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Adra

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(54) **GRANULOCYTE SUBTYPE-SELECTIVE RECEPTORS AND ION CHANNELS AND USES THEREOF**

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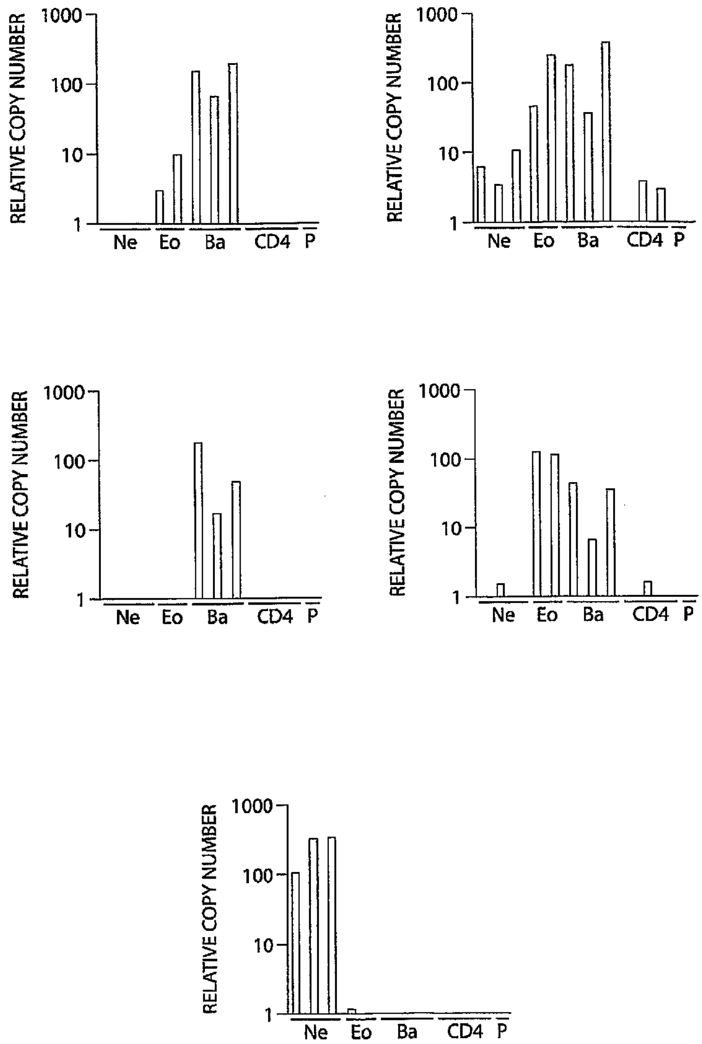
(57) **ABSTRACT**

The invention relates, in part, to granulocyte type selective markers that are preferentially expressed in granulocytes and their use in drug screening assays. Additionally, the granulocyte type selective markers are useful in the diagnosis and treatment of granulocyte disorders and in the assessment of the efficacy of therapies of granulocyte disorders.



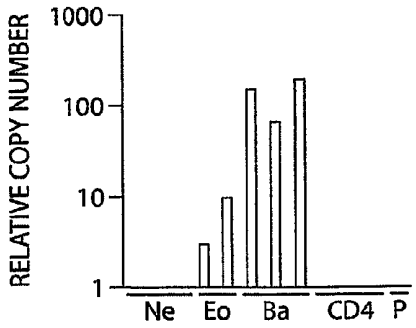


Fig. 1A

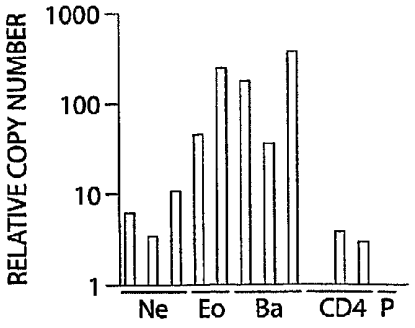


Fig. 1B

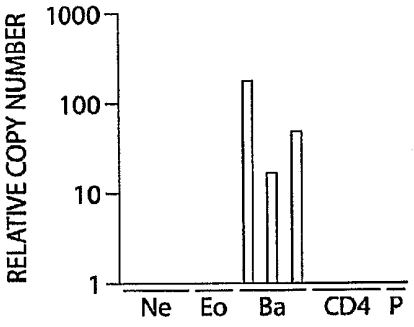


Fig. 1C

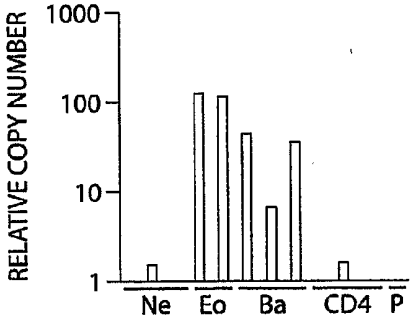


Fig. 1D

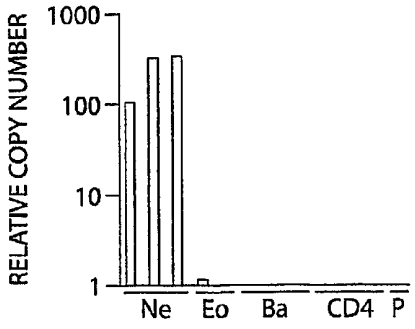


Fig. 1E

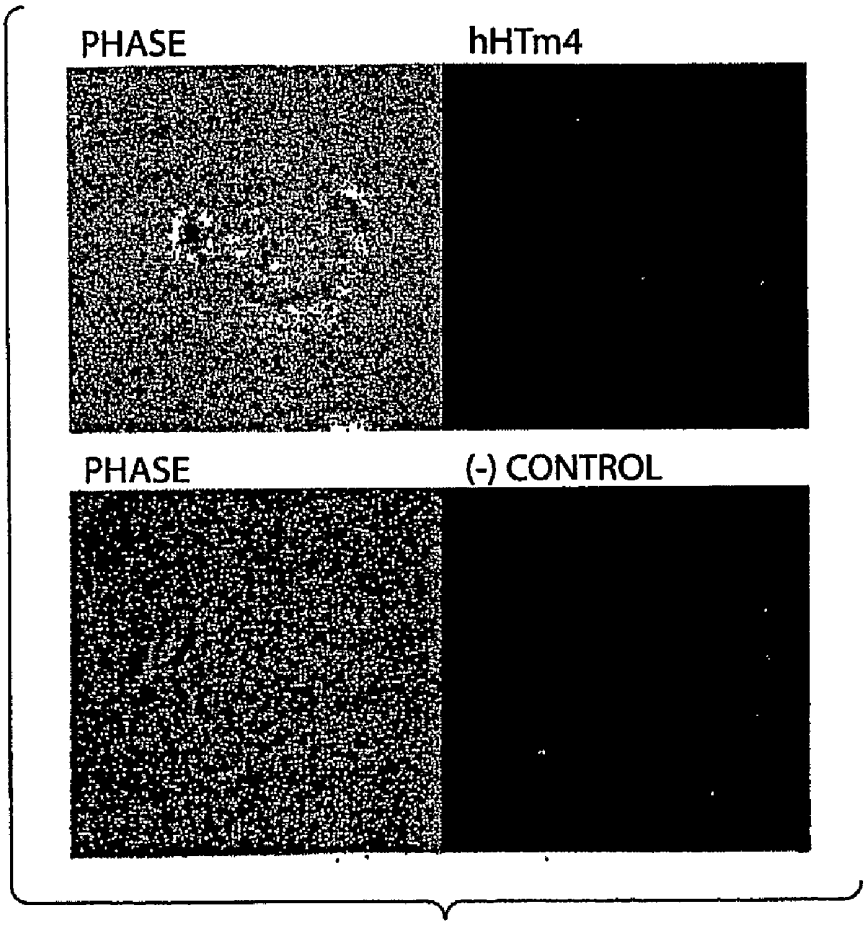


Fig. 2

Figure 3. Granulocyte subtype-specific transcripts for ion channels and receptors

Ion Channels Transcript (Accession #, GenBank)	Cell-type[a]	MC	Ba	Eo	Ne	Pl	CD4	CD8	CD14	CD19	Fb	TC[b]	*Gene Functions*
Ca^{2+} channel type A1 D (BE550599)	Ba, Eo	0.1	1.7	1.5	0.4	0.0	0.3	0.1	0.0	0.3	0.0	*0*	
aquaporin 9 (NM_020980) 602914	Ne	0.7	0.1	0.4	137.4	0.4	0.9	0.1	8.6	0.1	0.2	*7*	facilitates uptake of the metalloids arsenite and antimonite
K^+ channel Kir 1.3 (U73191) 600359	Ne	0.9	0.2	0.4	99.5	0.7	0.2	0.0	0.8	0.0	0.0	*5*	Andersen syndrome (170390) and Bartter syndrome (241200)
K^+ channel Kir 2.1 (AF153820) 600681	Ne	0.7	3.8	5.3	40.7	0.4	0.2	0.5	1.5	0.7	1.1	*6*	Andersen syndrome (170390) and Bartter syndrome (241200)
GPCR													
histamine H_4 R (AF312230) 606792	Ba	0.7	34.2	9.4	0.7	0.4	0.8	0.5	0.6	0.0	0.1	*0*	expression of HRH4 conferred sensitivity
PGE[c] R type 3a2 (X83858) 176806	Ba	0.8	10.3	0.1	0.7	0.6	0.3	0.2	0.2	0.5	1.7	*0*	signaling pathways
C3a R (U62027) 605246	Ba, Eo	11.8	55.7	39.4	2.0	1.6	1.6	1.5	3.0	0.6	0.5	*3*	anaphylatoxin receptor
CCR3 (NM_001837) 601268	Ba, Eo	0.6	117.4	90.9	24.9	0.2	0.5	0.4	0.2	0.2	0.4	*0*	importance for eosinophil responses
CRTH2 [c](NM_004778) 604837	Ba, Eo	1.1	26.0	38.2	2.0	0.8	1.4	1.0	1.2	0.9	0.5	*0*	mediate signals to the interior of the cell via activation of heterotrimeric G proteins
EMR-1 (NM_001974) 600493	Ba, Eo	0.8	33.5	90.9	4.2	3.4	1.7	0.8	7.1	1.6	0.5	*1*	Probably involved in cellular response to a hormone
adenosine A_3 R (NM_000677) 600445	Eo	2.6	2.9	15.4	2.3	1.2	1.6	0.5	2.0	0.5	0.5	*0*	cardioprotective function
P2Y2 purinergic R (NM_002564) 600041	Eo	0.1	0.1	5.5	0.1	0.2	0.1	0.3	1.2	0.2	0.1	*0*	P2RY2 may participate in control of the cell cycle of endometrial carcinoma cells
GPR 105 purinergic R (NM_014879)	Eo	2.6	2.9	15.4	2.3	1.2	1.6	0.5	2.0	0.5	0.5	*2*	GPR105 is a G-protein-coupled receptor identifying a quiescent, primitive population of hematopoietic cells restricted to bone marrow; GPR105 might play an important role in peripheral and neuroimmune function
GPR, Edg-4 (AF011466) 605110	Eo, Ne	1.3	2.8	15.9	24.2	0.1	3.6	5.0	3.8	1.9	0.9	*2*	edg-4 mrna was expressed in mouse islets; edg-4 (lpa2) r is a distinctive functional marker for ovarian carcinoma, and is expressed both as the wild-type and a carboxyl-terminally extended gain-of-function mutant.
PAR1-like GPR43 (NM_005306)	Eo, Ne	0.3	0.7	12.4	35.2	0.8	0.1	0.1	0.7	0.4	0.1	*0*	the highest levels of gpr43 were

Fig. 3A

603823												found in immune cells; gpr43 is highly restricted in hematopoietic tissues
C5a R (NM_001736) 113995	Ne	2.3	21.6	13.6	92.6	2.3	1.2	0.5	25.6	1.0	0.4	*5* receptor for the chemotactic and inflammatory peptide anaphylatoxin c5a. this receptor stimulates chemotaxis, granule enzyme release and superoxide anion production.
CXCR1 IL-8R (NM_000634) 146929	Ne	0.2	4.3	0.3	83.4	0.4	0.3	0.2	0.2	0.1	0.1	*0* receptor to interleukin-8, which is a powerful neutrophils chemotactic factor. binding of il-8 to the receptor causes activation of neutrophils. this response is mediated via a g-protein that activate a phosphatidylinositol-calcium second messenger system. this receptor binds to il-8 with a high affinity and to mgsa (gro) with a low affinity.
CXCR2 IL-8R (NM_001557)	Ne	0.2	1.1	1.5	112.1	2.7	0.3	0.8	0.7	0.6	0.0	*1* receptor to interleukin-8, which is a powerful neutrophils chemotactic factor. binding of il-8 to the receptor causes activation of neutrophils. this response is mediated via a g-protein that activate a phosphatidylinositol-calcium second messenger system. this receptor binds to il-8 with a high affinity and to gro/mgsa and nap-2 also with a high affinity.
formyl peptide R 1 (NM_002029) 136537	Ne	2.8	23.5	8.8	282.9	3.6	1.3	0.7	62.6	1.1	0.5	*0* HIGH AFFINITY RECEPTOR FOR N-FORMYL-METHIONYL PEPTIDES, WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED

Fig. 3B

Fig. 3C

formyl peptide R 2 (U81501)	Ne	0.4	0.5	0.6	75.5	0.1	1.0	0.6	6.0	0.8	0.1	*5*	VIA A G-PROTEIN THAT ACTIVATES PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. likely FPR2, mediates superoxide production at high concentrations of fMLF
GPR77 (NM_018485)	Ne	0.1	0.9	0.8	3.4	0.0	0.3	0.2	1.0	0.1	0.3	*2*	C5L2 is an anaphylatoxin-binding protein with unique ligand binding and signaling properties
GPR86 purinergic R (NM_023914)	Ne	0.3	0.2	17.9	88.2	1.9	0.1	0.2	12.3	0.6	0.0	*1*	GPR86 proved to be a G(i)-coupled receptor displaying a high affinity for ADP, similar to the P2Y(12) receptor and can therefore be tentatively called P2Y(13)
PAR2 (BE965369) **600933**	Ne	0.1	0.3	2.2	36.2	0.1	0.7	0.1	1.6	0.4	1.2	*15*	PAR2 plays a key role in chronic joint inflammation
Other Receptors													
Fc ε RI α (BC005912) 147138	Ba	19.4	219.0	4.6	5.5	1.4	5.1	0.8	1.4	0.4	0.2	*0*	responsible for initiating the allergic response
HTm4 (L35848) 606498	Ba	0.6	133.1	6.9	3.5	0.2	0.5	0.4	0.1	0.2	0.0	*1*	Cell cycle regulator
IL-3 R (NM_002183) **308385**	Ba	0.6	52.6	2.0	0.7	0.2	0.3	0.2	0.7	0.1	0.1	*0*	promotes the proliferation and differentiation of hematopoietic cells
CD244 NK cell R NM 016382 605554	Ba, Eo	0.3	56.0	16.5	1.2	0.1	0.4	3.5	5.2	1.1	0.1	*0*	engagement of 2B4 wih specific antibody activates NK cytolytic activity
fibroblast growth factor R 2 (NM_022969) 176943	Ba, Eo	0.1	27.9	12.1	0.2	0.1	0.1	0.2	0.1	0.1	1.0	*17*	Receptor for acidic and basic fibroblast growth factors.
IL-5R α **(M75914) 147851**	Ba, Eo	0.9	20.5	30.4	0.6	0.1	0.1	0.1	0.1	0.2	0.1	*0*	lacking either 115ra or Sox4 have defects in B-cell development
Siglec 8 (NM_014442) 605639	Eo	1.8	0.3	17.4	0.4	0.3	0.2	0.1	0.2	0.5	0.2	*0*	SIGLEC8 expression on eosinophils but not other leukocytes
CD117 c-KIT (NM_000222) **164920**	MC	89.0	7.2	4.2	1.2	0.8	0.2	0.5	0.1	0.1	0.5	*15*	Signaling from the KIT receptor tyrosine kinase is essential for primordial germ cell growth both in vivo and in vitro
SigtecB D86358 604405	MC	5.6	0.2	0.0	0.2	0.5	0.0	0.0	0.0	0.4	0.0	*0*	OBBP1 is almost exclusively expressed on B cells.
Fc ε RIβ (NM_000139) 147138	MC, Ba	22.3	44.3	0.4	0.6	1.6	0.5	0.2	0.0	0.3	0.1	*0*	MS4A2 Allergic disease
low density lipoprotein R	MC, Ba	20.7	20.4	1.3	1.8	2.3	2.1	3.4	3.5	0.8	6.3	*34*	receptor-mediated endocytosis

(NM_000527) 606945 TRK neurotrophin R (NM_002529) 191315	MC, Ba	4.6	7.3	0.1	0.1	0.1	0.1	0.1	0.1	0.0	0.0	*0*	participates in the primary signal transduction mechanism of NGF; is also an immunoregulatory cytokine acting on monocytes
butyrophilin like R (AK025267)	Ne	1.1	1.7	1.5	6.9	1.5	1.7	1.6	0.9	1.5	1.3	*1*	his gene is mainly expressed in small intestine, colon, testis, and leukocytes
CD120a, TNF-R-1 (NM_001065) 191190	Ne	1.7	1.2	7.8	74.7	1.3	2.2	5.9	17.4	0.6	16	*35*	Receptor for TNFSF2/TNF-alpha and homotrimeric TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling comlex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. Contributes to the induction of noncytocidal TNF effects including anti-viral state and activation of the acid sphingomyelinase.
CD95, Fas, APO-1 (AA164751) 134637	Ne	1.4	10.9	7.3	50.4	1.3	5.6	4.8	3.6	2.6	9.7	*7*	Receptor for TNFSF6/FASL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. FAS- mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T-cells, or both. The secreted

Fig. 3D

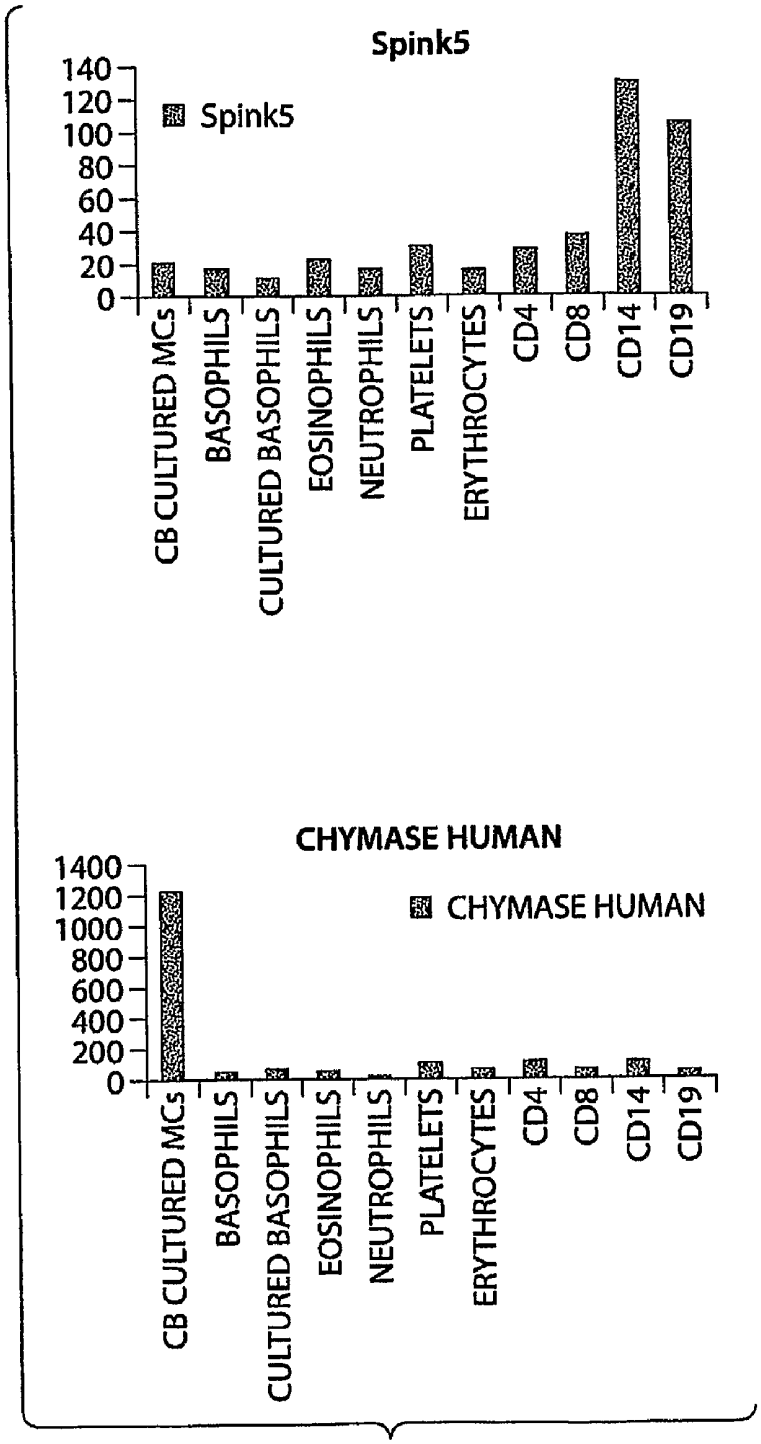
													isoforms 2 to 6 block apoptosis (in vitro). does not induce apoptosis.
decoy R1, TRAILR3 (AF012536) 603613	Ne	0.1	1.5	7.7	78.7	0.5	0.2	0.1	0.7	0.1	0.6	*0*	
FcγR IIc2 (U90939)	Ne	1.5	2.4	7.8	59.9	0.3	0.2	0.1	7.2	2.3	0.2	*2*	
FcγR IIc3 (U90940)	Ne	2.4	10.7	10.0	84.3	3.0	1.4	0.6	14.0	7.2	1.0	*5*	failure of the patient's
FcγR III (J04162) 146740	Ne	0.7	1.6	1.9	199.6	6.6	1.3	1.3	2.2	2.6	0.1	*4*	neutrophils to express Fc receptor III was associated with SLE
G-CSF R (NM_0007601) 138971	Ne	0.1	0.4	1.6	163.6	0.2	0.8	0.2	25.5	0.1	0.2	*3*	inhibits cell proliferation and survival in response to CSF3
IL-13 R (U81379) 308385	Ne	0.3	0.2	2.0	14.1	0.4	0.4	0.3	2.9	1.3	1.3	*0*	romotes the proliferation and differentiation of hematopoietic cells
IL-1R, type II (NM_004633) 147811	Ne	0.1	0.1	0.1	53.5	0.2	0.4	0.1	0.2	0.0	0.0	*3*	type II receptor inhibits IL1 activity by acting as a decoy target for IL1
IGFR 1 (NM_000875) 147370	Ne	0.3	3.5	5.0	17.4	1.6	0.1	2.8	2.4	2.0	3.5	*3*	IGFs may elicit a myogenic event which may be a key mechanism in the etiology of breast and ovarian cancer
IGFR 2 (NM_000876) 147280	Ne	4.6	0.9	5.4	85.3	1.7	2.9	8.7	8.4	4.8	15	*32*	Mutation in either MPRD or MPRI might result in a clinical disorder resembling a mucolipidosis
leukocyte immunoglobulin-like R A2 (NM_006866) 604812	Ne	0.5	5.8	4.3	41.2	1.8	0.0	0.1	11.6	0.5	0.1	*2*	Eosinophils may be activated through L1R7 for release of eosinophil-derived neurotoxin
Toll-like R 1 (AL050262) 601194	Ne	0.6	0.3	1.2	31.5	1.6	0.8	0.7	3.0	1.5	0.3	*0*	that TLR2-TLR1 heterodimers mediated the strongest cell activation
Toll-like R 2 (NM_003264) 603028	Ne	0.9	6.0	1.3	83.8	1.6	1.3	0.1	26.3	0.9	0.4	*0*	TLR2 is a molecular link between microbial products, apoptosis, and host defense mechanisms
Toll-like R 6 (NM_006068)	Ne	0.5	1.0	0.9	8.8	0.1	0.9	0.9	2.1	1.2	0.6	*0*	immunostimulatory activity

a. Cell-type specificity was obtained by comparing the "normalized AD" levels of each gene in mast cells (MC; average of 2 experiments), basophils (Ba; average of 3 experiments), eosinophils (Eo; average of 4 experiments), neutrophils (Ne; average of 4 experiments), platelets (Pl), $CD4^+$ cells (CD4), $CD8^+$ cells (CD8), $CD14^+$ cells (CD14), CD19+ cells (CD19) and nasal polyp-derived cultured fibroblasts (Fb).

Fig. 3E

	CB cultured MCs	Basophils	cultured basophils	Eosinophils	Neutrophils	platelets	Erythrocytes	CD4	CD8	CD14	CD19
Spink5	21	17	11	22	16	30	15	28	36	129	104
chymase human	1221	47	65	45	12	101	62	108	59	104	45
tryptase alpha	21179	212	40	33	25	184	139	104	17	52	39
tryptase beta	25414	195	113	49	28	152	10	122	113	93	6
tryptase delta	349	45	6	23	55	74	113	11	10	42	11
tryptase gamma	654	56	19	38	78	28	24	81	230	142	83
TRPV2	129	37	15	97	99	259	137	133	67	97	110
ANKTM1_	28	28	8	38	30	96	18	14	46	11	28
Cannabinoid receptor type 1	50	41	14	47	36	27	61	41	56	18	54
Cannabinoid receptor type 2	160	369	226	578	177	271	530	324	232	212	421

Fig. 4A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CD4
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CD14
CD19
CHYMASE HUMAN
CHYMASE HUMAN
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1200
1000
800
600
400
200
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BASOPHILS
CULTURED BASOPHILS
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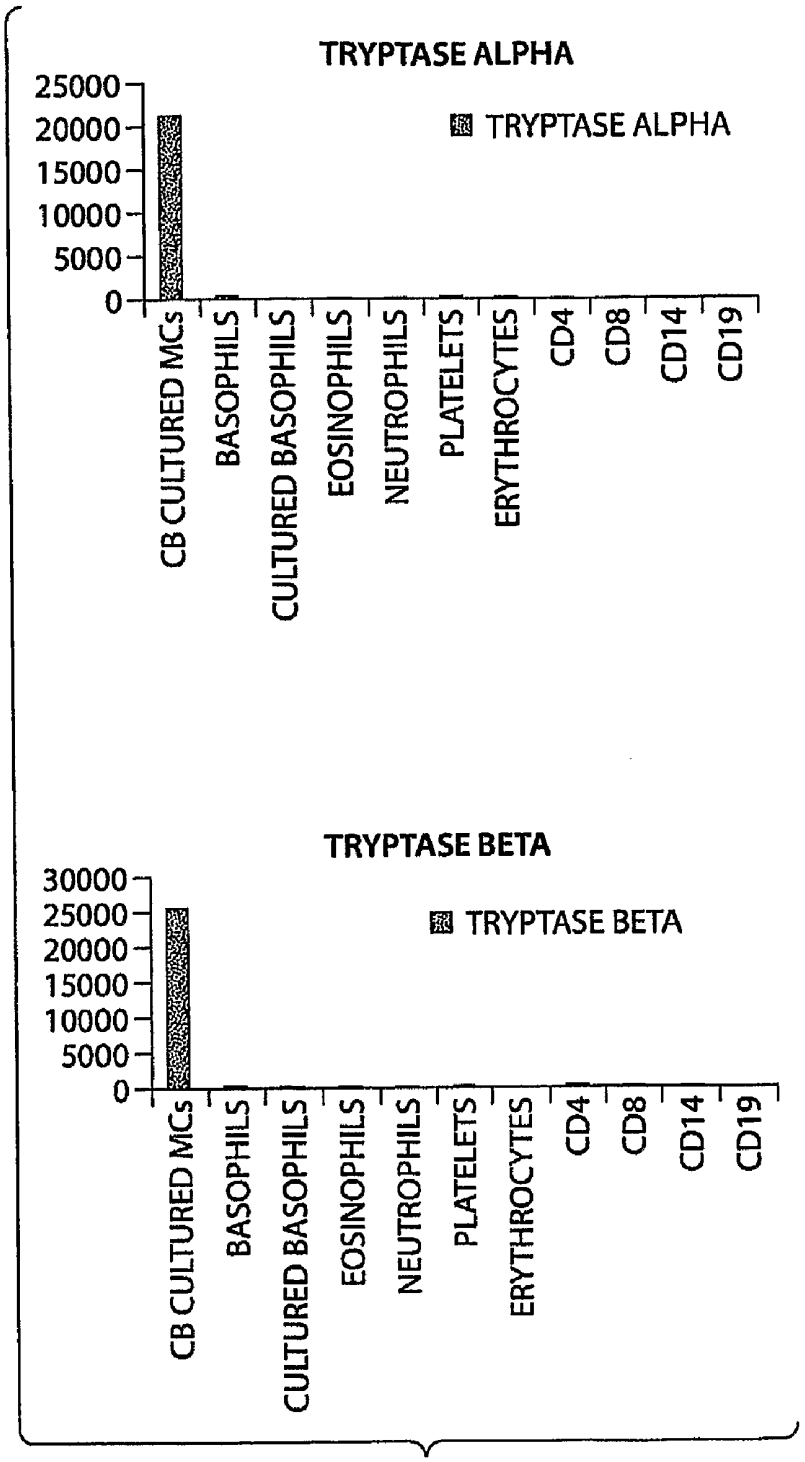
Fig. 4B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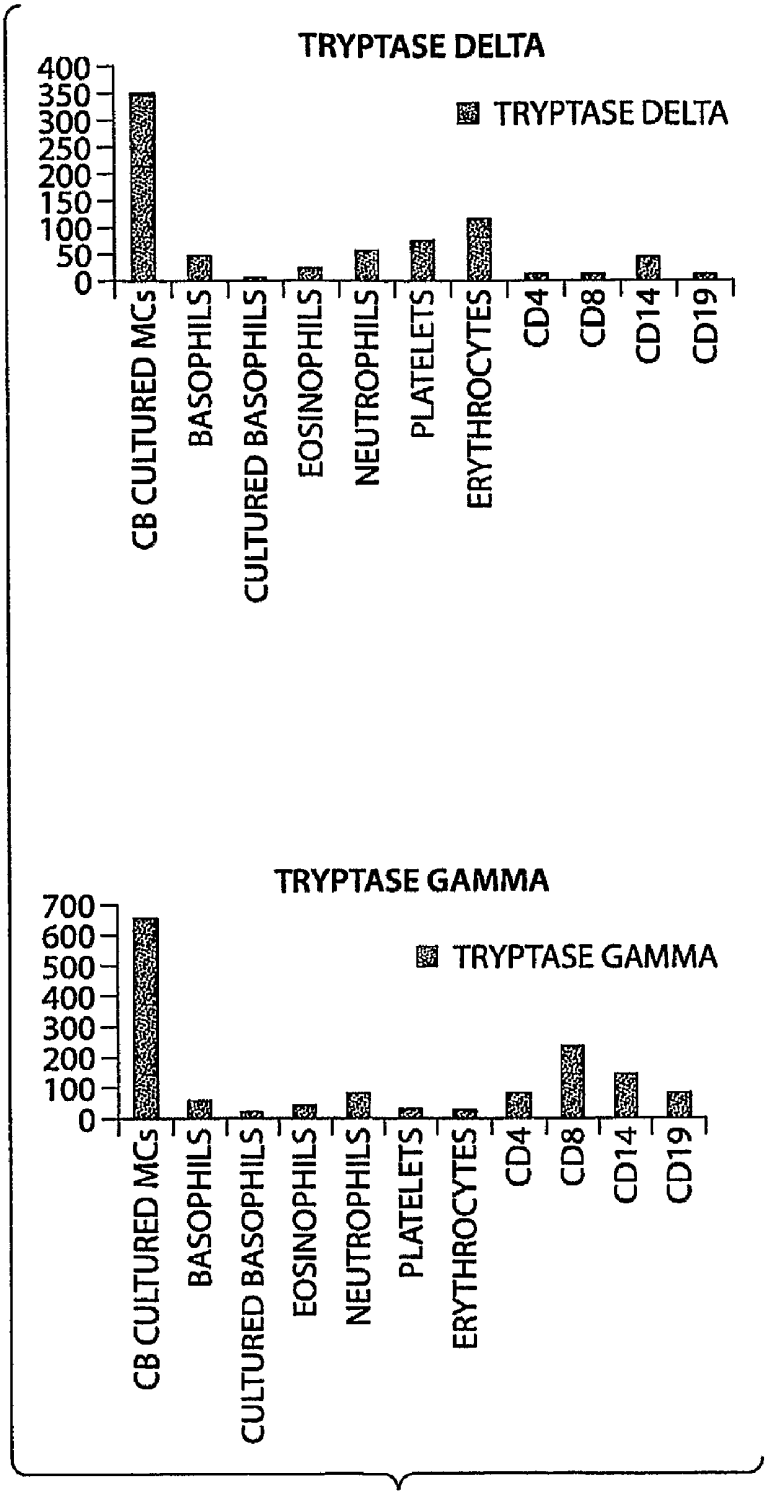
CD14
CD19

Fig. 4C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NEUTROPHILS
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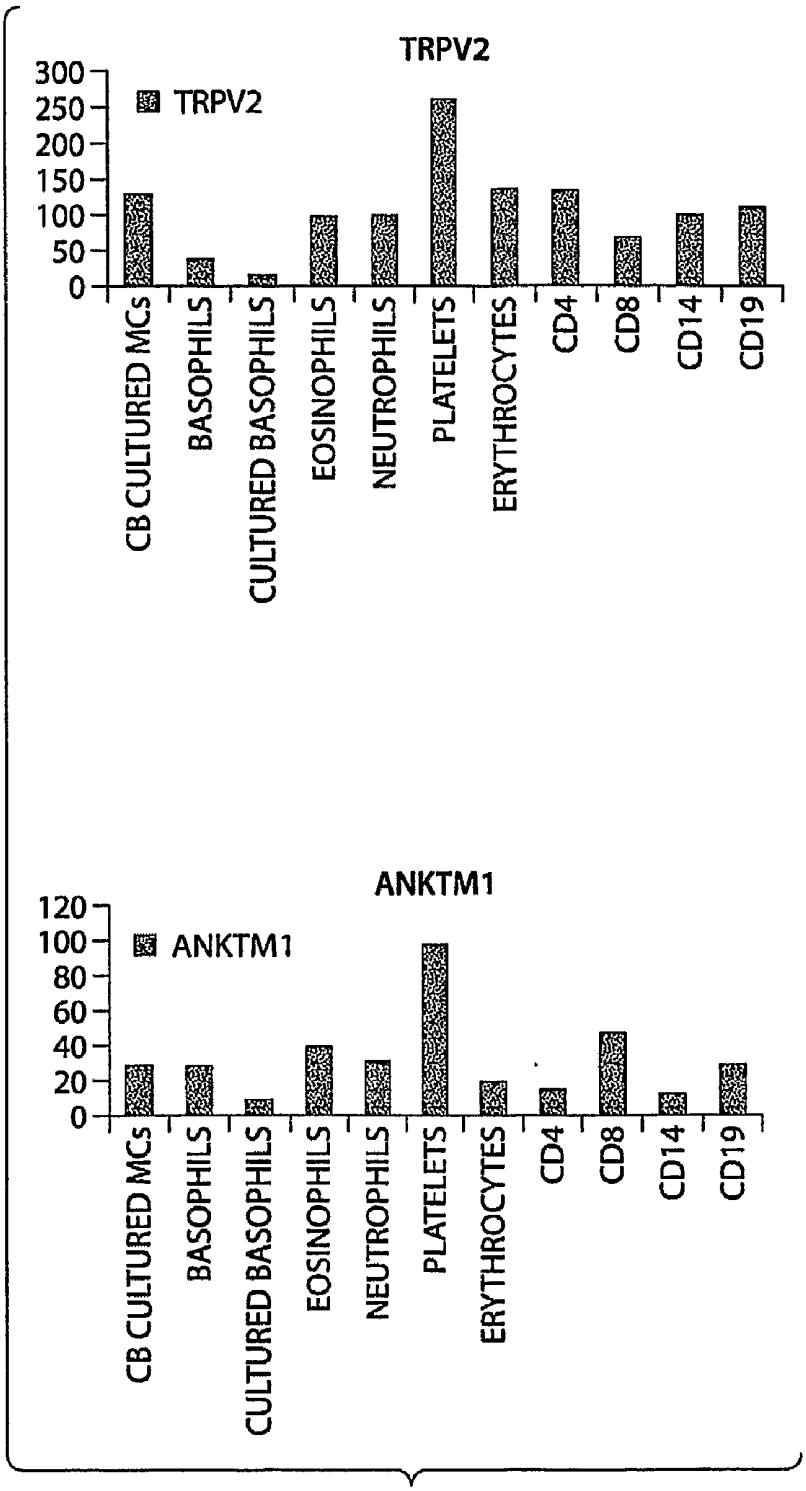
Fig. 4D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PLATELETS
ERYTHROCYTES
CD4
CD8
CD14
CD19
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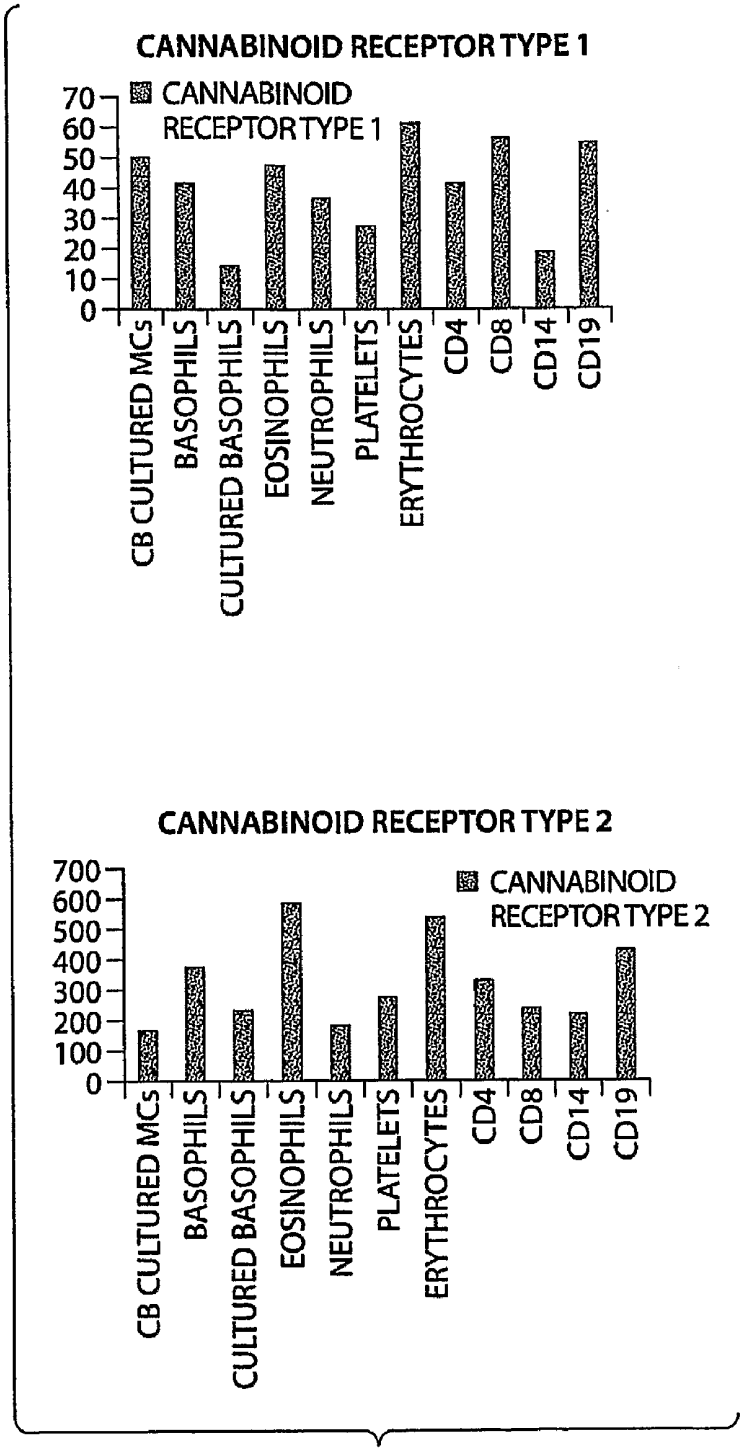
CD19

Fig. 4E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CANNABINOID RECEPTOR TYPE 2
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NEUTROPHILS
PLATELETS
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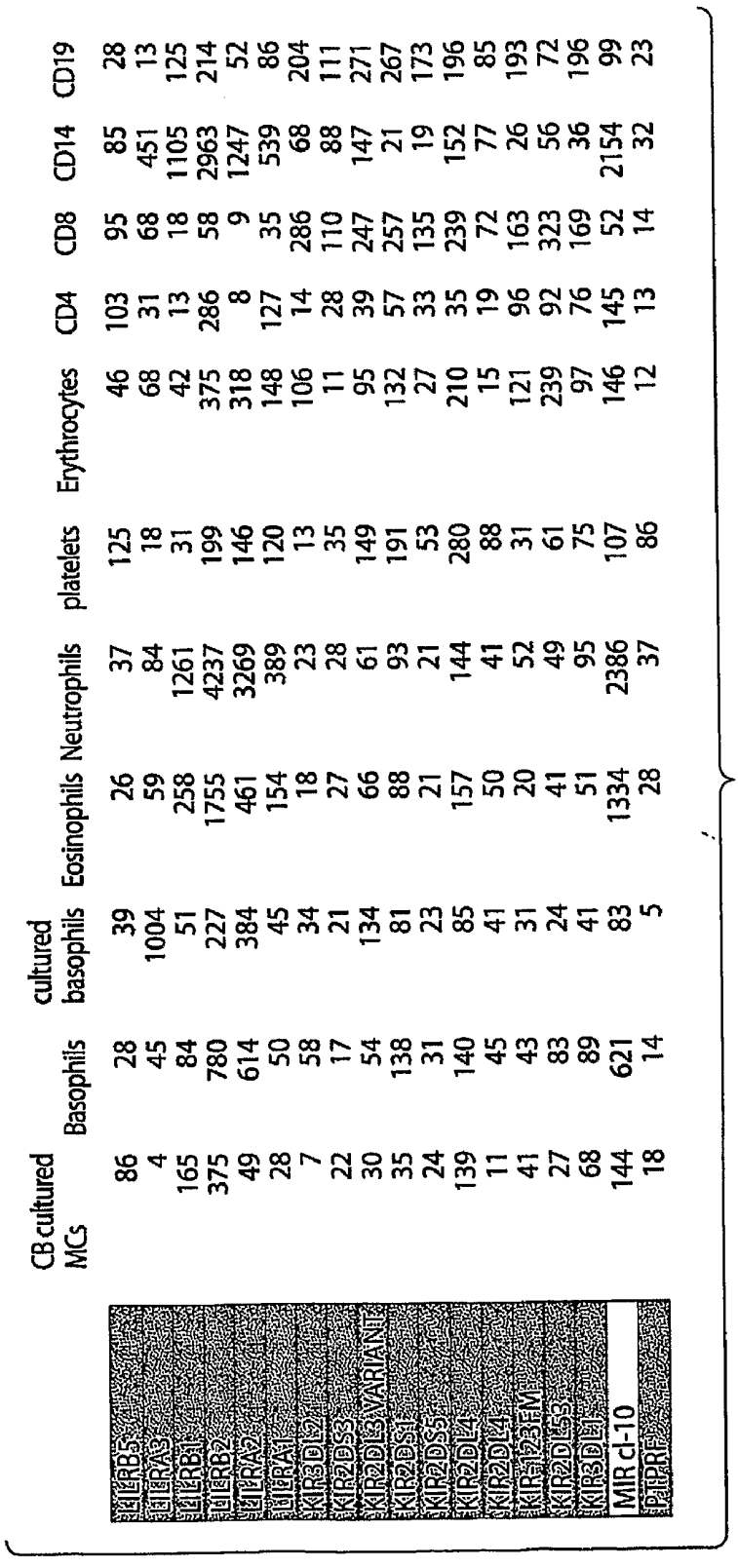
CD4
CD8
CD14
CD19

Fig. 4F


CB cultured MCs
Basophils
cultured basophils
Eosinophils
Neutrophils
platelets
Erythrocytes
CD4
CD8
CD14
CD19
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KIR2DS3 4 45 1004 59 84 18 68 31 68 451 13
KIR2DL3 VARIANT 165 84 51 258 1261 31 42 13 18 1105 125
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KIR2DS5 49 614 384 461 3269 146 318 8 9 1247 52
KIR2DL4 28 50 45 154 389 120 148 127 35 539 86
KIR2DL4 7 58 34 18 23 13 106 14 286 68 204
KIR2123EM 22 17 21 27 28 35 11 28 110 88 111
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MIR cl-10 24 31 23 21 21 53 27 33 135 19 173
PIPRF 139 140 85 157 144 280 210 35 239 152 196
24 11 41 50 41 88 15 19 72 77 85
41 45 31 20 52 31 121 96 163 26 193
27 43 24 41 49 61 239 92 323 56 72
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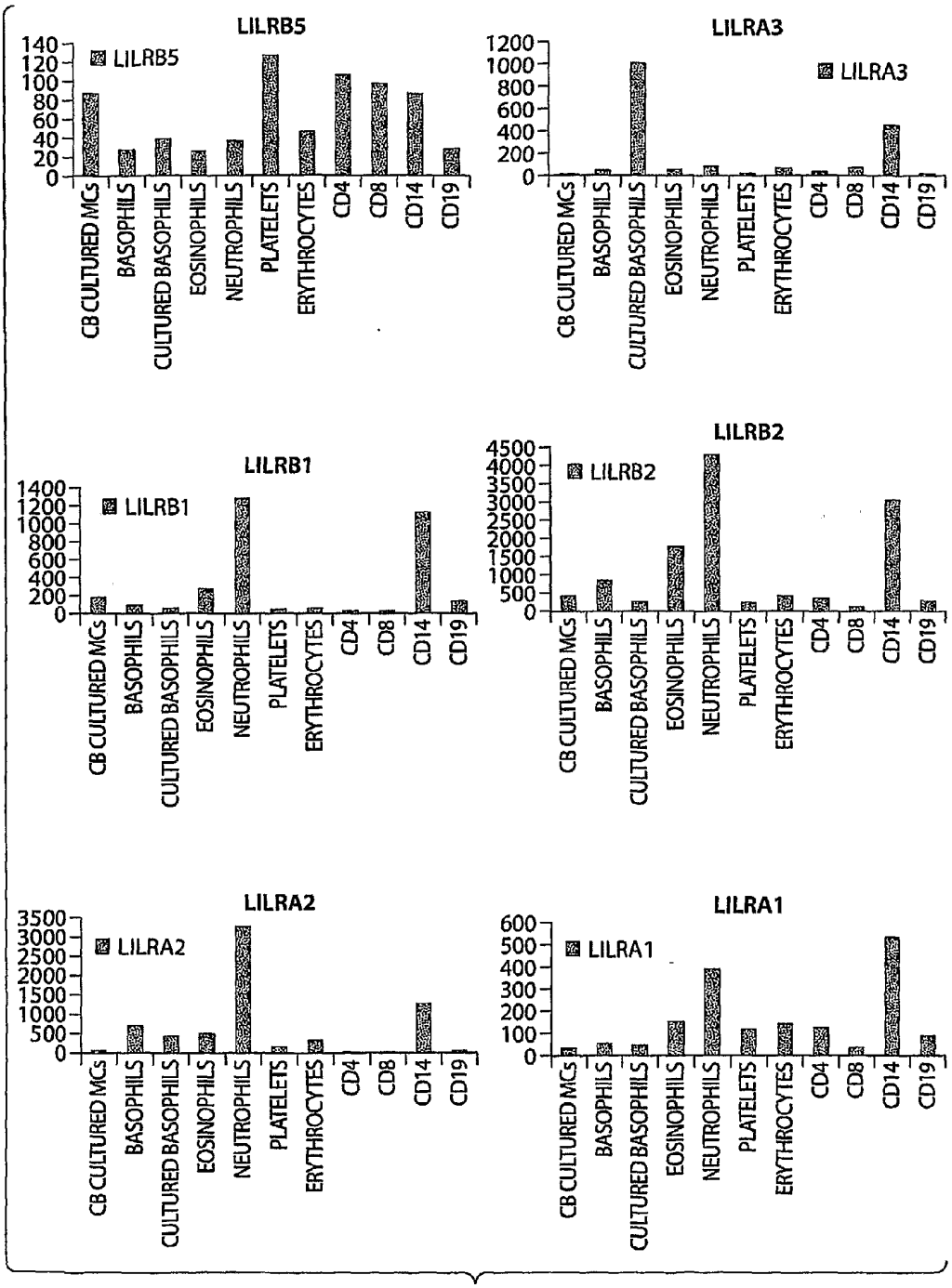
144 89 83 1334 2386 107 146 145 52 2154 99
18 621 5 28 37 86 12 13 14 32 23

Fig. 5A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80
60
40
20
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EOSINOPHILS
NEUTROPHILS
PLATELETS
ERYTHROCYTES
CD4
CD8
CD14
CD19
LILRA3
LILRA3
1200
1000
800
600
400
200
0
CB CULTURED MCs
BASOPHILS
CULTURED BASOPHILS
EOSINOPHILS
NEUTROPHILS
PLATELETS
ERYTHROCYTES
CD4
CD8
CD14
CD19
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LILRB1
1400
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1000
800
600
400
200
0
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BASOPHILS
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EOSINOPHILS
NEUTROPHILS
PLATELETS
ERYTHROCYTES
CD4
CD8
CD14
CD19
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LILRB2
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4000
3500
3000
2500
2000
1500
1000
500
0
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BASOPHILS
CULTURED BASOPHILS
EOSINOPHILS
NEUTROPHILS
PLATELETS
ERYTHROCYTES
CD4
CD8
CD14
CD19
LILRA2
LILRA2
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3000
2500
2000
1500
1000
500
0
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BASOPHILS
CULTURED BASOPHILS
EOSINOPHILS
NEUTROPHILS
PLATELETS
ERYTHROCYTES
CD4
CD8
CD14
CD19
LILRA1
LILRA1
600
500
400
300
200
100
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BASOPHILS
CULTURED BASOPHILS
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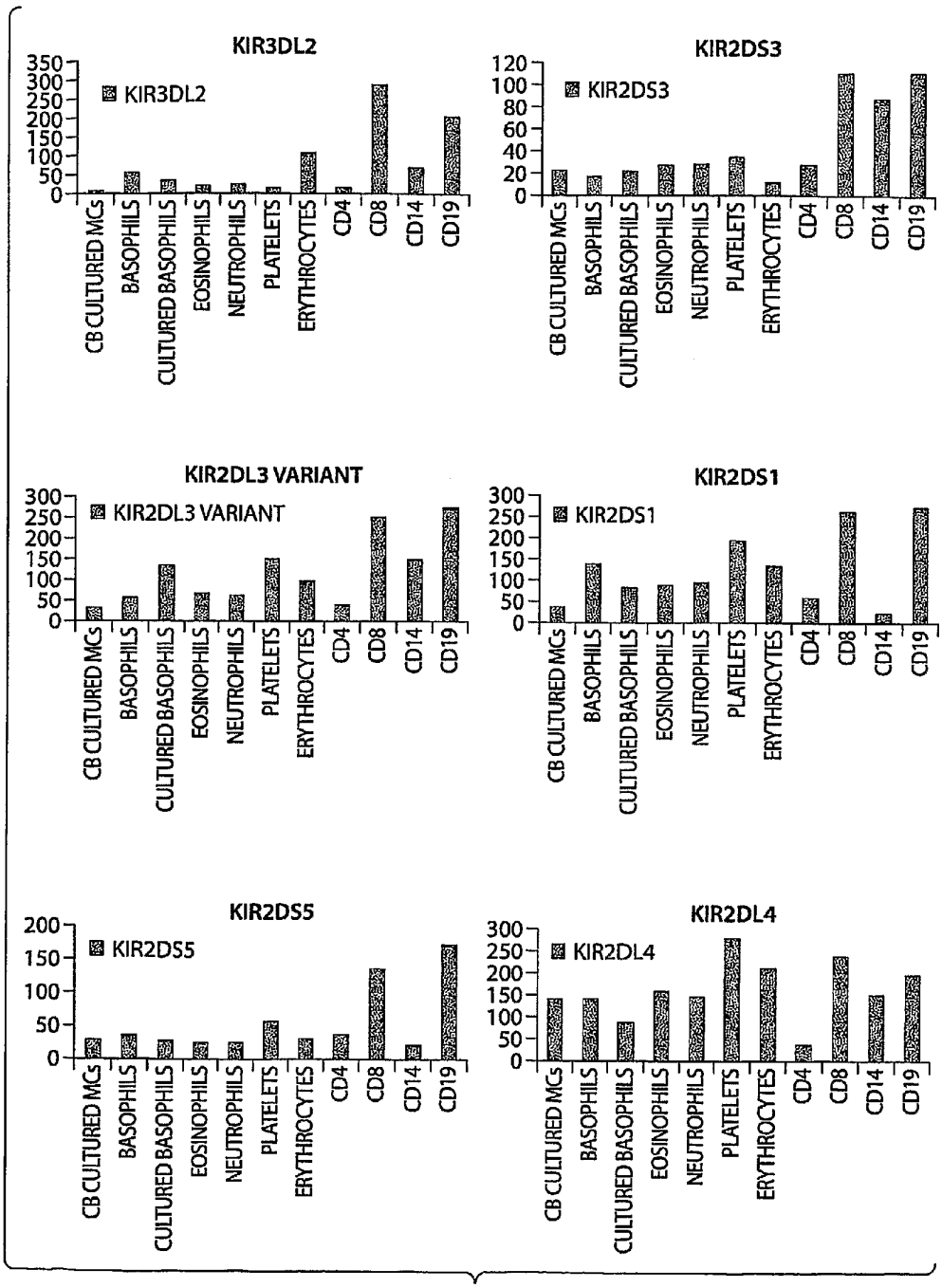
NEUTROPHILS
PLATELETS
ERYTHROCYTES
CD4
CD8
CD14
CD19

Fig. 5B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150
100
50
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BASOPHILS
CULTURED BASOPHILS
EOSINOPHILS
NEUTROPHILS
PLATELETS
ERYTHROCYTES
CD4
CD8
CD14
CD19
KIR2DS3
KIR2DS3
120
100
80
60
40
20
0
CB CULTURED MCs
BASOPHILS
CULTURED BASOPHILS
EOSINOPHILS
NEUTROPHILS
PLATELETS
ERYTHROCYTES
CD4
CD8
CD14
CD19
KIR2DL3 VARIANT
KIR2DL3 VARIANT
300
250
200
150
100
50
0
CB CULTURED MCs
BASOPHILS
CULTURED BASOPHILS
EOSINOPHILS
NEUTROPHILS
PLATELETS
ERYTHROCYTES
CD4
CD8
CD14
CD19
KIR2DS1
KIR2DS1
300
250
200
150
100
50
0
CB CULTURED MCs
BASOPHILS
CULTURED BASOPHILS
EOSINOPHILS
NEUTROPHILS
PLATELETS
ERYTHROCYTES
CD4
CD8
CD14
CD19
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KIR2DS5
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150
100
50
0
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BASOPHILS
CULTURED BASOPHILS
EOSINOPHILS
NEUTROPHILS
PLATELETS
ERYTHROCYTES
CD4
CD8
CD14
CD19
KIR2DL4
KIR2DL4
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250
200
150
100
50
0
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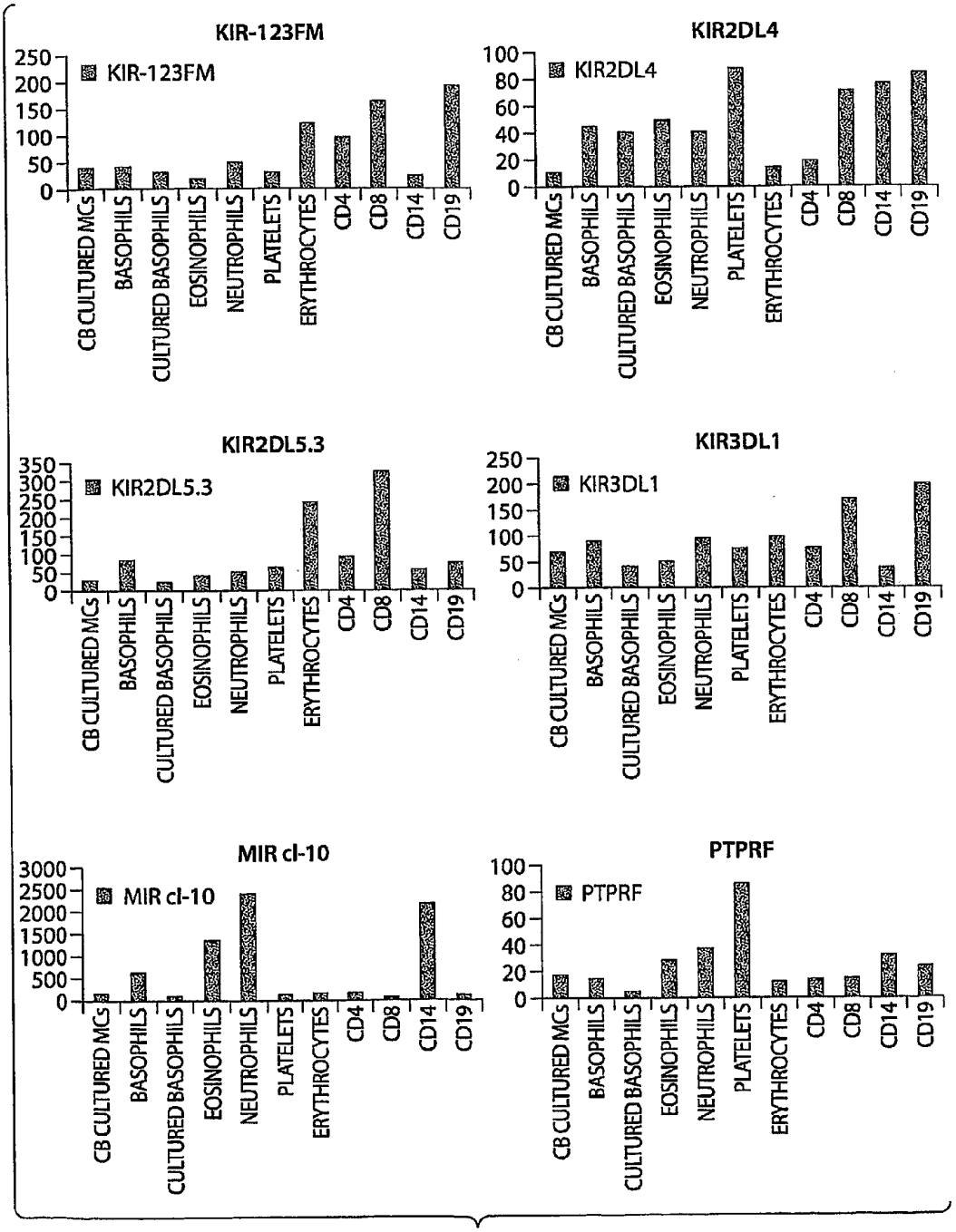
BASOPHILS
CULTURED BASOPHILS
EOSINOPHILS
NEUTROPHILS
PLATELETS
ERYTHROCYTES
CD4
CD8
CD14
CD19

Fig. 5C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KIR-123FM
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200
150
100
50
0
CB CULTURED MCs
BASOPHILS
CULTURED BASOPHILS
EOSINOPHILS
NEUTROPHILS
PLATELETS
ERYTHROCYTES
CD4
CD8
CD14
CD19
KIR2DL4
KIR2DL4
100
80
60
40
20
0
KIR2DL5.3
KIR2DL5.3
350
300
250
200
150
100
50
0
KIR3DL1
KIR3DL1
MIR cl-10
MIR cl-10
3000
2500
2000
1500
1000
500
0
PTPRF
PTPRF

Fig. 5D

Table E1. The complete list of granulocyte subtype-selective transcripts. Selectivity index (S.I.) was calculated by comparing the "normalized AD" level of a cell type or of two cell types with the maximal gene expression level of the other 8 or 9 cell types including platelets (Pl), $CD4^+$ cells, $CD8^+$ cells, $CD14^+$ cells, $CD19^+$ cells and nasal polyp-derived cultured fibroblasts (Fb). When the result was accompanied by presence call, it was shown as a bold numeral. Italic numerals show that the raw AD levels were associated with absence call by the GeneChip analysis software. Transcripts having S.I. >3-fold were shown in A-H. Abbreviations used in the table through A-I were (small); the results obtained by the small sample protocol (see materials and methods), R; receptor, and ICN; ion channel.

