SUPPLEMENTAL MATERIAL

Results

Linear Correlation Revealed High Correlation Between Datasets

To assess the quality of potential sources and degree of experimental variability, we calculated the correlation coefficients between datasets obtained after hybridization of the total RNA isolated from sorted BM subsets to Affymetrix HG-133A chips containing 22,283 probsets. All pairwise comparisons among 39 datasets (27 datasets from three diseased individuals D1-D3 and six control individuals C1-C6, and 12 repeated datasets from D2, C4, C5 and C6) revealed correlations with r=0.85-0.99. Correlations between datasets from repeated experiments from the same individuals were the highest (r=0.95-0.98). Also the correlation between samples within the populations P, E, and M were the highest with r=0.92-0.99 in the P and E populations, and r=0.95-0.99 in the M population. The lowest correlations were found between datasets from patient and control samples. For further analysis the 27 unique datasets with the highest intra-group correlations from individuals D1-D3 and C1-C6 were chosen.

Supplemental Material

Table S1. All significantly changed genes in DBA samples

Significantly changed genes in multipotential progenitors (P population) in DBA samples

Affymetrix ID	Symbol	LocusLink	GO molecular function*	**GFChA-f.ch.	***SAM -f.ch.
209967_s_at	*CREM*	1390	transcription	7.48	6.16
203290_at	*HLA-DQA1*	3117		6.81	-
209839_at	*KIAA0820*	26052		4.34	4.56
212589_at	*RRAS2*	22800	cancer	3.98	3.46
213537_at	*HLA-DPA1*	3113		3.72	3.71
211833_s_at	*BAX*	581	apoptosis/cancer	3.49	3.32
214508_x_at	*CREM*	1390	transcription	3.48	3.22
202377_at	*LEPR*	3953	cancer	3.22	3.07
205922_at	*VNN2*	8875		3.12	-
202499_s_at	*SLC2A3*	6515		3.12	-
218178_s_at	*GNAL*	2774		2.98	-
205501_at	-	-		2.93	-
203882_at	*ISGF3G*	10379	transcription	2.84	-
202858_at	*U2AF1*	7307		2.81	-
202004_x_at	*SDHC*	6391		2.68	2.60
220243_at	*HSPC063*	29068		2.68	-
204440_at	*CD83*	9308		2.62	-
203146_s_at	*GABBR1*	2550		2.58	2.51
220221_at	*FLJ10619*	55187		2.55	-
206118_at	*STAT4*	6775	transcription	2.53	2.40
210131_x_at	*SDHC*	6391		2.42	2.34
212051_at	*WIRE*	147179		2.41	2.35
206404_at	*FGF9*	2254		2.39	-
208789_at	*PTRF*	284119		2.33	-
213279_at	*DHRS1*	115817		2.27	-
201089_at	*ATP6V1B2*	526		2.25	2.24
201484_at	*SUPT4H1*	6827	transcription	2.25	-
200782_at	*ANXA5*	308		2.25	-
212199_at	*MGC9651*	114932		2.23	2.19
218607_s_at	*FLJ10498*	55153		2.21	2.16
211582_x_at	*LST1*	7940		2.20	-
212993_at	*MGC23427*	138151		2.19	-
217739_s_at	*PBEF*	10135		2.18	-
203528_at	*SEMA4D*	10507	apoptosis	2.12	-
203265_s_at	*MAP2K4*	6416	apoptosis	2.11	2.06
203885_at	*RAB21*	23011	cancer	2.11	-
36711_at	*MAFF*	23764	transcription/cancer	2.10	-
202322_s_at	*GGPS1*	9453		2.08	2.06
217897_at	*FXYD6*	53826		2.05	-
211528_x_at	*HLA-G*	3135		2.04	-
214211_at	*FTH1*	2495		2.02	2.04
201326_at	*CCT6A*	908		-2.02	-
201177_s_at	*UBA2*	10054		-2.03	-2.02
205361_s_at	*PFDN4*	5203		-2.04	-
201657_at	*ARL1*	400		-2.04	-
203675_at	*NUCB2*	4925		-2.05	-2.06
204528_s_at	*NAP1L1*	4673		-2.05	-2.03
202715_at	*CAD*	790		-2.05	-
210970_s_at	*IBTK*	25998		-2.05	-2.042
202469_s_at	*CPSF6*	11052		-2.06	-

Table S1. All significantly changed genes in DBA samples

200821_at	*LAMP2*	3920		-2.06	-2.066
209748_at	*SPG4*	6683		-2.09	-2.066
209513_s_at	*MGC10940*	84263		-2.10	-
212927_at	*SMC5L1*	23137		-2.11	-
219174_at	*CCDC2*	80173		-2.12	-
203581_at	*RAB4A*	5867	cancer	-2.12	-2.118
221553_at	*DKFZp564K142*	84061		-2.12	-
202823_at	*TCEB1*	6921	transcription	-2.16	-
207541_s_at	*PMSCL2*	5394		-2.16	-
208753_s_at	*NAP1L1*	4673		-2.16	-2.130
205347_s_at	*TMSNB*	11013		-2.20	-
213549_at	*SLC18A2*	6571		-2.21	-
211747_s_at	*LSM5*	23658		-2.22	-
211464_x_at	*CASP6*	839	apoptosis	-2.22	-
64432_at	*CDV-1*	28981	apoptosis	-2.23	-
201397_at	*PHGDH*	26227		-2.24	-
208694_at	*PRKDC*	5591		-2.24	-
218128_at	*NFYB*	4801	transcription	-2.25	-2.246
222297_x_at	*RPL18*	6141		-2.27	-
203132_at	*RB1*	5925	transcription/cancer	-2.30	-
204453_at	*ZNF84*	7637		-2.32	-2.379
201163_s_at	*IGFBP7*	3490		-2.33	-2.350
206674_at	*FLT3*	2322		-2.37	-
218256_s_at	*NUP54*	53371		-2.38	-
202345_s_at	*FABP5*	2171		-2.38	-2.391
200875_s_at	*NOL5A*	10528		-2.38	-
212449_s_at	*LYPLA1*	10434		-2.41	-2.388
202163_s_at	*CNOT8*	9337	transcription	-2.42	-
219762_s_at	*RPL36*	25873		-2.46	-
201284_s_at	*APEH*	327		-2.46	-
213129_s_at	-	2653		-2.46	-
202660_at	-	3709		-2.49	-
212709_at	*NUP160*	23279		-2.50	-2.41
203049_s_at	*KIAA0372*	9652		-2.53	-2.56
218334_at	*NIF3L1BP1*	80145		-2.55	-
208368_s_at	*BRCA2*	675	apoptosis/transcription/cancer	-2.59	-
207002_s_at	*PLAGL1*	5325	apoptosis/cancer	-2.61	-
213786_at	*TAX1BP1*	8887		-2.77	-2.83
214043_at	*PTPRD*	5789		-2.81	-
218609_s_at	*NUDT2*	318		-2.85	-
214678_x_at	*ZFX*	7543		-2.86	-
203440_at	*CDH2*	1000		-2.95	-
218637_at	*IMPACT*	55364		-3.02	-3.05
204120_s_at	*ADK*	132		-3.05	-
208794_s_at	*SMARCA4*	6597	transcription	-3.23	-
221797_at	*LOC339229*	339229		-3.30	-
221894_at	*ADCK2*	90956		-3.42	-3.27
213896_x_at	*KIAA0974*	317662		-3.44	-
205402_x_at	*PRSS2*	5645		-3.94	-
220085_at	*HELLS*	3070		-4.11	-
218480_at	*FLJ21839*	60509		-4.25	-
209739_s_at	*DXS1283E*	8228		-5.54	-

217716_s_at	*SEC61A1*	29927		-5.92	-
205830_at	*CLGN*	1047		-	-2.26
206922_at	*VCY1B /// VCY*	9084		-	2.39
219076_s_at	*PXMP2*	5827		-	-2.53
219583_s_at	*SPATA7*	55812		-	-2.48
221799_at	*CSGlcA-T*	54480		-	-3.07
55705_at	*C19orf22*	91300		-	2.00

Significantly changed genes in erythroid progenitors (E population) in DBA samples

