Supplementary

Table S1 Upregulated DEGs identified from GSE235516 and GSE268948 datasets

Gene IDs	Symbol	Description	log2 (fold change)	–log10 (P value)
23208	*SYT11*	synaptotagmin 11	1.743	18.675
51310	*SLC22A17*	solute carrier family 22 member 17	1.624	5.239
58985	*IL22RA1*	interleukin 22 receptor subunit alpha 1	1.61	2.632
6515	*SLC2A3*	solute carrier family 2 member 3	1.477	2.299
387856	*CCDC184*	coiled-coil domain containing 184	1.451	2.228
2049	*EPHB3*	EPH receptor B3	1.392	2.758
28514	*DLL1*	delta like canonical Notch ligand 1	1.313	2.419
8497	*PPFIA4*	PTPRF interacting protein alpha 4	1.249	4.276
253832	*ZDHHC20*	zinc finger DHHC-type palmitoyltransferase 20	1.231	56.531
9945	*GFPT2*	glutamine-fructose-6-phosphate transaminase 2	1.228	15.411
1293	*COL6A3*	collagen type VI alpha 3 chain	1.203	2.654
64220	*STRA6*	signaling receptor and transporter of retinol STRA6	1.182	8.847
230	*ALDOC*	aldolase, fructose-bisphosphate C	1.143	17.873
51286	*CEND1*	cell cycle exit and neuronal differentiation 1	1.129	21.218
57613	*FAM234B*	family with sequence similarity 234 member B	1.127	11.786
10148	*EBI3*	Epstein-Barr virus induced 3	1.127	2.733
114757	*CYGB*	Cytoglobin	1.122	1.912
5228	*PGF*	placental growth factor	1.08	5.096
18	*ABAT*	4-aminobutyrate aminotransferase	1.08	3.258
1958	*EGR1*	early growth response 1	1.078	13.167
80045	*GPR157*	G protein-coupled receptor 157	1.076	37.775
1.08E+08	*LOC107985317*	uncharacterized LOC107985317	1.066	1.308
4858	*NOVA2*	NOVA alternative splicing regulator 2	1.058	4.274
534	*ATP6V1G2*	ATPase H+ transporting V1 subunit G2	1.054	1.761
57333	*RCN3*	reticulocalbin 3	1.054	3.946
25789	*TMEM59L*	transmembrane protein 59 like	1.052	6.245
1.05E+08	*LOC105376033*	uncharacterized LOC105376033	1.037	1.353
1.01E+08	*MIR3614*	microRNA 3614	1.036	1.796
3398	*ID2*	inhibitor of DNA binding 2	1.032	6.079
55640	*FLVCR2*	FLVCR heme transporter 2	1.014	12.885
50509	*COL5A3*	collagen type V alpha 3 chain	2.925	9.803
7356	*SCGB1A1*	secretoglobin family 1A member 1	2.47	41.212
3897	*L1CAM*	L1 cell adhesion molecule	2.023	63.604
251	*ALPG*	alkaline phosphatase, germ cell	1.943	8.154
646960	*PRSS56*	serine protease 56	1.867	2.771

Table S1 (*continued*)

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Table S1 (*continued*)

