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Supplemental information

Adaptation of a mutual exclusivity framework to identify driver mutations within oncogenic pathways

Xinjun Wang, Caroline Kostrzewa, Allison Reiner, Ronglai Shen, and Colin Begg

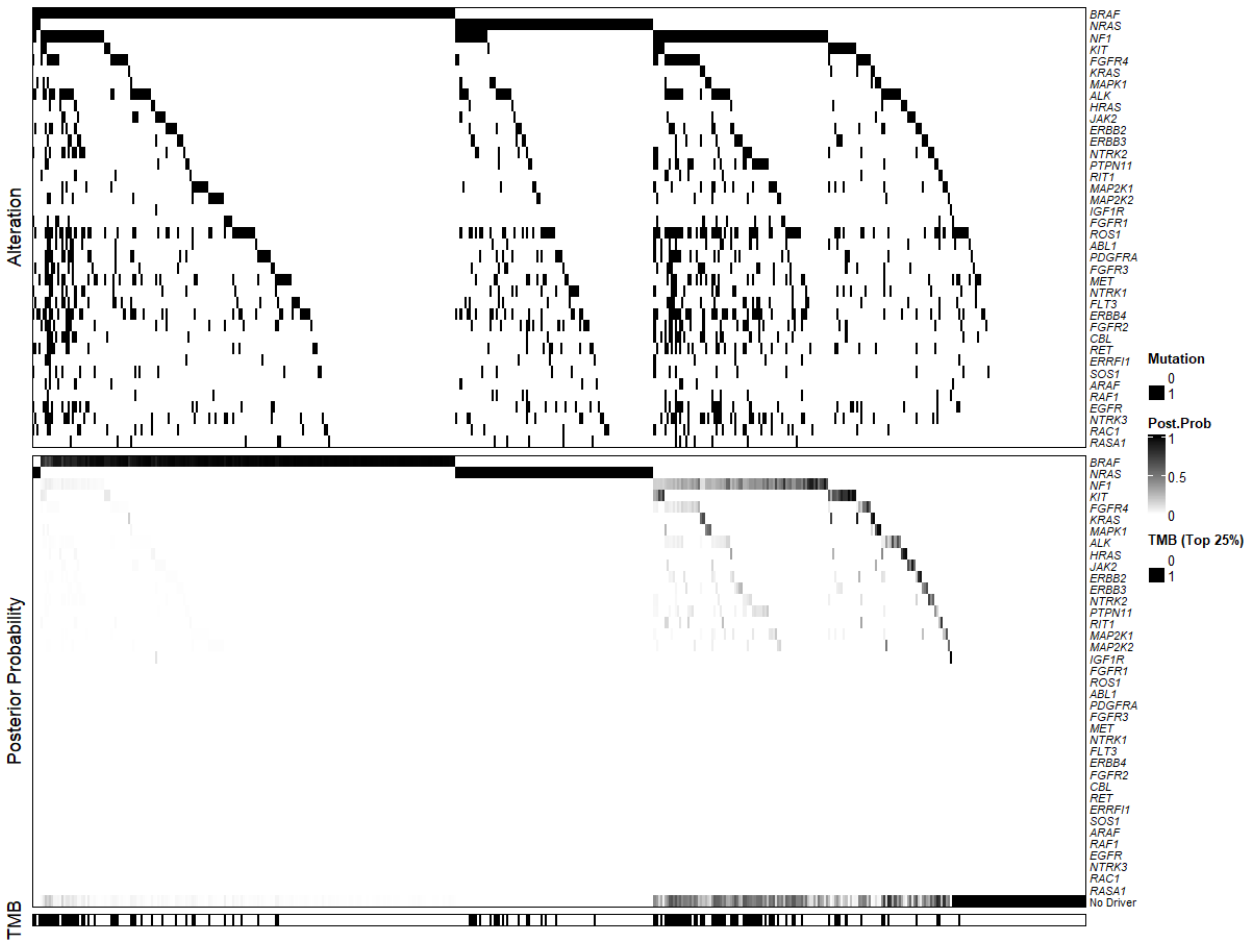

Figure S1: Illustration of the Observed Binary Mutation Status, Estimated Posterior Probability of Driver Mutation, and the Distribution of Binary Tumor Mutational Burden (TMB) for the RTK-RAS Pathway from the InterMEL Study. All 38 genes are included.

