

Northcott et al. Supplementary Table 5b

GSEA: Chemical & Genetic Perturbations --- Enriched in SHH vs Non-SHH					
#	Gene Set Name	Description	NES	pVal	FDR qValue
1	MYOD_BRG1_UP	Genes up-regulated following transduction of MyoD in NIH 3T3 cells that fail to achieve full induction with expression of a dominant-negative BRG1 allele; induction thought to require functional BRG1	1.845	0.002	0.127
2	HUMAN_TISSUE_LIVER	Genes expressed specifically in human liver tissue	1.718	0.014	0.635
3	LEE_TCELLS6_UP	Transcripts enriched more than 3-fold in DP compared to other lymphocytes, with average signal value differences of at least 100 between DP and every other lymphocyte subpopulation	1.704	0.000	0.522
4	BCNU_GLIOMA_NOMGMT_48HRS_UP	Up-regulated in an MGMT-deficient glioma cell line (A172) at 48 hours following treatment with BCNU	1.702	0.010	0.402
5	MUNSHI_MM_UP	Genes upregulated in multiple myeloma (MM) cells versus the normal plasma cells of patients' identical twins.	1.694	0.008	0.357
6	MUNSHI_MM_VS_PCS_UP	Selected up-regulated genes in patient MM cells versus normal twin PCs	1.651	0.008	0.546
7	AGUIRRE_PANCREAS_CHR19	Genes on chromosome 19 with copy-number-driven expression in pancreatic adenocarcinoma.	1.644	0.057	0.513
8	ZUCCHI_EPITHELIAL_DN	The 50 most downregulated genes in primary invasive breast ductal carcinoma or metastatic breast carcinoma isolated from lymph nodes, as compared to normal mammary epithelium.	1.619	0.012	0.622
9	HADDAD_CD45CD7_PLUS_VS_MINUS_UP	Genes enriched in CD45RA <sup>hi</sup> CD7 <sup>hi</sup> vs CD45RA <sup>int</sup> CD7 <sup>-</sup> HPCs	1.615	0.010	0.584
10	HADDAD_HSC_CD7_UP	Genes upregulated in human hematopoietic stem cells of the line CD45RA <sup>(hi)</sup> CD7 <sup>+</sup> , which are biased toward developing into T lymphocytes or natural killer cells, versus CD45RA <sup>(int)</sup> CD7 <sup>-</sup> .	1.615	0.010	0.526
11	TSA_CD4_DN	Down-regulated in mouse CD4 <sup>+</sup> T-cells following 4 hour treatment with 100 nM trichostatin A	1.604	0.023	0.547
12	GENOTOXINS_ALL_24HRS_REG	Genes most consistently regulated in mouse lymphocytes (TK 3.7.2C) at 24 hours by all six genotoxins tested (cisplatin, methyl methanesulfonate, mitomycin C, taxol, hydroxyurea and etoposide)	1.604	0.014	0.503
13	UVB_NHEK3_C3	Regulated by UV-B light in normal human epidermal keratinocytes, cluster 3	1.594	0.006	0.522
14	GAMMA-UV_FIBRO_DN	Down-regulated at any timepoint by treatment of human fibroblasts with UV light or gamma radiation, but not by 4-NQO	1.575	0.013	0.609
15	CMV_HCMV_TIMECOURSE_4HRS_DN	Down-regulated in fibroblasts following infection with human cytomegalovirus (at least 3-fold, with Affymetrix change call, in at least two consecutive timepoints), with maximum change at 4 hours	1.571	0.007	0.593
16	CHIARETTI_ZAP70_DIFF	Differentially expressed genes between high versus low ZAP70 cases with no known molecular aberrations	1.566	0.014	0.592
17	<b>POMEROY_DESMOPLASIC_VS_CLASSIC_MD_UP</b>	<b>Genes expressed in desmoplastic medulloblastomas. (p &lt; 0.01)</b>	<b>1.566</b>	<b>0.000</b>	<b>0.558</b>
18	WANG_MLL_CBP_VS_GMP_UP	MLL-CBP alters the genetic programs of GMP The top 50 genes most closely associated with MLL-CBP expression UP-regulated	1.559	0.014	0.576
19	IFN_ALL_UP	Upregulated 2-fold in HT1080 cells 6 hours following treatment with interferons alpha, beta and gamma	1.548	0.022	0.614
20	UVB_NHEK2_UP	Upregulated by UV-B light in normal human epidermal keratinocytes	1.540	0.051	0.638