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Biomarker discovery for asthma phenotyping: From gene expression to the clinic

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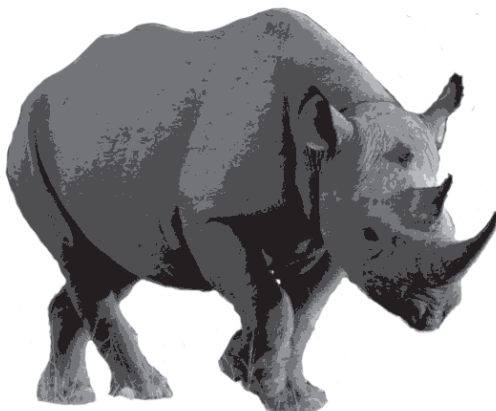
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CHAPTER 4

Supporting Information File

dsRNA-induced changes in gene expression profiles of primary nasal and bronchial epithelial cells from patients with asthma, rhinitis and controls



METHODS

Primary epithelial cell culture

Epithelial cell cultures were done as previously described (1). Primary cells were obtained by first digesting the biopsies and brushes with collagenase 4 (Worthington Biochemical Corp., Lakewood, NJ, USA) for 1 hour in Hanks' balanced salt solution (Sigma-Aldrich, Zwijndrecht, The Netherlands). Subsequently cells were washed with Hanks' balanced salt solution (HBSS) and resuspended in BEGM (Invitrogen, Breda, The Netherlands) and seeded in one well of a 6 wells plate. Cells were grown in fully humidified air containing 5% CO₂ at 37°C, and culture medium was replaced every other day. Cells were cultured to 80% confluence and were pre-incubated with BEBM for 24 hours prior to exposure to BEBM containing 20µg/ml poly(I:C) or with BEBM alone (control condition) for 24 hours before removal of supernatant and RNA extraction. For bronchial epithelial cells it took 14 days on average, and for nasal epithelial cells it took 24 days on average to grow to 80% confluence. There was no difference in time of culture between the three subject groups.

RNA extraction

Total RNA from each sample was extracted using Trizol (Life Technologies Inc., Gaithersburg, MD, USA) using manufacturer's protocol, followed by purification by nucleospin RNA II (Machery-Nagel, Düren, Germany). RNA concentration of all samples was measured on the nanodrop ND-1000 (NanoDrop Technologies Inc., Wilmington, DE, USA). The quality of the RNA was checked by using Agilent 2100 bio-analyser (Agilent Technologies, Palo Alto, CA, USA). All RIN scores were ≥9.5.

Microarray Affymetrix U133+ PM

Microarray analysis was done by previously published method [1]. Human Genome U133+ PM Genechip Array (Affymetrix inc., Santa Clara, CA, USA) representing more than 47,000 transcripts and variants, including over 33,000 well-characterized genes, was used in the analysis of the genes. The MicroArray Department (MAD) of the University of Amsterdam, a fully licensed microarray technologies centre for Affymetrix Genechip® platforms, performed the technical handling and the quality control of the microarray experiments. The quality of the images was checked by visual inspection and all raw data passed quality criteria based on borderplots, pseudocolor slide images, RNA degradation plots, box and density plots, RI plots (against a pseudoreference), correlation and PCA plots.

Real-time polymerase chain reaction and analysis

Quantitative real-time PCR was used to validate the differential expression of selected genes. A random selection of 9 genes was used that showed a variance of responses to Poly(I:C). PCR was performed on Bio-Rad CFX96 real-time PCR detection system (Bio-Rad, Veenendaal, The Netherlands). SYBR® Green primer sequences for *IL13-Ra2*, *EREG*, *PDE4D*, *IL1-β*, *IP-10*, *TIMP2*, *IL8*, β -actin and *GAPDH* were obtained from Sigma-Aldrich (Sigma-Aldrich, Zwijndrecht, The Netherlands). The following primers were used: *IL13-Ra2*; sense: TGC-TCA-GAT-GAC-GGA-ATT-TGG, antisense: TGG-TAG-CCA-GAA-ACG-TAG-CAA-AG, *EREG*; sense: ATC-CTG-GCA-TGT-GCT-AGG-GT, antisense: GTG-CTC-CAG-AGG-TCA-GCC-AT, *PDE4D*; sense: GGC-CTC-CAA-CAA-GTT-TAA-AA, antisense: ACC-AGA-CAA-CTC-TGC-TAT-TCT, *IL1-β*; sense: GGA-TAT-GGA-GCA-ACA-AGT-GG, antisense: ATG-TAC-CAG-TTG-GGG-AAC-TG, *IP-10*; sense: TGA-AAT-TAT-TCC-TGC-AAG-CCA-AT, antisense: CAG-ACA-TCT-CTT-CTC-ACC-CTT-CTT-T, *TIMP2*; sense: ATA-AGC-AGG-CCT-CCA-ACG-C, antisense: GAG-CTG-GAC-CAG-TCG-AAA-CC, *IL8*; sense: CCA-CAC-TGC-GCC-AAC-ACA-GAA-ATT-ATT-G, antisense: GCC-CTC-TTC-AAA-AAC-TTC-TCC-ACA-ACC-C, β -actin; sense: TGA-GCG-CGG-CTA-CAG-CTT, antisense: TCC-TTA-ATG-TCA-CGC-ACG-ATT-T, *GAPDH*; sense: GAA-GGT-GAA-GGT-CGG-AGT-C, antisense: GAA-GAT-GGT-GAT-GGG-ATT-TC. For *ATF3* and *DUSP1* we used TaqMan® gene expression assays from Applied Biosystems (Nieuwerkerk a/d IJssel, The Netherlands) with the following assay IDs: ATF3; HS00231069_M1, DUSP1; HS006102757_G1.

Correlations between fold changes (FC) within the microarray data and the real-time PCR data were determined using Pearson's correlation.

RESULTS

Validation of microarray data

The results of this microarray experiment were validated by independent real time PCR on the same starting material used for the microarray analysis. We first determined the expression of the housekeeping genes (ACTB and GAPDH) which were not statistically significantly induced by poly(I:C). Table S1 shows the fold changes (FC) calculated from the microarray data and the real-time PCR-derived expression. Statistical analysis revealed a high level of correspondence ($R=0.929$, $P<0.0001$) between the microarray data and the real-time PCR (Figure S1). FCs were logtransformed because of such large variances.

Table S1. Validatory PCR of housekeeping genes and significantly different genes

	Bronchial epithelial cells					
	Healthy		Allergic rhinitis		Allergic rhinitis & asthma	
	PCR FC	Microarray FC	PCR FC	Microarray FC	PCR FC	Microarray FC
ACTB	1.16	-1.03	1.52	1.04	1.38	-1.11
GAPDH	-1.83	-1.00	-1.82	-1.03	-1.49	-1.03
ATF3	1.43	2.37	-1.78	1.21	-2.10	1.51
CXCL10	568.10	263.55	214.38	121.34	170.31	88.92
DUSP1	5.78	6.71	4.01	2.35	4.96	4.16
EREG	1.37	2.07	-3.59	-1.83	-1.26	1.17
IL13RA2	10.59	14.62	7.32	8.66	7.41	13.44
IL1B	2.83	3.52	1.30	1.75	2.43	3.11
IL8	32.48	13.98	44.45	23.40	26.06	16.60
PDE4D	-3.63	-1.33	-6.19	-1.15	-3.81	-1.33
TIMP2	1.50	2.67	1.29	2.39	1.52	2.56

	Nasal epithelial cells					
	Healthy		Allergic rhinitis		Allergic rhinitis & asthma	
	PCR FC	Microarray FC	PCR FC	Microarray FC	PCR FC	Microarray FC
ACTB	-1.43	-1.04	1.04	-1.05	-1.03	-1.06
GAPDH	-1.92	-1.04	-2.45	-1.06	-1.77	-1.02
ATF3	9.61	5.02	4.35	3.97	1.69	2.75
CXCL10	465.72	74.79	587.32	175.30	161.27	72.35
DUSP1	11.45	17.60	7.48	15.22	5.98	7.17
EREG	3.90	3.13	1.67	3.24	1.03	1.35
IL13RA2	22.16	12.13	17.20	14.39	6.15	5.83
IL1B	5.25	3.33	3.02	4.04	4.14	3.75
IL8	178.73	73.41	122.11	64.77	63.85	23.72
PDE4D	-1.09	-1.03	-7.87	-1.29	-1.86	-1.04
TIMP2	3.02	4.25	1.77	5.73	1.31	2.97

PCR expression is given as fold change (FC).

