

# Hydroxyurea responsiveness in $\beta$ -thalassemic patients is determined by the stress response adaptation of erythroid progenitors and their differentiation propensity

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## Online Supplementary Design and Methods

### Patients

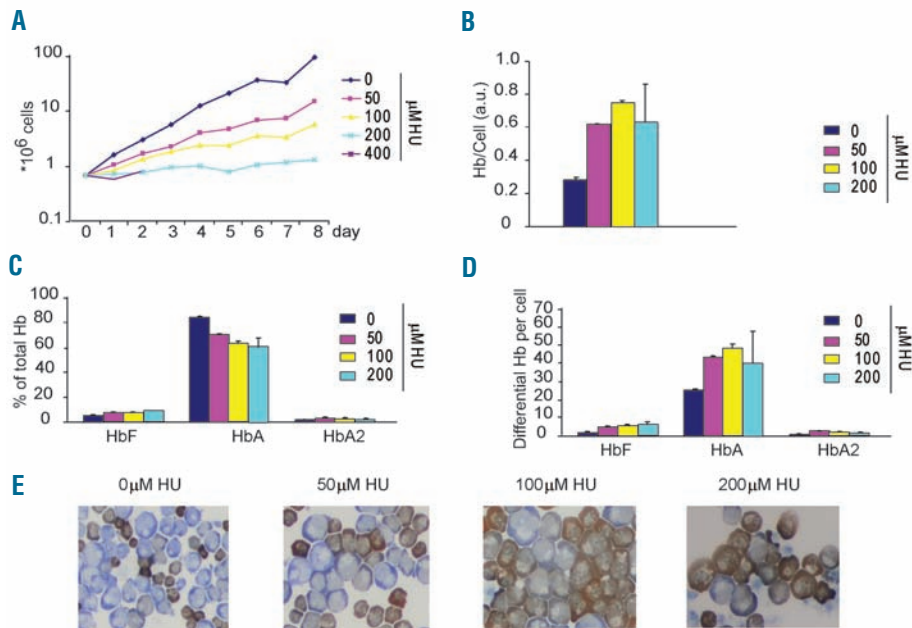
The studies reported here were approved by the local medical ethical review committee, and written informed consent was obtained from all the participating patients or their guardians. A large heterogeneous cohort of  $\beta$ -thalassemic patients were monitored for their clinical manifestation and response to hydroxyurea (HU) treatment.  $\beta$ -thalassemia patients, with milder phenotype, higher Hb level, less or no skeletal deformity, receiving similar amount of regular (18-30 day intervals) blood transfusions (average packed red blood cells (RBC) 800 mL) were selected for the study. Patients were also on parallel chelation therapy with Desferrioxamine (25-40 mg/kg/day). Transfusions were temporarily stopped at the start point of HU treatment, and hematologic indexes were analyzed at different time points. Clinical visits and laboratory tests for evaluation of HU response were performed weekly during the first month of treatment and monthly thereafter for a period of 2-6 months. Compliance was assessed by counting the HU pills at each return visit and by questionnaires. The patients were put on oral HU therapy at a starting dose of 5 mg/kg bodyweight per day. The dose was increased in increments of 5 mg/kg to a maximum of 20 mg/kg and was adjusted downward if evidence of hematopoietic suppression was observed (neutrophil count  $<2 \times 10^9/L$ , platelet count  $<150 \times 10^9/L$ ). The intervention was discontinued if neutrophil counts fell below  $1.5 \times 10^9/L$ , platelet counts  $<80 \times 10^9/L$ , or hemoglobin levels were below 80 g/L, and the patient was advised for blood transfusions. Details of clinical data, molecular analysis, hematologic indexes, transfusion and treatments are provided in the *Online Supplementary Table S1*. At this stage, two distinct groups were defined based on their response to HU: 'responders (R)' with a good response to HU treatment resulting in maintaining the mean hemoglobin level up to 8.5 g/dL (our threshold for transfusion) resulting in transfusion independency during the treatment period except during severe disease such as heavy flu. These patients had good clinical conditions, desire to

use HU and no side effects. 'Non-responders (NR)' with a poor response to HU treatment showing a mean Hb less than 8.5 g/dL. This group of patients developed side effects to HU therapy, had discomfort using the drug, and no or very little change in transfusion intervals during the treatment period. At this point, 27 patients (12 NR and 15 R) were selected for the follow-up study. At the same time, peripheral blood was collected from the patients for culture of erythroid progenitors used for subsequent studies. NR patients with a shorter treatment period (minimum 2 months) started the treatment process later and, since they did not benefit from it, they stopped taking HU and were put back on regular transfusion, while R patients became transfusion-independent and continued their HU treatment regimes.

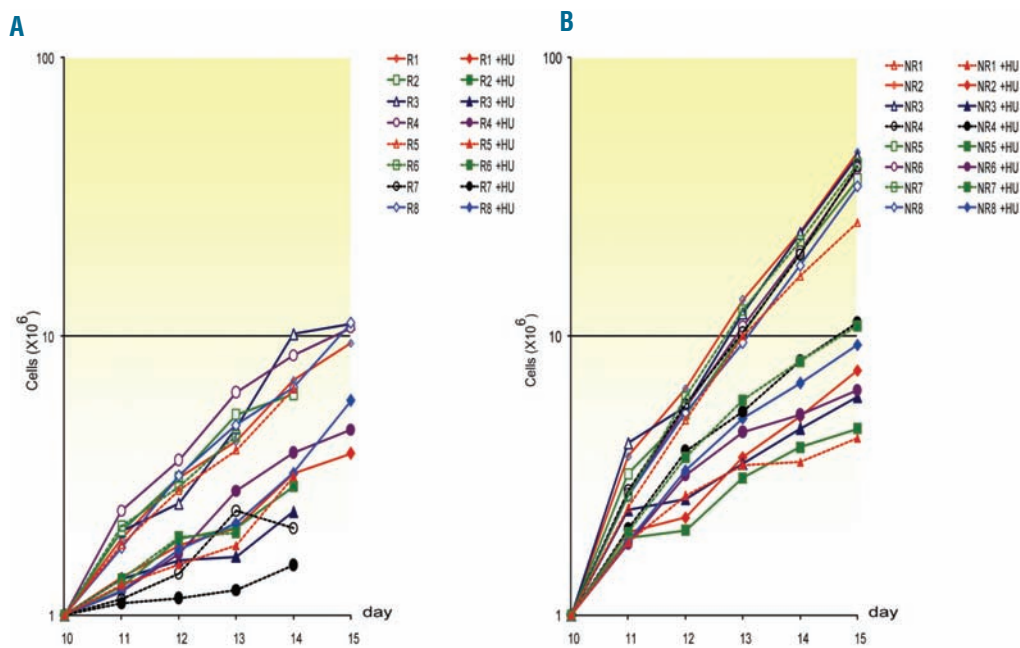
Mutations in the  $\alpha$ - and  $\beta$ -globin genes and the -158 XmnI G $\gamma$ -globin gene (C>T SNP) were determined as described previously.<sup>1,2</sup> Since positive correlation between  $\alpha$ -globin deletions and good response to HU therapy is reported,<sup>3,5</sup> patients with mutated or deleted  $\alpha$ -globin alleles were excluded from the study. Although a high HbF base line is correlated with the XmnI polymorphism as well other SNPs, HbF response to HU therapy does not seem to be correlated with the Xmn I polymorphism as well as  $\beta$ -globin gene mutation.<sup>4,6,7</sup> We, therefore, did not bias our study for these variables. We selected 8 patients from each group who comply with the above mentioned criteria for microarray analysis. Age, sex, HU treatment dose, transfusion start age and transfused blood volume, transfusion intervals were distributed similarly between the two groups (*Online Supplementary Table S1*).

### Cell culture

We collected 40 mL of blood from each patient and buffy coats were isolated by centrifugation. White cells were isolated from the interphase after Ficoll gradient purification, and washed with phosphate buffered saline (PBS). For initial expansion, cells were cultured at a density of  $1-2 \times 10^6$  cells/mL in serum-free medium (StemSpan; Stem Cell Technologies, Vancouver, BC, Canada) enriched with lipids (40 ng/mL cholesterol-rich lipid mix; Sigma,



**Online Supplementary Figure S1.** Hydroxyurea (HU) induces dose dependent hemoglobinization and reduces cell proliferation of healthy donor HEPs. (A) HEP growth curves on different HU doses (0 to 400  $\mu$ M). (B) Effect of different HU concentrations on total hemoglobin production after 8 days of HU treatment. Hb levels are represented in arbitrary units (a.u.). (C) HPLC Hb analysis of samples in (B). Note that the total amount of Hb does not add up to 100% because the P3 peak of the HPLC profile is not assigned to a specific Hb fraction. (D) Representation of Hb subtypes by distributing total hemoglobin (B) into HbF, HbA and HbA2 (C); expressed in arbitrary units (a.u.). (E) Representative cytopsin of HEPs treated with different HU concentrations, stained with histological dyes and neutral benzidine. Hemoglobinized cells are stained brown. Experiments were performed in triplicate, using cells from 2 healthy donors. Bars represent averages; error bars represent standard deviation of 6 measurements.



**Online Supplementary Figure S2.** Erythroblasts derived from responders are less sensitive to HU treatment. (A) Responder HEPs grown under proliferation conditions. (B) Non-responder HEPs grown under proliferation conditions. +HU: 100  $\mu$ M hydroxyurea added to the cultures. Note that the y-axis has a logarithmic scale.

St Louis, MO, USA) and supplemented with erythropoietin (2 u/mL, Orthobiotech, Tilburg, The Netherlands), dexamethasone (1  $\mu$ M; Sigma) and SCF (50 ng/mL).<sup>8,9</sup> The erythroblast cultures were expanded until Day 10 by daily partial medium changes and addition of fresh factors, keeping cell densities between 1.5-2x10<sup>6</sup> cells/mL. Proliferation kinetics and cell size distributions were monitored daily using an electronic cell counter (CASY-1, Schärfe-System, Reutlingen, Germany).

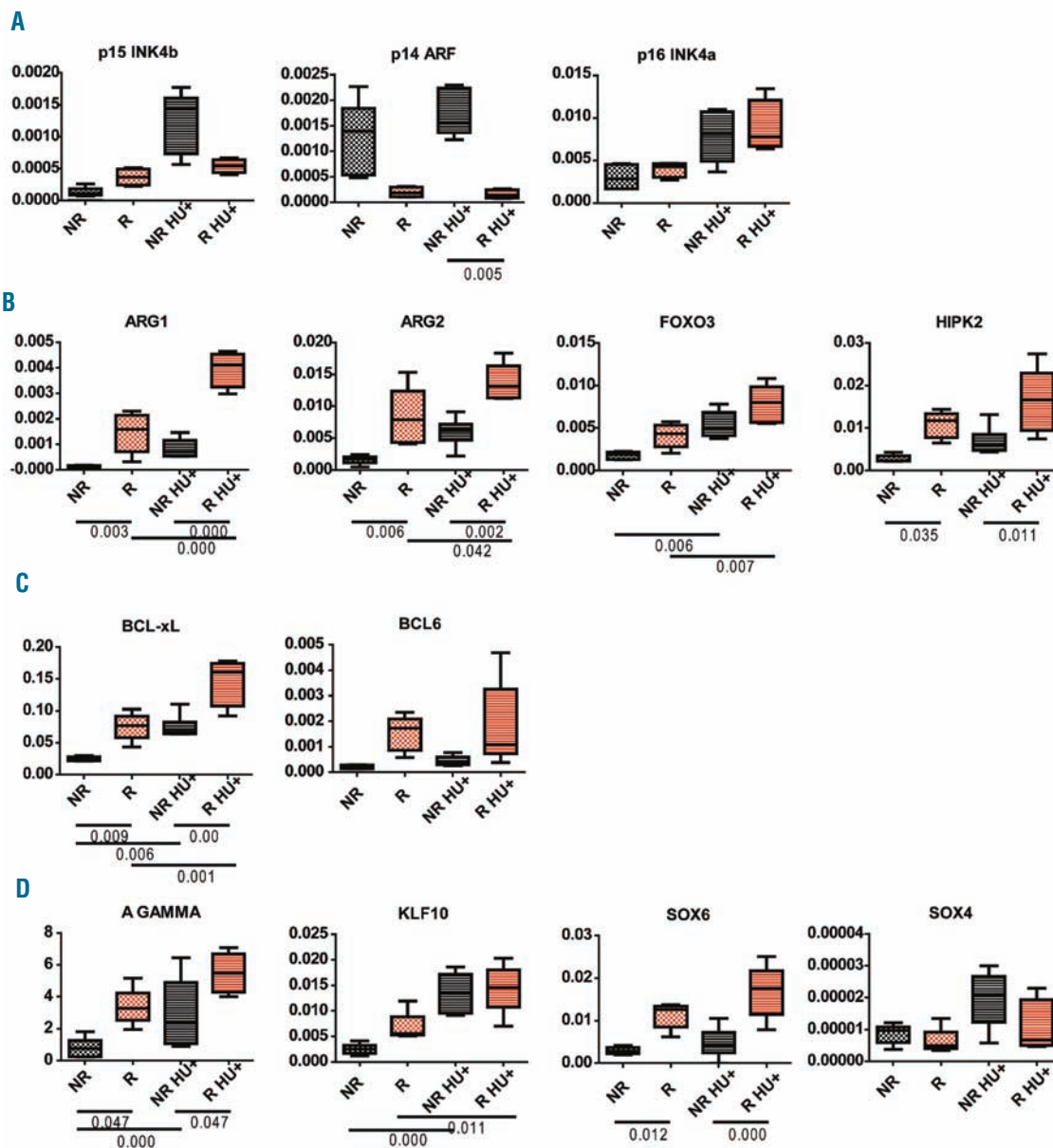
#### Quantitative PCR conditions and primers

Quantitative real-time PCR (MyIQ, Bio Rad) was performed using 0.75  $\mu$ L of SYBR Green I (Sigma S9430; 1/2500 dilution in DMSO), 0.5 u Platinum Taq (Invitrogen), 10 pmol of each primer and 4  $\mu$ L cDNA sample, in a final volume of 25  $\mu$ L. We used the following cycling conditions: 3 min at 95°C followed by 40

cycles of 30 s at 95°C, 20 s at 56°C, 40 s at 60°C, 15 s at 75°C. Human GAPDH and USP14 were used as endogenous references for normalization. Enrichment of specific sequences was calculated using the comparative CT method.<sup>10</sup>

#### Affymetrix microarrays

HEPs were lysed using the TRIzol Reagent (Invitrogen) and then incubated at room temperature for 5 min before adding 0.2 mL of chloroform to each 1 mL sample. After centrifugation (12,000 rpm) for 20 min to separate the phases, RNA was precipitated from the aqueous phase by the addition of 0.7 volume of isopropanol, and collected by centrifugation. The RNA pellets were washed with 75% ethanol and dissolved in RNase-free water. RNA samples were stored at -80 C until further use.



**Online Supplementary Figure S3.** qRT-PCR of selected genes validates expression profiling analysis. (A) *INK4B-ARF-INK4B* locus. (B) Stress response genes. (C) Apoptosis response genes. (D) Globin regulation-related genes. R: Responders; NR: non-responders; HU+: HU+ treated. *P*-values < 0.05 are indicated. At least 5 patients were analyzed in each group.

### Assessment of RNA quality and concentration

The integrity of the isolated total RNA was verified on the Agilent 2100 BioAnalyzer (Agilent Technologies, Palo Alto, CA, USA). Samples were kept for further processing if the 28s/18s ratio was higher than 1.8. The concentrations of RNA were measured with a NanoDrop ND-111 UV-VIS spectrophotometer.

