

Appendix 5. Top 50 highest expressed genes in fiber cells based on the fiber RPKM values

Gene symbol	Description	F_RPKM	E_RPKM	F_counts	E_counts	FC*	p_value
Cryaa	Crystallin, alpha A	177,267.7	29,373.3	6,264,319.1	366,616.4	17.1	9.11E-118
Cryba1	Crystallin, beta A1	155,230.3	5622.0	3,380,176.5	43,420.9	77.8	1.34E-240
Cryga	Crystallin, gamma A	83,496.3	2333.2	1,162,864.6	10,854.5	107.1	5.89E-270
Crybb3	Crystallin, beta B3	37,636.3	4743.1	736,007.9	34,717.7	21.2	4.45E-135
Crybb1	Crystallin, beta B1	34,662.8	1376.6	820,406.2	11,455.5	71.6	5.82E-233
Cryge	Crystallin, gamma E	26,992.7	886.4	475,263.1	5485.1	86.6	3.98E-249
Cryba4	Crystallin, beta A4	22,432.8	631.5	498,045.9	4819.9	103.3	2.86E-263
Crygb	Crystallin, gamma B	21,478.1	814.6	412,215.4	5314.1	77.6	6.08E-241
Crygc	Crystallin, gamma C	16,243.8	637.2	330,158.3	4479.6	73.7	2.31E-238
Crybb2	Crystallin, beta B2	15,803.8	846.3	224,744.9	4845.7	46.4	1.19E-201
Crygf	Crystallin, gamma F	13,203.3	466.8	229,454.8	2870.4	79.9	5.71E-231
Crygd	Crystallin, gamma D	13,116.7	511.9	262,189.6	3440.6	76.2	2.28E-239

Cryba2	Crystallin, beta A2	10,994.4	636.5	224,744.9	4845.7	46.4	1.19E-201
Cryab	Crystallin, alpha B	10,124.2	5673.3	333,597.9	65,971.7	5.1	2.71E-43
Crygs	Crystallin, gamma S	8549.3	397.9	168,257.2	2774.1	60.7	4.97E-88
Mip	Major intrinsic protein of eye lens fiber	6559.8	321.0	282,895.0	4661.4	60.7	2.09E-215
Crygn	Crystallin, gamma N	3550.3	193.1	76,140.3	1444.9	52.7	5.43E-204
Lim2	Lens intrinsic membrane protein 2	3088.4	260.6	76,713.9	2318.6	33.1	4.57E-169
RP23-81C12.3	Long intergenic non-coding RNA	2702.4	11,888.5	134,763.0	261,760.9	-1.9	1
mt-Nd1	NADH dehydrogenase, subunit 1	1798.9	5655.6	47,748.1	53,082.3	-1.1	0.838775756
Bfsp1	Beaded filament structural protein in lens-CP94	1412.9	57.6	86,017.9	1224.2	70.3	8.77E-228
Hsp90ab1	Heat shock protein 90 kDa alpha, class B member 1	1139.7	1480.7	35,901.2	18,998.2	1.9	3.84E-05
Cd24a	CD24a antigen	1024.6	114.0	51,768.2	2050.9	25.2	5.01E-148
Clu	Clusterin	1024.3	1102.0	39,596.3	19,662.2	2.0	1.34E-09
Nupr1	Nuclear protein 1	899.2	188.4	20,755.3	1533.6	13.5	1.74E-98
Mgarp	Mitochondria-localized glutamic acid-rich protein	897.2	791.0	27,793.2	8730.1	3.2	1.15E-22
Gnas	GNAS complex locus	882.1	969.0	6020.9	3106.4	1.9	2.34E-07
Sparc	Secreted acidic cysteine rich glycoprotein	809.8	2257.4	34,033.9	39,749.7	-1.2	0.462853

							166
Actb	Actin, beta, cytoplasmic	789.9	934.4	34,090.3	14,559.1	2.3	1.44E-12
Tdrd7	Tudor domain containing 7	674.5	52.9	37,986.7	1043.1	36.4	3.84E-175
Vim	Vimentin	673.4	1260.2	19,455.0	16,414.6	1.2	0.291463227
Gnb2l1	Guanine nucleotide binding protein, beta polypeptide 2 like 1	670.1	1293.3	21,652.1	14,495.1	1.5	0.001685952
Pla2g7	Phospholipase A2, group VII	665.0	11.9	23,289.7	167.1	139.4	4.43E-277
Atp5b	ATP synthase, beta subunit	648.6	686.8	22,537.8	8521.2	2.6	1.07E-16
mt-Nd2	NADH-ubiquinone oxidoreductase chain 2	615.2	1450.9	17,789.5	14,644.7	1.2	0.833748849
Malat1	Metastasis associated lung adenocarcinoma transcript 1	609.6	194.3	60,373.1	8753.2	6.9	2.44E-08
Eef1a1	Eukaryotic translation elongation factor 1 alpha 1	587.5	1389.1	12,607.2	11,489.2	1.1	0.754135917
Cox6b1	Cytochrome c oxidase, subunit VIb polypeptide 1	532.9	595.2	7495.4	2998.5	2.5	3.26E-14
Gja3	Gap junction protein, alpha 3	526.4	245.7	22,787.6	3733.9	6.1	4.02E-51
Rps5	Ribosomal protein S5	503.8	828.2	10,709.7	6372.8	1.7	1.35E-05
Gpx1	Glutathione peroxidase 1	491.4	161.5	14,213.5	1669.3	8.5	1.11E-69
Gas5	Growth arrest specific 5	475.0	500.9	6020.9	3106.4	1.9	2.34E-07
Cdkn1c	Cyclin-dependent kinase inhibitor 1C (P57)	472.1	1116.2	25,616.7	20,773.4	1.2	0.758028564
Capns1	Calpain, small subunit 1	462.0	278.7	8349.8	2421.0	3.4	5.70E-24

Pabpc1	Poly A binding protein, cytoplasmic 1	451.8	386.5	35,058.4	10,254.3	3.4	4.50E-12
Eef2	Eukaryotic translation elongation factor 2	443.6	1020.1	38,286.7	31,229.8	1.2	0.310362 469
Igfbp7	Insulin-like growth factor binding protein 7	428.3	1464.6	12,626.8	15,428.3	-1.2	0.154954 147
Ywhae	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	420.3	707.7	15,969.1	10,286.8	1.6	0.126038 482
Meg3	Maternally expressed 3	413.4	71.9	9342.9	590.6	15.8	2.50E-41
Gja8	Gap junction protein, alpha 8	412.8	531.4	19,487.6	8882.8	2.2	2.58E-05

Genes were ranked based on the RPKM (Reads Per Kilobase per Million mapped reads) values in the fiber cells (F) with F counts and E counts representing normalized read counts from DESeq software from the fiber and epithelial cell samples, respectively. *Fold-change (FC) was based on the expression level in the fiber cells relative to the epithelial cells in normalized 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.