Table S2. dsRNA-induced genes in upper and lower airways

	Healthy		Healthy		Rhinitis		Rhinitis		Asthma		Asthma	
	Nose		Bronchus		Nose		Bronchus		Nose		Bronchus	
<u>Probesets</u> <i>P</i> <0.05	17402		13424		15538		7517		6996		8560	
<u>Probesets</u> <i>P</i> <0.05 & FC>4	1255		550		1439		517		517		427	
<u>Genes</u> <i>P</i> <0.05	10163	↑4636 ↓5527	8342	↑3638 ↓4704	9353	↑4204 ↓5149	5190	↑2294 ↓2896	4919	↑2293 ↓2626	5810	↑2621 ↓3189
<u>Genes</u> <i>P</i> <0.05 & FC>4	894	↑528 ↓366	401	↑274 ↓127	1037	↑586 ↓451	391	↑244 ↓147	383	↑275 ↓108	319	↑227 ↓92

FC, fold change; *P*, *p*-value adjusted for multiple testing

Table S3A. Genes assigned to GO-cluster *response to virus* induced in the upper airways

Gene symbol	Venn diagram	FC Healthy	FC Rhinitis	FC Asthma
C7orf25 /// PSMA2	A	1.30		
CFL1	A	-1.17		
LILRB1	A	1.21		
PIM2	A	-1.32		
POLR3F	A	-1.22		
ACTA2	B	-1.27	-1.34	
BANF1	B	-1.56	-1.59	
BECN1	B	-1.25	-1.25	
BNIP3L	B	1.53	1.76	
CCL22	B	1.42	1.33	
CREBZF	B	-1.57	-1.53	
CYP1A1	B	-2.60	-1.73	
DNAJC3	B	1.95	1.81	
EEF1G /// TUT1	B	-1.77	-1.85	
ENO1	B	-1.33	-1.38	
FOSL1	B	3.39	3.90	
HBXIP	B	-1.23	-1.32	
IFNAR1	B	1.53	1.39	
IL12A	B	2.64	2.96	
IL28B	B	4.53	7.30	
LYST	B	1.99	1.73	
MAVS	B	-2.00	-1.69	
POLR3A	B	1.53	1.65	
POLR3H	B	-2.61	-2.44	
POLR3K	B	-2.95	-2.52	
TBK1	B	1.83	1.49	
ABCE1	C	-3.91	-4.42	-2.48
ACE2	C	15.24	12.25	7.55
AP1S1	C	-1.73	-1.63	-1.40
APOBEC3F	C	2.78	2.80	2.29
APOBEC3G	C	11.38	10.82	5.06
BCL2	C	-1.24	-1.40	-1.46
BCL3	C	3.08	3.17	2.43
BNIP3	C	2.05	2.05	1.66
BST2	C	45.73	79.99	27.17
C19orf2	C	-1.60	-1.90	-1.43
CCDC130	C	1.40	1.41	1.27
CCL4	C	255.13	243.83	39.32
CCL5	C	517.58	717.90	148.81
CCT5	C	-3.44	-3.23	-2.21
DDX58	C	25.21	38.03	14.32
DUOX2	C	3.01	3.86	2.03
EIF2AK2	C	4.09	6.12	3.56
GPAM	C	-4.25	-4.77	-2.70
GTF2F1	C	1.31	1.55	1.33
HERC5	C	46.50	72.10	26.64

Table S3A. (continued)

Gene symbol	Venn diagram	FC Healthy	FC Rhinitis	FC Asthma
HNRNPUL1	C	-1.35	-1.37	-1.27
HSPB1	C	-1.99	-2.25	-1.80
IFI16	C	1.70	1.59	1.74
IFI35	C	38.88	67.89	27.76
IFI44	C	64.88	164.77	42.51
IFIH1	C	18.03	22.18	10.42
IFITM1	C	8.15	10.90	6.25
IFITM2	C	2.92	2.99	2.45
IFITM3	C	2.27	2.25	1.93
IFNAR2	C	3.40	3.13	2.38
IFNB1	C	3.17	2.77	1.77
IFNE	C	-1.88	-2.68	-2.45
IFNGR1	C	1.82	1.48	1.68
IFNGR2	C	2.45	2.36	1.99
IFNK	C	3.23	4.05	3.67
IL23A	C	20.52	24.06	6.43
IL28A	C	13.29	15.78	4.49
IL29	C	25.01	20.48	7.40
IL6	C	20.34	11.13	10.02
IRF3	C	1.57	1.56	1.40
IRF7	C	28.26	40.73	16.88
IRF9	C	2.87	3.41	2.94
ISG15	C	23.50	46.89	15.63
ISG20	C	32.65	41.94	14.82
ITCH	C	2.67	3.02	2.43
IVNS1ABP	C	-5.44	-6.14	-2.57
MST1R	C	2.95	3.39	2.04
MX1	C	30.17	92.06	21.00
MX2	C	115.45	287.26	72.32
MYD88	C	2.60	2.98	2.37
NLRC5	C	38.61	38.77	12.56
ODC1	C	-2.23	-1.78	-2.04
PCBP2	C	-1.49	-1.56	-1.38
PLSCR1	C	6.38	8.28	5.22
POLR3B	C	-1.44	-1.63	-1.45
POLR3C	C	1.42	1.30	1.27
POLR3D	C	1.70	1.91	1.55
POLR3E	C	-2.14	-2.32	-1.67
POLR3G	C	-1.87	-2.15	-1.36
PRKRA	C	-1.90	-2.11	-1.61
PVR	C	1.93	1.81	1.54
RELA	C	2.38	2.45	1.98
RPS15A	C	-8.15	-9.98	-4.19
RSAD2	C	260.58	638.34	98.63
SAMHD1	C	16.36	31.76	12.09
SIVA1	C	-2.16	-2.48	-1.57

Table S3A. (continued)

Gene symbol	Venn diagram	FC Healthy	FC Rhinitis	FC Asthma
STAT1	C	13.66	17.43	10.47
STAT2	C	3.50	4.78	3.40
STMN1	C	-5.68	-4.89	-2.96
TICAM1	C	3.14	3.12	2.38
TLR3	C	11.82	10.00	6.68
TNF	C	8.16	6.72	4.38
TRIM11	C	1.73	1.78	1.59
TRIM22	C	4.90	5.16	4.61
TRIM25	C	6.43	8.67	4.13
TRIM5	C	3.81	3.90	2.94
UNC13D	C	1.60	1.76	1.53
UNC93B1	C	2.40	3.27	2.33
XPO1	C	-1.51	-1.63	-1.41
XPR1	C	-1.76	-2.49	-1.23
ZC3HAV1	C	16.13	18.83	9.78
ZNF175	C	1.67	1.80	1.32
ABCC9	E		1.23	
CLU	E		-1.26	
DMBT1	E		1.44	
MICA /// MICB	E		1.21	
PSMA2	E		-1.27	
PTPRC	E		1.24	
IRAK3	F		-1.82	1.38
CDK6	G			-1.41

Venn diagram: A, healthy specific; B, overlap healthy–rhinitis; C, overlap all groups; D, overlap healthy–asthma; E, rhinitis specific; F, overlap rhinitis–asthma; G, asthma specific; FC, fold change.

Table S3B. Genes assigned to GO-cluster *response to virus* induced in the lower airways

Gene symbol	Venn diagram	FC Healthy	FC Rhinitis	FC Asthma
BANF1	A	-1.36		
BECN1	A	-1.23		
BNIP3L	A	1.30		
CXCL12	A	-1.20		
ENO1	A	-1.21		
IRF3	A	1.31		
MAVS	A	-1.47		
MST1R	A	1.37		
POLR3D	A	1.40		
POLR3G	A	-1.62		
PSMA2	A	-1.30		
RNASEL	A	-1.35		
SIVA1	A	-1.73		
XPR1	A	-1.45		
BNIP3	B	1.55	1.69	
IFNAR1	B	1.23	1.42	
IFNB1	B	1.60	1.47	
IFNGR1	B	1.64	1.50	
IL28B	B	2.40	2.16	
LYST	B	1.73	1.68	
POLR3E	B	-1.62	-1.93	
POLR3K	B	-2.11	-2.00	
ZNF175	B	1.54	1.88	
ABCE1	C	-2.06	-2.49	-1.89
APOBEC3F	C	1.90	1.76	2.11
APOBEC3G	C	6.62	5.28	8.11
BCL3	C	2.44	2.45	1.98
BST2	C	24.79	48.02	13.00
C19orf2	C	-1.42	-1.56	-1.43
CCL4	C	83.19	20.90	35.57
CCL5	C	736.54	322.77	231.87
CCT5	C	-2.10	-1.80	-1.85
CDK6	C	-1.46	-1.30	-1.52
CREBZF	C	-1.29	-1.36	-1.38
CYP1A1	C	-1.91	-2.85	-2.10
DDX58	C	28.49	23.14	18.03
DNAJC3	C	1.48	1.36	1.40
DUOX2	C	9.56	4.80	7.87
EEF1G /// TUT1	C	-1.53	-1.57	-1.38
EIF2AK2	C	4.63	5.40	3.60
GPAM	C	-2.90	-2.26	-2.44
HERC5	C	35.87	25.29	27.95
HNRNPUL1	C	-1.26	-1.27	-1.25
HSPB1	C	-1.53	-1.74	-1.61
IFI35	C	48.10	39.73	31.80
IFI44	C	236.92	70.93	104.82
IFIH1	C	18.21	6.27	12.76
IFITM1	C	14.95	10.61	11.08
IFITM2	C	3.33	3.65	3.48
IFITM3	C	2.97	3.53	2.73
IFNAR2	C	2.43	2.54	2.36
IFNGR2	C	2.25	1.87	2.01
IL23A	C	9.34	12.37	7.90

Table S3B. (continued)

