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Original article

Comparison of gene expression profiles in eosinophilic esophagitis (EoE) between Japan and Western countries

Tetsuo Shoda^{a,*}, Hideaki Morita^a, Ichiro Nomura^a, Norihisa Ishimura^b, Shunji Ishihara^b, Akio Matsuda^a, Kenji Matsumoto^a, Yoshikazu Kinoshita^{a,**}^a Department of Allergy and Immunology, National Research Institute for Child Health and Development, Tokyo, Japan^b Department of Gastroenterology and Hepatology, Shimane University School of Medicine, Shimane, Japan

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Abbreviations:

ALOX15, arachidonate-15 lipoxigenase;
CAPN14, calpain 14; CCL26, C–C chemokine
ligand 26; CCR3, C–C chemokine receptor
type 3; CDH26, cadherin-like 26;
CLC, Charcot-Leyden crystals;
EG, eosinophilic gastritis; EGE, eosinophilic
gastroenteritis; EGID, eosinophilic
gastrointestinal disorders; EoE, eosinophilic
esophagitis; FLG, filaggrin;
GI, gastrointestinal; PMCH, pro-melanin-
concentrating hormone; POSTN, periostin;
TGF- β 1, transforming growth factor- β 1;
TSLP, thymic stromal lymphopoietin

ABSTRACT

Background: The prevalence rate of eosinophilic esophagitis (EoE) between Japan and Western countries is quite different. Although multiple factors, including the genetic background, lifestyle and dietary habits, may account for the difference, the pathogenic mechanism of EoE has not been fully clarified in Japanese. To elucidate whether EoE's pathogenic mechanisms differ between those populations, we performed transcriptome analysis of esophageal biopsy specimens from Japanese EoE patients and compared the identified gene signatures with published microarray data for EoE patients in the US.

Methods: We prospectively enrolled adult Japanese EoE patients ($n = 4$) according to the 2011 consensus guidelines for diagnosis of EoE. Age-matched healthy volunteer subjects ($n = 4$) were also enrolled as controls. We assessed the gene expression profiles of esophageal biopsies using microarray technology and then compared the identified gene signatures with earlier data generated in the US.

Results: Of 42,545 transcripts represented on the microarray, 385 were differentially expressed between the EoE and control samples (≥ 2 fold change and adjusted p -value of < 0.05). Our microarray data showed strong overlapping with the data from US patients with EoE. An EoE-specific-transcript signature is typically composed of IL-13-inducible and eosinophil-related genes, including eotaxin-3/C–C chemokine ligand 26 (CCL26).

Conclusions: This transcriptome study suggests that the pathogenetic mechanisms of EoE in Japan and Western countries are similar. Our findings may contribute to a better understanding of the pathogenesis of EoE and to more accurate diagnosis of this disease in Japanese individuals.

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Introduction

Eosinophilic gastrointestinal disorders (EGID) are clinicopathologically characterized by massive eosinophilic infiltration within

the gastrointestinal (GI) tract.¹ They are classified according to the site of infiltration as eosinophilic esophagitis (EoE), gastritis (EG), gastroenteritis (EGE), enteritis and colitis.² In Japan, the prevalence of EoE is reportedly quite low (estimated to be 0.01%),^{3,4} and much less than that of EGE.⁵ In contrast, the prevalence of EoE in Western countries, including the US and Europe, has been increasing in recent years, is now estimated to be 0.44–1%^{6,7} and is much higher than that of EGE.⁸ Notably, the prevalence of IgE-mediated food allergies (except for EGID) is increasing in Japan and shows a similar tendency to that in Western countries.^{9,10} Thus, the reason for the approximate 50– to 100–fold difference in the prevalence rates of EoE between Japan and Western countries is unclear.

* Corresponding author. Department of Allergy and Immunology, National Research Institute for Child Health and Development, 2-10-1, Okura, Setagaya-ku, Tokyo, 157-8535, Japan.

E-mail address: shoda-t@ncchd.go.jp (T. Shoda).

** Corresponding author. Department of Gastroenterology and Hepatology, Shimane University School of Medicine, 89-1, Enya, Izumo, Shimane, 693-8501, Japan.

E-mail address: kinoshita@med.shimane-u.ac.jp (Y. Kinoshita).

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Multiple factors, including the genetic background, lifestyle and dietary habits, may account for the difference in EoE between Japan and Western countries. To date, studies have suggested that EoE is more common in Caucasians than other racial groups.^{11,12} Interestingly, EoE may have different clinical presentations and endoscopic findings between racially distinct populations. Moreover, dietary habits, especially a Mediterranean diet, are reportedly associated with development of allergic diseases.¹³ The traditional diet of Japan is characterized by low fat content, even when consuming protein and dietary fiber, and it tends to prevent inflammatory bowel disease and colorectal cancer. In contrast, Western diets tend to promote those diseases. Since we have experienced EoE patients in spite of the Japanese genetic background and traditional Japanese dietary habits, the question arises as to whether EoE in Japan and Western countries is a different disease or not. A previous study of the pathogenic mechanism of EoE analyzed esophageal tissues by the transcriptome approach and found that eotaxin-3/C–C chemokine ligand 26 (CCL26) played a crucial role in inducing selective recruitment of eosinophils into the esophageal epithelium.¹⁴

In order to elucidate whether the pathogenic mechanism of EoE in Japan is similar to that in Western countries, we performed transcriptome analysis of esophageal biopsy specimens from Japanese EoE patients and compared the identified gene signatures with microarray data that have been published for EoE patients in the US.

Methods

We prospectively enrolled adult Japanese EoE patients ($n = 4$) who lived in the countryside and followed a traditional Japanese lifestyle and dietary habits. After granting informed consent, they underwent upper GI endoscopy due to their clinical symptoms. Diagnosis of EoE was defined as >15 eosinophils/HPF persisting in the distal esophagus even after proton pump inhibitor therapy, absence of treatment with oral or systemic steroids, in accordance with the 2011 consensus guidelines,¹⁵ and exclusion of other possible causes of esophageal eosinophilia. Age-matched healthy volunteer subjects ($n = 4$) were also enrolled as controls. Control specimens were defined as having <1 eosinophils/HPF, with no history of treatment with oral or systemic steroids or EoE. All esophageal biopsies were obtained from the Department of Gastroenterology, Shimane University Hospital (Shimane, Japan).

The study was performed according to a protocol approved by the institutional review board of National Center for Child Health and Development, Tokyo, Japan. Samples were placed in RNeasy[®] solution (QIAGEN, Valencia, CA, USA) at room temperature after biopsy and then stored at -80°C until gene expression profiling.

Microarray analysis (Agilent Technologies, Santa Clara, CA, USA) was performed according to the manufacturer's instructions. Briefly, total RNA was extracted with an RNeasy Micro kit (Qiagen) and then evaluated with an Agilent Bioanalyzer and an RNA 6000 Nano kit (Agilent Technologies). The gene expression profiles were assessed using microarray technology with Agilent SurePrint G3 Human GE 8 x 60k. Data analysis was performed using GeneSpring software ver. 12.5 (Agilent Technologies). To normalize variation in the staining intensity between microarrays, the average difference for all genes on a given microarray was divided by the median of all measurements on that microarray, and genes in EoE patient specimens that showed a significant difference in signal intensity compared with the same genes in the control specimens ($P < 0.05$, t test) were considered to be up-regulated or down-regulated. Hierarchical clustering was performed using the gene expression data, contrasting the EoE and control specimens (see Fig. 1). The differentially expressed genes of EoE in Japan and the US were compared by systematic analysis using the NextBio search engine (<http://www.nextbio.com/b/nextbio.nb>)¹⁶ (see Fig. 2).

Results

Characteristics of the subjects

The clinical and histopathological characteristics of all subjects are summarized in Table 1. All patients with EoE had a history of dysphagia, a common symptom observed among Japanese patients with EoE.⁵ The most frequent endoscopic finding in patients with EoE was linear furrows, the diagnostic usefulness of which was recently reported.¹⁷ Besides abnormal endoscopic findings, evidence of marked eosinophilic inflammation was observed in all patients with EoE.

Microarray analysis of differentially expressed genes in esophageal biopsies

Esophageal biopsy specimens from individual patients were subjected to whole-genome transcript expression profile analysis.

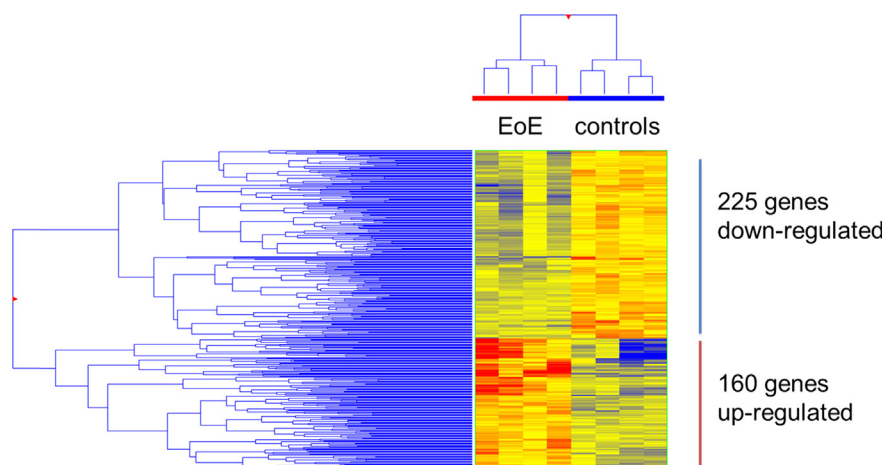


Fig. 1. Microarray analysis of differentially expressed genes in esophageal biopsies. The 385 genes differentially expressed ($P < 0.05$, fold difference ≥ 2) in the EoE group compared with control subjects are shown in a heatmap image. Up-regulated genes are represented in red and down-regulated genes in blue.