A. Basophil (Ba)-selective transcripts (1/2).

Probe set	Accession #		Transcripts	MC. cord blood	MC. lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ba S.I.
207539_s_at	NM_000589.1		IL-4	*0.2*	*0.1*	10.4	16.9	13.4	*0.1*	*0.0*	*0.2*	*0.1*	*0.1*	*0.3*	*0.0*	*1.2*	*0.2*	*0.0*	*0.2*	*0.1*	*0.0*	*0.0*	73.348
210254_at	L35848.1	R	HTm4	*0.8*	*0.4*	115.6	130.1	153.6	2.4	1.7	21.8	1.7	*0.1*	*0.9*	3.6	9.5	*0.2*	*0.5*	*0.4*	*0.1*	*0.2*	*0.0*	38.24
205513_at	NM_001062.1		vitamin B12 binding protein	1.5	*1.2*	98.9	149.3	110.9	3.2	2.2	16.1	*1.9*	4.9	4.5	6.3	8.1	*1.8*	*0.7*	*0.8*	*1.4*	*0.9*	*0.1*	20.322
206148_at	NM_002183.1	R	IL-3 R	*1.0*	*0.1*	6.2	80.2	71.3	*1.7*	*1.7*	*1.8*	2.9	*0.3*	*0.4*	*0.2*	*1.9*	*0.2*	*0.3*	*0.2*	*0.7*	*0.1*	*0.1*	16.62
214920_at	R33964		FLJ11022 fis	*0.1*	1.1	4.9	13.1	15.4	*0.1*	*0.2*	*0.7*	*0.5*	*1.0*	*0.4*	*0.5*	*0.7*	*0.1*	*0.1*	*0.2*	*0.1*	*0.3*	*0.1*	16.049
201825_s_at	AL572542		CGI-49	3.3	1.6	21.4	74.9	46.5	2.1	1.2	*0.1*	*1.2*	*0.1*	*0.1*	*0.2*	*0.1*	1.3	*0.7*	1.7	*1.4*	*0.8*	2.8	15.045
213238_at	AI478147		ATPase, Class V, type 10D	1.2	2.9	39.9	76.3	118.9	2.3	*1.7*	3.1	1.9	*2.1*	*1.4*	2.3	6.8	*0.7*	*0.9*	*0.9*	2.5	5.0	4.1	14.398
211734_s_at	BC005912.1	R	Fc epsilon R I alpha	10.5	28.4	210.0	220.8	226.2	8.4	2.1	4.8	2.9	*0.3*	*0.7*	4.5	16.6	1.4	5.1	*0.8*	1.4	*0.4*	*0.2*	12.703
213894_at	BF447246		KIAA0960	*0.1*	*0.0*	3.7	13.0	15.6	*0.3*	*0.4*	*0.4*	*0.4*	*0.9*	*0.7*	*0.7*	*0.6*	*0.5*	*0.6*	*0.1*	*0.1*	*0.2*	*0.2*	12.272
206363_at	NM_005360.2		c-MAF	3.7	*1.4*	36.5	75.7	66.4	1.2	*0.1*	*0.2*	*0.2*	*0.2*	*0.1*	*0.2*	*1.0*	*0.6*	4.8	2.7	*0.5*	1.0	*0.0*	11.927
203373_at	NM_003877.1		SOCS2	2.1	3.9	21.7	85.0	112.2	4.6	4.7	9.4	6.5	*0.7*	*1.2*	*0.3*	2.5	*1.6*	3.2	3.5	*0.8*	*0.9*	3.6	9.8282
207538_at	*NM_000589.1*		*IL-4*	*0.3*	*0.1*	5.4	9.8	9.2	*0.4*	*0.4*	*0.0*	*0.3*	*0.1*	*0.0*	*0.4*	*0.7*	*0.8*	*0.4*	*0.3*	*0.1*	*0.0*	*0.1*	9.8156
213684_s_at	BF671400		LIM-protein	*0.6*	*0.1*	11.1	21.0	20.6	1.9	*1.6*	2.4	1.8	*0.8*	*0.6*	1.5	2.5	*0.1*	*0.0*	*0.3*	*1.0*	*0.0*	*0.1*	8.9245
209360_s_at	D43968.1		AML 1b protein	10.4	2.4	53.2	131.1	90.5	8.5	7.0	13.8	11.3	*0.5*	*0.5*	*0.5*	*4.2*	1.3	*4.1*	5.9	1.3	2.5	3.1	8.7543
220234_at	NM_004056.2		carbonic anhydrase VIII	*0.4*	*0.1*	11.7	10.2	6.0	*1.2*	*0.1*	*0.2*	*0.4*	*0.8*	*0.9*	*0.1*	*0.5*	*0.5*	*1.1*	*0.1*	*0.1*	*0.8*	*0.0*	8.1309
210643_at	AF053712.1		osteoprotegerin ligand	*0.1*	*0.3*	1.8	3.4	6.0	*0.7*	*0.4*	*0.3*	*0.2*	*0.4*	*0.1*	*0.3*	*0.1*	*0.1*	*0.3*	*0.4*	*0.3*	*0.2*	*0.2*	7.6628
209211_at	AF132818.1		colon Kruppel-like factor	*0.1*	*0.0*	1.8	10.2	8.8	*0.3*	*0.5*	1.5	*0.8*	*1.1*	*0.7*	*0.8*	*0.5*	*0.2*	*0.2*	*0.4*	*0.2*	*0.1*	*0.3*	7.239
204309_at	NM_000781.1		CYP11A	*0.3*	*0.1*	2.6	6.1	5.6	*0.1*	*0.3*	*0.5*	*0.5*	*1.0*	*0.1*	*0.1*	*0.9*	*0.3*	*0.3*	*0.1*	*0.0*	*0.3*	*0.7*	6.8366
203372_s_at	AB004903.1		SOCS2	*0.6*	*1.6*	9.2	8.5	15.9	1.4	2.4	*0.9*	*0.2*	*0.7*	*0.6*	*0.4*	*0.8*	*0.8*	1.6	1.3	*0.3*	*0.3*	1.4	6.8271
207463_x_at	NM_002771.1		serine protease 3 (trypsin 3)	*1.0*	*1.0*	4.8	10.0	10.9	*0.4*	*1.0*	1.0	*1.2*	*1.2*	*0.9*	*1.0*	1.8	*0.4*	*0.6*	*0.4*	*0.3*	*0.7*	1.2	6.7218
			acid sphingomyelinase-like																				

Fig. 6A-1

Probe set	Accession #		Transcripts	MC. cord blood	MC. lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ba S.I.
213624_at	AA873600		phosphodiesterase	4.7	2.0	20.8	30.6	25.9	2.1	2.8	3.8	1.7	0.5	1.1	1.3	1.3	0.1	0.2	0.1	3.8	0.2	3.2	6.6846
214873_at	AL137651.1		clone DKFZp434O0213	0.1	0.4	3.7	15.5	24.4	2.0	0.9	2.5	2.3	0.2	0.1	0.7	0.6	0.1	1.1	1.5	0.5	0.6	0.7	6.2585
204928_s_at	NM_019848.2		protein P3	2.3	1.5	9.8	49.0	34.3	3.7	3.3	4.8	4.2	1.6	1.0	1.9	2.2	4.1	1.8	3.0	0.8	2.0	2.6	6.2142
208935_s_at	L78132.1		prostate carcinoma tumor antigen (pcta-1)	2.2	1.2	9.9	19.1	16.6	2.3	1.5	3.6	2.5	1.1	1.1	1.9	0.9	1.8	1.8	2.0	2.0	1.4	0.8	6.2011
203201_at	NM_000303.1		phosphomannomutase 2 (PMM2)	1.8	0.3	10.7	15.9	6.5	0.9	0.6	1.2	0.9	0.8	0.4	1.1	1.3	1.0	1.3	1.2	1.2	1.1	1.7	6.1557
201826_s_at	NM_016002.1		CGI-49	1.8	3.1	11.0	27.5	15.1	1.6	1.1	1.4	2.1	1.1	1.4	1.3	1.8	1.6	1.1	1.1	1.1	0.6	2.9	5.6407
213421_x_at	AW007273		serine protease 4 (trypsin 4)	1.8	1.7	5.9	12.5	11.4	1.0	0.5	1.2	0.5	1.2	1.7	1.2	1.2	0.9	1.0	1.2	1.0	0.4	1.7	5.4082
209348_s_at	AF055376.1		*c-MAF, short form*	6.4	4.9	29.6	47.7	42.3	0.8	0.3	0.4	0.6	0.3	0.0	0.9	1.4	1.0	7.3	3.1	0.9	0.7	1.4	5.3183
213343_s_at	AL041124		hypothetical protein PP1665	0.9	0.2	12.2	17.0	12.0	3.5	1.7	0.5	0.6	0.1	0.3	0.8	0.4	0.6	1.5	2.6	0.7	1.6	1.3	5.2721
202491_s_at	NM_003640.1		I kappa B-associated protein	1.6	3.8	23.9	51.9	43.5	4.6	4.0	7.1	7.3	1.6	2.1	2.5	2.3	1.7	3.7	7.4	3.2	4.7	4.2	5.107
221021_s_at	NM_030877.1		Bos taurus P14 protein	6.9	3.2	7.2	29.2	58.9	2.8	3.2	5.4	6.3	0.9	1.2	1.8	1.6	1.6	2.2	2.4	2.0	3.5	1.8	4.9129
213346_at	BE748563		hypothetical protein BC015148	2.7	1.8	17.5	38.8	25.8	4.0	6.7	6.2	4.8	1.4	0.9	0.8	1.1	0.2	1.2	1.5	0.6	1.1	1.9	4.8879
209764_at	AL022312		mannosyl (beta-1.4-)-glycoprotein beta-1.4-N-acetylglucosamiyltransferase	0.0	0.9	4.1	6.1	5.8	0.8	1.4	0.9	1.4	0.6	0.1	0.5	0.2	1.0	0.4	0.2	0.2	0.4	0.3	4.855
207067_s_at	NM_002112.1		histidine decarboxylase	64.1	14.7	105.2	164.9	165.7	3.4	1.4	4.1	2.8	2.1	1.2	4.6	14.0	2.4	0.8	0.9	1.1	0.7	0.2	4.6305
210375_at	X83858.1	GPR	prostaglandin E receptor, type 3a2	1.0	0.6	2.4	11.5	17.0	0.3	0.1	0.1	0.0	0.4	0.7	0.9	0.7	0.6	0.3	0.2	0.2	0.5	1.7	4.6103
206306_at	NM_001036.1		ryanodine receptor 3 (RYR3)	2.1	1.1	3.7	11.0	7.8	1.0	0.6	1.5	0.5	1.2	0.3	1.5	0.9	1.1	0.7	0.3	1.0	0.2	0.4	4.5552
210001_s_at	AB005043.1		SOCS1	5.2	0.2	3.0	24.1	29.9	2.1	3.0	3.2	3.4	0.3	1.0	0.8	1.3	0.8	0.8	0.8	0.0	0.8	0.9	4.5248
204614_at	NM_002575.1		serine (or cysteine) proteinase inhibitor, clase B (ovalbumin), member 2 (SERPIN82)	0.3	0.6	5.3	12.9	12.5	0.4	2.4	4.2	2.0	1.0	0.8	0.7	0.3	1.9	0.5	0.7	2.1	0.2	0.2	4.5061
209960_at	X16323.1		hepatocyte growth factor (HGF)	0.4	0.0	2.3	7.3	5.5	0.5	0.4	0.6	0.5	0.1	0.1	1.0	0.6	0.7	0.1	0.0	1.0	0.0	0.5	4.4335
209212_s_at	AB030824.1		transcription factor BTEB2	0.1	0.2	7.5	14.3	22.1	2.3	2.0	4.9	3.7	1.2	1.3	1.5	2.5	1.4	0.5	0.2	1.1	0.9	0.8	4.363

Fig. 6A-2

A. Basophil (Ba)-selective transcripts (2/2).

Probe set	Accession #		Transcripts	MC cord blood	MC lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ba S.I.
214651_S_at	U41813.1		class 1 homeoprotein (HOXA9)	0.6	0.6	1.7	6.3	8.3	0.3	0.5	0.8	0.5	0.1	0.1	0.5	1.0	1.0	0.1	0.1	0.3	0.1	0.1	4.3618
32502_at	AL041124		DKFZp434D0316_s1	1.6	1.9	14.6	22.5	17.4	4.0	2.1	0.7	1.4	1.1	1.0	0.4	0.4	2.3	2.5	4.1	2.5	2.3	1.8	4.3594
205373_at	NM_004389.1		catenin (cadherin-associated protein) alpha 2	0.2	0.1	1.1	3.9	3.2	0.6	0.1	0.1	0.1	0.1	0.1	0.2	0.1	0.1	0.1	0.6	0.2	0.2	0.2	4.2308
219676_at	NM_025231.1		FLJ22191	0.3	0.7	2.5	7.3	12.0	0.9	0.2	2.0	1.5	0.2	1.1	4.2	2.2	0.6	1.1	1.4	0.3	1.4	0.1	4.2135
213385_at	AK026415.1		beta2-chimaerin	4.7	3.1	8.3	22.9	21.8	1.1	0.8	0.9	1.0	0.2	1.5	0.8	1.0	0.1	0.9	1.6	3.3	0.2	0.4	4.2131
214637_at	BG437034		oncostatin M	0.4	0.0	0.9	5.4	4.4	0.2	0.7	0.1	0.7	0.5	1.8	0.2	1.1	0.4	0.1	0.1	0.2	0.1	0.0	4.1983
202490_at	AF153419.2		*I kappa B-associated protein*	0.2	0.2	1.3	3.6	2.2	0.4	0.4	0.5	0.1	0.3	0.0	0.2	0.0	0.3	0.3	0.5	0.2	0.4	0.2	4.1747
220416_at	NM_024837.1		FLJ21472	4.1	1.5	9.1	9.7	12.2	1.9	3.3	3.0	1.9	0.8	0.6	1.1	0.9	0.7	0.6	0.2	0.8	0.3	0.0	4.1718
218318_s_at	NM_016231.1		nemo-like kinase	1.4	1.3	6.2	7.0	7.1	0.8	0.9	0.8	0.6	0.5	1.0	0.1	0.1	1.6	1.3	0.9	1.2	1.1	0.4	4.1558
215201_at	AW166925		FLJ14135 fis; clone MAMMA1002728	0.1	0.1	2.1	3.5	5.1	0.5	0.7	0.8	0.9	0.0	0.1	0.1	0.1	0.5	0.3	0.8	0.4	0.5	0.1	4.1491
222303_at	AV700891		ETS2 intronic transcript 1 mRNA	0.6	1.4	31.1	86.8	63.8	3.6	2.2	2.9	3.2	10.8	10.5	16.6	19.0	1.2	0.7	0.7	8.1	0.3	0.8	4.0555
201664_at	AL136877.1		DKFZp434F205	2.8	5.0	17.3	27.7	31.8	4.4	5.3	9.1	8.3	4.3	3.9	5.7	5.5	0.1	4.8	4.2	2.5	4.1	4.8	3.8471
210252_s_at	AB002356.1		MAP-kinase activating death domain	5.6	4.6	12.7	35.0	40.7	6.2	6.1	7.0	8.3	2.2	1.3	1.9	3.3	5.2	2.7	5.4	3.0	3.5	1.1	3.8424
201328_at	AL575509		v-ets avian erythroblastosis virus E26 oncogene homolog 2	1.7	0.1	18.4	34.7	50.7	2.8	1.6	1.7	1.8	6.4	9.9	8.7	8.9	0.5	0.9	1.0	4.4	0.1	1.7	3.8075
218392_x_at	NM_022754		FLJ12876	1.2	1.0	3.5	7.5	7.4	1.4	1.0	2.7	1.5	1.0	0.6	0.9	0.1	0.9	1.4	0.4	0.7	0.5	1.4	3.7693
205046_at	NM_001813.1		FLJ14150 fis, clone MAMMA1003026	0.0	0.3	1.5	8.1	13.1	1.7	0.5	1.9	1.2	0.5	1.3	1.0	0.9	1.1	1.5	0.9	1.0	0.4	0.2	3.7324
221170_at	AF312230.1	GPR	histamine H4 receptor	0.6	0.8	35.9	34.2	32.5	7.8	11.9	8.7	9.3	0.2	0.8	0.8	1.0	0.4	0.8	0.5	0.6	0.0	0.1	3.6719
201663_s_at	NM_005496.1		chromosome-associated polypeptide C	2.2	4.3	17.6	15.1	18.1	3.4	6.6	4.9	4.2	4.0	3.7	2.2	2.7	1.7	4.1	2.9	1.7	3.7	4.2	3.6472
208933_s_at	AI659005		lectin, galactoside-binding, soluble, 8 (galectin 8)	11.8	4.9	26.7	28.3	28.2	5.9	6.6	10.1	4.8	3.8	4.5	5.5	2.1	4.3	7.6	7.4	7.2	4.3	2.7	3.6311
209710_at	AL563460		GATA-binding protein 2	50.4	38.9	141.1	189.2	154.7	4.4	1.3	3.8	3.1	0.7	1.2	5.4	10.8	2.5	0.7	0.9	0.3	0.1	6.3	3.6251
205769_at	NM_003645.1		fatty-acid-Coenzyme A ligase, very long-chain 1 (FACVL1)	3.3	2.5	7.0	16.2	9.2	0.3	0.3	0.3	0.5	0.1	0.4	0.2	0.3	0.2	0.4	0.7	0.1	0.3	0.1	3.5389
209409_at	D86962.1		KIAA0207	8.4	2.6	12.5	38.0	33.1	4.9	4.2	12.3	10.4	1.7	1.7	2.1	1.8	1.4	0.4	0.7	1.5	0.4	4.8	3.4907
38398_at	AB002356		KIAA0358	5.5	4.1	13.8	24.6	29.8	6.1	6.4	5.6	7.0	3.0	3.2	3.3	4.1	5.1	3.3	5.3	3.7	4.4	2.5	3.4534
205899_at	NM_003914.1		cyclin A1	5.6	3.6	16.2	20.6	10.5	0.1	0.6	0.9	0.1	1.6	0.1	0.8	0.4	1.9	0.7	0.1	0.1	0.3	0.8	3.3824
218150_at	NM_012097.1		ADP-ribosylation factor-like 5	8.2	5.3	37.6	56.6	54.6	9.1	8.6	14.0	12.1	3.9	5.0	7.7	9.6	3.8	8.3	8.1	14.5	9.9	8.1	3.3745
213097_s_at	AI338837		zuolin related factor 1	2.1	1.8	8.4	13.4	16.7	4.8	2.1	4.8	3.7	1.8	1.2	1.2	1.6	0.3	3.4	3.7	2.3	3.3	2.8	3.3672
208158_s_at	NM_018030.1		oxysterol-binding protein-related protein	1.2	2.3	8.8	18.0	15.3	0.6	0.8	1.6	1.4	1.5	2.3	2.7	1.8	2.0	0.2	0.7	1.3	0.5	4.0	3.342
210109_at	AF191492.1		nasopharyngeal carcinoma associated gene protein-8	1.2	0.7	3.6	6.4	4.2	1.2	1.6	1.0	0.3	0.6	1.1	1.7	0.6	0.2	1.3	0.5	1.4	0.6	0.1	3.2977
220918_at	NM_025143.1		FLJ20856	1.0	1.1	26.1	37.3	26.2	6.2	6.5	14.1	11.3	3.3	2.5	2.0	2.0	1.1	0.9	0.9	3.5	1.1	0.1	3.2902
209359_x_at	L34598.1		*aml 1 (acute myeloid leukemia 1) oncogene*	1.2	0.1	3.1	7.2	7.1	2.5	1.6	1.6	1.1	0.2	1.0	0.6	1.4	0.7	0.7	1.0	0.8	0.6	0.1	3.2789
208107_s_at	NM_030941.1		exonuclease NEF-sp	3.6	7.6	7.8	30.6	20.1	1.6	2.3	2.7	0.8	0.6	0.2	1.5	1.0	0.2	0.1	0.3	0.2	0.1	1.2	3.2356
212412_at	AV715767		DKFZp564A072	18.2	16.2	41.3	72.5	67.3	7.7	7.7	16.3	11.6	6.4	6.3	9.1	12.7	3.7	3.1	4.1	8.0	3.3	18.3	3.2017
215215_s_at	AC004381		chromosome 16 BAC clone CIT987SK-44M2	2.9	2.5	4.8	12.8	10.4	0.6	0.9	1.4	0.8	0.1	0.0	0.2	0.8	0.1	0.4	0.3	0.4	0.3	0.5	3.198
221509_at	AB014731.1		SMAP-3	7.6	5.4	13.2	48.5	32.4	5.2	5.7	18.1	10.7	3.5	3.8	11.4	8.1	2.8	5.6	6.0	4.1	7.5	8.0	3.1618
218637_at	NM_018439.1		hypothetical protein IMPACT	1.3	2.4	2.9	10.7	9.3	1.5	1.5	2.7	2.1	0.6	0.7	0.6	0.6	1.2	0.8	0.7	0.9	1.1	2.1	3.1587
218352_at	NM_018191.1		hypothetical protein FLJ10716	0.8	0.5	4.9	13.7	8.7	2.3	1.7	3.4	3.9	1.0	2.0	2.8	3.6	0.8	2.3	2.0	1.7	2.2	2.4	3.1058
213035_at	AI081194		KIAA0379	2.1	3.8	11.1	26.7	22.4	2.5	1.5	3.4	2.5	1.9	1.1	2.3	1.6	4.6	2.5	1.3	0.1	2.2	6.1	3.0937
211180_x_at	D89788.1		aml 1 (acute myeloid leukemia 1) oncogene	1.5	0.2	3.1	9.4	7.5	2.0	2.5	1.7	1.7	1.0	1.4	0.3	1.1	0.4	0.4	0.6	1.1	0.7	0.2	3.0936
210731_s_at	AL136105		*lectin, galactoside-binding, soluble, 8 (galectin 8)*	2.1	1.1	4.8	9.1	6.4	1.9	1.8	3.0	1.8	1.2	1.4	2.7	1.6	2.1	1.2	1.2	1.7	1.3	0.9	3.0876
203164_at	BE464756		acetyl-Coenzyme A transporter	2.3	1.9	3.7	12.6	12.4	2.5	1.9	4.0	2.7	1.1	0.6	1.2	1.7	1.4	2.3	2.6	2.1	2.7	2.5	3.063
205768_s_at	NM_003645.1		*fatty-acid-Coenzyme A ligase, very long-chain 1 (FACVL1)*	3.0	1.7	3.9	10.7	7.7	0.4	0.1	0.6	0.2	0.1	0.8	0.1	0.7	0.0	0.8	0.1	0.2	0.1	0.1	3.0353
210517_s_at	AB003476.1		A kinase (PRKA) anchor protein (gravin) 12	25.1	4.9	44.0	69.5	59.6	1.5	0.4	0.6	0.8	0.1	0.2	1.0	3.0	0.9	0.8	0.5	0.1	0.3	18.8	3.0146
210647_x_at	AF102988.1		Ca2+-independent phospholipase A2 short isoform	2.3	1.1	18.7	13.2	9.1	3.4	3.3	4.0	4.5	3.3	5.0	4.2	3.6	1.8	3.5	4.4	1.8	2.8	2.2	3.002

Fig. 6B

B. Eosinophil (Eo)-selective transcripts (1/1).

Probe set	Accession #		Transcripts	MC. cord blood	MC. lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Eo S.I.
207328_at	NM_001140.1		15-lipoxygenase	0.1	0.6	0.7	0.1	0.1	14.5	24.6	18.3	17.0	0.1	1.1	0.1	0.1	0.1	0.0	0.1	0.0	0.1	0.0	74.129
219695_at	NM_024703.1		FLJ22593	0.0	1.0	1.8	1.8	1.1	29.8	34.7	24.8	27.8	0.8	1.5	0.4	0.9	0.1	0.6	0.4	0.3	0.1	0.1	19.123
208253_at	NM_014442.1	R	sialic acid binding Ig-like lectin, Sigtec 8	1.3	2.4	0.4	0.4	0.2	17.1	23.1	17.6	11.8	0.1	0.4	0.1	0.8	0.3	0.2	0.1	0.2	0.5	0.2	9.8056
211922_s_at	AY028632.1		catalase	3.7	2.2	6.2	6.8	2.2	78.2	134.5	119.7	88.8	16.2	13.0	8.8	8.7	0.7	2.2	2.9	11.1	7.5	4.6	9.125
201802_at	NM_004955.1		solute carrier family 29 (nucleosidetransporters)	4.8	2.8	2.9	3.4	1.9	24.8	30.4	36.1	42.3	0.1	0.6	0.6	0.8	0.2	0.9	0.3	2.2	1.0	1.1	8.989
214523_at	NM_001805.1		CCAAT enhancer binding protein (CEBP), epsilon	0.1	0.1	0.7	1.2	1.2	7.9	11.4	23.4	17.3	1.8	1.5	1.9	1.1	1.4	0.5	0.4	1.0	0.1	0.1	8.9462
210029_at	M34455.1		interferon-gamma-inducible indoleamine 2,3-dioxygenase	0.7	0.1	5.3	4.2	2.6	20.0	39.0	33.4	29.5	1.6	2.1	2.3	1.8	1.7	1.5	1.7	0.3	1.4	0.9	7.7078
215573_at	AU147084		FLJ12072	0.1	0.1	0.5	0.3	1.1	9.8	8.4	16.9	7.2	0.4	1.9	1.8	2.0	0.1	0.1	0.0	0.1	0.4	0.0	7.5983
201801_s_at	AF079117.1		*solute carrier family 29 (nucleosidetransporters)*	3.5	1.9	1.7	0.5	0.9	29.7	47.1	7.4	11.0	0.1	0.5	0.4	0.7	1.1	0.4	0.1	1.4	0.6	1.0	7.0314
213825_at	AF221520.1		oligodendrocyte lineage transcription factor 2	0.4	0.6	0.2	0.4	0.6	6.0	10.9	18.7	12.5	0.8	0.9	1.5	1.0	0.6	1.7	0.3	0.4	0.3	0.3	6.5987
219821_s_at	NM_018988.1		glucose-fructose oxidoreductase domain containing	3.0	1.4	1.8	2.6	2.3	18.7	17.3	30.9	31.3	3.9	3.1	2.4	2.9	3.2	1.3	2.5	3.0	3.8	0.8	6.2284
205472_s_at	NM_004392.1		dachshund (Drosophila) homolog	0.0	0.1	0.1	0.4	0.1	2.7	1.4	2.2	1.7	0.3	0.1	0.1	0.1	0.2	0.1	0.1	0.1	0.3	0.0	6.0088
202188_at	NM_014669.1		KIAA0095	0.5	0.9	0.4	1.8	1.2	6.8	8.5	13.5	10.6	0.2	0.2	0.2	0.1	0.2	0.3	1.7	1.7	1.4	0.4	5.4499
210548_at	U58913.1		*chemokine CCL23*	0.6	1.8	0.4	1.1	0.5	5.5	6.2	4.2	6.9	0.1	0.9	0.1	0.2	0.3	0.1	0.2	0.6	0.1	0.0	5.3082
209447_at	AF043290.1		lymphocyte membrane associated protein (8B7)	0.6	0.5	2.5	3.4	3.6	41.8	49.7	66.2	60.1	0.2	0.9	0.5	1.2	2.6	5.1	10.4	1.6	6.3	2.7	5.1472
206171_at	NM_000677.2	GPR	ADORA3 adenosine A3 receptor	2.3	2.8	2.8	3.7	2.2	7.8	13.9	22.0	17.9	1.6	3.1	2.2	2.5	1.2	1.6	0.5	2.0	0.5	0.5	5.0469
210549_s_at	U58913.1		chemokine CCL23	1.1	1.1	0.1	1.3	0.6	7.9	5.6	2.7	8.1	0.0	0.6	0.0	0.2	0.1	0.1	0.1	0.2	0.0	0.4	4.9873
214183_s_at	X91817.1		transketolase-like protein	0.1	0.2	0.2	0.1	0.1	3.2	4.0	6.6	7.2	0.2	0.2	0.1	0.1	0.2	0.2	1.0	0.1	0.6	0.0	4.7894
215350_at	AB033088.1		spectrin repeat containing, nuclear envelope 1	0.1	0.1	0.5	0.1	0.1	3.8	4.2	3.0	2.8	0.0	0.1	0.2	0.4	0.7	0.2	0.1	0.0	0.1	0.2	4.7822
206277_at	NM_002564.1	GPR	P2Y2 purinergic receptor	0.1	0.1	0.1	0.2	0.1	3.4	4.7	8.1	5.9	0.1	0.3	0.1	0.1	0.2	0.1	0.3	1.2	0.2	0.1	4.3043
204776_at	NM_003248.1		thrombospondin 4 (THBS4)	0.8	0.1	1.5	0.1	0.8	3.2	5.9	10.0	6.4	1.8	1.4	0.6	0.9	0.3	0.2	0.3	1.4	1.1	1.2	4.1746
201563_at	L29008.1		L-iditol-2 dehydrogenase	4.1	2.6	3.5	11.4	12.8	22.5	29.9	49.0	37.0	1.8	3.0	4.4	2.2	2.1	1.6	1.2	2.7	2.5	1.8	4.1557
206637_at	NM_014879.1	GPR	P2YX purinergic receptor GPR105 for UDP-glucose	5.7	1.6	13.3	19.9	13.5	44.2	55.1	81.4	62.4	1.8	9.3	15.4	9.2	0.7	0.9	0.8	0.0	5.5	0.1	3.8761
213622_at	A1733465		collagen, type IX, alpha 2	1.5	1.4	1.9	1.2	1.3	10.3	9.6	6.6	8.8	2.7	2.1	2.1	2.2	0.7	1.2	1.2	2.2	1.7	0.9	3.8576
214705_at	AJ001306.1		PDZ domain protein	0.1	0.1	0.4	0.3	0.1	2.1	1.5	2.6	2.2	0.3	0.0	0.6	0.7	0.1	0.4	0.3	0.3	0.6	0.1	3.6532
266_s_at	L33930		*CD24 signal transducer*	0.2	0.1	3.0	0.3	0.8	11.9	14.0	18.8	13.9	0.1	0.1	0.3	0.8	0.9	0.0	0.1	0.1	4.3	0.2	3.3793
201432_at	NM_001752.1		catalase (CAT)	23.0	14.3	35.7	49.4	19.9	202.3	209.7	221.6	207.3	67.0	54.3	71.3	60.9	9.2	11.2	15.1	53.6	29.9	21.4	3.3325
209696_at	D26054.1		fructose-1,6-bisphosphatase	0.9	3.4	4.3	11.1	6.4	20.2	27.7	28.8	32.5	3.0	2.5	2.4	1.5	1.9	2.0	1.6	8.1	1.1	0.6	3.3089
216379_x_at	AK000168.1		CD24 signal transducer	1.3	1.4	16.2	0.9	1.5	66.1	70.1	81.9	77.9	1.7	2.8	2.6	4.1	4.8	0.5	0.6	0.9	22.5	0.5	3.2741
205569_at	NM_014398.1		lysosome-associated membrane glycoprotein (TSC403)	0.4	0.2	0.7	0.1	0.4	2.4	3.1	6.8	3.0	0.6	0.1	1.4	0.8	0.4	1.1	0.7	0.1	0.0	0.3	3.2308
219233_s_at	NM_018530.1		hypothetical protein PRO2521	0.1	1.9	2.1	4.6	5.4	7.5	8.5	21.8	21.2	0.8	0.1	1.5	2.1	0.1	1.1	4.1	0.1	1.4	0.5	3.2093
202286_s_at	J04152		gastrointestinal tumor-associated antigen GA733-1	0.9	0.7	1.3	0.3	0.1	1.1	2.5	8.7	1.8	0.4	0.8	0.6	0.6	0.2	0.2	0.7	0.3	0.5	0.1	3.1844
206442_at	NM_003007.1		semenogelin I (SEMG1)	0.6	0.1	0.4	0.0	0.1	1.2	3.2	4.9	3.4	0.3	0.2	1.1	1.9	0.1	0.2	0.2	0.9	0.4	0.1	3.1837
205733_at	NM_000057.1		Bloom syndrome	1.9	1.1	2.0	2.4	2.2	8.5	6.0	7.5	11.2	2.1	2.0	1.0	1.2	1.2	2.4	1.8	1.1	2.6	1.2	3.1427
204392_at	NM_003656.2		calciumcalmodulin-dependent protein kinase I (CAMK1)	4.0	1.1	6.3	8.9	6.4	17.8	19.3	24.9	26.5	0.6	0.2	1.8	1.5	0.1	1.4	1.0	3.0	0.6	1.8	3.0763
213497_at	AL050374.1		DKFZp586C1619	1.0	0.7	1.0	1.3	1.6	6.3	6.8	6.8	6.0	2.3	3.0	1.4	2.3	2.0	0.4	0.5	1.6	1.1	0.8	3.0099
219296_at	NM_019028.1		similar to ankyrinrepeat-containing protein AKR1	2.2	1.7	0.2	3.5	1.6	7.3	4.4	8.4	7.4	1.8	2.4	2.4	2.3	0.1	1.4	1.6	1.3	1.9	0.8	3.0018

Fig. 6C

C. Neutrophil (Ne)-selective transcripts (1/7).

Probe set	Accession #		Transcripts	MC cord blood	MC lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ne S.I.
205403_at	NM_004633.1	R	interleukin 1 R, type II	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	37.4	41.4	73.8	61.5	0.2	0.4	0.1	0.2	0.0	0.0	127.86
216782_at	AK026679.1		FLJ23026 fis	0.0	0.2	0.2	0.1	0.1	0.1	0.1	0.5	0.2	33.2	31.5	33.0	17.4	0.1	0.1	0.1	0.1	0.2	0.2	112.28
210119_at	U73191.1	ICN	KCNJ15 inward rectifier potassium channel Kir 1.3	0.7	1.1	0.1	0.1	0.5	0.1	0.1	0.9	0.6	81.6	98.6	129.0	88.8	0.7	0.2	0.0	0.8	0.0	0.0	107.47
209395_at	M80927.1		chitinase 3-like 1 (cartilage glycoprotein-39)	1.5	0.2	0.9	0.1	0.4	0.3	0.1	8.1	0.1	28.9	25.3	70.7	40.7	0.1	0.0	0.1	0.1	0.1	0.0	79.595
203691_at	NM_002638.1		protease inhibitor 3, skin-derived (SKALP)	0.2	0.1	0.1	0.1	0.8	0.5	0.2	0.4	0.1	16.9	36.7	27.7	24.5	0.1	0.1	0.1	0.1	0.5	0.1	51.901
211372_s_at	U64094.1	R	interleukin 1 R, type II	0.1	0.2	0.1	0.1	0.0	0.1	0.5	0.7	0.1	21.6	36.5	31.4	29.9	0.3	0.2	0.0	0.6	0.0	0.0	50.606
207008_at	NM_001557.1	GPR	CXCR2 interleukin 8 receptor, beta	0.0	0.4	1.1	1.2	1.0	1.3	1.3	2.1	1.2	129.8	168.4	81.5	68.8	2.7	0.3	0.8	0.7	0.6	0.0	39.316
206515_at	NM_000896.1		leukotriene B4 omega hydroxylase (CYP4F3)	0.3	0.1	1.1	0.7	1.2	0.5	0.8	5.9	1.7	56.8	40.3	57.2	48.9	0.2	0.9	0.0	0.7	0.3	0.3	34.919
204007_at	J04162.1	R	Fc gamma R IIIb (CD16)	0.8	0.7	1.4	1.6	1.8	1.1	1.8	2.8	1.9	204.5	226.5	194.0	173.3	6.6	1.3	1.3	2.2	2.6	0.1	29.895
204470_at	NM_001511.1		melanoma growth stimulating activity, alpha	1.2	0.0	0.7	0.9	0.1	0.6	0.5	1.2	0.7	19.1	23.0	26.3	48.1	0.1	0.2	0.2	1.0	0.1	0.2	28.189
206025_s_at	AW188198		tumor necrosis factor, alpha-induced protein 6	0.1	0.3	0.1	0.6	0.4	0.6	0.1	0.2	0.1	19.0	29.9	17.2	24.7	0.1	0.2	0.2	0.8	0.3	0.6	26.336
209396_s_at	M80927.1		chitinase 3-like 1 (cartilage glycoprotein-39)	1.8	0.2	1.6	0.4	0.5	0.8	0.5	5.6	0.9	37.9	32.2	52.8	26.7	1.4	0.0	0.0	0.1	0.1	0.4	25.669
211806_s_at	D87291.1	ICN	KCNJ15 inward rectifier potassium channel Kir1.3	0.9	1.7	2.0	1.4	1.4	2.1	1.3	1.8	1.7	62.2	77.2	77.5	56.8	3.0	1.0	1.1	1.7	0.9	0.7	22.254
221920_s_at	BE677761		mitochondrial solute carrier	0.4	0.8	6.9	0.0	0.2	2.4	1.5	2.2	1.5	59.0	43.2	57.4	46.8	2.5	0.7	0.3	1.8	1.1	1.0	20.163
207094_at	NM_000634.1	GPR	CXCR1 interleukin 8 receptor, alpha	0.3	0.1	4.2	4.3	4.4	0.3	0.3	0.2	0.3	69.2	81.9	95.3	87.4	0.4	0.3	0.2	0.2	0.1	0.1	19.325
213589_s_at	AW468201		23614 mRNA sequence	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.2	0.1	5.5	2.7	5.1	4.0	0.1	0.1	0.2	0.1	0.1	0.0	18.973
218963_s_at	NM_015515.1		DKFZP434G032	0.0	0.1	0.5	0.3	0.1	1.1	2.8	2.8	2.0	46.3	32.5	40.3	31.3	0.3	0.3	0.1	0.1	0.1	0.1	18.3
213506_at	BE965369	GPR	PAR2 proteinase activated receptor-2	0.1	0.0	0.0	0.4	0.3	1.2	1.3	4.1	2.3	33.4	35.7	42.4	33.4	0.1	0.7	0.1	1.6	0.4	1.2	18.208
220187_at	NM_024636.1		FLJ23153	0.3	0.1	0.3	0.1	0.1	0.0	0.1	0.5	0.5	16.5	26.3	5.7	7.0	0.0	0.1	0.1	0.7	0.1	0.2	17.111
206026_s_at	NM_007115.1		tumor necrosis factor, alpha-induced protein 6	0.1	0.8	0.4	0.8	0.6	1.1	0.5	0.9	0.1	18.2	23.3	20.0	17.0	0.6	1.0	1.0	1.1	0.1	1.0	17.051
41469_at	L10343		elafin	1.2	0.7	1.2	0.8	0.8	0.9	1.0	0.7	0.8	16.2	39.1	19.5	17.4	1.3	1.4	0.7	0.8	0.5	0.5	15.913
205568_at	NM_020980.2	ICN	aquaporin 9	0.5	0.9	0.1	0.1	0.1	0.3	0.1	1.0	0.1	133.3	136.7	169.0	110.5	0.4	0.9	0.1	8.6	0.1	0.2	15.805
210483_at	BC005043.1	R	decoy receptor 1, TRAILR3	0.1	0.1	0.4	0.9	0.7	1.0	0.9	1.3	1.2	25.8	23.2	9.7	8.6	0.2	0.4	0.3	0.2	0.2	0.1	13.337
215223_s_at	W46388		superoxide dismutase 2	4.4	1.9	1.7	4.9	8.7	5.8	3.3	6.0	8.3	124.6	153.1	142.4	151.8	11.0	1.6	1.1	7.3	2.2	1.5	13.008
210484_s_at	BC005043.1	R	decoy receptor 1, TRAILR3	0.9	0.9	0.9	0.2	0.1	2.2	4.8	0.8	0.6	60.1	86.3	4.7	5.9	0.5	0.6	0.4	0.9	0.4	0.5	12.748
205654_at	NM_000715.4		complement component 4-binding protein, alpha	0.5	1.1	1.3	0.7	0.7	1.5	1.0	1.3	1.4	2.1	20.7	43.6	33.7	1.2	0.3	1.3	1.2	1.2	0.9	12.161
210773_s_at	U81501.1	GPR	formyl peptide receptor 2	0.8	0.1	0.6	0.6	0.3	0.6	0.6	0.6	0.5	86.9	105.0	50.2	59.9	0.1	1.0	0.6	6.0	0.8	0.1	12.14
206222_at	NM_003841.1	R	decoy receptor 1, TRAILR3	1.5	0.8	1.9	0.7	0.7	3.6	13.7	3.4	3.9	121.0	137.1	37.5	22.5	0.0	0.1	0.1	1.8	0.5	0.7	12.034
202083_s_at	NM_003003.1		SEC14 (S. cerevisiae)-like1	0.8	0.2	0.9	1.8	3.0	2.2	2.6	3.8	2.6	36.7	25.9	33.9	32.6	1.3	0.1	0.1	1.1	1.0	0.7	11.729
211163_s_at	AF012536.1	R	decoy receptor 1, TRAILR3	0.2	0.1	2.2	1.5	0.6	2.6	12.3	9.4	6.4	87.9	110.9	60.4	55.8	0.5	0.2	0.1	0.7	0.1	0.6	11.404
205931_s_at	NM_004904.1		cAMP response element-binding protein CRE-BPa	0.0	0.1	0.3	0.1	0.6	0.6	0.6	0.6	0.7	23.2	14.5	20.5	12.9	1.6	0.8	0.1	1.6	0.1	0.1	10.618
205922_at	NM_004665.1		vanin 2	0.1	0.0	1.2	2.6	3.9	1.0	0.2	1.9	0.3	114.5	114.6	174.1	189.2	0.1	1.4	4.0	13.8	1.7	0.0	10.451
210176_at	AL050262.1	R	Toll-like receptor 1	0.7	0.6	0.2	0.3	0.3	0.5	1.1	1.9	1.2	29.5	38.6	25.1	32.6	1.6	0.8	0.7	3.0	1.5	0.3	10.418
215977_x_at	X68285.1		glycerol kinase	1.9	0.9	0.8	0.7	1.0	0.3	0.6	0.9	1.0	15.8	19.8	9.7	10.9	0.1	0.1	0.2	0.2	0.2	0.3	10.203
215783_s_at	X14174.1		liver-type alkaline phosphatase	0.5	1.2	0.7	0.9	0.4	0.7	0.5	1.0	0.6	21.2	42.8	11.6	12.8	1.2	0.7	0.2	0.5	0.5	1.9	10.167
217167_x_at	AJ252550		GK gene for glycerol kinase, exon 1	1.2	0.1	0.2	0.3	1.0	0.2	0.1	0.8	0.3	8.0	13.6	7.5	7.2	0.4	0.1	0.1	0.9	0.2	0.2	10.067
213349_at	AI934439		KIAA0779	0.9	0.7	0.9	1.4	1.0	1.9	1.4	2.3	2.1	15.6	15.3	19.5	23.8	0.1	1.4	1.5	1.6	1.2	1.2	9.7704

Fig. 6D

C. Neutrophil (Ne)-selective transcripts (2/7).

Probe set	Accession #		Transcripts	MC. cord blood	MC. lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ne S.I.
210789_x_at	L00692.1		carcinoembryonic antigen (CGM1)	1.1	0.4	1.9	1.4	1.5	2.0	1.5	2.5	0.4	19.4	18.6	22.6	15.5	0.7	1.6	0.9	2.0	0.3	1.1	9.2749
210772_at	M88107.1	GPR	formyl peptide receptor 2	0.1	0.2	0.4	0.7	0.7	0.7	0.3	0.8	0.7	51.4	67.7	44.8	46.4	0.5	0.5	0.5	5.6	0.1	0.1	9.2661
218978_s_at	NM_018586.1		PRO1584	0.7	0.5	1.6	0.2	0.5	1.1	0.9	0.7	0.5	26.3	20.5	6.6	2.8	0.2	0.7	0.4	1.1	0.2	0.4	9.1536
204006_s_at	NM_000570.1	R	Fc gamma R IIIb (CD16)	0.7	0.2	1.2	0.7	0.6	0.7	0.8	0.0	0.7	230.7	278.8	47.6	45.9	4.2	1.9	6.9	12.0	3.9	0.1	9.0769
207275_s_at	NM_001995.1		fatty-acid-Coenzyme A ligase, long-chain 1 (FACL1)	4.3	2.6	5.1	11.5	19.4	5.3	5.1	5.9	3.7	93.8	127.8	92.8	69.1	0.7	1.0	1.1	8.3	0.9	1.7	8.9855
220302_at	NM_005906.2		male germ cell-associated kinase	0.1	0.0	1.3	0.7	0.8	0.7	0.2	2.0	1.4	7.9	8.4	7.9	8.9	0.3	0.1	0.0	0.1	0.1	0.0	8.866
221803_s_at	AA883074		nuclear receptor binding factor-2	1.1	0.8	3.2	4.0	2.9	2.8	2.8	4.7	3.2	24.7	25.2	33.2	29.3	0.1	1.5	1.2	1.7	2.0	2.6	8.3788
206765_at	AF153820.1	ICN	KCNJ2 inwardly-rectifying potassium channel Kir2.1	1.0	0.4	2.5	4.4	4.4	2.4	4.7	6.1	8.0	25.8	36.2	52.4	48.3	0.4	0.2	0.5	1.5	0.7	1.1	8.108
213351_s_at	AI934469		KIAA0779	0.0	0.1	0.9	2.0	1.6	0.8	0.6	2.3	2.7	7.9	5.9	20.1	18.0	0.2	0.5	0.2	0.1	0.2	1.2	7.9705
214590_s_at	AL545760		ubiquitin-conjugating enzyme E2D1	0.1	1.5	0.3	0.4	0.5	1.1	1.0	0.5	0.4	7.9	10.7	10.1	4.4	0.1	0.4	0.3	1.0	0.4	0.9	7.8712
206522_at	NM_004668.1		leukotriene B4 omega hydroxytase (CYP4F3)	0.0	0.0	0.8	1.8	1.0	3.0	5.4	11.7	9.4	46.0	51.5	56.9	43.0	0.1	0.0	0.0	0.6	0.6	0.1	7.5773
210992_x_at	U90939.1	R	Fc gamma receptor IIc2	1.9	1.0	1.7	2.1	3.3	8.1	16.1	2.8	4.2	70.9	95.6	42.8	30.5	0.3	0.2	0.1	7.2	2.3	0.2	7.5239
220528_at	NM_018399.1		VNN3 protein	0.1	0.2	1.3	6.1	5.0	0.2	0.1	0.5	0.4	26.8	22.1	20.0	36.8	0.8	0.2	0.1	3.0	0.1	0.1	7.5216
200919_at	NM_004427.1		early development regulator 2	5.6	4.4	4.8	6.5	9.6	7.6	6.8	5.3	7.3	109.5	89.0	52.9	61.4	2.5	4.9	7.0	10.0	3.9	6.5	7.5056
207387_s_at	NM_000167.1		glycerol-kinase	2.1	1.5	1.0	1.5	1.6	1.1	1.4	1.6	1.4	14.3	20.3	10.7	10.3	0.9	0.6	0.3	1.7	0.6	0.6	7.4603
117_at	X51757		heat-shock protein HSP70B	1.1	0.2	0.8	0.6	0.9	5.9	8.3	2.1	4.1	46.3	41.2	25.1	25.8	0.4	0.9	0.6	3.7	1.6	0.5	7.4139
205174_s_at	NM_012413.2		glutaminyl-peptide cyclotransferas	0.4	0.0	0.4	0.7	0.9	0.7	0.0	0.4	0.3	30.1	47.7	36.4	24.7	0.7	0.6	0.0	4.6	0.1	1.5	7.3246
219434_at	NM_018643.1		triggering receptor expressed on myeloid cells 1	1.3	0.3	0.4	0.2	0.5	2.9	0.7	1.4	1.5	92.8	84.0	81.2	98.6	3.4	0.6	0.1	12.3	0.9	0.3	7.2368
203887_s_at	NM_000361.1		thrombomodulin	1.7	0.1	0.4	0.4	0.4	0.2	1.0	1.4	1.1	16.8	13.0	13.4	1.3	0.7	0.6	0.4	1.1	0.4	0.2	7.1328
205040_at	NM_000607.1		orosomucoid 1 (ORM1)	0.5	0.1	0.1	0.4	0.1	0.1	0.0	1.1	0.0	3.4	4.1	4.3	0.7	0.1	0.3	0.1	0.4	0.0	0.2	7.0823
214681_at	AI830490		glycerol kinase	0.2	0.4	0.1	1.2	1.7	0.8	1.1	0.6	1.2	7.8	14.2	24.0	12.1	0.9	0.0	0.1	1.9	1.0	0.3	6.966
218035_s_at	NM_019027.1		FLJ20273	2.9	1.0	0.9	1.5	0.8	0.9	0.4	1.3	1.1	47.2	54.4	91.9	94.0	1.7	0.7	0.4	9.9	1.5	0.3	6.9074
205068_s_at	BE671084		GTPase regulator associated with the focal adhesion kinase pp125(FAK)	1.2	1.4	3.5	5.9	5.1	6.5	5.1	8.5	7.1	43.7	40.6	45.2	56.0	0.7	1.3	2.9	5.1	0.8	1.2	6.8934
203021_at	NM_003064.1		secretory leukocyte protease inhibitor (antileukoproteinase) (SLPI)	1.7	0.8	4.6	1.5	1.1	1.2	2.2	8.5	0.8	16.2	19.8	13.9	8.7	1.8	0.6	1.2	1.7	1.1	2.1	6.7497
216316_x_at	X78713		glycerol kinase pseudogene, chromosome 1	2.0	0.9	0.4	0.6	1.0	0.7	0.6	0.5	1.0	10.3	18.6	5.8	5.8	0.5	0.2	0.2	0.8	0.3	0.1	6.6675
217209_at	X16454		carcinoembryonic antigen subdomains A and B	0.6	0.4	0.2	0.2	0.4	0.1	0.3	0.7	0.5	2.8	3.8	3.3	2.7	0.3	0.4	0.0	0.1	0.1	0.2	6.5382
220421_at	NM_024850.1		FLJ21458	0.3	0.6	0.1	0.1	0.1	0.3	0.8	0.4	0.3	8.9	7.2	9.1	7.0	1.2	0.6	0.0	0.1	0.1	0.2	6.4857
213524_s_at	NM_015714.1		putative lymphocyte G0G1 switch gene (G0S2)	0.8	0.8	1.3	0.9	0.5	8.0	8.5	18.7	10.1	118.0	52.0	39.6	92.5	1.7	0.8	0.1	6.0	0.2	3.4	6.4779
206472_s_at	NM_005078.1		transducin-like enhancer of split 3	2.2	2.6	1.3	0.7	0.5	1.6	0.6	0.5	1.0	22.6	25.0	11.3	8.3	1.3	1.2	1.5	1.8	1.5	0.9	6.4334
212769_at	AI567426		KIAA1547	1.4	1.5	0.5	1.3	2.3	1.1	1.0	2.2	1.9	17.9	15.9	15.1	12.8	2.4	0.8	1.1	1.3	1.2	0.5	6.4271
204307_at	AB002295.1		KIAA0329	0.7	0.0	0.1	2.6	2.1	1.8	1.5	2.4	2.0	10.3	11.2	15.4	12.8	1.9	0.1	0.5	0.2	0.1	0.5	6.3478
203591_s_at	NM_000760.1	R	granulocyte colony-stimulating factor receptor	0.1	0.0	1.0	0.1	0.2	2.3	0.6	2.4	1.0	220.3	187.2	134.9	112.1	0.2	0.8	0.2	25.5	0.1	0.2	6.2051
210210_at	AF181660.1		immunoglobulin superfamily member WM78	0.9	1.1	1.6	1.8	1.9	1.1	1.9	1.7	2.0	11.1	7.0	13.7	14.1	1.4	1.3	0.9	1.6	1.1	0.6	6.172
218610_s_at	NM_018340.1		FLJ11151	1.5	1.2	1.2	1.2	1.8	3.3	3.2	2.6	1.8	25.2	23.3	17.9	21.8	0.5	0.6	0.4	3.6	0.4	0.6	6.112
203561_at	NM_021642.1	R	Fc gamma receptor IIa (CD32)	4.7	1.2	0.9	1.2	2.4	19.5	22.8	19.4	21.4	104.3	129.0	153.0	123.9	4.0	0.7	0.7	16.3	2.2	0.2	6.1015
216841_s_at	X15132.1		superoxide dismutase 2	1.3	1.1	1.2	1.8	2.2	1.4	1.3	3.2	2.4	20.5	44.6	35.8	42.2	5.6	0.8	0.7	2.0	0.7	1.1	6.0724

