

Table SD1. Patient characteristics^a

Patient	Sex	Age (year)	Esophageal Disease	Treatment	Maximum eosinophils /hpf	Cell thickness in basal layer	Maximum mast cells /hpf	Maximum lymphocytes /hpf	Genotype	Food anaphylaxis	SPT/A ^b	SPT/F ^b	RAST ^b (positive reaction)	Rhinitis ^c	Atopic dermatitis ^c	Asthma ^c	Alternative diagnosis	Date ^d
1	M	11	NL	None	0	3	5	3	Unk	No	ND	ND	ND	Yes	No	No	Recurrent croup	December
2	M	11	NL	LTRA	0	3	4	3	Unk	No	ND	ND	ND	No	No	Yes	Functional abdominal pain	May
3	F	9	NL	None	0	3	4	3	Unk	Unk	ND	ND	ND	Unk	Unk	Unk	Functional abdominal pain	March
4	M	14	NL	None	0	2	6	4	Unk	No	ND	ND	ND	No	No	No	Vomiting/diarrhea	February
5	F	7	NL	LTRA	0	3	5	6	Unk	Yes	1	3	ND	Unk	Unk	Yes	Functional abdominal pain	March
6	F	13	NL	None	0	2	4	2	Unk	No	0	4	ND	No	No	No	Functional abdominal pain	August
7	M	17	CE	PPI	0	4	7	12	Unk	Yes	17	4	ND	No	No	Yes	None	November
8	M	6	CE	PPI	0	4	6	10	Unk	Unk	ND	ND	ND	Unk	Unk	Unk	None	June
9	F	16	CE	LTRA	3	4	6	8	Unk	No	ND	ND	ND	No	No	Yes	None	January
10	F	13	CE	LTRA+PPI	3	5	4	8	Unk	No	0	0	ND	No	No	No	None	August
11	F	11	CE	LTRA+PPI	6	4	6	9	Unk	Unk	ND	ND	ND	Unk	Unk	Unk	None	May
12	M	11	EE	PPI	24	6	6	12	TT	No	2	5	3	Yes	No	Yes	None	November
13	F	4	EE	PPI	25	6	15	15	TT	No	0	0	ND	No	No	No	None	November
14	M	15	EE	None	30	6	24	6	TG	Unk	1	1	ND	Unk	Unk	Yes	None	February
15	M	15	EE	None	31	6	15	11	TT	No	8	2	ND	Yes	No	Yes	None	March
16	M	13	EE	PPI	32	6	10	25	TG	No	0	0	ND	No	No	No	None	June
17	M	6	EE	PPI	40	7	10	21	TT	Yes	5	3	0	Unk	Unk	No	None	November
18	M	13	EE	LTRA	42	7	10	5	TT	No	4	5	2	Yes	Yes	Yes	None	November
19	F	16	EE	LTRA+PPI	50	9	9	23	TT	No	0	0	ND	No	No	No	None	December
20	M	15	EE	None	51	7	13	22	TG	No	0	0	ND	No	No	No	None	February
21	M	3	EE	PPI	56	7	15	20	TG	Yes	1	12	4	No	No	No	None	August
22	F	14	EE	PPI	72	8	11	12	TG	No	8	12	ND	Yes	Yes	No	None	September
23	M	2	EE	None	83	11	31	21	TG	Yes	0	12	9	No	No	No	None	May
24	F	4	EE	PPI	218	8	11	28	TT	No	2	4	5	Yes	No	No	None	November

Patient	Sex	Age (year)	Esophageal Disease	Treatment	Maximum eosinophils/h pf	Hyperplasia	SPT/A	SPT/F	Allergic Diseases	Genotype
25	M	7	CE	None	0	Yes	2	4	Yes	Unk
26	M	11	CE	PPI	0	Yes	Unk	Unk	Yes	Unk
27	M	7	CE	None	0	Yes	Unk	Unk	Unk	Unk
28	F	9	CE	pentasa	1	No	1	1	Yes	Unk
29	M	16	CE	None	5	Yes	Unk	Unk	Unk	Unk
30	F	4	CE	None	6	Yes	Unk	4	Yes	Unk
31	M	6	EE	PPI+LTRA	26	Yes	2	8	Yes	TG
32	M	12	EE	None	30	Yes	Unk	Unk	Unk	TG
33	M	15	EE	None	39	Yes	4	0	Yes	TG
34	M	8	EE	None	48	Yes	Unk	2	Yes	Unk
35	F	12	EE	PPI	55	Yes	0	0	Yes	TT
36	M	3	EE	None	79	Yes	0	6	Yes	TT
37	M	17	EE	None	126	Yes	Unk	Unk	Unk	Unk

^aPatient characteristics at the time the biopsy sample was obtained.

^bThe number of positive skin prick tests to aeroallergens (SPT/A) or foods (SPT/F) or positive food RAST results are reported as described in the Methods.

^cHistory of past or present atopic dermatitis, allergic rhinitis or asthma.

^dMonth when the biopsy was collected

Abbreviations: M, Male; F, Female; NL, Normal; CE, Chronic Esophagitis; EE, Eosinophilic Esophagitis; LTRA, Leukotriene Receptor Antagonist; PPI, Proton Pump Inhibitor; ND, Not Determined; Unk, Unknown.

Table SD2. Number of genes obtained using Welch and Student T-Test, Pearson correlation test and fold change filter.^a

Comparison	fold change			
	2	3	5	10
NL vs EE	1146	382	124	42
NL vs CE	25	7	0	0

	p value			
	0.05	0.01	0.005	0.001
NL vs EE				
Welch T test	9063	4183	3034	1527
student T test	7707	3283	2295	1017
Welch T test + FDR ^b	1928	574	333	69
student T test +FDR	958	236	134	59
NL vs CE				
Welch T test	1432	163	73	8
student T test	1618	216	105	8
Welch T test + FDR	0	0	0	0
student T test + FRD	0	0	0	0
EE Atopic vs EE non-Atopic				
Welch T test	1403	200	90	13
student T test	1543	216	88	14
Welch T test + FDR	0	0	0	0
student T test + FDR	0	0	0	0
EE female vs EE male				
Welch T test	4158	857	434	75
student T test	4185	691	298	49
Welch T test + FDR	1	1	1	1
student T test + FDR	8	5	5	5
EE treated vs EE untreated^c				
Welch T test	6487	1824	1022	275
student T test	5968	1785	984	141
Welch T test + FDR	0	0	0	0
student T test + FDR	0	0	0	0

Pearson correlation	p value				
	0.05	0.01	0.005	0.001	0.0005
Correlation to eosinophils	6261	2757	1943	899	615
Correlation to age	2257	334	136	16	10

^a The values in bold have been used in this study.

^b The FDR used was always Benjamini and Hochberg false discovery rate correction

Abbreviation: False rate discovery correction (FDR); EE, Eosinophilic esophagitis; CE, Chronic esophagitis; NL, normal.