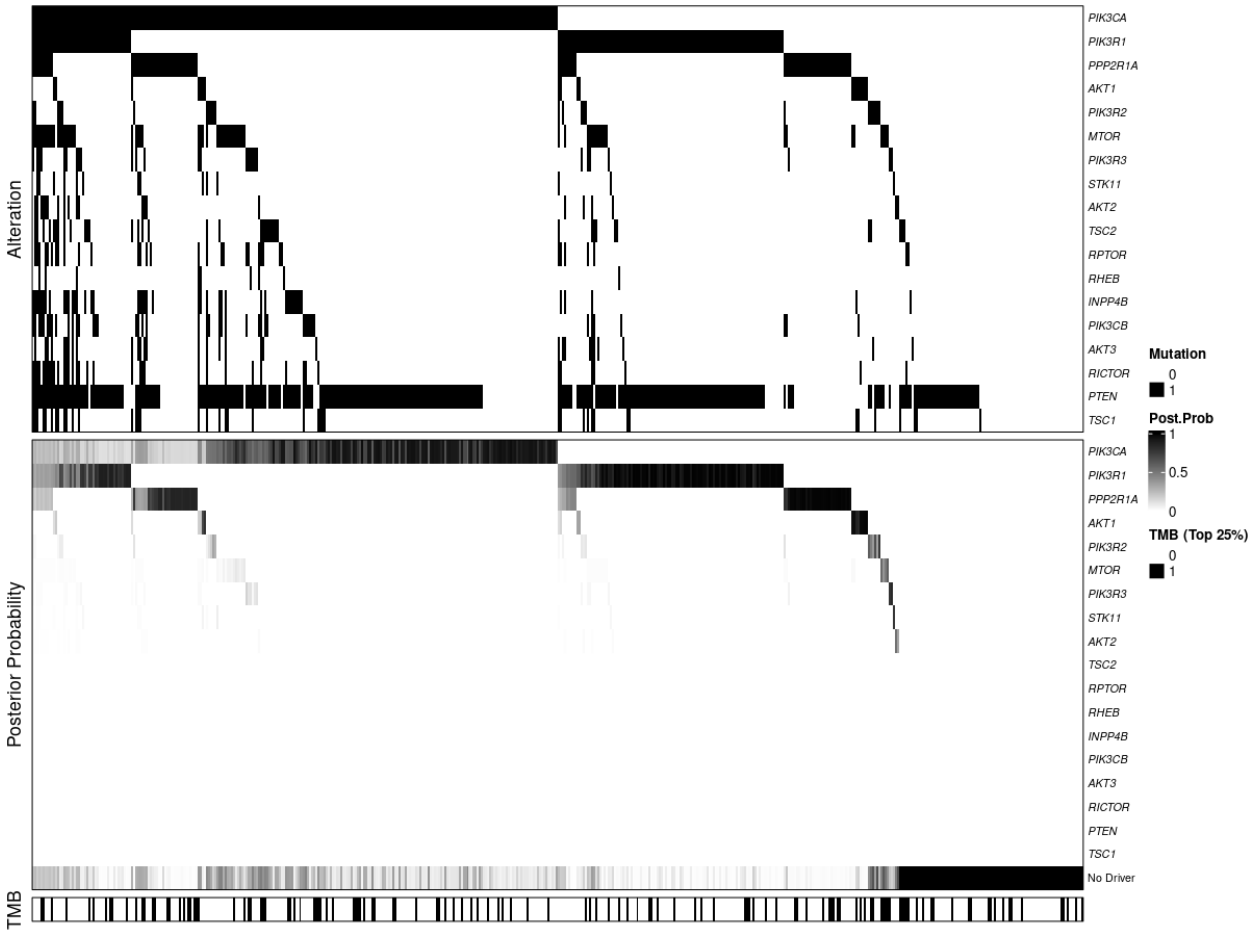

Figure S2. Illustration of the Observed Binary Mutation Status, Estimated Posterior Probability of Driver Mutation, and the Distribution of Binary Tumor Mutational Burden (TMB) for the PI3K Pathway from TCGA-UCEC Data.

