

Additional Table 9. Intensities of genes/ESTs differentially regulated only in males with a fold change of $\geq \pm 1.5$ for either of the comparisons Control vs MSG, Control vs TFA, Control vs TFA+MSG, or TFA vs TFA+MSG.

Name	Symbol Accesssion #	Control	MSG	TFA	TFA+MSG
NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1, 6kDa	Ndufc1 NM_025523	1732.1	2223.5	2994.3	2945.6
protein disulfide isomerase associated 4	Pdia4 NM_009787	642.5	487.9	1080.0	976.5
magnesium transporter 1	Magt1 NM_025952	307.5	413.2	636.9	642.8
5-methyltetrahydrofolate-homocysteine methyltransferase	Mtr NM_001081128	605.8	679.9	1239.4	843.5
thioredoxin 1	Txn1 NM_011660	1073.9	957.9	1333.4	1688.9
histone deacetylase 2	Hdac2 NM_008229	1278.2	1312.0	1955.7	1173.9
stearoyl-coenzyme A desaturase 4	Scd4 NM_183216	634.8	953.6	603.4	991.8
asporin	Aspn NM_025711	315.0	294.1	565.4	407.4
plastin 3 (T-isoform)	Pls3 NM_145629	963.0	1138.3	2244.4	1129.1
cullin 5	Cul5 NM_027807	1102.6	1513.7	1916.8	1492.7
tropomyosin 4	Tpm4 NM_001001491	1925.4	1641.2	2560.5	2889.4
DnaJ (Hsp40) homolog, subfamily A, member1	Dnaja1 NM_008298	132.2	55.2	303.3	200.2
epithelial membrane protein 1	Emp1 NM_010128	211.9	137.8	306.0	390.7
general transcription factor II H, polypeptide 2	Gtf2h2 NM_022011	172.1	331.5	305.9	204.1
glia maturation factor, beta	Gmfb NM_022023	281.3	297.5	562.9	507.4
topoisomerase (DNA) II binding protein 1	Topbp1 NM_176979	261.1	220.0	437.7	202.0
dystrophin, muscular dystrophy	Dmd NM_007868	3883.0	4230.5	4157.2	2621.6
dynein light chain Tctex-type 3	Dynlt3 NM_025975	380.7	464.6	617.6	635.8
microtubule-associated protein, RP/EB family, member 1	Mapre1 NM_007896	529.0	654.4	869.1	752.5
proteoglycan 4 (megakaryocyte stimulating factor)	Prg4 NM_021400	647.8	538.9	819.1	992.4
phospholipase B domain containing 1	Plbd1 NM_025806	424.0	524.3	667.7	737.4
enhancer of zeste homolog 1 (Drosophila)	Ezh1 NM_007970	1729.0	1695.6	1407.5	866.7
THO complex 2	Thoc2 NM_001033422	728.6	937.6	1163.0	1038.6
protein phosphatase 3 (formerly 2B), regulatory subunit B, alpha isoform	Ppp3r1 NM_024459	609.1	988.4	914.1	1032.6
predicted gene 14391	Gm14391 NM_001099308	766.5	1278.5	1627.5	1517.8
protein tyrosine phosphatase 4a2	Ptp4a2 NM_008974	1547.7	1631.5	2389.4	1950.8
basic leucine zipper & W2 domains 2	Bzw2 NM_025840	1366.8	2111.4	1917.4	1964.7
vacuolar protein sorting 13A (yeast)	Vps13a NM_173028	879.7	994.2	1390.8	952.8
COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis)	Cops3 NM_011991	985.7	1516.3	1277.4	1481.0
chemokine (C-C motif) lig& 9	Ccl9 NM_011338	1157.1	1025.5	1178.2	1831.8
Bmi1 polycomb ring finger oncogene	Bmi1 NM_007552	566.8	921.4	997.8	1053.3
Meis homeobox 2	Meis2 NM_001136072	892.6	901.1	987.8	646.0
cornichon homolog 4 (Drosophila)	Cnih4 NM_030131	510.6	696.1	834.4	849.1
RNA binding motif protein 28	Rbm28 NM_133925	703.8	751.8	820.8	517.0
related RAS viral (r-ras) oncogene homolog 2	Rras2 NM_025846	522.3	817.8	818.7	838.5