### cRNA amplification and labeling

Double stranded (ds) cDNA synthesis was performed according to the standardized protocol for One-Cycle cDNA synthesis from Affymetrix (Santa Clara, CA, USA). Approximately 5 µg of total RNA was first converted to single stranded cDNA in a 20 µL First-Strand Reaction Mix, containing poly-A control RNA, 100 µmol T7-Oligo primer, 1 x first strand buffer, 0.2 mmol DTT, 10 mmol dNTP mix and SuperScript II. The sample RNA, the poly-

A control RNA and the T7-Oligo Primer were mixed and incubated for 10 min at 70°C. Second, the first strand buffer, the DTT and the dNTP mix were added and incubated for 2 min at 42°C, followed by adding SuperScript II and incubation for 1 h at 42°C. The ds cDNA was prepared from the resultant First-Strand Reaction Mix, mixed with 1 x second strand reaction buffer, 30 mmol dNTP mix, *E. coli* DNA ligase, *E. coli* DNA Polymerase I and RNaseH. The mix was incubated for 2 h at 16°C, then supplemented with T4 DNA polymerase, and incubated for another 5 min at 16°C. The reaction was stopped by the addition of EDTA to a final concentration of 5 µM. The Sample Clean-up Module and GeneChip IVT Labeling Kit from Affymetrix were used to purify the synthesized ds cDNA, and this was used to generate biotin-labeled cRNA in the presence of 1 x IVT labeling buffer, IVT labeling NTP Mix, IVT labeling enzyme mix and

RNase-free water in a total volume of 40  $\mu$ l. After incubation for 16 h at 37°C, the concentration of the labeled cRNA was checked with a NanoDrop ND-1000 UV-VIS spectrophotometer. An A260/A280 ratio between 1.9 and 2.1 was considered acceptable. Approximately 20  $\mu$ g cRNA was fragmented to an average size of 35-200 nucleotides by heating at 94°C for 35 min, in the presence of a 1 x fragmentation buffer in a total volume of 40  $\mu$ l. The fragmented samples were stored at -20°C before being subjected to hybridization.

### Hybridization

Hybridization was conducted following Affymetrix instructions for GeneChip® Human Genome U133 Plus 2.0 arrays. The GeneArray scanner 3000 (Affymetrix) was used to detect the hybridization signals.

### Pre-processing microarray data

#### Array quality control

Microarrays that did not pass the quality assessment were removed from further analyses. The quality metrics used to exclude microarrays was the statistics summary calculated by the GCOS algorithm during the processing of probe level data. The primary inclusion criteria include: all arrays had to have comparable noise values (Raw Q, measurement for the pixel-to-pixel variation of probe cells on the chip); background values were within the range of 20 to 100; percent of present probe sets on the array should not be below 45%. The other criteria were: arrays with extremely high or low values for any of these parameters, e.g. values beyond the range of standard deviation  $\pm$  median, were excluded; signal ratio over 3 of the 3'/5' probe sets for GAPDH and Actin were used as a cut off; labeling and hybridization were controlled by using standard spike-in controls according to the Affymetrix protocol; if global scaling was applied, the scaling factors for each array were within a 3-fold range.

#### Array data analysis: quantile normalization

RMA (Robust Multi-Array average) is an integrated algorithm comprising background adjustment, quantile normalization, and expression summarization by median polish. The intensities of mismatch probes were entirely ignored due to their spurious estimation of non-specific binding. The intensities were background-corrected in such a way that all corrected values must be positive. The RMA algorithm utilized quantile normalization in which the signal value of individual probes was substituted by the average of all probes with the same rank of intensity on each array. Finally, Tukey's median polish algorithm was used to obtain the estimates of expression for normalized probe intensities.<sup>11</sup>

#### Other transformations

Intensities of probe sets lower than 30 were re-set to 30. The geometric mean for each probe set was calculated across all samples, or first for each subgroup of samples and then

across all samples (OmniViz, Maynard, MA, USA). The intensity values of individual probe sets in each sample were then displayed as the log<sub>2</sub> value of the deviations to the calculated geometric means.

### Probe set filtering

Probe sets were involved in further analysis only if their expression levels deviated from the overall mean in at least one array by a minimum factor of 1, because the remaining data were unlikely to be informative. The result was that 36,471 probe sets were eliminated and 18,204 probe sets remained for further analysis.

### Statistical analysis

The resulting list of 18,204 probe sets was the starting point for all supervised analyses which, for example, correlated gene expression with variables such as R *versus* NR, with or without HU treatment. Class comparison analysis was performed by using Significance Analysis of Microarray (SAM), integrated in OmniViz version 5.1.

### Functional annotation

Functional annotation was processed using Ingenuity Pathway Analysis with a Fisher's Exact test threshold *P* value of 0.05. (Ingenuity, Mountain View, CA, USA).

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Online Supplementary Table S1. Clinical data of  $\alpha$ -thalassaemia patients included in this study. NR: non-responders, R: Responders, F: female, M: male, ND: not determined; NA: not applicable.

Code	Age at sampling	Age at sampling (yr)	Sex (m/f)	Blood group	Height (cm)	Weight (kg)	Mutation	Xmnl polymorphism	HU (mg/kg/day)	Duration of HU Treatment (months)	Amount of blood transfusion (cc)	Transfusion start age (year)	Desferrioxamine mg/kg body weight/day	Transfusion intervals before HU (days)	Transfusion intervals after HU (days)	WBC (X10 <sup>9</sup> /l)	Hgb (g/l)	MCV (fl)	MCH (fmol/cell)	Platelet (X10 <sup>9</sup> /l)	Hba (%)	HbF (%)	HbA2 (%)
NR1	24	24	F	A+	162	50	IVS1-II/VS1-110	-/-	10	2	700	<2	20	21	18	5.3	92	86.6	1.76	380	ND/NA	ND/NA	ND/NA
NR2	25	25	F	A+	162	51	IVS1-II/VS1-II	-/-	10	4	800	<2	25	21	15	12.2	92	88.3	1.85	490	ND/NA	ND/NA	ND/NA
NR3	20	20	M	O+	120	48	C44/C27	-/-	15	6	800	<2	20	30	45	12.0	81	78.0	1.64	571	ND/NA	ND/NA	ND/NA
NR4	30	30	F	O+	168	48	IVS1-II/VS1-II	+/+	15	6	450	<2	20	28	35	10.3	92	85.4	1.75	424	ND/NA	ND/NA	ND/NA
NR5	15	15	F	O+	135	35	IVS1-II/VS1-II	-/-	5	4	800	<2	15	30	25	13.0	85	86.0	1.74	450	ND/NA	ND/NA	ND/NA
NR6	21	21	M	O+	168	55	IVS1-25/VS1-5	+/+	20	6	800	<2	10	20	18	4.8	69	79.5	1.61	332	ND/NA	ND/NA	ND/NA
NR7	21	21	M	O+	164	50	C39/C39	-/-	10	3	800	7	15	24	24	5.1	84	79.5	1.64	225	ND/NA	ND/NA	ND/NA
NR8	22	22	M	AB+	163	57	C22/C30	-/-	10	2	800	5	25	20	20	4.4	103	85.5	1.77	236	ND/NA	ND/NA	ND/NA
Mean	22.3	22.3	4/4		155.3	49.3		19% Xmnl +	11.9	4.1	743.8	3	18.8	24.6	25	8.4	84.6	83.6	1.72	389			
Median	21.5	21.5			162.5	50.0			10	4	800	2	20	24	22	7.8	83	85.5	1.74	402			
Min	15	15			120	35			5	2	460	2	10	20	15	4.4	68	78.0	1.61	225			
Max	30	30			168	57			20	6	800	7	25	30	45	13.0	103	88.3	1.85	571			
R1	14	14	M	AB+	175	48	IVS1-II/VS1-II	+/+	15	more than 6 month	900	4	30	30	no transfusion	8.2	119	90.1	1.92	699	21.6	75.0	3.4
R2	30	30	F	O+	149	50	C8/C8	+/+	10	more than 6 month	800	<2	35	30	no transfusion	11.3	87	94.2	1.84	433	28.9	68.0	3.1
R3	18	18	F	A+	137	27	IVS1-II/VS1-II	-/-	10	more than 6 month	800	5	20	30	no transfusion	10.5	89	65.6	1.35	400	43.1	54.0	2.9
R4	22	22	M	O+	164	49	IVS1-II/VS1-5	+/+	10	more than 6 month	800	<2	20	18	no transfusion	11.0	91	78.0	1.55	632	15.3	83.0	2.7
R5	25	25	F	B+	156	57	cd25-26/cd25-26	+/+	15	more than 6 month	800	<2	10	26	no transfusion	6.6	91	86.6	1.69	213	23.0	73.7	3.3
R6	21	21	M	O+	178	62	IVS1-II/VS1-II	+/+	10	more than 6 month	700	5	10	30	no transfusion	9.1	128	73.4	1.45	450	10.9	87.9	1.9
R7	30	30	F	A+	162	52	IVS1-II/VS1-II	+/+	10	more than 6 month	800	3	15	19	no transfusion	8.8	89	75.0	1.49	725	12.0	84.3	3.7
R8	25	25	M	AB+	155	61	IVS1-II/29bp deletion	-/-	10	more than 6 month	700	<2	10	18	no transfusion	12.7	116	84.0	1.69	564	39.1	56.0	4.9
Mean	23.1	23.1	4/4		159.6	50.8		69% Xmnl +	11.3	more than 6 month	787.5	3.1	20	26.1	no transfusion	9.8	101.3	80.9	1.62	515	24.2	72.7	3.2
Median	23.5	23.5			159.0	51.0			10		800	2.5	20	28		9.8	91	81.0	1.62	507	22.3	74.4	3.2
Min	14	14			137	27			10		700	2	10	18		6.6	87	65.6	1.35	213	10.9	64.0	1.9
Max	30	30			178	62			15		900	5	35	30		12.7	128	94.2	1.92	725	43.1	87.9	4.9

Online Supplementary Table S2. NR. vs. R. provided as single supplementary .pdf file.

ProbelD	Gene Title	Gene Symbol	Foldchange	qvalue%
206177_s_at	arginase, liver	ARG1	0,09829423	0,13717257
AFX-HUMRGE/M10098_5_at	---	---	0,13707349	2,38495135
202627_s_at	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibito	SERPINE1	0,15535468	1,3948219
205919_at	hemoglobin, epsilon 1	HBE1	0,15750912	0,13717257
204103_at	chemokine (C-C motif) ligand 4	CCL4	0,17903438	1,3948219
206447_at	chymotrypsin-like elastase family, member 2A	CELA2A	0,18664759	0,63176664
243737_at	ATPase, Na+/K+ transporting, beta 4 polypeptide	ATP1B4	0,19425806	0,85107329
AFX-HUMRGE/M10098_M_at	---	---	0,19601219	2,38495135
202628_s_at	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibito	SERPINE1	0,19766834	1,3948219
206446_s_at	chymotrypsin-like elastase family, member 2A /// chymotrypsin-like elas	CELA2A /// CELA	0,19873954	0,63176664
225207_at	pyruvate dehydrogenase kinase, isozyme 4	PKD4	0,23218808	4,1207969
207533_at	chemokine (C-C motif) ligand 1	CCL1	0,23930126	0,4846616
211207_s_at	acyl-CoA synthetase long-chain family member 6	ACSL6	0,24673187	0,13717257
212099_at	ras homolog gene family, member B	RHOB	0,25210128	0,13717257
205872_x_at	phosphodiesterase 4D interacting protein	PDE4DIP	0,25374269	0,13717257
232838_at	additional sex combs like 3 (Drosophila)	ASXL3	0,26542234	4,1207969
231078_at	---	---	0,26994434	0,13717257
205899_at	cyclin A1	CCNA1	0,27234542	4,51937074
214696_at	chromosome 17 open reading frame 91	C17orf91	0,27428881	0,13717257
203140_at	B-cell CLL/lymphoma 6	BCL6	0,27640233	0,13717257
202718_at	insulin-like growth factor binding protein 2, 36kDa	IGFBP2	0,28194234	1,21472295
242625_at	radical S-adenosyl methionine domain containing 2	RSAD2	0,28250739	0,13717257
211000_s_at	interleukin 6 signal transducer (gp130, oncostatin M receptor)	IL6ST	0,29029473	0,22870838
205984_at	corticotropin releasing hormone binding protein	CRHBP	0,29086541	0,13717257
240456_at	Ankyrin repeat domain 55	ANKRD55	0,29551725	0,13717257
242384_at	---	---	0,30079953	0,13717257
240168_at	exportin 7	XPO7	0,3011491	0,13717257
219630_at	PDZK1 interacting protein 1	PDZK1IP1	0,30203449	0,13717257
237739_at	---	---	0,30427037	0,13717257
217996_at	pleckstrin homology-like domain, family A, member 1	PHLDA1	0,30885797	4,51937074
221748_s_at	tensin 1	TNS1	0,30970833	0,13717257
204072_s_at	furry homolog (Drosophila)	FRY	0,31268127	0,13717257
238117_at	protoporphyrinogen oxidase	PPOX	0,3142431	0,13717257
213797_at	radical S-adenosyl methionine domain containing 2	RSAD2	0,31919312	0,13717257
241060_x_at	---	---	0,31967842	0,13717257
209047_at	aquaporin 1 (Colton blood group)	AQP1	0,32040166	0,13717257
1553589_a_at	PDZK1 interacting protein 1	PDZK1IP1	0,32123931	0,13717257
232035_at	histone cluster 1, H4h	HIST1H4H	0,32464211	2,79695557
200878_at	endothelial PAS domain protein 1	EPAS1	0,32529821	0,32270094
204863_s_at	interleukin 6 signal transducer (gp130, oncostatin M receptor)	IL6ST	0,32730687	0,13717257
215017_s_at	formin binding protein 1-like	FNBP1L	0,32858947	0,76883463
242496_at	---	---	0,33410888	0,13717257
202859_x_at	interleukin 8	IL8	0,33488998	1,3948219
239162_at	---	---	0,33870971	1,3948219
218332_at	brain expressed, X-linked 1	BEX1	0,34670495	1,00422607
208180_s_at	histone cluster 1, H4h	HIST1H4H	0,35185111	4,51937074
AFX-M27830_5_at	---	---	0,36222138	0,85107329
207077_at	chymotrypsin-like elastase family, member 2B	CELA2B	0,36237747	1,3948219
222420_s_at	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	UBE2H	0,3664732	0,13717257
237409_at	---	---	0,37065733	4,51937074
1569477_at	---	---	0,37424144	0,22870838
205076_s_at	myotubularin related protein 11	MTMR11	0,37482731	0,13717257
236302_at	protein phosphatase, Mg2+/Mn2+ dependent, 1E	PPM1E	0,38040323	0,13717257
212196_at	interleukin 6 signal transducer (gp130, oncostatin M receptor)	IL6ST	0,38171041	0,13717257
202686_s_at	AXL receptor tyrosine kinase	AXL	0,38181194	1,94055411
242280_x_at	cytoplasmic polyadenylation element binding protein 4	CPEB4	0,38300213	0,13717257
224829_at	cytoplasmic polyadenylation element binding protein 4	CPEB4	0,38548111	0,13717257
224237_at	---	---	0,38867357	1,3948219
229725_at	Acyl-CoA synthetase long-chain family member 6	ACSL6	0,39045274	0,22870838
200782_at	annexin A5	ANXA5	0,39150262	1,00422607
237849_at	---	---	0,39202188	0,13717257
227062_at	---	---	0,39471	3,63155925
206196_s_at	RUN domain containing 3A	RUNDC3A	0,39505641	0,13717257
205807_s_at	tuftelin 1	TUFT1	0,39557941	0,13717257
212195_at	interleukin 6 signal transducer (gp130, oncostatin M receptor)	IL6ST	0,39646356	0,13717257
208605_s_at	neurotrophic tyrosine kinase, receptor, type 1	NTRK1	0,39797032	0,13717257
237618_at	---	---	0,40178819	0,13717257
225368_at	homeodomain interacting protein kinase 2	HIPK2	0,40197504	0,13717257
208886_at	H1 histone family, member 0	H1F0	0,4068927	1,3948219
210357_s_at	spermine oxidase	SMOX	0,40915972	0,13717257
211458_s_at	GABA(A) receptor-associated protein like 1 /// GABA(A) receptors associ	GABARAPL1 ///	0,41020172	0,13717257
203946_s_at	arginase, type II	ARG2	0,41092632	0,13717257
223467_at	RAS, dexamethasone-induced 1	RASD1	0,41233754	0,13717257
225239_at	---	---	0,41249176	1,00422607
213096_at	transmembrane and coiled-coil domain family 2	TMCC2	0,41458556	0,13717257
1553962_s_at	ras homolog gene family, member B	RHOB	0,41497476	0,57337326
228573_at	anthrax toxin receptor 2	ANTXR2	0,41770615	4,51937074
224828_at	cytoplasmic polyadenylation element binding protein 4	CPEB4	0,42036204	0,13717257
224657_at	ERBB receptor feedback inhibitor 1	ERRFI1	0,42268928	0,50606127
209298_s_at	intersectin 1 (SH3 domain protein)	ITSN1	0,42302335	0,13717257
207542_s_at	aquaporin 1 (Colton blood group)	AQP1	0,4255778	0,40274237
229483_at	---	---	0,42710662	0,85107329
221747_at	tensin 1	TNS1	0,42726722	0,13717257
237568_at	---	---	0,42775034	0,13717257
221962_s_at	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	UBE2H	0,42873489	0,13717257
237590_at	---	---	0,4287692	0,13717257
213059_at	cAMP responsive element binding protein 3-like 1	CREB3L1	0,42926191	0,13717257
228181_at	solute carrier family 30 (zinc transporter), member 1	SLC30A1	0,43074842	0,13717257
229151_at	solute carrier family 14 (urea transporter), member 1 (Kidd blood group)	SLC14A1	0,43102228	0,13717257
236630_at	aquaporin 2 (collecting duct)	AQP2	0,43176462	0,85107329
236313_at	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	CDKN2B	0,43193654	4,1207969
203473_at	solute carrier organic anion transporter family, member 2B1	SLCO2B1	0,43375857	0,50606127
225116_at	homeodomain interacting protein kinase 2	HIPK2	0,43590803	0,13717257
209238_at	syntaxin 3	STX3	0,43658597	0,22870838
34210_at	CD52 molecule	CD52	0,43732341	4,51937074
1552713_x_at	solute carrier family 4, anion exchanger, member 1 (erythrocyte membr	SLC4A1	0,43833305	0,13717257
244358_at	---	---	0,43952132	0,13717257
204363_at	coagulation factor III (thromboplastin, tissue factor)	F3	0,44089687	3,12037782
205532_s_at	cadherin 6, type 2, K-cadherin (fetal kidney)	CDH6	0,44192844	0,13717257
208116_s_at	mannosidase, alpha, class 1A, member 1	MAN1A1	0,44205919	0,13717257
205533_s_at	cadherin 6, type 2, K-cadherin (fetal kidney)	CDH6	0,44273236	0,22870838
208869_s_at	GABA(A) receptor-associated protein like 1	GABARAPL1	0,44298237	0,13717257
205896_at	solute carrier family 22 (organic cation/ergothioneine transporter), mem	SLC22A4	0,44354292	0,4846616
201249_at	solute carrier family 2 (facilitated glucose transporter), member 1	SLC2A1	0,44400253	0,13717257

