

LIST OF ONLINE SUPPORTING INFORMATION

Table E1. Summary characteristics of patients with allergic rhinitis (n=19) and control subjects (n=11) in microarray analysis

Table E2. Up-regulated genes in inferior turbinate from patients with allergic rhinitis compared with control subjects.

Table E3. Down-regulated genes in inferior turbinate from patients with allergic rhinitis compared with control subjects.

Table E4. The seven canonical Gene Ontology categories were identified for differential expression genes.

Table E1. Summary characteristics of patients with allergic rhinitis (n=19, no. 1-19) and control subjects (n=11, no. 20-30) in microarray analysis

No.	Age, yr	Gender	Allergen sensitization*	Grade of atopy†	Total IgE, IU/ml
1	20	F	<i>D. pteronyssinus</i>	4	528.6
2	44	F	Mould fungi mixture	1	22.1
3	47	F	Tree mixture + Pigweed	3,3	279.4
4	22	M	<i>D. pteronyssinus</i> + House dust	4, 1	1597
5	51	M	<i>D. pteronyssinus</i>	2	869.8
6	43	F	<i>D. pteronyssinus</i>	4	5144
7	24	M	<i>D. pteronyssinus</i> + Cat epithelium and dander	6,2	65540
8	22	M	<i>D. pteronyssinus</i>	3	581.1
9	26	M	<i>D. pteronyssinus</i>	2	639.2
10	19	M	<i>D. pteronyssinus</i> + Mould fungi mixture	4,2	65540
11	17	M	<i>D. pteronyssinus</i>	5	1109
12	40	M	<i>D. pteronyssinus</i>	3	466.4
13	35	M	<i>D. pteronyssinus</i> + Cockroach	2, 2	786.1
14	41	M	<i>D. pteronyssinus</i>	2	1305
15	34	M	<i>D. pteronyssinus</i>	3	161.5
16	18	F	<i>D. pteronyssinus</i>	2	126.1
17	22	M	<i>D. pteronyssinus</i>	2	104.6
18	22	M	<i>D. pteronyssinus</i>	2	347
19	48	F	Mould fungi mixture + Tree mixture + Pigweed	5,4,5	208.5
20	57	M	Negative	-	30.4
21	38	M	Negative	-	337.2
22	48	M	Negative	-	58
23	27	M	Negative	-	176.4
24	30	M	Negative	-	30.4

25	31	M	Negative	-	12.2
26	26	F	Negative	-	320.2
27	32	F	Negative	-	81.3
28	28	F	Negative	-	1.2
29	20	M	Negative	-	255.1
30	29	F	Negative	-	140.4

* AR diagnosed was on the basis of a thorough history, physical examination, and serum specific IgE by using AllergyScreen[®] test.

The AllergyScreen[®] test include the following aeroallergens: D. pteronyssinus, pigweed, mould fungi mixture, tree mixture, house dust, weed mixture, dog epithelium and dander, cat epithelium and dander, cockroach, mulberry.

† The grades (G) of allergen-specific IgE were defined as follows: G0 (<0.35 IU/ml), G1 (0.35-0.70 IU/ml), G2 (0.71-3.5 IU/ml), G3 (5.6-17.5 IU/ml), G4 (17.6-50 IU/ml), G5 (51-100 IU/ml) and G6 (>100 IU/ml).

AR: allergic rhinitis; D. pteronyssinus: Dermatophagoides pteronyssinus; F: female; M: male

Table E2. Up-regulated genes in the inferior turbinate from AR patients as compared with control subjects

