Supplementary Table S4: Gene Ontology (GO) results. Interesting terms specifically enriched in one group are highlighted in red. The gene numbers of the different table sheets identify the groups shown in Figure 2.

194 specifically acetlylated genes in Hodgkin cell lines

Category	Term	p-value	Genes (Entrez Gene Id)
SP_PIR_KEYWORDS	phosphoprotein	4.5657497719809853E-7	4302, 3725, 146057, 55841, 137835, 94120, 8925, 10480, 23306, 535, 64319, 1822, 4929, 29911, 54910, 10614, 84926, 2010, 115004, 10133, 10538, 29780, 55958, 4835, 5554, 10000, 7733, 6553, 6776, 6607, 6606, 84910, 64135, 91010, 54880, 10526, 2625, 2316, 3748, 51393, 10010, 54331, 79026, 23118, 8440, 84790, 4782, 7185, 4233, 8233, 814, 116988, 79576, 65264, 6667, 10211, 997, 283987, 64343, 6595, 843, 1760, 1762, 5681, 57584, 4000, 10308, 22929, 55509, 8973, 55810, 7850, 5777, 22848, 85369, 3303, 64784, 6838, 7030, 57522, 24148, 10768, 30850, 54960, 3956, 4082, 6304, 1236, 117584, 55619, 7867, 5872, 65981, 23258, 1027, 54434, 2026, 29934, 3654, 958, 84667, 6624, 51741, 26509, 27436, 7159, 10553, 4065, 3663, 3569, 403313
GOTERM_BP_FAT	GO:0016265~death	2.5747617044847376E-5	3725, 843, 4049, 597, 146057, 8870, 57556, 65264, 93659, 1027, 3748, 10670, 7159, 3956, 10553, 1822, 4929, 117584, 7185, 5777, 6607, 3569, 6606, 10133
GOTERM_BP_FAT	GO:0008219~cell death	7.07462870475375E-5	3725, 843, 4049, 597, 146057, 8870, 57556, 65264, 93659, 1027, 3748, 10670, 7159, 3956, 10553, 1822, 117584, 7185, 5777, 6607, 3569, 6606, 10133
GOTERM_BP_FAT	GO:0006357~regulation of transcription from RNA polymerase II promoter	2.9625377864957603E-4	3725, 6595, 54880, 84441, 3223, 84667, 3398, 7030, 6667, 24148, 9480, 23433, 10553, 6304, 1822, 4929, 10614, 7716, 6776, 4782, 3569
GOTERM_MF_FAT	GO:0017016~Ras GTPase binding	5.209403921744636E-4	91010, 10526, 4688, 23258, 94120, 2316, 55619

UP_SEQ_FEATURE	mutagenesis site	5.902673954510979E-4	843, 7867, 64135, 1435, 54880, 1760, 5681, 57584, 1027, 54434, 4000, 10480, 22929, 10010, 10614, 8440, 2010, 3654, 121268, 51279, 54894, 814, 64784, 6624, 51741, 26509, 6667, 7159, 997, 4835, 23433, 10000, 10553, 6304, 117584, 55120, 3569, 4068
GOTERM_MF_FAT	GO:0030528~transcription regulator activity	8.09480354205556E-4	3725, 6595, 54880, 2625, 8320, 55509, 1822, 4929, 10614, 3221, 4211, 4782, 55810, 3654, 814, 56938, 3223, 84441, 10538, 84667, 3398, 6667, 7030, 24148, 9480, 10553, 6304, 467, 6776, 7716, 3663
GOTERM_MF_FAT	GO:0031267~small GTPase binding	9.101345310485304E-4	91010, 10526, 4688, 23258, 94120, 2316, 55619
GOTERM_BP_FAT	GO:0006355~regulation of transcription, DNA-dependent	9.120807975187316E-4	3725, 4302, 6595, 54880, 2625, 1027, 10308, 8320, 55509, 1822, 4929, 10614, 3221, 4211, 4782, 55810, 56938, 3223, 84441, 10538, 84667, 3398, 6667, 7030, 24148, 23433, 9480, 6304, 10553, 467, 7733, 6776, 7716, 3663, 3569
GOTERM_BP_FAT	GO:0002763~positive regulation of myeloid leukocyte differentiation	0.001117967002719667	3725, 1435, 3398, 6776
GOTERM_BP_FAT	GO:0002761~regulation of myeloid leukocyte differentiation	0.001290498934588769	3725, 1435, 3398, 6776, 7030
GOTERM_MF_FAT	GO:0051020~GTPase binding	0.0013579757601504185	91010, 10526, 4688, 23258, 94120, 2316, 55619
GOTERM_BP_FAT	GO:0051252~regulation of RNA metabolic process	0.0013724432478284783	3725, 4302, 6595, 54880, 2625, 1027, 10308, 8320, 55509, 1822, 4929, 10614, 3221, 4211, 4782, 55810, 56938, 3223, 84441, 10538, 84667, 3398, 6667, 7030, 24148, 23433, 9480, 6304, 10553, 467, 7733, 6776, 7716, 3663, 3569
GOTERM_BP_FAT	GO:0012501~programmed cell death	0.0017199873300760837	3725, 843, 4049, 597, 8870, 57556, 93659, 65264, 10670, 1027, 7159, 3956, 10553, 117584, 7185, 5777, 3569
KEGG_PATHWAY	hsa04620:Toll-like receptor signaling pathway	0.002241651634701385	3725, 958, 10000, 23118, 3654, 3663, 3569
SP_PIR_KEYWORDS	activator	0.0029956681536609706	6595, 56938, 2625, 84441, 64784, 7030, 6667, 8320, 9480, 4211, 7716, 6776, 4782, 55810
INTERPRO	IPR000837:Fos transforming protein	0.003004071748208487	55509, 10538, 467

