METHODS

RNA extraction and miRNA microarray analysis

Total RNA, including miRNA from patients' esophageal biopsy samples, was isolated with the miRNeasy Mini Kit, according to the manufacturer's instructions (Qiagen). RNA quality was assessed by using the Agilent 2100 Bioanalyzer (Agilent Technologies), and only samples with an RNA integrity number of greater than 8 were used. MiRNA expression was profiled by using TaqMan Human MicroRNA Array version 2.0, which includes probes for 667 human miRNAs in the miRBase microRNA Registry (release 10.0), according to the manufacturer's protocols (Applied Biosystems).[E1] Data analyses were carried out with GeneSpring software (Agilent Technologies). Expression data were normalized to the average of 2 endogenous control probes, U6 and RNU44, and then filtered on cycle threshold values of less than 30 and at least a 2-fold change between healthy control subjects and patients with EoE to identify miRNAs differentially regulated between healthy control subjects and patients with EoE. Statistical significance was determined at a *P* value of less than .05 with a Benjamini-Hochberg false discovery rate correction. The list of differentially expressed miRNAs was clustered by using hierarchic clustering, and a heat map was generated. Similar analyses were carried out comparing healthy control subjects with patients with chronic esophagitis and patients who did not receive glucocorticoid treatment with patients who received glucocorticoid treatment to identify differentially expressed miRNAs between the groups. The microarray data have been deposited into the Array Express database (www.ebi.ac.uk/arrayexpress; accession no. E-MEXP-3298) in compliance with minimum information about microarray experiment (MIAME) standards.

Quantitative RT-PCR for miRNA

MiRNA expression levels were measured quantitatively by using TaqMan MicroRNA Assays (Applied Biosystems), according to the manufacturer's protocol. The expression levels were normalized to the U6 endogenous control. Relative expression was calculated by using the comparative cycle threshold method, as previously described.[E2]

Correlation of miR-21 and miR-223 with major EoE signature genes

Esophageal mRNA from patients with EoE was reverse transcribed to cDNA by using a High Capacity cDNA Reverse Transcription Kit (Applied Biosystems), according to the manufacturer's protocol. The TaqMan reagents for amplification of EoE signature genes[E3-E5] were obtained from Applied Biosystems. The EoE signature genes are listed in Table E2. TaqMan real-time PCR amplification was performed with an Applied Biosystems 7900HT Real-Time PCR System. The amplification protocol consisted of a hot start of 95°C for 10 minutes, followed by 40 cycles of 15 seconds at 95°C and 1 minute at 60°C. The expression correlation study between miR-21 and miR-223 and 48 EoE genes was performed in GraphPad Prism software (GraphPad Software, Inc, La Jolla, Calif). Negative logs of *P* values from Pearson correlation analysis were plotted to demonstrate correlation significance with EoE genes. To control for the increased risk of false-positive results caused by the number of statistical tests performed, we applied a Bonferroni correction based on the number of gene expression profiles compared. Because the average pairwise correlation between gene expression profiles was 0.54, we applied principal components analysis to determine the effective number of independent comparisons, as previously described.[E6] By using this approach, a *P* value of .002 was required to achieve a family-wise error rate of 0.05.

Analysis of miR-21 and miR-223 coregulated genes by using RNA-Seq and gene expression microarray

RNA-Seq data were obtained from esophageal RNA samples from 11 patients with EoE by the Genomic Sequencing Core Laboratory at Cincinnati Children's Hospital Medical Center. The RNA-Seq was aligned to the GrCh37 build of the human genome by using the Ensembl annotations as a guide for TopHat.[E7] The resulting files were then analyzed with Cufflinks to test for differential expression and differential regulation.[E8] The region 3′ of miR-21 is identified as the best representation of pri-miR-21 (labeled as exon 3 in Fig E3, *A*). The region 3′ of miR-223 is identified as the best representation of pri-miR-223 (labeled as exon 2 in Fig E3, *B*).[E9] The pri-miR-21 region was found to be significantly enriched in patients with EoE compared with that seen in healthy control subjects. The expression pattern of the pri-miR-21 was then correlated with the other gene expression patterns present from the RNA-Seq expression profiles. MiR-223 was analyzed in a similar fashion. We also analyzed gene expression microarray experiments from patients with EoE.[E3,E5] MiR-21 and miR-223 were correlated by using the Affymetrix Human U133 probes (Affymetrix, Santa Clara, Calif) that best corresponded to the miRNA. A correlated gene is one the expression of which follows similar or inverse trends with the miRNA in question. These probes were correlated with microarray expression data, and 470 probes correlated well with at least 1 of the miRNA probes. The genes that showed the highest correlations and the top differentially regulated genes in the previously published EoE transcriptome were used as a training set alongside genes that are related to T_H1/T_H2 differentiation and eosinophilia and that are target genes of miR-21 and miR-223.[E10] The genes that showed patterns related to miR-21 or miR-223 were then analyzed to determine significant pathways and annotations related to T_H1/T_H2 differentiation and eosinophil development and function. The genes were then clustered based on the strength of the annotations that are associated with them. The results are rendered as a Cytoscape map.