Gene IDs	Symbol	Description	log2 (fold change)	–log10 (P value)
1.05E+08	*LOC105378009*	uncharacterized LOC105378009	1.866	3.879
5273	*SERPINB10*	serpin family B member 10	1.856	8.374
146547	*PRSS36*	serine protease 36	1.735	26.544
250	*ALPP*	alkaline phosphatase, placental	1.709	22.347
5596	*MAPK4*	mitogen-activated protein kinase 4	1.697	3.3
8817	*FGF18*	fibroblast growth factor 18	1.612	5.423
3684	*ITGAM*	integrin subunit alpha M	1.599	4.485
79919	*MAB21L4*	mab-21 like 4	1.591	3.867
404217	*CTXN1*	cortexin 1	1.567	2.926
170850	*KCNG3*	potassium voltage-gated channel modifier subfamily G member 3	1.547	1.697
404203	*SPINK6*	serine peptidase inhibitor Kazal type 6	1.534	11.712
1.08E+08	*LOC107985181*	uncharacterized LOC107985181	1.534	3.36
374918	*IGFL1*	IGF like family member 1	1.529	68.768
7447	*VSNL1*	visinin like 1	1.524	27.718
645638	*WFDC21P*	WAP four-disulfide core domain 21, pseudogene	1.516	8.817
94025	*MUC16*	mucin 16, cell surface associated	1.511	30.226
1081	*CGA*	glycoprotein hormones, alpha polypeptide	1.503	43.247
5055	*SERPINB2*	serpin family B member 2	1.503	31.767
3848	*KRT1*	keratin 1	1.498	1.605
4210	*MEFV*	MEFV innate immunity regulator, pyrin	1.481	4.359
85477	*SCIN*	scinderin	1.479	2.069
9235	*IL32*	interleukin 32	1.475	1.712
492307	*PPDPFL*	pancreatic progenitor cell differentiation and proliferation factor like	1.417	4.78
43847	*KLK14*	kallikrein related peptidase 14	1.41	1.654
1.05E+08	*MARCOL*	MARCO like	1.383	2.669
22979	*EFR3B*	EFR3 homolog B	1.343	24.451
619562	*SNORA3A*	small nucleolar RNA, H/ACA box 3A	1.342	1.503
248	*ALPI*	alkaline phosphatase, intestinal	1.319	1.334
63928	*CHP2*	calcineurin like EF-hand protein 2	1.314	4.927
5266	*PI3*	peptidase inhibitor 3	1.305	38.1
282763	*OR51B5*	olfactory receptor family 51 subfamily B member 5	1.3	2.198
8676	*STX11*	syntaxin 11	1.294	5.859
5918	*RARRES1*	retinoic acid receptor responder 1	1.293	35.959

Table S1 (*continued*)

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Table S1 (*continued*)

Gene IDs	Symbol	Description	log2 (fold change)	–log10 (P value)
340654	*LIPM*	lipase family member M	1.293	2.191
3627	*CXCL10*	C-X-C motif chemokine ligand 10	1.282	2.167
90139	*TSPAN18*	tetraspanin 18	1.263	3.999
2534	*FYN*	FYN proto-oncogene, Src family tyrosine kinase	1.26	12.517
4922	*NTS*	neurotensin	1.258	19.484
153218	*SPINK13*	serine peptidase inhibitor Kazal type 13	1.253	1.502
1.12E+08	*LOC112268457*	1.245	3.001	
1.05E+08	*HEATR6-DT*	HEATR6 divergent transcript	1.226	1.767
6317	*SERPINB3*	serpin family B member 3	1.215	40.64
6318	*SERPINB4*	serpin family B member 4	1.21	28.36
3672	*ITGA1*	integrin subunit alpha 1	1.202	18.719
84627	*ZNF469*	zinc finger protein 469	1.188	2.774
1.05E+08	*LOC105377945*	uncharacterized LOC105377945	1.175	2.363
79689	*STEAP4*	STEAP4 metalloreductase	1.168	30.44
4222	*MEOX1*	mesenchyme homeobox 1	1.133	15.294
50964	*SOST*	sclerostin	1.127	2.25
1.05E+08	*LINC02958*	long intergenic non-protein coding RNA 2958	1.127	1.318
79755	*ZNF750*	zinc finger protein 750	1.115	28.382
55824	*PAG1*	phosphoprotein membrane anchor with glycosphingolipid microdomains 1	1.107	12.989
80320	*SP6*	Sp6 transcription factor	1.098	28.808
1755	*DMBT1*	deleted in malignant brain tumors 1	1.087	38.307
28232	*SLCO3A1*	solute carrier organic anion transporter family member 3A1	1.087	11.09
11182	*SLC2A6*	solute carrier family 2 member 6	1.082	3.488
401647	*GOLGA7B*	golgin A7 family member B	1.078	3.017
118932	*ANKRD22*	ankyrin repeat domain 22	1.072	9.633
3687	*ITGAX*	integrin subunit alpha X	1.067	6.65
145788	*PIERCE2*	piercer of microtubule wall 2	1.057	3.733
57822	*GRHL3*	grainyhead like transcription factor 3	1.044	7.044
6662	*SOX9*	SRY-box transcription factor 9	1.044	14.698
79152	*FA2H*	fatty acid 2-hydroxylase	1.043	14.592
1.01E+08	*PYCARD-AS1*	PYCARD antisense RNA 1	1.033	9.348
9615	*GDA*	guanine deaminase	1.028	6.57