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244403_at	crumbs homolog 1 (Drosophila)	CRB1	0,44609447	0,22870838
202191_s_at	growth arrest-specific 7	GA57	0,44678327	3,12037782
218145_at	tribbles homolog 3 (Drosophila)	TRIB3	0,44684922	0,50606127
218864_at	tensin 1	TNS1	0,44980104	0,32270094
201631_s_at	immediate early response 3	IER3	0,4503119	3,12037782
202437_s_at	cytochrome P450, family 1, subfamily B, polypeptide 1	CYP1B1	0,45146204	0,32270094
206672_at	aquaporin 2 (collecting duct)	AQP2	0,45282691	0,13717257
241205_at	---	---	0,45342692	1,3948219
221577_x_at	growth differentiation factor 15 /// similar to growth differentiation fact	GDF15 /// LOC1C	0,45399936	0,40274237
204864_s_at	interleukin 6 signal transducer (gp130, oncostatin M receptor)	IL6ST	0,45496465	2,38495135
244205_at	aminolevulinatase, delta-, synthase 2	ALAS2	0,45580031	0,13717257
225685_at	---	---	0,45722506	0,57337326
240271_at	---	---	0,45876954	0,13717257
232978_at	---	---	0,45943449	0,57337326
39248_at	aquaporin 3 (Gill blood group)	AQP3	0,46118633	0,40274237
227498_at	SRY (sex determining region Y)-box 6	SOX6	0,46160585	0,13717257
228758_at	B-cell CLL/lymphoma 6	BCL6	0,4620285	0,13717257
211993_at	WNK lysine deficient protein kinase 1	WNK1	0,46350662	0,32270094
241542_at	---	---	0,46352309	0,22870838
1558518_at	TGF-beta activated kinase 1/MAP3K7 binding protein 3	TAB3	0,46411051	0,13717257
1559410_at	---	---	0,46532584	3,63155925
203502_at	2,3-bisphosphoglycerate mutase	BPGM	0,46685947	0,22870838
231616_at	---	---	0,46718403	0,22870838
225115_at	homeodomain interacting protein kinase 2	HIPK2	0,4678967	0,13717257
202435_s_at	cytochrome P450, family 1, subfamily B, polypeptide 1	CYP1B1	0,46818505	0,48466616
209288_s_at	CDC42 effector protein (Rho GTPase binding) 3	CDC42EP3	0,47197696	1,74547566
1569238_a_at	---	---	0,47212854	3,12037782
230688_at	---	---	0,47223298	0,13717257
235916_at	yippee-like 4 (Drosophila)	YPEL4	0,47308698	0,13717257
217799_x_at	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	UBE2H	0,47706414	0,13717257
236975_at	---	---	0,47714174	0,48466616
223179_at	yippee-like 3 (Drosophila)	YPEL3	0,47841388	0,13717257
214803_at	cadherin 6, type 2, K-cadherin (fetal kidney)	CDH6	0,47849207	0,50606127
215967_s_at	lymphocyte antigen 9	LY9	0,48005604	0,22870838
241561_at	---	---	0,48011593	0,13717257
234033_at	---	---	0,48055009	1,3948219
1558322_a_at	progesterin and adiponectin receptor family member IX	PAQR9	0,48069135	1,00422607
205266_at	leukemia inhibitory factor (cholinergic differentiation factor)	LIF	0,48230949	0,13717257
209795_at	CD69 molecule	CD69	0,48255543	3,12037782
212698_s_at	septin 10	10-set	0,48262512	4,1207969
205934_at	phospholipase C-like 1	PLCL1	0,4844806	0,85107329
200799_at	heat shock 70kDa protein 1A	HSPA1A	0,48454885	0,13717257
225097_at	homeodomain interacting protein kinase 2	HIPK2	0,4857077	0,13717257
1555680_a_at	spermine oxidase	SMOX	0,48572984	0,13717257
237207_at	---	---	0,48621249	0,13717257
213256_at	membrane-associated ring finger (C3HC4) 3	03-mar	0,48671707	0,13717257
202393_s_at	Kruppel-like factor 10	KLF10	0,48701	0,40274237
1558688_at	hypothetical LOC441461	LOC441461	0,48895229	0,13717257
205856_at	solute carrier family 14 (urea transporter), member 1 (Kidd blood group)	SLC14A1	0,49004622	0,50606127
209286_at	CDC42 effector protein (Rho GTPase binding) 3	CDC42EP3	0,49014217	0,22870838
238909_at	---	---	0,49037675	0,63176664
1569067_at	---	---	0,49148022	0,13717257
225957_at	chromosome 5 open reading frame 41	CSorf41	0,49150968	1,21472295
212907_at	Solute carrier family 30 (zinc transporter), member 1	SLC30A1	0,4917929	0,13717257
222421_at	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	UBE2H	0,49213281	0,13717257
213338_at	transmembrane protein 158 (gene/pseudogene)	TMEM158	0,49248499	0,22870838
233674_at	---	---	0,49325256	0,13717257
207220_at	ADP-ribosyltransferase 4 (Dombrock blood group)	ART4	0,49336199	0,13717257
242662_at	Protein convertase subtilisin/kexin type 6	PCSK6	0,49427502	0,13717257
243904_at	---	---	0,4953803	2,38495135
236439_at	---	---	0,49578922	1,00422607
1558950_at	---	---	0,49675673	0,40274237
202242_at	tetraspanin 7	TSPAN7	0,49859763	4,1207969
221760_at	Mannosidase, alpha, class 1A, member 1	MAN1A1	0,49877972	0,40274237
216101_at	---	---	0,49992252	0,50606127
224016_at	homeodomain interacting protein kinase 2	HIPK2	0,49996908	0,13717257
1568780_at	hypothetical LOC649305	LOC649305	0,50023304	1,3948219
224567_x_at	metastasis associated lung adenocarcinoma transcript 1 (non-protein co	MALAT1	0,50157012	1,3948219
227497_at	SRY (sex determining region Y)-box 6	SOX6	0,5018117	0,13717257
224831_at	cytoplasmic polyadenylation element binding protein 4	CPEB4	0,50303508	0,13717257
236808_at	FGFR1 oncogene partner 2	FGFR1OP2	0,50434151	2,38495135
202124_s_at	trafficking protein, kinesin binding 2	TRAK2	0,50506182	0,13717257
1569459_a_at	---	---	0,5055602	0,13717257
212390_at	phosphodiesterase 4D interacting protein	PDE4DIP	0,50556442	0,32270094
205592_at	solute carrier family 4, anion exchanger, member 1 (erythrocyte membr	SLC4A1	0,50567351	0,13717257
205730_s_at	actin binding LIM protein family, member 3	ABLIM3	0,50657681	0,63176664
238118_s_at	protoporphyrinogen oxidase	PPOX	0,50701513	0,13717257
211560_s_at	aminolevulinatase, delta-, synthase 2	ALAS2	0,50794867	0,13717257
39313_at	WNK lysine deficient protein kinase 1	WNK1	0,50858548	0,13717257
224889_at	forkhead box O3	FOXO3	0,50874823	0,13717257
237194_at	---	---	0,50876645	0,13717257
200800_s_at	heat shock 70kDa protein 1A /// heat shock 70kDa protein 1B	HSPA1A /// HSP1	0,50932179	0,85107329
238638_at	solute carrier family 37 (glycerol-3-phosphate transporter), member 2	SLC37A2	0,50957523	0,13717257
228170_at	oligodendrocyte transcription factor 1	OLIG1	0,50988747	1,00422607
201236_s_at	BTG family, member 2	BTG2	0,51004035	0,13717257
234989_at	---	---	0,51040848	3,12037782
238853_at	RAB3A interacting protein (rabin3)	RAB3IP	0,51126808	0,13717257
210370_s_at	lymphocyte antigen 9	LY9	0,51248178	0,48466616
203477_at	collagen, type XV, alpha 1	COL15A1	0,51254364	4,1207969
226675_s_at	metastasis associated lung adenocarcinoma transcript 1 (non-protein co	MALAT1	0,51283951	1,94055411
228854_at	---	---	0,51451989	1,00422607
239274_at	---	---	0,5158767	0,85107329
240178_at	---	---	0,51588908	0,13717257
243546_at	---	---	0,51721472	4,51937074
202436_s_at	cytochrome P450, family 1, subfamily B, polypeptide 1	CYP1B1	0,51784748	0,50606127
235730_at	---	---	0,51801026	0,50606127
236067_at	---	---	0,51874405	0,13717257
217523_at	CD44 molecule (Indian blood group)	CD44	0,51883314	1,74547566
203935_at	activin A receptor, type I	ACVR1	0,51999886	4,1207969
238476_at	chromosome 5 open reading frame 41	CSorf41	0,52063451	0,57337326
209890_at	tetraspanin 5	TSPAN5	0,5208872	0,13717257
212736_at	chromosome 16 open reading frame 45	Cl6orf45	0,52093616	0,22870838
216022_at	---	---	0,52128802	3,63155925
233648_at	---	---	0,52326312	0,50606127
221920_s_at	solute carrier family 25, member 37	SLC25A37	0,52533107	0,22870838

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219340_s_at	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation)	CLN8	0,52543091	0,13717257
222528_s_at	solute carrier family 25, member 37	SLC25A37	0,5256261	0,13717257
243509_at	---	---	0,52598229	0,13717257
236699_at	---	---	0,52757867	0,13717257
212828_at	synaptojanin 2	SYNJ2	0,52970281	0,40274237
239721_at	---	---	0,53010391	0,4846616
238176_at	Rap guanine nucleotide exchange factor (GEF) 2	RAPGEF2	0,53031298	1,00422607
223912_s_at	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation)	CLN8	0,53126395	0,13717257
235983_at	---	---	0,53223144	0,13717257
224891_at	forkhead box O3	FOXO3	0,53339679	0,13717257
228754_at	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	SLC6A6	0,53343996	0,40274237
226415_at	vesicle amine transport protein 1 homolog (T. californica)-like	VAT1L	0,53466327	1,00422607
224558_s_at	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	MALAT1	0,53564309	1,00422607
201250_s_at	solute carrier family 2 (facilitated glucose transporter), member 1	SLC2A1	0,53631829	0,13717257
215134_at	phosphatidylinositol 4-kinase type 2 alpha	PI4K2A	0,53635746	0,13717257
232138_at	Muscleblind-like 2 (Drosophila)	MBNL2	0,53668199	0,85107329
242320_at	---	---	0,53685868	0,13717257
207076_s_at	argininosuccinate synthase 1	ASS1	0,53695214	0,13717257
219270_at	ChaC, cation transport regulator homolog 1 (E. coli)	CHAC1	0,53757404	0,32270094
239661_at	---	---	0,53761287	1,74547566
210612_s_at	synaptojanin 2	SYNJ2	0,5379264	4,1207969
215992_s_at	Rap guanine nucleotide exchange factor (GEF) 2	RAPGEF2	0,53800664	1,3948219
244044_at	---	---	0,53804198	1,74547566
224897_at	WD repeat domain 26	WDR26	0,53909198	0,13717257
220120_s_at	erythrocyte membrane protein band 4.1 like 4A	EPB41L4A	0,53918227	2,38495135
232136_s_at	cortactin binding protein 2	CTTNBP2	0,53993266	2,79695557
235497_at	hypothetical LOC643837	LOC643837	0,54080366	0,63176664
211557_x_at	solute carrier organic anion transporter family, member 2B1	SLCO2B1	0,54086252	0,57337326
230000_at	ring finger protein 213	RNF213	0,5411234	0,22870838
222871_at	kelch domain containing 8A	KLHDC8A	0,54263459	0,13717257
209297_at	intersectin 1 (SH3 domain protein)	ITSN1	0,54274426	0,22870838
227762_at	---	---	0,54301802	0,63176664
229221_at	CD44 molecule (Indian blood group)	CD44	0,54310043	0,22870838
1559520_at	Glycophorin A (MNS blood group)	GYP A	0,54373546	0,85107329
225956_at	chromosome 5 open reading frame 41	CSorf41	0,54395508	0,85107329
222108_at	adhesion molecule with Ig-like domain 2	AMIGO2	0,54462215	0,50606127
228214_at	SRY (sex determining region Y)-box 6	SOX6	0,54494986	0,40274237
232823_at	---	---	0,54560738	2,79695557
239923_at	---	---	0,54645776	0,13717257
236266_at	RAR-related orphan receptor A	RORA	0,54676743	2,79695557
227959_at	---	---	0,54718183	0,13717257
223940_x_at	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	MALAT1	0,54803844	2,38495135
1561195_at	---	---	0,548246	0,40274237
239571_at	---	---	0,54980985	3,12037782
218686_s_at	rhomboid 5 homolog 1 (Drosophila)	RHBDF1	0,55024755	0,13717257
221269_s_at	SH3 domain binding glutamic acid-rich protein like 3	SH3BGR1	0,55033989	0,76883463
211005_at	linker for activation of T cells /// spinster homolog 1 (Drosophila)	LAT /// SPNS1	0,55050457	1,3948219
239872_at	---	---	0,55069509	0,13717257
235796_at	---	---	0,55106877	0,22870838
229958_at	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation)	CLN8	0,55124248	0,22870838
237626_at	---	---	0,55252869	0,32270094
207351_s_at	SH2 domain containing 2A	SH2D2A	0,55294238	0,32270094
201195_s_at	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	SLC7A5	0,55312381	0,13717257
232366_at	KIAA0232	KIAA0232	0,55371823	0,22870838
210579_s_at	tripartite motif-containing 10	TRIM10	0,55394583	0,4846616
221489_s_at	sprouty homolog 4 (Drosophila)	SPRY4	0,55446127	0,13717257
232631_at	Cadherin 6, type 2, K-cadherin (fetal kidney)	CDH6	0,55504201	0,13717257
204882_at	Rho GTPase activating protein 25	ARHGAP25	0,55562439	3,12037782
223217_s_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor 3	NFKBIZ	0,5556965	1,74547566
222816_s_at	zinc finger, CCHC domain containing 2	ZCCHC2	0,55608045	1,74547566
210479_s_at	RAR-related orphan receptor A	RORA	0,55609103	0,22870838
212223_at	iduronate 2-sulfatase	IDS	0,55706649	1,21472295
205920_at	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	SLC6A6	0,55724598	0,22870838
215819_s_at	Rh blood group, CcEe antigens /// Rh blood group, D antigen	RHCE /// RHD	0,55792317	0,13717257
239167_at	---	---	0,55969277	1,3948219
201733_at	chloride channel 3	CLCN3	0,55984833	0,13717257
215573_at	Catalase	CAT	0,56013584	0,4846616
243648_at	zinc finger, BED domain containing 6	ZBED6	0,56045179	2,79695557
231779_at	interleukin-1 receptor-associated kinase 2	IRAK2	0,56054316	0,76883463
234059_at	---	---	0,56108789	0,13717257
211067_s_at	growth arrest-specific 7	GAS7	0,5613972	4,51937074
204505_s_at	erythrocyte membrane protein band 4.9 (dematin)	EPB49	0,56200743	0,63176664
235567_at	RAR-related orphan receptor A	RORA	0,56216664	3,63155925
243646_at	---	---	0,56301228	0,13717257
1569617_at	oxysterol binding protein 2	OSBP2	0,56323622	0,13717257
1565701_at	---	---	0,56403127	0,13717257
239449_at	---	---	0,56469946	0,76883463
217966_s_at	family with sequence similarity 129, member A	FAM129A	0,56487166	0,50606127
228486_at	solute carrier family 44, member 1	SLC44A1	0,5649034	0,22870838
213998_s_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	DDX17	0,56528213	3,12037782
228256_s_at	erythrocyte membrane protein band 4.1 like 4A	EPB41L4A	0,56600718	2,38495135
226682_at	RAR-related orphan receptor A	RORA	0,56727446	4,51937074
1556203_a_at	SLIT-ROBO Rho GTPase activating protein 2	SRGAP2	0,56776476	0,13717257
211434_s_at	chemokine (C-C motif) receptor-like 2	CCRL2	0,56842029	0,13717257
225798_at	JAZF zinc finger 1	JAZF1	0,56890201	0,63176664
223218_s_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor 3	NFKBIZ	0,57085541	2,79695557
219341_at	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation)	CLN8	0,57144335	0,13717257
202083_s_at	SEC14-like 1 (S. cerevisiae)	SEC14L1	0,57171056	0,32270094
203303_at	dynein, light chain, Ctctex-type 3	DYNLT3	0,57181486	1,94055411
242239_at	---	---	0,57203195	0,4846616
205883_at	zinc finger and BTB domain containing 16	ZBTB16	0,57209712	1,21472295
1556034_s_at	myotubularin related protein 11	MTMR11	0,57286946	0,13717257
210426_x_at	RAR-related orphan receptor A	RORA	0,57334572	0,76883463
204132_s_at	forkhead box O3 /// forkhead box O3B pseudogene	FOXO3 /// FOXO	0,57447973	0,13717257
226541_at	F-box protein 30	FBXO30	0,5750065	0,22870838
201666_at	TIMP metalloproteinase inhibitor 1	TIMP1	0,57509293	0,85107329
215047_at	tripartite motif-containing 58	TRIM58	0,5753466	0,13717257
226794_at	syntaxin binding protein 5 (tomosyn)	STXBPS5	0,57568959	1,21472295
201732_s_at	chloride channel 3	CLCN3	0,57597943	0,13717257
221627_at	tripartite motif-containing 10	TRIM10	0,57673313	1,00422607
230180_at	---	---	0,57695524	3,12037782
235458_at	hepatitis A virus cellular receptor 2	HAVCR2	0,577564	4,1207969
224797_at	arrestin domain containing 3	ARRDC3	0,57784251	2,38495135
210598_at	---	---	0,57787315	0,13717257
242310_at	---	---	0,5784647	1,94055411

