



**Figure S3: Pathway specific heatmaps displaying log<sub>2</sub> transcripts per million (TPM) of the top differentially expressed transcripts comparing normal tissue against metastatic tissue. A) Top 30 differentially expressed transcripts related to WNT signaling. B) Top 12 differentially expressed transcripts related to EGFR signaling. This corresponds to the total number of differentially regulated EGFR pathway-related transcripts.**