

Supplemental Table 3

A

Gene	Parental vs Clone1		Parental vs Clone10	
	P-value	Fold change (log2)	P-value	Fold change (log2)
<i>MAL2</i>	0.0057	-10.36	0.00728	-9.26
<i>ESRP1</i>	0.0041	-7.73	0.00303	-8.85
<i>TMEM30B</i>	0.0014	-7.54	0.00159	-7.85
<i>GRHL2</i>	0.0032	-6.08	0.00064	-6.25
<i>CDH1</i>	0.0051	-5.77	0.00395	-6.48
<i>C1orf116</i>	0.0045	-5.72	0.00275	-6.68
<i>EPCAM</i>	0.0027	-4.31	0.00203	-5.05
<i>ERBB3</i>	0.0085	-4.21	0.00454	-6.04
<i>ARHGAP8</i>	0.0039	-3.83	0.00088	-3.36
<i>AP1M2</i>	0.0062	-3.75	0.00029	-5.18
<i>ST14</i>	0.0019	-3.73	0.00168	-4.05
<i>MAPK13</i>	0.0013	-2.42	0.00393	-2.28
<i>CRB3</i>	0.0036	-1.95	0.00452	-3.05
<i>RBPMS</i>	0.0065	0.63	0.00453	0.95
<i>AXL</i>	0.0053	1.83	0.00827	1.90

B

	Differentially expressed	Non-differentially expressed
Byers EMT+	15	61
Byers EMT-	459	27441

SI Table 3. Comparison of differentially expressed genes in the COR cell lines with the EMT signature of Byers *et al.* (2013). (A) Genes from Byers *et al.* (2013) 76-gene signature that display significantly altered gene expression in COR1-1 and COR10-1 compared to the parental NCI-H1975 cell line. (B) Analysis indicating the statistically significant enrichment of the Byers *et al.* (2013) gene set signature in differentially expressed genes comparing COR and parental NCI-H1975 cell line. Enrichment was determined by chi-square test ($p < 0.0001$) for the fraction of genes differentially expressed in the Byers EMT signature (EMT+) versus the genes not in the signature (EMT-; the rest of genes profiled in the RNA-seq assay).