Gene symbol	Venn diagram	FC Healthy	FC Rhinitis	FC Asthma
IL28A	C	4.21	4.48	4.99
IL29	C	6.80	3.95	4.96
IL6	C	8.80	4.92	7.60
IRF7	C	26.30	19.88	20.32
IRF9	C	4.44	3.44	3.67
ISG15	C	49.88	64.58	32.63
ISG20	C	10.51	7.46	8.46
ITCH	C	1.93	1.75	1.86
IVNS1ABP	C	-2.43	-2.16	-2.07
MX1	C	140.44	175.11	67.81
MX2	C	201.46	163.72	96.81
MYD88	C	2.17	2.32	2.19
NLRC5	C	17.88	12.59	11.61
ODC1	C	-2.02	-2.87	-2.11
PCBP2	C	-1.29	-1.29	-1.31
PLSCR1	C	7.77	7.54	5.70
POLR3A	C	1.49	1.61	1.29
PRKRA	C	-1.59	-1.41	-1.57
RELA	C	1.91	1.62	1.69
RPS15A	C	-4.45	-4.65	-3.17
RSAD2	C	363.02	304.55	167.47
SAMHD1	C	17.56	3.38	13.59
STAT1	C	16.34	6.17	11.13
STAT2	C	3.40	2.97	2.59
TBK1	C	1.44	1.42	1.30
TICAM1	C	2.30	2.15	2.31
TLR3	C	6.70	3.71	5.54
TNF	C	4.81	3.95	4.35
TRIM22	C	6.91	9.76	4.63
TRIM25	C	3.96	3.13	3.72
TRIM5	C	2.60	2.55	2.51
UNC13D	C	1.50	1.43	1.45
UNC93B1	C	2.52	1.82	2.21
ZC3HAV1	C	12.00	15.83	8.50
ACE2	D	6.49		5.12
ACTA2	D	-1.36		-1.38
AP1S1	D	-1.46		-1.34
BCL2	D	-1.43		-1.42
CCDC130	D	1.26		1.23
FOSL1	D	2.40		1.89
GTF2F1	D	1.25		1.29
IFI16	D	1.50		1.62
IRAK3	D	1.40		1.56
NLRP3	D	1.77		1.46
POLR3H	D	-1.74		-1.45
PVR	D	1.65		1.60
STMN1	D	-2.24		-1.93
TRIM11	D	1.59		1.54
XPO1	D	-1.25		-1.31
IFNE	E		-2.22	
CLU	G			-1.35

Venn diagram: A, healthy specific; B, overlap healthy–rhinitis; C, overlap all groups; D, overlap healthy–asthma; E, rhinitis specific; F, overlap rhinitis–asthma; G, asthma specific; FC, fold change.

Table S4. Genes induced in the upper airways of healthy controls and allergic rhinitis patients, assigned to GO cluster *Mitochondrion*

Gene alias	Gene name/description
AARS2	alanyl-tRNA synthetase 2, mitochondrial (putative)
ABCA12	ATP-binding cassette, sub-family A (ABC1), member 12
ABCF2	ATP-binding cassette, sub-family F (GCN20), member 2
ACACB	acetyl-CoA carboxylase beta
ACAD8	acyl-CoA dehydrogenase family, member 8
ACAD9	acyl-CoA dehydrogenase family, member 9
ACADM	acyl-CoA dehydrogenase, C-4 to C-12 straight chain
ACADVL	acyl-CoA dehydrogenase, very long chain
ACN9	ACN9 homolog (<i>S. cerevisiae</i>)
ACO2	aconitase 2, mitochondrial
ACOT13	acyl-CoA thioesterase 13
ACP6	acid phosphatase 6, lysophosphatidic
ACSF2	acyl-CoA synthetase family member 2
ACSL1	acyl-CoA synthetase long-chain family member 1
ACSS1	acyl-CoA synthetase short-chain family member 1
ADCK4	aarF domain containing kinase 4
ADH5	alcohol dehydrogenase 5 (class III), chi polypeptide
ADO	2-aminoethanethiol (cysteamine) dioxygenase
AIFM1	apoptosis-inducing factor, mitochondrion-associated, 1
AK2	adenylate kinase 2
AK3	adenylate kinase 3
AKAP10	A kinase (PRKA) anchor protein 10
AKT2	v-akt murine thymoma viral oncogene homolog 2
ALDH1B1	aldehyde dehydrogenase 1 family, member B1
ALDH1L1	aldehyde dehydrogenase 1 family, member L1
ALDH1L2	aldehyde dehydrogenase 1 family, member L2
ALDH2	aldehyde dehydrogenase 2 family (mitochondrial)
ALDH5A1	aldehyde dehydrogenase 5 family, member A1
ALKBH1	alkB, alkylation repair homolog 1 (<i>E. coli</i>)
ALKBH7	alkB, alkylation repair homolog 7 (<i>E. coli</i>)
AP2M1	adaptor-related protein complex 2, mu 1 subunit
APOA1BP	apolipoprotein A-I binding protein
ARG2	arginase, type II
ARMC10	armadillo repeat containing 10
ATIC	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase
ATP5B	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, beta polypeptide
ATP5C1	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, gamma polypeptide 1
ATP5D	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, delta subunit
ATP5G1	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit C1 (subunit 9)
ATP5G2	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit C2 (subunit 9)
ATP5G3	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit C3 (subunit 9)
ATP5H	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit d
ATP5I	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit E
ATP5J	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit F6

Table S4. (continued)

Gene alias	Gene name/description
ATP5J2	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit F2
ATP5L	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit G
ATP5S	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit s (factor B)
ATP5SL	ATP5S-like
ATPAF1	ATP synthase mitochondrial F1 complex assembly factor 1
BAX	BCL2-associated X protein
BBOX1	butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1
BCL2L1	BCL2-like 1
BCS1L	BCS1-like (yeast)
BDH2	3-hydroxybutyrate dehydrogenase, type 2
BNIP3L	BCL2/adenovirus E1B 19kDa interacting protein 3-like
BOLA1	boIA homolog 1 (E. coli)
BPHL	biphenyl hydrolase-like (serine hydrolase)
BRP44	brain protein 44
C10orf2	chromosome 10 open reading frame 2
C10orf58	chromosome 10 open reading frame 58
C12orf10	chromosome 12 open reading frame 10
C12orf62	chromosome 12 open reading frame 62
C14orf156	chromosome 14 open reading frame 156
C14orf159	chromosome 14 open reading frame 159
C15orf62	chromosome 15 open reading frame 62
C17orf61	chromosome 17 open reading frame 61
C17orf90	chromosome 17 open reading frame 90
C18orf19	chromosome 18 open reading frame 19
C19orf70	chromosome 19 open reading frame 70
C1orf151	chromosome 1 open reading frame 151
C20orf24	chromosome 20 open reading frame 24
C21orf33	chromosome 21 open reading frame 33
C2orf47	chromosome 2 open reading frame 47
C2orf64	chromosome 2 open reading frame 64
C3orf1	chromosome 3 open reading frame 1
C3orf31	Chromosome 3 open reading frame 31
C4orf46 /// TOMM7	chromosome 4 open reading frame 46 /// translocase of outer mitochondrial membrane 7 homolog (yeast)
C5orf54	chromosome 5 open reading frame 54
C6orf57	chromosome 6 open reading frame 57
C7orf55	chromosome 7 open reading frame 55
C7orf55 /// LUC7L2	chromosome 7 open reading frame 55 /// LUC7-like 2 (S. cerevisiae)
C9orf46	chromosome 9 open reading frame 46
CA5B	carbonic anhydrase VB, mitochondrial
CA5BP	Carbonic anhydrase VB pseudogene
CAV1	caveolin 1, caveolae protein, 22kDa
CBARA1	calcium binding atopy-related autoantigen 1
CCBL2	cysteine conjugate-beta lyase 2
CCDC123	coiled-coil domain containing 123

Table S4. (continued)