Affymetrix ID	***Symbol***	**LocusLink**		***GFChA-f.ch**	****SAM -f.ch.**
209295_at	*TNFRSF10B*	8795	apoptosis	10.11	6.24
209894_at	*LEPR*	3953	cancer	4.49	4.27
203409_at	*DDB2*	1643	DNA repair	3.73	3.56
221081_s_at	*FLJ22457*	79961		3.57	3.60
204780_s_at	*TNFRSF6*	355	apoptosis	3.03	2.97
218346_s_at	*SESN1*	27244		2.74	2.66
219361_s_at	*FLJ12484*	64782		2.69	2.59
218627_at	*FLJ11259*	55332		2.57	2.59
209716_at	*CSF1*	1435		2.55	2.43
220520_s_at	*FLJ20130*	54830		2.43	2.35
212780_at	*SOS1*	6654		2.40	2.28
212792_at	*KIAA0877*	23333		2.37	2.27
201089_at	*ATP6V1B2*	526		2.37	2.29
40273_at	*SPHK2*	56848	transcription	2.32	2.19
201462_at	*KIAA0193*	9805		2.26	2.22
202193_at	*LIMK2*	3985		2.25	2.12
203567_s_at	*TRIM38*	10475		2.24	2.04
201221_s_at	*SNRP70*	6625		2.22	2.20
219146_at	*FLJ22729*	79736		2.19	2.11
218715_at	*HCA66*	55813		2.19	2.11
204781_s_at	*TNFRSF6*	355	apoptosis	2.15	2.07
202395_at	*NSF*	4905		2.13	2.06
206348_s_at	*PDK3*	5165		2.07	2.05
200961_at	*SPS2*	22928		2.06	2.07
208765_s_at	*HNRPR*	10236		2.04	-
221957_at	*PDK3*	5165		2.03	2.05
204060_s_at	*PRKX*	5613		2.03	-
205136_s_at	*NUFIP1*	26747		2.00	-
217336_at	*RPS10*	-		-2.05	-2.04
221079_s_at	*METTL2*	55798		-2.05	-
200003_s_at	*RPL28*	6158		-2.07	-2.12
201627_s_at	*INSIG1*	3638		-2.32	-2.49
221192_x_at	*ET*	79157		-2.44	-2.49
209740_s_at	*DXS1283E*	8228		-2.49	-2.50
217269_s_at	*PRSS7*	5651		-2.57	-
206231_at	*KCNN1*	3780		-2.61	-
216175_at	*POLD2*	5425		-2.66	-
201439_at	*GBF1*	8729		-2.69	-
52651_at	*COL8A2*	1296		-2.70	-
221402_at	*OR1F1*	4992		-2.78	-
209152_s_at	*TCF3*	6929	transcription/cancer	-2.80	-
203305_at	*F13A1*	2162		-2.88	-2.94

Table S1. All significantly changed genes in DBA samples

214558_at	*GPR12*	2835		-2.90	-
220671_at	*CCRN4L*	25819	transcription	-2.92	-
205884_at	*ITGA4*	3676		-2.96	-
211364_at	*MTAP*	4507		-2.97	-
203686_at	*MPG*	4350		-2.97	-
222279_at	*HLA-F*	3134		-2.98	-2.97
214398_s_at	*IKBKE*	9641		-2.99	-
216092_s_at	*SLC7A8*	23428		-3.00	-
215071_s_at	-	-		-3.00	-3.33
64064_at	*IAN4L1*	55340		-3.02	-
210519_s_at	*NQO1*	1728		-3.08	-
208830_s_at	*SUPT6H*	6830	transcription	-3.09	-
206111_at	*RNASE2*	6036		-3.13	-3.31
213353_at	*ABCA5*	23461		-3.17	-
215167_at	*CRSP2*	9282	transcription	-3.18	-
203637_s_at	*MID1*	4281	transcription	-3.19	-
210568_s_at	*RECQL*	5965	DNA repair	-3.21	-
221553_at	*DKFZp564K142*	84061		-3.22	-3.08
209594_x_at	*PSG9*	5678		-3.24	-
211325_x_at	*na*	283345		-3.25	-
204638_at	*ACP5*	54	DNA repair	-3.26	-
204526_s_at	*TBC1D8*	11138		-3.29	-
214108_at	*MAX*	4149	transcription/cancer	-3.32	-
212776_s_at	*KIAA0657*	23363		-3.39	-
219968_at	*SZF1*	51385	transcription	-3.40	-
216580_at	-	-		-3.41	-
217473_x_at	*SLC11A1*	6556		-3.41	-
59433_at	-	-		-3.42	-
203586_s_at	*ARF4L*	379		-3.43	-
215528_at	-	-		-3.45	-
205815_at	*PAP*	5068		-3.45	-
204979_s_at	*SH3BGR*	6450		-3.46	-
203742_s_at	*TDG*	6996	DNA repair	-3.48	-
205586_x_at	*VGF*	7425		-3.52	-
208237_x_at	*ADAM22*	53616		-3.53	-
202445_s_at	*NOTCH2*	4853		-3.53	-
213422_s_at	*MGC3047*	84308		-3.56	-
59375_at	*MYO15B*	80022		-3.58	-
205881_at	*ZNF74*	7625		-3.58	-
205607_s_at	*PACE-1*	57147		-3.59	-3.77
206772_at	*PTHR2*	5746		-3.60	-
205144_at	*MYL5*	4636		-3.61	-
207061_at	*ERN1*	2081		-3.61	-
206212_at	*CPA2*	1358		-3.63	-12.70
206695_x_at	*ZNF43*	7594		-3.65	-
213996_at	*YPEL1*	29799		-3.67	-
204956_at	*MTAP*	4507		-3.68	-
220682_s_at	*KLHL5*	51088		-3.69	-
564_at	*GNA11*	2767		-3.74	-
219149_x_at	*DBR1*	51163		-3.75	-
207417_s_at	*ZNF177*	7730		-3.77	-
37586_at	*ZNF142*	7701	transcription	-3.78	-

Table S1. All significantly changed genes in DBA samples

210944_s_at	*CAPN3*	825		-3.78	-
204029_at	*CELSR2*	1952	cancer	-3.79	-
212427_at	*KIAA0368*	23392		-3.79	-
218553_s_at	*MGC2628*	79047		-3.80	-
208390_s_at	*GLP1R*	2740		-3.81	-
215372_x_at	*LOC151878*	151878		-3.85	-
204024_at	*C8orf1*	734		-3.85	-
214313_s_at	*IF2*	9669	translation	-3.85	-
212570_at	*KIAA0830*	23052		-3.87	-3.55
218174_s_at	*FLJ13263*	80195		-3.87	-
206197_at	*NME5*	8382	apoptosis	-3.89	-
203533_s_at	*CUL5*	8065	apoptosis/cancer	-3.90	-
206593_s_at	*SURF5*	6837		-3.92	-29.38
208250_s_at	*DMBT1*	1755	cancer	-3.94	-
219129_s_at	*FLJ11526*	79685		-3.95	-
220244_at	*NAG-7*	29931		-3.97	-
214955_at	*TMPRSS6*	164656		-3.98	-
208546_x_at	*HIST1H2BH*	8345		-3.98	-
212651_at	*RHOBTB1*	9886		-3.99	-
202183_s_at	*KIF22*	3835		-4.01	-8.21
220471_s_at	*FLJ21269*	80177		-4.03	-
209725_at	*DRIM*	27340		-4.06	-5.66
221082_s_at	*NDRG3*	57446		-4.07	-
204741_at	*BICD1*	636		-4.08	-
205002_at	*DJ159A19.3*	27245		-4.08	-
216960_s_at	*ZNF133*	7692	transcription	-4.08	-
201896_s_at	*CKS1B*	1163		-4.08	-
220494_s_at	*C14orf117*	55516		-4.13	-4.27
220953_s_at	*PIP3AP*	54545		-4.14	-
218221_at	*ARNT*	405	transcription	-4.15	-
219154_at	*na*	144404		-4.16	-
213124_at	*ZFP100*	25888		-4.18	-14.52
218144_s_at	*FLJ22056*	64423		-4.19	-4.18
218969_at	*Magmas*	51025		-4.23	-
214931_s_at	*SRPK2*	6733		-4.24	-
206613_s_at	*TAF1A*	9015	transcription	-4.27	-4.73
211815_s_at	*GGA3*	23163		-4.28	-
212531_at	*LCN2*	3934	cancer	-4.29	-
221616_s_at	*TAF9L*	51616	transcription	-4.31	-
221164_x_at	*CHST5*	23563		-4.33	-
212860_at	*ZDHHC18*	84243		-4.36	-
217715_x_at	-	-		-4.36	-38.99
219215_s_at	*SLC39A4*	55630		-4.37	-3.82
217367_s_at	*TIX1*	23051		-4.38	-
221419_s_at	-	-		-4.38	-
212398_at	*RDX*	5962		-4.38	-
203210_s_at	*RFC5*	5985	DNA repair	-4.39	-13.92
218621_at	*HEMK*	51409		-4.41	-
214918_at	*HNRPM*	4670		-4.42	-96.90
204109_s_at	*NFYA*	4800	transcription	-4.49	-21.59
212611_at	*KIAA0937*	23220		-4.57	-
208384_s_at	*MID2*	11043	transcription	-4.58	-6.08

