Cancer, driven by the accumulation of specific somatic mutations, is a global leading cause of death. Understanding these driver mutations and their interactions in individual patients is necessary for the personalization of cancer treatment. We assessed the connections between driver mutations on five protein-protein interaction networks (PPINs). Because driver mutations have been observed to be mutually exclusive in the same pathway, we expected to see few edges (interactions) between genes containing driver mutations in individual patients. We found that all five PPINs had patients with significantly few edges between driver mutations, but all PPINs had more patients with significantly many. While these patients were only a small fraction of the total patients in the dataset, we found that by performing the analysis for all patients of a given cancer type, all five PPINs had many significant cohorts that had fewer total edges than expected by chance. This observation indicates that mutual exclusivity on PPINs occurs across multiple patient samples rather than in one.