

Supplemental Figure 1: Levels of *SLC16A1* (MCT1), *SLC16A3* (MCT4) and *BSG* (CD147) Expression in Human Disc Tissue

A-C) qRT-PCR expression levels of *SLC16A1*, *SLC16A3*, and *BSG* mRNA in healthy (4), moderately-degenerate (4.6-6.9), severely-degenerate (7), and immune cell- infiltrated (INF) human discs. Graphs display the percent of disc samples expressing mRNA in each group. D-D") Representative immunohistochemical images showing MCT1-positive cells and MCT1-negative cells in healthy (D), moderately-degenerate (D'), and severely-degenerate (D") human samples. E) Percent MCT1 immunopositivity in healthy, moderately-, and severely- degenerate human discs. F-F") Representative immunohistochemical images showing CD147-positive cells and CD147-negative cells in healthy (F), mid-degenerate (F'), and severe degenerate (F") human samples. G). Percent CD147 immunopositivity in healthy, moderately-, and severe degenerate (F") human samples. G). Percent CD147 immunopositivity in healthy, moderately-, and severe legenerate (F") human samples. G). Percent CD147 immunopositivity in healthy, moderately-, and severely- degenerate human discs. H-J) Negative control IHC for MCT1 (H) and MCT4 (I) with Rabbit IgG, and CD147 (J) with Goat IgG. Lack of HRP-positive staining indicates antibody specificity. Statistical analysis on non-parametric IHC quantification was performed by Kruskall Wallis and Connover Ingman post hoc test. n.s.= not significant.



Supplemental Figure 2: Levels of MCT and CD147 Expression in Rodent Disc Tissue

A) Representative immunostaining showing MCT1 expression in the CEP. B, B') Representative immunostaining showing MCT4 expression in the NP compartment. C) Representative Western blot showing relative MCT1, MCT4, and CD147 expression in tissue protein lysate from rat NP.



Supplemental Figure 3: Histological Grades of Degeneration in WT and MCT4 KO Lumbar Spine

A, A') Safranin-O/Fast Green staining of the intervertebral disc in 8 mo WT and global MCT4 KO mice (Scale bar = 200  $\mu$ m). C) Average modified-Thompson grade of NP and AF degeneration. C, C') Safranin-O/Fast Green staining of the intervertebral disc in 14 mo WT and global MCT4 KO mice (Scale bar = 200  $\mu$ m). C) Average modified-Thompson grade of NP and AF degeneration. Statistical analysis: *t*-test, n.s.= not significant; \*, p-value ≤ 0.05.



Supplemental Figure 4: Characterization of NP phenotype and matrix composition in MCT4 KO mice.

Representative immunostaining in the intervertebral discs of 14 mo WT and MCT4 KO mice. NP phenotypic markers: A, A') GLUT1; B, B') CA3. (Scale bars= 100  $\mu$ m). Extracellular matrix molecules: C, C') ACAN; D-D') Chondroitin Sulfate, E-E) Collagen I. (Scale bars= 200  $\mu$ m). F-F''') Expression of MCT1 is not compensatory for loss of MCT4. G, G') MCT4 expression is lost in MCT4 KO animals. Imaged at 10X and 20X (Left scale bars= 200  $\mu$ m; Right scale bars= 50  $\mu$ m). Dotted lines were drawn to demarcate different tissue compartments within the disc. All staining was performed using at least 3 animals/genotype corresponding to Grade 2.

	Reference	Source	Age	IVD Level	Intact IVD?	Average	Classificati	
						Grade	on	
HD	40	PM	74	L2/L3	Yes	11	SD	
HD	65	Surgical	43	L4/L5	No	10	I	
HD	71	Surgical	42	L5/S1	Yes	3	ND	
HD	89	Surgical	21	L5/S1	No	4	ND	
HD	98	Surgical	65	L3/L4	Yes	11	SD	
HD	103	Surgical	45	C5/C6	No	9.5	SD	
HD	145	Surgical	38	L4/L5	No	11	I	
HD	154	Surgical	52	L4/L5	No	11	SD	
HD	158	Surgical	38	L4/L5	No	7	I	
HD	159	Surgical	39	L4/L5	No	9	I	
HD	203	Surgical	45	L5/S1	Yes	4	ND	
HD	219	Surgical	54	L5/S1	No	11	I	
HD	229	Surgical	56	L5	Yes	6	MD	
HD	233	Surgical	44	L5/S1	Yes	10	SD	
HD	234	Surgical	54	L5/S1	Yes	9	SD	
HD	254	Surgical	47	L4/L5	No	6	I	
HD	257	Surgical	46	L5/S1	No	3	I	
HD	264	Surgical	65	C3/C5	Yes	6	MD	
HD	266	Surgical	27	L5/S1	No	4	ND	
HD	270	Surgical	45	L5/S1	No	6	MD	
HD	282	Surgical	21	L5/S1	No	4	ND	
HD	310	Surgical	37	L4/L5	Yes	5	I	
HD	319	Surgical	47	L5/S1	No	5	MD	
HD	330	Surgical	32	L5/S1	Yes	5.5	MD	
HD	346	Surgical	46	C5/C6	Yes	6	MD	
HD	359	Surgical	40	L5/S1	No	4	ND	
HD	360	Surgical	50	C6		5.5	MD	
HD	370	Surgical	50	L5/S1	Yes	8	SD	
HD	375	Surgical	41	L5/S1	No	6	MD	
HD	380	PM	33	L2/L3	Yes	4	ND	

Supplemental Table S1: Human Intervertebral disc sample information.

Samples were separated into different grades, 0-4 (Non-degenerate, ND), 4.1-6.9 (Moderately-degenerate, MD) and 7-12 (Severely-degenerate, SD).

Grade	Nucleus pulposus	Annulus Fibrosus
Grade 1	Aggrecan-rich, bulging tissue	Discrete fibrous lamellae
Grade 2	Peripheral fibrous tissue	Mucinous material between lamellae
Grade 3	Consolidated fibrous tissue	Extensive mucinous material between lamellae and loss of NP-AF demarcation
Grade 4	Horizontal clefts parallel to the endplate	Focal lamellar disruptions (clefts)
Grade 5	Clefts through NP and AF	Clefts through NP and AF

Supplemental Table S2: Modified Thompson scale used for histological grading.

