

Appendix 4. **Top 50 highest expressed genes in epithelial cells based on RPKM values**

Gene symbol	Description	E_RPKM	F_RPKM	E_counts	F_counts	FC*	p_value
Cryaa	Crystallin, alpha A	29,373.3	177,267.7	366,616.4	6,264,319.1	17.09	9.11E-118
RP23-81C12.3	Long intergenic non-coding RNA	11,888.5	2702.4	261,760.9	134,763.0	-1.94	1
Cryab	Crystallin, alpha B	5673.3	10,124.2	65,971.7	333,597.9	5.06	2.71E-43
mt-Nd1	NADH dehydrogenase, subunit 1	5655.6	1798.9	53,082.3	47,748.1	-1.11	0.838775756
Cryba1	Crystallin, beta A1	5622.0	155,230.3	43,420.9	3,380,176.5	77.85	1.34E-240
Crybb3	Crystallin, beta B3	4743.1	37,636.3	34,717.7	736,007.9	21.20	4.45E-135
Cryga	Crystallin, gamma A	2333.2	83,496.3	10,854.5	1,162,864.6	107.13	5.89E-270
Sparc	Secreted acidic cysteine rich glycoprotein	2257.4	809.8	39,749.7	34,033.9	-1.17	0.462853166
Slc2a1	Solute carrier family 2, member 1	1832.8	162.9	43,031.4	10,654.8	-4.04	1.67E-05
Hsp90ab1	Heat shock protein 90 kDa alpha, class B member 1	1480.7	1139.7	18,998.2	35,901.2	1.89	3.84E-05
Igfbp7	Insulin-like growth factor binding protein 7	1464.6	428.3	15,428.3	12,626.8	-1.22	0.154954147
mt-Nd2	NADH-ubiquinone oxidoreductase chain 2	1450.9	615.2	14,644.7	17,789.5	1.21	0.833748849
Eef1a1	Eukaryotic translation elongation factor 1 alpha 1	1389.1	587.5	11,489.2	12,607.2	1.10	0.754135917
Crybb1	Crystallin, beta B1	1376.6	34,662.8	11,455.5	820,406.2	71.62	5.82E-233

Htra3	HtrA serine peptidase 3	1338.6	162.0	23,197.6	6433.9	-3.61	3.93E-05
Gnb2l1	Guanine nucleotide-binding protein subunit beta-2-like 1	1293.3	670.1	14,495.1	21,652.1	1.49	0.001685952
Vim	Vimentin	1260.2	673.4	16,414.6	19,455.0	1.19	0.291463227
Cdkn1c	Cyclin-dependent kinase inhibitor 1C (P57)	1116.2	472.1	20,773.4	25,616.7	1.23	0.758028564
Clu	Clusterin	1102.0	1024.3	19,662.2	39,596.3	2.01	1.34E-09
Hspg2	Perlecan (heparan sulfate proteoglycan 2)	1048.0	135.1	42,770.9	16,579.5	-2.58	2.92E-18
Eef2	Eukaryotic translation elongation factor 2	1020.1	443.6	31,229.8	38,286.7	1.23	0.310362469
Cst3	Cystatin C	998.4	179.8	5402.0	2642.7	-2.04	1.99E-09
Gnas	GNAS complex locus	969.0	882.1	3106.4	6020.9	1.94	2.34E-07
Actb	Actin, beta, cytoplasmic	934.4	789.9	14,559.1	34,090.3	2.34	1.44E-12
mt-Nd4	NADH dehydrogenase, subunit 4	896.4	407.5	12,709.5	15,947.4	1.25	0.123277652
Cryge	Crystallin, gamma E	886.4	26,992.7	5485.1	475,263.1	86.65	3.98E-249
Rpl8	Ribosomal protein L8	859.4	377.3	7500.7	9051.8	1.21	0.198740752
Lars2	Leucyl-tRNA synthetase, mitochondrial	854.0	225.6	41,010.2	24,625.8	-1.67	1
Crybb2	Crystallin, beta B2	846.3	15,803.8	5895.8	320,666.0	54.39	2.86E-207
Rps5	Ribosomal protein S5	828.2	503.8	6372.8	10,709.7	1.68	1.35E-05
Crygb	Crystallin, gamma B	814.6	21,478.1	5314.1	412,215.4	77.57	6.08E-241
Mgarp	Mitochondria-localized glutamic acid-rich protein	791.0	897.2	8730.1	27,793.2	3.18	1.15E-22

Rps26	Ribosomal protein S26	785.0	328.4	3510.0	4089.2	1.17	0.585260433
Bsg	Basigin	780.1	186.7	9134.2	6206.6	-1.47	0.001283268
Col4a1	Collagen, type IV, alpha 1	766.7	171.9	50,353.1	31,860.8	-1.58	5.33E-05
Col4a2	Collagen, type IV, alpha 2	762.9	142.8	49,587.7	25,861.6	-1.92	1.83E-07
mt-Nd5	NADH dehydrogenase 5	715.4	346.4	12,869.3	17,581.5	1.37	0.130253405
Ywhae	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	707.7	420.3	10,286.8	15,969.1	1.55	0.126038482
Tkt	Transketolase	692.8	64.8	14,188.6	3509.2	-4.04	9.72E-37
Atp5b	ATP synthase subunit beta	686.8	648.6	8521.2	22,537.8	2.64	1.07E-16
Tmsb4x	Thymosin, beta 4, X chromosome	672.2	199.8	5237.3	3939.1	0.75	0.924508074
mt-Cytb	Cytochrome b	665.3	314.4	7763.5	9996.1	1.29	0.048860755
mt-Tl1	tRNA leucine 1	659.0	366.7	479.8	776.2	1.62	0.182538593
Crygc	Crystallin, gamma C	637.2	16,243.8	4479.6	330,158.3	73.70	2.31E-238
Cryba2	Crystallin, beta A2	636.5	10,994.4	4845.7	224,744.9	46.38	1.19E-201
Cryba4	Crystallin, beta A4	631.5	22,432.8	4819.9	498,045.9	103.3 3	2.86E-263
Cox6b1	Cytochrome c oxidase, subunit VIb polypeptide 1	595.2	532.9	2998.5	7495.4	2.50	3.26E-14
Tubb5	Tubulin, beta 5	590.4	281.7	12,280.7	13,325.3	1.09	1
Rps9	Ribosomal protein S9	582.2	217.4	4247.0	4354.3	1.03	1
Nid1	Nidogen 1	581.8	168.6	34,758.1	28,381.8	0.82	0.118796771

Genes were ranked based on the RPKM (Reads Per Kilobase per Million mapped reads) values in the epithelial cells (E) with E counts and F counts representing normalized read counts from DESeq software from the epithelial and fiber cell samples, respectively. *Fold-change (FC) calculation was based on the expression level in the fiber cells relative to the epithelial cells in normalized read counts produced by DESeq. Negative values indicate expression lower in the fiber cells compared with the epithelial cells. Genes with a p-adjusted value less than 0.05 and more than a 1.5 fold-change in normalized read counts were considered as differential expression.