non-SMC element 1 homolog (S. cerevisiae)	Nsmce1 NM_026330	513.1	779.4	815.6	803.3
inositol polyphosphate-4-phosphatase, type I	Inpp4a NM_030266	553.9	545.5	790.6	518.4
family with sequence similarity 96, member A	Fam96a NM_026635	556.4	626.2	786.8	863.4
LAS1-like (S. cerevisiae)	Las1l NM_152822	506.3	694.6	761.3	727.5
amylase 1, salivary	Amy1 NM_007446	305.5	480.1	697.8	571.3
F-box protein 30	Fbxo30 NM_027968	435.4	625.2	676.4	589.3
poly (ADP-ribose) polymerase family, member 14	Parp14 NM_001039530	406.8	519.5	647.7	528.7
aspartylglucosaminidase	Aga NM_001005847	385.1	410.4	606.1	551.1
NEDD4 binding protein 2	N4bp2 NM_001024917	355.1	389.1	586.8	371.3
RIKEN cDNA 2310001A20 gene	2310001A20Rik AJ310638	381.3	478.2	576.0	647.6

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ER lipid raft associated 1	Erlin1 NM_145502	316.0	410.2	574.7	476.0
TIP41, TOR signalling pathway regulator-like (<i>S. cerevisiae</i>)	Tipr1 NM_145513	326.7	351.9	549.8	540.1
F-box protein 41	Fbxo41 NM_001001160	466.2	711.7	549.8	431.9
zinc finger protein 97	Zfp97 NM_011765	225.8	346.3	546.3	338.8
chromatin modifying protein 5	Chmp5 NM_029814	246.1	339.6	522.3	468.8
proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	Psm14 NM_021526	347.6	477.1	514.6	608.7
versican	Vcan NM_001081249	358.7	300.4	507.2	554.8
uroporphyrinogen decarboxylase	Urod NM_009478	315.4	471.0	504.6	500.4
CCR4-NOT transcription complex, subunit 8	Cnot8 NM_026949	294.5	375.6	493.5	421.8
phosphoglycerate mutase 1	Pgam1 NM_023418	370.9	442.8	455.0	640.9
PH domain & leucine rich repeat protein phosphatase 2	Fxyd6 NM_022004	359.9	302.4	449.2	572.0
reticulocalbin 1	Rcn1 NM_009037	322.6	353.7	448.3	568.7
BRCA2 & CDKN1A interacting protein	Bccip NM_025392	325.8	565.6	435.9	504.7
transmembrane protein 69	Tmem69 NM_177670	241.3	397.2	435.1	479.0
solute carrier family 35, member B1	Slc35b1 NM_016752	315.5	425.8	428.5	505.3
Rap guanine nucleotide exchange factor (GEF) 6	Rapgef6 NM_175258	379.3	441.6	422.6	587.7
inhibitor of growth family, member 4	Ing4 NM_133345	188.8	336.9	408.3	369.3
Family member 76b	Fam76b BC043120	242.6	314.7	405.9	304.9
histone cluster 1, H1e	Hist1h1e NM_015787	546.2	333.0	405.5	266.0
YY1 associated factor 2	Yaf2 NM_024189	272.4	352.3	391.6	426.9
TATA box binding protein (Tbp)-associated factor, RNA polymerase I, A	Taf1a NM_021466	214.9	305.4	386.5	336.0
MAPKinase3 member 15	Map3k15 ENSMUST00000033665	260.4	199.8	375.6	108.7
enhancer of yellow 2 homolog (<i>Drosophila</i>)	Eny2 NM_175009	220.1	301.9	374.3	273.5
ribosomal protein S11	Gm6394 XM_915925	238.3	235.8	369.4	267.7
ethanol induced 1	Etohi1 ENSMUST00000098999	128.3	241.3	367.8	286.4
general transcription factor IIB	Gtf2b NM_145546	120.2	185.7	362.4	211.6
recombination signal binding protein for immunoglobulin kappa J region-like	Rbpjl NM_009036	365.9	584.7	345.6	339.8
block of proliferation 1	Bop1 NM_013481	378.0	568.3	340.2	468.0
