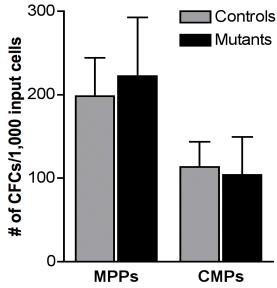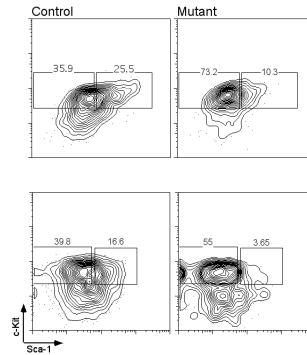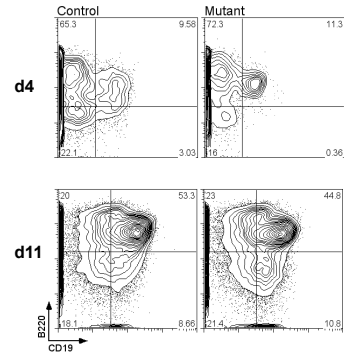# Ficara_Figure S1

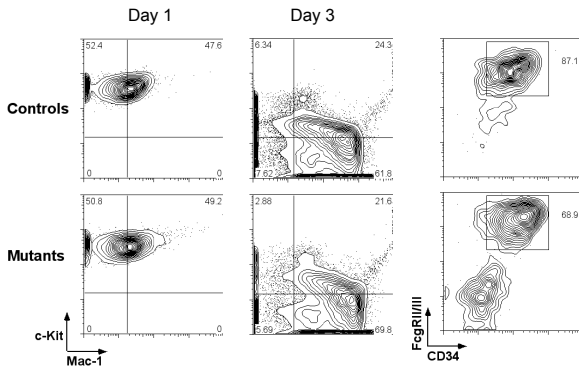**A** Methylcellulose colony assay

B Time-course FACS analysis on cultured MPPs
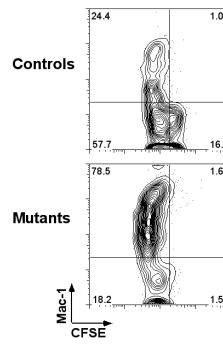

C In vitro B-cell differentiation from LMPPs

D GMPs - Time-course FACS analysis upon liquid culture

E CMPs two days after labelling with CFSE

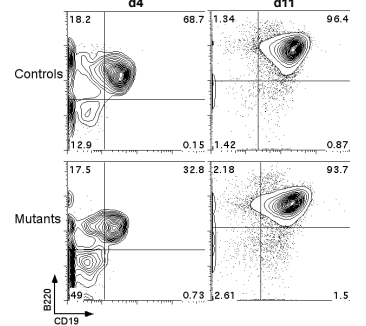**F** In vitro B-cell differentiation from CLPs

Figure S1. Differentiation of Pbx1-null progenitors. (A) Total number of colonies scored 7-9 days after plating prospectively isolated MPPs or CMPs, respectively, in methylcellulose. (B) Contour plots are referred to the Mac1-Gr1- gate shown in Fig. 2B (representative of two). (C) 1,000 prospectively isolated LMPPs (LKSFh) from control or mutant mice were seeded on GFP+ OP9 stromal cell layers and their progeny analyzed by FACS four or eleven days later for the presence of B cell markers. Representative contour plots are referred to the hematopoietic gate (stromal cells were excluded based on light scatter characteristics and GFP expression). (D) FACS analysis is shown for the progeny of GMPs prospectively isolated from control or mutant mice (representative of two). Dot plots on the right are relative to the cKit+Mac1- gate at day 3, showing a higher proportion of Pbx1-null cells lacking the GMP immunophenotype compared to control cells. (E) FACS analysis (representative of two) is shown for the progeny of control or mutant CMPs two days after sorting and labeling with CFSE. (F) Prospectively isolated CLPs from control or mutant mice were seeded on OP9 stromal cells as described in (C).

Ficara_Figure S2

A

B

C
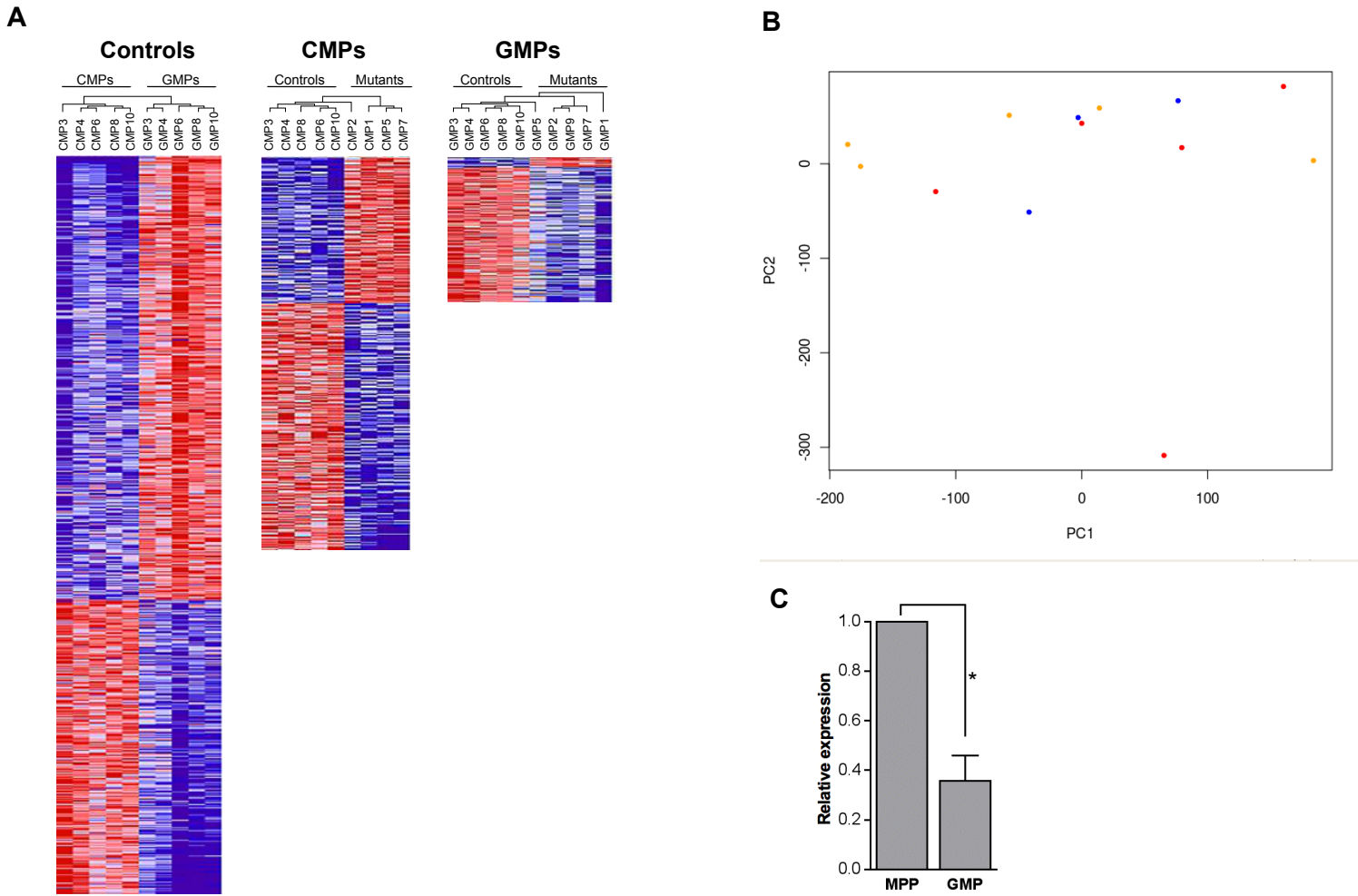
Figure S2. Gene expression profiles of CMPs and GMPs from control or Pbx1-null mice. (A) Heat maps show the expression of the CMP-to-GMP transition in control mice (left), and of Pbx1-regulated genes in CMPs (middle) and in GMPs (right) from control or mutant individual mice. Up-regulated and down-regulated genes are displayed in red and blue, respectively. (B) PCA analysis of control CMPs and GMPs (red and orange, respectively), and of Pbx1-null CMPs (blue). (C) The histogram shows Pbx1 transcript levels relative to MPPs as measured by real-time PCR (four biological replicates, each performed in duplicate; *p<0.01).

Ficara_Figure S3

A

CMP transcripts

(y-axis, top to bottom)
Response to drug
Helicase activity
Wound healing
Protein phosphatase
Protein kinase activity
Enzyme binding
Organ development
Chromatin binding
DNA binding
mRNA binding
Microtubule
Tgfb-receptor signaling
Regulation of cell cycle
Nucleotide excision repair
Protein N-terminus binding
Jak/Stat cascade
Actin cytoskeleton
Nuclear transport
Transcription
Hydrolase activity
RNA catabolic process

x-axis: Core enrichment size (0, 30, 60, 90, 120, 150)

C

Transcripts down-regulated in Pbx1-null CMPs

(y-axis, top to bottom)
G-protein coupled receptor
Protein domain-specific
Rhodopsin-like receptor
Receptor complex
Protein kinase activity
Cell activation
Lymphocyte differentiation
Molecular adaptor activity
Negative regulation of growth
Regulation of translational
Regulation of cellular
Protein dimerization activity
Homeostasis of number of
Signal transduction
Regulation of apoptosis
Regulation of metabolic
Behavior
Regulation of catalitic activity
C-AMP mediated signaling
Neuron differentiation
Chromosome
Positive regulation of binding
Cell development
Regulation of cell proliferation
Enzyme inhibitory activity
Negative regulation of cell
Enzyme binding
Cell-cell signaling
Jak/Stat cascade
Transmembrane receptor
Wound healing
Actin cytoskeleton
Organ development
DNA binding
Transcription
Tgfb-receptor signaling
Regulation of cell cycle

x-axis: Core enrichment size (0, 90, 180, 270)

B

GMP transcripts

(y-axis, top to bottom)
Cell surface
Vesicular fraction
Inflammatory response
Ion or cation transport
ER-Golgi intermediate compartment
Extracellular region
Oxidoreductase activity
Vescicle
Endoplasmic reticulum
Secretion
Cation binding
Membrane
Isomerase activity
Transferase activity
Lipid metabolic process
Vacuole
Peroxisome
Integral to orgalelle membrane
Peptidase activity
Cellular component disassembly
Organic acid metabolic process
Golgi apparatus
Gated channel activity
Cell-cell signaling
Hydrolase activity
Cofactor metabolic process
Alcohol metabolic process
Cytoplasmic part
Immune system process
Response ti biotic stimulus
Carbohydrate metabolic process

x-axis: Core enrichment size (0, 90, 180, 270)

D

Transcripts up-regulated in Pbx1-null CMPs

(y-axis, top to bottom)
Mitochondion
Lipoprotein biosyntetic process
Ribosome
Generation of precursor metabolites
Oxidoreductase activity
Transferase activity
Cofactor metabolic process
Ion or cation transport
Cellular component disassembly
Vesicular fraction
Cell surface
ER-Golgi intermediate compartment
Alcohol metabolic process
Inflammatory response

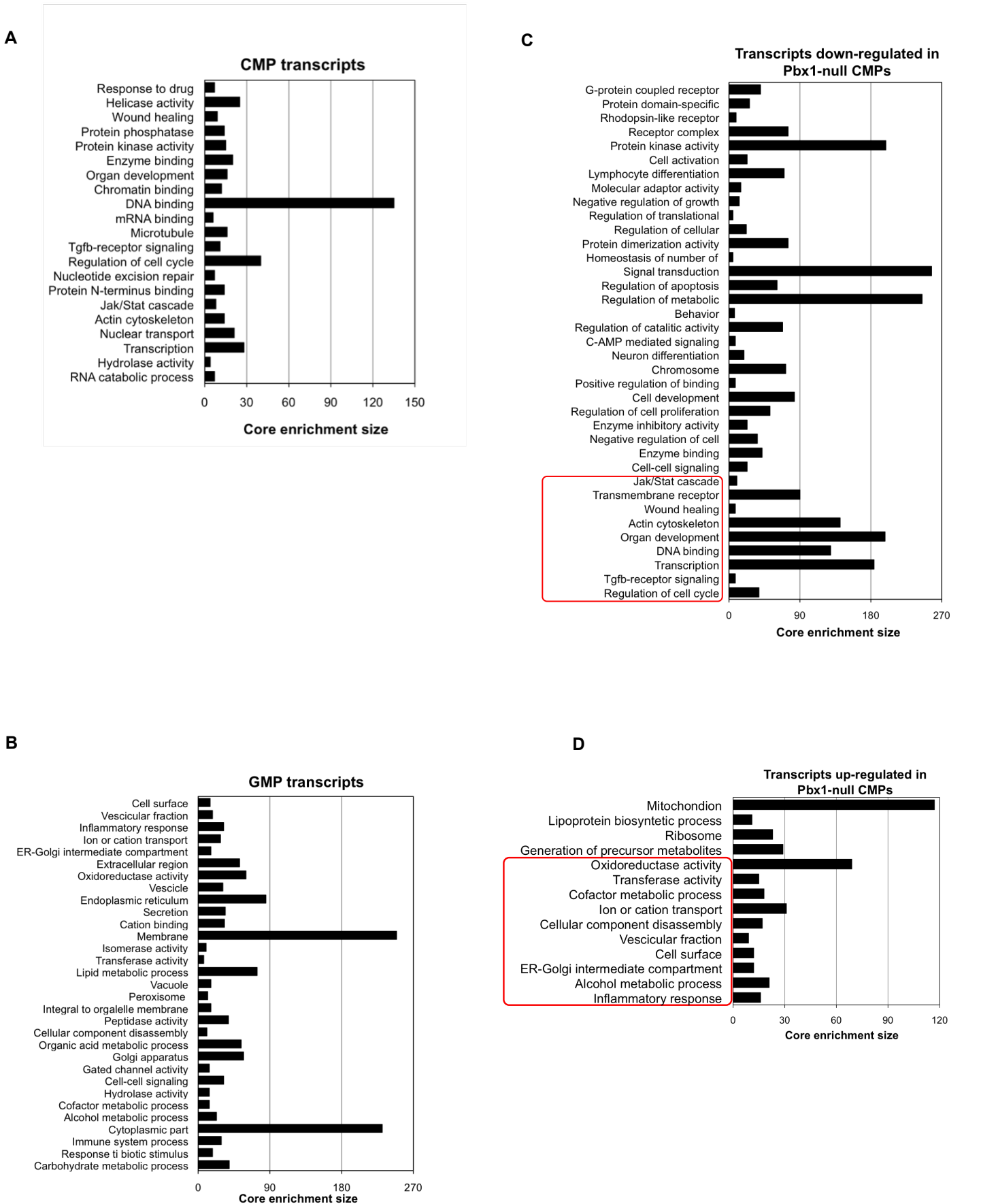x-axis: Core enrichment size (0, 30, 60, 90, 120)

Figure S3. GO analysis. The distribution into GO groups is shown for (A) normal CMP transcripts (= down-regulated in control GMPs compared to control CMPs), (B) normal GMP transcripts (= up-regulated in control GMPs compared to control CMPs), (C) transcripts down-regulated in Pbx1-null CMPs compared to control CMPs, (D) transcripts up-regulated in Pbx1-null CMPs compared to control CMPs, as determined by GSEA. Bars indicate the number of leading edge transcripts (core enrichment size) belonging to each functional group. GO groups with FDR q-value ≤0.23 and Nominal p-value ≤0.05 were considered significantly enriched. GO annotations highlighted in red in C, D represent GO groups in common with those in A and B, respectively.
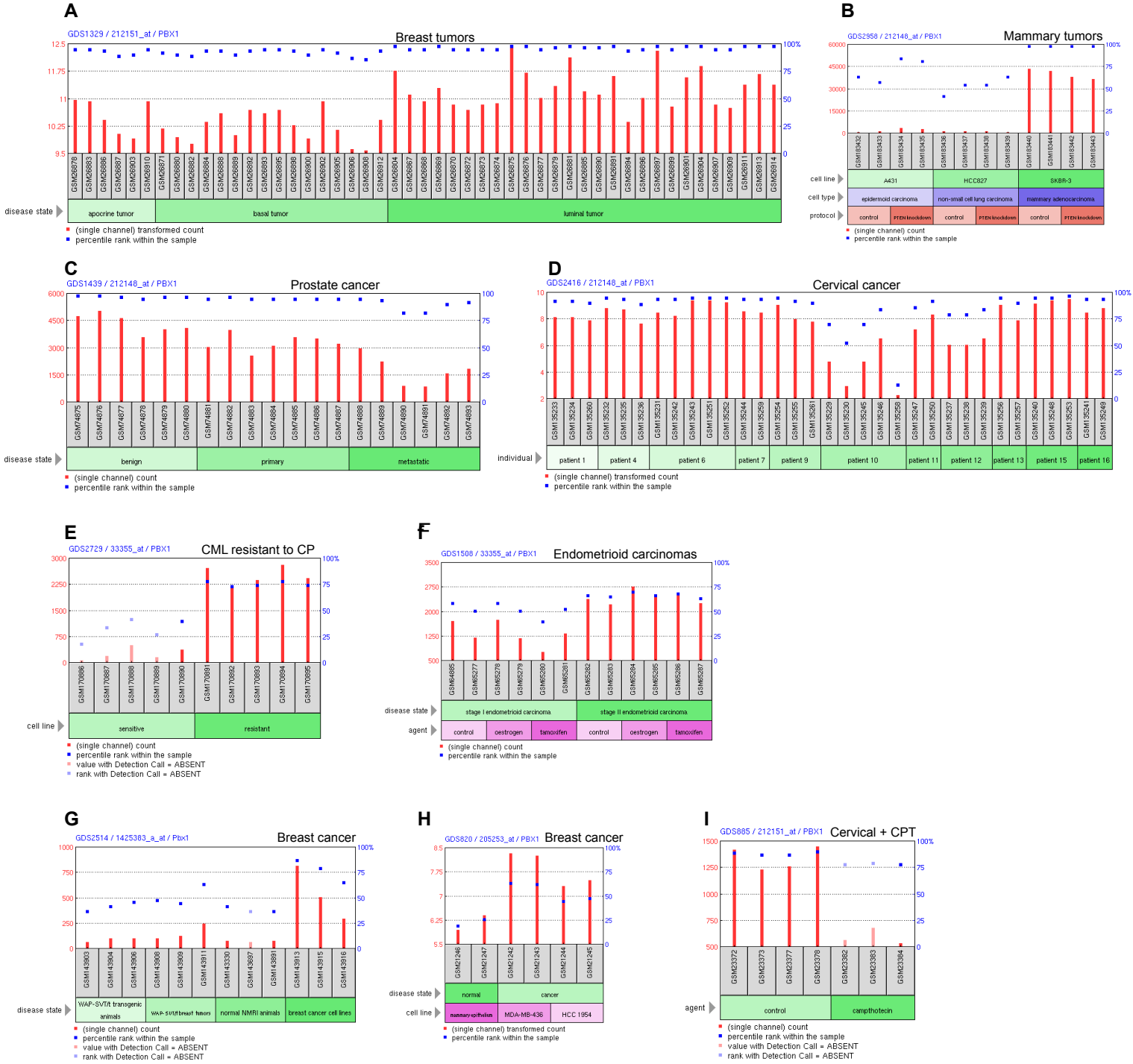
Ficara_Figure S4

Figure S4. Pbx1 expression in cancer cells within the GEO dataset. The images represent the abundance profile for Pbx1 across each Sample in a DataSet. GEO accession numbers are in the top left corner of each profile. (A) Analysis of tumors of 49 breast cancer patients. Tumors classified into luminal, basal, and molecular apocrine classes. Apocrine tumors are estrogen receptor negative (ER-) and androgen receptor positive (AR+), while luminal tumors are ER+ and AR+, and basal tumors are ER- and AR-. (B) Analysis of carcinoma cell lines depleted for the tumor suppressor PTEN, showing that Pbx1 is expressed in mammary adenocarcinoma. (C) Expression profiling of prostate cancer tumors that are benign, clinically localized, or metastatic and refractory to hormones. (D) Analysis of 33 biopsies from 11 cervical cancer patients. Biopsies were obtained from different areas of each tumor. (E) Analysis of chronic myelogenous leukemia (CML) cells resistant to cyclophosphamide (CP), an alkylating anticancer drug. (F) Analysis of endometrial epithelial cells from stage I or II endometrioid carcinomas after treatment with oestrogen or tamoxifen. (G) Analysis of mammary gland segments from WAP–SVT/t transgenic animals. These animals selectively synthesize the SV40 T/t antigen in mammary gland epithelial cells and develop breast cancer after the first lactation. (H) Expression profiling of breast cancer cell lines in reference to mammary epithelial cells. (I) HeLa tumor cells treated with 10 mM topoisomerase poison camptothecin (CPT) for 8 hours.
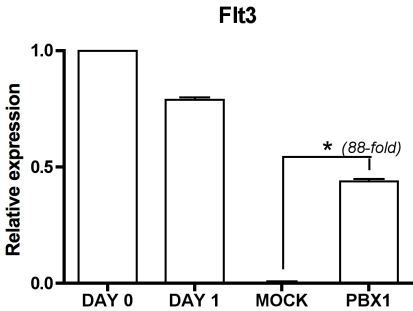
Figure S5. Flt3 expression level from the experiment described in Fig. 6B. *p=0.0007.

Table S1. CMP to GMP transition gene signature in control mice.

Genes up-regulated in GMPs compared to CMPs (= GMP gene signature)

Probe Set	Gene Symbol	CMPs					GMPs					Av Cont	Av Mut	Fold Diff	q-value(%)
		CMP3	CMP4	CMP6	CMP8	CMP10	GMP3	GMP4	GMP6	GMP8	GMP10				
1449846_at	Ear2	86.67	69.24	60	73.64	60	1855	7024	20000	10883	12871.2	69.91	10526.6	150.57	6.981670997
1422411_s_at	Ear1 /// Ear12 /// Ear2 /// Ear3	70.9	71.91	60	60	60	1856	11815	16104	9478	7965.49	64.562	9443.79	146.27	4.305363781
1422873_at	Prg2	60	173.2	60	60	60	7242	13836	8674.2	12344	8865.6	82.646	10192.4	123.33	0
1449136_at	Epx	60	60	60	60	60	1855	2766	4885.8	4949	4717.1	60	3834.63	63.91	1.132990469
1449924_at	Prg3	60	144	60	80.26	127.69	586.4	1573	2210.6	2620	2920.55	94.38	1982.23	21.00	2.81898819
1448620_at	Fcgr3	140.2	485.6	484.1	289.3	388.79	2367	2602	2191	2894	2491.7	357.586	2509.24	7.02	0
1454713_s_at	Hdc	580.9	1044	988.6	1169	800.59	5313	4807	5963.6	4744	6095.63	916.774	5384.7	5.87	0
1435749_at	Gda	526.9	899.6	397.8	420	153.38	1359	1291	4618.9	2734	3206.71	479.526	2641.98	5.51	6.981670997
1434510_at	Papss2	131	214.1	338.9	120.3	106.6	1164	789.2	900.17	966.5	832.34	182.188	930.338	5.11	0
1417389_at	Gpc1	103.6	239.6	259.9	103.2	92.56	385.8	451.2	1301.1	772.9	897	159.776	761.592	4.77	5.986067289
1438511_a_at	1190002H23Rik	504.4	695.9	558.6	486.7	243.03	1200	1651	3756.9	2120	2513.29	497.72	2248.31	4.52	4.305363781
1449184_at	Pglyrp1	60	158.9	173.5	131.6	85.44	211.6	323.4	942.82	669.6	603.8	121.888	550.232	4.51	8.934207489
1420572_at	Ms4a3	757.6	6415	4536	1656	1279.78	11740	11834	16868	12903	11569	2928.85	12982.9	4.43	0
1428781_at	Dmkn	60	165.2	163.3	66.4	60	389.7	406.6	781.98	345.1	292.94	102.984	443.244	4.30	5.876757684
1448330_at	Gstm1	252.2	1074	753.5	404.3	378.88	1724	2344	3438.3	2512	2146.32	572.632	2432.86	4.25	1.132990469
1415897_a_at	Mgst1	320.5	627.5	847.7	568.6	426.84	1560	1809	2683.5	3102	2437.77	558.228	2318.39	4.15	1.132990469
1460271_at	Trem3	180.9	777.4	826	395.2	281.4	1136	1482	3053.2	2618	1879.36	492.174	2033.67	4.13	3.863788009
1451796_s_at	Hdc	60	541.6	466	341.4	269.32	2414	1806	688.78	1160	831.73	335.664	1380.16	4.11	9.872171728
1418003_at	1190002H23Rik	111.4	386.8	219.3	102.7	104.86	973	637.6	744.81	599	597.21	185.018	710.304	3.84	1.132990469
1417679_at	Gfi1	122	430.3	546.3	333.4	301.13	809.8	849	2158.6	1364	1423.93	346.612	1321.07	3.81	5.118264635
1416416_x_at	Gstm1	856.9	3365	2246	1222	1110.41	7103	6240	8179.1	6086	5879.95	1759.88	6697.58	3.81	0
1418920_at	Cldn15	141.9	245.6	319.7	118.5	114.07	539.6	426.7	969.24	838.7	581.53	187.954	671.164	3.57	2.918890699
1418937_at	Dio2	206.3	566.8	381.7	220	181	1050	881.9	1543.8	947.8	1101.59	311.14	1105.08	3.55	1.132990469
1423954_at	C3	86.91	225.5	184.2	72.24	60.54	447.2	370.4	600.95	504.1	273.21	125.876	439.152	3.49	2.226912301
1416183_a_at	Ldhb	298.1	552.5	577.7	422.6	571.81	1001	998	2171.5	2022	1827.57	484.538	1604.06	3.31	3.376755907
1448881_at	Hp	1017	2504	2696	1880	1072.38	7945	5182	6202.7	5895	4766.98	1833.9	5998.56	3.27	0
1441930_x_at	Vat1	1385	1562	593	2444	822.25	1903	5045	4564	4572	5936.61	1361.21	4403.93	3.24	3.863788009
1425627_x_at	Gstm1	138.9	354.7	340	373.7	353.72	456.6	789.6	1722.3	907	1105.85	312.198	996.266	3.19	8.934207489
1421571_a_at	LOC100041546 /// LOC10004	1473	7528	10068	2567	3220.99	11280	15021	20000	17183	14206.3	4971.58	15538.2	3.13	2.226912301
1429189_at	Arsb	421.9	1114	1569	791.7	1030.18	2374	2762	3866.8	3791	2565.66	985.368	3071.75	3.12	1.132990469
1448237_x_at	Ldhb	346.3	425.7	481.3	466.6	372.15	636.8	630.6	1794.7	1491	1833.14	418.398	1277.23	3.05	8.934207489
1455235_x_at	Ldhb	475.6	461.9	585.3	479.5	447.19	811	838.8	2129.3	1569	1954	489.888	1460.37	2.98	5.986067289
1421408_at	Igsf6	123.4	513.9	622.6	318.6	248.81	1043	1059	1010.2	1241	1084.93	365.458	1087.69	2.98	0
1458703_at	---	61.65	102.4	69.67	65.63	60.97	117	108.5	338.99	208.8	298.48	72.06	214.356	2.97	11.33922971
1451858_at	LOC668727 /// Mrgpra2	60	160.1	248	112.8	214.09	496.8	293	623.99	395.4	540.34	158.99	469.914	2.96	2.460207875
1439651_at	---	102.6	104.1	111.6	153.7	129.74	285.8	232.3	314.9	319.3	603.68	120.35	351.186	2.92	6.981670997
1417542_at	Rps6ka2	238.4	590.1	423.9	572.2	293.62	644.4	817.5	2072.7	1100	1517.77	423.664	1230.43	2.90	9.872171728

Table S1. CMP to GMP transition gene signature in control mice.

Genes up-regulated in GMPs compared to CMPs (= GMP gene signature)

Probe Set	Gene Symbol	CMPs					GMPs					Av Cont	Av Mut	Fold Diff	q-value(%)
		CMP3	CMP4	CMP6	CMP8	CMP10	GMP3	GMP4	GMP6	GMP8	GMP10				
1448213_at	Anxa1	1433	3431	5578	3133	3482.01	9200	10756	9683.8	11773	7897.04	3411.43	9861.9	2.89	0
1429146_at	6620401M08Rik	512	535	566	726.9	549.66	880	909.3	2748.1	1807	1939.72	577.904	1656.77	2.87	9.872171728
1420641_a_at	Sqrdl	172.4	270.7	353.2	277.8	205.12	586.3	429.5	1087	691.5	836.68	255.834	726.198	2.84	4.305363781
1420621_a_at	App	60	123.1	212.8	67.03	94.52	273.7	208	500.74	305	287.57	111.494	314.99	2.83	5.986067289
1423726_at	Vat1	168.4	209.7	155.7	171.3	89.8	374.4	536.5	420.75	366.7	510.52	158.954	441.776	2.78	0
1457666_s_at	Ifi202b	238.7	558.3	442.5	315.2	288.99	486	897.4	1470.4	878.5	1308.53	368.722	1008.17	2.73	6.981670997
1424524_at	1200002N14Rik	164.5	473.2	434.9	350.9	235.23	578.4	611.9	1568.4	856.6	864.95	331.722	896.05	2.70	11.33922971
1435040_at	Irak3	152.8	479.2	426.8	363.6	275.21	780.9	864.1	987.25	905.1	1026.42	339.518	912.75	2.69	0
1444524_at	LOC100043424 /// OTTMUSG	115.7	306.3	227.9	260.9	156.18	352.7	464	694.96	566	790.14	213.418	573.572	2.69	3.376755907
1442025_a_at	---	211.1	215.8	138.1	254.8	205.02	427.8	410.2	592.28	418.7	871.25	204.968	544.044	2.65	5.876757684
1425626_at	Gstm1	62.03	90.69	105.8	60	141.47	149.3	149.7	381.33	233.7	293.59	91.988	241.498	2.63	8.934207489
1436584_at	Spry2	73.4	88.84	132.9	60	69.37	246.4	150.4	291.53	211.3	207.67	84.906	221.464	2.61	1.832069694
1453072_at	Gpr160	175.1	578	766.5	333.3	594.6	1206	992.6	1764.9	1246	1075.8	489.522	1256.89	2.57	2.81898819
1420407_at	Ltb4r1	432.8	394.1	301.8	355.8	256.5	923.1	650.5	1069.5	898	894.51	348.2	887.108	2.55	0
1439859_at	9630033F20Rik /// LOC67742	83.97	107.3	133.8	153.2	93.43	181.9	155.7	428.78	267.7	342.32	114.33	275.284	2.41	9.872171728
1421551_s_at	Ifi202b	89.53	339.1	341.9	79	162.16	357.7	612.4	593.07	388.9	427.8	202.33	475.968	2.35	6.981670997
1417124_at	Dstn	632.6	1947	2121	575.6	1041.91	3119	2606	3383.1	3708	1812.71	1263.61	2925.86	2.32	5.986067289
1460283_at	Mefv	108.4	149.8	184.7	133.3	84.47	273.6	226.2	461.75	292	274.58	132.146	305.602	2.31	4.305363781
1450753_at	Nkg7	2518	4290	3138	1517	1934.27	7000	7289	6855.5	5374	4392.76	2679.27	6182.14	2.31	2.226912301
1419537_at	Tcfec	142.8	349.5	449.3	248	160.69	665	626	672.21	698.5	431.87	270.05	618.702	2.29	2.460207875
1417741_at	Pygl	470.3	1007	1123	730.3	1012.85	1549	1688	2435.1	2466	1809.23	868.762	1989.46	2.29	2.226912301
1449392_at	Hsd17b1	66.98	140.4	141.1	172.7	147.95	247.1	219.7	378.44	271.6	406.66	133.812	304.676	2.28	3.863788009
1435477_s_at	Fcgr2b	214.1	772.6	1075	686.8	732.88	1560	1798	1549	1590	1417.06	696.222	1582.83	2.27	1.132990469
1454311_at	---	61.65	118.2	111.4	122.5	107.7	160.7	159.9	258.94	242.2	352.88	104.276	234.91	2.25	6.981670997
1422433_s_at	Idh1	2523	2658	3752	2898	2276.41	5581	5395	7122.6	7175	6368.19	2821.63	6328.35	2.24	0
1453049_at	6620401M08Rik	624.9	367.7	237.6	551.9	190.3	639.8	573	1143.3	862.1	1197.98	394.46	883.228	2.24	8.934207489
1418888_a_at	Sepx1	764	1433	1024	1222	835.76	2334	2410	2516.3	2266	2220.96	1055.69	2349.36	2.23	0
1450387_s_at	Ak3l1 /// LOC100047616 /// LO	206.3	483	367.2	277.6	180.5	582	768	779.82	560.2	676.04	302.92	673.2	2.22	1.832069694
1417702_a_at	Hnmt	60	107.5	82.29	60	60	194.7	200.1	190.45	158.6	77.51	73.952	164.276	2.22	5.986067289
1427747_a_at	Lcn2	60	60	64.61	60	60	126.7	97.21	153.83	198.3	97.98	60.922	134.814	2.21	5.118264635
1449773_s_at	Gadd45b	304.5	180.2	182.2	190.9	141.15	387.9	259.8	620.14	348.8	567.62	199.782	436.842	2.19	8.934207489
1424975_at	Siglec5	216.9	344.6	350.3	319.6	256.16	673.6	891.7	578.84	575.2	519.53	297.516	647.764	2.18	2.226912301
1460330_at	Anxa3	516.7	2385	2747	1473	1421.09	4384	4305	3036.7	4153	2696.19	1708.56	3714.85	2.17	5.118264635
1448914_a_at	Csf1	71.07	75.3	71.64	78.32	69.7	212.9	166.7	110.25	138.6	163.57	73.206	158.398	2.16	2.226912301
1423233_at	Cebpd	534.1	622.6	632.2	724.5	347.12	1500	1017	1229.9	1224	1200.69	572.098	1234.2	2.16	0
1421855_at	Fgl2	85.9	256.2	366.9	78.22	115.91	453.7	396.3	473.96	357.2	258.86	180.636	387.99	2.15	9.872171728
1424032_at	Hvcn1	260.6	458.9	476.1	258.5	297.24	910	717.7	806.97	696.6	628.28	350.256	751.902	2.15	1.132990469

Table S1. CMP to GMP transition gene signature in control mice.