GOTERM_BP_FAT	GO:0006915~apoptosis	0.0038184386639485445	3725, 843, 4049, 597, 8870, 57556, 93659, 65264, 10670, 7159, 3956, 10553, 117584, 7185, 5777, 3569
GOTERM_BP_FAT	GO:0070665~positive regulation of leukocyte proliferation	0.00383160575439426	958, 1435, 8440, 6776, 3569
GOTERM_BP_FAT	GO:0032946~positive regulation of mononuclear cell proliferation	0.00383160575439426	958, 1435, 8440, 6776, 3569
GOTERM_BP_FAT	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	0.004078964007730337	3725, 6595, 23433, 9480, 84441, 4929, 6776, 4782, 7030, 6667, 3569, 24148
UP_SEQ_FEATURE	compositionally biased region:Poly-Gln	0.004873560136234759	6595, 84441, 6304, 1822, 7716, 55810, 3748
SP_PIR_KEYWORDS	prenylation	0.00532226594546127	2790, 5872, 23433, 54331, 116442, 121268, 4000
SP_PIR_KEYWORDS	cytoplasm	0.0053765294789343675	5681, 57584, 8925, 10480, 79841, 51637, 10614, 29911, 5777, 10133, 29780, 4688, 64784, 3303, 54960, 4082, 4835, 10000, 117584, 6776, 55120, 6607, 6606, 7867, 824, 64135, 65981, 10526, 2316, 10670, 1027, 51393, 54434, 10010, 8440, 23118, 2026, 121268, 597, 814, 116988, 6624, 65264, 51741, 27436, 6667, 7159, 23433, 10553, 64343, 4068
GOTERM_MF_FAT	GO:0019899~enzyme binding	0.005836735570612088	958, 91010, 10526, 54880, 4688, 23258, 2316, 94120, 6667, 4082, 535, 1822, 3654, 55619
UP_SEQ_FEATURE	domain:Leucine-zipper	0.006048630054391508	3725, 4302, 55509, 10538, 467, 7030
SP_PIR_KEYWORDS	nucleus	0.006297601289336866	6595, 4302, 3725, 5681, 4000, 10308, 8320, 55509, 51637, 4929, 10614, 4211, 2010, 166815, 55810, 5777, 54894, 84441, 10538, 64784, 6838, 3398, 7030, 24148, 54960, 9480, 6304, 7733, 6776, 55120, 6607, 6606, 474382, 7867, 64135, 10526, 54880, 2625, 474381, 10670, 1027, 79026, 3221, 4782, 1847, 8233, 83740, 56938, 814, 3223, 286128, 84667, 79576, 65264, 51741, 26509, 6667, 7159, 10553, 467, 7716, 3663
GOTERM_BP_FAT	GO:0045639~positive regulation of myeloid cell differentiation	0.00657846823749763	3725, 1435, 3398, 6776
UP_SEQ_FEATURE	DNA-binding region:Basic motif	0.0066501669330518015	3725, 55509, 56938, 10538, 467, 84667, 7030
SP_PIR_KEYWORDS	macrophage	0.006719488426913112	1435, 4049, 3569

