

Supplementary Data

SUPPLEMENTARY TABLE S1. TOP 10 UP AND DOWN DIFFERENTIALLY REGULATED GENES IN EPIAIRWAY LUNG TISSUE, DAMS, AND OFFSPRING TISSUE AFTER MAINSTREAM CIGARETTE SMOKE EXPOSURE

	<i>Upregulated genes</i>			<i>Downregulated genes</i>		
	<i>Associated gene ID</i>	<i>p</i>	<i>Fold change</i>	<i>Associated gene ID</i>	<i>p</i>	<i>Fold change</i>
ELT	C-FOS	8.85E-05	3.3303	FN1	2.16E-02	5.3997
	CD300A	1.29E-02	2.8970	SPARC	8.55E-03	3.9802
	SAG	9.15E-03	2.5003	CRNN	1.18E-02	3.0898
	MATN1	2.19E-03	2.2019	ADAM19	1.38E-03	2.9293
	CXCR4	4.92E-03	2.1926	GPC6	1.06E-02	2.7941
	SCG3	7.13E-04	2.1032	MMP12	6.47E-03	2.7559
	FRMD1	2.14E-02	2.0700	MMP2	1.32E-02	2.7509
	ELMOD1	3.15E-03	1.8967	SRPX	2.36E-04	2.5735
	HERC2P9	2.20E-03	1.8487	APOE	1.33E-02	2.5694
	GLYATL2	3.67E-02	1.8263	SPOCK1	1.24E-02	2.4189
Dams	IGHG	1.28E-03	10.0077	IGKV8	4.55E-02	12.4052
	IGKV5	5.29E-04	2.7783	RETN	4.47E-03	4.5923
	GZMB	2.29E-04	2.5938	TMEM45B	3.93E-03	4.5373
	IGHV1	1.35E-03	2.4647	CAR3	8.08E-04	4.2618
	MTFR2	3.14E-03	2.1057	ADIPOQ	2.43E-03	4.2096
	IL1B	2.90E-03	2.0812	CFD	7.08E-03	3.3732
	HIST1HiB	4.13E-02	1.9907	TFF2	6.26E-03	2.7266
	KLRA17	6.94E-03	1.9576	THRSP	4.08E-03	2.4456
	ARNTL	1.08E-03	1.9509	PLIN1	1.07E-02	2.3777
	FEFV	7.98E-04	1.9452	MUC5B	3.06E-02	2.3440
Offspring	H2AB1	0.017866	17.57977	BEST1	8.17E-07	10.84912
	H2Q7	0.016136	15.42327	MBNL1	0.011763	10.23817
	TRMT61	0.0028	8.509253	AHDC1	8.64E-06	7.887322
	LY6D	0.010242	6.925174	BAIAP2L1	2.17E-05	7.718487
	STRA8	0.002144	6.818615	KCNQ1OT1	9.31E-06	7.359658
	H2DMB2	9.13E-04	6.113622	TNS1	5.16E-06	7.111162
	APOL7C	0.015917	5.175049	TJPs	2.51E-06	6.984259
	IFI44L	0.001521	5.093131	AGAP1	7.56E-06	6.975762
	HBB-BT	0.028783	4.819223	PITPNC1	0.00172	6.867369
	IKZF4	2.50E-04	4.78618	ZFHX3	7.63E-06	6.528332

ELT, EpiAirway lung tissue.

SUPPLEMENTARY TABLE S2. SOME OF THE LARGER GROUPS OF REVIGO-LINKED GENE ONTOLOGY TERMS OF CELLULAR COMPONENT AND MOLECULAR FUNCTION PROCESSES FOR THE EPIAIRWAY LUNG TISSUE

<i>CC-processes</i>	<i>Linked GO terms</i>	<i>MF-processes</i>	<i>Linked GO terms</i>
Extracellular region part	GO:0044421, GO:0005578, GO:0034361, GO:0005615, GO:0031012, GO:0005576.	Molecular binding.	GO:0001948, GO:0030674, GO:0003779, GO:0008092, GO:0008289, GO:0005488, GO:0005509, GO:0005543.
Basolateral plasma membrane.	GO:0016323, GO:0044459, GO:0005581, GO:0043234.	Structural molecule activity.	GO:0003777, GO:0008330, GO:0016817, GO:0017111, GO:0008233, GO:0003774, GO:0008237, GO:0004222, GO:0005198, GO:0005200, GO:0005201.
Cytoskeleton.	GO:0005856, GO:0043005, GO:0044463, GO:0005929, GO:0044449, GO:0044441, GO:0043292, GO:0043228, GO:0044430, GO:0043232, GO:0014069, GO:0001533, GO:0042995, GO:0070161, GO:0019861, GO:0030315.	Kinase, hydrolase and transferase activity.	GO:0008603, GO:0019207, GO:0047961, GO:0019205, GO:0016787.