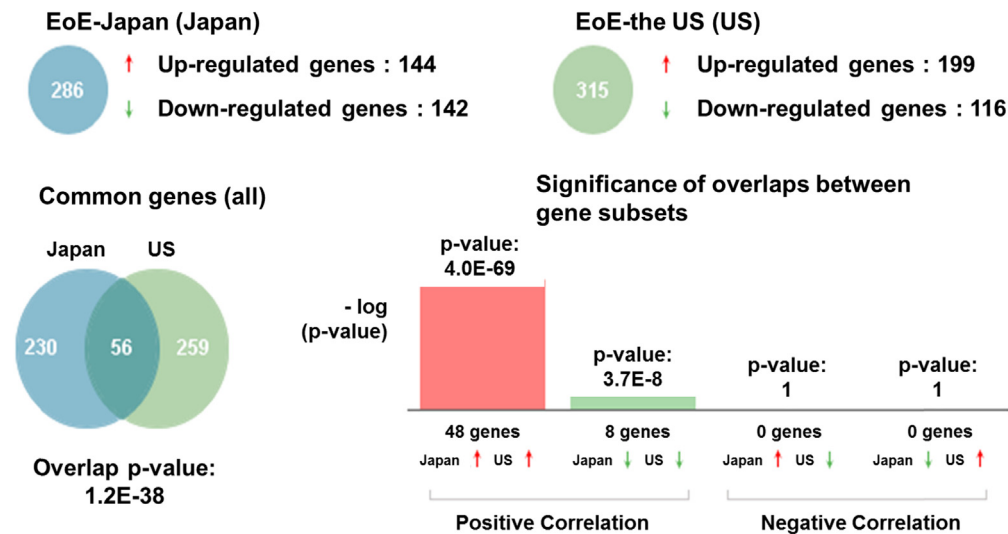


Fig. 2. Comparison of gene expression profiles in EoE between Japan and the US. NextBio was used to compare our list of dysregulated genes to those of Blanchard et al.,¹⁴ using the same fold difference (≥ 2 fold difference). Venn diagrams compare the number of genes identified as up-regulated and down-regulated in EoE across both datasets.

Of the 42,545 transcripts represented on the microarrays, 385 were differentially expressed (≥ 2 fold difference and adjusted p-value of < 0.05) in the Japanese EoE patients versus the normal control biopsy specimens (see [Supplementary Table 1](#)). Hierarchical clustering of the signal intensities of the individual transcripts in each group showed high similarity of transcript expression patterns among the EoE patients. Of those 385 transcripts, 160 were expressed more abundantly and 225 were expressed less abundantly in the EoE patients compared with the control group ([Fig. 1](#)). In agreement with a US study of EoE patients,¹⁴ cadherin-like 26 (CDH26), pro-melanin-concentrating hormone (PMCH), eotaxin-3/CCL26, arachidonate-15 lipoxygenase (ALOX15), periostin (POSTN) and Charcot-Leyden crystals (CLC) were highly up-regulated (> 10 fold) genes compared with in the control subjects.

Comparison of gene expression profiles in EoE between Japan and the US

We compared our list of unique up- and down-regulated genes to that of Blanchard et al. (2006),¹⁴ using the same fold difference (≥ 2 fold difference). After removing duplicate genes, expressed sequence tags and hypothetical genes, both the up- and down-regulated genes showed correlations between these datasets ([Fig. 2](#)). Fifty-six dysregulated genes were found to overlap between this study and the US data. Those genes are listed in [Table 2](#).

Discussion

Because the prevalence rates of EoE in Japan and Western countries are quite different, we compared the gene expression profiles in EoE patients between them. Our microarray data obtained from Japanese EoE patients substantially overlapped with earlier data from EoE patients in the US,¹⁴ suggesting that, even in different regions and countries with distinct dietary habits, EoE is the same disease entity.

Our results confirm that an EoE-specific-transcript signature is composed of dysregulated genes involved in type-2 inflammation, which plays a central role in the pathogenesis of EoE. Notably, IL-13, a type-2 cytokine that plays a pivotal role in allergic inflammation and eosinophil-associated tissue remodeling, is known to be responsible for various types of immune dysregulation.¹⁸ Importantly, our dataset confirmed that IL-13 transcript was significantly—although the level was quite low—upregulated in patients with EoE. In agreement with Blanchard et al.'s report,¹⁴ we identified eotaxin-3/CCL26, an IL-13-inducible chemokine that plays a crucial role in inducing selective recruitment of eosinophils into the esophageal epithelium, as one of the most highly induced genes in our Japanese EoE tissue biopsy specimens. A number of other IL-13-inducible genes also exhibited dysregulated expression in our Japanese patients with EoE. Interestingly, PMCH mRNA, an appetite-stimulating peptide, was significantly upregulated in both

Table 1
Characteristics of the subjects.

Age (y)	M/F	Diagnosis	Response to PPI therapy	Clinical symptoms			Endoscopic findings				Eosinophils		Atopic history
				Dysphagia	Heartburn	Other esophageal symptom	Furrow	Concentric ring	White plaque	Stricture	Histology eosinophils/HPF	Peripheral blood eosinophils (/μl)	
83	F	EoE	—	+	—	—	+	—	—	—	20	122	—
46	F	EoE	—	+	—	—	+	—	—	—	>20	NA	—
60	M	EoE	—	+	—	—	+	+	—	—	>20	169	AR
43	M	EoE	—	+	—	—	+	+	+	—	>50	308	BA, AR
59	M	control	NA	—	—	—	—	—	—	—	<1	NA	—
42	M	control	NA	—	—	—	—	—	—	—	<1	NA	—
44	M	control	NA	—	—	—	—	—	—	—	<1	NA	—
53	F	control	NA	—	—	—	—	—	—	—	<1	NA	—

EoE, Eosinophilic Esophagitis; PPI, Proton Pump Inhibitor; NA, Not Applicable

Table 2
Overlapping up- and down-regulated genes in EoE between Japan and the US.

ProbeName	Fold difference : EoE vs control		Gene symbol	Description
	Japan	US [†]		
Up-regulated genes				
A_23_P502957	26.4	23.4	CDH26	cadherin 26
A_23_P321223	22.5	19.0	PMCH	pro-melanin-concentrating hormone
A_23_P215484	22.3	53.2	CCL26	chemokine (C-C motif) ligand 26
A_23_P55373	21.5	20.9	ALOX15	arachidonate 15-lipoxygenase
A_24_P605563	19.7	17.6	IGLJ3	immunoglobulin lambda joining 3
A_33_P3511265	13.4	46.3	POSTN	periostin, osteoblast specific factor
A_23_P101683	12.0	12.7	CLC	Charcot-Leyden crystal protein
A_23_P167168	12.0	14.6	IGJ	immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides
A_24_P406754	11.7	2.6	LOXL4	lysyl oxidase-like 4
A_32_P315178	10.4	15.0	ATP13A5	ATPase type 13A5
A_33_P3304696	10.0	8.3	IGLV3-21	immunoglobulin lambda variable 3-21
A_24_P240259	8.9	10.9	LRRC31	leucine rich repeat containing 31
A_23_P81898	8.3	14.9	UBD	ubiquitin D
A_23_P105144	8.2	6.2	SCUBE2	signal peptide, CUB domain, EGF-like 2
A_23_P140384	6.4	3.6	CTSG	cathepsin G
A_23_P321354	5.6	14.0	TMEM71	transmembrane protein 71
A_23_P7212	5.4	5.7	CFI	complement factor I
A_23_P18017	4.9	13.1	CPA3	carboxypeptidase A3
A_23_P1904	4.8	4.2	MS4A2	membrane-spanning 4-domains, subfamily A, member 2
A_23_P117662	4.7	3.1	HDC	histidine decarboxylase
A_24_P263786	4.1	6.1	IGKC	immunoglobulin kappa constant
A_23_P330070	4.1	5.1	TFPI	tissue factor pathway inhibitor
A_23_P1552	3.9	9.0	CTSC	cathepsin C
A_23_P169092	3.7	4.3	CYP7B1	cytochrome P450, family 7, subfamily B, polypeptide 1
A_33_P3405728	3.3	5.3	PKP2	plakophilin 2
A_33_P3322804	3.2	7.4	NTRK2	neurotrophic tyrosine kinase, receptor, type 2
A_24_P3249	3.2	2.2	RARB	retinoic acid receptor, beta
A_23_P135548	3.1	3.4	DPYD	dihydropyrimidine dehydrogenase
A_33_P3373775	3.1	9.7	BCL2L15	BCL2-like 15
A_24_P157370	3.0	3.4	IL17RB	interleukin 17 receptor B
A_24_P419300	3.0	8.1	PP7080	uncharacterized LOC25845
A_33_P3224819	3.0	3.1	SLC45A4	solute carrier family 45, member 4
A_33_P3364268	2.9	3.1	LBH	limb bud and heart development homolog
A_24_P161018	2.8	2.3	PARP14	poly (ADP-ribose) polymerase family, member 14
A_23_P10506	2.7	5.3	HPGDS	hematopoietic prostaglandin D synthase
A_23_P27606	2.6	3.3	IL27RA	interleukin 27 receptor, alpha
A_24_P397489	2.6	2.9	GCNT2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme
A_24_P133253	2.5	3.9	KITLG	KIT ligand
A_23_P3532	2.5	3.6	LITAF	lipopolysaccharide-induced TNF factor
A_23_P121527	2.5	2.5	KLHL5	kelch-like 5
A_23_P144096	2.4	3.2	CISH	cytokine inducible SH2-containing protein
A_33_P3245908	2.4	2.2	C10orf128	chromosome 10 open reading frame 128
A_32_P53524	2.3	2.6	NTN1	netrin 1
A_23_P42718	2.2	2.9	NFE2L3	nuclear factor (erythroid-derived 2)-like 3
A_24_P408736	2.2	2.4	GALNT5	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 5
A_33_P3410093	2.2	2.2	LTA4H	leukotriene A4 hydrolase
A_33_P3342528	2.1	2.4	P2RY1	purinergic receptor P2Y, G-protein coupled, 1
A_23_P30655	2.0	2.1	NFKBIE	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon
Down-regulated genes				
A_24_P206776	-4.1	-6.3	CRYAB	crystallin, alpha B
A_33_P3293958	-3.8	-2.8	TUBB2A	tubulin, beta 2A class IIa
A_23_P69810	-3.0	-4.7	AGPAT9	1-acylglycerol-3-phosphate O-acyltransferase 9
A_23_P4536	-2.4	-14.6	EPB41L3	erythrocyte membrane protein band 4.1-like 3
A_24_P46130	-2.3	-5.0	ACPP	acid phosphatase, prostate
A_24_P152968	-2.1	-3.9	AKR1C1	aldo-keto reductase family 1, member C1
A_33_P3265030	-2.1	-2.4	GP1BB	glycoprotein Ib (platelet), beta polypeptide
A_33_P3231252	-2.1	-3.0	NHLH2	nescient helix loop helix 2

