Fold Change (FC) - Blue(-): fo Fold Difference (FD) - Blue(-)									
[C3H/HeN, Air](raw) [C3H/	HeN, O2](raw) [Gs	r-KO, Air)(raw) [G	r-KO, O2)(raw) RefSeq Transcript ID p (G	enotype-Exposure) FC (WT_	Air vs O2) FC (KC	Air vs O2) FD (WT O2	vs KO O2) Gene Symbol	Gene Title	Gene Ontology Biological Process
129.51744	23.972544	24.953693	863.6152 NM_001313949///NN	0.001502453	-5.403	34.609	36.025 Krt13	keratin 13	0007010 // cytoskeleton organization // not recorded///0009314 // response to radiation // inferred from electronic annotation///0043587 // tongue morphogenesis // in
420.56628	89.77674	92.97833	1910.9205 NM 008475	7.66E-04	-4.685	20.552	21.285 Krt4	keratin 4	0007010 // cytoskeleton organization // not recorded///0009790 // embryo development // traceable author satement///0030855 // epithelial cell differentiation // infer
249.79042 152.70363	147.60468 56.518883	58.468548 66.22598	2832.6384 NM_177369 523.25354 NM 027416	0.008138205 0.001268343	-1.692 -2.702	48.447 7.901	19.191 Myh8 9.258 Calml3	myosin, heavy polypeptide 8, skeletal muscle, perinatal calmodulin-like 3	0003009 // skeletal muscle contraction // not recorded///0006936 // muscle contraction /////0008152 // metabolic process // inferred from electronic annotation///00
1454.9548	968.98785	338.56406	7321.125 NM 001272041///NN	0.001268343	-2.702	21.624	7.555 Acta1	actin, alpha 1, skeletal muscle	0009612 // response to mechanical stimulus // inferred from electronic annotation//0009991 // response to extracellular stimulus // inferred from electronic annotation/
32.32457	24.188734	17.78789	143.10919 NM 001081123///XN	3.51E-04	-1.336	8.045	5.916 Arhgap36	Rho GTPase activating protein 36	0007165 // signal transduction // inferred from electronic annotation//0043547 // positive regulation of GTPase activity // inferred from electronic annotation
78.09718	36.344418	44.905346	188.82568 NM_028798	0.001839206	-2.149	4.205	5.195 Crct1	cysteine-rich C-terminal 1	0018149 // peptide cross-linking // not recorded///0030216 // keratinocyte differentiation // not recorded
149.9972	65.38318	71.152824	321.5579 NM_028216	0.008994052	-2.294	4.519	4.918 Psca	prostate stem cell antigen	
200.63406 82.520035	105.09884 73.845276	118.66843 49.759773	514.4454 NM_001101605///NN 345.17355 NM_013456	0.004987194 0.006323175	-1.909 -1.117	4.335 6.937	4.895 Ifit1bl1 4.674 Actn3	interferon induced protein with tetratricpeptide repeats 1B like 1 actinin alpha 3	0051607 // defense response to virus // not recorded//0060337 // type I interferon signaling pathway // not recorded 0001649 // osteoblast differentiation // inferred from mutant phenotype///0006936 // muscle contraction // inferred from direct assay///0014728 // regulation of the for
82.520035 646.0648	243.87666	49.759773 258.07495	1131.0095 NM 001164787///NN	0.006323175	-1.117	4.382	4.638 Sprr2a1///Sprr2a2///Sprr2a3		or 0008360 // regulation of cell shape // traceable author statement//0008544 // epidermis development // non-traceable author statement//0018149 // peptide cross-lin
30.519133	16.090836	12.981329	72.490616 NM 001033239	0.007458202	-1.897	5.584	4.505 Csta1	cystatin A1	10 0000500 // regulation of ten single // uscate authors statement//10005449 / prince into severaphients development // 10000000000000000000000000000000000
53.990597	35.14404	43.795063	158.04631 NM 173385	0.008461138	-1.536	3.609	4.497 Cilp	cartilage intermediate layer protein, nucleotide pyrophosphohydrolase	0043569 // negative regulation of insulin-like growth factor receptor signaling pathway // not recorded
58.237244	32.405205	38.48617	136.62178 NM_013505///XM_00	0.001027153	-1.797	3.550	4.216 Dsc2	desmocollin 2	0007155 // cell adhesion // inferred from electronic annotation///0007156 // homophilic cell adhesion via plasma membrane adhesion molecules // inferred from electron
40.16508	34.974964	32.55182	141.47806 NM_007582	0.001477798	-1.148	4.346	4.045 Cacng1	calcium channel, voltage-dependent, gamma subunit 1	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic annotation///0006816 // calcium ion transport // inferred from electronic annotation///0006816 // calcium ion transport // inferred from electronic annotation///0006816 // calcium ion transport // inferred from electronic annotation///0006816 // calcium ion transport // inferred from electronic annotation///0006816 // calcium ion transport // inferred from electronic annotation///0006816 // calcium ion transport // inferred from electronic annotation///0006816 // calcium ion transport // inferred from electronic annotation///0006816 // calcium ion transport // inferred from electronic annotation///0006816 // calcium ion transport // inferred from electronic annotation///0006816 // calcium ion transport // inferred from electronic annotation///0006816 // calcium ion transport // inferred from electronic annotation///0006816 // calcium ion transport // inferred from electronic annotation // inferred from e
69.31646	54.29826	52.8892	217.84296 NM_001199556///NN	0.008563411	-1.277	4.119	4.012 AW551984	expressed sequence AW551984	0055007 // cardiac muscle cell differentiation // inferred from mutant phenotype///0060923 // cardiac muscle cell fate commitment // inferred from genetic interaction
131.28381 45.802517	75.22613 33.401245	76.60803 30.585264	288.5503 NM_008476 118.26599 NM_008657///XM_00	0.003816715 0.008563787	-1.745 -1.371	3.767 3.867	3.836 Krt6a 3.541 Mvf6	keratin 6A myogenic factor 6	0002009 // morphogenesis of an epithelium // inferred from genetic interaction///0002009 // morphogenesis of an epithelium // inferred from mutant phenotype///0016 0001756 // somitogenesis // inferred from mutant phenotype///0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation///0006357
75.9061	63.03229	57.28121	213.16151 NM 021508	0.005267157	-1.204	3.721	3.382 Myoz1	myozenin 1	0001730 // Solintogeness // interieu nom marant priendype///0000333 // regulation or clariscription, prov-cemplated // interieu nom electronic annotation///0000337
110.10195	57.414654	62.484314	188.89784 NM 001081375///NN	0.003077287	-1.918	3.023	3.290 Cnfn	cornifelin	0031424 // keratinization // inferred from electronic annotation
36.20611	25.224588	29.133148	82.44814 NM 001081157///XN	0.004109589	-1.435	2.830	3.269 Lmod3	leiomodin 3 (fetal)	0006936 // muscle contraction // not recorded///007015 // actin filament organization // not recorded///0030239 // myofibril assembly // not recorded///0051694 // pc
34.98539	24.772469	26.90576	78.44409 NM_001033131	0.001616002	-1.412	2.916	3.167 Krtdap	keratinocyte differentiation associated protein	0008544 // epidermis development // not recorded///0030154 // cell differentiation // inferred from electronic annotation
50.355385	51.34201	32.838654	160.28629 NM 029569///XM 00	0.008152892	1.020	4.881	3.122 Asb5	ankyrin repeat and SOCs box-containing 5	0016567 // protein ubiquitination // inferred from electronic annotation///0035556 // intracellular signal transduction // inferred from electronic annotation
40.06156 64.72089	34.79185 49.354595	28.39306 45.98375	108.52695 NM_009109///XM_00 143.36182 NM 007812///NM 0I	0.004861059 0.002387153	-1.151 -1.311	3.822 3.118	3.119 Ryr1	ryanodine receptor 1, skeletal muscle	0001666 // response to hypoxia // not recorded///0003151 // outflow tract morphogenesis // inferred from mutant phenotype///0006810 // transport // inferred from eli
17.246458	11.09482	12.686517	32.053776 NM 001033233//XN	0.002387153	-1.554	2.527	2.905 Cyp2a4///Cyp2a5 2.889 Tmprss11a	transmembrane protease, serine 11a	5 0006805 // xenobiotic metabolic process // not recorded///0009804 // coumarin metabolic process // not recorded///0019373 // epoxygenase P450 pathway // not recorded/// epoxygenase P450 pathway // n
146.40717	138.79372	107.61155	400.9013 NM 026841	0.007172686	-1.055	3.725	2.888 Prr32	proline rich 32	6000000 If proceedings If mental non-electronic annotation/1000/040 If earliest If mental non-electronic annotation