Table S1. All significantly changed genes in DBA samples

202809_s_at	*FLJ21919*	65123		-4.59	-
210634_at	*AB026190*	27252		-4.60	-32.15
212916_at	*KIAA1111*	23133	transcription	-4.61	-
213550_s_at	*NDUFA2*	4695		-4.65	-
205194_at	*PSPH*	5723		-4.68	-
210160_at	*PAFAH1B2*	5049		-4.68	-
219583_s_at	*SPATA7*	55812		-4.74	-
214766_s_at	*AHCTF1*	25909	transcription	-4.74	-
221621_at	-	-		-4.75	-
221031_s_at	*DKFZP434F0318*	81575		-4.78	-
212567_s_at	*MAP4*	4134		-4.79	-8.05
206848_at	*HOXA7*	3204	transcription	-4.80	-
214169_at	*UNC84A*	23353		-4.80	-
207283_at	*SPTBN1*	6711		-4.80	-
205879_x_at	*RET*	5979	cancer	-4.81	-
219423_x_at	*TNFRSF25*	8718	apoptosis	-4.81	-
215023_s_at	*PEX1*	5189		-4.81	-
202009_at	*PTK9L*	11344		-4.82	-
336_at	*TBXA2R*	6915		-4.82	-
208368_s_at	*BRCA2*	675	apoptosis/transcription/cancer	-4.85	-
219048_at	*PIGN*	23556		-4.85	-26.41
208527_x_at	*HIST1H2BE*	8344		-4.86	-
218441_s_at	*DKFZP727M111*	26015		-4.87	-
213561_at	*ASF1A*	25842		-4.92	-5.24
212484_at	*SSSCA1*	10534		-4.93	-
214116_at	*BTD*	686		-4.94	-
222045_s_at	*C20orf67*	63935		-4.94	-
201602_s_at	*PPP1R12A*	4659		-4.95	-18.47
222065_s_at	*FLII*	2314		-4.95	-6.67
211781_x_at	-	-		-4.98	-
206878_at	*DAO*	1610		-4.99	-
213344_s_at	*H2AFX*	3014		-5.04	-
205037_at	*RABL4*	11020	cancer	-5.09	-
203576_at	*BCAT2*	587		-5.10	-
215492_x_at	*PTCRA*	171558		-5.12	-
201838_s_at	*STAF65(gamma)*	9913		-5.14	-14.22
211454_x_at	-	-		-5.15	-8.22
209057_x_at	*CDC5L*	988		-5.16	-
220048_at	*EDAR*	10913	apoptosis	-5.17	-
221311_x_at	*DJ122O8.2*	57226		-5.20	-
209865_at	*SLC35A3*	23443		-5.22	-
207206_s_at	*ALOX12*	239		-5.23	-
210276_s_at	*HRIHFB2122*	11078		-5.28	-
200884_at	*CKB*	1152		-5.31	-
35846_at	*THRA*	7067	transcription/cancer	-5.34	-
221960_s_at	*RAB2*	5862	cancer	-5.34	-
218958_at	*FLJ20850*	55049		-5.42	-
221788_at	*PGM3*	5238		-5.44	-
215128_at	-	-		-5.44	-10.35
212495_at	*KIAA0876*	23030	transcription	-5.45	-7.49
214469_at	*HIST1H2AE*	3012		-5.49	-
213087_s_at	*EEF1D*	1936	translation	-5.52	-

Table S1. All significantly changed genes in DBA samples

215190_at	*GA17*	10480		-5.56	-
217549_at	*HEM1*	3071		-5.58	-
204388_s_at	*MAOA*	4128		-5.60	-
201105_at	*LGALS1*	3956	apoptosis	-5.61	-
210883_x_at	*EFNB3*	1949		-5.68	-
202944_at	*NAGA*	4668		-5.69	-9.81
216205_s_at	*MFN2*	9927		-5.71	-7.41
213492_at	*COL2A1*	1280		-5.75	-
222233_s_at	*DCLRE1C*	64421		-5.82	-5.54
202912_at	*ADM*	133		-5.82	-7.32
212969_x_at	*MTA2*	256364		-5.85	-12.80
213826_s_at	*H3F3A*	3020		-5.85	-
203582_s_at	*RAB4A*	5867	cancer	-5.98	-5.70
203174_s_at	*ARFRP1*	10139		-6.00	-
206648_at	*HSPC059*	51276		-6.05	-
213297_at	*NOLA2*	55651		-6.05	-
41047_at	*C9orf16*	79095		-6.10	-
213879_at	*SMT3H2*	6613		-6.17	-
215152_at	*MYB*	4602	transcription/cancer	-6.20	-
209438_at	*PHKA2*	5256		-6.23	-63.13
209394_at	*ASMTL*	8623		-6.24	-7.21
208490_x_at	*HIST1H2BF*	8343		-6.24	-
218388_at	*PGLS*	25796		-6.26	-
201204_s_at	*RRBP1*	6238		-6.32	-
216667_at	*RNASE2*	6036		-6.33	-6.98
209972_s_at	*JTV1*	7965	translation	-6.35	-
222164_at	*FGFR1*	2260		-6.36	-67.29
206877_at	*MAD*	4084	transcription	-6.42	-
207598_x_at	*XRCC2*	7516	DNA repair	-6.54	-
212099_at	*ARHB*	388	cancer	-6.54	-
214252_s_at	*CLN5*	1203		-6.65	-14.96
217559_at	*RPL10L*	140801		-6.67	-6.25
215011_at	*CHC1*	1104		-6.67	-
201026_at	*IF2*	9669	translation	-6.68	-
216823_at	-	-		-6.68	-
219219_at	*FLJ20512*	54958		-6.74	-
202192_s_at	*GAS7*	8522	transcription	-6.78	-16.76
203945_at	*ARG2*	384		-6.80	-337.84
217672_x_at	-	350381		-6.93	-
212980_at	*AHSA2*	130872		-6.97	-6.16
209538_at	*ZNF32*	7580		-7.02	-
221155_x_at	*PRO1496*	55467		-7.11	-
211406_at	*HSPC039*	51124		-7.19	-
205653_at	*CTSG*	1511		-7.32	-12.41
207949_s_at	*ICA1*	3382		-7.47	-39.25
209383_at	*MARS*	4141	transcription	-7.55	-48.59
208579_x_at	*H2BFS*	54145		-7.76	-
57588_at	*SLC24A3*	57419		-8.03	-28.77
202112_at	*VWF*	7450		-8.21	-
203096_s_at	*PDZGEF1*	9693		-8.34	-
212952_at	*CALR*	811		-8.45	-
209369_at	*ANXA3*	306		-8.60	-