COTEM LC FAT     CONSTRUCT     114488511     318-20     117.61       COTEM LC FAT     CONSTRUT     14488511     348-10     388-20     137.61     388-20	Category	Term	Count	List	Fold	Bonferroni	FDR (%)
OCTERN CC FAT     0.0000081-0004 (asista) groups and provide state of the	GOTERM CC FAT	GO:0000786~nucleosome	29	274	11.48865113	3.89E-20	1.17E-19
REGO PATINAV     mund0322 systemic lups and professiona     28     146     0.24422007     0.5111     0.25211       COTTERN CC TAT     CON30009noclear anomain     9     774     0.30800220     0.3111-1     1.35211       COTTERN CC TAT     CON30009noclear anomain     9     744     0.30800221     0.3111-1     1.35213       COTTERN BP FAT     CON30009noclear anomain     9     746     0.30800221     0.3111-1     0.3111-1     1.35213     1.3581-0     0.3581     0.3581     0.3581     0.3581     0.3581     0.3581-0     0.3581     0.3581     0.3581-0     0.3581	GOTERM CC FAT	GO:0044815~DNA packaging complex	29	274	11.03515175	1.44E-19	4.31E-19
GOTERN, CC FAT, GO.000399-problem ONMA complex     30     274     0.4947/2002     5.915-14     1.552-13       DCTERN, CC FAT, GO.0000079-problem inclusions     41     274     7.9515002     5.915-14     1.552-13       DCTERN, CC FAT, GO.000079-problem inclusions     49     7.45     6.35612021     1.812-13     1.232-12       DCTERN, CC FAT, GO.000078-problem inclusions     49     7.44     7.83277362     1.016-13     2.232-12       DCTERN, CC FAT, GO.000178-problem inclusions     49     7.44     7.847964     1.142-68     1.142-68       DCTERN, CC FAT, GO.000128-problem inclusions     43     7.24     1.142-68	KEGG_PATHWAY	mmu05322:Systemic lupus erythematosus	28	145	9.244522043	1.36E-17	9.26E-17
GOTERNA DE PLAT     GOLDBARD     11     271     8.8820291     5.81E-14     1.95E-13       GOTERNA DE PLAT     GOTERNA DE PLAT     1.95E-13     2.92E-10	GOTERM_CC_FAT	GO:0032993~protein-DNA complex	30	274	6.940729927	5.31E-14	1.55E-13
Del GO EXTANUALY     Tomosofies Appointerm     49     1/16     1.93/2012     1.93/21     1.93/2	GOTERM_CC_FAT	GO:0000788~nuclear nucleosome	17	274	16.95293229	5.31E-14	1.55E-13
COTERN BP FAT     COUNTRAL FAT     COUNTRAL BP FAT     COUNTRAL FAT	GUIERM_CC_FAI	GO:0000790~nuclear chromatin	41	2/4	4.705190592	5.31E-14	1.55E-13
COTERN BP FAT     CO 200834	GOTERM CC FAT	GO:0000785~chromatin	29	27/	3 526703662	1.01E-13	2 99E-12
COTENN BP FAT     COUSSINGchromatin assembly     22     286     C 2249034     2.18E-38     1.04E-38       COTENN CC FAT     COUSSINGchromatin assembly     21     2248     C.1272134102     2.12E-38       COTENN DP FAT     COUSSINGchromatin assembly     22     2248     C.1272134102	GOTERM BP FAT	GO:0006334~nucleosome assembly	21	298	7.325542835	1.36E-08	6.48E-09
GOTERN, CC FAT     GOJONA4454-nuclear dromosome part     43     27.4     316708065     1.04E-08     4.18E-08       GOTERN, CC FAT     GOJONA232-nuclear dromosome parameter     44     27.4     316708065     1.04E-08     4.18E-08       GOTERN, BP FAT     GOJONA23-nuclear dromosome organization     22     29.6     5.757403971     5.66E-07     4.74E-07       GOTERN, BP FAT     GOJONA728-nucleasome organization     21     29.6     6.7724085     7.17E-07     7.17E-07       GOTERN, BP FAT     GOJONA728-nucleasome organization     21     29.6     6.9772485     7.11E-06     7.17E-07       GOTERN, BP FAT     GOJONA728-nucleasome organization     51     27.4     2.248108067     1.11E-05     3.34E-06       GOTERN, BP FAT     GOJONA322-chromatin silencing     18     2.98     2.428230398     1.31E-04     1.72E-04     7.25E-04     7	GOTERM BP FAT	GO:0031497~chromatin assembly	22	298	6.724970594	2.18E-08	1.04E-08
COTERN BP FAT     CODO0228-nuclear dynamosome     44     274     8.1116833     1.40E.03     4.10E.03     4.10E.03       COTERN BP FAT     COD000228-nuclear dynamics     23     236     5.57725234     1.00E.07     7.44E.07       COTERN BP FAT     COD000228-nuclear dynamics     22     298     5.57425047     3.1E.07     7.44E.07       COTERN BP FAT     COD000228-nuclear dynamics     21     298     5.57425047     3.1E.07     7.44E.07       COTERN BP FAT     COD000123-nuclear dynamics     1.81E.06     7.87E.07     7.87E.07 <t< td=""><td>GOTERM_CC_FAT</td><td>GO:0044454~nuclear chromosome part</td><td>43</td><td>274</td><td>3.196780065</td><td>1.04E-08</td><td>3.12E-08</td></t<>	GOTERM_CC_FAT	GO:0044454~nuclear chromosome part	43	274	3.196780065	1.04E-08	3.12E-08
COTERM BP FAT     GD 000803protein-DNA complex assembly     23     288     5.457540207     2.448-07       COTERM BP FAT     GD 000832brancesome organization     21     268     5.577440207     5.814-07     4.448-07       COTERM BP FAT     GD 000832brancesome organization     21     268     5.577440207     5.814-07     4.448-07       COTERM BP FAT     GD 000832brancesome organization     23     286     4.90775283     5.1574-01207     5.344-050       COTERM BP FAT     GD 000832brancesome organization     23     247     2.249338067     1.118-05     5.344-05       COTERM BP FAT     GD 000832brancesome organization     45     248     2.4497388     2.535-04     1.218-04     2.58E-04     1.28E-04     1.58E-04	GOTERM_CC_FAT	GO:0000228~nuclear chromosome	44	274	3.111166634	1.40E-08	4.19E-08
COLENU BP -A     COLOND333 - encodents assembly     22     288     E.7214112     SUPE UP     2.14.EU       COTERN BP FAT     COLOND340     SUPE UP     2.14.EU     SUPE UP     2.14.EU       COTERN BP FAT     COLONTAL Constantion of Lange     24     288     4.6710490021     1106.C6     SUPE Constantion     2.24     288     4.6710490021     1106.C6     SUPE Constantion     2.24     288     4.6710490021     1106.C6     SUPE Constantion     SUP	GOTERM_BP_FAT	GO:0065004~protein-DNA complex assembly	23	298	5.455785235	5.10E-07	2.43E-07
COTERN UP FAT     CONSTRUCT     200	GOTERM_BP_FAT	GO:0006333~chromatin assembly or disassembly	22	298	5.722124102	5.60E-07	2.67E-07
COTERN. BP FAT     CONTRACTOR     2001<	GOTERM_BP_FAT	GO:0006323~DNA packaging	22	298	5.575402971	9.31E-07	4.44E-07
COTERN LEP FAT     COTONIZ2S-protein-DNA complex subult organization     23     298     4.71149002     1116-05     5.28E-06       COTERN LCC FAT     CON0005684-chronomosome part     51     274     2.48198687     111E-05     3.38E-05       COTERN LEP FAT     CON000527-chronomatin organization     45     274     2.48199847     2.58E-04     1.21E-04       COTERN LEP FAT     CON00227-chronable momune response in mucosa     16     298     4.8497335     2.5E-04     1.21E-04       COTERN LEP FAT     CON00223-chronable momune response     18     298     1.48250336     0.001517429     7.38E-04       COTERN LEP FAT     CON00236-remucosal immune response     8     298     1.48250336     0.001517429     7.38E-04       COTERN LEP FAT     CO002317-chronosome organization     53     298     1.03541462     0.0025396     0.001218642     0.001218642     0.001218642     0.001218642     0.001218642     0.001218642     0.001218642     0.001218642     0.001218642     0.001218642     0.001218642     0.001218642     0.001218642     0.001218642     0.001218642     0.001218642     0.001218642	GOTERM BP_FAT	GO:0034726~nucleosome organization	21	290	2.0/4200047	9.94E-07	4.74E-07 7.97E-07
COTERN CC FAT CO008325-chromatin and mount synthesis and synthesynthesis and synthesis and synthesis and synthesis and	GOTERM BP FAT	GO:0071824~protain-DNA complex subunit organization	23	200	4.501132000	1.07 E-00	5.26E-06
GOTERM PFAT     COUD006894-chromatin organization     45     224633667     1111-05     3342-05       GOTERM BF FAT     COUD0842-chromatin ingenization     45     286     2.86179845     1315-04     6.2925       GOTERM BF FAT     COUD0842-chromatin ingenization     45     286     6.2427536     2.351-04     6.2925       GOTERM BF FAT     COUD0842-chromatin ingenization     6.8     1.81E-04     1.88E-04       GOTERM BF FAT     COUD0451-chipate macponization     8     286     1.8252401     2.12E-04       GOTERM BF FAT     COUD0451-chipate macponization     8     288     1.4252501     0.001217542       GOTERM BF FAT     COUD0451-chipate macponization     8     288     1.9534142     0.00255995     0.001217542       GOTERM BF FAT     COUD04072-genization inclusina macponization macponization macponization macponization macponization     8     288     1.9534142     0.00255995     0.001217542       GOTERM BF FAT     COUD03047-chipate macponization     1.928413755     1.9394703     0.011275425       GOTERM BF FA	GOTERM CC FAT	GO:0044427~chromosomal part	51	274	2 441895877	1.10E-05	4 76E-06
GOTERM BP FAT     GO:008325-chromatin inganization     45     288     248179945     1.318-04     6.2824.05       GOTERM BP FAT     GO:008227-innate immune response in mucosa     8     288     5.2825.058     1.582-04     1.218-04       GOTERM BP FAT     GO:002856-mucosal immune response     8     288     4.8256.038     0.00147429     7.38E-04       GOTERM BP FAT     GO:002867-mucosal immune response     8     288     1.42556.038     0.0012474-07     7.38E-04       GOTERM BP FAT     GO:0002167-chromato seme organic risuse genetic immune response     8     288     1.42556.038     0.0012474-07     7.37E-04       GOTERM BP FAT     GO:0001276-chromatoseme organic risuse genetic immune response     8     288     1.3855421     0.00126374     7.77E-04       GOTERM BP FAT     GO:0001276-chromatoseme organic seme segmese     9     288     3.45822316     0.032467809     0.017578583       GOTERM BP FAT     GO:0008105-chromatos guidance     7     288     6.30072477     1.7716.04       GOTERM MP FAT     GO:0008105-chromatos genetos in sempresion     9     288     3.45822316     0.049568142 <t< td=""><td>GOTERM CC FAT</td><td>GO:0005694~chromosome</td><td>53</td><td>274</td><td>2.254036067</td><td>1.11E-05</td><td>3.34E-05</td></t<>	GOTERM CC FAT	GO:0005694~chromosome	53	274	2.254036067	1.11E-05	3.34E-05
