		l decreased in neonate fold lower in neonate-	O2/Gsr-KO, Red : fold I		02/Gsr-KO.							
	p (Exposure) 0.48563203				[Gsr-KO, O2](raw) 700.8477	RefSeq Transcript ID p (Genotype-Expo NM 001177713///NM 17 0.004570393			FD (WT O2 vs KO O2)		Gene Title cytochrome P450, family 26, subfamily b, polypeptide 1	Gene Ontology Biological Process
0.003293092 2.37E-05	0.48563203		169.69853 4450.121	310.38336 6483.832	/00.84// 6646.392	NM_0011///13///NM_1: 0.0045/0393 NM_001166627///NM_0C_0.001643861	-1.73 -1.30	1.03	4.13 1.49	Cyp26b1 Dvnlt1-ns1///Dvnlt1a///Dvnlt1h///Dvn		0001709 // cell fate determination // inferred from mutant phenotype///0001768 // establishment of T cell polarity // inferred from mutant phe 0000132 // establishment of mitotic spindle orientation // inferred from mutant phenotype///0006810 // transport // inferred from electronic a
0.8882446	0.003401874			215.72896	241.59346	NM_010731///XM_00651 4.38E-04	-1.91	1.12	1.49	Zbtb7a	zinc finger and BTB domain containing 7a	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///0006351 // transcription, DNA-
	0.6627319			49.64675	64.59036	NM 144879///NR 02735 5.83E-04	-1.21	1.30	1.42	Vash2	vasohibin 2	0001938 // positive regulation of endothelial cell proliferation // not recorded///0045765 // regulation of angiogenesis // inferred from electron
0.039405506	0.114652224			34.55588 22.976355	45.49369 28.08051	NM_146244//XM_00651 4.96E-05 NM 022033 0.004433935	-1.15 -1.30	1.32	1.36 1.35	Rps6kl1 Oxct2a	ribosomal protein S6 kinase-like 1 3-oxoacid CoA transferase 2A	0006468 // protein phosphorylation // inferred from electronic annotation//0007165 // signal transduction // not recorded///0016310 // phosphorylation // succinyl-CoA metabolic process // not recorded///0008152 // metabolic process // inferred from electronic annotation///0046950 //
0.30519402	0.007108286		105.64493	139.5046	140.81895	NM_001039718///NM_05 0.00722072	-1.48	1.01	1.33	Cntf///Zfp91///Zfp91Cntf		0007250 // activation of NF-kappaB-inducing kinase activity // not recorded//0007259 // JAK-STAT cascade // not recorded//0007275 // multi-
0.4445606	0.002737228			434.0593	411.28082	NM_011917///XM_00649 0.008740946	-1.70	-1.06	1.33	Xrn2	5'-3' exoribonuclease 2	0000738 // DNA catabolic process, exonucleolytic // not recorded///0006139 // nucleobase-containing compound metabolic process // inferred l
	0.28360265 0.7949438	527.78656 68.77511	437.91776 58.98897	525.0143 64.54025	579.5629 77.71156	NM_008587//XM_00649 0.005747954 NM_001159925//NM_00 0.003418639	-1.21	1.10		Mertk Pax4	c-mer proto-oncogene tyrosine kinase	0001779 // natural killer cell differentiation // inferred from genetic interaction//0006468 // protein phosphorylation // not recorded//000690
		26.15641		23.438787	77.71156 30.67557	NM_001159925///NM_0L0.003418639 NM_183136///XM_00651_0.002949097	-1.17 -1.12	1.20	1.32	Pax4 Spink8	paired box 4 serine peptidase inhibitor, Kazal type 8	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///0006351 // transcription, DNA- 0010466 // negative regulation of peptidase activity // inferred from electronic annotation///0010951 // negative regulation of endopeptidase a
0.012796956	0.010678015	72.05801	71.83545	72.614784	94.12694	NM_144856 0.00194979	1.00	1.30	1.31	Slc22a7	solute carrier family 22 (organic anion transporter), member 7	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic annotation///0015711 // org
	0.14269932		934.57086	1118.2578	1206.1094	NM_001142916///NM_01 0.005038485	-1.21	1.08	1.29	Plod2	procollagen lysine, 2-oxoglutarate 5-dioxygenase 2	0001666 // response to hypoxia // inferred from electronic annotation///0032870 // cellular response to hormone stimulus // inferred from elec
3.61E-04 0.6471289		460.91266 46.36864		491.31323 37.452923	526.5961 51.131393	NM_172678///XM_01124 0.007030516 NM 023566 0.002995865	-1.12 -1.16	1.07	1.28	Acad9 Muc2	acyl-Coenzyme A dehydrogenase family, member 9 mucin 2	0008152 // metabolic process // inferred from electronic annotation///0032981 // mitochondrial respiratory chain complex I assembly // not rec 0002064 // epithelial cell development // inferred from mutant phenotype///0006915 // apoptotic process // inferred from mutant phenotype//
6.48E-06		2854.522		3188.5151	3512.0093	NM 001103165//NM 00 0.008336045	-1.16	1.10	1.27	Pcbp2	poly(rC) binding protein 2	0002376 // immune system process // inferred from electronic annotation///0043161 // proteasome-mediated ubiquitin-dependent protein cata
0.69512284		36.75465	30.798414	32.44561	38.811283	NM_026290///XM_01124 0.00461141	-1.19	1.20	1.26	Armc12	armadillo repeat containing 12	
0.52832735		67.78825 35.847717		62.141563 33.57702	77.11061 41.82455	NM_001045484///NM_00 0.006887504 NR 003248 0.003199265	-1.11 -1.08	1.24	1.26			$0006351 \ // \ transcription, \ DNA-templated \ // \ inferred \ from \ electronic \ annotation \ // \ // \ negulation \ of \ transcription, \ DNA-templated \ // \ inferred \ from \ electronic \ annotation \ // \ // \ negulation \ of \ transcription, \ DNA-templated \ // \ inferred \ from \ electronic \ annotation \ // \ negulation \ of \ transcription, \ DNA-templated \ // \ inferred \ from \ electronic \ annotation \ // \ negulation \ of \ transcription, \ DNA-templated \ // \ inferred \ from \ electronic \ annotation \ // \ negulation \ of \ transcription, \ DNA-templated \ // \ inferred \ from \ electronic \ annotation \ // \ negulation \ of \ transcription, \ DNA-templated \ // \ inferred \ from \ electronic \ annotation \ // \ negulation \ of \ transcription \ deleter \ from \ electronic \ ele$
0.19265433 1.53E-04		35.847717 550.1567		33.57702 584.98157	41.82455 625.4462	NR_003248 0.003199265 NM 025418//XM 00651 0.005756791	-1.08 -1.11	1.25	1.26 1.26	Foxi2os Vta1	forkhead box L2, opposite strand Vps20-associated 1 homolog (S. cerevisiae)	0006810 // transport // inferred from electronic annotation///0015031 // protein transport // inferred from electronic annotation///0046755 //
0.76190275	0.3137848	16.460617	13.221201	14.44999	16.570063	NM 029294 0.00900176	-1.25	1.15	1.25	Prps1l1	phosphoribosyl pyrophosphate synthetase 1-like 1	0008584 // male gonad development // inferred from electronic annotation///0009156 // ribonucleoside monophosphate biosynthetic process /
0.041302253		22.199343	21.526386	21.723131	26.868586	NM_001310617///NM_0; 0.003399813	-1.03	1.24	1.25	Akrid	aldo-keto reductase family 1, member C-like	0055114 // oxidation-reduction process // inferred from electronic annotation
0.0057146	0.002075208		29.465021 1060.6588	34.804962 1322 3085	36.534542 1311 1074	NM 016664///NR 01548 7.79E-04 NM_181322///XM_00653 0.002191061	-1.18 -1.28	1.05	1.24 1.24	Mtaq2 Ctcf	metastasis associated gene 2 CCCTC-binding factor	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0000122 // negative reg
0.571118	0.80810755			20.24656	24.865353	NM 019928 0.001790778	-1.21	1.23	1.23	Kik4		0006508 // proteolysis // inferred from electronic annotation///0006508 // proteolysis /////0022617 // extracellular matrix disassembly // inf
	0.001641556			46.57951	59.28458	NM_027105 9.92E-05	-1.03	1.27		Krtap26-1	keratin associated protein 26-1	
0.12472619 0.13595656	0.5566356 0.003541705	102.44889	92.46736 97.585464	100.074715	113.46666	NM 026152 0.002219897 NM_145419///XM_00651 0.002779155	-1.11	1.13	1.23	Hoga1 Hkdc1	4-hydroxy-2-oxoglutarate aldolase 1	0008152 // metabolic process // inferred from electronic annotation///0009436 // glyoxylate catabolic process // not recorded///0019470 // 4-1
0.13595656		93.56387 58.200413	97.585464 50.88851	91.39572 57.258442	119.6105 62.373695	NM_145419///XM_00651 0.0027/9155 NM_027790///XM_00651 0.007577031	1.04 -1.14	1.31	1.23 1.23	Dhrs2	hexokinase domain containing 1 dehydrogenase/reductase member 2	0001678 // cellular glucose homeostasis // not recorded///0005975 // carbohydrate metabolic process // inferred from electronic annotation///0008152 // metabolic process // inferred from electronic annotation///0009636 // response to toxic substance // inferred from electronic annotation
0.5152903		66.92564	62.118973	62.40638	75.72317	NM_001040136///NM_00 0.002372618	-1.08	1.21	1.22	Pdzd9	PDZ domain containing 9	
		11.494334		10.929648	13.085644	NM 010672 0.005041123	-1.07	1.20	1.22	Krtap6-1	keratin associated protein 6-1	
1.44E-04 0.06690413	0.97948813 0.055107508	14.270036	13.489722 22.84323	15.0711565 20.589144	16.34448 27.636942	NM_001001445///XM_00 0.001886785 NM 008900///NR 02789 9.35E-05	-1.06 -1.15	1.08	1.21 1.21	Trpv1 2900092D14Rik///Pou3f3	transient receptor potential cation channel, subfamily V, membe	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype///0001659 // temperature 0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded///0001822 // kidney development // inferred
	0.031227952			8.395976	9.7343645	NM 010133///XM 01124 0.009554812	1.00	1.16	1.21	En1	engrailed 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded///0006355 // regulation of transcription, DNA
0.6707818		107.63314		92.84797	114.21256	NM_019741///XM_00653 0.005664149	-1.14	1.23	1.21	Slc2a5		0006810 // transport // inferred from electronic annotation///0008643 // carbohydrate transport // inferred from electronic annotation///0015
0.51387125 0.3668665	0.40147555	44.488567	40.977566 441.66364	41.522038 506.08582	49.27595 527.9453	NM_001204371//NM_01 8.46E-04 NM_001008548//NM_0C 0.008909394	-1.09 -1.29	1.19	1.20 1.20	Oprk1 Pde2a	opioid receptor, kappa 1 phosphodiesterase 2A, cGMP-stimulated	0006955 // immune response // not recorded///0007165 // signal transduction // inferred from electronic annotation///0007186 // G-protein cc
0.7061665		88.39736	76.90627	83.18154	91.92827	NM 028130//XM 00650 0.005431023	-1.29 -1.15	1.11	1.20	Zfp157	zinc finger protein 157	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded///0003170 // heart valve development // infer 0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation///0010453 // regulation of cell fate commitment /
0.95593095		12.313707	10.163366	10.949724	12.143329	0.006872399	-1.21	1.11	1.19	D9Ertd292e	DNA segment, Chr 9, ERATO Doi 292, expressed	
		757.85187		574.4462	660.09265	NM_007528 8.58E-04	-1.37	1.15	1.19	Bcl6b	B cell CLL/lymphoma 6, member B	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay
0.93848526 0.89563096	0.001745556 0.47090113		17.066828 45.628708	14.723824 45.238667	20.316544 54.13659	NM_001003405///NM_01 0.008029391 NM 021408///XM 01123 0.005145514	1.05 -1.09	1.38	1.19 1.19	Try4///Try5 Ush2a	trypsin 4//trypsin 5 Usher syndrome 2A (autosomal recessive, mild)	0006508 // proteolysis // not recorded///0007586 // digestion // not recorded 0007601 // visual perception // inferred from electronic annotation///0007605 // sensory perception of sound // not recorded///0035315 // hair
	0.55132025		111.45675	121.82957	132.1195	NM 001163431//NM 0; 0.003416215	-1.05	1.08	1.19	Tmem258	transmembrane protein 258	0007001 // Visual perception // Illierred from electronic annotation///0007005 // Sensory perception of sound // flot recorded///0053515 // flail
0.116584465	0.001274807		35.54561	34.367138	42.11532	NM_020291 2.62E-04	-1.01	1.23	1.18	Olfr480	olfactory receptor 480	0007165 // signal transduction // inferred from electronic annotation///0007186 // G-protein coupled receptor signaling pathway // not recorde
0.54717433 0.18086573	0.012323908		23.484997 29.662539	20.952452 25.183386	27.734533 35.026917	NM_001276684//NM_01 0.004606338 NM_053095//XM_00652 0.004510169	-1.02 -1.08	1.32	1.18 1.18	Arc II24	activity regulated cytoskeletal-associated protein interleukin 24	0006897 // endocytosis // inferred from electronic annotation///0007010 // cytoskeleton organization // not recorded///0007275 // multicellula 0006915 // apoptotic process // inferred from electronic annotation///0006954 // inflammatory response // not recorded///0006955 // immune
0.18086573	0.002882958		33.15896	29.08609	38.90433	NM 030728//XM 00652 0.004510169	1.04	1.34	1.17	Cemip	cell migration inducing protein, hyaluronan binding	0007605 // sensory perception of sound // not recorded///0008152 // metabolic process // inferred from electronic annotation///0018800 // po
		41.55128	36.751213	35.570335	43.016304	NM 153079 0.002693375	-1.13	1.21	1.17	Nmur2	neuromedin U receptor 2	0002023 // reduction of food intake in response to dietary excess // inferred from mutant phenotype///0006816 // calcium ion transport // not
0.23873131		29.321762	25.632353	23.837547	29.975317	NM_145229 0.00920952	-1.14	1.26	1.17	AY074887	cDNA sequence AY074887	0007050 // cell cycle arrest // inferred from direct assay///0008285 // negative regulation of cell proliferation // inferred from direct assay///00!