Fig. 6E

C. Neutrophil (Ne)-selective transcripts (3/7).

Probe set	Accession #		Transcripts	MC cord blood	MC lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ne S.I.
207624_s_at	NM_000328.1		retinitis pigmentosa GTPase regulator (RPGR)	0.0	0.6	1.1	2.0	1.2	1.1	1.2	2.1	2.8	7.1	7.0	13.6	15.1	0.2	1.2	0.4	0.9	0.7	0.3	6.0348
209850_s_at	BC005406.1		Cdc42 effector protein 2	0.2	0.2	1.3	0.2	1.0	0.2	0.4	0.5	0.4	13.2	9.6	6.7	8.7	0.2	0.2	0.2	0.6	0.4	1.6	5.9313
203936_s_at	NM_004994.1		matrix metalloproeinase 9	47.7	0.6	1.6	1.9	1.4	1.2	2.4	15.5	1.5	36.5	35.1	36.8	21.9	1.7	2.0	1.4	1.9	1.3	1.4	5.9311
215966_x_at	AA292874		*glycerol kinase*	1.2	0.2	0.6	0.1	1.2	0.2	1.0	1.2	1.2	6.6	10.2	7.3	7.4	0.2	0.1	0.2	1.3	0.5	0.0	5.9077
206925_at	NM_005668.1		sialyltransferase 8	3.1	1.2	2.1	2.5	2.0	1.4	3.1	1.6	1.6	21.7	33.3	6.8	11.4	0.4	0.9	1.6	2.6	1.2	0.2	5.8688
211764_s_at	BC005980.1		ubiquitin-conjugating enzyme E2D 1	1.8	1.4	1.1	2.9	2.4	7.5	5.7	3.9	2.2	29.3	31.2	52.6	25.4	0.2	2.0	1.4	5.7	1.3	2.3	5.8143
201192_s_at	NM_006224.1		phosphotidylinositol transfer protein (PITPN)	3.0	3.1	1.9	5.0	4.6	3.9	5.4	6.6	5.4	27.9	26.9	32.9	35.2	2.0	3.5	3.7	5.0	3.2	2.8	5.811
205921_s_at	U16120.1		placental taurine transporter	1.2	0.7	0.5	0.2	0.4	0.3	1.6	0.5	0.9	14.8	17.2	2.8	2.6	0.0	0.1	0.3	1.1	0.3	0.4	5.7909
209137_s_at	BC000263.1		ubiquintin c-terminal hydrolase related polypeptide	3.6	4.1	2.0	2.6	1.9	1.5	0.9	2.7	0.9	25.0	24.5	37.6	29.7	3.5	5.0	2.5	3.5	2.7	3.0	5.7864
208052_x_at	NM_001815.1		carcinoembryonic antigen-related cell adhesion molecule 3 (CEACAM3)	1.7	1.4	2.9	2.7	1.9	3.0	2.6	2.8	2.1	14.3	16.5	20.0	13.7	2.5	1.3	2.3	2.8	2.5	1.6	5.7572
201393_s_at	NM_000876.1	R	insulin-like growth factor 2 receptor	6.4	2.8	0.2	0.8	1.8	4.1	5.4	6.8	5.4	82.4	106.9	80.1	71.7	1.7	2.9	8.7	8.4	4.8	14.8	5.7104
218614_at	NM_018169.1		FLJ10652	1.2	1.0	6.9	13.7	12.5	3.2	3.3	7.7	5.8	52.7	54.4	82.8	83.3	2.9	8.7	11.8	3.2	10.8	1.3	5.6442
202084_s_at	NM_003003.1		SEC14 (S. cerevisiae)-like 1	5.7	2.5	12.8	28.8	22.6	20.6	18.7	35.5	29.5	130.7	129.7	135.6	177.9	19.2	4.1	3.5	11.5	7.7	11.8	5.6423
32069_at	AB014515		*KIAA0615*	2.8	1.5	2.1	5.6	5.5	4.6	3.7	5.9	6.9	23.9	20.9	35.1	40.5	1.0	3.4	3.3	2.6	2.1	1.5	5.6348
205896_at	NM_003059.1		solute carrier family 22, member 4 (SLC22A4)	0.8	1.2	1.0	0.1	1.1	1.9	2.4	3.5	2.7	8.5	13.3	30.0	12.6	0.5	0.7	0.8	2.6	0.5	1.4	5.4612
206584_at	NM_015364.1		MD-2 protein	7.4	1.1	2.0	3.9	1.8	1.0	0.4	0.6	0.5	43.9	62.3	87.8	56.0	1.3	3.5	1.0	11.1	3.5	9.4	5.4459
202082_s_at	NM_003003.1		*SEC14 (S. cerevisiae)-like 1*	1.0	0.3	3.6	2.5	2.2	15.5	5.4	12.3	8.4	40.2	57.3	54.9	60.9	3.8	0.8	1.3	2.7	3.3	2.4	5.4422
204308_s_at	NM_014844.1		KIAA0329	2.9	1.1	2.2	2.8	2.8	2.1	3.1	3.1	4.3	16.5	18.7	19.9	19.0	3.4	1.3	1.7	1.8	1.3	2.5	5.4369
207500_at	NM_004347.1		caspase 5	0.3	1.1	0.1	0.0	0.1	0.1	0.3	0.2	0.5	4.2	6.2	4.6	2.9	0.3	0.3	0.4	0.8	0.1	0.3	5.379
203435_s_at	NM_007287.7		CD10, membrane metallo-endopeptidase	0.3	0.5	0.4	0.3	0.2	0.1	0.3	0.3	0.2	16.4	44.2	54.6	42.8	0.2	0.3	0.2	0.2	0.2	6.9	5.2591
205539_at	NM_006576.1		advillin	0.4	0.5	2.0	1.4	0.8	1.0	1.1	1.0	1.1	8.4	6.9	6.0	10.1	1.0	1.3	0.4	1.5	0.7	1.1	5.2541
204601_at	NM_014664.1		KIAA0615	1.9	1.2	1.3	3.2	2.3	3.0	2.7	3.7	3.0	12.9	12.8	20.2	20.0	0.1	2.2	2.6	1.3	1.9	1.0	5.2381
201963_at	NM_021122.2		*fatty-acid-Coenzyme A ligase, long-chain 1 (FACL1)*	2.9	2.1	5.0	19.9	33.4	6.6	3.8	10.3	6.1	58.8	86.6	92.2	80.2	0.1	1.1	1.1	10.8	1.5	2.4	5.2374
207064_s_at	NM_009590.1	GPR	*CXCR1 interleukin 8 receptor, alpha*	0.7	0.1	0.9	0.9	0.8	0.8	0.8	0.9	1.2	4.3	4.7	4.0	6.6	0.8	0.5	0.8	0.5	0.8	0.3	5.1905
220005_at	NM_023914.1	GPR	P2YX purinergic receptor GPR86 for UDP-glucose	0.6	0.0	0.1	0.5	0.1	19.7	9.6	25.1	17.3	76.5	77.1	100.7	98.6	1.9	0.1	0.2	12.3	0.6	0.0	5.1686
211395_x_at	U90940.1	R	Fc gamma receptor IIc3	4.6	0.3	7.3	9.7	15.1	9.7	19.5	4.4	6.6	115.0	140.3	42.9	38.9	3.0	1.4	0.6	14.0	7.2	1.0	5.1401
201780_s_at	NM_007282.1		ring finger protein 13 (RNF13)	4.4	2.8	3.5	9.2	6.6	6.8	6.2	8.9	7.1	27.1	36.6	52.5	35.7	0.8	4.1	3.7	7.2	7.2	4.6	5.1305
209864_at	AB045118.1		GSK-3 binding protein FRAT2	2.8	1.3	4.4	9.2	8.0	13.4	16.9	27.3	22.6	93.2	97.2	100.6	104.2	1.3	1.9	2.9	10.2	2.5	1.0	5.1047
218319_at	NM_020651.2		pellino (Drosophila) homolog 1 (PELI1)	3.4	2.9	5.9	17.5	33.5	17.7	11.7	12.6	15.1	64.9	88.3	73.0	80.2	2.4	6.3	2.9	13.8	12.6	1.1	5.0403
206632_s_at	NM_004900.1		phorbolin	0.6	1.1	1.0	1.2	2.6	1.3	0.8	3.9	0.5	19.6	11.1	30.8	0.5	1.5	0.2	0.4	0.4	1.0	1.2	5.0277
220990_s_at	NM_030938.1		DKFZp5661133	11.7	6.2	4.6	18.5	12.5	5.0	3.3	8.2	4.9	115.5	117.2	125.3	122.5	2.6	5.3	4.2	24.1	4.4	8.3	4.9858
221653_x_at	BC004395.1		apolipoprotein L	0.7	2.8	0.6	2.1	1.6	2.0	0.4	1.8	1.1	8.0	3.9	12.7	5.2	0.2	0.9	0.4	1.4	1.1	0.4	4.9332
204748_at	NM_00963.1		COX2 prostaglandin-endoperoxide synthase 2	6.5	16.2	0.6	2.4	2.0	4.5	2.3	3.4	3.4	35.8	44.1	44.6	91.8	0.4	0.6	0.2	4.3	0.3	0.5	4.9206
210423_s_at	L32185.1		integral membrane protein	2.0	0.2	1.4	1.6	1.3	1.3	2.2	1.5	2.0	85.0	78.5	75.2	52.9	1.9	0.4	1.9	14.7	1.0	1.0	4.8845
206429_at	NM_005242.2	GPR	PAR2 proteinase activated receptor-2	0.8	0.8	0.9	0.2	0.9	0.9	1.1	0.2	0.8	11.8	15.1	4.1	4.1	1.3	1.5	0.2	1.5	0.3	0.7	4.8608
213352_at	AI934469		KIAA0779	0.6	0.9	1.2	1.5	1.2	1.2	1.5	1.5	2.2	8.4	6.0	8.7	7.7	1.6	0.9	1.5	1.0	1.3	0.8	4.8373
201888_s_at	U81379.3	R	interleukin-13 receptor	0.1	0.6	0.3	0.2	0.0	1.7	2.7	1.7	2.0	8.6	19.0	15.0	13.9	0.4	0.4	0.3	2.9	1.3	1.3	4.746

Fig. 6F

C. Neutrophil (Ne)-selective transcripts (4/7).

Probe set	Accession #		Transcripts	MC. cord blood	MC. lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ba S.I.
204780_s_at	AA164751	R	CD95, Fas, APO-1	1.4	1.4	7.2	14.0	11.5	6.6	6.7	9.3	6.6	45.3	38.8	65.5	51.8	1.3	5.6	4.8	3.6	2.6	9.7	4.7254
209310_s_at	U25804.1		Ich-2 cysteine protease	2.5	1.9	2.1	7.7	7.0	1.4	1.3	1.3	1.4	19.1	17.5	36.7	23.5	2.9	4.1	4.5	4.9	3.9	2.2	4.6817
205452_at	NM_004855.1		phosphatidylinositol glycan, class B (PIGB)	2.3	2.7	2.3	6.4	7.7	2.3	1.4	3.0	3.0	16.3	17.6	22.2	39.3	1.7	2.0	2.9	2.8	3.5	2.2	4.6577
218298_s_at	NM_024952.1		FLJ20950	3.1	3.3	5.4	8.1	7.2	5.7	5.7	8.8	9.4	37.2	23.4	37.3	39.1	0.6	1.7	3.1	5.8	2.3	2.7	4.6558
221210_s_at	NM_030769.1		swineacylneuraminate lyase	3.8	1.2	0.8	1.2	1.4	3.0	4.7	3.2	4.6	20.4	23.6	23.5	18.3	0.6	0.1	0.3	4.6	0.5	0.1	4.6378
221497_x_at	BC005369.1		chromosome 1 open reading frame 12, clone MGC:12484	3.0	2.4	4.3	5.7	5.9	3.3	7.6	7.9	5.4	29.3	32.4	24.3	21.5	1.8	3.1	2.9	2.9	1.9	2.0	4.6333
204668_at	AL031670		ferritin, light polypeptide-like 1	0.8	0.5	1.8	1.0	1.2	0.3	1.5	1.7	0.9	8.4	8.1	7.0	6.5	1.4	1.3	1.0	1.5	0.5	1.6	4.614
201921_at	NM_004125.1		guanine nucleotide binding protein 10 (GNG10)	7.1	5.4	2.6	6.7	6.5	11.7	11.4	20.8	15.3	45.5	87.5	81.3	57.1	0.8	2.7	3.0	8.4	3.2	12.4	4.5644
209600_s_at	S69189.1		peroxisomal acyl-coenzyme A oxidase	2.9	1.7	2.8	5.3	4.7	1.4	1.0	1.2	1.3	15.0	17.7	21.4	21.2	0.4	1.0	0.8	2.1	0.7	1.5	4.5552
205119_s_at	NM_002029.1	GPR	formyl peptide receptor 1	4.1	1.4	11.2	26.6	32.7	14.0	11.1	4.2	6.0	288.2	315.8	274.7	252.9	3.6	1.3	0.7	62.6	1.1	0.5	4.505
217738_at	BF575514		*pre-B-cell colony-enhancing factor*	5.7	0.9	7.4	24.1	34.9	7.5	4.6	5.1	3.9	73.4	87.0	89.9	79.9	2.2	1.7	1.6	10.1	1.7	2.8	4.4839
215078_at	AL050388.1		DKFZp564M2422	0.0	0.1	0.0	0.1	0.4	0.9	0.5	0.8	0.3	7.1	12.9	4.5	7.9	0.1	0.5	0.5	1.7	0.1	0.1	4.4343
207545_s_at	NM_003744.1		numb (Drosophila) homolog	0.7	1.4	1.1	2.5	2.4	2.7	1.8	2.9	1.2	7.2	11.2	10.5	7.4	0.8	0.5	0.5	1.6	1.1	1.2	4.3728
213418_at	NM_002155.1		heat shock 70kD protein 6 (HSP70B)	1.1	0.4	0.7	1.5	1.6	25.3	28.8	10.5	17.0	104.0	91.6	70.0	70.8	0.5	1.1	1.1	12.8	4.7	0.5	4.3655
218023_s_at	NM_016605.1		putative nuclear protein (LOC51307)	5.7	3.8	6.6	13.0	12.6	8.5	10.3	13.0	10.9	40.1	39.7	47.0	59.7	3.0	4.4	5.9	7.0	6.0	6.8	4.3383
210386_s_at	BC001906.1		Similar to metaxin 1	6.2	1.9	2.7	5.4	4.0	1.4	2.2	1.8	3.6	19.5	15.8	23.4	23.8	2.5	3.6	2.6	4.1	2.6	4.7	4.3318
207643_s_at	NM_001065.1	R	CD120a, TNF-R-I p55	1.8	1.6	0.9	1.3	1.4	6.3	7.4	8.5	9.0	81.1	83.6	68.6	65.6	1.3	2.2	5.9	17.4	0.6	16.0	4.2796
203140_at	NM_001706.1		B-cell CLL/lymphoma 6 (BCL6)	6.2	2.9	9.1	13.5	19.8	23.5	16.7	28.7	33.1	99.1	107.8	115.8	101.1	2.2	3.4	3.4	23.4	6.7	6.5	4.2767
207253_s_at	NM_016936.1		ubinuclein 1	3.2	2.8	2.9	4.4	5.0	3.8	2.6	3.8	3.6	16.7	20.0	14.2	17.8	2.3	2.5	2.5	2.2	2.4	1.8	4.2556
202875_s_at	BE397715		pre-B-cell leukemia transcription factor 2	2.0	1.4	0.1	0.1	0.2	2.5	3.6	2.1	1.5	11.6	15.4	6.8	7.5	0.8	1.7	1.9	1.1	1.3	0.7	4.2425
218791_s_at	NM_024713.1		FLJ22557	1.2	0.7	2.5	2.7	1.8	0.9	1.5	1.6	1.0	6.9	8.7	13.2	11.2	1.4	1.0	0.5	1.3	0.8	1.2	4.2114
211862_x_at	AF015451.1		Usurpin-beta	3.5	2.6	16.8	9.7	10.1	5.6	10.2	7.7	7.1	65.7	67.7	36.1	37.9	3.1	6.8	8.7	10.1	6.9	2.0	4.2001
217986_s_at	NM_013448.1		bromodomain adjacent to zinc finger domain, 1A	3.5	3.0	3.5	9.2	8.4	6.1	8.5	14.5	13.1	39.0	35.1	43.5	51.6	2.5	5.9	6.5	7.0	5.0	1.7	4.1976
217966_s_at	NM_022083.1		*niban*	4.1	1.9	6.4	7.4	9.0	24.2	14.8	25.6	11.8	51.9	105.3	76.2	80.0	0.9	3.3	3.8	3.2	2.0	8.2	4.1858
212602_at	AI806395		*KIAA0993*	2.3	3.5	0.4	0.9	1.1	0.8	0.6	0.4	0.8	17.1	18.1	12.9	13.4	1.5	0.5	0.3	3.6	0.8	2.8	4.1806
208485_x_at	NM_003879.1		CASP8 and FADD-like apoptosis regulator (CFLAR)	3.2	2.5	19.2	9.8	9.9	6.2	13.0	8.1	8.3	70.8	69.7	33.8	41.4	3.5	6.4	8.4	11.5	6.6	2.0	4.1719
201942_s_at	D85390.1		gp 180-carboxypeptidase D-like enzyme	0.6	1.7	0.6	1.3	1.7	1.6	7.0	2.4	2.6	15.9	23.8	6.8	8.1	0.5	0.8	1.3	2.5	0.5	2.6	4.1525
220933_s_at	NM_024617.1		FLJ13409	2.1	2.0	9.6	14.2	14.0	7.1	7.2	10.9	12.5	38.1	37.3	81.5	57.8	1.9	3.1	4.8	6.2	3.8	3.0	4.1025
221764_at	AL574186		glycerol-3-phosphate dehydrogenase 1	6.3	4.4	16.5	18.6	15.0	10.4	15.8	21.9	22.7	80.9	99.2	46.3	60.3	9.5	8.9	9.4	5.7	9.4	2.5	4.0745
207446_at	NM_006068.1	R	Toll-like receptor 6	0.5	0.5	0.7	1.5	0.8	0.8	0.9	1.2	0.8	7.6	11.8	7.2	8.7	0.1	0.9	0.9	2.1	1.2	0.6	4.0697
219748_at	NM_024807.1		chromosome 6 open reading frame 76	0.2	0.3	0.3	0.4	0.6	1.9	2.6	1.6	1.6	9.1	9.1	6.7	6.4	0.2	0.3	0.6	0.5	1.1	0.0	4.0619
220945_x_at	NM_018050.1		FLJ10298	1.0	1.4	0.5	0.7	0.7	1.1	0.6	1.5	1.0	8.0	10.8	13.6	11.0	1.1	0.5	0.3	0.9	0.6	2.6	4.057
212577_at	AA868754		KIAA0650	1.9	1.3	6.4	8.0	9.9	10.1	24.0	8.1	9.4	74.0	98.6	42.2	57.4	4.4	10.8	9.5	7.5	16.0	3.2	4.0417
221732_at	AK026161.1		RIKEN cDNA 5830420C20	2.8	0.7	3.4	10.5	8.8	5.0	6.0	10.7	10.9	27.6	31.6	30.8	34.7	0.3	0.4	1.8	2.5	1.6	4.6	4.041
205986_at	NM_004920.1		apoptosis-associated tyrosine kinase	1.6	1.3	0.7	1.0	0.5	0.3	0.3	1.4	1.0	10.5	15.8	13.3	15.2	3.2	1.0	0.5	3.4	0.9	0.4	4.0322
213501_at	T62985		acyl-Coenzyme A oxidase 1, palmitoyl	1.3	1.1	2.0	2.6	2.8	1.3	0.9	1.2	0.6	8.5	11.5	12.4	7.5	0.1	1.1	0.3	1.8	0.5	1.1	4.0194
204542_at	NM_006456.1		sialyltransferase (STHM)	0.4	0.2	1.5	0.3	0.2	3.4	3.9	4.5	3.2	13.0	13.4	21.0	13.4	0.7	0.7	0.3	1.4	0.3	0.6	4.016

Fig. 6G

C. Neutrophil (Ne)-selective transcripts (5/7).

Probe set	Accession #		Transcripts	MC. cord blood	MC. lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ne S.I.
204071_s_at	NM_005802.1		tumor protein p53-binding protein	1.4	1.6	1.1	3.0	2.9	3.7	2.3	2.6	2.2	10.5	12.8	8.0	11.9	1.5	2.2	2.2	1.4	2.2	2.1	4.0148
210594_x_at	AF239756.1		myelin protein zero-like 1	1.2	0.5	0.6	1.5	1.2	0.1	0.4	0.8	1.9	15.3	13.9	7.1	10.9	0.3	0.2	0.6	1.0	0.7	2.8	3.9778
203063_at	NM_014634.1		protein phosphatase 1F (PP2C domain containing)	0.5	0.4	1.4	3.3	3.0	4.0	6.0	6.1	10.0	33.1	22.2	29.6	31.8	0.3	2.9	1.2	7.3	1.5	1.8	3.9764
201392_s_at	BG031974	R	*insulin-like growth factor 2 receptor*	1.7	0.7	0.1	0.0	0.1	2.6	3.0	1.9	1.5	51.1	59.1	12.8	15.0	1.1	1.2	4.0	3.8	2.2	7.0	3.9602
221477_s_at	BF575213		MGC:5618	2.9	1.4	3.4	4.3	9.0	4.2	4.2	4.2	4.2	56.8	63.6	36.1	46.6	7.9	3.2	1.2	12.6	2.7	2.1	3.9562
206756_at	NM_019886.1		carbohydrate (*N-acetylglucosamine* 6-O)sulfotransferase 7	0.2	0.1	0.1	0.0	0.1	0.1	0.1	0.1	0.1	5.0	3.9	3.5	10.5	0.1	1.3	1.0	1.0	0.2	0.5	3.9516
204994_at	NM_002463.1		myxovirus (influenza) resistance 2 (MX2)	1.3	2.3	5.4	7.8	8.2	9.2	11.6	15.2	12.3	49.8	46.6	77.6	80.8	2.4	7.5	6.0	15.6	4.8	1.8	3.9478
201943_s_at	NM_001304.2		carboxypeptidase D	0.9	0.9	0.5	2.1	3.6	1.7	7.6	7.2	4.6	16.4	21.3	18.7	15.2	0.7	1.0	1.7	3.3	0.4	3.8	3.8926
216252_x_at	Z70519.1	R	*CD95, Fas, APO-1*	0.3	0.8	4.3	2.5	1.1	1.8	4.7	1.8	1.7	18.5	31.2	10.3	8.4	2.2	3.8	2.4	1.9	1.4	3.9	3.8691
203066_at	NM_014863.1		B cell RAG associated protein (BRAG)	1.3	3.9	0.9	1.2	1.0	10.6	10.2	13.1	20.2	57.0	65.9	95.2	86.9	1.9	0.1	0.0	19.3	4.2	5.9	3.8667
212479_s_at	AL050139.1		FLJ13910	1.7	1.6	2.1	2.5	2.6	2.4	2.5	3.5	1.7	9.0	10.1	8.8	9.8	1.1	2.3	2.4	2.2	1.9	0.9	3.8422
209571_at	U03644.1		recepin	0.7	0.2	1.6	3.3	2.7	2.2	1.3	2.6	2.7	6.8	7.8	12.8	10.9	0.8	1.0	1.1	1.2	1.5	1.1	3.8367
211317_s_at	AF041461.1		*CASP8 and FADD-like apoptosis regulator*	1.6	1.8	9.5	3.6	4.0	3.7	6.8	3.2	2.8	33.1	44.8	15.2	17.6	2.4	4.7	6.5	5.7	4.9	1.1	3.8332
209732_at	BC005254.1		C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 2	8.1	5.9	10.0	18.6	23.6	9.0	10.0	8.9	7.3	72.9	77.0	99.7	75.5	4.1	14.4	21.2	10.2	16.4	1.3	3.8003
201779_s_at	AF070558.1		clone 24450 RING zinc finger protein RZF	14.8	5.9	13.0	13.3	13.9	21.8	27.0	25.3	13.1	88.2	108.1	116.5	81.8	6.0	9.6	11.3	25.7	15.7	8.5	3.7993
212441_at	D86985.2		KIAA0232	5.4	2.9	3.5	9.8	10.3	8.0	6.9	11.5	11.3	31.9	30.1	30.8	49.8	2.5	2.0	4.0	5.9	2.1	4.9	3.7868
205920_at	NM_003043.1		solute carrier family 6, member 6 (SLC6A6)	1.2	1.4	0.9	0.2	0.2	1.1	5.2	0.7	1.4	33.1	26.7	2.7	4.0	0.3	0.1	0.4	2.6	0.1	0.5	3.7836
213596_at	AL050391.1		DKFZp586A181	0.7	0.7	2.3	3.6	3.0	1.2	1.2	1.1	1.2	10.6	10.9	12.5	9.9	2.2	1.1	2.0	1.5	0.7	0.3	3.7615
209508_x_at	AF005774.1		caspase-like apoptosis regulatory protein (clarp)	1.7	2.7	10.8	7.6	11.5	4.9	6.3	6.0	8.4	37.0	34.8	34.7	40.8	2.7	4.0	5.1	6.3	3.4	1.3	3.7451
218115_at	NM_018154.1		FLJ10604	0.9	2.2	2.4	1.5	0.9	1.8	2.1	1.3	1.1	10.5	9.1	6.7	7.7	1.1	1.2	2.2	2.1	1.7	1.5	3.7435
215652_at	AK024382.1		FLJ14320	0.2	0.1	2.0	0.3	1.6	0.3	0.3	1.2	0.7	5.5	4.5	3.4	2.5	0.1	0.3	1.0	0.9	0.2	0.6	3.7249
212561_at	AA349595		RAB6 interacting protein 1	10.0	6.1	10.2	12.4	11.4	18.7	14.9	12.1	10.0	66.3	60.0	47.6	37.1	4.0	8.7	9.9	13.9	5.9	10.2	3.6962
204166_at	NM_014963.1		KIAA0963	3.6	0.4	1.1	0.0	0.1	1.0	1.3	0.1	0.8	11.8	12.5	4.0	2.9	0.3	0.9	1.7	1.7	1.2	0.2	3.6908
221874_at	AB037745.1		KIAA1324	0.3	0.3	0.7	1.1	0.3	0.8	0.8	0.7	0.5	9.1	5.1	5.1	1.2	0.9	1.1	0.7	0.5	0.6	0.4	3.6808
217207_s_at	AK025267.1	R	butyrophilin like receptor	1.2	1.1	1.4	2.1	1.7	1.2	1.9	0.6	2.4	10.9	3.4	7.2	6.1	1.5	1.7	1.6	0.9	1.5	1.3	3.6795
212579_at	AA868754		*KIAA0650*	1.3	1.6	5.3	9.8	15.5	7.3	7.8	11.3	8.3	32.8	42.9	40.0	39.7	2.0	5.4	5.7	3.1	10.5	2.2	3.6784
212657_s_at	AW083357		IL-1 receptor antagonist IL-1Ra (IL-1RN)	48.8	2.3	0.9	0.5	0.6	2.1	0.9	1.5	1.3	35.2	37.0	48.2	35.5	0.6	0.8	0.3	9.3	0.4	0.6	3.6759
202392_s_at	NM_014338.1		phosphatidylserine decarboxylase	3.4	2.7	6.2	11.7	6.8	3.4	4.7	5.4	4.7	32.8	31.0	22.0	32.3	0.8	1.6	1.4	4.2	1.4	1.2	3.6753
206177_s_at	NM_000045.2		arginase (ARG1)	0.5	1.3	2.2	0.4	0.6	0.9	0.8	7.2	0.7	3.9	4.3	8.1	5.0	1.1	0.1	0.4	0.6	0.7	0.0	3.6722
200706_s_at	NM_004862.1		LPS-induced TNF-alpha factor (PIG7)	31.2	39.0	20.7	64.6	62.5	15.6	13.4	31.8	21.7	173.2	148.5	172.0	150.2	8.5	13.3	42.7	14.3	16.7	18.2	3.6696
212478_at	AL050139.1		FLJ13910	0.	0.1	0.2	2.3	3.5	1.4	0.8	1.5	1.0	3.7	3.0	4.8	6.5	0.1	0.3	1.1	0.6	0.4	0.5	3.6623
218660_at	NM_003494.1		dysferlin	2.5	0.5	1.5	0.2	0.2	1.7	0.2	2.6	1.1	48.5	51.8	44.5	20.4	3.3	1.2	1.7	10.6	0.2	1.3	3.6616
211982_x_at	AL546600		exportin 6	9.8	6.7	14.9	31.8	27.8	24.6	24.0	34.0	24.0	107.2	101.1	86.6	90.2	6.6	17.5	17.4	9.6	11.5	7.7	3.6408
202748_at	NM_004120.2		guanylate binding protein 2, interferon-inducible (GBP2)	2.4	5.3	3.7	9.0	7.4	3.3	2.1	3.0	3.3	28.1	35.2	45.0	24.8	4.2	7.3	9.0	6.3	1.9	3.7	3.6111
220088_at	NM_001736.1	GPR	C5a receptor	2.2	2.3	15.4	24.6	24.8	17.1	15.6	9.8	12.0	90.5	104.5	84.4	91.1	2.3	1.2	0.5	25.6	1.0	0.4	3.6036
202890_at	T62571		microtubule-associated protein 7	0.9	0.1	0.7	1.4	1.1	0.1	0.0	0.2	0.1	2.5	3.1	3.2	7.1	0.0	0.1	0.4	0.1	0.1	0.0	3.6032
220987_s_at	NM_030952.1		DKFZP434J037	1.4	0.3	3.9	4.9	4.7	9.6	9.3	14.1	11.7	43.0	35.6	57.8	57.6	5.3	4.7	4.8	11.1	13.3	2.0	3.5748

Fig. 6H

C. Neutrophil (Ne)-selective transcripts (6/7).

Probe set	Accession #		Transcripts	MC. cord blood	MC. lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ne S.I.
207072_at	NM_003853.1		interleukin 18 receptor accessory protein (IL18RAP)	5.9	0.9	2.2	3.4	4.1	7.2	1.6	2.8	1.7	13.4	9.7	20.9	5.6	2.4	2.8	3.1	0.4	1.6	0.3	3.5722
215719_x_at	X83493.1	R	*CD95, Fas, APO-1*	1.0	0.6	3.1	2.7	1.6	2.2	5.2	1.8	1.7	19.0	31.9	11.4	9.4	1.0	4.5	2.2	1.6	1.1	4.4	3.5657
218404_at	NM_013322.1		sorting nexin 10	4.9	1.2	2.6	5.0	3.7	0.7	0.1	2.1	0.7	28.5	31.8	34.8	33.8	0.3	1.2	1.9	9.0	6.5	0.3	3.563
219394_at	NM_024419.1		phosphatidylglycerophosphate synthase (PGS1)	3.4	3.0	1.7	4.2	3.5	2.4	3.8	6.1	9.2	17.2	16.9	17.5	16.3	1.0	2.1	2.6	2.4	1.5	1.7	3.5544
216913_s_at	AK021460.1		KIAA0690	0.1	0.3	0.1	0.1	0.1	1.9	2.5	2.3	2.8	8.9	8.3	7.5	10.9	0.1	0.1	0.2	2.5	0.1	0.0	3.5402
205118_at	M60626.1	GPR	*formylpeptide receptor 1*	0.1	0.2	0.8	0.1	1.1	0.1	0.4	0.6	0.1	3.9	7.0	3.2	7.8	0.2	0.1	0.1	1.4	0.1	0.0	3.5295
210564_x_at	AF009619.1		*FLAME-1-delta*	1.4	1.5	5.3	6.6	7.0	4.3	4.2	5.9	3.5	21.2	30.3	18.4	19.6	2.1	2.9	4.0	4.6	3.0	1.8	3.5148
213607_x_at	BE551347		KIAA0134	1.3	1.3	2.9	2.0	1.7	8.7	15.8	3.5	4.3	42.7	42.5	11.1	15.3	0.6	1.3	1.9	6.2	1.7	0.9	3.514
203888_at	NM_000361.1		*thrombomodulin*	0.9	0.6	0.1	0.1	0.3	0.2	0.4	0.8	0.1	6.1	6.4	4.6	0.2	0.3	0.3	0.1	0.6	0.5	0.1	3.5126
210233_at	AF167343.1		interleukin-1 receptor accessory protein (IL1RAP)	0.5	0.1	0.0	0.1	0.6	0.8	0.4	0.6	0.7	1.8	3.0	2.0	2.3	0.6	0.0	0.0	0.0	0.0	0.3	3.5023
204959_at	NM_002432.1		myeloid cell nuclear differentiation antigen	1.2	0.6	24.2	50.0	26.2	17.5	17.9	49.8	22.3	249.8	290.2	186.0	217.0	3.4	1.6	0.6	66.6	2.5	0.0	3.4903
217967_s_at	AF288391.1		niban	6.3	3.7	16.3	42.4	35.9	27.9	29.5	43.0	30.9	107.4	115.3	117.9	110.3	2.6	7.5	9.9	4.9	3.4	20.4	3.4847
221763_at	A1694023		thyroid hormone receptor interactor 8	0.8	1.5	1.9	4.6	5.5	5.5	6.9	9.9	9.0	28.3	32.9	34.0	42.7	1.1	3.7	4.1	5.1	9.8	3.0	3.4777
207857_at	NM_006866.1	R	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain) member 2 (LILRA2)	0.4	0.5	3.6	8.5	5.3	4.5	4.9	1.6	6.3	33.5	34.3	46.2	50.8	1.8	0.0	0.1	11.6	0.5	0.1	3.4773
220740_s_at	NM_005135.1		solute carrier family 12 member 6 (SLC12A6)	1.6	1.0	2.5	3.3	3.4	3.5	5.6	3.2	3.2	12.6	19.0	10.7	14.4	4.0	2.9	2.2	2.9	3.5	0.8	3.4722
217739_s_at	NM_005746.1		pre-B-cell colony-enhancing factor	7.1	1.7	9.9	46.0	61.0	18.9	13.9	12.9	9.3	112.4	120.5	90.8	93.4	1.2	2.3	1.4	17.6	2.1	3.1	3.4242
205041_s_at	NM_000607.1		*orosomucoid 1 (ORM1)*	0.3	1.0	0.4	0.1	0.1	0.0	0.1	1.0	0.1	2.6	3.6	2.7	0.4	0.1	0.2	0.1	0.5	0.0	0.1	3.4189
214784_x_at	BE966299		*exportin 6*	7.4	5.0	10.0	23.7	23.9	13.0	16.7	23.3	20.5	60.3	67.8	57.2	60.8	2.9	8.7	7.8	6.6	5.9	5.4	3.4155
217985_s_at	AA102574		*bromodomain adjacent to zinc finger domain, 1A*	1.5	1.4	1.8	2.6	3.8	7.4	5.1	7.3	4.7	16.9	19.2	22.1	24.2	2.7	2.5	2.3	3.5	2.4	0.9	3.3999
212598_at	A1806395		*KIAA0993*	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	5.5	7.3	3.1	3.2	0.2	0.1	0.0	1.0	0.1	1.3	3.3933
219053_s_at	NM_017966.1		FLJ20847	2.6	2.0	1.9	2.3	2.3	2.6	2.1	3.0	2.8	11.3	7.6	22.2	34.1	1.6	0.5	0.9	4.7	1.3	2.9	3.3686
217475_s_at	AC002073		PAC clone RP3-515N1	0.6	0.5	0.6	0.2	0.4	1.3	1.3	0.5	1.2	5.9	9.8	1.6	1.4	0.7	0.3	0.1	0.5	0.7	0.2	3.3448
46323_at	AL120741		Ca2+-dependent endoplasmic reticulum nucleoside diphosphatase	4.4	3.2	4.2	8.3	7.2	5.3	6.7	11.4	7.9	20.0	21.5	33.9	26.3	2.5	2.8	3.6	4.3	3.4	5.0	3.3028
201965_s_at	NM_015046.1		KIAA0625	2.7	3.1	3.3	8.5	8.3	4.9	5.8	7.4	7.5	19.5	18.5	18.7	27.8	2.2	3.9	3.4	4.6	5.6	2.6	3.3019
203628_at	NM_000875.2	R	insulin-like growth factor 1 receptor	0.5	0.1	3.7	3.0	4.0	6.8	4.9	2.7	5.8	18.8	23.4	6.8	20.6	1.6	0.1	2.8	2.4	2.0	3.5	3.2989
202193_at	NM_005569.2		LIM domain kinase 2 (LIMK2) transcript variant 2a	1.8	1.5	1.9	5.6	5.6	6.4	4.8	11.3	8.9	17.0	20.5	36.5	28.2	0.1	1.3	1.1	0.6	0.5	0.8	3.2887
203042_at	NM_002294.1		lysosomal-associated membrane protein 2 (LAMP2)	2.4	3.1	1.1	1.7	1.3	5.9	6.4	12.4	10.7	21.3	27.0	44.1	35.4	0.8	0.6	0.5	3.2	0.8	9.4	3.282
220326_s_at	NM_018071.1		*FLJ10357*	5.1	4.5	1.9	1.2	1.9	6.3	8.9	5.2	8.5	25.3	28.1	19.2	21.0	0.9	0.1	0.7	6.4	0.1	4.1	3.2759
212470_at	AB011088.1		*sperm associated antigen 9*	4.0	2.9	3.3	6.3	7.2	4.5	4.0	4.7	4.9	13.2	17.0	18.1	24.0	1.2	2.5	2.2	3.9	3.0	5.4	3.2688
211133_x_at	AF009643.1		*clone 6 immunoglobulin-like transcript 5*	1.9	1.4	0.8	1.5	1.3	3.1	2.7	3.8	2.1	42.1	42.2	27.0	25.1	2.7	0.9	0.5	10.2	0.4	0.2	3.2526
219313_at	NM_017577.1		*DKFZp434C0328*	0.0	0.8	0.2	0.0	0.4	0.2	0.1	0.1	0.0	3.8	3.7	3.1	5.6	0.2	0.1	0.1	0.0	1.2	0.1	3.2404
221149_at	NM_018485.1	GPR	*G protein-coupled receptor GRP77*	0.2	0.1	0.8	0.7	1.2	0.7	0.9	0.9	0.6	3.3	3.2	4.2	2.9	0.0	0.3	0.2	1.0	0.1	0.3	3.2282
203433_at	NM_006441.1		*5, 10-methenyltetrahydrofolate synthetase*	1.4	1.8	1.5	2.5	1.6	3.1	4.2	3.5	3.1	15.8	11.4	9.6	9.0	1.6	1.8	1.9	2.9	1.7	1.5	3.2181
214486_x_at	AF041459.1		*FADD-like apoptosis regulator*	1.9	2.1	10.7	5.0	6.5	4.2	5.3	4.3	6.0	26.3	16.2	25.3	24.2	2.4	3.7	5.0	5.3	2.3	1.9	3.2114

Fig. 6I

C. Neutrophil (Ne)-selective transcripts (7/7).

Probe set	Accession #		Transcripts	MC cord blood	MC. lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ba S.I.
209222_s_at	BC000296.1		oxysterol binding protein-like 2	1.3	0.2	2.7	8.8	8.0	5.4	5.4	7.7	7.3	17.2	18.4	22.3	23.9	0.9	2.3	3.4	2.8	2.0	1.3	3.1877
202334_s_at	AA877765		ubiquitin-conjugating enzyme E2B	3.3	3.4	4.8	15.5	12.1	5.3	7.2	14.7	12.8	20.9	25.6	43.6	38.1	4.0	4.5	3.9	2.5	4.9	4.6	3.1871
203266_s_at	NM_003010.1		mitogen-activated protein kinase kinase 4	3.7	2.4	4.9	8.2	6.3	2.5	4.8	6.8	5.0	14.7	15.2	27.4	26.9	2.8	2.4	2.6	2.7	2.3	2.7	3.1804
58780_s_at	R42449		FLJ10357	4.5	5.4	1.5	3.9	3.0	7.8	9.6	12.8	16.4	28.0	27.6	46.7	44.1	1.2	0.6	0.1	6.5	0.2	5.7	3.1803
210582_s_at	AL117466.1		LIM domain kinase 2	3.8	1.9	4.3	5.1	4.8	8.7	10.3	10.8	9.4	33.9	36.5	30.8	23.8	1.3	1.7	1.8	1.9	0.9	1.4	3.1609
214766_s_at	AL080144.1		ELYS transcription factor-like protein TMBS62	1.3	0.2	2.0	3.1	4.2	1.9	1.4	2.1	2.4	9.4	9.5	9.9	11.3	3.2	1.3	0.8	0.5	1.0	1.3	3.1414
202266_at	NM_016614.1		TRAF and TNF receptor-associated protein (AD022)	9.8	6.2	9.4	23.7	20.9	8.6	9.9	16.5	14.0	36.1	56.5	64.5	57.5	4.5	7.7	9.4	5.3	8.2	6.3	3.1402
203278_s_at	NM_016621.1		BRAF35/HDAC2 complex (80 kDa)	2.1	2.8	2.7	14.8	11.0	5.7	5.0	7.4	4.9	21.0	16.6	31.0	30.6	0.1	3.0	4.5	3.1	2.7	3.0	3.1382
207291_at	NM_024081.1		transmembrane gamma-carboxyglutamic acid protein 4	0.1	1.2	1.3	1.4	1.1	0.9	0.2	0.4	0.2	3.8	7.9	4.5	8.5	0.2	0.8	0.1	1.9	1.1	0.4	3.1336
213229_at	BF590131		Dicer1, Dcr-1 homolog (Drosophila)	8.5	4.5	19.5	12.9	15.4	15.9	9.7	19.1	16.0	35.2	39.0	61.4	69.4	6.2	5.9	7.3	15.2	12.2	5.0	3.1306
204204_at	NM_001860.1		solute carrier family 31	1.7	1.7	1.3	0.3	0.8	1.7	0.9	2.3	1.2	22.6	23.8	31.3	36.0	2.0	1.2	1.2	8.9	0.2	0.4	3.1262
201364_s_at	AF242521.1		ornithine decarboxylase antizyme	8.3	7.3	4.4	2.2	1.9	11.5	21.9	8.0	7.7	61.9	59.1	21.0	27.7	2.2	5.1	6.3	12.2	6.2	9.6	3.1253
210784_x_at	AF009634.1		clone 17.6 immunoglobulin-like transcript	1.4	0.1	2.1	1.2	2.4	2.5	2.2	2.8	2.1	52.1	48.8	31.8	36.3	0.8	0.2	0.2	13.3	0.3	0.2	3.1236
202625_at	AI356412		*v-yes-1 Yamaguchi-sarcoma viral related oncogene homolog (LYN)*	6.9	6.9	5.0	18.2	14.9	20.7	21.7	27.7	28.6	74.7	76.3	77.5	75.7	7.5	1.7	0.9	17.1	23.6	0.5	3.1131
221895_at	AW469184		hypothetical protein MGC26706	2.2	0.5	5.4	5.2	5.8	5.2	3.4	7.6	5.1	14.8	12.0	24.6	19.2	2.0	2.4	2.1	5.2	1.5	1.6	3.11
37384_at	D13640		major histocompatibility complex, class I, B	2.5	3.0	3.4	3.8	3.8	6.7	6.6	7.6	6.6	25.2	17.9	21.3	29.4	2.6	2.5	2.5	7.4	1.8	2.8	3.0985
206608_s_at	NM_020366.1		retinitis pigmentosa GTPase regulator interacting protein 1 (RPGRIP1)	1.1	1.4	1.2	0.8	1.0	1.1	1.0	0.5	1.4	6.1	3.4	5.3	4.7	1.5	0.9	0.8	1.3	0.5	0.7	3.091
204924_at	NM_003264.1	R	Toll-like receptor 2	1.8	0.1	2.1	8.2	7.6	2.8	0.4	0.8	1.4	52.9	88.0	94.4	99.8	1.6	1.3	0.1	26.3	0.9	0.4	3.0909
204781_s_at	NM_000043.1	R	*CD95, Fas, APO-1*	2.0	1.1	5.9	11.0	8.9	5.4	4.4	6.8	7.0	20.6	27.1	27.0	29.1	0.3	5.2	5.3	4.0	2.0	3.8	3.0827
212606_at	AI806395		KIAA0993	2.0	2.0	0.0	0.7	0.6	0.7	0.0	0.1	0.1	18.0	14.3	25.0	26.9	0.1	0.2	0.3	6.6	0.0	3.4	3.0797
211316_x_at	AF009616.1		FLAME-1	3.1	2.9	20.1	19.4	31.9	11.6	11.9	20.6	19.1	58.8	74.1	72.8	81.0	4.1	6.8	8.7	10.3	5.5	2.6	3.0752
203045_at	NM_004148.1		ninjurin 1	4.4	2.5	3.2	6.4	4.8	10.7	9.7	18.5	12.1	29.3	34.1	44.7	46.1	0.5	1.2	1.7	8.3	0.2	2.9	3.0746
204949_at	NM_002162.2		intercellular adhesion molecule 3 (ICAM3)	3.0	3.7	5.7	46.3	34.5	38.9	51.6	94.5	93.7	161.1	168.3	239.1	241.1	4.5	13.6	21.0	17.6	19.9	1.3	3.0617
206208_at	NM_000717.2		*carbonic anhydrase IV (CA4)*	0.2	0.6	0.1	0.1	0.1	1.1	0.7	1.0	0.8	5.6	5.2	2.8	2.4	1.2	0.1	0.1	0.1	0.1	0.1	3.0572
213727_x_at	AI743654		metallo phosphoesterase	2.1	1.7	5.0	15.0	12.1	8.9	13.7	25.4	23.9	49.9	28.3	59.9	75.8	0.7	4.5	6.6	5.7	5.4	3.7	3.0554
202626_s_at	NM_002350.1		v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN)	15.5	9.5	12.1	12.7	14.8	32.6	31.6	54.0	41.0	110.1	115.1	122.7	127.2	18.4	2.1	1.5	36.8	33.0	0.6	3.0541
206420_at	NM_005849.1		immunoglobulin superfamily, member 6 (IGSF6)	1.1	0.3	0.2	0.4	0.7	1.9	1.2	1.1	1.0	17.5	24.2	30.6	33.3	1.4	0.4	0.4	8.4	0.3	0.3	3.0442
201651_s_at	NM_007229.1		protein kinase C and casein kinase substrate in neurons 2 (PACSIN2)	21.4	17.4	4.6	24.8	20.1	13.3	19.5	33.9	35.3	61.3	72.5	76.1	94.4	24.7	4.9	4.4	8.6	6.1	8.0	3.0391
219540_at	AU150728		zinc finger protein 267	2.0	1.0	1.3	3.7	3.6	2.0	1.5	4.4	3.7	6.7	6.9	9.2	9.9	1.0	2.1	1.3	1.0	1.6	0.1	3.0361
201244_s_at	NM_002880.1		v-raf-1 murine leukemia viral oncogene homolog 1 (RAF1)	6.0	5.4	12.4	32.8	33.1	14.9	19.0	27.3	25.7	60.4	58.2	89.2	86.2	2.2	6.6	11.3	12.8	7.6	7.3	3.0329
203265_s_at	AA810268		mitogen-activated protein kinase kinase 4	1.4	1.2	2.8	6.4	4.5	1.7	2.6	3.5	3.1	12.8	12.8	10.4	16.8	1.4	1.4	1.3	1.3	2.5	1.5	3.028
203030_s_at	AF007555.1		IAR receptor-like protein-tyrosine phosphatase	0.0	0.0	1.6	1.2	0.1	0.1	0.1	0.1	0.1	0.8	3.0	1.1	2.8	0.1	0.1	0.0	0.1	0.0	0.0	3.0269
203739_at	NM_006526.1		zinc finger protein 217	1.9	2.6	3.0	18.4	8.4	7.6	8.0	14.7	14.9	37.3	45.1	24.4	27.0	1.2	4.6	5.3	6.1	5.5	3.6	3.0158
204747_at	NM_001549.1		interferon-induced protein with tetratricopeptide repeats 4 (IFIT4)	2.0	3.0	4.9	6.0	3.5	4.3	12.4	4.4	3.0	24.2	27.0	15.4	12.0	0.3	1.8	1.2	6.2	1.4	2.6	3.0143
206209_s_at	NM_000717.2		carbonic anhydrase IV (CA4)	0.7	1.0	0.8	0.6	0.6	2.2	2.1	1.5	2.1	13.8	7.4	4.7	3.5	2.1	1.0	0.5	0.9	1.0	0.5	3.0112

Fig. 6J

D. Mast cell (MC)-selective transcripts (1/2).

Probe set	Accession #		Transcripts	MC. cord blood	MC. lung	Ba1	Ba2 (small)	Ba3 (small)	Eo 1	Eo 2	Eo3 (small)	Eo4 (small)	Ne 1	Ne 2	Ne3 (small)	Ne4 (small)	pl	CD4	CD8	CD14	CD19	Fb	MC.S.I.
217023_x_at	AF099143		*tryptase beta*	169.4	118.7	0.7	1.1	0.4	0.1	0.1	0.5	0.1	0.2	0.1	0.6	0.4	0.3	0.1	0.1	0.2	0.1	0.2	202.148
215382_x_at	AF206666.1		*tryptase beta*	168.1	108.4	1.7	0.7	0.4	0.2	0.2	0.2	0.1	0.1	0.3	0.1	0.1	0.7	0.1	0.1	0.1	0.1	0.5	172.668
204041_at	NM_000898.1		monoamine oxidase B	23.5	46.9	0.2	0.7	0.1	0.1	0.2	0.6	0.3	0.3	0.1	0.2	0.1	0.2	0.2	0.1	0.2	0.1	0.2	136.311
210084_x_at	AF206665.1		*tryptase alpha*	131.1	92.3	0.7	1.2	1.2	0.2	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.6	0.1	0.0	0.1	0.1	0.1	112.376
216474_x_at	AF206667.1		*tryptase beta*	210.0	120.9	2.4	2.0	1.4	1.2	0.4	0.2	0.1	0.2	1.1	0.1	0.1	1.8	0.8	0.9	0.9	0.1	0.1	84.3375
205683_x_at	NM_003294.2		*tryptase beta*	195.5	95.3	2.4	2.7	0.3	0.2	0.2	0.6	0.6	0.4	0.1	0.4	1.0	2.0	0.7	0.2	0.3	0.2	0.1	67.2617
207741_x_at	NM_003293.2		*tryptase alpha*	175.0	99.7	2.2	2.2	1.8	0.5	0.2	0.3	0.2	0.6	0.2	0.3	0.3	2.2	0.7	0.1	0.5	0.3	0.6	59.015
207134_x_at	NM_024164.2		*tryptase beta*	214.6	112.3	3.1	3.8	1.7	1.2	0.3	0.8	0.6	0.3	0.8	0.4	0.1	0.5	0.2	0.1	1.1	0.4	0.2	57.1834
205553_at	NM_001911.1		cathepsin G	91.2	57.0	2.7	1.1	0.9	0.9	0.4	3.1	0.8	0.3	1.4	1.6	0.6	0.7	0.2	0.4	1.3	0.3	0.2	51.4749
205266_at	NM_002309.2		leukemia inhibitary factor	17.0	9.8	0.2	0.2	0.3	0.3	0.1	0.2	0.2	0.1	0.2	0.4	0.7	0.1	0.2	0.1	0.1	0.1	0.1	44.3659
210324_at	M17263.1		complement protein C8 gamma	2.9	6.9	0.1	0.1	0.0	0.0	0.0	0.1	0.1	0.3	0.1	0.1	0.1	0.1	0.1	0.0	0.0	0.0	0.1	33.806
211743_s_at	BC005929.1		major basic protein	74.3	70.7	1.0	4.7	2.7	0.1	0.7	0.8	0.6	0.2	0.3	0.7	0.2	0.1	0.2	0.2	0.3	0.2	0.3	31.5959
211549_s_at	U63296.1		*15-hydroxyprostaglandin dehydrogenase*	48.3	48.3	2.1	2.5	1.4	1.5	1.3	0.8	0.9	0.1	0.1	0.2	0.1	1.1	0.5	0.8	0.5	0.5	0.0	24.8454
206726_at	NM_014485.1		prostaglandin D2 synthase	119.0	94.0	5.0	7.8	5.7	0.7	0.1	1.0	0.5	0.2	0.2	0.2	0.6	1.3	0.7	0.3	1.2	0.3	0.0	17.432
205011_at	NM_014622.1		loss of heterozygosity, 11, chromosomal region 2, gene A	76.1	70.9	3.0	6.8	4.5	2.3	1.0	1.4	1.9	0.2	1.1	1.2	1.8	2.9	2.2	1.3	1.7	2.0	2.6	16.2511
205428_s_at	NM_001740.2		calbindin 2	16.7	63.4	1.3	0.7	0.9	0.4	1.6	0.7	1.3	1.8	1.6	3.6	1.5	1.7	0.7	1.1	1.3	0.6	0.9	16.1621
219255_at	NM_024554.1		FLJ11413	10.0	9.2	0.1	0.1	0.1	0.2	0.1	0.6	0.6	0.1	0.6	0.1	0.2	0.1	0.6	0.1	0.6	0.0	0.2	15.639
204468_s_at	NM_005424.1		tyrosine kinase with immunoglobulin and epidermal growth factor homology domains	3.6	2.8	0.5	0.3	0.1	0.0	0.1	0.2	0.0	0.0	0.0	0.1	0.1	0.0	0.0	0.0	0.1	0.0	0.0	14.4259
208343_s_at	AF146343.1		CYP7A promoter binding factor	1.5	0.9	0.0	0.0	0.3	0.1	0.0	0.1	0.0	0.1	0.0	0.2	0.4	0.1	0.0	0.0	0.0	0.0	0.0	13.8025
205051_s_at	NM_000222.1	R	CD117 c-KIT	92.1	85.8	6.2	8.1	7.3	2.3	5.2	6.5	2.7	0.7	2.1	0.8	1.1	0.8	0.2	0.5	0.1	0.1	0.5	12.3815
210102_at	BC001234.1		*loss of heterozygosity, 11, chromosomal region 2, gene A*	40.9	41.1	2.8	3.7	4.5	0.3	0.4	0.3	0.6	0.7	0.9	0.2	0.6	1.8	0.8	0.7	1.2	0.6	1.3	11.3619
210796_x_at	D86359.1		*siatic acid binding Ig-like tectin, sigtec6*	17.8	26.0	1.5	1.0	1.1	1.2	1.5	1.3	1.4	1.4	2.3	1.7	1.3	2.0	1.4	1.5	1.8	1.0	0.8	10.5398
206519_x_at	D86358.1	R	siatic acid binding Ig-like tectin, sigtec6	3.4	7.9	0.0	0.3	0.4	0.0	0.0	0.0	0.1	0.0	0.1	0.5	0.2	0.5	0.0	0.0	0.0	0.4	0.0	10.13
206480_at	NM_000897.1		leukotriene C4 synthase	8.8	16.0	0.3	0.2	0.6	2.4	1.6	0.5	0.1	0.2	1.1	0.1	0.1	1.3	0.1	0.3	0.1	0.1	0.4	9.27381
206617_s_at	NM_002910.4		renin-binding protein	10.6	6.2	1.2	0.1	0.4	2.8	1.6	0.5	0.1	0.6	2.1	0.1	0.1	0.9	0.2	0.7	0.3	0.4	0.1	9.18529
208089_s_at	NM_030794.1		tudor domain containing 3	6.0	13.4	0.8	0.6	0.2	0.5	0.7	0.5	0.5	0.1	0.6	0.3	0.0	0.7	0.7	1.1	0.8	0.6	1.0	8.16897
205466_s_at	NM_005114.1		heparan sulfate 3-D-sulfotransferase	18.1	7.2	0.1	0.4	0.1	0.7	0.1	0.3	0.2	0.4	0.1	0.8	0.4	0.1	0.0	0.0	0.2	1.4	0.0	8.15381
214913_at	AB002364.1		ADAMTS3 a disintegrin-like and metalloprotease (reprotysin type) with thrombospondin type 1 motif, 3	6.8	4.3	0.5	0.7	0.8	0.5	0.7	0.6	0.4	0.5	0.4	0.7	1.2	0.7	0.6	0.5	0.4	0.5	0.5	7.2214
201860_s_at	NM_000930.1		tissue-plasminogen activator	22.2	29.7	0.2	0.4	0.1	0.1	0.3	0.5	0.5	0.1	0.1	1.3	0.4	1.6	0.1	0.2	0.6	0.1	3.6	7.10135
206520_x_at	NM_001245.1		*siatic acid binding Ig-like lectin, sigtec6*	19.0	22.7	2.4	1.1	0.8	1.1	1.5	1.3	1.0	2.0	2.0	0.4	1.4	2.9	2.1	2.3	1.9	1.9	1.2	7.10132
220532_s_at	NM_014020.1		LR8 protein	52.4	18.2	0.8	0.8	1.0	6.4	2.9	1.5	1.2	0.4	0.3	1.4	0.6	2.2	0.6	0.2	5.0	0.1	0.0	6.1662
218169_at	NM_018052.1		FLJ10305	6.2	14.6	0.3	0.2	0.4	0.4	0.3	0.3	0.4	0.6	0.5	0.1	0.1	0.5	0.2	1.4	1.6	0.3	1.0	6.04597
221728_x_at	AK025198.1		nuclear receptor subfamily 1, group I, member 3	5.6	5.5	0.6	0.9	1.0	0.4	3.6	0.9	0.8	0.7	0.6	1.4	0.9	0.9	0.8	0.7	0.7	0.8	0.5	5.70228
214028_x_at	AU156998		*tudor domain containing 3*	3.2	11.9	0.9	0.0	0.4	0.8	0.3	0.4	0.7	0.6	0.6	0.1	0.1	0.8	1.2	1.1	0.1	0.7	0.9	5.10738
221552_at	BC001698.1		lipase	10.6	3.4	0.9	1.8	1.1	0.9	1.1	1.0	0.9	0.2	0.2	0.7	0.1	0.1	0.2	0.7	0.9	0.3	1.1	5.02434
203367_at	NM_007026.1		MKP-1 like protein tyrosine phosphatase (MKP-L)	15.0	45.4	1.2	0.9	0.8	0.9	0.9	0.8	0.1	0.2	0.7	0.4	2.0	0.9	1.0	2.7	0.5	1.4	5.2	5.00514
206997_s_at	NM_004807.1		heparan sulfate 6-O-sulfotransferase	4.2	3.8	0.2	0.1	0.1	0.4	0.4	0.1	0.3	0.3	0.4	0.3	0.7	0.3	0.2	0.6	0.3	0.8	0.2	4.81127

