

Supplementary Information

Deep sequencing of early T stage colorectal cancers reveals disruption of homologous recombination repair in microsatellite stable tumours with high mutational burdens

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Table S1. Gene frequency differences amongst 69 Stage I and 12 Stage IIIA CRC specimens from TCGA COAD-READ projects.

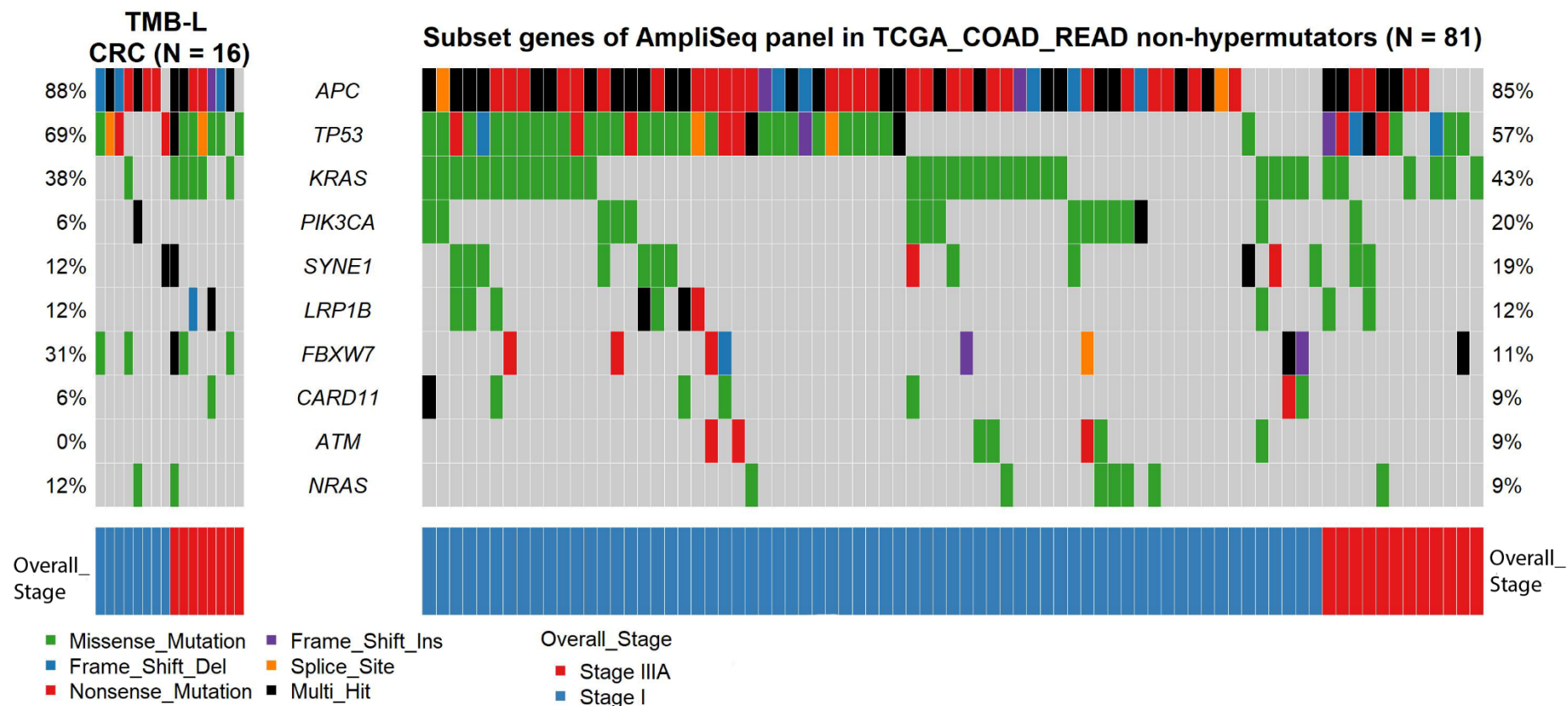
Table S2. Gene variants identified in TMB-H MSS CRC samples.