COTERM BP FAT     COD000342-chromatin ellinening     18     296     5.223530696     1.58E-04     7.58E-05       COTERM BP FAT     COD00251-chromatic immune response in mucces     8     298     14.2550336     0.00154742     7.38E-04       COTERM BP FAT     COD00251-crogan or fissue specific immune response     8     298     14.2550336     0.001547429     7.38E-04       COTERM BP FAT     CO00251-Crogan or fissue specific immune response     8     298     14.2550336     0.00151747429     7.38E-04       COTERM BP FAT     CO00025176     Deprove the specific immune response     8     298     1.0252516     0.02547695     0.001517653       COTERM BP FAT     CO00051076     Deprove the specific immune response immune response     6     288     3.0563216     0.02547653     CO101547653     CO101547653     CO101547653     CO101547643     0.03976533     COTERM BP FAT     CO000016971-ammine response immune response     19     298     1.0924073     0.07137233     COTERM SP FAT     CO00014971-ammine response immune response     1.0526767     COCO31480-dip metal meta	GOTERM_BP_FAT	GO:0006325~chromatin organization	45	298	2.46179945	1.31E-04	6.25E-05
COTERM BP_FAT     GO:000227-innate immune response in mucosa     8     28     19.24677338     2.53E-04     1.21E-04       COTERM BP_FAT     GO:0002365-mucosal immune response     8     298     14.8250338     0.001547429     7.38E-04       COTERM BP_FAT     GO:0001276-chromsome organization     53     298     14.8250338     0.001218542       COTERM BP_FAT     GO:001973-antinicrobal numoral response     8     298     13.9531422     0.00218542       GOTERM BP_FAT     GO:001973-antinicrobal numoral response     8     298     13.9531426     0.00218542       GOTERM BP_FAT     GO:001630-defense response to Gram-positive bacterium     10     298     5.006724852     0.0001803-defense response to Gram-positive bacterium     10     298     5.006724852     0.0000803-defense response     10.9386     10.938778	GOTERM_BP_FAT	GO:0006342~chromatin silencing	18	298	5.232530596	1.59E-04	7.59E-05
COTERM BP FAT     GO:0046914-negative regulation of gene expression, epigenetic     18     248     4.980019821     3.31E-04     1.58E-04       GOTERM BP FAT     GO:002251-organ or tissue specific immune response     8     288     14.8255038     0.001547429     7.38E-04       GOTERM BP FAT     GO:002157-organ or tissue specific immune response     8     298     13.9534142     0.00218542       GOTERM BP FAT     GO:0014765-chromosome or graphica     8     298     13.9534142     0.00218542       GOTERM BP FAT     GO:0016456-gene silencing     19     298     3.45625216     0.001218542       GOTERM BP FAT     GO:0006045-motor neuron axon guidance     7     298     10.9240561     0.095693142     0.01732033       GOTERM BP FAT     GO:0001645-gene silencing     8     277     28.914770     1.09647476     1.30947457     1.30947457     1.30947457     1.30947457     1.30947457     1.30947457     1.30947457     1.30947457     1.30947457     1.30947457     1.30947457     1.30947457     1.30947457     1.30947457     1.30947457     1.30947457     1.30947457     1.30947457     1.30947457 <t< td=""><td>GOTERM_BP_FAT</td><td>GO:0002227~innate immune response in mucosa</td><td>8</td><td>298</td><td>18.24677336</td><td>2.53E-04</td><td>1.21E-04</td></t<>	GOTERM_BP_FAT	GO:0002227~innate immune response in mucosa	8	298	18.24677336	2.53E-04	1.21E-04
COTERM PF FAT     GO:0002365-mucosal immune response     8     248     14.8255038     0.001517429     7.38E-04       COTERM PF FAT     GO:0001276-chromosame organization     53     248     2.073223424     0.001218542     7.38E-04       COTERM PF FAT     GO:0001773-antibacterial humoral response     8     288     13.9531142     0.02253995     0.001218542       COTERM PF FAT     GO:0001730-antibacterial humoral response     8     288     13.9531142     0.002553995     0.001218542       COTERM PF FAT     GO:0006030-defense response to Gram-positive bacterium     10     298     6.308724832     0.0897655312     0.047572583       GOTERM PF FAT     GO:0004002-reguitation of gene expression, epigenetic     19     298     3.096434767     0.19040531     0.10546258     0.105860719       GOTERM MF FAT     GO:0001720-haptoglobin binding     4     277     2.92418773     0.10546258     0.17572633       GOTERM MF FAT     GO:0001730-haptoglobin binding     4     274     2.81970803     0.27247755       GOTERM MF FAT     GO:0001730-haptoglobin binding     4     274     2.81970803     0.272477555<	GOTERM_BP_FAT	GO:0045814~negative regulation of gene expression, epigenetic	18	298	4.988019821	3.31E-04	1.58E-04
COTERM PF AT     GO:0002251-organ or tissue specific immune response     8     298     14.8255038     0.00157429     7.38E-04       COTERM PF AT     GO:0019730-antimicrobial humoral response     8     298     13.9531492     0.002253995     0.001218542       COTERM PF AT     GO:0019730-antimicrobial humoral response     8     298     13.9531492     0.002353995     0.01218542       COTERM PF AT     GO:0016458-gene silencing     19     298     3.45625216     0.095033142     0.03756533       COTERM PF AT     GO:00008045-motor neuron axon guidance     7     298     10.9240551     0.095033142     0.03756533       GOTERM PF AT     GO:0001392-nucleosomal DNA binding     8     277     7.491046931     0.02781732     1.07517132       GOTERM MF AT     GO:0000533-hemoglobin complex     4     274     2.91970803     0.02281763     0.1086071163     2.228427555       GOTERM MP FAT     GO:00000533-hemoglobin complex     4     274     2.91970803     0.02281763     0.022817163     2.228427555       GOTERM MP FAT     GO:0000053-hemoglobin complex     4     2777     2.9187183	GOTERM_BP_FAT	GO:0002385~mucosal immune response	8	298	14.82550336	0.001547429	7.38E-04
GOTERM BP FAT     GO:0061276-chromosome organization     53     298     2.073223424     0.001628717     7.77E-04       GOTERM BP FAT     GO:0019731-antibacterial humoral response     8     298     1.395314192     0.002553985     0.001218542       GOTERM BP FAT     GO:00196331-antibacterial humoral response     8     298     3.45625216     0.002563985     0.001218542       GOTERM BP FAT     GO:0005033-defense response to Gram-positive bacterium     10     298     5.308724321     0.090050312     0.037765373       GOTERM BP FAT     GO:0004029-regulation of gene expression, epigenetic     19     298     3.095343767     0.139043703     0.071817435       GOTERM MP FAT     GO:00031729-haptoglobin humding     4     277     2.9214773     0.105462586     0.21787248       GOTERM CP FAT     GO:00031383-hamptoglobin-hemoglobin-complex     4     274     2.81970803     0.072617163     0.22427555       GOTERM CP FAT     GO:000208-humoral immune response     10     298     4.86391724     0.7267763       GOTERM PFAT     GO:000208-humoral immune response     10     298     4.87174903     0.7267768 </td <td>GOTERM_BP_FAT</td> <td>GO:0002251~organ or tissue specific immune response</td> <td>8</td> <td>298</td> <td>14.82550336</td> <td>0.001547429</td> <td>7.38E-04</td>	GOTERM_BP_FAT	GO:0002251~organ or tissue specific immune response	8	298	14.82550336	0.001547429	7.38E-04
COTERM BP FAT     CO0019730-antimicrobial humoral response     8     288     13.98341492     0.00253998     0.001218542       COTERM BP FAT     CO00019731-antibacterial humoral response     19     288     3.456252316     0.032467800     0.01218542       COTERM BP FAT     CO0000802-defense response to Gram-positive bacterium     10     288     6.00874823     0.099003142     0.04758738       COTERM BP FAT     CO000002-engulation of gene expression, epigenetic     7     288     10.9240551     0.099003142     0.04758738       COTERM MP FAT     CO00003492-nucleosomal DNA binding     8     277     7.481046931     0.052862146     0.1058602146     0.015860246       COTERM MP FAT     CO0000333-hemoglobin complex     4     274     28.91970803     0.072817163     0.225427555       COTERM MP FAT     CO0000393-hemoglobin complex     4     274     28.91970803     0.072817163     0.225427555       COTERM MP FAT     CO00000393-hemoglobin complex     4     274     28.91970803     0.072817163     0.225427555       COTERM MP FAT     CO0000879-humoral immune response     10     287     1.050817899	GOTERM_BP_FAT	GO:0051276~chromosome organization	53	298	2.073223424	0.001628717	7.77E-04
GOTERM BP FAT     GO:0019731-entibacterial humoral response     8     8.288     13.9531492     0.00253980     0.001216542       GOTERM BP FAT     GO:0060832-defense response to Gram-positive bacterium     10     288     3.05242730     0.000763022     0.039765530       GOTERM BP FAT     GO:00040029-regulation of gene expression, epigenetic     19     288     3.095434767     0.139043703     0.071312835       GOTERM BP FAT     GO:00040029-regulation of gene expression, epigenetic     19     288     3.095434767     0.139043703     0.071312835       GOTERM MP FAT     GO:00031720-haptoglobin binding     4     274     28.91970803     0.072817163     0.224427555       GOTERM CP FAT     GO:00031389-haptoglobin-hemoglobin complex     4     274     28.91970803     0.072817163     0.224427555       GOTERM BP FAT     GO:0002098-neurogenesis     50     288     1.653917244     0.72775708     0.611097242     0.72877763     0.611097242       GOTERM MP FAT     GO:00031490-chromatin DNA binding     10     286     4.07714020     0.87894890     0.87894897     0.89894044     1.848719411     COTERM MP FAT     GO:0003	GOTERM_BP_FAT	GO:0019730~antimicrobial humoral response	8	298	13.95341492	0.002553995	0.001218542
GOTERM, BP_FAT     GO:0016458-gene silencing     19     298     3.486252316     0.032467809     0.015726583       GOTERM, BP_FAT     GO:0008045-motor neuron axon guidance     7     298     10.9240551     0.099083142     0.04759739       GOTERM, BP_FAT     GO:0008045-motor neuron axon guidance     19     298     3.095434767     0.0307181253       GOTERM, BP_FAT     GO:0005833-hemoglabin tomplex     4     277     29.92418773     0.04254274555       GOTERM, GP_FAT     GO:0005833-hemoglabin complex     4     274     28.91970803     0.072617168     0.228427555       GOTERM, GP_FAT     GO:000593-hemoglabin complex     4     274     28.91970803     0.072617168     0.228427555       GOTERM, BP_FAT     GO:000208-neurogenesis     50     286     1.86917524     0.7277051     0.61075252       GOTERM, BP_FAT     GO:00031490-chromatin DNA binding     10     277     4.38638801     0.28779208     0.6199847       GOTERM, BP_FAT     GO:00031490-chromatin DNA binding     10     277     4.38638801     0.28779208     0.69199847       GOTERM, BP_FAT     GO:00031490-chrom	GOTERM_BP_FAT	GO:0019731~antibacterial humoral response	8	298	13.95341492	0.002553995	0.001218542