Genes up-regulated in GMPs compared to CMPs (= GMP gene signature)

Probe Set	Gene Symbol	CMPs					GMPs					Av Cont	Av Mut	Fold Diff	q-value(%)
		CMP3	CMP4	CMP6	CMP8	CMP10	GMP3	GMP4	GMP6	GMP8	GMP10				
1447253_x_at	Nup54	116.7	119.9	149.8	130.1	154.6	235.9	199.2	440.09	258.2	304.76	134.214	287.636	2.14	5.986067289
1422645_at	Hfe	60	174.6	227	105.9	99.7	317	298	379.55	245.1	186.2	133.438	285.162	2.14	6.981670997
1419874_x_at	Zbtb16	106	86.36	70.37	82.25	74.57	183.3	119.8	171.29	162.7	257.39	83.914	178.888	2.13	3.863788009
1441850_x_at	Tcn2	332.4	353.8	262	340.6	241.86	642.7	635.8	663.76	682.5	635.38	306.126	652.016	2.13	0
1420678_a_at	Il17rb	151.4	105.7	108.9	98.95	77.37	237.8	197.7	246.68	203.5	268.6	108.45	230.856	2.13	0
1423141_at	Lipa	165	207.6	183	244.5	248.04	245.5	342	651.78	436.2	554.45	209.614	445.982	2.13	8.934207489
1455282_x_at	Alas1	365.6	573.7	690.6	340.1	333.13	1143	783.7	1017.8	975	976.56	460.624	979.236	2.13	1.132990469
1426261_s_at	LOC632297 /// Ugt1a1 /// Ugt1	98.4	260.8	372.7	206.3	221.16	431.4	471.2	449.67	676.3	434.43	231.86	492.576	2.12	3.863788009
1420981_a_at	Lmo4	475.4	385.2	516.1	311.5	380.29	1319	966.2	615.78	657.7	825.38	413.712	876.848	2.12	6.981670997
1453120_at	Txndc13	786.9	3078	3415	1199	1755.83	4359	4772	4754.4	4751	3052.98	2046.95	4337.97	2.12	5.876757684
1455889_at	Mlstd1	60	60	60	60	60	164.4	99.94	173.91	137.4	60	60	127.14	2.12	8.934207489
1419029_at	Ero1l	123.9	409.6	431.7	341.7	258.18	560.4	474.1	898.01	730.4	647.49	313.01	662.07	2.12	5.118264635
1423239_at	Impdh1	641.4	998.8	989.3	1238	1238.76	1140	1813	2559.4	2382	2848.12	1021.21	2148.5	2.10	6.981670997
1436305_at	Rnf217	60	101.8	109.8	74.13	91.33	161.1	168.1	200.75	175.5	213.54	87.41	183.778	2.10	0
1426223_at	2810439F02Rik	60	104.5	121.8	60	60	187.9	201.3	170.19	185.5	106.15	81.254	170.22	2.09	3.863788009
1434197_at	Atrn	60	113.4	241.2	79.2	155.63	309.1	221.2	323.57	309.9	194.84	129.874	271.704	2.09	6.981670997
1419609_at	Ccr1	86.76	478.9	387.7	312.6	398.65	622.3	904.8	436.75	851.9	655.77	332.93	694.312	2.09	8.035551262
1442118_at	---	60	65.72	95.03	77.71	64.17	156.6	100.1	149.05	174	176.43	72.526	151.248	2.09	1.832069694
1424783_a_at	LOC632297 /// Ugt1a1 /// Ugt1	1135	2376	2573	3141	2096.82	2193	4430	5732.3	5397	5825.6	2264.43	4715.57	2.08	8.934207489
1421824_at	Bace1	165.1	399.6	457.4	203.1	224.61	575.1	616.9	705.49	679.5	439.79	289.95	603.348	2.08	3.376755907
1456735_x_at	Acpl2	1021	1372	1864	1767	1016.56	2010	2590	4667.2	2917	2418.72	1408.02	2920.46	2.07	9.872171728
1457825_x_at	Tcn2	859.8	737.5	530.9	860	597.05	1561	1286	1627.2	1521	1413.24	717.044	1481.79	2.07	0
1449233_at	Bhlhb8	105.4	157.3	138.7	158.1	131.47	283.8	195.4	378.01	252	311.46	138.18	284.122	2.06	2.81898819
1441962_at	Alox5	253.5	346.1	242.1	492.8	270.33	567.4	658.6	594.77	634.3	841.79	320.97	659.374	2.05	1.832069694
1415901_at	Plod3	628.7	1035	1053	839.1	887.87	1723	1798	1732.5	2182	1686.6	888.596	1824.38	2.05	0
1460273_a_at	Naip2	335.1	304.6	238.3	201.6	119.26	439.9	411	609.46	500.4	498.59	239.768	491.858	2.05	2.226912301
1448200_at	Tcn2	353.6	751.2	628.9	647.3	620.32	1301	1307	1028.1	1456	1060.27	600.254	1230.52	2.05	1.132990469
1450639_at	RP23-357I14.1 /// Slc28a2	220.4	406.7	491.3	274.8	256.34	754.4	773.4	606.83	724.8	503.5	329.9	672.57	2.04	2.226912301
1457270_at	Gas7	60	60	64.76	63.65	60	115.9	80.58	190.69	105.1	135.43	61.682	125.532	2.04	6.981670997
1460401_at	Edem3	562.1	750.5	1049	661.8	980.62	2141	2003	931.18	1717	1344.08	800.782	1627.22	2.03	6.981670997
1441412_s_at	Trim45	290.4	347.3	276.9	257.6	183.66	555.3	492.1	637.19	562.8	496.34	271.186	548.722	2.02	0
1428749_at	Dmxl2	60	86.47	100.3	60	67.34	143.5	105.4	199.75	167	137.76	74.812	150.66	2.01	3.376755907
1435476_a_at	Fcgr2b	258.6	542.5	626.6	611.4	719.98	901.1	1058	1163.1	1211	1221.02	551.812	1110.83	2.01	1.132990469
1419078_at	Nin	136.7	409.2	428.8	325.9	251.31	696	633	640.22	637.1	513.56	310.384	623.97	2.01	1.832069694
1435259_s_at	Tmem141	151.4	231.6	186.2	220.1	154.4	425.2	360	428.4	340	340.77	188.718	378.87	2.01	0
1434362_at	---	363.1	460.6	641	672.7	513.61	664.7	738.5	1559.6	1154	1200.82	530.192	1063.48	2.01	9.872171728
1442798_x_at	Hk3	2263	2438	2403	2490	1416.92	4210	4162	5371.1	4026	4266.74	2202.23	4407.21	2.00	0

Table S1. CMP to GMP transition gene signature in control mice.

Genes up-regulated in GMPs compared to CMPs (= GMP gene signature)

Probe Set	Gene Symbol	CMPs					GMPs					Av Cont	Av Mut	Fold Diff	q-value(%)
		CMP3	CMP4	CMP6	CMP8	CMP10	GMP3	GMP4	GMP6	GMP8	GMP10				
1428154_s_at	Ppapdc1	171.2	284.8	334.9	118	167.91	404.1	410.7	519.61	469.3	350.08	215.36	430.768	2.00	3.376755907
1456792_at	LOC100045317 /// Tbc1d2	395.5	342.4	266.9	349.1	262.63	516.8	488.4	655.03	812.6	759.9	323.302	646.524	2.00	2.460207875
1418982_at	Cebpa	936.1	676.9	1026	1058	1150	1138	1688	2388.4	1913	2566.17	969.456	1938.55	2.00	5.986067289
1433833_at	Fndc3b	309.1	516.8	684	587.8	520.37	875	782.9	1358.7	1013	1203.57	523.622	1046.7	2.00	3.376755907
1455737_at	Ppm1h	676.2	1110	1517	1330	1355	1626	1731	3260.6	2663	2641.37	1197.56	2384.48	1.99	6.981670997
1431167_at	Dgkg	123	150.5	117.1	67.69	67.15	229	167.5	225.26	226.1	192.91	105.098	208.142	1.98	1.832069694
1434559_at	Stx3	60	137.3	181.1	78.42	141.37	285	215.1	172.02	281.1	221.05	119.622	234.844	1.96	5.876757684
1448355_at	Prss16	79.36	111.5	144.7	123	125.26	209.5	146.8	320.6	206.1	262.49	116.75	229.104	1.96	5.986067289
1448377_at	Slpi	1315	1960	1567	1537	1495.23	2103	2670	4525.1	3023	3100.8	1574.64	3084.34	1.96	5.986067289
1429190_at	Arsb	60	79.1	71.04	63.91	60	166.3	120.8	169.05	103.6	91.77	66.81	130.31	1.95	5.118264635
1454901_at	Ypel2	60	84.52	105.7	67.29	60	96.22	128.6	199.69	175.7	135.87	75.496	147.21	1.95	5.986067289
1455763_at	Rnf41	60	111.5	127	149.1	142.56	188.2	167.3	311.42	197.4	274.35	118.032	227.728	1.93	6.981670997
1455436_at	Diras2	166.3	167.5	139.7	103	136.17	329.1	225.2	245.7	245.5	326.98	142.528	274.504	1.93	1.832069694
1451006_at	Xdh	60	65.89	85.56	60	60	115.8	113.7	112.43	199.9	95.26	66.29	127.41	1.92	8.934207489
1416737_at	Gys1	227.4	402.6	425	475.7	346.75	577.1	554.6	934.35	830.8	698.71	375.492	719.116	1.92	3.863788009
1455660_at	Csf2rb	383.3	914.6	1367	1067	1290.63	1833	1625	1937	2192	2028.83	1004.48	1923.17	1.91	2.460207875
1431188_a_at	EG545878 /// Tom1	83.17	171	239.7	163.1	202.65	267.3	254.9	450.54	365.6	302.62	171.934	328.184	1.91	6.981670997
1439814_at	Atp8b4	1581	2470	3327	2422	2478.05	4365	5268	4634.8	4644	4407.45	2455.64	4663.85	1.90	0
1433832_at	Unc84b	2035	3390	3454	4596	3595.96	4592	5028	8254.9	7384	7111.18	3414.22	6473.92	1.90	5.876757684
1434630_at	Ankrd28	208.1	617.9	734.9	452.7	570.95	691	1094	1135.4	1013	937.09	516.88	974.102	1.88	5.118264635
1455332_x_at	Fcgr2b	60	336.3	394.9	228	277.09	459.7	572	545.73	528.5	326.57	259.258	486.5	1.88	8.934207489
1458040_at	---	101.9	96.96	105.6	93.52	86.25	185.7	130.8	208.36	171.4	212.36	96.854	181.718	1.88	1.132990469
1437119_at	Ern1	740.5	2657	2991	2626	2819.85	2934	4170	5911.1	4559	4550.01	2367.03	4424.78	1.87	8.035551262
1418099_at	Tnfrsf1b	271.9	704.5	621.4	519.8	723.75	1100	799.2	1317.9	1006	1087.01	568.272	1062.05	1.87	3.376755907
1427484_at	Eml5	84.69	60	63.14	61.52	60	105.6	79.84	169.86	134.5	123.7	65.87	122.69	1.86	5.986067289
1447284_at	Trem1	165.8	206.8	251.7	252.4	220.83	278.6	365.2	538.64	424.8	425.45	219.496	406.532	1.85	3.863788009
1433772_at	Stch	457.1	1094	1538	885.7	1151.91	1701	1697	2474.4	2056	1538.74	1025.49	1893.33	1.85	5.986067289
1424431_at	Csgalnact2	1117	1724	2207	1173	1441.39	2786	3842	2576.7	2627	2307.42	1532.28	2827.79	1.85	5.118264635
1437868_at	BC023892	831	749.4	624.7	932.4	633.37	1055	1378	1539.6	1494	1489.93	754.158	1391.21	1.84	1.132990469
1447800_x_at	---	3733	2702	1811	3498	2154.78	4861	4522	5760.9	4514	5935.44	2780.02	5118.54	1.84	2.226912301
1448470_at	Fbp1	133.7	240.1	247.2	299.9	216.4	378.6	427.4	625.9	315.2	341.31	227.468	417.688	1.84	9.872171728
1434418_at	Lass6	155.1	280.9	361.9	238.6	235.27	429.7	458.1	656.6	427.4	360.87	254.344	466.542	1.83	6.981670997
1429352_at	Mocos	83.83	96.05	120.5	136.4	116.04	175.4	180.8	232.01	204.7	219.8	110.58	202.538	1.83	0
1458718_at	---	249	343.9	386.7	408.7	299.51	432.4	474.1	776.85	685.6	718.39	337.568	617.446	1.83	5.876757684
1415741_at	Tmem165	922.6	2398	3203	1442	2608.05	2887	3419	4931.8	4591	3499.61	2114.8	3865.64	1.83	9.872171728
1428129_at	Lman1	77.99	146.2	153.9	79.56	97.47	198.3	187.8	245.28	201.9	175.1	111.03	201.67	1.82	2.81898819
1416635_at	Smpdl3a	653.3	714.4	659	316.1	407.54	1126	1100	1114.8	919.5	727.3	550.074	997.444	1.81	3.863788009

Table S1. CMP to GMP transition gene signature in control mice.

Genes up-regulated in GMPs compared to CMPs (= GMP gene signature)

Probe Set	Gene Symbol	CMPs					GMPs					Av Cont	Av Mut	Fold Diff	q-value(%)
		CMP3	CMP4	CMP6	CMP8	CMP10	GMP3	GMP4	GMP6	GMP8	GMP10				
1435084_at	C730049O14Rik	1973	2329	1040	1173	1047.82	2322	3294	3051.4	2499	2545.46	1512.52	2742.48	1.81	5.876757684
1449983_a_at	Nqo2	60	153.8	168.6	131.3	113.54	217.4	186.3	319.26	211.6	195.99	125.44	226.104	1.80	8.035551262
1426260_a_at	LOC632297 /// Ugt1a1 /// Ugt1	617.6	1771	2693	1537	2020.72	2926	2708	2919	4136	2876.55	1727.94	3113.05	1.80	8.934207489
1424650_at	Pdia5	256.2	564	494.8	506.8	510.87	854.5	668.4	917.18	910.5	841.68	466.538	838.462	1.80	1.832069694
1449084_s_at	Sh3d19	118.1	110.6	131.6	60	60	253.8	157	157.82	155.9	138.55	96.05	172.612	1.80	11.33922971
1444040_at	Lair1	103.3	104.7	109.1	60	66.79	197.3	127.8	213.33	158.2	99.91	88.782	159.282	1.79	11.33922971
1438164_x_at	Flot2	2597	1999	1532	2743	1314.51	2811	2835	4648.2	3684	4292.65	2037.26	3654.08	1.79	6.981670997
1446434_at	---	125.6	367.6	326.9	320	250.92	385.1	362.6	594.71	490	658.93	278.186	498.254	1.79	9.872171728
1460252_s_at	Zfp105	70.11	60	87.07	74.46	75.9	137.3	69.54	124.3	179.5	147.3	73.508	131.596	1.79	9.872171728
1426350_at	Mgat2	270	230.6	393.9	280.8	313.84	372.1	507.6	646.03	505.8	622.62	297.832	530.816	1.78	3.863788009
1419202_at	Cst7	3028	7742	6351	4731	5321.8	12432	12004	7576.5	9440	6849.75	5434.66	9660.49	1.78	9.872171728
1452054_at	Ube2w	331.4	315.3	370.7	362.4	342.33	430.1	551.9	773.96	608.7	689.3	344.436	610.78	1.77	2.81898819
1416843_at	Pde6d	341	433.9	412.1	309.9	269.32	880	729.8	482.37	605.6	427.21	353.234	624.982	1.77	9.872171728
1435490_at	Hk3	1026	2371	2773	1668	1329.12	4064	3615	2524.4	3583	2399.9	1833.33	3237.32	1.77	9.872171728
1445181_at	Eml5	66.9	86.47	94.12	74.23	91.62	115.2	109.7	197.29	152	155.25	82.668	145.886	1.76	5.876757684
1452783_at	Fndc3b	60	171.3	188.8	111.7	153.75	193.7	208.1	296.34	282	225.15	137.106	241.06	1.76	8.035551262
1417544_a_at	Flot2	736.1	756.4	754.2	735	861.83	1112	1309	1606.6	1418	1298.99	768.712	1349.07	1.75	0
1428544_at	0610007L01Rik	378.5	549.1	542	491.4	434.99	669.2	659.9	1075.7	899.8	891.66	479.192	839.264	1.75	3.376755907
1448744_at	Galns	159.5	255.3	306.5	284	250.08	472.8	436.9	384.63	439.9	462.67	251.084	439.38	1.75	0
1416381_a_at	Prdx5	2318	2461	2466	2435	2194.66	3355	3569	5674.1	4516	3645.77	2374.97	4151.83	1.75	3.863788009
1425128_at	B3gnt8	77.11	128.9	157.4	151.4	116.7	253.2	220.2	213.86	205.5	210.07	126.294	220.562	1.75	1.132990469
1437956_at	Pik3r6	71.92	102.9	174.6	83.9	97.67	217.7	142.3	225.39	193.8	146.68	106.188	185.18	1.74	8.934207489
1418076_at	St14	215.4	232.6	185.4	246.6	152.43	389	237.9	485.93	334.9	350.79	206.494	359.688	1.74	6.981670997
1416382_at	Ctsc	1724	2560	3354	1950	2877.7	3580	4684	4909.5	4882	3621.81	2492.85	4335.29	1.74	2.918890699
1448123_s_at	Tgfbi	270.6	166	305.7	370	249.55	479.5	350.5	371.5	625.2	535.04	272.392	472.36	1.73	8.035551262
1419030_at	Ero1l	60	96.5	173.3	74.29	85.8	165.6	162	198.33	179.9	139.72	97.968	169.1	1.73	8.934207489
1430718_s_at	Dph4	176.3	367.9	423.6	369.8	346.24	436.1	544.9	777.97	573.1	552.22	336.762	576.846	1.71	6.981670997
1456980_at	9830134C10Rik	1093	1080	1204	1192	1382.41	2052	2216	1203	2159	2552.64	1190.29	2036.64	1.71	5.876757684
1448439_at	D17Wsu104e	703.9	714.8	797.9	634	690.53	1116	778.8	1766.3	1182	1194.98	708.196	1207.53	1.71	9.872171728
1449324_at	Ero1l	506.1	766	1018	661.7	687.14	1069	1040	1521	1510	1057.12	727.862	1239.43	1.70	5.986067289
1429863_at	Lonrf3	60	99.63	115.2	76.61	65.87	148.7	116.1	150.21	156	134.5	83.462	141.112	1.69	2.81898819
1435091_at	Zfp568	337.8	570.4	573.3	561.4	637.56	634.3	727.5	1228.5	917	1014.86	536.088	904.442	1.69	8.934207489
1424835_at	Gstm4	294.1	281.7	241.6	324.1	252.74	316	365.1	646.72	519.4	491.6	278.836	467.76	1.68	9.872171728
1423706_a_at	Pgd	1698	2622	3949	2346	3305.37	4070	3962	5665.7	5469	4077.84	2784.18	4648.96	1.67	6.981670997
1417110_at	Man1a	146.7	566.2	559.4	459.5	413.5	784.6	707.3	627.81	839.4	612.35	429.058	714.276	1.66	8.934207489
1454934_at	Ppm1f	481.3	697.1	775.1	643.5	708.09	1169	1018	1010.2	1117	1176.52	661.028	1098.05	1.66	0
1437225_x_at	Gnai3	93.12	113.5	123.1	69.5	85.27	180.5	170.3	154.45	200.6	98.77	96.892	160.908	1.66	8.934207489

Table S1. CMP to GMP transition gene signature in control mice.

Genes up-regulated in GMPs compared to CMPs (= GMP gene signature)

Probe Set	Gene Symbol	CMPs					GMPs					Av Cont	Av Mut	Fold Diff	q-value(%)
		CMP3	CMP4	CMP6	CMP8	CMP10	GMP3	GMP4	GMP6	GMP8	GMP10				
1423883_at	Acsl1	1250	1593	1084	1424	1057.19	1698	1870	2522.1	2482	2056.38	1281.69	2125.62	1.66	2.918890699
1420703_at	Csf2ra	395.1	423.8	426.6	293.2	250.29	577.9	707.4	623.73	506.1	538.67	357.784	590.77	1.65	2.460207875
1425448_x_at	Atp6v0b	303.4	268.4	244.8	379.2	306.13	431.5	373.2	633.92	501	521.82	300.388	492.288	1.64	5.118264635
1416917_at	1700123O20Rik	1210	1695	1645	1102	1501.06	2997	2700	1759.7	2457	1808.18	1430.52	2344.36	1.64	8.035551262
1421947_at	Gng12	1029	982.3	891.3	839.3	729.85	1709	2002	1209.8	1204	1198.74	894.306	1464.89	1.64	8.035551262
1417588_at	Galnt3	124.9	159.1	177.2	154.8	141.32	180.2	200	315.66	264	278.74	151.458	247.716	1.64	5.986067289
1422519_at	Cask	91.46	118.6	126.4	179.4	152.18	169.2	188.1	266.24	263.9	199.24	133.602	217.34	1.63	8.035551262
1447842_x_at	---	1867	1434	930	2100	1177.27	2104	2180	2608.3	2576	2677.77	1501.71	2429.13	1.62	5.876757684
1416108_a_at	Tmed3	3319	4719	4586	2916	2942.33	7167	5704	6752.4	5404	4835.52	3696.36	5972.55	1.62	5.118264635
1417191_at	Dnajb9	364	655.4	656.8	509.1	865.43	850.1	843.3	1260.3	907.1	1063.78	610.148	984.91	1.61	8.934207489
1418437_a_at	Mlx	389.5	401	475.6	410.6	410.35	461.2	586.4	793.85	849	675.09	417.396	673.094	1.61	5.986067289
1416392_a_at	Atp6v0c /// Atp6v0c-ps2	4472	4823	6349	5708	5662.34	7115	7190	10429	9916	8893.57	5402.97	8708.75	1.61	2.918890699
1417441_at	Dnajc12	188.5	502.4	367.7	271.6	274.55	434	492.7	628.97	572	455.62	320.956	516.664	1.61	9.872171728
1455164_at	Cdgap	110.7	330.8	340.8	279.7	259.48	456.1	415.6	498.98	385.7	364.35	264.296	424.142	1.60	8.035551262
1436915_x_at	Laptm4b	136.2	194.6	212.3	274.7	162.52	260.8	327.7	426.06	253.4	303.58	196.056	314.298	1.60	9.872171728
1416654_at	Slc31a2	111.1	232	260.3	275.9	252.54	301	332.1	430.86	335.5	414.78	226.348	362.856	1.60	6.981670997
1433806_x_at	Calr	6659	9057	10650	9381	9239.85	13307	11806	15066	15398	16536.8	8997.16	14422.8	1.60	1.832069694
1449259_at	Rab3d	617.4	559.9	500.7	641.5	408.64	869.7	688.5	974.86	843.2	974.11	545.64	870.058	1.59	2.226912301
1417205_at	Kdelr2	219	405.4	471.2	359.6	346.43	452.7	559.8	659.67	682.3	513.39	360.322	573.558	1.59	5.986067289
1439616_at	---	613.9	625.5	536.8	807.7	415.21	681.9	944.8	1066.8	934.8	1123.99	599.814	950.448	1.58	5.986067289
1428600_at	Nin	658.9	1066	1079	922.1	1107.93	1117	1453	1693.2	1908	1462.3	966.804	1526.64	1.58	5.986067289
1447846_x_at	Mboat7	127.8	129.5	108.3	120	115.23	142	156.6	236.29	198.4	212.41	120.164	189.148	1.57	5.118264635
1451000_at	Tmem126a	1390	1559	1607	1707	1401.75	1872	2517	2504.3	2554	2612.86	1532.83	2412.12	1.57	1.132990469
1426746_at	1810026J23Rik	784.1	1753	2021	1515	2139.7	2077	2384	3071	2655	2725.01	1642.64	2582.2	1.57	8.934207489
1431997_at	3000002C10Rik	683.8	729.8	952.8	665.4	1063.65	1092	1347	1252.3	1519	1211.27	819.094	1284.47	1.57	2.918890699
1417266_at	Ccl6	195.6	111.3	249.4	268.3	252.54	253.4	329.8	414.44	333.7	357.53	215.44	337.768	1.57	8.934207489
1452281_at	Sos2	266	257.1	367	163.1	274.51	392.7	499.1	442.65	366	378.83	265.536	415.844	1.57	5.876757684
1427509_at	Baiap3	97.49	97.37	80.16	92.69	88.77	137.5	148.6	148.66	120.8	158.65	91.296	142.846	1.56	0
1452283_at	Rassf8	128.1	208	250	173.7	175.26	276	258.8	356.44	282.6	288.14	187.008	292.388	1.56	4.305363781
1437968_at	Grin1	82.05	91.54	78.63	130.7	104.59	124.8	122.3	192.21	155.2	166.6	97.51	152.226	1.56	8.035551262
1416592_at	Glrx	722	1052	934.9	866.7	737.97	1182	1645	1551.7	1297	1051.62	862.778	1345.39	1.56	5.876757684
1418520_at	LOC100038890 /// Tgoln1	60.55	128.9	105.3	70.92	90.31	149.8	164	120.46	164	108.85	91.182	141.424	1.55	11.33922971
1425099_a_at	Arntl	122.3	173.3	183.7	183	246.92	249.6	307.6	289.05	283.3	275.8	181.838	281.048	1.55	2.81898819
1437434_a_at	Gpr177	228.1	336.1	331.2	215.4	247.36	428.6	366	484.05	456.6	362.95	271.644	419.634	1.54	3.863788009
1439456_x_at	Atp6ap2	8128	9584	10144	8972	8079.3	10874	11382	18262	13944	14907.1	8981.45	13873.8	1.54	5.986067289
1429123_at	Rab27a	1042	1152	1050	834.8	1071.28	1545	1286	1661.4	2040	1411.05	1030.05	1588.8	1.54	4.305363781
1433451_at	Cdk5r1	338.1	339.6	270	343.5	247.97	417.4	352.4	587.34	502.3	509.33	307.832	473.744	1.54	5.876757684

Table S1. CMP to GMP transition gene signature in control mice.

Genes up-regulated in GMPs compared to CMPs (= GMP gene signature)

Probe Set	Gene Symbol	CMPs					GMPs					Av Cont	Av Mut	Fold Diff	q-value(%)
		CMP3	CMP4	CMP6	CMP8	CMP10	GMP3	GMP4	GMP6	GMP8	GMP10				
1434589_x_at	Surf4	1285	859.8	850	1121	849.92	1587	1337	1704.7	1331	1671.45	993.178	1526.24	1.54	2.918890699
1428643_at	Mgat5	1138	1456	1779	1569	1268.38	1809	2585	2612.2	2095	1956.94	1441.92	2211.56	1.53	5.118264635
1424988_at	Mylip	507.9	426.4	457.8	469.2	605.59	960.8	747.8	640.22	711.7	710.06	493.384	754.102	1.53	3.863788009
1425215_at	Ffar2	275.3	320.6	332.9	259.4	265.44	438.3	423.5	483.08	372.8	496.03	290.706	442.74	1.52	1.132990469
1434642_at	Hsd17b11	4448	5091	3460	4806	3122.3	7089	5660	6995.1	5626	6224.98	4185.49	6319.1	1.51	3.376755907
1426440_at	Dhrs7	320.9	618.1	719.2	629.2	742.3	809.1	742.2	1060.7	1078	883.64	605.926	914.74	1.51	9.872171728
1416511_a_at	Cdc42ep4	245.8	344.9	255.1	227.8	255.74	446	436	399.22	377.3	346.82	265.864	401.068	1.51	2.226912301
1437688_x_at	Atp6ap2	9922	12805	11710	10644	10551.1	14054	14720	20000	17022	18104.8	11126.3	16780.3	1.51	2.460207875
1447277_s_at	Pcyox1	2887	3359	4607	3303	4416.25	4409	4769	6997.3	5602	6162.02	3714.56	5587.9	1.50	8.934207489
1444089_at	Spnb2	60	90.9	89.38	71.93	71.42	113.3	80.97	120.97	123.8	138.04	76.726	115.42	1.50	6.981670997
1433887_at	Dnajc3a	604.2	693.2	757.4	565.5	533.82	1131	726.4	1161.3	880.6	838.95	630.816	947.74	1.50	8.035551262
1455072_at	Cep350	1296	2016	2086	1725	2382.63	2018	2531	3389.2	3147	3161.12	1900.92	2849.36	1.50	9.872171728
1415961_at	Itm2c	2155	2630	2483	3065	2293.17	4598	4640	2918.3	3727	3041.72	2525.1	3784.88	1.50	8.934207489
1428608_at	Mylc2b	8227	11408	11697	9649	8111.03	14257	15527	14740	14188	14841.6	9818.54	14710.8	1.50	0
1451475_at	Plxnd1	209.7	229.6	229.7	368.6	208.28	433.4	318.8	373.48	333.6	406.64	249.178	373.172	1.50	8.035551262
1417813_at	Ikbke	154.9	201.8	211.8	201.7	106.39	278.3	220.3	237.01	284.6	291.7	175.332	262.382	1.50	5.986067289
1448210_at	Rab1	412.4	581.8	623.2	423.6	605.5	850.9	734.1	1031.2	722	616.91	529.312	791.032	1.49	9.872171728
1455435_s_at	Chdh	1740	1993	2713	1722	1757.28	2553	2620	2728.1	3657	3240.22	1985.34	2959.55	1.49	6.981670997
1435230_at	Ankrd12 /// Ankrd12-like	245.9	351	358.1	234.9	262.97	468	478.8	447.3	337.1	431.98	290.564	432.654	1.49	5.118264635
1460316_at	Acsl1	169.3	112.7	123.8	135.3	152.26	184.7	179.4	198.64	254.6	214.46	138.662	206.372	1.49	4.305363781
1423394_at	Pcyox1	420.3	508.9	554.5	470.4	584.85	719	734	823.06	800.6	700.86	507.8	755.512	1.49	0
1422465_a_at	Nxn	350.8	545.1	521.8	362	569.05	702.9	674.8	657.85	825.1	625.23	469.766	697.168	1.48	5.118264635
1448477_at	Chst12	347.5	566.3	660.4	663.3	654.54	639.1	765.3	907.16	978.2	1001.27	578.404	858.196	1.48	9.872171728
1439506_at	Gm98	64.31	72.08	70.38	83.78	87.58	86.76	97.78	140.45	99.74	135.79	75.626	112.104	1.48	9.872171728
1439060_s_at	Wipi1	211.2	177.8	151	176.1	150.99	265.9	219.1	272.81	252.5	274.7	173.4	257.01	1.48	1.132990469
1422821_s_at	Stard5	129.7	222.4	206.2	263.1	228.64	279.9	250.5	363.72	318.5	338.69	209.986	310.268	1.48	8.035551262
1437741_at	Rab21	742.2	987.9	1432	876.5	1027.15	1112	1640	1760.3	1530	1434.22	1013.1	1495.25	1.48	11.33922971
1428690_at	Tysnd1	118.3	138.8	166.6	199.3	162.24	182.6	215.1	256.11	243.8	261.35	157.052	231.79	1.48	5.876757684
1457676_at	Tirap	344.8	302.4	321.8	351.3	393.15	423.9	421	584	519.3	576.15	342.696	504.852	1.47	3.376755907
1437223_s_at	Xbp1	3750	3183	3924	3397	3148.65	5686	4875	5687.8	4919	4435.08	3480.3	5120.63	1.47	1.132990469
1447223_at	---	68.67	88.08	90.61	121.3	104.1	133.5	137	158.65	142.2	123.51	94.556	138.988	1.47	3.376755907
1423871_at	Tmem63a	505.5	629.8	573.2	669.6	600.02	678.8	760.1	1044.1	911.8	981.03	595.63	875.162	1.47	5.118264635
1456876_at	P42pop	64.44	66.16	66.94	87.8	88.82	82.54	100.6	117.18	116.5	132.21	74.832	109.802	1.47	6.981670997
1450626_at	Manba	353.6	749.6	738.4	700.1	762.32	990.4	1090	891.12	1009	857.45	660.8	967.604	1.46	6.981670997
1423967_at	Palm	511.5	635.4	530.3	662.4	542.87	832.2	726.3	800.71	845.9	1015.22	576.49	844.072	1.46	2.226912301
1425187_at	Sel1l	147.4	157.7	208.3	225.8	205.86	274.5	232.1	333.57	272.5	270.69	189.016	276.664	1.46	5.118264635
1417632_at	Atp6v0a1	244.4	226.6	202.2	324.5	200.41	301.1	399.1	308.79	317.5	423.64	239.62	350.002	1.46	8.934207489

Table S1. CMP to GMP transition gene signature in control mice.