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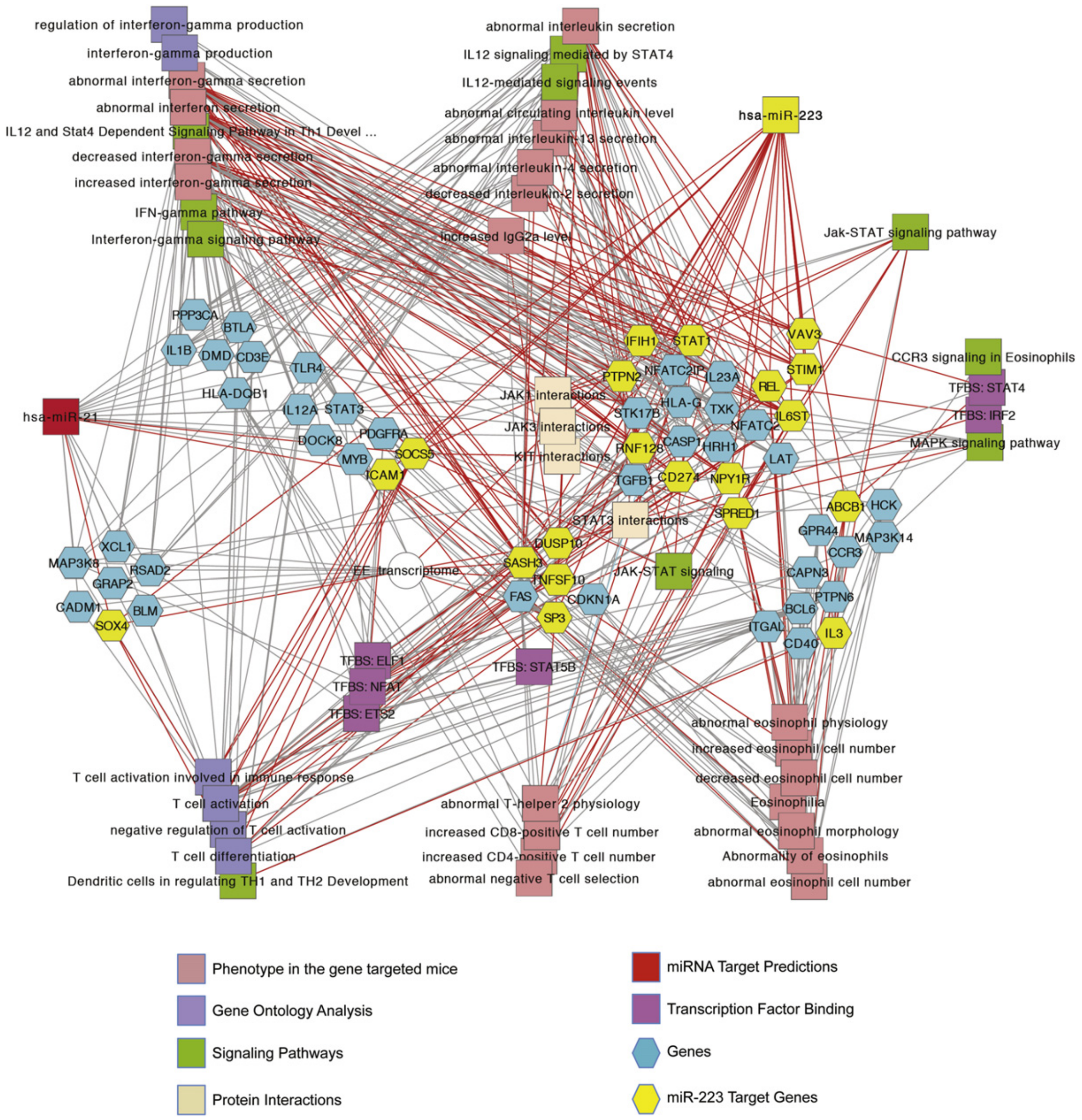

FIG E1. Gene enrichment analysis of miR-21 and miR-223 coregulated genes in patients with EoE. The miR-223 targets that are significantly correlated with miR-223 expression or in the EoE transcriptome are highlighted as *yellow hexagons*, and their respective feature and function relationships are shown connected through *red edges*. The features that are highly significant for other genes in the cluster are connected by *gray edges*. *TFBS*, Transcription factor binding sites.