GOTERM, BP FAT     GO.0050830-defense response to Gram-positive bacterium     10     298     6.306724632     0.00900322     0.03976536       GOTERM, BP FAT     GO.0040029-regulation of gene expression, epigenetic.     19     298     3.09543167     0.1934057     0.1934057     0.1934057     0.1934057     0.0901312935       GOTERM, MF FAT     GO.0031720-haptoplabin binding     8     277     28.9418773     0.105462586     0.21787281       GOTERM, CC, FAT     GO.0031838-hemoglobin complex     4     274     28.91970803     0.072617163     0.226427555       GOTERM, DC, FAT     GO.000289-humoral immune response     10     298     1.63619342     0.227773051     0.618072522       GOTERM, BP, FAT     GO.000289-humoral immune response     10     298     1.63619342     0.227773051     0.618072522       GOTERM, BP, FAT     GO.002189-humoral immune response     10     298     1.636193244     0.227733051     0.61807252       GOTERM, BP, FAT     GO.002089-humoral immune response     10     294     1.636193244     0.22773051     0.6180739464     0.93032971     0.930393271     0.930393271     0.93039	GOTERM_BP_FAT	GO:0016458~gene silencing	19	298	3.456252316	0.032467809	0.015726583
GOTERM, BP FAT     GO:0008045-motor neuron axon guidancia     7     298     10.9240551     0.0596083142     0.04759739       GOTERM, BP FAT     GO:0001492-muclassomal DNA binding     8     277     7.481046931     0.05634767     0.05963142     0.05634767     0.079132935       GOTERM, MF, FAT     GO:0005833-hemoglabin complex     4     274     28.91970803     0.072617168     0.224272555       GOTERM, GF, FAT     GO:000589-humoral immune response     10     298     4.941834452     0.460498080     0.2382547060       GOTERM, GF, FAT     GO:0002096-humoral immune response     10     298     4.941834452     0.460498080     0.2382547060       GOTERM, BP, FAT     GO:0002096-humoral immune response     10     298     4.941834452     0.460498080     0.2382547060       GOTERM, BP, FAT     GO:00031480-chromatin DNA binding     10     277     4.38638061     0.27777051     6.618072522       GOTERM, BP, FAT     GO:00031450-chromatin DNA binding     1277     4.38638061     0.278772089     0.73675270       GOTERM, BP, FAT     GO:00031757-back onder presponse     298     1.780653709     0.9395087	GOTERM BP FAT	GO:0050830~defense response to Gram-positive bacterium	10	298	6.308724832	0.080063022	0.039756536
GOTERM, BP_FAT     GO.0040029-regulation of gene expression, epigenetic.     19     298     3.095434767     0.139043703     0.071312305       GOTERM, MF_FAT     GO.001120-haptoplobin binding     8     277     7.841046831     0.055625144     0.105660719       GOTERM, MC_FAT     GO.0013120-haptoplobin complex     4     277     28.91970803     0.072611163     0.228427555       GOTERM, CC_FAT     GO.0003839-haptoplobin complex     4     274     28.91970803     0.072611163     0.228427555       GOTERM, BP_FAT     GO.00022006-neurogenesis     50     288     1.666317324     0.27815099     0.61807252       GOTERM, BP_FAT     GO.0007399-nervous system development     63     298     1.536195249     0.7815099     0.61993647       GOTERM, BP_FAT     GO.0003182-neuron differentiation     62     298     1.7106303     0.73589748     0.94540761     0.83877648     0.94540761     0.325098609     0.61993647       GOTERM, BP_FAT     GO.0003077-DNA binding     64     277     1.50325588     0.34309242     0.882704421     0.80317982       GOTERM, BP_FAT     GO.0004582-negative regulation	GOTERM BP FAT	GO:0008045~motor neuron axon guidance	7	298	10.9240551	0.095083142	0.04759739
GOTERM, MF, FAT     GO.0031492-nucleosomal DNA binding     8.     277     249241073     0.105462714     0.1052682154     0.1056807193       GOTERM, MF, FAT     GO.0031833-hanploploin-complex     4     274     28.91970803     0.072617163     0.222487555       GOTERM, CC, FAT     GO.0031833-hanploploin-toomplex     4     274     28.91970803     0.72617163     0.222487555       GOTERM, BP, FAT     GO.002008-neurogenesis     50     298     1.863917324     0.727773051     0.61807252       GOTERM, MF, FAT     GO.002008-neurogenesis     50     1.863917324     0.727773051     0.618072542       GOTERM, MF, FAT     GO.003189-nervona system development     63     298     1.20638716     0.837796484     0.945407611       GOTERM, MF, FAT     GO.0030754-detoxification     64     298     1.7165208     0.8430942     0.882709431       GOTERM, BP, FAT     GO.0031475-neuron projection development     37     298     1.786787049     0.3932239718     1.325739867       GOTERM, BP, FAT     GO.0048666-neuron development     37     298     1.786787649     0.3942043941     1.3248249435	GOTERM_BP_FAT	GO:0040029~regulation of gene expression, epigenetic	19	298	3.095434767	0.139043703	0.071312935
GOTERM CFAT     60.0031720-happtoglobin binding     4     277     29.92418773     0.105462586     0.21787281       GOTERM CC, FAT     60.000383-hemoglobin complex     4     274     28.91970803     0.072617163     0.225427555       GOTERM BP, FAT     60.000589-humoral immune response     10     284     49.4183452     40.409893     0.238624708       GOTERM BP, FAT     60.0007399-nerrous system     63     298     1.858317324     0.727773059     0.618075252       GOTERM BP, FAT     60.0007399-nerrous system     63     298     1.736638716     0.83779648     0.94540761       GOTERM BP, FAT     60.0007399-nerrous system     63     298     1.730638716     0.83779648     0.94540761       GOTERM BP, FAT     60.0003787-DNA binding     64     277     1.53255888     0.34309242     0.82709431       GOTERM BP, FAT     60.00045892-negative regulation of transcription, DNA-templated     42     298     1.700314613     0.9404344     1.33483208     1.32412244     1.33483208     1.33618972     0.96758424     1.03014613     0.9404344     1.334832081     1.324712344     1.334832	GOTERM MF FAT	GO:0031492~nucleosomal DNA binding	8	277	7.481046931	0.052682154	0.105860719
GOTERM CC_FAT     GO000833-hemoglobin complex     4     274     28.91970803     0.072617163     0.225427565       GOTERM CC_FAT     GO0008695-humoral immune response     10     284     4.94183452     0.40409893     0.238624708       GOTERM MP_FAT     GO.0002395-nervous system development     63     288     1.536195249     0.728752708       GOTERM MP_FAT     GO.0007395-nervous system development     63     288     1.536195249     0.7387537084     0.945407611       GOTERM MP_FAT     GO.0009739-nervous system development     63     288     1.7036716     0.828779848     0.945407611       GOTERM MP_FAT     GO.000977-DNA binding     64     277     1.50357084     0.945407611       GOTERM MP_FAT     GO.000977-DNA binding     64     278     1.7063503     0.925506245     1.232412244       GOTERM MP_FAT     GO.00031497-neuron projection development     37     288     1.7063703     0.925506245     1.232412244       GOTERM MP_FAT     GO.0048668-neuron development     37     288     1.70637061     0.82573988     0.36575028     1.6325739897     0.36575208     1.63257	GOTERM MF FAT	GO:0031720~haptoglobin binding	4	277	29.92418773	0.105462586	0.21787281
GOTERM BP_FAT     GO:0031838-happinglobin-hemoglobin complex     4     274     28.91970803     0.072617163     0.225427555       GOTERM BP_FAT     GO:0022008-neurogenesis     50     288     1.663917324     0.727773051     0.618072522       GOTERM BP_FAT     GO:0022008-neurogenesis     50     288     1.566195249     0.78150990     0.736752708       GOTERM MP_FAT     GO:003182-neuron differentiation     63     288     1.720538716     0.863779648     0.945407611       GOTERM MP_FAT     GO:0030757-DNA binding     64     277     1.530255989     0.3988609       GOTERM BP_FAT     GO:0045892-negative regulation of transcription, DNA-templated     42     288     1.710635003     0.925906245     1.232412284       GOTERM BP_FAT     GO:0045892-negative regulation of nucleic acid-templated transcription     42     288     1.710635003     0.925906245     1.232412284       GOTERM BP_FAT     GO:0045892-negative regulation of nucleic acid-templated transcription     42     288     1.710635003     0.925906245     1.232412284       GOTERM BP_FAT     GO:00405679-negative regulation of nucleic acid-templated transcription     42     1.76	GOTERM CC FAT	GO:0005833~hemoglobin complex	4	274	28.91970803	0.072617163	0.225427555
GOTERM_PF_AT     GO:0006959-humoral Immune response     10     298     4.941834452     0.460489933     0.293624706       GOTERM_BF_AT     GO:0007399-nervous system development     63     298     1.536195249     0.786752706       GOTERM_BF_AT     GO:0007399-nervous system development     63     298     1.536195249     0.786752706       GOTERM_MF_FAT     GO:000182-neuron differentiation     43     298     1.720638716     0.863779484     0.945407611       GOTERM_BF_FAT     GO:000877-DNA binding     64     277     1.503255896     0.946307614     0.882709431       GOTERM_BF_FAT     GO:000877-DNA binding     64     277     1.503255896     0.946307614     1.8827739367       GOTERM_BF_FAT     GO:000877-DNA binding     1.92247284     1.880747049     0.9322907243     1.32373387       GOTERM_BF_FAT     GO:0048666-neuron development     37     298     1.786787049     0.93929718     1.32373387       GOTERM_BF_FAT     GO:004812-neuron projection morphogenesis     23     298     1.786787049     0.93929718     1.32842985       GOTERM_BF_FAT     GO:00305-eliprojeaview regulatio	GOTERM CC FAT	GO:0031838~haptoglobin-hemoglobin complex	4	274	28.91970803	0.072617163	0.225427555
