

Supplemental Tables.

Supplemental Table S1. Allele specific expression (ASE) profile of neuroblastoma tumor samples from Pediatric Cancer Genome Project (PCGP) and Kids First Pediatric Research Program (KF).

Supplemental Table S2. For each tumor sample, we used FACETS to estimate allele-specific copy number from matched whole genome sequencing data. This table reports the sample-level statistics provided by FACETS. Columns report: sample, sample identifier; purity, estimated tumor cellular fraction; ploidy, estimated average tumor ploidy; dipLogR, the log-ratio value corresponding to the diploid copy-number state, used as a reference point for calling absolute copy number; flags, FACETS quality flags (e.g., low-purity or unreliable-estimate warnings; blank indicates no flag raised); n_seg, total number of copy-number segments called; n_loh, number of segments exhibiting loss of heterozygosity (LOH); and loh_frac, the fraction of the genome affected by LOH.

Supplemental Table S3. This table contains the segmental allele-specific copy number calls for tumor samples outputted by FACETS.

Supplemental Table S4. The table summarizes the total number of samples testable for allele-specific expression (ASE) and the number of samples exhibiting significant ASE ($FDR \leq 0.1$) for each gene. Genes were classified as neuroblastoma-specific ASE genes (`hard_filter = TRUE`) if they met all of the following criteria: (i) were testable for ASE in at least 10 neuroblastoma and adrenal gland samples, (ii) exhibited significant ASE in at least 3 neuroblastoma samples, and (iii) exhibited significant ASE in no more than 1 adrenal gland sample.

Supplemental Table S5. This table provides a comprehensive catalog of all single-nucleotide variants (SNVs) located within ± 1 Mb of transcription start sites of neuroblastoma-specific ASE genes and mapped to copy-neutral genomic regions in each sample. The table includes genomic coordinates, allelic information, and sample-level annotations for variants associated with neuroblastoma-specific ASE genes.

Supplemental Table S6. This table provides the raw prediction scores and quantile scores from AlphaGenome based variant effect predictions for SNVs located with ± 1 Mb of transcription start sites of neuroblastoma specific ASE genes within copy neutral regions.

Supplemental Table S7. For each transcription factor (TF), n_nbase is the number of NB-ASE genes with a nearby predicted TF-binding-disrupting SNV (AlphaGenome |quantile score| ≥ 0.95) used as that TF's target set; obs_mean is the observed mean GENIE3 edge weight among those genes; pval is the empirical permutation P-value (10,000 permutations, null generated by resampling from the TF's full target set); padj is the FDR-corrected P-value across all 30 TFs. Four TFs — GATA3, ZBTB33, GABPA, JUND — were significant at $\text{padj} \leq 0.1$ (Figure 4A).