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219331_s_at	kelch domain containing 8A	<b>KLHDC8A</b>	0,57859137	0,13717257
226811_at	family with sequence similarity 46, member C	<b>FAM46C</b>	0,57944326	0,13717257
201333_s_at	Rho guanine nucleotide exchange factor (GEF) 12	<b>ARHGEF12</b>	0,57969581	0,13717257
240855_at	---	---	0,58079721	0,13717257
1556352_at	---	---	0,58104535	0,63176664
203911_at	RAP1 GTPase activating protein	<b>RAP1GAP</b>	0,58112744	0,4846616
35776_at	intersectin 1 (SH3 domain protein)	<b>ITSN1</b>	0,58116723	0,22870838
233867_at	---	---	0,58137082	1,3948219
1569237_at	---	---	0,58138451	0,13717257
209881_s_at	linker for activation of T cells /// spinster homolog 1 (Drosophila)	<b>LAT /// SPNS1</b>	0,58202991	2,38495135
56748_at	tripartite motif-containing 10	<b>TRIM10</b>	0,58211991	1,21472295
202129_s_at	RIO kinase 3 (yeast)	<b>RIOK3</b>	0,58219922	0,13717257
215449_at	translocator protein 2	<b>TSPQ2</b>	0,58283981	0,76883463
213275_x_at	cathepsin B	<b>CTSB</b>	0,5829023	0,13717257
202131_s_at	RIO kinase 3 (yeast)	<b>RIOK3</b>	0,5831825	0,13717257
215071_s_at	histone cluster 1, H2ac	<b>HIST1H2AC</b>	0,58348043	3,12037782
202729_s_at	latent transforming growth factor beta binding protein 1	<b>LTBP1</b>	0,5837509	2,38495135
1555503_a_at	transmembrane and coiled-coil domain family 2	<b>TMCC2</b>	0,58384989	0,85107329
210586_x_at	Rh blood group, D antigen	<b>RHD</b>	0,58556867	0,13717257
232595_at	---	---	0,58561859	0,63176664
210305_at	phosphodiesterase 4D interacting protein	<b>PDE4DIP</b>	0,58567502	4,51937074
203725_at	growth arrest and DNA-damage-inducible, alpha	<b>GADD45A</b>	0,58631904	0,13717257
210001_s_at	suppressor of cytokine signaling 1	<b>Socs1</b>	0,58831816	0,22870838
217967_s_at	family with sequence similarity 129, member A	<b>FAM129A</b>	0,58836945	0,22870838
239208_s_at	Chromosome 21 open reading frame 57	<b>C21orf57</b>	0,58861507	1,00422607
1563454_at	SRY (sex determining region Y)-box 6	<b>SOX6</b>	0,58863956	0,76883463
210430_x_at	Rh blood group, D antigen	<b>RHD</b>	0,58914	0,13717257
1558515_at	non-protein coding RNA 182	<b>NCRNA00182</b>	0,58922532	4,51937074
229256_at	phosphoglucomutase 2-like 1	<b>PGM2L1</b>	0,58957265	2,79695557
209216_at	WD repeat domain 45	<b>WDR45</b>	0,58968025	0,13717257
222024_s_at	A kinase (PRKA) anchor protein 13	<b>AKAP13</b>	0,59014991	3,63155925
231205_at	---	---	0,59018878	3,63155925
234151_at	---	---	0,59099434	2,38495135
209383_at	DNA-damage-inducible transcript 3	<b>DDIT3</b>	0,59106885	0,13717257
233664_at	---	---	0,59133326	4,51937074
240274_at	---	---	0,59226161	0,32270094
225800_at	JAZF zinc finger 1	<b>JAZF1</b>	0,59264057	0,13717257
201739_at	serum/glucocorticoid regulated kinase 1	<b>SGK1</b>	0,59278747	3,12037782
215811_at	---	---	0,59296345	1,3948219
223658_at	potassium channel, subfamily K, member 6	<b>KCNK6</b>	0,59302474	0,40274237
203139_at	death-associated protein kinase 1	<b>DAPK1</b>	0,59307351	0,85107329
223471_at	RAB3A interacting protein (rabin3)	<b>RAB3IP</b>	0,59338433	0,22870838
204131_s_at	forkhead box O3	<b>FOXO3</b>	0,59373735	0,13717257
202125_s_at	trafficking protein, kinesin binding 2	<b>TRAK2</b>	0,59434521	0,13717257
208868_s_at	GABA(A) receptor-associated protein like 1	<b>GABARAPL1</b>	0,59441274	0,32270094
206160_at	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 2	<b>APOBEC2</b>	0,59533923	0,22870838
203882_at	interferon regulatory factor 9	<b>IRF9</b>	0,59536233	0,13717257
214129_at	phosphodiesterase 4D interacting protein	<b>PDE4DIP</b>	0,59569318	1,00422607
243424_at	---	---	0,59618803	0,22870838
210602_s_at	cadherin 6, type 2, K-cadherin (fetal kidney)	<b>CDH6</b>	0,59680457	1,21472295
212441_at	KIAA0232	<b>KIAA0232</b>	0,59696667	0,13717257
210075_at	membrane-associated ring finger (C3HC4) 2	---	0,59708031	0,32270094
243233_at	---	---	0,59725843	3,63155925
213274_s_at	cathepsin B	<b>CTSB</b>	0,59762053	0,13717257
223754_at	chromosome 2 open reading frame 88	<b>C2orf88</b>	0,59792977	0,22870838
201235_s_at	BTG family, member 2	<b>BTG2</b>	0,59888164	1,74547566
202500_at	DnaJ (Hsp40) homolog, subfamily B, member 2	<b>DNAJB2</b>	0,5989701	0,13717257
235683_at	sestrin 3	<b>SESN3</b>	0,59902336	1,3948219
243827_at	---	---	0,59906	0,22870838
235592_at	---	---	0,59920906	1,3948219
226657_at	chromosome 17 open reading frame 103	<b>C17orf103</b>	0,59930843	0,13717257
207528_s_at	solute carrier family 7, (cationic amino acid transporter, y+ system) mem	<b>SLC7A11</b>	0,59954198	0,13717257
228195_at	chromosome 2 open reading frame 88	<b>C2orf88</b>	0,59965942	0,32270094
203665_at	heme oxygenase (decycling) 1	<b>HMBOX1</b>	0,59978353	4,1207969
232737_s_at	ectonucleotide pyrophosphatase/phosphodiesterase 3	<b>ENPP3</b>	0,60053651	3,12037782
208891_at	dual specificity phosphatase 6	<b>DUSP6</b>	0,60093035	1,74547566
216317_x_at	Rh blood group, CcEe antigens	<b>RHCE</b>	0,60119903	0,13717257
220694_at	ASAP1 intronic transcript 1 (non-protein coding)	<b>ASAP1IT1</b>	0,60142085	2,79695557
237317_at	---	---	0,60154201	2,38495135
243751_at	---	---	0,60154981	2,38495135
200921_s_at	B-cell translocation gene 1, anti-proliferative	<b>BTG1</b>	0,60164845	1,21472295
1554229_at	chromosome 5 open reading frame 41	<b>C5orf41</b>	0,60221012	4,1207969
207459_x_at	glycophorin B (MNS blood group)	<b>GYPB</b>	0,60234782	0,13717257
208790_s_at	polymerase I and transcript release factor	<b>PTRF</b>	0,60248119	1,21472295
241396_at	neural precursor cell expressed, developmentally down-regulated 4-like	<b>NEDD4L</b>	0,60310202	0,57337326
238595_at	---	---	0,60334666	2,38495135
238883_at	---	---	0,60372049	4,51937074
226558_at	ankyrin repeat domain 57 pseudogene	<b>LOC389834</b>	0,60381008	4,51937074
224707_at	chromosome 5 open reading frame 32	<b>C5orf32</b>	0,60593661	0,13717257
1556493_a_at	lysine (K)-specific demethylase 4C	<b>KDM4C</b>	0,60615061	2,79695557
228628_at	SLIT-ROBO Rho GTPase activating protein 2 pseudogene 1	<b>SRGAP2P1</b>	0,60663701	0,13717257
202130_at	RIO kinase 3 (yeast)	<b>RIOK3</b>	0,60830068	0,22870838
203126_at	inositol(myo)-1(or 4)-monophosphatase 2	<b>IMPA2</b>	0,60945044	0,76883463
202940_at	WNK lysine deficient protein kinase 1	<b>WNK1</b>	0,60965314	0,13717257
214913_at	ADAM metalloproteinase with thrombospondin type 1 motif, 3	<b>ADAMTS3</b>	0,60966685	0,13717257
1570571_at	Coiled-coil domain containing 91	<b>CCDC91</b>	0,60981541	1,21472295
242565_x_at	Chromosome 21 open reading frame 57	<b>C21orf57</b>	0,61011855	1,21472295
206302_s_at	nudix (nucleoside diphosphate linked moiety X)-type motif 4 /// nudix (n	<b>NUDT4 /// NUD1</b>	0,61035405	0,63176664
223797_at	hypothetical protein PRO2852	<b>PRO2852</b>	0,61080961	1,74547566
230779_at	trinucleotide repeat containing 6B	<b>TNRC6B</b>	0,61095523	0,85107329
207331_at	---	---	0,6113231	2,79695557
202439_s_at	iduronate 2-sulfatase	<b>IDS</b>	0,61200685	2,38495135
213309_at	phospholipase C-like 2	<b>PLCL2</b>	0,61216529	0,63176664
208677_s_at	basigin (Ok blood group)	<b>BSG</b>	0,61248275	3,12037782
229553_at	phosphoglucomutase 2-like 1	<b>PGM2L1</b>	0,61274576	1,94055411
233937_at	gametogenin binding protein 2	<b>GGNBP2</b>	0,61285216	2,79695557
221985_at	kelch-like 24 (Drosophila)	<b>KLHL24</b>	0,61328002	2,38495135
239206_at	complement component (3b/4b) receptor 1-like	<b>CR1L</b>	0,6133924	3,12037782
207043_s_at	solute carrier family 6 (neurotransmitter transporter, glycine), member 5	<b>SLC6A9</b>	0,61362913	2,38495135
212181_s_at	nudix (nucleoside diphosphate linked moiety X)-type motif 4 /// nudix (n	<b>NUDT4 /// NUD1</b>	0,61389721	4,1207969
203989_x_at	coagulation factor II (thrombin) receptor	<b>F2R</b>	0,6147917	3,63155925
205489_at	crystallin, mu	<b>CRYM</b>	0,61490105	0,76883463
232238_at	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	<b>ASPM</b>	0,61500321	1,74547566
203543_s_at	Kruppel-like factor 9	<b>KLF9</b>	0,61503751	1,21472295
209159_s_at	NDRG family member 4	<b>NDRG4</b>	0,61560967	1,74547566