		31.236643 330.9814	28.152586 269.91238	29.631319 301.5427	32.8909 314.60266	NM 011377///XM 00652 0.007035035 NM 001081345///NR 03 6.17E-05	-1.11 -1.23	1.11	1.17 1.17	Sim2 Chd2///1810026B05Rik	single-minded homolog 2 (Drosophila) chromodomain helicase DNA hinding protein 2///RIKEN cDNA 18	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interaction///0006351 // transcription 0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated // infe
0.394392	0.944819	81.70685	73.00772	71.7649	85.05013	NM 182928 0.004702677	-1.12	1.19	1.16	Adm2	adrenomedullin 2	0001525 // angiogenesis // not recorded///0006468 // protein phosphorylation // not recorded///0007189 // adenylate cyclase-activating G-pro
0.8575528		40.253407	36.074856	37.484478	41.933167	NM_145707 0.001205893	-1.12	1.12	1.16	Obox3	oocyte specific homeobox 3	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
0.43670657 0.4146085		78.89765 67.04811	68.540306 60.07246	70.572914 58.634842	79.64475 69.69125	NM 001291076//NM 00 0.003071887 NM 145856//XM 00649 0.00989496	-1.15 -1.12	1.13 1.19	1.16 1.16	Snph II17f	syntaphilin interleukin 17F	0006906 // vesicle fusion // not recorded///0045806 // negative regulation of endocytosis // not recorded 0006029 // proteoglycan metabolic process // inferred from electronic annotation///0006954 // inflammatory response // inferred from electron
0.22492139		50.67753		44.02093	48.288906	NM 001033278///NM 00 0.001794563	-1.22	1.10	1.16	Rmi2		0006250 // DNA replication // inferred from electronic annotation
0.22742805		44.331467	37.66575	36.609924	43.64067	NM_001039653///NM_01 0.00792512	-1.18	1.19		Lhx3	LIM homeobox protein 3	0001890 // placenta development // inferred from genetic interaction///0006351 // transcription, DNA-templated // inferred from electronic an
0.81663543 0.22336788		26.842428 75.40404	25.280426 74.82741	24.652971 75.23498	29.229492 86.46951	NM_001077499//NM_01 4.30E-04 NM 199013//XM 00653 0.007373505	-1.06 -1.01	1.19 1.15	1.16 1.16	Scn8a Irgc1	sodium channel, voltage-gated, type VIII, alpha immunity-related GTPase family, cinema 1	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic annotation///0006814 // sod 0008152 // metabolic process // inferred from electronic annotation
0.23271957		23.048323	25.379147	19.538458	29.26495	NM 001311124//NM 00 0.006409707	1.10	1.50	1.15	Celf5	CUGBP, Elav-like family member 5	0008132 // Illectabolic process // Illiested from electronic annotation
0.6722247	0.008112337		672.4694	747.51886	774.4303	NM_181547 0.002821125	-1.38	1.04	1.15	Nostrin	nitric oxide synthase trafficker	0006897 // endocytosis // inferred from electronic annotation///0045892 // negative regulation of transcription, DNA-templated // inferred from
0.7991659 0.72802913		1715.7144 23.307806	1356.5481 21.989176	1481.2637 21.31298	1561.7902 25.283283	NM_001033141///XM_00 0.005054246 NM_008167///XM_00650 0.008907643	-1.26 -1.06	1.05	1.15 1.15	Ecscr Grid2		0001525 // angiogenesis // inferred from electronic annotation//0006915 // apoptotic process // inferred from electronic annotation//000693 0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0007157 // heti
0.35606194		35.14865	30.996437	30.44456	35.615616	NM 001110161//NM 00 0.009731988	-1.13	1.17	1.15	Ifitm7	glutamate receptor, ionotropic, delta 2 interferon induced transmembrane protein 7	0009607 // response to biotic stimulus // inferred from electronic annotation///outransport // inferred from electronic annotation///outransport // inferred from electronic annotation//outransport // inferred from electronic annotation
0.86263037	0.8260414	90.02369	83.921265	84.98351	96.36284	NM_001014425///NM_01 0.00167196	-1.07	1.13	1.15	Orc1	origin recognition complex, subunit 1	0006260 // DNA replication // traceable author statement//0048661 // positive regulation of smooth muscle cell proliferation // not recorded/j
		29.502851		26.45641	30.700249	NM_009602 0.004250879	-1.10	1.16	1.15	Chrnb2	cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal)	0001508 // action potential // inferred from genetic interaction///0001508 // action potential // inferred from mutant phenotype///0001661 //
0.98993367		70.01367 23.972599		66.583824 20.347387	78.41397 24.649916	NR_002866 0.00593322 NM 023383 0.002735607	-1.02 -1.11	1.18	1.14 1.14	Dio3os Aadac	deiodinase, iodothyronine type III, opposite strand arylacetamide deacetylase (esterase)	0008152 // metabolic process // inferred from electronic annotation///0010898 // positive regulation of triglyceride catabolic process // inferrec
0.99507153		37.48541	36.826965	35.359028	42.030254	NR 045613 0.008422628	-1.02	1.19	1.14	Zfp572	zinc finger protein 572	obolisk // metabolic process // microsi nom electronic annotation/// obstato regulation or trigglectric database process // microsi
0.7440081		9.215277	8.634481	8.737733	9.842344	NM_019545///XM_01124 0.008979796	-1.07	1.13	1.14	Hao2	hydroxyacid oxidase 2	0018924 // mandelate metabolic process // not recorded///0019395 // fatty acid oxidation // not recorded///0051260 // protein homooligomer
0.5942964	0.04901199 0.29877353	1717.6627		1436.4563 19.190685	1799.89 21.106476	NM 021604//XM 00653 0.002263975 NM 011039//XM 00653 0.009062278	-1.09 -1.14	1.25 1.10	1.14 1.14	Agrn Pax7	agrin paired box 7	0001932 // regulation of protein phosphorylation // not recorded///0001934 // positive regulation of protein phosphorylation // inferred from d 0006338 // chromatin remodeling // inferred from mutant phenotype///0006351 // transcription, DNA-templated // inferred from electronic an
0.90258646	0.29877353			477.97873	509.47058	NM 001039718//NM 05 1.78E-04	-1.14	1.07		Cntf///Zfp91///Zfp91Cntf		0007250 // activation of NF-kappaB-inducing kinase activity // not recorded///0007259 // JAK-STAT cascade // not recorded///0007275 // multi-
0.18218641	0.25977245	52.158714	45.412327	46.145092	51.591473	NM_019991 0.003396937	-1.15	1.12	1.14	Pri2a1	prolactin family 2, subfamily a, member 1	
0.27300724	0.116833754	48.984715 69.30272	42.617653 65.59545	44.3085 64.048584	48.40882 74.461334	NM 001290691//NM 00 0.002553866 NM 008899 0 006910339	-1.15 -1.06	1.09	1.14 1.14	Col9a1 Pou3f2	collagen, type IX, alpha 1 POU domain, class 3, transcription factor 2	0001894 // tissue homeostasis // inferred from mutant phenotype///0003417 // growth plate cartilage development // inferred from genetic int 0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated // not
0.5000591		52.150215		49.761337	74.461334 54.555252	NM_008899 0.006910339 NM 153390 3.31E-04	-1.06 -1.08	1.10	1.14	Pou3j2 Pxt1	POU domain, class 3, transcription factor 2 peroxisomal, testis specific 1	0007283 // spermatogenesis // inferred from expression pattern///0043065 // positive regulation of apoptotic process // inferred from genetic is
0.4610726	0.007499356			513.71375	515.4942	NM_001042592///NM_0; 0.005100506	-1.25	1.00	1.13	Arrdc4	arrestin domain containing 4	0051443 // positive regulation of ubiquitin-protein transferase activity // not recorded
0.10525096 0.29335374	0.033680357 0.7018843	74.57443 24.403536	72.093666 22.014418	64.72891 22.106756	81.76104 24.964632	NR 002855 0.001057235 NM 178243///XR 38748: 8.19E-04	-1.03 -1.11	1.26 1.13	1.13 1.13	Iqf2os Gm38440///Teddm2	insulin-like growth factor 2, opposite strand predicted gene, 38440///transmembrane epididymal family men	43
0.29335374		49.833412		48.432728	24.964632	NM_1/8243///XR_38/48: 8.19E-04 NM 001312906//NM 00 0.006724545	-1.11 -1.03	1.13	1.13	Gm38440///Tedam2 Hnf4a	predicted gene, 38440///transmembrane epididymai family men hepatic nuclear factor 4, alpha	iber 2 0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated // infe
0.63456523	0.3580214	47.442562	45.32026	44.883816	51.35316	NM 001159500//NM 01 0.0086279	-1.05	1.14	1.13	Esrrb	estrogen related receptor, beta	0001701 // in utero embryonic development // inferred from mutant phenotype///0001831 // trophectodermal cellular morphogenesis // inferred
	0.038657457			89.23327	99.574135	NM_001310066///NM_0C 0.005057832	-1.49	1.12	1.13	Atf7	activating transcription factor 7	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded///0006351 // transcription, DNA-templated //
		29.321878 91.09947	26.659689 78.68304	27.492811 75.50302	30.14563 88.8847	NM_020277///XM_00650 8.68E-04 NM_028799 0.005691088	-1.10 -1.16	1.10 1.18	1.13 1.13	Trpm5 Tgm5	transient receptor potential cation channel, subfamily M, member transglutaminase 5	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic annotation///0006812 // cati 0018149 // peptide cross-linking // inferred from electronic annotation
		23.46076	21.169271	20.408888	23.892548	NM 001081672 0.009096509	-1.11	1.17	1.13	Fam43b	family with sequence similarity 43, member B	0018149 // peptide closs-inixing // initeried from electronic annotation
0.03150445	0.69790673	48.53893	41.952534	37.60281	47.329327	NM_009580 0.002353815	-1.16	1.26	1.13	Zp1	zona pellucida glycoprotein 1	0007338 // single fertilization // inferred from electronic annotation
0.89034426 0.45206434	0.014128656 0.20258994		322.5736 81.68071	341.33212 84.77448	363.73895 92.052895	NM_011251//NM_02916 8.60E-04 NM_001081142//XM_00_0.008913822	-1.21	1.07	1.13 1.13	Rbm6	RNA binding motif protein 6 potassium voltage-gated channel, subfamily Q, member 4	PROCESS II AND
	0.20258994		81.68071 37.467113	84.77448 32.80692	92.052895 41.89809	NM_001081142///XM_00 0.008913822 0.004526713	-1.12 -1.03	1.09	1.13	Kcnq4 4933415J04Rik	potassium voltage-gated channel, subfamily Q, member 4 RIKEN cDNA 4933415J04 gene	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic annotation///0006813 // pot
0.54220176	0.047662996	21.320463	18.656109	19.82612	20.860659	NR_029552 0.007227177	-1.14	1.05	1.12	C78859///Mir138-2	expressed sequence C78859///microRNA 138-2	0042552 // myelination // inferred from direct assay///0071363 // cellular response to growth factor stimulus // inferred from direct assay
	0.030976031			412.5017	426.4249	NM_054078///XM_00651 0.003576975	-1.13	1.03	1.12	Baz2a	bromodomain adjacent to zinc finger domain, 2A	0000183 // chromatin silencing at rDNA // inferred from direct assay///0000183 // chromatin silencing at rDNA // inferred from mutant phenoty
0.92663634 0.4432998		722.4122		615.4656 55.56887	682.63086 63.36831	NM_144916 0.005345917 NM 001168521///NM 17 0.008979903	-1.18	1.11	1.12	Tmem150a	transmembrane protein 150A	0009056 // catabolic process // inferred from electronic annotation///0010506 // regulation of autophagy // not recorded
0.4432998 0.64183736		58.85158 63.74483	56.79175 61.250423	55.56887 63.278877	63.36831 68.30872	NM_001168521///NM_17 0.008979903 NM 130458///XM 00652 0.004144455	-1.04 -1.04	1.14	1.12 1.12	Sarm1 Sp7	sterile alpha and HEAT/Armadillo motif containing 1 Sp7 transcription factor 7	0002376 // immune system process // inferred from electronic annotation///0007165 // signal transduction // inferred from electronic annotatic 0001649 // osteoblast differentiation // inferred from mutant phenotype///0001649 // osteoblast differentiation // not recorded///0006351 // 1
0.08787782	0.3717486	106.0795	97.47567	85.90937	108.51428	NM 001033323///NM 00 0.005339456	-1.09	1.26	1.11	AI414108///iqsf9b	expressed sequence Al414108///immunoglobulin superfamily, m	0007156 // homophilic cell adhesion via plasma membrane adhesion molecules // inferred from direct assay///0097151 // positive regulation of