GOTERM_PF_FAT     GO:0022008-neurogenesis     50     298     1.663917324     0.72773051     0.618072522       GOTERM_MF_FAT     GO:0031490-chromatin DNA binding     10     277     4.33833801     0.287732089     0.661993647       GOTERM_MF_FAT     GO:003162-neuron differentiation     43     298     1.720638716     0.863779448     0.945407611       GOTERM_MF_FAT     GO:003677-DNA binding     64     277     1.503255898     0.364309242     0.882079431       GOTERM_BP_FAT     GO:003677-DNA binding     64     277     1.503255898     0.364309242     0.882079431       GOTERM_BP_FAT     GO:0045892-negative regulation of transcription, DNA-templated     42     298     1.706540503     0.93293718     1.32573367       GOTERM_BP_FAT     GO:0045892-negative regulation of nucleic acid-templated transcription     42     298     1.70614613     0.940403494     1.334832086       GOTERM_BP_FAT     GO:003547-negative regulation of nucleic acid-templated transcription     42     298     1.708614613     0.940403494     1.334832086       GOTERM_BP_FAT     GO:003540280     0.993059714     1.284948356     0.987587282	GOTERM BP FAT	GO:0006959~humoral immune response	10	298	4.941834452	0.460498993	0.293624708
COTERM MP FAT     GO:007399-nervous system development     63     298     1.536195249     0.788150999     0.736752708       COTERM MP FAT     GO:0031490-chromatin DNA binding     10     277     4.336838061     0.28772080     0.681993647       GOTERM MP FAT     GO:0030182-neuron differentiation     64     277     1.50325588     0.38430224     0.882709431       GOTERM MP FAT     GO:003017-DNA binding     64     277     1.50325588     0.38430242     0.882709431       GOTERM MP FAT     GO:003175-neuron projection development     34     298     1.7868615237     0.89766442     1.080217982       GOTERM MP FAT     GO:0048666-neuron development     37     298     1.786787049     0.939239718     1.325739367       GOTERM MP FAT     GO:013047-Inspative regulation of nucleic acid-templated transcription     42     298     1.70635067     0.483229381     1.23443208       GOTERM MP FAT     GO:013067-negative regulation of RNA biosynthetic process     42     298     1.68745664     1.240430365       GOTERM MP FAT     GO:0003030-cell projection organization     45     298     1.63256950     0.9873562	GOTERM_BP_FAT	GO:0022008~neurogenesis	50	298	1.663917324	0.727773051	0.618072522
COTERM_MF_FAT     GO:0031490-chromatin DNA binding     10     277     4.38633801     0.287792089     0.661993647       GOTERM_BP_FAT     GO:0030182-neuron differentiation     43     298     1.720638716     0.863779648     0.945407611       GOTERM_BP_FAT     GO:0030377-DNA binding     64     277     1.50325588     0.34309242     0.882709431       GOTERM_BP_FAT     GO:00303175-neuron projection development     34     298     1.710635003     0.925906245     1.22412244       GOTERM_BP_FAT     GO:0045892-negative regulation of transcription, DNA-templated transcription     42     298     1.710635003     0.925906245     1.22412244       GOTERM_BP_FAT     GO:0048666-neuron development     37     298     1.708614613     0.94043944     1.334832086       GOTERM_BP_FAT     GO:0031491-nucleosome binding     8     277     5.093478762     0.483229381     1.282443254       GOTERM_MP_FAT     GO:00304812-neuron projection organization     42     298     1.687455667     0.967593281     1.620843725       COTERM_MP_FAT     GO:00300-cell projection organization     45     298     1.687455667     0.	GOTERM BP FAT	GO:0007399~nervous system development	63	298	1.536195249	0.788150999	0.736752708
GOTERM BP_FAT     GC:0030182-neuron differentiation     43     298     1.720638716     0.863779648     0.945407611       GOTERM MP_FAT     GC:0003677-DNA binding     6     298     8.471716203     0.87838997     0.99886609       GOTERM MP_FAT     GC:0003677-DNA binding     64     277     1.50325598     0.364309242     0.882709431       GOTERM MP_FAT     GC:00048692-negative regulation of transcription, DNA-templated     42     298     1.710653003     0.92908245     1.324739367       GOTERM MP_FAT     GC:0036507-negative regulation of nucleic acid-templated transcription     42     298     1.786787049     0.939239718     1.325739367       GOTERM MP_FAT     GC:0031491-nucleosome binding     8     277     5.093478762     0.483229381     1.23649355       GOTERM MP_FAT     GC:002679-negative regulation of RNA biosynthetic process     42     228     1.87875667     0.96730562     1.616700812       GOTERM MP_FAT     GC:0003030-cell projection organization     45     298     1.612958856     0.98247822     1.91323061       GOTERM MP_FAT     GC:0000534-box/rate acrinogenesis     61     145     2.171899	GOTERM MF FAT	GO:0031490~chromatin DNA binding	10	277	4.336838801	0.287792089	0.661993647
COTERM BP_FAT     GO:0098754-detoxification     6     298     8.471716203     0.87836997     0.99868609       GOTERM MP_FAT     GO:0031775-neuron projection development     34     298     1.866915237     0.897664942     1.080317982       GOTERM BP_FAT     GO:0045892-negative regulation of transcription, DNA-templated     42     298     1.710635003     0.925906245     1.232412284       GOTERM BP_FAT     GO:0048666-neuron development     37     298     1.766787049     0.939239718     1.326739367       GOTERM BP_FAT     GO:0048812-neuron projection morphogenesis     23     298     1.710830027     0.96730562     1.826739367     1.67436844     1.240430365       GOTERM BP_FAT     GO:0048812-neuron projection organization     45     2.98     1.637456667     0.96730562     1.880034028       GOTERM BP_FAT     GO:0048812-neuron projection organization     6     145     5.250276391     1.612048925     1.880044028       GOTERM BP_FAT     GO:0003030-cell projection organization     6     145     2.52027630     1.820430365     1.88034028       GOTERM BP_FAT     GO:0000330-neugative regulation of cellular macromolecul	GOTERM BP FAT	GO:0030182~neuron differentiation	43	298	1.720638716	0.863779648	0.945407611
COTERM_MF_FAT     GO:0003677-DNA binding     64     277     1.503255898     0.364309242     0.882709431       GOTERM_BP_FAT     GO:00045892-negative regulation of transcription, DNA-templated     42     298     1.70635003     0.925906245     1.080317982       GOTERM_BP_FAT     GO:0045892-negative regulation of transcription, DNA-templated     42     298     1.706787049     0.939239718     1.32347323087       GOTERM_BP_FAT     GO:0048862-neuron development     37     298     1.706787049     0.939239718     1.32347323087       GOTERM_BP_FAT     GO:0048191-nucleosome binding     8     277     5.093478762     0.483229381     1.83649355       GOTERM_BP_FAT     GO:0048812-neuron projection morphogenesis     23     298     1.687455667     0.967593281     1.820843725       KEGG PATHWAY     mmu05203.Viral carcinogenesis     16     145     2.592075391     0.167436844     1.20433726       GOTERM_BP_FAT     GO:0003040-cell projection organization     6     145     7.114798024     0.89991897     1.452043725       GOTERM_BP_FAT     GO:0000344-oxygen transporter activity     4     277     17.09853844	GOTERM BP FAT	GO:0098754~detoxification	6	298	8.471716203	0.87836997	0.99886609
COTERM_BP_FAT     GO:0031175-neuron projection development     34     298     1.866915237     0.897664942     1.080317982       GOTERM_BP_FAT     GO:0048666-neuron development     42     298     1.70637003     0.925906245     1.322739367       GOTERM_BP_FAT     GO:0048666-neuron development     37     298     1.706371049     0.939239718     1.325739367       GOTERM_MP_FAT     GO:0048666-neuron development     42     298     1.703614613     0.94003494     1.33483208       GOTERM_MP_FAT     GO:0048812-neuron projection morphogenesis     23     298     2.171889027     0.96730562     1.616700812       GOTERM_MP_FAT     GO:0003491-neucleosome binding     8     277     5.09378716     1.620843725       GOTERM_MP_FAT     GO:0003403-cell projection organization     45     298     1.63717215     0.981725905     1.889034028       GOTERM_MP_FAT     GO:0000344-oxygen transporter activity     4     277     1.09953544     0.59553669     1.756183198       KEGG PATHWAY     muu05144:Malaria     6     145     7.113479624     0.18991897     1.425014745       GOTERM_MP	GOTERM MF FAT	GO:0003677~DNA binding	64	277	1.503255898	0.364309242	0.882709431
GOTERM_BP_FAT     GO:0045892-negative regulation of transcription, DNA-templated     42     298     1.710635003     0.925906245     1.322412284       GOTERM_BP_FAT     GO:0048866-neuron development     37     298     1.786787049     0.939239718     1.325739367       GOTERM_MP_FAT     GO:0031491-nucleosome binding     8     277     5.093478762     0.483229381     1.283649355       GOTERM_BP_FAT     GO:002679-negative regulation of RNA biosynthetic process     42     298     1.687455667     0.96730562     1.62043725       GOTERM_BP_FAT     GO:0003030-cell projection organization     45     298     1.61259856     0.982647822     1.913232061       GOTERM_BP_FAT     GO:00033030-cell projection organization     45     298     1.612959856     0.982647822     1.913232061       GOTERM_MP_FAT     GO:000344-oxygen transporter activity     4     277     1.710995354     0.59559369     1.756183198       KEGG PATIWAY     mun05144:Malania     6     145     2.7114241611     0.992760062     2.320929568       GOTERM_P_FAT     GO:0004369-generation of neurons     45     298     1.622300294     0.9	GOTERM BP FAT	GO:0031175~neuron projection development	34	298	1.866915237	0.897664942	1.080317982