Figure S1. Oncoplot showing the most frequently mutated genes from non-hypermutators in TCGA COAD-READ project compared with TMB-low CRC in this study.

Figure S2. Lollipop plot shows distributions of *APC* variants in hypermutated and non-hypermutated TCGA COAD-READ cohorts.

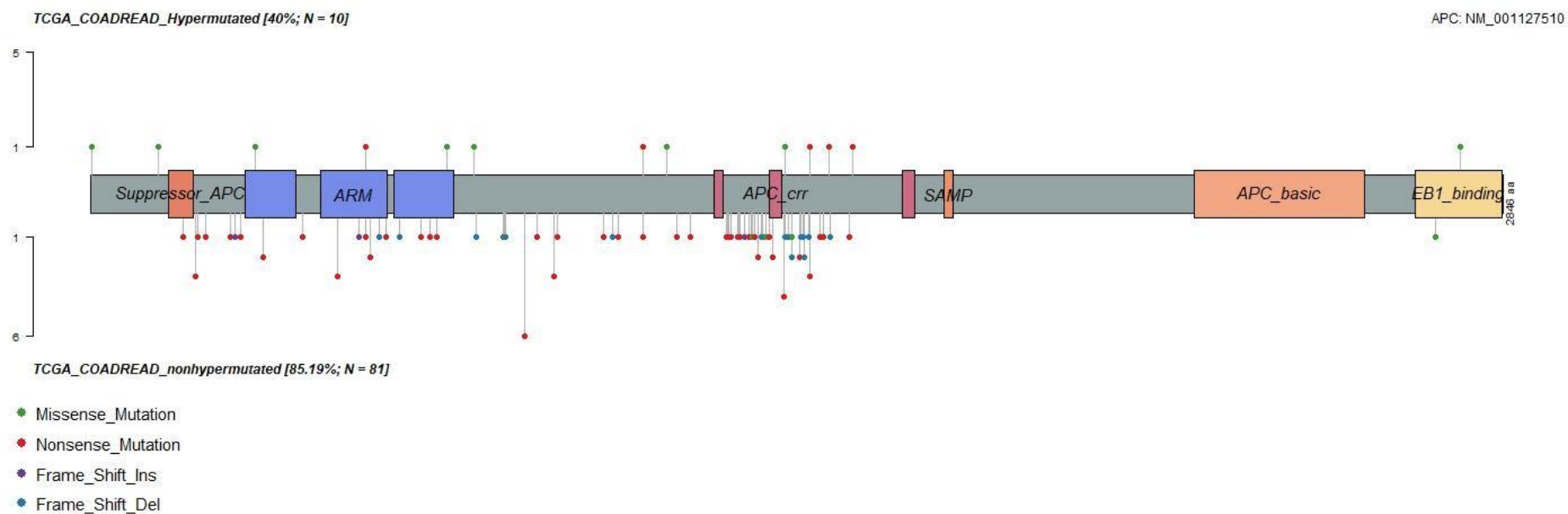
Figure S3. Oncoplot of HRR genes in the ten hypermutators of TCGA COAD-READ cohort.

Supplementary Figure S1. Oncoplot showing the most frequently mutated genes* from non-hypermutators in TCGA COAD-READ project compared with TMB-low CRC in this study.



*Considering mutation files of TCGA-COAD-READ projects were generated via WXS, we hereby focused on the subset of 409 genes on the Ion AmpliSeq™ Comprehensive Cancer Panel in order to do meaningful comparison between our data and TCGA-COAD-READ data. These figures demonstrate observations between our study and TCGA are mostly consistent.

Supplementary Figure S2. Lollipop plot shows distributions of APC variants in hypermutated and non-hypermutated TCGA COAD READ cohorts



Supplementary Figure S3. Oncoplot of HRR genes in the ten hypermutators of TCGA COAD-READ cohort