105.810394	68.14693	91.971664	187.01898 NM_001166030///XN	0.006050516	-1.553	2.033	2.744 Mylk4	myosin light chain kinase family, member 4	0006468 // protein phosphorylation // inferred from electronic annotation//0016310 // phosphorylation // inferred from electronic annotation
84.66858	56.89977	65.316025	152.30411 NM 027126///XM 00	0.003633969	-1.488	2.332	2.677 Hfe2	hemochromatosis type 2 (juvenile) (human homolog)	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype///0006879 // cellular iron ion homeostasis // inferre
65.19429	53.30556	51.451138	141.78748 NM_028202///XM_00	0.003266004	-1.223	2.756	2.660 KIhl40	kelch-like 40	0007275 // multicellular organismal development // inferred from electronic annotation///0016567 // protein ubiquitination ////0031397 // negative regulation of pro
34.193455 150.59355	20.290432 104.86743	21.105312 112.7098	53.855396 NM 025867 271.40237 NM 027011	0.004822153 2.82E-04	-1.685 -1.436	2.552 2.408	2.654 Serpinb11 2.588 Krt5	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 11 keratin 5	. 0010466 // negative regulation of peptidase activity // inferred from electronic annotation///0010951 // negative regulation of endopeptidase activity // not recorded
150.59355 74.690865	104.86743 66.81221	112.7098 62.840107	2/1.4023/ NM_02/011 167.70041 NM_146189///XM_00	2.82E-04 0.002593064	-1.436 -1.118	2.669	2.588 Krt5 2.510 Mybpc2	myosin binding protein C, fast-type	0006936 // muscle contraction // inferred from direct assay///0007155 // cell adhesion // inferred from electronic annotation
72.63135	46 58493	48 584885	115.7181 NM 001313701///NN	0.0025333004	-1.559	2 382	2.484 Pkp1	plakophilin 1	0007155 // cell adhesion // inferred from electronic annotation///0045337 // single organismal cell-cell adhesion // inferred from electronic annotation///0045110 // inte
936.2323	564.96075	704.48926	1400.4655 NM_001136062///NN	0.00623778	-1.657	1.988	2.479 Eno3	enolase 3, beta muscle	0006096 // glycolytic process // inferred from electronic annotation///0007568 // aging // inferred from electronic annotation///0042493 // response to drug // inferred f
148.86583	69.325676	134.74373	170.04344 NM_001013013	0.007874813	-2.147	1.262	2.453 Dhrs7c	dehydrogenase/reductase (SDR family) member 7C	0008152 // metabolic process // inferred from electronic annotation///0010880 // regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum
97.27986	61.803143	65.18649	150.86432 NM_001204427///NN	0.005044579	-1.574	2.314	2.441 Sprr3	small proline-rich protein 3	0018149 // peptide cross-linking // not recorded///0030216 // keratinocyte differentiation // not recorded///0031424 // keratinization // inferred from electronic annotat
22.339308	16.851057	17.868435	38.00067 NM_009257///XM_00	0.005070798	-1.326	2.127	2.255 Serpinb5	serine (or cysteine) peptidase inhibitor, clade B, member 5	0002009 // morphogenesis of an epithelium // inferred from mutant phenotype///0010951 // negative regulation of endopeptidase activity // not recorded///0030198 //
77.030876 39.625816	76.73347 29.538054	58.277485 29.245455	158.10065 NM_001007580///XN 59.957985 NM 133743	0.006615627 0.0082285	-1.004 -1.342	2.713 2.050	2.060 Fndc3c1 2.030 Lypd3	fibronectin type III domain containing 3C1 Ly6/Plaur domain containing 3	0006928 // movement of cell or subcellular component // not recorded//0007160 // cell-matrix adhesion // not recorded
62.41595	46.15705	49.297714	93.150215 NM_011097///XM_00	0.0082285	-1.342	1.890	2.030 Lypa3 2.018 Pitx1	paired-like homeodomain transcription factor 1	0001501 // skeletal system development // inferred from mutant phenotype///0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355
50.68309	48.111908	52.231308	95.71111 NM 010866	0.007260997	-1.053	1.832	1.989 Myod1	myogenic differentiation 1	0000381 // regulation of alternative mRNA splicing, via spliceosome // inferred from direct assay///0000381 // regulation of alternative mRNA splicing, via spliceosome //
73.02413	46.733673	50.67783	91.75521 NM_009660///XM_00	0.00955388	-1.563	1.811	1.963 Alox15	arachidonate 15-lipoxygenase	0001503 // ossification // inferred from mutant phenotype///0002820 // negative regulation of adaptive immune response // inferred from mutant phenotype///0006629
80.462364	57.460537	66.95816	111.818275 NM_029723	1.45E-04	-1.400	1.670	1.946 Dapl1	death associated protein-like 1	0006915 // apoptotic process // inferred from electronic annotation///0010507 // negative regulation of autophagy /////0030154 // cell differentiation // inferred from
57.67034	57.50089	57.15084	106.38834 NM_001313969///NN	0.008197373	-1.003	1.862	1.850 Vip	vasoactive intestinal polypeptide	0001878 // response to yeast // not recorded///0001938 // positive regulation of endothelial cell proliferation // not recorded///0007611 // learning or memory // not recorded///0007611 // learning or memory // not rec
129.59486 71.82227	96.229004 53.249424	127.3988 63.87838	175.15425 NM 182992 96.486305 NM_027158///XM_0C	0.005565609	-1.347 -1.349	1.375 1.510	1.820 Mypn 1.812 Upk3bl	myopalladin uroplakin 3B-like	0045214 // sarcomere organization // not recorded 0006979 // response to oxidative stress // inferred from electronic annotation///0055114 // oxidation-reduction process // inferred from electronic annotation
71.82227	60.432392	66.46184	109 29928 NM 001313956//NN	0.009496551	-1.349	1.510	1.809 Krt14//Krt17	keratin 14//keratin 17	000758 // sains // not recorded///000043 // response to sixia discovered annotation // voxatation-recurrence // interest or interest rom electronic annotation // 0007588 // sains // not recorded///000043 // response to init in inferred from electronic annotation // 00101212 // response to inniting radiation // inferred from electronic annotation // 00101212 // response to inniting radiation // inferred from electronic annotation // 00101212 // response to inniting radiation // inferred from electronic annotation // 00101212 // response to inniting radiation // inferred from electronic annotation // 00101212 // response to inniting radiation // inferred from electronic annotation // 00101212 // response to inniting radiation // inferred from electronic annotation // 00101212 // response to inniting radiation // inferred from electronic annotation // 00101212 // response to inniting radiation // inferred from electronic annotation // 00101212 // response to inniting radiation // inferred from electronic annotation // 00101212 // response to inniting radiation // inferred from electronic annotation // 00101212 // response to inniting radiation // inferred from electronic annotation // 00101212 // response to inniting radiation // inferred from electronic annotation // 00101212 // response to inniting radiation // inferred from electronic annotation // 00101212 // response to inniting radiation // inferred from electronic annotation // 00101212 // response to inniting radiation // inferred from electronic annotation // 00101212 // 0
64.75949	40.709656	25.22052	73.11003 NM 001174170//NN	6.95E-04	-1.591	2.899	1.796 Serpinb2	serine (or cysteine) peptidase inhibitor, clade B, member 2	0010466 // negative regulation of pertitabs activity // inferred from electronic annotation///0010951 // negative regulation of pertitabs activity // inferred from electronic annotation///0010951 // negative regulation of endopertitabs activity // inferred from electronic annotation///0010951 // negative regulation of endopertitabs activity // inferred from electronic annotation///0010951 // negative regulation of endopertitabs activity // inferred from electronic annotation///0010951 // negative regulation of endopertitabs activity // inferred from electronic annotation///0010951 // negative regulation of endopertitabs activity // inferred from electronic annotation///0010951 // negative regulation of endopertitabs activity // inferred from electronic annotation///0010951 // negative regulation of endopertitabs activity // inferred from electronic annotation///0010951 // negative regulation of endopertitabs activity // inferred from electronic annotation///0010951 // negative regulation of endopertitabs activity // inferred from electronic annotation///0010951 // negative regulation of endopertitabs activity // inferred from electronic annotation///0010951 // negative regulation of endopertitabs activity // inferred from electronic annotation///0010951 // negative regulation of endopertitable activity // inferred from electronic annotation///0010951 // negative regulation of endopertitable activity // inferred from electronic annotation///0010951 // negative regulation of endopertitable activity // inferred from electronic annotation///0010951 // negative regulation of endopertitable activity // inferred from electronic annotation///0010951 // negative regulation of endopertitable activity // inferred from electronic annotation///0010951 // negative regulation of endopertitable activity // inferred from electronic annotation/// negative regulation of endopertitable activity // inferred from electronic annotation/// on electronic annotation/// negative regulation of electronic annotation/// negative regulation