GOTERM BP FAT     GO:0048666-neuron development     37     298     1.786787049     0.393239718     1.325733367       GOTERM MP FAT     GO:0031491-nucleosome binding     8     277     5.0934787c     0.434232981     1.238649355       GOTERM MP FAT     GO:0031491-nucleosome binding     8     277     5.0934787c     0.433232981     1.28649355       GOTERM MP FAT     GO:0048812-neuron projection morphogenesis     23     298     2.171889027     0.96739522     1.616700812       GOTERM MP FAT     GO:0030300-cell projection organization     45     298     1.63717215     0.981725905     1.889034028       GOTERM MP FAT     GO:0005344- oxygen transporter activity     4     277     17.09955384     0.59550869     1.756183198       KEGG PATHWAY     mu05203.Viru ergulation of neurons     6     145     7.113479624     0.18991897     1.425014745       GOTERM MP FAT     GO:00043699-generation of neurons     45     298     1.620230294     0.991097292     2.224687786       GOTERM MP FAT     GO:00043699-generation of neurons     6     145     7.113479624     0.189991897     1.425014745 </td <td>GOTERM BP FAT</td> <td>GO:0045892~negative regulation of transcription, DNA-templated</td> <td>42</td> <td>298</td> <td>1.710635003</td> <td>0.925906245</td> <td>1.232412284</td>	GOTERM BP FAT	GO:0045892~negative regulation of transcription, DNA-templated	42	298	1.710635003	0.925906245	1.232412284
GOTERM_BP_FAT     GO:1903507-negative regulation of nucleic acid-templated transcription     42     298     1.703614613     0.940403494     1.334832098       GOTERM_MF_FAT     GO:0031491-nucleosome binding     8     277     5.093478762     0.483229381     1.283649355       GOTERM_BP_FAT     GO:0048812-neuron projection morphogenesis     23     298     1.87455667     0.967593281     1.620843725       GOTERM_BP_FAT     GO:003030-regative regulation of RNA biosynthetic process     42     298     1.887455667     0.967593281     1.620843725       GOTERM_BP_FAT     GO:003030-cell projection organization     45     298     1.6317215     0.987247822     1.913220061       GOTERM_BP_FAT     GO:00005344-oxygen transporter activity     4     277     17.09953584     0.595593669     1.756183198       KEGG_PATHWAY     mmu05144-Malaria     6145     7.113479624     0.189991897     1.425014745       GOTERM_BP_FAT     GO:00043699-generation of neurons     45     298     1.62320294     0.99109792     2.242687786       GOTERM_BP_FAT     GO:0004355-DNA replication-dependent nucleosome organization     6298     7.116241611 <t< td=""><td>GOTERM BP FAT</td><td>GO:0048666~neuron development</td><td>37</td><td>298</td><td>1.786787049</td><td>0.939239718</td><td>1.325739367</td></t<>	GOTERM BP FAT	GO:0048666~neuron development	37	298	1.786787049	0.939239718	1.325739367
GOTERM MF_FAT     GO:0031491~nucleosome binding     8     277     5.093478762     0.483229381     1.283649355       GOTERM BP_FAT     GO:0048812~neuron projection morphogenesis     23     298     1.61740612     0.96730362     1.616700612       GOTERM BP_FAT     GO:00300~cell projection organization     45     298     1.63717215     0.98730362     1.988034028       GOTERM BP_FAT     GO:000030-cell projection organization     45     298     1.63717215     0.98267822     1.938232061       GOTERM BP_FAT     GO:00005344~oxygen transporter activity     4     277     17.09953584     0.595593669     1.756183198       KEGG PATHWAY     mmu05144:Malaria     6     145     7.113479624     0.1899979     2.224687786       GOTERM BP_FAT     GO:0046699~generation of neurons     45     298     1.623230294     0.991097292     2.224687786       GOTERM BP_FAT     GO:004723~DNA replication-dependent nucleosome organization     6     298     7.116241611     0.992760062     2.320929568       GOTERM BP_FAT     GO:004723~negative regulation of RNA metabolic process     43     298     1.640918003     0.9	GOTERM BP FAT	GO:1903507~negative regulation of nucleic acid-templated transcription	42	298	1.703614613	0.940403494	1.334832098
GOTERM_BP_FAT     GO:0048812-neuron projection morphogenesis     23     298     2.171889027     0.96730562     1.616700812       GOTERM_BP_FAT     GO:1902679-negative regulation of RNA biosynthetic process     42     298     1.687455667     0.96730562     1.62084725       KEGG_PATHWAY     mmu05203:Viral carcinogenesis     16     145     2.592075391     0.167436844     1.240430365       GOTERM_BP_FAT     GO:0000304-cell projection organization     45     298     1.63717215     0.981725905     1.889034028       GOTERM_MP_FAT     GO:00005344-oxygen transporter activity     4     277     17.09953584     0.595593669     1.756183198       KEGG_PATHWAY     mmu05144.Malaria     6     145     7.113479624     0.189991897     1.425014745       GOTERM_BP_FAT     GO:0048699-generation of neurons     45     298     1.623230294     0.991097929     2.224687786       GOTERM_BP_FAT     GO:0043725-DNA replication-dependent nucleosome organization     6     298     7.116241611     0.992760062     2.320292668       GOTERM_BP_FAT     GO:0034725-DNA replication of RNA metabolic process     43     298     1.640918	GOTERM MF FAT	GO:0031491~nucleosome binding	8	277	5.093478762	0.483229381	1.283649355
GOTERM_BP_FAT     GO:1902679-negative regulation of RNA biosynthetic process     42     298     1.687455667     0.967593281     1.620843725       KEGG_PATHWAY     mmu05203:Viral carcinogenesis     16     145     2.592075391     0.167436844     1.240430365       GOTERM_BP_FAT     GO:003030-cell projection organization     45     298     1.63171215     0.98172505     1.88904028       GOTERM_MP_FAT     GO:0000334-oxygen transporter activity     4     277     17.09953584     0.982647822     1.913232061       GOTERM_BP_FAT     GO:0048699-generation of neurons     6     145     7.113479624     0.189991897     1.425014745       GOTERM_BP_FAT     GO:003355-DNA replication-dependent nucleosome assembly     6     298     7.116241611     0.992760062     2.320929568       GOTERM_BP_FAT     GO:0034723-DNA replication-dependent nucleosome organization     6     298     7.116241611     0.992760062     2.320929568       GOTERM_BP_FAT     GO:00342566-structure-specific DNA binding     11     277     3.393464587     0.66300335     2.106153885       GOTERM_BP_FAT     GO:00042566-structure-specific DNA binding     11     2	GOTERM BP FAT	GO:0048812~neuron projection morphogenesis	23	298	2.171889027	0.96730562	1.616700812
KEGG_PATHWAY     mmu05203:Viral carcinogenesis     16     145     2.592075391     0.167436844     1.240430365       GOTERM_BP_FAT     GO:030030-cell projection organization     45     298     1.632717215     0.981725905     1.889034028       GOTERM_BP_FAT     GO:0005344-oxygen transporter activity     4     277     17.09953584     0.5982647822     1.913232061       GOTERM_MF_FAT     GO:0005344-oxygen transporter activity     4     277     17.09953584     0.59953669     1.756183198       KEGG_PATHWAY     mmu05144:Malaria     6     145     7.113479624     0.189991897     1.425014745       GOTERM_BP_FAT     GO:0048609-generation of neurons     45     298     1.6123230294     0.991097929     2.24687786       GOTERM_BP_FAT     GO:00034723-DNA replication-dependent nucleosome organization     6     298     7.116241611     0.992760062     2.320929568       GOTERM_BP_FAT     GO:00043566-structure-specific DNA binding     11     277     3.393464587     0.66300335     2.106153885       GOTERM_BP_FAT     GO:00032276-DNA methylation on cytosine     6     298     6.84254010     0.997359314<	GOTERM BP FAT	GO:1902679~negative regulation of RNA biosynthetic process	42	298	1.687455667	0.967593281	1.620843725
GOTERM_BP_FAT     GO:0030030-cell projection organization     45     298     1.63717215     0.981725905     1.889034028       GOTERM_MP_FAT     GO:00005344-coxygen transporter activity     4     277     17.09953584     0.595593669     1.756183198       GOTERM_MP_FAT     GO:0006335-DNA replication-dependent nucleosome assembly     6     145     7.113479624     0.19991897     1.425014745       GOTERM_BP_FAT     GO:0006335-DNA replication-dependent nucleosome assembly     6     298     1.612958266     0.992760062     2.320929688       GOTERM_BP_FAT     GO:00043723-DNA replication-dependent nucleosome organization     6     298     7.116241611     0.992760062     2.320929568       GOTERM_BP_FAT     GO:00043723-DNA replication of RNA metabolic process     43     298     1.640918003     0.993940339     2.40372464       GOTERM_BP_FAT     GO:00032776-DNA methylation on cytosine     6     298     6.84254001     0.997359314     2.789240242       GOTERM_BP_FAT     GO:0005230-extracellular ilgand-gated ion channel activity     4     277     14.96209386     0.7993568313     2.72825013     2.498240242       GOTERM_BP_FAT     GO:0	KEGG PATHWAY	mmu05203:Viral carcinogenesis	16	145	2.592075391	0.167436844	1.240430365
GOTERM_BP_FAT     GO:2000113-negative regulation of cellular macromolecule biosynthetic process     47     298     1.612959856     0.982647822     1.913232061       GOTERM_MF_FAT     GO:0005344-oxygen transporter activity     4     277     17.09933544     0.595593669     1.756183198       KEGG_PATHWAY     mmu05144:Malaria     6     145     7.113479624     0.189991897     1.425014745       GOTERM_BP_FAT     GO:0048699-generation of neurons     45     298     1.623230294     0.991097929     2.224867786       GOTERM_BP_FAT     GO:000337-DNA replication-dependent nucleosome organization     6     298     7.116241611     0.992760062     2.320929568       GOTERM_BP_FAT     GO:0003276-DNA replication of RNA metabolic process     43     298     1.640918003     0.993940339     2.403724643       GOTERM_BP_FAT     GO:0003276-DNA methylation on cytosine     6     298     6.84254001     0.997359314     2.789240242       GOTERM_BP_FAT     GO:0008285-negative regulation of cell proliferation     25     298     1.982019165     0.998865808     3.179924089       GOTERM_BP_FAT     GO:0008285-negative regulation on charomelactivity <td< td=""><td>GOTERM BP FAT</td><td>GO:0030030~cell projection organization</td><td>45</td><td>298</td><td>1.63717215</td><td>0.981725905</td><td>1.889034028</td></td<>	GOTERM BP FAT	GO:0030030~cell projection organization	45	298	1.63717215	0.981725905	1.889034028