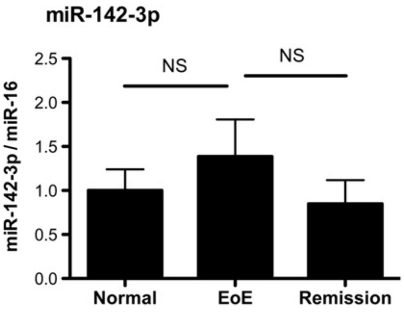

FIG E2. MiR-142-3p expression levels in patients' plasma samples. Expression of miR-142-3p was determined in plasma samples from patients with active EoE and patients with EoE remission compared with healthy control subjects. The relative expression levels were normalized to miR-16 (n = 13-14 plasma samples per group). Data are presented as mean ± SEM. *NS*, Not significant ($P > .05$).

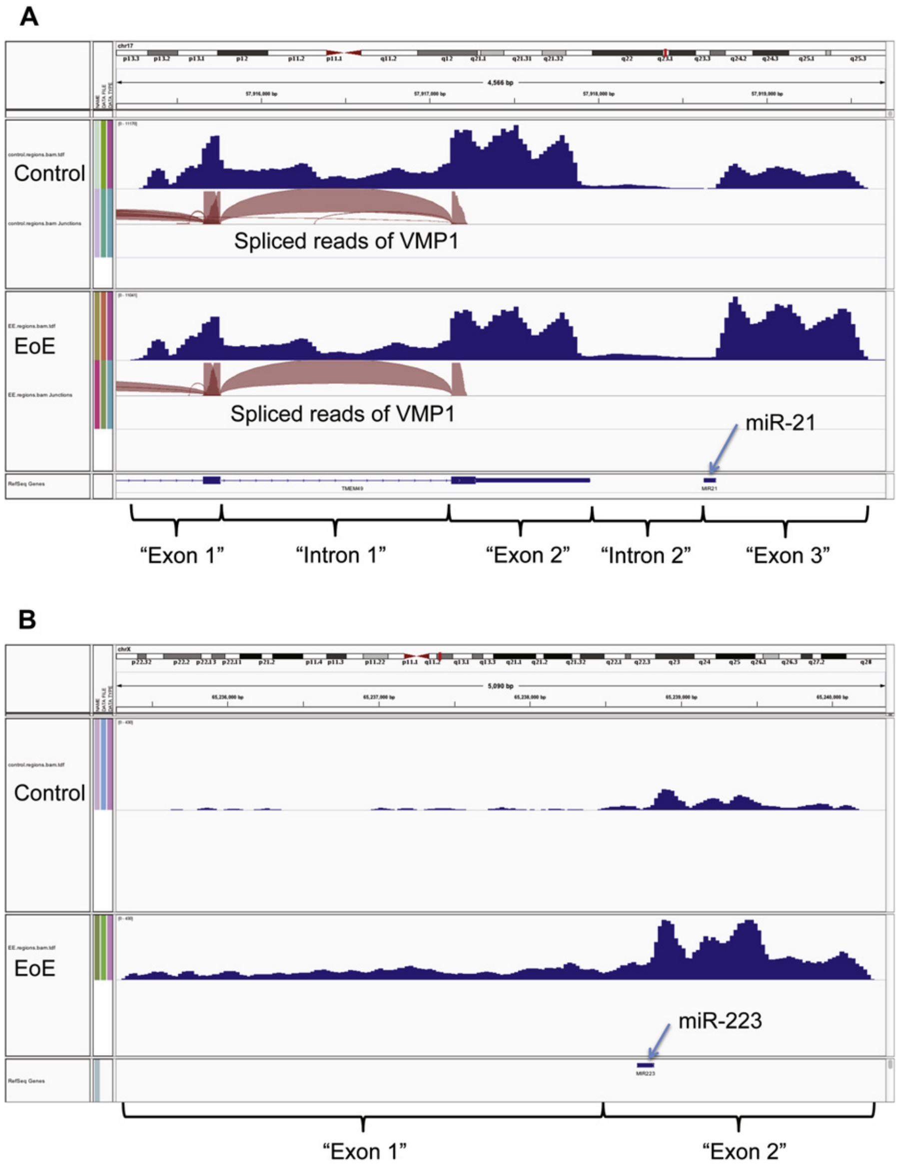

FIG E3. Regions identified as pri-miR-21 and pri-miR-223 in the RNA-Seq analysis. **A,** Identification of the pri-miR-21 region in the RNA-Seq analysis. The *blue regions* are normalized coverage tracks for the mRNA-seq. The *brown tracks* are spliced reads that are present in exons of *VMP1*. The lack of spliced reads present between the regions outside of the exons of *VMP1* leads to the assumption that it is a portion of pri-miR-21. The regions annotated as "exon" or "intron" are not necessarily true exons and introns of a gene but regions that showed significant expression patterns similar to those of a gene's exons and introns. They were annotated as this to facilitate the identification of the region to use for the correlation analysis. **B,** Identification of the pri-miR-223 region in the RNA-Seq analysis. The *blue regions* are normalized coverage tracks for the mRNA-seq. There are no reads spanning junctions because there are no splicing events present in this region. The regions annotated as "exon" are not necessarily true exons of a gene but regions that showed significant expression patterns similar to those of a gene's exons. They were annotated as this to facilitate the identification of the region to use for the correlation analysis.

TABLE E1. Patients' clinical characteristics

	Healthy control subjects	Patients with EoE	Patients with chronic esophagitis	Patients with EoE who responded to steroids	Patients with EoE who did not respond to steroids
No. of patients	23	31	9	20	8
Male sex, no. (%)	11 (48)	23 (74)	7 (78)	16 (80)	6 (75)
Age (y)					
Mean	9.26	9.29	9.06	8.32	10.96
Range	1.43-19.01	1.89-32.26	4.50-16.12	3.75-19.43	4.30-18.41
Medications					
PPI, no. (%)*	6 (26)	23 (74)	2 (22)	16 (80)	7 (88)
Steroids, no. (%)	0	0	0	20 (100)	8 (100)

PPI, Proton-pump inhibitor.

*Percentages listed reflect the total number of patients studied who had received at least 8 weeks of proton-pump inhibitor therapy before a diagnostic endoscopy.