GOTERM_MF_FAT	GO:0046983~protein dimerization activity	0.00768386222922303	3725, 1435, 10538, 2316, 51741, 10670, 6667, 3956, 55509, 283987, 467, 4929, 2026, 3654
GOTERM_BP_FAT	GO:0010628~positive regulation of gene expression	0.00791187495733176	6595, 3725, 1435, 84441, 7030, 6667, 24148, 9480, 23433, 4929, 6776, 4782, 55810, 3654, 3569
GOTERM_BP_FAT	GO:0045637~regulation of myeloid cell differentiation	0.00856811540823992	3725, 1435, 3398, 6776, 7030
GOTERM_MF_FAT	GO:0017048~Rho GTPase binding	0.00880531825984846	91010, 4688, 2316, 55619
SP_PIR_KEYWORDS	lymphokine	0.00913829859410145	1435, 4049, 3569
SP_PIR_KEYWORDS	DNA binding	0.00919909863666197	3725, 10308, 3223, 6304, 467, 3221, 7716, 4782, 7030, 6667
UP_SEQ_FEATURE	compositionally biased region:Poly-Pro	0.00925229272133810	9480, 6304, 1822, 64784, 3221, 85414, 55810, 3748, 6607, 57522, 6606, 79581
GOTERM_BP_FAT	GO:0045893~positive regulation of transcription, DNA-dependent	0.00988771006035289	6595, 3725, 84441, 7030, 6667, 24148, 9480, 23433, 4929, 6776, 4782, 55810, 3569
GOTERM_BP_FAT	GO:0051254~positive regulation of RNA metabolic process	0.0105199407316616	6595, 3725, 84441, 7030, 6667, 24148, 9480, 23433, 4929, 6776, 4782, 55810, 3569
GOTERM_BP_FAT	GO:0045449~regulation of transcription	0.0112039540002578	3725, 6595, 4302, 54880, 2625, 2316, 1027, 10308, 8320, 55509, 1822, 4929, 10614, 3221, 4211, 166815, 4782, 55810, 3654, 121268, 56938, 10538, 286128, 3223, 84441, 84667, 64784, 3398, 6667, 7030, 24148, 92806, 9480, 23433, 6304, 10553, 467, 7733, 6776, 7716, 3663, 3569
GOTERM_BP_FAT	GO:0006959~humoral immune response	0.0124890849249742	4049, 7030, 3569, 4068, 51279
GOTERM_MF_FAT	GO:0008134~transcription factor binding	0.0129071286234289	6595, 3725, 54880, 3223, 84441, 2625, 2316, 7159, 24148, 55509, 10553, 1822, 467
GOTERM_BP_FAT	GO:0010941~regulation of cell death	0.013445609863279	3725, 843, 64135, 4049, 597, 8870, 3303, 51741, 10670, 1027, 7159, 3956, 10553, 4929, 6776, 7185, 3654, 3569
GOTERM_BP_FAT	GO:0010740~positive regulation of protein kinase cascade	0.0135631842200943	958, 3956, 4049, 54910, 23118, 2316, 3569
GOTERM_BP_FAT	GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	0.0141863064545346	6595, 3725, 958, 84441, 7030, 6667, 24148, 9480, 23433, 4929, 6776, 4782, 55810, 3654, 3569

GOTERM_MF_FAT	GO:0043565~sequence-specific DNA binding	0.014542274159959566	3725, 2625, 10538, 3223, 7030, 6667, 9480, 55509, 6304, 467, 4929, 4211, 3221, 55810
GOTERM_BP_FAT	GO:0045941~positive regulation of transcription	0.014575884593619142	6595, 3725, 84441, 7030, 6667, 24148, 9480, 23433, 4929, 6776, 4782, 55810, 3654, 3569
GOTERM_BP_FAT	GO:0070663~regulation of leukocyte proliferation	0.016078036479005613	958, 1435, 8440, 6776, 3569
GOTERM_BP_FAT	GO:0032944~regulation of mononuclear cell proliferation	0.016078036479005613	958, 1435, 8440, 6776, 3569
GOTERM_BP_FAT	GO:0051173~positive regulation of nitrogen compound metabolic process	0.018178965439075094	6595, 3725, 958, 84441, 7030, 6667, 24148, 9480, 23433, 4929, 6776, 4782, 55810, 3654, 3569
GOTERM_MF_FAT	GO:0003700~transcription factor activity	0.018279791941505606	3725, 56938, 2625, 3223, 10538, 7030, 6667, 8320, 9480, 55509, 6304, 467, 4929, 4211, 3221, 6776, 4782, 55810, 3663
INTERPRO	IPR004827:Basic-leucine zipper (bZIP) transcription factor	0.018650807175211413	3725, 55509, 10538, 467
GOTERM_MF_FAT	GO:0005525~GTP binding	0.01942517461819985	5872, 22929, 51128, 23433, 116988, 84790, 10670, 116442, 121268, 55619
GOTERM_BP_FAT	GO:0002684~positive regulation of immune system process	0.01990821641319637	958, 8440, 6776, 3654, 3569, 4068, 51279, 1907
GOTERM_BP_FAT	GO:0032583~regulation of gene-specific transcription	0.020355669702514706	6595, 54880, 23433, 1027, 7030, 3569
UP_SEQ_FEATURE	region of interest:Docking domain	0.020852298737761205	474382, 83740, 474381
SP_PIR_KEYWORDS	dna-binding	0.021223443217162248	3725, 474382, 6595, 2625, 474381, 10308, 8320, 55509, 4929, 3221, 4211, 4782, 166815, 55810, 83740, 56938, 286128, 3223, 10538, 84667, 6838, 6667, 7030, 9480, 6304, 467, 7733, 6776, 7716, 3663
GOTERM_BP_FAT	GO:0009967~positive regulation of signal transduction	0.021608707811240302	958, 3956, 1435, 4049, 54910, 23118, 2316, 57045, 3569
GOTERM_MF_FAT	GO:0019001~guanyl nucleotide binding	0.02275617163017379	5872, 22929, 51128, 23433, 116988, 84790, 10670, 116442, 121268, 55619
GOTERM_MF_FAT	GO:0032561~guanyl ribonucleotide binding	0.02275617163017379	5872, 22929, 51128, 23433, 116988, 84790, 10670, 116442, 121268, 55619