Table S1 (*continued*)

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Table S1 (*continued*)

Gene IDs	Symbol	Description	log2 (fold change)	–log10 (P value)
7504	*XK*	X-linked Kx blood group antigen, Kell and VPS13A binding protein	1.028	4.683
1.02E+08	*LOC101929613*	replaced by ID 283875	1.021	1.343
525	*ATP6V1B1*	ATPase H+ transporting V1 subunit B1	1.018	3.908
10267	*RAMP1*	receptor activity modifying protein 1	1.018	3.9
80274	*SCUBE1*	signal peptide, CUB domain and EGF like domain containing 1	1.013	2.598
56925	*LXN*	latexin	1.005	13.697

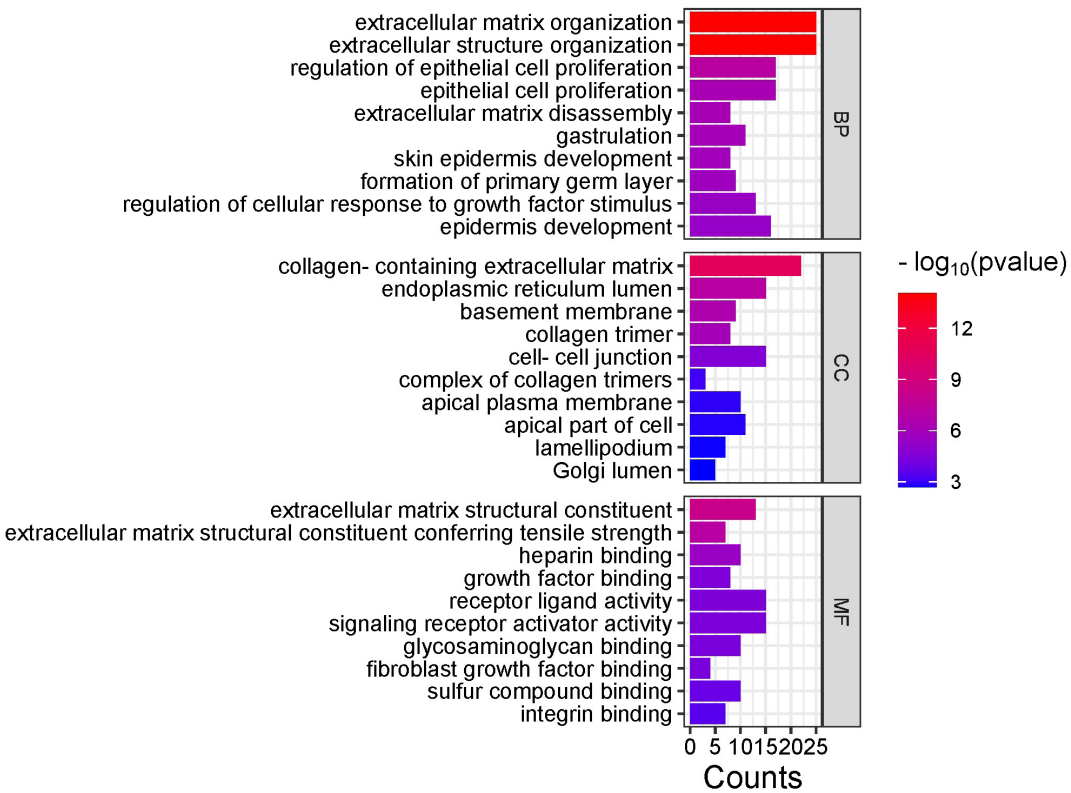

Figure S1 The plots illustrate the analysis results which are the 10 most enriched GO terms. The x-axis shows the name of the pathways while the y-axis shows the gene ratios of each pathway. The shade of grey from red to blue signifies the level of significance of enrichment from high to low.