0.9223647		60.853024		59.93177	65.38903	NM_001162906///XM_00 0.005057425	-1.04	1.09	1.11	2410089E03Rik	RIKEN cDNA 2410089E03 gene	0001736 // establishment of planar polarity // inferred from mutant phenotype///0001822 // kidney development // inferred from mutant phenotype
0.23332675 0.041049983		94.24121 47.09305		89.98954 39.3381	98.02602 43.720306	NM 174877//XM 00650 1.31E-04 NM 009925 0.003118436	-1.07 -1.19	1.09	1.11 1.11	Zar1 Col10a1	zygote arrest 1 collagen, type X, alpha 1	0007275 // multicellular organismal development // inferred from electronic annotation
		142.0818		125.68757	140.44292	NM 001005228//NM 01 0.001181073	-1.19	1.12	1.11	Hira	histone cell cycle regulation defective homolog A (S. cerevisiae)	0001649 // osteoblast differentiation // inferred from genetic interaction///0006336 // DNA replication-independent nucleosome assembly // no
0.040559206	0.55035543	20.591105	16.576937	15.338219	18.34955	NM_010983///XM_00650 0.006804544	-1.24	1.20	1.11	Olfr2	olfactory receptor 2	0007165 // signal transduction // inferred from electronic annotation///0007186 // G-protein coupled receptor signaling pathway // not recorde
	0.049480166 0.001954865		278.07797 4175.985	215.46759 4746.6978	307.74216 4616.7466	NM 146188///XM 00653 0.006559955 NM 001161854///NM 00 0.00215218	-1.06 -1.26	1.43 -1.03	1.11 1.11	Kctd15 Csde1	potassium channel tetramerisation domain containing 15 cold shock domain containing E1, RNA binding	0007275 // multicellular organismal development // inferred from electronic annotation///0051260 // protein homooligomerization // inferred from 0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation///0070966 // nuclear-transcribed mRNA catabolic
0.30/3/34	0.001334003	J204.0270	71,3,303	-,-0.05/0	-520.7400	002101034///HM_0t 0.00215218	-1.20	2.03			COTO STOCK SOMETH CONTRAINING EX, KIPA DINGING	2000222 // 10 Control of Control pulse, provident placed // interior from electronic annotation /// povidence // indicate -transcribed mixiva catabolic

	e) p (Expo	osure) [C	C3H/HeN, Air](raw) [C3H/HeN, O2](raw	Gsr-KO, Air](rav	/) [Gsr-KO, O2](raw	y) RefSeq Transcript ID p (Genotype-Expos	ure) FC in WT (Air	r:O2) FC in KO (Air:	:02) FD (WT 02 vs	KO O2) Gene Symbol	Gene Title	Gene Ontology Biological Process
0.9660949			11.8536 0.339832	271.29834 36.919514	281.71118 34.81693	299.49973 40.713478	NM 173013///XM 00650 0.002610634 NM 026834 9.92E-04	-1.15 -1.09	1.06 1.17	1.10	Map1s Krtap4-6	microtubule-associated protein 1S keratin associated protein 4-6	0000226 // microtubule cytoskeleton organization // inferred from direct assay///0001578 // microtubule bundle formation // not recorded///0
0.65375614			0.339832 88.20566	182.87846	176.93309	201.41908	NM 001038499//XM 01 0.004309912	-1.09	1.17	1.10	Arsi	arylsulfatase i	0008152 // metabolic process // inferred from electronic annotation
0.848567	0.15630	80399 12	20.39157	113.09846	117.759346	124.50309	NM_001122992///NM_0; 0.005040408	-1.06	1.06	1.10	Gmeb1	glucocorticoid modulatory element binding protein 1	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated // infe
0.81556433			8.84968	95.011246	97.553894	103.99177	NM 018780 0.00139039	-1.04	1.07	1.09	Sfrp5	secreted frizzled-related sequence protein 5	0007275 // multicellular organismal development // inferred from electronic annotation///0008285 // negative regulation of cell proliferation //
0.01280324 0.07868072				574.3703 19.075214	602.92554 18.45589	627.2328 20.82927	NM_007901 0.001283399 NM 145368///XM 00653 0.001136254	-1.79 -1.05	1.04	1.09 1.09	S1pr1 Acnat2	sphingosine-1-phosphate receptor 1 acyl-coenzyme A amino acid N-acyltransferase 2	0001525 // angiogenesis // inferred from direct assay///0001955 // blood vessel maturation // inferred from mutant phenotype///0003245 // c 0006629 // lipid metabolic process // inferred from electronic annotation///0006631 // fatty acid metabolic process // inferred from electronic
0.07808072			6.550192	24.917446	23.61244	27.164318	NM 178243//XR 38748: 0.007412531	-1.07	1.15	1.09	Gm38440///Teddm2	predicted gene, 38440//transmembrane epididymal family me	mber 2
0.2841015	0.0012	20769 52		405.39517	443.57333	441.38605	NM 001291059///NM 0(0.001709672	-1.30	1.00	1.09	Elf2	E74-like factor 2	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation ///0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation ///0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation ///0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation ///0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation ///0006355 // regulation of transcription inferred from electronic annotation ///0006355 // regulation of transcription inferred from electronic annotation ///0006355 // regulation of transcription inferred from electronic annotation ///0006355 // regulation of transcription inferred from electronic annotation ///0006355 // regulation of transcription // inferred from electronic annotation ///0006355 // regulation of transcription // inferred from electronic annotation
0.3574519 0.3023052	0.00509	99954 80	00.3792 03.58582	680.4418 378.5644	732.4097 380.14072	740.8121 412.0463	NM_025829 0.002868158 NM 080554///XM 00649 0.003082986	-1.18	1.01	1.09	Eif4e3	eukaryotic translation initiation factor 4E member 3	0006412 // translation // inferred from electronic annotation///0006413 // translational initiation // inferred from electronic annotation///0006
0.4950104		55024 40 55172 72		378.5644 681.27576	659.21136	741.49945	NM_080554//XM_00649 0.003082986 NM 138660 0.00801959	-1.07 -1.06	1.08	1.09	Psmd5 Casc3	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5 cancer susceptibility candidate 3	0043248 // proteasome assembly // inferred from electronic annotation///0070682 // proteasome regulatory particle assembly // not recorded 0000184 // nuclear-transcribed mRNA catabolic process, nonsense-mediated decay // inferred from electronic annotation///0006397 // mRNA process.
0.1251326			353.0845	2049.418	1867.3782	2229.5955	NM 133738 0.008024523	-1.15	1.19	1.09	Antxr2	anthrax toxin receptor 2	0022414 // reproductive process // inferred from mutant phenotype///1901998 // toxin transport // inferred from mutant phenotype
0.07348627			6.67318	14.377981	14.3655405	15.632002	NM_001289499///NM_0(0.008848611	-1.16	1.09	1.09	Adgrf4	adhesion G protein-coupled receptor F4	0007165 // signal transduction // inferred from electronic annotation///0007166 // cell surface receptor signaling pathway // inferred from electronic annotation
0.01473125			3.43518	40.016567	36.25204	43.4585	NM_026286 0.00264062	-1.09	1.20	1.09	Ftmt	ferritin mitochondrial	0006826 // iron ion transport // inferred from electronic annotation///0006879 // cellular iron ion homeostasis // not recorded///0006879 // cellular iron ion homeostasis // not recorded/// not
0.6661933			2.102196	94.14962 73.72451	93.541794 67.02662	102.23636 80.04983	NM_001039669//NM_00 0.009470357 NM 027597//NM 02906 0.00455572	1.02 -1.08	1.09	1.09	Iffo1 Fam71d	intermediate filament family orphan 1 family with sequence similarity 71, member D	
0.05363384				83.13764	77.04298	90.11794	NM 146155//XM 00653 0.003402894	-1.03	1.17	1.09	Ahdc1	AT hook, DNA binding motif, containing 1	
0.53285646	0.17170	70772 58	86.95667	564.1398	542.88727	611.41943	NM_021899 0.008767488	-1.04	1.13	1.08	Foxj2	forkhead box J2	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation ///0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation ///0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation ///0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation ///0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation ///0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation ///0006355 // regulation of transcription // DNA-templated // inferred from electronic annotation // DNA-templated // DNA-template
0.09697203		63058 10		764.56384	784.5656	828.5608	NM_028472 0.006768074	-1.42	1.06	1.08	Bmper	BMP-binding endothelial regulator	0001657 // ureteric bud development // inferred from expression pattern///0002043 // blood vessel endothelial cell proliferation involved in sp
0.03770556				9.889257 1980.404	8.36542 2049.8528	10.71021 2143.7866	NM_183015///XM_01124 0.003687942 NM_001301368///NM_0(_9.62E-04	-1.02 -1.27	1.28	1.08	Cenb3 Cdkn2c	cyclin B3 cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // inferred from electronic annotation///0007049 // cell cycle 0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // not recorded///0000082 // GI/S transition of mitotic cell of
0.05965313				14.342097	12.32475	15.473014	NM_207260///XM_00651 0.00529755	1.02	1.26	1.08	Ankrd34c	ankyrin repeat domain 34C	0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // not recorded///0000062 // G1/s transition of mitotic cell of
	9 0.02284			10.245452	14.448655	11.041299	0.008385799	1.05	-1.31	1.08	D8Ertd575e	DNA segment, Chr 8, ERATO Doi 575, expressed	
0.00195923				27.994698	24.09763	30.161198	NM_001093775///NM_0(4.63E-04	-1.06	1.25	1.08	Myt1I	myelin transcription factor 1-like	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated // infe
0.31317204		3591 12		121.34764	117.36472	130.5487	NM 001293689///NM 17 0.009114787	-1.04	1.11	1.08	Slc6a17		1: 0003333 // amino acid transmembrane transport /////0006810 // transport // inferred from electronic annotation///0006836 // neurotransm
0.03430631 0.03659862		971558 14 85669 33		11.776558 253.24078	12.056695 241.6893	12.66087 271.97943	NM_008777 0.006414984 NM 001115009//NM 15 0.003712319	-1.22 -1.33	1.05 1.13	1.08	Pah Synra	phenylalanine hydroxylase synergin, gamma	0006558 // L-phenylalanine metabolic process // not recorded///0006559 // L-phenylalanine catabolic process // inferred from electronic annot. 0006810 // transport // inferred from electronic annotation///0006897 // endocytosis // inferred from electronic annotation///0015031 // prot
	0.0938			117.68437	241.0893 96.96668	126.038	NM 033567 9.69E-04	1.03	1.13	1.07	Cecr6	cat eye syndrome chromosome region, candidate 6	0000810 // transport // interred from electronic annotation///0008897 // endocytosis // interred from electronic annotation///0015031 // protein
0.01114953	0.00570	704249 78	8.4429	80.22252	63.309254	85.780815	NM 010800//XM 00650 0.003037736	1.02	1.35	1.07	Bhlha15	basic helix-loop-helix family, member a15	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated // tra
0.19397871		8925 15		131.20175	139.97505	139.9449	NM_019950 0.00635217	-1.18	1.00	1.07	Chst5	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 5	0005975 // carbohydrate metabolic process // inferred from electronic annotation///0006044 // N-acetylglucosamine metabolic process // infer
6.16E-04	0.55634		86.07672	326.9245	403.5874	347.55518	NM 194269//XM 00652 0.007923021	1.14	-1.16	1.06	Morn2	MORN repeat containing 2	
0.06707997 4.72E-04	76 0.3436: 0.1614:		17.62371 008.36835	108.08736 985.57465	104.99603 1001.78296	114.51556 1042.8264	NM_026021///NM_1471; 0.009648492 NM_133968///XM_00650_0.005585942	-1.09 -1.02	1.09	1.06	Zmynd19 Snanc2	zinc finger, MYND domain containing 19 small nuclear RNA activating complex, polypeptide 2	0006351 // transcription. DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription. DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription.