SP_PIR_KEYWORDS	prenylated cysteine	0.0238898567122107	2790, 5872, 4000
GOTERM_BP_FAT	GO:0042981~regulation of apoptosis	0.0241757663084497	3725, 843, 64135, 4049, 597, 8870, 3303, 51741, 1027, 7159, 3956, 10553, 4929, 6776, 7185, 3654, 3569
GOTERM_BP_FAT	GO:0050671~positive regulation of lymphocyte proliferation	0.0250540400455152	958, 8440, 6776, 3569
GOTERM_BP_FAT	GO:0043067~regulation of programmed cell death	0.0262170944079535	3725, 843, 64135, 4049, 597, 8870, 3303, 51741, 1027, 7159, 3956, 10553, 4929, 6776, 7185, 3654, 3569
GOTERM_BP_FAT	GO:0043123~positive regulation of I-kappaB kinase/NF-kappaB cascade	0.0267807316994809	958, 3956, 4049, 23118, 2316
GOTERM_BP_FAT	GO:0034622~cellular macromolecular complex assembly	0.0271043334046139	474382, 54960, 83740, 10526, 474381, 2316, 8440, 84790, 6607, 6606, 24148
SP_PIR_KEYWORDS	SH2 domain	0.0285186194345507	8440, 6776, 1154, 5777, 4068
GOTERM_CC_FAT	GO:0019898~extrinsic to membrane	0.0290996311085728	2790, 22848, 51128, 10000, 54331, 117584, 94120, 23118, 57584, 8925, 10211
KEGG_PATHWAY	hsa04012:ErbB signaling pathway	0.0292455261148316	3725, 10000, 8440, 6776, 1027
GOTERM_BP_FAT	GO:0048872~homeostasis of number of cells	0.0295165035575088	1435, 3398, 6776, 6667, 3569
INTERPRO	IPR000980:SH2 motif	0.0296540378406475	8440, 6776, 1154, 5777, 4068
UP_SEQ_FEATURE	nucleotide phosphate-binding region:GTP	0.0319186940517425	5872, 51128, 23433, 116988, 84790, 10670, 116442, 121268
GOTERM_BP_FAT	GO:0006955~immune response	0.0321471946566359	64135, 4049, 4688, 5734, 9235, 7030, 8320, 1236, 7850, 4065, 3134, 3569, 4068, 51279
GOTERM_BP_FAT	GO:0051090~regulation of transcription factor activity	0.0324122468231819	2316, 3398, 3654, 121268, 3569
SMART	SM00338:BRLZ	0.0332309324252872	3725, 55509, 10538, 467
UP_SEQ_FEATURE	compositionally biased region:Poly-Arg	0.0334722678463416	6595, 3223, 3221, 29933, 26509, 57522
GOTERM_BP_FAT	GO:0045657~positive regulation of monocyte differentiation	0.0346052547489009	3725, 1435

GOTERM_BP_FAT	GO:0000122~negative regulation of transcription from RNA polymerase II promoter	0.03645488679339355	6595, 54880, 6304, 1822, 84667, 10614, 3398, 4782
GOTERM_BP_FAT	GO:0043122~regulation of I-kappaB kinase/NF-kappaB cascade	0.036523868450468205	958, 3956, 4049, 23118, 2316
GOTERM_BP_FAT	GO:0010647~positive regulation of cell communication	0.03792267101092399	958, 3956, 1435, 4049, 54910, 23118, 2316, 57045, 3569
UP_SEQ_FEATURE	domain:Sema	0.041649687023031075	57556, 54910, 4233
GOTERM_MF_FAT	GO:0016563~transcription activator activity	0.04180764205981084	6595, 8320, 814, 84441, 10553, 4929, 55810, 3654, 6667, 24148
GOTERM_BP_FAT	GO:0010557~positive regulation of macromolecule biosynthetic process	0.04191356566370287	6595, 3725, 84441, 7030, 6667, 24148, 9480, 23433, 4929, 6776, 4782, 55810, 3654, 3569
INTERPRO	IPR002165:Plexin	0.042555117643411355	57556, 54910, 4233
INTERPRO	IPR001627:Semaphorin/CD100 antigen	0.042555117643411355	57556, 54910, 4233
INTERPRO	IPR011616:bZIP transcription factor, bZIP-1	0.042555117643411355	3725, 55509, 10538
UP_SEQ_FEATURE	active site:Proton acceptor	0.04344264659245542	7867, 22848, 146057, 814, 1760, 219, 51741, 5681, 10000, 10553, 2026, 3654, 4233
SP_PIR_KEYWORDS	Apoptosis	0.04424142001051712	843, 597, 10553, 117584, 65264, 51741, 10670, 7185, 7159