^c The patients treated with PPI and/or LTRA+PPI has been compared to the untreated EE patients

Table SD3. Gene ontology of the upregulated genes in the EE transcript signature.^a

Classification	COUNT	%	PVALUE
Total upregulated	344		
CLASSIFIED (biological process)	270	100	
RESPONSE TO PEST/PATHOGEN/PARASITE	26	9.6	2.7E-09
RESPONSE TO STRESS	30	11.1	1.2E-06
INFLAMMATORY RESPONSE	13	4.8	6.2E-06
POSITIVE REGULATION OF I-KAPPAB KINASE/NF-KAPPAB CASCADE	8	3	6.6E-05
RESPONSE TO WOUNDING	14	5.2	6.8E-05
POSITIVE REGULATION OF SIGNAL TRANSDUCTION	8	3	9.7E-05
CELL COMMUNICATION	70	25.8	1.2E-04
SIGNAL TRANSDUCTION	59	21.8	1.8E-04
RESPONSE TO BIOTIC STIMULUS	49	18.1	3.0E-04
PROTEIN KINASE CASCADE	12	4.4	3.3E-04
HUMORAL IMMUNE RESPONSE	9	3.3	1.1E-03
IMMUNE RESPONSE	44	16.2	1.4E-03
RESPONSE TO EXTERNAL STIMULUS	54	19.9	3.0E-03
APOPTOSIS	14	5.2	3.7E-03
CARBOXYLIC ACID BIOSYNTHESIS	5	1.8	4.2E-03
ORGANIC ACID BIOSYNTHESIS	5	1.8	4.2E-03
PROTEOLYSIS AND PEPTIDOLYSIS	17	6.3	6.9E-03
ICOSANOID METABOLISM	4	1.5	7.2E-03
MONOCARBOXYLIC ACID TRANSPORT	3	1.1	7.9E-03
CATABOLISM	22	8.1	9.0E-03
PROTEIN CATABOLISM	17	6.3	9.3E-03
COMPLEMENT ACTIVATION	4	1.5	1.1E-02
CELL ADHESION	17	6.3	1.1E-02
ANTIGEN PROCESSING, ENDOGENOUS ANTIGEN VIA MHC CLASS I	3	1.1	1.5E-02
MACROMOLECULE CATABOLISM	18	6.6	1.6E-02
FATTY ACID BIOSYNTHESIS	4	1.5	1.6E-02
ICOSANOID BIOSYNTHESIS	3	1.1	2.5E-02
FATTY ACID METABOLISM	6	2.2	2.8E-02
BLOOD COAGULATION	5	1.8	2.9E-02
HEMOSTASIS	5	1.8	3.6E-02
CHOLESTEROL METABOLISM	4	1.5	4.0E-02
LIPID METABOLISM	13	4.8	4.6E-02
ANION TRANSPORT	7	2.6	4.7E-02
STEROL METABOLISM	4	1.5	4.9E-02
REGULATION OF BODY FLUIDS	5	1.8	5.0E-02
CLASSIFIED (molecular function)	271	100	
SIGNAL TRANSDUCER ACTIVITY	60	22.1	2.5E-04
SCAVENGER RECEPTOR ACTIVITY	5	1.8	4.5E-04
OXIDOREDUCTASE ACTIVITY, ACTING ON THE CH-NH2 GROUP OF DONORS	4	1.5	1.7E-03
PEPTIDE TRANSPORTER ACTIVITY	3	1.1	2.4E-03
PROTEIN BINDING	37	13.7	3.8E-03
PEPTIDASE ACTIVITY	16	5.9	5.1E-03
ENDOPEPTIDASE ACTIVITY	13	4.8	5.1E-03
CHYMOTRYPSIN ACTIVITY	6	2.2	1.0E-02
OBSOLETE MOLECULAR FUNCTION	15	5.5	1.2E-02
TRYPSIN ACTIVITY	6	2.2	2.6E-02
PROTEASOME ENDOPEPTIDASE ACTIVITY	3	1.1	3.1E-02
GLYCOSAMINOGLYCAN BINDING	5	1.8	3.3E-02
INTERLEUKIN RECEPTOR ACTIVITY	3	1.1	4.0E-02
RECEPTOR ACTIVITY	38	14	4.2E-02
INTERLEUKIN BINDING	3	1.1	4.3E-02
ENZYME ACTIVATOR ACTIVITY	6	2.2	4.3E-02
OLIGOPEPTIDE TRANSPORTER ACTIVITY	2	0.7	4.3E-02

^aThe functional annotations are generated by subjecting the data to DAVID software with the GoCharts (gene ontology charts) functional algorithm. Analysis is based on biological processes and molecular functions.

Table SD4. Gene ontology of the downregulated genes in the EE transcript signature^a

Classification	COUNT	%	PVALUE
Total downregulated	230		
CLASSIFIED (biological process)	180	100	
CARBOXYLIC ACID METABOLISM	11	6.1	1.1E-03
ORGANIC ACID METABOLISM	11	6.1	1.2E-03
METABOLISM	75	41.7	6.5E-03
INTRACELLULAR SIGNALING CASCADE	16	8.9	1.6E-02
FATTY ACID METABOLISM	5	2.8	2.2E-02
ICOSANOID METABOLISM	3	1.7	2.5E-02
MORPHOGENESIS	16	8.9	3.7E-02
PROTEIN KINASE CASCADE	6	3.3	4.7E-02
CLASSIFIED (molecular function)	180	100	
CATALYTIC ACTIVITY	63	35	3.1E-04
OXIDOREDUCTASE ACTIVITY, ACTING ON CH-OH GROUP OF DONORS	6	3.3	1.8E-03
ENZYME INHIBITOR ACTIVITY	8	4.4	2.5E-03
SERINE ESTERASE ACTIVITY	3	1.7	5.9E-03
ACTIN BINDING	7	3.9	6.0E-03
OXIDOREDUCTASE ACTIVITY	16	8.9	6.8E-03
CARBOXYLESTERASE ACTIVITY	3	1.7	8.3E-03
ENZYME REGULATOR ACTIVITY	11	6.1	8.3E-03
CYTOSKELETAL PROTEIN BINDING	7	3.9	2.5E-02
TRANS-1,2-DIHYDROBENZENE-1,2-DIOL DEHYDROGENASE ACTIVITY	2	1.1	2.9E-02
HYDROLASE ACTIVITY, ACTING ON ESTER BONDS	11	6.1	3.0E-02
ENDOPEPTIDASE INHIBITOR ACTIVITY	5	2.8	3.1E-02
PROTEASE INHIBITOR ACTIVITY	5	2.8	3.1E-02
CARBOXYLIC ACID TRANSPORTER ACTIVITY	4	2.2	3.4E-02
ORGANIC ACID TRANSPORTER ACTIVITY	4	2.2	3.4E-02
CYTOCHROME-B5 REDUCTASE ACTIVITY	2	1.1	3.6E-02
POLY(A) BINDING	2	1.1	3.6E-02
PHOSPHORIC MONOESTER HYDROLASE ACTIVITY	6	3.3	3.6E-02
PHOSPHOPROTEIN PHOSPHATASE ACTIVITY	5	2.8	4.1E-02
MAGNESIUM ION BINDING	5	2.8	4.3E-02

^aThe functional annotations are generated by subjecting the data to DAVID software with the GoCharts (gene ontology charts) functional algorithm. Analysis is based on biological processes and molecular functions.

