

Gene symbol	Peri-T/HC		Peri-T/T		T/HC	
	log2(FC)	q-values	log2(FC)	q-values	log2(FC)	q-values
Gfap	3.71	4.65E-23	2.85	5.04E-10	0.75	0.372
Noc4l	2.26	3.93E-09	2.53	6.73E-11	-0.42	0.649
Sall1	1.65	4.74E-05	1.62	7.00E-05	-0.11	0.997
Cdca7l	2.27	1.16E-04	1.36	2.20E-02	0.83	0.599
Slc22a8	1.44	3.50E-04	1.70	5.71E-03	-0.43	0.820
Lrrc61	1.56	4.65E-04	1.65	2.31E-04	-0.21	0.888
Lims2	2.77	1.07E-03	3.42	8.57E-05	-0.78	0.504
Zic2	1.57	1.16E-03	1.42	2.17E-03	0.00	1.000
Aqp4	1.67	1.59E-03	2.36	2.89E-06	-0.84	0.183
Slc16a13	1.80	3.00E-03	2.13	7.28E-04	-0.47	0.770
Tubb2b	1.20	5.83E-03	1.34	4.69E-03	-0.22	0.904
Pom121l2	-4.73	8.82E-03	-5.20	7.21E-03	0.23	1.000
Zic1	1.49	9.23E-03	1.76	2.14E-02	-0.41	0.883
Apod	1.32	1.14E-02	2.03	3.23E-05	-0.83	0.295
Plxnb3	1.22	1.21E-02	1.73	1.52E-03	-0.71	0.328
Cst3	1.65	2.16E-02	1.85	7.74E-03	-0.26	0.951
Igfbp7	1.14	2.73E-02	1.17	1.31E-02	-0.14	1.000
Gmppa	1.18	3.10E-02	1.51	3.13E-03	-0.48	0.588
Fxyd3	1.07	4.70E-02	2.01	3.98E-05	-1.05	0.177

Table 1. DEG list. Data obtained from LCM-seq were filtered to only include those results reaching q-values less than 0.05 between peritumoral tissues (Peri-T) and healthy tissues (HC) and between Peri-T and tumor (T), but not between HC and T. Genes are listed in order of decreasing q-values of Peri-T vs. HC. FC means fold change.