126 specifically acetlylated genes in MM cell lines

Category	Term	p-value	Genes (Entrez Gene Id)
SP_PIR_KEYWORDS	phosphoprotein	4.7558637382297557E-4	841, 2004, 8968, 92822, 79990, 7253, 79956, 389, 388, 2992, 151963, 1979, 55605, 29994, 122786, 51133, 4921, 56957, 23705, 64743, 2801, 146691, 2671, 54995, 4887, 3347, 28981, 91768, 201158, 1602, 860, 2620, 8987, 9368, 966, 25989, 80267, 1230, 114883, 3315, 51027, 80119, 667, 81563, 57619, 51808, 8345, 4783, 10771, 8994, 8506, 7015, 3572, 29969, 10252, 116987, 1407, 7525, 7764, 23528, 8087, 23189, 55105, 340061, 2826, 5996, 112574, 128153, 9338
SP_PIR_KEYWORDS	repressor	0.002762081769517555	1602, 639, 2004, 1407, 4783, 7764, 8110, 23528, 10771, 8994
GOTERM_CC_FAT	GO:0044459~plasma membrane part	0.0035210435310265077	841, 8987, 8516, 2913, 9368, 966, 1230, 667, 7253, 389, 57619, 9143, 10082, 83692, 122786, 51133, 4921, 8506, 23705, 1946, 3572, 23495, 4887, 2826, 112574, 2848, 124056
GOTERM_BP_FAT	GO:0019935~cyclic-nucleotide-mediated signaling	0.0036786077281772108	7253, 5996, 133, 1230, 1979, 4887
GOTERM_CC_FAT	GO:0031226~intrinsic to plasma membrane	0.004454578918478269	8506, 8987, 1946, 8516, 2913, 3572, 966, 1230, 23495, 4887, 7253, 2826, 9143, 2848, 10082, 124056, 51133, 4921
COG_ONTOLOGY	DNA replication, recombination, and repair	0.006710160006532249	1407, 84893, 80119, 667
GOTERM_BP_FAT	GO:0019933~cAMP-mediated signaling	0.006774158956747062	7253, 5996, 133, 1979, 4887
GOTERM_BP_FAT	GO:0030802~regulation of cyclic nucleotide biosynthetic process	0.01088793243876941	7253, 5996, 2913, 2982, 4887
GOTERM_BP_FAT	GO:0030808~regulation of nucleotide biosynthetic process	0.01088793243876941	7253, 5996, 2913, 2982, 4887

GOTERM_BP_FAT	GO:0030799~regulation of cyclic nucleotide metabolic process	0.01193980129591891	7253, 5996, 2913, 2982, 4887
GOTERM_BP_FAT	GO:0006140~regulation of nucleotide metabolic process	0.013054887846602267	7253, 5996, 2913, 2982, 4887
GOTERM_CC_FAT	GO:0005887~integral to plasma membrane	0.018612707611677787	8506, 8987, 8516, 2913, 3572, 1230, 23495, 4887, 7253, 2826, 9143, 2848, 10082, 124056, 51133, 4921
GOTERM_CC_FAT	GO:0032993~protein-DNA complex	0.020005563159134876	7015, 8968, 8345, 8369
PIR_SUPERFAMILY	PIRSF500586:GTP-binding protein Rho	0.022003077276448076	389, 388
GOTERM_BP_FAT	GO:0005996~monosaccharide metabolic process	0.02882716595384123	6675, 3572, 10891, 130589, 10402, 2992
GOTERM_BP_FAT	GO:0009968~negative regulation of signal transduction	0.030335665471170066	56957, 5996, 860, 3572, 80319, 9655
GOTERM_CC_FAT	GO:0009897~external side of plasma membrane	0.03188842824845704	3572, 10082, 966, 83692, 23495
INTERPRO	IPR007125:Histone core	0.03252850301191056	8968, 8345, 8369
SP_PIR_KEYWORDS	differentiation	0.036532329480117046	23705, 28981, 1946, 8516, 388, 23528, 6477, 8087
SP_PIR_KEYWORDS	nucleosome core	0.03671895370179349	8968, 8345, 8369
GOTERM_BP_FAT	GO:0019932~second-messenger-mediated signaling	0.03802979112669641	7253, 5996, 133, 1230, 1979, 4887
GOTERM_BP_FAT	GO:0045761~regulation of adenylate cyclase activity	0.039403739022075654	7253, 5996, 2913, 4887
INTERPRO	IPR003108:Growth-arrest-specific protein 2	0.040728865998390935	2620, 667
GOTERM_BP_FAT	GO:0031279~regulation of cyclase activity	0.04257888524909832	7253, 5996, 2913, 4887
SMART	SM00243:GAS2	0.042594752028174185	2620, 667
GOTERM_MF_FAT	GO:0030165~PDZ domain binding	0.04354999197414093	23705, 9368, 80319
GOTERM_BP_FAT	GO:0030817~regulation of cAMP biosynthetic process	0.04476509104426472	7253, 5996, 2913, 4887

GOTERM_BP_FAT	GO:0051339~regulation of lyase activity	0.04476509104426472	7253, 5996, 2913, 4887
SP_PIR_KEYWORDS	G protein-coupled receptor	0.04487290684719752	7253, 2826, 2848, 1230
GOTERM_BP_FAT	GO:0010648~negative regulation of cell communication	0.04615930923379334	56957, 5996, 860, 3572, 80319, 9655
INTERPRO	IPR009072:Histone-fold	0.046696593912854883	8968, 8345, 8369
GOTERM_BP_FAT	GO:0030814~regulation of cAMP metabolic process	0.04700635432691726	7253, 5996, 2913, 4887