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236386_at	Suppressor of zeste 12 homolog pseudogene	SUZ12P	0,61614759	1,94055411
205298_s_at	butyrophilin, subfamily 2, member A2	BTN2A2	0,61624785	1,74547566
203542_s_at	Kruppel-like factor 9	KLF9	0,61628342	0,13717257
203233_at	interleukin 4 receptor	IL4R	0,61648688	0,50606127
215224_at	small nucleolar RNA, H/ACA box 21	SNORA21	0,616563	2,38495135
1556202_at	SLIT-ROBO Rho GTPase activating protein 2	SRGAP2	0,61657046	1,94055411
232997_at	---	---	0,61666175	4,1207969
1555826_at	effector cell peptidase receptor 1 (non-protein coding)	EPR1	0,61679066	1,94055411
230053_at	---	---	0,61710739	0,13717257
200920_s_at	B-cell translocation gene 1, anti-proliferative	BTG1	0,61715791	1,3948219
240136_at	---	---	0,61718643	3,63155925
233981_at	---	---	0,61723327	0,63176664
227961_at	cathepsin B	CTSB	0,61754525	0,22870838
235556_at	chromosome 5 open reading frame 41	CSorf41	0,61758272	1,74547566
227357_at	TGF-beta activated kinase 1/MAP3K7 binding protein 3	TAB3	0,61792024	0,40274237
210655_s_at	forkhead box O3 /// forkhead box O3B pseudogene	FOXO3 /// FOXO	0,61802963	0,76883463
239946_at	---	---	0,61803032	1,00422607
242055_at	Proteasome (prosome, macropain) assembly chaperone 4	PSMG4	0,61837633	0,57337326
201824_at	ring finger protein 14	RNF14	0,61863898	1,21472295
204698_at	interferon stimulated exonuclease gene 20kDa	ISG20	0,61899442	1,21472295
208789_at	polymerase I and transcript release factor	PTRF	0,61900386	1,00422607
1570486_at	SRY (sex determining region Y)-box 6	SOX6	0,61934261	2,79695557
1560119_at	hypothetical LOC389634	LOC389634	0,61970777	1,00422607
225308_s_at	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1	TANC1	0,61972176	3,12037782
1559971_at	BSD domain containing 1	BSDC1	0,62013086	2,79695557
202728_s_at	latent transforming growth factor beta binding protein 1	LTPB1	0,62045125	0,22870838
213418_at	heat shock 70kDa protein 6 (HSP70B)	HSPA6	0,62069879	0,50606127
209921_at	solute carrier family 7, (cationic amino acid transporter, y+ system) mem	SLC7A11	0,62087484	2,79695557
1560342_at	---	---	0,62142283	2,38495135
1557197_a_at	lectin, galactoside-binding, soluble, 3	LGALS3	0,62150303	1,00422607
238988_at	---	---	0,62230268	1,21472295
208924_at	ring finger protein 11	RNF11	0,62236888	1,00422607
230607_at	---	---	0,62296278	3,63155925
217678_at	solute carrier family 7, (cationic amino acid transporter, y+ system) mem	SLC7A11	0,62324582	2,38495135
235028_at	---	---	0,62357059	4,51937074
229622_at	family with sequence similarity 132, member 8	FAM132B	0,62365951	0,40274237
223578_x_at	metastasis associated lung adenocarcinoma transcript 1 (non-protein co	MALAT1	0,62368839	4,51937074
209333_at	unc-51-like kinase 1 (C. elegans)	ULK1	0,62384534	0,13717257
203810_at	DnaJ (Hsp40) homolog, subfamily B, member 4	DNAJB4	0,62385822	2,79695557
231861_at	low density lipoprotein receptor-related protein 10	LRP10	0,6239431	0,22870838
221764_at	chromosome 19 open reading frame 22	C19orf22	0,62401943	0,13717257
209930_s_at	nuclear factor (erythroid-derived 2), 45kDa	NFE2	0,625063	0,50606127
242279_at	---	---	0,62520667	1,94055411
211433_x_at	KIAA1539	KIAA1539	0,62549742	0,13717257
211936_at	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	HSPA5	0,62616141	0,13717257
222529_at	solute carrier family 25, member 37	SLC25A37	0,62642666	0,13717257
218978_s_at	solute carrier family 25, member 37	SLC25A37	0,6265777	0,57337326
239050_s_at	---	---	0,62760579	0,50606127
222074_at	uroporphyrinogen decarboxylase	UROD	0,62771156	0,85107329
217572_at	---	---	0,62777583	0,13717257
233637_at	DDB1 and CUL4 associated factor 8	DCAF8	0,62804681	0,76883463
226756_at	---	---	0,62809992	0,85107329
214439_x_at	bridging integrator 1	BIN1	0,62827109	0,32270094
23259_at	enhancer of zeste homolog 1 (Drosophila)	EZH1	0,62881306	0,13717257
209217_s_at	WD repeat domain 45	WDR45	0,62902669	0,13717257
203395_s_at	hairy and enhancer of split 1, (Drosophila)	HES1	0,62907603	1,94055411
219168_s_at	proline rich 5 (renal)	PRRS	0,62915586	2,38495135
242471_at	---	---	0,62936227	1,74547566
243527_at	---	---	0,63047558	1,00422607
237762_at	---	---	0,63081875	1,00422607
223093_at	ankylosis, progressive homolog (mouse)	ANKH	0,63090742	0,13717257
232688_at	BMP2 inducible kinase	BMP2K	0,63094101	0,40274237
241027_at	optic atrophy 1 (autosomal dominant)	OPA1	0,63118333	0,32270094
241391_at	---	---	0,63126816	3,63155925
223649_s_at	solute carrier family 25, member 39	SLC25A39	0,63177698	2,79695557
227252_at	low density lipoprotein receptor-related protein 10	LRP10	0,63181023	0,13717257
213763_at	homeodomain interacting protein kinase 2	HIPK2	0,63185749	0,13717257
205938_at	protein phosphatase, Mg2+/Mn2+ dependent, 1E	PPM1E	0,63287719	4,51937074
239205_s_at	complement component (3b/4b) receptor 1 (Knops blood group) /// con	CR1 /// CR1L	0,6334374	1,21472295
208892_s_at	dual specificity phosphatase 6	DUSP6	0,63351917	3,12037782
228793_at	jumonji domain containing 1C	JMJD1C	0,63392772	1,3948219
221756_at	phosphoinositide-3-kinase interacting protein 1	PIK3IP1	0,63393479	1,00422607
240383_at	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	UBE2D3	0,63415148	1,94055411
213593_s_at	transformer 2 alpha homolog (Drosophila)	TRA2A	0,63423008	1,94055411
222874_s_at	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retar	CLN8	0,63453652	0,4846616
1557938_s_at	polymerase I and transcript release factor	PTRF	0,63500217	0,40274237
225931_s_at	ring finger protein 213	RNF213	0,63531148	1,74547566
1565867_a_at	zinc finger CCHC-type containing 11A	ZC3H11A	0,63533747	2,38495135
220751_s_at	chromosome 5 open reading frame 4	CSorf4	0,63583331	1,21472295
203845_at	K(llysine) acetyltransferase 2B	KAT2B	0,63629681	0,63176664
207765_s_at	KIAA1539	KIAA1539	0,63669498	1,21472295
223865_at	SRY (sex determining region Y)-box 6	SOX6	0,63683871	0,50606127
216063_at	hemoglobin, beta pseudogene 1	HBBP1	0,63698737	2,38495135
39249_at	aquaporin 3 (Gill blood group)	AQP3	0,63739353	0,40274237
230031_at	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	HSPA5	0,6375171	0,13717257
244086_at	---	---	0,63798681	0,13717257
243856_at	lanC lantibiotic synthetase component C-like 3 (bacterial)	LANCL3	0,63892309	0,57337326
47069_at	proline rich 5 (renal)	PRRS	0,63969717	1,3948219
1557193_at	---	---	0,63978029	1,21472295
209002_s_at	calcium binding and coiled-coil domain 1	CALCOCO1	0,63981184	0,13717257
225227_at	---	---	0,64015988	0,13717257
226599_at	FH2 domain containing 1	FHDC1	0,64070574	4,51937074
235227_at	---	---	0,64141668	3,63155925
243659_at	---	---	0,64183264	1,94055411
238021_s_at	colorectal neoplasia differentially expressed (non-protein coding)	CRNDE	0,64187279	0,22870838
206303_s_at	nudix (nucleoside diphosphate linked moiety X)-type motif 4	NUDT4	0,64259861	0,13717257
210162_s_at	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1	NFATC1	0,64295376	0,22870838
240440_at	N-acetylneuraminatase pyruvate lyase (dihydrodipicolinate synthase)	NPL	0,64303772	2,79695557
1555788_a_at	tribbles homolog 3 (Drosophila)	TRIB3	0,64398756	1,94055411
218660_at	dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive)	DYSF	0,64404346	0,13717257
231997_at	tubulin folding cofactor E-like	TBCEL	0,64442472	0,22870838
225929_s_at	ring finger protein 213	RNF213	0,644575	0,85107329
221718_s_at	A kinase (PRKA) anchor protein 13	AKAP13	0,64478491	1,74547566
206110_at	histone cluster 1, H3h	HIST1H3H	0,64479109	3,12037782
237498_at	Neural precursor cell expressed, developmentally down-regulated 4-like	NEDD4L	0,64483793	0,76883463

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33304_at	interferon stimulated exonuclease gene 20kDa	<b>ISG20</b>	0,6450005	1,21472295
233691_at	---	---	0,64501293	0,32270094
219557_s_at	nuclear receptor interacting protein 3	<b>NRIP3</b>	0,64523811	0,32270094
204689_at	hematopoietically expressed homeobox	<b>HHEX</b>	0,6458378	1,74547566
242736_at	---	---	0,64636496	0,40274237
205471_s_at	dachshund homolog 1 (Drosophila)	<b>DACH1</b>	0,64652635	4,1207969
1562529_s_at	---	---	0,64676208	0,63176664
244523_at	monocyte to macrophage differentiation-associated	<b>MMD</b>	0,64744775	1,00422607
235684_s_at	sestrin 3	<b>SESN3</b>	0,64782534	4,51937074
239489_at	---	---	0,6478617	1,74547566
202842_s_at	DnaJ (Hsp40) homolog, subfamily B, member 9	<b>DNAJB9</b>	0,64796642	0,22870838
1558678_s_at	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	<b>MALAT1</b>	0,64802988	1,21472295
227701_at	chromosome 10 open reading frame 118	<b>C10orf118</b>	0,64804358	0,13717257
216833_x_at	glycophorin B (MNS blood group)	<b>GYPB</b>	0,64812158	0,48466616
229736_at	transmembrane protein 86B	<b>TMEM86B</b>	0,64823997	0,85107329
243329_at	---	---	0,6483248	1,94055411
207042_at	E2F transcription factor 2	<b>E2F2</b>	0,64873617	1,3948219
202192_s_at	growth arrest-specific 7	<b>GAS7</b>	0,64890986	1,94055411
215435_at	---	---	0,64948441	4,51937074
209967_s_at	cAMP responsive element modulator	<b>CREM</b>	0,6495403	0,32270094
241885_at	---	---	0,64963939	2,79695557
202073_at	optineurin	<b>OPTN</b>	0,64968955	4,51937074
227226_at	melanocortin 2 receptor accessory protein 2	<b>MRAP2</b>	0,65010836	0,57337326
239049_at	---	---	0,65033109	3,63155925
204496_at	striatin, calmodulin binding protein 3	<b>STRN3</b>	0,65034625	4,51937074
231880_at	family with sequence similarity 40, member B	<b>FAM40B</b>	0,65035994	0,48466616
221246_x_at	tensin 1	<b>TNS1</b>	0,65051148	0,13717257
209345_s_at	phosphatidylinositol 4-kinase type 2 alpha	<b>PI4K2A</b>	0,65063061	0,13717257
242441_at	similar to ADAM metallopeptidase domain 21 preproprotein	<b>LOC646548</b>	0,65076981	1,3948219
235867_at	glutathione S-transferase mu 3 (brain)	<b>GSTM3</b>	0,65127313	1,94055411
215024_at	chromosome 7 open reading frame 28B	<b>C7orf28B</b>	0,6518495	1,94055411
243313_at	synaptopodin 2-like	<b>SYNPO2L</b>	0,65209779	0,13717257
229017_s_at	dual serine/threonine and tyrosine protein kinase	<b>DSTYK</b>	0,65228514	0,48466616
229696_at	ferrochelatase	<b>FECH</b>	0,65231	1,74547566
202887_s_at	DNA-damage-inducible transcript 4	<b>DDIT4</b>	0,65269111	0,13717257
1552928_s_at	TGF-beta activated kinase 1/MAP3K7 binding protein 3	<b>TAB3</b>	0,65271889	0,76883463
239163_at	ubiquitin-conjugating enzyme E2B (RAD6 homolog)	<b>UBE2B</b>	0,65278496	0,63176664
1562163_at	---	---	0,65345216	4,51937074
202460_s_at	lipin 2	<b>LPIN2</b>	0,65352983	0,32270094
238462_at	ubiquitin associated and SH3 domain containing B	<b>UBASH3B</b>	0,65375894	2,79695557
201735_s_at	chloride channel 3	<b>CLCN3</b>	0,65409144	0,13717257
224367_at	brain expressed X-linked 2	<b>BEX2</b>	0,65433899	3,63155925
202843_at	DnaJ (Hsp40) homolog, subfamily B, member 9	<b>DNAJB9</b>	0,65485658	1,21472295
242829_x_at	F-box and leucine-rich repeat protein 3	<b>FBXL3</b>	0,65588138	4,1207969
235376_at	---	---	0,65590404	0,40274237
238468_at	trinucleotide repeat containing 6B	<b>TNRC6B</b>	0,65595687	0,40274237
233219_at	---	---	0,65635885	4,51937074
216333_x_at	tenascin XA pseudogene, /// tenascin XB	<b>TNXA /// TNXB</b>	0,65669405	2,79695557
208335_s_at	Duffy blood group, chemokine receptor	<b>DARC</b>	0,65678772	1,94055411
212384_at	HLA-B associated transcript 1	<b>BAT1</b>	0,65742635	1,94055411
1561130_at	---	---	0,65770643	0,85107329
1554948_at	---	---	0,65798886	1,00422607
236475_at	Microtubule associated monooxygenase, calponin and LIM domain containing 2	<b>MICAL2</b>	0,65802714	0,13717257
214407_x_at	glycophorin B (MNS blood group)	<b>GYPB</b>	0,65803953	0,22870838
208763_s_at	TSC22 domain family, member 3	<b>TSC22D3</b>	0,65807318	0,22870838
225387_at	tetraspanin 5	<b>TSPAN5</b>	0,65840638	0,76883463
224254_x_at	---	---	0,65914448	2,38495135
240296_at	---	---	0,65950647	1,21472295
214145_s_at	spectrin, beta, erythrocytic	<b>SPTB</b>	0,66042797	0,85107329
236946_at	---	---	0,66058916	0,48466616
224898_at	WD repeat domain 26	<b>WDR26</b>	0,66061468	0,50606127
223669_at	hemogen	<b>HEMGN</b>	0,66196357	2,38495135
208997_s_at	uncoupling protein 2 (mitochondrial, proton carrier)	<b>UCP2</b>	0,66208072	0,63176664
202011_at	tight junction protein 1 (zona occludens 1)	<b>TJP1</b>	0,66227676	4,51937074
212430_at	RNA binding motif protein 38	<b>RBM38</b>	0,66228817	3,63155925
236621_at	ribosomal protein S27	<b>RPS27</b>	0,66250727	2,79695557
236552_at	---	---	0,66269055	1,3948219
205434_s_at	AP2 associated kinase 1	<b>AAK1</b>	0,66270334	0,40274237
232077_s_at	yippee-like 3 (Drosophila)	<b>YPEL3</b>	0,66314667	0,13717257
208937_s_at	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	<b>ID1</b>	0,6638539	3,12037782
225142_at	jumonji C domain containing histone demethylase 1 homolog D (S. cerevisiae)	<b>JHDM1D</b>	0,66399243	1,3948219
204568_at	KIAA0831	<b>KIAA0831</b>	0,66411111	0,40274237
1562903_at	family with sequence similarity 86, member A pseudogene	<b>FLJ10661</b>	0,66411943	0,13717257
237530_at	---	---	0,66495985	3,63155925
214815_at	tripartite motif-containing 33	<b>TRIM33</b>	0,66497036	0,22870838
215933_s_at	hematopoietically expressed homeobox	<b>HHEX</b>	0,66521454	1,3948219
1568857_a_at	Neighbor of BRCA1 gene 1	<b>NBR1</b>	0,66540267	1,3948219
244677_at	---	---	0,66561294	1,00422607
240176_at	---	---	0,66587372	1,3948219
224566_at	nuclear paraspeckle assembly transcript 1 (non-protein coding)	<b>NEAT1</b>	0,66621373	4,51937074
1561015_at	---	---	0,6666077	0,13717257
206347_at	pyruvate dehydrogenase kinase, isozyme 3	<b>PKD3</b>	1,50053249	0,13717257
228243_at	---	---	1,50057248	0,13717257
219355_at	chromosome X open reading frame 57	<b>CXorf57</b>	1,50063176	0,22870838
216262_s_at	TGF-beta-induced factor homeobox 2	<b>TGIF2</b>	1,50074967	0,13717257
212922_s_at	SET and MYND domain containing 2	<b>SMYD2</b>	1,5009239	0,13717257
224952_at	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	<b>TANC2</b>	1,50213735	0,22870838
226455_at	cAMP responsive element binding protein 3-like 4	<b>CREB3L4</b>	1,50310667	0,13717257
219457_s_at	Ras and Rab interactor 3	<b>RIN3</b>	1,50367561	0,13717257
212169_at	FK506 binding protein 9, 63 kDa	<b>FKBP9</b>	1,50389593	0,13717257
229305_at	MLF1 interacting protein	<b>MLF1IP</b>	1,50429161	0,22870838
223839_s_at	stearoyl-CoA desaturase (delta-9-desaturase)	<b>SCD</b>	1,50591525	4,51937074
217197_x_at	NEDD4 binding protein 2-like 1	<b>N4BP2L1</b>	1,50680803	0,13717257
209108_at	tetraspanin 6	<b>TSPAN6</b>	1,50701323	1,94055411
204379_s_at	fibroblast growth factor receptor 3	<b>FGFR3</b>	1,50740945	0,50606127
227446_s_at	chromosome 14 open reading frame 167	<b>C14orf167</b>	1,50746706	0,13717257
218633_x_at	abhydrolase domain containing 10	<b>ABHD10</b>	1,50751134	0,13717257
209864_at	frequently rearranged in advanced T-cell lymphomas 2	<b>FRAT2</b>	1,50847738	0,13717257
210114_at	inversin	<b>INVS</b>	1,50991832	0,22870838
213698_at	zinc finger, MYM-type 6	<b>ZMYM6</b>	1,51110608	0,13717257
209538_at	zinc finger protein 32	<b>ZNF32</b>	1,51135519	0,13717257
228708_at	RAB27B, member RAS oncogene family	<b>RAB27B</b>	1,51179902	2,79695557
209109_s_at	tetraspanin 6	<b>TSPAN6</b>	1,51216979	3,12037782
209576_at	guanine nucleotide binding protein (G protein), alpha inhibiting activity 4	<b>GNAI1</b>	1,51244032	2,79695557
204485_s_at	target of myb1 (chicken)-like 1	<b>TOM1L1</b>	1,51272731	0,13717257