Probe Set ID	Gene name	Fold difference	P-value
11723068_at	Corticotropin releasing hormone binding protein	3.316	0.001
11728717_at	Chemokine (C-X-C motif) ligand 5	3.313	0.017
11728716_x_at	Chemokine (C-X-C motif) ligand 5	3.119	0.041
11733115_a_at	Carbonic anhydrase II	3.043	0.012
11728715_at	Chemokine (C-X-C motif) ligand 5	2.922	0.039
11763851_a_at	Corticotropin releasing hormone binding protein	2.543	0.000
11757493_s_at	Histatin 3	2.453	0.037
11732995_a_at	Regulator of G-protein signaling 4	2.442	0.007
11723644_a_at	Phospholamban	2.410	0.047
11728521_a_at	ADP-ribosyltransferase 3	2.380	0.007
11760163_s_at	WD repeat and SOCS box containing 1	2.326	0.000
11722166_at	Regulator of G-protein signaling 5	2.319	0.001
11725653_a_at	Endomucin	2.301	0.018
11760162_at	WD repeat and SOCS box containing 1	2.267	0.000
11741572_a_at	Regulator of G-protein signaling 4	2.252	0.013
11737329_at	Solute carrier family 26, member 4	2.247	0.027
11747117_x_at	Folate hydrolase (prostate-specific membrane antigen) 1 /// folate hydrolase 1B	2.245	0.037
11744707_a_at	Angiopoietin-like 1	2.236	0.019
11731958_s_at	Folate hydrolase (prostate-specific membrane antigen) 1 /// folate hydrolase 1B	2.215	0.042
11731959_x_at	Folate hydrolase (prostate-specific membrane antigen) 1 /// folate hydrolase 1B	2.204	0.038
11750771_s_at	Folate hydrolase (prostate-specific membrane antigen) 1 /// folate hydrolase 1B	2.187	0.042
11751935_a_at	Epidermal growth factor	2.186	0.045
11722165_a_at	Regulator of G-protein signaling 5	2.141	0.001
11741222_a_at	Family with sequence similarity 198, member B	2.140	0.003
11756200_a_at	Chitinase 3-like 2	2.129	0.020
11740174_a_at	Neuregulin 3	2.128	0.049

11745434_a_at	Neuregulin 3	2.116	0.029
11727386_a_at	Neuropeptide Y receptor Y1	2.116	0.009
11750623_a_at	Filamin A interacting protein 1-like	2.100	0.022
11756201_x_at	Chitinase 3-like 2	2.092	0.025
11736281_a_at	Solute carrier family 22 (extraneuronal monoamine transporter), member 3	2.087	0.021
11757640_x_at	ADP-ribosyltransferase 3	2.061	0.003
11732994_a_at	Regulator of G-protein signaling 4	2.060	0.019
11758013_s_at	Chromosome 8 open reading frame 4	2.036	0.017
11724249_a_at	Solute carrier family 39 (zinc transporter), member 8	2.022	0.007
11722573_a_at	Endoplasmic reticulum aminopeptidase 2	2.019	0.043
11751576_a_at	Neuropeptide Y receptor Y1	2.016	0.002
11746069_a_at	Glycine amidinotransferase (L-arginine:glycineamidinotransferase)	2.015	0.015

Table E3. Down-regulated genes in the inferior turbinate in patients with allergic rhinitis as compared with control subjects

Probe Set ID	Gene name	Fold difference	P-value
11734525_a_at	Chromosome 11 open reading frame 88	4.525	0.034
11730044_a_at	Chromosome 9 open reading frame 24	4.273	0.036
11732909_at	Family with sequence similarity 183, member A	4.241	0.014
11756356_a_at	Family with sequence similarity 81, member B	4.096	0.048
11725562_at	Chromosome 20 open reading frame 85	4.047	0.047
11726535_a_at	MORN repeat containing 5	3.573	0.044
11732910_x_at	Family with sequence similarity 183, member A	3.550	0.040
11727983_a_at	Leucine rich repeat containing 46	3.541	0.013
11727734_at	Chromosome 1 open reading frame 192	3.462	0.036
11731323_a_at	A kinase (PRKA) anchor protein 14	3.446	0.039
11732908_a_at	Family with sequence similarity 183, member A	3.393	0.036
11733359_a_at	Coiled-coil domain containing 19	3.336	0.036
11723027_at	Intelectin 1 (galactofuranose binding)	3.302	0.043
11732678_a_at	Dynein, axonemal, heavy chain 12	3.248	0.047
11755367_s_at	Dynein, axonemal, assembly factor 3	3.086	0.020
11719767_a_at	Tubulin polymerization-promoting protein family member 3	3.041	0.017
11733934_a_at	Chromosome 1 open reading frame 88	3.029	0.046
11725875_at	WD repeat domain 66	3.023	0.021
11746662_a_at	Armadillo repeat containing 3	3.018	0.040
11728450_a_at	Armadillo repeat containing 3	2.997	0.049
11718722_at	Prostate stem cell antigen	2.985	0.029
11731660_a_at	von Willebrand factor A domain containing 3B	2.983	0.045
11755274_a_at	Catsper channel auxiliary subunit delta	2.937	0.038
11735554_at	Protein phosphatase 1, regulatory subunit 42	2.926	0.041
11733636_at	Family with sequence similarity 92, member B	2.924	0.030
11743595_at	Chromosome 5 open reading frame 49	2.911	0.046