Intersection of Hodgkin and MM cell lines (17 genes)

Category	Term	p-value	Genes (Entrez Gene Id)
SP_PIR_KEYWORDS	atp-binding	0.024977466577919886	3305, 225, 57198, 55750, 9928

Intersection of B1 and B2 (141 genes)

Category	**Term**	**P-value**	**Genes (Entrez Gene Id)**
SP_PIR_KEYWORDS	B-cell	1.589805097517102E-6	930, 933, 971, 952, 5452
GOTERM_BP_FAT	GO:0006955~immune response	5.537092678248269E-6	10346, 81793, 29760, 5079, 3603, 8744, 973, 974, 3981, 939, 9450, 3936, 10758, 653361, 23075, 397, 414062, 4064, 5452
KEGG_PATHWAY	hsa04662:B cell receptor signaling pathway	3.502912143306507E-5	29760, 6850, 930, 933, 971, 973, 974
SP_PIR_KEYWORDS	phosphoprotein	1.3513726303623566E-4	56098, 90338, 23031, 10791, 51225, 240, 23201, 22930, 3280, 84958, 51678, 640, 8673, 1523, 23406, 80183, 23075, 23231, 2011, 605, 604, 79788, 10163, 930, 8732, 5981, 933, 54468, 6688, 55362, 9815, 973, 8832, 5700, 85363, 9294, 974, 939, 27128, 88455, 284439, 6875, 1043, 5218, 5452, 29945, 400509, 9962, 79666, 3603, 3899, 51199, 284403, 6850, 114836, 26999, 221037, 9770, 137964, 57507, 29760, 8850, 5098, 11214, 7763, 54440, 55103, 5341, 3981, 3936, 3164, 54014, 653361, 51147, 7265, 7095, 397, 10783, 136647
GOTERM_BP_FAT	GO:0050871~positive regulation of B cell activation	1.689557809620484E-4	6850, 952, 54440, 604, 939
SP_PIR_KEYWORDS	surface antigen	2.7350128417059786E-4	930, 971, 952, 973, 939
GOTERM_BP_FAT	GO:0050864~regulation of B cell activation	7.878755516190904E-4	6850, 952, 54440, 604, 939
GOTERM_BP_FAT	GO:0050867~positive regulation of cell activation	0.0024717184536631473	6850, 952, 54440, 604, 5341, 939
GOTERM_BP_FAT	GO:0050853~B cell receptor signaling pathway	0.00249183010014401	6850, 930, 973
BIOCARTA	h_bcrPathway:BCR Signaling Pathway	0.002688016533119121	29760, 6850, 973, 974

UP_SEQ_FEATURE	mutagenesis site	0.003408189609790142	10346, 240, 22930, 3603, 11193, 5351, 11194, 57804, 10652, 1523, 23406, 2011, 23075, 114836, 604, 29760, 8850, 11214, 8732, 952, 8832, 85363, 973, 3936, 51144, 5452, 10783, 136647
SP_PIR_KEYWORDS	zinc-finger	0.0036572728962629537	126231, 57507, 10346, 8437, 90338, 55762, 199745, 1879, 11214, 79666, 7763, 11193, 9815, 85363, 147657, 55084, 3164, 1840, 51147, 6049, 221472, 604, 221037, 79788
UP_SEQ_FEATURE	domain:v-SNARE coiled-coil homology	0.0037011006277250357	10652, 10791, 8673
GOTERM_BP_FAT	GO:0042113~B cell activation	0.0038159826847179628	29760, 23075, 973, 604, 3981
GOTERM_MF_FAT	GO:0030695~GTPase regulator activity	0.0038814222464972556	8437, 22930, 11214, 221472, 84958, 79874, 397, 9815, 55103, 27128
INTERPRO	IPR001388:Synaptobrevin	0.0040724667795183946	10652, 10791, 8673
GOTERM_BP_FAT	GO:0006959~humoral immune response	0.0041939234064094924	29760, 10758, 5079, 5452, 9450
GOTERM_CC_FAT	GO:0031252~cell leading edge	0.004406595475309301	3936, 10163, 51225, 221472, 23075, 5341
GOTERM_MF_FAT	GO:0060589~nucleoside-triphosphatase regulator activity	0.004495837709420941	8437, 22930, 11214, 221472, 84958, 79874, 397, 9815, 55103, 27128
GOTERM_MF_FAT	GO:0005083~small GTPase regulator activity	0.005286773346775278	8437, 22930, 11214, 221472, 84958, 397, 9815, 27128
GOTERM_BP_FAT	GO:0046649~lymphocyte activation	0.006597804956515319	3936, 29760, 6850, 23075, 973, 604, 3981
INTERPRO	IPR001849:Pleckstrin homology	0.006823902503064348	8437, 11214, 79666, 221472, 23075, 55103, 5341, 27128
SP_PIR_KEYWORDS	transcription regulation	0.007812268627153368	10346, 126231, 90338, 55762, 3280, 3603, 3899, 1523, 604, 79788, 221037, 3203, 5079, 8850, 1879, 5981, 6688, 80237, 147657, 54014, 3164, 6875, 60468, 4066, 5452, 10745
GOTERM_BP_FAT	GO:0002520~immune system development	0.00895489143173021	90338, 29760, 6850, 23075, 973, 604, 5341, 3981
GOTERM_BP_FAT	GO:0006297~nucleotide-excision repair, DNA gap filling	0.009004236448322728	5981, 57804, 3981
GOTERM_BP_FAT	GO:0051251~positive regulation of lymphocyte activation	0.00910418531102421	6850, 952, 54440, 604, 939