Table S1. All significantly changed genes in DBA samples

214316_x_at	*CALR*	811		-9.78	-
210098_s_at	*RARG-1*	51406		-10.24	-
209890_at	*TM4SF9*	10098		-11.06	-
209788_s_at	*ARTS-1*	51752		-12.80	-
214146_s_at	*PPBP*	5473		-15.79	-
210140_at	*CST7*	8530		-22.43	-64.81
200041_s_at	*BAT1*	7919		-	2.02
200072_s_at	*HNRPM*	4670		-	2.03
200692_s_at	*HSPA9B*	3313		-	2.12
200696_s_at	*GSN*	2934		-	-2.53
200697_at	*HK1*	3098		-	2.32
200728_at	*ACTR2*	10097		-	2.03
200739_s_at	*SUMO3*	6612		-	-2.06
200788_s_at	*PEA15*	8682	apoptosis/cancer	-	-2.00
200806_s_at	*HSPD1*	3329		-	2.15
200855_at	*NCOR1*	9611		-	-2.47
200866_s_at	*PSAP*	5660		-	2.81
200920_s_at	*BTG1*	694		-	-2.03
201228_s_at	*ARIH2*	10425		-	-2.28
201330_at	*RARS*	5917		-	2.03
201460_at	*MAPKAPK2*	9261		-	-3.04
201566_x_at	*ID2*	3398		-	-2.88
201677_at	*DC12*	56941		-	-2.72
201688_s_at	*TPD52*	7163	cancer	-	-15.02
201794_s_at	*C1orf16*	9887		-	2.01
201848_s_at	*BNIP3*	664	apoptosis	-	-3.53
201950_x_at	*CAPZB*	832		-	-2.34
202049_s_at	*ZNF262*	9202		-	-2.05
202240_at	*PLK1*	5347	cancer	-	-2.83
202450_s_at	*CTSK*	1513		-	-2.46
202459_s_at	*LPIN2*	9663		-	2.06
202466_at	*POLS*	11044	DNA repair	-	2.02
202592_at	*BLOC1S1*	2647		-	-7.13
202743_at	*PIK3R3*	8503		-	-7.91
202784_s_at	*NNT*	23530		-	-2.77
202795_x_at	*HRIHFB2122*	11078		-	-2.61
202820_at	*AHR*	196	apoptosis/transcription	-	-4.20
202894_at	*EPHB4*	2050		-	2.16
202972_s_at	*FAM13A1*	10144		-	-12.98
203179_at	*GALT*	2592		-	-3.84
203187_at	*DOCK1*	1793	apoptosis	-	-3.68
203433_at	*MTHFS*	10588		-	-3.16
203489_at	*SIVA*	10572	apoptosis	-	-3.87
203521_s_at	*ZNF318*	24149		-	2.08
203634_s_at	*CPT1A*	1374		-	-2.48
203748_x_at	*RBMS1*	5937		-	2.21
203912_s_at	*DNASE1L1*	1774		-	-2.19
203948_s_at	*MPO*	4353	apoptosis	-	-4.54
204002_s_at	*ICA1*	3382		-	-189.04
204021_s_at	*PURA*	5813	transcription	-	-2.04
204121_at	*GADD45G*	10912	apoptosis/DNA repair	-	-3.79
204160_s_at	*ENPP4*	22875		-	2.16

Table S1. All significantly changed genes in DBA samples

204174_at	*ALOX5AP*	241		-	-2.62
204203_at	*CEBPG*	1054	transcription	-	-5.99
204246_s_at	*DCTN3*	11258		-	-2.39
204361_s_at	*SCAP2*	8935		-	-4.81
204460_s_at	*RAD1*	5810	DNA repair	-	-2.12
204479_at	*OSTF1*	26578	cancer	-	-7.83
204490_s_at	*CD44*	960		-	-4.60
204578_at	*KIAA0377*	9677		-	-59.99
204862_s_at	*NME3*	4832	apoptosis	-	-2.82
204871_at	*MTERF*	7978	transcription	-	-2.36
204906_at	*RPS6KA2*	6196		-	-49.24
204978_at	*SFRS16*	11129		-	-2.88
204994_at	*MX2*	4600		-	-11.64
205072_s_at	*XRCC4*	7518	DNA repair	-	-5.98
205308_at	*CGI-62*	51101		-	-6.85
205328_at	*CLDN10*	9071		-	-3.00
205347_s_at	*TMSNB*	11013		-	-3.59
205390_s_at	*ANK1*	286		-	2.82
205396_at	*SMAD3*	25856	transcription	-	-2.93
205483_s_at	*G1P2*	9636		-	-5.90
205518_s_at	*CMAH*	8418		-	-2.72
205612_at	*MMRN1*	22915		-	-7.03
205639_at	*AOAH*	313		-	-4.12
205682_x_at	*APOM*	55937		-	-2.27
205687_at	*UBPH*	56061		-	-2.05
205726_at	*DIAPH2*	1730		-	-2.98
205750_at	*BPHL*	670		-	-2.99
205776_at	*FMO5*	2330		-	-3.68
205804_s_at	*T3JAM*	80342		-	-11.07
205904_at	*MICA*	4276		-	-2.23
206023_at	*NMU*	10874		-	2.63
206059_at	*ZNF91*	7644	transcription	-	-2.57
206431_x_at	*KIAA0676*	23061		-	-5.22
206660_at	*IGLL1*	3543		-	-3.21
206707_x_at	*C6orf32*	9750		-	-2.98
206833_s_at	*ACYP2*	98		-	-2.73
206845_s_at	*RNF40*	9810		-	2.30
206851_at	*RNASE3*	6037		-	-5.23
206871_at	*ELA2*	1991		-	-10.64
206951_at	*HIST1H4E*	8361		-	-2.17
207136_at	*ARR3*	407		-	-16.46
207266_x_at	*RBMS1*	5937		-	2.12
207394_at	*ZNF137*	7696	transcription	-	-4.32
207496_at	*MS4A2*	2206		-	-4.06
207578_s_at	*HTR4*	3360		-	-14.98
207605_x_at	*ZNF117*	51351	transcription	-	-4.32
207608_x_at	*CYP1A2*	1544		-	-4.12
207760_s_at	*NCOR2*	9612		-	2.08
207839_s_at	*C9orf127*	51754		-	-14.59
208119_s_at	*ZNF505*	81931	transcription	-	-2.92
208365_s_at	*GRK4*	2868		-	-4.50
208686_s_at	*BRD2*	6046		-	-3.29

Table S1. All significantly changed genes in DBA samples

208853_s_at	*CANX*	821		-	-2.39
208903_at	*RPS28*	256949		-	-2.08
208935_s_at	*LGALS8*	3964	cancer	-	-2.72
209158_s_at	*PSCD2*	9266		-	-2.55
209217_s_at	*WDR45*	11152		-	-3.81
209310_s_at	*CASP4*	837	apoptosis	-	-2.06
209354_at	*TNFRSF14*	8764		-	-2.92
209398_at	*HIST1H1C*	3006		-	-17.11
209463_s_at	*TAF12*	6883	transcription	-	-2.08
209464_at	*AURKB*	9212		-	-2.48
209508_x_at	*CFLAR*	8837	apoptosis	-	-3.77
209511_at	*POLR2F*	5435	transcription	-	-2.10
209571_at	*CIR*	9541	transcription	-	-2.61
209575_at	*IL10RB*	3588		-	-2.28
209731_at	*NTHL1*	4913	DNA repair	-	-4.89
209739_s_at	*PNPLA4*	8228		-	-2.10
209901_x_at	*AIF1*	199		-	-3.95
209938_at	*TADA2L*	6871	transcription	-	-4.33
209943_at	*FBXL4*	26235		-	-4.53
209975_at	*CYP2E1*	1571		-	-3.49
210224_at	*MR1*	3140		-	-3.12
210232_at	*CDC42*	998		-	-2.73
210277_at	*AP4S1*	11154		-	-2.39
210377_at	*SAH*	6296		-	-2.53
210410_s_at	*MSH5*	4439	DNA repair	-	-10.16
210423_s_at	*SLC11A1*	6556		-	-3.55
210530_s_at	*NR2C1*	7181	transcription	-	-3.15
210639_s_at	*APG5L*	9474	apoptosis	-	-5.28
210733_at	*TRAM1*	23471		-	-2.27
210758_at	*PSIP1*	11168		-	-2.70
210829_s_at	*SSBP2*	23635		-	-2.46
210912_x_at	*GSTM4*	2948		-	-3.42
211144_x_at	*TARP /// TRGV9*	6965		-	-2.07
211168_s_at	*RENT1*	5976		-	2.04
211200_s_at	*MGC12458*	84288		-	-3.47
211252_x_at	*PTCRA*	171558		-	-5.08
211260_at	*BMP7*	655		-	-13.94
211328_x_at	*HFE*	3077		-	-16.73
211439_at	*SFRS7*	6432		-	-4.48
211697_x_at	*LOC56902*	56902		-	-3.18
211743_s_at	*PRG2*	5553		-	-4.24
211833_s_at	*BAX*	581	apoptosis/cancer	-	2.71
211992_at	*PRKWNK1*	65125		-	-3.15
212014_x_at	*CD44*	960		-	-3.12
212031_at	*RBM25*	58517		-	2.00
212044_s_at	---	6157		-	-3.52
212054_x_at	*KIAA0676*	23061		-	-6.41
212178_s_at	*POM121*	9883		-	2.79
212252_at	*CAMKK2*	10645		-	-5.77
212254_s_at	*DST*	667		-	-5.28
212314_at	*KIAA0746*	23231		-	2.83
212319_at	*RUTBC1*	9905		-	-9.90