158.7409	160.63313	179.4649	280.4809 NM 080451///XM 00	0.00320693	1.012	1.563	1.746 Synpo2	synaptopodin 2	
49.697514	46.69353	44.463757	79.22919 NM_024291///XM_00	0.001142978	-1.064	1.782	1.697 Ky	kyphoscoliosis peptidase	0006508 // proteolysis // inferred from electronic annotation///0007517 // muscle organ development // inferred from mutant phenotype///0007528 // neuromuscular ju
180.38297	152.09334	174.10493	253.77637 NM 009849	4.99E-04	-1.186	1.458	1.669 Entpd2	ectonucleoside triphosphate diphosphohydrolase 2	0007186 // G-protein coupled receptor signaling pathway // inferred from direct assay///0009181 // purine ribonucleoside diphosphate catabolic process // inferred from
521.4635 126.315	420.9284 102.665016	572.9062 109.64348	691.46515 NM_011224 167.64255 NM 009710//XM 01	8.91E-04 0.002272682	-1.239 -1.230	1.207 1.529	1.643 Pygm 1.633 Art1	muscle glycogen phosphorylase ADP-ribosyltransferase 1	0001666 // response to hypoxia // not recorded///0005975 // carbohydrate metabolic process // inferred from electronic annotation///0005977 // glycogen metabolic process // inferred from electronic annotation///0005977 // glycogen metabolic process // inferred from electronic annotation///0005977 // glycogen metabolic process // inferred from electronic annotation///0005977 // glycogen metabolic process // inferred from electronic annotation///0005977 // glycogen metabolic process // inferred from electronic annotation///0005977 // glycogen metabolic process // inferred from electronic annotation///0005977 // glycogen metabolic process // inferred from electronic annotation///0005977 // glycogen metabolic process // inferred from electronic annotation///0005977 // glycogen metabolic process // inferred from electronic annotation///0005977 // glycogen metabolic process // inferred from electronic annotation///0005977 // glycogen metabolic process // inferred from electronic annotation///0005977 // glycogen metabolic process // inferred from electronic annotation // inferred from electronic anno
275.78494	258.0456	238.4087	414.78268 NM 019417//XM 01	0.002272682	-1.230	1.740	1.607 Pdlim4	PDZ and LIM domain 4	0030036 // actin cytoskeleton organization // not recorded
131.85081	123.56234	100.15029	196.65428 NM 001029978///NN	3.74E-04	-1.067	1.964	1.592 Tceal3///Tceal5///Tceal6		as 0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated // inferred from electronic anno
131.85081	123.56234	100.15029	196.65428 NM_001029978///NN	3.74E-04	-1.067	1.964	1.592 Tceal3///Tceal5///Tceal6		ac 0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated // inferred from electronic anno
37.58786	34.016727	34.192394	53.54504 NM_011377///XM_00	1.98E-04	-1.105	1.566	1.574 Sim2	single-minded homolog 2 (Drosophila)	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interaction///0006351 // transcription, DNA-templated // inferr
180.35715 85.875786	148.49825 68.70731	176.43245 80.86911	230.24855 NM_028627///XM_00 105.50224 NM 009604///XM 00	0.008840978 0.008793402	-1.215 -1.250	1.305 1.305	1.551 Psd 1.536 Chrng	pleckstrin and Sec7 domain containing cholinergic receptor, nicotinic, gamma polypeptide	0016192 // vesicle-mediated transport ////0030182 // neuron differentiation // not recorded///0032012 // regulation of ARF protein signal transduction // inferred frc 0003009 // skeletal muscle contraction // not recorded///0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electron
85.875786 50.365475	58.70731 37.75751	80.86911 39.058052	105.50224 NM_009604///XM_00 57.88118 NM 011059	0.008793402	-1.250 -1.334	1.482	1.536 Chrng 1.533 Padi1	cholinergic receptor, nicotinic, gamma polypeptide peptidyl arginine deiminase, type I	0018101 // protein citrullination // not recorded // unlessed from electronic annotation // unle
138.31105	117.43096	78.13614	179.08975 NM 001122683///NN	0.007817438	-1.178	2.292	1.525 Bdh1	3-hydroxybutyrate dehydrogenase, type 1	008152 // metabolic process // inferred from electronic annotation//0055114 // oxidation-reduction process // not recorded
192.736	168.27196	172.62494	249.54987 NM 001290315///NN	0.001969149	-1.145	1.446	1.483 Igdcc4	immunoglobulin superfamily, DCC subclass, member 4	,
84.0216	65.99552	80.65314	97.54203 NM_145137///XM_00	0.00268434	-1.273	1.209	1.478 Mg/2	macrophage galactose N-acetyl-galactosamine specific lectin 2	
743.94934	635.7963	765.13666	932.85004 NM_001163487///NN	0.008761895	-1.170	1.219	1.467 Pfkm	phosphofructokinase, muscle	0005980 // glycogen catabolic process // inferred from mutant phenotype///0006002 // fructose 6-phosphate metabolic process // not recorded///0006096 // glycolytic p
170.75826	156.98477	125.14959	227.42311 NM_007994	2.54E-04	-1.088	1.817	1.449 Fbp2	fructose bisphosphatase 2	0005975 // carbohydrate metabolic process // inferred from electronic annotation///0006094 // gluconeogenesis // not recorded///0006470 // protein dephosphorylation
961.2245 92.90851	840.8235 64.9257	808.37354 71.817505	1209.0829 NM_010043 92.37193 NR 003964//NM 02	0.008571621 0.003581449	-1.143 -1.431	1.496 1.286	1.438 Des 1.423 Tubb2a-ps2///Tubb2b	desmin tubulin, beta 2a, pseudogene 2///tubulin, beta 2B class IIB	0007517 // muscle organ development // traceable author statement 0001764 // neuron migration // not recorded///0007017 // microtubule-based process // inferred from electronic annotation///0008152 // metabolic process // inferred f
106.68768	89.33396	92.56843	126.336464 NM 008125	5.92E-04	-1.194	1.365	1.414 Gib2	gap junction protein, beta 2	0007154 // cell communication // inferred from electronic annotation///0007267 // cell-cell signaling // inferred from direct assay//0007565 // female pregnancy // infer
195.32356	187.89755	209.39975	261.53027 NM_153098	0.005988242	-1.040	1.249	1.392 Cd109	CD109 antigen	0001933 // negative regulation of protein phosphorylation // inferred from mutant phenotype//0001942 // hair follicle development // inferred from mutant phenotype/
143.2621	131.40094	114.83265	181.92389 NM 023655///XM 00	0.008678827	-1.090	1.584	1.384 Trim29	tripartite motif-containing 29	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interaction///1900181 // negative regulation of protein localization
264.7405	281.6421	193.8662	387.0685 NM_025961	0.002840333	1.064	1.997	1.374 Gatm	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	0006601 // creatine biosynthetic process // not recorded///0006979 // response to oxidative stress // inferred from electronic annotation///0007584 // response to nutrie
376.26315 448.28677	302.0063 437.67813	306.78854 427.30783	412.1953 NM 001199113///NN 594.25494 NM 001081185///NN	0.009768182 0.001379344	-1.246 -1.024	1.344 1.391	1.365 Slc29a1 1.358 Finc	solute carrier family 29 (nucleoside transporters), member 1 filamin C, gamma	000681D // transport // inferred from electronic annotation///0007595 // lactation // inferred from electronic annotation///0015858 // nucleoside transport // inferred from 0030029 // actin filament-based process // traceable author statement//0048747 // muscle fiber development // inferred from direct assay