Table SD5. EE transcript Signature

Cytokines, cytokine receptors and cytokine signaling
Mast cell genes
Arachidonic acid metabolism and relatives
Cell growth and differentiation

Affy-ID	Fold Increase	Name	Complete name of the genes	GeneBank
223210 at	53.17	CCL26	[[MIP-4alpha][CCL26][TSC-1][SCYA26, FORMERLY][eotaxin-3 precursor][EOTAXIN 3][CC chemokine [MIP-4][thymic stroma chemokine-1][macrophage inflammatory protein 4-2]]	NM_006072
210809 s at	46.29	POSTN	[[OSF-2][POSTN][PNI][periostin, osteoblast specific factor][osteoblast specific factor 2 (fasciclin I-like)]]	NM_006475
206026 s at	23.59	TNFAIP6	[[TSG6][TNFAIP6][hyaluronate-binding protein][tumor necrosis factor-stimulated gene-6 protein][TUMOR NECROSIS FACTOR-ALPHA-INDUCED PROTEIN 6][tumor necrosis factor-stimulated gene-6 protein]]	NM_007115
233663 s at	23.42	CDH26	[[CDH26][cadherin-like 26]]	NM_177980
232306 at	21	CDH26	[[CDH26][cadherin-like 26]]	NM_177980
207328 at	20.89	ALOX15	[[1.13.11.33][ALOX15][arachidonate 15-lipoxygenase][15-LIPOXYGENASE, RETICULOCYTE ARACHIDONATE]]	NM_001140
206942 s at	19.81	PMCH	[[PMCH][pro-melanin-concentrating hormone]]	NM_002674
204470 at	18.79	CXCL1	[[MGSA-a][ANAP-3][CXCL1][SCYB1][GROa][GRO1, FORMERLY][GRO PROTEIN, ALPHA][GRO1 ONCOGENE, FORMERLY][MELANOMA GROWTH STIMULATORY ACTIVITY, ALPHA]]	NM_001511
214677 x at	17.57	IGLV@	[[IGLJ3][immunoglobulin lambda joining 3]]	NM_005174
211430 s at	16.42	IGHD	[[IGHM][immunoglobulin mu][IMMUNOGLOBULIN HEAVY MU CHAIN][immunoglobulin heavy constant mu][constant region of heavy chain of IgM]]	AK90461
243585 at	15	FLJ16025	[[FLJ16025]]	XM_293626
205890 s at	14.85	UBD	[[UBD][FAT10][diubiquitin][ubiquitin D1]]	NM_006398
212592 at	14.61	IGJ	[[IGCJ1][CHI][IGJ][immunoglobulin J chain][immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides]]	NM_144646
238429 at	14.01	FLJ33069	[[FLJ33069][hypothetical protein FLJ33069]]	NM_144649
205624 at	13.13	CPA3	[[CPA3][13.4.17.1][carboxypeptidase A3 (mast cell)][CARBOXYPEPTIDASE A3, MAST CELL][mast cell carboxypeptidase A3 precursor]]	NM_001870
206207 at	12.69	CLC	[[LPL, HUMAN][CLC1][galactin-10][1.3.1.5][GALS10][GALECTIN 10][lysocitichin acylhydrolase][eosinophil lysophospholipase][LYSOPHOSPHOLIPASE OF EOSINOPHIL][Charot]]	NM_001828
224795 x at	12.64	TCF12; HEB; HTF4; HsT17266	[[IGKC]]	BX647333
209138 x at	12.4	IGL@	[[IGL]]	NG_000002
225688 s at	12.05	PHLDB2	[[PHLDB2][pleckstrin homology-like domain, family B, member 2]]	NM_145753
1555778_a_a	11.84	POSTN	[[OSF-2][POSTN][PNI][periostin, osteoblast specific factor][osteoblast specific factor 2 (fasciclin I-like)]]	NM_006475
221671 x at	10.97	TCF12; HEB; HTF4; HsT17266	[[IGKC]]	BX647333
220622 at	10.94	FLJ23259	[[FLJ23259][hypothetical protein FLJ23259]]	NM_024727
221651 x at	10.2	TCF12; HEB; HTF4; HsT17266	[[IGKC]]	BX647333
232165 at	10.12	EPPK1	[[EPPK1][EPPK1][lepiplakin 1][450 kDa epidermal antigen]]	NM_031308
242013 at	9.701	na	[[na][hypothetical LOC148280 (LOC148280), mRNA]]	XM_097433
206529 x at	9.548	SLC26A4	[[SLC26A4][pendrin][PDS1][DFNB4][solute carrier family 26, member 4]]	NM_000441
232164 s at	9.334	EPPK1	[[EPPK1][EPPK1][lepiplakin 1][450 kDa epidermal antigen]]	NM_031308
225647 s at	9.008	CTSC	[[HMS1][CPPI13.4.14.1][DPP1][PALS1][DPP1][CTSC][PLS1][dipeptidyl transferase][cathepsin C][dipeptidyl-peptidase III][cathepsin J][Papillon-Lefevre syndrome][DIPPTIDYL PEP]]	NM_001814
220330 s at	8.687	SAMSN1	[[HACS1][SAMS1][HEMATOPOIETIC ADAPTOR CONTAINING SH3 AND SAM DOMAINS 1][SAM domain, SH3 domain and nuclear localisation signals, 1][SAM DOMAIN, SH3 DOMAIN]]	NM_022136
224412 s at	8.519	TRPM6	[[CHAK2][TRPM6][CHANNEL KINASE 2][transient receptor potential cation channel, subfamily M, member 6]]	NM_017662
215121 x at	8.317	IGLV@	[[IGL]]	AK051714
225458 at	8.068	SEC6L1	[[SEC6L1][SEC6-like 1 (S. cerevisiae)]]	NM_007277
223423 at	8.008	GPR160	[[GPR160][GPR160][putative G protein-coupled receptor][G protein-coupled receptor 160]]	NM_014373
227480 at	8.003	SUSD2	[[SUSD2][sushi domain containing 2]]	NM_019601
236979 at	7.996	KIAA0495	[[KIAA0495]]	AB007964
221796 at	7.355	NTRK2	[[NTRK2][NTRK2][TYROSINE KINASE RECEPTOR B][neurotrophic tyrosine kinase, receptor, type 2]]	NM_006180
225646 at	7.262	CTSC	[[HMS1][CPPI13.4.14.1][DPP1][PALS1][DPP1][CTSC][PLS1][dipeptidyl transferase][cathepsin C][dipeptidyl-peptidase III][cathepsin J][Papillon-Lefevre syndrome][DIPPTIDYL PEP]]	NM_001814
215379 x at	7.045	IGLV@	[[IGLJ3][immunoglobulin lambda joining 3]]	AK051714
235229 at	6.874	KIR216	[[KIR216][similar to Olfactory receptor 212 (LOC346170), mRNA]]	XM_294092
206765 at	6.696	KCNJ2	[[KCNJ2][inward rectifier channel 2][inward rectifier K+ channel KIR2.1][cardiac inward rectifier potassium channel][inward rectifier potassium channel 2]]	NM_000891
221795 at	6.56	NTRK2	[[NTRK2][NTRK2][TYROSINE KINASE RECEPTOR B][neurotrophic tyrosine kinase, receptor, type 2]]	NM_006180
216474 x at	6.429	TPSB2	[[TPSB2][trypsinase, alpha]]	NM_003294