Table S1. All significantly changed genes in DBA samples

212347_x_at	*MXD4*	10608		-	-5.29
212374_at	*FEM1B*	10116		-	-2.18
212409_s_at	*LAP1B*	26092		-	-2.33
212413_at	*SEPT6*	23157		-	-2.31
212423_at	*C10orf56*	219654		-	-2.42
212451_at	*KIAA0256*	9728		-	-24.27
212481_s_at	*TPM4*	7171		-	-3.82
212528_at	*D15Wsu75e*	-		-	-22.64
212557_at	*ZNF451*	26036		-	2.29
212649_at	*TRAM1834*	54505		-	-2.85
212717_at	*PLEKHM1*	9842		-	-3.54
212858_at	*PAQR4*	9088		-	-2.35
212911_at	*KIAA0962*	23341		-	-17.22
212991_at	*FBXO9*	26268		-	-2.50
213005_s_at	*ANKRD15*	23189		-	2.00
213076_at	*ITPKC*	80271		-	-5.72
213085_s_at	*KIBRA*	23286		-	-13.11
213095_x_at	*AIF1*	199		-	-2.26
213207_s_at	*GOSR2*	9570		-	-3.32
213269_at	*ZNF248*	57209		-	-3.65
213275_x_at	*FDFT1*	1508		-	-4.74
213281_at	*JUN*	3725	apoptosis/transcription	-	-2.55
213304_at	*KIAA0423*	23116		-	-3.59
213348_at	*CDKN1C*	1028	cancer	-	-2.71
213392_at	*MGC35048*	124152		-	-69.78
213431_x_at	*SFI1*	9814		-	-10.82
213551_x_at	*RNF110*	-	transcription	-	-32.14
213554_s_at	*H41*	55573		-	-3.37
213786_at	*TAX1BP1*	8887		-	-4.07
213789_at	*TRAM2959*	10682		-	-3.50
213858_at	*ZNF647*	58500		-	-85.47
213875_x_at	*C6orf62*	81688		-	-8.89
213897_s_at	*MRPL23*	6150		-	-4.08
213907_at	*EEF1E1*	9521	translation	-	-38.07
214036_at	*TRAM3204*	-		-	-6.05
214052_x_at	*TRAM3220*	23215		-	-4.78
214056_at	*TRAM3224*	4170	apoptosis	-	-4.07
214057_at	*TRAM3225*	4170	apoptosis	-	-2.25
214144_at	*POLR2D*	5433	transcription	-	-8.44
214194_at	*KIAA1008*	79866		-	-5.27
214330_at	*ATPAF2*	91647		-	-4.28
214364_at	*MGC61716*	130916		-	-160.00
214369_s_at	*RASGRP2*	10235		-	-4.43
214395_x_at	*EEF1D*	1936	translation	-	-22.97
214501_s_at	*H2AFY*	9555		-	2.04
214594_x_at	*ATP8B1*	5205		-	-2.05
214714_at	*ZNF394*	84124	transcription	-	-3.36
214780_s_at	*MYO9B*	4650		-	-10.60
214910_s_at	*APOM*	55937		-	-2.99
215022_x_at	*ZNF11B*	7558		-	-3.76
215082_at	*ELOVL5*	60481		-	-4.11
215273_s_at	*TADA3L*	10474	transcription	-	-130.55

Table S1. All significantly changed genes in DBA samples

215450_at	*TRAM4608*	6635		-	-2.42
215471_s_at	*MAP7*	9053		-	-2.01
215476_at	*TRAM4633*	-		-	-4.31
215532_x_at	*ZNF492*	57615		-	-3.38
215582_x_at	*TRAM4739*	8888		-	-4.01
215711_s_at	*WEE1*	7465		-	-7.30
215785_s_at	*CYFIP2*	26999		-	2.62
215832_x_at	*PICALM*	8301		-	-4.84
216008_s_at	*ARIH2*	10425		-	-32.06
216042_at	*TNFRSF25*	8718	apoptosis	-	-2.84
216354_at	---	-		-	-2.17
216383_at	*RPL18A*	-		-	-3.14
216548_x_at	*HMG4L*	-		-	-3.66
216570_x_at	---	-		-	-2.68
216620_s_at	*ARHGEF10*	9639		-	-5.68
216713_at	*CCM1*	-		-	-2.41
217107_at	---	-		-	-3.40
217346_at	---	-		-	-2.00
217347_at	---	-		-	-4.19
217501_at	*CIAO1*	9391		-	-2.62
217529_at	---	54784		-	-3.51
217579_x_at	---	-		-	-2.43
217650_x_at	*ST3GAL2*	6483		-	-11.76
217693_x_at	---	-		-	-4.62
217878_s_at	*CDC27*	996		-	-21.32
218013_x_at	*DCTN4*	51164	cancer	-	-12.61
218018_at	*PDXK*	8566		-	2.45
218043_s_at	*AZI2*	64343		-	-3.56
218122_s_at	*SENP2*	59343		-	-6.84
218145_at	*TRIB3*	57761	apoptosis	-	-8.06
218156_s_at	*FLJ10534*	55720		-	2.19
218291_at	*MAPBPIP*	28956		-	-3.45
218402_s_at	*HPS4*	89781		-	2.04
218414_s_at	*NDE1*	54820		-	-4.86
218531_at	*FLJ21749*	80194		-	-4.29
218607_s_at	*SDAD1*	55153		-	2.16
218609_s_at	*NUDT2*	318		-	-5.30
218766_s_at	*WARS2*	10352		-	-3.05
218801_at	*UGCGL2*	55757		-	-7.94
219001_s_at	*MGC10765*	79269		-	-2.20
219090_at	*SLC24A3*	57419		-	-2.72
219116_s_at	*C13orf17*	55208		-	-2.17
219118_at	*FKBP11*	51303		-	-2.19
219123_at	*ZNF232*	7775	transcription	-	-2.18
219138_at	*RPL14*	9045		-	-13.80
219155_at	*PITPNC1*	26207		-	-7.23
219204_s_at	*SRR*	63826		-	-4.45
219205_at	*SRR*	63826		-	-2.51
219240_s_at	*C10orf88*	80007		-	-2.89
219267_at	*GLTP*	51228		-	-5.14
219289_at	*FLJ20718*	55027		-	-6.50
219291_at	*MDS009*	56986		-	-2.52

Table S1. All significantly changed genes in DBA samples

219303_at	*C13orf7*	79596		-	2.33
219506_at	*FLJ23221*	79630		-	-51.60
219507_at	*MGC12197*	51319		-	-4.47
219548_at	*ZNF16*	7564		-	-2.47
219563_at	*C14orf139*	79686		-	2.14
219661_at	*RANBP17*	64901		-	-3.97
219706_at	*C20orf29*	55317		-	-3.58
219708_at	*NT5M*	56953		-	-6.13
219961_s_at	*C20orf19*	55857		-	-2.65
219992_at	*TAC3*	6866		-	-22.85
220036_s_at	*LIMR*	55716		-	-6.10
220058_at	*C17orf39*	79018		-	-3.62
220157_x_at	*PLEKHA9*	51054		-	-91.07
220183_s_at	*NUDT6*	11162		-	-11.39
220202_s_at	*MNAB*	54542		-	-2.25
220215_at	*FLJ12606*	79862		-	-2.30
220310_at	*TUBAL3*	79861		-	4.71
220319_s_at	*MYLIP*	29116		-	-2.40
220329_s_at	*C6orf96*	55005		-	-5.74
220377_at	*KIAA0125*	29064		-	-2.73
220417_s_at	*THAP4*	51078		-	-7.19
220496_at	*CLEC2*	51266		-	-4.21
220721_at	*ZNF614*	80110		-	-138.70
220951_s_at	*ACF*	29974		-	-15.65
221188_s_at	*CIDEB*	27141	apoptosis	-	-2.97
221216_s_at	*SCMH1*	22955	transcription	-	-2.76
221421_s_at	*ADAMTS12*	81792		-	-76.22
221435_x_at	*HT036*	81888		-	-2.20
221579_s_at	*NUDT3*	11165		-	-5.33
221587_s_at	*C19orf24*	55009		-	-2.24
221634_at	*RPL23AP7*	118433		-	-4.20
221706_s_at	*MDS032*	55850		-	-4.30
221740_x_at	---	9884		-	-9.93
221822_at	*LOC112869*	112869		-	-4.28
221833_at	*LONP*	6477	apoptosis	-	-3.05
221877_at	---	126298		-	2.35
221897_at	*TRIM52*	84851		-	-3.98
221912_s_at	*MGC1203*	79140		-	-7.73
221934_s_at	*FLJ10496*	55152		-	-2.55
222062_at	*IL27RA*	9466		-	-11.63
222067_x_at	*HIST1H2BD*	3017		-	-5.13
222294_s_at	*EIF2C2*	5873		-	-3.07
222297_x_at	*RPL18*	6141		-	-2.10
222360_at	*CGI-30*	51611		-	-2.05
34689_at	*TREX1*	11277	DNA repair	-	-3.72
37943_at	*ZFYVE26*	23503		-	-2.47
38069_at	*CLCN7*	1186		-	-425.53
41856_at	*UNC5B*	219699		-	-3.25
43427_at	*LOC283445*	32		-	-2.58
44669_at	---	-		-	-31.22
52005_at	*WIZ*	58525		-	-3.31
62212_at	*MGC955*	79078		-	-2.64