11748853_a_at	EF-hand calcium binding domain 1	2.885	0.032
11743952_a_at	Chromosome 6 open reading frame 165	2.884	0.036
11736917_at	LY6/PLAUR domain containing 2	2.881	0.010
11725494_at	Radial spoke head 9 homolog (Chlamydomonas)	2.873	0.021
11732667_x_at	Radial spoke head 10 homolog B (Chlamydomonas) /// radial spoke head 10 homolog B2 (Chlamydomonas)	2.866	0.047
11725724_a_at	Fatty acid binding protein 6, ileal	2.865	0.049
11756097_s_at	Zinc finger, MYND-type containing 10	2.862	0.043
11724109_a_at	Chromosome 9 open reading frame 116	2.858	0.032
11743003_a_at	Cytochrome P450, family 4, subfamily B, polypeptide 1	2.744	0.032
11727185_at	Coiled-coil domain containing 164	2.742	0.035
11755609_a_at	HYDIN, axonemal central pair apparatus protein	2.732	0.030
11733635_at	Family with sequence similarity 92, member B	2.724	0.026
11737141_a_at	Radial spoke head 1 homolog (Chlamydomonas)	2.723	0.038
11729503_at	Coiled-coil domain containing 11	2.719	0.049
11727921_a_at	Tektin 1	2.713	0.047
11742483_a_at	Chromosome 1 open reading frame 110	2.710	0.044
11735858_a_at	Regulatory subunit of type II PKA R-subunit (RIIa) domain containing 1	2.709	0.029
11718347_a_at	S100 calcium binding protein P	2.690	0.010
11730166_a_at	Chromosome 11 open reading frame 16	2.642	0.015
11736861_at	Chromosome X open reading frame 41	2.631	0.047
11721619_at	Forkhead box J1	2.613	0.036
11745292_a_at	Chromosome 22 open reading frame 15	2.599	0.031
11731945_a_at	WD repeat domain 38	2.585	0.017
11735637_a_at	Leucine rich repeat containing 23	2.578	0.032
11732658_a_at	Primary ciliary dyskinesia protein 1	2.578	0.050
11741932_a_at	Potassium channel regulator	2.572	0.041
11737400_s_at	Serine peptidase inhibitor-like, with Kunitz and WAP domains 1 (eppin) /// SPINLW1-WFDC6 readthrough /// WAP four-disulfide core domain 6	2.572	0.006
11729031_a_at	Chromosome 1 open reading frame 194	2.548	0.025
11746354_a_at	Chromosome 1 open reading frame 158	2.491	0.038

11745295_a_at	Uncharacterized LOC100287718	2.460	0.039
11763973_a_at	Chromosome 9 open reading frame 117	2.433	0.048
11740285_at	EF-hand calcium binding domain 1	2.432	0.034
11753938_a_at	Family with sequence similarity 166, member B	2.431	0.046
11728164_a_at	Serine peptidase inhibitor-like, with Kunitz and WAP domains 1 (eppin) /// SPINLW1-WFDC6 readthrough	2.414	0.034
11723899_a_at	Dehydrogenase/reductase (SDR family) member 9	2.391	0.033
11719321_a_at	Dynein, axonemal, light intermediate chain 1	2.386	0.034
11730944_a_at	Coiled-coil domain containing 65	2.376	0.041
11731924_a_at	Potassium channel regulator	2.376	0.038
11732856_at	Cadherin-related family member 4	2.375	0.033
11737119_a_at	NIMA (never in mitosis gene a)- related kinase 10	2.373	0.030
11729418_a_at	Tektin 2 (testicular)	2.371	0.042
11734055_a_at	Chromosome 20 open reading frame 26	2.369	0.010
11743030_at	Dynein, axonemal, heavy chain 3	2.368	0.034
11724349_at	Protein phosphatase 1, regulatory (inhibitor) subunit 14C	2.368	0.030
11739916_a_at	Serpin peptidase inhibitor, clade B (ovalbumin), member 11 (gene/pseudogene)	2.362	0.044
11717386_s_at	Metallothionein 1G	2.358	0.002
11755748_s_at	Placenta-specific 8	2.350	0.041
11729042_a_at	Deleted in lung and esophageal cancer 1	2.343	0.025
11734513_at	Leucine rich repeat containing 18	2.339	0.038
11730699_at	Group 10 secretory phospholipase A2-like /// phospholipase A2, group X	2.338	0.016
11732063_a_at	Chromosome 22 open reading frame 15	2.303	0.020
11727957_a_at	Dynein, axonemal, intermediate chain 1	2.295	0.019
11728116_at	Dynein, axonemal, heavy chain 10	2.291	0.039
11715263_at	Sperm flagellar 2	2.290	0.040
11732553_a_at	Enkurin, TRPC channel interacting protein	2.281	0.024
11733330_at	Coiled-coil domain containing 170	2.278	0.048
11732748_at	Dynein, axonemal, heavy chain 6	2.269	0.020
11735883_a_at	Dynein, axonemal, heavy chain 9	2.262	0.016
11737207_at	Chromosome 1 open reading frame 189	2.261	0.046