201487 at	6.299	CTSC	[[HMS1][CPPI13.4.14.1][DPP1][PALS1][DPP1][CTSC][PLS1][dipeptidyl transferase][cathepsin C][dipeptidyl-peptidase III][cathepsin J][Papillon-Lefevre syndrome][DIPPTIDYL PEP]]	NM_001814
219684 at	6.278	IFRG28	[[IFRG28][interferon responsive protein]]	NM_022147
205579 at	6.191	HRH1	[[HRH1][H1-1][hish1][histamine receptor H1][BPHS, MOUSE, HOMOLOG OF][histamine receptor, subclass H1]]	NM_000861
219197 s at	6.166	SCUBE2	[[SCUBE2][signal peptide, CUB domain, EGF-like 2]]	NM_020974
214669 x at	6.073	IGKC	[[Kml][HCAK1][IGKC1][immunoglobulin kappa constant][IMMUNOGLOBULIN IN V KAPPA-CHAIN DEFICIENCY][IMMUNOGLOBULIN KAPPA LIGHT CHAIN][immunoglobulin kappa constant]]	BM993907
207134 x at	6.028	TPSB2	[[TPSB2][trypsinase, alpha]]	NM_003294
204591 at	5.928	CHL1	[[CHL1][CAM2][CHL1][CALL][neural cell adhesion molecule][cell adhesion molecule L1-like][CHL1, MOUSE, HOMOLOG OF][L1 cell adhesion molecule 2][cell adhesion molecule with fibronectin type III repeats]]	NM_006614
203854 at	5.687	IF	[[IF][3.4.21.45][IF][IFACTOR 1][FACTOR 'EYE'][COMPLEMENT COMPONENT 1][factor (complement)]][C3 INACTIVATOR, DEFICIENCY OF][C3b INACTIVATOR, COMPLEMENT COMPO]]	NM_000204
204826 at	5.608	GLDC	[[GLDC][HYGN1][GCSPI][GCEI][NKH1][1.4.4.2][GLYCINE CLEAVAGE SYSTEM P PROTEIN][glycine dehydrogenase (decarboxylating); glycine decarboxylase, glycine cleavage syste]]	NM_000170
225457 s at	5.608	SEC6L1	[[SEC6L1][SEC6-like 1 (S. cerevisiae)]]	NM_007277
205683 x at	5.573	TPSB2	[[TPSB2][trypsinase, alpha]]	NM_003294
207717 s at	5.342	PKP2	[[PKP2][plakophilin 2]]	NM_004572
206726 at	5.265	PGDS	[[PGDS][15.3.99.2][prostaglandin-D synthase][prostaglandin D2 synthase, hematopoietic][hematopoietic prostaglandin D2 synthase]]	NM_014485
213258 at	5.108	TFPI	[[LAC1][TFPI][EPI][EXTRINSIC PATHWAY INHIBITOR][tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)]]	NM_006287
229975 at	5.094		[[Homo sapiens transcribed sequence with weak similarity to protein NP_060312.1]]	BQ004901
202357 s at	5.073	BF	[[GBG1][BF1][CAB1][PBF2][1.3.4.21.47][C3 proacelerator][glycine-rich beta-glycoprotein][B-factor, properdin][C3/C5 convertase][C3 proactivator][PROPERDIN FACTOR B][FACTO]]	NM_001710
221218 s at	5.033	TPK1	[[TPK1][TPK1][THIAMINE KINASE][thiamine pyrophosphokinase][mouse thiamine pyrophosphokinase homolog]]	NM_022445
202234 s at	4.941	SLC16A1	[[SLC16A1][MCT1][monocarboxylate transporter 1][solute carrier family 16, member 1][SOLUTE CARRIER FAMILY 16 (MONOCARBOXYLIC ACID TRANSPORTER), MEMBER 1]]	NM_003051
226695 at	4.819	PRRX1	[[PRRX1][PRRX1][homeobox protein PHOX1][PAIRED-RELATED HOMEBOX GENE 1][paired related homeobox 1][paired mesoderm homeo box 1][paired mesoderm hom]]	NM_006902
206932 at	4.732	CH25H	[[CH25H][C25H][cholesterol 25-hydroxylase]]	NM_003956
226702 at	4.61	LOC129607	[[LOC129607][hypothetical protein LOC129607]]	XM_059368
224916 at	4.603	LOC340061	[[LOC340061][hypothetical protein LOC340061]]	NM_198282
214836 x at	4.578	IGKC	[[Kml][HCAK1][IGKC1][immunoglobulin kappa constant][IMMUNOGLOBULIN IN V KAPPA-CHAIN DEFICIENCY][IMMUNOGLOBULIN KAPPA LIGHT CHAIN][immunoglobulin kappa constant]]	BM993907
236489 at	4.542	IGKC	[[Kml][HCAK1][IGKC1][immunoglobulin kappa constant][IMMUNOGLOBULIN IN V KAPPA-CHAIN DEFICIENCY][IMMUNOGLOBULIN KAPPA LIGHT CHAIN][immunoglobulin kappa constant]]	CA314541
206912 at	4.438	FOXE1	[[TFE-2][FOXE1][TFE2][TFE2][FKHL15][forkhead (Drosophila)-like 15][thyroid transcription factor-2][Forkhead, drosophila, homolog-like 15][forkhead box E1 (thyroid transc]]	NM_004473
202796 at	4.415	SYNPO	[[KIAA1029][synaptopodin][SYNPO]]	NM_007286
228771 at	4.385	ADRBK2	[[GRK3][IBARK2][12.7.1.126][ADRBK2][BETA-ADRENERGIC RECEPTOR KINASE 2][adrenergic, beta, receptor kinase 2][beta adrenergic receptor kinase 2]]	NM_005160
232277 at	4.349	SLC28A3	[[SLC28A3][CNT3][CONCENTRATIVE NUCLEOSIDE TRANSPORTER 3][solute carrier family 28 (sodium-coupled nucleoside transporter), member 3]]	NM_022127
207386 at	4.323	CYP7B1	[[1.14.13.1][CYP7B1][CYP7B1][oxysterol 7alpha-hydroxylase][OXYSTEROL 7-ALPHA-HYDROXYLASE][cytochrome P450, family 7, subfamily B, polypeptide 1][cytochrome P450]]	NM_004820
209546 s at	4.259	APOL1	[[APOL1][APOL1][APOL1][apolipoprotein L-1][apolipoprotein L1 isoform B precursor][apolipoprotein L1 isoform A precursor]]	NM_145343
204885 s at	4.254	MSLN	[[CAK1][SMR1][MSLN][mesothelin][MEGAKARYOCYTE-POTENTIATING FACTOR][SOLUBLE MPF][MESOTHELIN-RELATED PROTEIN][mesothelin isoform 2 precursor][mesothelin iso]]	NM_013404
202037 s at	4.239	SFRP1	[[SFRP1][IFRP-1][FrzA][SFRP1][secreted apoptosis-related protein 2][secreted frizzled-related protein 1]]	NM_003012
204396 s at	4.212	GRK5	[[2.7.1.1][GRK5][GRK5][G protein-coupled receptor kinase 5]]	NM_005308
207496 at	4.192	MS4A2	[[IFCER1][MS4A1][MS4A2][FCER1B][Fc epsilon receptor 1 beta-chain][Fc IqE RECEPTOR, BETA CHAIN][MEMBRANE-SPANNING 4 DOMAINS, SUBFAMILY A, MEMBER 2][immunol]]	NM_000139