Genes up-regulated in GMPs compared to CMPs (= GMP gene signature)

Probe Set	Gene Symbol	CMPs					GMPs					Av Cont	Av Mut	Fold Diff	q-value(%)
		CMP3	CMP4	CMP6	CMP8	CMP10	GMP3	GMP4	GMP6	GMP8	GMP10				
1434698_at	Mia3	169.6	297.4	258.4	231.4	293.37	306.5	400.8	352.1	390.2	375.23	250.01	364.966	1.46	4.305363781
1434815_a_at	Mapkapk3	8380	12472	10461	10444	5685.88	14283	15499	14851	13304	11313.5	9488.81	13849.9	1.46	8.934207489
1436143_at	4933425L03Rik	534.2	496	388.1	406.6	432.07	591.9	542	797.79	684.2	677.55	451.41	658.664	1.46	4.305363781
1449476_at	Rage	77.02	88.47	109.3	118.6	89.75	131.2	125.8	174.02	135.6	136.03	96.634	140.528	1.45	5.118264635
1444197_at	5830482F20Rik	60	60	60	60	60	73.3	78.78	108.79	78.41	95.17	60	86.89	1.45	3.863788009
1428518_at	Mlf1ip	657.3	770.1	628.6	953.7	644.05	923.8	1080	1098.1	990.1	1192.38	730.754	1056.89	1.45	3.376755907
1424654_at	Acp2	213.9	261.5	240.1	322.6	218.46	331.9	317.4	459.96	314	391.45	251.316	362.94	1.44	8.934207489
1427213_at	Pfkfb1	60	117.3	138.4	144	134.05	183.3	167.4	156.36	195.8	153.44	118.742	171.262	1.44	9.872171728
1424058_at	Prrc1	571	930.5	823.2	760.7	731.13	1121	895.7	1100.6	1267	1119.96	763.282	1100.88	1.44	4.305363781
1451382_at	Chac1	60	73.43	60.82	71.04	66.21	79	73.83	121.41	91.92	111.9	66.3	95.612	1.44	9.872171728
1424172_at	Hagh	488.5	513.1	500.3	376	459.85	651.7	613.5	711.9	725.5	661.77	467.55	672.86	1.44	0
1416385_a_at	M6pr	2115	3138	3939	2439	3182.29	4477	4074	4481.7	4862	3400.5	2962.85	4258.98	1.44	8.934207489
1427323_s_at	Wipi1	94.81	110.3	91.8	99.92	111.49	147.6	118.1	163.76	159.4	140.71	101.66	145.926	1.44	2.226912301
1435327_at	AW112037 /// Lpgat1	248.4	408.7	530.3	396.2	396.36	585.5	489.6	662.23	591.8	510.35	395.984	567.9	1.43	8.934207489
1435402_at	Gramd1b	67.46	106.1	107.2	85.53	90.27	151.6	125.7	144.81	126.4	105.97	91.3	130.902	1.43	5.986067289
1428667_at	Maoa	340	437.9	565.4	505.4	525.92	501.1	679.2	681	729.5	802.7	474.91	678.702	1.43	8.934207489
1450919_at	Mpp1	548.5	587.9	584.7	631.7	638.75	869.2	704.9	906.7	913.3	873.48	598.308	853.504	1.43	0
1456393_at	2310002J21Rik	9535	13353	11471	5795	10687.4	14212	13409	15584	16132	13015.3	10168.5	14470.7	1.42	9.872171728
1428644_at	Mgat5	1192	1135	1062	1069	1089.86	1136	1687	1963.3	1632	1473.43	1109.62	1578.23	1.42	6.981670997
1417203_at	Ethe1	451.9	573.7	731.5	663.5	600.14	889.6	780.9	826.28	963.4	834.82	604.152	859.01	1.42	2.81898819
1432845_at	---	76.44	88.98	78.7	84.85	96.62	102.4	102.3	160.4	121.4	118.38	85.118	120.966	1.42	8.934207489
1424655_at	Acp2	88.5	200	176.5	196.4	156.21	209.5	221	254.63	219.4	256.31	163.542	232.154	1.42	9.872171728
1434511_at	Phkb	283	386.5	373.8	339.5	289.04	477.9	435.6	621.15	406.1	429.58	334.364	474.056	1.42	8.934207489
1456170_x_at	Calr	10113	15271	14866	14549	15022.6	20000	18527	20000	20000	20000	13964.1	19705.4	1.41	1.132990469
1436225_at	Trpm2	87.95	87.68	84.88	109.1	88.63	120.2	107.6	173.32	115.4	129.87	91.646	129.274	1.41	9.872171728
1450498_at	Mthfr	76.73	88.19	92.97	132.4	103.79	116.8	119.5	146.44	159.3	154.25	98.812	139.238	1.41	9.872171728
1416059_at	LOC100048726 /// Sec23b	1640	2631	3369	2444	2897.84	3478	4128	3735.7	3901	3016.74	2596.42	3652.02	1.41	9.872171728
1428508_at	Tbc1d2b	669.2	635.1	530.4	493.1	627.49	657.6	692.6	976.24	908.9	916.35	591.054	830.34	1.40	8.035551262
1448339_at	Tmem30a	353.6	380.3	382.5	415.3	349.05	493.9	553.4	589.36	514.5	490.97	376.146	528.41	1.40	0
1415987_at	Hdlbp	1813	2592	2453	2064	2267.37	3161	3354	2852.3	3355	2993.81	2237.89	3143.27	1.40	1.832069694
1432332_a_at	Nudt19	279.1	400.9	453.8	354.2	390.11	586.7	572.7	492.25	549.7	431.92	375.62	526.65	1.40	5.876757684
1455590_at	Nqo2	234.4	286.2	365.4	247.5	292.63	429.8	398.6	408.57	333.1	428.82	285.228	399.758	1.40	4.305363781
1419513_a_at	Ect2	700.2	541.4	841.5	585.1	758.07	938.6	899.4	1209.7	869.4	878.68	685.258	959.144	1.40	8.934207489
1428240_at	Nrxn1	116.5	114.2	139.7	128.8	153.75	184.7	174.2	193.47	187.3	173.51	130.582	182.638	1.40	0
1429524_at	Myo1f	512.7	410.4	456.7	653.2	532.67	606.9	599.5	892.26	739.7	744.48	513.124	716.552	1.40	11.33922971
1449702_at	Zfand2a	198.2	338.6	308.2	322.5	350.3	378.9	399.8	434.06	422	481.97	303.554	423.346	1.39	5.876757684
1453974_at	1700023A20Rik	87.96	86.9	68.35	88.11	90.98	114.6	130.6	100.35	109.1	134.23	84.46	117.788	1.39	2.918890699

Table S1. CMP to GMP transition gene signature in control mice.

Genes up-regulated in GMPs compared to CMPs (= GMP gene signature)

Probe Set	Gene Symbol	CMPs					GMPs					Av Cont	Av Mut	Fold Diff	q-value(%)
		CMP3	CMP4	CMP6	CMP8	CMP10	GMP3	GMP4	GMP6	GMP8	GMP10				
1436797_a_at	Surf4	839.5	926	957.3	717	858.2	1372	1085	1122.9	1197	1208.72	859.614	1197.16	1.39	1.832069694
1434223_at	1810007P19Rik /// LOC10004	74.5	64.79	80.22	64.56	83.79	121.9	85.33	97.63	109.6	97.52	73.572	102.394	1.39	5.118264635
1424495_a_at	Cklf	475.4	657.8	639.7	546	592.44	759	781.7	1071.2	775	664.72	582.258	810.322	1.39	11.33922971
1418392_a_at	Gbp3	867.1	1069	1395	888.4	1019.87	1241	1507	1732	1396	1407.94	1047.88	1456.68	1.39	8.035551262
1452056_s_at	Ppp3ca	719.2	575.6	559.2	543.3	629.08	737.8	745	1029	833.9	859.42	605.28	841.022	1.39	5.118264635
1444486_at	Klhl5	60	60	83.77	65.57	60	96.76	86.53	108.25	97.54	67.81	65.868	91.378	1.39	9.872171728
1436102_at	Sec22c	178.7	315.5	226.9	288.6	210.77	372.2	330.8	376.2	309.9	304.26	244.12	338.662	1.39	8.934207489
1459522_s_at	Gyg	6707	8032	7436	8322	6793.76	11739	11447	8467.3	10660	9379.74	7458.16	10338.5	1.39	3.863788009
1423140_at	Lipa	106	104.2	121.1	116.9	90.61	180.1	121.3	155.4	152.3	137.51	107.754	149.316	1.39	5.876757684
1423333_at	Ergic1	351.7	420.6	416.5	431.9	401.29	441.6	484	593.44	581.7	692.13	404.37	558.562	1.38	8.035551262
1438188_x_at	Slc25a29	81.59	83.38	87.78	83.3	74.69	139.1	106.6	100.41	126.8	93.89	82.148	113.352	1.38	5.986067289
1456036_x_at	Gsto1	3656	4060	4138	4575	2956.23	4193	5574	6007.2	5135	5784.8	3877.04	5338.72	1.38	6.981670997
1454268_a_at	Cyba	2683	3238	3900	3303	4243.16	4457	4710	5598.8	5147	3966.17	3473.58	4775.84	1.37	8.035551262
1418956_at	Tssk6	60	72.31	69.99	74.81	60.54	82.7	80.59	106.44	97.54	96.53	67.53	92.76	1.37	2.918890699
1415853_at	Def8	361.4	369.1	439	294.1	357.48	460.6	478.8	518.88	624.7	417.58	364.21	500.122	1.37	8.934207489
1452440_at	LOC100048347 /// Tnfsf12 ///	61.65	60.23	60	88.53	62.46	97.64	81.37	104.45	79.31	94.27	66.574	91.408	1.37	8.035551262
1428502_at	Actr6	620.6	585.8	641.1	621.1	724.75	796.5	898.6	1034.5	846.4	806.25	638.644	876.454	1.37	2.226912301
1436623_at	Entpd7	92.73	109.9	141.9	107.3	98.78	166.3	124.1	175.6	148.1	140.57	110.108	150.922	1.37	8.934207489
1421846_at	Wsb2	135.7	103.4	109.4	82.59	95.58	139.7	136.8	139.69	136.6	167.08	105.338	143.984	1.37	5.986067289
1448967_at	Nipsnap3a	651	697.3	998.9	746.5	866.48	1064	1105	1288.1	958.1	993.64	792.032	1081.78	1.37	6.981670997
1428385_at	March8	365	348.4	432.3	217.5	288.03	451.6	439	504.37	423.3	431.52	330.236	449.954	1.36	9.872171728
1451243_at	Rnpep	726.8	895.1	1016	760.3	862.48	1424	1147	1188.2	1014	1027.09	852.14	1160.25	1.36	6.981670997
1424708_at	Tmed10	1209	1189	1046	1201	1092.38	1415	1577	1685.7	1450	1663.08	1147.35	1558.19	1.36	0
1447226_at	---	118.4	94.27	88.66	129.2	120.91	135.6	130.6	160.14	137.9	184.67	110.294	149.774	1.36	9.872171728
1453949_s_at	Lypla1	105.5	171.8	183.9	203.8	160.59	247.5	222.6	233.39	189.7	225.68	165.126	223.772	1.36	9.872171728
1451307_at	Mrpl14	289.5	338.7	269.7	359.9	293.72	435	463.4	425.3	328.7	447.17	310.318	419.92	1.35	5.876757684
1418890_a_at	Rab3d	605.3	509.8	432.2	453.8	444.18	695.1	634.4	634.71	669.5	668.91	489.068	660.508	1.35	1.832069694
1460194_at	Phyh	345.1	375.5	301.7	267.8	242.63	452.3	450.7	442.37	370.9	348.95	306.518	413.03	1.35	8.934207489
1418319_at	Ufsp2	658.5	790.5	1024	629.3	808.93	1025	921	1194.1	1060	1067.15	782.326	1053.51	1.35	8.035551262
1448378_at	Fscn1	89.89	102.6	94.09	132.1	122.52	119.2	128.7	165.87	161.4	152.99	108.25	145.628	1.35	9.872171728
1418621_at	Rab2a	2522	3061	3667	2494	3087.01	4013	4222	4048.9	4293	3354.65	2966.01	3986.27	1.34	5.876757684
1423252_at	Hdgfrp3	91.79	105.4	104.3	116.1	106.82	164	121.4	153.05	128.6	137.64	104.888	140.928	1.34	3.863788009
1420174_s_at	Tax1bp1	286.5	375.2	376	417.2	443.28	524.3	506.4	590.08	435.6	493.21	379.644	509.914	1.34	5.986067289
1429012_at	Arhgef6	1576	2138	2133	2300	2063.44	2190	2638	3314.3	2849	2697.43	2042.05	2737.72	1.34	8.934207489
1417426_at	Srgn	12297	18575	14743	12100	13267.6	20000	20000	18560	19365	17065.5	14196.6	18998	1.34	5.876757684
1441281_s_at	Ninj1	1104	1067	1076	1267	1254.38	1163	1536	1436.1	1786	1799.69	1153.92	1544.04	1.34	9.872171728
1450987_a_at	2310004I24Rik	421.3	560.5	557.4	612.2	547.78	784.3	676	880.7	689.4	579.21	539.814	721.932	1.34	9.872171728

Table S1. CMP to GMP transition gene signature in control mice.

Genes up-regulated in GMPs compared to CMPs (= GMP gene signature)

Probe Set	Gene Symbol	CMPs					GMPs					Av Cont	Av Mut	Fold Diff	q-value(%)
		CMP3	CMP4	CMP6	CMP8	CMP10	GMP3	GMP4	GMP6	GMP8	GMP10				
1436301_at	Ripk5	367.2	409.4	426.1	325.6	397.05	538	379.6	600.83	547.7	502.65	385.06	513.752	1.33	9.872171728
1418857_at	Slc13a2	78.12	69.93	69.89	73.53	60.09	82.77	84.63	106.15	91.47	103.78	70.312	93.76	1.33	3.863788009
1458132_at	ENSMUSG00000067124	67.74	94.49	65.18	88.16	90.31	84.18	122.1	111.39	107.9	115.47	81.176	108.21	1.33	9.872171728
1423358_at	Ece2	812.2	1039	1121	811	1117.34	1251	1580	1184.1	1299	1203.95	980.214	1303.67	1.33	8.934207489
1428146_s_at	Acaa2	1570	1835	1779	1453	1599.8	1983	2162	2138.3	2531	2134.85	1647.38	2189.7	1.33	2.226912301
1456896_at	6720462K09Rik	87.89	84.65	69.93	91.1	87.53	116.8	90.34	140.46	104.8	107.08	84.22	111.906	1.33	9.872171728
1456251_x_at	Tspo	6924	5047	5219	5714	3700.77	7540	7074	7054.4	6916	6686.74	5321.07	7054.18	1.33	8.934207489
1417386_at	Npepps	806.2	905.1	686.9	716	796.71	1085	853.5	1184.9	979.1	1074.98	782.162	1035.46	1.32	5.876757684
1434031_at	Zfp692	619.5	582	556.1	437.1	587.81	605.6	633.3	808.64	758.5	873.78	556.514	735.962	1.32	11.33922971
1448318_at	Adfp	3356	3425	3459	3081	2930.74	4619	4511	4545.5	4213	3528.65	3250.16	4283.5	1.32	2.81898819
1450792_at	Tyrobp	6107	5771	6495	7283	6828.35	8042	9154	8577.5	8939	8078.4	6496.94	8558.26	1.32	1.132990469
1448583_at	AA960436	555.7	450	466.1	469.2	530.51	629.6	567.9	615.68	679.2	759.67	494.298	650.394	1.32	3.863788009
1416465_a_at	Vapa	6853	5418	6354	6112	5388.96	6681	7287	8492.8	9098	8048.62	6025.14	7921.39	1.31	5.876757684
1427737_a_at	1200011M11Rik	173.5	222.3	245.6	263.8	239.82	306.2	323.8	342.39	258.9	272.07	229.02	300.676	1.31	8.035551262
1452139_at	Slc35c1	384.9	439.1	477.3	381.1	453.6	520.1	508.1	597.9	666.5	505.49	427.206	559.616	1.31	5.986067289
1439375_x_at	Aldoa /// Aldoart1	6140	7170	6373	5843	5886.29	8929	7499	7763.3	9229	7723.73	6282.42	8228.89	1.31	2.81898819
1427870_x_at	Igh-6	157	111.1	120.4	137.3	156.95	174.9	149.1	207.42	190.8	172.12	136.558	178.866	1.31	9.872171728
1449712_s_at	Atp6v1e1	2454	2433	2583	2450	2535.09	2701	2904	4157.4	3357	3125.17	2490.98	3249	1.30	11.33922971
1426434_at	Tmem43	424.9	434.3	554.2	420.4	467.92	646.3	571.2	612.72	607.8	559.68	460.324	599.524	1.30	2.226912301
1444601_at	---	140.4	158.1	129.2	167.4	142.34	158.1	172.4	221.44	188.9	219.39	147.482	192.048	1.30	9.872171728
1451557_at	Tat	61.69	60	60	64.99	72.79	80.17	70.63	77.6	95	92.53	63.894	83.186	1.30	5.876757684
1417781_at	Lass4	122.2	120.5	125.6	149.8	144.19	151.4	165.3	199.93	174.3	171.25	132.446	172.414	1.30	4.305363781
1456867_x_at	Ergic3	3001	3138	2699	3493	3457.53	4196	4674	4433.9	3752	3432.58	3157.55	4097.72	1.30	6.981670997
1435089_at	2010111I01Rik	118.1	154.9	153.3	157.1	140.74	198.4	203.7	197.7	188.7	148.88	144.836	187.48	1.29	6.981670997
1416328_a_at	Atp6v0e	3931	4274	3666	4610	3530.56	4697	6107	5088.9	4622	5308.04	4002.35	5164.57	1.29	6.981670997
1420012_at	Xbp1	61.4	71.62	78.79	79.39	65.36	106.6	81.22	104.09	78.91	89.07	71.312	91.976	1.29	9.872171728
1423833_a_at	Brp44	2106	3111	3419	3019	3115.7	3416	4182	3788.5	4208	3434.13	2954.14	3805.74	1.29	9.872171728
1418929_at	Ift57	406.2	420.3	413.7	399.7	511.22	540.4	558.5	567.52	549.1	554.2	430.224	553.93	1.29	1.132990469
1449140_at	Nudcd2	331.9	366.3	500.8	410.6	434.86	522.5	560.6	584.15	468.3	492.84	408.87	525.664	1.29	8.934207489
1448391_at	Rab9	1304	1174	1261	919.3	1194.68	1573	1451	1735.6	1416	1338.55	1170.54	1503	1.28	6.981670997
1440520_a_at	1700051A21Rik	75.79	70.52	80.42	101.2	99.7	100.1	108.3	123.31	108	108.85	85.524	109.702	1.28	8.035551262
1438640_x_at	Pgk1	12203	13839	14381	15105	13210.8	14287	16014	20000	18113	19693.9	13747.7	17621.6	1.28	8.934207489
1426697_a_at	Lrpap1	344.9	408.2	362.4	398.5	392.83	515.1	410.2	499.65	490.1	523.54	381.356	487.72	1.28	2.81898819
1445614_at	---	60	76.51	73.81	73.79	91.76	96.75	86.8	93.41	91.26	112.37	75.174	96.118	1.28	9.872171728
1415941_s_at	Zfand2a	188.2	163.1	181.8	187.1	203.82	252.2	197.6	243.99	225	262.04	184.772	236.154	1.28	5.118264635
1451624_a_at	Phospho2	124.8	160.2	178	133.5	162.43	182.8	173.7	216.12	218.3	178.37	151.782	193.868	1.28	9.872171728
1422467_at	Ppt1	335.5	512.3	456.1	508.4	499.53	627.2	569.4	554.13	658.7	528.53	462.356	587.6	1.27	9.872171728

Table S1. CMP to GMP transition gene signature in control mice.

Genes up-regulated in GMPs compared to CMPs (= GMP gene signature)

Probe Set	Gene Symbol	CMPs					GMPs					Av Cont	Av Mut	Fold Diff	q-value(%)
		CMP3	CMP4	CMP6	CMP8	CMP10	GMP3	GMP4	GMP6	GMP8	GMP10				
1456520_at	Zfp652	194.1	214.4	228.7	183.4	209.84	266.8	246.8	314.68	245.9	233.46	206.092	261.53	1.27	8.035551262
1426558_x_at	0610010B08Rik /// LOC10003	338.4	260.5	344.1	331.5	269.41	389.7	387	422.48	344	415.78	308.796	391.794	1.27	5.986067289
1425950_at	1700019H03Rik	123.9	126.8	138.9	131.3	109.28	168.5	130.4	189.02	154.1	156.94	126.018	159.786	1.27	9.872171728
1437055_x_at	Mfsd1	135.1	144	163.6	150.1	130.33	181.1	167.4	214.38	191.5	161.48	144.632	183.164	1.27	6.981670997
1449024_a_at	Hexa	7266	11515	10986	9287	9351.09	12737	11401	12604	12977	11494.5	9680.88	12242.8	1.26	9.872171728
1418096_at	Dok3	383.3	349.6	349.4	421.8	347.7	460.1	429.2	421.11	550.4	477.36	370.348	467.642	1.26	5.986067289
1453318_at	Tmem102	85.53	88.8	89.22	105.1	107.66	123.9	112.5	145.04	113.5	106.55	95.268	120.276	1.26	9.872171728
1455714_at	Vstm2l	96.59	93.35	91.35	110	101.13	118.6	105.4	121.3	130.1	145.06	98.484	124.104	1.26	6.981670997
1440442_at	Map2k7	115.4	129.4	129.4	161.7	142.05	146	162.6	193.43	183.9	167.07	135.568	170.608	1.26	9.872171728
1422484_at	Cycs	5377	4877	6105	4557	4630.01	7275	6260	6623	5921	6051.55	5109.29	6426.03	1.26	6.981670997
1460695_a_at	2010111I01Rik	538.6	733.6	612.1	710.5	767.06	727.2	911.9	877.28	870.5	828.74	672.34	843.142	1.25	8.934207489
1417606_a_at	Calr	12535	17557	16264	16527	16877.3	20000	20000	20000	20000	20000	15952	20000	1.25	2.460207875
1436120_at	Setdb2	620.6	562.6	500.8	528	654.59	659.8	634.1	810.92	698.8	788.72	573.308	718.476	1.25	8.934207489
1452143_at	Spnb2	2832	3619	4113	3141	3950.77	4767	4244	4363.7	4706	3999.85	3531.06	4415.97	1.25	8.934207489
1448948_at	Rag1ap1	302	365.4	315.2	339.5	393.87	422.2	409.4	447.17	400.2	463.87	343.198	428.576	1.25	3.863788009
1452375_at	Aldh4a1	70.51	93.01	91.51	99.27	91.18	117.6	119.9	103.88	112	102.69	89.096	111.216	1.25	5.876757684
1417182_at	Dnaja2	373.4	380.9	424.1	318	437.11	495	465.8	546.18	428.7	476.55	386.718	482.44	1.25	8.035551262
1431893_a_at	Pdss1	269.4	268.8	330.7	276	298.19	319	389.4	374.56	311.5	405.66	288.604	360.008	1.25	8.934207489
1419429_at	Cntfr	74.86	65.72	60.05	73.2	70.89	89.79	83.37	78.51	87.82	90.28	68.944	85.954	1.25	2.226912301
1422241_a_at	Ndufa1	13460	15622	14500	14392	15111.9	18281	16949	20000	17078	18805.4	14617.3	18222.7	1.25	1.832069694
1448422_at	Tmed4	1351	1467	1284	1576	1423.12	1847	1794	1796.7	1860	1531.32	1420.14	1765.71	1.24	2.918890699
1416547_at	Ndufb3	2606	3122	2364	2816	2424.51	3470	3752	3122.6	3096	3080.7	2666.47	3304.37	1.24	8.035551262
1451031_at	Sfrp4	100.9	102.3	98.27	103.5	99.15	132.9	123.4	146.94	112.3	108.49	100.816	124.802	1.24	8.035551262
1416189_a_at	Sec61a1	11540	11002	10625	12153	9355.41	12333	11955	14959	13304	15129.9	10935.1	13536.3	1.24	8.934207489
1429568_x_at	Ube2f	894.4	677.2	744.6	787.9	783.27	943	918.2	1073.2	898.9	977.99	777.456	962.258	1.24	4.305363781
1438753_at	---	84.43	76.83	77.21	71.24	83.98	91.87	87.01	106.6	103.7	95.89	78.738	97.004	1.23	3.863788009
1436452_x_at	LOC100042343 /// Tmed2	9786	13004	12445	10341	9703.7	12334	14178	14207	14149	13227.6	11055.7	13619.2	1.23	8.934207489
1456865_x_at	Rrs1	6956	6745	6354	7197	6183.19	7369	7492	8305.8	9967	8013.72	6686.98	8229.46	1.23	9.872171728
1447399_at	---	71.36	71.16	67.62	79.7	91.83	87.4	85.83	101.57	91.91	101.66	76.334	93.674	1.23	9.872171728
1416441_at	Pgcp	807.2	896.3	797.5	689.1	826.63	1081	1086	943.28	933.2	883	803.366	985.402	1.23	6.981670997
1454676_s_at	Ticam1	181.6	247.3	210.5	222.6	249.18	280.1	265.1	300.82	239.3	275.65	222.234	272.186	1.22	9.872171728
1441175_at	Arx	65.45	76.36	80.14	85.84	76.07	80.85	87.04	99.07	100.9	101.73	76.772	93.908	1.22	8.934207489
1460204_at	Tec	720.3	682.6	632.2	669.3	791.17	919.9	799.7	818.48	834.8	896.86	699.118	853.952	1.22	2.918890699
1427503_at	AI324046	75.44	67.27	62.43	77.23	68.16	75.17	84.54	88.67	80.39	98.7	70.106	85.494	1.22	8.934207489
1424026_s_at	BC013529	169.2	165.7	158.5	178.5	138.11	220.9	191.4	198.36	191.9	182.41	162.014	197.012	1.22	5.876757684
1452758_s_at	Eif4g2	15646	13503	12811	12606	11954	15348	15667	16561	15906	17336.8	13303.8	16163.7	1.21	4.305363781
1449272_at	Cadm3	60	61.21	60	72.77	66.32	69.1	72.92	76.37	79.49	91.03	64.06	77.782	1.21	9.872171728

Table S1. CMP to GMP transition gene signature in control mice.

Genes up-regulated in GMPs compared to CMPs (= GMP gene signature)

Probe Set	Gene Symbol	CMPs					GMPs					Av Cont	Av Mut	Fold Diff	q-value(%)
		CMP3	CMP4	CMP6	CMP8	CMP10	GMP3	GMP4	GMP6	GMP8	GMP10				
1449441_a_at	Wbp1	660.4	649.8	612.7	642.3	737.94	673.7	772.8	919.88	828.2	810.27	660.64	800.964	1.21	9.872171728
1452753_at	Foxk2	280.8	288.3	256.3	292.9	274.71	371.5	333.3	345.76	281.7	353.16	278.594	337.088	1.21	5.986067289
1427965_at	Ssbp1	10619	10853	11032	10770	11169.9	11172	11859	14829	13509	14340	10888.7	13141.8	1.21	8.934207489
1416727_a_at	Cyb5	2002	2356	1923	2463	2276.86	2480	3029	2635.2	2588	2563.32	2204.34	2659.18	1.21	8.934207489
1437278_a_at	Uba2	5270	4826	4773	5354	4086.06	5187	6580	5790.4	5821	5699.93	4861.9	5815.58	1.20	11.33922971
1449593_at	---	111.1	133.1	110.8	137.4	130.28	160.3	139.3	142.56	156.3	145.16	124.52	148.722	1.19	6.981670997
1436443_a_at	Kdelc1	3876	3553	3106	3430	3058.24	3798	3974	4471.6	3942	4010.16	3404.59	4039.1	1.19	8.035551262
1454661_at	Atp5g3	14516	17667	16903	14773	18191.4	20000	19565	20000	19110	18177.7	16410.2	19370.7	1.18	5.986067289
1428075_at	LOC100041273 /// LOC10004	4109	3369	3571	3581	3414.16	4089	4494	4312.7	3953	4394.13	3608.97	4248.55	1.18	5.118264635
1419644_at	Cstf2	205.8	216.3	208.4	214.7	188.55	281.4	235.2	220.2	239.4	237.42	206.73	242.72	1.17	8.934207489
1455968_x_at	LOC100042343 /// Tmed2	12809	15690	15392	14052	12364.8	15404	16245	17651	15724	17069.6	14061.7	16418.8	1.17	11.33922971
1448795_a_at	LOC100046166 /// Tbrg4	734.1	679.2	668	685.8	660.14	711	775.3	789.98	872.1	828.37	685.444	795.35	1.16	5.876757684
1426606_at	Crtac1	71.13	71.12	64.14	67.15	74.71	76.39	76.2	84.95	86.23	78.63	69.65	80.48	1.16	5.876757684
1426346_at	Prepl	75.84	83.75	74.05	74.13	70.68	91.21	85.01	85.52	78.41	89.31	75.69	85.892	1.13	8.934207489
1438794_x_at	EG625298 /// LOC100039924	17370	15717	14876	16873	17152.4	17300	19027	18617	17769	18776	16397.7	18298.1	1.12	8.035551262
1439270_x_at	LOC100045999 /// LOC64020	14734	15320	14598	14605	14909.2	15771	16476	16040	16224	16474.9	14833.3	16197.3	1.09	0

Table S1. CMP to GMP transition gene signature in control mice.

Genes down-regulated in GMPs compared to CMPs (= CMPs gene signature)

Probe Set	Gene Symbol	CMPs					GMPs					Av Cont	Av Mut	Fold Diff	q-value(%)
		CMP3	CMP4	CMP6	CMP8	CMP10	GMP3	GMP4	GMP6	GMP8	GMP10				
1449757_x_at	Dntt	627.99	338.64	406.35	847.91	917.21	60	60	60	60	60	627.62	60	10.46	2.583218269
1428114_at	Slc14a1	2145.6	2007.1	1090.4	671.68	1077.8	563.66	222.65	60	62.3	60	1398.52	193.72	7.22	5.876757684
1448640_at	Slc14a1	1078.2	1099.2	607.72	277.16	587.76	228.48	104.17	60	60	60	730.01	102.53	7.12	5.876757684
1454630_at	Samd14	1325.1	928.22	381.98	434.06	437.15	219.79	113.54	60	60	60	701.302	102.67	6.83	11.33922971
1442000_at	Gm1964	2191.2	2125.9	966.65	687.18	1064.9	494.1	360.76	60	60	60	1407.16	206.97	6.80	6.981670997
1422817_at	Gp5	1284.1	975.48	432.9	423.15	512.31	287.59	101.28	60	60	60	725.59	113.77	6.38	8.934207489
1448995_at	Pf4	18559	15072	9858.7	11817	11546	7331.5	3419	453.17	215.78	169.41	13370.5	2317.8	5.77	2.583218269
1450545_a_at	Dntt	147.95	338.9	407.31	249.78	579.49	60	60	60	60	60	344.686	60	5.74	5.876757684
1421461_at	Mpl	1012	697.79	532.25	681.3	1002.6	162.53	127.34	86.34	131.45	185	785.176	138.53	5.67	1.655909147
1451046_at	Zfpm1	1784.2	1601	851.4	842.59	1303.7	458.01	393.56	60	116.12	130.49	1276.56	231.64	5.51	2.583218269
1440037_at	Pbx1	1372.3	1249.9	368.78	1297.2	1025.1	218.66	196.03	145.25	154.74	270.75	1062.68	197.09	5.39	2.81898819
1417155_at	Mycn	328.18	583.72	448.81	298.64	704.17	164.92	108.56	60	60	60	472.704	90.696	5.21	2.81898819
1418199_at	Hemgn	1197.8	1176.7	863.49	833.65	1181.1	425.98	364.05	61.97	87.55	72.21	1050.53	202.35	5.19	0
1455900_x_at	Tgm2	544.15	350.82	186.39	320.36	143.42	60	60	60	60	60	309.028	60	5.15	8.035551262
1417235_at	Ehd3	1001.3	1111.7	407.09	466.75	443.58	283.43	127.61	137.55	60	64.96	686.086	134.71	5.09	8.035551262
1450852_s_at	F2r	3621.8	2590.4	1237.7	1882.9	1648.3	1063.2	480.32	220.04	188.83	214.62	2196.21	433.4	5.07	5.876757684
1433428_x_at	Tgm2	383.04	350.21	197.32	335.76	177.17	60	60	60	60	60	288.7	60	4.81	2.583218269
1437308_s_at	F2r	16274	15397	12740	14415	15134	8162.4	4708.2	651.8	691.01	1622.8	14792	3167.2	4.67	0
1455257_at	Itgb3	2573.4	1712.6	599.81	1326.3	1054	600.7	319.38	232.01	258.66	272.55	1453.22	336.66	4.32	9.872171728
1448748_at	Plek	3085.7	3762.7	2379.7	2379.2	3005.5	1136.1	905.46	386.58	515.17	519.53	2922.57	692.56	4.22	0
1428209_at	Bex4	760.5	629.53	453.87	350.23	408.12	252.69	125.44	66.98	101.39	94.1	520.45	128.12	4.06	2.81898819
1437277_x_at	Tgm2	341.14	335.79	143.34	242.79	126.75	60	60	60	60	60	237.962	60	3.97	5.876757684
1448471_a_at	Ctla2a	3957.1	1974.8	1040.2	1884.1	2587.1	1121.8	855.41	175.4	308.79	555.65	2288.67	603.42	3.79	9.872171728
1452352_at	Ctla2b	1720.6	913.63	476.66	858.67	848.59	372.43	377.57	152.91	214.58	253.41	963.638	274.18	3.51	9.872171728
1457933_at	Gm1964	366.45	245.44	151.74	153.4	220.39	86.24	60.03	60	60	60	227.484	65.254	3.49	5.118264635
1419538_at	Flt3	2276.5	1964.5	2318.3	3822	3114.8	1148.9	1182.3	479.23	561.59	503.96	2699.24	775.19	3.48	2.583218269
1423213_at	Plxnc1	1726	2028.4	1605.8	1088.5	1323.4	714.99	572.3	371.5	361.77	299.62	1554.42	464.04	3.35	1.655909147
1450992_a_at	Meis1	1131	1129	954.09	689.23	989.26	504.11	422.15	99.36	233.2	240.8	978.528	299.92	3.26	1.655909147
1428647_at	Pbx1	3159.8	4136.2	1799.8	1769.1	2368.5	1141.9	1006.3	813.3	490.64	605.68	2646.69	811.56	3.26	5.876757684
1428867_at	Exoc3l2	417.21	365.98	246.41	127.63	185.51	165.39	62.32	60	62.03	65.54	268.548	83.056	3.23	11.33922971
1416811_s_at	Ctla2a /// Ctla2b	1958	1820.2	941.36	1052.6	1654.8	1060	725.15	60	224.02	230.69	1485.38	459.98	3.23	6.981670997
1457052_at	Kcng1	397	241.36	238.21	336.98	367.95	179.91	131.33	60	66.93	68.82	316.3	101.4	3.12	2.583218269
1425742_a_at	Tsc22d1	2989.6	3056.3	1591.4	2072.9	2404.8	1244.9	1228	438.05	498.3	505.16	2422.97	782.89	3.09	2.583218269
1450644_at	Zfp36l1	558.78	396.06	376.96	368.23	358.03	180.7	186.38	90.03	102.86	111.83	411.612	134.36	3.06	1.655909147
1424923_at	Serpina3g	6916.9	4386.3	4632.4	4793.4	5275.9	2688.7	1730.6	1144.6	1336.6	1641.6	5200.96	1708.4	3.04	1.655909147
1426801_at	Sept8	508.59	396.28	429.92	154.83	421.57	250.39	171.62	60	84.68	68.23	382.238	126.98	3.01	6.981670997
1436515_at	Bach2	231.37	304.17	264.46	423.11	300.34	149.39	175.41	60	62.36	69.08	304.69	103.25	2.95	2.583218269

Table S1. CMP to GMP transition gene signature in control mice.