Fig. 6K

D. Mast cell (MC)-selective transcripts (2/2).

Probe set	Accession #	Transcripts	MC. cord blood	MC. lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	MCS.I.
207480_s-at	NM_020149.1	TALE homeobox protein Meis2e	14.0	14.9	1.9	3.6	4.0	1.7	1.9	5.3	3.8	0.3	0.6	1.0	0.3	0.5	0.8	0.4	0.6	0.4	0.8	4.72642
45288_at	AA209239	*lipase*	10.9	3.0	0.2	2.1	0.8	0.5	0.5	1.3	0.9	0.1	0.1	0.2	0.1	0.4	0.5	0.5	1.3	1.0	0.9	4.52869
207039_at	NM_000077.1	*cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)*	7.5	3.6	0.7	0.7	0.1	0.6	0.4	0.3	0.5	0.1	1.2	0.6	1.1	0.1	0.9	0.5	0.8	0.1	1.2	4.35629
201650_at	NM_002276.1	keratin 19	6.2	12.0	0.0	0.0	0.3	0.1	0.0	0.0	0.0	0.1	0.1	0.1	0.1	0.1	0.0	0.1	0.1	0.0	2.0	4.35547
214533_at	NM_001836.1	chymase	10.1	2.7	0.4	0.2	0.8	0.1	0.1	0.8	0.6	0.1	0.1	0.2	0.2	1.2	0.7	0.5	1.0	0.4	0.3	4.27984
218211_s_at	NM_024101.1	melanophilin	24.8	29.6	2.7	2.5	1.8	3.0	2.5	1.9	2.2	4.6	4.1	3.3	4.1	6.4	4.0	3.2	2.4	3.4	2.7	4.24499
203916_at	NM_003635.1	N-deacetylaseN-sulfotransferase	17.9	26.7	3.2	6.5	6.8	2.5	2.7	3.6	3.1	4.2	3.4	5.5	5.2	0.9	3.1	4.9	3.3	2.7	2.4	4.20693
212336_at	AB002336.1	erythrocyte membrane protein band 4.1-like 1	3.8	6.4	0.1	0.2	0.1	0.5	0.1	0.2	0.4	0.1	0.1	0.1	0.5	0.1	0.4	0.2	0.4	0.4	1.2	4.12758
200766_at	NM_001909.1	cathepsin D	42.6	39.5	2.5	5.3	4.3	4.3	4.8	3.4	2.7	4.0	6.7	3.1	1.9	2.6	1.6	2.5	10.0	1.6	5.9	4.1037
202218_s_at	NM_004265.1	delta-6 fatty acid desaturase (FADSD6)	18.8	24.5	0.4	0.2	1.0	0.3	0.1	0.8	0.5	0.2	0.1	0.1	0.1	1.6	0.1	0.6	0.1	0.6	5.3	4.08548
204066_s_at	NM_014914.1	centaurin, gamma 2	5.3	7.9	0.4	0.4	0.7	0.2	0.2	0.6	0.6	0.3	0.5	0.4	0.4	0.8	0.6	1.6	0.6	1.0	1.6	4.06712
209644_x_at	U38945.1	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	14.0	6.4	1.0	1.4	0.7	1.2	1.3	1.7	1.5	1.0	1.6	1.5	2.1	2.3	1.8	1.5	0.9	0.3	2.4	3.88459
221679_s_at	AF225418.1	*lipase*	2.8	1.9	0.4	0.9	0.1	0.3	0.4	0.4	0.1	0.1	0.5	0.0	0.5	0.5	0.1	0.6	0.6	0.5	0.2	3.83039
211538_s_at	U56725.1	heat shock protein 70kD	4.4	7.4	0.3	0.6	0.4	0.6	0.3	0.3	0.9	1.4	0.4	1.0	0.8	1.5	0.5	0.5	0.1	0.5	0.7	3.80423
211548_s_at	J05594.1	*15-hydroxyprostaglandin dehydrogenase*	82.6	60.0	19.4	26.0	16.3	3.2	2.9	1.8	1.7	0.8	0.5	0.9	0.2	4.1	1.2	0.9	0.1	0.6	0.2	3.49258
210174_at	AF228413.1	nuclear receptor subfamily 5, group A, member 2	2.9	3.4	0.5	0.5	0.6	0.8	1.1	0.7	1.2	1.1	0.4	0.1	0.4	0.9	0.7	0.2	0.2	0.6	0.3	3.47124
219412_at	NM_022337.1	RAB38, member RAS oncogene	3.9	4.0	0.1	0.4	0.3	0.7	0.1	0.2	0.3	0.2	0.2	1.1	0.1	1.2	0.1	0.8	0.4	0.1	0.5	3.32805
201850_at	NM_001747.1	gelsolin-like capping protein (actin filament)	70.5	64.5	9.6	30.8	28.8	8.1	7.8	11.5	9.9	2.6	3.6	3.0	2.4	1.6	1.1	1.0	17.0	5.8	5.3	3.29919
205888_s_at	AI962693	KIAA0555	5.4	4.6	0.7	1.6	1.2	0.8	0.7	0.1	1.0	1.3	0.3	0.2	0.6	1.2	0.3	1.5	0.7	1.2	0.4	3.25197
221750_at	BG035985	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	5.0	3.8	0.9	1.5	1.1	1.1	1.2	1.3	1.0	1.3	0.5	0.7	1.2	0.7	0.5	1.1	0.7	1.4	1.2	3.1926
214218_s_at	AV699347	*nuclear receptor subfamily 1, group I, member 3*	3.5	3.5	0.7	0.6	0.7	0.5	2.2	0.5	0.5	0.7	1.2	0.6	0.1	1.1	0.9	0.3	0.6	0.8	0.4	3.15254
218788_s_at	NM_022743.1	FLJ21080	16.1	23.7	0.5	2.3	2.5	0.9	1.1	2.7	2.1	1.1	1.0	0.8	0.9	2.3	2.1	2.9	0.6	2.0	6.3	3.07851
218087_s_at	NM_015385.1	SH3-domain protein 5 (ponsin)	1.4	1.9	0.4	0.9	0.4	0.5	0.0	0.0	0.1	0.0	0.1	0.1	0.2	0.1	0.0	0.2	0.2	0.2	0.1	3.07366
221577_x_at	AF003934.1	prostate differentiation factor	7.8	5.5	0.6	0.3	0.5	0.6	0.1	0.2	0.6	0.0	0.2	0.3	0.1	0.1	0.2	0.0	0.1	0.4	2.1	3.05532
35820_at	X62078	GM2 activator protein	21.8	17.6	1.4	3.3	1.3	0.3	0.3	0.2	0.5	0.5	0.8	1.9	0.3	0.4	0.2	0.2	6.5	5.0	2.7	3.01647
208744_x_at	BG403660	heat shock 105kD	7.3	4.8	0.5	0.2	0.2	0.9	0.1	0.4	0.6	0.1	0.1	0.3	0.1	0.8	1.7	2.0	0.9	0.9	2.0	3.00671

Fig. 6L

E. Basophil and eosinophil-selective transcripts (1/1).

Probe set	Accession #		Transcripts	MC cord blood	MC lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ba+Eo S.I.
211517_s_at	M96651.1		*IL-5R interleukin 5 receptor alpha*	*0.6*	*0.1*	11.8	28.2	17.9	16.4	25.3	32.6	29.5	*0.0*	*0.7*	*0.0*	*1.0*	*0.0*	*0.4*	*0.2*	*0.0*	*0.2*	*0.0*	61.956
210744_s_at	M75914.1	R	IL-5R interleukin 5 receptor alpha	*0.2*	*1.6*	15.4	30.8	15.3	18.7	40.2	29.7	33.0	*0.3*	*0.2*	*1.5*	*0.5*	*0.1*	*0.1*	*0.1*	*0.1*	*0.2*	*0.1*	42.811
206361_at	NM_004778.1	GPR	CRTH2 chemoattractant receptor-homologous molecule expressed on Th2 cells	1.8	*0.3*	22.0	40.5	15.3	33.7	37.9	38.9	42.3	*1.0*	*2.6*	2.2	*2.1*	*0.8*	*1.4*	*1.0*	*1.2*	*0.9*	*0.5*	16.642
206207_at	NM_001828.3		Charcot-Leyden crystal protein	*1.1*	*0.1*	270.0	219.1	203.6	226.8	233.8	179.7	163.1	*2.1*	19.4	19.1	49.3	*2.8*	*1.0*	*1.4*	*0.9*	*0.7*	*0.4*	15.164
203638_s_at	NM_022969.1	R	fibroblast growth factor R 2	*0.2*	*0.1*	7.3	43.5	33.0	4.1	8.8	12.3	23.3	*0.1*	*0.1*	*0.3*	*0.3*	*0.1*	*0.1*	*0.2*	*0.1*	*0.1*	*1.0*	13.357
207111_at	NM_001974.1	GPR	egf-like module containing, mucin-like, hormone receptor-like sequence 1 (EMR-1)	*1.5*	*0.1*	16.4	49.5	34.5	85.9	93.1	91.2	93.5	*2.7*	*3.7*	5.4	5.1	*3.4*	*1.7*	*0.8*	7.1	1.6	*0.5*	8.0092
215248_at	AU145003		FLJ11581 fis, clone HEMBA1003598	*0.7*	*0.3*	5.7	4.7	5.2	4.5	2.1	2.8	2.1	*1.0*	*0.1*	*0.1*	*0.1*	*0.2*	*0.1*	*0.1*	*0.1*	*0.1*	*0.2*	7.2618
205471_s_at	AW772082		dachshund (Drosophila) homolog Hs.63931	*0.1*	*0.6*	5.1	4.1	3.7	6.4	8.3	9.0	7.6	*0.8*	*0.9*	1.0	0.8	*0.1*	*0.1*	*0.3*	0.5	*0.0*	*0.1*	6.8198
218857_s_at	NM_025080.1		FLJ22316	*1.0*	7.0	18.0	35.3	18.6	13.7	12.5	16.3	15.4	*1.3*	*1.7*	*0.9*	*1.9*	*0.3*	*0.5*	*0.4*	*2.4*	*0.2*	*0.2*	6.5045
221169_s_at	NM_021624.1		*histamine receptor H4*	*0.2*	*0.5*	4.5	12.5	8.9	1.9	2.6	4.2	2.9	*0.5*	*0.6*	1.1	*0.6*	*0.4*	*0.7*	*0.5*	*0.7*	*0.0*	*0.3*	5.9783
201769_at	NM_014666.1		enthoprotin	7.8	9.1	41.7	101.5	76.0	26.8	34.1	40.5	35.7	*3.0*	2.9	3.6	4.2	4.5	6.3	6.9	8.0	9.0	7.9	5.1015
208228_s_at	M87771.1		secreted fibroblast growth factor receptor (K-sam_III)	*0.3*	*1.4*	3.7	10.2	8.3	3.9	8.9	4.5	8.3	*0.8*	*1.4*	*1.1*	*0.5*	1.3	*0.4*	*0.7*	*0.3*	*0.5*	1.1	4.9922
213605_s_at	AL049987.1		hypothetical protein, MNCb-4779	*0.8*	*0.0*	10.8	46.8	44.7	6.7	6.1	25.8	20.6	1.3	*1.4*	4.5	4.2	2.9	*1.1*	2.1	3.7	2.0	*0.3*	4.7426
205382_s_at	NM_001928.1		adipsin	3.5	*0.1*	62.0	206.0	176.5	62.4	48.1	60.5	44.8	7.1	32.5	20.5	16.3	*0.1*	*0.6*	*0.1*	15.6	*0.1*	3.8	4.7202
49452_at	AI057637		*hypothetical protein LOC283445*	*0.6*	*0.2*	5.2	7.7	6.6	6.9	5.9	10.2	12.7	*1.1*	*0.2*	*0.3*	*1.3*	*0.1*	*1.6*	*1.6*	*0.5*	*1.3*	*0.8*	4.7183
220307_at	NM_016382.1	R	CD244 natural killer cell receptor 2B4	*0.5*	*0.1*	15.7	87.0	65.4	9.9	10.8	26.6	18.5	*0.3*	*0.4*	*1.2*	*3.0*	*0.1*	*0.4*	3.5	5.2	*1.1*	*0.1*	4.6297
210108_at	BE550599	ICN	calcium channel, voltage-dependent, L type, alpha 1D subunit	*0.2*	*0.1*	1.0	1.7	2.4	*0.9*	0.8	2.4	1.8	*0.0*	*0.6*	*0.5*	*0.5*	*0.0*	*0.3*	*0.1*	*0.0*	*0.3*	*0.0*	4.5958
209193_at	M24779.1		protein kinase-related oncogene (PIM1)	6.8	7.1	61.3	110.3	100.1	47.0	79.7	91.6	79.5	19.2	18.8	21.1	16.1	4.1	12.7	13.9	4.6	4.0	1.2	4.1983
202794_at	NM_002194.2		inositol polyphosphate-1-phosphatase (INPP1)	5.7	6.2	7.1	25.8	20.5	17.9	24.8	53.6	57.8	2.8	2.7	2.6	4.0	1.9	1.8	2.6	4.8	1.9	4.8	4.1158
208304_at	NM_001837.1	GPR	CCR3 chemokine (C-C motif) receptor 3	*0.2*	*1.1*	107.2	142.9	102.2	46.4	91.7	118.1	107.5	28.3	20.0	26.3	25.1	*0.2*	*0.5*	*0.4*	*0.2*	*0.2*	*0.4*	3.9525
206111_at	NM_002934.1		eosinophil-derived neurotoxin	2.2	2.0	33.7	71.4	38.4	104.7	80.8	47.7	45.1	*2.0*	2.3	3.1	2.8	*1.4*	*0.7*	*0.4*	14.8	*0.7*	*0.5*	3.7641
43427_at	AI970898		hypothetical protein LOC283445	*0.8*	*0.7*	*2.1*	4.8	4.3	5.1	4.6	8.0	6.4	*1.0*	*0.8*	*0.7*	*0.8*	*1.1*	*1.0*	1.3	*0.6*	1.1	*1.1*	3.7554
213804_at	AI039084		inositol polyphosphate-5-phosphatase, 75kD	*0.6*	*1.2*	4.3	8.0	6.8	8.6	5.6	6.3	9.7	*0.7*	*0.5*	2.2	*1.7*	*1.4*	*1.2*	*1.4*	*1.0*	*1.9*	*1.3*	3.6088
209906_at	U62027.1	GPR	C3a receptor	12.4	11.2	44.1	72.3	50.5	18.8	38.8	70.3	29.9	*1.2*	*1.2*	*1.8*	3.8	*1.6*	*1.6*	*1.5*	3.0	*0.6*	*0.5*	3.6039
202804_at	AI539710		ATP-binding cassette, sub-family C (CFTR/MRP), member 1	8.5	7.0	24.2	56.2	48.9	14.2	20.0	30.1	20.7	3.0	3.6	4.3	6.0	3.8	3.5	5.4	5.1	5.5	5.3	3.5673
221675_s_at	AF195624.1		cholinephosphotransferase 1 beta	7.0	6.8	31.6	79.7	55.8	26.9	32.6	43.8	41.8	5.2	7.5	5.9	9.6	2.4	3.1	3.3	7.7	11.8	5.7	3.5626
201562_s_at	NM_003104.1		sorbitol dehydrogenase (SORD)	2.0	*1.5*	2.9	4.2	4.1	7.4	11.6	8.3	11.2	*1.7*	*2.5*	*1.5*	*1.3*	*1.3*	*1.4*	*1.8*	*1.2*	*1.8*	*1.1*	3.5098
210230_at	BC003629.1		FLJ23438 fis, clone HRC13275	*1.1*	*0.1*	8.3	11.0	13.3	2.4	5.1	5.1	4.1	*0.1*	*0.5*	*0.2*	*0.7*	*0.3*	*0.2*	*0.6*	*0.8*	1.9	*0.5*	3.2532
219919_s_at	NM_018276.1		FLJ10928	*0.1*	*0.2*	3.1	1.8	2.5	1.7	4.3	*1.7*	2.1	*0.1*	*0.5*	*0.4*	*0.3*	*0.1*	*0.1*	*0.1*	*0.1*	*0.1*	*0.7*	3.2497
204301_at	NM_014867.1		KIAA0711	0.6	*0.1*	3.8	14.3	10.7	5.3	6.8	12.6	10.5	*1.2*	*0.6*	*1.6*	*1.6*	*1.0*	*0.8*	1.2	2.6	*0.8*	*0.1*	3.2398
210999_s_at	U66065.1		Grb 10- and Grb-IR-related splice variant 1	3.6	1.7	8.4	13.6	11.8	7.3	4.6	4.8	6.4	2.2	1.7	1.9	2.0	1.9	1.2	1.2	1.6	*0.4*	1.6	3.1044
209539_at	D25304.1		RacCdc42 guanine exchange factor (GEF) 6	13.1	24.8	28.8	74.7	73.0	53.8	35.5	92.9	59.6	9.2	6.1	18.5	13.7	3.1	10.8	12.9	7.1	7.8	1.0	3.0943
208921_s_at	L12387.1		sorcin (SRI)	19.2	11.4	20.2	88.6	67.0	37.4	42.4	86.3	85.4	6.9	8.9	17.6	21.5	2.6	11.1	12.7	8.4	8.6	17.8	3.0628
209043_at	AF033026.1		bifunctional ATP sulfurylase/adenosine 5-phosphosulfate kinase	19.9	16.1	39.0	87.1	75.2	66.4	68.7	89.4	71.4	13.8	20.0	46.5	8.9	6.3	6.7	4.4	10.6	11.0	22.7	3.0385

Fig. 6M

E. Eosinophil and neutrophil-selective transcripts (1/1).

Probe set	Accession #		Transcripts	MC. cord blood	MC. lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Eo+Ne S.I.
221345_at	NM_005306.1	GPR	GPR43 PAR1-like	0.1	0.4	0.9	0.6	0.6	7.0	16.6	15.4	10.5	49.7	45.7	22.5	23.0	0.8	0.1	0.1	0.7	0.4	0.1	21.742
212860_at	BG168720		zinc finger, DHHC domain containing 18	2.2	0.8	4.1	3.9	4.0	16.0	17.4	14.8	16.7	59.2	53.9	30.9	39.8	1.1	2.4	3.8	2.6	1.5	1.3	6.5842
211576_s_at	BC003068.1		solute carrier family 19 member 1	1.4	0.1	0.7	1.4	0.7	5.1	5.9	11.5	12.4	19.8	18.7	27.1	28.1	1.8	0.9	0.4	2.7	0.5	0.8	4.99
214321_at	BF440025		nephroblastoma overexpressed gene	1.3	1.0	0.8	0.2	0.7	6.2	7.2	17.0	13.7	4.5	7.6	10.7	11.3	0.1	0.1	0.0	0.1	0.1	1.8	4.9823
218950_at	NM_022481.1		ARF-GAP, RHO-GAP, ankyrin repeat and plekstrin homology domains-containing protein 3	1.4	3.1	2.4	3.7	2.1	15.5	15.9	18.3	15.5	28.0	24.3	15.9	20.6	0.7	0.2	0.8	3.9	0.9	1.0	4.829
205681_at	NM_004049.1		BCL2-related protein A1	0.5	1.9	1.0	3.2	2.4	52.4	40.2	35.9	30.5	46.5	49.2	35.5	33.5	1.5	2.2	1.9	8.3	4.3	0.2	4.7782
203765_at	NM_012198.1		grancalcin	2.0	1.8	4.5	11.7	8.3	27.5	39.8	46.7	34.8	71.6	85.2	80.5	77.9	1.0	1.0	1.2	12.1	3.1	0.5	4.4403
213241_at	AF035307.1		cDNA FLJ36416 fis, clone THYMU2011053	5.0	2.4	1.6	1.0	1.0	33.2	37.1	68.7	40.6	63.2	77.8	89.2	80.9	3.0	3.0	2.8	13.5	4.1	7.8	4.2603
221815_at	BE671816		hypothetical protein PRO2831	1.2	1.4	1.3	0.5	1.6	10.1	8.8	11.2	6.4	5.0	6.2	4.0	3.8	1.6	0.8	0.2	1.4	0.9	0.6	4.1325
214153_at	BE467941		homolog of yeast long chain polyunsaturated fatty acid elongation enzyme 2	1.0	0.6	1.0	2.0	3.1	9.1	10.4	18.2	16.6	9.7	9.7	14.5	15.2	0.8	0.9	1.2	0.7	2.3	0.1	4.0797
212821_at	AU147160		KIAA0599	0.1	0.1	0.4	1.2	0.9	4.6	2.8	4.7	3.4	4.4	3.5	6.0	7.9	0.4	0.2	0.4	0.3	0.0	0.2	3.727
206723_s_at	AF011466.1	GPR	Edg4, endothelial differentiation lysophosphatidic acid G-protein-coupled receptor, 4	1.2	1.4	2.1	3.6	2.6	13.7	8.0	19.6	22.3	24.6	17.0	26.1	29.1	0.1	3.6	5.0	3.8	1.9	0.9	3.7119
212360_at	AI916249		adenosine monophosphate deaminase 2 (isoform L)	1.0	2.0	2.6	5.9	4.6	26.6	18.7	30.2	31.9	78.7	63.1	79.5	91.3	3.4	5.8	6.1	12.6	3.7	5.8	3.5888
218308_at	NM_006342.1		transforming, acidic coiled-coil containing protein 3 (TACC3)	0.4	0.4	4.8	8.3	9.5	3.3	2.4	3.3	4.7	17.6	14.8	23.5	22.8	2.4	2.3	1.6	3.6	1.0	0.7	3.4769
212629_s_at	AK023692.1		protein kinase C-like 2	1.9	0.6	3.1	3.7	5.1	11.8	7.6	17.7	13.8	16.7	23.6	27.0	28.4	1.1	2.1	2.2	4.2	4.2	2.9	3.2963
201739_at	NM_005627.1		serumglucocorticoid regulated kinase (SGK)	30.2	25.2	1.9	18.5	25.4	114.1	116.0	150.9	164.8	60.2	77.1	105.8	156.3	1.1	3.7	0.7	34.6	1.6	18.9	3.2456
209473_at	AV717590		ectonucleoside triphosphate diphosphohydrolase 1	1.4	0.6	2.1	1.6	2.0	15.9	22.3	39.5	29.1	14.1	13.7	23.7	13.8	2.6	2.6	1.3	6.5	4.8	0.6	3.0752
209304_x_at	AF087853.1		growth arrest and DNA damage inducible protein beta (GADD45B)	2.0	0.3	2.7	4.5	3.6	15.5	11.9	16.3	34.4	7.0	12.0	13.5	9.4	0.4	3.1	4.2	4.1	3.7	0.6	3.0295
210666_at	AF050145.1		iduronate 2-sulfatase	0.1	0.3	1.3	0.5	1.7	7.1	2.9	3.3	3.8	6.1	5.1	5.2	10.8	0.4	0.1	0.9	0.7	0.4	0.1	3.0005

Fig. 6N

G. Basophil and neutrophil-selective transcripts (1/1).

Probe set	Accession #	Transcripts	MC. cord blood	MC. lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ba+Ne S.I.
218739_at	NM_016006.1	CGI-58 protein	1.8	1.8	7.2	16.3	17.3	2.6	3.3	3.2	2.5	20.7	23.6	21.4	19.3	1.3	1.2	0.7	2.9	0.7	1.5	5.81398
219242_at	NM_025180.1	FLJ13386	1.0	0.3	10.1	23.5	18.8	2.4	3.7	4.5	4.2	13.7	14.0	26.1	27.7	0.1	0.5	1.6	1.0	0.6	2.5	4.97025
219157_at	NM_007246.1	kelch (Drosophila)-like 2	2.4	1.7	4.2	16.2	19.2	3.6	2.5	4.3	3.8	15.5	24.4	24.5	22.5	0.7	2.0	1.5	3.0	2.2	1.7	4.61523
206643_at	NM_002108.2	histidine ammonia-lyase	0.1	1.4	8.5	13.7	25.4	0.2	0.6	1.3	0.6	31.4	32.8	61.7	37.0	1.6	0.5	0.1	5.6	0.6	0.5	4.57355
213935_at	AF007132.1	clone 23551 mRNA	0.8	0.1	5.0	26.2	26.4	2.4	1.7	2.9	1.2	4.5	6.7	11.2	9.0	0.1	0.1	0.2	2.3	0.5	0.8	4.33664
222151_s_at	AK023738.1	FLJ13676 fis	1.0	0.9	4.5	5.5	4.7	1.8	1.7	1.4	1.6	8.4	10.2	8.4	7.6	0.5	0.8	1.3	0.8	1.0	1.3	4.14372
207907_at	NM_003807.1	tumor necrosis factor (ligand) superfamily member 14 (TNFSF 14)	0.1	0.1	3.9	10.4	6.3	1.2	1.5	4.0	4.1	15.8	7.3	15.8	11.5	0.2	0.4	0.1	0.6	0.0	0.1	3.89177
202530_at	NM_001315.1	mitogen-activated protein kinase 14	5.0	3.0	28.8	82.2	70.8	4.0	7.1	13.9	11.1	13.6	23.0	25.7	22.3	5.3	2.9	3.5	7.3	2.6	4.5	3.8469
217521_at	N54942	Hs.276590 ESTs	0.1	0.1	5.5	18.9	20.9	0.3	0.3	1.6	0.1	19.6	14.5	29.9	18.4	0.4	0.8	0.9	4.3	1.0	0.3	3.84207
203693_s_at	NM_001949.2	E2F transcription factor 3	2.5	1.7	4.3	16.2	13.2	2.1	1.9	5.7	3.3	8.8	11.7	13.3	15.4	1.5	1.4	2.5	2.3	1.1	1.2	3.7116
203420_at	NM_016255.1	autosomal highly conserved protein (AHCP)	2.4	3.3	15.6	31.5	32.4	7.3	6.6	14.3	11.0	37.2	37.2	48.5	50.0	6.1	5.0	9.8	4.5	3.3	9.8	3.48188
218308_at	NM_006342.1	transforming acidic coiled-coil containing protein 3	0.4	0.4	4.8	8.3	9.5	3.3	2.4	3.3	4.7	17.6	14.8	23.5	22.8	2.4	2.3	1.6	3.6	1.0	0.7	3.4769
203080_s_at	NM_013450.1	bromodomain adjacent to zinc finger domain, 2B	2.2	2.4	10.4	22.8	22.9	4.9	6.6	10.0	9.5	29.5	30.7	33.5	40.6	1.1	1.7	1.9	4.6	2.3	1.5	3.401
219999_at	NM_018621.1	hypothetical protein PRO2198	0.4	0.6	3.9	7.6	8.0	2.0	1.5	3.9	2.7	9.8	6.5	11.7	12.3	0.2	1.3	1.8	2.4	1.7	0.9	3.31991
213805_at	AI692428	clone 23551 mRNA	0.3	0.1	13.8	11.0	8.7	3.2	3.0	1.4	1.4	19.7	16.7	5.3	7.0	0.7	0.2	0.8	3.3	0.4	0.7	3.29317
204669_s_at	NM_007219.2	ring finger protein 24	0.9	0.2	4.4	27.9	34.3	2.1	5.9	16.1	14.5	18.8	14.4	60.7	56.1	0.5	0.1	0.1	0.1	0.1	0.8	3.18834
215555_at	AK023774.1	FLJ13712 fis	0.0	0.4	5.0	4.3	5.8	1.5	1.9	1.5	1.5	7.6	8.2	3.3	3.2	0.9	1.0	1.5	1.5	1.0	0.1	3.1591

Fig. 60

H. Mast cell and basophil-selective transcripts (1/1).

Probe set	Accession #		Transcripts	MC. cord blood	MC. lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	MC+Ba S.I.
205624_at	NM_001870.1		carboxypeptidase A3	137.1	91.0	107.6	139.0	173.1	2.5	1.6	2.8	1.9	0.1	1.4	2.0	12.4	0.2	1.2	0.2	0.2	0.5	0.5	59.1989
208605_s_at	NM_002529.2	R	TRK neurotrophin receptor	8.0	1.2	4.6	9.3	8.1	0.2	0.2	0.0	0.1	0.2	0.0	0.1	0.1	0.1	0.1	0.1	0.1	0.0	0.0	34.7309
210258_at	AF030107.1		regulator of G protein signaling (RGS13)	6.2	8.4	5.6	7.1	10.9	0.3	0.1	0.4	0.5	0.5	0.0	0.1	0.3	0.1	0.0	0.0	0.2	0.3	0.0	21.7762
207496_at	NM_000139.1	R	Fc epsilon R I beta	19.9	24.7	35.4	51.9	45.6	0.9	0.1	0.5	0.3	0.1	0.1	0.5	1.8	1.6	0.5	0.2	0.0	0.3	0.1	21.1783
205857_at	AI269290		solute carrier family 18	24.3	27.1	8.1	22.3	25.0	1.3	1.0	0.8	0.9	1.3	0.9	0.5	0.7	0.9	0.4	0.3	0.2	0.3	0.3	20.3301
210358_x_at	BC002557.1		GATA-binding protein 2	18.4	12.8	55.0	31.7	24.7	2.0	1.6	1.9	1.7	0.9	1.9	1.3	3.7	2.6	0.8	0.8	0.9	0.4	2.7	9.46893
207497_s_at	D10583.1		*Fc epsilon R I beta*	10.7	28.6	34.9	12.6	6.8	1.5	1.0	0.8	0.8	1.9	0.9	1.7	1.5	1.7	0.7	0.7	0.1	0.3	0.5	9.39967
203914_x_at	NM_000860.1		*15-hydroxyprostaglandin dehyrogenase (PDGH)*	63.9	51.4	24.8	36.0	23.3	4.1	4.6	4.6	2.6	1.3	0.9	1.3	1.2	6.0	1.4	1.5	0.4	0.8	0.4	6.14285
219557_s_at	NM_020645.1		chromosome 11 open reading frame 14	7.4	4.2	4.4	7.4	6.6	1.2	1.6	2.0	2.4	0.9	1.9	1.1	2.1	1.1	1.4	1.4	1.5	0.4	1.6	3.38029
204061_at	NM_005044.1		protein kinase, X-linked	6.2	5.2	5.2	12.8	16.9	2.3	2.7	2.5	2.4	0.8	0.4	0.7	1.2	1.9	1.5	2.1	2.5	2.0	0.8	3.26062
202068_s_at	NM_000527.2	R	low density lipoprotein receptor	24.6	16.8	19.3	28.5	13.5	1.6	1.0	1.6	0.9	0.8	2.4	1.5	2.5	2.3	2.1	3.4	3.5	0.8	6.3	3.1679

Fig. 6P

I. Specific transcripts markers for non-granulocytes.

Probe set	Accession #	Transcripts	MC. cord blood	MC. lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb
203547_at	U47924	CD4	5.5	4.7	2.2	1.1	1.2	2.0	1.6	0.4	0.9	0.7	1.1	0.7	0.8	3.5	15.0	0.3	17.6	1.2	0.4
205758_at	AW006735	CD8	0.5	1.7	2.6	2.3	3.2	1.3	1.1	2.2	1.7	0.3	0.5	1.8	0.3	4.2	3.0	76.1	0.8	0.6	0.4
206398_s_at	NM_001770.1	CD19	0.7	0.1	0.7	0.4	0.7	0.8	0.5	0.5	0.2	0.6	1.5	1.1	0.7	4.0	0.0	0.1	0.1	19.1	0.4
211644_x_at	L14458.1	IgG V-J region	0.2	0.1	0.1	0.1	0.2	0.2	0.2	0.2	0.3	0.1	0.3	0.2	0.2	3.8	0.1	0.2	0.1	70.9	0.1
201743_at	NM_000591.1	CD14	18.4	2.4	0.3	0.1	0.6	8.8	0.6	1.1	3.2	40.7	49.6	58.7	68.2	2.9	0.4	0.0	97.2	1.1	0.9
203104_at	NM_005211.1	v-fms M-CSF receptor	3.8	0.2	0.6	0.7	0.3	3.0	1.1	1.7	1.5	8.8	8.7	6.3	6.4	5.2	2.8	0.7	42.1	1.4	0.9
209968_s_at	U63041.1	CD56	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.2	0.1	0.1	0.1	0.2	0.1	0.1	0.1	0.1	0.2	0.1	0.0
204627_s_at	M35999.1	CD61 glycoprotein IIIa	1.7	9.4	0.2	0.1	0.3	0.1	0.1	0.1	0.1	0.1	0.4	0.1	0.2	48.3	0.1	0.3	0.1	0.2	0.5
216442_x_at	AK026737.1	fibronectin	0.3	1.5	0.3	0.3	0.2	0.1	1.0	0.3	0.6	0.1	0.1	0.2	0.1	0.3	0.1	1.0	0.3	0.1	92.6

Fig. 6Q

J. Raw AD levels for the median values used to normalize the raw AD levels, and the housekeeping genes.

Probe set	Accession #	Transcripts	MC cord blood	MC lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb
AFFX-HSAC07/X00351_3_at	X00351	beta-actin	18534	19383	14638	20922	19151	22019	18638	21153	18568	19406	22302	16589	17569	18295	18782	20805	20661	17542	20399
AFFX-HSAC07/X00351_M_at	X00351	beta-actin	22898	21777	12940	11533	7608	22560	18785	14861	13431	23106	23373	6861	8019	19368	20362	22761	22294	19087	22757
AFFX-HSAC07/X00351_5_at	X00351	beta-actin	15642	15838	9516	2927	2066	17186	21061	4861	3771	18772	19768	2165	2193	14887	16381	18218	17583	15063	16795
AFFX-HUMGAPDH/M33197_3_at	M33197	GAPDH	14906	13632	3640	10477	9332	2649	2844	5498	2605	2549	3186	3586	3538	5929	6429	6098	9756	5180	19674
AFFX-HUMGAPDH/M33197_M_at	M33197	GAPDH	15891	16852	3218	7587	6963	2382	2565	3720	1838	2194	2796	2312	2154	6182	5931	5921	11464	4344	17013
AFFX-HUMGAPDH/M33197_5_at	M33197	GAPDH	16298	16701	3479	4559	5110	1827	3121	2127	1168	2492	3476	1636	1355	4655	6826	6260	9905	5636	23350
The median value of 22283 transcripts			121	169.3	85.3	112.2	110.9	93.7	102.1	127.3	114	62.7	73.1	87.4	87.3	82.3	152.5	121.3	107.1	114.1	183.8

Abbreviations used in the table A-I were (small); the results obtained by the small sample protocol (see materials and methods), R; receptor, and ICN; ion channel.

Fig. 6R

GRANULOCYTE SUBTYPE-SELECTIVE RECEPTORS AND ION CHANNELS AND USES THEREOF

FIELD OF THE INVENTION

[0001] The present invention relates to the identification of granulocyte-selective markers that can be used as targets for drug discovery.

BACKGROUND OF THE INVENTION

[0002] Three types of human blood granulocytes, eosinophils, basophils and neutrophils, play roles in protecting against microbial infection by releasing cell type-specific mediators and proteases. Specifically, eosinophils and basophils evoke allergic reactions as well as damage nematodes.[1,2] As well as killing bacteria, neutrophils sometimes induce systemic vasculitis or multiple organ damage under certain conditions.[3,4] Thus, targeting granulocyte type-selective functions is considered an important strategy for drug discovery.

[0003] Activation of blood granulocytes and tissue mast cells is generally characterized by an influx of extracellular calcium (Ca^{2+}), which is essential for subsequent release of granule-derived mediators, newly generated lipid mediators and cytokines.[5] The mechanism by which granulocyte mediator secretion is sustained is therefore likely to include modulation of various types of ion channels. Flow of ions including K^+ and Cl^- may play an important role during granulocyte responses because they regulate cell membrane potential and thus influence Ca^{2+} influx.[6] Treatment of mast cells and basophils with pertussis toxin inactivates the Gi-type of G-proteins and abolishes degranulation induced by non-immunological ligands such as thrombin and N-formylpeptide; however, it fails to inhibit the influx of Ca^{2+}.[7] Thus, Ca^{2+}-independent stimulation of Gi is also involved in granulocyte degranulation. The thrombin (protease) activated receptors and formylpeptide receptors are classified as G protein-coupled receptors (GPR), having an extracellular N-terminal segment, a seven transmembrane region, which forms the transmembrane core; three exoloops, three cytoloops, and a C-terminal segment.[8] Thus, ion channels and GPR both play essential roles in degranulation as well as other cellular function important for granulocytes. As a result, both ion channels and GPR are targets of drug development.[9]

[0004] As the human genome project nears completion, the identification of potential drug targets using gene expression profiles from specific cell types is becoming practical and important for drug discovery.[10,11] The sequencing of the human genome is offering an unprecedented opportunity for the pharmaceutical development of drugs. Receptor genes and ion channel genes are found only in 5% and 1.3% of all genes present in the human genome,[10] respectively. However, receptors and ion channels are respectively found in 45% and 5% of the molecular targets of all known drugs.[9,12,13] Thus, receptors including GPR and ion channels are now considered as the most important drug targets.

[0005] Until recently, it has been impractical to analyze genome-wide expression of leukocytes. Newly developed technology, the microarray or high density oligonucleotide probe array (GeneChip) is one of the latest breakthroughs in experimental molecular biology, which allows approximately 39,000 transcripts derived from a cells transcriptome to be simultaneously monitored. Using this technology, we previously reported the transcriptome profiling of various types of mast cells and eosinophils.[14-16] However, there is still a need in the art to identify drug targets that are selectively, or preferentially, expressed in specific cell types such that efforts required for pharmaceutical development are minimized.

SUMMARY OF THE INVENTION

[0006] In the present study, we used GeneChip (version U133A containing approximately 22,000 gene probes) to examine the granulocyte type-selective transcriptome expression of 7 types of leukocytes (basophils, eosinophils, neutrophils, $CD4^+$ cells, $CD8^+$ cells, $CD14^+$ cells and $CD19^+$ cells), platelets, mast cells and fibroblasts by focusing on the expression of granulocyte-selective genes for ion channels, GPR and other receptors. We identified many novel granulocyte subtype-selective transcripts (markers) that are useful for drug development.

[0007] Granulocyte subtype selective transcripts were chosen based on several conditions such as the transcript having 5-fold or greater expression level compared to the maximum level of other leukocytes. Fifty-one transcripts were chosen to be preferentially expressed by each granulocyte subtype. Seventeen out of the 51 transcripts have not been previously reported as granulocyte subtype-selective. Among the 17 receptors and ion channels, six were basophil- and/or eosinophil-selective and were not highly expressed by other organs, indicating that they may be potential targets for anti-allergic drugs, for example.

[0008] Utilization of this database of potential granulocyte type-selective drug targets will minimize the efforts required for pharmaceutical development of drugs for treatment of diseases of the immune system, cancer, cardiac diseases, as well as other diseases.

[0009] Accordingly, the invention provides methods and compositions that are useful for drug discovery, disease diagnosis and/or prognosis, granulocyte type detection and/or selection and/or manipulation, and/or therapeutic applications.

[0010] Accordingly, in one aspect, methods of the invention include diagnosing a granulocyte disorder by detecting, in a biological sample obtained from a subject, a level of expression of one or more granulocyte-selective markers, and comparing the level of expression of each of the one or more granulocyte-selective markers with a reference level of expression. A statistically significant difference between the level of expression of at least one granulocyte-selective marker and an expected level of expression for the at least one granulocyte-selective marker is indicative of a granulocyte disorder in the subject. The reference level of expression for a granulocyte-selective marker may be, for example, a normal level of expression of the granulocyte-selective marker in a normal granulocyte. A higher level of expression of at least one of the one or more granulocyte-selective markers in the biological sample compared to the expected level of expression for the at least one granulocyte-selective marker may be indicative of the granulocyte disorder. A lower level of expression of at least one of the one or more granulocyte-selective markers in the biological sample compared to the expected level of expression for the at least one granulocyte-selective marker also may be indicative of the granulocyte disorder. In one embodiment, the granulocyte disorder may be an abnormally high number of one or more types of granulocyte in the biological sample. In another embodiment, the granulocyte disorder may be an abnormally low number of one or more types of granulocyte in the biological sample. In

yet another embodiment, the granulocyte may be an abnormal pattern of expression of one or more granulocyte selective markers in one or more types of granulocyte in the biological sample.

[0011] In another aspect, methods of the invention include diagnosing a non-neutrophil granulocyte disorder or mast cell disorder by detecting, in a biological sample from a subject, a level of expression of one or more non-neutrophil granulocyte or mast cell selective markers, and comparing the level of expression of each of the one or more non-neutrophil granulocyte or mast cell selective markers with a reference level of expression. A statistically significant difference between the level of expression of at least one non-neutrophil granulocyte or mast cell selective marker and an expected level of expression for the at least one non-neutrophil granulocyte or mast cell selective marker may be indicative of a non-neutrophil granulocyte disorder or mast cell disorder in the subject. In one embodiment, the non-neutrophil granulocyte disorder may be a basophil disorder. The basophil disorder may be one or more of the diseases described herein, including a tumor or cancer. In another embodiment, the non-neutrophil granulocyte disorder may be an eosinophil disorder. The eosinophil disorder may be one or more of the diseases described herein, including a tumor or cancer. In other embodiments, a mast cell disorder may be one or more of the diseases described herein, including a tumor or cancer.

[0012] A higher level of expression of one or more non-neutrophil granulocyte or mast cell-selective marker in the biological sample compared with the control level of expression of the one or more non-neutrophil granulocyte or mast cell-selective marker may be diagnostic of the non-neutrophil granulocyte disorder or mast cell disorder. Alternatively, a lower level of expression of one or more non-neutrophil granulocyte or mast cell-selective marker in the biological sample compared with the control level of expression of the one or more non-neutrophil granulocyte or mast cell-selective marker also may be diagnostic of the non-neutrophil granulocyte disorder or mast cell disorder.

[0013] In another aspect, methods of the invention include determining onset, progression, or regression, of a granulocyte disorder in a subject, by i) detecting in a first biological sample from a subject a first level of expression of one or more granulocyte-selective markers, ii) detecting in a second biological sample comprising blood and obtained from the subject at a time later than the first biological sample, a second level of expression of the one or more granulocyte-selective markers, and iii) comparing the first level of expression with the second level of expression. A statistically significant difference between the first and second levels may be an indication of onset, progression, or regression of the granulocyte disorder.

[0014] In another aspect, methods of the invention include selecting a course of treatment for a subject having or suspected of having a granulocyte disorder by i) detecting in a biological sample from a subject a level of expression of one or more granulocyte-selective markers, ii) comparing the level of expression of the one or more granulocyte-selective markers to a reference level of expression, iii) determining the status of the granulocyte disorder of the subject based on the difference in the level of expression of one or more granulocyte-selective marker in the sample compared to the reference level of expression, and iv) selecting a course of treatment for the subject appropriate to the status of the granulocyte disorder of the subject.

[0015] In another aspect, methods of the invention includes monitoring responses to treatment in a subject with a granulocyte disorder by i) detecting in a biological sample from a subject that has received treatment for the granulocyte disorder, a level of expression of one or more granulocyte-selective markers, and ii) comparing the level of expression of the one or more granulocyte-selective marker with a reference level of expression. A statistically significant change in the level of expression of one or more of the granulocyte-selective markers in the biological sample relative to the reference level of expression may indicate that the subject is responding to the treatment for the granulocyte disorder.

[0016] In another aspect, methods of the invention include identifying a compound that alters at least one physiological property of a granulocyte by i) contacting a granulocyte with a candidate compound that interacts with a granulocyte-selective marker, ii) determining at least one physiological property of the granulocyte after contact with the candidate compound, and iii) comparing the at least one physiological property to one at least one reference property to determine whether the candidate compound alters at least one physiological property of the granulocyte. In one embodiment, the effect of the candidate compound on a granulocyte may be compared to its effect on a second cell type to determine whether the candidate compound has a cell-type selective effect on the granulocyte. The second cell type may be another granulocyte cell type. Alternatively, the second cell type may be a non-granulocyte cell type (including a mast cell or other leukocyte). In one embodiment, a physiological property may be an expression level of one or more granulocyte-selective markers. In another embodiment, a physiological property may be the growth rate and/or proliferation rate of the granulocyte. In one embodiment, the candidate compound may be cytostatic or cytotoxic (e.g., it may kill the granulocyte). It should be appreciated that the candidate compound may have cell type selective effects (e.g., cell type selective cytotoxic and/or cytostatic effects).

[0017] In another aspect, methods of the invention include treating a granulocyte-associated disease, by administering to a subject having a granulocyte-associated disease a compound that interacts with a granulocyte-selective marker in an amount sufficient to treat the granulocyte-associated disease. Similarly, the invention provides methods for treating a mast cell-associated disease by administering to a subject having a mast cell-associated disease a compound that interacts with a mast cell-selective marker in an amount sufficient to treat the mast cell-associated disease. In some embodiments, a plurality (e.g., any whole number between 1 and 50, for example 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) of granulocyte-selective or mast cell-selective compounds may be administered. Compounds may be administered in physiologically acceptable (e.g., biologically compatible) solutions or carrier. Therapeutic preparations of the invention may be sterilized using any appropriate technique including filtration, heat treatment, radiation, chemical treatment, and/or other suitable techniques.

[0018] In another aspect, methods of the invention include treating a granulocyte-associated disease by modulating the activity or expression of a granulocyte-selective marker to an extent that is sufficient to treat the granulocyte-associated disease. Similarly, the invention also provides methods of treating a mast cell-associated disease by modulating the activity or expression of a mast cell-selective marker thereby to treat the mast cell-associated disease. Modulating the

activity or expression of a marker may involve activating or inactivating and/or increasing or decreasing the expression levels.

[0019] In any of the therapeutic methods described herein, one or more therapeutic compounds may be identified as described herein by screening for one or more compounds that alter at least one physiological property of a granulocyte and/or a mast cell.

[0020] In another aspect, the invention provides compounds that alter a physiological property of a granulocyte and/or a mast cell. One or more compounds may be identified as described herein by screening compounds that are known to interact (e.g., specifically, selectively, etc.) with a granulocyte-selective marker and/or a mast cell-selective marker. Compounds of the invention may be formulated in a physiologically acceptable preparation.

[0021] In any of the aspects described herein, the level of expression of each of the one or more granulocyte-selective markers (including neutrophil-selective markers, basophil-selective markers, eosinophil-selective markers, or a combination thereof) may be determined by determining an amount of an mRNA in the biological sample corresponding to each of the one or more granulocyte-selective markers. The amount of mRNA may be determined by reverse transcription polymerase chain reaction (RT-PCR) amplification or any other suitable method including microarray analysis or other hybridization or primer extension assays (e.g., using labeled probes and/or nucleotides). In other embodiments, the level of expression of each of the one or more granulocyte-selective markers may be determined by determining an amount of a protein in the biological sample corresponding to each of the one or more granulocyte-selective markers (e.g., using antibody binding assays with labeled antibodies, including ELISA assays or other antibody binding assays). Other suitable methods of determining expression levels of granulocyte-selective markers may be used (including activity levels). Similarly, expression levels of non-neutrophil granulocyte or mast cell-selective markers may be determined by determining mRNA and/or protein levels or using any other appropriate assay (including functional assays).

[0022] In any of the aspects described herein, the biological sample may be a blood sample, a tissue sample, or any other suitable biological sample.

[0023] In any of the aspects described herein, the subject may be human.

[0024] In any of the aspects described herein, a granulocyte may be a neutrophil, a basophil, or an eosinophil. It should be appreciated that aspects of the invention described herein in the context of granulocytes may be applied to non-neutrophil granulocytes and/or mast cells. Similarly, aspects of the invention described herein in the context of granulocytes or mast cells may be applied to other leukocytes including those described in the examples and for which cell-type selective expression is shown in the experiments including the Figures attached hereto.

[0025] According to aspects of the invention, one or more methods described herein may involve a combination of two or more markers. In one embodiment, markers that are more selective as described herein may be used. In some embodiments, a combination of two or more (e.g., 3, 4, 5, 6, 7, 8, 9, or 10 or more) markers may be used to increase the cell-selectivity of a screening or diagnostic method. It should be appreciated that different combinations of markers disclosed herein may be used (e.g., panels of two or more markers). Accordingly, compositions of the invention may include compounds that interact with two or more markers (e.g., a single compound that interacts with two or more markers, or two or more compounds each of which interacts with a single marker, or any combination thereof).

[0026] Methods and compositions described herein may include or involve nucleic acids that hybridize to one or more nucleic acids that encode a granulocyte or mast cell-selective marker (e.g., DNA or RNA). The nucleic acids may be oligonucleotides (e.g., synthetic oligodeoxynucleotides). The oligonucleotides may be between 10 and 100 nucleotides in length (e.g., between about 20 and about 50). The oligonucleotides may include sequences that are complementary to sequences of one or more markers described herein (or the complement thereof). In some embodiments, nucleic acids may be antisense or siRNA nucleic acids that are useful to decrease the expression of one or more granulocyte or mast cell-selective markers. Similarly, methods and compositions described herein may include or involve agents that bind or interact with one or more proteins that are granulocyte or mast cell-selective markers. Binding agents may be antibodies or fragments thereof (including single chain antibodies, synthetic antibodies, humanized antibodies), aptamers, and/or other molecules including naturally occurring or synthetic molecules (e.g., low molecular weight molecules), that bind to one or more peptide epitopes of one or more granulocyte and/or mast cell-selective marker. Examples of nucleic acid and peptide sequences for certain granulocyte and/or mast cell-selective markers are provided in the sequence listing. These and others are described in the examples, tables, and figures. In the sequence listing, the nucleic acid sequences are presented as cDNA sequences. The following list of sequences in the sequence listing includes the description of the molecule and the genbank accession number is indicated in parentheses.

SEQ ID NO: 1	Ca^{2+} channel type A1 D (BE550599) cDNA
SEQ ID NO: 2	K^+ channel Kir1.3 (U73191.1) cDNA
SEQ ID NO: 3	K^+ channel Kir1.3 (U73191.1) translation
SEQ ID NO: 4	K^+ channel Kir2.1 (AF153820.1) cDNA
SEQ ID NO: 5	K^+ channel Kir2.1 (AF153820.1) translation
SEQ ID NO: 6	PGE R type 3a2 (X83858.1) cDNA
SEQ ID NO: 7	PGE R type 3a2 (X83858.1) translation
SEQ ID NO: 8	EMR-1 (NM_001974.1) cDNA
SEQ ID NO: 9	EMR-1 (NM_001974.1) translation
SEQ ID NO: 10	GPR105 purinergic R (NM_014879.1) cDNA
SEQ ID NO: 11	GPR105 purinergic R (NM_014879.1) translation
SEQ ID NO: 12	GPR, Edg-4 (AF011466.1) cDNA
SEQ ID NO: 13	GPR, Edg-4 (AF011466.1) translation
SEQ ID NO: 14	PAR1-like GPR43 (NM_005306.1) cDNA
SEQ ID NO: 15	PAR1-like GPR43 (NM_005306.1) translation
SEQ ID NO: 16	GPR77 (018485.1) cDNA
SEQ ID NO: 17	GPR77 (018485.1) translation
SEQ ID NO: 18	GPR86 purinergic R (NM_023914.1) cDNA
SEQ ID NO: 19	GPR86 purinergic R (NM_023914.1) translation
SEQ ID NO: 20	PAR2 (BE965369) cDNA
SEQ ID NO: 21	HTm4 (L35848.1) cDNA
SEQ ID NO: 22	HTm4 (L35848.1) translation
SEQ ID NO: 23	CD244 NK cell R (NM_016382.1) cDNA
SEQ ID NO: 24	CD244 NK cell R (NM_016382.1) translation
SEQ ID NO: 25	Fibroblast growth factor R 2 (NM_022969.1) cDNA
SEQ ID NO: 26	Fibroblast growth factor R 2 (NM_022969.1) translation
SEQ ID NO: 27	Low-density lipoprotein R (NM_000527.2) cDNA
SEQ ID NO: 28	Low-density lipoprotein R (NM_000527.2) translation
SEQ ID NO: 29	Butyrophilin-like R (AK025267.1) cDNA

-continued

SEQ ID NO: 30	Leukocyte Ig-like R A2 (NM_006866.1) cDNA
SEQ ID NO: 31	Leukocyte Ig-like R A2 (NM_006866.1) translation

BRIEF DESCRIPTION OF THE DRAWINGS

[0027] FIG. **1** shows Real-time quantitative PCR analysis of granulocyte-selective gene expression. The relative mRNA expression level by each cell type against PBMNC was shown after normalization of mRNA levels for A. HTm4 (0.42 per 100 GAPDH), B. Ca^{2+} receptor alpha 1D subunit (0.003), C. prostaglandin E receptor type 3a2 (0.12), D. EMR-1 (0.62), and E. aquaporin 9 (0.92) expressed by PBMNC. Ne; neutrophils (n=3), Eo; eosinophils (n=2), Ba, basophils (n=3), CD4; CD4+ cells (n=3), P; PBMNC (n=1).