0.5848929	0.04693	3181 24	49.08206	250.13692	232.23848	263.91074	NM_024264///XM_00649 0.008359906	1.00	1.14	1.06	Cyp27a1	cytochrome P450, family 27, subfamily a, polypeptide 1	0008203 // cholesterol metabolic process // not recorded///0036378 // calcitriol biosynthetic process from calciol // not recorded///0055114 //
0.01687426	55 0.1851	1177 9.3	.209656	8.440748	8.41108	8.892763	NM_008648///XM_01123 0.001331851	-1.09	1.06	1.05	Mup4	major urinary protein 4	0006112 // energy reserve metabolic process // inferred from sequence or structural similarity///0006810 // transport // inferred from electronic
0.04522990			882.4314	2980.9773	2933.7688	3135.7078	NM_001243008///NM_00 0.007453924	-1.30	1.07	1.05	Col6a3	collagen, type VI, alpha 3	0010951 // negative regulation of endopeptidase activity // inferred from electronic annotation
0.00948331			0.799442 9.05768	29.97391 54.935993	27.757368 52.773865	31.516876 57.75429	NR_046034 0.007820836 NM 001114322///NM 0i 0.001740048	-1.03 -1.08	1.14	1.05 1.05	Slc36a1os Cdhr5	solute carrier family 36 (proton/amino acid symporter), membe cadherin-related family member 5	r 1, opposite strand 0007155 // cell adhesion // not recorded//0007156 // homophilic cell adhesion via plasma membrane adhesion molecules // inferred from elec
0.31260055		32354 21		204.0594	194.82393	213.80855	NM 013581//XM 00653 0.007871569	-1.04	1.10	1.05	Cog1///LOC102641618		ric 0000301 // retrograde transport, vesicle recycling within Golgi // not recorded///0006810 // transport // inferred from electronic annotation///
0.00215529			3.67772	58.288177	70.06932	61.04129	NM_001033240///NM_0C 0.002195059	-1.44	-1.15	1.05	Wfdc6a	WAP four-disulfide core domain 6A	0010466 // negative regulation of peptidase activity // not recorded///0010951 // negative regulation of endopeptidase activity // inferred from
0.00247887		98013 58		58.44567	54.50324	61.202744	NM_001080963 0.002409674	-1.01	1.12	1.05	Plpp4	phospholipid phosphatase 4	0006470 // protein dephosphorylation // inferred from electronic annotation///0006644 // phospholipid metabolic process // not recorded///00
0.05325356 0.00322542			211.9332	820.30225 32.68169	910.3361	857.19507 34.045612	NM_025807///XM_00651 0.005290066	-1.48 -1.10	-1.06	1.04	Slc16a9 Mami2	solute carrier family 16 (monocarboxylic acid transporters), me	m 0006810 // transport // inferred from electronic annotation///0015718 // monocarboxylic acid transport /////0034220 // ion transmembrane
0.00322542 0.07112506		759033 35		32.68169	29.854433 313.30557	34.045612 361.47385	NM_001013813///NM_0(0.004069697 NM_001311087///NM_0(0.001640848	-1.10 -1.02	1.14	1.04	Mami2 Kihdc10	mastermind like 2 (Drosophila) kelch domain containing 10	0007219 // Notch signaling pathway // inferred from sequence or structural similarity///0007219 // Notch signaling pathway // inferred from el
	73 0.28789			2385.698	2157.7024	2483.2341	NM_001276481//NM_00 0.00318391	-1.36	1.15	1.04	Dag1	dystroglycan 1	0002011 // morphogenesis of an epithelial sheet // inferred from mutant phenotype///0006509 // membrane protein ectodomain proteolysis /
	77 0.49170		3.637882	16.198849	18.331953	16.85446	0.008269064	1.19	-1.09	1.04	DXErtd242e	DNA segment, Chr X, ERATO Doi 242, expressed	
	19 0.1518		4.45757	32.358948	27.718523	33.62654	NM_013596///XR_38597! 0.002299439	-1.06	1.21	1.04	Mc5r	melanocortin 5 receptor	0007165 // signal transduction // inferred from electronic annotation///0007186 // G-protein coupled receptor signaling pathway // inferred from
2.82E-04 0.00691600		11737 11	1.8060055 7.81132	11.107412 76.53294	10.400521 80.070465	11.518471 79.10811	NM 001305058//NM 0; 1.32E-04 NM 053261 0.006069575	-1.06 1.13	1.11 -1.01	1.04	Spata19	spermatogenesis associated 19 inositol (myo)-1(or 4)-monophosphatase 2	0007275 // multicellular organismal development // inferred from electronic annotation///0007283 // spermatogenesis // inferred from electro 0006020 // inositol metabolic process // traceable author statement///0006021 // inositol biosynthetic process // inferred from electronic anno
0.00652573			7.81132 09.9736	100.84757	93.15693	103.577866	NM 001164609//NM 00 0.005994563	-1.09	1.11	1.03	Impa2 Smpd4	sphingomyelin phosphodiesterase 4	0006085 // sphingomyelin catabolic process // not recorded///0006085 // sphingomyelin catabolic process // inferred from sequence or structure.
0.00315120				2414.2622	2900.0547	2479.2979	NM 026684 0.008661822	1.05	-1.17	1.03	Ndufb10	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10	0006810 // transport // inferred from electronic annotation///0055114 // oxidation-reduction process // inferred from electronic annotation
0.11026668			76.0358	745.24384	665.63293	763.21606	NM 001114098///NM 17 0.008244759	-1.04	1.15	1.02	Mtcl1	microtubule crosslinking factor 1	0001578 // microtubule bundle formation // inferred from direct assay///0010506 // regulation of autophagy // inferred from electronic annotation
0.01588900				208.59314	189.36949	213.61388	NM_001030306///NM_00 0.004193304	-1.14	1.13	1.02	Fam193a	family with sequence similarity 193, member A	
0.02546469				64.1107 125.18318	63.41889	65.28747 127.43953	NM 170599//XM 00652 0.006957558 NM 001081349//NM 0(0.008336377	1.25 -1.21	1.03	1.02	Iqsf11 SIc43a1	immunoglobulin superfamily, member 11 solute carrier family 43, member 1	0007155 // cell adhesion // inferred from electronic annotation///0040008 // regulation of growth // inferred from electronic annotation 0006810 // transport // inferred from electronic annotation//001580
0.01040030				1069.1632	1000.7835	1086.5745	NM 001164272//NM 17 0.004722597	-1.21	1.09	1.02	Cosf7	cleavage and polyadenylation specific factor 7	0006397 // mRNA processing // inferred from electronic annotation///0051262 // protein tetramerization // not recorded
0.04603104		199676 17		1404.5717	1442.226	1427.3601	NM_010197///XM_00652 0.009466414	-1.23	-1.01	1.02	Fgf1	fibroblast growth factor 1	0001525 // angiogenesis // inferred from electronic annotation///0001759 // organ induction // inferred from direct assay///0001934 // positiv
0.01505160			94.70502	268.93658	239.24835	272.9282	NM 173439 0.004116373	-1.10	1.14	1.01	Fbxo45	F-box protein 45	0001764 // neuron migration // inferred from mutant phenotype///0006974 // cellular response to DNA damage stimulus // not recorded///000
0.00725441		17741 14		145.55875 391.10498	130.4085 391.94247	147.09398 394.95135	NM_001039466///NM_1E 0.005407464 NM 011258///XM 00650 0.009747389	1.00 -1.09	1.13	1.01 1.01	Trim46 Rfc1	tripartite motif-containing 46 replication factor C (activator 1) 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded///0006260 // DNA replication // inferred from
0.02036071		112988 94		700.0069	732.43396	705.4339	NM 001282967//NM 01 0.005971064	-1.34	-1.04	1.01	Elk3	ELK3, member of ETS oncogene family	0001525 // angiogenesis // inferred from mutant phenotype///0006351 // transcription, DNA-templated // inferred from electronic annotation,
	0.1503			2160.1028	2119.829	2155.785	NM_025356///XM_00650 0.002261581	-1.09	1.02	-1.00	Ube2d3	ubiquitin-conjugating enzyme E2D 3	0000209 // protein polyubiquitination // not recorded///0006281 // DNA repair // inferred from electronic annotation///0006511 // ubiquitin-d
	64 0.59650		728.2175	2453.692	2210.798	2444.296	NM_001198859///NM_0C 0.009438206	-1.11	1.11	-1.00	Ctbp1	C-terminal binding protein 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype///0000122 // negative regulation
0.00469338		134868 28		349.1069	346.42804 729.2377	346.8006	NM_028448///XM_00653 0.005394633	1.22	1.00	-1.01	Cenpv	centromere protein V	0001667 // ameboidal-type cell migration // not recorded///0007049 // cell cycle // inferred from electronic annotation///0007067 // mitotic n
	18 0.2368 34 0.6196		53.87537 10.9478	771.7917 462.88144	729.2377 395.21826	766.36414 457.75577	NM_007555 0.0057721 NM_139311///XM_00653 0.009106273	-1.11 -1.10	1.05 1.16	-1.01 -1.01	Bmp5 Mllt6	bone morphogenetic protein 5 myeloid/lymphoid or mixed-lineage leukemia (trithorax homolo	0001501 // skeletal system development // inferred from mutant phenotype///0001503 // ossification // inferred from electronic annotation/// g, Drosophila); translocated to, 6
	0.2257		9.97545	21.27163	23.113716	20.93768	NM 023048 0.006746996	1.06	-1.10	-1.02	Asb4	ankyrin repeat and SOCS box-containing 4	0016567 // protein ubiquitination // inferred from electronic annotation//0016567 // protein ubiquitination // inferred from direct assay///00
	97 0.7974		129.99	5532.0796	6043.648	5437.1147	NM_019766///XM_00654 7.27E-05	1.08	-1.11	-1.02	LOC102641464///Ptges3	prostaglandin E synthase 3///prostaglandin E synthase 3 (cytos	oli 0001516 // prostaglandin biosynthetic process // inferred from mutant phenotype///0001516 // prostaglandin biosynthetic process // not record
0.22935818			3.379087	13.981436	15.521217	13.733013	NM_026256///NM_02761 0.007059423	1.05	-1.13	-1.02	Poteg	POTE ankyrin domain family, member G	
0.00105980 0.00536731		09109 81 889694 84		602.78564 791.4012	562.7438 655.079	591.48413 776.13275	NM_001313977//NM_0(0.00110689 NM_001286630//NM_0; 0.005097861	-1.36 -1.06	1.05	-1.02 -1.02	Prkch Brd4	protein kinase C, eta	0006468 // protein phosphorylation // not recorded///0010744 // positive regulation of macrophage derived foam cell differentiation // inferre
0.00536731 0.00253122				791.4012 151.04512	655.079 134.0023	776.13275 148.04895	NM_001286630///NM_0; 0.005097861 NM_001304965///NM_0; 0.009570044	-1.06 -1.04	1.18	-1.02 -1.02	Brd4 Pou6f1	bromodomain containing 4	0000083 // regulation of transcription involved in G1/S transition of mitotic cell cycle // not recorded///0001833 // inner cell mass cell prolifera
0.00233122												POU domain class 6 transcription factor 1	0006351 // transcription_DNA-templated // inferred from electronic apportation ///0006355 // regulation of transcription_DNA-templated // inferred from electronic apportation ///0006355 // regulation of transcription_DNA-templated // inferred from electronic apportation ///0006355 // regulation of transcription_DNA-templated // inferred from electronic apportation ///0006355 // regulation of transcription_DNA-templated // inferred from electronic apportation ///0006355 // regulation of transcription_DNA-templated // inferred from electronic apportation_DNA-templated // inferred fro
0.00789343	0.84404	397 39	56.66724 95.74374	297.45526	222.1195	291.49307	NM 008317///NM 01975 0.009533374	-1.33	1.31	-1.02	Hyal1///Nat6	POU domain, class 6, transcription factor 1 hyaluronoglucosaminidase 1///N-acetyltransferase 6	0000302 // response to reactive oxygen species // not recorded///0005975 // carbohydrate metabolic process // inferred from electronic annot.