448.28677 260.79483	437.67813 259.3912	427.30783 245.13454	594.25494 NM_001081185///NN 351.577 NM 001083334///NN	0.001379344	-1.024 -1.005	1.391 1.434	1.358 Finc 1.355 Bin1	filamin C, gamma bridging integrator 1	0030029 // actin filament-based process // traceable author statement///0048747 // muscle fiber development // inferred from direct assay  0006897 // endocytosis // inferred from electronic annotation///0007275 // multicellular organismal development // inferred from electronic annotation///0030100 // res
260.79483 53.708904	259.3912 43.13493	245.13454 50.740044	57.446808 NM 001109761//NN	0.001/54/33	-1.005 -1.245	1.434	1.355 Bin1 1.332 Capn3	oringing integrator 1 calpain 3	UUUba97 // endocytobis // interred from electronic annotation//UUU2/25 // multicellular organismal development // interred from electronic annotation//UU03101 // rej 0001896 // autolysis // inferred from direct assay//0006461 // protein complex assembly // inferred from multant phenotype///0006508 // protein-drophysis // inferred from direct assay///00066451 // protein complex assembly // inferred from multant phenotype///0006508 // protein-drophysis // inferred from direct assay///00066451 // protein complex assembly // inferred from multant phenotype///0006508 // protein-drophysis // inferred from direct assay///0006451 // protein complex assembly // inferred from multant phenotype///0006508 // protein-drophysis // inferred from direct assay/// inferred from direct assay// i
71.7336	64.51345	64.93632	85.38805 NM 008596///XM 00	6.92E-04	-1.112	1.315	1.324 Sypl2	synaptophysin-like 2	0006810 // transport // inferred from electronic annotation///0006874 // cellular calcium ion homeostasis // inferred from mutant phenotype///0021762 // substantia nij
410.01532	298.67725	304.813	392.7135 NM_001291185///NN	0.006490774	-1.373	1.288	1.315 Aurka	aurora kinase A	0000212 // meiotic spindle organization // inferred from mutant phenotype///0000226 // microtubule cytoskeleton organization // inferred from genetic interaction///00
56.49337	46.752335	53.880287	61.27484 NM 031169///XM 00	7.77E-05	-1.208	1.137	1.311 Kcnmb1		el 0005513 // detection of calcium ion // not recorded///0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic a
319.36285	287.22388	305.7263	375.90765 NM_001289677///NN	3.37E-04	-1.112	1.230	1.309 Pacsin3	protein kinase C and casein kinase substrate in neurons 3	0006897 // endocytosis // inferred from electronic annotation//0007010 // cytoskeleton organization // not recorded///0016310 // phosphorylation // inferred from elec
69.21607	59.9288 156.40622	60.878212 221.54189	78.397514 NM 023485///XM 00 199.62935 NM 001271402///NN	0.002857046 3.44E-04	-1.155 -1.590	1.288	1.308 Sync 1.276 Ephx2	syncoilin epoxide hydrolase 2, cytoplasmic	0045103 // intermediate filament-based process // inferred from direct assay 0002539 // prostaglandin production involved in inflammatory response // not recorded///0006470 // protein dephosphorylation // inferred from electronic annotation///
248.65813 73.13846	156.40622 70.503555	221.54189 63.14047	199.62935 NM_001271402///NN 89.07153 NM 153776///XM 00	3.44E-04 0.00781204	-1.590 -1.037	-1.110 1.411	1.276 Ephx2 1.263 Tmem121	epoxide hydrolase 2, cytoplasmic transmembrane protein 121	unicasing production involved in inflammatory response // not recorded///UUUb4/U // protein dephosphorylation // inferred from electronic annotation//
73.13846 558.83105	532.1112	528.922	665.83356 NM 016696//XM 00	0.00781204	-1.037	1.259	1.253 Imem121 1.251 Gpc1	glypican 1	0014037 // Schwann cell differentiation // not recorded///0030200 // heparan sulfate proteoglycan catabolic process // not recorded///0032288 // myelin assembly // not
263.56796	226.98973	279.40796	283.37735 NM_177857//XM_00	0.001291332	-1.161	1.014	1.248 Dennd2c	DENN/MADD domain containing 2C	0043547 // positive regulation of GTBss activity // not recorded
66.96741	60.685833	59.45699	75.61617 NM_009626///XM_00	0.002682331	-1.104	1.272	1.246 Adh7	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide	0001523 // retinoid metabolic process // not recorded///0006067 // ethanol metabolic process // not recorded///0006068 // ethanol catabolic process // inferred from mi
46.65424	40.316757	44.015057	49.84326 NM_010425	0.009711027	-1.157	1.132	1.236 Foxd3	forkhead box D3	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///0000122 // negative regulation of transcription from RNA
259.0079	284.35574	213.22421	350.23697 NM_001310604///NN	0.009136112	1.098	1.643	1.232 Lgi2	leucine-rich repeat LGI family, member 2	
373.84296	314.02383	319.44034	384.72855 NM_019699	0.0057259	-1.190	1.204	1.225 Fads2	fatty acid desaturase 2	0006629 // lipid metabolic process // inferred from electronic annotation///0006631 // fatty acid metabolic process // inferred from electronic annotation///0006633 // fatty acid metabolic process // inferred from electronic annotation///0006633 // fatty acid metabolic process // inferred from electronic annotation///0006633 // fatty acid metabolic process // inferred from electronic annotation///0006633 // fatty acid metabolic process // inferred from electronic annotation///0006633 // fatty acid metabolic process // inferred from electronic annotation///0006633 // fatty acid metabolic process // inferred from electronic annotation///0006633 // fatty acid metabolic process // inferred from electronic annotation///0006633 // fatty acid metabolic process // inferred from electronic annotation///0006633 // fatty acid metabolic process // inferred from electronic annotation/// fatty acid metabolic process // inferred from electronic annotation/// fatty acid metabolic process // inferred from electronic annotation/// fatty acid metabolic process // inferred from electronic annotation/// fatty acid metabolic process // inferred from electronic annotation// fatty acid metabolic process // inferred from electronic annotation// fatty acid metabolic process // inferred from electronic annotation// fatty acid metabolic process // inferred from electronic annotation// inferred from electr
178.86964 468.33282	165.57704 435.09576	171.01756 452.36975	202.77391 NM_026865///XM_00 529.13464 NM_028030///XM_00	0.002685172 0.003395482	-1.080 -1.076	1.186 1.170	1.225 Ptges3l 1.216 Rbpms2	prostaglandin E synthase 3 (cytosolic)-like RNA binding protein with multiple splicing 2	0006419 // alanyl-tRNA aminoacylation // inferred from electronic annotation///0006450 // regulation of translational fidelity /////0043039 // tRNA aminoacylation //
468.33282 351.65115	435.09576 301.02887	452.36975 311.71408	366.01175 NM 022419	0.003395482	-1.076 -1.168	1.170	1.216 Rbpms2 1.216 Abhd8	abhydrolase domain containing 8	0008152 // metabolic process // not recorded
157.88878	128.87108	117.20409	156.49934 NM_007634///XM_00	0.005477267	-1.108	1.335	1.216 Abnas 1.214 Ccnf	cyclin F	000322 // metabolic process // not recorded 000320 // re-entry into mitotic cell cycle // inferred from mutant phenotype///0001890 // placenta development // inferred from mutant phenotype///0007049 // cell cy
126.325775	119.45886	126.431366	140.9552 NM_008712///XM_00	0.0081487	-1.057	1.115	1.180 Nos1	nitric oxide synthase 1, neuronal	0001666 // response to hypoxia // inferred from electronic annotation///0002028 // regulation of sodium ion transport // inferred from mutant phenotype///0006527 // i
612.7535	590.14026	608.2461	693.18225 NM_001313906///NN	0.003380457	-1.038	1.140	1.175 Prmt5	protein arginine N-methyltransferase 5	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype///0000387 // spliceosomal snRNP assembly // not re
490.67093	433.45343	468.3034	504.26685 NM 001141930///NN	0.004160284	-1.132	1.077	1.163 Ctnnbip1	catenin beta interacting protein 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///0001658 // branching involved in ureteric bud morphoge
82.33252	68.92149	77.07697	80.02457 NM_026725 3448.2847 NM 009503	0.007670673	-1.195	1.038	1.161 Dusp23 1.144 Vcp	dual specificity phosphatase 23	0006470 // protein dephosphorylation // inferred from electronic annotation//0016311 // dephosphorylation // inferred from electronic annotation//0016311 // dephosphorylation // inferred from electronic annotation//0035335 // peptid
