

**Supp. Table 14. Overlap of stem cell gene signatures in *Cftr* KO tumors with *Apc*<sup>Min</sup> tumors.** GSEA was used to identify leading edge genes enriched in *Cftr* KO or *Apc*<sup>Min</sup> tumors. Leading edge genes enriched in *Cftr* KO that overlap with those in *Apc*<sup>Min</sup> are shown in red.

Geneset Tissue Enriched in NES	EphB2-ISC SI		Hu-LGR5-ISC colon	
	Cftr-KO tumor	Apc Min tumor	Cftr-KO tumor	Apc Min tumor
	1.78	2.37	2.23	1.71
Genes in leading edge	TUBB2B	SOAT1	ABTB2	FMNL2
	PSRC1	PXDN	AXIN2	KIF12
	CENPF	TUBB2B	EPHA4	FGFR4
	TEAD2	PSRC1	FAM64A	SCN2B
	FSTL1	TEAD2	FGFR4	DTL
	EPHB3	FSTL1	FMNL2	MPP3
	SORCS2	EPHB3	FSTL1	NPNT
	ST3GAL3	LGR5	GRAMD1A	SOX4
	CD44	SORCS2	IGFBP4	FSTL1
	CHST11	ASCL2	IL17RD	APCDD1
	PHGDH	KLHL8	KIF12	IL17RD
	ESAM	ST3GAL3	LGR5	LGR5
	ARL4C	NAV1	LIFR	EPHA4
	IGFBP4	CD44	MPP3	FAM64A
		CHST11	NPNT	RNF157
		PHGDH	PITPNC1	TNFRSF19
		ASRGL1	RNF157	PITPNC1
		TGIF2	SERTAD4	AXIN2
		LFNG	SOX4	IGFBP4
		ARL4C	TNFRSF19	
	IGFBP4	UTRN		