Table S1. All significantly changed genes in DBA samples

64942_at	*GPR153*	387509		-	-3.52
65521_at	*LOC51619*	-		-	-3.94
78383_at	*TOPORS*	-		-	-2.11

Significantly changed genes in myeloid progenitors (M population) in DBA samples

Affymetrix ID	*Symbol*	LocusLink		*GFChA-f.ch	**SAM -f.ch.
209959_at	*NR4A3*	8013	transcription	15.80	-
203887_s_at	*THBD*	7056		13.71	13.06
203888_at	*THBD*	7056		7.81	-
209967_s_at	*CREM*	1390	transcription	6.97	-
209301_at	*CA2*	760		5.32	4.61
219628_at	*WIG1*	64393		4.75	5.23
203357_s_at	*CAPN7*	23473		3.62	-
214735_at	-	26034		3.61	-
204735_at	*PDE4A*	5141		3.39	-
218880_at	*FOSL2*	2355	transcription	3.37	2.91
209295_at	*TNFRSF10B*	8795	apoptosis	3.10	3.08
202955_s_at	*BIG1*	10565		3.09	-
212902_at	*SEC24A*	10802		2.86	-
209147_s_at	*PPAP2A*	8611	cancer	2.67	-
203567_s_at	*TRIM38*	10475		2.57	2.58
203821_at	*DTR*	1839		2.55	-
205076_s_at	*CRA*	10903		2.51	-
212557_at	*ZNF451*	26036		2.48	-
211833_s_at	*BAX*	581	apoptosis/cancer	2.43	-
212861_at	*MGC11308*	84975		2.34	2.31
219622_at	*RAB20*	55647	cancer	2.34	-
202466_at	*POLS*	11044	DNA repair	2.29	-
203553_s_at	*MAP4K5*	11183		2.28	-
204160_s_at	*ENPP4*	22875		2.27	2.21
204072_s_at	*13CDNA73*	10129		2.22	2.22
222118_at	*BM039*	55839		2.22	-
201776_s_at	*KIAA0494*	9813		2.19	-
208863_s_at	*SFRS1*	6426	transcription	2.18	-
207604_s_at	*SLC4A7*	9497		2.11	-
209300_s_at	*DKFZP566B183*	25977		2.10	2.10
203409_at	*DDB2*	1643	DNA repair	2.08	2.04
208630_at	*HADHA*	3030		-2.01	-
217266_at	*RPL15*	6138		-2.04	-
208970_s_at	*UROD*	7389		-2.05	-2.06
206059_at	*ZNF91*	7644	transcription	-2.06	-
214349_at	-	-		-2.08	-
200983_x_at	*CD59*	966		-2.10	-
218572_at	*C14orf123*	29082		-2.13	-
212781_at	*RBBP6*	5930		-2.16	-
204559_s_at	*LSM7*	51690		-2.18	-
214527_s_at	*PQBP1*	10084		-2.20	-
203582_s_at	*RAB4A*	5867	cancer	-2.22	-
211698_at	*CRI1*	23741		-2.23	-2.23
220494_s_at	*C14orf117*	55516		-2.25	-
212605_s_at	-	11165		-2.31	-
220319_s_at	*MIR*	29116		-2.31	-

Table S1. All significantly changed genes in DBA samples

208646_at	*RPS14*	6208		-2.32	-2.31
202343_x_at	*COX5B*	1329		-2.33	-
201844_s_at	*RYBP*	23429		-2.35	-
203551_s_at	*COX11*	1353		-2.36	-2.33
221831_at	*KIAA0601*	23028		-2.44	-
209739_s_at	*DXS1283E*	8228		-2.45	-
200003_s_at	*RPL28*	6158		-2.45	-2.41
200658_s_at	*PHB*	5245	cancer	-2.48	-
213786_at	*TAX1BP1*	8887		-2.53	-
211025_x_at	*COX5B*	1329		-2.65	-
204246_s_at	*DCTN3*	11258		-2.65	-
214321_at	*NOV*	4856		-2.68	-
219762_s_at	*RPL36*	25873		-2.82	-2.79
220375_s_at	*H2AFY*	9555		-2.88	-
208851_s_at	*THY1*	7070		-3.17	-
213897_s_at	*MRPL23*	6150		-3.74	-
212884_x_at	*APOE*	348		-5.46	-
201228_s_at	*ARIH2*	10425		-5.77	-
217559_at	*RPL10L*	140801		-9.19	-7.53
220646_s_at	*KLRF1*	51348		-10.52	-
202545_at	*PRKCD*	5580		-	3.72
211405_x_at	*IFNA17*	3451		-	-2.91
212271_at	*MAPK1*	5594	apoptosis	-	2.02
212955_s_at	*POLR2I*	5438	transcription	-	-2.03
213385_at	*CHN2*	1124		-	2.98
219076_s_at	*PXMP2*	5827		-	-2.01
219678_x_at	*DCLRE1C*	64421		-	-2.06
220395_at	*DNAJA4*	55466		-	2.24

GO molecular function* - Gene Ontology molecular function is only indicated if the gene is annotated to: apotosis, transcription, translation, cancer and DNA repair categories
****GFChA - f.ch.** - Geometric Fold Change Analysis- fold change
*****SAM - f.ch.**- Significance Analysis of Microarrays- fold change

Supplemental Material.

Table S2. Twenty-nine significantly changed genes in two or more cell types in DBA samples.

				Fold Changes					
				P population		E population		M population	
Affymetrix ID	**Symbol**	**LocusLink**	**GO molecular function***	****G-f.ch.**	*****SAM -f.ch.**	**G-f.ch.**	**SAM -f.ch.**	**G-f.ch.**	**SAM -f.ch.**
211833_s_at	*BAX*	581	apoptosis/cancer	3.49	3.32	-	2.71	2.43	-
213786_at	*TAX1BP1*	8887		-2.77	-2.83	-	-4.07	-2.53	-
209739_s_at	*DXS1283E*	8228		-5.54	-	-	-2.10	-2.45	-2.41
201089_at	*ATP6V1B2*	526		2.25	2.24	2.37	2.29	-	-
218607_s_at	*FLJ10498*	55153		2.21	2.16	-	2.16	-	-
221553_at	*DKFZp564K142*	84061		-2.12	-	-3.22	-3.08	-	-
205347_s_at	*TMSNB*	11013		-2.20	-	-	-3.59	-	-
222297_x_at	*RPL18*	6141		-2.27	-	-	-2.10	-	-
208368_s_at	*BRCA2*	675	apoptosis/transcription/cancer	-2.59	-	-4.85	-	-	-
218609_s_at	*NUDT2*	318		-2.85	-	-	-5.30	-	-
219583_s_at	*SPATA7*	55812		-	-2.48	-4.74	-	-	-
209295_at	*TNFRSF10B*	8795	apoptosis	-	-	10.11	6.24	3.10	3.08
203567_s_at	*TRIM38*	10475		-	-	2.24	2.04	2.57	2.58
212557_at	*ZNF451*	26036		-	-	-	2.29	2.48	-
202466_at	*POLS*	11044	DNA repair	-	-	-	2.02	2.29	-
204160_s_at	*ENPP4*	22875		-	-	-	2.16	2.27	2.21
203409_at	*DDB2*	1643	DNA repair	-	-	3.73	3.56	2.08	2.04
206059_at	*ZNF91*	7644	transcription	-	-	-	-2.57	-2.06	-
203582_s_at	*RAB4A*	5867	cancer	-	-	-5.98	-5.70	-2.22	-
220494_s_at	*C14orf117*	55516		-	-	-4.13	-4.27	-2.25	-
220319_s_at	*MYLIP*	29116		-	-	-	-2.40	-2.31	-
200003_s_at	*RPL28*	6158		-	-	-2.07	-2.12	-2.45	-2.41
204246_s_at	*DCTN3*	11258		-	-	-	-2.39	-2.65	-
213897_s_at	*MRPL23*	6150		-	-	-	-4.08	-3.74	-
201228_s_at	*ARIH2*	10425		-	-	-	-2.28	-5.77	-
217559_at	*RPL10L*	140801		-	-	-6.67	-6.25	-9.19	-7.53
209967_s_at	*CREM*	1390	transcription	7.48	6.16	-	-	6.97	-
219762_s_at	*RPL36*	25873		-2.46	-	-	-	-2.82	-2.79
219076_s_at	*PXMP2*	5827		-	-2.53	-	-	-	-2.01