Genes down-regulated in GMPs compared to CMPs (= CMPs gene signature)

Probe Set	Gene Symbol	CMPs					GMPs					Av Cont	Av Mut	Fold Diff	q-value(%)
		CMP3	CMP4	CMP6	CMP8	CMP10	GMP3	GMP4	GMP6	GMP8	GMP10				
1453841_at	2310050P20Rik	510.55	368.37	176.19	499.82	355.7	87.69	135.67	60	135.62	229.08	382.126	129.61	2.95	5.986067289
1451428_x_at	Egfl7	1237.9	1050.4	1282.1	1554.1	2055.7	637.5	630.8	286.58	389.14	496.9	1436.04	488.18	2.94	2.583218269
1451506_at	Mef2c	1460.2	968.22	834.52	841.17	1305.3	421.06	379.25	369.25	362.86	345.38	1081.87	375.56	2.88	2.583218269
1416333_at	Dok2	633.65	383.34	337.51	284.54	242.65	154.3	128.09	145.96	117.81	108.22	376.338	130.88	2.88	8.035551262
1421498_a_at	2010204K13Rik	942.52	665.9	432.11	839.64	496.88	325.85	231.54	177.77	187.72	267.17	675.41	238.01	2.84	3.863788009
1449198_a_at	St3gal5	436.3	218.38	286.94	295.03	317.2	128.73	123.12	120.53	89.45	103.41	310.77	113.05	2.75	2.583218269
1428284_at	8430427H17Rik	850.21	507.74	369.77	518.18	432.82	344.41	174.67	119.14	160.68	193.42	535.744	198.46	2.70	6.981670997
1447584_s_at	Myct1	279.17	164.07	190.12	202.41	190.98	110.35	92.85	60	60	61.06	205.35	76.852	2.67	2.002494782
1417872_at	Fhl1	264.64	179.23	144.58	122.09	114.56	70.34	60	60	60	60	165.02	62.068	2.66	5.986067289
1460651_at	Lat	685.45	703.27	345.06	423.85	363.86	369.13	228.81	107.54	121.65	131.54	504.298	191.73	2.63	8.934207489
1418294_at	Epb4.1l4b	342.51	567.98	523.51	470.57	754.76	236.48	339.33	95.22	188.97	153.27	531.866	202.65	2.62	4.305363781
1433645_at	Slc44a1	408.09	277.63	194.93	265.31	218.19	138.79	117.17	85.18	102.71	79.31	272.83	104.63	2.61	3.863788009
1418773_at	Fads3	217.21	160.74	144.6	157.5	187.63	78.07	77.25	60	60	60	173.536	67.064	2.59	0
1424852_at	Mef2c	4256	5658.5	4329.7	3459	5660.1	1838.1	1864.9	1729.6	1812.4	1784	4672.66	1805.8	2.59	1.655909147
1428650_at	Tns1	455.86	643.77	448.28	643.23	888.03	323.39	286.55	106.42	243.94	230.95	615.834	238.25	2.58	3.863788009
1440285_at	Ppp1r9a	819.38	422.33	303.44	491.19	403.99	115.26	238.44	249.12	175.34	168.78	488.066	189.39	2.58	9.872171728
1451507_at	Mef2c	123.47	254.79	228.17	237.98	266.32	123.78	107.06	60	79.74	65.06	222.146	87.128	2.55	2.81898819
1454971_x_at	Tsc22d1	8484.7	8045.7	5477.1	8323.2	7767.3	3285.5	4093	1961	2569.3	3055.3	7619.58	2992.8	2.55	0
1437667_a_at	Bach2	234.76	255.25	184.96	278.81	201.62	151.42	122.94	60	60	60	231.08	90.872	2.54	2.583218269
1448765_at	Fyn	882.78	510.5	456.02	352.93	587.14	373.16	252.19	87.13	184.72	204.96	557.874	220.43	2.53	9.872171728
1456634_at	9830001H06Rik	260.9	253.75	208.75	185.75	117.1	139.32	85.36	60	60	64.43	205.25	81.822	2.51	5.118264635
1420649_at	Zfhx3	562.96	316.93	198.33	418.46	262.28	151.88	121.08	150.55	124.31	154.66	351.792	140.5	2.50	9.872171728
1428572_at	Basp1 /// LOC100	1014.6	484.83	958.82	805.38	831.04	377.7	434.15	227.12	233.86	368	818.942	328.17	2.50	2.81898819
1419137_at	Shank3	240.2	163.49	146.03	108.86	119.51	72.74	60	60	60	60	155.618	62.548	2.49	5.876757684
1439449_at	Satb1	443.97	213.7	245.38	362.23	291.44	96.4	133.94	73.55	159.32	163.78	311.344	125.4	2.48	5.118264635
1450905_at	Plxnc1	1826.3	1759.9	1021.2	1346.7	1134.4	548.81	591.24	783.14	367.38	589.7	1417.69	576.05	2.46	2.81898819
1418012_at	Sh3glb1	368.59	510.15	349.63	416.23	316.04	271.08	193.61	71.6	136.16	132.95	392.128	161.08	2.43	2.81898819
1456072_at	Ppp1r9a	644.04	369.73	241.44	366.14	322.06	116.03	181.17	212.69	152.68	137.89	388.682	160.09	2.43	9.872171728
1425503_at	Gcnt2	409.95	532.76	464.94	678.45	731.77	330.28	401.59	123.31	194.55	135.83	563.574	237.11	2.38	5.876757684
1451427_a_at	Egfl7	751.09	693.74	800.99	1033.6	1198.4	465.41	464.95	347.92	321.38	298.09	895.568	379.55	2.36	2.583218269
1418123_at	Unc119	1059.4	986.96	537.14	589.59	545.27	445.41	435.04	278.66	251.73	179.84	743.676	318.14	2.34	8.934207489
1417065_at	Egr1	261.13	266.37	305.72	198.06	245.74	187.62	126.52	80.16	73.32	79.16	255.404	109.36	2.34	2.583218269
1424588_at	Srgap3	336.91	399.08	229.22	332.88	240.39	242.93	114.59	99.53	104.14	97.78	307.696	131.79	2.33	5.118264635
1417558_at	Fyn	1256.7	1144.8	777.61	1057.5	1254	629.68	620.2	256.74	352.77	494.17	1098.11	470.71	2.33	2.583218269
1417236_at	Ehd3	385.25	310.5	139.22	315.54	247.88	90.46	128.96	188.92	102.29	95	279.678	121.13	2.31	8.035551262
1425268_a_at	Pear1	435.73	288.03	209.9	295.35	217.32	166.96	126.33	78.51	106.57	149.09	289.266	125.49	2.31	5.986067289
1429089_s_at	2900026A02Rik	1224.7	714.42	472.46	1068.6	673.51	274.39	467.48	301.5	281.66	488.93	830.732	362.79	2.29	11.33922971

Table S1. CMP to GMP transition gene signature in control mice.

Genes down-regulated in GMPs compared to CMPs (= CMPs gene signature)

Probe Set	Gene Symbol	CMPs					GMPs					Av Cont	Av Mut	Fold Diff	q-value(%)
		CMP3	CMP4	CMP6	CMP8	CMP10	GMP3	GMP4	GMP6	GMP8	GMP10				
1449389_at	Tal1	2959.5	2236.4	1425.4	2133.9	2176.3	1103.6	1203.8	601.21	872.06	1044.6	2186.28	965.04	2.27	2.918890699
1418181_at	Ptp4a3	1611.4	2019	1963.8	1736.7	2489.3	1277.3	1108.1	578.75	836.41	616.98	1964.03	883.52	2.22	2.583218269
1428577_at	Ppfia4	243.2	211.7	234.03	193.95	267.87	143.75	115.19	66.69	109.63	89.07	230.15	104.87	2.19	1.655909147
1417219_s_at	Tmsb10	133.96	161.03	122.97	210.07	101.21	81.2	74.14	60	60	60	145.848	67.068	2.17	5.118264635
1418401_a_at	Dusp16	216.36	148.13	166.87	113.84	141.83	99.02	83.35	60	60	60	157.406	72.474	2.17	3.376755907
1460239_at	Tspan13	1004.5	699.44	641.74	859.79	828.25	625.4	471.85	194.24	297.89	272.09	806.748	372.29	2.17	3.863788009
1434384_at	Nrip1	862.55	848.92	744.85	580.68	889.16	465.31	541.92	216.22	308.23	281.17	785.232	362.57	2.17	2.583218269
1433695_at	Cnrip1	209.54	120.15	186.47	128.91	188.78	92.03	84.57	69.58	74.71	65.61	166.77	77.3	2.16	2.81898819
1428340_s_at	Atp13a2	3771.6	2537.6	2888.2	2866.4	3196.6	1815.8	1689.2	1123	1232.1	1232	3052.06	1418.4	2.15	1.655909147
1446484_at	---	431.69	375.66	227.81	507.53	514.47	150.76	145.38	154.45	240.59	275.84	411.432	193.4	2.13	6.981670997
1418741_at	Itgb7	1046.4	777.41	969.62	1070	1124.3	676.66	668.22	257.75	358.48	388.15	997.538	469.85	2.12	2.583218269
1434472_at	Dusp3	617.41	412.77	254.58	506.57	340.97	187.08	167.83	232.93	192.09	228.74	426.46	201.73	2.11	8.035551262
1438125_at	C230085N15Rik	146.67	169.79	171.03	310.49	262.81	125.22	87.33	66.64	134.8	88.53	212.158	100.5	2.11	9.872171728
1455349_at	LOC100048397	2168.5	2457.2	1597.5	1430.3	1421.9	1051.2	863.52	897.25	847.2	653.77	1815.08	862.58	2.10	3.863788009
1443394_at	---	220.88	102.5	104.71	153.84	126.12	60	60	60	68.94	92.54	141.61	68.296	2.07	11.33922971
1443832_s_at	Sdpr	202.48	199.88	106.34	146.44	132.57	60	60	115.24	69.32	75.67	157.542	76.046	2.07	5.986067289
1418011_a_at	Sh3glb1	266.08	315.68	190.06	318.74	232.59	190.15	136.97	96.94	88.62	126.94	264.63	127.92	2.07	3.376755907
1419406_a_at	Bcl11a	3116	2021.9	1266	2478.2	2053	1071.2	1291.4	984.73	859.96	1087	2187	1058.8	2.07	6.981670997
1458370_at	Bmp2k	513.01	630.55	437.4	453.53	409.42	414.65	290.13	111.71	238.98	139.03	488.782	238.9	2.05	6.981670997
1416257_at	Capn2	472.61	277.76	327.31	321.98	359.18	284.55	218.84	69.45	182.42	104.6	351.768	171.97	2.05	8.035551262
1428510_at	Lphn1	418.31	458.67	330.31	655.57	585.63	255.21	186.01	239.13	199.27	317.59	489.698	239.44	2.05	5.876757684
1445338_at	---	200.82	144.5	120.4	108.4	136.97	75.2	80.77	60	60	72.71	142.218	69.736	2.04	3.863788009
1455161_at	AI504432	2678.1	1659.9	1312.7	1784.8	1774.9	1056.9	1061.1	648	812.96	957.3	1842.08	907.25	2.03	5.876757684
1424704_at	Runx2	2326.6	2833.8	3081.1	3102.4	3453.7	1705.3	2338.8	1039.4	1159.6	1066	2959.52	1461.8	2.02	2.81898819
1429196_at	Rabgap1l	3056.5	2307.6	1565.2	2490.4	1679.3	1058.4	904.4	1207.4	1033.4	1303.3	2219.82	1101.4	2.02	5.876757684
1438242_at	Usp40	252.28	211.92	145.02	141.18	159.25	106.63	86.98	69.16	116.43	79.06	181.93	91.652	1.99	5.876757684
1455773_at	---	177.2	266.08	247.24	129.93	191.24	102.72	128.81	70.75	133.46	80.29	202.338	103.21	1.96	6.981670997
1416724_x_at	Tcf4	1776.5	1147.7	703.98	1479.4	1161.5	559.01	735.99	492.34	661.12	763.39	1253.82	642.37	1.95	9.872171728
1428468_at	3110043O21Rik	143.11	145.05	161.72	71.65	139.58	83.77	76.07	60	60	60	132.222	67.968	1.95	5.876757684
1434036_at	Mtss1	294.71	333.42	256.55	214.95	242.8	194.26	204.66	104.24	109.38	82.22	268.486	138.95	1.93	5.876757684
1436499_at	Sgms1	551.45	420.74	440.34	258.42	392.25	268.24	290.67	156.87	219.41	135.72	412.64	214.18	1.93	8.035551262
1416872_at	Tspan6	196.32	271.25	257.75	199.5	290.8	187.1	122.21	79.95	127.67	116.59	243.124	126.7	1.92	3.376755907
1453395_at	5330403D14Rik	169.97	158.16	128.03	132.71	154.14	95.18	76.61	60	78.42	77.06	148.602	77.454	1.92	0
1435195_at	Vash1	484.56	510.21	343.6	497.08	406.82	273.06	203.43	232.81	186.15	275.03	448.454	234.1	1.92	2.002494782
1451608_a_at	Tspan33	176.53	172.34	136.26	107.61	92.41	84.21	84.27	71.82	60	60	137.03	72.06	1.90	6.981670997
1441971_at	---	395.06	342.17	199.58	291.55	212.99	177.93	210.73	112.15	115.73	145.15	288.27	152.34	1.89	9.872171728
1450675_at	Smap2	1139.7	961.89	987.84	704.65	884.22	674.51	633.71	449.36	368.93	354.3	935.66	496.16	1.89	3.376755907

Table S1. CMP to GMP transition gene signature in control mice.

Genes down-regulated in GMPs compared to CMPs (= CMPs gene signature)

Probe Set	Gene Symbol	CMPs					GMPs					Av Cont	Av Mut	Fold Diff	q-value(%)
		CMP3	CMP4	CMP6	CMP8	CMP10	GMP3	GMP4	GMP6	GMP8	GMP10				
1437421_at	---	174.02	194.4	204.37	117.78	171.24	144.06	104.69	60	89.12	60	172.362	91.574	1.88	6.981670997
1456686_at	---	263.39	173.61	154.89	254.63	217.19	97.3	126.74	102.07	87.07	155.65	212.742	113.77	1.87	5.118264635
1416326_at	Crip1	6444.9	6347.8	5437.6	7602.8	3780.6	3283	4744	2653.2	2623.7	2539.4	5922.74	3168.7	1.87	6.981670997
1442655_at	Dnmt3b	194.06	231.13	227.58	280.58	160.27	159.81	132.8	60	110.94	122.41	218.724	117.19	1.87	5.876757684
1424089_a_at	Tcf4	536.79	436.25	280.62	554.52	405.49	274.91	330.75	90.71	221.39	268.68	442.734	237.29	1.87	11.33922971
1457072_at	Bcl11a	185.41	222.34	260.85	283.13	285.25	173.53	140.43	120.63	110.88	122.51	247.396	133.6	1.85	2.583218269
1418643_at	Tspan13	4183.2	2922.5	2100.9	3446.7	2903.7	1667.2	2581	1192.5	1207.1	1763.9	3111.37	1682.3	1.85	8.934207489
1419031_at	Fads2	383.14	429.93	377.44	365.52	502.03	333.71	360.86	92.97	185.38	141.18	411.612	222.82	1.85	11.33922971
1452231_x_at	Ifi203	5763.4	6223.6	4588.5	6037.1	4925.8	3319.7	4190.2	2328.3	2368	2709.1	5507.66	2983.1	1.85	2.583218269
1443682_at	AI662476	169.55	97.9	85.62	115.85	112.22	60	60	62.21	60	72.72	116.228	62.986	1.85	6.981670997
1433883_at	Tpm4	2218.5	2463.8	2814.4	2589.1	3073	1495.1	2266.9	978.37	1243.4	1155.2	2631.73	1427.8	1.84	3.376755907
1429159_at	Itih5	496.38	548.24	501.37	628.32	663.26	434.53	378.57	300.51	202.26	226.68	567.514	308.51	1.84	2.918890699
1435745_at	5031439G07Rik	1263.7	1129.1	1131.2	2079.3	1422.5	924.19	717.43	643.31	845.56	693.97	1405.14	764.89	1.84	8.035551262
1423702_at	H1f0	925.14	1782.8	1670.3	1424.7	1389.4	1099.7	1015	380.71	894.59	543.38	1438.47	786.68	1.83	11.33922971
1416457_at	Ddah2	487.95	568.49	374.57	428.84	421.95	383.59	374.24	128.44	188.67	175.59	456.36	250.11	1.82	9.872171728
1430127_a_at	Ccnd2	2637.3	2692.4	2087.7	2042	2575	1749.4	1868	636.32	1224.4	1133.5	2406.86	1322.3	1.82	5.118264635
1416008_at	Satb1	1940.9	1489.5	2314.3	2369.7	2559.7	1472.1	1405.8	809.03	1123.6	1074.7	2134.79	1177.1	1.81	3.863788009
1442700_at	Pde4b	478.28	412.41	398.33	500.14	310.38	212.03	214.59	250.13	205.94	276.26	419.908	231.79	1.81	2.583218269
1416167_at	Prdx4	1095.5	2081.7	1728.3	1709.4	1980.8	1072.7	1312.6	689.49	990.34	685.74	1719.13	950.17	1.81	6.981670997
1422474_at	Pde4b	195.87	205.57	240.95	218.54	284.05	167.94	151.39	83.23	130.82	107.33	228.996	128.14	1.79	2.918890699
1427819_at	---	463.87	345.25	229.74	330.22	278.49	193.58	135.71	175.7	159.76	262.02	329.514	185.35	1.78	11.33922971
1424554_at	Ppp1r8	899.52	908.57	744.9	629.22	839.59	673.2	633.57	453.44	300.48	202.76	804.36	452.69	1.78	9.872171728
1433939_at	Aff3	3695.9	3448.5	3744.8	3997.2	3782.4	3091.1	2661.9	1130.3	1533.5	2146.3	3733.76	2112.6	1.77	3.376755907
1433546_at	Gns	423.35	414.78	423.35	335.42	424.56	347.95	347.95	113.68	190.11	148.05	404.292	229.55	1.76	9.872171728
1423597_at	Atp8a1	289.79	215.8	328.6	186.73	263.95	152.92	105.18	132.23	189.08	151.9	256.974	146.26	1.76	5.986067289
1426633_s_at	Kctd14	957.35	618.53	511.66	842.87	642.62	369.72	354.76	447.97	316.34	551.59	714.606	408.08	1.75	8.934207489
1448960_at	Cxxc5	1650.9	1152	1145.3	1720.1	1882.9	1109.8	892.03	589.72	891.37	833.95	1510.22	863.38	1.75	6.981670997
1455135_at	2610014I16Rik	644.36	944.29	560.81	718.52	848.84	436.53	435.68	426.75	355.92	473.63	743.364	425.7	1.75	3.376755907
1422938_at	Bcl2 /// LOC1000	451.65	268.61	357.22	409.92	310.29	185.79	177.84	224.88	216.04	226.75	359.538	206.26	1.74	3.376755907
1420905_at	Il17ra	1589.3	1780.8	1727.4	1404.7	1975	1522.5	1084.9	631.46	849	798.14	1695.41	977.19	1.73	5.876757684
1429097_at	C030044C12Rik	84.69	122.09	149.15	152.65	137	79.19	78.5	66.95	69.74	78.41	129.116	74.558	1.73	3.863788009
1415698_at	Golm1	1430.4	1141.1	918.03	1223.8	1122	1029.6	750.01	426.33	619.54	544.84	1167.08	674.06	1.73	6.981670997
1427185_at	Mef2a	392.58	505.55	564.64	506.74	555.01	461.01	355.41	199.28	264.48	184.67	504.904	292.97	1.72	8.035551262
1423393_at	Clic4	2776.8	3276	2149.4	2426.3	2992	1645.6	1852.6	1008.4	1685.1	1758.5	2724.1	1590	1.71	3.376755907
1460555_at	6330500D04Rik	1527.3	1645.1	1669.1	1081.8	1579.7	1110.4	1018.3	596.16	839.87	824.12	1500.62	877.77	1.71	3.376755907
1448325_at	Myd116	304.15	279.74	247.45	240.68	167.21	185.37	180.5	110.16	137.96	110.92	247.846	144.98	1.71	6.981670997
1447164_at	---	307.5	247.33	172.68	217.41	157.01	129.68	123.93	102.3	142.55	146.49	220.386	128.99	1.71	9.872171728

Table S1. CMP to GMP transition gene signature in control mice.

Genes down-regulated in GMPs compared to CMPs (= CMPs gene signature)

Probe Set	Gene Symbol	CMPs					GMPs					Av Cont	Av Mut	Fold Diff	q-value(%)
		CMP3	CMP4	CMP6	CMP8	CMP10	GMP3	GMP4	GMP6	GMP8	GMP10				
1426906_at	Ifi203	4186	4151.2	3789.4	4990.3	3681.1	2655.5	4075.5	1800.7	1649.6	1996	4159.59	2435.4	1.71	8.035551262
1423754_at	Ifitm3	6386.7	6595.2	4697.7	5722.1	4508.2	4656.9	4139.7	2177.5	2530.5	2860.8	5581.97	3273.1	1.71	6.981670997
1425267_a_at	Pear1	375.13	264.33	227.15	316.39	260.77	176.49	175.78	159.92	172.14	164.1	288.754	169.69	1.70	3.376755907
1451143_at	1110006G06Rik	912	729.52	631.38	845.02	816.37	630.38	563.84	379.33	389.49	365.93	786.858	465.79	1.69	3.863788009
1419649_s_at	Myo1c	1293.5	894.8	816.57	1424	1013.6	695.87	632.95	584.95	675.89	655.5	1088.51	649.03	1.68	6.981670997
1437341_x_at	Cnp	7933.6	7993.6	6283	10113	6189.2	6816.4	5233.6	3191.5	3936.3	3825.5	7702.5	4600.6	1.67	11.33922971
1418634_at	Notch1	2443.2	3074.7	3111.5	3236.5	4223	2270.8	1830.8	1735.4	2066.5	1738.4	3217.77	1928.4	1.67	4.305363781
1442310_at	Pip4k2a	186.75	143.48	151.52	157.49	170.13	86.57	86.86	93.52	102.98	117.21	161.874	97.428	1.66	1.655909147
1421963_a_at	Cdc25b	627.94	774.45	689.02	578.69	712.14	593.89	572.71	344.79	281.98	253.72	676.448	409.42	1.65	9.872171728
1423680_at	Fads1	923.02	721.24	640.87	632.24	690.91	635.22	529.71	342.65	356.37	328.34	721.656	438.46	1.65	8.035551262
1451352_s_at	Mta3	897.26	780.64	1022.9	954.37	1169.7	731.91	777.39	346.96	533.92	551.86	964.98	588.41	1.64	5.986067289
1448229_s_at	Ccnd2	4127.1	2940.4	2667.9	3502.6	3897.1	1291.2	1730.6	1993.3	2530.5	2919.1	3427.01	2093	1.64	9.872171728
1416123_at	Ccnd2	415.72	354.73	373.41	319.24	514.64	207.28	201.45	238.4	276.39	288.48	395.548	242.4	1.63	5.118264635
1448452_at	Irf8	4199.4	3656.4	3712.2	6008.8	5044.9	2629.9	2602.7	2688.4	3003.3	2959	4524.31	2776.7	1.63	5.986067289
1443156_at	---	191.06	177.46	127.43	153.15	149.72	85.22	80.92	70.86	143.57	110.52	159.764	98.218	1.63	8.035551262
1418582_at	Cbfa2t3	1001.9	861.15	557.93	818.09	950.63	662.95	499.67	493.75	360.83	559.85	837.934	515.41	1.63	8.035551262
1426297_at	Tcfe2a	1167.7	1109.3	1670.6	1050.1	1333.9	1010.1	900.91	524.03	855.08	604.81	1266.32	778.99	1.63	8.934207489
1439323_a_at	Map4k1	1132.8	1007.8	821.02	814.91	804.78	719.71	636.58	568.21	418.95	481.53	916.27	565	1.62	5.118264635
1425506_at	Mylk	220.57	346.67	221.18	271.83	265.14	216.56	154.58	152.3	151.81	144.04	265.078	163.86	1.62	5.986067289
1446088_at	9430081I23Rik	179.02	158.19	105.31	133.35	133.58	110.73	87.62	60	79.12	101.18	141.89	87.73	1.62	8.035551262
1438606_a_at	Clic4	1512.1	1697.4	2119.9	1464.4	2015.7	1194.4	1149.8	995.74	1038.2	1079.7	1761.9	1091.6	1.61	2.583218269
1416683_at	Plxnb2	545.39	422.99	535.75	669.08	785.85	373.89	430.71	312.87	355.21	364.45	591.812	367.43	1.61	8.035551262
1418010_a_at	Sh3glb1	2156.8	2199.8	2162.8	1675.1	2031	1803.1	1590.7	1009.2	947.65	1012.2	2045.1	1272.6	1.61	5.986067289
1440400_at	Rnf157	111.95	137.62	129.36	152.82	160.97	120.44	73.47	60	87.17	90.34	138.544	86.284	1.61	5.876757684
1434400_at	Tgif2	712.18	550.63	428.74	644.16	592.51	449.37	415.27	253.14	320.83	387.65	585.644	365.25	1.60	6.981670997
1434603_at	Med13l	1507.9	1849.4	1263.4	1665.4	1370	1042	1063.7	626.24	1003.3	1072.7	1531.24	961.6	1.59	4.305363781
1418942_at	Ift74	197.01	176.63	177.01	208.1	136.39	168.46	127.86	96.7	96.14	73.17	179.028	112.47	1.59	9.872171728
1448926_at	Hoxa5	174.64	168.4	124.31	157.65	151.89	132.23	115.1	66.19	106.53	70.62	155.378	98.134	1.58	6.981670997
1428096_at	Ipo11	919.68	927.62	999.12	683.96	1041.9	653.35	650.2	456.48	627.3	504.87	914.462	578.44	1.58	3.376755907
1449404_at	Pip4k2a	2146.6	1873.2	1731	2522.3	2059.1	1293	1300.3	1453.8	1095.8	1403.6	2066.44	1309.3	1.58	2.583218269
1458126_at	D030041H20Rik	170.35	104.42	108.04	120.69	124.19	90.18	70.97	60	72.63	104.57	125.538	79.67	1.58	11.33922971
1423212_at	Phc1	841.62	743.8	642.55	811.49	860.39	661.16	486.72	470.33	363.51	503.87	779.97	497.12	1.57	3.376755907
1448775_at	Ifi203	2722.3	2728.7	2913.9	3947.9	3465	2011.7	2472.3	1757.2	1550	2267.6	3155.54	2011.8	1.57	5.876757684
1436836_x_at	Cnn3 /// LOC100	5287.8	4899.3	7564.8	8115.8	7859	4057.6	4061.4	4679.2	4318.7	4413.2	6745.34	4306	1.57	8.035551262
1440227_at	Slc5a3	200.22	225.96	183.72	195.35	162.19	89.44	120.12	116.53	138.31	153.2	193.488	123.52	1.57	2.918890699
1417548_at	Sart3	159.25	133.45	171.48	125.39	89.4	89.25	80.69	73.79	103.71	88.19	135.794	87.126	1.56	11.33922971
1448027_at	Ncoa3	818.77	537.42	490.59	656.59	643.62	500.45	367.21	368.39	380.6	402.75	629.398	403.88	1.56	6.981670997

Table S1. CMP to GMP transition gene signature in control mice.