[0028] FIG. **2** shows the demonstration of HTm4 protein on human basophils. Cells on the glass slide were incubated with 2 μg/ml polyclonal rabbit anti-hHTm4 antibody or 2 μg/ml rabbit IgG (H+L) as a control followed by incubation with a secondary antibody, highly cross-adsorbed Alexa Fluor® 546 conjugated goat anti-rabbit IgG (H+L). After mounting using the Prolong AntiFade Kit, slides were scanned by Zeiss Laser Scanning Microscope 5 Pascal.

[0029] FIGS. **3**A through **3**E shows granulocyte subtype-specific transcripts for ion channels and receptors.

[0030] FIGS. **4**A through **4**F show a table of "normalized AD" expression levels of various genes in indicated cells and shows corresponding graphs; x axis represents "normalized AD" expression levels.

[0031] FIGS. **5**A through **5**D show a table of "normalized AD" levels of various genes in indicated cells and shows corresponding graphs; x axis represents "normalized AD" expression levels.

[0032] FIG. **6**A through FIG. **6**R show the complete list of granulocyte subtype-selective transcripts.

DETAILED DESCRIPTION OF THE INVENTION

[0033] In one aspect of the invention, one or more granulocyte-selective markers may be used for drug discovery. For example, a granulocyte-selective marker (e.g., a cell type selective transcript, its protein product, or the gene encoding the marker) may be used as a target for drug identification. Drug identification may involve a random screen of potential drug candidates (including peptides, nucleic acids, small molecules, etc.). In one embodiment, one or more granulocyte-selective markers may be used as targets for drug identification. For example, a single drug molecule that interacts (e.g., that activates, or inactivates, and/or binds to) with one or more markers may be identified. However, in some embodiments, more than one drug molecule may be identified, each one interacting with a different granulocyte-selective marker. According to aspects of the invention, drug(s) that target a specific granulocyte may be used to stimulate or inhibit activity or growth of that cell type. A cell type specific drug also may be used to kill or slow or stop the growth of a specific cell type.

[0034] Examples of markers for different granulocyte types include: Ca^{2+} channel type A1 D (GenBank accession no. BE550599), K^+ channel Kir1.3 (GenBank accession no. U73191.1), K^+ channel Kir2.1 (GenBank accession no. AF153820.1), PGE R type 3a2 (GenBank accession no. X83858.1), EMR-1 (GenBank accession no. NM_001974.1), GPR105 purinergic R (GenBank accession no. NM_014879.1), GPR, Edg-4 (GenBank accession no. AF011466.1), PAR1-like GPR43 (GenBank accession no. NM_005306.1), GPR77 (GenBank accession no. NM_018485.1), GPR86 purinergic R (GenBank accession no. NM_023914.1), PAR2 (GenBank accession no. BE965369), HTm4 (GenBank accession no. L35848.1), CD244 NK cell R (GenBank accession no. NM_016382.1), Fibroblast growth factor R 2 (GenBank accession no. NM_022969.1), Low-density lipoprotein R (GenBank accession no. NM_000527.2), Butyrophilin-like R (GenBank accession no. AK025267.1), and Leukocyte Ig-like R A2 (GenBank accession no. NM_006866.1).

[0035] Some of these markers are specific for one cell type only (e.g., HTm4 (GenBank accession no. L35848.1) is preferentially expressed in basophils, and GPR105 purinergic R (GenBank accession no. NM_014879.1) is preferentially expressed in eosinophils). Others are preferentially expressed in two or three cell types (e.g., Ca^{2+} channel type A1 D (GenBank accession no. BE550599), and EMR-1 (GenBank accession no. NM_001974.1) are expressed in both basophils and eosinophils.

[0036] In one aspect, the invention provides methods for screening compounds to identify those that interact with one or more cell type selective markers disclosed herein. Cell type selective markers of the invention include receptors, ion channels (including calcium channels) and other molecules. Accordingly, candidate drug compounds may include one or more receptor binding compounds, ion channel binding compounds (including calcium channel binding compounds) and compounds that bind to one or more of the other molecules. Candidate drug compounds also may include compounds that can be transported across/through one or more ion channels. Candidate drug compounds also may include compounds that block ion transport (e.g., calcium transport).

[0037] In one embodiment, drug compounds may be agents that selectively or specifically bind to one or more cell type selective markers of the invention. For example, drug compounds may be antibodies or aptamers that bind to one or more cell type selective markers of the invention. A marker binding drug may directly inactivate the marker. Alternatively, a marker binding agent may activate the marker. In another embodiment, a marker binding agent may be used to target a second compound to cells that selectively express that marker. For example, the marker binding agent may be conjugated to one or more additional moieties to alter the physiology of the target cell (e.g., to activate, inactivate, or kill the target cell). For example, radioactive moieties, heavy metal moieties, certain enzymes, toxins, and other toxic compounds (e.g., other cytostatic or cytotoxic compounds) may be used to inactivate or kill a target cell. In contrast, activating moieties (e.g., cytokines, growth factors, etc.) may be used to activate a target cell. In certain embodiments, a binding agent (e.g., an antibody, aptamer, etc.) may be bispecific, trispecific, or multispecific (meaning that it binds to two, three, or more cell selective markers). Multispecific binding agents may be better targeting moieties if they bind to a specific combination of markers that is selectively or specifically present on the target cell type. Preferred markers for binding agents are those that are accessible to the binding agents (e.g., extracellular, membrane bound, or transmembrane proteins). However, any of the markers described herein (or combinations thereof) may be used as the invention is not limited in this respect. Antibodies to one or more leukocyte (e.g., granulo-

cyte, granulocyte subtype, mast cell, etc.) marker may be used in several aspects of the invention. Antibodies may be monoclonal, polyclonal, humanized, synthetic, single-chained, etc., or any useful combination thereof. Selective marker binding agents also may be conjugated to one or more detection moieties (e.g., fluorescent, radioactive, enzyme mediated, etc.) and used as detection agents to detect one or more leukocyte cell types.

[0038] In another aspect of the invention, one or more granulocyte-selective markers may be used for diagnostic and/or prognostic applications. For example, a single cell type-selective marker may be used as a marker of the presence of a specific granulocyte type-selective marker in diseased tissue. Similarly, a panel of granulocyte-selective markers (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, etc.) may be used as markers indicating the presence of a specific granulocyte-selective marker in diseased tissue (e.g., in a tumor or cancerous growth). Accordingly, any one or more of Ca^{2+} channel type A1 D (GenBank accession no. BE550599), EMR-1 (GenBank accession no. NM_001974.1), or GPR105 purinergic R (GenBank accession no. NM_014879.1) may be used to detect, for example, the presence of eosinophils in a biological sample. Similarly, one or more markers of the invention may be used to determine the ratio of different granulocyte types in a biological tissue or sample from a subject.

[0039] A biological sample includes, but is not limited to: cells, tissue, body fluid (e.g. blood, serum, etc.). The tissue may be in a subject, obtained from a subject, or may be grown in culture (e.g. from a cell line). A cell or tissue used in the invention can be a blood cell or other cell type. As used herein, cell samples, tissue samples, and/or blood samples, etc., may be obtained using methods well known to those of ordinary skill in the related medical arts. A biological sample may be, for example, a tissue biopsy sample or a biological fluid or solid.

[0040] As used herein, a subject is a mammal, preferably a human, non-human primate, cow, horse, pig, sheep, goat, dog, cat, or rodent. In all embodiments, human subjects are particularly preferred. In some embodiments, the subject is suspected of having a granulocyte disorder. In other embodiments the subject has been diagnosed with a granulocyte disorder.

[0041] The detection of one or more particular granulocyte types or granulocyte-selective markers in a biological sample, or the determination of an abnormal ratio of different cell types in a biological sample, may be useful for disease diagnostic or prognostic purposes. Allergies, cancers and infections are some examples of diseases characterized by an altered proliferation of one or more granulocyte cell type(s). Granulocyte disorders include basophil cell disorders and eosinophil cell disorders. Examples of basophil cell disorders include myeloproliferative disorders such as polycythemia vera and myelofibrosis.

[0042] Examples of basophil cell disorders include asthma, eosinophilic pneumonia, helminthic infestations and Eosinophilic Gastrointestinal Disorders. Examples of Eosinophilic Gastrointestinal Disorders include Eosinophilic Esophagitis (EE), Eosinophilic Gastritis (EG), Eosinophilic Duodenitis (ED), Eosinophilic Colitis (EC), Eosinophilic Gastroenteritis (EGE), and Eosinophilic Ileitis (EI).

[0043] Diagnosis and treatment of mast cell disorders are also encompassed by this invention. Examples of Mast Cell Disorders include Systemic Mastocytosis (with or without cutaneous manifestations such as Urticaria Pigmentosa) such as Aggressive Mastocytosis, Indolent Mastocytosis, Mastocytosis with associated Hematologic Disorder, Mast Cell Leukemia, Cutaneous Mastocytosis such as Urticaria Pigmentosa (UP), Telengiecstasia Macularis Eruptive Perstans (TMEP), Mast Cell Activation Syndrome/Disorder, and Pediatric mast cell disorders such as Solitary Mastocytoma, Urticaria Pigmentosa, and Diffuse Cutaneous Mastocytosis.

[0044] In some embodiments, the detection of an abnormal level of one of more granulocyte-selective marker(s) may be used to determine appropriate drug or therapeutic regimens (e.g., abnormal growth of a particular cell type may suggest the use of one or more drugs that inhibit that growth of, or kill, that particular cell type).

[0045] In another aspect, diagnostic methods of the invention may be used to determine whether an abnormal expression pattern of one or more granulocyte-selective marker(s) is present on a particular granulocyte type. An abnormal pattern may be indicative of a disease (e.g., cancer, allergic response, infection, etc.). An abnormal pattern of expression of a granulocyte-selective marker may be an increase or decrease in the level of expression (at the level of transcription, translation, activity, or a combination of two or more thereof) of one or more granulocyte-specific markers relative to a reference level of expression.

[0046] The reference level may be a level of the same marker(s) in a reference cell or tissue. The reference level may be a level of one or more other granulocyte-selective marker (s). The reference level may the level of expression of one or more markers that are not granulocyte-selective. The reference level may be a predetermined control value. The reference level may be a combination of two or more of the above.

[0047] Levels of expression may be compared to controls. The control may be a predetermined value, which can take a variety of forms. It can be a single value, such as a median or mean. A control value can be established based upon comparative groups (e.g. comparative cell types), such as in cells having normal levels of expression of one or more granulocyte-selective marker. These types of control values can serve as control values for substantially similar cells that are contacted with a treatment compound. In some embodiments of the invention, a control level of expression of a granulocyte selective marker(s) is the level of expression of the granulocyte selective marker(s) in a non-granulocyte cell or tissue.

[0048] In a further aspect of the invention, one or more granulocyte-selective markers may be used for specific cell type detection, selection, and or manipulation. For example, an antibody or specific binding agent (e.g., aptamer etc.) that binds to a granulocyte-selective marker (e.g., a protein, including a membrane bound or a surface protein) may be detectably labeled (e.g., with a fluorescent label, a radioactive label, or any other detectable label or combination thereof) and used to bind to a particular cell type. The detectably labeled antibody (or other binding agent) may be used to detect a particular cell type directly in vivo (e.g., via an MRI, PET, or CAT scan or other in vivo imaging technique) or ex vivo (e.g., via microscopy such as fluorescent microscopy or other ex vivo imaging technique). The detectably labeled antibody (or other binding agent) may be used to detect the presence of markers indicative of particular cell types (e.g., in an assay for nucleic acid, protein, and/or activity levels performed on a processed sample obtained from a biological sample that includes cells or cellular debris). The detectably labeled antibody (or other binding agent) may be used to select (for or against) the presence of certain granulocyte cell

types in a cell preparation (e.g., via a cell sorting technique such as FACS). Accordingly, granulocyte or cell preparations may be enriched or depleted for one or more granulocyte subtypes (e.g., basophil, neutrophil, or eosinophil) or mast cells using methods of the invention. In one embodiment, stem cell preparations may be enriched or depleted for one or more types of granulocyte or granulocyte precursor using one or more granulocyte-selective markers described herein.

[0049] In another aspect, markers of the invention may be used as targets for molecules that alter the function and development of certain granulocyte subtypes (e.g., may change their development path and direct them from one type of granulocyte to another, particularly for stem cells and other precursor cells).

[0050] In yet another aspect of the invention, one or more granulocyte-selective markers may be useful for therapeutic applications and particularly for cell type selective or specific therapies. This can be done by targeting one or more of the granulocyte-selective markers. Accordingly, one or more compounds that bind or interact with one or more cell type-specific markers may be used therapeutically. Treatment methods of the invention may be therapeutic (e.g., they reduce or cure symptoms of a disease) or prophylactic (e.g., they prevent symptoms of the disease).

[0051] The invention also provides for methods for selecting a course of treatment of a subject having or suspected of having a granulocyte disorder. In this aspect of the invention, the selection of the course of treatment involves determining the status of the granulocyte disorder in the subject. As used herein the "status" of a granulocyte disorder means the physiological stage or clinical condition of the cell, tissue, or the subject with the granulocyte disorder. It will be understood by those of ordinary skill that the status may reflect a number of different factors relating to the granulocyte disorder in the cell, tissue, or subject. These factors include, but are not limited to: the genotype of the cell, tissue, or subject, the genetic penetrance of the disorder, the length of time the disease has been manifested in the subject, and individual cell, tissue, and/or subject parameters that define the presentation of the granulocyte disorder in the cell, tissue, or subject. The status of the granulocyte disorder in a subject, cell, or tissue may change over time and thus the determination of a subject, cell, or tissue's status at a first time point may differ from the status of the cell, tissue, or subject's status at a second, subsequent time point.

[0052] The status of granulocyte disorder in a cell, tissue, or subject may be classified using general categories such as early-stage, mid-stage, or late-stage granulocyte disorder and the physiological manifestation of the granulocyte disorder may be generally classified as mild, medium, or severe, with various gradations in between. In some embodiments, the status of the disease means the level of pathogenesis from the disease. Thus, at early stages of a granulocyte disorder, pathogenesis may be mild or non-detectable and at mid and late stages the pathogenesis may be more pronounced. As used herein, the term "pathogenesis" means the clinical and physiological process and effects of the disease.

[0053] Accordingly, aspects of the invention may be used to treat any number of diseases including cancer, allergy, inflammation, infectious diseases, cardiovascular diseases, and other diseases associated with one or more leukocyte cell types (e.g., a mast cell and/or one or more granulocyte subtypes). Methods and compositions described herein in the context of mast cells and granulocytes may by applied to other leukocytes and leukocyte-selective markers that are described in the following examples and figures. For example, one or more $CD4^+$ and/or $CD8^+$ selective cell markers (e.g., with a value of 1.5 or more, 2 or more, 3 or more, 4 or more, 5 or more, in the tables included in the figures) may be used as targets to develop drugs that inactivate $CD4^+$ and/or $CD8^+$ cells and are thereby useful to promote allograft tolerance (e.g., tolerance of cell tissue and/or organ transplants) and/or tolerance of an implanted medical device or artificial structure). In addition, to enhancing transplantation tolerance, methods and compositions that modulate $CD4^+$, $CD8^+$ and/or other leukocytes, may be useful to treat cancer, infection, allergy, and other diseases described herein.

EXAMPLE

[0054] In this study, we have used high density oligonucleotide probe array (GeneChip) to measure the expression levels of approximately 20,000 different transcripts in highly purified cells. These cells were basophils, eosinophils, neutrophils, monocytes ($CD14^+$), T lymphocytes ($CD4^+$ and $CD8^+$ cells), B lymphocytes ($CD19^+$), lung-derived mast cells, cord blood-derived cultured mast cells, and nasal polyp-derived fibroblasts. The GeneChip assay allows the simultaneous measurement of large numbers of transcripts using relatively small numbers of cells. Using this technology, we could even measure triplicate transcriptome levels of basophils, the most rare granulocytes in peripheral blood.

[0055] Cell type-selective transcripts were selected based on the following criteria; (1) the average "normalized AD" expression level of each gene in a certain cell type must be 3-fold or greater than the maximal level in other cell types, and (2) must be significantly ($p<0.01$) greater than that in other cell types. (3) The "AD" expression level provided with "absence" or "marginal" call by GeneChip Suite Software should be observed only once or not at all in the three or four independent experiments (3 experiments for basophils, 4 experiments for eisinophils and neutrophils) using different cell populations performed. (4) For the transcripts preferentially expressed for the two different cell types such as basophils and eosinophils, the average "normalized AD" expression levels in the two cell types should be within 3-fold of each other. Using these standards, we found 83 basophil-selective, 37 eosinophil-selective, 257 neutrophil-selective, 34 basophil-eosinophil-selective, 19 eosinophil-neutrophil-selective, and 17 basophil-neutrophil-selective transcripts. Due to the functional similarity with basophils, mast cell-selective transcripts were also examined, and 63 mast cell-selective and 11 mast cell-basophil-selective transcripts were also detected (Table 1, and FIGS. **6**A-**6**R). Since mast cells, basophils and eosinophils play similar roles in allergic inflammation, the transcripts preferentially expressed for the three granulocytes by comparing their average "normalized AD" levels to other leukocytes. Thirty-four transcripts were then selected; however, most of them were overlapped with the transcripts listed in FIGS. **6**A-**6**R. Only four transcripts (MYB, SAMSN1, BACE2, and CASP3) were found not overlapped, and they were not receptors or ion channels.

[0056] Among the 491 granulocyte-selective transcripts listed in FIGS. **6**A-**6**R, 4 ion channels, 19 GPR and 28 other receptors were further selected (FIG. **3**). When plural transcripts obtained by different probe sets had identical Genebank or Unigene accession numbers (http://www.ncbi.nlm.nih.gov/), the transcript showing the highest expression level was selected.

Ion Channels and Receptors Preferentially Expressed by Granulocytes other than Neutrophils

[0057] Eosinophils, basophils and mast cells play an important role in the pathogenesis of allergic diseases, but do not play an essential role in killing microbes except for nematodes. On the other hand, neutrophils play a crucial role in killing microbes such as bacteria. Caution should be taken in regulating neutrophil function even in the case of neutrophil-induced inflammation. Therefore, the molecules present only in granulocytes except for neutrophils would be important pharmaceutical targets for allergic disorders.[1,2]

[0058] Among the 51 granulocyte-selective transcripts for ion channels and receptors, we identified 17 granulocyte-selective transcripts that have not been reported for their selective expression (shown in bold letters in FIG. **3**). Of these 17 transcripts, eight were preferentially expressed by granulocytes other than neutrophils. Among these eight transcripts, the two transcripts for fibroblast growth factor receptor 2 and low density lipoprotein receptor were found to be expressed by multiple tissue cell types (shown at the Web site http://www.lsbm.org/index_e.html), which displays genomic expression of 55 different human tissue cells such as brain, heart and lung cells using the same experimental system. Affymetrix, U133A as ourts. Thus, they may not be suitable as a drug target because important organs that are unrelated to allergic inflammation (such as the brain) express it. Among the six novel transcripts found to be preferentially expressed by granulocytes except for neutrophils, we focus on the following four transcripts expressed by granulocytes including basophils. They were Ca^{2+} channel (CACNA1D), a prostaglandin E receptor, (EP3A2), epidermal growth factor-like module-containing mucin-like receptor (EMR) 1 (EMR1), and HTm4 (MS4A3).

[0059] Basophils are the rarest granulocytes present in human peripheral blood and as such their complete transcriptional profiles remain unclear and no basophil-selective transcripts have previously been reported.[21] Although eosinophils and mast cells have been considered as important therapeutic targets for allergic diseases for a long time, recent studies suggest the importance of basophils in pathogenesis of severe allergic diseases such as fatal asthma.[2,22] Therefore, we further examined the selective expression of these four basophil-, or basophil-eosinophil-selective transcripts by using real-time RT-PCR. As shown in the FIG. **1**, including a known molecule preferentially expressed by neutrophils, aquaporin 9,[23] the results obtained with GeneChip assay were confirmed by using this highly accurate and reproducible method.[24]

[0060] Among these four molecules, we could obtain a suitable antibody against HTm4, which is a member of a family of four transmembrane-proteins which include CD 20 and high affinity Fc receptor for IgE (FcϵRI) β-chain.[25] Genetics provided evidence for the existence of multiple loci relevant to atopic asthma on chromosome 11q13, including HTm4.[26] Most recently, we have published data identifying HTm4 as a hematopoietic cell cycle regulator.[27] Using specific antibody against HTm4, we could detect the expression of HTm4 at the protein level in basophils (FIG. **2**). To confirm whether these ion channels and receptors could be potential drug targets for diseases involving basophil activation, the amount of molecules expressed by various cell types should be quantified and the effect of any identified antagonists should be tested on the cell types found to express these molecules.

[0061] As has been well documented and expected, Fc ϵ RI β, IL-3 receptors, IL-5 receptors, chemokine receptor CCR3,[1,2] sialic acid binding Ig-like lectin (Siglec)-8,[28] Siglec-6,[15] histamine H4 receptor[29] and chemoattractant receptor-homologous molecule expressed on Th2 cells (CRTH2)[30] were preferentially expressed by basophils and/or eosinophils or mast cells. These consistent observations strengthened the reliability of the present methods and research strategy. Indeed, the antibody against Siglec-8 can induce selective apoptosis of eosinophils, and is expected to be useful therapeutically.[28]

Ion Channels and Receptors Preferentially Expressed by Granulocytes Including Neutrophils

[0062] Of the 17 transcripts that have not been reported as granulocyte-selective, nine were preferentially expressed by granulocytes including neutrophils. Pharmaceutical targets of selective granulocyte transcripts should treat inflammatory diseases without affecting the function of important organs that are unrelated to inflammation as well as the function of lymphocytes. However, four of the nine neutrophil-selective transcripts were expressed by multiple organ tissues. One of the four neutrophil-selective transcripts encoded proteinase-activated receptor (PAR)-2, a receptor for mast cell tryptase, which is linked to the pathogenesis of allergic diseases such as asthma.[31,32] PAR-2 transcripts are also abundantly expressed by tissue types including skin and intestine which are often the target organs for allergic diseases. But the development of PAR-2 antagonists for use as anti-allergic drugs may be unsuitable because it may down regulate neutrophil function and thereby induce bacterial infection.

General Discussion

[0063] We identified 51 granulocyte-selective genes for ion channels and receptors by examining approximately 20,000 kinds of transcripts derived from 16,000 genes from 10 different types of cells using U133A GeneChip, which covers approximately half of the genes present in the human genome. The majority of these transcripts encoded molecules known or expected to be granulocyte subtype-selective such as the IL-3 receptor and Fc ϵ receptors.

[0064] Mast cells expressed low levels of Fc ϵ RI α compared to basophils, and that even neutrophils expressed a substantial level of the receptor (FIG. **3**). This raises the possibility that GeneChip assay may not be suitable for detecting selective molecules. In the present study, however, only the GeneChip data obtained using cord blood-derived mast cells and lung mast cells could be employed due to the strict data selection based on the RNA quality (see Methods). As has been reported,[14,33] peripheral blood-derived cultured mast cells or skin-derived mast cells expressed approximately 10-fold Fc ϵ RI α mRNA compared to cord blood-derived mast cells (data not shown). Also, as shown in FIGS. **6**A-**6**R, only 2 of the 4 neutrophil samples expressed Fc ϵ RI α mRNA. This may be explained by the observation that only neutrophils obtained from some allergic donors express the molecule.[34]

[0065] We unexpectedly found 17 granulocyte-selective transcripts including HTm4. Basophil- and/or eosinophil-selective transcripts identified in our study could be potential

therapeutic targets for allergic diseases because these granulocytes play a crucial role in allergic inflammation.[1,2] Granulocyte-selective transcripts could also be drug targets for other inflammatory diseases such as systemic vasculitis.[3,4] Analysis of cell type-selective transcripts from database searches is expected to minimize the efforts required for drug discovery. The public database (http)://www.lsbm.org/index_e.html) shows that some granulocyte-selective transcripts (18 out of 51) detected in our study are abundantly expressed by multiple (more than 3) organ tissue cell types using the same GeneChip U133A probe array. Thus, the safety of any candidate drug must be evaluated by comparing its efficacy (on granulocytes) with its toxicity (to organs). Six out of the 17 novel granulocyte-selective molecules may be excluded from drug development due to their expression in multiple organs unrelated to the diseases. Thus, our approach has identified 11 receptors and ion channels with therapeutic potential. Especially, among the 11 receptors and ion channels, seven were basophil- and/or eosinophil-selective and were not expressed by other organs, indicating that they may be potential targets for anti-allergic drugs.

[0066] Finally, it should be stressed that basophils, the rarest leukocytes, have recently been found to play a more crucial role than we ever proposed in the pathogenesis of intractable allergic diseases such as fatal asthma.[35,36] Thus, targeting basophil receptors and ion channels such as HTm4 and Ca^{2+} channel CACNA1D is particularly expected for the future drug discovery. The importance of molecules known to be expressed by basophils may be reevaluated regarding its selectivity. Freshly-isolated resting basophils expressed the highest level of IL-4 compared to other cell types. Because the basophil purification procedure requires more isolation steps, ex vivo manipulation may activate the cells. However, it should also be noted that basophils have been recently found as the major source of IL-4 at least in asthma models.[37,38]

Materials and Methods

Purification of Leukocytes

[0067] All human subjects in this study provided written, informed consent, and the Ethical Review Boards at the relevant hospitals (National Center for Child Health and Development, and Jikei University School of Medicine) approved the study. The subjects used in this study were all healthy volunteers, especially having no allergic diseases.

[0068] Granulocytes and mononuclear cells were separated from venous blood of normal volunteers. Human basophils were semipurified by means of Percoll (Pharmacia, Uppsala, Sweden) density gradient centrifugation, and the cells were further purified by negative selection through use of a MACS Basophil Isolation Kit (Miltenyi BioTech, Bergisch-Gladbach, Germany), as described previously.[17] Eosinophils were isolated by using Percoll (1.090 g/mL) density centrifugation. The eosinophils were further purified by negative selection with anti-CD16-bound micromagnetic beads, as described previously.[18] Neutrophils were isolated by using Percoll (1.085 g/mL) density centrifugation and further purified by negative selection using anti-CD81 antibody and antimouse IgG-bound micromagnetic beads to eliminate contaminating eosinophils. These granulocytes purified from human peripheral blood were spun down onto slide glass by Cytospin II (Shandon Southern Instruments, Inc., Sewickley, Pa.). The purity of these cells was evaluated based on 500 cells stained with May-Grünwald and Giemsa solutions.

[0069] For preparation of lymphocytes and monocytes, peripheral blood mononuclear cells (PBMNC) were isolated by centrifugation on lymphocyte separation medium (Organon Teknika Corp., Durham, N.C.). Monocytes ($CD14^+$ cells) were prepared using magnetic beads-conjugated $CD14^+$ antibody (CD14 MicroBeads; Miltenyi Biotec) from PBMNC. $CD4^+$ and $CD8^+$ cells were also respectively sorted using magnetic beads-conjugated $CD4^+$ (CD4 MicroBeads; Miltenyi Biotec) and $CD8^+$ antibodies (CD8 MicroBeads; Miltenyi Biotec) from PBMNC after depletion of $CD14^+$ cells with MACS CD14 MicroBeads (Miltenyi Biotec). The purity of $CD4^+$, $CD8^+$ and $CD14^+$ cells was evaluated by staining the magnetic beads—conjugated cells compared to feasible control cell preparations such as unpurified cells with FITC-labeled goat anti-mouse Immunoglobulin (BD Pharmingen, Tokyo, Japan). Peripheral B cells were purified by a combination of negative (MicroBeads—conjugated antibodies to CD3, CD7, CD14, CD42b, and CD56; Miltenyi Biotec) and positive (CD19 MicroBeads; Miltenyi Biotec) selection using MicroBeads (Miltenyi Biotec). To obtain platelet rich plasma, blood samples were mixed with 3.8% (w/v) sodium citrate solution (9:1) and centrifuged at 260×g for 15 min. at 20° C. To remove any contaminating erythrocytes and leukocytes, the plasma was centrifuged again at 260×g for 15 min.

[0070] Human mast cells were derived from cord blood $CD34^+$ progenitor cells as described previously.[11-14] Briefly, progenitor cells purified from peripheral blood by $CD34^+$ isolation kits (Miltenyi Biotec), were cultured in Iscove's modified Dulbecco medium supplemented with 1% insulin-transferrin-selenium supplements (Life Technologies), 50 μM 2-mercaptoethanol, antibiotics, and 2% fetal calf serum in the presence of 100 ng/ml stem cell factor and 50 ng/ml IL-6. After 11 to 14 weeks of culture, tryptase positive cells represented more than 99% of the cells.

Purification of Human Lung Mast Cells and Nasal Polyp-derived Fibroblasts

[0071] Normal human lung tissue dissected during surgery was obtained macroscopically after informed consent. Human lung mast cells were dispersed from chopped lung specimens by an enzymatic procedure and were purified by magnetic bead affinity selection using the mAb anti-kit, YB5. B8 (BD PharMingen, San Diego, Calif.) as described previously.[19] The cells were further cultured in the presence of SCF and interleukin 6 (IL-6) for several weeks. Human nasal polyp-derived fibroblasts were obtained as previously reported.[20]

GeneChip Expression Analysis

[0072] Human genome-wide gene expression was examined using the Human Genome U133A probe array (GeneChip, Affymetrix, Santa Clara, Calif.), which contains the oligonucleotide probe set for 22,000 full-length genes. Experiments were performed in accordance with the manufacturer's protocol (Expression Analysis Technical Manual) and previous reports.[11-14] Total RNA (3-10 μg) was extracted from 10^7 cells. Double-stranded cDNA was synthesized using a SuperScript Choice system (Life Technologies) and a T7-(dT)24 primer (Amersham Pharmacia Biotech, Bucking-

hamshire, UK). The cDNA was subjected to in vitro transcription in the presence of biotinylated nucleoside triphosphates using a BioArray high-yield RNA transcript labeling kit (Enzo Diagnostics, Farmingdale, N.Y.). The biotinylated cRNA was hybridized with a probe array for 16 h at 45° C. In some experiments as indicated in the supplementary table, biotinylated cRNA was prepared using two-cycles of cDNA synthesis and in vitro transcription for target amplification was performed according to the manufacturer's "The Small Sample Labeling Protocol version II" (Affymetrix, Inc). For the latter protocol, we employed 100 ng total RNA. After washing, the hybridized, biotinylated cRNA was stained with streptavidin-phycoerythrin (Molecular Probes, Eugene, Oreg.) and then scanned with a HP gene array scanner. The fluorescence intensity of each probe was quantified using a computer program, GeneChip Analysis Suite 5.0 (Affymetrix). The expression level of single mRNA was determined as the average fluorescence intensity among the intensities obtained by 11 paired (perfect-matched and single nucleotide-mismatched) probes. If the intensities of mismatched probes were very high, gene expression was judged to be absent, even if a high average fluorescence was obtained with the GeneChip Analysis Suite 5.0 program. The level of gene expression was determined as the average difference (AD) using the GeneChip software. Each AD level was then normalized by dividing it with the median value of 22,283 AD levels obtained in an experiment ("normalized AD" level).

Real-Time Reverse Transcriptase (RT)-PCR

[0073] Total RNA was isolated using Isogen (Nippon gene, Tokyo, Japan) according to the manufacturer's instructions and quantified by measuring the absorbance at 260 nm. RNA was subsequently treated with DNase I (Life Technologies) reverse transcribed using Superscript II reverse transcriptase (Life Technologies). Real-time RT-PCR was performed 10 ng cDNA in 25 μl of final volume using the primers and probes supplied by "Assays-on-Demand Gene Expression system" (PE Applied Biosystem) according to the manufacturer's instructions. Measurement of gene expression was performed using the ABI PRISM 7700 Sequence Detector. The expression level of each gene was normalized to a GAPDH.

Staining of Basophils with Anti-HTm4

[0074] Basophils purified from human peripheral blood with Basophil Isolation Kit (Miltenyi Biotec) were spun down onto slide glass by Cytospin II (Shandon Southern Instruments Inc., Sewickley, Pa.). Cells were fixed with aceton for 1 minute and then blocked in goat serum in 50 mm TRS-Cl, pH 7.4 for 1 hour. Cells were further incubated for 2 hours with 2 μg/ml of the polyclonal antibody rabbit anti-hHTm4. Cells were then washed three times with PBS and incubated with a secondary antibody, highly cross-adsorbed Alexa Fluor® 546-conjugated goat anti-rabbit IgG (H+L) (Red) (Molecular Probes, Eugene, Oreg.) for one hour. After three PBS washes, air dried cells were further mounted using the Prolong Anti-Fade Kit (Molecular Probes, Eugene, Oreg.). Slides were scanned by Zeiss Laser Scanning Microscope 5 Pascal (Carl Zeiss Microimaging Inc, Thornwood, N.Y.).

Purity and Viability of the Leukocytes, and RNA Quality

[0075] We used leukocyte samples in this study only if the purity of each cell type was at least 98%, but there are >0.5% contaminated cells in any of the samples. We could not evaluate the purity of $CD19^+$ cells and platelets due to lack of feasible controls or methods. However, specific transcript markers for non-granulocytes (CD4, CD8, CD14, CD19, IgG, etc.) as well as granulocyte subtype-specific transcripts were reasonably expressed by each leukocyte type as shown in FIGS. **6**A-**6**R. Regarding the viability, we qualified the RNA before GeneChip assay using Array Quality Metrics Comparisons Software (Affymetrix) as well as trypan blue staining (they were always >95% viable), since RNAse-rich granules derived from degenerating cells rapidly destroy RNA transcripts. Briefly, to evaluate the quality of RNA, the ratio of 3'-probe set and 5'-probe set of housekeeping genes were compared as shown in FIGS. **6**A-**6**R. According to the above software's guidance, the ratio of >2:1 at standard sample (5 μg total RNA) protocol and that of >10:1 at small sample (50 ng total RNA) protocol were recommended. As shown in FIGS. **6**A-**6**R, the cells used in the present study had the appropriate ratios of 3'-probe set and 5'-probe set of housekeeping genes, suggesting that these cells were highly viable.

Statistical Analysis

[0076] Since logarithmic "normalized AD" levels were normally distributed within each group, unpaired parametric Student's two-tailed t-test was employed to analyze the data on a logarithmic scale.

TABLE 1

Representative cell type-selective transcripts in granulocytes

Accession #[a]	Transcript	S.I.[b]	Normalized AD level
	Basophil-selective		
NM_000589.1	IL-4	73.3	13.3
L35848.1	HTm4	38.2	132.1
BC005912.1	Fc ϵ RI α	12.7	218.9
	Eosinophil-selective		
NM_001140.1	Arachidonate 15-lipoxygenase	74.1	18.3
NM_024703.1	FLJ22593	19.1	29.1
NM_014442.1	Siglec-8	9.8	16.9
	Neutrophil-selective		
NM_004633.1	IL-1 R, type II	127.9	51.5
U73191.1	inward rectifier K^+ channel Kir1.3	107.5	98
NM_001557.1	CXCR2 (IL-8 receptor β)	39.3	105.2
	Mast cell-selective		
AF206667.1	tryptase β	84.3	159.4
NM_001911.1	cathepsin G	51.5	72.1
BC005929.1	major basic protein	31.6	72.5
	Basophil-eosinophil-selective		
M75914.1	IL-5R α	42.8	19.4(B), 29.3(E)
NM_004778.1	CRTH2	16.6	23.9(B), 38.1(E)
NM_001828.3	Charcot-Leyden crystal protein	15.2	229.2(B), 198.6(E)
	Eosinophil-neutrophil-selective		
NM_005306.1	GPR 43 (PAR1-like)	21.7	11.7(E), 32.9(N)
NM_004668.1	DHHC domain containing 18	6.6	16.2(E), 44.5(N)
	Basophil-neutrophil-selective		
NM_016006.1	CGI-58 protein	5.8	12.6(B), 21.2(N)

TABLE 1-continued

Representative cell type-selective transcripts in granulocytes

Accession #[a]	Transcript	S.I.[b]	Normalized AD level
	Basophil-mast cell-selective		
NM_001870.1	carboxypeptidase A3	59.2	111.7(M), 137.3(B)
NM_002529.2	TRK neurotrophin receptor	34.7	3.1(M), 7 (B)
NM_000139.1	Fc ϵ RI β	21.2	22.2(M), 43.8(B)

[a]The GenBank accession number (http://www.ncbi.nlm.nih.gov).
[b]Selectivity index (S.I.) was calculated by comparing the "normalized AD" level in a cell type or of two cell types with the maximal gene expression level of the other 8 or 9 cell types. The complete list of the genes having >3 S.I. is shown in Supplementary Table 1.

[0077] FIGS. **6**A-**6**R show the complete list of granulocyte subtype-selective transcripts. Selectivity index (S.I.) was calculated by comparing the "normalized AD" level of a cell type or of two cell types with the maximal gene expression level of the other 8 or 9 cell types including platelets (P1), $CD4^+$ cells (CD4), $CD8^+$ cells (CD8), $CD14^+$ cells (CD14), $CD19^+$ cells (CD19) and nasal polyp-derived cultured fibroblasts (Fb). Transcripts having S.I. >3-fold were shown in FIGS. **6**A-**6**R A-H. A. Basophil (Ba)-selective transcripts. B. Eosinophil (Eo)-selective transcripts. C. Neutrophil (Ne)-selective transcripts. D. Mast cell (MC)-selective transcripts. E. Basophil and eosinophil-selective transcripts. F. Eosinophil and neutrophil-selective transcripts. G. Basophil and neutrophil-selective transcripts. H Mast cell and basophil-selective transcripts. I. Raw AD levels for the median values used to normalize the raw AD levels, and the housekeeping genes. When the result was accompanied by presence call, it was shown as a bold numeral. Italic numerals show that the raw AD levels were associated with absence call by the GeneChip analysis software. 1. Abbreviations used in the tables were (small); the results obtained by the small sample protocol (see materials and methods), R; receptor, and ICN; ion channel.

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[0078] Useful techniques and compositions described in the references cited herein are incorporated herein by reference. In addition, U.S. Ser. No. 60/549,865, filed on Mar. 3, 2004, the benefit of the filing date of which is claimed under 35 U.S.C. §119(e), is incorporated herein by reference in its entirety.

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15 20 25

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Met Ser Lys Ser Gly His Ser Asn Val Arg Ile Asp Lys Val Asp Gly
30 35 40 45

ata tac cta ctc tac ctg caa gac ctg tgg acc aca gtt atc gac atg 253
Ile Tyr Leu Leu Tyr Leu Gln Asp Leu Trp Thr Thr Val Ile Asp Met
50 55 60

aag tgg aga tac aaa ctc acc ctg ttc gct gcc act ttt gtg atg acc 301
Lys Trp Arg Tyr Lys Leu Thr Leu Phe Ala Ala Thr Phe Val Met Thr
65 70 75

tgg ttc ctt ttt gga gtc atc tac tat gcc atc gcg ttt att cat ggg 349
Trp Phe Leu Phe Gly Val Ile Tyr Tyr Ala Ile Ala Phe Ile His Gly
80 85 90

gac tta gaa ccc gat gag ccc att tca aat cat acc ccc tgc atc atg 397
Asp Leu Glu Pro Asp Glu Pro Ile Ser Asn His Thr Pro Cys Ile Met
95 100 105

aaa gtg gac tct ctc act ggg gcg ttt ctc ttt tcc ctg gaa tcc cag 445
Lys Val Asp Ser Leu Thr Gly Ala Phe Leu Phe Ser Leu Glu Ser Gln
110 115 120 125

aca acc att ggc tat gga gtc cgt tcc atc aca gag gaa tgt cct cat 493
Thr Thr Ile Gly Tyr Gly Val Arg Ser Ile Thr Glu Glu Cys Pro His
130 135 140

gcc atc ttc ctg ttg gtt gct cag ttg gtc atc acg acc ttg att gag 541
Ala Ile Phe Leu Leu Val Ala Gln Leu Val Ile Thr Thr Leu Ile Glu
145 150 155

atc ttc atc acc gga acc ttc ctg gcc aaa atc gcc aga ccc aaa aag 589
Ile Phe Ile Thr Gly Thr Phe Leu Ala Lys Ile Ala Arg Pro Lys Lys
160 165 170

cgg gct gag acc atc aag ttc agc cac tgt gca gtc atc acc aag cag 637
Arg Ala Glu Thr Ile Lys Phe Ser His Cys Ala Val Ile Thr Lys Gln
175 180 185

aat ggg aag ctg tgc ttg gtg att cag gta gcc aat atg agg aag agc 685
Asn Gly Lys Leu Cys Leu Val Ile Gln Val Ala Asn Met Arg Lys Ser
190 195 200 205

ctc ttg att cag tgc cag ctc tct ggc aag ctc ctg cag acc cac gtc 733
Leu Leu Ile Gln Cys Gln Leu Ser Gly Lys Leu Leu Gln Thr His Val
210 215 220

acc aag gag ggg gag cgg att ctc ctc aac caa gcc act gtc aaa ttc 781
Thr Lys Glu Gly Glu Arg Ile Leu Leu Asn Gln Ala Thr Val Lys Phe
225 230 235

cac gtg gac tcc tcc tct gag agc ccc ttc ctc att ctg ccc atg aca 829
His Val Asp Ser Ser Ser Glu Ser Pro Phe Leu Ile Leu Pro Met Thr
240 245 250

ttc tac cat gtg ctg gat gag acg agc ccc ctg aga gac ctc aca ccc 877
Phe Tyr His Val Leu Asp Glu Thr Ser Pro Leu Arg Asp Leu Thr Pro

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    255                 260                 265

caa aac cta aag gag aag gag ttt gag ctt gtg gtc ctc ctc aat gcc      925
Gln Asn Leu Lys Glu Lys Glu Phe Glu Leu Val Val Leu Leu Asn Ala
270                 275                 280                 285

act gtg gaa tcc acc agc gct gtc tgc cag agc cga aca tct tat atc      973
Thr Val Glu Ser Thr Ser Ala Val Cys Gln Ser Arg Thr Ser Tyr Ile
                290                 295                 300

cca gag gaa atc tac tgg ggt ttt gag ttt gtg cct gtg gta tct ctc     1021
Pro Glu Glu Ile Tyr Trp Gly Phe Glu Phe Val Pro Val Val Ser Leu
            305                 310                 315

tcc aaa aat gga aaa tat gtg gct gat ttc agt cag ttt gaa cag att     1069
Ser Lys Asn Gly Lys Tyr Val Ala Asp Phe Ser Gln Phe Glu Gln Ile
        320                 325                 330

cgg aaa agc cca gat tgc aca ttt tac tgt gca gat tct gag aaa cag     1117
Arg Lys Ser Pro Asp Cys Thr Phe Tyr Cys Ala Asp Ser Glu Lys Gln
    335                 340                 345

caa ctc gag gag aag tac agg cag gag gat cag agg gaa aga gaa ctg     1165
Gln Leu Glu Glu Lys Tyr Arg Gln Glu Asp Gln Arg Glu Arg Glu Leu
350                 355                 360                 365

agg aca ctt tta tta caa cag agc aat gtc tga tcacaggggc gccatccagg   1218
Arg Thr Leu Leu Leu Gln Gln Ser Asn Val
                370                 375

tttaaccctg caagctgttt ccacatcaga actcccttca aacacaaaga ttgctgtgaa   1278

aacgaaaatg tgtagacgca ctctcaaaaa ctgcacggac atacaaaatc aatcttttcc   1338

tttgatcttg tggctaaacc agcatttctg tgtttgagag atttcctgtt aggtgcttcg   1398

tctgaaagtg aactctcata attcaaattg tataaaataa agctacattt ctaagagctt   1458

ggtgtagggc aattggaata atgtcctgtt agataaacag acatttagca atgctgacat   1518

taaaaggaaa tgtatttcta tacaagatta ttagctgtaa tacaagatat ttatttaacc   1578

aatgacctta tggctgagag ttgaattgtg gttca                              1613


<210> SEQ ID NO 3
<211> LENGTH: 375
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 3

Met Asp Ala Ile His Ile Gly Met Ser Ser Thr Pro Leu Val Lys His
1               5                   10                  15

Thr Ala Gly Ala Gly Leu Lys Ala Asn Arg Pro Arg Val Met Ser Lys
            20                  25                  30

Ser Gly His Ser Asn Val Arg Ile Asp Lys Val Asp Gly Ile Tyr Leu
        35                  40                  45

Leu Tyr Leu Gln Asp Leu Trp Thr Thr Val Ile Asp Met Lys Trp Arg
    50                  55                  60

Tyr Lys Leu Thr Leu Phe Ala Ala Thr Phe Val Met Thr Trp Phe Leu
65                  70                  75                  80

Phe Gly Val Ile Tyr Tyr Ala Ile Ala Phe Ile His Gly Asp Leu Glu
                85                  90                  95

Pro Asp Glu Pro Ile Ser Asn His Thr Pro Cys Ile Met Lys Val Asp
            100                 105                 110

Ser Leu Thr Gly Ala Phe Leu Phe Ser Leu Glu Ser Gln Thr Thr Ile
        115                 120                 125
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Gly Tyr Gly Val Arg Ser Ile Thr Glu Glu Cys Pro His Ala Ile Phe
    130                 135                 140

Leu Leu Val Ala Gln Leu Val Ile Thr Thr Leu Ile Glu Ile Phe Ile
145                 150                 155                 160

Thr Gly Thr Phe Leu Ala Lys Ile Ala Arg Pro Lys Lys Arg Ala Glu
                165                 170                 175

Thr Ile Lys Phe Ser His Cys Ala Val Ile Thr Lys Gln Asn Gly Lys
            180                 185                 190

Leu Cys Leu Val Ile Gln Val Ala Asn Met Arg Lys Ser Leu Leu Ile
        195                 200                 205

Gln Cys Gln Leu Ser Gly Lys Leu Leu Gln Thr His Val Thr Lys Glu
    210                 215                 220

Gly Glu Arg Ile Leu Leu Asn Gln Ala Thr Val Lys Phe His Val Asp
225                 230                 235                 240

Ser Ser Ser Glu Ser Pro Phe Leu Ile Leu Pro Met Thr Phe Tyr His
                245                 250                 255

Val Leu Asp Glu Thr Ser Pro Leu Arg Asp Leu Thr Pro Gln Asn Leu
            260                 265                 270

Lys Glu Lys Glu Phe Glu Leu Val Val Leu Leu Asn Ala Thr Val Glu
        275                 280                 285

Ser Thr Ser Ala Val Cys Gln Ser Arg Thr Ser Tyr Ile Pro Glu Glu
    290                 295                 300

Ile Tyr Trp Gly Phe Glu Phe Val Pro Val Val Ser Leu Ser Lys Asn
305                 310                 315                 320

Gly Lys Tyr Val Ala Asp Phe Ser Gln Phe Glu Gln Ile Arg Lys Ser
                325                 330                 335

Pro Asp Cys Thr Phe Tyr Cys Ala Asp Ser Glu Lys Gln Gln Leu Glu
            340                 345                 350

Glu Lys Tyr Arg Gln Glu Asp Gln Arg Glu Arg Glu Leu Arg Thr Leu
        355                 360                 365

Leu Leu Gln Gln Ser Asn Val
    370                 375


<210> SEQ ID NO 4
<211> LENGTH: 5397
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (384)..(1667)

<400> SEQUENCE: 4

gcgcactgga gccctggcca gcgcgcagcc ttcccggcgc cggcgggctg ggtcttggga     60

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acccccccact tccactccat gtccccatgc tcctgcgcca gcaacaggac atgttctctg    180

gatgtcagct gagtcattaa agtaactctg catgtcagta gacagacctt ggtagaacca    240

caaggctccc agagacaccc atctctcctc atttttttgg tgtgtgtgtc ttcaccgaac    300

attcaaaact gtttctccaa agcgttttgc aaaaactcag actgttttcc aaagcagaag    360

cactggagtc cccagcagaa gcg atg ggc agt gtg cga acc aac cgc tac agc    413
                          Met Gly Ser Val Arg Thr Asn Arg Tyr Ser
                          1               5                   10

atc gtc tct tca gaa gaa gac ggt atg aag ttg gcc acc atg gca gtt      461
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Ile Val Ser Ser Glu Glu Asp Gly Met Lys Leu Ala Thr Met Ala Val
                15                  20                  25

gca aat ggc ttt ggg aac ggg aag agt aaa gtc cac acc cga caa cag      509
Ala Asn Gly Phe Gly Asn Gly Lys Ser Lys Val His Thr Arg Gln Gln
            30                  35                  40

tgc agg agc cgc ttt gtg aag aaa gat ggc cac tgt aat gtt cag ttc      557
Cys Arg Ser Arg Phe Val Lys Lys Asp Gly His Cys Asn Val Gln Phe
        45                  50                  55

atc aat gtg ggt gag aag ggg caa cgg tac ctc gca gac atc ttc acc      605
Ile Asn Val Gly Glu Lys Gly Gln Arg Tyr Leu Ala Asp Ile Phe Thr
    60                  65                  70

acg tgt gtg gac att cgc tgg cgg tgg atg ctg gtt atc ttc tgc ctg      653
Thr Cys Val Asp Ile Arg Trp Arg Trp Met Leu Val Ile Phe Cys Leu
75                  80                  85                  90

gct ttc gtc ctg tca tgg ctg ttt ttt ggc tgt gtg ttt tgg ttg ata      701
Ala Phe Val Leu Ser Trp Leu Phe Phe Gly Cys Val Phe Trp Leu Ile
                95                  100                 105

gct ctg ctc cat ggg gac ctg gat gca tcc aaa gag ggc aaa gct tgt      749
Ala Leu Leu His Gly Asp Leu Asp Ala Ser Lys Glu Gly Lys Ala Cys
            110                 115                 120

gtg tcc gag gtc aac agc ttc acg gct gcc ttc ctc ttc tcc att gag      797
Val Ser Glu Val Asn Ser Phe Thr Ala Ala Phe Leu Phe Ser Ile Glu
        125                 130                 135

acc cag aca acc ata ggc tat ggt ttc aga tgt gtc acg gat gaa tgc      845
Thr Gln Thr Thr Ile Gly Tyr Gly Phe Arg Cys Val Thr Asp Glu Cys
    140                 145                 150

cca att gct gtt ttc atg gtg gtg ttc cag tca atc gtg ggc tgc atc      893
Pro Ile Ala Val Phe Met Val Val Phe Gln Ser Ile Val Gly Cys Ile
155                 160                 165                 170

atc gat gct ttc atc att ggc gca gtc atg gcc aag atg gca aag cca      941
Ile Asp Ala Phe Ile Ile Gly Ala Val Met Ala Lys Met Ala Lys Pro
                175                 180                 185

aag aag aga aac gag act ctt gtc ttc agt cac aat gcc gtg att gcc      989
Lys Lys Arg Asn Glu Thr Leu Val Phe Ser His Asn Ala Val Ile Ala
            190                 195                 200

atg aga gac ggc aag ctg tgt ttg atg tgg cga gtg ggc aat ctt cgg     1037
Met Arg Asp Gly Lys Leu Cys Leu Met Trp Arg Val Gly Asn Leu Arg
        205                 210                 215

aaa agc cac ttg gtg gaa gct cat gtt cga gca cag ctc ctc aaa tcc     1085
Lys Ser His Leu Val Glu Ala His Val Arg Ala Gln Leu Leu Lys Ser
    220                 225                 230

aga att act tct gaa ggg gag tat atc cct ctg gat caa ata gac atc     1133
Arg Ile Thr Ser Glu Gly Glu Tyr Ile Pro Leu Asp Gln Ile Asp Ile
235                 240                 245                 250

aat gtt ggg ttt gac agt gga atc gat cgt ata ttt ctg gtg tcc cca     1181
Asn Val Gly Phe Asp Ser Gly Ile Asp Arg Ile Phe Leu Val Ser Pro
                255                 260                 265

atc act ata gtc cat gaa ata gat gaa gac agt cct tta tat gat ttg     1229
Ile Thr Ile Val His Glu Ile Asp Glu Asp Ser Pro Leu Tyr Asp Leu
            270                 275                 280

agt aaa cag gac att gac aac gca gac ttt gaa atc gtg gtc ata ctg     1277
Ser Lys Gln Asp Ile Asp Asn Ala Asp Phe Glu Ile Val Val Ile Leu
        285                 290                 295

gaa ggc atg gtg gaa gcc act gcc atg acg aca cag tgc cgt agc tct     1325
Glu Gly Met Val Glu Ala Thr Ala Met Thr Thr Gln Cys Arg Ser Ser
    300                 305                 310

tat cta gca aat gaa atc ctg tgg ggc cac cgc tat gag cct gtg ctc     1373
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Tyr Leu Ala Asn Glu Ile Leu Trp Gly His Arg Tyr Glu Pro Val Leu
315                 320                 325                 330

ttt gaa gag aag cac tac tac aaa gtg gac tat tcc agg ttc cac aaa     1421
Phe Glu Glu Lys His Tyr Tyr Lys Val Asp Tyr Ser Arg Phe His Lys
                335                 340                 345

act tac gaa gtc ccc aac act ccc ctt tgt agt gcc aga gac tta gca     1469
Thr Tyr Glu Val Pro Asn Thr Pro Leu Cys Ser Ala Arg Asp Leu Ala
            350                 355                 360

gaa aag aaa tat atc ctc tca aat gca aat tca ttt tgc tat gaa aat     1517
Glu Lys Lys Tyr Ile Leu Ser Asn Ala Asn Ser Phe Cys Tyr Glu Asn
        365                 370                 375

gaa gtt gcc ctc aca agc aaa gag gaa gac gac agt gaa aat gga gtt     1565
Glu Val Ala Leu Thr Ser Lys Glu Glu Asp Asp Ser Glu Asn Gly Val
    380                 385                 390

cca gaa agc act agt acg gac acg ccc cct gac ata gac ctt cac aac     1613
Pro Glu Ser Thr Ser Thr Asp Thr Pro Pro Asp Ile Asp Leu His Asn
395                 400                 405                 410

cag gca agt gta cct cta gag ccc agg ccc tta cgg cga gag tcg gag     1661
Gln Ala Ser Val Pro Leu Glu Pro Arg Pro Leu Arg Arg Glu Ser Glu
                415                 420                 425

ata tga ctgactgatt ccttctctgg aatagttact ttacaacacg gtctgttggt      1717
Ile

cagaggccca aaacagttat acagatgacg gtactggtca agatgggtca agcaagcggc   1777

cacaagggac tgaggcaagc acaatggttt caaagaaaga ctgtaagctc catgattagc   1837

ataaagcact aaccatgtct ccatgtgacc cgatggcaca tagatgttgt agaataagtt   1897

atgggttttt atgttttgtt ttgtgttttt ccaaaacttg aacttgcagg caagccttgg   1957

ttgggtattt gatttatcca gaatgcttct ctttagggaa caaggatgtt tttaatggca   2017

taacaaaggc aagactctgc cttaatttttt gaaaagctgc taactacatg aacacaaatg   2077

tgtatttttg ttgcagtgta gttttccttt tgtgtaattt taaagtcagt gttgaatttt   2137

attgaaagct catgatgcgc ttcaaagtgg caagtatttg gctattaact gccaaaacaa   2197

gagcctgatt ttttgaggcc agtaattcgt ttgctagaat tgatttttttt tctctctctc   2257

tttgttacat aagggcatta tgtaacacta gccgaatggt agcctctggg ttgttgtttt   2317

tttcttttcc tccatgatgt taatgggtta tctcaaattt taagttaaac tacctaaaat   2377

aaataccaaa gataatgcat atttttgcac agtggagctt acacttaaaa gaaaacaaag   2437

ccccatgggc tgccttgaaa tcaagagaca ataactttga acctcagcaa gaccttgaac   2497

cgccggttca ttttgcacct tattcagaaa atagagcatc atactcaccg agtctagtca   2557

gtgtagtgct tttaaaaatt ttgtcctttc atgtaacttt tttattttaa gaggaagaag   2617

aagaaagggg cacacacaca caataccgac gtctatcctt tcctgctagg cagtgctggc   2677

caggctcatg tgtagtgtgc gagatggtga tgtactctta tatttttctg ggcttttcct   2737

tttgcacatt ccaaaattca tttcataaga caagatcttc ataggacctc cttggcatcc   2797

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tgaatttatt gcctggactg tcaggacatc accagcccac cttcacctta gggaagatgc   2917

cacacctggc ctccacactt gctcttctga tcagtctgtc tggattgagt cctacagtgt   2977

cagatagggc ggcaaatgcc aaagcaggga aacagggagg tgtggacaag ccagtttgat   3037

gcagcacttc agatcaagtg cttaggaagg agaggaaact tgccttttttt atggcagagg   3097
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atagtaatga aaatgtctca gtattttagg gtcaatgaga gccataaaaa tataacataa 3157

tcacaagtaa aggagataat ggtctaaaac agctatttcc cttttctgtg tgcatactta 3217

tgactgaatg tgagctaagc attttctcct gtggagccct agagcaggtt actaaggaag 3277

gacacattgt tttccagaag cctcccctgc ctggctgact gccttgctag aaacataatt 3337

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aactgaggtg ttattttcaa tgaaacaaag aaagagatgt taagcaagtg gttgttttag 3697