[†] US data: Previously reported by Blanchard et al.¹⁴

datasets, although its pathophysiological role in EoE is not yet known. We previously reported that PMCH was the most strongly induced gene (over 1200-fold up-regulation) in the human vascular endothelial cell transcriptome in response to such type-2 cytokines as IL-4 and IL-13, in a STAT6-dependent manner.¹⁹ Since PMCH is an endothelial, but not an epithelial, cell-specific transcript, over-expression of PMCH may imply that an IL-13-mediated inflammatory response might extend to esophageal endothelial cells, in part

because of esophageal epithelial barrier dysfunction. Greater understanding of the pathophysiological roles of MCH in EoE patients may lead to serum MCH becoming a useful surrogate biomarker for IL-13 in EoE patients.

Our microarray data also showed that a number of eosinophil-specific genes were dramatically upregulated in EoE patients, including CLC (12 fold), ALOX15 (21 fold) and C–C chemokine receptor type 3 (CCR3) (3.5 fold). CLC likely promotes

proinflammatory changes, including epithelial hyperplasia, and it correlates with mucosal inflammation in EoE.²⁰ Matoso et al. recently reported that ALOX15 may be a useful diagnostic marker for EoE.²¹ CCR3 is known to contribute to accumulation and activation of eosinophils, and it binds and responds to eotaxin-3/CCL26.¹⁴ Furthermore, Transforming growth factor (TGF)- β 1 produced by eosinophils is responsible for overexpression of various molecules involved in the tissue remodeling process. Notably, periostin, a matricellular protein, is known to be critically involved in the pathogenesis of allergic diseases,²² not only as a component in subepithelial fibrosis but also by playing a key role in the amplification and chronic nature of allergic skin inflammation.²³ We previously reported that both IL-13 and TGF- β 1 play a role in inducing periostin production by subepithelial cells, including endothelial cells, in a corticosteroid-insensitive manner.²⁴ Indeed, periostin expression remains increased in corticosteroid-treated patients with EoE.²⁵ The genes identified in this study were also identified by Wen et al.,²⁶ using an EoE diagnostic panel based on a 96-gene expression profile. These observations further support our present findings suggesting that EoE in both Japan and Western countries should be considered to be the same disease entity.

The findings of our dataset confirmed almost exactly the findings of the earlier EoE dataset from the US. There were small discrepancies, probably due in part to the use of different microarray platforms in the studies. For instance, a recent genome-wide association study by Kottyan et al. showed that calpain 14 (CAPN14) is closely associated with EoE.²⁷ It was also identified as a significantly increased gene in our Japanese EoE patients, but not in Blanchard's study. On the other hand, filaggrin (FLG), which might disrupt normal esophageal barrier function,²⁸ was identified as a significantly decreased gene in Blanchard's dataset, but not in our study. Despite recent evidence showing that thymic stromal lymphopoietin (TSLP) plays a crucial role in the pathogenesis of EoE,¹⁸ TSLP expression was not significantly increased in our EoE patients when compared with the healthy control subjects, as in Blanchard et al.'s study.¹⁴

Several mechanisms might explain the regional differences in prevalence of EoE. The reported low prevalence of EoE in Japan might be due not only to a lack of awareness of this illness but also different genetic and environmental factors between Japan and Western countries. EoE was recently recognized as a form of food allergy.² Although Japanese dietary habits, which have been different from those of Westerners for a long time, might be associated with the low prevalence of EoE in Japan, our data suggest that the mechanism underlying the pathogenesis of EoE is similar. In that scenario, once disease develops, dietary habits would no longer play any role in the progression of EoE. Currently, EGE is more prevalent than EoE in Japan, from children to adults.^{5,29} Application of our microarray analysis to the entire GI tract might lead to elucidation of the precise mechanisms of EGID, and more studies are clearly warranted.

In conclusion, this transcriptome study suggests that the pathogenetic mechanisms of EoE in Japan and Western countries are similar. Our findings may contribute to a better understanding of the pathogenesis of EoE and to more accurate diagnosis of this disease in Japanese individuals.

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Appendix A. Supplementary data

Supplementary data related to this article can be found at <http://dx.doi.org/10.1016/j.alit.2015.03.002>.

Conflict of interest

The authors have no conflicts of interest to declare.

Authors' contributions

TS and HM contributed equally to this work. TS designed the study, analyzed the data and wrote the manuscript. HM designed the study, performed the experiments and analyzed the data. IN designed the study and received grant support. NI and SI contributed to sample collection. AM interpreted the results and critically revised the manuscript. KM designed the study and critically revised the manuscript. YK designed the study, provided overall supervision and edited the manuscript. All authors read and approved the final manuscript.

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Supplementary Table 1. List of 385 genes differentially expressed genes ($P < 0.05$, ≥ 2 fold) between eosinophilic esophagitis (EoE) and control in Japan

ProbeName	Fold difference	GeneSymbol	Description
	EoE vs control		
Up-regulated genes [†]			
A_33_P3263319	69.1		immunoglobulin heavy constant gamma 3 (G3m marker) [Source:HGNC Symbol;Acc:5527] [ENST00000390551]
A_33_P3226154	41.2		immunoglobulin kappa constant [Source:HGNC Symbol;Acc:5716] [ENST00000390237]
A_23_P502957	26.4	CDH26	Homo sapiens cadherin 26 (CDH26), transcript variant b, mRNA [NM_021810]
A_33_P3379039	23.2	IGLL5	Homo sapiens immunoglobulin lambda-like polypeptide 5 (IGLL5), transcript variant 1, mRNA [NM_001178126]
A_23_P321223	22.5	PMCH	Homo sapiens pro-melanin-concentrating hormone (PMCH), mRNA [NM_002674]
A_23_P215484	22.3	CCL26	Homo sapiens chemokine (C-C motif) ligand 26 (CCL26), mRNA [NM_006072]
A_33_P3422298	21.6		{pseudogene} Ig V lambda IJ psi C lambda 6=Ig lambda chain surface Ig receptor VJC region {truncated light chain constant region} [human, B lymphoma cell line OCI LY8, mRNA Partial, 623 nt]. [S77011]
A_23_P55373	21.5	ALOX15	Homo sapiens arachidonate 15-lipoxygenase (ALOX15), mRNA [NM_001140]
A_33_P3424754	19.7		immunoglobulin lambda variable 1-47 [Source:HGNC Symbol;Acc:5880] [ENST00000390294]
A_24_P605563	19.7		immunoglobulin lambda constant 2 (Kern-Oz- marker) [Source:HGNC Symbol;Acc:5856] [ENST00000390323]
A_23_P61042	19.2		immunoglobulin heavy constant alpha 2 (A2m marker) [Source:HGNC Symbol;Acc:5479] [ENST00000390539]
A_33_P3768930	18.6		MYE4344 Myeloma (MYE) cDNA library Homo sapiens cDNA, mRNA sequence [BF175071]
A_23_P21800	17.8		immunoglobulin kappa variable 3-20 [Source:HGNC Symbol;Acc:5817] [ENST00000492167]
A_24_P626951	16.3		immunoglobulin kappa variable 1-16 [Source:HGNC Symbol;Acc:5732] [ENST00000479981]
A_33_P3424591	16.2		immunoglobulin heavy constant gamma 1 (G1m marker) [Source:HGNC Symbol;Acc:5525] [ENST00000390549]
A_24_P110242	15.4		immunoglobulin heavy variable 3/OR16-8 (non-functional) [Source:HGNC Symbol;Acc:5643] [ENST00000438532]
A_33_P3364959	15.2		Homo sapiens isolate N1408L immunoglobulin lambda light chain variable region (IGLV2) mRNA, IGLV2-23*02 allele, partial cds. [DQ098707]
A_33_P3714341	14.8		Homo sapiens IGK mRNA for immunoglobulin kappa light chain, partial cds, clone: F010-014L. [AB363267]
A_33_P3395675	14.7		immunoglobulin lambda constant 2 (Kern-Oz- marker) [Source:HGNC Symbol;Acc:5856] [ENST00000390323]
A_23_P201211	14.0	FCRL5	Homo sapiens Fc receptor-like 5 (FCRL5), transcript variant 1, mRNA [NM_031281]