0.00222619	0.84404	0497 39 16893 61	95.74374 10.40424	649.19037	695.1485	634.8921	NM 008317///NM 01975 0.009533374 NM_026308 0.001724925	-1.33 1.06	1.31 -1.09	-1.02 -1.02	Hyal1///Nat6 Rpp21	hyaluronoglucosaminidase 1///N-acetyltransferase 6 ribonuclease P 21 subunit	0000302 // response to reactive oxygen species // not recorded///0005975 // carbohydrate metabolic process // inferred from electronic annotation///0090501 // RNA processing // not recorded///0042493 // response to drug // inferred from electronic annotation///0090501 // RNA phosphod
0.00222619 0.00345232	0.84404 0.30644 22 0.03354	0497 39 16893 61 50567 27	95.74374 10.40424 721.9685	649.19037 2034.5537	695.1485 1930.0481	634.8921 1982.3739	NM 008317//NM 0197: 0.009533374 NM_026308 0.001724925 NM 001164572//NM 1: 0.008320594	-1.33 1.06 -1.34	1.31 -1.09 1.03	-1.02 -1.02 -1.03	Hyal1//Nat6 Rpp21 Snrk	hyaluronoglucosaminidase 1///N-acetyltransferase 6 ribonuclease P 21 subunit SNF related kinase	0000302 // response to reactive oxygen species // not recorded///0005975 // carbohydrate metabolic process // inferred from electronic annot. 0008033 // tRNA processing // not recorded///0042493 // response to drug // inferred from electronic annotation///0090501 // RNA phosphod
0.00222619 0.00345232 0.09677315	0.84404 0.30640 22 0.03350 0.1962	0497 39 16893 61 50567 27 21791 26	95.74374 10.40424 721.9685 6.14927	649.19037 2034.5537 28.889297	695.1485 1930.0481 33.634277	634.8921 1982.3739 28.103666	NM 008317///NM 0197: 0.009533374 NM_026308 0.001724925 NM 001164572///NM 1: 0.008320594 NR_027799 0.006529678	-1.33 1.06 -1.34 1.10	1.31 -1.09 1.03 -1.20	-1.02 -1.02 -1.03 -1.03	Hya11///Nat6 Rpp21 Snrk Tbrg3	hyaluronoglucosaminidase 1///N-acetyltransferase 6 ribonuclease P 21 subunit SNF related kinase transforming growth factor beta regulated gene 3	0000302 // response to reactive oxygen species // not recorded///0005975 // carbohydrate metabolic process // inferred from electronic annot. 0008033 // tRNA processing // not recorded///0042493 // response to drug // inferred from electronic annotation///0090501 // RNA phosphod
0.00222619 0.00345232 0.09677315 6.98E-04	0.84404 0.30644 22 0.03354 0.1962: 0.97234	0497 39 16893 61 50567 27 21791 26 8012 28	95.74374 10.40424 721.9685 6.14927 85.37033	649.19037 2034.5537 28.889297 276.36328	695.1485 1930.0481 33.634277 251.56847	634.8921 1982.3739 28.103666 268.67432	NM 008317//NM 0197: 0.009533374 NM_026308 0.001724925 NM 001164572//NM 1: 0.008320594 NR_027799 0.006529678 NM 028447//XM 00652 0.003934787	-1.33 1.06 -1.34 1.10 -1.03	1.31 -1.09 1.03 -1.20 1.07	-1.02 -1.02 -1.03 -1.03	Hydi1///Nat6 Rpp21 Snrk Tbrg3 Prrc1	hyaluronoglucosaminidase 1//N-acetyltransferase 6 ribonuclease P 21 subunit SNF related kinase transforming growth factor beta regulated gene 3 proline-rich coiled-coil 1	0000302 // reponse to reactive exques species / not recorded//10005757 // carbohydate metabolic process // inferred from electronic annotation //0008033 // 18NA processing // not recorded//0042493 // reponse to drug // inferred from electronic annotation//00090501 // 8NAA phosphodo
0.00222619 0.00345232 0.09677315 6.98E-04 0.94456345	8 0.84404 9 0.30644 22 0.03354 6 0.1962 0.97234 6 0.00774	0497 39 16893 61 50567 27 21791 26 8012 28 741772 35	95.74374 10.40424 721.9685 6.14927 85.37033 5.00311	649.19037 2034.5537 28.889297	695.1485 1930.0481 33.634277	634.8921 1982.3739 28.103666	NM 008317///NM 0197: 0.009533374 NM 026308 0.001724925 NM 001164572//NM 1: 0.008320594 NR_027799 NM 00652 0.006529678 NM 028447//XM 00652 0.003934787 NM_010213///XM_00650 0.009358832 NM 019729 0.005424981	-1.33 1.06 -1.34 1.10	1.31 -1.09 1.03 -1.20	-1.02 -1.02 -1.03 -1.03	Hya11///Nat6 Rpp21 Snrk Tbrg3	hyaluronoglucosaminidase 1///N-acetyltransferase 6 ribonuclease P 21 subunit SNF related kinase transforming growth factor beta regulated gene 3	0006313 / Iranscription, DNA-templated / Inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated / Inferred from electronic annotation/opension for transcription, DNA-templated / Inferred from electronic annotation/opens
0.00222619 0.00345232 0.09677315 6.98E-04 0.94456345 0.00223183 0.00838929	8 0.84404 9 0.30640 22 0.03350 5 0.1962: 0.97230 6 0.00774 34 0.12379 94 0.9158	0497 39 16893 61 50567 27 21791 26 3012 28 741772 35 79128 74 3313 27	95.74374 10.40424 721.9685 6.14927 85.37033 5.00311 442.302 70.7018	649.19037 2034.5537 28.889297 276.36328 35.442886 5272.0146 323.78555	695.1485 1930.0481 33.634277 251.56847 39.242416 4567.4497 366.2005	634.8921 1982.3739 28.103666 268.67432 34.403652 5094.78 312.59354	NM 008317//NM 01975 0.009533374 NM_026308 0.001724925 NM 001164572//NM 15 0.008320594 NR 027799 0.006529678 NM 028447//NM 00652 0.009358832 NM 010929 0.005424981 NM 007929 0.005424981	-1.33 1.06 -1.34 1.10 -1.03 1.01 -1.41 1.20	1.31 -1.09 1.03 -1.20 1.07 -1.14 1.12 -1.17	-1.02 -1.02 -1.03 -1.03 -1.03 -1.03 -1.03	Hyal1///Nat6 Rpp21 Snrk Tbrg3 Prrc1 Fh13 Emp2 Timmdc1	hyalurongukosamindase 1//N-acetyltranderase 6 ribonuclases P1 subunit SIF related kinsse trandoming growth factor beta regulated gene 3 proline-rich collect-coll 1 four and a half UM domains 2 epithelial membrane protein 2 trandozase of inner mitochondriál membrane domain containi	0000302 // response to reactive exques species // nor recorded///0005975 // carbohydrate metabolic process // inferred from electronic annotation//000305 // NRAP shoopshord 00006488 // protein phosphonylation // not recorded///0016310 // phosphonylation // inferred from electronic annotation//000305 // NRAP shoopshord 00006488 // protein phosphonylation // not recorded///0016310 // phosphonylation // inferred from electronic annotation///00035556 // intracell 0000006488 // actin cytoskeleton organization // inferred from direct assay // 0001767 // membrane raft assembly // inferred from direct assay // 0001767 // membrane raft assembly // inferred from direct assay // 0001767 // membrane raft assembly // inferred from direct assay // 0001767 // membrane raft assembly // inferred from direct assay // 0001767 // membrane raft assembly // inferred from direct assay // 0001767 // membrane raft assembly // inferred from direct assay // 0001767 // membrane raft assembly // inferred from direct assay // 0001767 // membrane raft assembly // inferred from direct assay // 0001767 // membrane raft assembly // inferred from direct assay // 0001767 // membrane raft assembly // inferred from direct assay // 0001767 // membrane raft assembly // inferred from direct assay // 0001767 // membrane raft assembly // inferred from direct assay // 0001767 // membrane raft assembly // inferred from direct assay // 0001767 // membrane raft assembly // inferred from direct assay // 0001767 // membrane raft assembly // inferred from direct assay // 0001767 // membrane raft assembly // inferred from direct assay // 0001767 // membrane raft assembly // inferred from direct assay // 0001767 // membrane raft assembly // inferred from direct assay // 0001767 // membrane raft assembly // inferred from direct assay // 0001767 // membrane raft assembly // inferred from direct assay // 0001767 // 0001767 // 0001767 // 0001767 // 0001767 // 0001767 // 0001767 // 0001767 // 0001767 // 0001767 // 0001767 // 0001767 // 0001767 // 0001767 // 0001767 /
0.00222619 0.00345232 0.09677315 6.98E-04 0.94456345 0.00223183 0.00838929 0.05075565	3 0.84404 9 0.30644 22 0.03356 5 0.1962: 0.97236 5 0.00774 34 0.12379 94 0.9158: 54 2.91E-0	0497 39 16893 61 160567 27 11791 26 1012 28 1741772 35 179128 74 18313 27 104 51	95.74374 10.40424 721.9685 6.14927 85.37033 5.00311 442.302 70.7018 1.08518	649.19037 2034.5537 28.889297 276.36328 35.442886 5272.0146 323.78555 47.711773	695.1485 1930.0481 33.634277 251.56847 39.242416 4567.4497 366.2005 70.8504	634.8921 1982.3739 28.103666 268.67432 34.403652 5094.78 312.59354 46.041767	NM 008317//NM 01977 0.009533374 NM 008317//NM 01977 0.009533374 NM 001164572//NM 1: 0.00820598 NR 027799	-1.33 1.06 -1.34 1.10 -1.03 1.01 -1.41 1.20 -1.07	1.31 -1.09 1.03 -1.20 1.07 -1.14 1.12 -1.17 -1.54	-1.02 -1.02 -1.03 -1.03 -1.03 -1.03 -1.03 -1.04 -1.04	Hyal1///Nat6 Rpp21 Snrk Tbrg3 Prrc1 Fhl3 Emp2 Timmdc1 Cnqo2	haluuronalucoaminidase 1//N-acetyltranderase 6 ribonuclases 2-1 subumit SF related tinase transforming growth factor beta regulated gene 3 profine-rich collect-coil 1 four and a half LIM domains 3 eothelial membrane protein 9 translocase of inner mitochondrial membrane domain containiry cyclic nucleotide gated chamen alapha 2	0000302 // response to reactive exques species // not recorded//1000597 // cathohydate metabolic process // inferred from electronic annotation/0005031 // 1884 posspoked 00006468 // protein phosphorylation // not recorded//70016310 // phosphorylation // inferred from electronic annotation/10005031 // 1884 phosphorylation // not recorded//70016310 // phosphorylation // inferred from electronic annotation/1/003556 // instruced 00006468 // protein phosphorylation // not recorded//70016310 // phosphorylation // inferred from electronic annotation///0035556 // instruced 00000764 // actin cytoskeleton organization // inferred from direct assay // 0001765 // membrane raft assembly // inferred from direct assay // 0001765 // membrane raft assembly // inferred from direct assay // 0001765 // membrane raft assembly // inferred from direct assay // 0001765
0.00222619 0.00345232 0.09677315 6.98E-04 0.94456345 0.00223183 0.00838929 0.05075565 0.00129835	3 0.84404 9 0.30644 12 0.03356 15 0.1962: 16 0.097236 17 0.00774 18 0.12379 19 0.91583 19 0.91583 10 0.91583	0497 39 16893 61 160567 27 121791 26 13012 28 141772 35 19128 74 13313 27 104 51 113117 13	95.74374 10.40424 721.9685 6.14927 85.37033 5.00311 442.302 70.7018 1.08518 367.6346	649.19037 2034.5537 28.889297 276.36328 35.442886 5272.0146 323.78555 47.711773 1145.2308	695.1485 1930.0481 33.634277 251.56847 39.242416 4567.4497 366.2005 70.8504 1092.1595	634.8921 1982.3739 28.103666 268.67432 34.403652 5094.78 312.59354 46.041767 1104.2035	NM 008317//NM 0197 0.009533374 NM 008117/NM 0197 0.009533374 NM 001164572//NM 10.008320594 NM 002799 0.005529678 NM 0284471//NM 00552 0.003943787 NM 007929 0.005424981 NM 007929 0.005424981 NM 007724//NM 00552 0.003428325 NM 007724//NM 00552 0.003428325 NM 007724//NM 00552 0.00345837	-1.33 1.06 -1.34 1.10 -1.03 1.01 -1.41 1.20 -1.07 -1.19	1.31 -1.09 1.03 -1.20 1.07 -1.14 1.12 -1.17 -1.54	-1.02 -1.02 -1.03 -1.03 -1.03 -1.03 -1.03 -1.04 -1.04	Hyaf1//Nat6 Rpp21 Snrk Tbrg3 PrrC1 FhB Emp2 Timmdc1 Cng02 Rnf14da	hyaluronajkucosamindase 1//N-acetyltranderase 6 ribonuclases P21 subunit SSF related kinsuse trandoming growth factor beta regulated gene 3 proline-rich collect-coll 1 four and a half UM domains 3 epithelial membrane protein 2 trandouses of inner mitochondrial membrane domain containit cyclic nucleotide gated channel alpha 2 ring finger protein 144A.	0000302 // reaponse to reactive exygen species // not recorded///0000597 // carbohydrate metabolic process // inferred from electronic annotation//0000501 // NRAP shoopshod 00006333 // ISBAN processing // not recorded///0016310 // phosphonylation // inferred from electronic annotation//000305 // NRAP shoopshod 00064688 // protein phosphonylation // not recorded///0016310 // phosphonylation // inferred from electronic annotation///0035556 // intracel 0030376 // actin cytokeleton organization // inferred from direct assay 0001765 // membrane raft assembly // inferred from direct assay // 0001765 // membrane raft assembly // inferred from direct assay // 0001765 // membrane raft assembly // inferred from direct assay // 0001765 // membrane raft assembly // inferred from direct assay // 0001765 // inferred from directronic annotation/// 003500000000000000000000000000000000