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gttgtaaaga aaacttacag aagaggcaac aatttggttc ttgacagtga gaggatattg 3817

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ctgagagcta gtacctatat gctaccggtt agcatggttt tagcaaatat ataccagcct 4297

tataaggttc gtattgctat gttcttctgt tatttatttc agcatggact gttcatttga 4357

aacctttttc tagttattag cgttttaaca gttacaagct ttaaatggca attttttttt 4417

ttttttttt ttttttttt tttttgtcaa gagccaagac acaggtaatg cacgacattg 4477

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ccctttttaaa gaatttttgc ccatatctgg aagggcacta tatttttggg aggagccata 4717

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gtttccgctc tgggctctgg caagttgaac aatcctagcc attgacaatc gtgatagtta 5257

ttattttccc atttgctgtc tttttgtatc taaagtcttc ctattgtact gcacaaacca 5317

tggattgtac atatttttat atattatgtc ttatttttatt atttctaaat aaaaaaatta 5377

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aaaattgaaa aaaaaaaaaa 5397

<210> SEQ ID NO 5
<211> LENGTH: 427
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 5

Met Gly Ser Val Arg Thr Asn Arg Tyr Ser Ile Val Ser Ser Glu Glu
1 5 10 15

Asp Gly Met Lys Leu Ala Thr Met Ala Val Ala Asn Gly Phe Gly Asn
20 25 30

Gly Lys Ser Lys Val His Thr Arg Gln Gln Cys Arg Ser Arg Phe Val
35 40 45

Lys Lys Asp Gly His Cys Asn Val Gln Phe Ile Asn Val Gly Glu Lys
50 55 60

Gly Gln Arg Tyr Leu Ala Asp Ile Phe Thr Thr Cys Val Asp Ile Arg
65 70 75 80

Trp Arg Trp Met Leu Val Ile Phe Cys Leu Ala Phe Val Leu Ser Trp
85 90 95

Leu Phe Phe Gly Cys Val Phe Trp Leu Ile Ala Leu Leu His Gly Asp
100 105 110

Leu Asp Ala Ser Lys Glu Gly Lys Ala Cys Val Ser Glu Val Asn Ser
115 120 125

Phe Thr Ala Ala Phe Leu Phe Ser Ile Glu Thr Gln Thr Thr Ile Gly
130 135 140

Tyr Gly Phe Arg Cys Val Thr Asp Glu Cys Pro Ile Ala Val Phe Met
145 150 155 160

Val Val Phe Gln Ser Ile Val Gly Cys Ile Ile Asp Ala Phe Ile Ile
165 170 175

Gly Ala Val Met Ala Lys Met Ala Lys Pro Lys Lys Arg Asn Glu Thr
180 185 190

Leu Val Phe Ser His Asn Ala Val Ile Ala Met Arg Asp Gly Lys Leu
195 200 205

Cys Leu Met Trp Arg Val Gly Asn Leu Arg Lys Ser His Leu Val Glu
210 215 220

Ala His Val Arg Ala Gln Leu Leu Lys Ser Arg Ile Thr Ser Glu Gly
225 230 235 240

Glu Tyr Ile Pro Leu Asp Gln Ile Asp Ile Asn Val Gly Phe Asp Ser
245 250 255

Gly Ile Asp Arg Ile Phe Leu Val Ser Pro Ile Thr Ile Val His Glu
260 265 270

Ile Asp Glu Asp Ser Pro Leu Tyr Asp Leu Ser Lys Gln Asp Ile Asp
275 280 285

Asn Ala Asp Phe Glu Ile Val Val Ile Leu Glu Gly Met Val Glu Ala
290 295 300

Thr Ala Met Thr Thr Gln Cys Arg Ser Ser Tyr Leu Ala Asn Glu Ile
305 310 315 320

Leu Trp Gly His Arg Tyr Glu Pro Val Leu Phe Glu Glu Lys His Tyr
325 330 335

Tyr Lys Val Asp Tyr Ser Arg Phe His Lys Thr Tyr Glu Val Pro Asn
340 345 350

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Thr Pro Leu Cys Ser Ala Arg Asp Leu Ala Glu Lys Lys Tyr Ile Leu
        355                 360                 365

Ser Asn Ala Asn Ser Phe Cys Tyr Glu Asn Glu Val Ala Leu Thr Ser
    370                 375                 380

Lys Glu Glu Asp Asp Ser Glu Asn Gly Val Pro Glu Ser Thr Ser Thr
385                 390                 395                 400

Asp Thr Pro Pro Asp Ile Asp Leu His Asn Gln Ala Ser Val Pro Leu
                405                 410                 415

Glu Pro Arg Pro Leu Arg Arg Glu Ser Glu Ile
            420                 425


<210> SEQ ID NO 6
<211> LENGTH: 2344
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (208)..(1380)

<400> SEQUENCE: 6

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acgccgacct ccgccgccgc ccgcgcccgt ctgccccctc ccgctgcggc tctctggacg    180

ccatcccctc ctcacctcga agccaac atg aag gag acc cgg ggc tac gga ggg    234
                              Met Lys Glu Thr Arg Gly Tyr Gly Gly
                              1               5

gat gcc ccc ttc tgc acc cgc ctc aac cac tcc tac aca ggc atg tgg      282
Asp Ala Pro Phe Cys Thr Arg Leu Asn His Ser Tyr Thr Gly Met Trp
10                  15                  20                  25

gcg ccc gag cgt tcc gcc gag gcg cgg ggc aac ctc acg cgc cct cca      330
Ala Pro Glu Arg Ser Ala Glu Ala Arg Gly Asn Leu Thr Arg Pro Pro
                30                  35                  40

ggg tct ggc gag gat tgc gga tcg gtg tcc gtg gcc ttc ccg atc acc      378
Gly Ser Gly Glu Asp Cys Gly Ser Val Ser Val Ala Phe Pro Ile Thr
            45                  50                  55

atg ctg ctc act ggt ttc gtg ggc aac gca ctg gcc atg ctg ctc gtg      426
Met Leu Leu Thr Gly Phe Val Gly Asn Ala Leu Ala Met Leu Leu Val
        60                  65                  70

tcg cgc agc tac cgg cgc cgg gag agc aag cgc aag aag tcc ttc ctg      474
Ser Arg Ser Tyr Arg Arg Arg Glu Ser Lys Arg Lys Lys Ser Phe Leu
    75                  80                  85

ctg tgc atc ggc tgg ctg gcg ctc acc gac ctg gtc ggg cag ctt ctc      522
Leu Cys Ile Gly Trp Leu Ala Leu Thr Asp Leu Val Gly Gln Leu Leu
90                  95                  100                 105

acc acc ccg gtc gtc atc gtc gtg tac ctg tcc aag cag cgt tgg gag      570
Thr Thr Pro Val Val Ile Val Val Tyr Leu Ser Lys Gln Arg Trp Glu
                110                 115                 120

cac atc gac ccg tcg ggg cgg ctc tgc acc ttt ttc ggg ctg acc atg      618
His Ile Asp Pro Ser Gly Arg Leu Cys Thr Phe Phe Gly Leu Thr Met
            125                 130                 135

act gtt ttc ggg ctc tcc tcg ttg ttc atc gcc agc gcc atg gcc gtc      666
Thr Val Phe Gly Leu Ser Ser Leu Phe Ile Ala Ser Ala Met Ala Val
        140                 145                 150

gag cgg gcg ctg gcc atc agg gcg ccg cac tgg tat gcg agc cac atg      714
Glu Arg Ala Leu Ala Ile Arg Ala Pro His Trp Tyr Ala Ser His Met
    155                 160                 165
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aag acg cgt gcc acc cgc gct gtg ctg ctc ggc gtg tgg ctg gcc gtg      762
Lys Thr Arg Ala Thr Arg Ala Val Leu Leu Gly Val Trp Leu Ala Val
170                 175                 180                 185

ctc gcc ttc gcc ctg ctg ccg gtg ctg ggc gtg ggc cag tac acc gtc      810
Leu Ala Phe Ala Leu Leu Pro Val Leu Gly Val Gly Gln Tyr Thr Val
                190                 195                 200

cag tgg ccc ggg acg tgg tgc ttc atc agc acc ggg cga ggg ggc aac      858
Gln Trp Pro Gly Thr Trp Cys Phe Ile Ser Thr Gly Arg Gly Gly Asn
            205                 210                 215

ggg act agc tct tcg cat aac tgg ggc aac ctt ttc ttc gcc tct gcc      906
Gly Thr Ser Ser Ser His Asn Trp Gly Asn Leu Phe Phe Ala Ser Ala
        220                 225                 230

ttt gcc ttc ctg ggg ctc ttg gcg ctg aca gtc acc ttt tcc tgc aac      954
Phe Ala Phe Leu Gly Leu Leu Ala Leu Thr Val Thr Phe Ser Cys Asn
    235                 240                 245

ctg gcc acc att aag gcc ctg gtg tcc cgc tgc cgg gcc aag gcc acg     1002
Leu Ala Thr Ile Lys Ala Leu Val Ser Arg Cys Arg Ala Lys Ala Thr
250                 255                 260                 265

gca tct cag tcc agt gcc cag tgg ggc cgc atc acg acc gag acg gcc     1050
Ala Ser Gln Ser Ser Ala Gln Trp Gly Arg Ile Thr Thr Glu Thr Ala
                270                 275                 280

att cag ctt atg ggg atc atg tgc gtg ctg tcg gtc tgc tgg tct ccg     1098
Ile Gln Leu Met Gly Ile Met Cys Val Leu Ser Val Cys Trp Ser Pro
            285                 290                 295

ctc ctg ata atg atg ttg aaa atg atc ttc aat cag aca tca gtt gag     1146
Leu Leu Ile Met Met Leu Lys Met Ile Phe Asn Gln Thr Ser Val Glu
        300                 305                 310

cac tgc aag aca cac acg gag aag cag aaa gaa tgc aac ttc ttc tta     1194
His Cys Lys Thr His Thr Glu Lys Gln Lys Glu Cys Asn Phe Phe Leu
    315                 320                 325

ata gct gtt cgc ctg gct tca ctg aac cag atc ttg gat cct tgg gtt     1242
Ile Ala Val Arg Leu Ala Ser Leu Asn Gln Ile Leu Asp Pro Trp Val
330                 335                 340                 345

tac ctg ctg tta aga aag atc ctt ctt cga aag ttt tgc cag atc agg     1290
Tyr Leu Leu Leu Arg Lys Ile Leu Leu Arg Lys Phe Cys Gln Ile Arg
                350                 355                 360

tac cac aca aac aac tat gca tcc agc tcc acc tcc tta ccc tgc cag     1338
Tyr His Thr Asn Asn Tyr Ala Ser Ser Ser Thr Ser Leu Pro Cys Gln
            365                 370                 375

tgt tcc tca acc ttg atg tgg agc gac cat ttg gaa aga taa             1380
Cys Ser Ser Thr Leu Met Trp Ser Asp His Leu Glu Arg
        380                 385                 390

tgaaagaacg gagttggaca ttttattgca attcctgctt ccctgaattt gcatatttct   1440

tcccacctga gaaggataat tatatatttt aatttggatt atttcttcat ttttatcttt   1500

ttattttaat gattgttttg tcagtaatac ccatggagat caactttatt attataatcc   1560

atgcctctga atattagagg gtttcttgga tgggattttg aatatgcatt taagaacgtt   1620

gggaacaatt tcacagatga tgattggagg aaaagtgatg aaaagaaaga cctgtgttcc   1680

aggagttttc tccaacttca aacctttacg tgaatcttaa ccaaagtgga catctttaca   1740

tttcatgata gcttgctttt gcaatatgag tttgaaaaat cagtataagc ttatgatggt   1800

gaaaagtcaa catattgaga gtgataattc aattaatagg atatgaactt aacgacatat   1860

aaaagataaa cttaacgaca tataaaagca aataagggca ggagggaatc gtgacaaaaa   1920

atatttgtgc ccaattataa ccaatgtttt agagatgttg tgtccctgtg gcttagcatg   1980
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gaactaaaag ttctaagtct caattctagt tatgtgtcat ttagtaactc aggaatctgc 2040

ttaattgtta tttctaagct tttgatgaca aaggagtgat gcagctaagg gcatccttgg 2100

agtgtcataa aaaacaaatt tgaggttgaa tgattagctg ccagttagag tgataaaaaa 2160

atccaggtag gccttctgat tcaccatgac caagtcagga tttcttaata tttcttttct 2220

ggcagcatat acaaaggcaa aattaataaa taacagttgt tgaataacaa actttattac 2280

gtttttataa aataaaagaa tctattttgt ctgtattaaa ataaaaagct ttgtggactt 2340

ctaa 2344

<210> SEQ ID NO 7
<211> LENGTH: 390
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 7

Met Lys Glu Thr Arg Gly Tyr Gly Gly Asp Ala Pro Phe Cys Thr Arg
1 5 10 15

Leu Asn His Ser Tyr Thr Gly Met Trp Ala Pro Glu Arg Ser Ala Glu
20 25 30

Ala Arg Gly Asn Leu Thr Arg Pro Pro Gly Ser Gly Glu Asp Cys Gly
35 40 45

Ser Val Ser Val Ala Phe Pro Ile Thr Met Leu Leu Thr Gly Phe Val
50 55 60

Gly Asn Ala Leu Ala Met Leu Leu Val Ser Arg Ser Tyr Arg Arg Arg
65 70 75 80

Glu Ser Lys Arg Lys Lys Ser Phe Leu Leu Cys Ile Gly Trp Leu Ala
85 90 95

Leu Thr Asp Leu Val Gly Gln Leu Leu Thr Thr Pro Val Val Ile Val
100 105 110

Val Tyr Leu Ser Lys Gln Arg Trp Glu His Ile Asp Pro Ser Gly Arg
115 120 125

Leu Cys Thr Phe Phe Gly Leu Thr Met Thr Val Phe Gly Leu Ser Ser
130 135 140

Leu Phe Ile Ala Ser Ala Met Ala Val Glu Arg Ala Leu Ala Ile Arg
145 150 155 160

Ala Pro His Trp Tyr Ala Ser His Met Lys Thr Arg Ala Thr Arg Ala
165 170 175

Val Leu Leu Gly Val Trp Leu Ala Val Leu Ala Phe Ala Leu Leu Pro
180 185 190

Val Leu Gly Val Gly Gln Tyr Thr Val Gln Trp Pro Gly Thr Trp Cys
195 200 205

Phe Ile Ser Thr Gly Arg Gly Gly Asn Gly Thr Ser Ser Ser His Asn
210 215 220

Trp Gly Asn Leu Phe Phe Ala Ser Ala Phe Ala Phe Leu Gly Leu Leu
225 230 235 240

Ala Leu Thr Val Thr Phe Ser Cys Asn Leu Ala Thr Ile Lys Ala Leu
245 250 255

Val Ser Arg Cys Arg Ala Lys Ala Thr Ala Ser Gln Ser Ser Ala Gln
260 265 270

Trp Gly Arg Ile Thr Thr Glu Thr Ala Ile Gln Leu Met Gly Ile Met
275 280 285

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Cys Val Leu Ser Val Cys Trp Ser Pro Leu Leu Ile Met Met Leu Lys
    290                 295                 300

Met Ile Phe Asn Gln Thr Ser Val Glu His Cys Lys Thr His Thr Glu
305                 310                 315                 320

Lys Gln Lys Glu Cys Asn Phe Phe Leu Ile Ala Val Arg Leu Ala Ser
                325                 330                 335

Leu Asn Gln Ile Leu Asp Pro Trp Val Tyr Leu Leu Leu Arg Lys Ile
            340                 345                 350

Leu Leu Arg Lys Phe Cys Gln Ile Arg Tyr His Thr Asn Asn Tyr Ala
        355                 360                 365

Ser Ser Ser Thr Ser Leu Pro Cys Gln Cys Ser Ser Thr Leu Met Trp
    370                 375                 380

Ser Asp His Leu Glu Arg
385                 390


<210> SEQ ID NO 8
<211> LENGTH: 3150
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (39)..(2699)

<400> SEQUENCE: 8

aaaagtttct tttctttgaa tgacagaact acagcata atg cgt ggc ttc aac ctg     56
                                          Met Arg Gly Phe Asn Leu
                                          1               5

ctc ctc ttc tgg gga tgt tgt gtt atg cac agc tgg gaa ggg cac ata      104
Leu Leu Phe Trp Gly Cys Cys Val Met His Ser Trp Glu Gly His Ile
            10                  15                  20

aga ccc aca cgg aaa cca aac aca aag ggt aat aac tgt aga gac agt      152
Arg Pro Thr Arg Lys Pro Asn Thr Lys Gly Asn Asn Cys Arg Asp Ser
        25                  30                  35

acc ttg tgc cca gct tat gcc acc tgc acc aat aca gtg gac agt tac      200
Thr Leu Cys Pro Ala Tyr Ala Thr Cys Thr Asn Thr Val Asp Ser Tyr
    40                  45                  50

tat tgc gct tgc aaa caa ggc ttc ctg tcc agc aat ggg caa aat cac      248
Tyr Cys Ala Cys Lys Gln Gly Phe Leu Ser Ser Asn Gly Gln Asn His
55                  60                  65                  70

ttc aag gat cca gga gtg cga tgc aaa gat att gat gaa tgt tct caa      296
Phe Lys Asp Pro Gly Val Arg Cys Lys Asp Ile Asp Glu Cys Ser Gln
                75                  80                  85

agc ccc cag ccc tgt ggt cct aac tca tcc tgc aaa aac ctg tca ggg      344
Ser Pro Gln Pro Cys Gly Pro Asn Ser Ser Cys Lys Asn Leu Ser Gly
            90                  95                  100

agg tac aag tgc agc tgt tta gat ggt ttc tct tct ccc act gga aat      392
Arg Tyr Lys Cys Ser Cys Leu Asp Gly Phe Ser Ser Pro Thr Gly Asn
        105                 110                 115

gac tgg gtc cca gga aag ccg ggc aat ttc tcc tgt act gat atc aat      440
Asp Trp Val Pro Gly Lys Pro Gly Asn Phe Ser Cys Thr Asp Ile Asn
    120                 125                 130

gag tgc ctc acc agc agc gtc tgc cct gag cat tct gac tgt gtc aac      488
Glu Cys Leu Thr Ser Ser Val Cys Pro Glu His Ser Asp Cys Val Asn
135                 140                 145                 150

tcc atg gga agc tac agt tgc agc tgt caa gtt gga ttc atc tct aga      536
Ser Met Gly Ser Tyr Ser Cys Ser Cys Gln Val Gly Phe Ile Ser Arg
                155                 160                 165
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aac tcc acc tgt gaa gac gtg gat gaa tgt gca gat cca aga gct tgc      584
Asn Ser Thr Cys Glu Asp Val Asp Glu Cys Ala Asp Pro Arg Ala Cys
            170                 175                 180

cca gag cat gca act tgt aat aac act gtt gga aac tac tct tgt ttc      632
Pro Glu His Ala Thr Cys Asn Asn Thr Val Gly Asn Tyr Ser Cys Phe
        185                 190                 195

tgc aac cca gga ttt gaa tcc agc agt ggc cac ttg agt ttc cag ggt      680
Cys Asn Pro Gly Phe Glu Ser Ser Ser Gly His Leu Ser Phe Gln Gly
    200                 205                 210

ctc aaa gca tcg tgt gaa gat att gat gaa tgc act gaa atg tgc ccc      728
Leu Lys Ala Ser Cys Glu Asp Ile Asp Glu Cys Thr Glu Met Cys Pro
215                 220                 225                 230

atc aat tca aca tgc acc aac act cct ggg agc tac ttt tgc acc tgc      776
Ile Asn Ser Thr Cys Thr Asn Thr Pro Gly Ser Tyr Phe Cys Thr Cys
                235                 240                 245

cac cct ggc ttt gca cca agc aat gga cag ttg aat ttc aca gac caa      824
His Pro Gly Phe Ala Pro Ser Asn Gly Gln Leu Asn Phe Thr Asp Gln
            250                 255                 260

gga gtg gaa tgt aga gat att gat gag tgc cgc caa gat cca tca acc      872
Gly Val Glu Cys Arg Asp Ile Asp Glu Cys Arg Gln Asp Pro Ser Thr
        265                 270                 275

tgt ggt cct aat tct atc tgc acc aat gcc ctg ggc tcc tac agc tgt      920
Cys Gly Pro Asn Ser Ile Cys Thr Asn Ala Leu Gly Ser Tyr Ser Cys
    280                 285                 290

ggc tgc att gca ggc ttt cat ccc aat cca gaa ggc tcc cag aaa gat      968
Gly Cys Ile Ala Gly Phe His Pro Asn Pro Glu Gly Ser Gln Lys Asp
295                 300                 305                 310

ggc aac ttc agc tgc caa agg gtt ctc ttc aaa tgt aag gaa gat gtg     1016
Gly Asn Phe Ser Cys Gln Arg Val Leu Phe Lys Cys Lys Glu Asp Val
                315                 320                 325

ata ccc gat aat aag cag atc cag caa tgc caa gag gga acc gca gtg     1064
Ile Pro Asp Asn Lys Gln Ile Gln Gln Cys Gln Glu Gly Thr Ala Val
            330                 335                 340

aaa cct gca tat gtc tcc ttt tgt gca caa ata aat aac atc ttc agc     1112
Lys Pro Ala Tyr Val Ser Phe Cys Ala Gln Ile Asn Asn Ile Phe Ser
        345                 350                 355

gtt ctg gac aaa gtg tgt gaa aat aaa acg acc gta gtt tct ctg aag     1160
Val Leu Asp Lys Val Cys Glu Asn Lys Thr Thr Val Val Ser Leu Lys
    360                 365                 370

aat aca act gag agc ttt gtc cct gtg ctt aaa caa ata tcc acg tgg     1208
Asn Thr Thr Glu Ser Phe Val Pro Val Leu Lys Gln Ile Ser Thr Trp
375                 380                 385                 390

act aaa ttc acc aag gaa gag acg tcc tcc ctg gcc aca gtc ttc ctg     1256
Thr Lys Phe Thr Lys Glu Glu Thr Ser Ser Leu Ala Thr Val Phe Leu
                395                 400                 405

gag agt gtg gaa agc atg aca ctg gca tct ttt tgg aaa ccc tca gca     1304
Glu Ser Val Glu Ser Met Thr Leu Ala Ser Phe Trp Lys Pro Ser Ala
            410                 415                 420

aat atc act ccg gct gtt cgg acg gaa tac tta gac att gag agc aaa     1352
Asn Ile Thr Pro Ala Val Arg Thr Glu Tyr Leu Asp Ile Glu Ser Lys
        425                 430                 435

gtt atc aac aaa gaa tgc agt gaa gag aat gtg acg ttg gac ttg gta     1400
Val Ile Asn Lys Glu Cys Ser Glu Glu Asn Val Thr Leu Asp Leu Val
    440                 445                 450

gcc aag ggg gat aag atg aag atc ggg tgt tcc aca att gag gaa tct     1448
Ala Lys Gly Asp Lys Met Lys Ile Gly Cys Ser Thr Ile Glu Glu Ser
455                 460                 465                 470
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gaa tcc aca gag acc act ggt gtg gct ttt gtc tcc ttt gtg ggc atg     1496
Glu Ser Thr Glu Thr Thr Gly Val Ala Phe Val Ser Phe Val Gly Met
                475                 480                 485

gaa tcg gtt tta aat gag cgc ttc ttc aaa gac cac cag gct ccc ttg     1544
Glu Ser Val Leu Asn Glu Arg Phe Phe Lys Asp His Gln Ala Pro Leu
            490                 495                 500

acc acc tct gag atc aag ctg aag atg aat tct cga gtc gtt ggg ggc     1592
Thr Thr Ser Glu Ile Lys Leu Lys Met Asn Ser Arg Val Val Gly Gly
        505                 510                 515

ata atg act gga gag aag aaa gac ggc ttc tca gat cca atc atc tac     1640
Ile Met Thr Gly Glu Lys Lys Asp Gly Phe Ser Asp Pro Ile Ile Tyr
    520                 525                 530

act ctg gag aac att cag cca aag cag aag ttt gag agg ccc atc tgt     1688
Thr Leu Glu Asn Ile Gln Pro Lys Gln Lys Phe Glu Arg Pro Ile Cys
535                 540                 545                 550

gtt tcc tgg agc act gat gtg aag ggt gga aga tgg aca tcc ttt ggc     1736
Val Ser Trp Ser Thr Asp Val Lys Gly Gly Arg Trp Thr Ser Phe Gly
                555                 560                 565

tgt gtg atc ctg gaa gct tct gag aca tat acc atc tgc agc tgt aat     1784
Cys Val Ile Leu Glu Ala Ser Glu Thr Tyr Thr Ile Cys Ser Cys Asn
            570                 575                 580

cag atg gca aat ctt gcc gtt atc atg gcg tct ggg gag ctc acg atg     1832
Gln Met Ala Asn Leu Ala Val Ile Met Ala Ser Gly Glu Leu Thr Met
        585                 590                 595

gac ttt tcc ttg tac atc att agc cat gta ggc att atc atc tcc ttg     1880
Asp Phe Ser Leu Tyr Ile Ile Ser His Val Gly Ile Ile Ile Ser Leu
    600                 605                 610

gtg tgc ctc gtc ttg gcc atc gcc acc ttt ctg ctg tgt cgc tcc atc     1928
Val Cys Leu Val Leu Ala Ile Ala Thr Phe Leu Leu Cys Arg Ser Ile
615                 620                 625                 630

cga aat cac aac acc tac ctc cac ctg cac ctc tgc gtg tgt ctc ctc     1976
Arg Asn His Asn Thr Tyr Leu His Leu His Leu Cys Val Cys Leu Leu
                635                 640                 645

ttg gcg aag act ctc ttc ctc gcc ggt ata cac aag act gac aac aag     2024
Leu Ala Lys Thr Leu Phe Leu Ala Gly Ile His Lys Thr Asp Asn Lys
            650                 655                 660

atg ggc tgc gcc atc atc gcg ggc ttc ctg cac tac ctt ttc ctt gcc     2072
Met Gly Cys Ala Ile Ile Ala Gly Phe Leu His Tyr Leu Phe Leu Ala
        665                 670                 675

tgc ttc ttc tgg atg ctg gtg gag gct gtg ata ctg ttc ttg atg gtc     2120
Cys Phe Phe Trp Met Leu Val Glu Ala Val Ile Leu Phe Leu Met Val
    680                 685                 690

aga aac ctg aag gtg gtg aat tac ttc agc tct cgc aac atc aag atg     2168
Arg Asn Leu Lys Val Val Asn Tyr Phe Ser Ser Arg Asn Ile Lys Met
695                 700                 705                 710

ctg cac atc tgt gcc ttt ggt tat ggg ctg ccg atg ctg gtg gtg gtg     2216
Leu His Ile Cys Ala Phe Gly Tyr Gly Leu Pro Met Leu Val Val Val
                715                 720                 725

atc tct gcc agt gtg cag cca cag ggc tat gga atg cat aat cgc tgc     2264
Ile Ser Ala Ser Val Gln Pro Gln Gly Tyr Gly Met His Asn Arg Cys
            730                 735                 740

tgg ctg aat aca gag aca ggg ttc atc tgg agt ttc ttg ggg cca gtt     2312
Trp Leu Asn Thr Glu Thr Gly Phe Ile Trp Ser Phe Leu Gly Pro Val
        745                 750                 755

tgc aca gtt ata gtg atc aac tcc ctt ctc ctg acc tgg acc ttg tgg     2360
Cys Thr Val Ile Val Ile Asn Ser Leu Leu Leu Thr Trp Thr Leu Trp
    760                 765                 770
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atc ctg agg cag agg ctt tcc agt gtt aat gcc gaa gtc tca acg cta     2408
Ile Leu Arg Gln Arg Leu Ser Ser Val Asn Ala Glu Val Ser Thr Leu
775                 780                 785                 790

aaa gac acc agg tta ctg acc ttc aag gcc ttt gcc cag ctc ttc atc     2456
Lys Asp Thr Arg Leu Leu Thr Phe Lys Ala Phe Ala Gln Leu Phe Ile
                795                 800                 805

ctg ggc tgc tcc tgg gtg ctg ggc att ttt cag att gga cct gtg gca     2504
Leu Gly Cys Ser Trp Val Leu Gly Ile Phe Gln Ile Gly Pro Val Ala
            810                 815                 820

ggt gtc atg gct tac ctg ttc acc atc atc aac agc ctg cag ggg gcc     2552
Gly Val Met Ala Tyr Leu Phe Thr Ile Ile Asn Ser Leu Gln Gly Ala
        825                 830                 835

ttc atc ttc ctc atc cac tgt ctg ctc aac ggc cag gta cga gaa gaa     2600
Phe Ile Phe Leu Ile His Cys Leu Leu Asn Gly Gln Val Arg Glu Glu
    840                 845                 850

tac aag agg tgg atc act ggg aag acg aag ccc agc tcc cag tcc cag     2648
Tyr Lys Arg Trp Ile Thr Gly Lys Thr Lys Pro Ser Ser Gln Ser Gln
855                 860                 865                 870

acc tca agg atc ttg ctg tcc tcc atg cca tcc gct tcc aag acg ggt     2696
Thr Ser Arg Ile Leu Leu Ser Ser Met Pro Ser Ala Ser Lys Thr Gly
                875                 880                 885

taa agtcctttct tgctttcaaa tatgctatgg agccacagtt gaggacagta          2749

gtttcctgca ggagcctacc ctgaaatctc ttctcagctt aacatggaaa tgaggatccc   2809

accagcccca gaaccctctg gggaagaatg ttgggggcgg tcttcctgtg gttgtatgca   2869

ctgatgagaa atcaggcgtt tctgctccaa acgaccattt tatcttcgtg ctctgcaact   2929

tcttcaattc cagagtttct gagaacagac ccaaattcaa tggcatgacc aagaacacct   2989

ggctaccatt ttgttttctc ctgcccttgt tggtgcatgg ttctaagcat gcccctccag   3049

agcctatcat acgcctgata cagagaacct ctcaataaat gatttgtcgc ctgtctgact   3109

gatttaccct aggaaaaaaa aaaaaaaaaa aaaaaaaaaa a                       3150


<210> SEQ ID NO 9
<211> LENGTH: 886
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 9

Met Arg Gly Phe Asn Leu Leu Leu Phe Trp Gly Cys Cys Val Met His
1               5                   10                  15

Ser Trp Glu Gly His Ile Arg Pro Thr Arg Lys Pro Asn Thr Lys Gly
            20                  25                  30

Asn Asn Cys Arg Asp Ser Thr Leu Cys Pro Ala Tyr Ala Thr Cys Thr
        35                  40                  45

Asn Thr Val Asp Ser Tyr Tyr Cys Ala Cys Lys Gln Gly Phe Leu Ser
    50                  55                  60

Ser Asn Gly Gln Asn His Phe Lys Asp Pro Gly Val Arg Cys Lys Asp
65                  70                  75                  80

Ile Asp Glu Cys Ser Gln Ser Pro Gln Pro Cys Gly Pro Asn Ser Ser
                85                  90                  95

Cys Lys Asn Leu Ser Gly Arg Tyr Lys Cys Ser Cys Leu Asp Gly Phe
            100                 105                 110

Ser Ser Pro Thr Gly Asn Asp Trp Val Pro Gly Lys Pro Gly Asn Phe
        115                 120                 125
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Ser Cys Thr Asp Ile Asn Glu Cys Leu Thr Ser Ser Val Cys Pro Glu
    130                 135                 140

His Ser Asp Cys Val Asn Ser Met Gly Ser Tyr Ser Cys Ser Cys Gln
145                 150                 155                 160

Val Gly Phe Ile Ser Arg Asn Ser Thr Cys Glu Asp Val Asp Glu Cys
                165                 170                 175

Ala Asp Pro Arg Ala Cys Pro Glu His Ala Thr Cys Asn Asn Thr Val
            180                 185                 190

Gly Asn Tyr Ser Cys Phe Cys Asn Pro Gly Phe Glu Ser Ser Ser Gly
        195                 200                 205

His Leu Ser Phe Gln Gly Leu Lys Ala Ser Cys Glu Asp Ile Asp Glu
    210                 215                 220

Cys Thr Glu Met Cys Pro Ile Asn Ser Thr Cys Thr Asn Thr Pro Gly
225                 230                 235                 240

Ser Tyr Phe Cys Thr Cys His Pro Gly Phe Ala Pro Ser Asn Gly Gln
                245                 250                 255

Leu Asn Phe Thr Asp Gln Gly Val Glu Cys Arg Asp Ile Asp Glu Cys
            260                 265                 270

Arg Gln Asp Pro Ser Thr Cys Gly Pro Asn Ser Ile Cys Thr Asn Ala
        275                 280                 285

Leu Gly Ser Tyr Ser Cys Gly Cys Ile Ala Gly Phe His Pro Asn Pro
    290                 295                 300

Glu Gly Ser Gln Lys Asp Gly Asn Phe Ser Cys Gln Arg Val Leu Phe
305                 310                 315                 320

Lys Cys Lys Glu Asp Val Ile Pro Asp Asn Lys Gln Ile Gln Gln Cys
                325                 330                 335

Gln Glu Gly Thr Ala Val Lys Pro Ala Tyr Val Ser Phe Cys Ala Gln
            340                 345                 350

Ile Asn Asn Ile Phe Ser Val Leu Asp Lys Val Cys Glu Asn Lys Thr
        355                 360                 365

Thr Val Val Ser Leu Lys Asn Thr Thr Glu Ser Phe Val Pro Val Leu
    370                 375                 380

Lys Gln Ile Ser Thr Trp Thr Lys Phe Thr Lys Glu Glu Thr Ser Ser
385                 390                 395                 400

Leu Ala Thr Val Phe Leu Glu Ser Val Glu Ser Met Thr Leu Ala Ser
                405                 410                 415

Phe Trp Lys Pro Ser Ala Asn Ile Thr Pro Ala Val Arg Thr Glu Tyr
            420                 425                 430

Leu Asp Ile Glu Ser Lys Val Ile Asn Lys Glu Cys Ser Glu Glu Asn
        435                 440                 445

Val Thr Leu Asp Leu Val Ala Lys Gly Asp Lys Met Lys Ile Gly Cys
    450                 455                 460

Ser Thr Ile Glu Glu Ser Glu Ser Thr Glu Thr Thr Gly Val Ala Phe
465                 470                 475                 480

Val Ser Phe Val Gly Met Glu Ser Val Leu Asn Glu Arg Phe Phe Lys
                485                 490                 495

Asp His Gln Ala Pro Leu Thr Thr Ser Glu Ile Lys Leu Lys Met Asn
            500                 505                 510

Ser Arg Val Val Gly Gly Ile Met Thr Gly Glu Lys Lys Asp Gly Phe
        515                 520                 525

Ser Asp Pro Ile Ile Tyr Thr Leu Glu Asn Ile Gln Pro Lys Gln Lys
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    530                 535                 540

Phe Glu Arg Pro Ile Cys Val Ser Trp Ser Thr Asp Val Lys Gly Gly
545                 550                 555                 560

Arg Trp Thr Ser Phe Gly Cys Val Ile Leu Glu Ala Ser Glu Thr Tyr
                565                 570                 575

Thr Ile Cys Ser Cys Asn Gln Met Ala Asn Leu Ala Val Ile Met Ala
            580                 585                 590

Ser Gly Glu Leu Thr Met Asp Phe Ser Leu Tyr Ile Ile Ser His Val
        595                 600                 605

Gly Ile Ile Ile Ser Leu Val Cys Leu Val Leu Ala Ile Ala Thr Phe
    610                 615                 620

Leu Leu Cys Arg Ser Ile Arg Asn His Asn Thr Tyr Leu His Leu His
625                 630                 635                 640

Leu Cys Val Cys Leu Leu Leu Ala Lys Thr Leu Phe Leu Ala Gly Ile
                645                 650                 655

His Lys Thr Asp Asn Lys Met Gly Cys Ala Ile Ile Ala Gly Phe Leu
            660                 665                 670

His Tyr Leu Phe Leu Ala Cys Phe Phe Trp Met Leu Val Glu Ala Val
        675                 680                 685

Ile Leu Phe Leu Met Val Arg Asn Leu Lys Val Val Asn Tyr Phe Ser
    690                 695                 700

Ser Arg Asn Ile Lys Met Leu His Ile Cys Ala Phe Gly Tyr Gly Leu
705                 710                 715                 720

Pro Met Leu Val Val Val Ile Ser Ala Ser Val Gln Pro Gln Gly Tyr
                725                 730                 735

Gly Met His Asn Arg Cys Trp Leu Asn Thr Glu Thr Gly Phe Ile Trp
            740                 745                 750

Ser Phe Leu Gly Pro Val Cys Thr Val Ile Val Ile Asn Ser Leu Leu
        755                 760                 765

Leu Thr Trp Thr Leu Trp Ile Leu Arg Gln Arg Leu Ser Ser Val Asn
    770                 775                 780

Ala Glu Val Ser Thr Leu Lys Asp Thr Arg Leu Leu Thr Phe Lys Ala
785                 790                 795                 800

Phe Ala Gln Leu Phe Ile Leu Gly Cys Ser Trp Val Leu Gly Ile Phe
                805                 810                 815

Gln Ile Gly Pro Val Ala Gly Val Met Ala Tyr Leu Phe Thr Ile Ile
            820                 825                 830

Asn Ser Leu Gln Gly Ala Phe Ile Phe Leu Ile His Cys Leu Leu Asn
        835                 840                 845

Gly Gln Val Arg Glu Glu Tyr Lys Arg Trp Ile Thr Gly Lys Thr Lys
    850                 855                 860

Pro Ser Ser Gln Ser Gln Thr Ser Arg Ile Leu Leu Ser Ser Met Pro
865                 870                 875                 880

Ser Ala Ser Lys Thr Gly
                885


<210> SEQ ID NO 10
<211> LENGTH: 2428
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (213)..(1229)
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<400> SEQUENCE: 10

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agtgttacct tggagcctac aatgagaggt atttcaaaat gagtgaagca tgactctcac     60

agatgaaggc ctagacgcag gatctttaat gaaaaaacac ttgggccact tcaagacgac    120

aaacgctcac tgggcaaaac accttcactg aaaagagacc tcatattatg caaaaaaaat    180

cttaaaaggc ctctgccttc agaagttaca ag atg atc aat tca acc tcc aca      233
                                  Met Ile Asn Ser Thr Ser Thr
                                  1               5

cag cct cca gat gaa tcc tgc tct cag aac ctc ctg atc act cag cag      281
Gln Pro Pro Asp Glu Ser Cys Ser Gln Asn Leu Leu Ile Thr Gln Gln
        10                  15                  20

atc att cct gtg ctg tac tgt atg gtc ttc att gca gga atc cta ctc      329
Ile Ile Pro Val Leu Tyr Cys Met Val Phe Ile Ala Gly Ile Leu Leu
    25                  30                  35

aat gga gtg tca gga tgg ata ttc ttt tac gtg ccc agc tct gag agt      377
Asn Gly Val Ser Gly Trp Ile Phe Phe Tyr Val Pro Ser Ser Glu Ser
40                  45                  50                  55

ttc atc atc tat ctc aag aac att gtt att gct gac ttt gtg atg agc      425
Phe Ile Ile Tyr Leu Lys Asn Ile Val Ile Ala Asp Phe Val Met Ser
                60                  65                  70

ctg act ttt cct ttc aag atc ctt ggt gac tca ggc ctt ggt ccc tgg      473
Leu Thr Phe Pro Phe Lys Ile Leu Gly Asp Ser Gly Leu Gly Pro Trp
            75                  80                  85

cag ctg aac gtg ttt gtg tgc agg gtc tct gcc gtg ctc ttc tac gtc      521
Gln Leu Asn Val Phe Val Cys Arg Val Ser Ala Val Leu Phe Tyr Val
        90                  95                  100

aac atg tac gtc agc att gtg ttc ttt ggg ctc atc agc ttt gac aga      569
Asn Met Tyr Val Ser Ile Val Phe Phe Gly Leu Ile Ser Phe Asp Arg
    105                 110                 115

tat tat aaa att gta aag cct ctt tgg act tct ttc atc cag tca gtg      617
Tyr Tyr Lys Ile Val Lys Pro Leu Trp Thr Ser Phe Ile Gln Ser Val
120                 125                 130                 135

agt tac agc aaa ctt ctg tca gtg ata gta tgg atg ctc atg ctc ctc      665
Ser Tyr Ser Lys Leu Leu Ser Val Ile Val Trp Met Leu Met Leu Leu
                140                 145                 150

ctt gct gtt cca aat att att ctc acc aac cag agt gtt agg gag gtt      713
Leu Ala Val Pro Asn Ile Ile Leu Thr Asn Gln Ser Val Arg Glu Val
            155                 160                 165

aca caa ata aaa tgt ata gaa ctg aaa agt gaa ctg gga cgg aag tgg      761
Thr Gln Ile Lys Cys Ile Glu Leu Lys Ser Glu Leu Gly Arg Lys Trp
        170                 175                 180

cac aaa gca tca aac tac atc ttc gtg gcc atc ttc tgg att gtg ttt      809
His Lys Ala Ser Asn Tyr Ile Phe Val Ala Ile Phe Trp Ile Val Phe
    185                 190                 195

ctt ttg tta atc gtt ttc tat act gct atc aca aag aaa atc ttt aag      857
Leu Leu Leu Ile Val Phe Tyr Thr Ala Ile Thr Lys Lys Ile Phe Lys
200                 205                 210                 215

tcc cac ctt aag tca agt cgg aat tcc act tcg gtc aaa aag aaa tct      905
Ser His Leu Lys Ser Ser Arg Asn Ser Thr Ser Val Lys Lys Lys Ser
                220                 225                 230

agc cgc aac ata ttc agc atc gtg ttt gtg ttt ttt gtc tgt ttt gta      953
Ser Arg Asn Ile Phe Ser Ile Val Phe Val Phe Phe Val Cys Phe Val
            235                 240                 245

cct tac cat att gcc aga atc ccc tac aca aag agt cag acc gaa gct     1001
Pro Tyr His Ile Ala Arg Ile Pro Tyr Thr Lys Ser Gln Thr Glu Ala
        250                 255                 260
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cat tac agc tgc cag tca aaa gaa atc ttg cgg tat atg aaa gaa ttc     1049
His Tyr Ser Cys Gln Ser Lys Glu Ile Leu Arg Tyr Met Lys Glu Phe
    265                 270                 275

act ctg cta cta tct gct gca aat gta tgc ttg gac cct att att tat     1097
Thr Leu Leu Leu Ser Ala Ala Asn Val Cys Leu Asp Pro Ile Ile Tyr
280                 285                 290                 295

ttc ttt cta tgc cag ccg ttt agg gaa atc tta tgt aag aaa ttg cac     1145
Phe Phe Leu Cys Gln Pro Phe Arg Glu Ile Leu Cys Lys Lys Leu His
                300                 305                 310

att cca tta aaa gct cag aat gac cta gac att tcc aga atc aaa aga     1193
Ile Pro Leu Lys Ala Gln Asn Asp Leu Asp Ile Ser Arg Ile Lys Arg
            315                 320                 325

gga aat aca aca ctt gaa agc aca gat act ttg tga gttcctaccc          1239
Gly Asn Thr Thr Leu Glu Ser Thr Asp Thr Leu
        330                 335

tcttccaaag aaagaccacg tgtgcatgtt gtcatcttca attacataac agaaatcaat   1299

aagatatgtg ccctcatcat aaatatcatc tctagcactg ccatccaatt tagttcaata   1359

aaattcaaat ataagtttcc atgctttttt gtaacatcaa agaaaacata cccatcagta   1419

atttctctaa tactgacctt tctattctct attaataaaa aattaataca tacaattatt   1479

caattctatt atattaaaat aagttaaagt ttataaccac tagtctggtc agttaatgta   1539

gaaatttaaa tagtaaataa aacacaacat aatcaaagac aactcactca ggcatcttct   1599

ttctctaaat accagaatct agtatgtaat tgttttcaac actgtcctta aagactaact   1659

tgaaagcagg cacagtttga tgaagggcta gagagctgtt tgcaataaaa agtcaggttt   1719

ttttcctgat ttgaagaagc aggaaaagct gacacccaga caatcactta agaaacccct   1779

tattgatgta tttcatggca ctgcaaagga agaggaatat taattgtata cttagcaaga   1839

aaatttttt tttctgatag cactttgagg atattagata catgctaaat atgttttcta   1899

caaagactta cgtcatttaa tgagcctggg gttctggtgt tagaatattt ttaagtaggc   1959

tttactgaga gaaactaaat attggcatac gttatcagca acttcccctg ttcaatagta   2019

tgggaaaaat aagatgactg ggaaaaagac acacccacac cgtagaacat atattaatct   2079

actggcgaat gggaaaggag accattttct tagaaagcaa ataaacttga ttttttaaa    2139

tctaaaattt acattaatga gtgcaaaata acacataaaa tgaaaattca cacatcacat   2199

ttttctggaa aacagacgga ttttacttct ggagacatgg catacggtta ctgacttatg   2259

agctaccaaa actaaattct ttctctgcta ttaactggct agaagacatt catctatttt   2319

tcaaatgttc tttcaaaaca tttttataag taatgtttgt atctatttca tgctttactg   2379

tctatatact aataaagaaa tgttttaata ccgaaaaaaa aaaaaaaaa              2428


<210> SEQ ID NO 11
<211> LENGTH: 338
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 11

Met Ile Asn Ser Thr Ser Thr Gln Pro Pro Asp Glu Ser Cys Ser Gln
1               5                   10                  15

Asn Leu Leu Ile Thr Gln Gln Ile Ile Pro Val Leu Tyr Cys Met Val
            20                  25                  30

Phe Ile Ala Gly Ile Leu Leu Asn Gly Val Ser Gly Trp Ile Phe Phe
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        35                  40                  45

Tyr Val Pro Ser Ser Glu Ser Phe Ile Ile Tyr Leu Lys Asn Ile Val
    50                  55                  60

Ile Ala Asp Phe Val Met Ser Leu Thr Phe Pro Phe Lys Ile Leu Gly
65                  70                  75                  80

Asp Ser Gly Leu Gly Pro Trp Gln Leu Asn Val Phe Val Cys Arg Val
                85                  90                  95

Ser Ala Val Leu Phe Tyr Val Asn Met Tyr Val Ser Ile Val Phe Phe
            100                 105                 110

Gly Leu Ile Ser Phe Asp Arg Tyr Tyr Lys Ile Val Lys Pro Leu Trp
        115                 120                 125

Thr Ser Phe Ile Gln Ser Val Ser Tyr Ser Lys Leu Leu Ser Val Ile
    130                 135                 140

Val Trp Met Leu Met Leu Leu Leu Ala Val Pro Asn Ile Ile Leu Thr
145                 150                 155                 160

Asn Gln Ser Val Arg Glu Val Thr Gln Ile Lys Cys Ile Glu Leu Lys
                165                 170                 175

Ser Glu Leu Gly Arg Lys Trp His Lys Ala Ser Asn Tyr Ile Phe Val
            180                 185                 190

Ala Ile Phe Trp Ile Val Phe Leu Leu Leu Ile Val Phe Tyr Thr Ala
        195                 200                 205

Ile Thr Lys Lys Ile Phe Lys Ser His Leu Lys Ser Ser Arg Asn Ser
    210                 215                 220

Thr Ser Val Lys Lys Lys Ser Ser Arg Asn Ile Phe Ser Ile Val Phe
225                 230                 235                 240

Val Phe Phe Val Cys Phe Val Pro Tyr His Ile Ala Arg Ile Pro Tyr
                245                 250                 255

Thr Lys Ser Gln Thr Glu Ala His Tyr Ser Cys Gln Ser Lys Glu Ile
            260                 265                 270

Leu Arg Tyr Met Lys Glu Phe Thr Leu Leu Leu Ser Ala Ala Asn Val
        275                 280                 285

Cys Leu Asp Pro Ile Ile Tyr Phe Phe Leu Cys Gln Pro Phe Arg Glu
    290                 295                 300

Ile Leu Cys Lys Lys Leu His Ile Pro Leu Lys Ala Gln Asn Asp Leu
305                 310                 315                 320

Asp Ile Ser Arg Ile Lys Arg Gly Asn Thr Thr Leu Glu Ser Thr Asp
                325                 330                 335

Thr Leu


<210> SEQ ID NO 12
<211> LENGTH: 1734
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (85)..(1233)

<400> SEQUENCE: 12

ggcacgaggc gccgggccat gggcctcgag cccgccccga acccccgcga gcccgccttg     60

tctgcggcgt gactggaggc ccag atg gtc atc atg ggc cag tgc tac tac       111
                          Met Val Ile Met Gly Gln Cys Tyr Tyr
                          1               5

aac gag acc atc ggc ttc ttc tat aac aac agt ggc aaa gag ctc agc      159
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Asn Glu Thr Ile Gly Phe Phe Tyr Asn Asn Ser Gly Lys Glu Leu Ser
10                  15                  20                  25

tcc cac tgg cgg ccc aag gat gtg gtc gtg gtg gca ctg ggg ctg acc      207
Ser His Trp Arg Pro Lys Asp Val Val Val Val Ala Leu Gly Leu Thr
                30                  35                  40

gtc agc gtg ctg gtg ctg ctg acc aat ctg ctg gtc ata gca gcc atc      255
Val Ser Val Leu Val Leu Leu Thr Asn Leu Leu Val Ile Ala Ala Ile
            45                  50                  55

gcc tcc aac cgc cgc ttc cac cag ccc atc tac tac ctg ctc ggc aat      303
Ala Ser Asn Arg Arg Phe His Gln Pro Ile Tyr Tyr Leu Leu Gly Asn
        60                  65                  70

ctg gcc gcg gct gac ctc ttc gcg ggc gtg gcc tac ctc ttc ctc atg      351
Leu Ala Ala Ala Asp Leu Phe Ala Gly Val Ala Tyr Leu Phe Leu Met
    75                  80                  85

ttc cac act ggt ccc cgc aca gcc cga ctt tca ctt gag ggc tgg ttc      399
Phe His Thr Gly Pro Arg Thr Ala Arg Leu Ser Leu Glu Gly Trp Phe
90                  95                  100                 105

ctg cgg cag ggc ttg ctg gac aca agc ctc act gcg tcg gtg gcc aca      447
Leu Arg Gln Gly Leu Leu Asp Thr Ser Leu Thr Ala Ser Val Ala Thr
                110                 115                 120

ctg ctg gcc atc gcc gtg gag cgg cac cgc agt gtg atg gcc gtg cag      495
Leu Leu Ala Ile Ala Val Glu Arg His Arg Ser Val Met Ala Val Gln
            125                 130                 135

ctg cac agc cgc ctg ccc cgt ggc cgc gtg gtc atg ctc att gtg ggc      543
Leu His Ser Arg Leu Pro Arg Gly Arg Val Val Met Leu Ile Val Gly
        140                 145                 150

gtg tgg gtg gct gcc ctg ggc ctg ggg ctg ctg cct gcc cac tcc tgg      591
Val Trp Val Ala Ala Leu Gly Leu Gly Leu Leu Pro Ala His Ser Trp
    155                 160                 165

cac tgc ctc tgt gcc ctg gac cgc tgc tca cgc atg gca ccc ctg ctc      639
His Cys Leu Cys Ala Leu Asp Arg Cys Ser Arg Met Ala Pro Leu Leu
170                 175                 180                 185

agc cgc tcc tat ttg gcc gtc tgg gct ctg tcg agc ctg ctt gtc ttc      687
Ser Arg Ser Tyr Leu Ala Val Trp Ala Leu Ser Ser Leu Leu Val Phe
                190                 195                 200

ctg ctc atg gtg gct gtg tac acc cgc att ttc ttc tac gtg cgg cgg      735
Leu Leu Met Val Ala Val Tyr Thr Arg Ile Phe Phe Tyr Val Arg Arg
            205                 210                 215

cga gtg cag cgc atg gca gag cat gtc agc tgc cac ccc cgc tac cga      783
Arg Val Gln Arg Met Ala Glu His Val Ser Cys His Pro Arg Tyr Arg
        220                 225                 230

gag acc acg ctc agc ctg gtc aag act gtt gtc atc atc ctg ggg gcg      831
Glu Thr Thr Leu Ser Leu Val Lys Thr Val Val Ile Ile Leu Gly Ala
    235                 240                 245

ttc gtg gtc tgc tgg aca cca ggc cag gtg gta ctg ctc ctg gat ggt      879
Phe Val Val Cys Trp Thr Pro Gly Gln Val Val Leu Leu Leu Asp Gly
250                 255                 260                 265

tta ggc tgt gag tcc tgc aat gtc ctg gct gta gaa aag tac ttc cta      927
Leu Gly Cys Glu Ser Cys Asn Val Leu Ala Val Glu Lys Tyr Phe Leu
                270                 275                 280

ctg ttg gcc gag gcc aac tca ctg gtc aat gct gct gtg tac tct tgc      975
Leu Leu Ala Glu Ala Asn Ser Leu Val Asn Ala Ala Val Tyr Ser Cys
            285                 290                 295

cga gat gct gag atg cgc cgc acc ttc cgc cgc ctt ctc tgc tgc gcg     1023
Arg Asp Ala Glu Met Arg Arg Thr Phe Arg Arg Leu Leu Cys Cys Ala
        300                 305                 310

tgc ctc cgc cag tcc acc cgc gag tct gtc cac tat aca tcc tct gcc     1071
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Cys Leu Arg Gln Ser Thr Arg Glu Ser Val His Tyr Thr Ser Ser Ala
    315                 320                 325

cag gga ggt gcc agc act cgc atc atg ctt ccc gag aac ggc cac cca     1119
Gln Gly Gly Ala Ser Thr Arg Ile Met Leu Pro Glu Asn Gly His Pro
330                 335                 340                 345

ctg atg act cca ccc ttt agc tac ctt gaa ctt cag cgg tac gcg gca     1167
Leu Met Thr Pro Pro Phe Ser Tyr Leu Glu Leu Gln Arg Tyr Ala Ala
                350                 355                 360

agc aac aaa tcc aca gcc cct gat gac ttg tgg gtg ctc ctg gct caa     1215
Ser Asn Lys Ser Thr Ala Pro Asp Asp Leu Trp Val Leu Leu Ala Gln
            365                 370                 375

ccc aac caa cag gac tga ctgactggca ggacaaggtc tggcatggca            1263
Pro Asn Gln Gln Asp
        380

cagcaccact gccaggcctc cccaggcaca ccactctgcc cagggaatgg gggctttggg   1323

tcatctccca ctgcctgggg gagtcagatg gggtgcagga atctggctct tcagccatct   1383

caggtttagg gggtttgtaa cagacattat tctgttttca ctgcgtatcc ttggtaagcc   1443

ctgtggactg gttcctgctg tgtgatgctg agggttttaa ggtggggaga gataagggct   1503

ctctcgggcc atgctacccg gtatgactgg gtaatgagga cagactgtgg acaccccatc   1563

tacctgagtc tgattcttta gcagcagaga ctgaggggtg cagagtgtga gctgggaaag   1623

gtttgtggct ccttgcagcc tccagggact ggcctgtccc caatagaatt gaagcagtcc   1683

acggggaggg gatgatacaa ggagtaaacc tttctttaca ctcaaaaaaa a            1734


<210> SEQ ID NO 13
<211> LENGTH: 382
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 13

