

Table S2. Gene Ontology GO enriched pathways in Mg2800 vs Mg500_synovial tissues and spleens table

GO Category	GOID	Description	GeneRatio	BgRatio	pvalue	padj	-log10(adj p)	geneID	geneName	Count	Down	Up
SYNOVIAL TISSUES												
CC	GO:0000781	nucleosome	8/362	62/17361	4.19E-05	0.0123833	1.9071631	ENSMUSG0	Hist1h3e/Hi	8	8	0
CC	GO:0005831	proteasome core complex	5/362	21/17361	5.93E-05	0.0123833	1.9071631	ENSMUSG0	Psmb3/Psm	5	5	0
CC	GO:0044811	DNA packaging complex	8/362	70/17361	0.0001012	0.0140993	1.8508024	ENSMUSG0	Hist1h3e/Hi	8	8	0
CC	GO:0032991	protein-DNA complex	11/362	154/17361	0.0003924	0.0410011	1.3872049	ENSMUSG0	Hist1h3e/Hi	11	11	0
SPLEENS												
MF	GO:0140091	catalytic activity, acting on DNA	26/790	181/16652	4.37E-07	0.000358	3.4460753	ENSMUSG0	Dnnt1/Isg20/	26	7	19
MF	GO:0016641	oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor	7/790	17/16652	6.74E-06	0.002762	2.5587792	ENSMUSG0	Aldh112/Mt	7	3	4
MF	GO:0003671	DNA helicase activity	10/790	42/16652	2.01E-05	0.0042313	2.3735221	ENSMUSG0	Cdc45/Twnl	10	1	9
MF	GO:0003691	single-stranded DNA binding	16/790	101/16652	2.07E-05	0.0042313	2.3735221	ENSMUSG0	Smug1/Cdc	16	4	12
MF	GO:0005541	phospholipid binding	36/790	379/16652	6.05E-05	0.0099114	2.0038652	ENSMUSG0	Syt5/Rundc	36	21	15
MF	GO:0016641	oxidoreductase activity, acting on the CH-NH group of donors	7/790	25/16652	0.0001195	0.0163079	1.7876017	ENSMUSG0	Aldh112/Mt	7	3	4
BP	GO:0042021	protein refolding	8/800	23/16895	6.34E-06	0.0185548	1.7315428	ENSMUSG0	Hsp90aa1/I	8	0	8
BP	GO:0014901	smooth muscle cell migration	15/800	85/16895	9.59E-06	0.0185548	1.7315428	ENSMUSG0	Itga2/Myc/I	15	14	1
BP	GO:0014811	muscle cell migration	16/800	97/16895	1.20E-05	0.0185548	1.7315428	ENSMUSG0	Itga2/Myc/I	16	15	1
MF	GO:0031071	heat shock protein binding	17/790	134/16652	0.0002032	0.023769	1.6239889	ENSMUSG0	Ppid/Hsph1	17	2	15
MF	GO:0030211	semaphorin receptor binding	6/790	20/16652	0.0002445	0.0250345	1.6014615	ENSMUSG0	Sema3d/Sei	6	6	0
MF	GO:0008091	DNA-dependent ATPase activity	12/790	79/16652	0.0003279	0.029835	1.5252736	ENSMUSG0	Chtf18/Erc	12	1	11
BP	GO:0046651	tetrahydrofolate metabolic process	7/800	21/16895	3.37E-05	0.0317668	1.4980268	ENSMUSG0	Aldh112/Mt	7	3	4
BP	GO:0014911	positive regulation of smooth muscle cell migration	11/800	54/16895	3.70E-05	0.0317668	1.4980268	ENSMUSG0	Itga2/Myc/I	11	10	1
BP	GO:0000721	telomere maintenance	17/800	120/16895	4.96E-05	0.0317668	1.4980268	ENSMUSG0	Hsp90aa1/I	17	3	14
BP	GO:0051081	chaperone cofactor-dependent protein refolding	8/800	30/16895	5.64E-05	0.0317668	1.4980268	ENSMUSG0	Hsph1/Hsp	8	0	8
BP	GO:0006261	DNA replication	27/800	250/16895	5.73E-05	0.0317668	1.4980268	ENSMUSG0	Chtf18/Cdc	27	7	20
BP	GO:0032201	telomere organization	17/800	122/16895	6.14E-05	0.0317668	1.4980268	ENSMUSG0	Hsp90aa1/I	17	3	14
BP	GO:0014911	regulation of smooth muscle cell migration	13/800	78/16895	6.94E-05	0.0323008	1.4907865	ENSMUSG0	Itga2/Myc/I	13	12	1
MF	GO:0004001	ATP-dependent DNA helicase activity	7/790	31/16652	0.0005097	0.0417444	1.3794022	ENSMUSG0	Recql4/Xrcc	7	1	6
BP	GO:0000721	double-strand break repair via homologous recombination	15/800	104/16895	0.0001104	0.0427995	1.3685609	ENSMUSG0	Tex15/Cdc4	15	4	11
BP	GO:0000721	recombinational repair	15/800	104/16895	0.0001104	0.0427995	1.3685609	ENSMUSG0	Tex15/Cdc4	15	4	11
CC	GO:0005651	replication fork	12/808	69/16943	9.16E-05	0.0483525	1.3155814	ENSMUSG0	Cdc45/Mcrr	12	1	11