coenzyme Q10 homolog B (<i>S. cerevisiae</i>)	Coq10b NM_001039710	242.4	317.7	338.0	388.0
cysteine-rich with EGF-like domains 2	Creld2 NM_029720	257.1	195.4	334.0	397.9
integral membrane protein 2A	Itm2a NM_008409	144.6	92.0	302.0	234.5
mitochondrial ribosomal protein L35	Mrpl35 NM_025430	233.6	272.7	298.6	352.2
guanine nucleotide binding protein (G protein), beta 4	Gnb4 NM_013531	196.1	197.8	296.2	283.4
dicarbonyl L-xylulose reductase	Dcxr NM_026428	312.2	480.4	272.0	371.2
tetraspanin 6	Tspan6 NM_019656	145.8	145.9	270.0	277.2
reticulocalbin 3, EF-h& calcium binding domain	Rcn3 NM_026555	173.4	153.7	268.0	287.6
glutathione S-transferase, mu 4	Gstm4 NM_026764	144.9	293.6	260.0	256.9
mediator of RNA polymerase II transcription, subunit 31	Med31 NM_026068	150.8	148.7	260.0	249.2
mitochondrial ribosomal protein S14	Mrps14 NM_025474	164.7	155.9	257.3	286.2
cartilage oligomeric matrix protein	Comp NM_016685	140.1	87.5	244.6	304.2
keratin 75	Krt75 NM_133357	148.1	123.0	234.1	193.7
transmembrane protein 106A	Tmem106a NM_144830	184.3	241.6	226.4	341.5
tachykinin receptor 3	Tacr3 NM_021382	91.6	94.7	217.9	87.1
phosphodiesterase 3B, cGMP-inhibited	Pde3b NM_011055	144.2	117.5	205.5	249.8
hairy & enhancer of split 2 (<i>Drosophila</i>)	Hes2 NM_008236	91.3	121.2	203.6	169.6
eukaryotic translation initiation factor 2 alpha kinase 4	Eif2ak4 AF193344	105.7	255.7	200.0	168.9

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Name	Symbol Accesssion #	Control	MSG	TFA	TFA+MSG
exosome component 8	Exosc8 NM_027148	120.5	141.0	198.6	216.0
ribosomal protein S27-like	Rps27l NM_026467	169.1	131.0	178.7	255.2
proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	Psmc9 NM_026000	160.9	210.0	168.6	290.7
phosphodiesterase 6A, cGMP-specific, rod, alpha	Pde6a NM_146086	321.3	199.6	166.0	99.1
LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae)	Lsm6 NM_030145	109.1	101.2	164.9	142.5
sine oculis-related homeobox 4 homolog (Drosophila)	Six4 NM_011382	84.2	106.0	141.6	119.5
hyperpolarization-activated, cyclic nucleotide-gated K+ 1	Hcn1 NM_010408	76.7	29.0	135.1	138.9
asparagine-linked glycosylation 6 homolog (yeast, alpha-1,3,-glucosyltransferase)	Alg6 NM_001081264	62.3	68.4	128.4	101.2
secretogranin V	Scg5 NM_009162	75.7	112.6	121.5	90.5
activity regulated cytoskeletal-associated protein	Arc NM_018790	79.9	102.5	120.2	138.2
histone cluster 1, H2ak	Hist1h2ak NM_178183	77.0	83.6	119.9	116.0
Unknown	OTTMUSG00000016609 NM_001100416	130.9	225.0	384.0	284.9
Unknown	Gm14305 NM_001099327	130.9	225.0	384.0	284.9
Unknown	Gm14403 ENSMUST00000108947	203.4	355.3	442.7	309.1
Unknown	Gm10828 ENSMUST00000100068	212.3	382.6	478.5	403.2
Unknown	Gm14325 ENSMUST00000108939	217.9	456.5	654.1	518.9
Unknown	3100002L24Rik U62393	239.0	399.3	701.3	520.4
Unknown	2410015M20Rik BC056164	567.3	638.8	895.2	862.4
Unknown	Gm5532 ENSMUST00000097531	552.9	787.4	857.4	914.0
Unknown	Gm14434 NM_001101804	766.5	1278.5	1627.5	1517.8