

Supplemental Table 3. The commonly up-regulated genes in lungs of A/J mice exposed to CS for different time periods.

Genbank ID	Gene Title	Gene Symbol	1.5 mos		
			5 h FC ± SEM	8 d FC ± SEM	FC ± SEM 6 mos
AA419994	Zinc finger and btb domain containing 16*	Zbtb16	3.4 ± 0.5	7.1 ± 0.4	4.8 ± 0.4
AV124537	Extra cellular link domain-containing 1*	Xlkd1	3.0 ± 0.4	2.1 ± 0.4	2.6 ± 0.4
AW108044	Uncoupling protein 2 (mitochondrial, proton carrier)*	Ucp2	1.6 ± 0.4	2.0 ± 0.4	1.5 ± 0.4
BB284199	Thioredoxin reductase 1*	Txnr1	5.6 ± 0.5	1.8 ± 0.4	2.0 ± 0.3
BB449960	Transcobalamin 2*	Tcn2	1.6 ± 0.4	1.6 ± 0.4	2.1 ± 0.3
AA144045	Sema domain, immunoglobulin domain (ig), and gpi membrane anchor, (semaphorin) 7a*	Sema7a	2.0 ± 0.4	1.9 ± 0.4	1.5 ± 0.4
NM_019414	Selenium binding protein 1	Selenbp1	1.7 ± 0.4	2.1 ± 0.4	2.6 ± 0.4
BC006809	Phosphomannomutase 1	Pmm1	2.7 ± 0.4	1.7 ± 0.4	1.5 ± 0.4
AI391218	Glutamate-ammonia ligase (glutamine synthase)*	Glul	1.7 ± 0.4	2.0 ± 0.4	1.9 ± 0.3
BB364488	Forkhead box o3a*	Foxo3a	1.9 ± 0.4	2.2 ± 0.4	1.8 ± 0.4
NM_007647	Ectonucleoside triphosphate diphosphohydrolase 5	Entpd5	2.8 ± 0.4	1.6 ± 0.4	1.9 ± 0.4
AV117919	Ectonucleoside triphosphate diphosphohydrolase 1	Entpd1	2.6 ± 0.5	1.6 ± 0.5	1.8 ± 0.4
BI251808	Cytochrome p450, family 1, subfamily b, polypeptide 1*	Cyp1b1	19.7 ± 0.4	8.5 ± 0.4	0.4
NM_009992	Cytochrome p450, family 1, subfamily a, polypeptide 1	Cyp1a1	57.7 ± 0.4	7.4 ± 0.4	0.4
AK003232	Carbonyl reductase 3	Cbr3	4.4 ± 0.4	1.5 ± 0.4	2.4 ± 0.4
BF682848	Cdna sequence bc055107*	BC05510	5.1 ± 0.4	2.1 ± 0.4	7.8 ± 0.4
NM_007436	Aldehyde dehydrogenase family 3, subfamily a1	7	10.6 ± 0.4	2.0 ± 0.5	5.0 ± 0.6
AI64939		Aldh3a1			11.8 ± 0.4
BB258019	Expressed sequence ai649393*	3	5.4 ± 0.4	1.6 ± 0.4	1.8 ± 0.4
NM_009626	Alcohol dehydrogenase 7 (class iv), mu or sigma polypeptide	Adh7	2.8 ± 0.4	2.1 ± 0.5	3.5 ± 0.5
BB144704	ATP-binding cassette, sub-family A (ABC1), member 1*	Abca1	2.2 ± 0.4	1.8 ± 0.4	1.7 ± 0.4
NM_025427	1190002H23 gene	1190002	2.5 ± 0.4	2.4 ± 0.4	3.2 ± 0.4
	*Expressed Sequence Tags (ESTs)	H23Rik			1.7 ± 0.4