Gene alias	Gene name/description
CCDC58	coiled-coil domain containing 58
CCT7	chaperonin containing TCP1, subunit 7 (eta)
CDS2 /// LOC149832	CDP-diacylglycerol synthase (phosphatidate cytidyltransferase) 2
CECR5	cat eye syndrome chromosome region, candidate 5
CHCHD1	coiled-coil-helix-coiled-coil-helix domain containing 1
CHCHD2	coiled-coil-helix-coiled-coil-helix domain containing 2
CHCHD7	coiled-coil-helix-coiled-coil-helix domain containing 7
CISD2	CDGSH iron sulfur domain 2
CISD3	CDGSH iron sulfur domain 3
CKMT1A /// CKMT1B	creatine kinase, mitochondrial 1A /// creatine kinase, mitochondrial 1B
CLN3	ceroid-lipofuscinosis, neuronal 3
COL4A3BP	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein
COMTD1	catechol-O-methyltransferase domain containing 1
COQ10A	coenzyme Q10 homolog A (<i>S. cerevisiae</i>)
COQ3	coenzyme Q3 homolog, methyltransferase (<i>S. cerevisiae</i>)
COQ5	coenzyme Q5 homolog, methyltransferase (<i>S. cerevisiae</i>)
COQ6	coenzyme Q6 homolog, monooxygenase (<i>S. cerevisiae</i>)
COQ9	coenzyme Q9 homolog (<i>S. cerevisiae</i>)
COX10	COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransferase (yeast)
COX15	COX15 homolog, cytochrome c oxidase assembly protein (yeast)
COX4I1	cytochrome c oxidase subunit IV isoform 1
COX4NB	COX4 neighbor
COX5B	cytochrome c oxidase subunit Vb
COX6B1	cytochrome c oxidase subunit VIb polypeptide 1 (ubiquitous)
COX6C	cytochrome c oxidase subunit VIc
COX7A2L	cytochrome c oxidase subunit VIIa polypeptide 2 like
COX7B	cytochrome c oxidase subunit VIIb
COX7C	cytochrome c oxidase subunit VIIc
CPOX	coproporphyrinogen oxidase
CPS1	carbamoyl-phosphate synthase 1, mitochondrial
CPT2	carnitine palmitoyltransferase 2
CRAT	carnitine O-acetyltransferase
CS	citrate synthase
CYB5B	cytochrome b5 type B (outer mitochondrial membrane)
CYC1	cytochrome c-1
CYP1A1	cytochrome P450, family 1, subfamily A, polypeptide 1
CYP2A1	cytochrome P450, family 24, subfamily A, polypeptide 1
DAB1 /// OMA1	disabled homolog 1 (<i>Drosophila</i>) /// OMA1 homolog, zinc metallopeptidase (<i>S. cerevisiae</i>)
DARS2	aspartyl-tRNA synthetase 2, mitochondrial
DBI	diazepam binding inhibitor (GABA receptor modulator, acyl-CoA binding protein)
DECR1	2,4-dienoyl CoA reductase 1, mitochondrial
DHODH	dihydroorotate dehydrogenase
DHRS4 /// DHRS4L2	dehydrogenase/reductase (SDR family) member 4 /// dehydrogenase/reductase (SDR family) member 4 like 2

Table S4. (continued)

Gene alias	Gene name/description
DLD	dihydrolipoamide dehydrogenase
DLST	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)
DNAJA3	DnaJ (Hsp40) homolog, subfamily A, member 3
DNAJC19	DnaJ (Hsp40) homolog, subfamily C, member 19
DNLZ	DNL-type zinc finger
DNM3	dynamain 3
DRG2	developmentally regulated GTP binding protein 2
DYNLL1	dynein, light chain, LC8-type 1
EARS2	glutamyl-tRNA synthetase 2, mitochondrial (putative)
ECH1	enoyl CoA hydratase 1, peroxisomal
EHHADH	enoyl-CoA, hydratase/3-hydroxyacyl CoA dehydrogenase
ELAC2	elaC homolog 2 (E. coli)
ENDOG	endonuclease G
ENO1	enolase 1, (alpha)
ETFA	electron-transfer-flavoprotein, alpha polypeptide
ETFB	electron-transfer-flavoprotein, beta polypeptide
FAHD1	fumarylacetoacetate hydrolase domain containing 1
FAM110B	family with sequence similarity 110, member B
FAM136A	family with sequence similarity 136, member A
FAM175A	family with sequence similarity 175, member A
FAM82B	Family with sequence similarity 82, member B
FANCG	Fanconi anemia, complementation group G
FARS2	Phenylalanyl-tRNA synthetase 2, mitochondrial
FASTK	Fas-activated serine/threonine kinase
FDPS	farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase)
FDX1	ferredoxin 1
FECH	ferrochelataase
FEZ1	fasciculation and elongation protein zeta 1 (zygin I)
FIBP	fibroblast growth factor (acidic) intracellular binding protein
FIS1	fission 1 (mitochondrial outer membrane) homolog (<i>S. cerevisiae</i>)
FUNDC2	FUN14 domain containing 2
FXC1	fracture callus 1 homolog (rat)
FXN	frataxin
GABBR1 /// UBD	gamma-aminobutyric acid (GABA) B receptor, 1 /// ubiquitin D
GAD1	glutamate decarboxylase 1 (brain, 67kDa)
GADD45GIP1	growth arrest and DNA-damage-inducible, gamma interacting protein 1
GAS8	growth arrest-specific 8
GBAS	glioblastoma amplified sequence
GCDH	glutaryl-CoA dehydrogenase
GHITM	growth hormone inducible transmembrane protein
GJA1	gap junction protein, alpha 1, 43kDa
GK	glycerol kinase
GK /// GK3P	glycerol kinase /// glycerol kinase 3 pseudogene
GK3P	glycerol kinase 3 pseudogene
GLOD4	glyoxalase domain containing 4

Table S4. (continued)

Gene alias	Gene name/description
GLS2	glutaminase 2 (liver, mitochondrial)
GLT8D1	Glycosyltransferase 8 domain containing 1
GLYCTK	glycerate kinase
GM2A	GM2 ganglioside activator
GNPAT	glyceronephosphate O-acyltransferase
GPX4	glutathione peroxidase 4 (phospholipid hydroperoxidase)
GRAMD4	GRAM domain containing 4
GRN	granulin
GTF2H4	general transcription factor IIH, polypeptide 4, 52kDa
GTPBP3	GTP binding protein 3 (mitochondrial)
HCCS	holocytochrome c synthase
HDDC2	HD domain containing 2
HEBP1	heme binding protein 1
HEBP2	heme binding protein 2
HEMK1	HemK methyltransferase family member 1
HIBADH	3-hydroxyisobutyrate dehydrogenase
HINT2	histidine triad nucleotide binding protein 2
HK1	hexokinase 1
HK2	hexokinase 2
HLCS	holocarboxylase synthetase (biotin-(propionyl-CoA-carboxylase (ATP-hydrolysing)) ligase)
HRSP12	Heat-responsive protein 12
HSD17B10	hydroxysteroid (17-beta) dehydrogenase 10
HSD17B8	hydroxysteroid (17-beta) dehydrogenase 8
HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1
HSPE1	heat shock 10kDa protein 1 (chaperonin 10)
ICT1	immature colon carcinoma transcript 1
IDH1	Isocitrate dehydrogenase 1 (NADP+), soluble
IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial
IDH3A	isocitrate dehydrogenase 3 (NAD+) alpha
IDH3B	isocitrate dehydrogenase 3 (NAD+) beta
IMMP2L	IMP2 inner mitochondrial membrane peptidase-like (<i>S. cerevisiae</i>)
ISCA1	iron-sulfur cluster assembly 1 homolog (<i>S. cerevisiae</i>)
ISOC2	isochorismatase domain containing 2
KARS	lysyl-tRNA synthetase
KIAA0141	KIAA0141
KMO	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)
KRT5	keratin 5
L2HGDH	L-2-hydroxyglutarate dehydrogenase
LARS2	leucyl-tRNA synthetase 2, mitochondrial
LETM1	leucine zipper-EF-hand containing transmembrane protein 1
LETMD1	LETM1 domain containing 1
LGALS3	Lectin, galactoside-binding, soluble, 3
LIMK2	LIM domain kinase 2
LIPT1	lipoyltransferase 1
LONP1	lon peptidase 1, mitochondrial

Table S4. (continued)

Gene alias	Gene name/description
LRP5	Low density lipoprotein receptor-related protein 5
LYRM1	LYR motif containing 1
LYRM2	LYR motif containing 2
LYRM4	LYR motif containing 4
LYRM5	LYR motif containing 5
MARS2	methionyl-tRNA synthetase 2, mitochondrial
MAT2B	Methionine adenosyltransferase II, beta
MAVS	mitochondrial antiviral signaling protein
MCAT	malonyl CoA:ACP acyltransferase (mitochondrial)
MCEE	methylmalonyl CoA epimerase
MCL1	myeloid cell leukemia sequence 1 (BCL2-related)
ME3	malic enzyme 3, NADP(+)-dependent, mitochondrial
MECR	mitochondrial trans-2-enoyl-CoA reductase
MFF	mitochondrial fission factor
MIPEP	mitochondrial intermediate peptidase
MLXIP	MLX interacting protein
MMACHC	methylmalonic aciduria (cobalamin deficiency) cblC type, with homocystinuria
MOSC1	MOCO sulphurase C-terminal domain containing 1
MPST	mercaptopyruvate sulfurtransferase
MPV17	MpV17 mitochondrial inner membrane protein
MPV17L2	MPV17 mitochondrial membrane protein-like 2
MRPL1	mitochondrial ribosomal protein L1
MRPL11	mitochondrial ribosomal protein L11
MRPL12	Mitochondrial ribosomal protein L12
MRPL13	mitochondrial ribosomal protein L13
MRPL16	mitochondrial ribosomal protein L16
MRPL18	mitochondrial ribosomal protein L18
MRPL19	mitochondrial ribosomal protein L19
MRPL2	mitochondrial ribosomal protein L2
MRPL20	mitochondrial ribosomal protein L20
MRPL21	mitochondrial ribosomal protein L21
MRPL22	mitochondrial ribosomal protein L22
MRPL23	mitochondrial ribosomal protein L23
MRPL30	mitochondrial ribosomal protein L30
MRPL32	mitochondrial ribosomal protein L32
MRPL35	mitochondrial ribosomal protein L35
MRPL4	mitochondrial ribosomal protein L4
MRPL40	mitochondrial ribosomal protein L40
MRPL41	mitochondrial ribosomal protein L41
MRPL42	mitochondrial ribosomal protein L42
MRPL45	mitochondrial ribosomal protein L45
MRPL48	mitochondrial ribosomal protein L48
MRPL49	mitochondrial ribosomal protein L49
MRPL50	mitochondrial ribosomal protein L50
MRPL51 /// SPTLC1	mitochondrial ribosomal protein L51 /// serine palmitoyltransferase, long chain base subunit 1

