

Table S2. Significantly over-represented biological processes embedded in the post-TX mRNA signature (245 mRNAs).

Biological process	Genes	adjusted <i>p</i> -value (Benjamini-Hochberg)
response to wounding	KNG1, F11, NFKBIZ, NMI, PTGER3, GATM, S100A8, KL, TNC, EPHX2, TLR2, ITGA2, ITGB3, PLG, CD163, TNFAIP6, LYVE1, FGA, FGB, ITGB6, SERPINA3, PEBP1, VCAN, NEFL	6.82E-04
response to toxin	DDC, CYP17A1, TRPM6, SLC23A1, EPHX2, PEBP1, BPHL, NQO1, NEFL	9.00E-04
response to metal ion	KHK, TNFRSF11B, AQP9, FGA, GATM, FGB, SLC34A1, ABAT, PEBP1, CAPN3, MT1X	3.70E-03
oxidation reduction	ACOX2, ALDH6A1, SORD, HSD17B14, NELL1, PIPOX, PXDNL, IYD, FMO4, RDH12, PRUNE2, CYP17A1, FMO1, AKR1B10, MIOX, HAO2, HSD11B2, DAO, CYP4F2, DIO1, NQO1, HADH, DCXR, NQO2	3.97E-03
fatty acid metabolic process	ACOX2, LPL, CRYL1, ACSM2A, HAO2, EPHX2, FABP3, ECHS1, CYP4F2, HADH, ACSF2, ACSM5	1.77E-02
response to inorganic substance	KHK, TNFRSF11B, AQP9, FGA, GATM, FGB, SLC34A1, ABAT, PEBP1, CAPN3, MT1X, PXDNL	2.02E-02