0.00222619 0.00345232 0.09677315 6.98E-04 0.94456345 0.00223183 0.00838929 0.05075565 0.00129835	3 0.84404 9 0.30644 12 0.03356 15 0.1962: 16 0.00774 17 0.9158: 18 0.0074: 18 0.1237! 18 0.9158: 18 0.9158: 18 0.0074: 19 0.0121:	0497 39 16893 61 160567 27 121791 26 13012 28 141772 35 19128 74 13313 27 104 51 113117 13	95.74374 10.40424 721.9685 6.14927 85.37033 5.00311 442.302 70.7018 1.08518 367.6346 259.2003	649.19037 2034.5537 28.889297 276.36328 35.442886 5272.0146 323.78555 47.711773	695.1485 1930.0481 33.634277 251.56847 39.242416 4567.4497 366.2005 70.8504	634.8921 1982.3739 28.103666 268.67432 34.403652 5094.78 312.59354 46.041767	NM 008317//NM 0197: 000933374 NM 025308 0.00172925 NM 001146572//NM 1 0.008230594 NM 012467//NM 00552 000333678 NM 028471//NM 00552 0003338787 NM 0102131//NM 00552 0003338787 NM 0724731//NM 00552 0003428357 NM 0724731//NM 00552 000342837 NM 0724731/NM 00552 000342837 NM 0724731/NM 00552 0003475577 NM 0010819771/NM 0100537098	-1.33 1.06 -1.34 1.10 -1.03 1.01 -1.41 1.20 -1.07	1.31 -1.09 1.03 -1.20 1.07 -1.14 1.12 -1.17 -1.54	-1.02 -1.02 -1.03 -1.03 -1.03 -1.03 -1.03 -1.04 -1.04	Hyal1///Nat6 Rpp21 Snrk Tbrg3 Prrc1 Fhl3 Emp2 Timmdc1 Cnqo2	helauronaph.coaminidase 1//N-acetyltranderase 6 ribonuclases P1 subunit SNF related kinase trandoming growth factor beta regulated gene 3 proline-rich collect-coll 1 four and a half this demans 3 trandocase of inner mitochondrial membrane domain contains cyclin cucleotide gated channel alpha 2 ring finger protein 144A. Kruppel-like factor 11	0000302 // response to reactive exques species // not recorded//1000597 // cathohydate metabolic process // inferred from electronic annotation/0005031 // 1884 posspoked 00006468 // protein phosphorylation // not recorded//70016310 // phosphorylation // inferred from electronic annotation/10005031 // 1884 phosphorylation // not recorded//70016310 // phosphorylation // inferred from electronic annotation/1/003556 // instruced 00006468 // protein phosphorylation // not recorded//70016310 // phosphorylation // inferred from electronic annotation///0035556 // instruced 00000764 // actin cytoskeleton organization // inferred from direct assay // 0001765 // membrane raft assembly // inferred from direct assay // 0001765 // membrane raft assembly // inferred from direct assay // 0001765 // membrane raft assembly // inferred from direct assay // 0001765
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.00222619 .00345232 .09677315 .98E-04 .94456345 .00223183 .00838929 .05075565 .00129835 .00587357 .94E-04 .42E-05 .33E-04 .64E-05 .19652016 .04219629 .11604464	8 0.84404 9 0.306448 5 0.1962 0.09723 0.00774 44 0.1237 44 0.9158 45 2.916-0 55 0.0074 9 0.0121 0.11819 0.1591 0.1592 0.5915 5 0.80851 1 0.08891 1 0.08891	0497 39 16893 61 1690567 27 1791 26 18012 28 1841772 35 19128 74 183313 27 18413117 13 174163 12 199114 29 19914 29 199956 37 166805 65 18266 15 196221 10 197312 96 195554 65	95.74374 10.40424 721.9685 6.14927 85.37033 5.00311 442.302 70.7018 1.08518 367.6346 159.2003 96.84476 5.229904 77.6963 50.3084 5.460045 0.013593 68.47174 56.559503	649.19037 2034.5537 276.36328 35.442886 5272.0146 323.78555 47.711773 1145.2308 804.66504 264.96505 95.400215 315.73477 596.51166 18.032099 10.964676	695.1485 1930.0481 33.634277 251.56847 39.242416 4567.4497 366.2005 70.8504 1092.1595 758.28534 238.76695 85.62417 270.7512 532.7627 19.240032 12.281892	634.8921 1982.3739 28.103666 268.67432 34.403652 5094.78 312.59354 46.041767 1104.2035 775.3405 255.03049 91.635345 303.12955 572.6741 17.299839 10.511552 1055.6401 422.91534	NM 008317//NM 0197' 0.00533374 NM 001817/0.00533374 NM 001164572//NM 11 0.00532054 NM 001164572//NM 11 0.00532054 NM 0238471//NM 00551 0.005342691 NM 0284471/NM 00551 0.005342891 NM 07939	-1.33 1.06 -1.34 1.10 -1.03 1.01 -1.41 1.20 -1.07 -1.19 -1.56 -1.12 1.00 -1.20 -1.09 -1.17 1.09 1.14	1.31 -1.09 1.03 -1.20 1.07 -1.14 1.12 -1.17 -1.54 1.01 1.02 1.07 1.07 1.17 -1.17	-1.02 -1.02 -1.03 -1.03 -1.03 -1.03 -1.03 -1.04 -1.05	Hwall//Net6 Rpg21 Sonk Thrg3 Prv1 Frw1 Frm2 Timmdc1 Croin2 Rff1460 Rff147 Rff2 Frw2 Frdm1 Akap13 Igf1ix Gm7173	helauronaghucosamindase 1//N-acetyltranderase 6 ribonuclases P.1 subunit SNF related kinase trandoming growth factor beta regulated gene 3 proline-rich collect-coll 1 four and a half till 4 domains 3 epithelial membrane potein 2 trandocase of inner mitochonorial membrane domain containit cyclic nucleotide gated channel alpha 2 mg finege protein 144A Nousel-like factor 11 againtig enzyme 12 binding protein homo hypermethylated in curacre 2 PR domain containing 1, with ZNF domain A kinase (PRA) anohor protein 3 insulin-like growth factor 1 in insulin-like growth factor 1, intronic transcript predicted gene 7/13 guanosine diphosphate (GDP) dissociation inhibitor 1 serie (or cyclerice) perdiates inhibitor, dade A, member 3N serie (or cyclerice) perdiates inhibitor, dade A, member 3N serie (or cyclerice) perdiates inhibitor, dade A, member 3N serie (or cyclerice) perdiates inhibitor, dade A, member 3N serie (or cyclerice) perdiates inhibitor, dade A, member 3N series (or cyclerice) perdiates inhibitor, dade A, member 3N series (or cyclerice) perdiates inhibitor, dade A, member 3N series (or cyclerice) perdiates inhibitor, dade A, member 3N series (or cyclerice) perdiates inhibitor, dade A, member 3N series (or cyclerice) perdiates inhibitor.	0000302 // response to reactive exques species // nor recorded//0002957 // carbohydrate metabolic process // Inferred from electronic amount of the processing // nar recorded//0002498 // protein phosphorylation // not recorded//0016310 // phosphorylation // inferred from electronic annotation//000305 // RNA phosphorylation // not recorded//0016310 // phosphorylation // inferred from electronic annotation//0035556 // intrace 0000376 // membrane raft assembly // inferred from direct assay//0001765 // membrane raft assembly // inferred from direct assay///0001763 // membrane raft assembly // inferred from direct assay///0001763 // inferred from electronic annotation//0003501 // inferred from electronic annotation//0003511 // inferred from electronic annotation//0003611 // inferred from electronic annotation//0003611 // inferred from electronic annotation//0003611 // inferred from electronic annotation///0003611 // inferred f
0.00222619 0.00345232 0.09677315 6.98E-04 0.94456345 0.00223183 0.003838929 0.05075565 0.00129835 0.00587357 0.94E-04 0.42E-05 0.33E-04 0.64E-05 0.19652016 0.04219629 0.11604464 0.00582774 0.00582774	8 0.84404 9 0.30644 5 0.1962; 0.97236 5 0.97236 5 0.0774; 84 0.1237; 84 0.9158; 64 2.916-0 0.1181; 0.9361; 0.1599; 0.59156 0.0058; 3 0.80856 1 0.0058; 3 0.30849;	0497 39 16893 61 16893 61 169012 28 16912 28 179128 74 179128 74 179128 74 179128 74 179128 74 179128 74 179129 79 179129 37 179129 37 17912	95.74374 10.40424 10.10.40424 10.10.40424 10.10.40424 10.10.40424 10.10.40427 10.10.85.37033 10.00311 10.442.302 10.7018 10.8518 367.6346 10.9518 367.6346 10.9518 10.75.9904 10.75.9904 10.10.9593 10.3084 10.450045 10.013593 10.47174 10.55.59503 10.481.12473	649.19037 2034.5537 228.889297 276.36328 35.442886 5272.0146 223.78555 47.711773 1145.2308 804.66504 264.96585 95.400215 315.73477 996.51166 18.032099 10.964676 1102.4196 443.1589	695.1485 1930.0481 33.634277 251.56847 39.242416 4567.4497 366.2005 70.8504 1092.1595 758.28534 238.76695 85.62417 270.7512 532.7627 19.240032 12.281892 1049.8877 334.79 485.6149	634,8921 1982,3739 28.103666 268,67432 34.403652 5094,78 312.59354 46.041767 1104.2035 775.3405 255.03049 91.635345 303.12955 572.6741 17.299839 10.511552 1055.6401 422.91534 464.42245	NM 008317//NM 0197' 0.005333374 MM 008317//NM 110.00533054 MM 00116572//NM 110.00532054 MM 00116572//NM 110.00532054 MM 002467//NM 10052 0.00532678 MM 028467//NM 00652 0.00338387 MM 02734//NM 00652 0.00338387 MM 02734//NM 00652 0.00338387 MM 02734//NM 00652 0.00348387 MM 02734//NM 00652 0.00342837 MM 02734//NM 00652 0.00342837 MM 02734//NM 00652 0.00342837 MM 02734//NM 00652 0.003756139 MM 12837 0.007756139 MM 12837 0.007756139 MM 12837 0.007576139 MM 12837 0.007576139 MM 12837 0.007576139 MM 028321//NM 00654 2.006743132 MM 028321//NM 00654 2.00674313 MM 028321//NM 00654 2.00674313 MM 028321//NM 00654 2.00674313 MM 028321//NM 00654 0.00674313 MM 028321//NM 00654 0.006743134 MM 028321//NM 00654 0.006743134	-1.33 1.06 -1.34 1.10 -1.03 1.01 -1.41 1.20 -1.07 -1.19 -1.56 -1.12 1.00 -1.20 -1.09 1.17 1.09 1.14 1.48 1.42	1.31 1.09 1.03 -1.20 1.07 -1.14 1.12 -1.17 -1.54 1.01 1.02 1.07 1.07 1.12 1.07 1.11 -1.11 -1.11 -1.11 -1.11 -1.11 -1.15	-1.02 -1.02 -1.03 -1.03 -1.03 -1.03 -1.03 -1.04 -1.05	Hwall//Net6 Rpp21 Snrk Thrp3 Prrc1 FNB Emp2 Timmdc1 Crone2 Rnf1440 Klf11 Arhil/fm20199 HkG Prdm1 Akop13 Igfitt Gm7173 Gdf1 Serpina0n Kdm60	helauronaghucosaminidase 1//N-acetyltranderase 6 ribonuclases P1 subunit SNF related kinsuse trandoming growth factor beta regulated gene 3 proline-rich collect-coll 3 proline-rich collect-colle	0000303 // response to reactive exques species // not recorded//1000375 // carbohydrate metabolic process // inferred from electronic amotosion/0003031 // stills species/ii/ not recorded//10003631 // shopshon/dation // inferred from electronic amotosion/1000305 // shopshon/dation // inferred from electronic amotosion/1000305 // shopshon/dation // inferred from electronic amotosion/100035556 // intrace 0000365 // actin cytoskelecton organization // inferred from direct assay// 0001765 // membrane raft assembly // inferred from direct assay// 0001765 // membrane raft assembly // inferred from direct assay// 0001765 // membrane raft assembly // inferred from direct assay// 0001765 // membrane raft assembly // inferred from direct assay// 0001765 // membrane raft assembly // inferred from direct assay/// 0000000000000000000000000000000000
