

Dataset S2: Functional enrichment analysis of genes that are differentially expressed between NIH and Tgfbm2/3 mice

A. OVA treatment (NIH x Tgfbm2/3)

Term	Count	P-Value
inflammatory response	9	6.20E-07
secreted	30	4.60E-05
macrophage	4	1.30E-04
cytokine	9	2.00E-04
immunoregulation	3	5.20E-04
lymphokine	3	5.40E-03
disulfide bond	36	5.80E-03
inflammation	3	1.10E-02
pyrogen	2	1.90E-02
chemotaxis	4	1.90E-02
acute phase	3	1.90E-02
signal	39	2.00E-02
glycoprotein	45	2.90E-02
receptor	32	3.90E-02
ribonucleoprotein	7	3.90E-02
mitogen	3	4.30E-02

B. Saline treatment (NIH x Tgfbm2/3)

Term	Count	P-Value
cell cycle	15	2.40E-03
ribonucleoprotein	10	8.60E-03
ribosomal protein	8	8.80E-03
protein kinase inhibitor	3	1.00E-02
endoplasmic reticulum	17	1.70E-02
methylation	8	2.50E-02
acetylation	42	2.80E-02
mitosis	7	3.10E-02
mitochondrion inner mem	7	3.30E-02
respiratory chain	4	4.60E-02