Met Val Ile Met Gly Gln Cys Tyr Tyr Asn Glu Thr Ile Gly Phe Phe
1               5                   10                  15

Tyr Asn Asn Ser Gly Lys Glu Leu Ser Ser His Trp Arg Pro Lys Asp
            20                  25                  30

Val Val Val Val Ala Leu Gly Leu Thr Val Ser Val Leu Val Leu Leu
        35                  40                  45

Thr Asn Leu Leu Val Ile Ala Ala Ile Ala Ser Asn Arg Arg Phe His
    50                  55                  60

Gln Pro Ile Tyr Tyr Leu Leu Gly Asn Leu Ala Ala Ala Asp Leu Phe
65                  70                  75                  80

Ala Gly Val Ala Tyr Leu Phe Leu Met Phe His Thr Gly Pro Arg Thr
                85                  90                  95

Ala Arg Leu Ser Leu Glu Gly Trp Phe Leu Arg Gln Gly Leu Leu Asp
            100                 105                 110

Thr Ser Leu Thr Ala Ser Val Ala Thr Leu Leu Ala Ile Ala Val Glu
        115                 120                 125

Arg His Arg Ser Val Met Ala Val Gln Leu His Ser Arg Leu Pro Arg
    130                 135                 140

Gly Arg Val Val Met Leu Ile Val Gly Val Trp Val Ala Ala Leu Gly
145                 150                 155                 160

Leu Gly Leu Leu Pro Ala His Ser Trp His Cys Leu Cys Ala Leu Asp
                165                 170                 175
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Arg Cys Ser Arg Met Ala Pro Leu Leu Ser Arg Ser Tyr Leu Ala Val
            180                 185                 190

Trp Ala Leu Ser Ser Leu Leu Val Phe Leu Leu Met Val Ala Val Tyr
        195                 200                 205

Thr Arg Ile Phe Phe Tyr Val Arg Arg Arg Val Gln Arg Met Ala Glu
    210                 215                 220

His Val Ser Cys His Pro Arg Tyr Arg Glu Thr Thr Leu Ser Leu Val
225                 230                 235                 240

Lys Thr Val Val Ile Ile Leu Gly Ala Phe Val Val Cys Trp Thr Pro
                245                 250                 255

Gly Gln Val Val Leu Leu Leu Asp Gly Leu Gly Cys Glu Ser Cys Asn
            260                 265                 270

Val Leu Ala Val Glu Lys Tyr Phe Leu Leu Leu Ala Glu Ala Asn Ser
        275                 280                 285

Leu Val Asn Ala Ala Val Tyr Ser Cys Arg Asp Ala Glu Met Arg Arg
    290                 295                 300

Thr Phe Arg Arg Leu Leu Cys Cys Ala Cys Leu Arg Gln Ser Thr Arg
305                 310                 315                 320

Glu Ser Val His Tyr Thr Ser Ser Ala Gln Gly Gly Ala Ser Thr Arg
                325                 330                 335

Ile Met Leu Pro Glu Asn Gly His Pro Leu Met Thr Pro Pro Phe Ser
            340                 345                 350

Tyr Leu Glu Leu Gln Arg Tyr Ala Ala Ser Asn Lys Ser Thr Ala Pro
        355                 360                 365

Asp Asp Leu Trp Val Leu Leu Ala Gln Pro Asn Gln Gln Asp
    370                 375                 380


<210> SEQ ID NO 14
<211> LENGTH: 993
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(993)

<400> SEQUENCE: 14

atg ctg ccg gac tgg aag agc tcc ttg atc ctc atg gct tac atc atc       48
Met Leu Pro Asp Trp Lys Ser Ser Leu Ile Leu Met Ala Tyr Ile Ile
1               5                   10                  15

atc ttc ctc act ggc ctc cct gcc aac ctc ctg gcc ctg cgg gcc ttt       96
Ile Phe Leu Thr Gly Leu Pro Ala Asn Leu Leu Ala Leu Arg Ala Phe
            20                  25                  30

gtg ggg cgg atc cgc cag ccc cag cct gca cct gtg cac atc ctc ctg      144
Val Gly Arg Ile Arg Gln Pro Gln Pro Ala Pro Val His Ile Leu Leu
        35                  40                  45

ctg agc ctg acg ctg gcc gac ctc ctc ctg ctg ctg ctg ctg ccc ttc      192
Leu Ser Leu Thr Leu Ala Asp Leu Leu Leu Leu Leu Leu Leu Pro Phe
    50                  55                  60

aag atc atc gag gct gcg tcg aac ttc cgc tgg tac ctg ccc aag gtc      240
Lys Ile Ile Glu Ala Ala Ser Asn Phe Arg Trp Tyr Leu Pro Lys Val
65                  70                  75                  80

gtc tgc gcc ctc acg agt ttt ggc ttc tac agc agc atc tac tgc agc      288
Val Cys Ala Leu Thr Ser Phe Gly Phe Tyr Ser Ser Ile Tyr Cys Ser
                85                  90                  95

acg tgg ctc ctg gcg ggc atc agc atc gag cgc tac ctg gga gtg gct      336
Thr Trp Leu Leu Ala Gly Ile Ser Ile Glu Arg Tyr Leu Gly Val Ala
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           100                 105                 110

ttc ccc gtg cag tac aag ctc tcc cgc cgg cct ctg tat gga gtg att      384
Phe Pro Val Gln Tyr Lys Leu Ser Arg Arg Pro Leu Tyr Gly Val Ile
        115                 120                 125

gca gct ctg gtg gcc tgg gtt atg tcc ttt ggt cac tgc acc atc gtg      432
Ala Ala Leu Val Ala Trp Val Met Ser Phe Gly His Cys Thr Ile Val
    130                 135                 140

atc atc gtt caa tac ttg aac acg act gag cag gtc aga agt ggc aat      480
Ile Ile Val Gln Tyr Leu Asn Thr Thr Glu Gln Val Arg Ser Gly Asn
145                 150                 155                 160

gaa att acc tgc tac gag aac ttc acc gat aac cag ttg gac gtg gtg      528
Glu Ile Thr Cys Tyr Glu Asn Phe Thr Asp Asn Gln Leu Asp Val Val
                165                 170                 175

ctg ccc gtg cgg ctg gag ctg tgc ctg gtg ctc ttc ttc atc ccc atg      576
Leu Pro Val Arg Leu Glu Leu Cys Leu Val Leu Phe Phe Ile Pro Met
            180                 185                 190

gca gtc acc atc ttc tgc tac tgg cgt ttt gtg tgg atc atg ctc tcc      624
Ala Val Thr Ile Phe Cys Tyr Trp Arg Phe Val Trp Ile Met Leu Ser
        195                 200                 205

cag ccc ctt gtg ggg gcc cag agg cgg cgc cga gcc gtg ggg ctg gct      672
Gln Pro Leu Val Gly Ala Gln Arg Arg Arg Arg Ala Val Gly Leu Ala
    210                 215                 220

gtg gtg acg ctg ctc aat ttc ctg gtg tgc ttc gga cct tac aac gtg      720
Val Val Thr Leu Leu Asn Phe Leu Val Cys Phe Gly Pro Tyr Asn Val
225                 230                 235                 240

tcc cac ctg gtg ggg tat cac cag aga aaa agc ccc tgg tgg cgg tca      768
Ser His Leu Val Gly Tyr His Gln Arg Lys Ser Pro Trp Trp Arg Ser
                245                 250                 255

ata gcc gtg gtg ttc agt tca ctc aac gcc agt ctg gac ccc ctg ctc      816
Ile Ala Val Val Phe Ser Ser Leu Asn Ala Ser Leu Asp Pro Leu Leu
            260                 265                 270

ttc tat ttc tct tct tca gtg gtg cgc agg gca ttt ggg aga ggg ctg      864
Phe Tyr Phe Ser Ser Ser Val Val Arg Arg Ala Phe Gly Arg Gly Leu
        275                 280                 285

cag gtg ctg cgg aat cag ggc tcc tcc ctg ttg gga cgc aga ggc aaa      912
Gln Val Leu Arg Asn Gln Gly Ser Ser Leu Leu Gly Arg Arg Gly Lys
    290                 295                 300

gac aca gca gag ggg aca aat gag gac agg ggt gtg ggt caa gga gaa      960
Asp Thr Ala Glu Gly Thr Asn Glu Asp Arg Gly Val Gly Gln Gly Glu
305                 310                 315                 320

ggg atg cca agt tcg gac ttc act aca gag tag                          993
Gly Met Pro Ser Ser Asp Phe Thr Thr Glu
                325                 330


<210> SEQ ID NO 15
<211> LENGTH: 330
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 15

Met Leu Pro Asp Trp Lys Ser Ser Leu Ile Leu Met Ala Tyr Ile Ile
1               5                   10                  15

Ile Phe Leu Thr Gly Leu Pro Ala Asn Leu Leu Ala Leu Arg Ala Phe
            20                  25                  30

Val Gly Arg Ile Arg Gln Pro Gln Pro Ala Pro Val His Ile Leu Leu
        35                  40                  45

Leu Ser Leu Thr Leu Ala Asp Leu Leu Leu Leu Leu Leu Leu Pro Phe
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    50                  55                  60

Lys Ile Ile Glu Ala Ala Ser Asn Phe Arg Trp Tyr Leu Pro Lys Val
65                  70                  75                  80

Val Cys Ala Leu Thr Ser Phe Gly Phe Tyr Ser Ser Ile Tyr Cys Ser
                85                  90                  95

Thr Trp Leu Leu Ala Gly Ile Ser Ile Glu Arg Tyr Leu Gly Val Ala
            100                 105                 110

Phe Pro Val Gln Tyr Lys Leu Ser Arg Arg Pro Leu Tyr Gly Val Ile
        115                 120                 125

Ala Ala Leu Val Ala Trp Val Met Ser Phe Gly His Cys Thr Ile Val
    130                 135                 140

Ile Ile Val Gln Tyr Leu Asn Thr Thr Glu Gln Val Arg Ser Gly Asn
145                 150                 155                 160

Glu Ile Thr Cys Tyr Glu Asn Phe Thr Asp Asn Gln Leu Asp Val Val
                165                 170                 175

Leu Pro Val Arg Leu Glu Leu Cys Leu Val Leu Phe Phe Ile Pro Met
            180                 185                 190

Ala Val Thr Ile Phe Cys Tyr Trp Arg Phe Val Trp Ile Met Leu Ser
        195                 200                 205

Gln Pro Leu Val Gly Ala Gln Arg Arg Arg Arg Ala Val Gly Leu Ala
    210                 215                 220

Val Val Thr Leu Leu Asn Phe Leu Val Cys Phe Gly Pro Tyr Asn Val
225                 230                 235                 240

Ser His Leu Val Gly Tyr His Gln Arg Lys Ser Pro Trp Trp Arg Ser
                245                 250                 255

Ile Ala Val Val Phe Ser Ser Leu Asn Ala Ser Leu Asp Pro Leu Leu
            260                 265                 270

Phe Tyr Phe Ser Ser Ser Val Val Arg Arg Ala Phe Gly Arg Gly Leu
        275                 280                 285

Gln Val Leu Arg Asn Gln Gly Ser Ser Leu Leu Gly Arg Arg Gly Lys
    290                 295                 300

Asp Thr Ala Glu Gly Thr Asn Glu Asp Arg Gly Val Gly Gln Gly Glu
305                 310                 315                 320

Gly Met Pro Ser Ser Asp Phe Thr Thr Glu
                325                 330


<210> SEQ ID NO 16
<211> LENGTH: 1287
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (72)..(1085)

<400> SEQUENCE: 16

cctgtgtgcc acgtgctgga caaatcttaa ctcctcaagg actcccaaaa ccagagacac     60

caggagcctg a atg ggg aac gat tct gtc agc tac gag tat ggg gat tac     110
             Met Gly Asn Asp Ser Val Ser Tyr Glu Tyr Gly Asp Tyr
             1               5                   10

agc gac ctc tcg gac cgc cct gtg gac tgc ctg gat ggc gcc tgc ctg      158
Ser Asp Leu Ser Asp Arg Pro Val Asp Cys Leu Asp Gly Ala Cys Leu
    15                  20                  25

gcc atc gac ccg ctg cgc gtg gcc ccg ctc cca ctg tat gcc gcc atc      206
Ala Ile Asp Pro Leu Arg Val Ala Pro Leu Pro Leu Tyr Ala Ala Ile
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30                  35                  40                  45

ttc ctg gtg ggg gtg ccg ggc aat gcc atg gtg gcc tgg gtg gct ggg      254
Phe Leu Val Gly Val Pro Gly Asn Ala Met Val Ala Trp Val Ala Gly
                50                  55                  60

aag gtg gcc cgc cgg agg gtg ggt gcc acc tgg ttg ctc cac ctg gcc      302
Lys Val Ala Arg Arg Arg Val Gly Ala Thr Trp Leu Leu His Leu Ala
            65                  70                  75

gtg gcg gat ttg ctg tgc tgt ttg tct ctg ccc atc ctg gca gtg ccc      350
Val Ala Asp Leu Leu Cys Cys Leu Ser Leu Pro Ile Leu Ala Val Pro
        80                  85                  90

att gcc cgt gga ggc cac tgg ccg tat ggt gca gtg ggc tgt cgg gcg      398
Ile Ala Arg Gly Gly His Trp Pro Tyr Gly Ala Val Gly Cys Arg Ala
    95                  100                 105

ctg ccc tcc atc atc ctg ctg acc atg tat gcc agc gtc ctg ctc ctg      446
Leu Pro Ser Ile Ile Leu Leu Thr Met Tyr Ala Ser Val Leu Leu Leu
110                 115                 120                 125

gca gct ctc agt gcc gac ctc tgc ttc ctg gct ctc ggg cct gcc tgg      494
Ala Ala Leu Ser Ala Asp Leu Cys Phe Leu Ala Leu Gly Pro Ala Trp
                130                 135                 140

tgg tct acg gtt cag cgg gcg tgc ggg gtg cag gtg gcc tgt ggg gca      542
Trp Ser Thr Val Gln Arg Ala Cys Gly Val Gln Val Ala Cys Gly Ala
            145                 150                 155

gcc tgg aca ctg gcc ttg ctg ctc acc gtg ccc tcc gcc atc tac cgc      590
Ala Trp Thr Leu Ala Leu Leu Leu Thr Val Pro Ser Ala Ile Tyr Arg
        160                 165                 170

cgg ctg cac cag gag cac ttc cca gcc cgg ctg cag tgt gtg gtg gac      638
Arg Leu His Gln Glu His Phe Pro Ala Arg Leu Gln Cys Val Val Asp
    175                 180                 185

tac ggc ggc tcc tcc agc acc gag aat gcg gtg act gcc atc cgg ttt      686
Tyr Gly Gly Ser Ser Ser Thr Glu Asn Ala Val Thr Ala Ile Arg Phe
190                 195                 200                 205

ctt ttt ggc ttc ctg ggg ccc ctg gtg gcc gtg gcc agc tgc cac agt      734
Leu Phe Gly Phe Leu Gly Pro Leu Val Ala Val Ala Ser Cys His Ser
                210                 215                 220

gcc ctc ctg tgc tgg gca gcc cga cgc tgc cgg ccg ctg ggc aca gcc      782
Ala Leu Leu Cys Trp Ala Ala Arg Arg Cys Arg Pro Leu Gly Thr Ala
            225                 230                 235

att gtg gtg ggg ttt ttt gtc tgc tgg gca ccc tac cac ctg ctg ggg      830
Ile Val Val Gly Phe Phe Val Cys Trp Ala Pro Tyr His Leu Leu Gly
        240                 245                 250

ctg gtg ctc act gtg gcg gcc ccg aac tcc gca ctc ctg gcc agg gcc      878
Leu Val Leu Thr Val Ala Ala Pro Asn Ser Ala Leu Leu Ala Arg Ala
    255                 260                 265

ctg cgg gct gaa ccc ctc atc gtg ggc ctt gcc ctc gct cac agc tgc      926
Leu Arg Ala Glu Pro Leu Ile Val Gly Leu Ala Leu Ala His Ser Cys
270                 275                 280                 285

ctc aat ccc atg ctc ttc ctg tat ttt ggg agg gct caa ctc cgc cgg      974
Leu Asn Pro Met Leu Phe Leu Tyr Phe Gly Arg Ala Gln Leu Arg Arg
                290                 295                 300

tca ctg cca gct gcc tgt cac tgg gcc ctg agg gag tcc cag ggc cag     1022
Ser Leu Pro Ala Ala Cys His Trp Ala Leu Arg Glu Ser Gln Gly Gln
            305                 310                 315

gac gaa agt gtg gac agc aag aaa tcc acc agc cat gac ctg gtc tcg     1070
Asp Glu Ser Val Asp Ser Lys Lys Ser Thr Ser His Asp Leu Val Ser
        320                 325                 330

gag atg gag gtg tag gctggagaga cattgtgggt gtgtatcttc ttatctcatt     1125
Glu Met Glu Val
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335

tcacaagact ggcttcaggc atagctggat ccaggagctc aatgatgtct tcattttatt 1185

ccttccttca ttcaacagat atccatcatg cacttgctat gtgcaaggcc tttttaggca 1245

ctagagatat agcagtgacc aaaacagaca caaatcctgc cc 1287

<210> SEQ ID NO 17
<211> LENGTH: 337
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 17

Met Gly Asn Asp Ser Val Ser Tyr Glu Tyr Gly Asp Tyr Ser Asp Leu
1 5 10 15

Ser Asp Arg Pro Val Asp Cys Leu Asp Gly Ala Cys Leu Ala Ile Asp
20 25 30

Pro Leu Arg Val Ala Pro Leu Pro Leu Tyr Ala Ala Ile Phe Leu Val
35 40 45

Gly Val Pro Gly Asn Ala Met Val Ala Trp Val Ala Gly Lys Val Ala
50 55 60

Arg Arg Arg Val Gly Ala Thr Trp Leu Leu His Leu Ala Val Ala Asp
65 70 75 80

Leu Leu Cys Cys Leu Ser Leu Pro Ile Leu Ala Val Pro Ile Ala Arg
85 90 95

Gly Gly His Trp Pro Tyr Gly Ala Val Gly Cys Arg Ala Leu Pro Ser
100 105 110

Ile Ile Leu Leu Thr Met Tyr Ala Ser Val Leu Leu Leu Ala Ala Leu
115 120 125

Ser Ala Asp Leu Cys Phe Leu Ala Leu Gly Pro Ala Trp Trp Ser Thr
130 135 140

Val Gln Arg Ala Cys Gly Val Gln Val Ala Cys Gly Ala Ala Trp Thr
145 150 155 160

Leu Ala Leu Leu Leu Thr Val Pro Ser Ala Ile Tyr Arg Arg Leu His
165 170 175

Gln Glu His Phe Pro Ala Arg Leu Gln Cys Val Val Asp Tyr Gly Gly
180 185 190

Ser Ser Ser Thr Glu Asn Ala Val Thr Ala Ile Arg Phe Leu Phe Gly
195 200 205

Phe Leu Gly Pro Leu Val Ala Val Ala Ser Cys His Ser Ala Leu Leu
210 215 220

Cys Trp Ala Ala Arg Arg Cys Arg Pro Leu Gly Thr Ala Ile Val Val
225 230 235 240

Gly Phe Phe Val Cys Trp Ala Pro Tyr His Leu Leu Gly Leu Val Leu
245 250 255

Thr Val Ala Ala Pro Asn Ser Ala Leu Leu Ala Arg Ala Leu Arg Ala
260 265 270

Glu Pro Leu Ile Val Gly Leu Ala Leu Ala His Ser Cys Leu Asn Pro
275 280 285

Met Leu Phe Leu Tyr Phe Gly Arg Ala Gln Leu Arg Arg Ser Leu Pro
290 295 300

Ala Ala Cys His Trp Ala Leu Arg Glu Ser Gln Gly Gln Asp Glu Ser
305 310 315 320

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Val Asp Ser Lys Lys Ser Thr Ser His Asp Leu Val Ser Glu Met Glu
                325                 330                 335

Val


<210> SEQ ID NO 18
<211> LENGTH: 2858
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (174)..(1175)

<400> SEQUENCE: 18

aacagtattt tccttttcaa cacatctatt gaaagtgttg gataaatgca ggatgttaat     60

atgctataaa cataaagtct gtttttaaaa aatagcattt gaaaatcatg aagggctttt    120

tgttttcttt tgtttgtata tatgtttatt ggtaacaggt gacactggaa gca atg       176
                                                          Met
                                                          1

aac acc aca gtg atg caa ggc ttc aac aga tct gag cgg tgc ccc aga      224
Asn Thr Thr Val Met Gln Gly Phe Asn Arg Ser Glu Arg Cys Pro Arg
          5                  10                  15

gac act cgg ata gta cag ctg gta ttc cca gcc ctc tac aca gtg gtt      272
Asp Thr Arg Ile Val Gln Leu Val Phe Pro Ala Leu Tyr Thr Val Val
      20                  25                  30

ttc ttg acc ggc atc ctg ctg aat act ttg gct ctg tgg gtg ttt gtt      320
Phe Leu Thr Gly Ile Leu Leu Asn Thr Leu Ala Leu Trp Val Phe Val
  35                  40                  45

cac atc ccc agc tcc tcc acc ttc atc atc tac ctc aaa aac act ttg      368
His Ile Pro Ser Ser Ser Thr Phe Ile Ile Tyr Leu Lys Asn Thr Leu
50                  55                  60                  65

gtg gcc gac ttg ata atg aca ctc atg ctt cct ttc aaa atc ctc tct      416
Val Ala Asp Leu Ile Met Thr Leu Met Leu Pro Phe Lys Ile Leu Ser
              70                  75                  80

gac tca cac ctg gca ccc tgg cag ctc aga gct ttt gtg tgt cgt ttt      464
Asp Ser His Leu Ala Pro Trp Gln Leu Arg Ala Phe Val Cys Arg Phe
          85                  90                  95

tct tcg gtg ata ttt tat gag acc atg tat gtg ggc atc gtg ctg tta      512
Ser Ser Val Ile Phe Tyr Glu Thr Met Tyr Val Gly Ile Val Leu Leu
      100                 105                 110

ggg ctc ata gcc ttt gac aga ttc ctc aag atc atc aga cct ttg aga      560
Gly Leu Ile Ala Phe Asp Arg Phe Leu Lys Ile Ile Arg Pro Leu Arg
  115                 120                 125

aat att ttt cta aaa aaa cct gtt ttt gca aaa acg gtc tca atc ttc      608
Asn Ile Phe Leu Lys Lys Pro Val Phe Ala Lys Thr Val Ser Ile Phe
130                 135                 140                 145

atc tgg ttc ttt ttg ttc ttc atc tcc ctg cca aat acg atc ttg agc      656
Ile Trp Phe Phe Leu Phe Phe Ile Ser Leu Pro Asn Thr Ile Leu Ser
              150                 155                 160

aac aag gaa gca aca cca tcg tct gtg aaa aag tgt gct tcc tta aag      704
Asn Lys Glu Ala Thr Pro Ser Ser Val Lys Lys Cys Ala Ser Leu Lys
          165                 170                 175

ggg cct ctg ggg ctg aaa tgg cat caa atg gta aat aac ata tgc cag      752
Gly Pro Leu Gly Leu Lys Trp His Gln Met Val Asn Asn Ile Cys Gln
      180                 185                 190

ttt att ttc tgg act gtt ttt atc cta atg ctt gtg ttt tat gtg gtt      800
Phe Ile Phe Trp Thr Val Phe Ile Leu Met Leu Val Phe Tyr Val Val
  195                 200                 205
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att gca aaa aaa gta tat gat tct tat aga aag tcc aaa agt aag gac      848
Ile Ala Lys Lys Val Tyr Asp Ser Tyr Arg Lys Ser Lys Ser Lys Asp
210                 215                 220                 225

aga aaa aac aac aaa aag ctg gaa ggc aaa gta ttt gtt gtc gtg gct      896
Arg Lys Asn Asn Lys Lys Leu Glu Gly Lys Val Phe Val Val Val Ala
                230                 235                 240

gtc ttc ttt gtg tgt ttt gct cca ttt cat ttt gcc aga gtt cca tat      944
Val Phe Phe Val Cys Phe Ala Pro Phe His Phe Ala Arg Val Pro Tyr
            245                 250                 255

act cac agt caa acc aac aat aag act gac tgt aga ctg caa aat caa      992
Thr His Ser Gln Thr Asn Asn Lys Thr Asp Cys Arg Leu Gln Asn Gln
        260                 265                 270

ctg ttt att gct aaa gaa aca act ctc ttt ttg gca gca act aac att     1040
Leu Phe Ile Ala Lys Glu Thr Thr Leu Phe Leu Ala Ala Thr Asn Ile
    275                 280                 285

tgt atg gat ccc tta ata tac ata ttc tta tgt aaa aaa ttc aca gaa     1088
Cys Met Asp Pro Leu Ile Tyr Ile Phe Leu Cys Lys Lys Phe Thr Glu
290                 295                 300                 305

aag cta cca tgt atg caa ggg aga aag acc aca gca tca agc caa gaa     1136
Lys Leu Pro Cys Met Gln Gly Arg Lys Thr Thr Ala Ser Ser Gln Glu
                310                 315                 320

aat cat agc agt cag aca gac aac ata acc tta ggc tga caactgtaca      1185
Asn His Ser Ser Gln Thr Asp Asn Ile Thr Leu Gly
            325                 330

tagggttaac ttctatttat tgatgagact tccgtagata atgtggaaat caaatttaac   1245

caagaaaaaa agattggaac aaatgctctc ttacatttta ttatcctcgt gtacagaaaa   1305

gattatataa aatttaaatc cacatagatc tattcataag ctgaatgaac cattactaag   1365

agaatgcaac aggatacaaa tggccactag aggtcattat ttctttcttt ctttttttt    1425

ttttttaatt tcaagagcat ttcactttaa cattttggaa aagactaagg agaaacgtat   1485

atccctacaa acctcccctc caaacacctt ctcacattct tttccacaat tcacataaca   1545

ctactgcttt tgtgcccctt aaatgtagat atgtgctgaa agaaaaaaaa aacgcccaac   1605

tcttgaagtc cattgctgaa aactgcagcc aggggttgaa agggatgcag acttgaagag   1665

tctgaggaac tgaagtgggt cagcaagacc tctgaaatcc tgggtaaagg attttctcct   1725

tacaattaca aacagcctct ttcacattac aataatatac cataggaggc acaagcacca   1785

ttattaagcc actttgctta caccttaagt gtgtacaatt caagtgtgag aatgctgtgt   1845

taactattct ttggaattct ccttctgtcc agcaaatact ctaatgatgg ttaaacatgg   1905

cacctactca gcaatgcctt cctggaccac aacccctatc cccctgcccc accctcctca   1965

ttaaaaacaa atacttctac tgtttgggtg tgtgataggg ttctcaatgc agatctccct   2025

tttctagtta gctatattct tgactgcatc cgctaaaaat gttaaagctt cttgagagac   2085

agacatgcca gattttcttg gtatctccca taatacgacc tacagtccat ggtctacaga   2145

tgttttaaat agaattgcta ttctcgatac atacaaagac gtaattgctg acccacaatc   2205

agtaacatcc atattgagag atttttcaaa ggatggtgac cctgcttgta tttatttacc   2265

ttggtatttt ttcttgcatc cttctgtgat tcaaaaaagt aaaatgtggc tttctgaaat   2325

gatggataag agtctacatc ttctagaaaa aatacataaa ggagtagtta agctctgtaa   2385

atgtgccacg agctccaaca cgaccatcgt agggtgaagc ccacgttttc ttccatggcc   2445

tcaaaggccc tagaacttgc ctacctttct ggccttacct cctagctact tatccatctc   2505
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ttgaacttta tactcttgta taaatttcta actttcagaa aatgccatac tctgttttgg 2565

caccacacat gtatatttcc ccctggtaca cttggaagac tcttatccat ctgtgaaacc 2625

ctatgttgtc atcacttggt ccatgaaata ttacctggcc aatatcccac catcacctca 2685

aacccaatca ccccctcctc tgtatgctgt cacacctata ttattaaact tatcacattg 2745

cattgtaatt acttcctgac ctttgtatct actcttttag taactgatgt atatatctga 2805

aaggagagat tgtttcattg tgcaatcaat aaatgtttga taaaataaag ccc 2858

<210> SEQ ID NO 19
<211> LENGTH: 333
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 19

Met Asn Thr Thr Val Met Gln Gly Phe Asn Arg Ser Glu Arg Cys Pro
1 5 10 15

Arg Asp Thr Arg Ile Val Gln Leu Val Phe Pro Ala Leu Tyr Thr Val
20 25 30

Val Phe Leu Thr Gly Ile Leu Leu Asn Thr Leu Ala Leu Trp Val Phe
35 40 45

Val His Ile Pro Ser Ser Ser Thr Phe Ile Ile Tyr Leu Lys Asn Thr
50 55 60

Leu Val Ala Asp Leu Ile Met Thr Leu Met Leu Pro Phe Lys Ile Leu
65 70 75 80

Ser Asp Ser His Leu Ala Pro Trp Gln Leu Arg Ala Phe Val Cys Arg
85 90 95

Phe Ser Ser Val Ile Phe Tyr Glu Thr Met Tyr Val Gly Ile Val Leu
100 105 110

Leu Gly Leu Ile Ala Phe Asp Arg Phe Leu Lys Ile Ile Arg Pro Leu
115 120 125

Arg Asn Ile Phe Leu Lys Lys Pro Val Phe Ala Lys Thr Val Ser Ile
130 135 140

Phe Ile Trp Phe Phe Leu Phe Phe Ile Ser Leu Pro Asn Thr Ile Leu
145 150 155 160

Ser Asn Lys Glu Ala Thr Pro Ser Ser Val Lys Lys Cys Ala Ser Leu
165 170 175

Lys Gly Pro Leu Gly Leu Lys Trp His Gln Met Val Asn Asn Ile Cys
180 185 190

Gln Phe Ile Phe Trp Thr Val Phe Ile Leu Met Leu Val Phe Tyr Val
195 200 205

Val Ile Ala Lys Lys Val Tyr Asp Ser Tyr Arg Lys Ser Lys Ser Lys
210 215 220

Asp Arg Lys Asn Asn Lys Lys Leu Glu Gly Lys Val Phe Val Val Val
225 230 235 240

Ala Val Phe Phe Val Cys Phe Ala Pro Phe His Phe Ala Arg Val Pro
245 250 255

Tyr Thr His Ser Gln Thr Asn Asn Lys Thr Asp Cys Arg Leu Gln Asn
260 265 270

Gln Leu Phe Ile Ala Lys Glu Thr Thr Leu Phe Leu Ala Ala Thr Asn
275 280 285

Ile Cys Met Asp Pro Leu Ile Tyr Ile Phe Leu Cys Lys Lys Phe Thr
290 295 300

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Glu Lys Leu Pro Cys Met Gln Gly Arg Lys Thr Thr Ala Ser Ser Gln
305                 310                 315                 320

Glu Asn His Ser Ser Gln Thr Asp Asn Ile Thr Leu Gly
                325                 330
```

<210> SEQ ID NO 20
<211> LENGTH: 878
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 20