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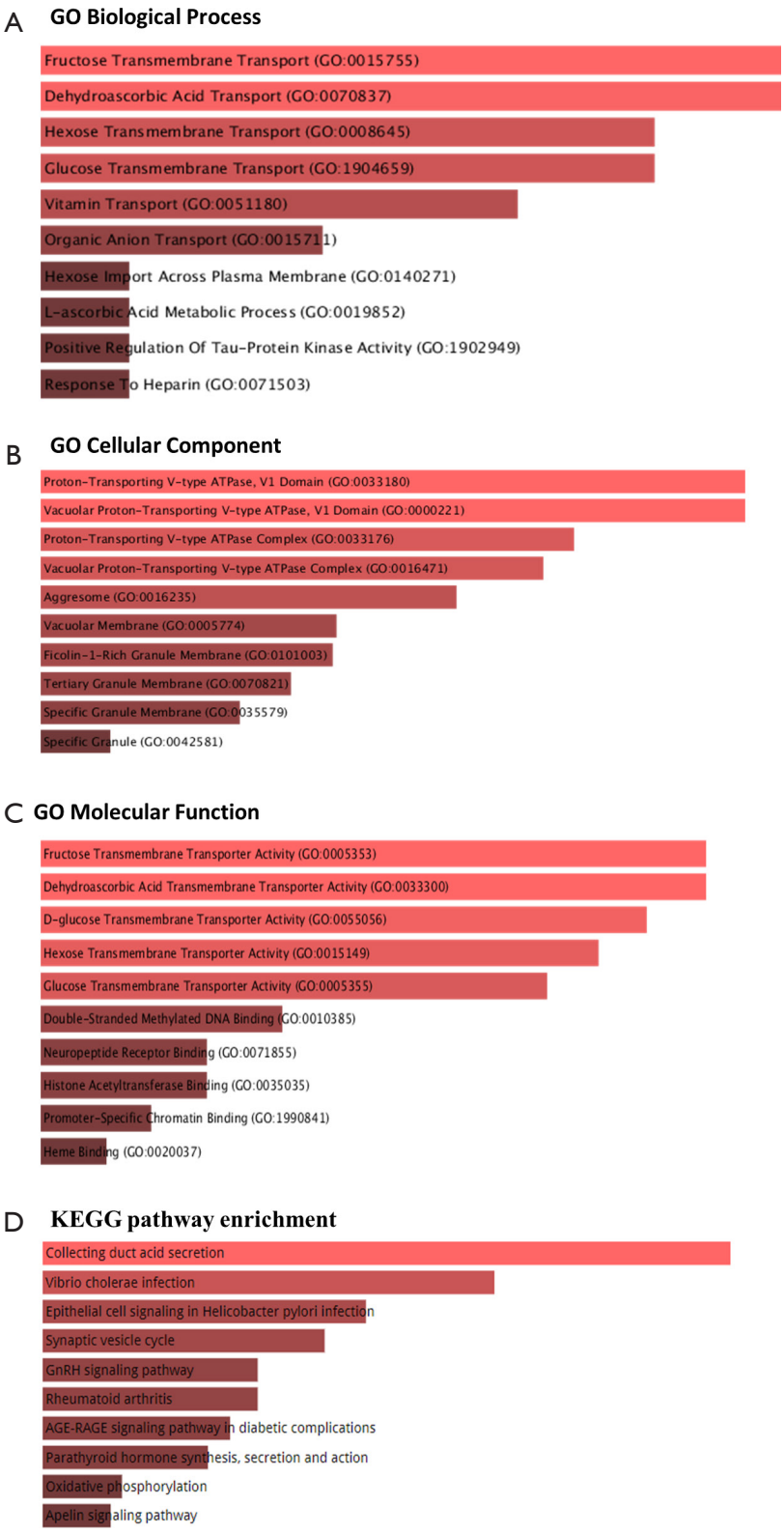

Figure S2 The GO and KEGG pathways analysis of all DE-FRGs. (A) represents the GO biological process, (B) represents the GO cellular components and (C) represents the GO molecular function. (D) represents the KEGG pathways enriched by DR-FRGs.