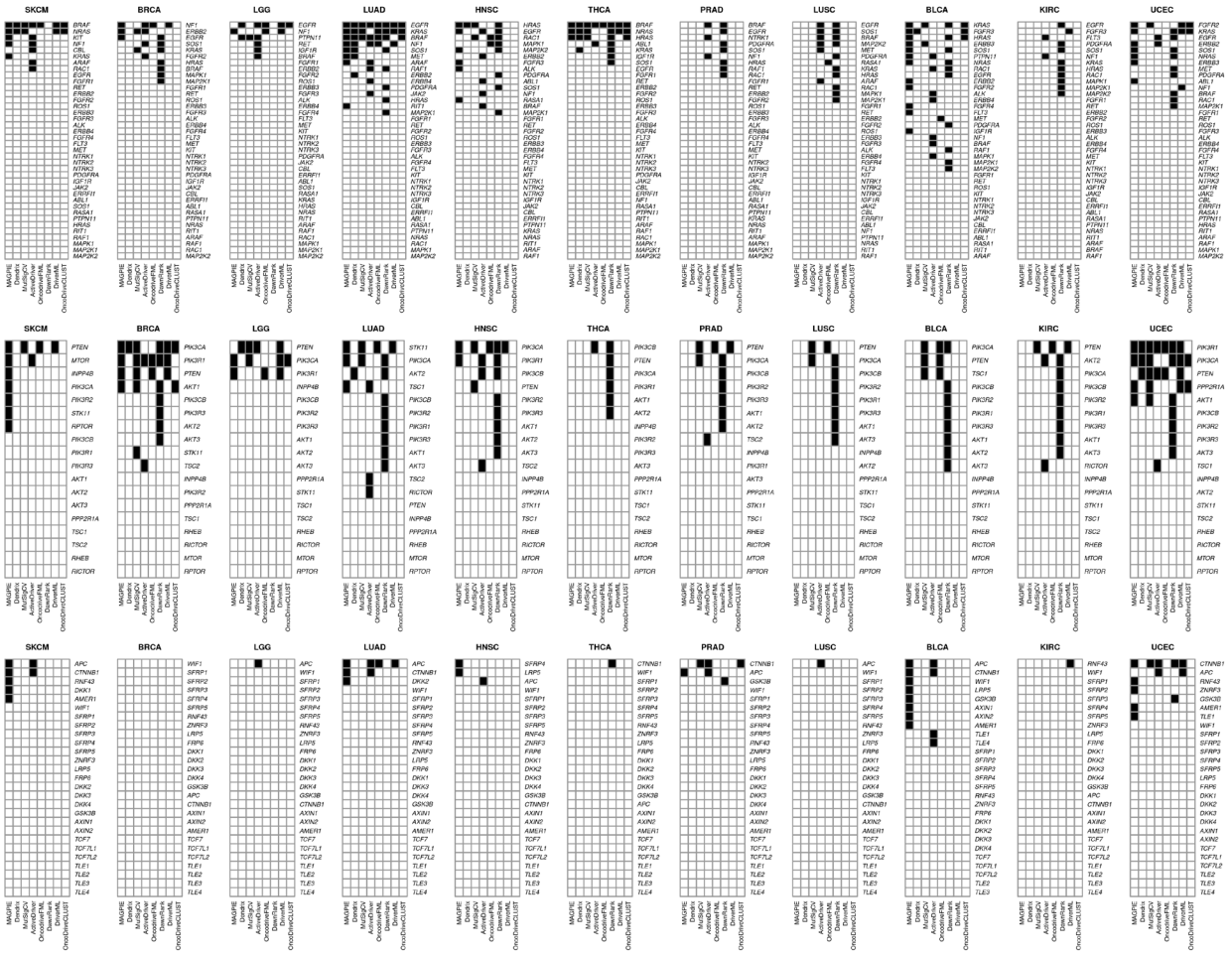

Figure S3. Driver Gene Nomination by Different Methods for All Eleven Cancer Sites. A: RTK-RAS pathway; B: PI3K pathway; C: Wnt pathway. TCGA disease codes and abbreviations: BRCA, breast cancer; LGG, lower grade glioma; UCEC, uterine corpus endometrial carcinoma; LUAD, lung adenocarcinoma; HNSC, head and neck squamous cell carcinoma; THCA, papillary thyroid carcinoma; PRAD: Prostate adenocarcinoma; LUSC, lung squamous cell carcinoma; BLCA, urothelial bladder cancer; SKCM, cutaneous melanoma; KIRC: clear cell kidney carcinoma.