3122.6555 224.42886	3013.3027 217.59578	2826.07 188.8137	3448.2847 NM 009503 247.98503 NM 001291105///NN	0.005723821 0.008722606	-1.036 -1.031	1.220 1.313	1.144 Vcp 1.140 E2f1	valosin containing protein E2F transcription factor 1	0006281 // DNA repair // inferred from electronic annotation//0006302 // double-strand break repair // not recorded///0006511 // ubiquitin-dependent protein cataboli 0000077 // DNA damage checkpoint // not recorded///0006351 // tra
224.42886 52.61245	217.59578 48.188713	188.8137 48.467705	247.98503 NM_001291105///NN 54.63674 NM 007843	0.008722606	-1.031 -1.092	1.313	1.140 E2f1 1.134 Defb1	tzr transcription factor 1 defensin beta 1	UUUUU/// UNA damage checkpoint // not recorded//UUUU012// negative regulation of transcription from kNA polymerase II promoter // not recorded//UUUl0351 // tra 0002227 // innate imnune ressonse in mucosa // inferred from electronic annotation// 0002256 // innate imnune ressonse in mucosa // inferred from electronic annotation// 0002256 // innate imnune ressonse in mucosa // inferred from electronic annotation// 0002257 // innate imnune ressonse in mucosa // inferred from electronic annotation// 0002257 // innate imnune ressonse in mucosa // inferred from electronic annotation// 0002257 // innate imnune ressonse in mucosa // inferred from electronic annotation// 0002257 // innate imnune ressonse in mucosa // inferred from electronic annotation// 0002257 // innate imnune ressonse in mucosa // inferred from electronic annotation// 0002257 // innate imnune ressonse in mucosa // inferred from electronic annotation// 0002257 // innate imnune ressonse in mucosa // inferred from electronic annotation// 0002257 // innate imnune ressonse in mucosa // inferred from electronic annotation// 0002257 // innate imnune ressonse in mucosa // inferred from electronic annotation// 000257 // innate imnune ressonse in mucosa // inferred from electronic annotation// 000257 // innate imnune ressonse in mucosa // inferred from electronic annotation// 000257 // innate imnune ressonse in mucosa // inferred from electronic annotation// 000257 // innate imnune ressonse in mucosa // inferred from electronic annotation// 000257 // innate imnune ressonse in mucosa // inferred from electronic annotation// 000257 // innate imnune ressonse in mucosa // inferred from electronic annotation// innate imnune ressonse in mucosa // inferred from electronic annotation// innate imnune ressonse in mucosa // inferred from electronic annotation// innate imnune ressonse in mucosa // inferred from electronic annotation// innate imnune ressonse in mucosa // inferred from electronic annotation// innate imnune ressonse in mucosa // innate imnune ressonse in muco
162.12201	153.19641	151.29774	171.50165 NM 144816//XM 00	0.005241432	-1.058	1.134	1.134 Dejb1 1.119 Rhbdl1	rhomboid, veinlet-like 1 (Drosophila)	0005227 // innate immune response in mucosa // innerred from electronic annotation///0002526 // scare innaminatory response // innerred from electronic annotation///0008152 // 0006508 // proteolysis // inferred from electronic annotation///0008152 /
270.08713	231.91049	245.01318	259.54437 NM 001290461///NN	0.001249709	-1.165	1.059	1.119 Zfp428	zinc finger protein 428	
803.40485	759.7564	665.82654	848.7779 NM_009272	0.007591147	-1.057	1.275	1.117 Srm	spermidine synthase	0006595 // polyamine metabolic process // inferred from electronic annotation///0006596 // polyamine biosynthetic process // inferred from electronic annotation///000

Methods	[C2H/HoM Air/from) [C2	I/HoN O31/sout IGes	VO Airlianu) (Ge	r KO O31(rous) Bolton Transcript ID in (G	constant Eventure) EC (MC	T Airus (23) EC/VO	Lieuw O2\ ED (MT O2 :	s KO O3) Cone Sumbal	Gene Title	Gene Ontology Biological Process
March   Marc	652.65674	633.9833	615.2309	707.957 NM 025891//XM 00	0.002069692	-1.029	1.151	1.117 Smarcd3		
March   Marc				115.940834 NM_138684			1.120		WAP four-disulfide core domain 12	0010466 // negative regulation of peptidase activity // inferred from electronic annotation///0010951 // negative regulation of endopeptidase activity // inferred from ele
Prof.   Prof				123.78757 NM 001290753///NN		-1.069				0000902 // cell morphogenesis // inferred from genetic interaction///0001525 // angiogenesis // inferred from mutant phenotype///0001655 // urogenital system develop
March   Marc				221.348 NM_026021///NM_1						2000 CO // Control of CO / DNA for a feet and a DNA for DNA fo
March   Marc										
Mathematical   Math	80.40162	70.798485	72.135735	77.92661 XM 011243061	0.001379849	-1.136	1.080	1.101 Fbxw23	F-box and WD-40 domain protein 23	
Property										
Prop										
Property				249.49503 NM 023637//XM 00						OU06508 // proceosyss // interfeed from electronic annotation//O006418 // IRNA aminoacytation for protein translation // inferred from electronic annotation//O006418 // IRNA aminoacytation for protein translation // inferred from electronic annotation///0006434
Column										
Mathematical   Math									sulfotransferase family, cytosolic, 2B, member 1	0000103 // sulfate assimilation // inferred from direct assay///0006629 // lipid metabolic process // inferred from electronic annotation///0008202 // steroid metabolic pr
Column					9.33E-04				SRY (sex determining region Y)-box 10	0001701 // in utero embryonic development // inferred from genetic interaction///0001755 // neural crest cell migration // inferred from mutant phenotype///0002052 /
Mathematical Content										
Mathematical Content										0000038 // very long-chain fatty add metabolic process // not recorded///0001676 // long-chain fatty add metabolic process // traceable author statement//0006629 //
Mathematical   Math				239.21056 NM_133694///XM_00	0.007227812					000086 // G2/M transition of mitotic cell cycle // not recorded///0009953 // dorsal/ventral pattern formation // inferred from sequence or structural similarity///001656
Mathematical Content										
March   Marc										0001967 // suckling behavior // inferred from genetic interaction///0006878 // cellular copper ion homeostasis // inferred from mutant phenotype///0007176 // regulatio
Mathematical   Math										
March   Marc	61.56107	54.149185	53.570972	57.598965 NM_001081099	0.005286331	-1.137		1.064 Aunip	aurora kinase A and ninein interacting protein	
March   Marc										
March   Marc										
April										0001501 // selected system development // inferred from microt penotype///0001506 // action potential // inferred from an action action action of the property
March   Marc				34.907173 NM 146167				1.057 Gimap7	GTPase, IMAP family member 7	0008152 // metabolic process // inferred from electronic annotation
March   Marc				34.545444 NM_001025388///NN						a 0001701 // in utero embryonic development // inferred from mutant phenotype///0006096 // glycolytic process // inferred from sequence or structural similarity///00510
1.5   1.5		48.33125	49.8485	50.98181 NM 001289442///NN	0.006410688			1.055 Grap2		
1965   1967   1967   1968   1969		493.94446	504./63/6 1503.0845	521.0304 NM_01123////XR_8/!					KAD9 nomolog A	UUUUU/5 // cell cycle checkpoint // interred from electronic annotation///UUUUU/6 // DNA replication checkpoint // not recorded///UUUUU/7 // DNA damage checkpoint // DNA d
Mary   1965   1967   1968   1968   1968   1969									eukaryotic translation elongation factor 1 gamma	0005412 // translation // inferred from electronic annotation///0006414 // translation // not recorded//0006749 // glutathione metabolic process // not rec
Part										0006629 // lipid metabolic process // inferred from electronic annotation///0016042 // lipid catabolic process // inferred from electronic annotation
Part										0000733 // DNA strand renaturation // not recorded///0001501 // skeletal system development // inferred from mutant phenotype///0006260 // DNA replication // not r
