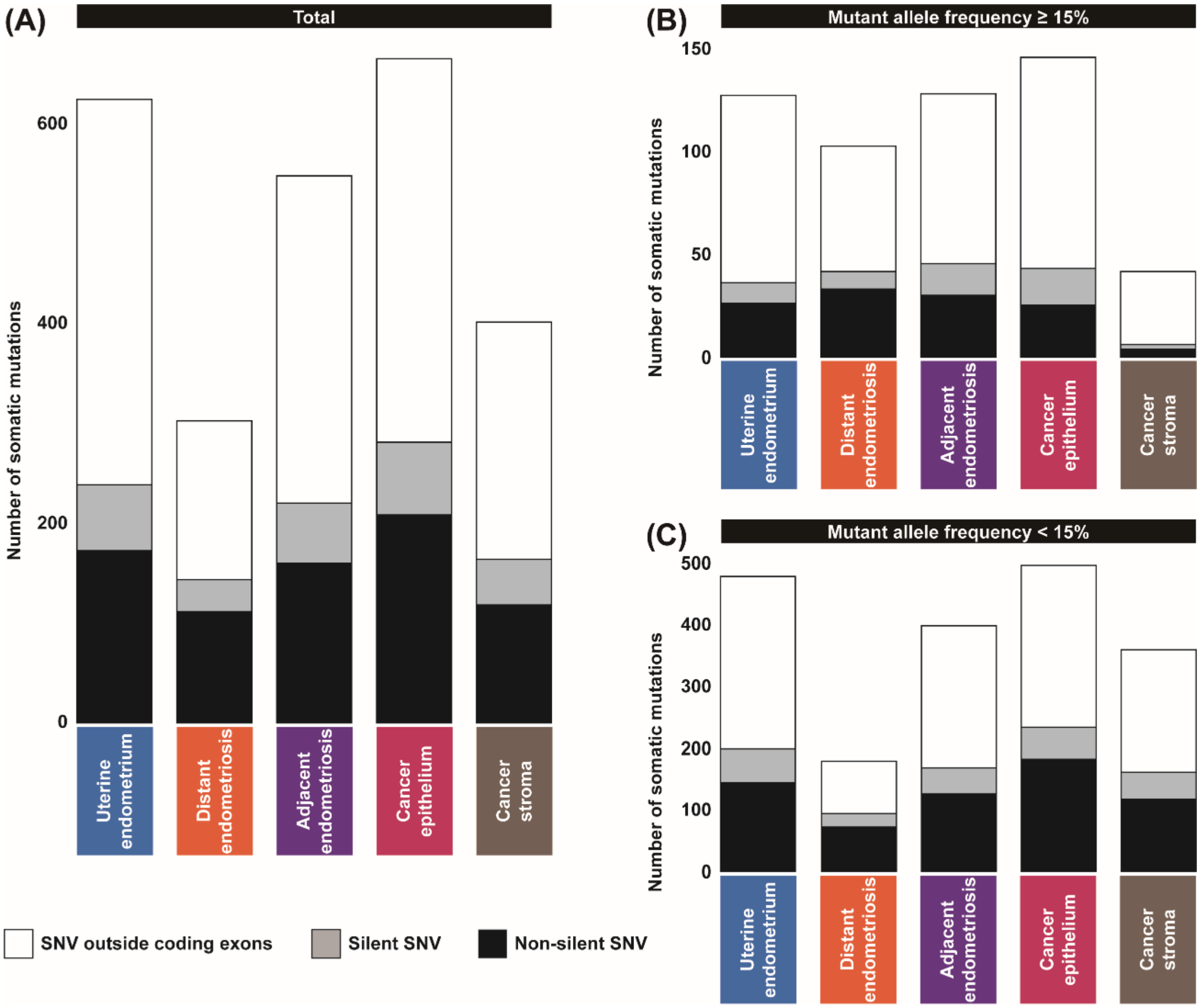

Figure S4. Number of somatic mutations in each sample subjected to whole-exome sequencing. The bar colors indicate the mutation types: black, nonsilent mutations (missense, nonsense, or splice site); gray, silent mutations (synonymous); and white, mutations outside of protein-coding exons. A, All somatic mutations. B, Somatic mutations with a high (≥0.15) MAF. C, Somatic mutations with a low (<0.15) MAF.