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Supplemental Data

Evaluation of DNA Methylation Episignatures for Diagnosis and Phenotype Correlations in 42 Mendelian Neurodevelopmental Disorders

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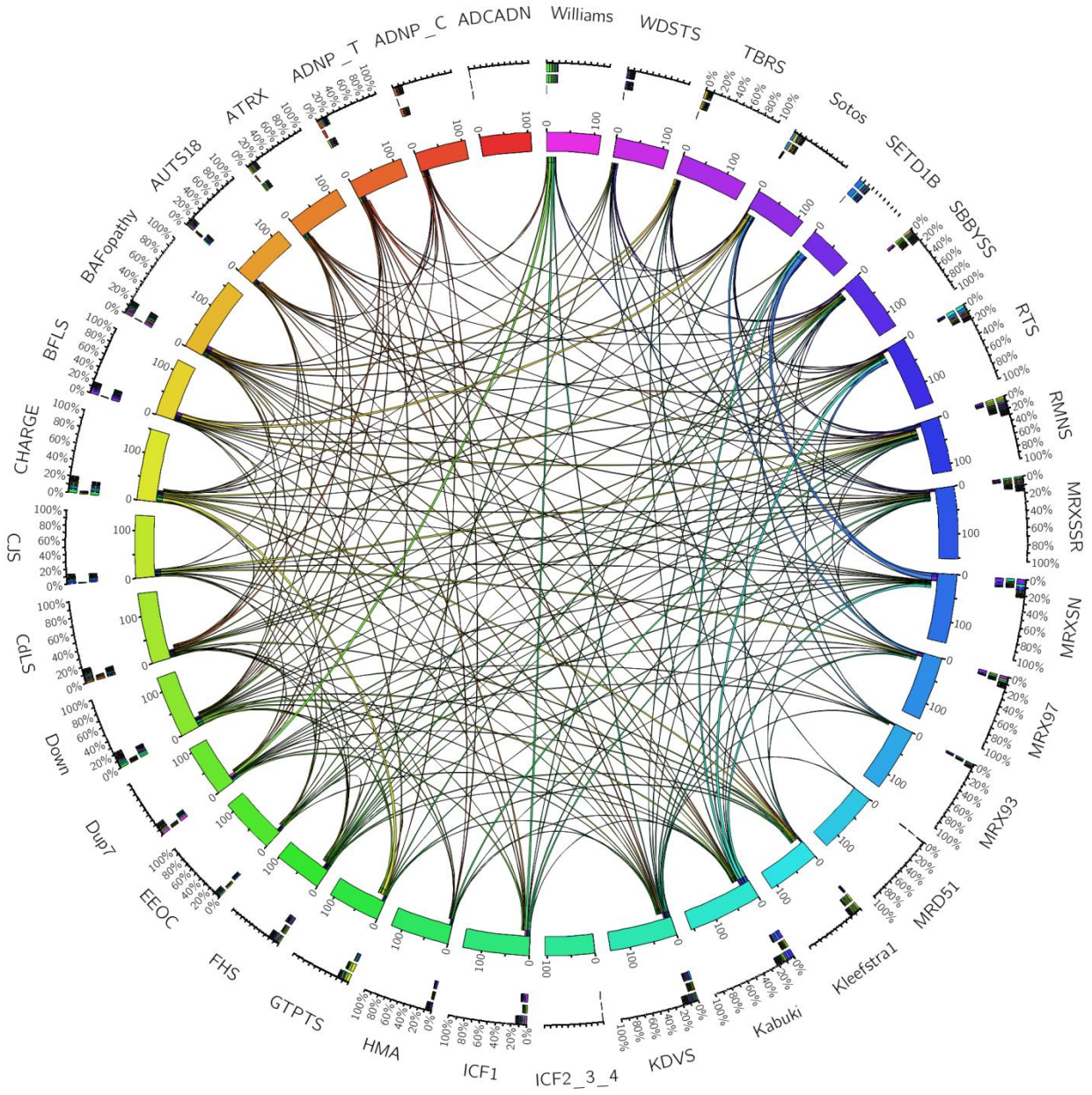

Figure S1- Co-occurrence of CpG sites between different episignatures

Circos plot showing the number of probes co-occurring between any two episignatures as demonstrated using the thickness of the connecting lines; The probe counts per episignature is scaled from 0 to 100%. The connecting lines show the percentage of probes from each signatures being shared with the others. All of the shared components are summed as stacks of bars on the right side of each episignature. As seen, only a small fraction of differentially methylated probes are common among disorders and the portion of shared probes from each episignatures with all others does not reach 5%.