CC, cellular component; GO, gene ontology.

SUPPLEMENTARY TABLE S3. SOME OF THE LARGER GROUPS OF REVIGO-LINKED GENE ONTOLOGY TERMS OF CELLULAR COMPONENT AND MOLECULAR FUNCTION PROCESSES FOR THE DAMS

<i>CC-processes</i>	<i>Linked GO terms</i>	<i>MF processes</i>	<i>Linked GO terms</i>
Chromosome, centromeric region and protein DNA interaction.	GO:0005694, GO:0000775, GO:0032133, GO:0030141, GO:0019814, GO:0032993.	Protein activity.	GO:0004144, GO:0003924, GO:0060089, GO:0004872, GO:0004869, GO:0004950, GO:0004896, GO:0004871, GO:0015144, GO:0005384, GO:0015291, GO:0015294.
Cell surface.	GO:0009897, GO:0005887, GO:0005886, GO:0044459, GO:0009986.	Cytokine activity.	GO:0008009, GO:0019956, GO:0005125, GO:0019955, GO:0001664, GO:0043515, GO:0005102, GO:0005070.
Extracellular space.	GO:0044421, GO:0044421, GO:0005615, GO:0042571, GO:0005576.	Binding.	GO:0001872, GO:0003823, GO:0005488, GO:0060090, GO:0030246, GO:0005515, GO:0001871.

MF, molecular function.

SUPPLEMENTARY TABLE S4. SOME OF THE LARGER GROUPS OF REVIGO LINKED GENE ONTOLOGY
TERMS OF CELLULAR COMPONENT AND MOLECULAR FUNCTION PROCESSES FOR THE OFFSPRING

<i>CC processes</i>	<i>Linked GO terms</i>	<i>MF processes</i>	<i>Linked GO terms</i>
Mitochondrion.	GO:0015629, GO:0032432 GO:0042641, GO:0016327, GO:0005938, GO:0044448, GO:0005832, GO:0044427, GO:0005694, GO:0005905, GO:0005581, GO:0043292, GO:0005737, GO:0016023, GO:0000932, GO:0044444, GO:0009898, GO:0005856, GO:0005829, GO:0044445, GO:0022626, GO:0022627, GO:0030286, GO:0005793, GO:0000178, GO:0005794, GO:0000792, GO:0043232, GO:0043229, GO:0044424, GO:0005770, GO:0005811, GO:0030117, GO:0034708, GO:0042613, GO:0042611, GO:0042579, GO:0044455, GO:0044429, GO:0005746, GO:0005739, GO:0032982, GO:0016460, GO:0043228, GO:0005720, GO:0031981, GO:0044428, GO:0005634, GO:0000313, GO:0031090, GO:0044422, GO:0048471, GO:0005777, GO:0046930, GO:0000502, GO:0005839, GO:0043234, GO:0045259, GO:0016469, GO:0030529, GO:0030880, GO:0030017, GO:0000803, GO:0015935, GO:0001725, GO:0042825, GO:0000151, GO:0005774, GO:0005773, GO:0031982.	Cytoskeletal protein binding	GO:0003779, GO:0003785, GO:0008013, GO:0005516, GO:0051087, GO:0008092, GO:0019899, GO:0051020, GO:0051427, GO:0042802, GO:0043560, GO:0005178, GO:0035257, GO:0048407, GO:0030674, GO:0032403, GO:0046983, GO:0019904, GO:0046982, GO:0017048, GO:0017124, GO:0046332, GO:0008134, GO:0051082.
		Motor activity	GO:0004559, GO:0042623, GO:0003689, GO:0004521, GO:0016817, GO:0016820, GO:0016788, GO:0015923, GO:0000146, GO:0003774, GO:0016791, GO:0034595, GO:0042578, GO:0033170, GO:0004540, GO:0004298, GO:0070003.
		Ubiquitin-protein transferase activity.	GO:0019200, GO:0003899, GO:0004364, GO:0004402, GO:0042054, GO:0004468, GO:0016278, GO:0004709, GO:0008168, GO:0008080, GO:0019205, GO:0004550, GO:0016773, GO:0016776, GO:0004672, GO:0008276, GO:0004674, GO:0004713, GO:0034062, GO:0016765, GO:0016741, GO:0016772, GO:0004714, GO:0004842.
Cell projection part.	GO:0044463, GO:0005929, GO:0030027, GO:0043005.	Zinc ion binding.	GO:0005524, GO:0043169, GO:0019992, GO:0005525, GO:0019001, GO:0043167, GO:0000287, GO:0030145, GO:0046872, GO:0003676, GO:0035091, GO:0017076, GO:0046914, GO:0008270.
Basement membrane.	GO:0005604, GO:0030935.		