Supplemenatry Table 3. Complete list of enriched pathways associated with airflow obstruction. Gene sets are grouped into modules based on functional overlap. An FDR less than 0.1% was used to designate significance for a given pathway. For each gene set, the number of significant genes (i.e., loci with an associated SNP with GWA P-value < 0.05) and the total number of pathway-associated genes mapped from the airflow obstruction GWAS are shown. Gene sets identical to those identified from the staged lung function pathway analysis are highlighted in bold.

Pathway/Gene set	Functional Module	FDR (%)	Significant genes	All mapped genes
HSA04514 CELL ADHESION MOLECULES	Adhesion	0	84	121
SYNAPSE	Adhesion	0	19	25
CELL RECOGNITION	Adhesion	0	14	17
SYNAPSE PART	Adhesion	0	11	12
HSA04510 FOCAL ADHESION	Adhesion	1.46E-04	113	183
APICOLATERAL PLASMA MEMBRANE	Adhesion	3.68E-04	18	28
APICAL JUNCTION COMPLEX	Adhesion	3.68E-04	18	28
CERAMIDEPATHWAY	Apoptosis	0	16	21
APOPTOSIS GO	Apoptosis	2.12E-04	195	408
PROGRAMMED CELL DEATH	Apoptosis	3.53E-04	195	409
HSA04210 APOPTOSIS	Apoptosis	5.78E-04	39	76
REGULATION OF APOPTOSIS	Apoptosis	8.98E-04	157	324
VOLTAGE GATED CALCIUM CHANNEL ACTIVITY	Channel/Transporter	0	15	17
ION CHANNEL ACTIVITY	Channel/Transporter	0	87	139
SUBSTRATE SPECIFIC CHANNEL ACTIVITY	Channel/Transporter	1.79E-05	89	146
CATION CHANNEL ACTIVITY	Channel/Transporter	1.11E-04	73	113
POTASSIUM CHANNEL ACTIVITY	Channel/Transporter	1.14E-04	34	49
VOLTAGE GATED CHANNEL ACTIVITY	Channel/Transporter	1.38E-04	48	70
SUBSTRATE SPECIFIC TRANSPORTER ACTIVITY	Channel/Transporter	1.39E-04	196	366
ACETYLCHOLINE BINDING	Channel/Transporter	1.41E-04	10	16
PHOSPHATE TRANSMEMBRANE TRANSPORTER ACTIVITY	Channel/Transporter	1.43E-04	10	12
VOLTAGE GATED CALCIUM CHANNEL COMPLEX	Channel/Transporter	1.61E-04	12	14
SUBSTRATE SPECIFIC TRANSMEMBRANE TRANSPORTER ACTIVITY	Channel/Transporter	1.65E-04	175	319
VOLTAGE GATED CATION CHANNEL ACTIVITY	Channel/Transporter	1.67E-04	46	64
LIPID TRANSPORTER ACTIVITY	Channel/Transporter	1.67E-04	16	27
INORGANIC ANION TRANSPORT	Channel/Transporter	1.69E-04	11	16
TRANSMEMBRANE TRANSPORTER ACTIVITY	Channel/Transporter	1.78E-04	188	348
CALCIUM CHANNEL ACTIVITY	Channel/Transporter	2.06E-04	24	31
GATED CHANNEL ACTIVITY	Channel/Transporter	4.48E-04	72	113
ION TRANSMEMBRANE TRANSPORTER ACTIVITY	Channel/Transporter	4.65E-04	143	258
CATION TRANSMEMBRANE TRANSPORTER ACTIVITY	Channel/Transporter	8.78E-04	114	199
VOLTAGE GATED POTASSIUM CHANNEL COMPLEX	Channel/Transporter	9.53E-04	27	39
POSITIVE REGULATION OF DEVELOPMENTAL PROCESS	Development	8.06E-05	112	206
REGULATION OF DEVELOPMENTAL PROCESS	Development	3.81E-04	211	415
HSA04330 NOTCH SIGNALING PATHWAY	Development	5.55E-04	23	41
INTEGRINPATHWAY	ECM	0	24	33
PROTEINACEOUS EXTRACELLULAR MATRIX	ECM	1.45E-04	62	92
EXTRACELLULAR MATRIX PART	ECM	1.75E-04	39	53
EXTRACELLULAR MATRIX	ECM	2.50E-04	62	93
COLLAGEN	ECM	2.52E-04	17	22
EXTRACELLULAR MATRIX STRUCTURAL CONSTITUENT	ECM	9.48E-04	19	25
GLUTAMATE SIGNALING PATHWAY	Glutamate	0	14	16
