

Overexpressed somatic alleles are enriched in functional elements in Breast Cancer

Paula Restrepo,^{1,2+} Mercedeh Movassagh,^{2,3+} Nawaf Alomran,^{2,4+} Christian Miller,^{2,+} Muzi Li,^{2,4+} Chris Trenkov,² Yulian Manchev,² Sonali Bahl,¹ Stephanie Warnken,¹ Liam Spurr,^{1,2} Tatiyana Apanasovich,⁵ Keith Crandall,⁶ Nathan Edwards,³ and Anelia Horvath^{1,2,6,7*}

¹Department of Pharmacology and Physiology, School of Medicine and Health Sciences, The George Washington University, Washington, DC 20037, USA

²McCormick Genomics and Proteomics Center, School of Medicine and Health Sciences, The George Washington University, Washington, DC 20037, USA

³University of Massachusetts Medical School, Program in Bioinformatics and Integrative Biology, Worcester, MA 01605, USA

⁴Department of Biochemistry and Molecular and Cellular Biology, Georgetown University, School of Medicine, Washington, DC 20057, USA

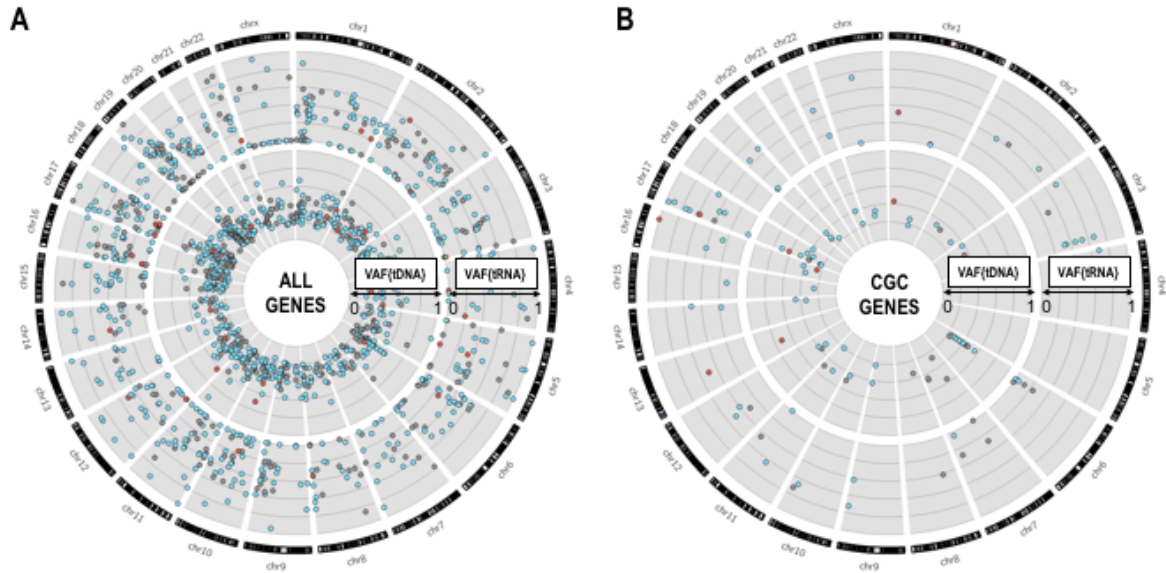
⁵Department of Statistics, The George Washington University, Washington, DC 20037, USA

⁶Department of Biochemistry and Molecular Medicine, School of Medicine and Health Sciences, The George Washington University, Washington, DC 20037, USA

⁷Computational Biology Institute, The George Washington University, Washington, DC 20037, USA

* Correspondence to: horvatha@gwu.edu

⁺these authors contributed equally to this work



Supplementary Figure 1. Circos plots of VAF{tRNA} (outer layer) and VAF{tDNA} (inner layer) of somatic mutations called in the entire dataset (A) and in the CGC genes (B) in the 72 TCGA BRCA samples. VAF{tRNA} and VAF{tDNA} (scale 0 to 1, center-outwards). The different types of nucleotide substitutions are distinguished by colors: nonsense - red, missense - blue, and synonymous - gray.



Supplementary Figure 2. Molecular function (left) and biological process (right) of genes hosting SOM-E, SOM-L and SOM variants (GO annotations).