Genes down-regulated in GMPs compared to CMPs (= CMPs gene signature)

Probe Set	Gene Symbol	CMPs					GMPs					Av Cont	Av Mut	Fold Diff	q-value(%)
		CMP3	CMP4	CMP6	CMP8	CMP10	GMP3	GMP4	GMP6	GMP8	GMP10				
1435484_at	Slc5a3	647.27	509.66	441.77	535.54	386.32	371.36	322.86	371.5	257.97	301.82	504.112	325.1	1.55	6.981670997
1417240_at	Zyx	2543.6	3054.6	2327.6	2486.1	3028.9	2316.5	2296.8	1014.7	1589.5	1453.7	2688.14	1734.2	1.55	9.872171728
1452746_at	Atp13a2	2486.6	2552.2	3191.1	3232	3522.4	2181.5	1872.9	1712.9	1800.7	2115.5	2996.86	1936.7	1.55	2.81898819
1420824_at	Sema4d	700.68	999.71	813.91	1197.6	1112.5	571.19	687.27	599.98	670.47	589.09	964.872	623.6	1.55	6.981670997
1445665_at	---	140.61	111.01	108.13	118.17	123.4	86.08	95.11	60	71.03	78.76	120.264	78.196	1.54	2.583218269
1449089_at	Nrip1	1079.9	865.93	593.45	815.27	933.29	569.75	575.45	456.55	573.68	613.49	857.568	557.78	1.54	8.035551262
1450052_at	Kif2a	374.96	301.07	426.99	297.97	263.14	266.37	204.35	214.63	190.69	210.57	332.826	217.32	1.53	8.035551262
1441131_at	---	160.5	147.83	158.57	112.69	134.81	106.55	81.34	79.76	100.91	98.12	142.88	93.336	1.53	2.81898819
1434359_at	6330500D04Rik	235.87	255.82	243.27	233.5	245.78	194.45	198.58	151.9	157.77	91.1	242.848	158.76	1.53	4.305363781
1417039_a_at	Cul7	1086.1	873.41	990.92	1393.6	1222.8	991.48	727.69	555.42	717.21	661.81	1113.36	730.72	1.52	9.872171728
1455495_at	Abl2	1471.8	1351.7	1048	1897.9	1424.1	858.14	1088.6	859.31	915.77	1004.2	1438.69	945.19	1.52	8.934207489
1450897_at	Arhgap5	253.67	181.6	253.6	281.18	208.8	146.06	153.84	156.27	178.38	139.94	235.77	154.9	1.52	4.305363781
1416723_at	Tcf4	637.13	936.27	783.39	867.62	928.04	597.89	654.93	390.6	575.9	520.83	830.49	548.03	1.52	5.876757684
1417622_at	Slc12a2	302.87	403.19	388.41	368.39	338.2	177.12	246.43	256.29	258.06	251.53	360.212	237.89	1.51	2.583218269
1452843_at	Il6st	1653.2	1145.3	1208.5	1053.3	1176.5	1076.2	869.91	622.46	879.91	674.72	1247.36	824.63	1.51	11.33922971
1448390_a_at	Dhrs3	717.96	643.18	956.61	818.75	706.96	529.59	561.29	601.51	366.37	487.48	768.692	509.25	1.51	5.986067289
1448956_at	Stard10	1564.3	1094.7	1090.1	948.12	1260.1	652.48	819.92	792.8	921.01	761.06	1191.45	789.45	1.51	8.035551262
1416940_at	Ppif	1135.6	1801.9	1717.1	1315	1692.2	1135.5	997.12	958.28	972.19	1025.9	1532.34	1017.8	1.51	5.876757684
1427691_a_at	Ifnar2	802.31	1107.4	1281.7	1057.4	1296.3	660.34	799.63	601.49	876.31	754.54	1109.01	738.46	1.50	6.981670997
1428479_at	Nfatc1	828.82	547.68	674.55	678.18	881.58	625.57	517.3	435.68	392.62	440.61	722.162	482.36	1.50	9.872171728
1429085_at	Vezf1	3386.1	2565.4	2063.9	2433.4	2835	1856.3	1870.6	1387.4	1799.9	2061.1	2656.78	1795.1	1.48	8.035551262
1455741_a_at	Ece1	351.7	346.61	482.05	521.92	405.77	304.94	330.6	264.91	249.19	275.41	421.61	285.01	1.48	6.981670997
1417892_a_at	Sirt3	3061.3	2361.5	1984.4	1977.8	2388.6	1820.9	1868.1	1157.2	1672.4	1459	2354.7	1595.5	1.48	11.33922971
1417676_a_at	Ptpro	184.89	180.73	248.24	252.62	246.73	169.98	160.2	168.97	159.81	101.14	222.642	152.02	1.46	8.934207489
1440841_at	---	231.86	255.98	246.27	226.04	218.71	172.07	144.1	98.02	173	217.85	235.772	161.01	1.46	6.981670997
1435970_at	Nlk	984.57	891.05	740.91	752.74	644.34	525.08	510.75	685.46	481.04	546.11	802.722	549.69	1.46	6.981670997
1423206_s_at	2310003F16Rik	3051	2624.2	2702.8	3025.4	2248.1	1831.7	2631.2	1313.3	1805.1	1808.1	2730.3	1877.9	1.45	9.872171728
1422580_at	Myl4	82.67	110.58	92.94	120.69	94.31	88.98	67.84	60	67.92	60	100.238	68.948	1.45	6.981670997
1460576_at	Exoc6	2343	1892.9	1570.1	2372.4	1626.9	1134.5	1299.8	1506.6	1401.1	1408.1	1961.07	1350	1.45	8.934207489
1426662_at	Cmas	2599.9	3352.9	2636.9	2661.4	2943.2	1967.2	2529.5	1495.7	2092.3	1690.3	2838.86	1955	1.45	5.876757684
1433711_s_at	Sesn1	2369.2	3057.2	3251.4	3437.1	3532.3	2426.7	2393.7	2103.2	1931.8	1957.9	3129.43	2162.7	1.45	4.305363781
1454967_at	---	396.09	429.94	289.86	339.25	332.51	276.76	274.72	210.39	243.7	229.86	357.53	247.09	1.45	5.876757684
1453360_a_at	Tex9	153.72	153.48	197.96	131.49	183.72	144.74	113.2	91.19	126.91	91.01	164.074	113.41	1.45	11.33922971
1452745_at	Trappc9	514.93	411.05	385.88	413.76	404.9	384.79	361.74	219.54	263.3	246.19	426.104	295.11	1.44	9.872171728
1455701_at	Snx26	90.78	101.87	121.77	121.62	100.7	62.8	64.39	72.31	74.98	97.45	107.348	74.386	1.44	5.986067289
1417271_a_at	Eng	935.89	691.34	887.06	900.87	1031.3	564.62	633.11	625.8	681.25	580.23	889.298	617	1.44	2.918890699
1441753_at	4921505C17Rik	203.89	171.98	167.97	140.37	153.15	139.52	94.45	82	128.26	137.77	167.472	116.4	1.44	11.33922971

Table S1. CMP to GMP transition gene signature in control mice.

Genes down-regulated in GMPs compared to CMPs (= CMPs gene signature)

Probe Set	Gene Symbol	CMPs					GMPs					Av Cont	Av Mut	Fold Diff	q-value(%)
		CMP3	CMP4	CMP6	CMP8	CMP10	GMP3	GMP4	GMP6	GMP8	GMP10				
1418084_at	Nrp1	398.54	356.54	334.76	294.38	351.72	221.02	263.79	253.82	261.47	207.45	347.188	241.51	1.44	2.583218269
1423462_at	Map3k7ip2	3908.4	2516.6	3537.8	2674.8	3138.6	2288.7	1852.3	2150	2294.8	2406.6	3155.22	2198.5	1.44	8.035551262
1421469_a_at	Stat5a	511.89	387.49	607.33	432.81	570.64	401.06	391.54	340.91	339	285.39	502.032	351.58	1.43	9.872171728
1450857_a_at	Col1a2	97.34	97.72	96.73	63.17	77.74	61.51	61.55	60	60	60	86.54	60.612	1.43	6.981670997
1418710_at	Cd59a	310.43	257.25	227.06	298.97	268.79	205	197.05	158.63	156.85	237.99	272.5	191.1	1.43	5.986067289
1437253_at	A630054L15Rik	224.39	221.11	218.2	229.36	215	148.02	140.94	173.28	176.4	138.98	221.612	155.52	1.42	0
1454739_at	Cdc27	705.41	678.74	806.86	673.62	684.51	574.05	586.44	434.34	444.27	452.03	709.828	498.23	1.42	2.583218269
1429749_at	Sfmbt1	157.47	158.69	142.52	161.02	143.42	118.59	91.98	93.95	121.65	109.81	152.624	107.2	1.42	1.655909147
1458980_at	---	525.96	410.67	466.23	409.12	508.04	281.83	304.02	295.78	322.86	426.95	464.004	326.29	1.42	5.876757684
1440033_at	---	168.66	150.95	135.9	166.07	186.55	97.98	107.23	97.86	131.26	135.17	161.626	113.9	1.42	5.118264635
1420493_a_at	Pcyt2	863.54	731.78	623.68	808.06	598.6	544.91	621.23	446.39	442.12	501.44	725.132	511.22	1.42	8.035551262
1443889_at	9030619P08Rik	221.92	228.14	219.13	233.52	292.57	151.89	203.64	168.53	193.39	125.93	239.056	168.68	1.42	6.981670997
1434745_at	Ccnd2	5765.6	5594.8	4763.9	4781.2	6293	3703.5	3981.7	2713.4	4229.2	4672.2	5439.69	3860	1.41	6.981670997
1423622_a_at	Ccnl1	4081.6	3122	3441.8	2688.9	3524.2	1869	2352.4	2198.1	2599.3	3013.7	3371.71	2406.5	1.40	11.33922971
1419642_at	Purb	868.15	886.61	920.31	636.32	878.34	466.29	558.83	606.7	657.04	708.41	837.946	599.45	1.40	6.981670997
1435069_at	BC064078	144.49	107.68	169.14	130.05	158.3	116.28	86.78	104.63	110.96	90.45	141.932	101.82	1.39	9.872171728
1452310_at	Tada2l	557.7	600.96	506.19	539.91	551.8	509.04	412.23	378.96	320.16	363.42	551.312	396.76	1.39	3.863788009
1425615_a_at	Pck2	1275.2	1632.6	1595.2	1511.2	1664.7	1209.8	1280.3	978.34	1157	908.64	1535.77	1106.8	1.39	3.863788009
1455042_at	---	779.51	735.39	689.83	831.33	640.02	603.59	630.12	590.73	431.43	398.89	735.216	530.95	1.38	8.035551262
1422737_at	Ncoa3	221.42	245.19	214.63	245.48	215.42	197.52	152.92	198.63	167.05	109.7	228.428	165.16	1.38	8.035551262
1435762_at	Pacs1	485.76	413.1	399.47	397.52	431.03	298.51	310.06	344.14	259.76	336.12	425.376	309.72	1.37	2.583218269
1451564_at	Parp14	680.39	573.61	560.85	590.26	651.65	615.01	419.72	399.99	353.28	441.98	611.352	446	1.37	9.872171728
1458218_s_at	Pde7a	383.62	324.72	426.39	355.08	397.1	290.69	220.09	350.66	244.96	276.03	377.382	276.49	1.36	8.035551262
1417295_at	Mta1	658.38	525.84	610.17	553.46	684.03	486.04	493.3	462.58	347.75	432.72	606.376	444.48	1.36	5.118264635
1417302_at	Rcor2	127.66	161.23	132.97	157.57	135.28	113.47	109.91	107.57	98.36	95.91	142.942	105.04	1.36	2.583218269
1434564_at	E2f3	660.12	762.55	851.14	780.09	784.92	484.93	604.37	582.3	603.07	558.78	767.764	566.69	1.35	2.583218269
1422675_at	Smarce1	2639.8	1879.1	2039.3	1895.1	2070.9	1666.8	1713.4	1274.6	1613.2	1578.3	2104.83	1569.2	1.34	8.934207489
1429588_at	2810474O19Rik	928.03	923.47	850.83	977.04	848.02	712.02	753.49	632.5	676.25	614.33	905.478	677.72	1.34	1.655909147
1416532_at	Trrap	1439.1	1209.3	1146.7	1543.4	1289	941.25	893.99	1010.1	1004	1122.7	1325.49	994.39	1.33	5.118264635
1445161_at	Usp6nl	201.31	161.76	175.86	160.95	180.88	139.67	103.78	144.84	124.93	149.06	176.152	132.46	1.33	5.876757684
1455481_at	Ids	620.44	470.52	619.96	587.34	651.04	497.16	456.71	458.4	375.32	437.95	589.86	445.11	1.33	5.876757684
1417223_at	Cd2bp2	1037	890.04	1002.2	1037.5	1140.5	907.62	774.45	644.86	837.32	694.31	1021.47	771.71	1.32	5.118264635
1454919_at	Nmt2	1129.5	962.54	745.41	1051	886.38	687.62	723.41	671.56	741.49	790.97	954.958	723.01	1.32	9.872171728
1454636_at	Cbx5	3078.7	3011.5	3482.7	2981	3119.7	2225.5	2606.1	2131.5	2603.3	2301.9	3134.71	2373.7	1.32	2.002494782
1421923_at	Sh3bp5	169.65	158.15	174.35	152.93	166.45	151.93	140.88	111.29	112.25	106.19	164.306	124.51	1.32	5.876757684
1453095_at	Rab10	2513.2	2495.5	2832.7	2360.6	2505.3	1748.3	1806.3	1967.1	2053	2119.9	2541.44	1938.9	1.31	2.002494782
1426241_a_at	Scmh1	265.8	244.13	260.23	304.2	250.98	250.39	215.96	194.97	191.88	160.45	265.068	202.73	1.31	8.934207489

Table S1. CMP to GMP transition gene signature in control mice.

Genes down-regulated in GMPs compared to CMPs (= CMPs gene signature)

Probe Set	Gene Symbol	CMPs					GMPs					Av Cont	Av Mut	Fold Diff	q-value(%)
		CMP3	CMP4	CMP6	CMP8	CMP10	GMP3	GMP4	GMP6	GMP8	GMP10				
1425014_at	Nr2c2	77.81	101.45	92.31	117.17	92.96	76.7	77.59	66.35	75.25	73.12	96.34	73.802	1.31	9.872171728
1428881_at	Klc1 /// LOC1000	390.47	411.04	444.89	394.93	399.25	399.03	354.22	259.98	279.33	274.59	408.116	313.43	1.30	9.872171728
1417038_at	Sept9	1909.3	2159.8	2720.4	2373.1	2356.8	1862.2	1823.8	1747.9	1670.3	1774.5	2303.87	1775.7	1.30	5.986067289
1446107_at	---	94.78	105.83	91.35	97.41	81.78	67.13	60	69.66	85.8	80.93	94.23	72.704	1.30	8.035551262
1428787_at	Nckap1l	1010.6	986.46	1029.5	981.03	1026.2	860.24	776.18	686.34	908.15	659.86	1006.77	778.15	1.29	2.918890699
1433759_at	Dpy19l1	920.84	858.7	814.8	682.99	760.57	593.65	621.81	571.43	667.41	674.72	807.58	625.8	1.29	5.118264635
1451459_at	Ahctf1	922.16	886.57	830.58	817.19	888.34	721.47	695.61	650.64	689.49	676.37	868.968	686.72	1.27	0
1416963_at	Ubac1	1183.6	1219.1	1082	1234.7	1124.9	1172.2	902.96	811.18	923.86	828.67	1168.85	927.77	1.26	8.934207489
1427981_a_at	Csad	284.48	248.11	231.64	244.92	269.71	206.26	183.52	191.74	210.81	227.58	255.772	203.98	1.25	4.305363781
1433951_at	Arl5a	783.69	762.53	748.51	817.3	757.33	674.36	633.86	665.37	524.34	590.04	773.872	617.59	1.25	2.583218269
1428854_at	Tmed8	452.55	366.93	447.03	446.61	425.91	315.95	331.83	371.4	362.24	331.35	427.806	342.55	1.25	3.376755907
1418261_at	Syk	4562.1	4050.1	3358.3	3863.3	3645.1	3241.6	3425	2769.4	3129.1	3035.3	3895.79	3120.1	1.25	8.934207489
1419359_at	Hexim1	228.61	215.17	228.04	210.94	181.4	182.22	173.83	182.85	172.55	143.12	212.832	170.91	1.25	6.981670997
1429499_at	Fbxo5	2613.6	2160.8	2111.6	2295.5	2251.4	1720.6	2164.3	1800.1	1752.7	1777.4	2286.57	1843	1.24	6.981670997
1415726_at	Ankrd17	1186.9	1197.8	1113.9	1098.4	1049.2	1078.8	890.84	848.36	839.97	908.29	1129.24	913.24	1.24	4.305363781
1416419_s_at	Gabarapl1	1530.3	1625.6	1420.7	1471.3	1698.7	1245	1290.6	982.48	1340.2	1414.9	1549.32	1254.6	1.23	9.872171728
1448361_at	Ttc3	3317.7	3367.9	3467	3031.5	3613	2324.9	2734.4	2531.6	3151.6	2912.9	3359.42	2731.1	1.23	6.981670997
1437633_at	Ankrd11 /// LOC6	605.31	557.77	646.97	538.74	602.43	414.03	503.2	434.2	566.88	483.36	590.244	480.33	1.23	9.872171728
1423975_s_at	Numa1	1999.5	1816.2	1977.4	1889.6	1898.3	1909.3	1564.9	1293.1	1513.8	1549.4	1916.17	1566.1	1.22	8.934207489
1455035_s_at	Nol5a	5690.6	4483.1	5334.5	5723.7	4994.3	4440.1	3977.8	4007.6	4261.6	4841.6	5245.25	4305.7	1.22	9.872171728
1453032_at	Mobkl3	965.89	863.73	958.06	954.12	971.4	711.28	835.74	822.83	686.47	841	942.64	779.46	1.21	4.305363781
1434997_at	Cdc2l6	1196	1414.8	1477.4	1540	1472.1	1149.1	1237.8	1226.3	1147.1	1192.6	1420.07	1190.6	1.19	6.981670997
1426525_at	Arid2	3416.5	3178.1	3089.6	2681.8	2902.2	2421.5	2587.3	2660.5	2613.4	2641.6	3053.61	2584.9	1.18	8.035551262

Table S2. Pbx1-regulated genes in CMPs

Genes up-regulated in the absence of Pbx1

Probe Set	Gene Symbol	Controls					Mutants				Average Cont	Average Mut	Fold Diff.	q-value(%)
		CMP3	CMP4	CMP6	CMP8	CMP10	CMP1	CMP2	CMP5	CMP7				
1437745_at	Chd7	97.03	161.22	183.23	89.43	73.57	1121.5	373.76	815.42	612.36	120.896	730.76	6.04	10.42419758
1449184_at	Pglyrp1	60	158.85	173.53	131.62	85.44	772.85	289.44	1046.8	735.49	121.888	711.155	5.83	10.58793513
1438511_a_at	1190002H23Rik	504.43	695.87	558.6	486.67	243.03	2648.8	1831.5	3236	1507.7	497.72	2305.9975	4.63	7.013521794
1429764_at	1500005K14Rik	82.94	175.01	177.85	228.61	147.58	776.27	546.26	851.02	505.11	162.398	669.665	4.12	4.172804729
1456765_at	6430511F03 /// EG	236.95	243.84	200.06	324.27	191.5	1052.4	483.34	645.88	1214.9	239.324	849.13	3.55	12.71951321
1434499_a_at	Ldhb	639.73	376.82	366.4	509.15	254.65	1748.5	1048.3	1194.9	1949.2	429.35	1485.225	3.46	6.965891765
1441092_at	9330159M07Rik	99.36	60	60	60	60	241.46	276.05	109.24	190.52	67.872	204.3175	3.01	11.91840305
1419029_at	Ero1l	123.88	409.59	431.67	341.73	258.18	879.12	675.95	981.26	979.96	313.01	879.0725	2.81	4.172804729
1451970_at	Daglb	147.05	132.32	203.38	72.81	125.41	283.1	347.1	392.14	375.13	136.194	349.3675	2.57	4.172804729
1420407_at	Ltb4r1	432.82	394.05	301.83	355.8	256.5	1192.2	645.76	970.17	743.24	348.2	887.845	2.55	8.766902243
1449773_s_at	Gadd45b	304.51	180.18	182.2	190.87	141.15	666.55	357.12	472.25	448.57	199.782	486.1225	2.43	10.42419758
1428289_at	Klf9	1179.4	1146.9	752.36	1441.4	986.21	2833.4	3600.4	2045.2	2172.3	1101.254	2662.815	2.42	8.766902243
1424032_at	Hvcn1	260.56	458.89	476.06	258.53	297.24	1093.4	760.29	735.95	765.97	350.256	838.89	2.40	6.965891765
1428129_at	Lman1	77.99	146.21	153.92	79.56	97.47	289.78	200.09	319.48	245.79	111.03	263.785	2.38	6.965891765
1435055_a_at	Tom1	952.77	777.48	693.51	1067.4	666.37	2160.4	1677.8	1835.9	2140.8	831.502	1953.7175	2.35	0
1435462_at	Plcxd2	60	104.62	112.74	101.73	87.19	218.46	181.85	269.2	199.28	93.256	217.1975	2.33	4.172804729
1429190_at	Arsb	60	79.1	71.04	63.91	60	194.92	131.42	160.58	132.61	66.81	154.8825	2.32	4.172804729
1426343_at	Stt3b	447.71	445.38	561.74	506.58	409.45	909.16	1086.4	1205.8	1081.7	474.172	1070.77	2.26	0
1460273_a_at	Naip2	335.14	304.59	238.29	201.56	119.26	547.55	611.64	430.08	518.91	239.768	527.045	2.20	6.965891765
1428544_at	0610007L01Rik	378.51	549.1	541.97	491.39	434.99	1229.9	781.01	1150.2	1052.1	479.192	1053.275	2.20	4.172804729
1420822_s_at	Sgpp1	479.93	416.38	454.15	426.3	342.84	815.41	663.8	1307.6	907.03	423.92	923.45	2.18	12.10755341
1449221_a_at	Rrbp1	337.71	358.96	362.51	647.42	385.84	909.86	724.9	990.29	1019.3	418.488	911.0775	2.18	6.061547922
1421957_a_at	Pcyt1a	244.76	369.04	320.17	379.2	260.7	834.48	538.54	642.41	703.66	314.774	679.7725	2.16	4.798725438
1444090_at	Pram1	157.97	129.02	178.08	136.53	136.29	295.68	214.71	333.62	387.5	147.578	307.8775	2.09	8.766902243
1426123_a_at	Rrbp1	380.03	256.14	234.6	403.14	231.66	586.18	582.21	623.56	696.53	301.114	622.12	2.07	4.172804729
1424058_at	Prrc1	570.95	930.45	823.19	760.69	731.13	1508.2	1666.1	1430.1	1665.2	763.282	1567.3875	2.05	0
1427509_at	Baiap3	97.49	97.37	80.16	92.69	88.77	159.17	254.47	174.29	151.93	91.296	184.965	2.03	9.641274853
1435259_s_at	Tmem141	151.35	231.59	186.2	220.05	154.4	342.24	384.44	304.92	494.54	188.718	381.535	2.02	8.766902243
1457287_at	---	164.92	322.02	365.85	403	341.59	797.75	453.3	632.41	695.59	319.476	644.7625	2.02	11.91840305
1448571_a_at	Gmfb	218.99	161.87	176.85	218.57	152	341.75	332.82	342.75	454.8	185.656	368.03	1.98	4.297366064
1439163_at	Zbtb16	352.8	347.42	237.9	332.39	262.46	546.53	661.89	485	700.25	306.594	598.4175	1.95	6.061547922
1434223_at	1810007P19Rik ///	74.5	64.79	80.22	64.56	83.79	161.44	134.35	137.15	138.76	73.572	142.925	1.94	0
1418888_a_at	Sepx1	764	1432.7	1023.5	1222.5	835.76	2029.6	1451.8	2296.7	2319.3	1055.688	2024.3325	1.92	10.42419758
1443870_at	Abcc4	659.46	785.25	651.17	622.14	522.29	1351.9	792.85	1332.8	1492.1	648.062	1242.4025	1.92	10.58793513
1427299_at	Rps6ka3	157.18	173.31	211.58	134.14	183.2	391.77	373.01	265.35	282.77	171.882	328.225	1.91	8.097849177
1423883_at	Acsl1	1249.9	1593.3	1084	1424.1	1057.19	2609.6	2242.2	2390.1	2512.5	1281.694	2438.61	1.90	0
1436531_at	Metap2	688.5	569.09	606.04	697.36	641.46	1147.9	998.34	1128.6	1593.2	640.49	1217.01	1.90	8.48555108

Table S2. Pbx1-regulated genes in CMPs

Genes up-regulated in the absence of Pbx1

Probe Set	Gene Symbol	Controls					Mutants				Average Cont	Average Mut	Fold Diff.	q-value(%)
		CMP3	CMP4	CMP6	CMP8	CMP10	CMP1	CMP2	CMP5	CMP7				
1427200_at	Zranb1	108.75	194.71	197.4	214.83	153.36	322.31	298.62	282.26	412.1	173.81	328.8225	1.89	8.766902243
1445181_at	Eml5	66.9	86.47	94.12	74.23	91.62	130.99	146.53	145.64	190.49	82.668	153.4125	1.86	6.337939258
1455244_at	Daam1	478.53	350.78	348.65	306.07	266.33	661.23	713.27	597.22	626.34	350.072	649.515	1.86	4.172804729
1427364_a_at	Odc1	850.46	939.22	603.48	1053.8	774.29	1488.4	1829.6	1633.3	1286.7	844.256	1559.5175	1.85	6.337939258
1437868_at	BC023892	830.99	749.38	624.69	932.36	633.37	1204.5	1698.8	1108.7	1488.5	754.158	1375.12	1.82	8.766902243
1418226_at	Orc2l	421.68	421.29	495.92	670.31	579.25	792.8	1064.3	839.85	1009.5	517.69	926.6025	1.79	6.965891765
1419798_at	2610019E17Rik	60	96.96	92.29	92.34	78.44	119.64	147.56	183.87	149.17	84.006	150.06	1.79	8.766902243
1423233_at	**Cebpd**	534.06	622.63	632.2	724.48	347.12	1244	872.75	1021.7	907.63	572.098	1011.51	1.77	10.42419758
1435091_at	Zfp568	337.84	570.4	573.26	561.38	637.56	976.46	742.96	1004.3	1066.7	536.088	947.6	1.77	8.48555108
1420548_a_at	2310008H09Rik	143.43	142.39	144.11	102.63	125.49	189.99	286.9	220.75	227.57	131.61	231.3025	1.76	8.097849177
1428667_at	Maoa	340.02	437.88	565.35	505.38	525.92	808.25	669.78	859.64	902.88	474.91	810.1375	1.71	6.965891765
1457825_x_at	Tcn2	859.8	737.52	530.89	859.96	597.05	1508.7	1079.1	1141.5	1154	717.044	1220.82	1.70	10.42419758
1442025_a_at	---	211.1	215.79	138.12	254.81	205.02	361.24	380	256.14	391.14	204.968	347.13	1.69	11.91840305
1458431_at	Eif4g2	60	70.25	70.19	74.26	67.74	125.14	126.77	101.99	109.8	68.488	115.925	1.69	0
1418703_at	Rbms1	296.97	512.61	597.52	376.69	526.95	657.77	857.14	718.28	880.59	462.148	778.445	1.68	11.91840305
1423747_a_at	Pdk1	2157.1	1911.1	1740	2659.6	1720.36	3828.4	2561.8	3448.4	3771.3	2037.628	3402.495	1.67	10.58793513
1439060_s_at	Wipi1	211.15	177.78	150.98	176.1	150.99	349.77	318.96	244.49	244.05	173.4	289.3175	1.67	10.42419758
1417764_at	Ssr1	563.56	670.77	637.26	798.06	646.29	1144	848.35	1311.6	1094.6	663.188	1099.6375	1.66	8.766902243
1441272_at	Matr3	947.54	574.41	550.6	775.71	846.79	1104.2	1103.7	1383.8	1273	739.01	1216.1625	1.65	9.641274853
1417513_at	Evi5	650.16	608.92	603.41	678.77	615.9	1163.6	886.57	825.94	1280.2	631.432	1039.0775	1.65	10.58793513
1431064_at	Dpp8	268.71	245.74	265.32	224.46	167.64	339.42	457.43	349.08	364.78	234.374	377.6775	1.61	8.766902243
1423196_at	Nedd1	70.3	115.75	140.94	122.27	96.28	182.29	190.97	176.29	153.15	109.108	175.675	1.61	10.42419758
1434942_at	Esf1	711.52	930.74	853.9	1062.3	1018.36	1238.9	1399.1	1676.1	1581.3	915.366	1473.8325	1.61	7.270796118
1422570_at	Yy1	447.89	411.66	384.19	523.86	496.72	732.42	812.19	559.39	779.56	452.864	720.89	1.59	8.766902243
1458040_at	---	101.94	96.96	105.6	93.52	86.25	136.09	119.65	176.17	181.19	96.854	153.275	1.58	11.91840305
1435430_at	Tmem1	1443.2	1268.2	1544.9	1435.5	1380.53	2402.1	1744.1	2404.3	2373.7	1414.442	2231.0375	1.58	6.337939258
1444705_at	---	116.04	114.01	108.5	113.23	81.83	198.14	126.39	169.34	176.93	106.722	167.7	1.57	12.10755341
1423943_at	Dus1l	1787.9	2003.1	2016.3	1955.5	1907.14	2767.2	3769.7	3112.8	2454.1	1933.978	3025.975	1.56	10.42419758
1441850_x_at	Tcn2	332.35	353.79	262.01	340.62	241.86	548.77	425.16	457.85	483.2	306.126	478.745	1.56	7.270796118
1423394_at	Pcyox1	420.29	508.93	554.54	470.39	584.85	845.12	664.43	713.32	937.12	507.8	789.9975	1.56	10.42419758
1451776_s_at	Hopx	60	60	60	63.72	60	78.53	86.66	96.35	116.01	60.744	94.3875	1.55	8.766902243
1452145_at	H6pd	1133.1	941.15	733.63	1054	803.46	1621.8	1494.3	1191.5	1483.8	933.054	1447.8525	1.55	9.641274853
1418899_at	Ufm1	654.6	515.65	435.4	714.58	597.05	888	1059.5	856.68	815.04	583.456	904.81	1.55	10.42419758
1426977_at	Usp47	583.9	840.01	877.77	646.61	848.1	986.59	1241.3	1202.5	1275.2	759.278	1176.3725	1.55	8.766902243
1423967_at	Palm	511.46	635.39	530.33	662.4	542.87	966.17	713.03	880.67	1012.5	576.49	893.08	1.55	8.766902243
1449694_s_at	Commd5	264.14	241.68	228.39	258.52	228.61	375.68	439.9	323.11	368.77	244.268	376.865	1.54	4.798725438
1455658_at	Cggbp1	266.51	326.38	297.63	277.49	298.78	402.97	404.45	427.34	563.33	293.358	449.5225	1.53	10.42419758

Table S2. Pbx1-regulated genes in CMPs

Genes up-regulated in the absence of Pbx1

Probe Set	Gene Symbol	Controls					Mutants				Average Cont	Average Mut	Fold Diff.	q-value(%)
		CMP3	CMP4	CMP6	CMP8	CMP10	CMP1	CMP2	CMP5	CMP7				
1418339_at	Recql	893.66	657.47	698.92	858.07	957.37	1151.9	1178.6	1126.6	1526	813.098	1245.7575	1.53	11.91840305
1428232_at	Cpsf6	981.65	557.94	616.52	714.22	718.71	1144.8	1114.9	1136	985.44	717.808	1095.2775	1.53	10.42419758
1434870_at	2810004N23Rik	562.52	506.34	511.35	580.56	724.4	843.89	858.61	768.22	1039.4	577.034	877.54	1.52	9.641274853
1423871_at	Tmem63a	505.52	629.77	573.21	669.63	600.02	853.93	994.23	810.75	959.14	595.63	904.5125	1.52	4.172804729
1437982_x_at	Cox15	749.86	524.24	570.12	704.84	628.53	929.22	907.98	1099.5	905.96	635.518	960.665	1.51	6.965891765
1415697_at	G3bp2	1243.3	1154.1	1239.8	1716.8	1228.41	2000.3	1703.6	2016.5	2193	1316.466	1978.3275	1.50	8.766902243
1428508_at	Tbc1d2b	669.21	635.06	530.38	493.13	627.49	931.63	825.73	893.21	894.59	591.054	886.29	1.50	3.427661027
1448795_a_at	Tbrg4	734.13	679.2	668	685.75	660.14	1193.4	1143.7	936.74	835.26	685.444	1027.27	1.50	9.641274853
1428146_s_at	Acaa2	1569.8	1834.8	1779.4	1453.2	1599.8	2367	2761.5	2187.6	2528.3	1647.384	2461.08	1.49	4.297366064
1416610_a_at	Clcn3	222.04	330.99	281.52	264.41	319.19	365.38	391.35	435.19	497.85	283.63	422.4425	1.49	11.91840305
1434216_a_at	Nudt19	831.57	921.33	753	655.17	612.24	1212.2	1095.7	1138.6	1048.8	754.662	1123.81	1.49	6.965891765
1450847_at	Ncbp2	822.25	757.02	857.97	834.61	804.95	1033.2	1312.5	1292.2	1214.3	815.36	1213.0825	1.49	4.172804729
1426265_x_at	Dlat	473.28	485.78	451.34	541.04	422.92	703.23	601.54	813.1	696.64	474.872	703.6275	1.48	6.965891765
1459900_at	C79468	411.96	410.97	409.33	506.19	407.76	778.39	589.17	551.23	602.65	429.242	630.36	1.47	11.91840305
1438922_x_at	Slc25a5	1698.2	1137.6	1291.3	1191.7	1360.43	1946	1728.3	2123.4	1982.4	1335.826	1945.0175	1.46	8.766902243
1460495_s_at	Htra2	1266.5	1420.3	1329.4	1112.3	1128.33	1971.6	1891.5	1797.9	1610	1251.372	1817.7275	1.45	4.297366064
1448914_a_at	**Csf1**	71.07	75.3	71.64	78.32	69.7	115.95	107.58	96.24	101.8	73.206	105.3925	1.44	3.427661027
1448302_at	Kctd20	1313.1	970.61	1067.2	1015.2	902.28	1697.9	1416.7	1380.4	1531.5	1053.68	1506.6225	1.43	9.641274853
1418437_a_at	Mlx	389.48	400.98	475.56	410.61	410.35	526.62	542.17	710.2	602.23	417.396	595.305	1.43	10.42419758
1424571_at	Ddx46	284.29	346.45	418.56	355.2	390.69	446.51	513.78	525.63	548.71	359.038	508.6575	1.42	8.766902243
1439262_x_at	2310001A20Rik	171.55	134.72	141.3	130.62	125.89	189.51	215.79	190.47	200.97	140.816	199.185	1.41	6.337939258
1428518_at	Mlf1ip	657.3	770.11	628.64	953.67	644.05	1030.1	974.99	1018.2	1095.4	730.754	1029.66	1.41	11.91840305
1429092_at	Vkorc1l1	318.33	258.62	371.3	310.49	244.6	409.67	395.19	459.2	428.15	300.668	423.0525	1.41	10.42419758
1436788_at	Acp2	157.98	175.91	162.14	118.37	127.28	208.13	209.41	204.01	210.98	148.336	208.1325	1.40	8.766902243
1448610_a_at	Sod2	4504.7	3400.1	3552.4	3240.4	3105.2	5063.9	5552.2	4692	4643.8	3560.564	4987.985	1.40	10.42419758
1423333_at	Ergic1	351.66	420.56	416.45	431.89	401.29	623.8	536.73	531.56	570.65	404.37	565.685	1.40	4.172804729
1420977_at	Man1a2	317.61	348.34	320.44	392.43	295.7	524.03	477.14	410.69	458.56	334.904	467.605	1.40	8.766902243
1425011_x_at	Stx18	1029.7	889.99	1030.3	869.99	979.3	1293.9	1122.5	1487.1	1439.9	959.848	1335.82	1.39	8.766902243
1452839_at	Dph5	456.35	566.92	632.7	559.7	670.34	819.18	896.87	713.61	779.57	577.202	802.3075	1.39	10.58793513
1451368_at	Alg1	527.71	491.87	378.25	405.21	369.34	582.6	622.69	633.38	557.94	434.476	599.1525	1.38	10.58793513
1419363_a_at	Mrpl35	1285.1	1484.5	1477.3	1201.1	1293.23	1617.7	1871.4	1911	1945.9	1348.244	1836.475	1.36	6.965891765
1459522_s_at	Gyg	6707.5	8031.6	7435.5	8322.5	6793.76	11159	8358.9	10457	10533	7458.164	10126.8475	1.36	11.91840305
1448583_at	AA960436	555.73	449.95	466.11	469.19	530.51	675.18	655.95	685.35	659.7	494.298	669.045	1.35	3.427661027
1436732_s_at	Fbxw8	794.78	938.67	971.91	1032.9	989.81	1158.6	1366.8	1199.8	1384.2	945.616	1277.3375	1.35	8.48555108
1438769_a_at	Thyn1	608.66	620.64	526.58	787.53	597.24	885.14	793.23	807.63	905.53	628.13	847.8825	1.35	12.10755341
1456520_at	Zfp652	194.06	214.43	228.69	183.44	209.84	257.48	294.95	304.83	249.54	206.092	276.7	1.34	8.766902243
1442465_s_at	Strbp	610.28	557.22	622.39	674.44	607.75	695.26	879.62	837.08	887.23	614.416	824.7975	1.34	8.766902243