TABLE E2. List of EoE signature genes used for correlation analysis

Entrez gene ID	Gene name	Description
55	*ACPP*	Acid phosphatase, prostate
72	*ACTG2*	Actin, gamma 2, smooth muscle, enteric
246	*ALOX15*	Arachidonate 15-lipoxygenase
383	*ARG1*	Arginase, liver
10344	*CCL26*	Chemokine (C-C motif) ligand 26
1232	*CCR3*	Chemokine (C-C motif) receptor 3
131450	*CD200R1*	CD200 receptor 1
978	*CDA*	Cytidine deaminase
60437	*CDH26*	Cadherin-like 26
3426	*CFI*	Complement factor I
10370	*CITED2*	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2
1178	*CLC*	Charcot-Leyden crystal protein
9071	*CLDN10*	Claudin 10
1215	*CMA1*	Chymase 1, mast cell
1296	*COL8A2*	Collagen, type VIII, alpha 2
1359	*CPA3*	Carboxypeptidase A3 (mast cell)
10321	*CRISP3*	Cysteine-rich secretory protein 3
8727	*CTNNAL1*	Catenin (cadherin-associated protein), alpha-like 1
1828	*DSG1*	Desmoglein 1
2009	*EML1*	Echinoderm microtubule-associated protein-like 1
2312	*FLG*	Filaggrin
9245	*GCNT3*	Glucosaminyl (N-acetyl) transferase 3, mucin type
134266	*GRPEL2*	GrpE-like 2, mitochondrial (E. coli)
27306	*HPGDS*	hematopoietic prostaglandin D synthase
3269	*HRH1*	Histamine receptor H1
3512	*IGJ*	Immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides
3596	*IL13*	Interleukin 13
3565	*IL4*	Interleukin 4
3567	*IL5*	Interleukin 5 (colony-stimulating factor, eosinophil)
3568	*IL5RA*	Interleukin 5 receptor, alpha
3576	*IL8*	Interleukin 8
3759	*KCNJ2*	Potassium inwardly-rectifying channel, subfamily J, member 2
25984	*KRT23*	Keratin 23 (histone deacetylase inducible)
4321	*MMP12*	Matrix metallopeptidase 12 (macrophage elastase)
4585	*MUC4*	Mucin 4, cell surface associated
4747	*NEFL*	Neurofilament, light polypeptide 68kDa
5367	*PMCH*	Pro-melanin-concentrating hormone
10631	*POSTN*	Periostin, osteoblast-specific factor
64092	*SAMSN1*	SAM domain, SH3 domain and nuclear localization signals 1
9120	*SLC16A6*	Solute carrier family 16, member 6 (monocarboxylic acid transporter 7)
5172	*SLC26A4*	Solute carrier family 26, member 4
84651	*SPINK7*	Serine peptidase inhibitor, Kazal type 7 (putative)
7130	*TNFAIP6*	Tumor necrosis factor, alpha-induced protein 6
7177	*TPSAB1*	Tryptase alpha/beta 1
85480	*TSLP*	Thymic stromal lymphopoietin
23554	*TSPAN12*	Tetraspanin 12
11045	*UPK1A*	Uroplakin 1A
7348	*UPK1B*	Uroplakin 1B