Proc.   Proc										0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated // inferred from electronic anno
March   Marc										0006915 // appototic process // inferred from electronic annotation///0032088 // negative regulation of NF-kaopaB transcription factor activity // inferred from mutant p
Section   Control   Cont				11627.55 NM_019865						0006412 // translation // inferred from electronic annotation
Post		86.06967		89.453445 NM_001081220///NN	0.004898137	-1.270				0007186 // G-protein coupled receptor signaling pathway // not recorded///0007601 // visual perception // not recorded///0072659 // protein localization to plasma men
Mary										
1.150    1				249.829/3 NM_024199///XM_0C						
March   Control   Contro				261.6003 NM 033573				1.035 Proc		0007932 // regulation in protein prospring visitority in clean despite of the large y/ miletted from indiant prenotype//outdate/ // protein depite 0007093 // mitotic cell cycle checkopist // not recorded
64-1501   64-1501   65-150						1.000			TELO2 interacting protein 2	
A. STORT   C. STORT						1.055				
1.05.000   10.0000   10.00000   1.000000   1.0000000   1.00000000   1.000000000   1.0000000000				662.49164 NM_031373///XM_00				1.030 Ogfr	opioid growth factor receptor	0040008 // regulation of growth // inferred from electronic annotation
\$4,000   \$										0007000 // nucleables commission // inferred from direct accase
2 17 20 20 27 20 20 27 20 20 27 20 20 27 20 20 20 20 20 20 20 20 20 20 20 20 20										0006308 // DNA catabolic process // inferred from electronic annotation///0006309 // apoptotic DNA fragmentation // inferred from direct assay///0006915 // apoptotic
1941-148   1941-149										0000209 // protein polyubiquitination // not recorded///0016567 // protein ubiquitination // inferred from mutant phenotype///0023035 // CD40 signaling pathway // ini
69-365   69-275   79-255   7										
19.11/15/15   19.11/15/15   19.11/15/15   19.11/15/15   19.11/15/15   19.11/15/15   19.11/15/15   19.11/15/15   19.11/15/15   19.11/15/15   19.11/15/15   19.11/15/15   19.11/15/15   19.11/15/15   19.11/15/15   19.11/15/15   19.11/15/15   19.11/15/15/15/15/15/15/15/15/15/15/15/15/1									solute carrier family 25 (mitochondrial carrier, adenine nucleotide transic	5 UUUbattu // transport // inferred from electronic annotation//UUUbats // apoptotic miticonondrial changes // inferred from genetic interaction//UUUbats // apoptotic miticonondrial changes // inferred from genetic interaction//UUIbats // apoptotic miticonondrial changes // inferred from genetic interaction//UUIbats // apoptotic miticonondrial changes // inferred from genetic interaction//UUIbats // apoptotic miticonondrial changes // inferred from genetic interaction//UUIbats // apoptotic miticonondrial changes // inferred from genetic interaction//UUIbats // apoptotic miticonondrial changes // inferred from genetic interaction//UUIbats // apoptotic miticonondrial changes // inferred from genetic interaction//UUIbats // apoptotic miticonondrial changes // inferred from genetic interaction//UUIbats // apoptotic miticonondrial changes // inferred from genetic interaction//UUIbats // apoptotic miticonondrial changes // inferred from genetic interaction//UUIbats // apoptotic miticonondrial changes // inferred from genetic interaction//UUIbats // apoptotic miticonondrial changes // inferred from genetic interaction//UUIbats // apoptotic miticonondrial changes // inferred from genetic interaction//UUIbats // apoptotic miticonondrial changes // inferred from genetic interaction//UUIbats // apoptotic miticonondrial changes // interaction//UUIbats // apoptotic miticonondr
297-146   297-179   297-									CDS antigen-like	
1312776   1312976   1312976   131297   1312976   131297			2380.7717			-1.151	1.065	1.016 Acat1	acetyl-Coenzyme A acetyltransferase 1	0001889 // liver development // inferred from electronic annotation///0007420 // brain development // inferred from electronic annotation///0008152 // metabolic proo
\$2,000   \$										0001701 // in utero embryonic development // inferred from genetic interaction///0006810 // transport // inferred from electronic annotation///0015671 // oxygen trans
## 15/2016   19.00   1										
1931-075   1931-075										
1981/250   1981/250   2315-000   1991/250									cysteine-rich perinuclear theca 3	•
1813.18   1812.07   1817.18   1812.07   1817.18   1812.08   1812									zinc binding alcohol dehydrogenase, domain containing 2	
1806.467   1807.06   180										0007275 // multicellular organismal development // inferred from electronic annotation
4.4.6757   14.6572   14.6757   14.67								-1.002 Artey///Gm4/3/		
\$2,3775 7, 7,1811 Mr. (1918-11) Mr. (1918-11								-1.002 Ugt2b34	UDP glucuronosyltransferase 2 family, polypeptide B34	0008152 // metabolic process // inferred from electronic annotation///0009813 // flavonoid biosynthetic process // not recorded///0032870 // cellular response to hormo
14.1541   1.154   1.156   1.					0.002536024					0006810 // transport // not recorded///0006869 // lipid transport // not recorded///0008152 // metabolic process // inferred from electronic annotation///0055085 // tra
\$45,5735   \$45,5531   \$40,5411   \$40,52   Mr. (2011)132/l/m   \$20,000   \$11,11   \$1.00   \$40,000   \$10,000   \$11,11   \$1.00   \$40,000   \$40,000   \$10,000   \$11,11   \$1.00   \$40,000   \$										
128-1279   131-2548   134-047   130-2547   130-2548   130-2547   130-2548   130-2547   130-2548									RPTOR independent companion of MTOR, complex 2	0001932 // regulation of protein phosphorylation // inferred from mutant phenotype///0001938 // positive regulation of endothelial cell proliferation // not recorded///0
Pall   298										0006412 // translation // inferred from direct assay///0032543 // mitochondrial translation // inferred from sequence or structural similarity
\$5.51.00   \$95.015   \$60.0154   \$5.55.01   \$10.0000155   \$-1.00										
34.5931 30.6848 403.1955 32.86.003 Mt, 2008.45(1/Mt, 200.000) 34.5931 30.6848 403.1955 32.86.003 Mt, 200.0000 10.0000 10.000000 10.0000000 10.00000000						1.048				a 0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated // not recorded///0006359 // re
Fig. 17:15   Fig. 23:23   73				585.862 NM 026817//XM 00 324.6203 NM 008434//XM 00	0.004683933	1.016				UUUSS86 // Intracellular protein transport // not recorded///0007264 // small GTPase mediated signal transduction // interred from electronic annotation///0007338 // sis 0002730 // nositive repulsation of defense response to vivin by host // not recorded///0006740 // repulsation of again against imministration // single against imministration // single repulsation of against against imministration // single repulsation of against imministration
C030-619   079-99807   79-95304   059-99807   079-95304   059-99807   079-95304   059-99807   079-99						1.089				
101.4 601.4   100.5	630.6419	679.69507	719.55304	664.3967 NM_027225///NM_1	0.008468187	1.078	-1.083	-1.023 Cobll1	Cobl-like 1	0030041 // actin filament polymerization // not recorded///0051639 // actin filament network formation // not recorded
## 473.455   473.4854   Mil.1941/J.M.D. K   Co.005432/75.5   1.03   1.071   1.032   Modebal   million   Mi				1018.29816 NM 019786					TANK-binding kinase 1	0002218 // activation of innate immune response // inferred from mutant phenotype///0002376 // immune system process // inferred from electronic annotation///0006
986.315   513.182   396.787 NM, 008384/I/NM, 05   0.0044393   1.003										
843.2024 773.0616 633.4454 773.0617 M3 (255954 C) 0.0042038 1.091 1.109 1.0318 par phosphosphosphosphosphosphosphosphosphos										
5.1,000.00 5.4,375.484 5.7,483.486 5.2,128914 NM, 17778 0.000.002371576, 765.1579 62,10.09 NM, 0.00232105/1,Nb. 0.0015808 1.00 6.00232175 133,623.81 1.00 1.00252177 1.003.81 1.002 6.0025277 1.003.81 1.002 6.0025277 1.003.81 1.00	843.2024	773.0616	639.34454	747.6671 NM 025954	0.00442038	-1.091	1.169	-1.034 Pap	phosphoglycolate phosphatase	0005975 // carbohydrate metabolic process // inferred from electronic annotation///0008152 // metabolic process // inferred from electronic annotation///0016311 // de