```
ttttttttt ttttaagtgg taaaaaaaat ttggttattt ataaatcaat tacacaataa     60

aataattatt tttaaaagtc acaaatacaa tcgtggtata aagtcatttg ggcatcaagt    120

atctcttaaa tatgtggcaa actatttgtc caaagagatg tggtccaaac ccgtcgaagg    180

ctttataatt tggtattaga taacaaggtg aacaaaactg acaataaata ctccaacgaa    240

ttatttttta aaatactaag gggcaaaggc tattctaagg ggcaaaacaa tctattactc    300

agacctacct gaaaatttca cgtgaagtcg atcaaaagtt atacaaaatt ggtatttaca    360

tgtttaaaat ccggattggc atttttcttt aataataata catacaaaaa ctcagagggt    420

taataaagaa ataattcaaa gtcctaataa gtcaacaaac agatttcatt ataagctgga    480

acataaaaga gacaccatgg ttggctgtct cttttcaaaa attatcacgg ccacttggtc    540

aaacgggaag cagcattcag aacaatggtt ctcaaatctc ggggtggcat aaacaccatg    600

caggttggtt accacacaga ttcctgggcc tgttcccagt ctgaagctct cataaaggat    660

ctgaggaatc tgcttcgtga caagattcag actatttatt tatttatcac ccaagctgga    720

gtgcaggggt gcaacccggt caggaaacct cgcctcggag taaaagggaa accaaatcgg    780

ggcccaggcc ctgagaatgg gttcaaacgg gcccaccacc ggtaacggta tcagaaaaaa    840

acggtccaga aggccagggg tcaaccgaac caagaagc                            878
```

<210> SEQ ID NO 21
<211> LENGTH: 1646
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (99)..(743)

<400> SEQUENCE: 21

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tagtgatctt ttctgagtgt ctcctacttg cgacaaggtg gacttgggag gaaagccgtc     60

tgccaaagcc tgaagcctcc aagccataaa caacccca atg gcc tcc cac gaa gtt    116
                                        Met Ala Ser His Glu Val
                                        1               5

gat aat gca gag ctg ggg tca gcc tct gcc cat ggt acc cca ggc agt      164
Asp Asn Ala Glu Leu Gly Ser Ala Ser Ala His Gly Thr Pro Gly Ser
            10                  15                  20

gag acg gga cca gaa gag ctg aat act tct gtc tac cac ccc ata aat      212
Glu Thr Gly Pro Glu Glu Leu Asn Thr Ser Val Tyr His Pro Ile Asn
        25                  30                  35

gga tca cca gat tat cag aaa gca aaa tta caa gtt ctt ggg gcc atc      260
Gly Ser Pro Asp Tyr Gln Lys Ala Lys Leu Gln Val Leu Gly Ala Ile
    40                  45                  50

cag atc ctg aat gca gca atg att ctg gct ttg ggt gtc ttt ctg ggt      308
Gln Ile Leu Asn Ala Ala Met Ile Leu Ala Leu Gly Val Phe Leu Gly
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55                  60                  65                  70

tcc ttg caa tac cca tac cac ttc caa aag cac ttc ttt ttc ttc acc      356
Ser Leu Gln Tyr Pro Tyr His Phe Gln Lys His Phe Phe Phe Phe Thr
                75                  80                  85

ttc tac aca ggc tac ccg att tgg ggt gct gtg ttt ttc tgt agt tca      404
Phe Tyr Thr Gly Tyr Pro Ile Trp Gly Ala Val Phe Phe Cys Ser Ser
            90                  95                  100

gga acc ttg tct gtt gta gca ggg ata aaa ccc aca aga aca tgg ata      452
Gly Thr Leu Ser Val Val Ala Gly Ile Lys Pro Thr Arg Thr Trp Ile
        105                 110                 115

cag aac agt ttt gga atg aac att gcc agt gct aca att gca cta gtg      500
Gln Asn Ser Phe Gly Met Asn Ile Ala Ser Ala Thr Ile Ala Leu Val
    120                 125                 130

ggg act gct ttt ctc tca cta aat ata gca gtt aat atc cag tca tta      548
Gly Thr Ala Phe Leu Ser Leu Asn Ile Ala Val Asn Ile Gln Ser Leu
135                 140                 145                 150

agg agt tgt cac tct tca tca gag tca ccg gac cta tgc aat tac atg      596
Arg Ser Cys His Ser Ser Ser Glu Ser Pro Asp Leu Cys Asn Tyr Met
                155                 160                 165

ggc tcc ata tca aat ggc atg gtg tct cta ctg ctg att ctc acc ttg      644
Gly Ser Ile Ser Asn Gly Met Val Ser Leu Leu Leu Ile Leu Thr Leu
            170                 175                 180

ctg gaa tta tgc gta act atc tct acc ata gcc atg tgg tgc aat gca      692
Leu Glu Leu Cys Val Thr Ile Ser Thr Ile Ala Met Trp Cys Asn Ala
        185                 190                 195

aac tgc tgt aat tca aga gag gaa att tcc tca cct ccc aat tct gtg      740
Asn Cys Cys Asn Ser Arg Glu Glu Ile Ser Ser Pro Pro Asn Ser Val
    200                 205                 210

taa tcaagaatac ctccttatga aaataattct gagagcatga atatttgacc           793

ttaaatctcc agtgactcag agcttcaccc acaaactcag gagaacataa gcctgctcgt    853

aaagctcaat ccttctatca tggcaccaat cacaagaacc ttggacgttt gactgactct    913

atcctttctc tcctaactat aaatcctatt tgtgtgtcgt gggtatggaa ggacagatat    973

atttctttag gcattcttgg atatctgtaa cttctatgat cattactcca aagttgtttc   1033

cagaaattgg ttctatttct tcttatccac ctactccatt gctttatgag gtttaaggaa   1093

ggaaggcggt ataatcccta ttcaatatat tttttctaaa atccaacttc tgaccgccca   1153

gtaggaagaa aaatgagaca ttttttccat tacagagaaa tgcttcttga ctttaacatc   1213

agcattataa aaagtgtcaa ataaaaaatt accatcatta tcattaaaat aaattttcac   1273

tgtatttgag atgggagggt taaggctcag ggattttatt tcagtgaact gctggaactc   1333

acacatgccc tgatatgtaa atgatgattt atgttggcga gtctgagagc aagcccaaat   1393

gtgttcttca aaggacaatg ggaaactgta aagtagagaa ctaaagaata aggcctttag   1453

aatctgacac atctgggttc aaattctgaa actgtcactt attacctgta tgaacatggg   1513

caaattatct aatctctctg atctatttttt cctcatctgt aaaataggtg taataataac   1573

aactactttg tcggttgctc tgagggttaa atgaaaataa aaagaaaatg tgaaacagca   1633

ccacaggtac ttg                                                      1646
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<210> SEQ ID NO 22
<211> LENGTH: 214
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 22

Met Ala Ser His Glu Val Asp Asn Ala Glu Leu Gly Ser Ala Ser Ala
1 5 10 15

His Gly Thr Pro Gly Ser Glu Thr Gly Pro Glu Glu Leu Asn Thr Ser
20 25 30

Val Tyr His Pro Ile Asn Gly Ser Pro Asp Tyr Gln Lys Ala Lys Leu
35 40 45

Gln Val Leu Gly Ala Ile Gln Ile Leu Asn Ala Ala Met Ile Leu Ala
50 55 60

Leu Gly Val Phe Leu Gly Ser Leu Gln Tyr Pro Tyr His Phe Gln Lys
65 70 75 80

His Phe Phe Phe Phe Thr Phe Tyr Thr Gly Tyr Pro Ile Trp Gly Ala
85 90 95

Val Phe Phe Cys Ser Ser Gly Thr Leu Ser Val Val Ala Gly Ile Lys
100 105 110

Pro Thr Arg Thr Trp Ile Gln Asn Ser Phe Gly Met Asn Ile Ala Ser
115 120 125

Ala Thr Ile Ala Leu Val Gly Thr Ala Phe Leu Ser Leu Asn Ile Ala
130 135 140

Val Asn Ile Gln Ser Leu Arg Ser Cys His Ser Ser Ser Glu Ser Pro
145 150 155 160

Asp Leu Cys Asn Tyr Met Gly Ser Ile Ser Asn Gly Met Val Ser Leu
165 170 175

Leu Leu Ile Leu Thr Leu Leu Glu Leu Cys Val Thr Ile Ser Thr Ile
180 185 190

Ala Met Trp Cys Asn Ala Asn Cys Cys Asn Ser Arg Glu Glu Ile Ser
195 200 205

Ser Pro Pro Asn Ser Val
210

<210> SEQ ID NO 23
<211> LENGTH: 2481
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (179)..(1276)

<400> SEQUENCE: 23

ggccttgtca gctcacagca ggcgttaaca gcctctaatt gaggaaactg tggctggaca 60

ggttgcaagg cagttctgct ccccatcgtc ctcttgctga ctggggactg ctgagcccgt 120

gcacggcaga gagtctggtg gggtggaggg gctggcctgg cccctctgtc ctgtggaa 178

atg ctg ggg caa gtg gtc acc ctc ata ctc ctc ctg ctc ctc aag gtg 226
Met Leu Gly Gln Val Val Thr Leu Ile Leu Leu Leu Leu Leu Lys Val
1 5 10 15

tat cag ggc aaa gga tgc cag gga tca gct gac cat gtg gtt agc atc 274
Tyr Gln Gly Lys Gly Cys Gln Gly Ser Ala Asp His Val Val Ser Ile
20 25 30

tcg gga gtg cct ctt cag tta caa cca aac agc ata cag acg aag gtt 322
Ser Gly Val Pro Leu Gln Leu Gln Pro Asn Ser Ile Gln Thr Lys Val
35 40 45

gac agc att gca tgg aag aag ttg ctg ccc tca caa aat gga ttt cat 370
Asp Ser Ile Ala Trp Lys Lys Leu Leu Pro Ser Gln Asn Gly Phe His
50 55 60

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cac ata ttg aag tgg gag aat ggc tct ttg cct tcc aat act tcc aat      418
His Ile Leu Lys Trp Glu Asn Gly Ser Leu Pro Ser Asn Thr Ser Asn
65                  70                  75                  80

gat aga ttc agt ttt ata gtc aag aac ttg agt ctt ctc atc aag gca      466
Asp Arg Phe Ser Phe Ile Val Lys Asn Leu Ser Leu Leu Ile Lys Ala
                85                  90                  95

gct cag cag cag gac agt ggc ctc tac tgc ctg gag gtc acc agt ata      514
Ala Gln Gln Gln Asp Ser Gly Leu Tyr Cys Leu Glu Val Thr Ser Ile
            100                 105                 110

tct gga aaa gtt cag aca gcc acg ttc cag gtt ttt gta ttt gat aaa      562
Ser Gly Lys Val Gln Thr Ala Thr Phe Gln Val Phe Val Phe Asp Lys
        115                 120                 125

gtt gag aaa ccc cgc cta cag ggg cag ggg aag atc ctg gac aga ggg      610
Val Glu Lys Pro Arg Leu Gln Gly Gln Gly Lys Ile Leu Asp Arg Gly
    130                 135                 140

aga tgc caa gtg gct ctg tct tgc ttg gtc tcc agg gat ggc aat gtg      658
Arg Cys Gln Val Ala Leu Ser Cys Leu Val Ser Arg Asp Gly Asn Val
145                 150                 155                 160

tcc tat gct tgg tac aga ggg agc aag ctg atc cag aca gca ggg aac      706
Ser Tyr Ala Trp Tyr Arg Gly Ser Lys Leu Ile Gln Thr Ala Gly Asn
                165                 170                 175

ctc acc tac ctg gac gag gag gtt gac att aat ggc act cac aca tat      754
Leu Thr Tyr Leu Asp Glu Glu Val Asp Ile Asn Gly Thr His Thr Tyr
            180                 185                 190

acc tgc aat gtc agc aat cct gtt agc tgg gaa agc cac acc ctg aat      802
Thr Cys Asn Val Ser Asn Pro Val Ser Trp Glu Ser His Thr Leu Asn
        195                 200                 205

ctc act cag gac tgt cag aat gcc cat cag gaa ttc aga ttt tgg ccg      850
Leu Thr Gln Asp Cys Gln Asn Ala His Gln Glu Phe Arg Phe Trp Pro
    210                 215                 220

ttt ttg gtg atc atc gtg att cta agc gca ctg ttc ctt ggc acc ctt      898
Phe Leu Val Ile Ile Val Ile Leu Ser Ala Leu Phe Leu Gly Thr Leu
225                 230                 235                 240

gcc tgc ttc tgt gtg tgg agg aga aag agg aag gag aag cag tca gag      946
Ala Cys Phe Cys Val Trp Arg Arg Lys Arg Lys Glu Lys Gln Ser Glu
                245                 250                 255

acc agt ccc aag gaa ttt ttg aca att tac gaa gat gtc aag gat ctg      994
Thr Ser Pro Lys Glu Phe Leu Thr Ile Tyr Glu Asp Val Lys Asp Leu
            260                 265                 270

aaa acc agg aga aat cac gag cag gag cag act ttt cct gga ggg ggg     1042
Lys Thr Arg Arg Asn His Glu Gln Glu Gln Thr Phe Pro Gly Gly Gly
        275                 280                 285

agc acc atc tac tct atg atc cag tcc cag tct tct gct ccc acg tca     1090
Ser Thr Ile Tyr Ser Met Ile Gln Ser Gln Ser Ser Ala Pro Thr Ser
    290                 295                 300

caa gaa cct gca tat aca tta tat tca tta att cag cct tcc agg aag     1138
Gln Glu Pro Ala Tyr Thr Leu Tyr Ser Leu Ile Gln Pro Ser Arg Lys
305                 310                 315                 320

tct gga tcc agg aag agg aac cac agc cct tcc ttc aat agc act atc     1186
Ser Gly Ser Arg Lys Arg Asn His Ser Pro Ser Phe Asn Ser Thr Ile
                325                 330                 335

tat gaa gtg att gga aag agt caa cct aaa gcc cag aac cct gct cga     1234
Tyr Glu Val Ile Gly Lys Ser Gln Pro Lys Ala Gln Asn Pro Ala Arg
            340                 345                 350

ttg agc cgc aaa gag ctg gag aac ttt gat gtt tat tcc tag             1276
Leu Ser Arg Lys Glu Leu Glu Asn Phe Asp Val Tyr Ser
        355                 360                 365
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ttgctgcagc aattctcacc tttcttgcac atcagcatct gctttgggaa ttggcacagt   1336

ggatgacggc acaggagtct ctatagaaca gttcctagtc tggagaggat atggaaattt   1396

gttcttgttc tatattttgt tttgaaaatg atgtctaaca accatgataa gagcaaggct   1456

gttaaataat atcttccaat ttacagatca gacatgaatg ggtggagggg ttaggttgtt   1516

cacaaaaggc cacattccaa gtatttgtaa tctagaaagt gttatgtaag tgatgttatt   1576

agcatcgaga ttccctccac ctgattttca agctgtcact tgtttccttt tctcccctct   1636

ctgggttgac tgcatttcta gactctcgcc ggcccaggcc catcttccaa agcaagagga   1696

aggaatgata atggtgactc aggggaagaa gaaacagccc tcctctgaaa gcctggactg   1756

tccggctgtg aactggctgg caggttctgc acgtgggtgg gggccagggc ctgggcttta   1816

ctcaattgca gagaaaaaac tttctccctg catctcatac ctttacctct ggccagttgg   1876

ccaccagggg gagtgggctg aagggagagt agatggtgca aagcaagccc atctctaagt   1936

agaaaaatca cccagagcac atgctgacct gataactggg gtgttgagac cagctttgtc   1996

catggtatga tgtttgattt atgaagacgc attgttagaa atccatttgg cttcttcata   2056

gaagtggctt cccagaggaa gaggcctctc agaaaccatg ttctatttaa gttctgagtc   2116

ctgatgagtg ttccccagga tgcacattga agggagggct caggcagctg agggctgaga   2176

atgaggcagt tggaatctag acactatgct gggttccctg agtcgtcagg ccagacattt   2236

caacaaggct gtggggagca gggctgtgac tctggctgag cccaggaaag cgacaagggt   2296

gaactgggag aggacttact cagagacccc aacaggtgat actgcacaaa gcctggttct   2356

tcaattttcc taccctgtat ctaacatagg agtttcatat aaaacggtga tatcatgcag   2416

atgcagtctg aattccttgc ctgaattaaa tttatgtatc ctctccaaaa aaaaaaaaaa   2476

aaaaa                                                               2481
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<210> SEQ ID NO 24
<211> LENGTH: 365
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 24

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Met Leu Gly Gln Val Val Thr Leu Ile Leu Leu Leu Leu Lys Val
1               5                  10                  15

Tyr Gln Gly Lys Gly Cys Gln Gly Ser Ala Asp His Val Val Ser Ile
            20                  25                  30

Ser Gly Val Pro Leu Gln Leu Gln Pro Asn Ser Ile Gln Thr Lys Val
        35                  40                  45

Asp Ser Ile Ala Trp Lys Lys Leu Leu Pro Ser Gln Asn Gly Phe His
    50                  55                  60

His Ile Leu Lys Trp Glu Asn Gly Ser Leu Pro Ser Asn Thr Ser Asn
65                  70                  75                  80

Asp Arg Phe Ser Phe Ile Val Lys Asn Leu Ser Leu Leu Ile Lys Ala
                85                  90                  95

Ala Gln Gln Gln Asp Ser Gly Leu Tyr Cys Leu Glu Val Thr Ser Ile
            100                 105                 110

Ser Gly Lys Val Gln Thr Ala Thr Phe Gln Val Phe Val Phe Asp Lys
        115                 120                 125

Val Glu Lys Pro Arg Leu Gln Gly Gln Gly Lys Ile Leu Asp Arg Gly
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    130                 135                 140

Arg Cys Gln Val Ala Leu Ser Cys Leu Val Ser Arg Asp Gly Asn Val
145                 150                 155                 160

Ser Tyr Ala Trp Tyr Arg Gly Ser Lys Leu Ile Gln Thr Ala Gly Asn
                165                 170                 175

Leu Thr Tyr Leu Asp Glu Glu Val Asp Ile Asn Gly Thr His Thr Tyr
            180                 185                 190

Thr Cys Asn Val Ser Asn Pro Val Ser Trp Glu Ser His Thr Leu Asn
        195                 200                 205

Leu Thr Gln Asp Cys Gln Asn Ala His Gln Glu Phe Arg Phe Trp Pro
    210                 215                 220

Phe Leu Val Ile Ile Val Ile Leu Ser Ala Leu Phe Leu Gly Thr Leu
225                 230                 235                 240

Ala Cys Phe Cys Val Trp Arg Arg Lys Arg Lys Glu Lys Gln Ser Glu
                245                 250                 255

Thr Ser Pro Lys Glu Phe Leu Thr Ile Tyr Glu Asp Val Lys Asp Leu
            260                 265                 270

Lys Thr Arg Arg Asn His Glu Gln Glu Gln Thr Phe Pro Gly Gly Gly
        275                 280                 285

Ser Thr Ile Tyr Ser Met Ile Gln Ser Gln Ser Ser Ala Pro Thr Ser
    290                 295                 300

Gln Glu Pro Ala Tyr Thr Leu Tyr Ser Leu Ile Gln Pro Ser Arg Lys
305                 310                 315                 320

Ser Gly Ser Arg Lys Arg Asn His Ser Pro Ser Phe Asn Ser Thr Ile
                325                 330                 335

Tyr Glu Val Ile Gly Lys Ser Gln Pro Lys Ala Gln Asn Pro Ala Arg
            340                 345                 350

Leu Ser Arg Lys Glu Leu Glu Asn Phe Asp Val Tyr Ser
        355                 360                 365


<210> SEQ ID NO 25
<211> LENGTH: 4574
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (593)..(3061)

<400> SEQUENCE: 25

gagcgggcga gggagcgcgc gcggccgcca caaagctcgg gcgccgcggg gctgcatgcg     60

gcgtacctgg cccggcgcgg cgactgctct ccgggctggc gggggccggc cgcgagcccc    120

gggggccccg aggccgcagc ttgcctgcgc gctctgagcc ttcgcaactc gcgagcaaag    180

tttggtggag gcaacgccaa gcctgagtcc tttcttcctc tcgttcccca aatccgaggc    240

agcccgcggg cgtcatgccc gcgctcctcc gcagcctggg gtacgcgctg aagcccggga    300

ggcttggcgc cggcgaagac ccaaggacca ctcttctgcg tttggagttg ctccccacaa    360

ccccgggctc gtcgctttct ccatcccgac ccagccgggg cgcggggaca acacaggtcg    420

cggaggagcg ttgccattca agtgactgca gcagcagcgg cagcgcctcg gttcctgagc    480

ccaccgcagg ctgaaggcat tgcgcgtagt ccatgcccgt agaggaagtg tgcagatggg    540

attaacgtcc acatggagat atggaagagg accggggatt ggtaccgtaa cc atg gtc    598
                                                          Met Val
                                                          1
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agc tgg ggt cgt ttc atc tgc ctg gtc gtg gtc acc atg gca acc ttg      646
Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala Thr Leu
        5                  10                  15

tcc ctg gcc cgg ccc tcc ttc agt tta gtt gag gat acc aca tta gag      694
Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr Leu Glu
    20                  25                  30

cca gaa gag cca cca acc aaa tac caa atc tct caa cca gaa gtg tac      742
Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu Val Tyr
35                  40                  45                  50

gtg gct gcg cca ggg gag tcg cta gag gtg cgc tgc ctg ttg aaa gat      790
Val Ala Ala Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu Lys Asp
                55                  60                  65

gcc gcc gtg atc agt tgg act aag gat ggg gtg cac ttg ggg ccc aac      838
Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly Pro Asn
            70                  75                  80

aat agg aca gtg ctt att ggg gag tac ttg cag ata aag ggc gcc acg      886
Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly Ala Thr
        85                  90                  95

cct aga gac tcc ggc ctc tat gct tgt act gcc agt agg act gta gac      934
Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr Val Asp
    100                 105                 110

agt gaa act tgg tac ttc atg gtg aat gtc aca gat gcc atc tca tcc      982
Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile Ser Ser
115                 120                 125                 130

gga gat gat gag gat gac acc gat ggt gcg gaa gat ttt gtc agt gag     1030
Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu
                135                 140                 145

aac agt aac aac aag aga gca cca tac tgg acc aac aca gaa aag atg     1078
Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu Lys Met
            150                 155                 160

gaa aag cgg ctc cat gct gtg cct gcg gcc aac act gtc aag ttt cgc     1126
Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys Phe Arg
        165                 170                 175

tgc cca gcc ggg ggg aac cca atg cca acc atg cgg tgg ctg aaa aac     1174
Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu Lys Asn
    180                 185                 190

ggg aag gag ttt aag cag gag cat cgc att gga ggc tac aag gta cga     1222
Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys Val Arg
195                 200                 205                 210

aac cag cac tgg agc ctc att atg gaa agt gtg gtc cca tct gac aag     1270
Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser Asp Lys
                215                 220                 225

gga aat tat acc tgt gtg gtg gag aat gaa tac ggg tcc atc aat cac     1318
Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile Asn His
            230                 235                 240

acg tac cac ctg gat gtt gtg gag cga tcg cct cac cgg ccc atc ctc     1366
Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile Leu
        245                 250                 255

caa gcc gga ctg ccg gca aat gcc tcc aca gtg gtc gga gga gac gta     1414
Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly Asp Val
    260                 265                 270

gag ttt gtc tgc aag gtt tac agt gat gcc cag ccc cac atc cag tgg     1462
Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp
275                 280                 285                 290

atc aag cac gtg gaa aag aac ggc agt aaa tac ggg ccc gac ggg ctg     1510
Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp Gly Leu
                295                 300                 305
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ccc tac ctc aag gtt ctc aag cac tcg ggg ata aat agt tcc aat gca     1558
Pro Tyr Leu Lys Val Leu Lys His Ser Gly Ile Asn Ser Ser Asn Ala
            310                 315                 320

gaa gtg ctg gct ctg ttc aat gtg acc gag gcg gat gct ggg gaa tat     1606
Glu Val Leu Ala Leu Phe Asn Val Thr Glu Ala Asp Ala Gly Glu Tyr
        325                 330                 335

ata tgt aag gtc tcc aat tat ata ggg cag gcc aac cag tct gcc tgg     1654
Ile Cys Lys Val Ser Asn Tyr Ile Gly Gln Ala Asn Gln Ser Ala Trp
    340                 345                 350

ctc act gtc ctg cca aaa cag caa gcg cct gga aga gaa aag gag att     1702
Leu Thr Val Leu Pro Lys Gln Gln Ala Pro Gly Arg Glu Lys Glu Ile
355                 360                 365                 370

aca gct tcc cca gac tac ctg gag ata gcc att tac tgc ata ggg gtc     1750
Thr Ala Ser Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile Gly Val
                375                 380                 385

ttc tta atc gcc tgt atg gtg gta aca gtc atc ctg tgc cga atg aag     1798
Phe Leu Ile Ala Cys Met Val Val Thr Val Ile Leu Cys Arg Met Lys
            390                 395                 400

aac acg acc aag aag cca gac ttc agc agc cag ccg gct gtg cac aag     1846
Asn Thr Thr Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala Val His Lys
        405                 410                 415

ctg acc aaa cgt atc ccc ctg cgg aga cag gta aca gtt tcg gct gag     1894
Leu Thr Lys Arg Ile Pro Leu Arg Arg Gln Val Thr Val Ser Ala Glu
    420                 425                 430

tcc agc tcc tcc atg aac tcc aac acc ccg ctg gtg agg ata aca aca     1942
Ser Ser Ser Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile Thr Thr
435                 440                 445                 450

cgc ctc tct tca acg gca gac acc ccc atg ctg gca ggg gtc tcc gag     1990
Arg Leu Ser Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val Ser Glu
                455                 460                 465

tat gaa ctt cca gag gac cca aaa tgg gag ttt cca aga gat aag ctg     2038
Tyr Glu Leu Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp Lys Leu
            470                 475                 480

aca ctg ggc aag ccc ctg gga gaa ggt tgc ttt ggg caa gtg gtc atg     2086
Thr Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Met
        485                 490                 495

gcg gaa gca gtg gga att gac aaa gac aag ccc aag gag gcg gtc acc     2134
Ala Glu Ala Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala Val Thr
    500                 505                 510

gtg gcc gtg aag atg ttg aaa gat gat gcc aca gag aaa gac ctt tct     2182
Val Ala Val Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp Leu Ser
515                 520                 525                 530

gat ctg gtg tca gag atg gag atg atg aag atg att ggg aaa cac aag     2230
Asp Leu Val Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His Lys
                535                 540                 545

aat atc ata aat ctt ctt gga gcc tgc aca cag gat ggg cct ctc tat     2278
Asn Ile Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr
            550                 555                 560

gtc ata gtt gag tat gcc tct aaa ggc aac ctc cga gaa tac ctc cga     2326
Val Ile Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Arg
        565                 570                 575

gcc cgg agg cca ccc ggg atg gag tac tcc tat gac att aac cgt gtt     2374
Ala Arg Arg Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn Arg Val
    580                 585                 590

cct gag gag cag atg acc ttc aag gac ttg gtg tca tgc acc tac cag     2422
Pro Glu Glu Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr Tyr Gln
595                 600                 605                 610
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ctg gcc aga ggc atg gag tac ttg gct tcc caa aaa tgt att cat cga     2470
Leu Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile His Arg
                615                 620                 625

gat tta gca gcc aga aat gtt ttg gta aca gaa aac aat gtg atg aaa     2518
Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val Met Lys
            630                 635                 640

ata gca gac ttt gga ctc gcc aga gat atc aac aat ata gac tat tac     2566
Ile Ala Asp Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp Tyr Tyr
        645                 650                 655

aaa aag acc acc aat ggg cgg ctt cca gtc aag tgg atg gct cca gaa     2614
Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu
    660                 665                 670

gcc ctg ttt gat aga gta tac act cat cag agt gat gtc tgg tcc ttc     2662
Ala Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp Ser Phe
675                 680                 685                 690

ggg gtg tta atg tgg gag atc ttc act tta ggg ggc tcg ccc tac cca     2710
Gly Val Leu Met Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro
                695                 700                 705

ggg att ccc gtg gag gaa ctt ttt aag ctg ctg aag gaa gga cac aga     2758
Gly Ile Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg
            710                 715                 720

atg gat aag cca gcc aac tgc acc aac gaa ctg tac atg atg atg agg     2806
Met Asp Lys Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met Met Arg
        725                 730                 735

gac tgt tgg cat gca gtg ccc tcc cag aga cca acg ttc aag cag ttg     2854
Asp Cys Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu
    740                 745                 750

gta gaa gac ttg gat cga att ctc act ctc aca acc aat gag gaa tac     2902
Val Glu Asp Leu Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu Glu Tyr
755                 760                 765                 770

ttg gac ctc agc caa cct ctc gaa cag tat tca cct agt tac cct gac     2950
Leu Asp Leu Ser Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr Pro Asp
                775                 780                 785

aca aga agt tct tgt tct tca gga gat gat tct gtt ttt tct cca gac     2998
Thr Arg Ser Ser Cys Ser Ser Gly Asp Asp Ser Val Phe Ser Pro Asp
            790                 795                 800

ccc atg cct tac gaa cca tgc ctt cct cag tat cca cac ata aac ggc     3046
Pro Met Pro Tyr Glu Pro Cys Leu Pro Gln Tyr Pro His Ile Asn Gly
        805                 810                 815

agt gtt aaa aca tga atgactgtgt ctgcctgtcc ccaaacagga cagcactggg     3101
Ser Val Lys Thr
    820

aacctagcta cactgagcag ggagaccatg cctcccagag cttgttgtct ccacttgtat   3161

atatggatca gaggagtaaa taattggaaa agtaatcagc atatgtgtaa agatttatac   3221

agttgaaaac ttgtaatctt ccccaggagg agaagaaggt ttctggagca gtggactgcc   3281

acaagccacc atgtaacccc tctcacctgc cgtgcgtact ggctgtggac cagtaggact   3341

caaggtggac gtgcgttctg ccttccttgt taattttgta ataattggag aagatttatg   3401

tcagcacaca cttacagagc acaaatgcag tatataggtg ctggatgtat gtaaatatat   3461

tcaaattatg tataaatata tattatatat ttacaaggag ttatttttg tattgatttt   3521

aaatggatgt cccaatgcac ctagaaaatt ggtctctctt tttttaatag ctatttgcta   3581

aatgctgttc ttacacataa tttcttaatt ttcaccgagc agaggtggaa aaatactttt   3641

gctttcaggg aaaatggtat aacgttaatt tattaataaa ttggtaatat acaaaacaat   3701
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taatcattta tagtttttt tgtaatttaa gtggcatttc tatgcaggca gcacagcaga 3761

ctagttaatc tattgcttgg acttaactag ttatcagatc ctttgaaaag agaatattta 3821

caatatatga ctaatttggg gaaaatgaag ttttgattta tttgtgttta aatgctgctg 3881

tcagacgatt gttcttagac ctcctaaatg ccccatatta aaagaactca ttcataggaa 3941

ggtgtttcat tttggtgtgc aaccctgtca ttacgtcaac gcaacgtcta actggacttc 4001

ccaagataaa tggtaccagc gtcctcttaa aagatgcctt aatccattcc ttgaggacag 4061

accttagttg aaatgatagc agaatgtgct tctctctggc agctggcctt ctgcttctga 4121

gttgcacatt aatcagatta gcctgattct cttcagtgaa ttttgataat ggcttccaga 4181

ctctttgcgt tggagacgcc tgttaggatc ttcaagtccc atcatagaaa attgaaacac 4241

agagttgttc tgctgatagt tttggggata cgtccatctt tttaagggat tgctttcatc 4301

taattctggc aggacctcac caaaagatcc agcctcatac ctacatcaga caaaatatcg 4361

ccgttgttcc ttctgtacta aagtattgtg ttttgctttg gaaacaccca ctcactttgc 4421

aatagccgtg caagatgaat gcagattaca ctgatcttat gtgttacaaa attggagaaa 4481

gtatttaata aaacctgtta atttttatac tgacaataaa aatgtttcta cagatattaa 4541

tgttaacaag acaaaataaa tgtcacgcaa ctt 4574

<210> SEQ ID NO 26
<211> LENGTH: 822
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 26

Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala
1 5 10 15

Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr
20 25 30

Leu Glu Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu
35 40 45

Val Tyr Val Ala Ala Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu
50 55 60

Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly
65 70 75 80

Pro Asn Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly
85 90 95

Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr
100 105 110

Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile
115 120 125

Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val
130 135 140

Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu
145 150 155 160

Lys Met Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys
165 170 175

Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu
180 185 190

Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys

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        195                 200                 205

Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser
    210                 215                 220

Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile
225                 230                 235                 240

Asn His Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro
                245                 250                 255

Ile Leu Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly
            260                 265                 270

Asp Val Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile
        275                 280                 285

Gln Trp Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp
    290                 295                 300

Gly Leu Pro Tyr Leu Lys Val Leu Lys His Ser Gly Ile Asn Ser Ser
305                 310                 315                 320

Asn Ala Glu Val Leu Ala Leu Phe Asn Val Thr Glu Ala Asp Ala Gly
                325                 330                 335

Glu Tyr Ile Cys Lys Val Ser Asn Tyr Ile Gly Gln Ala Asn Gln Ser
            340                 345                 350

Ala Trp Leu Thr Val Leu Pro Lys Gln Gln Ala Pro Gly Arg Glu Lys
        355                 360                 365

Glu Ile Thr Ala Ser Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile
    370                 375                 380

Gly Val Phe Leu Ile Ala Cys Met Val Val Thr Val Ile Leu Cys Arg
385                 390                 395                 400

Met Lys Asn Thr Thr Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala Val
                405                 410                 415

His Lys Leu Thr Lys Arg Ile Pro Leu Arg Arg Gln Val Thr Val Ser
            420                 425                 430

Ala Glu Ser Ser Ser Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile
        435                 440                 445

Thr Thr Arg Leu Ser Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val
    450                 455                 460

Ser Glu Tyr Glu Leu Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp
465                 470                 475                 480

Lys Leu Thr Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val
                485                 490                 495

Val Met Ala Glu Ala Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala
            500                 505                 510

Val Thr Val Ala Val Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp
        515                 520                 525

Leu Ser Asp Leu Val Ser Glu Met Glu Met Met Lys Met Ile Gly Lys
    530                 535                 540

His Lys Asn Ile Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro
545                 550                 555                 560

Leu Tyr Val Ile Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr
                565                 570                 575

Leu Arg Ala Arg Arg Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn
            580                 585                 590

Arg Val Pro Glu Glu Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr
        595                 600                 605
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Tyr Gln Leu Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile
    610                 615                 620

His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val
625                 630                 635                 640

Met Lys Ile Ala Asp Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp
                645                 650                 655

Tyr Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala
            660                 665                 670

Pro Glu Ala Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp
        675                 680                 685

Ser Phe Gly Val Leu Met Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro
    690                 695                 700

Tyr Pro Gly Ile Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly
705                 710                 715                 720

His Arg Met Asp Lys Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met
                725                 730                 735

Met Arg Asp Cys Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys
            740                 745                 750

Gln Leu Val Glu Asp Leu Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu
        755                 760                 765

Glu Tyr Leu Asp Leu Ser Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr
    770                 775                 780

Pro Asp Thr Arg Ser Ser Cys Ser Ser Gly Asp Asp Ser Val Phe Ser
785                 790                 795                 800

Pro Asp Pro Met Pro Tyr Glu Pro Cys Leu Pro Gln Tyr Pro His Ile
                805                 810                 815

Asn Gly Ser Val Lys Thr
            820


<210> SEQ ID NO 27
<211> LENGTH: 5175
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (94)..(2676)

<400> SEQUENCE: 27

gccccgagtg caatcgcggg aagccagggt ttccagctag gacacagcag gtcgtgatcc     60

gggtcgggac actgcctggc agaggctgcg agc atg ggg ccc tgg ggc tgg aaa     114
                                    Met Gly Pro Trp Gly Trp Lys
                                    1               5

ttg cgc tgg acc gtc gcc ttg ctc ctc gcc gcg gcg ggg act gca gtg      162
Leu Arg Trp Thr Val Ala Leu Leu Leu Ala Ala Ala Gly Thr Ala Val
        10                  15                  20

ggc gac aga tgt gaa aga aac gag ttc cag tgc caa gac ggg aaa tgc      210
Gly Asp Arg Cys Glu Arg Asn Glu Phe Gln Cys Gln Asp Gly Lys Cys
    25                  30                  35

atc tcc tac aag tgg gtc tgc gat ggc agc gct gag tgc cag gat ggc      258
Ile Ser Tyr Lys Trp Val Cys Asp Gly Ser Ala Glu Cys Gln Asp Gly
40                  45                  50                  55

tct gat gag tcc cag gag acg tgc ttg tct gtc acc tgc aaa tcc ggg      306
Ser Asp Glu Ser Gln Glu Thr Cys Leu Ser Val Thr Cys Lys Ser Gly
                60                  65                  70
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gac ttc agc tgt ggg ggc cgt gtc aac cgc tgc att cct cag ttc tgg      354
Asp Phe Ser Cys Gly Gly Arg Val Asn Arg Cys Ile Pro Gln Phe Trp
            75                  80                  85

agg tgc gat ggc caa gtg gac tgc gac aac ggc tca gac gag caa ggc      402
Arg Cys Asp Gly Gln Val Asp Cys Asp Asn Gly Ser Asp Glu Gln Gly
        90                  95                  100

tgt ccc ccc aag acg tgc tcc cag gac gag ttt cgc tgc cac gat ggg      450
Cys Pro Pro Lys Thr Cys Ser Gln Asp Glu Phe Arg Cys His Asp Gly
    105                 110                 115

aag tgc atc tct cgg cag ttc gtc tgt gac tca gac cgg gac tgc ttg      498
Lys Cys Ile Ser Arg Gln Phe Val Cys Asp Ser Asp Arg Asp Cys Leu
120                 125                 130                 135

gac ggc tca gac gag gcc tcc tgc ccg gtg ctc acc tgt ggt ccc gcc      546
Asp Gly Ser Asp Glu Ala Ser Cys Pro Val Leu Thr Cys Gly Pro Ala
                140                 145                 150

agc ttc cag tgc aac agc tcc acc tgc atc ccc cag ctg tgg gcc tgc      594
Ser Phe Gln Cys Asn Ser Ser Thr Cys Ile Pro Gln Leu Trp Ala Cys
            155                 160                 165

gac aac gac ccc gac tgc gaa gat ggc tcg gat gag tgg ccg cag cgc      642
Asp Asn Asp Pro Asp Cys Glu Asp Gly Ser Asp Glu Trp Pro Gln Arg
        170                 175                 180

tgt agg ggt ctt tac gtg ttc caa ggg gac agt agc ccc tgc tcg gcc      690
Cys Arg Gly Leu Tyr Val Phe Gln Gly Asp Ser Ser Pro Cys Ser Ala
    185                 190                 195

ttc gag ttc cac tgc cta agt ggc gag tgc atc cac tcc agc tgg cgc      738
Phe Glu Phe His Cys Leu Ser Gly Glu Cys Ile His Ser Ser Trp Arg
200                 205                 210                 215

tgt gat ggt ggc ccc gac tgc aag gac aaa tct gac gag gaa aac tgc      786
Cys Asp Gly Gly Pro Asp Cys Lys Asp Lys Ser Asp Glu Glu Asn Cys
                220                 225                 230

gct gtg gcc acc tgt cgc cct gac gaa ttc cag tgc tct gat gga aac      834
Ala Val Ala Thr Cys Arg Pro Asp Glu Phe Gln Cys Ser Asp Gly Asn
            235                 240                 245

tgc atc cat ggc agc cgg cag tgt gac cgg gaa tat gac tgc aag gac      882
Cys Ile His Gly Ser Arg Gln Cys Asp Arg Glu Tyr Asp Cys Lys Asp
        250                 255                 260

atg agc gat gaa gtt ggc tgc gtt aat gtg aca ctc tgc gag gga ccc      930
Met Ser Asp Glu Val Gly Cys Val Asn Val Thr Leu Cys Glu Gly Pro
    265                 270                 275

aac aag ttc aag tgt cac agc ggc gaa tgc atc acc ctg gac aaa gtc      978
Asn Lys Phe Lys Cys His Ser Gly Glu Cys Ile Thr Leu Asp Lys Val
280                 285                 290                 295

tgc aac atg gct aga gac tgc cgg gac tgg tca gat gaa ccc atc aaa     1026
Cys Asn Met Ala Arg Asp Cys Arg Asp Trp Ser Asp Glu Pro Ile Lys
                300                 305                 310

gag tgc ggg acc aac gaa tgc ttg gac aac aac ggc ggc tgt tcc cac     1074
Glu Cys Gly Thr Asn Glu Cys Leu Asp Asn Asn Gly Gly Cys Ser His
            315                 320                 325

gtc tgc aat gac ctt aag atc ggc tac gag tgc ctg tgc ccc gac ggc     1122
Val Cys Asn Asp Leu Lys Ile Gly Tyr Glu Cys Leu Cys Pro Asp Gly
        330                 335                 340

ttc cag ctg gtg gcc cag cga aga tgc gaa gat atc gat gag tgt cag     1170
Phe Gln Leu Val Ala Gln Arg Arg Cys Glu Asp Ile Asp Glu Cys Gln
    345                 350                 355

gat ccc gac acc tgc agc cag ctc tgc gtg aac ctg gag ggt ggc tac     1218
Asp Pro Asp Thr Cys Ser Gln Leu Cys Val Asn Leu Glu Gly Gly Tyr
360                 365                 370                 375
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aag tgc cag tgt gag gaa ggc ttc cag ctg gac ccc cac acg aag gcc     1266
Lys Cys Gln Cys Glu Glu Gly Phe Gln Leu Asp Pro His Thr Lys Ala
                380                 385                 390

tgc aag gct gtg ggc tcc atc gcc tac ctc ttc ttc acc aac cgg cac     1314
Cys Lys Ala Val Gly Ser Ile Ala Tyr Leu Phe Phe Thr Asn Arg His
            395                 400                 405

gag gtc agg aag atg acg ctg gac cgg agc gag tac acc agc ctc atc     1362
Glu Val Arg Lys Met Thr Leu Asp Arg Ser Glu Tyr Thr Ser Leu Ile
        410                 415                 420

ccc aac ctg agg aac gtg gtc gct ctg gac acg gag gtg gcc agc aat     1410
Pro Asn Leu Arg Asn Val Val Ala Leu Asp Thr Glu Val Ala Ser Asn
    425                 430                 435

aga atc tac tgg tct gac ctg tcc cag aga atg atc tgc agc acc cag     1458
Arg Ile Tyr Trp Ser Asp Leu Ser Gln Arg Met Ile Cys Ser Thr Gln
440                 445                 450                 455

ctt gac aga gcc cac ggc gtc tct tcc tat gac acc gtc atc agc agg     1506
Leu Asp Arg Ala His Gly Val Ser Ser Tyr Asp Thr Val Ile Ser Arg
                460                 465                 470

gac atc cag gcc ccc gac ggg ctg gct gtg gac tgg atc cac agc aac     1554
Asp Ile Gln Ala Pro Asp Gly Leu Ala Val Asp Trp Ile His Ser Asn
            475                 480                 485

atc tac tgg acc gac tct gtc ctg ggc act gtc tct gtt gcg gat acc     1602
Ile Tyr Trp Thr Asp Ser Val Leu Gly Thr Val Ser Val Ala Asp Thr
        490                 495                 500

aag ggc gtg aag agg aaa acg tta ttc agg gag aac ggc tcc aag cca     1650
Lys Gly Val Lys Arg Lys Thr Leu Phe Arg Glu Asn Gly Ser Lys Pro
    505                 510                 515

agg gcc atc gtg gtg gat cct gtt cat ggc ttc atg tac tgg act gac     1698
Arg Ala Ile Val Val Asp Pro Val His Gly Phe Met Tyr Trp Thr Asp
520                 525                 530                 535

tgg gga act ccc gcc aag atc aag aaa ggg ggc ctg aat ggt gtg gac     1746
Trp Gly Thr Pro Ala Lys Ile Lys Lys Gly Gly Leu Asn Gly Val Asp
                540                 545                 550

atc tac tcg ctg gtg act gaa aac att cag tgg ccc aat ggc atc acc     1794
Ile Tyr Ser Leu Val Thr Glu Asn Ile Gln Trp Pro Asn Gly Ile Thr
            555                 560                 565

cta gat ctc ctc agt ggc cgc ctc tac tgg gtt gac tcc aaa ctt cac     1842
Leu Asp Leu Leu Ser Gly Arg Leu Tyr Trp Val Asp Ser Lys Leu His
        570                 575                 580

tcc atc tca agc atc gat gtc aat ggg ggc aac cgg aag acc atc ttg     1890
Ser Ile Ser Ser Ile Asp Val Asn Gly Gly Asn Arg Lys Thr Ile Leu
    585                 590                 595

gag gat gaa aag agg ctg gcc cac ccc ttc tcc ttg gcc gtc ttt gag     1938
Glu Asp Glu Lys Arg Leu Ala His Pro Phe Ser Leu Ala Val Phe Glu
600                 605                 610                 615

gac aaa gta ttt tgg aca gat atc atc aac gaa gcc att ttc agt gcc     1986
Asp Lys Val Phe Trp Thr Asp Ile Ile Asn Glu Ala Ile Phe Ser Ala
                620                 625                 630

aac cgc ctc aca ggt tcc gat gtc aac ttg ttg gct gaa aac cta ctg     2034
Asn Arg Leu Thr Gly Ser Asp Val Asn Leu Leu Ala Glu Asn Leu Leu
            635                 640                 645

tcc cca gag gat atg gtc ctc ttc cac aac ctc acc cag cca aga gga     2082
Ser Pro Glu Asp Met Val Leu Phe His Asn Leu Thr Gln Pro Arg Gly
        650                 655                 660

gtg aac tgg tgt gag agg acc acc ctg agc aat ggc ggc tgc cag tat     2130
Val Asn Trp Cys Glu Arg Thr Thr Leu Ser Asn Gly Gly Cys Gln Tyr
    665                 670                 675
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ctg tgc ctc cct gcc ccg cag atc aac ccc cac tcg ccc aag ttt acc     2178
Leu Cys Leu Pro Ala Pro Gln Ile Asn Pro His Ser Pro Lys Phe Thr
680                 685                 690                 695

tgc gcc tgc ccg gac ggc atg ctg ctg gcc agg gac atg agg agc tgc     2226
Cys Ala Cys Pro Asp Gly Met Leu Leu Ala Arg Asp Met Arg Ser Cys
                700                 705                 710

ctc aca gag gct gag gct gca gtg gcc acc cag gag aca tcc acc gtc     2274
Leu Thr Glu Ala Glu Ala Ala Val Ala Thr Gln Glu Thr Ser Thr Val
            715                 720                 725

agg cta aag gtc agc tcc aca gcc gta agg aca cag cac aca acc acc     2322
Arg Leu Lys Val Ser Ser Thr Ala Val Arg Thr Gln His Thr Thr Thr
        730                 735                 740

cgg cct gtt ccc gac acc tcc cgg ctg cct ggg gcc acc cct ggg ctc     2370
Arg Pro Val Pro Asp Thr Ser Arg Leu Pro Gly Ala Thr Pro Gly Leu
    745                 750                 755

acc acg gtg gag ata gtg aca atg tct cac caa gct ctg ggc gac gtt     2418
Thr Thr Val Glu Ile Val Thr Met Ser His Gln Ala Leu Gly Asp Val
760                 765                 770                 775

gct ggc aga gga aat gag aag aag ccc agt agc gtg agg gct ctg tcc     2466
Ala Gly Arg Gly Asn Glu Lys Lys Pro Ser Ser Val Arg Ala Leu Ser
                780                 785                 790

att gtc ctc ccc atc gtg ctc ctc gtc ttc ctt tgc ctg ggg gtc ttc     2514
Ile Val Leu Pro Ile Val Leu Leu Val Phe Leu Cys Leu Gly Val Phe
            795                 800                 805

ctt cta tgg aag aac tgg cgg ctt aag aac atc aac agc atc aac ttt     2562
Leu Leu Trp Lys Asn Trp Arg Leu Lys Asn Ile Asn Ser Ile Asn Phe
        810                 815                 820

gac aac ccc gtc tat cag aag acc aca gag gat gag gtc cac att tgc     2610
Asp Asn Pro Val Tyr Gln Lys Thr Thr Glu Asp Glu Val His Ile Cys
    825                 830                 835

cac aac cag gac ggc tac agc tac ccc tcg aga cag atg gtc agt ctg     2658
His Asn Gln Asp Gly Tyr Ser Tyr Pro Ser Arg Gln Met Val Ser Leu
840                 845                 850                 855

gag gat gac gtg gcg tga acatctgcct ggagtcccgc ccctgcccag           2706
Glu Asp Asp Val Ala
                860

aacccttcct gagacctcgc cggccttgtt ttattcaaag acagagaaga ccaaagcatt   2766

gcctgccaga gctttgtttt atatatttat tcatctggga ggcagaacag gcttcggaca   2826

gtgcccatgc aatggcttgg gttgggattt tggtttcttc ctttcctgtg aaggataaga   2886

gaaacaggcc cgggggggacc aggatgacac ctccatttct ctccaggaag ttttgagttt   2946

ctctccaccg tgacacaatc ctcaaacatg gaagatgaaa gggcagggga tgtcaggccc   3006

agagaagcaa gtggctttca acacacaaca gcagatggca ccaacgggac cccctggccc   3066

tgcctcatcc accaatctct aagccaaacc cctaaactca ggagtcaacg tgtttacctc   3126

ttctatgcaa gccttgctag acagccaggt tagcctttgc cctgtcaccc ccgaatcatg   3186

acccacccag tgtctttcga ggtgggtttg taccttcctt aagccaggaa agggattcat   3246

ggcgtcggaa atgatctggc tgaatccgtg gtggcaccga gaccaaactc attcaccaaa   3306

tgatgccact tcccagaggc agagcctgag tcaccggtca cccttaatat ttattaagtg   3366

cctgagacac ccggttacct tggccgtgag gacacgtggc ctgcacccag gtgtggctgt   3426

caggacacca gcctggtgcc catcctcccg acccctaccc acttccattc ccgtggtctc   3486

cttgcacttt ctcagttcag agttgtacac tgtgtacatt tggcatttgt gttattattt   3546
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tgcactgttt tctgtcgtgt gtgttgggat gggatcccag gccagggaaa gcccgtgtca   3606

atgaatgccg gggacagaga ggggcaggtt gaccgggact tcaaagccgt gatcgtgaat   3666

atcgagaact gccattgtcg tctttatgtc cgcccaccta gtgcttccac ttctatgcaa   3726

atgcctccaa gccattcact tccccaatct tgtcgttgat gggtatgtgt ttaaaacatg   3786

cacggtgagg ccgggcgcag tggcctcacg cctgtaatcc cagcactttg ggaggccgag   3846

gcgggtggat catgaggtca ggagatcgag accatcctgg ctaacaaggt gaaaccccgt   3906

ctctactaaa aatacaaaaa attagccggg cgcggtggtg ggcacctgta gtcccagcta   3966

ctcgggaggc tgaggcagga gaatggtgtg aacccgggaa gcggagcttg cagtgagccg   4026

agattgcgcc actgcagtcc gcagtctggc ctgggcgaca gagcgagact ccgtctcaaa   4086

aaaaacaaaa caaaaaaaaa ccatgcatgg tgcatcagca gcccatggcc tctggccagg   4146

catggcgagg ctgaggtggg aggatggttt gagctcaggc atttgaggct gtcgtgagct   4206

atgattatgc cactgctttc cagcctgggc aacatagtaa gaccccatct cttaaaaaat   4266

gaatttggcc agacacaggt gcctcacgcc tgtaatccca gcactttggg aggctgagct   4326

ggatcacttg agttcaggag ttggagacca ggcctgagca acaaagcgag atcccatctc   4386

tacaaaaacc aaaaagttaa aaatcagctg ggtatggtgg cacgtgcctg tgatcccagc   4446

tacttgggag gctgaggcag gaggatcgcc tgagcccagg aggtggaggt tgcagtgagc   4506

catgatcgag ccactgcact ccagcctggg caacagatga agaccctatt tcagaaatac   4566

aactataaaa aaaataaata aatcctccag tctggatcgt ttgacgggac ttcaggttct   4626

ttctgaaatc gccgtgttac tgttgcactg atgtccggag agacagtgac agcctccgtc   4686

agactcccgc gtgaagatgt cacaagggat tggcaattgt ccccagggac aaaacactgt   4746

gtccccccca gtgcagggaa ccgtgataag cctttctggt ttcggagcac gtaaatgcgt   4806

ccctgtacag atagtgggga ttttttgtta tgtttgcact ttgtatattg gttgaaactg   4866

ttatcactta tatatatata tacacacata tatataaaat ctatttattt ttgcaaaccc   4926

tggttgctgt atttgttcag tgactattct cggggccctg tgtagggggt tattgcctct   4986

gaaatgcctc ttctttatgt acaaagatta tttgcacgaa ctggactgtg tgcaacgctt   5046

tttgggagaa tgatgtcccc gttgtatgta tgagtggctt ctgggagatg ggtgtcactt   5106

tttaaaccac tgtatagaag gtttttgtag cctgaatgtc ttactgtgat caattaaatt   5166

tcttaaatg                                                          5175
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<210> SEQ ID NO 28
<211> LENGTH: 860
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 28

```
Met Gly Pro Trp Gly Trp Lys Leu Arg Trp Thr Val Ala Leu Leu Leu
1               5                   10                  15

Ala Ala Ala Gly Thr Ala Val Gly Asp Arg Cys Glu Arg Asn Glu Phe
            20                  25                  30

Gln Cys Gln Asp Gly Lys Cys Ile Ser Tyr Lys Trp Val Cys Asp Gly
        35                  40                  45

Ser Ala Glu Cys Gln Asp Gly Ser Asp Glu Ser Gln Glu Thr Cys Leu
    50                  55                  60
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Ser Val Thr Cys Lys Ser Gly Asp Phe Ser Cys Gly Gly Arg Val Asn
65                  70                  75                  80

Arg Cys Ile Pro Gln Phe Trp Arg Cys Asp Gly Gln Val Asp Cys Asp
                85                  90                  95

Asn Gly Ser Asp Glu Gln Gly Cys Pro Pro Lys Thr Cys Ser Gln Asp
            100                 105                 110

Glu Phe Arg Cys His Asp Gly Lys Cys Ile Ser Arg Gln Phe Val Cys
        115                 120                 125

Asp Ser Asp Arg Asp Cys Leu Asp Gly Ser Asp Glu Ala Ser Cys Pro
    130                 135                 140

Val Leu Thr Cys Gly Pro Ala Ser Phe Gln Cys Asn Ser Ser Thr Cys
145                 150                 155                 160

Ile Pro Gln Leu Trp Ala Cys Asp Asn Asp Pro Asp Cys Glu Asp Gly
                165                 170                 175

Ser Asp Glu Trp Pro Gln Arg Cys Arg Gly Leu Tyr Val Phe Gln Gly
            180                 185                 190

Asp Ser Ser Pro Cys Ser Ala Phe Glu Phe His Cys Leu Ser Gly Glu
        195                 200                 205

Cys Ile His Ser Ser Trp Arg Cys Asp Gly Gly Pro Asp Cys Lys Asp
    210                 215                 220

Lys Ser Asp Glu Glu Asn Cys Ala Val Ala Thr Cys Arg Pro Asp Glu
225                 230                 235                 240

Phe Gln Cys Ser Asp Gly Asn Cys Ile His Gly Ser Arg Gln Cys Asp
                245                 250                 255

Arg Glu Tyr Asp Cys Lys Asp Met Ser Asp Glu Val Gly Cys Val Asn
            260                 265                 270

Val Thr Leu Cys Glu Gly Pro Asn Lys Phe Lys Cys His Ser Gly Glu
        275                 280                 285

Cys Ile Thr Leu Asp Lys Val Cys Asn Met Ala Arg Asp Cys Arg Asp
    290                 295                 300

Trp Ser Asp Glu Pro Ile Lys Glu Cys Gly Thr Asn Glu Cys Leu Asp
305                 310                 315                 320

Asn Asn Gly Gly Cys Ser His Val Cys Asn Asp Leu Lys Ile Gly Tyr
                325                 330                 335

Glu Cys Leu Cys Pro Asp Gly Phe Gln Leu Val Ala Gln Arg Arg Cys
            340                 345                 350

Glu Asp Ile Asp Glu Cys Gln Asp Pro Asp Thr Cys Ser Gln Leu Cys
        355                 360                 365

Val Asn Leu Glu Gly Gly Tyr Lys Cys Gln Cys Glu Glu Gly Phe Gln
    370                 375                 380

Leu Asp Pro His Thr Lys Ala Cys Lys Ala Val Gly Ser Ile Ala Tyr
385                 390                 395                 400

Leu Phe Phe Thr Asn Arg His Glu Val Arg Lys Met Thr Leu Asp Arg
                405                 410                 415

Ser Glu Tyr Thr Ser Leu Ile Pro Asn Leu Arg Asn Val Val Ala Leu
            420                 425                 430

Asp Thr Glu Val Ala Ser Asn Arg Ile Tyr Trp Ser Asp Leu Ser Gln
        435                 440                 445

Arg Met Ile Cys Ser Thr Gln Leu Asp Arg Ala His Gly Val Ser Ser
    450                 455                 460

Tyr Asp Thr Val Ile Ser Arg Asp Ile Gln Ala Pro Asp Gly Leu Ala
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465                 470                 475                 480

Val Asp Trp Ile His Ser Asn Ile Tyr Trp Thr Asp Ser Val Leu Gly
                485                 490                 495

Thr Val Ser Val Ala Asp Thr Lys Gly Val Lys Arg Lys Thr Leu Phe
            500                 505                 510

Arg Glu Asn Gly Ser Lys Pro Arg Ala Ile Val Val Asp Pro Val His
        515                 520                 525

Gly Phe Met Tyr Trp Thr Asp Trp Gly Thr Pro Ala Lys Ile Lys Lys
    530                 535                 540

Gly Gly Leu Asn Gly Val Asp Ile Tyr Ser Leu Val Thr Glu Asn Ile
545                 550                 555                 560

Gln Trp Pro Asn Gly Ile Thr Leu Asp Leu Leu Ser Gly Arg Leu Tyr
                565                 570                 575

Trp Val Asp Ser Lys Leu His Ser Ile Ser Ser Ile Asp Val Asn Gly
            580                 585                 590

Gly Asn Arg Lys Thr Ile Leu Glu Asp Glu Lys Arg Leu Ala His Pro
        595                 600                 605

Phe Ser Leu Ala Val Phe Glu Asp Lys Val Phe Trp Thr Asp Ile Ile
    610                 615                 620

Asn Glu Ala Ile Phe Ser Ala Asn Arg Leu Thr Gly Ser Asp Val Asn
625                 630                 635                 640

Leu Leu Ala Glu Asn Leu Leu Ser Pro Glu Asp Met Val Leu Phe His
                645                 650                 655

Asn Leu Thr Gln Pro Arg Gly Val Asn Trp Cys Glu Arg Thr Thr Leu
            660                 665                 670

Ser Asn Gly Gly Cys Gln Tyr Leu Cys Leu Pro Ala Pro Gln Ile Asn
        675                 680                 685

Pro His Ser Pro Lys Phe Thr Cys Ala Cys Pro Asp Gly Met Leu Leu
    690                 695                 700

Ala Arg Asp Met Arg Ser Cys Leu Thr Glu Ala Glu Ala Ala Val Ala
705                 710                 715                 720

Thr Gln Glu Thr Ser Thr Val Arg Leu Lys Val Ser Ser Thr Ala Val
                725                 730                 735

Arg Thr Gln His Thr Thr Thr Arg Pro Val Pro Asp Thr Ser Arg Leu
            740                 745                 750

Pro Gly Ala Thr Pro Gly Leu Thr Thr Val Glu Ile Val Thr Met Ser
        755                 760                 765

His Gln Ala Leu Gly Asp Val Ala Gly Arg Gly Asn Glu Lys Lys Pro
    770                 775                 780

Ser Ser Val Arg Ala Leu Ser Ile Val Leu Pro Ile Val Leu Leu Val
785                 790                 795                 800

Phe Leu Cys Leu Gly Val Phe Leu Leu Trp Lys Asn Trp Arg Leu Lys
                805                 810                 815

Asn Ile Asn Ser Ile Asn Phe Asp Asn Pro Val Tyr Gln Lys Thr Thr
            820                 825                 830

Glu Asp Glu Val His Ile Cys His Asn Gln Asp Gly Tyr Ser Tyr Pro
        835                 840                 845

Ser Arg Gln Met Val Ser Leu Glu Asp Asp Val Ala
    850                 855                 860
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<210> SEQ ID NO 29

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<211> LENGTH: 2070
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 29

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tcatctgttt tcatagtgtg agatcaaccc acaggaatat ccatggcttt tgtgctcatt 180

ttggttctca gtttctacga gctggtgtca ggacagtggc aagtcactgg accgggcaag 240

tttgtccagg ccttggtggg ggaggacgcc gtgttctcct gctccctctt tcctgagacc 300

agtgcagagg ctatggaagt gcggttcttc aggaatcagt tccatgctgt ggtccacctc 360

tacagagatg gggaagactg ggaatctaag cagatgccac agtatcgagg gagaactgag 420

tttgtgaagg actccattgc agggggggcgt gtctctctaa ggctaaaaaa catcactccc 480

tcggacatcg gcctgtatgg gtgctggttc agttcccaga tttacgatga ggaggccacc 540

tgggagctgc gggtggcagc actgggctca cttcctctca tttccatcgt gggatatgtt 600

gacggaggta tccagttact ctgcctgtcc tcaggctggt tcccccagcc cacagccaag 660

tggaaaggtc cacaaggaca ggatttgtct tcagactcca gagcaaatgc agatgggtac 720

agcctgtatg atgtggagat ctccattata gtccaggaaa atgctgggag catattgtgt 780

tccatccacc ttgctgagca gagtcatgag gtggaatcca aggtattgat aggagagacg 840

tttttccagc cctcaccttg gcgcctggct tctattttac tcgggttact ctgtggtgcc 900

ctgtgtggtg ttgtcatggg gatgataatt gttttcttca aatccaaagg gaaaatccag 960

gcggaactgg actggagaag aaagcacgga caggcagaat tgagagacgc ccggaaacac 1020

gcagtggagg tgactctgga tccagagacg gctcacccga agctctgcgt ttctgatctg 1080

aaaactgtaa cccatagaaa agctccccag gaggtgcctc actctgagaa gagatttaca 1140

aggaagagtg tggtggcttc tcagggtttc caagcaggga aacattactg ggaggtggac 1200

gtgggacaaa atgtagggtg gtatgtggga gtgtgtcggg atgacgtaga caggggggaag 1260

aacaatgtga ctttgtctcc caacaatggg tattgggtcc tcagactgac aacagaacat 1320

ttgtatttca cattcaatcc ccatttttatc agcctccccc ccagcacccc tcctacacga 1380

gtaggggtct tcctggacta tgagggtggg accatctcct tcttcaatac aaatgaccag 1440

tcccttattt ataccctgct gacatgtcag tttgaaggct tgttgagacc ctatatccag 1500

catgcgatgt atgacgagga aaaggggact cccatattca tatgtccagt gtcctgggga 1560

tgagacagag aagaccctgc ttaaagggcc ccacaccaca gacccagaca cagccaaggg 1620

agagtgctcc cgacaggtgg ccccagcttc ctctccggag cctgcgcaca gagagtcacg 1680

ccccccactc tcctttaggg agctgaggtt cttctgccct gagccctgca gcagcggcag 1740

tcacagcttc cagatgaggg gggattggcc tgaccctgtg ggagtcagaa gccatggctg 1800

ccctgaagtg gggacggaat agactcacat taggtttagt ttgtgaaaac tccatccagc 1860

taagcgatct tgaacaagtc acaacctccc aggctcctca tttgctagtc acggacagtg 1920

attcctgcct cacaggtgaa gattaaagag acaacgaatg tgaatcatgc ttgcaggttt 1980

gagggcacag tgtttgctaa tgatgtgttt ttatattata cattttccca ccataaactc 2040

tgtttgctta ttccaaaaaa aaaaaaaaaa 2070

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<210> SEQ ID NO 30
<211> LENGTH: 1696
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (88)..(1488)

<400> SEQUENCE: 30

ccgagtgtcc acaccctgtg cgtctctctg tcctgccagc actgagggct catccatccg 60

cagagcaggg cagtgggagg agacgcc atg acc ccc atc ctc acg gtc ctg atc 114
Met Thr Pro Ile Leu Thr Val Leu Ile
1 5

tgt ctc ggg ctg agt ctg ggc ccc agg acc cac gtg cag gca ggg cac 162
Cys Leu Gly Leu Ser Leu Gly Pro Arg Thr His Val Gln Ala Gly His
10 15 20 25

ctc ccc aag ccc acc ctc tgg gct gag cca ggc tct gtg atc atc cag 210
Leu Pro Lys Pro Thr Leu Trp Ala Glu Pro Gly Ser Val Ile Ile Gln
30 35 40

gga agt cct gtg acc ctc agg tgt cag ggg agc ctt cag gct gag gag 258
Gly Ser Pro Val Thr Leu Arg Cys Gln Gly Ser Leu Gln Ala Glu Glu
45 50 55

tac cat cta tat agg gaa aac aaa tca gca tcc tgg gtt aga cgg ata 306
Tyr His Leu Tyr Arg Glu Asn Lys Ser Ala Ser Trp Val Arg Arg Ile
60 65 70

caa gag cct ggg aag aat ggc cag ttc ccc atc cca tcc atc acc tgg 354
Gln Glu Pro Gly Lys Asn Gly Gln Phe Pro Ile Pro Ser Ile Thr Trp
75 80 85

gaa cac gca ggg cgg tat cac tgt cag tac tac agc cac aat cac tca 402
Glu His Ala Gly Arg Tyr His Cys Gln Tyr Tyr Ser His Asn His Ser
90 95 100 105

tca gag tac agt gac ccc ctg gag ctg gtg gtg aca gga gcc tac agc 450
Ser Glu Tyr Ser Asp Pro Leu Glu Leu Val Val Thr Gly Ala Tyr Ser
110 115 120

aaa ccc acc ctc tca gct ctg ccc agc cct gtg gtg acc tta gga ggg 498
Lys Pro Thr Leu Ser Ala Leu Pro Ser Pro Val Val Thr Leu Gly Gly
125 130 135

aac gtg acc ctc cag tgt gtc tca cag gtg gca ttt gac ggc ttc att 546
Asn Val Thr Leu Gln Cys Val Ser Gln Val Ala Phe Asp Gly Phe Ile
140 145 150

ctg tgt aag gaa gga gaa gat gaa cac cca caa cgc ctg aac tcc cat 594
Leu Cys Lys Glu Gly Glu Asp Glu His Pro Gln Arg Leu Asn Ser His
155 160 165

tcc cat gcc cgt ggg tgg tcc tgg gcc atc ttc tcc gtg ggc ccc gtg 642
Ser His Ala Arg Gly Trp Ser Trp Ala Ile Phe Ser Val Gly Pro Val
170 175 180 185

agc ccg agt cgc agg tgg tcg tac agg tgc tat gct tat gac tcg aac 690
Ser Pro Ser Arg Arg Trp Ser Tyr Arg Cys Tyr Ala Tyr Asp Ser Asn
190 195 200

tct ccc tat gtg tgg tct cta ccc agt gat ctc ctg gag ctc ctg gtc 738
Ser Pro Tyr Val Trp Ser Leu Pro Ser Asp Leu Leu Glu Leu Leu Val
205 210 215

cca ggt gtt tct aag aag cca tca ctc tca gtg cag cca ggt cct atg 786
Pro Gly Val Ser Lys Lys Pro Ser Leu Ser Val Gln Pro Gly Pro Met
220 225 230

gtg gcc cct ggg gag agc ctg acc ctc cag tgt gtc tct gat gtc ggc 834
Val Ala Pro Gly Glu Ser Leu Thr Leu Gln Cys Val Ser Asp Val Gly
235 240 245

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tac gac aga ttt gtt ctg tat aag gag gga gaa cgt gac ttc ctc cag      882
Tyr Asp Arg Phe Val Leu Tyr Lys Glu Gly Glu Arg Asp Phe Leu Gln
250                 255                 260                 265

cgc cct ggt tgg cag ccc cag gct ggg ctc tcc cag gcc aac ttc acc      930
Arg Pro Gly Trp Gln Pro Gln Ala Gly Leu Ser Gln Ala Asn Phe Thr
                270                 275                 280

ctg ggc cct gtg agc ccc tcc cac ggg ggc cag tac aga tgc tac agt      978
Leu Gly Pro Val Ser Pro Ser His Gly Gly Gln Tyr Arg Cys Tyr Ser
            285                 290                 295

gca cac aac ctc tcc tcc gag tgg tcg gcc ccc agt gac ccc ctg gac     1026
Ala His Asn Leu Ser Ser Glu Trp Ser Ala Pro Ser Asp Pro Leu Asp
        300                 305                 310

atc ctg atc aca gga cag ttc tat gac aga ccc tct ctc tcg gtg cag     1074
Ile Leu Ile Thr Gly Gln Phe Tyr Asp Arg Pro Ser Leu Ser Val Gln
    315                 320                 325

ccg gtc ccc aca gta gcc cca gga aag aac gtg acc ctg ctg tgt cag     1122
Pro Val Pro Thr Val Ala Pro Gly Lys Asn Val Thr Leu Leu Cys Gln
330                 335                 340                 345

tca cgg ggg cag ttc cac act ttc ctt ctg acc aag gag ggg gca ggc     1170
Ser Arg Gly Gln Phe His Thr Phe Leu Leu Thr Lys Glu Gly Ala Gly
                350                 355                 360

cat ccc cca ctg cat ctg aga tca gag cac caa gct cag cag aac cag     1218
His Pro Pro Leu His Leu Arg Ser Glu His Gln Ala Gln Gln Asn Gln
            365                 370                 375

gct gaa ttc cgc atg ggt cct gtg acc tca gcc cac gtg ggg acc tac     1266
Ala Glu Phe Arg Met Gly Pro Val Thr Ser Ala His Val Gly Thr Tyr
        380                 385                 390

aga tgc tac agc tca ctc agc tcc aac ccc tac ctg ctg tct ctc ccc     1314
Arg Cys Tyr Ser Ser Leu Ser Ser Asn Pro Tyr Leu Leu Ser Leu Pro
    395                 400                 405

agt gac ccc ctg gag ctc gtg gtc tca gca tcc cta ggc caa cac ccc     1362
Ser Asp Pro Leu Glu Leu Val Val Ser Ala Ser Leu Gly Gln His Pro
410                 415                 420                 425

cag gat tac aca gtg gag aat ctc atc cgc atg ggt gtg gct ggc ttg     1410
Gln Asp Tyr Thr Val Glu Asn Leu Ile Arg Met Gly Val Ala Gly Leu
                430                 435                 440

gtc ctg gtg gtc ctc ggg att ctg cta ttt gag gct cag cac agc cag     1458
Val Leu Val Val Leu Gly Ile Leu Leu Phe Glu Ala Gln His Ser Gln
            445                 450                 455

aga agc cta caa gat gca gcc ggg agg tga acagcagaga ggacaatgca       1508
Arg Ser Leu Gln Asp Ala Ala Gly Arg
        460                 465

tacttcagcg tggtggagcc tcagggacag atctgatgat cccaggaggc tctggaggac   1568

aatctaggac ctacattatc tggactgtat gctggtcatt tctagagaca gcaatcaata   1628

tttgagtgta aggaaactgt ctggggtgat tcctagaaga tcattaaact gtggtacatt   1688

tttttgtc                                                           1696


<210> SEQ ID NO 31
<211> LENGTH: 466
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 31

Met Thr Pro Ile Leu Thr Val Leu Ile Cys Leu Gly Leu Ser Leu Gly
1               5                   10                  15
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Pro Arg Thr His Val Gln Ala Gly His Leu Pro Lys Pro Thr Leu Trp
            20                  25                  30

Ala Glu Pro Gly Ser Val Ile Ile Gln Gly Ser Pro Val Thr Leu Arg
        35                  40                  45

Cys Gln Gly Ser Leu Gln Ala Glu Glu Tyr His Leu Tyr Arg Glu Asn
    50                  55                  60

Lys Ser Ala Ser Trp Val Arg Arg Ile Gln Glu Pro Gly Lys Asn Gly
65                  70                  75                  80

Gln Phe Pro Ile Pro Ser Ile Thr Trp Glu His Ala Gly Arg Tyr His
                85                  90                  95

Cys Gln Tyr Tyr Ser His Asn His Ser Ser Glu Tyr Ser Asp Pro Leu
            100                 105                 110

Glu Leu Val Val Thr Gly Ala Tyr Ser Lys Pro Thr Leu Ser Ala Leu
        115                 120                 125

Pro Ser Pro Val Val Thr Leu Gly Gly Asn Val Thr Leu Gln Cys Val
    130                 135                 140

Ser Gln Val Ala Phe Asp Gly Phe Ile Leu Cys Lys Glu Gly Glu Asp
145                 150                 155                 160

Glu His Pro Gln Arg Leu Asn Ser His Ser His Ala Arg Gly Trp Ser
                165                 170                 175

Trp Ala Ile Phe Ser Val Gly Pro Val Ser Pro Ser Arg Arg Trp Ser
            180                 185                 190

Tyr Arg Cys Tyr Ala Tyr Asp Ser Asn Ser Pro Tyr Val Trp Ser Leu
        195                 200                 205

Pro Ser Asp Leu Leu Glu Leu Leu Val Pro Gly Val Ser Lys Lys Pro
    210                 215                 220

Ser Leu Ser Val Gln Pro Gly Pro Met Val Ala Pro Gly Glu Ser Leu
225                 230                 235                 240

Thr Leu Gln Cys Val Ser Asp Val Gly Tyr Asp Arg Phe Val Leu Tyr
                245                 250                 255

Lys Glu Gly Glu Arg Asp Phe Leu Gln Arg Pro Gly Trp Gln Pro Gln
            260                 265                 270

Ala Gly Leu Ser Gln Ala Asn Phe Thr Leu Gly Pro Val Ser Pro Ser
        275                 280                 285

His Gly Gly Gln Tyr Arg Cys Tyr Ser Ala His Asn Leu Ser Ser Glu
    290                 295                 300

Trp Ser Ala Pro Ser Asp Pro Leu Asp Ile Leu Ile Thr Gly Gln Phe
305                 310                 315                 320

Tyr Asp Arg Pro Ser Leu Ser Val Gln Pro Val Pro Thr Val Ala Pro
                325                 330                 335

Gly Lys Asn Val Thr Leu Leu Cys Gln Ser Arg Gly Gln Phe His Thr
            340                 345                 350

Phe Leu Leu Thr Lys Glu Gly Ala Gly His Pro Pro Leu His Leu Arg
        355                 360                 365

Ser Glu His Gln Ala Gln Gln Asn Gln Ala Glu Phe Arg Met Gly Pro
    370                 375                 380

Val Thr Ser Ala His Val Gly Thr Tyr Arg Cys Tyr Ser Ser Leu Ser
385                 390                 395                 400

Ser Asn Pro Tyr Leu Leu Ser Leu Pro Ser Asp Pro Leu Glu Leu Val
                405                 410                 415

Val Ser Ala Ser Leu Gly Gln His Pro Gln Asp Tyr Thr Val Glu Asn
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-continued

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            420                 425                 430

Leu Ile Arg Met Gly Val Ala Gly Leu Val Leu Val Val Leu Gly Ile
        435                 440                 445

Leu Leu Phe Glu Ala Gln His Ser Gln Arg Ser Leu Gln Asp Ala Ala
    450                 455                 460

Gly Arg
465
```

We claim:

1. A method for diagnosing a granulocyte disorder comprising:

detecting in a biological sample from a subject a level of expression of one or more granulocyte-selective markers,

comparing the level of expression of each of the one or more granulocyte-selective markers with a reference level of expression, wherein a statistically significant difference between the level of expression of at least one granulocyte-selective marker and an expected level of expression for the at least one granulocyte-selective marker is indicative of a granulocyte disorder in the subject.

2. The method of claim **1**, wherein the reference level of expression for a granulocyte-selective marker is a normal level of expression of the granulocyte-selective marker in a normal granulocyte.

3. The method of claim **1**, wherein the biological sample is a blood sample.

4. The method of claim **1**, wherein the biological sample is a tissue sample.

5. The method of claim **1**, wherein the level of expression of each of the one or more granulocyte-selective markers is determined by determining an amount of an mRNA in the biological sample corresponding to each of the one or more granulocyte-selective markers.

6. The method of claim **5**, wherein the method of determining the amount of mRNA comprises reverse transcription polymerase chain reaction (RT-PCR) amplification.

7. The method of claim **1**, wherein the level of expression of each of the one or more granulocyte-selective markers is determined by determining an amount of a protein in the biological sample corresponding to each of the one or more granulocyte-selective markers.

8. The method of claim **7**, wherein the method of determining the amount of a protein that corresponds to a granulocyte-selective marker comprises contacting the biological sample with an antibody that binds to the protein.

9. The method of claim **1**, wherein a higher level of expression of at least one of the one or more granulocyte-selective markers in the biological sample compared to the expected level of expression for the at least one granulocyte-selective marker is indicative of the granulocyte disorder.

10. The method of claim **1**, wherein a lower level of expression of at least one of the one or more granulocyte-selective markers in the biological sample compared to the expected level of expression for the at least one granulocyte-selective marker is indicative of the granulocyte disorder.

11. The method of claim **1**, wherein the granulocyte disorder comprises an abnormally high number of one or more types of granulocyte in the biological sample.

12. The method of claim **1**, wherein the granulocyte disorder comprises an abnormally low number of one or more types of granulocyte in the biological sample.

13. The method of claim **1**, wherein the granulocyte disorder comprises an abnormal pattern of expression of one or more granulocyte selective markers in one or more types of granulocyte in the biological sample.

14. A method for diagnosing a non-neutrophil granulocyte disorder or mast cell disorder comprising:

detecting in a biological sample from a subject a level of expression of one or more non-neutrophil granulocyte or mast cell selective markers,

comparing the level of expression of each of the one or more non-neutrophil granulocyte or mast cell selective markers with a reference level of expression, wherein a statistically significant difference between the level of expression of at least one non-neutrophil granulocyte or mast cell selective marker and an expected level of expression for the at least one non-neutrophil granulocyte or mast cell selective marker is indicative of a non-neutrophil granulocyte disorder or mast cell disorder in the subject.

15. The method of claim **14**, wherein the non-neutrophil granulocyte disorder is a basophil disorder.

16. The method of claim **15**, wherein the basophil disorder is a basophil-associated tumor or cancer.

17. The method of claim **14**, wherein the non-neutrophil granulocyte disorder is an eosinophil disorder.

18. The method of claim **17**, wherein the eosinophil disorder is an eosinophil-associated tumor or cancer.

19. The method of claim **14**, wherein the mast cell disorder is a mast cell-associated tumor or cancer.

20-48. (canceled)

49. An assay for identifying a compound that alters at least one physiological property of a granulocyte comprising:

contacting a granulocyte with a candidate compound that interacts with a granulocyte-selective marker,

determining at least one physiological property of the granulocyte after contact with the candidate compound,

comparing the at least one physiological property to one at least one reference property to determine whether the candidate compound alters at least one physiological property of the granulocyte.

50-71. (canceled)

* * * * *

专利名称(译)	粒细胞亚型选择性受体和离子通道及其用途		
公开(公告)号	US20080187908A1	公开(公告)日	2008-08-07
申请号	US10/591628	申请日	2005-03-03
[标]申请(专利权)人(译)	安泽CHAKERñ		
申请(专利权)人(译)	安泽CHAKERñ		
当前申请(专利权)人(译)	安泽CHAKERñ		
[标]发明人	ADRA CHAKER N		
发明人	ADRA, CHAKER N.		
IPC分类号	C12Q1/68 G01N33/53		
CPC分类号	C12Q1/6809 C12Q1/6883 C12Q2600/158 C12Q2565/501		
优先权	60/549865 2004-03-03 US		
外部链接	Espacenet USPTO		

摘要(译)

本发明部分涉及优先在粒细胞中表达的粒细胞型选择标记及其在药物筛选试验中的用途。另外，粒细胞型选择标记可用于诊断和治疗粒细胞病症和评估粒细胞病症治疗的功效。