GOTERM_MF_FAT	GO:0030528~transcription regulator activity	0.009804927308522452	10346, 3203, 5079, 8850, 1879, 3280, 5981, 6688, 80237, 1523, 3164, 54014, 1840, 6875, 51147, 6049, 60468, 4066, 5452, 604, 10745
SP_PIR_KEYWORDS	Transcription	0.010291482040294547	10346, 126231, 90338, 55762, 3280, 3603, 3899, 1523, 604, 79788, 221037, 3203, 5079, 8850, 1879, 5981, 6688, 80237, 147657, 54014, 3164, 6875, 60468, 4066, 5452, 10745
GOTERM_BP_FAT	GO:0001775~cell activation	0.010580036330019565	3936, 29760, 6850, 23075, 973, 604, 5341, 3981
GOTERM_BP_FAT	GO:0050671~positive regulation of lymphocyte proliferation	0.01090188703911347	6850, 952, 54440, 604
INTERPRO	IPR011993:Pleckstrin homology-type	0.01094422974109705	8437, 11214, 79666, 221472, 23075, 55103, 5341, 27128
GOTERM_BP_FAT	GO:0030098~lymphocyte differentiation	0.011204379920095979	29760, 6850, 973, 604, 3981
GOTERM_BP_FAT	GO:0070665~positive regulation of leukocyte proliferation	0.01146048397530865	6850, 952, 54440, 604
GOTERM_BP_FAT	GO:0032946~positive regulation of mononuclear cell proliferation	0.01146048397530865	6850, 952, 54440, 604
GOTERM_BP_FAT	GO:0002696~positive regulation of leukocyte activation	0.0123622924982572	6850, 952, 54440, 604, 939
GOTERM_BP_FAT	GO:0030890~positive regulation of B cell proliferation	0.012372215403919248	952, 54440, 604
GOTERM_BP_FAT	GO:0002684~positive regulation of immune system process	0.014951068930314483	6850, 930, 952, 54440, 973, 604, 939
GOTERM_BP_FAT	GO:0045619~regulation of lymphocyte differentiation	0.015155762399572477	6850, 54440, 604, 939
GOTERM_BP_FAT	GO:0030097~hemopoiesis	0.01523932949884163	90338, 29760, 6850, 973, 604, 5341, 3981
GOTERM_CC_FAT	GO:0001726~ruffle	0.015266554951006605	3936, 10163, 221472, 5341
GOTERM_CC_FAT	GO:0019815~B cell receptor complex	0.015501111577715906	6850, 973
GOTERM_CC_FAT	GO:0019814~immunoglobulin complex	0.015501111577715906	6850, 973
GOTERM_BP_FAT	GO:0050865~regulation of cell activation	0.01616630090904346	6850, 952, 54440, 604, 5341, 939

GOTERM_BP_FAT	GO:0045321~leukocyte activation	0.016431096215471154	3936, 29760, 6850, 23075, 973, 604, 3981
COG_ONTOLOGY	Transcription / Cell division and chromosome partitioning	0.017071430471099595	57507, 126231, 90338, 55762
GOTERM_CC_FAT	GO:0030027~lamellipodium	0.017156935994426095	10163, 51225, 221472, 23075
GOTERM_CC_FAT	GO:0000267~cell fraction	0.01782671890993378	137964, 56098, 240, 22930, 11214, 5098, 84958, 952, 11194, 5341, 939, 8673, 653361, 1043, 120227, 26999, 9962
GOTERM_BP_FAT	GO:0046637~regulation of alpha-beta T cell differentiation	0.0190030720708737	6850, 54440, 604
GOTERM_CC_FAT	GO:0005624~membrane fraction	0.02062777767558213	137964, 56098, 11214, 5098, 84958, 952, 11194, 5341, 939, 8673, 1043, 120227, 9962, 26999
GOTERM_BP_FAT	GO:0030888~regulation of B cell proliferation	0.021989961992807124	952, 54440, 604
BIOCARTA	h_bcrmolecule:B Cell Receptor Complex	0.022654135109559666	973, 974
GOTERM_BP_FAT	GO:0051336~regulation of hydrolase activity	0.023040397034028885	2782, 3164, 22930, 80183, 221472, 9815, 604, 5341
GOTERM_BP_FAT	GO:0048534~hemopoietic or lymphoid organ development	0.02336490554156863	90338, 29760, 6850, 973, 604, 5341, 3981
SMART	SM00233:PH	0.023687044177774067	8437, 11214, 79666, 221472, 23075, 55103, 5341, 27128
GOTERM_BP_FAT	GO:0002521~leukocyte differentiation	0.025021808982289315	29760, 6850, 973, 604, 3981
GOTERM_BP_FAT	GO:0002377~immunoglobulin production	0.02515733868580664	10758, 23075, 3981
GOTERM_CC_FAT	GO:0005626~insoluble fraction	0.026599943511557225	137964, 56098, 11214, 5098, 84958, 952, 11194, 5341, 939, 8673, 1043, 120227, 9962, 26999
GOTERM_BP_FAT	GO:0002440~production of molecular mediator of immune response	0.02680655551103266	10758, 23075, 3981
GOTERM_BP_FAT	GO:0050851~antigen receptor-mediated signaling pathway	0.03200624733737255	6850, 930, 973
GOTERM_BP_FAT	GO:0050670~regulation of lymphocyte proliferation	0.032824706501664275	6850, 952, 54440, 604

