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Supplemental information

Truncating *SRCAP* variants outside the Floating-Harbor syndrome locus cause a distinct neurodevelopmental disorder with a specific DNA methylation signature

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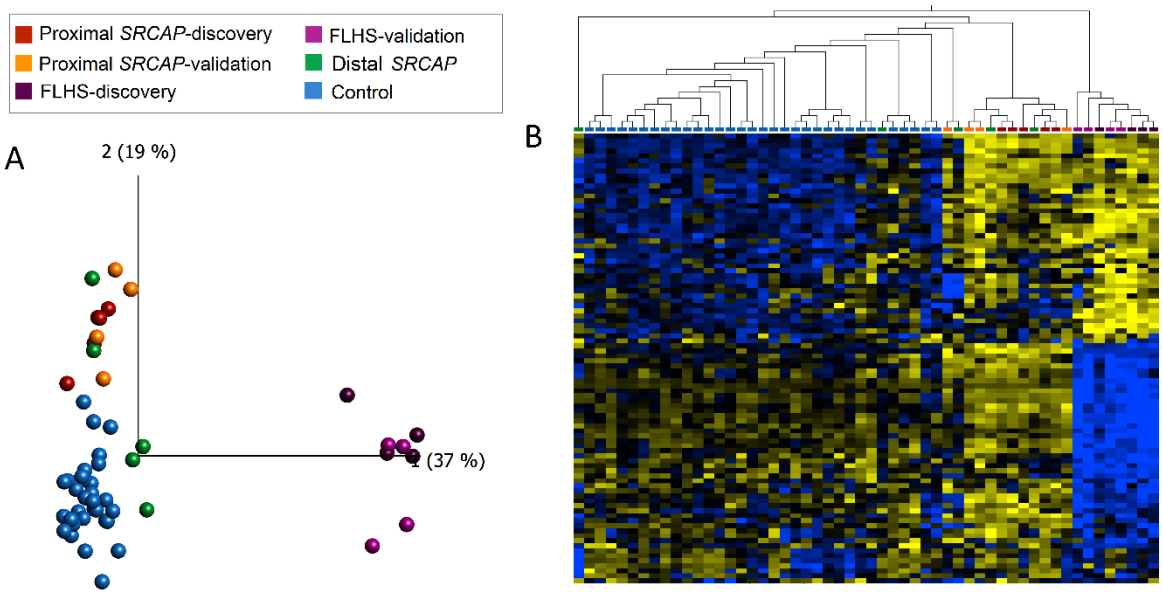

Figure S1. Clustering of *SRCAP* cohort and control samples using previous DNAm signature. All plots show the discovery, validation, and test samples used in this study. **A)** PCA using the DNAm values at n=99 CpG sites making up the FLHS DNAm signature from Hood et al., (2016) applied to the samples from the present study. Clustering of all samples is very similar to that of the FLHS signature from this study shown in Figure 1. **B)** The heatmap shows hierarchical clustering of DNAm values at the FLHS signature sites from Hood et al., (2016) for all *SRCAP* samples and discovery controls from the present study. A similar pattern of DNAm to the FLHS signature described in the present study is evident across all samples, including the intermediate, hypermethylated profile of the proximal-*SRCAP* cases. Euclidian distance metric is used for the clustering dendrogram.