.00222619 .00345232 .09677315 .998-04 .94456345 .00223183 .00838929 .05075565 .00129835 .00587357 .94E-04 .42E-05 .33E-04 .64E-05 .11660466 .04219629 .11604464 .00582774 .002138473 .02138473	8 0.84404 9 0.30644 2 0.03365 5 0.1962; 0.9723 6 0.0077, 84 0.1237, 94 0.9158; 44 0.9158; 45 0.0071, 0.1181; 0.9361; 0.1999; 0.5915; 0.0805; 92 0.0889; 94 0.0058; 94 0.0058; 95 0.0058; 96 0.0058; 97 0.0058; 98 0.0058; 98 0.0058; 98 0.0058; 99 0.0058; 90 0.0058; 90 0.0058; 90 0.0058; 91 0.0	0497 39 16893 61 16893 61 16893 61 16893 61 171791 26 171791 27 171791	95.74374 10.40424 771.9685 6.14927 85.37033 5.00311 442.302 70.7018 1.08518 367.6346 259.2003 6.84476 5.229904 77.6963 50.3084 5.460045 0.013593 68.47174 56.59503 43.12473 13.4429	649 19037 2024 5337 28.889297 276.6328 55.442885 5272.0146 323.78555 47.711773 1145.2308 80.4.65504 56.905585 95.400215 315.73477 596.51166 18.032099 10.964676 1102.4196 443.1189 487.0162	695.1485 1930.0481 33.634277 251.56847 39.242416 4567.4497 366.2005 70.8504 1092.1595 758.28534 238.76695 85.62417 270.7512 532.7627 19.240032 12.281892 1049.8877 334.79 485.6149 949.09674	634.8921 1982.3739 28.103666 268.67432 34.403652 5094.78 312.59354 46.041767 1104.2035 775.3405 255.03049 91.635345 303.1295 572.6741 17.299839 10.511552 1055.6401 422.91534 464.42245 818.8622	NM 008317//NM 0197' 0.00933374 MM 008317//NM 110 0.00933374 MM 001164572//NM 11 0.008320594 MM 001164572//NM 11 0.008320594 MM 0238471//NM 0.0051 0.00334787 MM 024271/MM 0.0051 0.00334787 MM 0.003734//NM 0.0051 0.003348237 MM 0.07939 0.00542981 MM 0.003724//NM 0.0051 0.003245237 MM 0.079374//NM 0.0051 0.003245237 MM 0.079374//NM 0.0051 0.00324527 MM 0.003937/MM 0.0051 0.00324527 MM 0.079348//NM 0.0051 0.00324527 MM 0.079348//NM 0.0051 0.00324527 MM 0.079348//NM 0.0051 0.00034529 MM 0.003937/MM 0.0051 0.00034529 MM 0.003937/MM 0.0051 0.00034529 MM 0.003937/MM 0.0051 0.0003459 MM 0.003937/MM 0.0051 0.0003459 MM 0.00331031444//MM 0.0051 0.00739345	-1.33 -1.34 -1.10 -1.03 -1.03 -1.01 -1.44 -1.20 -1.07 -1.19 -1.56 -1.12 -1.00 -1.20 -1.09 -1.17 -1.09 -1.14 -1.48 -1.48 -1.42 -1.06	1.31 -1.09 1.03 -1.20 1.07 -1.14 1.12 -1.17 -1.54 1.01 1.07 1.07 1.07 1.17 1.07 1.11 1.07 -1.11 1.17 1.01 1.05 -1.16	-1.02 -1.02 -1.03 -1.03 -1.03 -1.03 -1.03 -1.04 -1.04 -1.04 -1.04 -1.04 -1.04 -1.04 -1.04 -1.04 -1.04 -1.04 -1.04 -1.04 -1.05 -1.05 -1.05	Hwall / / Nea	helauronaghucosamindase 1//N-acetyltranderase 6 ribonuclases P.1 subunit SNF related kinase trandoming growth factor beta regulated gene 3 proline-rich collect-coll 1 four and a half UM domains 3 epithelial membrane protein 2 trandocase of inner mitochondorial membrane domain containit cyclic nucleotide gated channel alpha 2 randocase of inner mitochondorial membrane domain containit cyclic nucleotide gated channel alpha 2 randocase protein ta4An Kuupel-like factor 11 auriden Wedglicht conjugating enzyme E2 binding protein homo ariden in the containing 1, with ZNF domain containing 1, with ZNF domain a familie provide factor 13 insulin-like growth factor 1, intronic transcript predicted gene 7173 guanosine diphosphate (GIP) dissociation inhibitor 1 serie (or cyteriole peptidase inhibitor, dale A, member 3N lysine (X)-specific demethylase 6A hydroxyag (butathone hydrosae	0000303 // response to reactive exques species // not recorded//1000575 // carbohydrate metabolic process // inferred from electronic amount of the processing // not recorded//1000476 // response to drug // inferred from electronic amountation//1000505 // Rhay hospiday 0000533 // fishing processing // not recorded///0016310 // phosphorylation // inferred from electronic amountation///0003555 // intrace 0000535 // actin cytoskeleton organization // inferred from direct assay 0001765 // membrane raft assembly // inferred from direct assay // // 0001765 // membrane raft assembly // inferred from direct assay // // 0001765 // membrane raft assembly // inferred from direct assay // 0001765 // membrane raft assembly // inferred from direct assay // 0001765 // membrane raft assembly // inferred from direct assay // 0000000000000000000000000000000000
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0.00222619 0.00345322 0.09677315 0.98E-04 0.94456345 0.00223183 0.00838929 0.05075565 0.00129835 0.00129835 0.00587357 0.005075565 0.00129835 0.00587357 0.04219629 0.11604464 0.00582774 0.00582774 0.02138473 0	8 0.8440.0 9 0.30644 22 0.03356 5 0.1962: 0.9723 6 0.0077. 844 0.9158: 0.0737. 945 0.9121: 0.1181: 0.9361: 0.9361: 0.9361: 0.05891 0.05913: 0.05913	M497 39 66893 61 66893 61 66893 61 600567 27 611791 26 6012 28 6012 28 60141772 35 6012 28 60141772 35 6014 51 6014 51 6014 61	95.74374 10.40424 771.9685 6.14927 85.37033 85.37033 85.37033 85.37033 10.00311 442.302 70.7018 10.0518 367.6346 5259.2003 96.84476 96.84476 96.84476 85.279904 77.6963 90.3084 5.460045 90.3084 5.460045 90.3084 31.44429 71.11872 7.756661 13.4429 71.11872 7.756661 13.4429 71.11872 7.756661 13.4429 71.11872 7.756661	649.19037 2034.5537 28.889297 270.36328 35.442886 5272.0146 323.78555 47.71173 1145.2308 804.66504 264.96585 95.400215 315.73477 396.31166 18.032099 1109.46676 487.0162 861.08417 31.374862 44.28484 467.0162 48.2894753 560.99963	695,1485 139,0481 33,642477 52,15,5884 39,242416 4557,4497 366,2005 70,8504 70,8504 70,8504 70,8504 88,62417 270,7512 70,2002 70,2004	G34.8921 1982.3739 28.103666 28.67432 28.1036652 2506478 312.59354 312.59354 312.59354 312.59354 312.59354 312.59354 312.59354 312.59354 312.59354 313.29355	NM 008371//NM 0197' 0.00533374 NM 00164572//NM 11 0.00532054 NM 001164572//NM 11 0.00532054 NM 001164572//NM 11 0.00532058 NM 002478/NM 0052 0.00532678 NM 028471/NM 00552 0.00334787 NM 007329 0.00552098 NM 007329 0.00542981 NM 0073274/NM 00551 0.00242934 NM 12827 0.00573772 NM 007548//NM 00551 0.00243934 NM 007548//NM 00551 0.00343938 NM 007548//NM 00551 0.00343938 NM 007548//NM 00551 0.00343939 NM 007548//NM 00551 0.00363299	-1.33 1.06 -1.14 1.10 -1.03 1.01 -1.01 -1.01 -1.01 -1.01 -1.01 -1.01 -1.00 -1.07 -1.19 -1.19 -1.19 -1.10 -1.00 -1.09 -1.14 -1.48 -1.48 -1.48 -1.48 -1.06 -1.15 -1.08 -1.09 -1.08 -1.01 -1.16 -1.08 -1.09 -1.01 -1.16 -1.07	131 -1.09 -1.09 -1.09 -1.03 -1.10 -1.07 -1.11 -1	-102 -102 -103 -103 -103 -103 -103 -103 -104 -104 -104 -104 -104 -104 -104 -105 -105 -105 -105 -105 -105 -105 -105	Hyadi//Net6 Rpp21 Sork Targ3 Prvc1 Find Emg2 Timmedc1 Coub2 Right Archil/Gm20199 Nic2 Prdm1 Akap13 Igflit Gm1723 Gdi SerphedIn Komida SerphedIn Komida SerphedIn Komida SerphedIn Komida SerphedIn Komida SerphedIn Komida DSFrdd102 Admrt18 D2Wau107e Nanos1 Ube2v1	helauronaghucosamindase 1//N-acetyltranderase 6 ribonuclases P.1 subunit SNF related kinase trandoming growth factor beta regulated gene 3 proline-rich collect-coll 1 four and a half UM domains 3 estitelial membrane protein 2 trandocuses of inner mitochendrical membrane domain contains cycle nucleotide gated channel alpha 2 trandocuses of inner mitochendrical membrane domain contains cycle nucleotide gated channel alpha 2 trandocuses of inner mitochendrical membrane protein homo hypermethylated in cancer 2 PR domain containing 1, with ZNF domain A kinase (PRA) anothor protein 3 insulin-like growth factor 1, intronic transcript predicted gene 2713 guanosine diphosphate (GPP) dissociation inhibitor 1 serie for cyteriole peptidase inhibitor, clade A, member 3N lytine (K)-specific demethylase 6A hydroxycol glutathorine hydroxia of the control of the con	0000303 // response to reactive expens species // not recorded//10003575 // carbohydrate metabolic process // inferred from electronic amount of the processing // not recorded//10003673 // carbohydrate metabolic process // inferred from electronic amount of the processing // not recorded//10016310 // phosphorylation // inferred from electronic amount of the processing // not recorded//10016310 // phosphorylation // inferred from electronic amount of the processing // not recorded//10016310 // phosphorylation // inferred from electronic amount of the processing // interactive // inferred from direct assay/// 10001731 // registronic phosphorylation // inferred from direct assay/// 10001731 // registronic phosphorylation // intered from direct assay/// 10001731 // registronic phosphorylation/// index moderate // 10016031 // intered from electronic amount of the processing // intered from elec
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0.00222619 0.00345322 0.009677315 0.98450345 0.00223183 0.00838929 0.05075565 0.00129835 0.00587357 0.04219629 0.1160446 0.06219629 0.1160446 0.050754010 0.02138473	8 0.8440.0 9 0.30644 22 0.0335 5 0.1962: 0.9723 44 0.1237 44 0.1218 0.9158: 5 0.0074 45 0.1818 0.9361: 0.1818 0.9361: 0.1818 0.0058: 3 0.3884 0.0058: 3 0.3884 0.0058: 3 0.3884 0.0058: 3 0.3884 0.0058: 3 0.3884 0.0058: 3 0.3884 0.0058: 3 0.3884 0.0058: 3 0.3884 0.0058: 3 0.3884 0.0058: 3 0.3884 0.0058: 3 0.3884 0.0058: 3 0.3884 0.0058: 3 0.3884 0.0058: 3 0.3884 0.0058: 3 0.0058: 3 0.0058: 3 0.0058: 3 0.0058: 3 0.0058: 3 0.0058: 3 0.0058: 3 0.0058: 3 0.0058: 3 0.0058: 3 0.0058: 3 0.0058: 3 0.0058: 3 0.0058:	M497 39 66893 61 66893 61 66893 61 600567 27 611791 26 6012 28 6012 28 60141772 35 6012 28 60141772 35 6014 51 6014 51 6014 61	95.74374 10.40424 7721.9685 16.14927 18.5.37033 15.00311 442.302 70.70718 10.08518 279.2003 28.64476 29.2003 29.6460045 20.013093 20.013093 20.140045 20.013093 20.13	649.19037 2034.5537 28.889297 276.36328 35.442886 5272.0146 323.78555 47.71173 1145.2308 35.400215 315.73477 596.51166 18.032099 10.964676 1102.4196 443.1589 487.0162 861.08417 313.734594 443.1589 442.1589 442.1589 443.1589 560.09963 560.99963 560.99963 560.99963 560.99963 560.99963 560.299963 560.299963 560.299963 560.299963 560.299963 560.299963	695,1485 133,04851 33,634277 39,242416 39,242416 70,8504 1092,1595 758,12854 1092,1595 758,12854 1270,7512 152,1605 1092,1595 758,12854 128,7605 192,2408 193,1595 193,2408 193,24	G34.8921 1982.3739 28.103666 28.67432 34.403652 5094.78 312.59354 46.041767 1104.2035 303.12595 572.6741 17.729889 10.511552 10.55.6401 472.91534 464.42245 818.8622 12.5517698 11.5517698 11.5517698 11.5517698 11.5517698 11.5517698 11.5517698 11.5517698 11.5517698 11.5517698 11.5517698 11.5517698 11.5517698 11.5517698 11.5517698 11.5517698 11.5517698 11.5517698	NM 0.08331//NM 0.197' 0.00533314* NM 0.08337//NM 110.0832054 NM 0.0116572//NM 11.00532054 NM 0.0165727475 NM 0.016572//NM 11.00532054 NM 0.0532054 NM 0.053210/NM 0.05320034557 NM 0.053210/NM 0.053256107 NM 0.03326107 NM 0.0532056107 NM 0.0532056107 NM 0.053200563044 NM 0.031311311/NM 0.055200563264 NM 0.031311311/NM 0.055200563264 NM 0.031311311/NM 0.0552005632661 NM 0.03203205/NM 0.05520056508	-1.33 1.06 -1.14 1.10 -1.03 1.01 -1.01 -1.01 -1.01 -1.01 -1.01 -1.01 -1.00 -1.07 -1.19 -1.19 -1.19 -1.10 -1.00 -1.09 -1.14 -1.48 -1.48 -1.48 -1.48 -1.06 -1.15 -1.08 -1.09 -1.08 -1.01 -1.16 -1.08 -1.09 -1.01 -1.16 -1.07	131 -1.09 -1.09 -1.09 -1.03 -1.10 -1.07 -1.11 -1	-102 -102 -103 -103 -103 -103 -103 -103 -104 -104 -104 -104 -104 -104 -104 -105 -105 -105 -105 -105 -105 -105 -105	Healt	helauronaghucosamindase 1//N-acetyltranderase 6 ribonuclases P.1 subunit SNF related kinase trandoming growth factor beta regulated gene 3 proline-rich collect-coll 1 four and a half UM domains 3 estitelial membrane protein 2 trandocuses of inner mitochendrical membrane domain contains cycle nucleotide gated channel alpha 2 trandocuses of inner mitochendrical membrane domain contains cycle nucleotide gated channel alpha 2 trandocuses of inner mitochendrical membrane protein homo hypermethylated in cancer 2 PR domain containing 1, with ZNF domain A kinase (PRA) anothor protein 3 insulin-like growth factor 1, intronic transcript predicted gene 2713 guanosine diphosphate (GPP) dissociation inhibitor 1 serie for cyteriole peptidase inhibitor, clade A, member 3N lytine (K)-specific demethylase 6A hydroxycol glutathorine hydroxia of the control of the con	0000303 // response to reactive expens species // not recorded//10003575 // carbohydrate metabolic process // inferred from electronic amount of the processing // not recorded//10003673 // carbohydrate metabolic process // inferred from electronic amount of the processing // not recorded//10016310 // phosphorylation // inferred from electronic amount of the processing // not recorded//10016310 // phosphorylation // inferred from electronic amount of the processing // not recorded//10016310 // phosphorylation // inferred from electronic amount of the processing // interactive // inferred from direct assay/// 10001731 // registronic phosphorylation // inferred from direct assay/// 10001731 // registronic phosphorylation // intered from direct assay/// 10001731 // registronic phosphorylation/// index moderate // 10016031 // intered from electronic amount of the processing // intered from elec

p (Genotype)	p (Exposure)	[C3H/HeN, Air](raw)	[C3H/HeN, O2](raw)	[Gsr-KO, Air](raw)	[Gsr-KO, O2](raw)	RefSeq Transcript ID	p (Genotype-Exposure)	FC in WT (Air:O2)	FC in KO (Air:O2)	FD (WT O2 vs KO O2)	Gene Symbol	Gene Title
0.2903104	0.025998186	318.0659	331.1289	335.27103	298.3071	NM 001100591///NM 0	0.007281573	1.04	-1.12	-1.11	Rc3h2	ring finger and CCCH-type zinc finger domains 2
0.07800728	0.8453955	16.240852	17.858604	17.32233	16.055773	NM_023135	0.007376966	1.10	-1.08	-1.11	Sult1e1	sulfotransferase family 1E, member 1
0.47713605	0.08072522	798.17804	827.0046	824.9663	742.5771	NM 027098///XM 0064	9 0.005984975	1.04	-1.11	-1.11	Mrpl30	mitochondrial ribosomal protein L30
0.33910736	0.8743928	23.702065	26.93612	26.731722	24.161081	NM_183030///NR_02808	0.001805932	1.14	-1.11	-1.11	Smim10l2a	small integral membrane protein 10 like 2A
0.037662134	0.3203201	218.51404	234.4993	226.00665	210.28682	NM 025578	0.009090482	1.07	-1.07	-1.12	Mrps25	mitochondrial ribosomal protein S25
0.076956056	0.97664875	5885.496	6235.394	6097.597	5551.961	NM_011653	0.003223013	1.06	-1.10	-1.12	Tuba1a	tubulin, alpha 1A
0.11579136	0.57086194	13.383798	14.869218	14.763236	13.233142	NM 170597//XM 0064	9 0.001420977	1.11	-1.12	-1.12	Creg2	cellular repressor of E1A-stimulated genes 2
0.001559537	7.75E-04	33.4198	39.426548	51.94689	35.05513	NM_009162	3.89E-06	1.18	-1.48	-1.12	Scg5	secretogranin V
0.07675284	0.02617646	259.37936	280.8956	406.44058	248.93655	NM 001099774	0.008754982	1.08	-1.63	-1.13	Krtap17-1	keratin associated protein 17-1
0.7924486	0.64331704	120.54288	143.55579	147.13474	127.162674	NM_016866///XM_0064	9 0.002123031	1.19	-1.16	-1.13	Stk39	serine/threonine kinase 39
0.5320976	0.005739873	309.65298	326.20502	338.36047	288.9452	NM_026844///XM_0065	3 7.07E-04	1.05	-1.17	-1.13	Cmc2	COX assembly mitochondrial protein 2
0.46572787	0.43188995	2822.9985	2983.197	2988.9175	2642.2893	NM_011327///XM_0112	4 0.00789655	1.06	-1.13	-1.13	Scp2	sterol carrier protein 2, liver
0.9860367	0.44730213	53.07649	62.51307	65.57573	55.15674	NM_016662///XR_87343	4 0.00125412	1.18	-1.19	-1.13	Mxd3	Max dimerization protein 3
0.005637219	0.08278733	57.3333	66.9638	60.187172	59.00381	NM 001113478///NM 0	(0.003351502	1.17	-1.02	-1.13	Frrs1	ferric-chelate reductase 1
0.003472009	0.09408813	102.89054	120.43201	107.66417	106.05429	NM_001301407///NM_1	4 0.007864923	1.17	-1.02	-1.14	Tspan33	tetraspanin 33
0.10661421	0.4775329	11.898493	13.12598	12.987627	11.551271	NM 175488///XM 0065	1 0.002101263	1.10	-1.12	-1.14	Ccdc38	coiled-coil domain containing 38
0.9901541	0.19400911	45.44407	51.24861	56.275387	44.9879	NM_007662	0.008350538	1.13	-1.25	-1.14	Cdh15	cadherin 15
7.41E-04	0.08986641	1001.4492	724.69794	580.7146	635.4509	NM 033563///XM 0064	9 0.009038049	-1.38	1.09	-1.14	KIf7	Kruppel-like factor 7 (ubiquitous)
0.038364775	0.5657878	7.312391	8.018694	7.751234	6.9740005	NM_177162	0.005708666	1.10	-1.11	-1.15	Tmprss11g	transmembrane protease, serine 11g
0.5911136	0.47230577	67.01783	81.80634	89.667046	70.985016	NR 015349	0.008672642	1.22	-1.26	-1.15	Etohd2	ethanol decreased 2
0.5868689	0.63585263	8.808447	10.484583	10.233674	9.079129	NM_177774///XM_0065	3 0.00723779	1.19	-1.13	-1.15	Srsf12	serine/arginine-rich splicing factor 12
0.09555525	0.048695326	39.95345	44.094017	45.47682	38.13308	NM 016982///NM 0169	£ 4.94E-04	1.10	-1.19	-1.16	Vpreb1///Vpreb2	pre-B lymphocyte gene 1///pre-B lymphocyte gene 2
0.9539284	0.20049705	28.868834	38.72149	36.402557	33.1805	NM_001290397///NM_0	0.007991966	1.34	-1.10	-1.17	Mybl1	myeloblastosis oncogene-like 1
0.61671585	0.008956795	398.17203	548.8051	482.23813	467.35214	NM 001294302///NM 0	1 0.003081697	1.38	-1.03	-1.17	Preb	prolactin regulatory element binding
0.47870213	0.21939896	300.20813	347.8457	348.97882	281.4759	NM_009293///XM_0010	0.001818157	1.16	-1.24	-1.24	Sts	steroid sulfatase
1.76E-04	0.49507868	7399.8096	7760.3833	6742.2266	6219.299	NM 011125///XM 0064	9 0.008738595	1.05	-1.08	-1.25	Pltp	phospholipid transfer protein
0.5122295	0.22264111	32.784462	45.97425	41.877045	36.10311	NM_001103182///NM_1	0.00214569	1.40	-1.16	-1.27	Lin9	lin-9 homolog (C. elegans)
0.32234672	2.97E-04	28.481337	75.41425	47.716915	59.164722	NM 009140	0.003614375	2.65	1.24	-1.27	Cxcl2	chemokine (C-X-C motif) ligand 2
0.24736327	0.50653183	24.590448	32.157936	29.573622	25.206078	NM_001290779///NM_1	0.001707604	1.31	-1.17	-1.28	Zfp879	zinc finger protein 879
0.043703277	0.2729481	55.983547	72.03841	61.92984	56.35559	NM 025637///NM 0284	5 0.006108716	1.29	-1.10	-1.28	Rwdd3	RWD domain containing 3
2.15E-04	0.05562703	322.78778	394.3657	308.66342	293.3602	NM_001033272///NM_0	0.002134426	1.22	-1.05	-1.34	Spata13	spermatogenesis associated 13
0.10320588	0.028435951	40.14017	60.255722	47.371956	44.777042	NM 013738///XM 0065	1 0.003471293	1.50	-1.06	-1.35	Plek2	pleckstrin 2
0.45284718	0.0739012	37.68251	59.952892	48.501804	44.39286	NM_009100	0.008385968	1.59	-1.09	-1.35	Rptn	repetin
0.16815148	0.5074813	685.0561	814.30096	764.7367	601.46423	NM 001081322///XM 0	0.003057414	1.19	-1.27	-1.35	Myo5c	myosin VC
0.03992995	9.96E-05	73.78068	138.49205	83.03101	101.89759	NM_019810	0.006027912	1.88	1.23	-1.36	Slc5a1	solute carrier family 5 (sodium/glucose cotransporter), member
0.05897384	0.049493894	94.72826	112.03129	113.171745	80.16662	NM_201638	0.002128884	1.18	-1.41	-1.40	Metti14	methyltransferase like 14
0.004151421	0.21870469	27.880014	37.659985	30.380669	26.246265	NM_019514///NM_2071	C 6.26E-04	1.35	-1.16	-1.43	Astn2	astrotactin 2
0.14543886	0.75992215	94.96745	135.1971	116.40971	92.20429	XM_006504243///XM_00	0.009329869	1.42	-1.26	-1.47	Tmem156	transmembrane protein 156
7.40E-04	0.21091159	80.28159	109.415375	85.37532	74.47691	NM_010780	6.16E-04	1.36	-1.15	-1.47	Cma1	chymase 1, mast cell
0.86537766	0.009022173	65.09017	70.67845	133.38834	40.061073	NM_010861///XM_0065	3 0.005792308	1.09	-3.33	-1.76	Myl2	myosin, light polypeptide 2, regulatory, cardiac, slow
0.7730397	0.001061631	15.179602	79.0113	33.033127	43.647808	NM_203320	0.005966249	5.21	1.32	-1.81	Cxcl3	chemokine (C-X-C motif) ligand 3

Gene Ontology Biological Process

0000209 // protein polyubiquitination // not recorded///0001782 // B cell homeostasis // inferred from genetic interaction///0009791 // post-ei 0007565 // female pregnancy // inferred from mutant phenotype///0008210 // estrogen metabolic process // inferred from direct assay///0008.

0032543 // mitochondrial translation // inferred by curator

0007017 // microtubule-based process // inferred from electronic annotation///0008152 // metabolic process // inferred from electronic annotation 00051114 // oxidation-reduction process // inferred from electronic annotation 00058101 // transport // inferred from electronic annotation

0001933 // negative regulation of protein phosphorylation // inferred from direct assay//0006468 // protein phosphorylation // not recorded//,

000633 // acyl-CoA metabolic process // traceable author statement//0006694 // steroid biosynthetic process // not recorded///0006701 // p
0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated // infe
0006810 // transport // inferred from electronic annotation///0055114 // oxidation-reduction process // inferred from electronic annotation
0045747 // positive regulation of Notch Signaling pathway // not recorded///0051604 // protein maturation // inferred from mutant phenotype,

0007155 // cell adhesion // inferred from electronic annotation///0007156 // homophilic cell adhesion via plasma membrane adhesion molecule 0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated // infe

000081, // regulation of alternative mBNA splicing, via splicesozeme // Inferred from electronic annotation///0000385 // mBNA 5*-uplice via the root operation international report of the responsibility of the responsibil

0008152 // metabolic process // inferred from electronic annotation ///0032254 // establishment of scretory granule localization // not recorde
ember 1 0001656 // metanephros development // inferred from mutant phenotype//0006810 // transport // inferred from electronic annotation///0000
000398 // mRNA splicing, via splicessome // not recorded//10006139 // nucleobase-containing compound metabolic process // inferred from e
2000009 // negative regulation of portion localization to elisa uffice // inferred from direct assay

0006508 // proteolysis // not recorded///0006518 // peptide metabolic process // inferred from electronic annotation///0016485 // protein pro 0000202 // regulation of the force of heart contraction // not recorded//0003007 // heart morphogenesis // inferred from genetic interaction/ 00002699 // positive regulation of leukocyte hemotastis // not recorded//0000958 // chemotassis // inferred from electronic annotation///00065