Table S4. (continued)

Gene alias	Gene name/description
MRPL55	mitochondrial ribosomal protein L55
MRPL9	mitochondrial ribosomal protein L9
MRPS12	mitochondrial ribosomal protein S12
MRPS14	mitochondrial ribosomal protein S14
MRPS17 /// ZNF713	mitochondrial ribosomal protein S17 /// zinc finger protein 713
MRPS18A	mitochondrial ribosomal protein S18A
MRPS2	mitochondrial ribosomal protein S2
MRPS21	mitochondrial ribosomal protein S21
MRPS23	mitochondrial ribosomal protein S23
MRPS25	mitochondrial ribosomal protein S25
MRPS27	mitochondrial ribosomal protein S27
MRPS28	mitochondrial ribosomal protein S28
MRPS31	mitochondrial ribosomal protein S31
MRPS33	mitochondrial ribosomal protein S33
MRPS34	mitochondrial ribosomal protein S34
MRPS7	mitochondrial ribosomal protein S7
MRPS9	mitochondrial ribosomal protein S9
MSRB2	methionine sulfoxide reductase B2
MSTO1	misato homolog 1 (<i>Drosophila</i>)
MTERFD1	MTERF domain containing 1
MTERFD3	MTERF domain containing 3
MTG1	mitochondrial GTPase 1 homolog (<i>S. cerevisiae</i>)
MTHFD1L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like
MTIF2	mitochondrial translational initiation factor 2
MTOR	mechanistic target of rapamycin (serine/threonine kinase)
MTUS1	Microtubule associated tumor suppressor 1
MUT	methylmalonyl CoA mutase
MUTYH	mutY homolog (<i>E. coli</i>)
NCRNA00219	non-protein coding RNA 219
NDUFA1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa
NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa
NDUFA11	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 11, 14.7kDa
NDUFA12	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12
NDUFA13	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13
NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa
NDUFA3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3, 9kDa
NDUFA4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa
NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa
NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7, 14.5kDa
NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa
NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 39kDa
NDUFAB1	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa
NDUFAF2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 2
NDUFB3	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa
NDUFB5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa
NDUFB7	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 18kDa

Table S4. (continued)

Gene alias	Gene name/description
NDUFB8	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa
NDUFB9	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa
NDUFC2	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kDa
NDUF55 /// RPL10	NADH dehydrogenase (ubiquinone) Fe-S protein 5, (NADH-coenzyme Q reductase) /// ribosomal protein L10
NDUF57	NADH dehydrogenase (ubiquinone) Fe-S protein 7, 20kDa (NADH-coenzyme Q reductase)
NDUFV1	NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa
NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa
NEFH	neurofilament, heavy polypeptide
NFS1	NFS1 nitrogen fixation 1 homolog (<i>S. cerevisiae</i>)
NFU1	NFU1 iron-sulfur cluster scaffold homolog (<i>S. cerevisiae</i>)
NIT2	nitrilase family, member 2
NLRX1	NLR family member X1
NOP14	NOP14 nucleolar protein homolog (yeast)
NR3C1	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)
NRAS	neuroblastoma RAS viral (v-ras) oncogene homolog
NRD1	nardilysin (N-arginine dibasic convertase)
NT5DC3	5'-nucleotidase domain containing 3
NUDT13	nudix (nucleoside diphosphate linked moiety X)-type motif 13
NUDT19	nudix (nucleoside diphosphate linked moiety X)-type motif 19
NUDT6	nudix (nucleoside diphosphate linked moiety X)-type motif 6
NUDT9	nudix (nucleoside diphosphate linked moiety X)-type motif 9
OAT	ornithine aminotransferase
OCIAD1	OCIA domain containing 1
OGDH	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)
OGG1	8-oxoguanine DNA glycosylase
OMA1	OMA1 homolog, zinc metallopeptidase (<i>S. cerevisiae</i>)
OXA1L	oxidase (cytochrome c) assembly 1-like
OXR1	oxidation resistance 1
OXSM	3-oxoacyl-ACP synthase, mitochondrial
P4HA1	prolyl 4-hydroxylase, alpha polypeptide I
PACS2	phosphofurin acidic cluster sorting protein 2
PARG	poly (ADP-ribose) glycohydrolase
PARK7	Parkinson disease (autosomal recessive, early onset) 7
PARL	presenilin associated, rhomboid-like
PARS2	prolyl-tRNA synthetase 2, mitochondrial (putative)
PCCB	propionyl CoA carboxylase, beta polypeptide
PCK2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)
PDK1	pyruvate dehydrogenase kinase, isozyme 1
PDSS2	prenyl (decaprenyl) diphosphate synthase, subunit 2
PECI	peroxisomal D3,D2-enoyl-CoA isomerase
PEMT	phosphatidylethanolamine N-methyltransferase
PERP	PERP, TP53 apoptosis effector
PET112L	PET112-like (yeast)
PGAM5	phosphoglycerate mutase family member 5

Table S4. (continued)

Gene alias	Gene name/description
PHYH	phytanoyl-CoA 2-hydroxylase
PHYHIPL	phytanoyl-CoA 2-hydroxylase interacting protein-like
PICK1	protein interacting with PRKCA 1
PIGY	phosphatidylinositol glycan anchor biosynthesis, class Y
PINK1	PTEN induced putative kinase 1
PITRM1	pitrilysin metalloproteinase 1
PMPCA	peptidase (mitochondrial processing) alpha
PNKD	paroxysmal nonkinesigenic dyskinesia
POLDIP2	polymerase (DNA-directed), delta interacting protein 2
POLG	polymerase (DNA directed), gamma
POLG2	polymerase (DNA directed), gamma 2, accessory subunit
POLRMT	polymerase (RNA) mitochondrial (DNA directed)
PON2	paraoxonase 2
PPIF	peptidylprolyl isomerase F
PPOX	protoporphyrinogen oxidase
PPP1CA	protein phosphatase 1, catalytic subunit, alpha isozyme
PPP2CA	protein phosphatase 2, catalytic subunit, alpha isozyme
PPP3CB	protein phosphatase 3, catalytic subunit, beta isozyme
PRDX1	peroxiredoxin 1
PRDX2	peroxiredoxin 2
PRDX5	peroxiredoxin 5
PRKACA	protein kinase, cAMP-dependent, catalytic, alpha
PTGR2	prostaglandin reductase 2
PTRF	polymerase I and transcript release factor
PTRH1	Peptidyl-tRNA hydrolase 1 homolog (<i>S. cerevisiae</i>)
PTRH2	peptidyl-tRNA hydrolase 2
PTS	6-pyruvoyltetrahydropterin synthase
PUS1	pseudouridylate synthase 1
PYCR1	pyrroline-5-carboxylate reductase 1
QTRT1	queuine tRNA-ribosyltransferase 1
QTRTD1	queuine tRNA-ribosyltransferase domain containing 1
RAF1	v-raf-1 murine leukemia viral oncogene homolog 1
RAI14	retinoic acid induced 14
RARS2	arginyl-tRNA synthetase 2, mitochondrial
RBFA	ribosome binding factor A
RDBP	RD RNA binding protein
RDH13	Retinol dehydrogenase 13 (all-trans/9-cis)
RG9MTD1	RNA (guanine-9-) methyltransferase domain containing 1
RNF5	ring finger protein 5
RPL9	ribosomal protein L9
RPP21 /// TRIM39 ///	ribonuclease P/MRP 21kDa subunit /// tripartite motif-containing 39 /// TRIM39-like
TRIM39R	protein
RPS6KB1	ribosomal protein S6 kinase, 70kDa, polypeptide 1
RPUSD4	RNA pseudouridylate synthase domain containing 4
SAMM50	sorting and assembly machinery component 50 homolog (<i>S. cerevisiae</i>)
SARS	Seryl-tRNA synthetase

Table S4. (continued)