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222761_at	basic, immunoglobulin-like variable motif containing	BIVM	1,51359857	0,13717257
64900_at	transmembrane protein 231	TMEM231	1,51373938	0,13717257
200644_at	MARCKS-like 1	MARCKSL1	1,51393636	1,94055411
222587_s_at	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosamin	GALNT7	1,51397458	3,12037782
208885_at	lymphocyte cytosolic protein 1 (L-plastin)	LCP1	1,51422226	1,3948219
235315_at	TSC22 domain family, member 1	TSC22D1	1,51431606	1,00422607
241416_at	---	---	1,51502846	0,13717257
225458_at	hypothetical LOC25845	LOC25845	1,51598343	0,22870838
230741_at	---	---	1,51622093	2,38495135
1555037_s_at	isocitrate dehydrogenase 1 (NADP+), soluble	IDH1	1,51680622	0,13717257
203294_s_at	lectin, mannose-binding, 1	LMAN1	1,51754601	0,57337326
219155_at	phosphatidylinositol transfer protein, cytoplasmic 1	PITPNC1	1,51782077	0,22870838
204321_at	neogenin homolog 1 (chicken)	NEO1	1,51827318	0,50606127
211220_s_at	heat shock transcription factor 2	HSF2	1,51917788	0,13717257
214857_at	---	---	1,51927309	0,13717257
226743_at	schlafen family member 11	SLFN11	1,52011197	0,22870838
218897_at	transmembrane protein 177	TMEM177	1,52035862	0,13717257
207543_s_at	prolyl 4-hydroxylase, alpha polypeptide I	P4HA1	1,52084902	0,13717257
1554466_a_at	chromosome 16 open reading frame 13	Cl6orf13	1,52123719	0,85107329
235773_at	zinc finger protein interacting with K protein 1 homolog (mouse)	ZIK1	1,52183832	0,13717257
202702_at	tripartite motif-containing 26	TRIM26	1,52222702	0,57337326
222603_at	endoplasmic reticulum metalloproteinase 1	ERMP1	1,52240816	1,21472295
243808_at	---	---	1,52284897	0,13717257
213012_at	neural precursor cell expressed, developmentally down-regulated 4	NEDD4	1,52371425	0,13717257
1554679_a_at	lysosomal protein transmembrane 4 beta	LAPTM4B	1,52410107	3,12037782
207045_at	coiled-coil domain containing 132	CDC132	1,52417114	0,57337326
1554489_a_at	centrosomal protein 70kDa	CEP70	1,52430002	0,85107329
227533_at	---	---	1,52431833	0,32270094
230937_at	hypothetical protein LOC285835	LOC285835	1,52506526	0,13717257
242264_at	---	---	1,52553647	0,50606127
222001_x_at	hypothetical LOC728855	LOC728855	1,52644358	0,50606127
205356_at	ubiquitin specific peptidase 13 (isopeptidase T-3)	USP13	1,52654685	0,32270094
228799_at	---	---	1,52666304	0,13717257
224345_x_at	family with sequence similarity 162, member A	FAM162A	1,52772521	0,13717257
222752_at	ubiquitin specific peptidase 30	USP30	1,52794363	0,13717257
210154_at	malic enzyme 2, NAD(+)-dependent, mitochondrial	ME2	1,52881229	0,13717257
228479_at	sterol O-acyltransferase 1	SOAT1	1,52988139	0,13717257
210145_at	phospholipase A2, group IVA (cytosolic, calcium-dependent)	PLA2G4A	1,53133398	0,63176664
224150_s_at	centrosomal protein 70kDa	CEP70	1,53134353	0,76883463
209494_s_at	POZ (BTB) and AT hook containing zinc finger 1	PATZ1	1,53203488	0,76883463
60471_at	Ras and Rab interactor 3	RIN3	1,53204275	0,13717257
212377_s_at	Notch homolog 2 (Drosophila)	NOTCH2	1,53420802	0,76883463
221573_at	chromosome 7 open reading frame 25 /// proteasome (prosome, macro	C7orf25 /// PSM	1,53431059	0,13717257
222146_s_at	transcription factor 4	TCF4	1,53437225	0,13717257
225564_at	spermatogenesis associated 13	SPATA13	1,53456237	1,21472295
228174_at	suppressor of cancer cell invasion	SCAI	1,53474591	0,63176664
239001_at	Microsomal glutathione S-transferase 1	MGST1	1,53549907	0,13717257
223193_x_at	family with sequence similarity 162, member A	FAM162A	1,53554733	0,13717257
218764_at	protein kinase C, eta	PRKCH	1,53571678	0,76883463
206777_s_at	crystallin, beta B2 /// crystallin, beta B2 pseudogene 1	CRYBB2 /// CRYE	1,53587258	4,1207969
223206_s_at	NmrA-like family domain containing 1	NMRAL1	1,5359375	0,13717257
225764_at	ets variant 6	ETV6	1,53607185	0,13717257
209213_at	carbonyl reductase 1	CBR1	1,53678128	0,50606127
219957_at	RUN and FYVE domain containing 2	RUFY2	1,53702339	0,13717257
243495_s_at	---	---	1,53711354	2,79695557
232149_s_at	neutral sphingomyelinase (N-SMase) activation associated factor	NSMAF	1,53776406	0,13717257
210006_at	abhydrolase domain containing 14A	ABHD14A	1,5381262	0,13717257
213854_at	synaptogyrin 1	SYNGR1	1,53848649	0,13717257
218627_at	DNA-damage regulated autophagy modulator 1	DRAM1	1,53947362	0,13717257
225619_at	SLAIN motif family, member 1	SLAIN1	1,54054584	1,94055411
1554037_a_at	zinc finger and BTB domain containing 24	ZBTB24	1,54073523	0,40274237
204624_at	ATPase, Cu++ transporting, beta polypeptide	ATP7B	1,54125656	0,63176664
211991_s_at	major histocompatibility complex, class II, DP alpha 1	HLA-DPA1	1,54127612	2,79695557
206572_x_at	zinc finger protein 85	ZNF85	1,54513933	0,76883463
213562_s_at	squalene epoxidase	SQLE	1,54558164	0,13717257
209537_at	exostosins (multiple)-like 2	EXTL2	1,54608515	0,13717257
216956_s_at	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen C	ITGA2B	1,54726603	2,38495135
236918_s_at	leucine rich repeat containing 34	LRR34	1,54796636	1,00422607
201193_at	isocitrate dehydrogenase 1 (NADP+), soluble	IDH1	1,54866564	0,13717257
207949_s_at	islet cell autoantigen 1, 69kDa	ICA1	1,54911312	0,13717257
211379_x_at	beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)	B3GALNT1	1,55038993	4,1207969
219889_at	frequently rearranged in advanced T-cell lymphomas	FRAT1	1,55114631	0,13717257
226068_at	spleen tyrosine kinase	SYK	1,55249737	0,63176664
238681_at	glycerophosphodiester phosphodiesterase domain containing 1	GDPD1	1,5530227	0,13717257
213891_s_at	transcription factor 4	TCF4	1,5535578	0,13717257
201874_at	myelin protein zero-like 1	MPZL1	1,5545969	0,13717257
214931_s_at	SFRS protein kinase 2	SRPK2	1,55497011	0,13717257
204454_at	protein phosphatase 1, regulatory (inhibitor) subunit 3D	PPP1R3D	1,55630979	0,13717257
227119_at	CCR4-NOT transcription complex, subunit 6-like	CNOT6L	1,55651388	0,13717257
203761_at	Src-like-adaptor	SLA	1,5569085	1,94055411
208767_s_at	lysosomal protein transmembrane 4 beta	LAPTM4B	1,55777077	1,74547566
1566472_s_at	retinol saturase (all-trans-retinol 13,14-reductase)	RETSAT	1,55803763	0,13717257
227220_at	nuclear transcription factor, X-box binding-like 1	NFXL1	1,5582479	0,4846616
222931_s_at	threonine synthase-like 1 (S. cerevisiae)	THNSL1	1,55868872	0,13717257
238448_at	mitochondrial ribosomal protein L19	MRPL19	1,55919543	3,63155925
202443_x_at	Notch homolog 2 (Drosophila)	NOTCH2	1,55989443	0,57337326
226741_at	solute carrier family 12 (potassium/chloride transporters), member 6	SLC12A6	1,55994634	0,13717257
217988_at	cyclin B1 interacting protein 1	CCNB1IP1	1,56039997	0,13717257
236635_at	zinc finger protein 667	ZNF667	1,56138602	1,3948219
49452_at	acetyl-CoA carboxylase beta	ACACB	1,56271881	1,3948219
222240_s_at	inositol-3-phosphate synthase 1	ISYNA1	1,56314835	1,21472295
225700_at	glucocorticoid induced transcript 1	GLCC1	1,56365933	0,40274237
40472_at	lysophosphatidylcholine acyltransferase 4	LPCAT4	1,56432048	0,13717257
215723_s_at	phospholipase D1, phosphatidylcholine-specific	PLD1	1,56436753	0,22870838
240063_at	glucuronidase, beta pseudogene	LOC441046	1,56581372	0,13717257
201328_at	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	ETS2	1,56630298	1,74547566
202234_s_at	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	SLC16A1	1,5669508	1,94055411
222594_s_at	spermatogenesis associated, serine-rich 2	SPATS2	1,56735904	0,13717257
212719_at	PH domain and leucine rich repeat protein phosphatase 1	PHLPP1	1,56785948	0,22870838
205830_at	calmegin	CLGN	1,56857586	2,79695557
229644_at	prolyl endopeptidase	PREP	1,57059833	0,13717257
210756_s_at	Notch homolog 2 (Drosophila)	NOTCH2	1,57110178	0,13717257
210933_s_at	fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)	FSCN1	1,57118747	1,74547566
236400_at	---	---	1,57150499	0,13717257
200785_s_at	low density lipoprotein receptor-related protein 1	LRP1	1,57165572	0,4846616

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222614_at	---	---	1,57234378	0,13717257
209608_s_at	acetyl-CoA acetyltransferase 2	ACAT2	1,57247884	0,13717257
226038_at	LON peptidase N-terminal domain and ring finger 1	LONRF1	1,57252603	0,22870838
210613_s_at	synaptogyrin 1	SYNGR1	1,57295133	0,13717257
204044_at	quinolinate phosphoribosyltransferase	QPRT	1,573007	0,13717257
200952_s_at	cyclin D2	CCND2	1,57466877	1,94055411
243957_at	hypothetical LOC100128108	LOC100128108	1,57473017	0,13717257
220255_at	Fanconi anemia, complementation group E	FANCE	1,57487827	0,13717257
209916_at	dehydrogenase E1 and transketolase domain containing 1	DHTKD1	1,57496318	0,13717257
201689_s_at	tumor protein D52	TPD52	1,57547162	3,12037782
203221_at	transducin-like enhancer of split 1 (E[sp1] homolog, Drosophila)	TLE1	1,57633832	0,13717257
225224_at	chromosome 20 open reading frame 112	C20orf112	1,57726806	0,13717257
228869_at	sorting nexin 20	SNX20	1,57761642	0,22870838
209239_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1	NFKB1	1,57825477	0,22870838
225421_at	peptidase M20 domain containing 2	PM20D2	1,57924478	1,21472295
206752_s_at	DNA fragmentation factor, 40kDa, beta polypeptide (caspase-activated)	DFFB	1,57987604	0,13717257
213386_at	chromosome 9 open reading frame 125	C9orf125	1,58005155	0,32270094
209431_s_at	POZ (BTB) and AT hook containing zinc finger 1	PATZ1	1,58086431	0,13717257
1555167_s_at	nicotinamide phosphoribosyltransferase	NAMPT	1,58121353	0,13717257
226946_at	chromosome 5 open reading frame 33	C5orf33	1,58145642	0,13717257
219211_at	ubiquitin specific peptidase 18	USP18	1,58168441	0,13717257
1552470_a_at	abhydrolase domain containing 11	ABHD11	1,58185064	0,85107329
229700_at	zinc finger protein 738	ZNF738	1,5845407	1,00422607
205798_at	interleukin 7 receptor	IL7R	1,58457474	0,13717257
210547_x_at	islet cell autoantigen 1, 69kDa	ICA1	1,58458281	0,13717257
229391_s_at	family with sequence similarity 26, member F	FAM26F	1,58517144	1,21472295
229429_x_at	hypothetical LOC728855	LOC728855	1,58611892	0,22870838
206167_s_at	Rho GTPase activating protein 6	ARHGAP6	1,5861579	2,38495135
222697_s_at	abhydrolase domain containing 10	ABHD10	1,58683646	0,13717257
225081_s_at	cell division cycle associated 7-like	CDCA7L	1,58690825	0,13717257
201790_s_at	7-dehydrocholesterol reductase	DHCR7	1,58920589	0,40274237
225270_at	neogenin homolog 1 (chicken)	NEO1	1,58939691	0,22870838
212838_at	dynamitin binding protein	DNMBP	1,59051896	0,13717257
222819_at	CTP synthase II	CTPS2	1,59083159	0,13717257
1556242_a_at	hypothetical LOC100310756	LOC100310756	1,59161613	0,13717257
208637_x_at	actinin, alpha 1	ACTN1	1,59248807	1,3948219
208636_at	actinin, alpha 1	ACTN1	1,59261785	0,85107329
225532_at	Cdk5 and Abl enzyme substrate 1	CABLES1	1,59348845	0,13717257
1552256_a_at	scavenger receptor class B, member 1	SCARB1	1,59351194	0,57337326
226649_at	pantothenate kinase 1	PANK1	1,5940272	2,38495135
204062_s_at	unc-51-like kinase 2 (C. elegans)	ULK2	1,59424452	0,13717257
222559_s_at	regulation of nuclear pre-mRNA domain containing 1A	RPRD1A	1,59439207	0,13717257
225841_at	chromosome 1 open reading frame 59	C1orf59	1,59523193	0,13717257
206695_x_at	zinc finger protein 43	ZNF43	1,59582731	0,40274237
231926_at	epidermal growth factor receptor pathway substrate 15-like 1	EPS15L1	1,5961813	0,13717257
203182_s_at	SFRS protein kinase 2	SRPK2	1,59664294	0,57337326
202540_s_at	3-hydroxy-3-methylglutaryl-CoA reductase	HMGCR	1,59822727	1,3948219
215143_at	dpv-19-like 2 pseudogene 2 (C. elegans)	DPY19L2P2	1,59866203	0,85107329
228430_at	---	---	1,59874179	0,13717257
225604_s_at	GLI pathogenesis-related 2	GLIPR2	1,59899549	0,57337326
212186_at	acetyl-CoA carboxylase alpha	ACACA	1,59973965	0,13717257
229715_at	---	---	1,60027581	0,13717257
204412_s_at	neurofilament, heavy polypeptide	NEFH	1,60071901	0,13717257
235027_at	---	---	1,60165793	1,74547566
218176_at	melanoma antigen family F, 1	MAGEF1	1,6026525	0,22870838
200762_at	dihydropyrimidinase-like 2	DPYSL2	1,6032539	3,12037782
230051_at	chromosome 10 open reading frame 47	C10orf47	1,60380495	0,63176664
226301_at	chromosome 6 open reading frame 192	C6orf192	1,60410223	0,22870838
202071_at	syndecan 4	SDC4	1,60463774	0,13717257
203988_s_at	fucosyltransferase 8 (alpha 1,6) fucosyltransferase)	FUT8	1,60521526	0,76883463
210473_s_at	G protein-coupled receptor 125	GPR125	1,60554299	0,22870838
213964_x_at	---	---	1,60567433	0,85107329
202662_s_at	inositol 1,4,5-trisphosphate receptor, type 2	ITPR2	1,60578082	0,63176664
1552716_at	sperm flagellar 2	SPEF2	1,60595063	0,13717257
235142_at	zinc finger and BTB domain containing 8A	ZBTB8A	1,60636055	0,40274237
206493_at	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen	ITGA2B	1,60725936	2,38495135
244050_at	protein tyrosine phosphatase-like A domain containing 2	PTPLAD2	1,60861709	0,32270094
225579_at	PQ loop repeat containing 3	PQLC3	1,6096414	0,40274237
206544_x_at	SWI/SNF related, matrix associated, actin dependent regulator of chrom	SMARCA2	1,60988212	0,63176664
207275_s_at	acyl-CoA synthetase long-chain family member 1	ACSL1	1,61100639	0,40274237
219703_at	meiosis-specific nuclear structural 1	MNS1	1,61125984	0,63176664
212385_at	transcription factor 4	TCF4	1,61127391	0,13717257
1569107_s_at	zinc finger protein 642	ZNF642	1,61264134	0,4846616
221082_s_at	NDRG family member 3	NDRG3	1,61293674	0,13717257
202016_at	mesoderm specific transcript homolog (mouse)	MEST	1,61338603	0,57337326
218988_at	solute carrier family 35, member E3	SLC35E3	1,61338781	0,4846616
228720_at	sortilin-related VPS10 domain containing receptor 2	SORCS2	1,61340577	2,38495135
203188_at	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1	B3GNT1	1,613427	0,13717257
202741_at	protein kinase, cAMP-dependent, catalytic, beta	PRKACB	1,61458107	1,21472295
213787_s_at	emopamil binding protein (sterol isomerase)	EBP	1,61474589	0,57337326
202735_at	emopamil binding protein (sterol isomerase)	EBP	1,61491911	0,13717257
210451_at	pyruvate kinase, liver and RBC	PKLR	1,61502329	0,32270094
229693_at	transmembrane protein 220	TMEM220	1,61561868	1,21472295
220952_s_at	pleckstrin homology domain containing, family A member 5	PLEKHA5	1,61664099	0,76883463
211715_s_at	3-hydroxybutyrate dehydrogenase, type 1	BDH1	1,61679911	0,32270094
202326_at	euchromatic histone-lysine N-methyltransferase 2	EHMT2	1,61697258	0,22870838
231769_at	F-box protein 6	FBXO6	1,61786784	0,22870838
1569040_s_at	hypothetical LOC645784	FLJ40330	1,61823546	1,74547566
221586_s_at	E2F transcription factor 5, p130-binding	E2F5	1,61857573	0,13717257
1556183_at	hypothetical LOC645784	FLJ40330	1,61864415	0,13717257
201329_s_at	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	ETS2	1,61920213	0,13717257
222446_s_at	beta-site APP-cleaving enzyme 2	BACE2	1,61932814	2,38495135
210653_s_at	branched chain keto acid dehydrogenase E1, beta polypeptide	BCKDHB	1,62002528	0,13717257
209310_s_at	caspase 4, apoptosis-related cysteine peptidase	CASP4	1,62013907	0,63176664
232774_x_at	zinc finger protein interacting with K protein 1 homolog (mouse)	ZIK1	1,62238428	0,13717257
219869_s_at	solute carrier family 39 (zinc transporter), member 8	SLC39A8	1,6233826	0,13717257
205706_s_at	ankyrin repeat domain 26	ANKRD26	1,62349048	0,13717257
201819_at	scavenger receptor class B, member 1	SCARB1	1,62500876	0,22870838
203576_at	branched chain amino-acid transaminase 2, mitochondrial	BCAT2	1,62552006	0,63176664
203148_s_at	tripartite motif-containing 14	TRIM14	1,6258175	0,13717257
207018_s_at	RAB27B, member RAS oncogene family	RAB27B	1,62615954	0,85107329
200951_s_at	cyclin D2	CCND2	1,6266824	3,12037782
212087_s_at	Era G-protein-like 1 (E. coli)	ERAL1	1,62697089	1,00422607
237291_at	PrdX deacylase domain containing 1, pseudogene	PRDXDD1P	1,62715079	0,40274237
223596_at	solute carrier family 12 (potassium/chloride transporters), member 6	SLC12A6	1,62810971	0,13717257