TABLE E3. Log$_2$ fold change of all miRNAs expressed at greater than background levels

Gene symbol	Healthy control subjects	Patients with chronic esophagitis	Patients with EoE	Fluticasone responders
U6	0.005	0.010	0.070	−0.065
RNU24	0.052	−0.203	0.040	0.170
RNU43	−3.572	−3.124	−0.249	0.020
RNU44	−0.005	−0.010	−0.070	0.065
RNU48	−0.023	−0.031	0.249	0.093
RNU6B	0.055	−0.319	−0.050	−0.039
hsa-let-7a	−0.046	0.026	−0.019	0.007
hsa-let-7b	0.254	0.140	−0.057	−0.230
hsa-let-7c	0.114	−0.092	−0.973	−0.099
hsa-let-7d	0.065	0.033	0.001	0.152
hsa-let-7e	−0.074	−0.141	−0.390	−0.103
*hsa-let-7f-2**	−0.033	−0.259	−0.153	−0.109
hsa-let-7f	−0.138	0.146	−0.250	0.151
hsa-let-7g	−0.005	0.261	0.089	0.553
hsa-miR-1	−0.960	−1.173	−2.695	−2.563
hsa-miR-100	−0.027	−0.144	−0.602	0.333
hsa-miR-101	−0.029	−0.117	−0.060	0.353
hsa-miR-103	−0.099	−0.178	−0.184	0.254
hsa-miR-106a	−0.155	0.034	−0.055	0.189
*hsa-miR-106b**	−0.749	0.676	2.046	1.049
hsa-miR-106b	−0.111	0.210	0.234	0.628
hsa-miR-107	0.089	0.190	−0.677	0.192
hsa-miR-10a	0.129	−0.352	−0.076	−0.210
*hsa-miR-10b**	−0.172	−0.278	−0.183	−0.199
hsa-miR-10b	−0.258	−0.063	−0.083	−0.029
hsa-miR-125a-5p	−0.009	−0.428	0.016	−0.469
hsa-miR-125b	0.170	0.216	−0.067	0.505
*hsa-miR-126**	0.146	−0.294	−0.240	0.041
hsa-miR-126	0.160	−0.108	−0.200	−0.188
hsa-miR-127	0.067	−0.726	−0.248	−0.936
hsa-miR-128a	0.019	0.266	0.185	0.369
hsa-miR-130a	0.215	0.323	0.328	1.002
hsa-miR-130b	−0.012	0.359	0.509	0.753
hsa-miR-132	0.062	0.321	1.858	−0.013
hsa-miR-133a	−0.694	−0.988	−2.194	−2.236
*hsa-miR-135a**	0.163	−0.495	−0.379	−0.780
hsa-miR-135a	0.278	0.607	−0.381	0.505
*hsa-miR-135b**	0.004	0.024	0.465	0.436
hsa-miR-135b	0.076	0.271	−0.243	0.551
*hsa-miR-138-1**	0.154	−0.393	0.257	−0.244
hsa-miR-138	−0.241	−0.183	0.684	−0.348
hsa-miR-139-5p	0.184	−0.092	−0.415	0.067
hsa-miR-140-3p	0.101	−0.250	0.203	−0.106
hsa-miR-140	0.199	−0.206	0.521	−0.281
hsa-miR-141	−0.061	0.091	−0.203	0.712
hsa-miR-142-3p	0.184	0.521	2.219	0.489
hsa-miR-142-5p	−0.087	0.206	1.854	0.411
hsa-miR-143	0.420	−0.177	−0.180	−0.706
*hsa-miR-144**	−0.112	−0.996	−1.429	0.021
*hsa-miR-145**	0.377	−0.590	−0.711	−0.982
hsa-miR-145	0.184	−0.904	−1.032	−1.493
hsa-miR-146a	0.150	0.114	1.635	−0.280
hsa-miR-146b	0.042	0.249	2.153	−0.046
hsa-miR-148a	−0.059	0.132	−0.365	0.372
*hsa-miR-148b**	0.072	−0.064	0.174	0.140
hsa-miR-148b	0.024	0.067	−0.033	0.292
hsa-miR-149	0.021	0.007	−0.366	−0.230