223078 s at	0.346			TMOD3	[[TMOD3]] TROPOMODULIN, UBIQUITOUS [[tropomodulin 3 (ubiquitous)]]	NM_014547
201397 at	0.343			PHGDH	[[PHGDH]] PHOSPHOGLYCERATE DEHYDROGENASE [[3-phosphoglycerate dehydrogenase]] phosphoglycerate dehydrogenase	NM_006623
203946 s at	0.334			ARG2	[[ARG2]] 3,5,3,1 A-III kidney arginase nonhepatic arginase L-arginine amidinohydrolase L-arginine ureahydrolase [[ARGINASE III]] arginase, type III arginase, type II precursor	NM_001172
203675 at	0.331			NUCB2	[[NUCB2]] NEFA1 nucleobindin 2	NM_005013
208539 x at	0.329			SPRR2B	[[SPRR2B]] small proline-rich protein 2B	NM_006945
215228 at	0.329			NHLH2	[[NSC2]] NHLH2 HEN2 NEURONAL SCL-LIKE PROTEIN 2 nescient helix loop helix 2	NM_005599
209426 s at	0.328			AMACR	[[AMACR]] 5,9,4 ALPHA-METHYLACYL-CoA RACEMASE AMACR DEFICIENCY [[alpha-methylacyl-CoA racemase isomerase]]	NM_014324
227280 s at	0.314			FLJ40432	[[FLJ40432]] hypothetical protein FLJ40432	NM_153253
211922 at	0.302			PKWINK1	[[PKWINK1]] PRKWK PROTEIN KINASE, LYSINE-DEFICIENT 1 KDP PSEUDOHYPOALDOSTERONISM, TYPE I [[protein kinase, lysine deficient 1]]	NM_018979
210609 s at	0.3			TP53I3	[[TP53I3]] PIG3 lipoxygenase oxidoreductase homolog p53-induced gene 3 protein [[tumor protein p53 inducible protein 3]]	NM_004881
206595 at	0.286			CST6	[[CST6]] cystatin 6 cystatin E/MICYSTATIN M/E cystatin M precursor	NM_001323
155264 a a	0.29			ZNF101	[[ZNF101]] zinc finger protein 101	NM_033204
1564307 a a	0.286			FLJ25179	[[FLJ25179]] hypothetical protein FLJ25179	NM_144670
203225 s at	0.282			RFK	[[RFK]] 1149 riboflavin kinase	NM_018339
209160 at	0.281			AKR1C3	[[HA1753]] 1.1.1.188 DD3 HluPGFS HSD17B5 1.3.1.20 1.1.1.213 AKR1C3 KIAA0119 HAKRB HAKRE trans-1,2-dihydrobenzene-1,2-diol dehydrogenase chlordecone reductase	NM_003739
216594 x at	0.281			AKR1C1	[[1.1.1.213]] 2-ALPHA-HSD 1.3.1.20 20-ALPHA-HSD MGCR954 H-37 HAKRC MBAB C9 DDH1 AKR1C1 trans-1,2-dihydrobenzene-1,2-diol dehydrogenase chlordecone reductase	NM_001353
201468 s at	0.28			NOO1	[[NMOR1]] diaphorase-4 NQO1 OR1 DDT DHOU NMOR1 DIA4 DIAPHORASE 4 NAD(P)H dehydrogenase, quinone 1 diaphorase (NADH/NADPH) (cytochrome b-5 reductase)	NM_000903
213725 x at	0.279			LOC283824	[[LOC283824]] hypothetical protein LOC283824	BX647541
204048 s at	0.268			C6orf56	[[C6orf56]] KIAA0680 KIAA0680 gene product chromosome 6 open reading frame 56	NM_014721
227410 at	0.263			FAM43A	[[FAM43A]] hypothetical protein FLJ90022	NM_153690
205637 s at	0.26			SH3GL3	[[EEN-B2]] SH3D2 SH3GL3 SH3P1 Hst1 9371 CN3A3 ENDOPHILIN A3 SH3-domain GRB2-like 3 SH3 DOMAIN, GRB2-LIKE, 3	NM_003027
204151 x at	0.257			AKR1C1	[[1.1.1.213]] 2-ALPHA-HSD 1.3.1.20 20-ALPHA-HSD MGCR954 H-37 HAKRC MBAB C9 DDH1 AKR1C1 trans-1,2-dihydrobenzene-1,2-diol dehydrogenase chlordecone reductase	NM_001353
211653 x at	0.256			AKR1C2	[[BAPB]] DD2 1.3.1.20 HBAB 1.1.1.213 HAKRD MCDR2 AKR1C2 DDH2 AKR1C-pseudo pseudo-chlordecone reductase trans-1,2-dihydrobenzene-1,2-diol dehydrogenase	NM_001354
1553960 at	0.255			C20orf161	[[C20orf161]] chromosome 20 open reading frame 161	NM_033421
231711 at	0.254			ACPP	[[3.1.3.2]] ACPP PAP acid phosphatase, prostate PHOSPHATASE, PROSTATE-SPECIFIC ACID prostatic acid phosphatase precursor	NM_001099
209699 x at	0.251			AKR1C2	[[BAPB]] DD2 1.3.1.20 HBAB 1.1.1.213 HAKRD MCDR2 AKR1C2 DDH2 AKR1C-pseudo pseudo-chlordecone reductase trans-1,2-dihydrobenzene-1,2-diol dehydrogenase	NM_001354
1553929 at	0.251			ASAH3	[[ASAH3]] N-acylsphingosine amidohydrolase (alkaline ceramidase) 3	NM_133492
223074 s at	0.25			C9orf58	[[C9orf58]] chromosome 9 open reading frame 58	NM_031426
210519 s at	0.248			NOO1	[[NMOR1]] diaphorase-4 NQO1 OR1 DDT DHOU NMOR1 DIA4 DIAPHORASE 4 NAD(P)H dehydrogenase, quinone 1 diaphorase (NADH/NADPH) (cytochrome b-5 reductase)	NM_000903
205863 at	0.247			S100A12	[[MRP6]] CAEF1 ENRAGE ICGRP S100A12 CALGRANULIN-RELATED PROTEIN S100 calcium-binding protein A12 CALCIUM-BINDING PROTEIN IN AMNIOTIC FLUID EXTRACTABLE S100	NM_005621
243871 at	0.247					BG218400
213652 at	0.246			PCSK5	[[PCGA]] 3.4.21-1 PCSK5 SPC6 protease PC6 proprotein convertase PC5 subtilisin/kexin-like protease PC5 prohormone convertase 5 PROPROTEIN CONVERTASE, SUBTILISIN-LIKE 5	NM_006200
204797 s at	0.244			EBH1	[[EBH1]] EAPL EML1 HHEPAR ECHINODERM MICROTUBULE-ASSOCIATED PROTEIN-LIKE 1 ECHINODERM MICROTUBULE ASSOCIATED PROTEIN LIKE 1	NM_004434
201467 s at	0.241			NOO1	[[NMOR1]] diaphorase-4 NQO1 OR1 DDT DHOU NMOR1 DIA4 DIAPHORASE 4 NAD(P)H dehydrogenase, quinone 1 diaphorase (NADH/NADPH) (cytochrome b-5 reductase)	NM_000903
241137 at	0.238			DPCR1	[[DPCR1]] PBL1 PANBRONCHIOLITIS, DIFFUSE diffuse panbronchiolitis critical region 1	NM_080870
227626 at	0.232			C6orf33	[[MPRB]] MPB1 C6orf33 MEMBRANE PROGESTIN RECEPTOR, BETA ALLOSOMAL MEMBRANE PROTEIN, BRAIN-EXPRESSED, 1 chromosome 6 open reading frame 33	NM_133367