GOTERM_MF_FAT     GO:0005344-oxygen transporter activity     4     277     17.09953584     0.595593669     1.756183198       KEGG_PATHWAY     mmu05144:Malaria     6     145     7.113479624     0.189991897     1.425014745       GOTERM_BP_FAT     GO:0006335-DNA replication-dependent nucleosome assembly     6     298     7.116241611     0.992760062     2.320929568       GOTERM_BP_FAT     GO:00051253-negative regulation of RNA metabolic process     43     298     1.640918003     0.993940339     2.403724643       GOTERM_BP_FAT     GO:0051253-negative regulation of RNA metabolic process     43     298     1.640918003     0.993940339     2.403724643       GOTERM_BP_FAT     GO:0052776-DNA methylation on cytosine     6     298     6.84254001     0.997359314     2.789240242       GOTERM_BP_FAT     GO:0005230-extracellular ligand-gated ion channel activity     4     277     14.96209386     0.766693103     2.728250104       GOTERM_BP_FAT     GO:0005230-extracellular ligand-gated ion channel activity     4     277     14.96209386     0.766693103     2.728250104       GOTERM_BP_FAT     GO:0005687-integral component of plasma membrane	GOTERM BP FAT	GO:2000113~negative regulation of cellular macromolecule biosynthetic process	47	298	1.612959856	0.982647822	1.913232061
KEGG_PATHWAY     mmu05144:Malaria     6     145     7.113479624     0.189991897     1.425014745       GOTERM_BP_FAT     GO:00048699-generation of neurons     45     298     1.623230294     0.991097929     2.224687786       GOTERM_BP_FAT     GO:000335-DNA replication-dependent nucleosome organization     6     298     7.116241611     0.992760062     2.320929568       GOTERM_BP_FAT     GO:0051253-negative regulation of RNA metabolic process     43     298     1.640918003     0.993940339     2.403724643       GOTERM_BP_FAT     GO:0032776-DNA methylation on cytosine     6     298     6.84254001     0.997359314     2.789240242       GOTERM_BP_FAT     GO:0005230-extracellular ligand-gated ion channel activity     4     277     1.496209386     0.756693103     2.728250104       GOTERM_BP_FAT     GO:0005230-extracellular ligand-gated ion channel activity     4     277     1.964654078     0.598711543     2.696339101       GOTERM_BP_FAT     GO:0005887-integral component of plasma membrane     25     274     1.964654078     0.598711543     2.696339101       GOTERM_BP_FAT     GO:0005887-integative regulation of macromolecule biosynthetic pro	GOTERM MF FAT	GO:0005344~oxygen transporter activity	4	277	17.09953584	0.595593669	1.756183198
GOTERM_BP_FAT     GO:0048699-generation of neurons     45     298     1.623230294     0.991097929     2.224687786       GOTERM_BP_FAT     GO:0006335-DNA replication-dependent nucleosome organization     6     298     7.116241611     0.992760062     2.320929568       GOTERM_BP_FAT     GO:0051253-negative regulation of RNA metabolic process     43     298     1.640918003     0.993940339     2.403724643       GOTERM_BP_FAT     GO:0032776-DNA methylation on cytosine     6     298     6.84254001     0.993759314     2.789240242       GOTERM_BP_FAT     GO:0008285-negative regulation of cell proliferation     25     298     1.842019165     0.99886508     3.179924089       GOTERM_BP_FAT     GO:0005230-extracellular ligand-gated ion channel activity     4     277     14.96209386     0.756693103     2.728250104       GOTERM_BP_FAT     GO:0005842-defense response to other organism     19     298     2.25347651     0.999367238     3.448714516       GOTERM_BP_FAT     GO:0005887-integral component of plasma membrane     25     274     1.964654078     0.598711543     2.696339101       GOTERM_BP_FAT     GO:0005887-integral component of macromole	KEGG PATHWAY	mmu05144:Malaria	6	145	7.113479624	0.189991897	1.425014745
GOTERM_BP_FAT     GO:000335-DNA replication-dependent nucleosome assembly     6     298     7.116241611     0.992760062     2.320929568       GOTERM_BP_FAT     GO:0034723-DNA replication-dependent nucleosome organization     6     298     7.116241611     0.992760062     2.320929568       GOTERM_BP_FAT     GO:0051253-negative regulation of RNA metabolic process     43     298     1.640918003     0.99394039     2.403724643       GOTERM_MF_FAT     GO:0043566-structure-specific DNA binding     11     277     3.393464587     0.66300335     2.106153885       GOTERM_BP_FAT     GO:0008285-negative regulation on cytosine     6     298     6.84254001     0.997359314     2.789240242       GOTERM_BP_FAT     GO:0008285-negative regulation on cytosine     6     298     1.982019165     0.998865808     3.179924089       GOTERM_BP_FAT     GO:0008285-negative regulation on chem cyganism     19     298     2.25347651     0.999367138     3.448714516       GOTERM_BP_FAT     GO:0005887-integral component of plasma membrane     25     274     1.964654078     0.598711543     2.696339101       GOTERM_BP_FAT     GO:0010558-negative regulation of macromol	GOTERM BP FAT	GO:0048699~generation of neurons	45	298	1.623230294	0.991097929	2.224687786
GOTERM_BP_FAT     GO:0034723-DNA replication-dependent nucleosome organization     6     298     7.116241611     0.992760062     2.320929568       GOTERM_BP_FAT     GO:0051253-negative regulation of RNA metabolic process     43     298     1.640918003     0.993940339     2.403724643       GOTERM_MP_FAT     GO:0043566-structure-specific DNA binding     11     277     3.393464587     0.66300335     2.106153885       GOTERM_BP_FAT     GO:0032776-DNA methylation on cytosine     6     298     6.84254001     0.997359314     2.782240242       GOTERM_BP_FAT     GO:0005230-extracellular ligand-gated ion channel activity     4     277     14.96209386     0.756693103     2.728250104       GOTERM_BP_FAT     GO:000587-integral component of plasma membrane     25     274     1.964654078     0.598711543     2.66833101       GOTERM_BP_FAT     GO:0005887-integral component of plasma membrane     25     274     1.964654078     0.598711543     2.698331011       GOTERM_BP_FAT     GO:00048468-cell development     59     298     1.462716866     0.999765405     3.04020281       GOTERM_BP_FAT     GO:00015276-ligand-gated ion channel activity	GOTERM BP FAT	GO:0006335~DNA replication-dependent nucleosome assembly	6	298	7.116241611	0.992760062	2.320929568
GOTERM_BP_FAT     GO:0051253-negative regulation of RNA metabolic process     43     298     1.640918003     0.993940339     2.403724643       GOTERM_MF_FAT     GO:0043566-structure-specific DNA binding     11     277     3.393464587     0.66300335     2.106153885       GOTERM_BP_FAT     GO:0032776-DNA methylation on cytosine     6     298     6.84254001     0.997359314     2.789240242       GOTERM_BP_FAT     GO:0008285-negative regulation of cell proliferation     25     298     1.982019165     0.998865808     3.179924089       GOTERM_MF_FAT     GO:0005230-extracellular ligand-gated ion channel activity     4     277     14.96209386     0.756693103     2.728220104       GOTERM_BP_FAT     GO:0005887-integral component of plasma membrane     25     274     1.964654078     0.598711543     2.696639101       GOTERM_BP_FAT     GO:0005887-integral component of plasma membrane     25     274     1.964654078     0.598711543     2.696639101       GOTERM_BP_FAT     GO:0005887-integral component of plasma membrane     25     28     1.462716886     0.999765405     3.94209281       GOTERM_BP_FAT     GO:00048468-cell development	GOTERM BP FAT	GO:0034723~DNA replication-dependent nucleosome organization	6	298	7.116241611	0.992760062	2.320929568
GOTERM_MF_FAT     GO:0043566-structure-specific DNA binding     11     277     3.393464587     0.66300335     2.106153885       GOTERM_BP_FAT     GO:0032776-DNA methylation on cytosine     6     298     6.84254001     0.997359314     2.789240242       GOTERM_BP_FAT     GO:0008285-negative regulation of cell proliferation     25     298     1.982019165     0.998865808     3.179924089       GOTERM_BP_FAT     GO:0005230-extracellular ligand-gated ion channel activity     4     277     14.96209386     0.756693103     2.7282260104       GOTERM_BP_FAT     GO:0005830-extracellular ligand-gated ion channel activity     4     277     14.96209386     0.756693103     2.7282260104       GOTERM_BP_FAT     GO:0005887-integral component of plasma membrane     25     274     1.964654078     0.598711543     2.696339101       GOTERM_BP_FAT     GO:0010558-negative regulation of macromolecule biosynthetic process     47     298     1.4602716886     0.999765405     3.904209281       GOTERM_BP_FAT     GO:0005065-response to external stimulus     53     298     1.4692716886     0.999765405     3.904209281       GOTERM_MF_FAT     GO:00050605-response t	GOTERM BP FAT	GO:0051253~negative regulation of RNA metabolic process	43	298	1.640918003	0.993940339	2.403724643
GOTERM_BP_FAT     GO:0032776-DNA methylation on cytosine     6     298     6.84254001     0.997359314     2.789240242       GOTERM_BP_FAT     GO:0008285-negative regulation of cell proliferation     25     298     1.982019165     0.998865808     3.179924089       GOTERM_MF_FAT     GO:0008285-negative regulation of cell proliferation     25     298     1.982019165     0.998865808     3.179924089       GOTERM_MF_FAT     GO:00082842-defense response to other organism     19     298     2.25347651     0.999367138     3.448714516       GOTERM_BP_FAT     GO:0005887integral component of plasma membrane     25     274     1.964654078     0.598711543     2.696339101       GOTERM_BP_FAT     GO:0010558-negative regulation of macromolecule biosynthetic process     47     298     1.560579301     0.999867298     3.7050617       GOTERM_BP_FAT     GO:00105860-response to external stimulus     53     298     1.462716886     0.999765405     3.904209281       GOTERM_MF_FAT     GO:0015276-ligand-gated ion channel activity     53     298     1.462716886     0.999765405     3.094209281       GOTERM_MF_FAT     GO:0022834-ligand-gated ion channel act	GOTERM MF FAT	GO:0043566~structure-specific DNA binding	11	277	3.393464587	0.66300335	2.106153885