hsa-miR-150	−0.143	−0.156	0.692	0.155
hsa-miR-151-3p	0.008	−0.311	0.335	0.238
hsa-miR-152	0.046	−0.006	0.413	0.000
hsa-miR-155	−4.901	−2.608	−4.867	0.547
*hsa-miR-15a**	−0.096	−0.469	−0.102	−0.108
hsa-miR-15a	−0.157	−0.097	0.677	−5.024
*hsa-miR-15b**	−4.120	−2.228	−6.134	0.968
hsa-miR-15b	−0.055	0.034	0.048	0.675
*hsa-miR-16-1**	−0.301	−0.355	0.559	−0.062
hsa-miR-16	−0.074	−0.228	−0.223	−0.182
*hsa-miR-17**	−0.185	−0.392	−0.473	0.006
hsa-miR-17	−0.121	0.022	−0.037	0.257
*hsa-miR-181a-2**	0.021	−0.356	−0.905	0.052
hsa-miR-181a	0.262	0.375	0.407	0.511
hsa-miR-182	0.125	0.342	−0.595	−0.155
*hsa-miR-183**	−0.243	−0.314	−1.218	0.182
hsa-miR-183	−0.077	0.052	−0.637	0.135
hsa-miR-185	0.071	0.091	0.930	0.226
hsa-miR-186	−0.203	−0.496	−0.586	−0.520
hsa-miR-188-5p	0.198	−0.605	0.261	−0.333
hsa-miR-18a	0.067	0.444	0.787	0.426
hsa-miR-18b	−3.585	−1.188	−3.780	0.876
hsa-miR-190	−0.061	0.336	−0.107	0.804
hsa-miR-191	0.049	−0.127	0.013	−0.034
hsa-miR-192	0.535	2.019	0.286	1.957
hsa-miR-193a-3p	−0.119	−0.791	−1.513	−0.406
hsa-miR-193a-5p	−0.050	−0.603	−1.261	−0.243
*hsa-miR-193b**	−1.347	−1.035	−7.696	0.082
hsa-miR-193b	0.048	−0.346	−1.910	−0.190
hsa-miR-194	0.487	2.388	0.125	1.506
hsa-miR-195	0.157	−0.176	−0.034	−0.107
hsa-miR-197	0.001	−0.021	0.137	0.306
hsa-miR-199a-3p	0.160	−0.182	0.327	−0.202
hsa-miR-19a	−0.010	0.123	0.288	0.119
*hsa-miR-19b-1**	0.027	0.074	0.379	0.169
hsa-miR-19b	0.005	0.022	0.071	0.222
*hsa-miR-200a**	0.056	−0.064	0.066	0.210
hsa-miR-200a	0.036	0.220	0.003	0.476
*hsa-miR-200b**	−0.105	−0.157	−0.270	0.400
hsa-miR-200b	−0.063	0.036	−0.409	0.247
hsa-miR-200c	0.017	0.233	−0.240	0.126
hsa-miR-203	−0.059	−0.324	−1.843	0.099
hsa-miR-204	−0.035	1.078	−1.204	0.139
hsa-miR-205	−0.159	−0.037	−0.283	−0.227
*hsa-miR-20a**	0.020	−0.282	−0.181	0.088
hsa-miR-20a	−0.001	0.140	0.047	0.325
hsa-miR-20b	0.028	−0.086	0.094	0.022
*hsa-miR-21**	0.019	0.506	2.639	0.227
hsa-miR-21	−0.058	0.840	2.332	0.596
hsa-miR-210	0.038	−0.240	−1.570	0.200
hsa-miR-211	−0.099	−0.728	−2.985	−0.028
hsa-miR-212	0.005	0.377	1.914	0.290
hsa-miR-214	0.158	−0.554	0.644	−0.686
hsa-miR-215	−0.516	1.547	−3.082	1.916
hsa-miR-218	0.090	−0.234	−0.494	0.193
*hsa-miR-22**	−0.186	−0.621	−0.697	−0.010
hsa-miR-22	−1.148	1.084	0.308	1.058
hsa-miR-221	−0.144	−0.172	0.286	−0.085
*hsa-miR-222**	−0.076	−0.093	1.057	−0.063
hsa-miR-222	0.071	0.118	0.425	−0.019
*hsa-miR-223**	0.249	−0.076	3.303	0.183

