



**Supplementary Figure S1.** Association between GNAQ status and genetic indicators of tumor progression. **(A)** Comparison of mean tumor aneuploidy (measured as the % of non-diploid chromosomal arms by array CGH) versus GNAQ mutation status. **(B)** PCA analysis of 30 tumors with respect to GNAQ status (blue, wildtype; red, mutant). Illumina and Affymetrix datasets were analyzed separately, as indicated. **(C)** SAM analysis to identify genes differentially expressed based on GNAQ status. In the Affymetrix class 1 dataset, two genes (CPNE6 and SARM1) were expressed at lower levels in mutant tumors (arrows). In the Illumina class 1 dataset, one gene (UGCG) was expressed at higher levels in the mutant tumors (arrow). In the Illumina class 2 dataset, no differentially expressed genes were identified. Overall, no consistently differentially expressed genes (indicated by points located above or below the parallel diagonal lines) were identified.