A_33_P3511265	13.4	POSTN	Homo sapiens periostin, osteoblast specific factor (POSTN), transcript variant 1, mRNA [NM_006475]
A_23_P101683	12.0	CLC	Homo sapiens Charcot-Leyden crystal protein (CLC), mRNA [NM_001828]
A_23_P167168	12.0	IGJ	Homo sapiens immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides (IGJ), mRNA [NM_144646]
A_33_P3301075	12.0		immunoglobulin heavy variable 3-33 [Source:HGNC Symbol;Acc:5596] [ENST00000390615]
A_24_P406754	11.7	LOXL4	Homo sapiens lysyl oxidase-like 4 (LOXL4), mRNA [NM_032211]
A_23_P84596	11.5	MZB1	Homo sapiens marginal zone B and B1 cell-specific protein (MZB1), mRNA [NM_016459]
A_24_P357847	11.4	LOC100510044	immunoglobulin kappa variable 3-15 [Source:HGNC Symbol;Acc:5816] [ENST00000390252]
A_33_P3336822	11.3		immunoglobulin lambda variable 1-44 [Source:HGNC Symbol;Acc:5879] [ENST00000390297]
A_33_P3368334	11.2	FCRL3	Fc receptor-like 3 [Source:HGNC Symbol;Acc:18506] [ENST00000368186]
A_24_P87036	11.0	ANO1	Homo sapiens anoctamin 1, calcium activated chloride channel (ANO1), transcript variant 1, mRNA [NM_018043]
A_33_P3337609	11.0		GB
A_32_P315178	10.4	ATP13A5	Homo sapiens ATPase type 13A5 (ATP13A5), mRNA [NM_198505]
A_24_P15388	10.2		immunoglobulin heavy variable 3-74 [Source:HGNC Symbol;Acc:5624] [ENST00000424969]
A_33_P3304696	10.0		Homo sapiens clone ASPBLL50 immunoglobulin lambda light chain VJ region mRNA, partial cds. [AF058072]
A_32_P159192	9.3		immunoglobulin kappa variable 3-7 (non-functional) [Source:HGNC Symbol;Acc:5821] [ENST00000390247]
A_23_P161458	9.2	OLAH	Homo sapiens oleoyl-ACP hydrolase (OLAH), transcript variant 2, mRNA [NM_001039702]
A_24_P240259	8.9	LRR31	Homo sapiens leucine rich repeat containing 31 (LRR31), mRNA [NM_024727]
A_33_P3335506	8.7	FCRL5	Fc receptor-like 5 [Source:HGNC Symbol;Acc:18508] [ENST00000368190]
A_23_P251031	8.4	IL13	Homo sapiens interleukin 13 (IL13), mRNA [NM_002188]
A_24_P110831	8.4	ANO1	anoctamin 1, calcium activated chloride channel [Source:HGNC Symbol;Acc:21625] [ENST00000316296]
A_23_P81898	8.3	UBD	Homo sapiens ubiquitin D (UBD), mRNA [NM_006398]
A_23_P105144	8.2	SCUBE2	Homo sapiens signal peptide, CUB domain, EGF-like 2 (SCUBE2), transcript variant 1, mRNA [NM_020974]
A_23_P328545	8.0	GABRP	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, pi (GABRP), mRNA [NM_014211]
A_24_P239076	8.0	IGLL1	Homo sapiens immunoglobulin lambda-like polypeptide 1 (IGLL1), transcript variant 1, mRNA [NM_020070]
A_24_P212024	7.8		immunoglobulin kappa variable 1-27 [Source:HGNC Symbol;Acc:5735] [ENST00000498435]
A_33_P3424612	7.8		immunoglobulin kappa variable 3-11 [Source:HGNC Symbol;Acc:5815] [ENST00000483158]
A_32_P34826	7.8	C21orf88	Homo sapiens chromosome 21 open reading frame 88 (C21orf88), transcript variant 2, non-coding RNA [NR_026543]
A_24_P510357	7.6		immunoglobulin lambda variable 2-14 [Source:HGNC Symbol;Acc:5888] [ENST00000390312]
A_33_P3227400	7.5	COL4A4	Homo sapiens collagen, type IV, alpha 4 (COL4A4), mRNA [NM_000092]

A_33_P3375145	7.4	C9orf150	Homo sapiens chromosome 9 open reading frame 150 (C9orf150), mRNA [NM_203403]
A_33_P3281444	7.3		immunoglobulin kappa variable 1D-43 [Source:HGNC Symbol;Acc:5758] [ENST00000468879]
A_33_P3304707	7.0		immunoglobulin lambda variable 2-8 [Source:HGNC Symbol;Acc:5895] [ENST00000390317]
A_23_P13753	6.8	NFE2	Homo sapiens nuclear factor (erythroid-derived 2), 45kDa (NFE2), transcript variant 1, mRNA [NM_006163]
A_23_P92909	6.7	SPINK6	Homo sapiens serine peptidase inhibitor, Kazal type 6 (SPINK6), transcript variant 1, mRNA [NM_205841]
A_23_P140384	6.4	CTSG	Homo sapiens cathepsin G (CTSG), mRNA [NM_001911]
A_24_P24053	6.0		immunoglobulin heavy variable 3-66 [Source:HGNC Symbol;Acc:5619] [ENST00000390632]
A_32_P722809	5.7		immunoglobulin kappa variable 2D-28 [Source:HGNC Symbol;Acc:5799] [ENST00000453166]
A_23_P321354	5.6	TMEM71	Homo sapiens transmembrane protein 71 (TMEM71), transcript variant 1, mRNA [NM_144649]
A_33_P3289246	5.5		immunoglobulin heavy variable 3-9 [Source:HGNC Symbol;Acc:5628] [ENST00000390600]
A_23_P7212	5.4	CFI	Homo sapiens complement factor I (CFI), mRNA [NM_000204]
A_23_P18017	4.9	CPA3	Homo sapiens carboxypeptidase A3 (mast cell) (CPA3), mRNA [NM_001870]
A_32_P148122	4.8		immunoglobulin kappa variable 1D-33 [Source:HGNC Symbol;Acc:5753] [ENST00000390265]
A_33_P3235876	4.8		immunoglobulin heavy variable 3-66 [Source:HGNC Symbol;Acc:5619] [ENST00000390632]
A_23_P1904	4.8	MS4A2	Homo sapiens membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for; beta polypeptide) (MS4A2), mRNA [NM_000139]
A_23_P117662	4.7	HDC	Homo sapiens histidine decarboxylase (HDC), mRNA [NM_002112]
A_32_P161762	4.6	RUNX2	Homo sapiens runt-related transcription factor 2 (RUNX2), transcript variant 3, mRNA [NM_004348]
A_24_P400324	4.6	THSD7A	Homo sapiens thrombospondin, type I, domain containing 7A (THSD7A), mRNA [NM_015204]
A_23_P39067	4.3	SPIB	Homo sapiens Spi-B transcription factor (Spi-1/PU.1 related) (SPIB), mRNA [NM_003121]
A_24_P263786	4.1		immunoglobulin kappa variable 2D-30 [Source:HGNC Symbol;Acc:5801] [ENST00000474213]
A_23_P330070	4.1	TFPI	Homo sapiens tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor) (TFPI), transcript variant 2, mRNA [NM_001032281]
A_23_P1552	3.9	CTSC	Homo sapiens cathepsin C (CTSC), transcript variant 1, mRNA [NM_001814]
A_24_P944253	3.9	KLHL6	Homo sapiens kelch-like 6 (Drosophila) (KLHL6), mRNA [NM_130446]
A_33_P3295313	3.8	MS4A2	Homo sapiens membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for; beta polypeptide) (MS4A2), mRNA [NM_000139]
A_33_P3373960	3.8	RD3	Homo sapiens retinal degeneration 3 (RD3), transcript variant 1, mRNA [NM_183059]
A_32_P424761	3.7	C12orf28	chromosome 12 open reading frame 28 [Source:HGNC Symbol;Acc:26316] [ENST00000299350]

A_33_P3733417	3.7	DRD2	Homo sapiens dopamine receptor D2 (DRD2), transcript variant 1, mRNA [NM_000795]
A_23_P169092	3.7	CYP7B1	Homo sapiens cytochrome P450, family 7, subfamily B, polypeptide 1 (CYP7B1), mRNA [NM_004820]
A_33_P3258274	3.6	TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor) [Source:HGNC Symbol;Acc:11760] [ENST00000481132]
A_23_P376060	3.6	IKZF3	Homo sapiens IKAROS family zinc finger 3 (Aiolos) (IKZF3), transcript variant 1, mRNA [NM_012481]
A_19_P00316385	3.6		lincRNA:chr18:39081199-39212092 reverse strand
A_33_P3424489	3.6		immunoglobulin lambda variable 3-25 [Source:HGNC Symbol;Acc:5908] [ENST00000390305]
A_33_P3381821	3.6	CAPN14	Homo sapiens calpain 14 (CAPN14), mRNA [NM_001145122]
A_23_P250302	3.5	CCR3	Homo sapiens chemokine (C-C motif) receptor 3 (CCR3), transcript variant 1, mRNA [NM_001837]
A_32_P167076	3.5	CAPN14	Homo sapiens calpain 14 (CAPN14), mRNA [NM_001145122]
A_23_P159335	3.5	CD8B	Homo sapiens CD8b molecule (CD8B), transcript variant 5, mRNA [NM_004931]
A_33_P3234546	3.5	CD8B	Homo sapiens CD8b molecule (CD8B), transcript variant 5, mRNA [NM_004931]
A_19_P00810352	3.4		lincRNA:chr15:96788096-96828896 reverse strand
A_24_P115932	3.4	GPR44	Homo sapiens G protein-coupled receptor 44 (GPR44), mRNA [NM_004778]
A_24_P107317	3.3	USP2	Homo sapiens ubiquitin specific peptidase 2 (USP2), transcript variant 1, mRNA [NM_004205]
A_24_P33895	3.3	ATF3	Homo sapiens activating transcription factor 3 (ATF3), transcript variant 4, mRNA [NM_001040619]
A_24_P262127	3.3	RRAD	Homo sapiens Ras-related associated with diabetes (RRAD), transcript variant 2, mRNA [NM_004165]
A_32_P128258	3.3	SIGLECP3	Homo sapiens sialic acid binding Ig-like lectin, pseudogene 3 (SIGLECP3), non-coding RNA [NR_002804]
A_23_P209129	3.3	LAIR2	Homo sapiens leukocyte-associated immunoglobulin-like receptor 2 (LAIR2), transcript variant 1, mRNA [NM_002288]
A_33_P3405728	3.3	PKP2	Homo sapiens plakophilin 2 (PKP2), transcript variant 2b, mRNA [NM_004572]
A_33_P3369436	3.2	LOC100130111	PREDICTED: Homo sapiens hypothetical LOC100130111 (LOC100130111), partial miscRNA [XR_109206]
A_33_P3322804	3.2	NTRK2	Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2), transcript variant c, mRNA [NM_001018064]
A_23_P128281	3.2	KLRC3	Homo sapiens killer cell lectin-like receptor subfamily C, member 3 (KLRC3), transcript variant 2, mRNA [NM_007333]
A_24_P3249	3.2	RARB	Homo sapiens retinoic acid receptor, beta (RARB), transcript variant 1, mRNA [NM_000965]
A_24_P318990	3.1		immunoglobulin lambda variable 1-50 (non-functional) [Source:HGNC Symbol;Acc:5881] [ENST00000390291]
A_23_P135548	3.1	DPYD	Homo sapiens dihydropyrimidine dehydrogenase (DPYD), transcript variant 1, mRNA [NM_000110]
A_23_P95640	3.1	C1orf186	Homo sapiens chromosome 1 open reading frame 186 (C1orf186), mRNA [NM_001007544]
A_24_P396167	3.1	CTSW	Homo sapiens cathepsin W (CTSW), mRNA [NM_001335]
A_33_P3373775	3.1	BCL2L15	Homo sapiens BCL2-like 15 (BCL2L15), mRNA [NM_001010922]
A_23_P357881	3.1	CD8B	Homo sapiens CD8b molecule (CD8B), transcript variant 4, mRNA [NM_172102]