201848 s at	0.23			BNIP3	[[BNIP3]] BCL2 adenovirus E1B 19kD-interacting protein 3 BCL2 adenovirus E1B 19kDa interacting protein 3 BCL2 ADENOVIRUS E1B 19-KD PROTEIN-INTERACTING PROTEIN 3	NM_004052
226423 at	0.228			C6orf33	[[MPRB]] MPB1 C6orf33 MEMBRANE PROGESTIN RECEPTOR, BETA ALLOSOMAL MEMBRANE PROTEIN, BRAIN-EXPRESSED, 1 chromosome 6 open reading frame 33	NM_133367
228810 at	0.227			FLJ40432	[[FLJ40432]] hypothetical protein FLJ40432	NM_152523
1563894 at	0.218			na		XM_379456
242998 at	0.216			RDH12	[[RDH12]] retinol dehydrogenase 12 (all-trans and 9-cis)	NM_152443
223075 s at	0.215			C9orf58	[[C9orf58]] chromosome 9 open reading frame 58	NM_031426
224480 s at	0.212			MGC11324	[[MGC11324]] hypothetical protein MGC11324	NM_032717
205560 at	0.212			PCSK5	[[PCGA]] 3.4.21-1 PCSK5 SPC6 protease PC6 proprotein convertase PC5 subtilisin/kexin-like protease PC5 prohormone convertase 5 PROPROTEIN CONVERTASE, SUBTILISIN-LIKE 5	NM_006200
211538 s at	0.211			HSPA2	[[HSPA1A]] heat shock-induced protein HEAT-SHOCK 70-KD PROTEIN 1A dnaK-type molecular chaperone HSP70-1 HEAT-SHOCK PROTEIN, 70-KD, 1 heat shock 70kDa protein	NM_056725
205964 at	0.209			ZNF426	[[ZNF426]] zinc finger protein 426	NM_024106
238724 at	0.205			BGM		BG030612
204059 s at	0.204			ME1	[[MES1]] 1.1.40 HUMNDME ME1 pyruvic-malic carboxylase MALIC ENZYME, SOLUBLE malic enzyme, cytoplasmic NADP-dependent malic enzyme cytosolic malic enzyme	NM_002395
1559028 at	0.202			LOC284233		BC037172
218843 at	0.2			FNDC4	[[FNDC4]] fibronectin type III domain containing 4	NM_022823
204393 s at	0.199			ACPP	[[3.1.3.2]] ACPP PAP acid phosphatase, prostate PHOSPHATASE, PROSTATE-SPECIFIC ACID prostatic acid phosphatase precursor	NM_001099
218484 at	0.194			LOC56901	[[LOC56901]] NADH:ubiquinone oxidoreductase MLRQ subunit homolog	NM_020142
220723 s at	0.191			FLJ21511	[[FLJ21511]] hypothetical protein FLJ21511	NM_025087
205559 s at	0.19			PCSK5	[[PCGA]] 3.4.21-1 PCSK5 SPC6 protease PC6 proprotein convertase PC5 subtilisin/kexin-like protease PC5 prohormone convertase 5 PROPROTEIN CONVERTASE, SUBTILISIN-LIKE 5	NM_006200
204058 at	0.186			ME1	[[MES1]] 1.1.40 HUMNDME ME1 pyruvic-malic carboxylase MALIC ENZYME, SOLUBLE malic enzyme, cytoplasmic NADP-dependent malic enzyme cytosolic malic enzyme	NM_002395
206448 at	0.173			ZNF365	[[ZNF365C]] ZNF365D KIAA0844 ZNF365 ITLN1 Talanin ZNF365B ZNF365 ZNF365A zinc finger protein 365 zinc finger protein 365 isoform B zinc finger protein 365 isoform C	NM_199450
233534 at	0.167			KRTAP3-2	[[KRTAP3-2]] keratin associated protein 3-2	NM_031959
243313 at	0.166			SYNP02L	[[SYNP02L]] synaptotagmin 2-like	NM_024875
201849 at	0.166			BNIP3	[[BNIP3]] BCL2 adenovirus E1B 19kD-interacting protein 3 BCL2 adenovirus E1B 19-KD PROTEIN-INTERACTING PROTEIN 3	NM_004052
209283 at	0.158			CRYAB	[[CTP2]] CRYAB CRYSTALLIN, ALPHA-B CRYSTALLIN, ALPHA-B crystallin, alpha B heat-shock 20 kD like-protein CRYA2 CATARACT, POSTERIOR POLAR 2	NM_001885
220724 at	0.154			FLJ21511	[[FLJ21511]] hypothetical protein FLJ21511	NM_025087
218507 at	0.148			HIG2	[[HIG2]] hypoxia-inducible protein 2	NM_013332
219804 at	0.139			SYNP02L	[[SYNP02L]] synaptotagmin 2-like	NM_024875
239430 at	0.138			IGFL1	[[APRG644]] UNQ644	NM_198541
1557016 a a	0.129			FLJ40201	[[FLJ40201]] hypothetical protein FLJ40201	NM_152607
223720 at	0.128			ECG2	[[ECG2]] esophagus cancer-related gene-2	NM_032566
207206 s at	0.105			ALOX12	[[112(S)]] lipoxygenase 12-@LIPXYGENASE 1.13.11.31 ALOX12 LOG12 12@LO ARACHIDONATE 12-OXIDOREDUCTASE arachidonate 12-lipoxygenase	NM_000697
211776 s at	0.0956			EPB41L3	[[IDAL]] KIAA0987 EPB41L3 4.1B IDAL-1 NONERYTHROID PROTEIN 4.1, BRAIN TYPE liverthocyte membrane protein band 4.1-like 3 differentially expressed in adenocarcinoma	NM_012307
244620 at	0.0946			SNX19	[[KIAA0254]] CHETB SNX19 sorting nexin 19 KIAA0254 gene product	NM_014758
206605 at	0.0934			P1	[[IPRS26]] PENDING P1 PP1 22 serine protease 26 serine protease placental protein 11 precursor	NM_006025
209616 s at	0.0881			CE54	[[CE54]] carboxylesterase 1 (monocyte/macrophage serine esterase 1)	NM_016380
212681 at	0.0709			EPB41L3	[[IDAL]] KIAA0987 EPB41L3 4.1B IDAL-1 NONERYTHROID PROTEIN 4.1, BRAIN TYPE liverthocyte membrane protein band 4.1-like 3 differentially expressed in adenocarcinoma	NM_012307
206710 s at	0.0687			EPB41L3	[[IDAL]] KIAA0987 EPB41L3 4.1B IDAL-1 NONERYTHROID PROTEIN 4.1, BRAIN TYPE liverthocyte membrane protein band 4.1-like 3 differentially expressed in adenocarcinoma	NM_012307
214621 at	0.0662			GYS2	[[IGYS2]] 2.4.1.11 LIVER GLYCOGEN SYNTHASE GLYCOGEN SYNTHASE, LIVER glycogen synthase 2 (liver)	NM_021957
205627 at	0.0587			CDA	[[3.5.4.4]] CDA CDD cytidine deaminase	NM_001785
244056 at	0.0555					BF514741
1558920 at	0.0387					AK125406
207802 at	0.0306			CRISP3	[[d442L6.3]] CRS3 CRISP-3 SGP28 Aeg2 CRISP3 cysteine-rich secretory protein-3 cysteine-rich secretory protein 3 specific granule protein (28 kDa)	NM_006061