GOTERM_BP_FAT     GO:0008285-negative regulation of cell proliferation     25     298     1.982019165     0.998865808     3.179924089       GOTERM_MF_FAT     GO:0005230-extracellular ligand-gated ion channel activity     4     277     14.96209386     0.756693103     2.728250104       GOTERM_BP_FAT     GO:0005230-extracellular ligand-gated ion channel activity     4     277     14.96209386     0.756693103     2.728250104       GOTERM_BP_FAT     GO:0008587-integral component of plasma membrane     25     274     1.964654078     0.598711543     2.666339101       GOTERM_BP_FAT     GO:0010558-negative regulation of macromolecule biosynthetic process     47     298     1.560579301     0.999867298     3.73050617       GOTERM_BP_FAT     GO:00048468-cell development     59     298     1.462716886     0.999765405     3.904209281       GOTERM_BP_FAT     GO:0009605-response to external stimulus     53     298     1.499526103     0.99988074     4.2135072       GOTERM_MF_FAT     GO:0015276-ligand-gated ion channel activity     5     277     7.874786244     0.914425545     4.697250525       GOTERM_MF_FAT     GO:0022834-ligand-gated ion channel	GOTERM BP FAT	GO:0032776~DNA methylation on cytosine	6	298	6.84254001	0.997359314	2.789240242
GOTERM_MF_FAT     GO:0005230-extracellular ligand-gated ion channel activity     4     277     14.96209386     0.756693103     2.728250104       GOTERM_BP_FAT     GO:0005887-integral component of plasma membrane     19     298     2.25347651     0.999367138     3.448714516       GOTERM_BP_FAT     GO:0005887-integral component of plasma membrane     25     274     1.964654078     0.598711543     2.696339101       GOTERM_BP_FAT     GO:0010588-negative regulation of macromolecule biosynthetic process     47     298     1.560579301     0.999657298     3.73050617       GOTERM_BP_FAT     GO:0048468-cell development     59     298     1.462716886     0.999765405     3.094209281       GOTERM_BP_FAT     GO:0009605-response to external stimulus     53     298     1.499526103     0.99988074     4.2135072       GOTERM_MF_FAT     GO:0015276-ligand-gated ion channel activity     5     277     7.874786244     0.914425545     4.697250525       GOTERM_MF_FAT     GO:0022834-ligand-gated ion channel activity     5     277     7.874786244     0.914425545     4.697250525       GOTERM_MF_FAT     GO:00202834-ligand-gated ion channel activity	GOTERM BP FAT	GO:0008285~negative regulation of cell proliferation	25	298	1.982019165	0.998865808	3.179924089
GOTERM_BP_FAT     GO:0098542-defense response to other organism     19     298     2.25347651     0.999367138     3.448714516       GOTERM_CC_FAT     GO:0005887-integral component of plasma membrane     25     274     1.964654078     0.598711543     2.696339101       GOTERM_BP_FAT     GO:0010558-negative regulation of macromolecule biosynthetic process     47     298     1.560579301     0.999657298     3.73050617       GOTERM_BP_FAT     GO:0010558-negative regulation of macromolecule biosynthetic process     47     298     1.462716886     0.999765405     3.904209281       GOTERM_BP_FAT     GO:0009605-response to external stimulus     53     298     1.469526103     0.99986074     4.2135072       GOTERM_MF_FAT     GO:0015276-ligand-gated ion channel activity     5     277     7.874786244     0.914425545     4.697250525       GOTERM_MF_FAT     GO:0022834-ligand-gated channel activity     5     277     7.874786244     0.914425545     4.697250525       GOTERM_MF_FAT     GO:0022034-ligand-gated channel activity     5     277     7.874786244     0.914425545     4.697250525       GOTERM_MF_FAT     GO:0020037-heme binding <t< td=""><td>GOTERM MF FAT</td><td>GO:0005230~extracellular ligand-gated ion channel activity</td><td>4</td><td>277</td><td>14.96209386</td><td>0.756693103</td><td>2.728250104</td></t<>	GOTERM MF FAT	GO:0005230~extracellular ligand-gated ion channel activity	4	277	14.96209386	0.756693103	2.728250104
GOTERM_CC_FAT     GO:0005887-integral component of plasma membrane     25     274     1.964654078     0.598711543     2.696339101       GOTERM_BP_FAT     GO:0010558-negative regulation of macromolecule biosynthetic process     47     298     1.560579301     0.999657298     3.73050617       GOTERM_BP_FAT     GO:0048468-cell development     59     298     1.462716886     0.999765405     3.904209281       GOTERM_BP_FAT     GO:0009605-response to external stimulus     53     298     1.499526103     0.99986774     4.215072       GOTERM_MP_FAT     GO:0015276-ligand-gated ion channel activity     5     277     7.874786244     0.914425545     4.697250525       GOTERM_MF_FAT     GO:0022834-ligand-gated channel activity     5     277     7.874786244     0.914425545     4.697250525       KEGG_PATHWAY     mmu040808.Neuroactive ligand-receptor interaction     7     145     4.681520778     0.436956509     3.836983827       GOTERM_MF_FAT     GO:0020037-heme binding     8     277     4.05751698     0.922210935     4.87491139	GOTERM BP FAT	GO:0098542~defense response to other organism	19	298	2.25347651	0.999367138	3.448714516
GOTERM_BP_FAT     GO:0010558-negative regulation of macromolecule biosynthetic process     47     298     1.560579301     0.999657298     3.73050617       GOTERM_BP_FAT     GO:0010558-negative regulation of macromolecule biosynthetic process     47     298     1.560579301     0.999657298     3.73050617       GOTERM_BP_FAT     GO:0010558-negative regulation of macromolecule biosynthetic process     59     298     1.462716886     0.999765405     3.904209281       GOTERM_BP_FAT     GO:0009605-response to external stimulus     53     298     1.499526103     0.99988074     4.2135072       GOTERM_MF_FAT     GO:0022834-ligand-gated ion channel activity     5     277     7.874786244     0.914425545     4.697250525       GOTERM_MF_FAT     GO:0022834-ligand-gated channel activity     5     277     7.874786244     0.914425545     4.697250525       KEGG_PATHWAY     mmu04080:Neuroactive ligand-receptor interaction     7     145     4.681520778     0.436956509     3.836983827       GOTERM_MF_FAT     GO:0020037-heme binding     8     277     4.05751698     0.922210935     4.874991139	GOTERM CC FAT	GO:0005887~integral component of plasma membrane	25	274	1.964654078	0.598711543	2.696339101
GOTERM_BP_FAT     GO:0048468-cell development     59     298     1.462716886     0.999765405     3.904209281       GOTERM_BP_FAT     GO:00048468-cell development     53     298     1.462716886     0.999765405     3.904209281       GOTERM_BP_FAT     GO:0015276-ligand-gated ion channel activity     5     277     7.874786244     0.914425545     4.697250525       GOTERM_MF_FAT     GO:0022834-ligand-gated channel activity     5     277     7.874786244     0.914425545     4.697250525       GOTERM_MF_FAT     GO:0022037-ligand-gated channel activity     5     277     7.874786244     0.914425545     4.697250525       GOTERM_MF_FAT     GO:0020037-heme binding     7     145     4.681520778     0.436956509     3.836983827       GOTERM_MF_FAT     GO:0020037-heme binding     8     277     4.05751698     0.922210935     4.87491139	GOTERM BP FAT	GO:0010558~negative regulation of macromolecule biosynthetic process	47	298	1.560579301	0.999657298	3,73050617
GOTERM_BP_FAT     GO:0009605-response to external stimulus     53     298     1.499526103     0.99988074     4.2135072       GOTERM_MF_FAT     GO:0015276-ligand-gated ion channel activity     5     277     7.874786244     0.914425545     4.697250525       GOTERM_MF_FAT     GO:0022834-ligand-gated ion channel activity     5     277     7.874786244     0.914425545     4.697250525       KEGG_PATHWAY     mm040808.Neuroactive ligand-receptor interaction     7     145     4.681520778     0.436956509     3.836983827       GOTERM MF_FAT     GO:0020037-heme binding     8     277     4.05751698     0.922210935     4.87491139	GOTERM BP FAT	GO:0048468~cell development		298	1.462716886	0.999765405	3.904209281
GOTERM_MF_FAT     GO:0015276-ligand-gated ion channel activity     5     277     7.874786244     0.914425545     4.697250525       GOTERM_MF_FAT     GO:002834-ligand-gated channel activity     5     277     7.874786244     0.914425545     4.697250525       KEGG_PATHWAY     mmu04080:Neuroactive ligand-receptor interaction     7     145     4.681520778     0.436986509     3.836983827       GOTERM_MF_FAT     GO:0020037-heme binding     8     277     4.05751698     0.922210935     4.874991139	GOTERM BP FAT	GO:0009605~response to external stimulus	53	298	1,499526103	0.99988074	4,2135072
GOTERM_MF_FAT     GO:0022834-ligand-gated channel activity     5     277     7.874786244     0.914425545     4.697250525       KEGG_PATHWAY     mmu04080:Neuroactive ligand-receptor interaction     7     145     4.681520778     0.4369656509     3.836983827       GOTERM_MF_FAT     GO:0020037-heme binding     8     277     4.05751698     0.922210935     4.874991139	GOTERM ME FAT	GO:0015276~ligand-gated ion channel activity	5	277	7.874786244	0.914425545	4.697250525
KEGG_PATHWAY     mmu04080:Neuroactive ligand-receptor interaction     7     145     4.681520778     0.436956509     3.836983827       GOTERM MF_FAT     GO:0020037-heme binding     8     277     4.05751698     0.922210935     4.87491139	GOTERM MF FAT	GO:0022834~ligand-gated channel activity	5	277	7.874786244	0.914425545	4.697250525
GOTERM MF FAT G0:0020037-heme binding 8 277 4.05751698 0.922210325 4.87491139	KEGG PATHWAY	mmu04080:Neuroactive ligand-receptor interaction	7	145	4.681520778	0.436956509	3.836983827
	GOTERM MF FAT	GO:0020037~heme binding		277	4.05751698	0.922210935	4.874991139

Supplemental Table S3: Functional Annotation Analysis of DEGs from Microarray Data.

Gene Name	Primer Location		Primer Sequence			
HRE Region	Start	End	Forward	Reverse		
SLC16A3 Promoter	-1399	-1231	5'-ccccgttaagtggagaatgg-3'	5'-ggcgactttaagtgctctca-3'		
SLC16A3 Intron	+775	+902	5'-cctactccaggcaatacgg-3'	5'-tggaagtagtggtccagtcg-3'		
Car12	-172	-24	5'-gagtcgccacataaaaagca-3'	5'- ccgctggctctaagctgt-3'		

Supplemental Table S4: Primer Sequences used for Chromatin Immunoprecipitations