A_24_P157370	3.0	IL17RB	Homo sapiens interleukin 17 receptor B (IL17RB), mRNA [NM_018725]
A_23_P121657	3.0	HS3ST1	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), mRNA [NM_005114]
A_24_P419300	3.0	PP7080	Homo sapiens hypothetical LOC25845 (PP7080), non-coding RNA [NR_024158]
A_33_P3224819	3.0	SLC45A4	Homo sapiens solute carrier family 45, member 4 (SLC45A4), mRNA [NM_001080431]
A_23_P346093	3.0	TMC8	Homo sapiens transmembrane channel-like 8 (TMC8), mRNA [NM_152468]
A_23_P79155	2.9	GPR39	Homo sapiens G protein-coupled receptor 39 (GPR39), mRNA [NM_001508]
A_33_P3223964	2.9		immunoglobulin heavy variable 1-24 [Source:HGNC Symbol;Acc:5551] [ENST00000390610]
A_33_P3240843	2.9	TMEM71	Homo sapiens transmembrane protein 71 (TMEM71), transcript variant 1, mRNA [NM_144649]
A_33_P3364268	2.9	LBH	Homo sapiens limb bud and heart development homolog (mouse) (LBH), mRNA [NM_030915]
A_24_P345846	2.9	ANTXR2	Homo sapiens anthrax toxin receptor 2 (ANTXR2), transcript variant 1, mRNA [NM_058172]
A_24_P245838	2.9	MGAT3	Homo sapiens mannosyl (beta-1,4-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase (MGAT3), transcript variant 1, mRNA [NM_002409]
A_23_P132515	2.9	SIDT1	Homo sapiens SID1 transmembrane family, member 1 (SIDT1), mRNA [NM_017699]
A_23_P137139	2.8	BTK	Homo sapiens Bruton agammaglobulinemia tyrosine kinase (BTK), mRNA [NM_000061]
A_32_P101352	2.8	CXorf65	Homo sapiens chromosome X open reading frame 65 (CXorf65), transcript variant 1, mRNA [NM_001025265]
A_33_P3212615	2.8	TFPI	Homo sapiens tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor) (TFPI), transcript variant 1, mRNA [NM_006287]
A_33_P3252326	2.8		HCG1981372, isoform CRA_cNovel protein [Source:UniProtKB/TrEMBL;Acc:B1B108] [ENST00000483918]
A_24_P161018	2.8	PARP14	Homo sapiens poly (ADP-ribose) polymerase family, member 14 (PARP14), mRNA [NM_017554]
A_23_P10506	2.7	HPGDS	Homo sapiens hematopoietic prostaglandin D synthase (HPGDS), mRNA [NM_014485]
A_33_P3359771	2.7	ATP1A2	Homo sapiens ATPase, Na+/K+ transporting, alpha 2 polypeptide (ATP1A2), mRNA [NM_000702]
A_23_P217269	2.7	VSIG4	Homo sapiens V-set and immunoglobulin domain containing 4 (VSIG4), transcript variant 1, mRNA [NM_007268]
A_33_P3797820	2.6		full-length cDNA clone CS0DK001YC14 of HeLa cells Cot 25-normalized of Homo sapiens (human). [CR609725]
A_23_P502336	2.6	EMR2	Homo sapiens egf-like module containing, mucin-like, hormone receptor-like 2 (EMR2), transcript variant 1, mRNA [NM_013447]
A_23_P27606	2.6	IL27RA	Homo sapiens interleukin 27 receptor, alpha (IL27RA), mRNA [NM_004843]
A_33_P3331641	2.6	NCRNA00245	Homo sapiens non-protein coding RNA 245 (NCRNA00245), transcript variant 1, non-coding RNA [NR_024421]
A_23_P88559	2.6	LIPC	Homo sapiens lipase, hepatic (LIPC), mRNA [NM_000236]
A_24_P397489	2.6	GCNT2	Homo sapiens glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood group) (GCNT2), transcript variant 2, mRNA [NM_001491]
A_24_P133253	2.5	KITLG	Homo sapiens KIT ligand (KITLG), transcript variant b, mRNA [NM_000899]
A_33_P3402783	2.5		

A_23_P3532	2.5	LITAF	Homo sapiens lipopolysaccharide-induced TNF factor (LITAF), transcript variant 1, mRNA [NM_004862]
A_23_P121527	2.5	KLHL5	Homo sapiens kelch-like 5 (Drosophila) (KLHL5), transcript variant 1, mRNA [NM_015990]
A_33_P3300965	2.5	HOXC6	Homo sapiens homeobox C6 (HOXC6), transcript variant 2, mRNA [NM_153693]
A_23_P383118	2.4	ZSWIM5	Homo sapiens zinc finger, SWIM-type containing 5 (ZSWIM5), mRNA [NM_020883]
A_23_P144096	2.4	CISH	Homo sapiens cytokine inducible SH2-containing protein (CISH), transcript variant 2, mRNA [NM_145071]
A_33_P3245908	2.4	C10orf128	Homo sapiens chromosome 10 open reading frame 128 (C10orf128), mRNA [NM_001010863]
A_23_P148473	2.3	IL2RG	Homo sapiens interleukin 2 receptor, gamma (IL2RG), mRNA [NM_000206]
A_23_P414654	2.3	RAB37	Homo sapiens RAB37, member RAS oncogene family (RAB37), transcript variant 3, mRNA [NM_175738]
A_32_P53524	2.3	NTN1	Homo sapiens netrin 1 (NTN1), mRNA [NM_004822]
A_33_P3277514	2.3	BTK	Homo sapiens Bruton agammaglobulinemia tyrosine kinase (BTK), mRNA [NM_000061]
A_23_P208302	2.3	APOC2	Homo sapiens apolipoprotein C-II (APOC2), mRNA [NM_000483]
A_33_P3280531	2.3	CRAT	Homo sapiens carnitine O-acetyltransferase (CRAT), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA [NM_000755]
A_23_P42718	2.2	NFE2L3	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA [NM_004289]
A_23_P11201	2.2	GPR34	Homo sapiens G protein-coupled receptor 34 (GPR34), transcript variant 4, mRNA [NM_001097579]
A_24_P408736	2.2	GALNT5	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 5 (GalNAc-T5) (GALNT5), mRNA [NM_014568]
A_24_P363408	2.2	HEY2	Homo sapiens hairy/enhancer-of-split related with YRPW motif 2 (HEY2), mRNA [NM_012259]
A_33_P3281567	2.2	CMAHP	Homo sapiens cytidine monophospho-N-acetylneuraminic acid hydroxylase, pseudogene (CMAHP), transcript variant 1, non-coding RNA [NR_002174]
A_33_P3410093	2.2	LTA4H	Homo sapiens leukotriene A4 hydrolase (LTA4H), mRNA [NM_000895]
A_23_P30223	2.1	SRD5A1	Homo sapiens steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1) (SRD5A1), mRNA [NM_001047]
A_33_P3245415	2.1	N4BP2L1	Homo sapiens NEDD4 binding protein 2-like 1 (N4BP2L1), transcript variant 1, mRNA [NM_052818]
A_33_P3325229	2.1	LOC389906	Homo sapiens hypothetical LOC389906 (LOC389906), non-coding RNA [NR_034031]
A_33_P3342528	2.1	P2RY1	Homo sapiens purinergic receptor P2Y, G-protein coupled, 1 (P2RY1), mRNA [NM_002563]
A_19_P00803558	2.1		lincRNA:chr12:4958789-4970589 forward strand
A_33_P3330952	2.1	ATP8A1	Homo sapiens ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1 (ATP8A1), transcript variant 1, mRNA [NM_006095]
A_23_P143713	2.0	APOBEC3G	Homo sapiens apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G (APOBEC3G), mRNA [NM_021822]