SP_PIR_KEYWORDS	zinc	0.033079054754739684	10346, 126231, 8437, 90338, 55762, 79666, 11193, 55084, 1840, 6049, 221472, 604, 79788, 221037, 57507, 199745, 1879, 11214, 7763, 85363, 9815, 147657, 79691, 3164, 51147
GOTERM_BP_FAT	GO:0032944~regulation of mononuclear cell proliferation	0.03385021715645091	6850, 952, 54440, 604
GOTERM_BP_FAT	GO:0070663~regulation of leukocyte proliferation	0.03385021715645091	6850, 952, 54440, 604
GOTERM_BP_FAT	GO:0006350~transcription	0.03454726559833697	126231, 90338, 55762, 3280, 3603, 3899, 1523, 1840, 604, 79788, 221037, 3203, 5079, 8850, 1879, 5981, 6688, 80237, 147657, 54014, 3164, 6875, 60468, 4066, 5452, 10745
GOTERM_BP_FAT	GO:0007242~intracellular signaling cascade	0.03498587983461538	8437, 10163, 29760, 81793, 23221, 11214, 55103, 640, 9294, 5341, 939, 10758, 2782, 6850, 51147, 2011, 397, 79602
GOTERM_MF_FAT	GO:0003677~DNA binding	0.03500843802909279	10346, 126231, 90338, 55762, 3280, 3899, 1523, 6049, 23075, 604, 79788, 3203, 5079, 199745, 1879, 5981, 7763, 6688, 3981, 3164, 6875, 60468, 10186, 4066, 5452, 10745
KEGG_PATHWAY	hsa05340:Primary immunodeficiency	0.03543961523369738	29760, 930, 973
UP_SEQ_FEATURE	domain:PH	0.03557458044242405	8437, 11214, 79666, 23075, 55103, 27128
GOTERM_BP_FAT	GO:0046634~regulation of alpha-beta T cell activation	0.03567456670641246	6850, 54440, 604
GOTERM_BP_FAT	GO:0045621~positive regulation of lymphocyte differentiation	0.03567456670641246	6850, 54440, 939
GOTERM_BP_FAT	GO:0051249~regulation of lymphocyte activation	0.036129518190091	6850, 952, 54440, 604, 939
GOTERM_CC_FAT	GO:0005654~nucleoplasm	0.03954066711220151	8850, 8732, 5981, 11193, 80237, 7979, 9815, 57804, 3164, 6875, 51147, 6049, 29945
KEGG_PATHWAY	hsa04130:SNARE interactions in vesicular transport	0.041206929585764995	10652, 10791, 8673
GOTERM_BP_FAT	GO:0002429~immune response-activating cell surface receptor signaling pathway	0.0414639577215053	6850, 930, 973

GOTERM_BP_FAT	GO:0030036~actin cytoskeleton organization	0.042601779149096866	3936, 10163, 221472, 397, 604, 5341
PIR_SUPERFAMILY	PIRSF005409:Synaptobrevin_euk	0.04353095616612639	10791, 8673
SP_PIR_KEYWORDS	activator	0.0450993792571044	54014, 60468, 1879, 5981, 6688, 3899, 147657, 604, 5452
SP_PIR_KEYWORDS	ascorbic acid	0.04533561079994961	5351, 9962
GOTERM_BP_FAT	GO:0002768~immune response-regulating cell surface receptor signaling pathway	0.04550586759547533	6850, 930, 973
GOTERM_BP_FAT	GO:0006355~regulation of transcription, DNA-dependent	0.04704299164194051	126231, 10346, 3203, 90338, 55762, 5079, 8850, 1879, 3280, 6688, 80237, 147657, 1523, 54014, 3164, 6875, 51147, 6049, 60468, 5452, 604, 221037
INTERPRO	IPR016444:Synaptobrevin, metazoa/fungi	0.047621803370933885	10791, 8673
GOTERM_BP_FAT	GO:0048584~positive regulation of response to stimulus	0.048255562704003795	6850, 930, 3603, 54440, 973, 939
SP_PIR_KEYWORDS	metal-binding	0.04956613657094476	126231, 10346, 8437, 90338, 55762, 240, 79666, 11193, 5351, 55084, 1840, 6049, 221472, 2011, 604, 79788, 221037, 57507, 199745, 1879, 11214, 7763, 9815, 85363, 147657, 3981, 79691, 3164, 51147, 120227, 10783