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202245_at	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	LSS	1,62872435	0,57337326
206494_s_at	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CIIb)	ITGA2B	1,63215264	4,51937074
202504_at	tripartite motif-containing 29	TRIM29	1,63229013	3,63155925
225545_at	eukaryotic elongation factor-2 kinase	EEF2K	1,63339475	0,13717257
210115_at	ribosomal protein L39-like	RPL39L	1,63563333	0,13717257
228771_at	adrenergic, beta, receptor kinase 2	ADRBK2	1,63667131	0,22870838
212386_at	transcription factor 4	TCF4	1,63990297	0,63176664
228499_at	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 4	PFKFB4	1,64075227	0,13717257
232693_s_at	F-box protein 16 /// zinc finger protein 395	FBXO16 /// ZNF3	1,64092582	0,13717257
223216_x_at	zinc finger protein 395	ZNF395	1,64186754	0,13717257
213547_at	cullin-associated and neddylation-dissociated 2 (putative)	CAND2	1,64316767	0,13717257
232553_at	phosphate cytidyltransferase 1, choline, beta	PCYT1B	1,64351539	0,57337326
201791_s_at	7-dehydrocholesterol reductase	DHCR7	1,64392238	0,13717257
206683_at	zinc finger protein 165	ZNF165	1,64453275	0,13717257
221123_x_at	zinc finger protein 395	ZNF395	1,64486333	0,13717257
1554704_at	ATPase, aminophospholipid transporter, class I, type 8B, member 3	ATP8B3	1,64495108	1,94055411
226431_at	family with sequence similarity 117, member B	FAM117B	1,64507787	0,63176664
210290_at	zinc finger protein 174	ZNF174	1,64693605	0,13717257
218285_s_at	3-hydroxybutyrate dehydrogenase, type 2	BDH2	1,64803525	0,13717257
201127_s_at	ATP citrate lyase	ACLY	1,6516258	0,13717257
204063_s_at	unc-51-like kinase 2 (C. elegans)	ULK2	1,65167987	0,13717257
225193_at	---	---	1,65178209	0,13717257
204975_at	epithelial membrane protein 2	EMP2	1,6519235	0,32270094
236917_at	leucine rich repeat containing 34	LRRC34	1,65225862	1,00422607
220459_at	MCM3AP antisense RNA (non-protein coding)	MCM3APAS	1,65271824	0,13717257
207559_s_at	zinc finger, MYM-type 3	ZMYM3	1,65623018	0,13717257
201626_at	insulin induced gene 1	INSIG1	1,65677971	1,74547566
230944_at	chromosome 6 open reading frame 223	C6orf223	1,65966056	0,85107329
210233_at	interleukin 1 receptor accessory protein	IL1RAP	1,66160252	1,21472295
224925_at	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 1	PREX1	1,66475416	0,13717257
220418_at	ubiquitin associated and SH3 domain containing A	UBASH3A	1,6657331	0,13717257
222719_s_at	platelet derived growth factor C	PDGFC	1,66586852	1,3948219
210087_s_at	myelin protein zero-like 1	MPZL1	1,66860126	0,13717257
202022_at	aldolase C, fructose-bisphosphate	ALDOC	1,66902689	0,76883463
227224_at	Ral GEF with PH domain and SH3 binding motif 2	RALGPS2	1,67014027	0,13717257
223714_at	zinc finger protein 256	ZNF256	1,67307499	0,13717257
227812_at	tumor necrosis factor receptor superfamily, member 19	TNFRSF19	1,67364116	1,94055411
225710_at	guanine nucleotide binding protein (G protein), beta polypeptide 4	GNB4	1,67513773	0,32270094
227985_at	---	---	1,68078855	0,13717257
204545_at	peroxisomal biogenesis factor 6	PEX6	1,6823767	3,12037782
226820_at	zinc finger protein 362	ZNF362	1,68361241	0,13717257
209276_s_at	glutaredoxin (thioltransferase)	GLRX	1,6933598	0,50606127
200953_s_at	cyclin D2	CCND2	1,69398779	0,50606127
230466_s_at	---	---	1,69449386	0,32270094
224221_s_at	vav 3 guanine nucleotide exchange factor	VAV3	1,69599377	0,13717257
201625_s_at	insulin induced gene 1	INSIG1	1,69629116	0,50606127
206465_at	acyl-CoA synthetase bubblegum family member 1	ACSBG1	1,69724037	2,38495135
222939_s_at	solute carrier family 16, member 10 (aromatic amino acid transporter)	SLC16A10	1,69983706	0,13717257
1558254_s_at	SFRS protein kinase 2	SRPK2	1,7007677	0,13717257
228293_at	DEP domain containing 7	DEPDC7	1,70415882	0,13717257
218795_at	acid phosphatase 6, lysosphosphatidic	ACP6	1,70593118	0,13717257
210567_s_at	S-phase kinase-associated protein 2 (p45)	SKP2	1,7062867	0,13717257
204294_at	aminomethyltransferase	AMT	1,70765767	0,13717257
220183_s_at	nudix (nucleoside diphosphate linked moiety X)-type motif 6	NUDT6	1,71238428	0,13717257
208029_s_at	lysosomal protein transmembrane 4 beta	LAPTM4B	1,71355608	1,74547566
219470_x_at	cyclin J	CCNJ	1,7174083	0,13717257
220740_s_at	solute carrier family 12 (potassium/chloride transporters), member 6	SLC12A6	1,71841067	0,13717257
212387_at	transcription factor 4	TCF4	1,71864965	0,13717257
223492_s_at	leucine rich repeat (in FLII) interacting protein 1	LRRFIP1	1,71933611	0,22870838
221522_at	ankyrin repeat domain 27 (VPS9 domain)	ANKRD27	1,71974889	0,13717257
213160_at	dedicator of cytokinesis 2	DOCK2	1,7207978	3,12037782
210337_s_at	ATP citrate lyase	ACLY	1,72304472	0,13717257
1555310_a_at	p21 protein (Cdc42/Rac)-activated kinase 6	PAK6	1,72695556	0,32270094
224904_at	pyruvate dehydrogenase phosphatase regulatory subunit	PDPDR	1,72918374	0,32270094
231152_at	INO80 complex subunit D	INO80D	1,73151544	1,94055411
227976_at	hypothetical protein LOC644538	LOC644538	1,73207966	0,13717257
201719_s_at	erythrocyte membrane protein band 4.1-like 2	EPB41L2	1,73527978	1,21472295
232594_at	heat shock factor binding protein 1-like 1	HSBP1L1	1,73828001	0,13717257
221773_at	ELK3, ETS-domain protein (SRF accessory protein 2)	ELK3	1,73953428	1,21472295
228717_at	---	---	1,74219211	0,13717257
203626_s_at	S-phase kinase-associated protein 2 (p45)	SKP2	1,74547924	0,40274237
210993_s_at	SMAD family member 1	SMAD1	1,74582988	0,13717257
229390_at	family with sequence similarity 26, member F	FAM26F	1,74638673	3,12037782
216705_s_at	adenosine deaminase	ADA	1,74648117	0,13717257
212538_at	dedicator of cytokinesis 9	DOCK9	1,74781759	0,40274237
224428_s_at	cell division cycle associated 7	CDCA7	1,74835264	3,12037782
1554930_a_at	fucosyltransferase 8 (alpha (1,6) fucosyltransferase)	FUT8	1,75071439	0,13717257
218404_at	sorting nexin 10	SNX10	1,75220285	0,57337326
211002_s_at	tripartite motif-containing 29	TRIM29	1,75439274	1,74547566
227094_at	dehydrogenase E1 and transketolase domain containing 1	DHTKD1	1,75581909	0,13717257
224909_s_at	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 1	PREX1	1,76003428	0,85107329
214240_at	galanin prepropeptide	GAL	1,76154429	1,94055411
228617_at	XIAP associated factor 1	XAF1	1,76172338	0,22870838
202813_at	TAR (HIV-1) RNA binding protein 1	TARBP1	1,76218898	0,13717257
218935_at	EH-domain containing 3	EHD3	1,76398787	0,13717257
211990_at	major histocompatibility complex, class II, DP alpha 1	HLA-DPA1	1,76401066	4,51937074
1555606_a_at	glycerophosphodiester phosphodiesterase domain containing 1	GDDP1	1,76480763	0,13717257
204550_x_at	glutathione S-transferase mu 1	GSTM1	1,76558503	4,1207969
228624_at	transmembrane protein 144	TMEM144	1,76621627	0,40274237
201809_s_at	endoglin	ENG	1,76946511	0,40274237
209790_s_at	caspase 6, apoptosis-related cysteine peptidase	CASP6	1,77014585	0,13717257
225274_at	prenylcysteine oxidase 1	PCYOX1	1,77068671	0,13717257
218486_at	Kruppel-like factor 11	KLF11	1,77194506	0,50606127
201849_at	BCL2/adenovirus E1B 19kDa interacting protein 3	BNIP3	1,77590463	1,94055411
238444_at	zinc finger protein 618	ZNF618	1,77662655	0,13717257
228153_at	ring finger protein 144B	RNF144B	1,77726378	0,22870838
202747_s_at	integral membrane protein 2A	ITM2A	1,77742998	0,13717257
224902_at	pyruvate dehydrogenase phosphatase regulatory subunit	PDPDR	1,77876439	0,76883463
204418_x_at	glutathione S-transferase mu 2 (muscle)	GSTM2	1,78053752	4,1207969
232024_at	GTPase, IMAP family member 2	GIMAP2	1,78494242	0,85107329
218149_s_at	zinc finger protein 395	ZNF395	1,78635698	0,13717257
225351_at	family with sequence similarity 45, member A	FAM45A	1,7864587	0,13717257
214788_x_at	dendrin	DDN	1,78648117	0,13717257
215333_x_at	glutathione S-transferase mu 1	GSTM1	1,7882563	4,1207969
201315_x_at	interferon induced transmembrane protein 2 (1-8D)	IFITM2	1,79489998	0,76883463