A_33_P3322363	2.0	HMSD	Homo sapiens histocompatibility (minor) serpin domain containing (HMSD), mRNA [NM_001123366]
A_33_P3385842	2.0	CCDC7	Homo sapiens coiled-coil domain containing 7 (CCDC7), transcript variant 1, mRNA [NM_145023]
A_23_P30655	2.0	NFKBIE	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon (NFKBIE), mRNA [NM_004556]

Down-regulated genes[†]

A_33_P3368193	-14.6	PNLIPRP3	Homo sapiens pancreatic lipase-related protein 3 (PNLIPRP3), mRNA [NM_001011709]
A_33_P3265189	-8.3	DSG1	Homo sapiens desmoglein 1 (DSG1), mRNA [NM_001942]
A_23_P116850	-7.9	KRT2	Homo sapiens keratin 2 (KRT2), mRNA [NM_000423]
A_23_P146294	-7.8	EFCAB1	Homo sapiens EF-hand calcium binding domain 1 (EFCAB1), transcript variant 1, mRNA [NM_024593]
A_33_P3362826	-7.4	ANKRD31	Homo sapiens ankyrin repeat domain 31 (ANKRD31), mRNA [NM_001164443]
A_19_P00316714	-6.3	XLOC_005285	BROAD lincRNAs version v2 (http://www.broadinstitute.org/genome_bio/human_lincrnas/)
A_33_P3242623	-5.6	SLC7A11	Homo sapiens solute carrier family 7 (anionic amino acid transporter light chain, xc- system), member 11 (SLC7A11), mRNA [NM_014331]
A_24_P230938	-5.4	MORN4	Homo sapiens MORN repeat containing 4, mRNA (cDNA clone IMAGE:4690584), complete cds. [BC022054]
A_33_P3270826	-4.9	THEM5	Homo sapiens thioesterase superfamily member 5 (THEM5), mRNA [NM_182578]
A_19_P00317556	-4.8		lincRNA:chr8:129082331-129113343 forward strand
A_19_P00810003	-4.7		lincRNA:chrX:10933204-10941554 reverse strand
A_32_P91546	-4.5	TDRG1	Homo sapiens testis development related protein 1 (TDRG1), non-coding RNA [NR_024015]
A_24_P141707	-4.5	INHBE	Homo sapiens inhibin, beta E (INHBE), mRNA [NM_031479]
A_23_P38735	-4.4	CDH19	Homo sapiens cadherin 19, type 2 (CDH19), mRNA [NM_021153]
A_33_P3269423	-4.2	C13orf35	Homo sapiens chromosome 13 open reading frame 35 (C13orf35), mRNA [NM_207440]
A_24_P206776	-4.1	CRYAB	Homo sapiens crystallin, alpha B (CRYAB), mRNA [NM_001885]
A_19_P00812320	-4.1		lincRNA:chr5:133837051-133848098 reverse strand
A_33_P3285877	-4.0	C9orf146	Homo sapiens chromosome 9 open reading frame 146 (C9orf146), non-coding RNA [NR_038194]
A_23_P77908	-4.0	SLC47A2	Homo sapiens solute carrier family 47, member 2 (SLC47A2), transcript variant 1, mRNA [NM_152908]
A_23_P146233	-4.0	LPL	Homo sapiens lipoprotein lipase (LPL), mRNA [NM_000237]
A_19_P00810302	-4.0		lincRNA:chr4:79623626-79634676 reverse strand
A_33_P3380850	-3.9	PAX2	Homo sapiens paired box 2 (PAX2), transcript variant e, mRNA [NM_003990]
A_19_P00808332	-3.8		lincRNA:chr4:38197205-38433455 forward strand

A_33_P3262167	-3.8		
A_33_P3293958	-3.8		Homo sapiens cDNA clone IMAGE:40109262. [BC131577]
A_33_P3397865	-3.8	TNNT1	Homo sapiens troponin T type 1 (skeletal, slow) (TNNT1), transcript variant 1, mRNA [NM_003283]
A_23_P42397	-3.7	PRSS35	Homo sapiens protease, serine, 35 (PRSS35), transcript variant 2, mRNA [NM_153362]
A_23_P58770	-3.7	HAND1	Homo sapiens heart and neural crest derivatives expressed 1 (HAND1), mRNA [NM_004821]
A_19_P00813444	-3.7		lincRNA:chr11:3362099-3372424 reverse strand
A_33_P3297907	-3.6	FGF22	Homo sapiens fibroblast growth factor 22 (FGF22), mRNA [NM_020637]
A_23_P348264	-3.6	LETM2	Homo sapiens leucine zipper-EF-hand containing transmembrane protein 2 (LETM2), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA [NM_144652]
A_19_P00322379	-3.6		lincRNA:chr2:216542746-216554494 reverse strand
A_33_P3314511	-3.6	SNRPD3	small nuclear ribonucleoprotein D3 polypeptide 18kDa [Source:HGNC Symbol;Acc:11160] [ENST00000402849]
A_19_P00804592	-3.5		lincRNA:chr3:194190336-194206786 forward strand
A_33_P3367550	-3.5	LOC401242	Homo sapiens hypothetical LOC401242 (LOC401242), non-coding RNA [NR_033379]
A_19_P00321979	-3.5		lincRNA:chr15:58538381-58623829 reverse strand
A_23_P148990	-3.5	HMCN1	Homo sapiens hemicentin 1 (HMCN1), mRNA [NM_031935]
A_19_P00326930	-3.5		lincRNA:chr6:111806107-111823857 reverse strand
A_33_P3273424	-3.4	RETSAT	retinol saturase (all-trans-retinol 13,14-reductase) [Source:HGNC Symbol;Acc:25991] [ENST00000490291]
A_33_P3388148	-3.4	CHRNA3	Homo sapiens cholinergic receptor, nicotinic, alpha 3 (CHRNA3), transcript variant 2, mRNA [NM_001166694]
A_19_P00321084	-3.4		lincRNA:chr4:74582924-74600402 reverse strand
A_23_P393880	-3.4	KIAA1244	Homo sapiens KIAA1244 (KIAA1244), mRNA [NM_020340]
A_19_P00812722	-3.4		lincRNA:chrX:7532690-7533018 forward strand
A_23_P345564	-3.3	OPRL1	Homo sapiens opiate receptor-like 1 (OPRL1), transcript variant 1, mRNA [NM_182647]
A_33_P3289596	-3.3	EFR3B	Homo sapiens EFR3 homolog B (S. cerevisiae) (EFR3B), mRNA [NM_014971]
A_19_P00316268	-3.3		lincRNA:chr2:208091672-208093032 reverse strand
A_19_P00324627	-3.3		lincRNA:chr22:32115350-32145824 forward strand
A_19_P00805514	-3.3		lincRNA:chr4:106271676-106286376 reverse strand
A_33_P3267150	-3.3		
A_23_P214079	-3.3	SPINK1	Homo sapiens serine peptidase inhibitor, Kazal type 1 (SPINK1), mRNA [NM_003122]
A_23_P131330	-3.2	LRRTM1	Homo sapiens leucine rich repeat transmembrane neuronal 1 (LRRTM1), mRNA [NM_178839]

A_33_P3355230	-3.2	LAIR1	Homo sapiens leukocyte-associated immunoglobulin-like receptor 1 (LAIR1), transcript variant a, mRNA [NM_002287]
A_33_P3281171	-3.2	LOC100130987	Homo sapiens hypothetical LOC100130987 (LOC100130987), non-coding RNA [NR_024469]
A_23_P341527	-3.2	DCST1	Homo sapiens DC-STAMP domain containing 1 (DCST1), transcript variant 1, mRNA [NM_152494]
A_33_P3237260	-3.2	C11orf53	Homo sapiens chromosome 11 open reading frame 53 (C11orf53), mRNA [NM_198498]
A_23_P111978	-3.2	KCNK9	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA [NM_016601]
A_19_P00327388	-3.2		lincRNA:chr3:162445031-162502906 reverse strand
A_19_P00328058	-3.1		lincRNA:chr6:167382710-167411729 reverse strand
A_23_P425332	-3.1	PPP4R4	Homo sapiens protein phosphatase 4, regulatory subunit 4 (PPP4R4), transcript variant 1, mRNA [NM_058237]
A_23_P114084	-3.1	PHEX	Homo sapiens phosphate regulating endopeptidase homolog, X-linked (PHEX), mRNA [NM_000444]
A_24_P293114	-3.1	SPTBN4	Homo sapiens spectrin, beta, non-erythrocytic 4 (SPTBN4), transcript variant sigma1, mRNA [NM_020971]
A_19_P00320754	-3.0		lincRNA:chr15:40338196-40349201 reverse strand
A_19_P00802954	-3.0		lincRNA:chr7:64336915-64348765 reverse strand
A_23_P300087	-3.0	FKSG83	Homo sapiens FKSG83 (FKSG83), mRNA [NM_032030]
A_23_P69810	-3.0	AGPAT9	Homo sapiens 1-acylglycerol-3-phosphate O-acyltransferase 9 (AGPAT9), mRNA [NM_032717]
A_19_P00810806	-3.0		lincRNA:chr13:44717350-44723025 forward strand
A_19_P00804899	-3.0		lincRNA:chr6:43946747-43965218 forward strand
A_19_P00320499	-3.0		lincRNA:chr6:132224787-132228642 forward strand
A_19_P00320970	-3.0	XLOC_005020	BROAD lincRNAs version v2 (http://www.broadinstitute.org/genome_bio/human_lincnas/)
A_33_P3266783	-3.0		Q66I89_BRARE (Q66I89) PQ loop repeat containing 3, partial (6%) [THC2736258]
A_19_P00332443	-3.0		lincRNA:chr12:57808558-57820783 forward strand
A_23_P101564	-3.0	FGF21	Homo sapiens fibroblast growth factor 21 (FGF21), mRNA [NM_019113]
A_19_P00812045	-3.0		lincRNA:chr4:129215150-129232550 forward strand
A_33_P3384502	-3.0	LOC100128946	Homo sapiens hypothetical LOC100128946 (LOC100128946), non-coding RNA [NR_038944]
A_33_P3401813	-2.9		Homo sapiens cDNA FLJ44636 fis, clone BRACE2025452. [AK126599]
A_24_P32627	-2.9		PREDICTED: Homo sapiens hCG1981531 (LOC728586), partial miscRNA [XR_110564]
A_24_P66312	-2.9	KRTAP12-1	Homo sapiens keratin associated protein 12-1 (KRTAP12-1), mRNA [NM_181686]
A_33_P3210180	-2.9	TLE1	Homo sapiens clone FP17926 unknown mRNA. [AY129016]
A_19_P00324586	-2.9		lincRNA:chr2:134880005-134978205 reverse strand
A_24_P924836	-2.9	CRYZL1	Homo sapiens crystallin, zeta (quinone reductase)-like 1, mRNA (cDNA clone IMAGE:3632782), partial cds. [BC022827]