Table SD6. Gene ontology of the genes of the cluster 1 and 2 of the CE transcript signature^a

Classification	COUNT	%	PVALUE
Total Cluster 1			
CLASSIFIED (biological process)	48	100	
INTRACELLULAR SIGNALING CASCADE	5	10.4	8.4E-02
BIOSYNTHESIS	5	10.4	1.1E-01
MACROMOLECULE BIOSYNTHESIS	4	8.3	1.4E-01
NEUROPEPTIDE SIGNALING PATHWAY	2	4.2	1.7E-01
MUSCLE DEVELOPMENT	2	4.2	1.9E-01
LIPID METABOLISM	3	6.3	2.2E-01
LIPID BIOSYNTHESIS	2	4.2	2.5E-01
METABOLISM	15	31.3	3.4E-01
SIGNAL TRANSDUCTION	7	14.6	3.4E-01
REGULATION OF CELLULAR PROCESS	3	6.3	3.8E-01
RNA PROCESSING	2	4.2	3.9E-01
NUCLEOBASE, NUCLEOSIDE, NUCLEOTIDE AND NUCLEIC ACID METABOLISM	7	14.6	4.0E-01
RNA METABOLISM	2	4.2	4.8E-01
CARBOXYLIC ACID METABOLISM	2	4.2	4.8E-01
ORGANIC ACID METABOLISM	2	4.2	4.8E-01
CLASSIFIED (molecular function)	48	100	
PHOSPHATIDYLINOSITOL 3-KINASE ACTIVITY	2	4.2	2.1E-02
PHOSPHOINOSITIDE 3-KINASE ACTIVITY	2	4.2	2.1E-02
OXIDOREDUCTASE ACTIVITY, ACTING ON THE CH-NH GROUP	2	4.2	3.7E-02
LIPID KINASE ACTIVITY	2	4.2	4.3E-02
INOSITOL/PHOSPHATIDYLINOSITOL KINASE ACTIVITY	2	4.2	5.7E-02
CATALYTIC ACTIVITY	14	29.2	7.3E-02
HYDROLASE ACTIVITY, ACTING ON ESTER BONDS	4	8.3	8.6E-02
PHOSPHOTRANSFERASE ACTIVITY, ALCOHOL GROUP AS ACCEPTOR	4	8.3	1.2E-01
TRANSFERASE ACTIVITY	6	12.5	1.3E-01
KINASE ACTIVITY	4	8.3	1.9E-01
TRANSFERASE ACTIVITY	4	8.3	2.1E-01
RNA BINDING	3	6.3	2.1E-01
HYDROLASE ACTIVITY	6	12.5	2.4E-01
MAGNESIUM ION BINDING	2	4.2	2.4E-01
NUCLEIC ACID BINDING	8	16.7	2.5E-01
CAMP-DEPENDENT PROTEIN KINASE ACTIVITY	2	4.2	2.8E-01
STRUCTURAL CONSTITUENT OF RIBOSOME	2	4.2	3.0E-01
PHOSPHORIC MONOESTER HYDROLASE ACTIVITY	2	4.2	3.2E-01
STRUCTURAL MOLECULE ACTIVITY	3	6.3	3.6E-01
PHOSPHORIC ESTER HYDROLASE ACTIVITY	2	4.2	4.2E-01
DNA BINDING	5	10.4	4.2E-01
PROTEIN SERINE/THREONINE KINASE ACTIVITY	2	4.2	4.9E-01
ELECTRON TRANSPORTER ACTIVITY	2	4.2	4.9E-01
Classification	COUNT	%	PVALUE
Total Cluster 2			
CLASSIFIED (biological process)	40	100	
BIOLOGICAL_PROCESS UNKNOWN	3	7.5	0.10798584
PROTEIN METABOLISM	8	20	0.13128147
PROTEIN MODIFICATION	5	12.5	0.17677815
PROTEIN FOLDING	2	5	0.20216705
CELL GROWTH AND/OR MAINTENANCE	9	22.5	0.23926263
MACROMOLECULE METABOLISM	8	20	0.27079597
PROTEIN UBIQUITINATION	2	5	0.35281222
CELLULAR PHYSIOLOGICAL PROCESS	9	22.5	0.39093985
UBIQUITIN CYCLE	2	5	0.43916213
INTRACELLULAR SIGNALING CASCADE	3	7.5	0.48780127
SIGNAL TRANSDUCTION	6	15	0.49792254
CLASSIFIED (molecular function)	40	100	
PROTEIN METHYLTRANSFERASE ACTIVITY	2	5	0.02618582
CYCLOPHILIN	2	5	0.04104433
CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE ACTIVITY	2	5	0.04104433
FK506-SENSITIVE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE	2	5	0.04104433
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE ACTIVITY	2	5	0.04639337
CATALYTIC ACTIVITY	13	32.5	0.08352889
S-ADENOSYLMETHIONINE-DEPENDENT METHYLTRANSFERASE ACTIVITY	2	5	0.11462364
METHYLTRANSFERASE ACTIVITY	2	5	0.16651771
TRANSFERASE ACTIVITY, TRANSFERRING ONE-CARBON GROUPS	2	5	0.16885902
TRANSITION METAL ION BINDING	5	12.5	0.17813991
ISOMERASE ACTIVITY	2	5	0.17931714
OBSOLETE MOLECULAR FUNCTION	3	7.5	0.22712857
ZINC ION BINDING	4	10	0.32123001
PROTEIN BINDING	5	12.5	0.33017209
UBIQUITIN-PROTEIN LIGASE ACTIVITY	2	5	0.3947534
MOLECULAR_FUNCTION UNKNOWN	2	5	0.44285498
LIGASE ACTIVITY, FORMING CARBON-NITROGEN BONDS	2	5	0.44524061
ION BINDING	5	12.5	0.45830473
METAL ION BINDING	5	12.5	0.45830473