HSA04612 ANTIGEN PROCESSING AND PRESENTATION	Immunity	0	31	70
HSA04620 TOLL LIKE RECEPTOR SIGNALING PATHWAY	Immunity	0	55	97
TCRPATHWAY	Immunity	0	29	41
CD40PATHWAY	Immunity	1.10E-04	10	12
NKCELLSPATHWAY	Immunity	2.43E-04	14	19
HEMATOPOIETIN INTERFERON CLASS D200 DOMAIN CYTOKINE RECEPTOR ACTIVITY	Immunity	2.57E-04	23	29
NTHIPATHWAY	Immunity	3.59E-04	16	22
HSA04670 LEUKOCYTE TRANSENDOTHELIAL MIGRATION	Immunity	4.13E-04	57	97
INTERLEUKIN BINDING	Immunity	4.37E-04	15	22
INTERLEUKIN RECEPTOR ACTIVITY	Immunity	4.76E-04	13	17
TNFR1PATHWAY	Immunity	8.15E-04	17	28
SETPATHWAY	Immunity	8.73E-04	6	10
CARBOHYDRATE TRANSMEMBRANE TRANSPORTER ACTIVITY	Metabolism	0	11	15
PHOSPHORIC MONOESTER HYDROLASE ACTIVITY	Metabolism	0	67	103
PHOSPHOPROTEIN PHOSPHATASE ACTIVITY	Metabolism	0	53	76
HSA04940 TYPE I DIABETES MELLITUS	Metabolism	0	30	42
PHOSPHORIC ESTER HYDROLASE ACTIVITY	Metabolism	0	91	143
PHOSPHORUS OXYGEN LYASE ACTIVITY	Metabolism	0	9	9
HYDROLASE ACTIVITY ACTING ON ESTER BONDS	Metabolism	0	135	245
FRUCTOSE AND MANNOSE METABOLISM	Metabolism	1.75E-05	13	23
HSA00860 PORPHYRIN AND CHLOROPHYLL METABOLISM	Metabolism	1.16E-04	27	37
GLYCOSPHINGOLIPID METABOLISM	Metabolism	1.76E-04	15	21
INSULINPATHWAY	Metabolism	2.04E-04	14	20
HSA04930 TYPE II DIABETES MELLITUS	Metabolism	2.08E-04	27	42
MITOCHONDRIAPATHWAY	Metabolism	3.42E-04	11	19
HEME BIOSYNTHESIS	Metabolism	3.50E-04	5	8
DNA CATABOLIC PROCESS	Metabolism	3.66E-04	12	22
PORPHYRIN AND CHLOROPHYLL METABOLISM	Metabolism	6.07E-04	17	21
HSA00600 SPHINGOLIPID METABOLISM	Metabolism	7.72E-04	21	33
GLUCOSE METABOLIC PROCESS	Metabolism	7.74E-04	13	22
SMOOTH MUSCLE CONTRACTION	Other	0	85	134
NEGATIVE REGULATION OF SECRETION	Other	3.28E-05	9	12
AMINE BINDING	Other	1.20E-04	13	20

OXYGEN BINDING	**Other**	1.74E-04	15	21
PROTEIN N TERMINUS BINDING	**Other**	6.09E-04	23	37
PROTEIN HETERODIMERIZATION ACTIVITY	**Other**	7.45E-04	45	76
ENZYME REGULATOR ACTIVITY	**Other**	9.59E-04	154	293
CARDIACEGFPATHWAY	**Proliferation**	0	13	15
CHROMATIN BINDING	**Proliferation**	0	16	28
CHROMATIN	**Proliferation**	0	24	32
PROTEIN TYROSINE PHOSPHATASE ACTIVITY	**Proliferation**	0	38	52
HSA05214 GLIOMA	**Proliferation**	0	37	60
CYCLASE ACTIVITY	**Proliferation**	0	10	10
HSA04115 P53 SIGNALING PATHWAY	**Proliferation**	0	44	65
FBW7PATHWAY	**Proliferation**	0	7	8
PDGFPATHWAY	**Proliferation**	0	18	24
CDMACPATHWAY	**Proliferation**	0	14	15
P27PATHWAY	**Proliferation**	0	7	10
NUCLEAR CHROMATIN	**Proliferation**	0	10	13
KERATINOCYTEPATHWAY	**Proliferation**	0	30	42
IGF1PATHWAY	**Proliferation**	0	15	19
SKP2E2FPATHWAY	**Proliferation**	0	8	9
RACCYCDPATHWAY	**Proliferation**	0	18	22
CHROMOSOME	**Proliferation**	1.08E-04	62	112
CELL PROLIFERATION GO 0008283	**Proliferation**	1.13E-04	237	468
METPATHWAY	**Proliferation**	1.23E-04	24	34
EGFPATHWAY	**Proliferation**	1.70E-04	18	25
CDC42RACPATHWAY	**Proliferation**	1.70E-04	10	14
MICROTUBULE POLYMERIZATION OR DEPOLYMERIZATION	**Proliferation**	1.73E-04	8	10
DNA MODIFICATION	**Proliferation**	2.10E-04	8	10
BETA TUBULIN BINDING	**Proliferation**	2.63E-04	5	7