A_23_P207537	-2.9	DUSP14	Homo sapiens dual specificity phosphatase 14 (DUSP14), mRNA [NM_007026]
A_19_P00322953	-2.9	XLOC_002319	BROAD lincRNAs version v2 (http://www.broadinstitute.org/genome_bio/human_lincnas/)
A_23_P315964	-2.9	UMODL1	Homo sapiens uromodulin-like 1 (UMODL1), transcript variant 2, mRNA [NM_173568]
A_23_P104224	-2.9	A1CF	Homo sapiens APOBEC1 complementation factor (A1CF), transcript variant 3, mRNA [NM_138933]
A_19_P00319266	-2.9		lincRNA:chr3:106940579-106949939 reverse strand
A_33_P3252441	-2.8		
A_33_P3346331	-2.8		
A_23_P47125	-2.8	OR5P2	Homo sapiens olfactory receptor, family 5, subfamily P, member 2 (OR5P2), mRNA [NM_153444]
A_19_P00811216	-2.8		lincRNA:chr19:28213935-28328635 forward strand
A_19_P00323668	-2.8		lincRNA:chr6:132228532-132259157 forward strand
A_33_P3254761	-2.8		
A_33_P3379001	-2.8	UNC5A	Homo sapiens unc-5 homolog A (C. elegans) (UNC5A), mRNA [NM_133369]
A_23_P25674	-2.8	CKB	Homo sapiens creatine kinase, brain (CKB), mRNA [NM_001823]
A_19_P00802200	-2.8		lincRNA:chr8:43518693-43531493 forward strand
A_19_P00802304	-2.7		lincRNA:chr2:216473880-216713730 forward strand
A_33_P3405349	-2.7	C7orf43	chromosome 7 open reading frame 43 [Source:HGNC Symbol;Acc:25604] [ENST00000448720]
A_23_P414281	-2.7	C16orf71	Homo sapiens chromosome 16 open reading frame 71 (C16orf71), mRNA [NM_139170]
A_33_P3212804	-2.7	C22orf42	Homo sapiens chromosome 22 open reading frame 42 (C22orf42), mRNA [NM_001010859]
A_19_P00801362	-2.7		lincRNA:chr3:139139360-139147910 reverse strand
A_23_P135669	-2.7	SLCO5A1	Homo sapiens solute carrier organic anion transporter family, member 5A1 (SLCO5A1), transcript variant 1, mRNA [NM_030958]
A_19_P00808394	-2.7		lincRNA:chr8:58115146-58143017 reverse strand
A_23_P37676	-2.7	GPR176	Homo sapiens G protein-coupled receptor 176 (GPR176), mRNA [NM_007223]
A_23_P168551	-2.7	SLC29A4	Homo sapiens solute carrier family 29 (nucleoside transporters), member 4 (SLC29A4), transcript variant 1, mRNA [NM_001040661]
A_19_P00801960	-2.7		lincRNA:chr6:107185182-107197657 reverse strand
A_19_P00318932	-2.7		lincRNA:chrX:110800399-110828053 reverse strand
A_33_P3272663	-2.6		PREDICTED: Homo sapiens hypothetical protein LOC100506093 (LOC100506093), mRNA [XM_003118587]
A_23_P149946	-2.6	CDHR1	Homo sapiens cadherin-related family member 1 (CDHR1), transcript variant 1, mRNA [NM_033100]
A_23_P370666	-2.6	GLYATL1	Homo sapiens glycine-N-acyltransferase-like 1 (GLYATL1), transcript variant 1, mRNA [NM_080661]
A_19_P00802461	-2.6		lincRNA:chr1:182101177-182132002 forward strand

A_23_P133474	-2.6	GPX3	Homo sapiens glutathione peroxidase 3 (plasma) (GPX3), mRNA [NM_002084]
A_19_P00809354	-2.6		lincRNA:chr5:133837051-133848098 forward strand
A_23_P104054	-2.6	C1orf9	Homo sapiens chromosome 1 open reading frame 9 (C1orf9), transcript variant 2, mRNA [NM_016227]
A_33_P3349265	-2.5	GLYATL3	Homo sapiens glycine-N-acyltransferase-like 3 (GLYATL3), mRNA [NM_001010904]
A_23_P9869	-2.5	CNDP1	Homo sapiens carnosine dipeptidase 1 (metallopeptidase M20 family) (CNDP1), mRNA [NM_032649]
A_33_P3230798	-2.5	MUSK	muscle, skeletal, receptor tyrosine kinase [Source:HGNC Symbol;Acc:7525] [ENST00000374441]
A_33_P3406370	-2.5		KB-EST0005989 BPS7 Homo sapiens cDNA, mRNA sequence [DT220905]
A_19_P00805333	-2.5		lincRNA:chr15:40828033-40834483 reverse strand
A_23_P19291	-2.5	TUBB2A	Homo sapiens tubulin, beta 2A (TUBB2A), mRNA [NM_001069]
A_19_P00809109	-2.5		lincRNA:chr4:295700-311175 forward strand
A_19_P00324432	-2.5		lincRNA:chr19:48146663-48181363 forward strand
A_19_P00324030	-2.5		lincRNA:chr1:79897287-79954287 reverse strand
A_33_P3369371	-2.5	GPX3	Homo sapiens glutathione peroxidase 3 (plasma) (GPX3), mRNA [NM_002084]
A_33_P3336273	-2.5	NAV3	Homo sapiens neuron navigator 3 (NAV3), mRNA [NM_014903]
A_23_P24676	-2.5	OR8U1	Homo sapiens olfactory receptor, family 8, subfamily U, member 1 (OR8U1), mRNA [NM_001005204]
A_33_P3331992	-2.5		Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:B5MCR4] [ENST00000401694]
A_19_P00809814	-2.5		lincRNA:chr11:69216919-69339519 reverse strand
A_33_P3219596	-2.5	LOC254559	Homo sapiens hypothetical LOC254559 (LOC254559), non-coding RNA [NR_015411]
A_19_P00804757	-2.5		lincRNA:chr3:48327371-48332931 forward strand
A_19_P00807207	-2.5	XLOC_007052	BROAD lincRNAs version v2 (http://www.broadinstitute.org/genome_bio/human_lincnas/)
A_24_P623782	-2.4	FRG2	Homo sapiens FSHD region gene 2 (FRG2), mRNA [NM_001005217]
A_33_P3361267	-2.4	LOC100128386	Homo sapiens cDNA FLJ42335 fis, clone TUTER2001286. [AK124326]
A_19_P00318923	-2.4		lincRNA:chr13:20268546-20269862 forward strand
A_23_P162288	-2.4	MYO1A	Homo sapiens myosin IA (MYO1A), mRNA [NM_005379]
A_23_P13713	-2.4	PRPH	Homo sapiens peripherin (PRPH), mRNA [NM_006262]
A_23_P105862	-2.4	FRY	Homo sapiens furry homolog (Drosophila) (FRY), mRNA [NM_023037]
A_23_P4536	-2.4	EPB41L3	Homo sapiens erythrocyte membrane protein band 4.1-like 3 (EPB41L3), mRNA [NM_012307]
A_19_P00805063	-2.4		lincRNA:chr22:41324879-41330529 reverse strand
A_33_P3288491	-2.4	KLHL38	Homo sapiens kelch-like 38 (Drosophila) (KLHL38), mRNA [NM_001081675]