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221804_s_at	family with sequence similarity 45, member A /// family with sequence s FAM45A /// FAN	1,80264076	0,13717257
1557196_a_at	---	1,80307885	0,13717257
214136_at	nudix (nucleoside diphosphate linked moiety X)-type motif 13	1,80831785	0,13717257
202742_s_at	protein kinase, cAMP-dependent, catalytic, beta	1,80862585	0,85107329
225792_at	hook homolog 1 (Drosophila)	1,81082196	1,3948219
225079_at	epithelial membrane protein 2	1,81145713	0,85107329
212657_s_at	interleukin 1 receptor antagonist	1,81187994	0,13717257
1555600_s_at	apolipoprotein L, 4	1,81450747	0,32270094
227210_at	Scm-like with four mbt domains 2	1,81451857	0,50606127
226319_s_at	THO complex 4	1,81581848	0,13717257
201718_s_at	erythrocyte membrane protein band 4.1-like 2	1,8185813	0,85107329
205147_x_at	neutrophil cytosolic factor 4, 40kDa	1,82108776	0,13717257
202119_s_at	copine III	1,82438686	0,13717257
221690_s_at	NLR family, pyrin domain containing 2	1,82827302	4,51937074
235333_at	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6	1,8293338	0,13717257
236198_at	---	1,83139382	0,13717257
228906_at	tet oncogene 1	1,83181336	0,13717257
227609_at	epithelial stromal interaction 1 (breast)	1,8326659	0,13717257
242245_at	---	1,83290535	0,22870838
206295_at	interleukin 18 (interferon-gamma-inducing factor)	1,83365839	0,22870838
219412_at	RAB38, member RAS oncogene family	1,83592603	1,74547566
218656_s_at	lipoma HMGIC fusion partner	1,83663651	0,57337326
228090_at	nicotinamide nucleotide adenylyltransferase 3	1,83876909	0,13717257
221750_at	3-hydroxy-3-methylglutaryl-CoA synthase 1 (soluble)	1,84056148	0,22870838
227798_at	SMAD family member 1	1,84255971	0,85107329
210663_s_at	kynureninase (L-kynurenine hydrolase)	1,84410651	0,57337326
1559826_a_at	hypothetical LOC401074	1,84545034	0,76883463
202345_s_at	fatty acid binding protein 5 (psoriasis-associated)	1,84630681	0,40274237
202118_s_at	copine III	1,84661676	0,48466616
210762_s_at	deleted in liver cancer 1	1,84850936	0,40274237
219479_at	KDEL (Lys-Asp-Glu-Leu) containing 1	1,8508244	0,13717257
223457_at	coatamer protein complex, subunit gamma 2	1,85831617	0,22870838
228716_at	thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) c	1,85997505	0,13717257
225078_at	epithelial membrane protein 2	1,86596259	0,40274237
229091_s_at	cyclin J	1,86705183	0,13717257
204867_at	GTP cyclohydrolase I feedback regulator	1,86787579	0,13717257
201627_s_at	insulin induced gene 1	1,8696846	0,63176664
208964_s_at	fatty acid desaturase 1	1,8760869	0,48466616
229100_s_at	translocase of inner mitochondrial membrane 22 homolog (yeast)	1,87758324	0,13717257
214453_s_at	interferon-induced protein 44	1,87964165	0,22870838
1565162_s_at	microsomal glutathione S-transferase 1	1,88437454	0,13717257
225525_at	KIAA1671	1,88490438	0,13717257
201309_x_at	chromosome 5 open reading frame 13	1,88710153	0,13717257
201688_s_at	tumor protein D52	1,89298848	2,38495135
229657_at	thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) c	1,89899189	0,50606127
208963_x_at	fatty acid desaturase 1	1,89916584	0,40274237
209040_s_at	proteasome (prosome, macropain) subunit, beta type, 8 (large multifu	1,89960519	0,13717257
226592_at	zinc finger protein 618	1,89978622	0,13717257
218806_s_at	vav 3 guanine nucleotide exchange factor	1,91192194	0,22870838
237265_at	chromosome 16 open reading frame 73	1,91215378	0,22870838
223812_at	family with sequence similarity 178, member B	1,91343799	1,3948219
204305_at	mitochondrial intermediate peptidase	1,92066453	0,76883463
211019_s_at	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	1,92266971	0,63176664
222592_s_at	acyl-CoA synthetase long-chain family member 5	1,92701633	0,13717257
204639_at	adenosine deaminase	1,9291041	0,13717257
214039_s_at	lysosomal protein transmembrane 4 beta	1,93237035	2,38495135
201647_s_at	scavenger receptor class B, member 2	1,93457632	1,3948219
202746_at	integral membrane protein 2A	1,94599817	0,13717257
200832_s_at	stearoyl-CoA desaturase (delta-9-desaturase)	1,94744828	0,50606127
220911_s_at	NYN domain and retroviral integrase containing	1,94772866	0,13717257
224918_x_at	microsomal glutathione S-transferase 1	1,94849845	0,13717257
226117_at	TRAF-interacting protein with forkhead-associated domain	1,95472863	0,13717257
218807_at	vav 3 guanine nucleotide exchange factor	1,96043716	0,22870838
221524_s_at	Ras-related GTP binding D	1,96257905	0,76883463
36830_at	mitochondrial intermediate peptidase	1,97037426	0,50606127
231736_x_at	microsomal glutathione S-transferase 1	1,97112238	0,13717257
219184_x_at	translocase of inner mitochondrial membrane 22 homolog (yeast)	1,97392913	0,13717257
1570153_at	chromosome 13 open reading frame 38	1,97408027	0,13717257
226568_at	family with sequence similarity 102, member B	1,97737453	0,22870838
228959_at	pyruvate dehydrogenase kinase, isozyme 3	1,97863127	0,13717257
224848_at	cyclin-dependent kinase 6	1,98029579	0,13717257
206693_at	interleukin 7	1,98195627	0,13717257
223204_at	family with sequence similarity 198, member B	1,982939	3,12037782
217478_s_at	major histocompatibility complex, class II, DM alpha	1,98651527	1,94055411
226438_at	syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic comp	1,98830257	0,13717257
212218_s_at	fatty acid synthase	1,99275351	0,57337326
201646_at	scavenger receptor class B, member 2	1,99786846	0,63176664
227692_at	guanine nucleotide binding protein (G protein), alpha inhibiting activity	2,00110911	1,3948219
207858_s_at	pyruvate kinase, liver and RBC	2,00452787	0,22870838
226590_at	zinc finger protein 618	2,00577394	0,13717257
208962_s_at	fatty acid desaturase 1	2,0082901	0,50606127
1556211_a_at	---	2,00961924	0,13717257
213757_at	Eukaryotic translation initiation factor 5A	2,01391142	4,51937074
222955_s_at	family with sequence similarity 45, member A /// family with sequence s	2,01615221	0,13717257
200831_s_at	stearoyl-CoA desaturase (delta-9-desaturase)	2,02060434	0,22870838
224822_at	deleted in liver cancer 1	2,02667155	0,22870838
209200_at	myocyte enhancer factor 2C	2,02954135	0,13717257
207677_s_at	neutrophil cytosolic factor 4, 40kDa	2,03423563	0,13717257
205229_s_at	coagulation factor C homolog, cochlilin (Limulus polyphemus)	2,05225419	0,13717257
218976_at	DnaJ (Hsp40) homolog, subfamily C, member 12	2,05605968	0,13717257
209199_s_at	myocyte enhancer factor 2C	2,05693863	0,13717257
212203_x_at	interferon induced transmembrane protein 3 (1-8U)	2,0597393	0,22870838
224847_at	cyclin-dependent kinase 6	2,06317786	0,13717257
201562_s_at	sorbitol dehydrogenase	2,06486507	0,48466616
221558_s_at	lymphoid enhancer-binding factor 1	2,07226677	0,50606127
1552703_s_at	caspase recruitment domain family, member 16 /// caspase 1, apoptosis	2,07624829	0,22870838
243000_at	cyclin-dependent kinase 6	2,07626711	0,13717257
201848_s_at	BCL2/adenovirus E1B 19kDa interacting protein 3	2,07658714	0,13717257
201163_s_at	insulin-like growth factor binding protein 7	2,08462327	0,76883463
224983_at	scavenger receptor class B, member 2	2,09192599	0,13717257
227231_at	KIAA1211	2,09818776	0,57337326
221024_s_at	solute carrier family 2 (facilitated glucose transporter), member 10	2,09939095	0,22870838
224851_at	cyclin-dependent kinase 6	2,09966765	0,13717257
219288_at	chromosome 3 open reading frame 14	2,10115478	0,32270094
230085_at	pyruvate dehydrogenase kinase, isozyme 3	2,10123234	0,13717257

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235099_at	CKLF-like MARVEL transmembrane domain containing 8	CMTM8	2,1099624	1,74547566
231897_at	prostaglandin reductase 1	PTGR1	2,12512598	0,22870838
228824_s_at	prostaglandin reductase 1	PTGR1	2,14049956	0,13717257
217388_s_at	kynureninase (L-kynurenine hydrolase)	KYNU	2,15238675	2,38495135
229402_at	sterile alpha motif domain containing 13	SAMD13	2,15650397	0,13717257
1555989_at	---	---	2,16264355	2,79695557
203153_at	interferon-induced protein with tetratricopeptide repeats 1	IFIT1	2,16695144	0,13717257
221957_at	pyruvate dehydrogenase kinase, isozyme 3	PKD3	2,17305818	0,13717257
211162_x_at	stearoyl-CoA desaturase (delta-9-desaturase)	SCD	2,17319398	0,13717257
211708_s_at	stearoyl-CoA desaturase (delta-9-desaturase)	SCD	2,17461925	0,13717257
230925_at	amyloid beta (A4) precursor protein-binding, family B, member 1 interact	APBB1IP	2,17537504	0,40274237
205698_s_at	mitogen-activated protein kinase kinase 6	MAP2K6	2,18698967	0,13717257
205822_s_at	3-hydroxy-3-methylglutaryl-CoA synthase 1 (soluble)	HMGCS1	2,19560673	0,32270094
235287_at	cyclin-dependent kinase 6	CDK6	2,19741132	0,13717257
202597_at	interferon regulatory factor 6	IRF6	2,23926098	0,13717257
1552478_a_at	interferon regulatory factor 6	IRF6	2,24798023	0,13717257
214022_s_at	interferon induced transmembrane protein 1 (9-27)	IFITM1	2,25309524	0,76883463
201839_s_at	epithelial cell adhesion molecule	EPCAM	2,27105307	0,13717257
227230_s_at	KIAA1211	KIAA1211	2,2949441	0,13717257
206348_s_at	pyruvate dehydrogenase kinase, isozyme 3	PKD3	2,29821871	0,13717257
211812_s_at	beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)	B3GALNT1	2,33160219	0,13717257
206740_x_at	synaptonemal complex protein 1	SYCP1	2,36143496	0,22870838
201310_s_at	chromosome 5 open reading frame 13	CSorf13	2,36507659	0,13717257
203799_at	CD302 molecule	CD302	2,37545891	0,13717257
223360_at	chromosome 21 open reading frame 56	C21orf56	2,38394668	0,57337326
219676_at	zinc finger and SCAN domain containing 16	ZSCAN16	2,38859015	0,13717257
1552701_a_at	caspase recruitment domain family, member 16	CARD16	2,41405483	0,22870838
218322_s_at	acyl-CoA synthetase long-chain family member 5	ACSL5	2,41685171	0,13717257
223125_s_at	chromosome 1 open reading frame 21	C1orf21	2,42228672	0,13717257
213005_s_at	KN motif and ankyrin repeat domains 1	KANK1	2,43317902	0,13717257
224579_at	solute carrier family 38, member 1	SLC38A1	2,45917147	1,3948219
208146_s_at	carboxypeptidase, vitellogenic-like	CPVL	2,46042338	1,00422607
33767_at	neurofilament, heavy polypeptide	NEFH	2,48313891	0,13717257
221081_s_at	DENN/MADD domain containing 2D	DENN2D	2,48344294	0,13717257
201601_x_at	interferon induced transmembrane protein 1 (9-27)	IFITM1	2,54465143	0,22870838
1552477_a_at	interferon regulatory factor 6	IRF6	2,54844044	0,13717257
209574_s_at	chromosome 18 open reading frame 1	C18orf1	2,55063155	0,13717257
225060_at	low density lipoprotein receptor-related protein 11	LRP11	2,58933201	0,13717257
202479_s_at	tribbles homolog 2 (Drosophila)	TRIB2	2,59278319	0,13717257
212686_at	protein phosphatase, Mg2+/Mn2+ dependent, 1H	PPM1H	2,65206259	3,63155925
1559131_a_at	---	---	2,66443752	0,57337326
1558871_at	---	---	2,72757937	0,13717257
1559827_at	hypothetical LOC401074	LOC401074	2,8026957	1,3948219
223374_s_at	beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)	B3GALNT1	2,84336098	0,13717257
216917_s_at	synaptonemal complex protein 1	SYCP1	2,8942953	0,50606127
218237_s_at	solute carrier family 38, member 1	SLC38A1	2,93423722	0,22870838
210262_at	cysteine-rich secretory protein 2	CRISP2	3,02337005	0,13717257
227759_at	proprotein convertase subtilisin/kexin type 9	PCSK9	3,10753734	0,13717257
202478_at	tribbles homolog 2 (Drosophila)	TRIB2	3,25650174	0,13717257
201563_at	sorbitol dehydrogenase	SORD	3,43878171	0,13717257
202934_at	hexokinase 2	HK2	3,45574281	0,13717257
204042_at	WAS protein family, member 3	WASF3	3,50712579	2,38495135
218217_at	serine carboxypeptidase 1	SCPEP1	3,52066003	1,00422607
223599_at	tripartite motif-containing 6	TRIM6	3,78897161	0,13717257
212543_at	absent in melanoma 1	AIM1	3,87152909	1,3948219
202411_at	interferon, alpha-inducible protein 27	IFI27	4,05626764	0,4846616

**Online Supplementary Table S3.** Genes in this Table belong to one of the following categories: (A) differentiation and globin expression related genes or possibly involved in  $\gamma$ -globin regulation based on literature or similarities with genes in the same gene family (B) stress response or apoptosis genes. Differential expression is calculated as fold-change, comparing responders over non-responders. Expression profiling data were confirmed for selected genes by qRT-PCR, as indicated.

Gene Title	Gene Symbol	R vs. NR	qRT-PCR Confirmed	Function
<b>Differentiation and globin expression related genes</b>				
Arginase, liver	ARG1	10.1	12.7	SNP associated with high HbF
Arginase, type II	ARG2	2.4	5.1	SNP associated with high HbF
Argininosuccinate synthetase 1	ASS1	1.9		SNP associated with high HbF
cAMP responsive element binding protein 3-like 1	CREB3L1	2.3		sequence-specific DNA binding transcription factor
Glycophorin A	GYP A	1.8		glycophorin
Glycophorin B	GYP B	1.7		glycophorin
JAZF zinc finger 1	JAZF1	1.7		zinc fingers, functions as a transcriptional repressor
Hematopoietically expressed homeobox	HHEX	1.5		hematopoietic transcription factor
Inhibitor of DNA binding 1, dominant negative helix-loop-helix	ID1	1.5		transcription factor
Interleukin 6 signal transducer (gp130, oncostatin M receptor)	IL6ST	2.5		proliferation, growth, differentiation
Interleukin 7	IL7	-1.9		proliferation, survival,
Interleukin 7 receptor	IL7R	-1.6		proliferation, differentiation, growth
Interleukin 8	IL8	2.9		chemotaxis, activation, migration
Kruppel-like factor 10	KLF10	2.0	2.7	proliferation, differentiation
Kruppel-like factor 9	KLF9	1.6		transcription factor that binds to GC box elements
Mitogen-activated protein kinase kinase 6	MAP2K6	-2.1		apoptosis, proliferation
Nuclear factor (erythroid-derived 2), 45kDa	NFE2	1.5		sequence-specific DNA binding transcription factor
RAR-related orphan receptor A	RORA	1.8		differentiation
Sorbitol dehydrogenase	SORD	-3.4		enzyme in sorbitol pathway
SRV (sex determining region Y)-box 6	SOX6	2.0	3.8	sequence-specific DNA binding transcription factor
SRV (sex determining region Y)-box 4	SOX4	-1.7	-1.4	sequence-specific DNA binding transcription factor
Tripartite motif-containing 10	TRIM10	1.8		differentiation
WD repeat domain 26	WDR26	1.9		facilitate multiprotein complex formation
WD repeat domain 45	WDR45	1.7		facilitate multiprotein complex formation
Exportin 7	XPO7	3.3		nuclear export signal receptor
Zinc finger and BTB domain containing 16	ZBTB16	1.7		differentiation, binds SP1, BCL6 etc.
<b>Stress and proliferation related genes</b>				
BCL2-like 1	BCL2L1	2.0	3.0	pro-apoptotic
B-cell CLL/lymphoma 6 (zinc finger protein 51)	BCL6	3.6	7.3	apoptosis, proliferation
BTG family, member 1	BTG1	1.7		apoptosis, proliferation
BTG family, member 2	BTG2	2.0		apoptosis, proliferation
Caspase 4, apoptosis-related cysteine peptidase	CASP4	-1.6		apoptosis, proliferation
Caspase 6, apoptosis-related cysteine peptidase	CASP6	-1.8		apoptosis, proliferation
Cyclin-dependent kinase 6	CDK6	-2.1		apoptosis, proliferation, growth, differentiation
Cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	CDKN2B	2.3	3.0	apoptosis, proliferation, growth, differentiation
DnaJ (Hsp40) homolog, subfamily C, member 12	DNAJ12	-2.0		complex assembly, protein folding, and export
Forkhead box O3	FOXO3	1.9	2.3	apoptosis, cell cycle progression
Homeodomain interacting protein kinase 2	HIPK2	2.5	3.9	apoptosis, proliferation, growth