## **Supplemental Note 3**

Our decision to remap the segmented array data from the two genomic array platforms enabled a GISTIC analysis of the composite collection of 486 tumors. However, this decision risked the loss of the ability to detect highly focal SCNAs or precisely identify SCNA boundaries, especially for the higher density SNP6.0 arrays. We therefore also performed a GISTIC analysis across our collection of 271 SNP6.0 samples without remapping of the segmented data, including 112 EA, 97 GC, and 62 CRC tumors. Twenty-seven significant focal amplifications were observed, as compared to 35 significant focal amplifications in the combined analysis. Twenty-five of these peaks overlapped; peaks at 8q11.1 and 2q21.2 were restricted to SNP6.0 only (Supplementary Table S6A).

Twenty-seven focal deletion peaks were observed in the SNP6.0 dataset (Supplementary Table S6B), as compared to 30 identified in the combined group. Twenty-two of these overlapped; four peaks (3q26.31, 1p13.1, 1p33, 11q25) were restricted to samples analyzed with SNP6.0 arrays. Among these SNP6-restricted peaks, two were highly significant, including LRRN3 (7q31.1) and *NAALADL2* (3p26.31), a gene whose footprint spans ~1Mb. These appear often to be affected by small deletions that are lost when the data are filtered in the combined dataset. Eight peaks were identified only in the combined analysis. One reason for the lack of significance in these peaks may be attributed to the decreased power of the CRC tumor cohort as fewer CRC's were profiled with SNP6 arrays.

Overall, this analysis of the SNP6 alone GISTIC data reveals that while there are some differences introduced by our remapping of the segmented SNP6 data to the probes

shared by the SNP6 and Styl 250K platforms, most of the biologically salient features of the analysis are preserved in the composite analysis. In many cases, the augmented sample set in the composite data provides greater power to identify significant aberrations despite the sacrifice in SCNA resolution per sample.