Table S2. Pbx1-regulated genes in CMPs

Genes up-regulated in the absence of Pbx1

Probe Set	Gene Symbol	Controls					Mutants				Average Cont	Average Mut	Fold Diff.	q-value(%)
		CMP3	CMP4	CMP6	CMP8	CMP10	CMP1	CMP2	CMP5	CMP7				
1423060_at	Pa2g4	3341.2	3378.9	3759.7	3915.9	3408.89	5185	3920.1	5115.6	4869.6	3560.93	4772.5725	1.34	10.58793513
1454996_at	Hsdl1	1535.3	1412.2	1460.3	1085.5	1318.73	1782.9	1721.4	1878	1916.2	1362.41	1824.62	1.34	8.48555108
1420013_s_at	Lss	216.91	255.52	247.83	261.46	276.47	342.51	378.89	324.7	298.26	251.638	336.09	1.34	8.766902243
1433646_at	Mrps27	511.22	501.23	514.33	588.74	623.45	675.66	811.29	740.16	683.53	547.794	727.66	1.33	8.766902243
1453048_at	Nhlrc2	336.39	350.02	414.2	350.22	378.59	474.3	536.6	452.08	426.33	365.884	472.3275	1.29	11.91840305
1424904_at	1300010F03Rik	190.58	200.8	207.67	206.49	189.34	254.87	223.12	252.42	293.06	198.976	255.8675	1.29	10.42419758
1452579_at	Iscu	1371	1445.4	1177.9	1256.8	1370.03	1592.2	1614	1789.7	1731.8	1324.222	1681.9275	1.27	6.965891765
1417287_at	H13	3157.2	3577.2	3788.2	3245.4	3070.5	4415.9	4253.3	4257.7	4041.5	3367.71	4242.0825	1.26	6.965891765
1448517_at	Timm22	880.47	917.68	799.81	703.73	908.85	1063.8	999.98	1101.3	1067.7	842.108	1058.1825	1.26	10.42419758
1455420_at	Rad23b	162.68	152.99	178.31	165.42	140.04	194.86	211.78	190.35	206.36	159.888	200.8375	1.26	8.48555108
1448488_at	Mrps5	566.52	628.74	540.78	574.24	578.91	709.42	808.9	734.04	643.37	577.838	723.9325	1.25	10.42419758

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Genes down-regulated in the absence of Pbx1

Probe Set	Gene Symbol	Controls					Mutants				Average Cont	Average Mut	Fold Diff.	q-value(%)
		CMP3	CMP4	CMP6	CMP8	CMP10	CMP1	CMP2	CMP5	CMP7				
1449757_x_at	Dntt	627.99	338.64	406.35	847.91	917.21	60	60	60	60	627.62	60	10.46	8.097849177
1417155_at	Mycn	328.18	583.72	448.81	298.64	704.17	60	136.18	65.67	60	472.704	80.4625	5.87	7.270796118
1421461_at	Mpl	1012	697.79	532.25	681.3	1002.57	107.9	348.62	149.41	120.78	785.176	181.6775	4.32	5.141491541
1428647_at	Pbx1	3159.8	4136.2	1799.8	1769.1	2368.54	685.73	672.49	470.15	719.46	2646.694	636.9575	4.16	10.52884906
1448995_at	Pf4	18559	15072	9858.7	11817	11545.6	4218.8	9788.1	727.14	194.88	13370.504	3732.235	3.58	10.58793513
1448748_at	Plek	3085.7	3762.7	2379.7	2379.2	3005.51	560.94	1316.4	727.7	665.95	2922.574	817.7375	3.57	3.69132726
1424588_at	Srgap3	336.91	399.08	229.22	332.88	240.39	118.87	60	93.24	76.48	307.696	87.1475	3.53	4.265533723
1439066_at	Angpt1	1544.6	1897.2	1159.5	1495	1876.31	352.44	750.07	332.06	386.58	1594.514	455.2875	3.50	3.69132726
1437667_a_at	Bach2	234.76	255.25	184.96	278.81	201.62	71.32	80.82	60	60	231.08	68.035	3.40	0
1423213_at	Plxnc1	1726	2028.4	1605.8	1088.5	1323.44	355.72	733.83	334.39	426.13	1554.42	462.5175	3.36	5.141491541
1425503_at	Gcnt2	409.95	532.76	464.94	678.45	731.77	195.69	172.86	173.57	158.89	563.574	175.2525	3.22	5.141491541
1449988_at	Gimap1	291.04	314.19	242.41	127.32	249.78	81.22	112.47	60.63	60	244.948	78.58	3.12	8.097849177
1450992_a_at	Meis1	1131	1129	954.09	689.23	989.26	404.98	550.33	237.25	207.9	978.528	350.115	2.79	5.141491541
1424852_at	Mef2c	4256	5658.5	4329.7	3459	5660.12	1780.9	981.61	1877.9	2160.3	4672.662	1700.1875	2.75	5.141491541
1433485_x_at	Gpr56	3245	5970.6	5119.9	3676.1	5292.57	1851.6	2218.8	1443.7	1299.7	4660.832	1703.4575	2.74	6.061547922
1424923_at	Serpina3g	6916.9	4386.3	4632.4	4793.4	5275.87	2336.7	2790.4	1165.5	1353.7	5200.964	1911.57	2.72	5.141491541
1419538_at	Flt3	2276.5	1964.5	2318.3	3822	3114.83	954.56	1174	1040.5	891.04	2699.242	1015.0025	2.66	8.097849177
1447584_s_at	Myct1	279.17	164.07	190.12	202.41	190.98	60	131.95	60	60	205.35	77.9875	2.63	6.337939258
1437308_s_at	F2r	16274	15397	12740	14415	15133.6	7051.7	13001	2487.1	921.21	14792.02	5865.1425	2.52	11.91840305
1419722_at	Klk8	1091.9	708.7	632.87	710.35	736.04	234.9	381.89	276.78	343.13	775.976	309.175	2.51	6.061547922
1435144_at	---	820.76	912.94	579.14	466.18	723.2	204.14	486.34	155.34	271.87	700.444	279.4225	2.51	10.52884906
1428650_at	Tns1	455.86	643.77	448.28	643.23	888.03	198.78	342.51	203.89	249.41	615.834	248.6475	2.48	10.52884906
1446484_at	---	431.69	375.66	227.81	507.53	514.47	226.05	70.2	169.52	205.9	411.432	167.9175	2.45	11.91840305
1425742_a_at	Tsc22d1	2989.6	3056.3	1591.4	2072.9	2404.79	747.78	1679.9	623.67	905.61	2422.974	989.2275	2.45	10.52884906
1433883_at	Tpm4	2218.5	2463.8	2814.4	2589.1	3072.96	998.56	612.43	1085.8	1634.5	2631.734	1082.82	2.43	3.69132726
1417558_at	Fyn	1256.7	1144.8	777.61	1057.5	1253.96	489.88	673.05	305.96	352.36	1098.114	455.3125	2.41	5.141491541
1457052_at	Kcng1	397	241.36	238.21	336.98	367.95	119.24	193.37	130.01	84.66	316.3	131.82	2.40	7.270796118
1460719_a_at	P2rx1	193.12	255.05	277.53	129	231.94	65.49	106.79	109.17	81.12	217.328	90.6425	2.40	8.771863704
1428510_at	Lphn1	418.31	458.67	330.31	655.57	585.63	181.96	252.19	176.28	211.53	489.698	205.49	2.38	8.48555108
1421118_a_at	Gpr56	2287.9	2499.4	3433.1	2327.9	3052.77	1168.7	1655.4	1043.7	709.91	2720.196	1144.425	2.38	5.141491541
1423350_at	Socs5	429.64	332.56	336.37	340.21	338.96	202.24	90.63	219.17	88.7	355.548	150.185	2.37	5.141491541
1455161_at	AI504432	2678.1	1659.9	1312.7	1784.8	1774.93	901.12	1029.8	517.56	669.64	1842.076	779.525	2.36	10.52884906
1425506_at	Mylk	220.57	346.67	221.18	271.83	265.14	124.12	98.36	96.22	131.42	265.078	112.53	2.36	5.141491541
1428572_at	Basp1 /// LOC1000	1014.6	484.83	958.82	805.38	831.04	332.15	296.19	306.51	461.94	818.942	349.1975	2.35	8.097849177
1456064_at	AI504432	592.76	637.59	733.37	419.67	841.25	313.81	298.61	237.81	251.02	644.928	275.3125	2.34	7.013521794
1456634_at	9830001H06Rik	260.9	253.75	208.75	185.75	117.1	74.23	132.09	89.18	60	205.25	88.875	2.31	12.10755341
1437122_at	Bcl2	332.82	471.36	378.62	202.66	406.55	199.05	168.85	142.77	111.27	358.402	155.485	2.31	10.52884906

Genes down-regulated in the absence of Pbx1

Probe Set	Gene Symbol	Controls					Mutants				Average Cont	Average Mut	Fold Diff.	q-value(%)
		CMP3	CMP4	CMP6	CMP8	CMP10	CMP1	CMP2	CMP5	CMP7				
1421937_at	Dapp1	3057.5	1956.7	1918.7	2243.5	2511.26	1162.9	1071.8	965.06	902.63	2337.518	1025.6025	2.28	5.141491541
1427819_at	---	463.87	345.25	229.74	330.22	278.49	207.51	114.69	156.67	103.77	329.514	145.66	2.26	10.58793513
1456795_at	D330027G24Rik	93.6	186.65	177.37	122.62	186.26	77.62	60	65.71	71.61	153.3	68.735	2.23	10.52884906
1435083_at	Ctxn1	151.79	157.3	135.86	241.99	239.98	104.43	76.29	71.77	80.04	185.384	83.1325	2.23	10.52884906
1451506_at	Mef2c	1460.2	968.22	834.52	841.17	1305.25	352.18	438.79	509.03	663.24	1081.872	490.81	2.20	10.52884906
1415995_at	Casp6	554.89	703.03	590.88	548.17	593.13	254.64	255.5	280.92	301.4	598.02	273.115	2.19	0
1460555_at	Fam65b	1527.3	1645.1	1669.1	1081.8	1579.74	666.46	641.49	680.91	762.82	1500.624	687.92	2.18	3.69132726
1435745_at	5031439G07Rik	1263.7	1129.1	1131.2	2079.3	1422.51	817.06	446.82	589.42	734.69	1405.136	646.9975	2.17	12.10755341
1443832_s_at	Sdpr	202.48	199.88	106.34	146.44	132.57	70.88	99.55	60	60	157.542	72.6075	2.17	10.58793513
1436515_at	Bach2	231.37	304.17	264.46	423.11	300.34	159.22	203.95	97.54	102.31	304.69	140.755	2.16	10.52884906
1452823_at	Gstk1	335.3	264.82	204.39	209.48	181.92	99.21	119.32	116.6	107.4	239.182	110.6325	2.16	8.771863704
1425517_s_at	Ogt	354.06	251.71	436.5	248.26	298.11	140.83	91.13	199.69	160.1	317.728	147.9375	2.15	10.52884906
1428479_at	Nfatc1	828.82	547.68	674.55	678.18	881.58	297.19	184.47	368.31	527.55	722.162	344.38	2.10	8.771863704
1433719_at	Slc9a9	141.28	177.97	184.22	174.41	148.28	74.32	60	77.8	103.61	165.232	78.9325	2.09	3.69132726
1433939_at	Aff3	3695.9	3448.5	3744.8	3997.2	3782.44	2097.1	2555	1267.7	1270.1	3733.764	1797.48	2.08	3.69132726
1418741_at	Itgb7	1046.4	777.41	969.62	1070	1124.3	429.39	748.12	330.83	416.27	997.538	481.1525	2.07	6.061547922
1426397_at	Tgfbr2	671.95	1253.6	709.53	762.82	890.49	406.67	470.26	347.15	443.66	857.684	416.935	2.06	11.91840305
1427918_a_at	Rhoq	369.59	282.04	359.27	418.3	362.49	263.34	60.89	191.76	180.81	358.338	174.2	2.06	8.771863704
1436836_x_at	Cnn3 /// LOC1000	5287.8	4899.3	7564.8	8115.8	7858.96	2679.4	2338.9	4279.8	3904.9	6745.336	3300.74	2.04	10.52884906
1435195_at	Vash1	484.56	510.21	343.6	497.08	406.82	242.19	297.13	147.27	197.02	448.454	220.9025	2.03	5.645559339
1416257_at	Capn2	472.61	277.76	327.31	321.98	359.18	170.46	162.33	153.68	207.14	351.768	173.4025	2.03	6.965891765
1427185_at	Mef2a	392.58	505.55	564.64	506.74	555.01	160.31	124.92	343.63	374.88	504.904	250.935	2.01	10.52884906
1416872_at	Tspan6	196.32	271.25	257.75	199.5	290.8	74.13	174.72	131.19	105.22	243.124	121.315	2.00	8.48555108
1449856_at	Rgs18	1942	2151.9	1913.6	1005.7	1800.29	791.08	858.36	938.76	933.2	1762.69	880.35	2.00	10.52884906
1436181_at	Ddef2	213.23	293.11	174.56	216.88	185.73	104.16	82.84	118.45	127.51	216.702	108.24	2.00	8.097849177
1421891_at	St3gal2	235.18	203.51	257.49	150.81	218.38	106.66	119.42	117.59	82.1	213.074	106.4425	2.00	5.645559339
1428577_at	Ppfia4	243.2	211.7	234.03	193.95	267.87	96.37	69.39	132.74	163.15	230.15	115.4125	1.99	5.645559339
1433501_at	Ctso	838.47	620.69	560.3	431.3	577.75	295.35	282.73	341.18	296.32	605.702	303.895	1.99	9.641274853
1419222_at	Tbxa2r	141.39	172.87	139.22	245.78	229.24	96.56	95.25	82.37	99.31	185.7	93.3725	1.99	11.91840305
1448398_s_at	Rpl22	3242.2	3087	2741.6	2492.7	3277.98	1182.5	1600.5	1360.5	1852.8	2968.298	1499.0875	1.98	3.69132726
1448960_at	Cxxc5	1650.9	1152	1145.3	1720.1	1882.88	754.23	903.35	766.14	653.66	1510.224	769.345	1.96	8.771863704
1437421_at	---	174.02	194.4	204.37	117.78	171.24	71.82	60	107.55	112.11	172.362	87.87	1.96	8.771863704
1453261_at	2610035D17Rik	153.43	129.94	114.62	195.87	143.22	71.64	88.2	60	81.19	147.416	75.2575	1.96	8.097849177
1451427_a_at	Egfl7	751.09	693.74	800.99	1033.6	1198.39	344.47	630.04	413.15	448.16	895.568	458.955	1.95	11.91840305
1445895_at	---	182.89	163.37	135.13	134.2	106.27	62.39	86.92	60	86.8	144.372	74.0275	1.95	8.097849177
1424455_at	Gprasp1	428.13	487.33	367.29	667.99	424.98	258.42	168.73	268.99	286.94	475.144	245.77	1.93	11.91840305
1422737_at	Ncoa3	221.42	245.19	214.63	245.48	215.42	106.51	60	155.58	153.66	228.428	118.9375	1.92	5.141491541

Table S2. Pbx1-regulated genes in CMPs

Genes down-regulated in the absence of Pbx1

Probe Set	Gene Symbol	Controls					Mutants				Average Cont	Average Mut	Fold Diff.	q-value(%)
		CMP3	CMP4	CMP6	CMP8	CMP10	CMP1	CMP2	CMP5	CMP7				
1433695_at	Cnrip1	209.54	120.15	186.47	128.91	188.78	60	106.08	95.48	86.09	166.77	86.9125	1.92	11.91840305
1416683_at	Plxnb2	545.39	422.99	535.75	669.08	785.85	315.07	236.17	288.88	398.3	591.812	309.605	1.91	10.58793513
1418004_a_at	Tmem176b	5678.3	8145.4	7039.6	5935.8	8095.12	4916.8	3138.8	2930.6	3621.5	6978.846	3651.9175	1.91	6.337939258
1433711_s_at	Sesn1	2369.2	3057.2	3251.4	3437.1	3532.3	1558.3	1447.5	1627	1927.6	3129.426	1640.085	1.91	3.69132726
1454899_at	Lpp	220.93	155.88	171.01	127.74	203.52	94.58	71.24	99.63	105.09	175.816	92.635	1.90	8.771863704
1417240_at	Zyx	2543.6	3054.6	2327.6	2486.1	3028.86	1334.5	1901	1056.7	1393	2688.138	1421.295	1.89	5.141491541
1458370_at	Bmp2k	513.01	630.55	437.4	453.53	409.42	257.88	190.71	338.3	253.11	488.782	260	1.88	7.270796118
1454727_at	Afap1l1	901.38	1019.5	1123.6	1054.2	1165.11	515.79	550.29	616.32	566.47	1052.768	562.2175	1.87	0
1454971_x_at	Tsc22d1	8484.7	8045.7	5477.1	8323.2	7767.3	3887.8	6377.7	2105.2	4114.6	7619.582	4121.3125	1.85	12.10755341
1424704_at	Runx2	2326.6	2833.8	3081.1	3102.4	3453.66	1741.2	1047.3	1772.8	1843.3	2959.524	1601.145	1.85	5.141491541
1434457_at	Sp100	282.46	191.62	214.15	200.02	232.01	123.95	87.71	136.78	142.57	224.052	122.7525	1.83	6.061547922
1422474_at	Pde4b	195.87	205.57	240.95	218.54	284.05	114.1	124.86	133.5	129.68	228.996	125.535	1.82	4.265533723
1422527_at	H2-DMa	3286.5	2793.4	2695.1	2806.3	2727.65	1987.1	1922.5	908.51	1507.4	2861.774	1581.365	1.81	5.141491541
1449303_at	Sesn3	293.03	215.86	213.75	216.06	222.46	135.18	103.38	126.34	150.22	232.232	128.78	1.80	5.141491541
1417218_at	Calhm2	369.7	342.41	335.69	266.76	294.02	188.81	213.23	159.78	154.5	321.716	179.08	1.80	3.69132726
1416007_at	Satb1	963.87	1098.2	723.31	1031.3	818.22	706.97	574.75	368.68	415.67	926.984	516.5175	1.79	9.641274853
1457687_at	Bcl2	3234.2	3534.6	3858.8	4517.7	4654.02	2578.2	1644.1	2240.8	2408.3	3959.862	2217.8475	1.79	6.061547922
1417336_a_at	Sytl4	177.62	160.35	157.05	124.37	182.44	67.49	106.54	110.94	77.05	160.366	90.505	1.77	6.337939258
1438999_a_at	Nfat5	116.38	189.64	161.05	134.91	148.89	110.47	60	93.22	75.8	150.174	84.8725	1.77	10.52884906
1434058_at	Mtmr12	462.94	406.15	424.22	348.69	411.04	225.5	121.05	290.75	292.67	410.608	232.4925	1.77	8.097849177
1440226_at	Zfp760	340.47	429.88	411.78	333.22	409.17	200.82	204.87	240.8	229.23	384.904	218.93	1.76	3.69132726
1448892_at	Dock7	341.75	340.42	371.56	230.42	268.4	122.41	174.14	183.84	233.34	310.51	178.4325	1.74	11.91840305
1415850_at	Rasa3	1425.1	2044	1989.9	1320.7	1987.52	1086.9	943.88	963.87	1076.4	1753.446	1017.7575	1.72	8.771863704
1433546_at	Gns	423.35	414.78	423.35	335.42	424.56	198.9	292.3	227.54	221.33	404.292	235.0175	1.72	3.69132726
1428517_at	Wdfy3	477.25	346.73	460.58	285.57	364.53	202.16	219.48	209.4	268.94	386.932	224.995	1.72	10.52884906
1455481_at	Ids	620.44	470.52	619.96	587.34	651.04	300.78	243.99	399.44	429.92	589.86	343.5325	1.72	6.337939258
1420756_at	Fut7	700.84	637.18	639.43	660.6	785.57	449.79	389.73	331.02	432.43	684.724	400.7425	1.71	3.69132726
1418634_at	Notch1	2443.2	3074.7	3111.5	3236.5	4222.97	2153.6	1402	1750	2231.2	3217.77	1884.17	1.71	11.91840305
1452746_at	Atp13a2	2486.6	2552.2	3191.1	3232	3522.35	1669.8	1905.8	1510	1949.3	2996.856	1758.73	1.70	5.645559339
1434063_at	Zfp664	421.07	443.21	527.97	354.57	505.01	253.5	316.4	304.74	193.25	450.366	266.9725	1.69	8.097849177
1437111_at	Zc3h12c	234.35	254.45	231.46	277.02	244.1	126.24	88.17	175.25	199.63	248.276	147.3225	1.69	8.48555108
1448775_at	Ifi203	2722.3	2728.7	2913.9	3947.9	3464.96	2022.8	1721	1690.5	2086.6	3155.54	1880.2475	1.68	7.270796118
1434576_at	Tsga14	238.21	350.92	371.27	253.16	295.12	193.82	149.46	190.26	185.65	301.736	179.7975	1.68	10.52884906
1434179_at	Mll3	448.88	640.39	578.3	438.45	531.98	338.58	340.86	324.01	254.18	527.6	314.4075	1.68	7.013521794
1418181_at	Ptp4a3	1611.4	2019	1963.8	1736.7	2489.32	1126.4	1531	1132.5	902.24	1964.032	1173.0375	1.67	10.52884906
1417609_at	Ube2a	505.31	556.53	494.28	373.23	424.43	255.21	275.69	324.58	275.44	470.756	282.73	1.67	6.061547922
1434359_at	Fam65b	235.87	255.82	243.27	233.5	245.78	151.18	170.79	119.62	142.58	242.848	146.0425	1.66	0

Table S2. Pbx1-regulated genes in CMPs

Genes down-regulated in the absence of Pbx1

Probe Set	Gene Symbol	Controls					Mutants				Average Cont	Average Mut	Fold Diff.	q-value(%)
		CMP3	CMP4	CMP6	CMP8	CMP10	CMP1	CMP2	CMP5	CMP7				
1435564_at	EG240055	122.46	161.89	155.54	147.45	143.71	94.6	75.85	90.75	90.9	146.21	88.025	1.66	3.69132726
1434036_at	Mtss1	294.71	333.42	256.55	214.95	242.8	117.21	174.6	192.99	163.12	268.486	161.98	1.66	10.52884906
1433514_at	Etnk1	2422.6	3889.8	3605.8	2659.5	3680.34	2059.4	1580.2	2294.8	1925.1	3251.61	1964.8725	1.65	12.10755341
1433668_at	Pnrc1	1627.8	2153.4	1601.3	1463.6	1797.16	983.23	1292.8	849.4	1058.2	1728.644	1045.92	1.65	8.097849177
1452222_at	Utrn	879.44	546.13	593.75	659.45	691.19	406.61	331.46	391.7	513.37	673.992	410.785	1.64	11.91840305
1434444_s_at	Anapc1	463.25	615.38	652.92	645.57	730.55	441.5	271.97	407.92	394.66	621.534	379.0125	1.64	8.771863704
1456380_x_at	Cnn3 /// LOC1000	442.73	310.04	405.55	514.47	454.06	206.31	212.52	304.53	321.42	425.37	261.195	1.63	12.71951321
1421963_a_at	Cdc25b	627.94	774.45	689.02	578.69	712.14	395.28	608.11	317.78	341.73	676.448	415.725	1.63	10.58793513
1428064_at	Arap1	704.99	1013.7	874.72	835.95	809.43	650.98	446.58	496.54	500.01	847.762	523.5275	1.62	6.337939258
1437161_x_at	Rbpms	189.54	265.91	238.66	296.18	249.76	190.81	143.01	144.5	138.19	248.01	154.1275	1.61	8.771863704
1417791_a_at	Zfml	844	850.08	846.36	719.86	815.78	465.26	456.47	629.27	479.5	815.216	507.625	1.61	3.69132726
1451352_s_at	Mta3	897.26	780.64	1022.9	954.37	1169.69	524.13	759.03	608.3	514.84	964.98	601.575	1.60	8.771863704
1416844_at	Prmt2	216.71	215.7	175.26	209.41	153.27	163.38	107.25	118.74	95.84	194.07	121.3025	1.60	10.58793513
1460728_s_at	Ing4	342.61	362.99	418.7	259.85	312.54	223.09	213.72	203.41	208.69	339.338	212.2275	1.60	8.48555108
1453360_a_at	Tex9	153.72	153.48	197.96	131.49	183.72	84.86	95.54	125.42	106.88	164.074	103.175	1.59	10.52884906
1436067_at	Zbtb10	158.47	116.99	137.9	173.87	156.58	60	109	104.86	100.7	148.762	93.64	1.59	10.58793513
1445546_at	AI844685	208.51	175.5	203.16	177.35	162.96	123.42	118.43	118.57	112.19	185.496	118.1525	1.57	3.69132726
1428789_at	Ralgps2	1376.5	1148.4	1102.5	1688.7	1402.59	924.26	807.19	711.9	997.37	1343.736	860.18	1.56	10.58793513
1452186_at	Rbm5	3093.3	3421.9	4467.2	2891.5	3501.27	2571.4	1717.7	2457.6	2188.5	3475.04	2233.78	1.56	12.10755341
1433826_at	Tspyl3	589.11	512.98	560.77	571.05	613.94	331.07	256.61	406	481.38	569.57	368.765	1.54	8.097849177
1423678_at	BC017643	1276.5	1288.2	1217.6	922.71	1099.62	867.09	729.22	753.81	658.18	1160.928	752.075	1.54	6.337939258
1430127_a_at	Ccnd2	2637.3	2692.4	2087.7	2042	2575.04	1814.3	1724.7	1560.5	1141.9	2406.864	1560.355	1.54	8.771863704
1426832_at	Ddx26b	1781.8	2201.4	1712.5	1757.8	1796.42	1507.9	1450.5	959.36	903.39	1849.96	1205.2725	1.53	10.58793513
1449404_at	Pip4k2a	2146.6	1873.2	1731	2522.3	2059.08	1251	1540	1130.4	1502.4	2066.442	1355.935	1.52	8.771863704
1434027_at	Rcan3	206.56	173.15	178.86	184.19	200.95	97.65	144.67	99.39	154	188.742	123.9275	1.52	8.097849177
1436161_at	Pds5b	1394.3	1233.2	1312.1	1548.7	1333.23	1033.4	544.69	1071.6	939.45	1364.302	897.2875	1.52	10.52884906
1426662_at	Cmas	2599.9	3352.9	2636.9	2661.4	2943.23	2163.9	1639.6	1776.6	1899.6	2838.86	1869.9425	1.52	5.141491541
1421194_at	Itga4	163.19	162.53	198.33	157.14	211.29	106.51	112.47	144	110.53	178.496	118.3775	1.51	8.771863704
1452231_x_at	Ifi203	5763.4	6223.6	4588.5	6037.1	4925.8	4142.6	3338.5	3073.9	4070.8	5507.662	3656.42	1.51	8.097849177
1418261_at	Syk	4562.1	4050.1	3358.3	3863.3	3645.14	3108.7	2312.4	2283.7	2679.5	3895.79	2596.0625	1.50	6.965891765
1419259_at	Rsu1	2002.7	2519.6	2658.5	2058	2531.36	1439.7	1336.9	1784.5	1722.2	2354.026	1570.8525	1.50	8.097849177
1445665_at	---	140.61	111.01	108.13	118.17	123.4	91.32	60	101.86	68.83	120.264	80.5025	1.49	10.58793513
1451176_at	Mavs	715.35	627.72	548.94	548.42	618.97	330.32	519.82	367.3	426.59	611.88	411.0075	1.49	9.641274853
1452085_at	Gatad1	740.37	653.67	708.41	648.91	831.9	395.12	456.41	564.42	510.96	716.652	481.7275	1.49	6.337939258
1426906_at	Ifi203	4186	4151.2	3789.4	4990.3	3681.09	3128.1	2435.2	2373.3	3281.3	4159.592	2804.4525	1.48	8.771863704
1416968_a_at	Hsd3b7	1194.2	1270.7	1342.2	1116.4	1343.65	840.3	912.35	725.31	912.46	1253.438	847.605	1.48	3.69132726
1424015_at	Dennd5a	2175.9	2312.5	2418.9	1741.6	2042.68	1505	1381.2	1383.9	1518	2138.322	1447.02	1.48	5.141491541

Table S2. Pbx1-regulated genes in CMPs

Genes down-regulated in the absence of Pbx1

Probe Set	Gene Symbol	Controls					Mutants				Average Cont	Average Mut	Fold Diff.	q-value(%)
		CMP3	CMP4	CMP6	CMP8	CMP10	CMP1	CMP2	CMP5	CMP7				
1458980_at	---	525.96	410.67	466.23	409.12	508.04	273.57	277.58	311.64	393.48	464.004	314.0675	1.48	8.771863704
1430028_at	2210018M11Rik	216.91	176.23	179.38	161.56	154.93	128.13	127.65	122.39	103.43	177.802	120.4	1.48	8.097849177
1448926_at	Hoxa5	174.64	168.4	124.31	157.65	151.89	136.95	88.46	96.23	101.67	155.378	105.8275	1.47	11.91840305
1417503_at	Rfc2	3518.5	3661.6	3530.1	4452.4	3325.49	3179.8	2037.5	2131.7	2731.6	3697.586	2520.135	1.47	11.91840305
1423999_at	Abl1	1064.5	1422.4	1000.7	1131.1	1216.92	926.13	852.64	696.32	712.93	1167.128	797.005	1.46	10.52884906
1425104_at	Kctd1	541.56	398.06	403.4	413.58	429.49	278.75	294.36	304.27	320.14	437.218	299.38	1.46	7.270796118
1433756_at	S100pbp	500.35	413.05	417.3	423.21	355.03	330.7	265.9	275.2	285.43	421.788	289.3075	1.46	7.013521794
1423070_at	Rpl21	297.65	326.54	342.69	243.27	307.9	188.14	161.43	227.79	255.64	303.61	208.25	1.46	12.10755341
1426957_at	Trp53bp1	439.13	582.32	468.78	528.94	509.89	360.29	414.41	330.78	285.43	505.812	347.7275	1.45	8.097849177
1423609_a_at	Mgat1	2279.7	2959.1	2156.9	2562.7	2645.41	1916.6	1750.6	1614.6	1688.1	2520.75	1742.4725	1.45	6.965891765
1426365_at	2810403A07Rik	719.92	942.05	737.2	769.03	770.25	664.8	484.94	618	419.47	787.69	546.8025	1.44	12.10755341
1451075_s_at	Ctdsp2	4036.2	4172.7	4162.2	4137.5	4760.96	2836.1	2988.6	2422	3627.2	4253.924	2968.4675	1.43	6.061547922
1434361_at	Snx33	127.27	124.45	125.01	137.05	126.08	99.64	93.86	87.91	76.31	127.972	89.43	1.43	0
1427317_at	Kin	432.46	411.33	425.9	389.89	428.08	320.63	298.97	329.46	228.62	417.532	294.42	1.42	5.141491541
1436121_a_at	Nsmce1	1281	1441.7	1255.5	1134.6	1178.68	870.3	780.63	901.21	1021.2	1258.288	893.3325	1.41	5.645559339
1416118_at	Trim59	1386.3	1751.7	1640.4	1674.4	1944.61	1219.2	1132.8	1247.8	1183.1	1679.474	1195.705	1.40	6.337939258
1454979_at	Diap1	3918.3	4705.9	3562.3	4170.8	3940.21	3305.7	3246.9	2417.2	2633.9	4059.494	2900.9175	1.40	8.771863704
1423655_a_at	1500010J02Rik	732.1	642.54	747.8	722.87	715.6	529.66	457.1	453.71	602.13	712.182	510.65	1.39	5.141491541
1455502_at	Madd	2178.9	1762.2	1752.7	1912.3	2186.91	1275.4	1475	1310.1	1575.9	1958.578	1409.1	1.39	7.270796118
1416662_at	Sardh	132.98	122.84	119.82	147.3	168.75	104.36	99.27	98.78	99.95	138.338	100.59	1.38	11.91840305
1451519_at	Rnf2	538.31	628.53	598.1	633.75	634.9	393.03	397.37	529.14	446.16	606.718	441.425	1.37	6.061547922
1428881_at	Klc1 /// LOC10004	390.47	411.04	444.89	394.93	399.25	335.92	275.66	328.99	249.14	408.116	297.4275	1.37	5.141491541
1452214_at	Skil	589.36	506.75	472.95	523.52	600.27	367.15	322.63	424.19	461.82	538.57	393.9475	1.37	10.58793513
1453095_at	Rab10	2513.2	2495.5	2832.7	2360.6	2505.29	1956.2	1612	1953.4	1920.5	2541.438	1860.5025	1.37	3.69132726
1448928_at	Hdac6	405.9	368.12	444.8	364.64	415.6	298.51	297.89	287.27	289.76	399.812	293.3575	1.36	3.69132726
1416406_at	Pea15a	147.94	120.41	147.11	144.89	148.24	107.6	101.76	101.62	106.05	141.718	104.2575	1.36	3.69132726
1453032_at	Mobkl3	965.89	863.73	958.06	954.12	971.4	764.97	553.38	749.52	707.51	942.64	693.845	1.36	5.141491541
1423269_a_at	Nedd4l	347.03	424.58	364.4	348.36	332.11	305.66	215.2	277.37	272.33	363.296	267.64	1.36	10.52884906
1434373_at	Fam168a	236.85	267.51	262.52	284.28	261.27	193.19	166.84	221.56	192.04	262.486	193.4075	1.36	5.141491541
1422517_a_at	Znrd1	2811.4	2785.6	2716.4	2864.6	2839.62	2084.5	1700.1	2141.3	2391.7	2803.518	2079.4	1.35	5.141491541
1460334_at	Dbnl	1088.3	1144.3	1058.8	1098.4	1127.61	923.24	821.32	835.94	700.54	1103.484	820.26	1.35	3.69132726
1424971_at	Ccdc99	404	419.14	418.77	325.43	364.76	252.99	284.15	323.93	296.09	386.42	289.29	1.34	9.641274853
1449705_x_at	Mcm3	2903.2	3915.7	3739.7	3310.9	3153.46	2822.2	2532.4	2464.1	2383.5	3404.584	2550.5625	1.33	10.58793513
1426241_a_at	Scmh1	265.8	244.13	260.23	304.2	250.98	203.83	162.99	223.22	204.32	265.068	198.59	1.33	8.771863704
1434320_at	Gtf3c4	2233	2508.9	2024.1	2315.6	2475.64	2004.2	1666	1832.2	1426	2311.45	1732.085	1.33	9.641274853
1418262_at	Syk	678.89	565.15	568.99	584.6	630.59	523.28	347.1	451.58	496.73	605.644	454.6725	1.33	12.10755341
1448361_at	Ttc3	3317.7	3367.9	3467	3031.5	3613.01	2625.4	2574.2	2066.2	2892	3359.42	2539.4525	1.32	7.270796118