Gene alias	Gene name/description
SCCPDH	saccharopine dehydrogenase (putative)
SDHA	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)
SDHA /// SDHAP1 /// SDHAP2	succinate dehydrogenase complex, subunit A, flavoprotein (Fp) /// succinate dehydrogenase complex, subunit A, flavoprotein pseudogene 1 /// succinate dehydrogenase complex, subunit A, flavoprotein pseudogene 2
SDHAF1	succinate dehydrogenase complex assembly factor 1
SDHC	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa
SDHD	succinate dehydrogenase complex, subunit D, integral membrane protein
SFXN1	sideroflexin 1
SFXN2	sideroflexin 2
SHC1	SHC (Src homology 2 domain containing) transforming protein 1
SIRT5	sirtuin (silent mating type information regulation 2 homolog) 5 (<i>S. cerevisiae</i>)
SLC1A3	solute carrier family 1 (glial high affinity glutamate transporter), member 3
SLC25A12	solute carrier family 25 (mitochondrial carrier, Aralar), member 12
SLC25A14	solute carrier family 25 (mitochondrial carrier, brain), member 14
SLC25A25	solute carrier family 25, member 25
SLC25A26	solute carrier family 25, member 26
SLC25A29	solute carrier family 25, member 29
SLC25A3	solute carrier family 25, member 3
SLC25A32	solute carrier family 25, member 32
SLC25A36	Solute carrier family 25, member 36
SLC25A38	solute carrier family 25, member 38
SLC25A39	solute carrier family 25, member 39
SLC25A44	solute carrier family 25, member 44
SLC25A6	solute carrier family 25, member 6
SLC27A3	solute carrier family 27 (fatty acid transporter), member 3
SLIT3	slit homolog 3 (<i>Drosophila</i>)
SLMO2	slowmo homolog 2 (<i>Drosophila</i>)
SNN	stannin
SOD1	superoxide dismutase 1, soluble
STAR	steroidogenic acute regulatory protein
STOML2	stomatin (EPB72)-like 2
SUCLG1	succinate-CoA ligase, alpha subunit
SURF1	surfeit 1
TATDN3	TatD DNase domain containing 3
TBC1D15	TBC1 domain family, member 15
TBRG4	transforming growth factor beta regulator 4
THG1L	tRNA-histidine guanylyltransferase 1-like (<i>S. cerevisiae</i>)
TIMM13	translocase of inner mitochondrial membrane 13 homolog (yeast)
TIMM17A	translocase of inner mitochondrial membrane 17 homolog A (yeast)
TIMM22	Translocase of inner mitochondrial membrane 22 homolog (yeast)
TIMM23 /// TIMM23B	translocase of inner mitochondrial membrane 23 homolog (yeast) /// translocase of inner mitochondrial membrane 23 homolog B (yeast)
TIMM8A	translocase of inner mitochondrial membrane 8 homolog A (yeast)
TMEM126A	transmembrane protein 126A
TMEM14B /// TMEM14C	transmembrane protein 14B /// transmembrane protein 14C

Table S4. (continued)

Gene alias	Gene name/description
TMEM14C	transmembrane protein 14C
TMEM160	transmembrane protein 160
TMEM223	transmembrane protein 223
TMTC1	transmembrane and tetratricopeptide repeat containing 1
TOMM22	translocase of outer mitochondrial membrane 22 homolog (yeast)
TOMM34	translocase of outer mitochondrial membrane 34
TOMM70A	translocase of outer mitochondrial membrane 70 homolog A (<i>S. cerevisiae</i>)
TP53	tumor protein p53
TRAP1	TNF receptor-associated protein 1
TRIT1	tRNA isopentenyltransferase 1
TRNT1	tRNA nucleotidyl transferase, CCA-adding, 1
TXNDC12	thioredoxin domain containing 12 (endoplasmic reticulum)
TXNRD1	thioredoxin reductase 1
UQCC	ubiquinol-cytochrome c reductase complex chaperone
UQCR10	ubiquinol-cytochrome c reductase, complex III subunit X
UQCR11	ubiquinol-cytochrome c reductase, complex III subunit XI
UQCRB	ubiquinol-cytochrome c reductase binding protein
UQCRH	ubiquinol-cytochrome c reductase hinge protein
UQCRC	ubiquinol-cytochrome c reductase, complex III subunit VII, 9.5kDa
USP30	ubiquitin specific peptidase 30
VARS2	valyl-tRNA synthetase 2, mitochondrial (putative)
VHL	von Hippel-Lindau tumor suppressor
WARS2	tryptophanyl tRNA synthetase 2, mitochondrial
WASF1	WAS protein family, member 1
YME1L1	YME1-like 1 (<i>S. cerevisiae</i>)
YWHAE	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide
YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide

Table S5. Genes induced in the lower airways of healthy controls, assigned to GO cluster *Mitochondrion*

Gene alias	Gene name/description
ABCB6	ATP-binding cassette, sub-family B (MDR/TAP), member 6
ACADVL	acyl-CoA dehydrogenase, very long chain
ACP6	acid phosphatase 6, lysophosphatidic
ADH5	alcohol dehydrogenase 5 (class III), chi polypeptide
ADO	2-aminoethanethiol (cysteamine) dioxygenase
AIFM1	apoptosis-inducing factor, mitochondrion-associated, 1
AK1	adenylate kinase 1
AKT2	v-akt murine thymoma viral oncogene homolog 2
ALDH18A1	aldehyde dehydrogenase 18 family, member A1
ALKBH7	AlkB, alkylation repair homolog 7 (E. coli)
ARAF	v-raf murine sarcoma 3611 viral oncogene homolog
ARSB	arylsulfatase B
ASS1	argininosuccinate synthase 1
ATP5C1	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, gamma polypeptide 1
ATP5G3	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit C3 (subunit 9)
ATP5H	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit d
ATP5I	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit E
ATP5J2	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit F2
ATP5SL	ATP5S-like
ATP6V1A	ATPase, H ⁺ transporting, lysosomal 70kDa, V1 subunit A
AURKAIP1	aurora kinase A interacting protein 1
BCL2L10	BCL2-like 10 (apoptosis facilitator)
BCL2L2	BCL2-like 2
BLOC1S1	biogenesis of lysosomal organelles complex-1, subunit 1
BNIP3L	BCL2/adenovirus E1B 19kDa interacting protein 3-like
C10orf58	chromosome 10 open reading frame 58
C12orf10	chromosome 12 open reading frame 10
C12orf62	chromosome 12 open reading frame 62
C14orf159	chromosome 14 open reading frame 159
C15orf62	chromosome 15 open reading frame 62
C17orf61	chromosome 17 open reading frame 61
C18orf19	chromosome 18 open reading frame 19
C1orf31	chromosome 1 open reading frame 31
C22orf32	chromosome 22 open reading frame 32
C2orf56	chromosome 2 open reading frame 56
C9orf46	chromosome 9 open reading frame 46
CA5B	carbonic anhydrase VB, mitochondrial
CCDC142 /// MRPL53	coiled-coil domain containing 142 /// mitochondrial ribosomal protein L53
CCDC58	coiled-coil domain containing 58
CDS2 /// LOC149832	CDP-diacylglycerol synthase (phosphatidate cytidyltransferase) 2
CHAF1B	chromatin assembly factor 1, subunit B (p60)
CHCHD1	coiled-coil-helix-coiled-coil-helix domain containing 1
CHCHD2	coiled-coil-helix-coiled-coil-helix domain containing 2
CHCHD4	coiled-coil-helix-coiled-coil-helix domain containing 4
CIDEA	cell death-inducing DFFA-like effector a
CISD3	CDGSH iron sulfur domain 3

Table S5. (continued)

Gene alias	Gene name/description
CLPX	ClpX caseinolytic peptidase X homolog (E. coli)
CLTC	Clathrin, heavy chain (Hc)
COL4A3BP	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein
COMTD1	catechol-O-methyltransferase domain containing 1
COQ5	coenzyme Q5 homolog, methyltransferase (<i>S. cerevisiae</i>)
COQ9	coenzyme Q9 homolog (<i>S. cerevisiae</i>)
COX10	COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransferase (yeast)
COX15	COX15 homolog, cytochrome c oxidase assembly protein (yeast)
COX16	COX16 cytochrome c oxidase assembly homolog (<i>S. cerevisiae</i>)
COX4NB	COX4 neighbor
COX5B	Cytochrome c oxidase subunit Vb
COX6B1	cytochrome c oxidase subunit VIb polypeptide 1 (ubiquitous)
COX7C	cytochrome c oxidase subunit VIIc
CRAT	carnitine O-acetyltransferase
CROT	carnitine O-octanoyltransferase
CXorf23	chromosome X open reading frame 23
CYB5R1	cytochrome b5 reductase 1
CYB5R3	cytochrome b5 reductase 3
DDX28	DEAD (Asp-Glu-Ala-Asp) box polypeptide 28
DHODH	dihydroorotate dehydrogenase
DHX29	DEAH (Asp-Glu-Ala-His) box polypeptide 29
DHX30	DEAH (Asp-Glu-Ala-His) box polypeptide 30
DLST	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)
DNAJC15	DnaJ (Hsp40) homolog, subfamily C, member 15
DNAJC4	DnaJ (Hsp40) homolog, subfamily C, member 4
DPYSL2	dihydropyrimidinase-like 2
DRG2	developmentally regulated GTP binding protein 2
DYNLL1	dynein, light chain, LC8-type 1
EHHADH	enoyl-CoA, hydratase/3-hydroxyacyl CoA dehydrogenase
ELAC2	elaC homolog 2 (E. coli)
ENDOG	endonuclease G
ENO1	enolase 1, (alpha)
FAHD1	fumarylacetoacetate hydrolase domain containing 1
FASTK	Fas-activated serine/threonine kinase
FOXRED1	FAD-dependent oxidoreductase domain containing 1
FTSJ2	FtsJ homolog 2 (E. coli)
FUNDC2	FUN14 domain containing 2
FXC1	fracture callus 1 homolog (rat)
FXN	frataxin
GADD45GIP1	Growth arrest and DNA-damage-inducible, gamma interacting protein 1
GATC	Glutamyl-tRNA(Gln) amidotransferase, subunit C homolog (bacterial)
GATM	Glycine amidinotransferase (L-arginine:glycine amidinotransferase)
GHITM	growth hormone inducible transmembrane protein
GK /// GK3P	glycerol kinase /// glycerol kinase 3 pseudogene
GK3P	glycerol kinase 3 pseudogene
GLUL	glutamate-ammonia ligase