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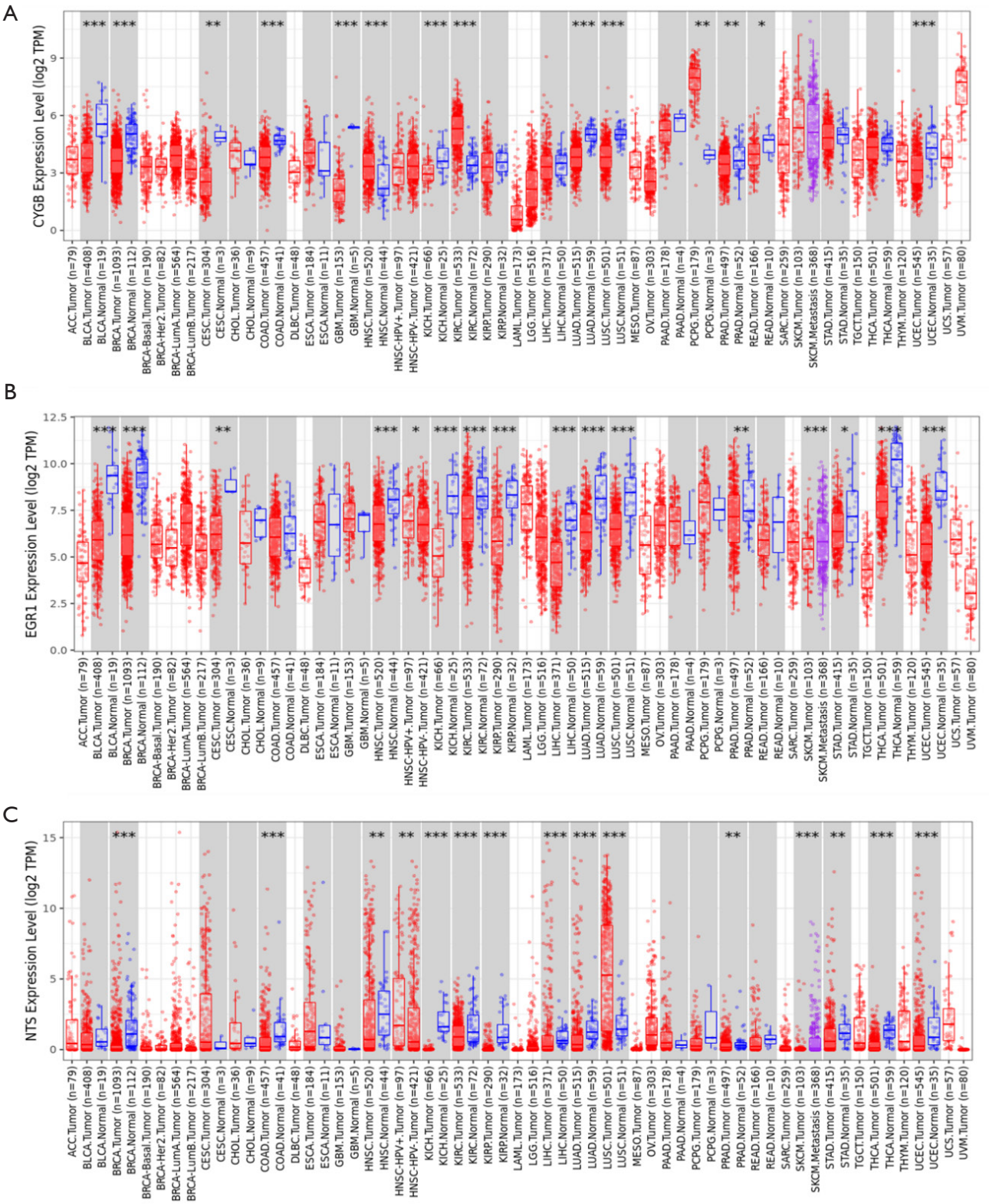

Figure S3 Expression level of normal and tumor tissues of (A) CYGB, (B) EGR1, (C) NTS. The red shows the highly expressed and blue shows low expression of DE-FRGs in various types of cancer.