Table S2. Pbx1-regulated genes in CMPs

Genes down-regulated in the absence of Pbx1

Probe Set	Gene Symbol	Controls					Mutants				Average Cont	Average Mut	Fold Diff.	q-value(%)
		CMP3	CMP4	CMP6	CMP8	CMP10	CMP1	CMP2	CMP5	CMP7				
1448946_at	Kif3c	274.82	266.67	247.52	320.76	257.56	205.98	201.05	178.68	242.77	273.466	207.12	1.32	12.10755341
1434561_at	Asxl1	2409	2553.6	3030.3	2528.7	2809.48	2362	1852.8	1894.5	1983.4	2666.212	2023.14	1.32	9.641274853
1454641_at	Cggbp1	7519.2	7962.1	8213.8	7253.3	6751.91	6279.1	6078.8	5930.6	4818.8	7540.054	5776.8	1.31	8.097849177
1455269_a_at	Coro1a	12262	11791	12084	10764	11100.3	10133	9868.1	7631	8055.5	11600.316	8921.9125	1.30	8.771863704
1415726_at	Ankrd17	1186.9	1197.8	1113.9	1098.4	1049.15	986.04	746.81	954.65	806.72	1129.236	873.555	1.29	8.097849177
1429613_at	Dusp28	151.55	141.25	134.55	147.91	132.64	99.29	99.58	119.37	122.17	141.58	110.1025	1.29	6.965891765
1423975_s_at	Numa1	1999.5	1816.2	1977.4	1889.6	1898.26	1498.7	1849.9	1332.7	1292.6	1916.17	1493.46	1.28	11.91840305
1454851_at	Nr2c2	3029.5	3791.7	3292.9	3505.8	3516.7	3036.5	2507.5	2419.8	2732.2	3427.3	2674.005	1.28	8.771863704
1455020_at	Snx25	223.19	253.61	228.92	267.35	242.26	195.42	174.59	187.51	202.55	243.066	190.0175	1.28	5.645559339
1417815_a_at	Serinc3	6767.3	6390.5	6436.7	5687.2	6989.33	4305.4	5182.2	5696.6	5042.5	6454.198	5056.7	1.28	10.52884906
1425224_at	Slmo1	84.71	89.43	105.27	87.89	101.86	67.48	69.85	80.99	76.95	93.832	73.8175	1.27	10.58793513
1426479_a_at	Cnpy3	645.74	607.43	647.41	651.23	729.14	595.92	443.66	498.66	533.12	656.19	517.84	1.27	10.52884906
1429499_at	Fbxo5	2613.6	2160.8	2111.6	2295.5	2251.41	1914.8	1887.2	1602	1895.7	2286.572	1824.93	1.25	10.52884906
1423656_x_at	1500010J02Rik	809.17	715.53	800.82	721.1	739.09	581.16	566.98	609.08	666.05	757.142	605.8175	1.25	5.141491541
1423392_at	Clic4	3570	2973.2	3442.2	4453.7	3511.16	3530.4	1928.7	2588.1	3619	3590.072	2916.5275	1.23	5.141491541
1454977_at	C2cd3	398.32	424.61	366.95	421.03	399.31	361.23	338.02	312.64	299.47	402.044	327.84	1.23	7.270796118
1451459_at	Ahctf1	922.16	886.57	830.58	817.19	888.34	737.16	727.15	741.37	650.13	868.968	713.9525	1.22	5.141491541
1451125_at	Paip2b	576.55	649.55	635.11	674.22	738.16	544.87	533.74	506.19	570.37	654.718	538.7925	1.22	11.91840305
1454636_at	Cbx5	3078.7	3011.5	3482.7	2981	3119.67	2562.1	2601.3	2483.6	2758.1	3134.71	2601.265	1.21	6.337939258
1424078_s_at	Pex6	1037.6	1144.4	1000.8	1005.1	1014.14	855.41	905.13	856.22	844.02	1040.402	865.195	1.20	5.141491541
1448252_a_at	Eef1b2	17117	20000	20000	18335	18927.3	16263	15633	16964	16595	18875.982	16363.79	1.15	10.52884906
1442828_at	Ifi203	69.94	71.8	69.46	72.5	76.37	62.08	60	65.95	62.38	72.014	62.6025	1.15	5.141491541

Table S3. Pbx1-regulated genes in GMPs

Genes up-regulated in the absence of Pbx1

Probe Set	Gene Symbol	Controls					Mutants					Av Cont	Av Mut	Fold Diff	q-value(%)
		GMP3	GMP4	GMP6	GMP8	GMP10	GMP1	GMP2	GMP5	GMP7	GMP9				
1430156_at	4930520O04Rik	60	60	71.33	65.64	80.84	113.52	134.71	124.9	148.23	132.03	67.562	130.678	1.93	0
1448256_at	Gosr1	213.32	149.12	193.73	194.37	107.06	275.91	338.5	262.76	267.07	366.64	171.52	302.176	1.76	12.80530892
1421498_a_at	2010204K13Rik	325.85	231.54	177.77	187.72	267.17	418.47	379.73	405.33	401.91	414.2	238.01	403.928	1.70	9.68401487
1416974_at	Stam2	280.04	246.48	333.93	259.45	273.41	567.64	467.5	386.91	380.63	490.74	278.662	458.684	1.65	10.26738926
1422476_at	Ifi30	623.74	640.27	712.56	859.82	684.05	1228.8	1032.1	1011.2	928.41	1073	704.088	1054.716	1.50	10.26738926
1455658_at	Cggbp1	373.39	328.86	294.21	281.77	289.54	404.6	472.55	459.18	399.04	526.09	313.554	452.292	1.44	10.26738926
1424519_at	Mtg1	436.82	426.49	462.57	368.29	459.21	563.68	517.75	511.17	536.44	538.29	430.676	533.466	1.24	10.26738926
1423992_at	Gatad2a	664.59	616.75	629.85	688.66	659.99	806.67	768.68	732.93	839.33	811.03	651.968	791.728	1.21	9.68401487

Table S3. Pbx1-regulated genes in GMPs

Genes down-regulated in the absence of Pbx1

Probe Set	Gene Symbol	Controls					Mutants					Av Cont	Av Mut	Fold Diff	q-value(%)
		GMP3	GMP4	GMP6	GMP8	GMP10	GMP1	GMP2	GMP5	GMP7	GMP9				
1457722_at	Klrb1f	270.48	367.57	208.83	231.86	256.38	60	91.67	123.3	129.9	69.2	267.024	94.808	2.82	9.68401487
1455698_at	Sec62	383.65	245.2	252.83	236.38	189.55	60	91.28	173.4	92.2	60	261.522	95.384	2.74	9.68401487
1424033_at	Sfrs7	2237.6	2540	1720.2	1842.4	1556.7	558.7	582.3	1153	1158	422.8	1979.376	775.096	2.55	9.68401487
1434243_s_at	Tomm70a	400.91	339.23	295.62	264.05	212.85	70.21	88.19	184.6	188.1	101	302.532	126.422	2.39	9.68401487
1428985_at	Ints12	285.56	296.04	193.2	219.04	110.25	60	91.51	146	109	60	220.818	93.292	2.37	11.5384007
1435331_at	Pyhin1	549.69	528.31	418.69	415.55	461.98	60	141.7	395.3	219.4	199.3	474.844	203.132	2.34	9.68401487
1423547_at	Lyz2	1709.9	1761	1226.7	1221.8	924.09	344.2	730	766.9	562.3	562.4	1368.69	593.126	2.31	9.68401487
1456063_at	ORF34	272.2	226.59	159.91	197.12	108.82	63.74	82.85	99.42	111.3	67.58	192.928	84.978	2.27	9.68401487
1452657_at	Ap1s2	635.69	646.84	722.94	680	499.22	60	278.7	534.3	263.1	269.9	636.938	281.19	2.27	9.68401487
1435912_at	Ubxd7	297.08	360.91	193.21	271.61	185.1	60	79.24	164.3	156.7	124.6	261.582	116.968	2.24	9.68401487
1416618_at	Ppox	274.17	128.39	154.22	157.5	128.82	60	81.45	69.75	72.95	99.95	168.62	76.82	2.20	12.34069152
1431067_at	2210012G02Rik	129.71	163.95	190.79	102.38	130.9	60	83.37	69	60	71.77	143.546	68.828	2.09	9.68401487
1417702_a_at	Hnmt	194.72	200.08	190.45	158.62	77.51	60	82.16	124	70.49	60	164.276	79.322	2.07	12.34069152
1455336_at	Thap2	631.59	631.17	386.59	453.11	297.68	187.5	272	329.8	249.2	125.5	480.028	232.822	2.06	12.34069152
1452080_a_at	Dcun1d1	214	205.14	254.7	171.85	177.01	71.92	60	172.8	106.3	86.69	204.54	99.528	2.06	9.68401487
1415937_s_at	Pdcd6ip	277.7	222.67	234.19	239.32	138.55	60	78.7	125.8	197	92.13	222.486	110.718	2.01	11.5384007
1448502_at	Slc16a7	300.33	273.24	196.65	233.6	188.65	78.37	80.8	147.9	171.5	124.9	238.494	120.678	1.98	9.68401487
1454666_at	LOC100046855	264.36	343.57	344.45	241.73	245.61	65.3	148.3	216.1	175.9	129.6	287.944	147.02	1.96	9.68401487
1416029_at	Klf10	293.1	431.88	296.58	282.08	294.29	127.7	130	249.8	231.8	88.64	319.586	165.596	1.93	9.68401487
1450095_a_at	Acyp1	726.73	751.33	438.4	655.54	491.63	60	363.6	351.8	416.8	414.3	612.726	321.298	1.91	12.80530892
1450484_a_at	Cmpk2	138.29	173.09	222.55	132.94	133.51	60	61.51	141.1	96.13	60.99	160.076	83.952	1.91	12.80530892
1450020_at	Cx3cr1 /// LOC1000⁴	378.5	367.18	258.24	334.93	429.72	293	145.2	102.2	274.7	112.9	353.714	185.594	1.91	11.5384007
1434144_s_at	2410187C16Rik	867.39	716.5	588.23	549.37	502.16	90.31	522.4	388.9	358	332.7	644.73	338.446	1.90	12.80530892
1452094_at	P4ha1	372.51	348.87	294.7	371.23	273.51	60	157.4	235.2	259.7	168.7	332.164	176.18	1.89	9.68401487
1425993_a_at	Hsph1	6959.8	6460.4	6962.1	5266.7	6063.2	4000	2538	5352	2751	2342	6342.418	3396.64	1.87	9.68401487
1417594_at	Gkap1	484.38	392.33	269.41	309.13	315.07	147.4	133	171.8	197.6	302.4	354.064	190.42	1.86	11.5384007
1432431_s_at	Macrod2	174.87	155.67	103.43	160.14	101.31	60	60	102.2	76.89	80.6	139.084	75.928	1.83	9.68401487
1430034_at	Cct4	197.02	141.51	199.99	171.57	167.3	89.8	100.3	110.2	107.7	72.32	175.478	96.068	1.83	0
1442118_at	---	156.64	100.1	149.05	174.02	176.43	60	147.2	72.95	62.85	72.84	151.248	83.164	1.82	12.80530892
1434510_at	Papss2	1163.5	789.17	900.17	966.47	832.34	418.9	556.8	648.3	273	667.6	930.338	512.906	1.81	9.68401487
1418520_at	Tgoln1	149.82	164	120.46	163.99	108.85	60	81.79	121.8	67.23	60	141.424	78.17	1.81	9.68401487
1434373_at	B930006L02Rik	312.73	267.03	249.07	219.6	191.4	64.78	168.8	166.6	163.6	126.5	247.966	138.07	1.80	9.68401487
1448170_at	Siah2	297.39	269.82	273.17	311.21	275.62	60	111.2	277.8	182.7	165	285.442	159.322	1.79	11.5384007
1449303_at	Sesn3	211.88	210.12	143.8	160.3	137.32	60	78.89	114.6	129.3	99.39	172.684	96.428	1.79	9.68401487
1440303_at	Slc7a6os	215.74	140.79	137.01	128.51	145.28	60	75.23	126.9	85.72	85.96	153.466	86.764	1.77	11.5384007
1433649_at	Aof1	255.56	306.17	229.48	217.25	178.09	61.93	134.1	166.9	190.7	121.4	237.31	135.008	1.76	12.34069152
1439815_at	Heatr5b	483.24	394.53	422.48	365.58	346.63	94.55	199.8	349.8	270.4	243.4	402.492	231.59	1.74	10.26738926

Table S3. Pbx1-regulated genes in GMPs

Genes down-regulated in the absence of Pbx1

Probe Set	Gene Symbol	Controls					Mutants					Av Cont	Av Mut	Fold Diff	q-value(%)
		GMP3	GMP4	GMP6	GMP8	GMP10	GMP1	GMP2	GMP5	GMP7	GMP9				
1448944_at	Nrp1	177.63	205.02	167.73	155.24	120.37	99.39	60	100.4	140.1	76.24	165.198	95.222	1.73	9.68401487
1429059_s_at	Tmem107	280.05	219.14	197.68	208.45	185.07	76.57	139.2	166.1	142.1	105.3	218.078	125.85	1.73	9.68401487
1427978_at	4732418C07Rik	204.06	202.16	144.87	156.13	136.31	60	86.4	102.6	122.4	125.8	168.706	99.446	1.70	9.68401487
1449267_at	Chid1	272.78	200.92	303.67	259.49	187.36	177	113.1	177.2	138.5	117.3	244.844	144.59	1.69	9.68401487
1455548_at	Dlgap4	131.91	89.37	111.94	136.27	135.38	60	60	83.49	93.93	60	120.974	71.484	1.69	9.68401487
1427730_a_at	Zfp148	138.69	113.34	117.03	100.37	76.36	60	60	72.9	69.75	60	109.158	64.53	1.69	9.68401487
1435384_at	Ube2n	233.99	172.94	155.57	193.97	166.29	80.51	89.74	138.3	161.6	78.21	184.552	109.662	1.68	11.5384007
1417534_at	Itgb5	158.55	190.41	155.06	163.7	165.62	60	60	106.6	128.4	141.6	166.668	99.306	1.68	9.68401487
1435914_at	Ncor1	151.56	140.33	144.17	137.62	91.38	60	84.96	79.19	110.3	64.28	133.012	79.746	1.67	9.68401487
1435490_at	Hk3	4064.4	3615.3	2524.4	3582.6	2399.9	1970	1953	2052	2178	1553	3237.322	1941.112	1.67	9.68401487
1433699_at	Tnfaip3	275.27	217.49	199.02	185.36	131.56	112.7	148.3	133.2	97.14	121	201.74	122.46	1.65	12.80530892
1455544_at	Zranb3	242.08	195.02	215.32	195.74	180.27	87.46	69.32	151.3	167.8	149.9	205.686	125.146	1.64	9.68401487
1415901_at	Plod3	1723.3	1797.7	1732.5	2181.8	1686.6	623.1	1127	1451	1214	1138	1824.376	1110.522	1.64	9.68401487
1452155_a_at	Ddx17	5171.4	6048.5	5626.8	5597.2	4491.2	1739	3103	3545	3795	4350	5387.02	3306.506	1.63	9.68401487
1428873_a_at	Casc3 /// LOC10004	168.71	120.86	130.16	133.81	148.69	60	130.7	109.8	69.59	62.47	140.446	86.498	1.62	12.80530892
1418806_at	Csf3r	1111.5	1153.5	796.93	914.34	825.8	490.6	618.8	666.8	670.1	539	960.428	597.056	1.61	9.68401487
1425769_x_at	Cklf	168.36	139.41	198.42	159.67	152.38	60	90.59	157.2	115.9	85.85	163.648	101.904	1.61	12.80530892
1416289_at	Plod1	130.73	102.73	113.62	113.63	92.65	60	68.16	96.65	60	60	110.672	68.962	1.60	9.68401487
1452821_at	Tial1	435.83	428.05	329.76	363.32	382.09	167.6	258.4	299.1	321	170.1	387.81	243.22	1.59	9.68401487
1416059_at	Sec23b	3478.2	4128	3735.7	3901.5	3016.7	1180	1846	2944	2854	2693	3652.022	2303.53	1.59	11.06744557
1419269_at	Dut	138.64	140.51	152.91	126.92	131.66	103.6	96.69	103.7	71.85	60	138.128	87.166	1.58	9.68401487
1415692_s_at	Canx	13473	14912	14451	14119	11989	4432	8284	10732	11222	9142	13788.636	8762.478	1.57	9.68401487
1428930_at	Tmem29	371.27	259.51	297.8	256.64	267.49	182.7	138.1	235.4	237.9	137.2	290.542	186.262	1.56	11.5384007
1434444_s_at	Anapc1	578.11	588.94	350.43	615.17	534.19	313.6	326.6	386.3	449.9	242.4	533.368	343.748	1.55	12.80530892
1436597_at	Ankhd1 /// Eif4ebp3	201.85	170.91	166.39	162.03	141.82	60	129.9	121.8	109.1	124.8	168.6	109.126	1.55	9.68401487
1421022_x_at	Acyp1	634.41	767.91	632.41	687.8	599.7	225.5	473.8	426.7	498	531.6	664.446	431.126	1.54	9.68401487
1450186_s_at	Gnas	8035.1	8487.2	5694.7	6325.4	5557.9	3185	4815	4041	5783	4493	6820.066	4463.386	1.53	12.80530892
1444343_at	A130064L14Rik	130.72	87.05	99.93	107.31	86.91	60	60	75.72	79.94	60	102.384	67.132	1.53	9.68401487
1440886_at	Cdc37l1	164.36	174.91	176.42	144.43	135.56	60	132.9	134.4	92.31	103.2	159.136	104.55	1.52	11.5384007
1449419_at	Dock8	1071.9	1114.9	831.31	875.01	730.44	378.6	717.7	684.3	656.7	606.6	924.702	608.78	1.52	12.34069152
1423233_at	Cebpd	1499.7	1016.6	1229.9	1224	1200.7	534.5	919	923.2	733.7	957	1234.2	813.474	1.52	9.68401487
1422433_s_at	Idh1	5581.4	5394.9	7122.6	7174.7	6368.2	3875	3861	5245	3670	4299	6328.348	4189.884	1.51	9.68401487
1426886_at	Cln5	1082.8	824.77	755.76	866.1	733.24	342.1	738.9	612.1	588.1	560.2	852.536	568.268	1.50	12.80530892
1429524_at	Myo1f	606.85	599.48	892.26	739.69	744.48	293.3	544.5	511.8	526.4	515.5	716.552	478.3	1.50	11.5384007
1450034_at	Stat1	674.22	591.27	668.95	517.2	590.35	425.3	455.2	522.8	295.2	343.6	608.398	408.424	1.49	9.68401487
1451243_at	Rnpep	1424.5	1147.1	1188.2	1014.5	1027.1	524.5	874.3	994.7	767	740.5	1160.25	780.206	1.49	10.26738926
1448905_at	Nme3	1126.7	1063	793.26	830.65	733.49	632.4	737.9	614	534.7	546	909.412	613.01	1.48	11.06744557

Table S3. Pbx1-regulated genes in GMPs

Genes down-regulated in the absence of Pbx1

Probe Set	Gene Symbol	Controls					Mutants					Av Cont	Av Mut	Fold Diff	q-value(%)
		GMP3	GMP4	GMP6	GMP8	GMP10	GMP1	GMP2	GMP5	GMP7	GMP9				
1421000_at	Cnot4	167.59	196.33	202.53	192.3	156.26	84.18	126.9	119.5	130.9	156.3	183.002	123.55	1.48	9.68401487
1435328_at	Cyhr1	760.94	651.49	635.43	693.85	806.59	299.2	556.8	578.3	593.5	381.6	709.66	481.878	1.47	11.5384007
1454882_at	L3mbtl3	1123.6	1127	1212.7	1238.7	1025.3	790.7	536.3	733.4	1025	824.5	1145.45	781.908	1.46	9.68401487
1433464_at	Ipo13	1060.1	981.49	1001.5	883.88	1063.2	558.1	583.5	818.1	757.5	718.7	998.042	687.166	1.45	9.68401487
1416151_at	Sfrs3	840.63	806.74	985.87	793.92	878.16	530.6	551.6	757	661.3	464.8	861.064	593.04	1.45	9.68401487
1424672_at	Dmxl1	151.96	173.86	159.3	176.26	144.01	71.78	122.3	144.8	111	106.7	161.078	111.33	1.45	9.68401487
1452869_at	Prpf38b	1061.9	912.38	1006.5	906.23	1033.6	576.7	561.8	930.5	809	560.7	984.118	687.752	1.43	10.26738926
1447923_at	1810026B05Rik	686.66	779.08	657.32	702.98	725.03	287.6	571.9	626	534.1	477.5	710.214	499.42	1.42	11.5384007
1449024_a_at	Hexa	12737	11401	12604	12977	11495	4968	10482	9819	9232	8552	12242.77	8610.414	1.42	10.26738926
1428108_x_at	Tmcc2	259.95	188.21	192.57	202.08	171.45	119.5	140.6	172.1	133.1	151.7	202.852	143.404	1.41	11.5384007
1425323_a_at	BC008155	3324.8	3517.6	2917.4	3148.9	2645.1	1965	1876	2372	2596	2197	3110.754	2201.222	1.41	9.68401487
1428385_at	March8	451.59	438.95	504.37	423.34	431.52	269.6	328.7	420.4	283.5	306.9	449.954	321.828	1.40	9.68401487
1429058_at	Tmem107	2983.9	3552.8	3122.1	3318.9	3274.2	2026	1841	2769	2490	2576	3250.364	2340.568	1.39	9.68401487
1428890_at	Fem1c	1151.4	1299.1	1032.8	1084.5	1093.6	559.2	859.6	916.6	963.5	799.6	1132.272	819.7	1.38	9.68401487
1438865_at	H13	157.94	160.06	167.99	166.76	171.05	104.8	112.2	142.5	117.6	122	164.76	119.822	1.38	0
1436047_at	Gm672	179.32	168.27	217.83	187.55	173.42	115.2	99.5	152.5	154.8	152.7	185.278	134.944	1.37	11.06744557
1420081_s_at	D2Ertd750e	1201.1	1176.8	999.91	1027	896.11	931.9	773.2	785.3	804.7	588.1	1060.162	776.648	1.37	9.68401487
1436836_x_at	Cnn3 /// LOC100047	4057.6	4061.4	4679.2	4318.7	4413.2	3928	2134	2698	3751	3318	4306.002	3165.91	1.36	12.80530892
1454920_at	Uhrf2	661.67	715.98	765.9	659.51	604.31	424.3	404.5	644.7	557	481.4	681.474	502.364	1.36	11.5384007
1427897_s_at	Suds3	944.76	898.62	1116.5	1008.4	1050.3	603.3	670.6	898.9	821.6	720.9	1003.722	743.034	1.35	9.68401487
1426878_at	Pbrm1	1282.1	1101.8	1145.5	1151.1	1121.5	543.5	898.9	1040	869.7	956.7	1160.386	861.834	1.35	12.34069152
1426364_at	Mrrf	1117.1	1122.6	1005.5	898.73	1061.7	819.9	677.1	878.7	759.5	748.2	1041.14	776.666	1.34	9.68401487
1451207_at	Cbara1	950.15	882.43	855.75	948.53	824.52	579.9	672.8	678.5	753.2	662.6	892.276	669.384	1.33	0
1433442_at	Klhl9	1693.6	1777	1531.1	1497.9	1351.4	1316	1021	1249	1412	922	1570.198	1184.026	1.33	12.34069152
1423075_at	Lman2	1132.6	1289.7	1028.5	1051.3	1082.3	1019	935.2	899.8	734	633.9	1116.848	844.476	1.32	12.80530892
1451202_at	C330007P06Rik	1108.8	1058.8	1093.8	1017.7	1092.2	527.7	797.2	919.1	891.7	928.2	1074.24	812.768	1.32	11.5384007
1418254_at	Apip /// LOC100044	1054.4	899.4	813.39	891.37	814.35	674	576.5	701	820.6	635	894.576	681.43	1.31	10.26738926
1456046_at	Cd93	5026.1	5379.6	3867.8	4833.1	4669.5	4176	3764	2816	3844	3663	4755.21	3652.574	1.30	12.34069152
1434750_at	Exoc3	989.43	745.1	997.06	856.76	869.7	530.7	756	759.1	688.3	691.2	891.61	685.058	1.30	12.34069152
1433702_at	Ermp1	1971.5	2104.6	2096.7	1977.6	1867.4	1122	1612	1734	1867	1400	2003.548	1547.052	1.30	12.34069152
1426488_at	Bfar	544.91	477.76	567.87	523.26	478.15	445.5	411.7	428	395	321.5	518.39	400.322	1.29	9.68401487
1426845_at	Pdcd2l	1022.6	822.91	784.13	852.66	938.63	694.8	775.3	734.4	624.8	681.9	884.194	702.246	1.26	9.68401487
1422484_at	Cycs	7274.7	6260.3	6623	5920.7	6051.6	4645	4972	6108	5330	4751	6426.034	5161.266	1.25	10.26738926
1426964_at	3110003A17Rik	7403.6	7736.9	7261.6	7397	6693.3	5124	5455	5921	6507	6599	7298.474	5921.278	1.23	9.68401487
1455236_x_at	Serf2	9413.8	9620.5	10395	9117.7	9394.1	7377	8155	8271	6802	8583	9588.198	7837.596	1.22	9.68401487
1436783_x_at	Ywhab	12831	14465	11575	12634	13303	9346	11928	9553	10618	11772	12961.714	10643.26	1.22	12.80530892
1436116_x_at	Appl1	73.49	72.35	82	67.08	73.7	60	60	63.24	60	60	73.724	60.648	1.22	9.68401487

Table S3. Pbx1-regulated genes in GMPs

Genes down-regulated in the absence of Pbx1

Probe Set	Gene Symbol	Controls					Mutants					Av Cont	Av Mut	Fold Diff	q-value(%)
		GMP3	GMP4	GMP6	GMP8	GMP10	GMP1	GMP2	GMP5	GMP7	GMP9				
1428507_at	Hdhd2	671.49	637.68	639.97	737.38	692.36	446	576	635.5	557.7	569.4	675.776	556.912	1.21	12.34069152
1460621_x_at	Ywhaq	11750	12911	13402	11669	12912	9760	10463	9379	11364	11246	12528.878	10442.44	1.20	9.68401487
1456071_a_at	Cycs /// LOC672195	12359	12534	11910	10794	11584	9893	10344	11350	8671	9352	11836.346	9922.096	1.19	11.06744557
1439814_at	Atp8b4	4365.5	5268	4634.8	4643.5	4407.5	3947	3907	3919	3787	4040	4663.852	3919.95	1.19	9.68401487
1435738_x_at	Serf2	9431.4	9848.7	8574.3	8638.1	8373.6	7249	8171	7766	6511	8079	8973.222	7555.086	1.19	11.5384007
1429197_s_at	Rabgap1l	724.3	722.69	760.74	725.63	667.87	630	677.4	564.1	562.7	663.9	720.246	619.61	1.16	10.26738926
1454925_x_at	Mdh1	6569.3	6900.4	7052.4	6567.2	6627.4	5415	6159	6000	5932	5667	6743.334	5834.678	1.16	9.68401487
1454813_at	Ccdc72	16171	16757	16096	15097	15813	12252	14974	14423	13955	14114	15986.804	13943.4	1.15	9.68401487
1426434_at	Tmem43	646.25	571.2	612.72	607.77	559.68	545.9	557.2	545	523.6	479.5	599.524	530.226	1.13	12.34069152
1438794_x_at	Rps13	17300	19027	18617	17769	18776	16909	16751	17227	17160	17117	18298.052	17032.85	1.07	9.68401487

gsea_report_for_Cont

NAME	Core enrich. SIZE	NOM p-val	FDR q-val	DESCRIPTION	FUNCTIONAL GROUP
Report for CMP - Phenotype:Cont					
BRUNO_IL3_DN	18	0.003	0.026	Annotated list of commonly downreg. genes in differentiation pathways	**Differentiation**
IDX_TSA_DN_CLUSTER1	13	0.002	0.031	Down-reg during differentiation of fibroblasts into adipocytes, vs. fibroblasts treated to prevent diff.	**Differentiation**
TAVOR_CEBP_DN	10	0.007	0.052	C/EBP down-regulated genes in KCL22 cells	**Differentiation**
IDX_TSA_DN_CLUSTER2	19	0.010	0.077	Down-reg during differentiation of fibroblasts into adipocytes, vs. fibroblasts treated to prevent differentiation	**Differentiation**
MYOD_NIH3T3_DN	18	0.018	0.089	Down-reg in NIH 3T3 following transduction with MyoD and incubation in differentiation medium	**Differentiation**
HOHENKIRK_MONOCYTE_DEND_DN	28	0.005	0.093	Down-regulated mRNAs in monocyte-derived DCs	**Differentiation**
NADLER_OBESITY_UP	20	0.015	0.094	Genes with increased expression with obesity (decrease in expression of genes normally involved in adipogenesis)	**Differentiation**
IGF_VS_PDGF_DN	8	0.030	0.098	Down-regulated in myoblasts by treatment with IGF1 (it facilitates differentiation), vs treatment with PDGF	**Differentiation**
NADLER_OBESITY_HYPERGLYCEMIA	13	0.028	0.115	Genes correlated with the development of hyperglycemia (decrease in expression of genes involved in adipogenesis)	**Differentiation**
IDX_TSA_DN_CLUSTER5	10	0.050	0.146	Down-reg during differentiation of 3T3-L1 fibroblasts into adipocytes with IDX, vs. fibroblasts treated to prevent differentiation	**Differentiation**
ADDYA_K562_HEMIN_TREATMENT	18	0.000	0.012	Differentially expressed genes in K562 cells after hemin treatment	**Erythroid**
PLATELET_EXPRESSED	13	0.000	0.012	50 genes most strongly expressed in human platlets from 3 healthy donors	**Platelets**
GNATENKO_PLATELET	17	0.000	0.013	Top expressed genes in human platelet cells.	**Platelets**
GNATENKO_PLATELET_UP	17	0.002	0.014	Top 50 human platelet-expressed genes	**Platelets**
TENEDINI_MEGAKARYOCYTIC_GENES	16	0.000	0.036	Genes essential to the development of megakaryocytes	**Platelets**
TPOPATHWAY	8	0.014	0.069		**Platelets/HSC**
TARTE_BCELL	13	0.000	0.013	Genes overexpressed in B cells as compared to mature plasma cells	**B Lymphoid**
HOFFMANN_BIVSBII_BI	31	0.000	0.014	Genes with at least 5-fold change between Pre-BI and Large Pre-BII cells	**B Lymphoid**
HOFFMANN_BIVSBII_BI_TABLE2	67	0.000	0.036	Genes with at least 5-fold change between Pre-BI and Large Pre-BII cells	**B Lymphoid**
HADDAD_HPCLYMPHO_ENRICHED	43	0.000	0.045	Enriched in CD45RAhiLin-CD10+ ("B skewed) vs CD45RAintCD7- and CD45RAhiCD7hi HPCs	**B Lymphoid**
HADDAD_HSC_CD10_UP	40	0.000	0.051	Genes upregulated in hHSCs of the line CD45RA(hi)Lin-CD10+, biased toward B cells	**B Lymphoid**
ZHAN_MMPC_LATEVS	11	0.005	0.052	Differentially expressed in comparison of CD138-enriched tonsil PCs and CD138-enriched BM PCs	**B Lymphoid**
LU_IL4BCELL	20	0.003	0.052	Genes induced in peripheral B cells by 4 hours of incubation with IL-4	**B Lymphoid**
ST_B_CELL_ANTIGEN_RECEPTOR	10	0.009	0.072		**B Lymphoid**

