

Dataset S4: Functional enrichment analysis of genes with greater saline-to-OVA gene expression differentials ($\Delta S-O$) in one strain than another

A. $\Delta S-O$ Tgfbm2/3 > S-O NIH			B. $\Delta S-O$ NIH > S-O Tgfbm2/3		
Term	Count	P-Value	Term	Count	P-Value
microsome	13	4.00E-06	acetylation	132	2.20E-13
endoplasmic reticulum	33	1.80E-04	protein biosynthesis	16	2.00E-05
cytoplasm	101	2.30E-04	centromere	9	2.10E-05
disulfide bond	83	5.60E-04	Chromosome partition	8	3.80E-05
cytokine	13	7.40E-04	cell cycle	30	9.50E-05
phosphoprotein	182	8.50E-04	ribonucleoprotein	21	1.60E-04
signal	95	9.70E-04	chromosomal protein	14	1.60E-04
membrane	160	1.50E-03	atp synthesis	5	2.30E-04
inflammatory response	8	2.40E-03	phosphoprotein	228	3.80E-04
chemotaxis	7	3.00E-03	kinetochore	9	4.60E-04
synaptosome	5	7.50E-03	lysosome	13	1.40E-03
oxidoreductase	24	9.90E-03	rrna processing	8	1.90E-03
Secreted	47	1.70E-02	hydrogen ion transport	7	2.20E-03
plasma	4	1.90E-02	ribosomal protein	14	2.60E-03
cytoskeleton	23	2.30E-02	mitosis	14	3.10E-03
macrophage	3	2.70E-02	cell division	17	4.90E-03
monooxygenase	7	4.30E-02	methylation	15	6.40E-03
coiled coil	53	4.40E-02	atp-binding	53	1.70E-02
			mitochondrion inner membrane	12	2.20E-02
			nucleotide-binding	63	3.00E-02
			er-golgi transport	7	3.20E-02
			DNA damage	12	3.20E-02
			dna repair	11	3.60E-02
			ATP	10	3.90E-02
			oxidoreductase	26	3.90E-02
			proto-oncogene	7	4.30E-02
			dna replication	7	4.30E-02
			nucleotide binding	6	4.30E-02
			sh3 domain	12	4.50E-02
			p-loop	6	4.60E-02
			iron-sulfur	5	4.60E-02
			exosome	3	4.90E-02

N.B. $\Delta S-O$ indicates differential in gene expression between saline and OVA