A_33_P3245348	-2.4	KRTAP4-1	Homo sapiens keratin associated protein 4-1 (KRTAP4-1), mRNA [NM_033060]
A_33_P3240094	-2.4	NGEF	neuronal guanine nucleotide exchange factor [Source:HGNC Symbol;Acc:7807] [ENST00000409079]
A_33_P3255409	-2.4	PIH1D1	Homo sapiens PIH1 domain containing 1 (PIH1D1), mRNA [NM_017916]
A_33_P3217356	-2.4	LOC388630	Homo sapiens UPF0632 protein A (LOC388630), mRNA [NM_001194986]
A_33_P3308299	-2.4		
A_19_P00329189	-2.4		lincRNA:chr4:3676927-3688227 forward strand
A_19_P00812769	-2.4		lincRNA:chr8:125471969-125486269 forward strand
A_33_P3304268	-2.4	LOC643327	Homo sapiens cDNA FLJ39230 fis, clone OCBBF2007485. [AK096549]
A_24_P289404	-2.4	RPS26	Homo sapiens ribosomal protein S26 (RPS26), mRNA [NM_001029]
A_19_P00319133	-2.4	XLOC_004558	BROAD lincRNAs version v2 (http://www.broadinstitute.org/genome_bio/human_lincrnas/)
A_23_P167129	-2.4	HHIP	Homo sapiens hedgehog interacting protein (HHIP), mRNA [NM_022475]
A_23_P23502	-2.4	OR6N1	Homo sapiens olfactory receptor, family 6, subfamily N, member 1 (OR6N1), mRNA [NM_001005185]
A_24_P383762	-2.4	RASGEF1C	Homo sapiens RasGEF domain family, member 1C (RASGEF1C), mRNA [NM_175062]
A_23_P41888	-2.3	AGXT2L2	Homo sapiens alanine-glyoxylate aminotransferase 2-like 2 (AGXT2L2), mRNA [NM_153373]
A_33_P3381621	-2.3	PLB1	phospholipase B1 [Source:HGNC Symbol;Acc:30041] [ENST00000329020]
A_24_P49597	-2.3		
A_23_P105691	-2.3	GPRC5D	Homo sapiens G protein-coupled receptor, family C, group 5, member D (GPRC5D), mRNA [NM_018654]
A_33_P3278330	-2.3	FLJ16124	Homo sapiens FLJ16124 protein, mRNA (cDNA clone MGC:43245 IMAGE:5264239), complete cds. [BC033059]
A_24_P365015	-2.3	HOXB13	Homo sapiens homeobox B13 (HOXB13), mRNA [NM_006361]
A_24_P7652	-2.3	MAP7D2	Homo sapiens MAP7 domain containing 2 (MAP7D2), transcript variant 2, mRNA [NM_152780]
A_23_P140475	-2.3	NOX5	Homo sapiens NADPH oxidase, EF-hand calcium binding domain 5 (NOX5), transcript variant 1, mRNA [NM_024505]
A_19_P00324546	-2.3		lincRNA:chr6:22183421-22200496 forward strand
A_33_P3309741	-2.3	CCDC108	coiled-coil domain containing 108 [Source:HGNC Symbol;Acc:25325] [ENST00000441164]
A_33_P3384284	-2.3	FAM48B1	Homo sapiens family with sequence similarity 48, member B1 (FAM48B1), mRNA [NM_001136234]
A_19_P00808283	-2.3		lincRNA:chr8:60062921-60832721 forward strand
A_33_P3324786	-2.3	TCFL5	transcription factor-like 5 (basic helix-loop-helix) [Source:HGNC Symbol;Acc:11646] [ENST00000217162]
A_33_P3369829	-2.3	LOC154822	Homo sapiens hypothetical LOC154822 (LOC154822), non-coding RNA [NR_024394]
A_24_P46130	-2.3	ACPP	Homo sapiens acid phosphatase, prostate (ACPP), transcript variant 1, mRNA [NM_001099]
A_33_P3242039	-2.3		

A_19_P00804846	-2.3		lincRNA:chr6:28134146-28139947 reverse strand
A_33_P3256550	-2.3	MST152	Homo sapiens MSTP152 (MST152) mRNA, complete cds. [AF190155]
A_19_P00328024	-2.3		lincRNA:chr17:29887612-29925137 reverse strand
A_23_P22647	-2.2	FAM155B	Homo sapiens family with sequence similarity 155, member B (FAM155B), mRNA [NM_015686]
A_19_P00804827	-2.2		lincRNA:chr1:9209361-9210752 reverse strand
A_19_P00316210	-2.2		lincRNA:chr19:56794715-56824749 forward strand
A_32_P217655	-2.2	LOC645166	Homo sapiens lymphocyte-specific protein 1 pseudogene (LOC645166), transcript variant 2, non-coding RNA [NR_027355]
A_19_P00802019	-2.2		lincRNA:chr6:3897476-3911792 forward strand
A_19_P00325810	-2.2		lincRNA:chr6:73983629-73998029 reverse strand
A_24_P165205	-2.2	MORN1	Homo sapiens MORN repeat containing 1 (MORN1), mRNA [NM_024848]
A_19_P00321571	-2.2		lincRNA:chr6:14283035-14285450 reverse strand
A_33_P3221888	-2.2		
A_33_P3375358	-2.2	GPR31	Homo sapiens G protein-coupled receptor 31 (GPR31), mRNA [NM_005299]
A_23_P23839	-2.2	LGR6	Homo sapiens leucine-rich repeat containing G protein-coupled receptor 6 (LGR6), transcript variant 1, mRNA [NM_001017403]
A_33_P3315979	-2.2	OR4Q3	Homo sapiens olfactory receptor, family 4, subfamily Q, member 3 (OR4Q3), mRNA [NM_172194]
A_19_P00812538	-2.2		lincRNA:chr12:89931569-89946444 reverse strand
A_23_P159721	-2.1	GPR50	Homo sapiens G protein-coupled receptor 50 (GPR50), mRNA [NM_004224]
A_33_P3298861	-2.1	SLC12A8	Homo sapiens solute carrier family 12 (potassium/chloride transporters), member 8 (SLC12A8), transcript variant 1, mRNA [NM_024628]
A_23_P75647	-2.1	HYOU1	Homo sapiens hypoxia up-regulated 1 (HYOU1), transcript variant 1, mRNA [NM_006389]
A_33_P3394993	-2.1	PREX2	Homo sapiens phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 2 (PREX2), transcript variant 2, mRNA [NM_025170]
A_33_P3221111	-2.1	PGA3	Homo sapiens mRNA; cDNA DKFZp666J2410 (from clone DKFZp666J2410). [AL832946]
A_33_P3287310	-2.1		
A_23_P133637	-2.1	HTR4	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 4 (HTR4), transcript variant d, mRNA [NM_001040172]
A_19_P00327794	-2.1		lincRNA:chrX:130874594-130963544 forward strand
A_19_P00812657	-2.1		lincRNA:chr5:81707769-81713444 reverse strand
A_23_P202034	-2.1	GUCY2GP	Homo sapiens guanylate cyclase 2G homolog (mouse), pseudogene (GUCY2GP), non-coding RNA [NR_028134]
A_19_P00331765	-2.1		lincRNA:chr1:234861727-234869377 forward strand
A_19_P00326869	-2.1		lincRNA:chr8:37183617-37193667 forward strand
ERCC-00022_66	-2.1		Unknown

A_33_P3481113	-2.1	CECR3	Homo sapiens cat eye syndrome chromosome region, candidate 3 (non-protein coding) (CECR3), non-coding RNA [NR_038398]
A_33_P3210418	-2.1	SLC5A10	Homo sapiens solute carrier family 5 (sodium/glucose cotransporter), member 10 (SLC5A10), transcript variant 1, mRNA [NM_152351]
A_19_P00803126	-2.1		lincRNA:chr7:106224664-106257564 reverse strand
A_19_P00326463	-2.1		lincRNA:chr12:97010269-97032694 reverse strand
A_23_P21990	-2.1	SLC23A1	Homo sapiens solute carrier family 23 (nucleobase transporters), member 1 (SLC23A1), transcript variant 2, mRNA [NM_152685]
A_23_P339818	-2.1	ARRDC4	Homo sapiens arrestin domain containing 4 (ARRDC4), mRNA [NM_183376]
A_19_P00810701	-2.1		lincRNA:chr18:10552875-10561233 forward strand
A_24_P152968	-2.1	AKR1C1	Homo sapiens aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase) (AKR1C1), mRNA [NM_001353]
A_19_P00322420	-2.1		lincRNA:chr4:79567056-79584458 forward strand
A_32_P197621	-2.1	GEMIN8P4	Homo sapiens gem (nuclear organelle) associated protein 8 pseudogene 4 (GEMIN8P4), non-coding RNA [NR_002830]
A_33_P3265030	-2.1	GP1BB	Homo sapiens glycoprotein Ib (platelet), beta polypeptide (GP1BB), mRNA [NM_000407]
A_19_P00804601	-2.1		lincRNA:chr11:3402374-3408174 forward strand
A_33_P3231252	-2.1	NHLH2	Homo sapiens nescient helix loop helix 2 (NHLH2), transcript variant 1, mRNA [NM_005599]
A_19_P00806087	-2.1		lincRNA:chr5:5357650-5384825 forward strand
A_33_P3287258	-2.1		
A_19_P00801515	-2.1		lincRNA:chr2:232366756-232372381 reverse strand
A_33_P3465703	-2.0	SNORA60	601888042F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121819 5', mRNA sequence [BF304636]
A_19_P00324132	-2.0		lincRNA:chr7:105546714-105564714 reverse strand
A_23_P210690	-2.0	TRIB3	Homo sapiens tribbles homolog 3 (Drosophila) (TRIB3), mRNA [NM_021158]
A_19_P00806914	-2.0		lincRNA:chr21:44907647-44916222 reverse strand
A_19_P00318078	-2.0		lincRNA:chr5:39521667-39524810 reverse strand
A_19_P00319011	-2.0		lincRNA:chr2:235358561-235363194 reverse strand
A_23_P139965	-2.0	SERP2	Homo sapiens stress-associated endoplasmic reticulum protein family member 2 (SERP2), mRNA [NM_001010897]
A_23_P316085	-2.0	C13orf43	chromosome 13 open reading frame 43 [Source:HGNC Symbol;Acc:39933] [ENST00000493739]
A_33_P3415678	-2.0	MKL1	megakaryoblastic leukemia (translocation) 1 [Source:HGNC Symbol;Acc:14334] [ENST00000402630]
A_19_P00329963	-2.0		lincRNA:chr11:102257165-102265615 forward strand
A_33_P3365002	-2.0	TUBB2A	Homo sapiens tubulin, beta 2A (TUBB2A), mRNA [NM_001069]
A_19_P00804710	-2.0		lincRNA:chr6:158658787-158724862 forward strand

A_19_P00318438

-2.0

lincRNA:chr9:470310-473357 forward strand

[†]160 unique up-regulated genes.

[‡]225 unique down-regulated genes.

Overlapping up- and down-regulated gene in EoE between Japan and the US.