Table S5. (continued)

Gene alias	Gene name/description
GLYCTK	glycerate kinase
GNPAT	glyceronephosphate O-acyltransferase
GOT2	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)
GRN	granulin
GRPEL1	GrpE-like 1, mitochondrial (E. coli)
GRPEL2	GrpE-like 2, mitochondrial (E. coli)
GSTZ1	glutathione transferase zeta 1
GTF2H4	general transcription factor IIH, polypeptide 4, 52kDa
GTPBP5	GTP binding protein 5 (putative)
GTPBP8	GTP-binding protein 8 (putative)
HEBP2	heme binding protein 2
HEMK1	HemK methyltransferase family member 1
HK2	hexokinase 2
HSCB	HscB iron-sulfur cluster co-chaperone homolog (E. coli)
HTRA2	HtrA serine peptidase 2
ICT1	immature colon carcinoma transcript 1
IDH1	Isocitrate dehydrogenase 1 (NADP+), soluble
IDH3B	isocitrate dehydrogenase 3 (NAD+) beta
ISCA1	iron-sulfur cluster assembly 1 homolog (S. cerevisiae)
ISCA2	iron-sulfur cluster assembly 2 homolog (S. cerevisiae)
IVD	isovaleryl-CoA dehydrogenase
JMJD7	jumonji domain containing 7
KIAA0141	KIAA0141
KIF1B	kinesin family member 1B
KMO	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)
LARS2	leucyl-tRNA synthetase 2, mitochondrial
LETM1	leucine zipper-EF-hand containing transmembrane protein 1
LETMD1	LETM1 domain containing 1
LGALS3	lectin, galactoside-binding, soluble, 3
LIMK2	LIM domain kinase 2
LOC100510009 ///	Williams-Beuren syndrome chromosome region 16
WBSCR16	
LYRM2	LYR motif containing 2
MAVS	mitochondrial antiviral signaling protein
MCAT	malonyl CoA:ACP acyltransferase (mitochondrial)
MCL1	myeloid cell leukemia sequence 1 (BCL2-related)
MECR	mitochondrial trans-2-enoyl-CoA reductase
MMACHC	methylmalonic aciduria (cobalamin deficiency) cblC type, with homocystinuria
MRPL11	mitochondrial ribosomal protein L11
MRPL13	mitochondrial ribosomal protein L13
MRPL16	mitochondrial ribosomal protein L16
MRPL17	mitochondrial ribosomal protein L17
MRPL18	mitochondrial ribosomal protein L18
MRPL20	mitochondrial ribosomal protein L20
MRPL22	mitochondrial ribosomal protein L22
MRPL32	mitochondrial ribosomal protein L32
MRPL33	mitochondrial ribosomal protein L33

Table S5. (continued)

Gene alias	Gene name/description
MRPL36	mitochondrial ribosomal protein L36
MRPL4	mitochondrial ribosomal protein L4
MRPL41	mitochondrial ribosomal protein L41
MRPL43	mitochondrial ribosomal protein L43
MRPL45	mitochondrial ribosomal protein L45
MRPL50	mitochondrial ribosomal protein L50
MRPL55	Mitochondrial ribosomal protein L55
MRPL9	mitochondrial ribosomal protein L9
MRPS12	Mitochondrial ribosomal protein S12
MRPS14	mitochondrial ribosomal protein S14
MRPS15	mitochondrial ribosomal protein S15
MRPS17 /// ZNF713	mitochondrial ribosomal protein S17 /// zinc finger protein 713
MRPS2	mitochondrial ribosomal protein S2
MRPS24	mitochondrial ribosomal protein S24
MRPS26	mitochondrial ribosomal protein S26
MRPS28	mitochondrial ribosomal protein S28
MRPS9	mitochondrial ribosomal protein S9
MSTO1 /// MSTO2P	misato homolog 1 (<i>Drosophila</i>) /// misato homolog 2 pseudogene
MTFMT	mitochondrial methionyl-tRNA formyltransferase
MTG1	mitochondrial GTPase 1 homolog (<i>S. cerevisiae</i>)
MTOR	Mechanistic target of rapamycin (serine/threonine kinase)
MUT	methylmalonyl CoA mutase
NAGS	N-acetylglutamate synthase
NDUFA1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa
NDUFA11	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 11, 14.7kDa
NDUFA12	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12
NDUFA13	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13
NDUFA3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3, 9kDa
NDUFA4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa
NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa
NDUFAB1	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa
NDUFB1	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7kDa
NDUFB3	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa
NDUFB5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa
NDUFB7	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 18kDa
NDUFB9	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa
NDUFS5 /// RPL10	NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase) /// ribosomal protein L10
NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase)
NFS1	NFS1 nitrogen fixation 1 homolog (<i>S. cerevisiae</i>)
NLRX1	NLR family member X1
NR3C1	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)
NRAS	neuroblastoma RAS viral (v-ras) oncogene homolog
NRD1	nardilysin (N-arginine dibasic convertase)
NT5C	5', 3'-nucleotidase, cytosolic
OAT	ornithine aminotransferase

Table S5. (continued)

Gene alias	Gene name/description
OCIAD1	OCIA domain containing 1
OXSM	3-oxoacyl-ACP synthase, mitochondrial
P4HA1	prolyl 4-hydroxylase, alpha polypeptide I
PAM16	presequence translocase-associated motor 16 homolog
PANK2	Pantothenate kinase 2
PARG	poly (ADP-ribose) glycohydrolase
PARL	presenilin associated, rhomboid-like
PARS2	prolyl-tRNA synthetase 2, mitochondrial (putative)
PCCA	Propionyl Coenzyme A carboxylase, alpha polypeptide
PDK1	pyruvate dehydrogenase kinase, isozyme 1
PDS52	prenyl (decaprenyl) diphosphate synthase, subunit 2
PECR	peroxisomal trans-2-enoyl-CoA reductase
PET112L	PET112-like (yeast)
PIN4	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)
PMPCA	peptidase (mitochondrial processing) alpha
POLDIP2	polymerase (DNA-directed), delta interacting protein 2
PPP1CA	protein phosphatase 1, catalytic subunit, alpha isozyme
PPP1CC	protein phosphatase 1, catalytic subunit, gamma isozyme
PPP3CA	protein phosphatase 3, catalytic subunit, alpha isozyme
PROSC	Proline synthetase co-transcribed homolog (bacterial)
PTRH1	peptidyl-tRNA hydrolase 1 homolog (S. cerevisiae)
PTRH2	peptidyl-tRNA hydrolase 2
PUS1	pseudouridylate synthase 1
RAB11A	RAB11A, member RAS oncogene family
RAB3D	RAB3D, member RAS oncogene family
RAI14	retinoic acid induced 14
RARS2	arginyl-tRNA synthetase 2, mitochondrial
RBFA	ribosome binding factor A
RDBP	RD RNA binding protein
RDH13	Retinol dehydrogenase 13 (all-trans/9-cis)
RNASEL	ribonuclease L (2,5'-oligoadenylate synthetase-dependent)
RNF5	ring finger protein 5
RPP21 /// TRIM39 /// TRIM39R	ribonuclease P/MRP 21kDa subunit /// tripartite motif-containing 39 /// TRIM39-like protein
SACS	spastic ataxia of Charlevoix-Saguenay (sacsin)
SARDH	Sarcosine dehydrogenase
SARS2	seryl-tRNA synthetase 2, mitochondrial
SEC61A1	Sec61 alpha 1 subunit (S. cerevisiae)
SFXN5	sideroflexin 5
SH3BP5	SH3-domain binding protein 5 (BTK-associated)
SIVA1	SIVA1, apoptosis-inducing factor
SLC1A3	solute carrier family 1 (glial high affinity glutamate transporter), member 3
SLC25A13	Solute carrier family 25, member 13 (citrin)
SLC25A14	solute carrier family 25 (mitochondrial carrier, brain), member 14
SLC25A25	solute carrier family 25, member 25
SLC25A26	solute carrier family 25, member 26
SLC25A29	Solute carrier family 25, member 29

Table S5. (continued)