388.34814 389.82489 424.5300 372.8178 1M, 00.035925177 153.8253.81 153.824.83 M, 00.075340 0.00651279 1.018 1.139 1.056 (Cold/3) 1.056 (Cold/		54.375484				1.066	-1.101	-1.041 Lhfpl4	lipoma HMGIC fusion partner-like protein 4	
1324.7793   1603.9137   1593.7876   1533.6233   MN_007734   0.006152298   1.121   1.039   1.068   CoMag   collagen, type // Lapha 3   0.00615279   St. 153.6233   MN_00773576   1.353.6233   MN_00773576   1.007   1.008   7.0						1.005				
82.25932 87.85.84 85.75.854 87.85.25 87						1.058			ninna (never in mitosis gene a)-related expressed kinase 1 collagen, type IV, alpha 3	uuuuuso // mark cassae /////uuuuso // activation of Mark activity // not recorded///uuusakk/ kidney development // interred from mutant phenotype///000646 0006319 // activation of cysteine-type endopoetidase activity involved in aboototic propess // not recorded///uusakk/ interred from mutant phenotype///000646
PRE-9937   PRE-9556   498-2001   1.12   1.029   1.02	822.5932	855.3894	905.3091	816.192 NM 001312868///NN	0.009435071	1.040	-1.109	-1.048 Tqfbr1		0000186 // activation of MAPKK activity // not recorded///0001501 // skeletal system development // inferred from genetic interaction///0001525 // angiogenesis // infer
904.9856 993.9992 995.19986 943.2021 Mt (0.000603998) 1.008 1.002 1.005 Birght 1.002 1.002 Birght 1.002 1.005 Birght 1.002 1.002 Birght 1.002 1.002 Birght 1.002 1.002 Birght 1	782.9937	878.6584	857.4552	833.63544 NM_198037	0.001479376	1.122	-1.029	-1.054 Cachd1	cache domain containing 1	0006810 // transport // inferred from electronic annotation///0006816 // calcium ion transport // inferred from electronic annotation///0006816 // calcium ion transport // inferred from electronic annotation///0006816 // calcium ion transport // inferred from electronic annotation//
506.0052   589.2048   541.0913   556.5524   Mt. [00139890/]/(Nh.   0.0008153]   1.164   1.077   1.104   1.075   1.066   Ahr   Ah						1.098			BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, (Mot1	
158.5236 158.51772 171.128 Nr. (0.013140271/Nr. 0.00856331 1.09 1.165 A. Propherosity of the complete of the c										
## 47.6698   \$77.26447   108.915   \$79.5447   108.915   \$79.54447   108.915   \$79.54447   108.915   \$79.54447   108.915   \$79.54447   108.915   \$79.54447   108.915   \$79.54447   108.915   \$79.54447   108.915   \$79.54447   108.915   \$79.54447   108.915   \$79.54447   108.915   \$79.54447   108.915   \$79.54447   108.915   \$79.54447   108.915   \$79.54447   108.915   \$79.54447   108.915   \$79.54447   108.915   \$79.54447   108.915   \$79.54447   108.915   \$79.54447   108.915   10										
880,5015   970,547   108,9155   970,64845   Mt, 001114328///Mth   0.0068374025   1.102   1.147   1.077   Cogs   cell cyde progression 1   0.007499 / (regl. cyd. lineterd from electronic annotation///0000384 / positive regulation of cell proliferation of cell pro	474.6698	567.26447	535.0716	531.4275 NM_001038602///NN	0.002360535	1.195	-1.007	-1.067 Marveld2	MARVEL (membrane-associating) domain containing 2	0007605 // sensory perception of sound // inferred from mutant phenotype///0007605 // sensory perception of sound // not recorded///0045216 // cell-cell junction orga
1298.1542   1290.077   1399.4392   1197.6648 NI, 001005588/I/N, 0 0.004552883   -1.056   -1.0										0007049 // cell cycle // inferred from electronic annotation///0008284 // positive regulation of cell proliferation // not recorded///0045787 // positive regulation of cell c
\$18.5223 \$41.728 \$5.28.356 \$50.126.4 Mt, 0011466555/[Mh 0.00345704 \$1.055 \$1.05										
14460.339				1137.0048 NM_001005868///NN 500.12454 NM_001146085///NA						vocuous // procent rangering // interred from direct assay///vutuozo // positive regulation of gene expression // not recorded///vutuus/s/ negative regulation of NF-kap
44.586.1 45.2878 45.22842 27.149 NN, 00.00377272//NN. 0.008212957 1.047 -1.15 1.089 Typu5 18NA-WP symboxims protein 5 576.595.863 612.796 636.4848 55.850.92 (NO.00031272)/N, 0.00757279 1.04 43.51082 494.6944 51.50.37 47.70752 NN, 0.10632 (0.0037697) 1.15 1.109 Exect establishment of chesion in homologa 15, cerevisiae) 0.006273/ regulation of DNA registration / not recorded//0007049 // regulation of DNA registration / not recorded//0007049 // regulation of DNA registration of DNA re										
576 55636 612 7976 636 348 55.58.042 NM 001081222///NM 0,007504778 1.062 -1.145 -1.103 Exat establishment of cohesion / Inferred from electronic annotation // 10007062 // sizer chromatid cohesion / Inferred from electronic annotation // 10007062 // sizer chromatid cohesion / Inferred from electronic annotation // 10007062 // sizer chromatid cohesion / Inferred from electronic annotation // 10007062 // sizer chromatid cohesion / Inferred from electronic annotation // 10007062 // sizer chromatid cohesion // Inferred from electronic annotation // 10007062 // sizer chromatid cohesion // Inferred from electronic annotation // 10007062 // sizer chromatid cohesion // Inferred from electronic annotation // 10007062 // sizer chromatid cohesion // Inferred from electronic annotation // 10007062 // sizer chromatid cohesion // Inferred from electronic annotation // 10007062 // sizer chromatid cohesion // Inferred from electronic annotation // 10007062 // sizer chromatid cohesion // Inferred from electronic annotation // 10007062 // sizer chromatid cohesion // Inferred from electronic annotation // 10007052 // anjoigenesis // Inferred from electronic annotation // 10007052 // anjoigenesis // Inferred from electronic annotation // 10007052 // anjoigenesis // Inferred from electronic annotation // 10007052 // anjoigenesis // Inferred from electronic annotation // 10007052 // anjoigenesis // Inferred from electronic annotation // 10007052 // anjoigenesis // Inferred from electronic annotation // 10007052 // anjoigenesis // Inferred from electronic annotation // 10007052 // anjoigenesis // Inferred from electronic annotation // 10007052 // anjoigenesis // Inferred from electronic annotation // 10007052 // anjoigenesis // Inferred from electronic annotation // 10007052 // anjoigenesis // Inferred from electronic annotation // 10007052 // anjoigenesis // Inferred from electronic annotation // 10007052 // anjoigenesis // Inferred from electronic annotation // 10007052 // anjoigenesis // Inferred from electronic annotation // 10007								-1.088 Atp8b3	ATPase, class I, type 8B, member 3	0006810 // transport // inferred from electronic annotation///0006869 // lipid transport // inferred from electronic annotation///0007030 // Golgi organization // not reo
493.52182 494.4844 15.12182 494.4844 15.12182 494.4844 15.12182 494.4844 15.12182 494.6944 15.12182 49						1.047				0008033 // tRNA processing // inferred from electronic annotation///0031591 // wybutosine biosynthetic process // not recorded///0055114 // oxidation-reduction proce
4895.975 5487.877 5731.7095 4946.1793 MN 021471/[NM 2] 0.006913814 1121 -1.159 -1.110 Renared from househouse, Rhisee A family 4 0001525 // langiogenesis // inferred from electronic annotations/ [N0001352 // langiogenesis // inferred from electronic annotations/ [N001352 // langiogenesis // inferred fro									establishment of cohesion 1 homolog 1 (S. cerevisiae)	0006275 // regulation of DNA replication // not recorded///0007049 // cell cycle // inferred from electronic annotation///0007062 // sister chromatid cohesion // inferred
28.532837 31.41317 32.565186 28.230968 NNL 0020209 0.008405672 1.105 -1.154 5.113 Off6500 offstcory receptor 6500 0007155/ // signit manageation // not recorded///0007165/ // not r										0001525 // angiogenesis // inferred from electronic annotation///0001525 // angiogenesis /////0001575 // angiogenesis // inferred from sequence or structural similar