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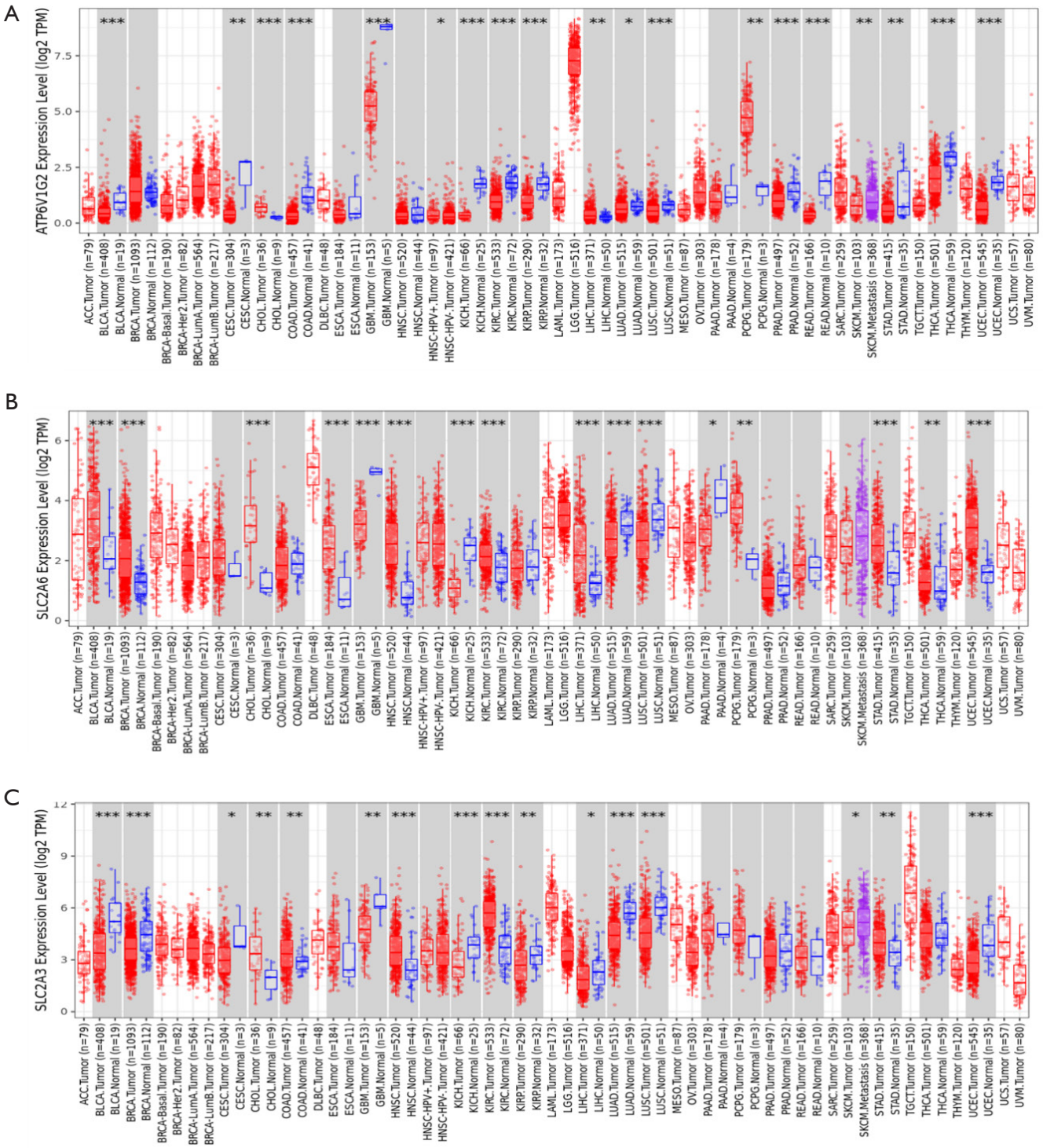

Figure S4 Expression level of normal and tumor tissues of (A) ATP6V1G2, (B) SLC2A3, and (C) SLC2A6. The red shows the highly expressed and blue shows low expression of DE-FRGs in various types of cancer.

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