Gene alias	Gene name/description
SLC25A30	solute carrier family 25, member 30
SLC25A32	solute carrier family 25, member 32
SLC25A38	solute carrier family 25, member 38
SLC25A44	solute carrier family 25, member 44
SLC25A45	solute carrier family 25, member 45
SLC27A1	solute carrier family 27 (fatty acid transporter), member 1
SLC27A3	solute carrier family 27 (fatty acid transporter), member 3
SLMO2	slowmo homolog 2 (Drosophila)
SND1	staphylococcal nuclease and tudor domain containing 1
SOD1	superoxide dismutase 1, soluble
SRGAP2	SLIT-ROBO Rho GTPase activating protein 2
SSSCA1	Sjogren syndrome/scleroderma autoantigen 1
STAR	steroidogenic acute regulatory protein
SURF1	surfeit 1
SYNJ2BP	synaptojanin 2 binding protein
TAOK3	TAO kinase 3
TATDN3	TatD DNase domain containing 3
TBC1D15	TBC1 domain family, member 15
TBRG4	transforming growth factor beta regulator 4
TDRKH	tudor and KH domain containing
TIMM17A	translocase of inner mitochondrial membrane 17 homolog A (yeast)
TIMM23	translocase of inner mitochondrial membrane 23 homolog (yeast)
TMEM126A	transmembrane protein 126A
TMEM14B /// TMEM14C	transmembrane protein 14B /// transmembrane protein 14C
TMEM14C	transmembrane protein 14C
TMEM186	transmembrane protein 186
TMEM223	transmembrane protein 223
TOMM40	translocase of outer mitochondrial membrane 40 homolog (yeast)
TXNIP	thioredoxin interacting protein
UQCRC1	ubiquinol-cytochrome c reductase, complex III subunit XI
UQCRC2	ubiquinol-cytochrome c reductase core protein II
UQCRCFS1	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1
WARS2	tryptophanyl tRNA synthetase 2, mitochondrial
ZFHX3	Zinc finger homeobox 3

Table S6. Genes induced in the lower airways of healthy controls and allergic rhinitis patients, assigned to GO cluster *Mitochondrion*

Gene alias	Gene name/description
AASS	aminoadipate-semialdehyde synthase
ADCK2	aarF domain containing kinase 2
AK3	adenylate kinase 3
AK4	adenylate kinase 4
ATP5J	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6
ATP5L	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit G
BBOX1	butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1
BCAT1	branched chain amino-acid transaminase 1, cytosolic
BNIP3	BCL2/adenovirus E1B 19kDa interacting protein 3
C10orf2	chromosome 10 open reading frame 2
C14orf156	chromosome 14 open reading frame 156
C19orf70	chromosome 19 open reading frame 70
C2orf47	chromosome 2 open reading frame 47
C3orf1	chromosome 3 open reading frame 1
C3orf78	small integral membrane protein 4
C4orf14	chromosome 4 open reading frame 14
C6orf203	chromosome 6 open reading frame 203
C7orf55 /// LUC7L2	chromosome 7 open reading frame 55 /// LUC7-like 2 (<i>S. cerevisiae</i>)
CCBL2	cysteine conjugate-beta lyase 2
CCT7	chaperonin containing TCP1, subunit 7 (eta)
CKB	creatine kinase, brain
CKMT1A /// CKMT1B	creatine kinase, mitochondrial 1A /// creatine kinase, mitochondrial 1B
COX11	COX11 cytochrome c oxidase assembly homolog (yeast)
COX3	mitochondrially encoded cytochrome c oxidase III
COX7A2L	cytochrome c oxidase subunit VIIa polypeptide 2 like
CPS1	carbamoyl-phosphate synthase 1, mitochondrial
CS	citrate synthase
CYCS	cytochrome c, somatic
DARS2	aspartyl-tRNA synthetase 2, mitochondrial
DHRS1	dehydrogenase/reductase (SDR family) member 1
DLAT	dihydrolipoamide S-acetyltransferase
EFHD1	EF-hand domain family, member D1
FIS1	fission 1 (mitochondrial outer membrane) homolog (<i>S. cerevisiae</i>)
GCAT	glycine C-acetyltransferase
GCDH	glutaryl-CoA dehydrogenase
GLRX2	glutaredoxin 2
HERC2	hect domain and RLD 2
KARS	lysyl-tRNA synthetase
KRT4	keratin 4
LONP1	lon peptidase 1, mitochondrial
LYRM4	LYR motif containing 4
MARS2	methionyl-tRNA synthetase 2, mitochondrial
MCCC2	Methylcrotonoyl-Coenzyme A carboxylase 2 (beta)
METT11D1	methyltransferase like 17

Table S6. (continued)

Gene alias	Gene name/description
METTL12	methyltransferase like 12
MMAA	methylmalonic aciduria (cobalamin deficiency) cblA type
MPST	mercaptopyruvate sulfurtransferase
MRPL12	mitochondrial ribosomal protein L12
MRPL2	mitochondrial ribosomal protein L2
MRPL21	mitochondrial ribosomal protein L21
MRPL35	mitochondrial ribosomal protein L35
MRPL42	mitochondrial ribosomal protein L42
MRPS16	mitochondrial ribosomal protein S16
MRPS23	mitochondrial ribosomal protein S23
MRPS25	mitochondrial ribosomal protein S25
MRPS33	mitochondrial ribosomal protein S33
MRPS34	mitochondrial ribosomal protein S34
MRPS35	mitochondrial ribosomal protein S35
MRPS7	mitochondrial ribosomal protein S7
MSTO1	misato homolog 1 (Drosophila)
MTERFD1	MTERF domain containing 1
MTHFD2	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase
MTPAP	mitochondrial poly(A) polymerase
NAPG	N-ethylmaleimide-sensitive factor attachment protein, gamma
NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 39kDa
NDUFB8	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa
NDUFC1	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1, 6kDa
NDUF57	NADH dehydrogenase (ubiquinone) Fe-S protein 7, 20kDa (NADH-coenzyme Q reductase)
NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa
NIPSNAP1	nipsnap homolog 1 (C. elegans)
NIT2	nitrilase family, member 2
NOP14	NOP14 nucleolar protein homolog (yeast)
NR1D1 /// THRA	nuclear receptor subfamily 1, group D, member 1 /// thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog, avian)
NUDT19	nudix (nucleoside diphosphate linked moiety X)-type motif 19
NUDT9	nudix (nucleoside diphosphate linked moiety X)-type motif 9
PITRM1	pitriysin metalloproteinase 1
POLG2	polymerase (DNA directed), gamma 2, accessory subunit
PPOX	protoporphyrinogen oxidase
PRDX1	peroxiredoxin 1
QTRTD1	queuine tRNA-ribosyltransferase domain containing 1
RARS	arginyl-tRNA synthetase
REXO2	REX2, RNA exonuclease 2 homolog (S. cerevisiae)
SFXN4	Sideroflexin 4
SLC22A4	solute carrier family 22 (organic cation/ergothioneine transporter), member 4
SLC25A15	solute carrier family 25 (mitochondrial carrier; ornithine transporter), member 15
SLC25A19	solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier), member 19
SMCR7L	Smith-Magenis syndrome chromosome region, candidate 7-like
SUPV3L1	suppressor of var1, 3-like 1 (S. cerevisiae)

Table S6. (continued)

Gene alias	Gene name/description
TFB1M	transcription factor B1, mitochondrial
TFB2M	transcription factor B2, mitochondrial
TIMM44	translocase of inner mitochondrial membrane 44 homolog (yeast)
TK2	thymidine kinase 2, mitochondrial
TMEM160	transmembrane protein 160
TMLHE	trimethyllysine hydroxylase, epsilon
TOMM70A	translocase of outer mitochondrial membrane 70 homolog A (<i>S. cerevisiae</i>)
TXNDC12	thioredoxin domain containing 12 (endoplasmic reticulum)
UQCRB	ubiquinol-cytochrome c reductase binding protein
UQCRCQ	ubiquinol-cytochrome c reductase, complex III subunit VII, 9.5kDa
VARS	valyl-tRNA synthetase
YME1L1	YME1-like 1 (<i>S. cerevisiae</i>)
YWHAE	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide

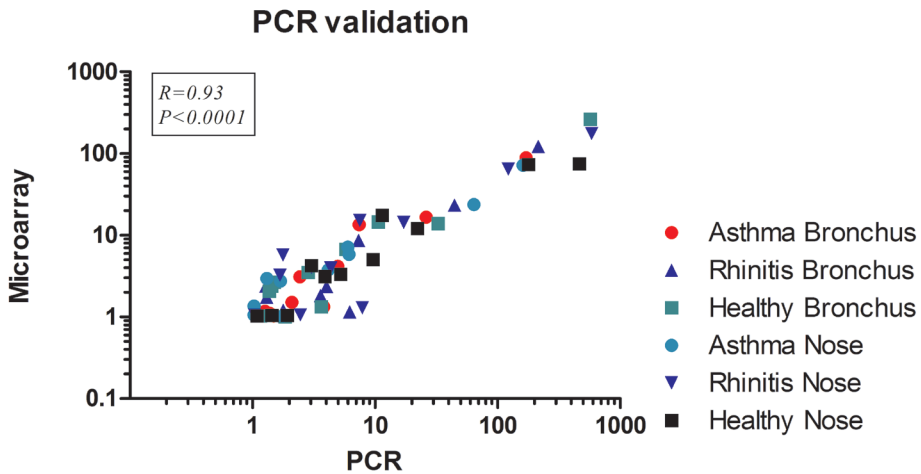


Figure S1. Correlation plot of real-time PCR data and microarray results.

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