11743801_at	Dynein, axonemal, heavy chain 2	2.254	0.031
11728981_at	Chromosome 8 open reading frame 47	2.253	0.026
11737031_a_at	Kallikrein-related peptidase 13	2.250	0.005
11731722_a_at	Aldehyde dehydrogenase 3 family, member B1	2.228	0.022
11739440_a_at	Keratin 4	2.219	0.047
11737637_a_at	Chromosome 9 open reading frame 171	2.205	0.031
11752329_a_at	Dynein, axonemal, intermediate chain 2	2.203	0.039
11731273_a_at	Potassium voltage-gated channel, Isk-related family, member 1	2.201	0.045
11746427_a_at	WD repeat domain 66	2.195	0.044
11728604_at	Rhabdoid tumor deletion region gene 1	2.191	0.014
11733903_a_at	Spermatogenesis associated 4	2.191	0.042
11739797_a_at	Regulatory factor X, 2 (influences HLA class II expression)	2.189	0.032
11738889_at	IQ motif containing D	2.180	0.020
11752019_a_at	YSK4 Sps1/Ste20-related kinase homolog (<i>S. cerevisiae</i>)	2.139	0.039
11724350_s_at	Protein phosphatase 1, regulatory (inhibitor) subunit 14C	2.125	0.014
11757570_s_at	Proline rich 15	2.125	0.014
11723635_s_at	Matrix metalloproteinase 3 (stromelysin 1, progelatinase)	2.124	0.045
11726521_a_at	Spermatogenesis associated 17	2.117	0.047
11732367_a_at	Fibroblast growth factor 14	2.113	0.031
11757615_a_at	Microtubule-associated protein 6	2.113	0.012
11732954_at	Coiled-coil domain containing 153	2.111	0.022
11726922_a_at	EF-hand calcium binding domain 6	2.077	0.009
11751078_s_at	Cytochrome P450, family 2, subfamily F, polypeptide 1	2.075	0.019
11737415_at	BPI fold containing family B, member 4	2.074	0.021
11720867_x_at	Placenta-specific 8	2.070	0.044
11725908_at	Leucine rich repeat containing 10B	2.070	0.014
11735530_a_at	PIH1 domain containing 2	2.066	0.034
11730456_at	Coiled-coil domain containing 96	2.065	0.029
11736275_x_at	Carboxyl ester lipase (bile salt-stimulated lipase)	2.064	0.017
11742263_a_at	Sperm associated antigen 8	2.031	0.031
11722994_s_at	Alcohol dehydrogenase 1A (class I), alpha polypeptide /// alcohol dehydrogenase 1B	2.028	0.049

	(class I), beta polypeptide /// alcohol dehydrogenase 1C (class I), gamma polypeptide		
11730244_at	Flavin containing monooxygenase 2 (non-functional)	2.024	0.004
11759102_at	UBX domain protein 10	2.013	0.036
11734262_a_at	Adenylate kinase 8	2.006	0.011
11741397_a_at	Dynein, axonemal, intermediate chain 2	2.006	0.042
11739893_a_at	Cyclin N-terminal domain containing 1	2.005	0.019
11727658_s_at	Kallikrein-related peptidase 10	2.002	0.038

Table E4. The seven canonical Gene Ontology categories were identified for the differentially expressed genes

Gene Ontology term	Associated Genes identified	No. of genes	False discovery rate
1. Motile cilium assembly	<i>CFAP221, DNAAF3, FOXJ1, RSPH9, ZMYND10</i>	5	<0.001
2. Axonemal dynein complex assembly	<i>DNAAF3, DNAI1, DNAI2, DRC1, PIH1D3, TEKT2, ZMYND10</i>	7	<0.001
3. Cilium or flagellum-dependent cell motility	<i>DNAH2, DNAH3, DNAH6, DRC1, RSPH9, TEKT1, TEKT2</i>	7	<0.001
4. Cilium movement	<i>CFAP206, CFAP221, CFAP53, CFAP61, DNAH9, DNAI1, DNAI2, HYDIN, RSPH9, TEKT1, TEKT2, WDR66</i>	12	<0.001
5. Negative regulation of transporter activity	<i>KCNE1, KCNRG, PLN</i>	3	0.009
6. Response to zinc ion	<i>CA2, MT1G, PLN</i>	3	0.010
7. C-terminal protein lipidation	<i>ART3, LYPD2, PSCA</i>	3	0.013