165.3509 136.11333 107.76688 122.215126 NIM 011270 0.005920866 -1.215 1.134 -1.114 Rhd Rh blood group, D antigen 0015696 // ammonium transport // inferred from mutant phenotype///0068821 // erythrocyte development // inferred from mutant phenotype///0060586 // multicelluk	28.532837	31.41317	32.565186	28.230968 NM_020290	0.008405672	1.101	-1.154	-1.113 Olfr690	olfactory receptor 690	0007165 // signal transduction // not recorded///0007186 // G-protein coupled receptor signaling pathway // not recorded///0007608 // sensory perception of smell // nc
102.04454 107.09461 110.80449 95.35772 NM_001013387//NM 0.002132295 1.049 -1.162 -1.123 Zfp182 zinc finger protein 182 0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated // not recorded										0015696 // ammonium transport // inferred from mutant phenotype///0048821 // erythrocyte development // inferred from mutant phenotype///0060586 // multicellula
	102.04454	107.09461	110.80449	95.35772 NM_001013387///NN	0.002132295	1.049	-1.162	-1.123 Zfp182	zinc finger protein 182	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated // not recorded

			r-KO, O2](raw) RefSeq Transcript ID p (G					Gene Title	Gene Ontology Biological Process
78.50476	83.57728	81.85938	74.15306 NM 153061///XR 10!	0.009946417	1.065	-1.104	-1.127 Tiaf2	TGF-beta1-induced anti-apoptotic factor 2	
548.4758	680.0645	770.6171	601.928 NM_001039181///NN	0.005818703	1.240	-1.280	-1.130 Npr3	natriuretic peptide receptor 3	0001501 // skeletal system development // inferred from direct assay///0001501 // skeletal system development // inferred from mutant phenotype///0002158 // osteoc
499.83173	577.6723	542.535	504.32684 NM 001039215///NN	0.001658322	1.156	-1.076	-1.145 Pfkfb4	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	0006000 // fructose metabolic process // inferred from electronic annotation///0006003 // fructose 2,6-bisphosphate metabolic process // inferred from electronic annotation
760.32666	871.6596	893.9743	759.65546 NM_001081150	0.001133994	1.146	-1.177	-1.147 Lonrf1	LON peptidase N-terminal domain and ring finger 1	0006508 // proteolysis // inferred from electronic annotation
385.27368	449.73163	483.1919	387.40793 NM 013867///XM 00	1.30E-04	1.167	-1.247	-1.161 Bcar3	breast cancer anti-estrogen resistance 3	0002089 // lens morphogenesis in camera-type eye // inferred from mutant phenotype///0007165 // signal transduction // inferred from electronic annotation///0007264
554.0281	765.62036	619.1688	656.87244 NM_001114098///NN	0.00805221	1.382	1.061	-1.166 Mtcl1	microtubule crosslinking factor 1	0001578 // microtubule bundle formation // inferred from direct assay///0010506 // regulation of autophagy // inferred from electronic annotation///0045197 // establis
110.14734	123.800865	115.75199	105.61347	0.008094004	1.124	-1.096	-1.172 C77097	expressed sequence C77097	
67.583115	38.96788	36.072266	33.06806 NM_145146	0.005742774	-1.734	-1.091	-1.178 Afm	afamin	0006810 // transport // inferred from electronic annotation///0051180 // vitamin transport // not recorded
2915.611	3436.7405	3575.5144	2819.8708 NM 133725///NM 1:	0.009999848	1.179	-1.268	-1.219 Secisbp2l	SECIS binding protein 2-like	
1710.4757	2207.7852	1961.248	1809.4072 NM_001025250///NN	0.003167039	1.291	-1.084	-1.220 Vegfa	vascular endothelial growth factor A	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded///0001525 // angiogenesis // inferred from direct assay///0001525 // arg
355.8095	425.62427	379.70926	347.82846 NM_175187///NR_02	0.004542276	1.196	-1.092	-1.224 Tmem161b	transmembrane protein 161B	
37.44921	44.33614	38.355804	36.149307	0.009915507	1.184	-1.061	-1.226 D1Ertd646e	DNA segment, Chr 1, ERATO Doi 646, expressed	
66.743034	73.25703	68.7475	59.705116 NM_177052///XM_00	0.004596748	1.098	-1.151	-1.227 Kif6	kinesin family member 6	0007018 // microtubule-based movement // not recorded///0008152 // metabolic process // inferred from electronic annotation
605.0476	679.1741	614.92474	544.8614 NM_026368///XM_00	0.001098655	1.123	-1.129	-1.247 Caap1	caspase activity and apoptosis inhibitor 1	0006915 // apoptotic process // inferred from electronic annotation
32.1485	32.640057	30.868538	25.986841	0.008977985	1.015	-1.188	-1.256 9430087J23Rik	RIKEN cDNA 9430087J23 gene	
28.196205	36.272247	32.59862	28.606833	0.005570435	1.286	-1.140	-1.268 D7Ertd558e	DNA segment, Chr 7, ERATO Doi 558, expressed	
166.81755	211.61995	168.47212	166.18628 NM_030110///XM_00	0.006348874	1.269	-1.014	-1.273 Micu3	mitochondrial calcium uptake family, member 3	
143.05722	28.310953	20.604244	21.480125 NM_001150749///NN	0.007889654	-5.053	1.043	-1.318 Rdh7	retinol dehydrogenase 7	0008152 // metabolic process // inferred from electronic annotation///0042572 // retinol metabolic process // inferred from electronic annotation///0055114 // oxidation
511.498	723.33057	550.2367	547.33636 NM_007707///XM_01	0.006182605	1.414	-1.005	-1.322 Socs3	suppressor of cytokine signaling 3	0001666 // response to hypoxia // inferred from electronic annotation///0001932 // regulation of protein phosphorylation // inferred from direct assay///0006469 // nega
1531.4441	1833.0116	1756.8998	1347.1793 NM_001012766///NN	0.003918618	1.197	-1.304	-1.361 Ear-ps2///Ear1///Ear12///Ea	ar2///E eosinophil-associated, ribonuclease A family, pseudogene 2///eosinop	hil-i 0006935 // chemotaxis // inferred from direct assay///0008152 // metabolic process // inferred from electronic annotation///0090305 // nucleic acid phosphodiester bond
128.37373	20.784555	15.921132	15.120894 NM_029562///XM_00	0.005814837	-6.176	-1.053	-1.375 Cyp2d26	cytochrome P450, family 2, subfamily d, polypeptide 26	0006805 // xenobiotic metabolic process // not recorded///0007565 // female pregnancy // inferred from electronic annotation///0019369 // arachidonic acid metabolic process // not recorded // 0007565 // female pregnancy // inferred from electronic annotation///0019369 // arachidonic acid metabolic process // not recorded // 0007565 // female pregnancy // inferred from electronic annotation // 0019369 // arachidonic acid metabolic process // not recorded // 0007565 // female pregnancy // inferred from electronic annotation // 0019369 // arachidonic acid metabolic process // not recorded // 0007565 // female pregnancy // inferred from electronic annotation // 0019369 // arachidonic acid metabolic process // not recorded // 0007565 // female pregnancy // inferred from electronic annotation // 0019369 // arachidonic acid metabolic process // not recorded // 0007565 // female pregnancy // inferred from electronic annotation // 0019369 // arachidonic acid metabolic process // not recorded // 0007565 // female pregnancy // inferred from electronic annotation // 0019369 // arachidonic acid metabolic process // not recorded // 0007565 // female pregnancy // inferred from electronic annotation // 0019369 // arachidonic acid metabolic process // not recorded // 0007565 // acid metabolic process // not recorded // 0007565 // acid metabolic process // not recorded // 0007565 // acid metabolic process // not recorded // 0007565 // acid metabolic process // not recorded // 0007565 // acid metabolic process // not recorded // 0007565 // acid metabolic process // not recorded // 0007565 // acid metabolic process // not recorded // 0007565 // acid metabolic process // not recorded // 0007565 // acid metabolic process // not recorded // 0007565 // acid metabolic process // not recorded // 0007565 // acid metabolic process // not recorded // 0007565 // acid metabolic process // not recorded // 0007565 // acid metabolic process // not recorded // 0007565 // acid metabolic process // not recorded // 0007565 // acid metabolic process
125.92949	179.2413	2265.6091	118.197014 NM_008725	0.008516206	1.423	-19.168	-1.516 Nppa	natriuretic peptide type A	0001666 // response to hypoxia // inferred from electronic annotation///0003085 // negative regulation of systemic arterial blood pressure // not recorded///0006182 //
481.74808	49.186993	36.431168	30.955608 NM_007376	0.004647014	-9.794	-1.177	-1.589 Pzp	pregnancy zone protein	0007566 // embryo implantation // inferred from genetic interaction///0010466 // negative regulation of peptidase activity // inferred from electronic annotation///0010