^aThe functional annotations are generated by subjecting the data to DAVID software with the GoCharts (gene ontology charts) functional algorithm. Analysis is based on biological processes and molecular functions.

Table SD7. List of the 40 genes significantly different in EE and CE compared to NL

NL	CE	EE	Affy ID	Fold increase in EE	Name	Complete Name
			232113_at	2.432		AK095791
			238865_at	2.047	LOC132430	XR_000195
			226055_at	1.887	ARRDC2	NM_015683
			227271_at	1.868	FGF11	FGF11 MGC45269 FHF3 fibroblast growth factor 11 fibroblast growth factor 11
			215184_at	1.695	DAPK2	DRP-1 DAPK2 death-associated protein kinase 2
			210542_s_at	1.623	SLCO3A1	SLC21A11 OATP-D SLCO3A1 OATP3A1 solute carrier organic anion transport
			203753_at	1.547	TCF4	SEF2-1B TCF4 E2-2 ITF2 transcription factor 4 IMMUNOGLOBULIN TRANSC
			233634_at	1.517	MARVELD3	LOC91862 MRVLDC3 MARVEL (membrane-associating) domain containing 3 s
			239227_at	1.507	EXT1	BX115875
			212676_at	1.506	NF1	NFNS WSS NF1 VRNF Neurofibromin (neurofibromatosis, type I) VON RECK
			202326_at	1.45	BAT8	Em:AF134726.3 BAT8 NG36/G9a NG36 protein ankyrin repeat-containing pr
			1562948_at	1.332	SMC5L1	BC035661
			216699_s_at	1.28	KLK1	Klk6 KLKR 3.4.21.35 KLK1 KALLIKREIN, RENAL/PANCREATIC/SALIVARY tis
			1554430_at	1.263	C21orf51	C21orf51 chromosome 21 open reading frame 51
			226212_s_at	1.25	INSR	INSR insulin receptor IRAN, TYPE A DIABETES MELLITUS, INSULIN-RESISTAN
			230941_at	1.225		LOC400988 (LOC400988), mRNA
			213204_at	1.206	PARC	H7AP1 KIAA0708 PARC Ubch7-associated protein 1 p53-ASSOCIATED PARK
			1568785_a_at	1.192		BC033938
			225037_at	1.145	SLC35C2	SLC35C2 solute carrier family 35, member C2
			1559833_at	0.884	ARHGEF12	ARHGEF12 PRO2792 KIAA0382 LARG LARG/MLL FUSION GENE leukemia-ass
			244095_at	0.869	na	Similar to hypothetical protein 4932411E22 (LOC342600), mRNA
			214754_at	0.864	MGC22014	MGC22014 hypothetical protein MGC22014
			237399_at	0.861	MTA3	AW594033
			1563809_a_at	0.851	MCF2L	ARHGEF14 KIAA0362 FLJ12122 MCF2L OST DBL's big sister MCF2 transfor
			216712_at	0.844	SLC25A30	LOC253512 hypothetical protein LOC253512
			234658_at	0.843	TARP	AK026401
			225812_at	0.842		BC044912
			239249_at	0.84		BM723387
			205088_at	0.831	CXorf6	CG1 CXorf6 F18 GENE chromosome X open reading frame 6
			234145_at	0.823	PBX3	AK027170
			213098_at	0.811	RQCD1	CNOT9 RQCD1 RCD1+ protein involved in sexual development rcd1 (require
			1556978_a_at	0.81	TBN	TBN taube nuss homolog (mouse)
			244768_at	0.802	DNCH1	DNCH1 HL-3 KIAA0325 Dnchc1 p22 DYHC DHC1a DNCL DNECL dynein
			243382_at	0.793	na	LOC388952 (LOC388952), mRNA
			233582_at	0.78	LOC115110	AL359943
			242774_at	0.779	SYNE2	DKFZP434H2235 Nesprin-2 SYNE2 NUANCE SYNE-2 KIAA1011 nesprin 2
			200638_s_at	0.654	YWHAZ	KCIP-1 14-3-3-ZETA YWHAZ phospholipase A2 14-3-3 zeta BRAIN PROTEIN
			230286_at	0.653		BE562274
			238780_s_at	0.65		BM993105
			219509_at	0.452	MYOZ1	MYOZ1 myozenin 1 CALSAARCIN 2