REGULATION OF CELL CYCLE	**Proliferation**	3.41E-04	91	173
CELL FATE COMMITMENT	**Proliferation**	3.45E-04	9	11
TGFBPATHWAY	**Proliferation**	3.62E-04	11	14
MICROTUBULE BASED PROCESS	**Proliferation**	3.68E-04	43	73
GHPATHWAY	**Proliferation**	4.00E-04	16	25
CDC42 PROTEIN SIGNAL TRANSDUCTION	**Proliferation**	4.40E-04	8	10
CHROMOSOMAL PART	**Proliferation**	7.29E-04	48	88
NUCLEAR CHROMOSOME	**Proliferation**	8.40E-04	25	46
POSITIVE REGULATION OF CELL PROLIFERATION	**Proliferation**	8.87E-04	76	136
REGULATION OF MITOTIC CELL CYCLE	**Proliferation**	8.92E-04	13	21
PHOSPHATIDYLINOSITOL SIGNALING SYSTEM	**Signaling**	0	49	79
RANKLPATHWAY	**Signaling**	0	11	12
PROTEIN KINASE REGULATOR ACTIVITY	**Signaling**	0	22	36
CALCIUM REGULATION IN CARDIAC CELLS	**Signaling**	0	81	130
HSA04720 LONG TERM POTENTIATION	**Signaling**	0	45	62
KINASE REGULATOR ACTIVITY	**Signaling**	0	26	43
ENZYME BINDING	**Signaling**	0	89	161
REGULATION OF RHO GTPASE ACTIVITY	**Signaling**	0	8	8
NOS1PATHWAY	**Signaling**	0	15	20
HSA04730 LONG TERM DEPRESSION	**Signaling**	0	50	70
HSA04070 PHOSPHATIDYLINOSITOL SIGNALING SYSTEM	**Signaling**	0	43	69
HSA04740 OLFACTORY TRANSDUCTION	**Signaling**	0	20	29
WNT SIGNALING	**Signaling**	1.67E-05	38	56
HSA04310 WNT SIGNALING PATHWAY	**Signaling**	1.69E-05	88	138
BREAST CANCER ESTROGEN SIGNALING	**Signaling**	1.82E-05	55	90
CK1PATHWAY	**Signaling**	1.89E-05	12	16
ACTIVATION OF PROTEIN KINASE ACTIVITY	**Signaling**	1.19E-04	18	24
HSA04916 MELANOGENESIS	**Signaling**	1.68E-04	60	94
REGULATION OF RAS GTPASE ACTIVITY	**Signaling**	1.72E-04	8	9
GUANYL NUCLEOTIDE EXCHANGE FACTOR ACTIVITY	**Signaling**	1.72E-04	30	41
REGULATION OF RAS PROTEIN SIGNAL TRANSDUCTION	**Signaling**	2.17E-04	13	16
G PROTEIN SIGNALING	**Signaling**	2.41E-04	53	85
PROTEIN KINASE BINDING	**Signaling**	2.48E-04	33	58
ST WNT CA2 CYCLIC GMP PATHWAY	**Signaling**	2.87E-04	12	19
HSA04912 GNRH SIGNALING PATHWAY	**Signaling**	3.39E-04	54	91
PROTEIN SERINE THREONINE PHOSPHATASE ACTIVITY	**Signaling**	3.62E-04	13	21
PLCPATHWAY	**Signaling**	4.16E-04	6	7
GTPASE REGULATOR ACTIVITY	**Signaling**	4.19E-04	66	109
INOSITOL PHOSPHATE METABOLISM	**Signaling**	4.43E-04	15	22
KINASE BINDING	**Signaling**	4.46E-04	37	66
RAS GUANYL NUCLEOTIDE EXCHANGE FACTOR ACTIVITY	**Signaling**	5.81E-04	15	18
MAPKPATHWAY	**Signaling**	6.04E-04	47	82
REGULATION OF SMALL GTPASE MEDIATED SIGNAL TRANSDUCTION	**Signaling**	6.71E-04	15	20
HSA04910 INSULIN SIGNALING PATHWAY	**Signaling**	7.50E-04	61	121
HSA04020 CALCIUM SIGNALING PATHWAY	**Signaling**	7.75E-04	97	155
PGC1APATHWAY	**Signaling**	9.94E-04	15	23
CARM1PATHWAY	**Transcription**	1.72E-05	10	12
TRANSCRIPTION FACTOR ACTIVITY	**Transcription**	1.11E-04	175	326
RNA POLYMERASE II TRANSCRIPTION FACTOR ACTIVITY	**Transcription**	1.25E-04	92	170
REGULATION OF TRANSCRIPTION DNA DEPENDENT	**Transcription**	2.10E-04	213	422
REGULATION OF RNA METABOLIC PROCESS	**Transcription**	3.47E-04	214	428
HSA03022 BASAL TRANSCRIPTION FACTORS	**Transcription**	3.63E-04	16	29
TRANSCRIPTION ELONGATION REGULATOR ACTIVITY	**Transcription**	7.27E-04	8	11