Table S4. GSEA Report

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NAME	Core enrich. SIZE	NOM p-val	FDR q-val	DESCRIPTION	FUNCTIONAL GROUP
ZHAN_TONSIL_BONEMARROW	8	0.027	0.090	Diifferentially expressed in CD138-enriched tonsil plasma cells and CD138-enriched BM plasma cells	**B Lymphoid**
ZHAN_MMPC_EARLYVS	13	0.022	0.094	Differentiation genes differentially expressed in comparison of CD19-enriched tonsil BCs and CD138-enriched tonsil PCs	**B Lymphoid**
YU_CMYC_DN	21	0.013	0.094	Myc-repressed genes during B-lymphomagenesis	**B Lymphoid**
SIG_BCR_SIGNALING_PATHWAY	11	0.020	0.119		**B Lymphoid**
HOFFMANN_BIVSBII_IMVM	20	0.019	0.122	Genes with at least 5-fold change between immature and mature B cells	**B Lymphoid**
HOFFMANN_BIVSBII_LGBII	32	0.020	0.134	Genes with at least 5-fold change between large and small Pre-BII cells	**B Lymphoid**
HSA04662_B_CELL_RECEPTOR_ SIGNALING_PATHWAY	14	0.039	0.142		**B Lymphoid**
BASSO_GERMINAL_CENTER_CD40_DN	8	0.055	0.165	CD40 down-regulated genes	**B Lymphoid**
FLECHNER_KIDNEY_TRANSPLANT_ REJECTION_PBL_UP	16	0.009	0.076	Upreg in PBLs of patients who rejected a kidney TX relative to patients with a well functioning kidney TX	**Lymphoid**
IL2RBPATHWAY	10	0.016	0.082		**Lymphoid**
FLECHNER_KIDNEY_TRANSPLANT_ REJECTION_UP	31	0.016	0.107	Upreg in rejection transplanted kidney biopsies relative to well functioning transplanted kidney biopsies	**Lymphoid**
IL2PATHWAY	11	0.042	0.127		**Lymphoid**
HSA04612_ANTIGEN_PROCESSING_AND_ PRESENTATION	12	0.051	0.134		**Lymphoid**
FLECHNER_KIDNEY_TRANSPLANT_WELL _UP	105	0.004	0.191	Upreg in well functioning transplanted kidneys from stable, immunosuppressed recipients relative to normal kidneys	**Lymphoid**
LINDSTEDT_DEND_8H_VS_48H_DN	15	0.009	0.078	Genes up-reg in DC stimulated for 48 h vs to DC stimulated for 8 h	**Lymphoid (DC)**
LINDSTEDT_DEND_UP	17	0.048	0.135	Genes up-regulated in DC stimulated for 8 and 48 h	**Lymphoid (DC)**
LINDSTEDT_DEND_8H_VS_48H_UP	15	0.049	0.142	Genes up-reg in DC stimulated for 8h vs to DC stimulated for 48h	**Lymphoid (DC)**
HSA04650_NATURAL_KILLER_CELL_ MEDIATED_CYTOTOXICITY	15	0.019	0.117	Genes involved in natural killer cell mediated cytotoxicity	**NK Lymphoid**
LEE_TCELLS2_UP	209	0.000	0.030	Transcripts enriched in more mature cells (SP4, CB4, and AB4)	**T Lymphoid**
LEE_TCELLS3_UP	28	0.005	0.050	Transcripts enriched in both ITTP and DP (less mature)	**T Lymphoid**
GOLDRATH_CELLCYCLE	11	0.005	0.052	Cell cycle genes induced during antigen activation of CD8+ T cells	**T Lymphoid**
LEE_TCELLS4_UP	14	0.018	0.070	Transcripts enriched in more mature cells (SP4, CB4, and AB4)	**T Lymphoid**
HSA04660_T_CELL_RECEPTOR_ SIGNALING_PATHWAY	19	0.024	0.117	Genes involved in T cell receptor signaling pathway	**T Lymphoid**
HADDAD_CD45CD7_PLUS_VS_MINUS_UP	13	0.040	0.153	Genes enriched in CD45RAhiCD7hi vs CD45RAintCD7- HPCs	**T Lymphoid**
HADDAD_HSC_CD7_UP	13	0.047	0.159	Upreg in hHSCs of the line CD45RA(hi)CD7+, biased toward developing into T or NK cells, vs CD45RA(int) CD7-	**T Lymphoid**
LEE_TCELLS1_UP	42	0.027	0.159	Transcripts enriched in more mature cells (SP4, CB4, and AB4) vs less	**T Lymphoid**

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NAME	Core enrich. SIZE	NOM p-val	FDR q-val	DESCRIPTION	FUNCTIONAL GROUP
				mature (ITTP, DP)	
LEE_TCELLS8_UP	42	0.015	0.168	Enriched in naive CD4 T cells	**T Lymphoid**
LEE_TCELLS10_UP	42	0.027	0.172		**T Lymphoid**
FICARA_LT_PBX1WT	34	0.000	0.001	Down-regulated in Pbx1-null LT-HSCs	**HSC**
HEMATOP_STEM_ALL_UP	9	0.000	0.010	Up-regulated in CD34+/CD38-/Lin- cells, compared to CD34+/[CD38/Lin++	**HSC**
HSC_LTHSC_ADULT	56	0.000	0.011	Up-reg in mouse HSC from adult bone marrow (LT-HSC Shared + Adult)	**HSC**
HSC_LTHSC_FETAL	48	0.000	0.012	Up-regulated in mouse HSC from fetal liver (LT-HSC Shared)	**HSC**
HSC_LTHSC_SHARED	47	0.000	0.012	Up-reg in mouse HSC from adult BM and FL (Cluster i, LT-HSC Shared)	**HSC**
PARK_MSCS_BOTH	20	0.002	0.015	Genes commonly expressed in both HSCs and MPPs	**HSC**
HSC_HSCANDPROGENITORS_SHARED	104	0.000	0.032	Up-reg in mouse HSC and progenitors from both adult BM and fetal liver	**HSC**
HSC_HSCANDPROGENITORS_FETAL	104	0.000	0.035	Up-reg in mouse hematopoietic stem cells and progenitors from fetal liver	**HSC**
HSC_HSCANDPROGENITORS_ADULT	104	0.000	0.038	Up-reg in mouse hematopoietic stem cells and progenitors from adult bone	**HSC**
HSC_HSC_SHARED	39	0.000	0.042	Up-reg in mouse HSCs from both adult BM and fetal liver	**HSC**
PARK_MSCS_LIN2	14	0.009	0.048	Genes analyzed after negative selection of the cDNA library generated from Lin2/loSca-11Thy-11loc-kit1 cells ("self-renewal genes")	**HSC**
HSC_HSC_ADULT	46	0.000	0.050	Up-regulated in mouse hematopoietic stem cells from adult bone marrow	**HSC**
HSC_STHSC_FETAL	8	0.015	0.069	Up-reg in mouse short-term functional HSCs from fetal liver	**HSC**
HSC_STHSC_SHARED	8	0.011	0.070	Up-reg in mouse ST functional HSCs from both adult BM and fetal liver	**ST-HSC**
HSC_HSC_FETAL	39	0.002	0.077	Up-regulated in mouse hematopoietic stem cells from fetal liver	**HSC**
HSC_STHSC_ADULT	9	0.018	0.088	Up-reg in mouse short-term functional HSCs from adult bone marrow	**ST-HSC**
FETAL_LIVER_ENRICHED_ TRANSCRIPTION_FACTORS	26	0.005	0.098		**HSC**
BOQUEST_CD31PLUS_VS_CD31MINUS_ DN	25	0.009	0.116	Overexpressed in CD31- vs CD31+ cells (transcripts associated with cell cycle quiescence and stemness)	***HSC***
HUMAN_CD34_ENRICHED_ TRANSCRIPTION_FACTORS	45	0.017	0.164		**HSC/ST-HSC**
STEMCELL_HEMATOPOIETIC_UP	265	0.000	0.170	Enriched in mouse HSCs, vs differentiated brain and bone marrow cells	**HSC**
HOX_GENES	10	0.000	0.042	HOX genes related to hematopoiesis	**Hox**
TAKEDA_NUP8_HOXA9_3D_UP	34	0.000	0.001	Up-regulated in CD34+ cells 3d after transduction with NUP98-HOXA9	**Cancer**
TAKEDA_NUP8_HOXA9_8D_UP	21	0.000	0.001	Up-regulated in CD34+ cells 8d after transduction with NUP98-HOXA9	**Cancer**
POMEROY_DESMOPLASIC_VS_CLASSIC_ MD_UP	6	0.000	0.003	Genes expressed in desmoplastic medulloblastomas	**Cancer**
BASSO_GERMINAL_CENTER_CD40_UP	24	0.000	0.003	CD40 up-regulated genes in human transformed GC B cells	**Cancer**
CHIARETTI_T_ALL	61	0.000	0.003	Genes overexpressed in leukemia cells	**Cancer**
CHIARETTI_T_ALL_DIFF	66	0.000	0.009	Genes expressed in T-cell acute lymphocytic leukemia	**Cancer**

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Table S4. GSEA Report

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NAME	Core enrich. SIZE	NOM p-val	FDR q-val	DESCRIPTION	FUNCTIONAL GROUP
HCC_SURVIVAL_GOOD_VS_POOR_DN	44	0.000	0.013	Genes highly expressed in hepatocellular carcinoma with poor survival	**Cancer**
FSH_OVARY_MCV152_UP	12	0.000	0.013	Up-regin ovarian epithelial cells following FSH (follicle-stimulating hormone	**Cancer**
BRG1_ALAB_UP	9	0.000	0.018	Up-reg with expression of BRG1 in breast cancer cells with inactive BRG1	**Cancer**
CROMER_HYPOPHARYNGEAL_MET_VS_ NON_UP	27	0.000	0.018	Genes increased in metastatic hypopharyngeal cancer tumours	**Cancer**
HSA05220_CHRONIC_MYELOID_LEUKEMIA	27	0.000	0.022	Genes involved in chronic myeloid leukemia	**Cancer**
ROSS_FAB_M7	16	0.004	0.036	Genes upregulated in AML samples of the FAB class M7	**Cancer**
BRENTANI_SIGNALING	36	0.000	0.041	Cancer related genes involved in the cell signaling	**Cancer**
BREASTCA_TWO_CLASSES	39	0.000	0.044	Gene set that can be used to differentiate BRCA1-linked and BRCA2-linked breast cancers	**Cancer**
CHAUHAN_2ME2	22	0.003	0.044	Genes influenced by 2ME2, a metabolite that has antitumor activity, in multiple myeloma cells	**Cancer**
P21_P53_ANY_DN	20	0.005	0.046	Down-regulated following ectopic expression of p21 (CDKN1A) in OvCa cells, p53-dependent	**Cancer**
GLEEVECPATHWAY	8	0.002	0.050	Gleevec specifically targets the abnormal bcr-abl protein, an apoptosis inhibitor present in CML	**Cancer**
RAS_ONCOGENIC_SIGNATURE	51	0.003	0.068	Genes selected to discriminate cells expressing activated H-Ras from control cells (epithelial cells)	**Cancer**
BRENTANI_DEATH	12	0.005	0.069	Cancer related genes involved in cell death	**Cancer**
CHIARETTI_ZAP70_DIFF	9	0.010	0.070	Differentially expressed genes between high/low ZAP70 cases with T-ALL	**Cancer**
IFNALPHA_HCC_UP	10	0.017	0.072	Upreg by interferon alpha treatment in Hep3B hepatocellular carcinoma	**Cancer**
BRG1_H1299_UP	12	0.007	0.072	Up-reg by expression of BRG1 (SMARCA4) in lung cancer cells with mutant, inactive BRG1	**Cancer**
FLOTHO_CASP8AP2_MRD_DIFF	20	0.009	0.082	Genes significantly associated with MRD (minimal residual disease) in ALL	**Cancer**
P21_P53_MIDDLE_DN	9	0.025	0.088	Down-reg following ectopic expression of p21 (CDKN1A) in OvCa cells, p53-dependent	**Cancer**
ZHAN_MM_CD138_MF_VS_REST	6	0.029	0.095	50 top ranked SAM-defined over-expressed genes in each subgroup_MF (multiple myeloma)	**Cancer**
YAGI_AML_PROG_FAB	37	0.003	0.095	FAB type-specific probe sets (AML)	**Cancer**
ZHAN_MM_CD138_HP_VS_REST	16	0.033	0.098	50 top ranked SAM-defined over-expressed genes in each subgroup_HP (multiple myeloma)	**Cancer**
HSA05210_COLORECTAL_CANCER	26	0.007	0.098		**Cancer**
BECKER_TAMOXIFEN_RESISTANT_UP	9	0.040	0.102	Genes up-reg in a tamoxifen-resistant mammary carcinoma compared with a tamoxifen-sensitive mammary carcinoma	**Cancer**
BASSO_HCL_DIFF	14	0.017	0.116	HCL (Hairy cell leukemia)-specific genes. HCL is a chronic B cell malignancy characterized by infiltration of BM and spleen	**Cancer**
HSA05219_BLADDER_CANCER	13	0.029	0.117	Genes involved in bladder cancer	**Cancer**
KUMAR_HOXA_DIFF	53	0.000	0.122	Genes that were significantly different between wild-type, preleukemic,	**Cancer**

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NAME	Core enrich. SIZE	NOM p-val	FDR q-val	DESCRIPTION	FUNCTIONAL GROUP
				and leukemic mice	
BRENTANI_TRANSCRIPTION_FACTORS	10	0.033	0.130	Cancer related genes that are also transcription factors	**Cancer**
RADMACHER_AMLNORMALKARYTYPE_ SIG	16	0.048	0.159	Bullinger Validation Signature (Patients with AML and normal karyotype)	**Cancer**
RAY_P210_DIFF	15	0.049	0.160	Classification of p210BCR-ABL (CML) differentially regulated genes	**Cancer**
KRETZSCHMAR_IL6_DIFF	30	0.011	0.167	Probe sets that report an expression change in response to IL-6 addition to INA-6 cells (human myeloma cell line)	**Cancer**
BROCKE_IL6	30	0.022	0.172	Genes whose expression was modulated at least 1.5-fold in multiple myeloma INA-6 cells on addition of interleukin-6	**Cancer**
ET743_SARCOMA_24HRS_DN	35	0.035	0.174	Down-reg following treatment with Et-743 (anticancer agent) in sarcoma cell lines	**Cancer**
CORDERO_KRAS_KD_VS_CONTROL_UP	8	0.050	0.175	Genes upregulated in kras knockdown vs control in a human cell line	**Cancer**
ALCALAY_AML_NPMC_UP	28	0.040	0.179	Increased expression in NPMc+ leukemias (nucleophosmin+ AML)	**Cancer**
SHEPARD_CRASH_AND_BURN_MUT_VS_ WT_DN	36	0.036	0.187	Upreg in zebra fish wt compared to the crash&burn mutant (cell proliferation mutant with increased cancer susceptibility)	**Cancer**
WANG_HOXA9_VS_MEIS1_DN	14	0.000	0.000	Increased expression in Hoxa9+Meis1-immortalized progenitors vs Hoxa9 alone	**Transformation (Meis1)**
ARGIROPOULUS_MEIS1_UP	11	0.000	0	Up-regulated in pre-leukemic progenitors overexpressing Meis-1	**Transformation (Meis1)**
TAKEDA_NUP8_HOXA9_10D_UP	32	0.000	0.013	Up-regulated in CD34+ cells 10d after transduction with NUP98-HOXA9	**Transformation**
TAKEDA_NUP8_HOXA9_6H_UP	17	0.002	0.018	Up-regulated in CD34+ cells 6h after transduction with NUP98-HOXA9	**Transformation**
HTERT_UP	15	0.027	0.122	Upreg in hTERT-immortalized fibroblasts vs. non-immortalized controls	**Transformation**
TAKEDA_NUP8_HOXA9_16D_UP	23	0.027	0.129	Effect of NUP98-HOXA9 on gene transcription at 16d after transduction UP	**Transformation**
INTEGRIN_MEDIATED_CELL_ADHESION_ KEGG	26	0.000	0.014		**Cell adhesion**
PASSERINI_TRANSCRIPTION	13	0.000	0.019	Cellular adhesion genes differentially expressed in EC of aortas from different flow areas	**Cell adhesion**
HSA04510_FOCAL_ADHESION	38	0.000	0.021	Genes involved in focal adhesion	**Cell adhesion**
HSA04540_GAP_JUNCTION	28	0.000	0.028	Genes involved in gap junction	**Cell adhesion**
RHOPATHWAY	7	0.000	0.032	RhoA is a G protein whose active form stabilizes actin structures such as focal adhesions.	**Cell adhesion**
PASSERINI_PROLIFERATION	15	0.002	0.032	Genes associated with cellular adhesion in EC	**Cell adhesion**
ECMPATHWAY	6	0.000	0.040	ECM induces integrin-mediated phosphorylation in epithelial cells, leading to PI3 and MAP kinase activation and actin reorganization.	**Cell adhesion**
CELL_ADHESION_RECEPTOR_ACTIVITY	5	0.018	0.044		**Cell adhesion**
HSA04810_REGULATION_OF_ACTIN_ CYTOSKELETON	47	0.000	0.051	Genes involved in regulation of actin cytoskeleton	**Cell adhesion**

Table S4. GSEA Report

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NAME	Core enrich. SIZE	NOM p-val	FDR q-val	DESCRIPTION	FUNCTIONAL GROUP
CELL_ADHESION	22	0.003	0.053		**Cell adhesion**
INTEGRINPATHWAY	8	0.009	0.072		**Cell adhesion**
METPATHWAY	14	0.019	0.077	The hepatocyte growth factor receptor c-Met stimulates proliferation and alters cell motility and adhesion	**Cell adhesion**
HSA04520_ADHERENS_JUNCTION	18	0.009	0.082		**Cell adhesion**
HSA04512_ECM_RECEPTOR_INTERACTIO	14	0.009	0.090	Genes involved in ECM-receptor interaction	**Cell adhesion**
BRENTANI_CELL_ADHESION	8	0.015	0.094	Cancer related genes involved in cell adhesion and metalloproteinases	**Cell adhesion**
MCALPAINPATHWAY	8	0.033	0.095	In integrin-mediated cell migration, calpains digest links between the actin cytoskeleton and focal adhesion proteins.	**Cell migration**
PASSERINI_SIGNAL	46	0.000	0.097	Genes associated with adhesion differentially expressed in EC of aortas from disturbed flow vs undisturbed laminar flow	**Cell adhesion**
ST_INTEGRIN_SIGNALING_PATHWAY	13	0.024	0.116		**Cell adhesion**
SIG_REGULATION_OF_THE_ACTIN_ CYTOSKELETON_BY_RHO_GTPASES	6	0.032	0.119	Genes related to regulation of the actin cytoskeleton	**Cell adhesion/cytoskeleton**
PASSERINI_ADHESION	6	0.050	0.141	Genes associated with adhesion differentially expressed in EC from regions of disturbed flow vs regions of undisturbed flow	**Cell adhesion/cytoskeleton**
ROTH_HTERT_DIFF	10	0.000	0.011	Genes involved in DNA repair and cell-cycle control in hTERT-transduced T cells	**DNA repair**
ATMPATHWAY	7	0.000	0.020	ATM responds to radiation-induced DNA damage by blocking cell-cycle and activating DNA repair	**DNA repair**
STRESS_GENOTOXIC_SPECIFIC_DN	12	0.002	0.031	Genes down-reg following genotoxic stress (B-lymphoblastoid cell line)	**DNA repair**
UVC_TTD_ALL_DN	100	0.000	0.038	Down-regulated following treatment of XPB/TTD fibroblasts (defective in DNA repair) with UVC	**DNA repair**
CHEMICALPATHWAY	7	0.012	0.040	DNA damage promotes Bid cleavage, mitochondrial cyt c release and caspase activation	**DNA repair**
CMV-UV_HCMV_6HRS_DN	22	0.000	0.044	Down-regulated in fibroblasts at 6 hours following infection with UV-inactivated human CMV	**DNA repair**
UVC_TTD_4HR_DN	77	0.000	0.050	Downreg at 4h upon treatment of XPB/TTD fibroblasts with 3 J/m^2 UVC	**DNA repair**
UVB_SCC_DN	29	0.002	0.052	Downregulated by UV-B light in squamous cell carinoma cells	**DNA repair**
OXSTRESS_RPE_HNETBH_DN	14	0.004	0.052	Downregulated by HNE and t-BH in retinal pigment epithelium cells	**DNA repair**
UVB_NHEK1_DN	72	0.000	0.068	Downregulated by UV-B light in normal human epidermal keratinocytes	**DNA repair**
BLEO_HUMAN_LYMPH_HIGH_24HRS_UP	22	0.000	0.072	Up-reg following treatment of human lymphocytes (TK6) with bleomycin (DNA-damaging agent)	**DNA repair**
JISON_SICKLE_CELL	10	0.016	0.073	Genes differentially expressed in blood mononuclear cells of clinically stable sickle-cell patients	**DNA repair**
AS3_FIBRO_DN	8	0.027	0.088	Downreg by sodium arsenite (known to induce oxidative damage chromosome aberrations)	**DNA repair**

Table S4. GSEA Report

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NAME	Core enrich. SIZE	NOM p-val	FDR q-val	DESCRIPTION	FUNCTIONAL GROUP
UVC_HIGH_ALL_DN	71	0.000	0.103	Down-regulated at any timepoint following treatment of WS1 human skin fibroblasts with UVC at a high dose	**DNA repair**
FMLPPATHWAY	16	0.031	0.110	The fMLP receptor is a G-protein coupled receptor in neutrophils activates NADPH oxidase	**DNA repair**
OXSTRESS_RPETWO_DN	22	0.011	0.115	Downreg by two of H2O2, HNE and t-BH in retinal pigment epithelium cells	**DNA repair**
UVC_XPCS_ALL_DN	105	0.000	0.116	Downreg at any timepoint upon treatment of XPB/CS fibroblasts with 3 J/m^2 UV	**DNA repair**
CIS_XPC_UP	21	0.005	0.140	Increased in XPC (a DNA damage recognition protein)-defective fibroblasts vs normal, following treatment with cisplatin	**DNA repair**
CELL_CYCLE_CHECKPOINT	5	0.046	0.146		**DNA repair**
PROLIFERATION_GENES	57	0.000	0.037	Proliferation related genes	**Proliferation**
SHEPARD_NEG_REG_OF_CELL_PROLIFEI	16	0.000	0.044	Negative regulators of cell proliferation in zebra fish	**Neg reg of proliferation**
CELL_PROLIFERATION	34	0.002	0.077		**Proliferation**
SHEPARD_CELL_PROLIFERATION	34	0.002	0.089	Cell proliferation genes determined in zebra fish	**Proliferation**
PEART_HISTONE_UP	15	0.012	0.092	Cell-proliferation-related genes upregulated by SAHA and depsipeptide (histone deacetylase inhibitors)	**Proliferation**
CELL_CYCLE_ARREST	6	0.047	0.116		**Neg reg of proliferation**
APOPTOSIS_GENMAPP	17	0.036	0.126		**Apoptosis**
APOPTOSIS	12	0.042	0.160		**Apoptosis**
ERK5PATHWAY	5	0.050	0.103	Erk5 induces transcription of anti-apoptotic factors	**Erk**
TGF_BETA_SIGNALING_PATHWAY	18	0.002	0.017		**Tgfb**
HSA04350_TGF_BETA_SIGNALING_PATHW	24	0.015	0.113		**Tgfb**
WNT_SIGNALING	20	0.022	0.103		**Wnt**
HSA04310_WNT_SIGNALING_PATHWAY	32	0.032	0.191		**Wnt**
IFNA_HCMV_6HRS_UP	14	0.033	0.115	Up-reg in fibroblasts at 6 hours following treatment with interferon-alpha	**Ifna**
RADAEVA_IFNA_UP	10	0.032	0.116	Genes up-regulated by interferon-alpha in primary hepatocyte	**Ifna**
IFN_ALPHA_UP	10	0.048	0.142	Upreg 2-fold in HT1080 cells (human fibrosarcoma cell line) 6h upon treatment with interferon alpha	**Ifna**
DER_IFNA_UP	13	0.052	0.166	Genes up-regulated by interferon-alpha in HT1080 (fibrosarcoma)	**Ifna**
HSA04630_JAK_STAT_SIGNALING_PATHW	33	0.000	0.012		**Jack/Stat**
MAPK_CASCADE	9	0.007	0.040		**Mapk**

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NAME	Core enrich. SIZE	NOM p-val	FDR q-val	DESCRIPTION	FUNCTIONAL GROUP
P38MAPKPATHWAY	9	0.028	0.115	The Rho GTPases activate the p38 MAPKs under environmental stress or in the presence of pro-inflammatory cytokines	**Mapk**
MEF2DPATHWAY	5	0.050	0.115	Mef2 promote calcium-induced apoptosis in T cells and are regulated by MAP kinases and histone deacetylases	**Mapk**
NTHIPATHWAY	8	0.020	0.076	Hemophilus influenzae infections activate NF-kB inducing the inflammatory response.	**NF-kB**
NFATPATHWAY	9	0.029	0.122	Cardiac hypertrophy is induced by NF-ATc4 and GATA4, which are stimulated through calcineurin activated by CaMK	**NFAT**
IRITANI_ADPROX_LYMPH	29	0.000	0.014	Genes repressed by Mad1 (80% of which are induced by Myc)	**Myc**
YU_CMYC_UP	14	0.003	0.055	Myc-activated genes (during B-lymphomagenesis)	**Myc**

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NAME	Core enrich. SIZE	NOM p-val	FDR q-val	DESCRIPTION	FUNCTIONAL GROUP
Report for CMP - Phenotype:Mut					
WANG_MLL_CBP_VS_GMP_UP	20	0.000	0.020	MLL-CBP alters the genetic programs of GMP The top 50 genes most closely associated with MLL-CBP expression UP-regulated	**Cancer/GMP phenptype**
LEE_DENA_DN	11	0.041	0.224	Genes down-regulated in hepatoma induced by diethylnitrosamine	**Cancer**
IDX_TSA_UP_CLUSTER6	59	0.000	0.012	Up-reg during differentiation of 3T3-L1 fibroblasts into adipocytes with IDX, vs. fibroblasts treated to prevent differentiation	**Differentiation**
LIAN_MYELOID_DIFF_GRANULE	10	0.007	0.073	Granule constituents expressed during mouse promyelocytic cell line cell differentiation	**Differentiation**
LIAN_MYELOID_DIFF_RECEPTORS	14	0.026	0.137	Receptors expressed during myeloid differentiation process	**Differentiation**
FLAGELLAR_ASSEMBLY	8	0.049	0.178		**Differentiation**
TYPE_III_SECRETION_SYSTEM	8	0.038	0.186		**Differentiation**
GERY_CEBP_TARGETS	18	0.016	0.206	Complete list of differentially regulated C/EBP-target genes	**Differentiation**
HOUSTIS_ROS	11	0.014	0.080	nes known to modulate ROS or whose expression changes in response to R	**DNA repair**
UVB_NHEK3_C7	11	0.025	0.169	Regulated by UV-B light in normal human epidermal keratinocytes	**DNA repair**
BHATTACHARYA_ESC_UP	12	0.002	0.071	Genes upregulated in undifferentiated human embryonic stem cells	**ESC**
HSC_LATEPROGENITORS_SHARED	100	0.000	0.071	Upreg in mouse hematopoietic late progenitors from both adult BM and FL	**Late progenitors**
HSC_LATEPROGENITORS_FETAL	100	0.000	0.072	Up-regulated in mouse hematopoietic late progenitors from fetal liver	**Late progenitors**
HSC_LATEPROGENITORS_ADULT	104	0.000	0.074	Up-reg in mouse hematopoietic late progenitors from adult bone marrow	**Late progenitors**
HSC_INTERMEDIATEPROGENITORS_ADU	45	0.000	0.075	Up-reg in mouse hematopoietic intermediate progenitors from adult BM	**Late progenitors**
HSC_INTERMEDIATEPROGENITORS_SHAF	41	0.000	0.076	in mouse hematopoietic intermediate progenitors from both adult BM and fe	**Late progenitors**
HSC_INTERMEDIATEPROGENITORS_FETA	38	0.000	0.092	Up-reg in mouse hematopoietic intermediate progenitors from fetal liver	**Late progenitors**
HSC_MATURE_ADULT	60	0.000	0.211	Upreg in mouse mature bood cells from adult BM, compared to progenitors	**Late progenitors**
WANG_HOXA9_VS_MEIS1_UP	14	0.000	0.000	Genomic signature of progenitors immortalized by Hoxa9 versus Hoxa9 plus Meis1 Increased expression in Hoxa9-immortalized progenitors	**Transformation (Meis1)**
ARGIROPOULUS_MEIS1_DOWN	24	0.000	0.000	Down-regulated in pre-leukemic progenitors overexpressing Meis-1	**Transformation (Meis1)**
HSA00600_SPHINGOLIPID_METABOLISM	11	0.000	0.000		**Metabolism**
GLUTATHIONE_METABOLISM	10	0.000	0.007		**Metabolism**
GLUCONEOGENESIS	13	0.000	0.011		**Metabolism**
GLYCOLYSIS	13	0.000	0.015		**Metabolism**
HSA00010_GLYCOLYSIS_AND_ GLUCONEOGENESIS	14	0.002	0.019		**Metabolism**

Table S4. GSEA Report

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NAME	Core enrich. SIZE	NOM p-val	FDR q-val	DESCRIPTION	FUNCTIONAL GROUP
HSA00340_HISTIDINE_METABOLISM	15	0.000	0.019		**Metabolism**
ELECTRON_TRANSPORTER_ACTIVITY	25	0.000	0.031		**Metabolism**
PYRUVATE_METABOLISM	11	0.000	0.031		**Metabolism**
HSA00450_SELENOAMINO_ACID_ METABOLISM	12	0.009	0.036		**Metabolism**
HSA00561_GLYCEROLIPID_METABOLISM	13	0.000	0.047		**Metabolism**
HSA00480_GLUTATHIONE_METABOLISM	9	0.006	0.064		**Metabolism**
HSA00030_PENTOSE_PHOSPHATE_PATHV	8	0.009	0.068		**Metabolism**
HSA00150_ANDROGEN_AND_ESTROGEN _METABOLISM	9	0.006	0.070		**Metabolism**
HSA00590_ARACHIDONIC_ACID_ METABOLISM	6	0.014	0.070		**Metabolism**
HSA00620_PYRUVATE_METABOLISM	10	0.004	0.071		**Metabolism**
PENTOSE_PHOSPHATE_PATHWAY	8	0.014	0.075		**Metabolism**
GLYCOLYSIS_AND_GLUCONEOGENESIS	9	0.007	0.076		**Metabolism**
GLYCEROLIPID_METABOLISM	7	0.015	0.077		**Metabolism**
HSA00970_AMINOACYL_TRNA_ BIOSYNTHESIS	10	0.018	0.125		**Metabolism**
HSA00220_UREA_CYCLE_AND_ METABOLISM_OF_AMINO_GROUPS	9	0.030	0.159		**Metabolism**
HSA00260_GLYCINE_SERINE_AND_ THREONINE_METABOLISM	8	0.034	0.166		**Metabolism**
HSA00252_ALANINE_AND_ASPARTATE_ METABOLISM	11	0.037	0.168		**Metabolism**
ATP_SYNTHESIS	8	0.035	0.168		**Metabolism**
GALACTOSE_METABOLISM	8	0.050	0.175		**Metabolism**
GLYCINE_SERINE_AND_THREONINE_ METABOLISM	8	0.046	0.187		**Metabolism**
SIG_INSULIN_RECEPTOR_PATHWAY_IN_ CARDIAC_MYOCYTES	5	0.040	0.224	Genes related to the insulin receptor pathway	**Metabolism**
PROPANOATE_METABOLISM	8	0.054	0.226		**Metabolism**
HSA00380_TRYPTOPHAN_METABOLISM	11	0.037	0.230		**Metabolism**
MITOCHONDRIA	120	0.000	0.072	Mitochondrial genes	**Mitochondria**
HUMAN_MITODB_6_2002	115	0.000	0.078	Mitochondrial genes	**Mitochondria**