GO molecular function* - Gene Ontology molecular function is only indicated if the gene is annotated to: apotosis, transcription, translation, cancer and DNA repair categories

****G - f.ch.** - Geometric Fold Change Analysis- fold change

*****SAM - f.ch.**- Significance Analysis of Microarrays- fold change

Table S3. Supplemental Material. Expression of MYB RNA related to GAPDH in three BM subsets in diseased and control samples.

BM cell population	Sample ID	MYB Average C_T	GAPDH Average C_T	ΔC_T MYB-GAPDH	$\Delta\Delta C_T$ (ΔC_T-$\Delta C_{T,C}$)	MYB Rel. to GAPDH ($2^{-\Delta\Delta CT}$)
P	(C1-C4)	26.56±0.25	23.69±0.27	2.87±0.37	0.00±0.37	1.00 (0.78-1.29)
	D1	29.84±0.27	26.62±0.41	3.22±0.49	0.35±0.61	0.78 (0.51-1.20)
	D2	27.53±0.02	25.54±0.26	1.99±0.26	-0.88±0.45	1.84 (1.35-2.52)
	D3	23.26±0.12	19.56±0.32	3.70±0.34	0.83±0.50	0.56 (0.40-0.80)
E	(C1-C4)	25.57±0.50	23.26±0.39	2.31±0.63	0.00±0.63	1.00 (0.64-1.55)
	D1	29.09±0.07	24.91±0.12	4.18±0.14	1.88±0.65	0.27 (0.17-0.43)
	D2	33.32±0.04	28.69±0.07	4.63±0.08	2.32±0.64	0.20 (0.13-0.31)
	D3	22.89±0.12	18.62±0.05	4.27±0.51	1.97±0.81	0.26 (0.15-0.45)
M	(C1-C3)	25.60±0.25	21.54±0.13	4.06±0.28	0.00±0.28	1.00 (0.82-1.21)
	D2	26.15±0.10	22.40±0.11	3.76±0.15	-0.30±0.32	1.23 (0.99-1.53)
	D3	27.62±0.22	23.59±0.18	4.04±0.29	-0.02±0.40	1.01 (0.77-1.34)

C – Control samples, D1 – diseased # 1, D2 – diseased # 2, D3 – diseased # 3, P – multipotential progenitors, E – erythroid progenitors, M – myeloid progenitors; C_T - number of cycles; $C_{T,C}$ - number of control cycles

Table S4. Supplemental Material. Expression of TNFRSF10B related to GAPDH in three BM subsets in diseased and control samples.

BM cell population	Sample ID	TNFRSF10B Average C_T	GAPDH Average C_T	ΔC_T TNFRSF10B-GAPDH	$\Delta\Delta C_T$ (ΔC_T-$\Delta C_{T,C}$)	TNFRSF10B Rel. to GAPDH ($2^{-\Delta\Delta CT}$)
P	(C1-C4)	35.40	23.64	11.76	0.00	1.00
	D1	38.04	26.87	11.17	-0.59	1.41
	D2	34.76	23.31	11.45	-0.31	1.69
	D3	32.11	19.74	12.37	0.61	0.65
E	(C1-C4)	34.21	21.07	13.13	0.00	1.00
	D1	34.58	24.85	9.73	-3.40	10.55
	D3	29.98	19.92	10.06	-3.07	8.39
M	(C1-C3)	33.16	19.86	13.30	0.00	1.00
	D2	33.88	22.59	11.29	-2.01	4.02
	D3	35.62	23.55	12.07	-1.23	2.34

C – Control samples, D1 – diseased # 1, D2 – diseased # 2, D3 – diseased # 3, P – multipotential progenitors, E – erythroid progenitors, M – myeloid progenitors; C_T - number of cycles; $C_{T,C}$ - number of control cycles

Table S5. Supplemental Material. Expression of TNFRSF6 related to GAPDH in three BM subsets in diseased and control samples.

BM cell population	Sample ID	TNFRSF6 Average C_T	GAPDH Average C_T	ΔC_T TNFRSF6-GAPDH	$\Delta\Delta C_T$ (ΔC_T-$\Delta C_{T,C}$)	TNFRSF6 Rel. to GAPDH ($2^{-\Delta\Delta CT}$)
P	(C1-C4)	33.67	21.95	11.71	0.00	1.00
	D2	35.02	23.48	11.54	-0.17	1.12
	D3	31.55	20.01	11.54	-0.17	1.12
E	(C1-C4)	31.89	20.91	10.98	0.00	1.00
	D1	34.17	24.77	9.40	-1.58	2.98
	D2	37.79	28.90	8.89	-2.09	4.25
	D3	30.39	21.15	9.24	-1.74	3.34
M	(C1-C3)	32.88	21.90	10.98	0.00	1.00
	D2	33.10	22.69	10.41	-0.57	1.48
	D3	33.44	23.07	10.37	-0.61	1.52

C – Control samples, D1 – diseased # 1, D2 – diseased # 2, D3 – diseased # 3, P – multipotential progenitors, E – erythroid progenitors, M – myeloid progenitors; C_T - number of cycles; $C_{T,C}$ - number of control cycles

Table S6. Supplemental Material. Expression of RPL18 RNA related to GAPDH in three BM subsets in diseased and control samples.

BM cell population	Sample ID	RPL18 Average C_T	GAPDH Average C_T	ΔC_T RPL18-GAPDH	$\Delta\Delta C_T$ (ΔC_T-$\Delta C_{T,C}$)	RPL18 Rel. to GAPDH ($2^{-\Delta\Delta CT}$)
P	(C1-C4)	27.39	24.09	3.30	0.00	1.00
	D1	29.09	25.16	3.93	0.63	0.65
	D2	27.94	23.76	4.18	0.88	0.54
	D3	23.85	19.13	4.72	1.42	0.37
E	(C1-C4)	26.96	22.95	4.02	0.00	1.00
	D1	27.41	22.22	5.19	1.17	0.44
	D2	33.13	28.31	4.82	0.80	0.57
	D3	24.21	18.78	5.43	1.41	0.38
M	(C1-C3)	26.15	21.63	4.52	0.00	1.00
	D2	26.12	22.02	4.10	-0.42	0.75
	D3	30.25	25.29	4.96	0.44	1.35

C – Control samples, D1 – diseased # 1, D2 – diseased # 2, D3 – diseased # 3, P – multipotential progenitors, E – erythroid progenitors, M – myeloid progenitors; C_T - number of cycles; $C_{T,C}$ - number of control cycles

Table S7. Supplemental Material. Expression of RPS19 RNA related to GAPDH in three BM subsets in diseased and control samples.