(Continued)

TABLE E3. *(Continued)*

Gene symbol	Healthy control subjects	Patients with chronic esophagitis	Patients with EoE	Fluticasone responders
hsa-miR-223	0.042	0.125	3.348	0.223
hsa-miR-224	−0.024	−0.066	−0.455	0.259
hsa-miR-23b	0.040	0.084	−0.265	−0.169
hsa-miR-24	−0.067	−0.062	−0.317	0.165
hsa-miR-25	−0.084	0.041	0.303	0.342
*hsa-miR-26a-1**	0.074	−0.096	0.081	0.184
*hsa-miR-26a-2**	0.025	−0.433	1.020	0.434
hsa-miR-26a	0.004	0.017	−0.132	0.336
*hsa-miR-26b**	0.082	−0.131	0.375	0.114
hsa-miR-26b	−0.024	0.024	−0.115	0.367
*hsa-miR-27a**	−0.027	−0.220	0.338	0.153
hsa-miR-27a	−0.081	0.151	0.376	0.414
*hsa-miR-27b**	−0.079	−0.130	0.756	0.027
hsa-miR-27b	−0.074	0.227	0.330	0.514
hsa-miR-28-3p	−0.114	−0.221	−0.164	0.146
hsa-miR-28	−0.120	−0.187	0.245	0.067
hsa-miR-296	−0.114	0.207	−0.397	0.756
*hsa-miR-29a**	−0.054	−0.524	0.511	−0.266
hsa-miR-29a	0.292	0.414	1.205	0.441
hsa-miR-29b	0.120	0.391	1.290	0.761
*hsa-miR-29c**	0.119	−0.226	0.207	−0.057
hsa-miR-29c	−0.166	0.085	−0.067	0.671
hsa-miR-301	0.028	0.035	0.241	0.084
hsa-miR-301b	−0.105	0.141	0.492	0.312
hsa-miR-30a-3p	0.300	−0.599	−0.900	−0.349
hsa-miR-30a-5p	0.254	−0.368	−0.345	0.221
hsa-miR-30b	−0.129	−0.103	−0.399	0.371
hsa-miR-30c	−0.005	−0.013	−0.364	0.220
*hsa-miR-30d**	0.011	−0.322	−0.010	0.255
hsa-miR-30d	0.283	−0.406	−0.138	0.155
hsa-miR-30e-3p	0.139	−0.532	−0.413	−0.190
hsa-miR-30e	0.120	−0.367	−0.194	0.070
hsa-miR-31	−0.183	0.077	−0.961	−0.117
hsa-miR-32	0.017	0.297	−0.142	0.299
hsa-miR-320	−0.119	−0.229	−0.331	−0.101
hsa-miR-324-3p	0.024	0.003	−0.348	0.121
hsa-miR-324-5p	−0.038	0.256	0.109	0.583
hsa-miR-328	0.270	−0.074	−0.150	−0.043
hsa-miR-331	0.094	0.230	−0.152	0.418
*hsa-miR-335**	−0.246	−0.405	−0.215	0.413
hsa-miR-335	−0.098	−0.256	0.065	0.143
hsa-miR-339-3p	−0.094	−0.140	−0.094	0.037
hsa-miR-339-5p	−0.070	0.592	1.144	1.286
*hsa-miR-33a**	−0.059	−0.031	−0.097	0.062
*hsa-miR-340**	−0.080	−0.299	0.439	0.018
hsa-miR-340	−0.068	0.209	0.793	0.139
hsa-miR-342-3p	−0.021	0.043	0.754	−0.007
hsa-miR-345	−0.110	0.214	0.626	0.297
*hsa-miR-34a**	−0.044	−0.492	0.141	−0.140
hsa-miR-34a	−0.090	−0.132	0.000	0.295
hsa-miR-34c	0.746	−0.396	3.306	0.526
hsa-miR-361	0.020	0.362	0.272	0.389
hsa-miR-362-3p	0.064	0.079	0.143	0.310
hsa-miR-362	0.006	0.136	0.016	0.076
hsa-miR-365	−0.044	−0.564	−1.684	−0.107
hsa-miR-374	−0.017	−0.035	−0.177	0.154
hsa-miR-374-5p	0.025	0.145	−0.151	0.427
hsa-miR-375	−0.032	−0.363	−4.953	0.073
hsa-miR-376c	0.455	−0.335	0.399	−0.088
hsa-miR-378	−0.115	−0.311	−0.219	0.220

(Continued)

