

S5 Table. Alterations in genes related to epithelial-to-mesenchymal transition (EMT) in the primary tumor components and metastatic samples

	TCD	TSD	MD
No. of genes	107	85	60
Top 10 enriched pathways	KEGG_Pathways in cancer KEGG_PI3K-AKT signaling pathway KEGG_Bladder cancer	KEGG_Bladder cancer KEGG_Pathways in cancer Reactome_Signal transduction Reactome_Signaling by NOTCH3	KEGG_Pathways in cancer KEGG_Bladder cancer KEGG_Melanoma KEGG_PI3K-AKT signaling pathway
	KEGG_Breast cancer	KEGG_Human papillomavirus infection	Reactome_Signal transduction
	KEGG_Focal adhesion	Reactome_Transcriptional regulation by RUNX3	Reactome_Constitutive signaling by aberrant PI3K in cancer
	Reactome_Signal transduction	Reactome_Signaling by NOTCH	KEGG_Human papillomavirus infection
	KEGG_MicroRNAs in cancer	Reactome_Signaling by TGFbeta receptor complex	KEGG_Focal adhesion
	KEGG_Human Papillomavirus infection	Reactome_Diseases of signal transduction by growth factor receptors and second messengers	KEGG_Proteoglycans in cancer
	KEGG_Melanoma	KEGG_Adherens junction	KEGG_Breast cancer
Top 5 enriched GO terms	Cell death	Anatomical structure morphogenesis	Regulation of molecular function
	Cellular developmental process	Signal transduction	Cell death
	Multicellular organism development	Cell communication	Signal transduction
	Anatomical structure morphogenesis	Cellular response to stimulus	Multicellular organism development
	Anatomical structure development	Regulation of biological process	Cell communication

A total of 1,184 EMT-related genes were analyzed. Enrichment analysis was performed on ConsensusPathDB (<http://cpdb.molgen.mpg.de/>). The enriched pathways and gene ontology terms listed have p-values < 0.001 and q-values < 0.001. EMT, epithelial-mesenchymal transition; GO, gene ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; MD, metastatic tumor; No. of genes, number of altered EMT-related genes; PI3K, phosphoinositide 3-kinase; TCD, primary carcinomatous component; TSD, primary sarcomatous component.