BM cell population	**Sample ID**	**RPS19 Average C_T**	**GAPDH Average C_T**	**ΔC_T RPS19-GAPDH**	**$\Delta\Delta C_T$ (ΔC_T-$\Delta C_{T,C}$)**	**RPS19 Rel. to GAPDH ($2^{-\Delta\Delta CT}$)**
P	(C1-C4)	20.92	22.80	-1.88	0.00	1.00
	D2	19.40	21.33	-1.93	-0.05	1.03
	D3	19.29	21.55	-2.26	-0.31	1.23
E	(C1-C4)	18.55	20.16	-1.61	0.00	1.00
	D2	17.46	19.41	-1.95	0.33	1.25
	D3	19.22	20.92	-1.70	0.10	1.07
M	(C1-C4)	18.66	19.91	-1.33	0.00	1.00
	D2	18.71	21.51	-2.80	-1.47	2.77
	D3	20.11	22.68	-2.57	-1.24	2.36

C – Control samples, D2 – diseased # 2, D3 – diseased # 3, P – multipotential progenitors, E – erythroid progenitors, M – myeloid progenitors; C_T - number of cycles; $C_{T,C}$ - number of control cycles

Fig. S1 (Supplemental Material)

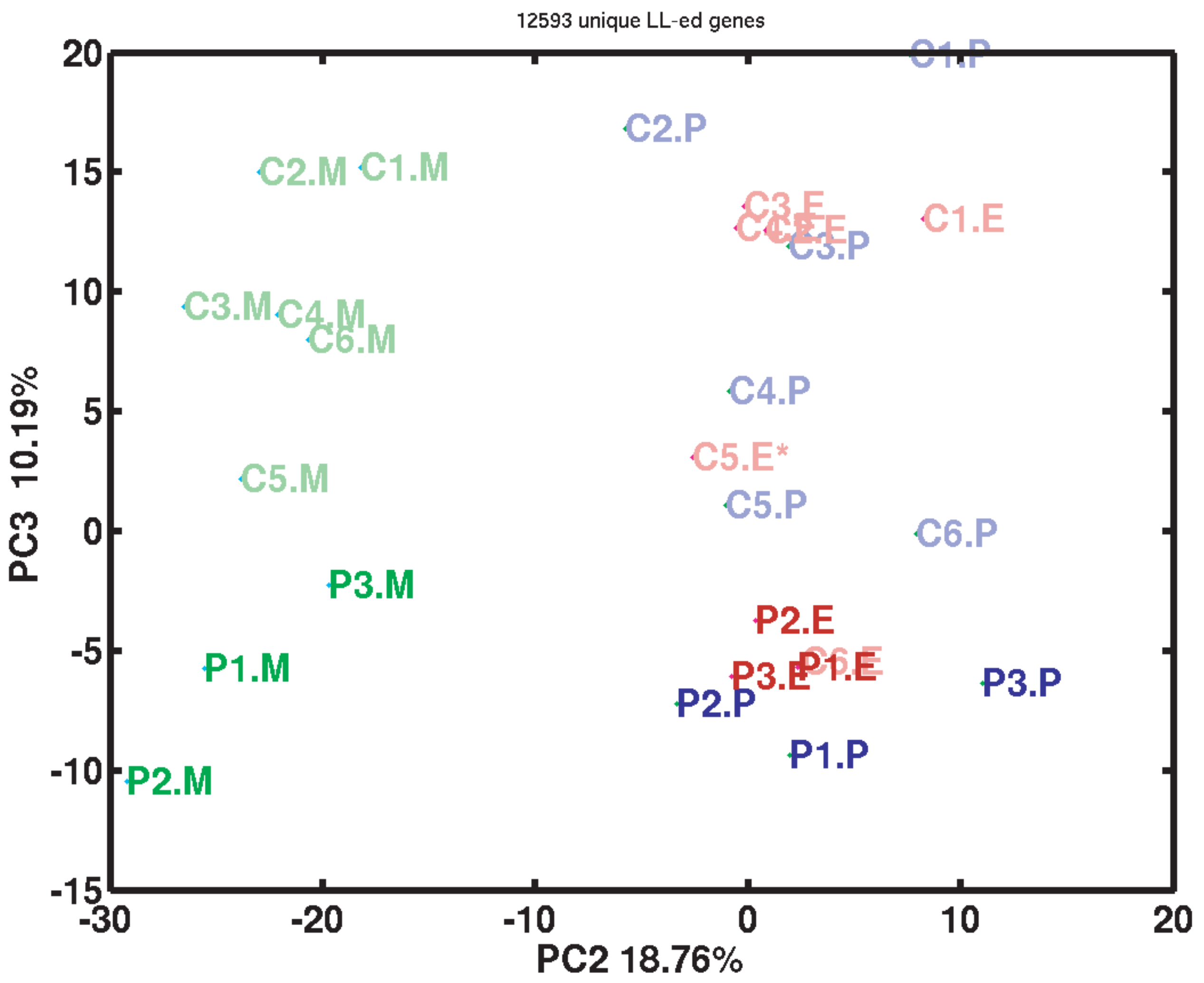

Fig. S2 (Supplemental Material)

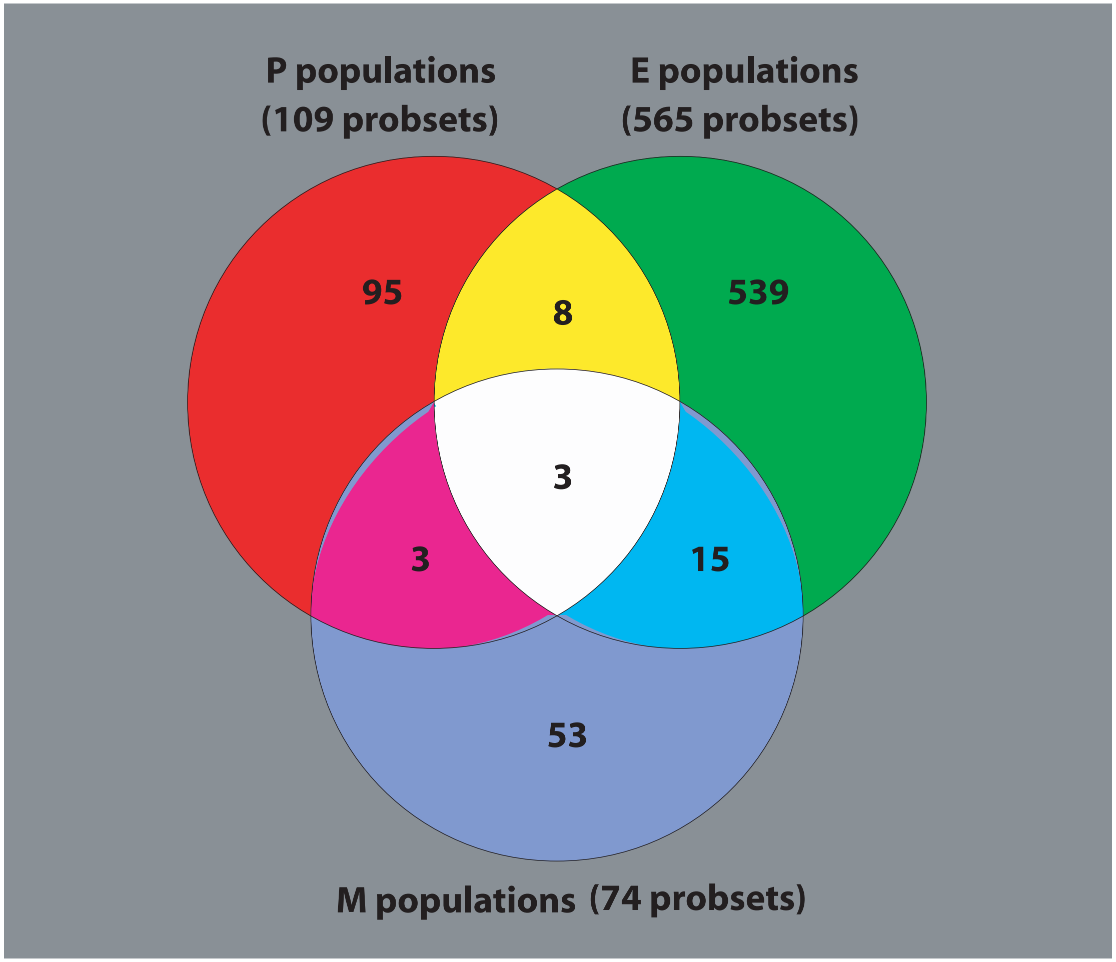

Figure Legend (Supplemental Material)

Fig. S1. PC3 performed on 12,593 genes (with LocusLink ID) and 27 samples clearly distinguished the diseased and control three cell populations P, E, and M. Blue color indicates P population, light blue - control samples (C1-C6), dark blue – diseased samples (D1-D3) samples; red color shows E population, light red - control samples, dark red – diseased samples; green color shows M population, light green - control samples, dark green - diseased samples. B)

Fig. S2. The overlap between the significantly changed genes in the P, E an M diseased BM populations.