TABLE E3. *(Continued)*

Gene symbol	Healthy control subjects	Patients with chronic esophagitis	Patients with EoE	Fluticasone responders
hsa-miR-378	0.011	−0.378	0.025	0.124
hsa-miR-380-5p	−0.109	−0.638	0.067	−0.462
hsa-miR-411	0.028	−0.413	−0.433	−0.746
hsa-miR-422a	−0.006	0.030	0.210	−0.079
hsa-miR-423-5p	−0.065	−0.254	0.194	0.221
*hsa-miR-425**	−0.008	0.205	0.871	0.278
hsa-miR-425-5p	0.021	0.367	0.419	0.443
hsa-miR-429	0.041	0.266	−0.125	0.463
hsa-miR-451	−0.179	−0.586	−1.137	0.210
hsa-miR-452	0.070	0.051	−0.338	0.248
hsa-miR-454	−0.074	0.055	0.436	−0.100
hsa-miR-455-3p	−0.105	0.274	0.742	0.478
hsa-miR-455	0.084	0.246	0.605	0.535
hsa-miR-483-5p	0.751	0.744	0.759	−0.391
hsa-miR-484	0.031	−0.202	0.070	0.001
hsa-miR-491	0.013	−0.162	−0.168	0.141
hsa-miR-494	0.945	1.112	0.886	0.306
hsa-miR-495	−0.057	−0.345	−0.226	−0.848
hsa-miR-497	0.094	−0.847	−0.727	−0.440
hsa-miR-500	−0.709	−0.105	−2.617	0.970
hsa-miR-500	−0.060	0.109	0.228	0.370
hsa-miR-501	0.023	3.372	1.185	5.325
hsa-miR-502-3p	−0.003	−0.068	0.068	0.294
hsa-miR-502	−0.050	0.414	0.395	0.874
*hsa-miR-505**	0.090	−0.424	0.469	−0.065
hsa-miR-532-3p	−0.012	−0.071	−0.142	0.239
hsa-miR-532	0.036	−0.263	−0.024	−0.019
hsa-miR-545	0.024	1.117	0.560	1.007
hsa-miR-565	0.039	−0.143	0.907	0.143
hsa-miR-574-3p	0.051	−0.452	−0.657	−0.234
hsa-miR-576-3p	−0.150	−0.269	−0.008	0.064
hsa-miR-579	−0.015	0.073	−0.291	0.445
hsa-miR-590-5p	0.009	−0.127	0.056	0.016
hsa-miR-592	−0.135	0.816	1.663	0.054
hsa-miR-597	0.244	0.582	0.668	0.774
hsa-miR-598	0.003	0.037	−0.302	0.285
*hsa-miR-625**	0.129	−0.100	0.664	0.168
hsa-miR-625	0.034	0.236	0.839	0.516
hsa-miR-628-5p	0.041	0.079	0.863	−0.103
hsa-miR-629	−0.013	−0.114	−0.200	0.226
hsa-miR-629	−0.068	−0.584	−0.378	0.187
hsa-miR-642	−0.041	0.403	1.165	1.110
hsa-miR-650	0.166	−3.439	9.602	1.714
hsa-miR-652	0.206	0.504	0.366	0.622
hsa-miR-660	−0.046	0.002	0.038	0.433
hsa-miR-661	0.329	−0.214	0.820	−0.477
hsa-miR-671-3p	0.012	0.069	0.522	0.062
hsa-miR-675	0.150	−0.208	−4.643	7.873
*hsa-miR-7-1**	−0.259	−0.202	0.257	0.229
hsa-miR-7	0.158	0.399	1.221	0.640
hsa-miR-708	0.079	−0.180	−0.563	0.407
*hsa-miR-744**	−0.005	−0.212	−0.678	0.095
hsa-miR-744	0.055	0.034	−0.335	0.107
hsa-miR-760	0.194	−0.633	−0.054	−0.896
hsa-miR-766	−2.682	−0.455	1.014	0.580
hsa-miR-768-3p	−0.005	−0.081	0.770	0.167
hsa-miR-769-5p	−0.064	−0.285	0.263	0.196
hsa-miR-801	0.084	−0.460	3.908	−0.568
hsa-miR-877	0.233	−0.078	0.571	−0.423
hsa-miR-885-5p	−0.184	0.003	−0.027	0.781

(Continued)

TABLE E3. *(Continued)*

Gene symbol	Healthy control subjects	Patients with chronic esophagitis	Patients with EoE	Fluticasone responders
hsa-miR-886-3p	−0.032	−0.099	1.583	−0.316
hsa-miR-886-5p	0.094	0.177	1.528	−0.277
hsa-miR-9	−0.123	0.018	−0.222	0.145
hsa-miR-923	0.853	0.445	−0.866	−0.802
*hsa-miR-92a-1**	−0.333	0.151	1.129	0.872
hsa-miR-92a	−0.052	0.107	0.198	0.491
*hsa-miR-93**	−0.051	0.006	0.242	0.308
hsa-miR-93	−0.008	0.004	0.385	−0.081
hsa-miR-942	−0.347	0.008	0.164	0.530
hsa-miR-944	0.007	−0.182	−0.081	0.130
hsa-miR-95	−0.051	0.229	0.301	0.565
hsa-miR-96	−0.063	−0.129	−0.525	0.195
*hsa-miR-99a**	0.158	−0.326	−0.600	0.285
hsa-miR-99a	−0.052	−0.113	−0.619	0.274
*hsa-miR-99b**	−0.088	0.298	0.204	1.290
hsa-miR-99b	0.043	−0.055	0.131	−0.018

Asterisks (*) after the name of the miRNA indicate the minor form of the miRNA derived from the passenger strand.