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Supplemental Information

Deep whole-genome sequencing of multiple proband tissues and parental blood reveals the complex genetic etiology of congenital diaphragmatic hernias

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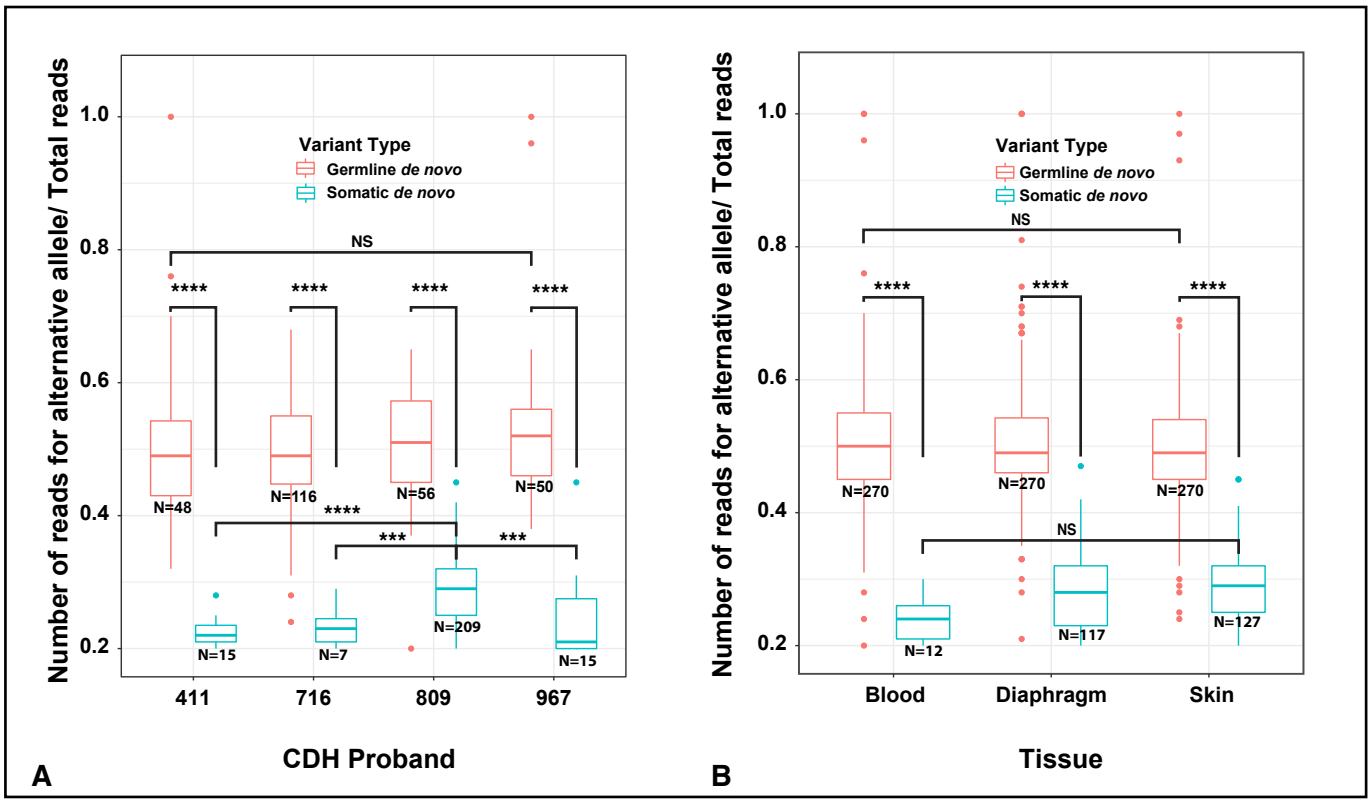

Figure S1: Alternative allele read depth of somatic *de novo* variants is significantly lower than germline *de novo* variants across CDH probands (A) and tissues (B). Box plots represent quartiles, with outliers as single points. One-way ANOVA with multiple comparisons used to test differences between somatic or germline de novo variants found across probands or tissues and unpaired t tests used to compare somatic and germline de novo variants within probands or tissues. NS- Not Significant, ***- $P < 0.001$, ****- $P < 0.0001$.

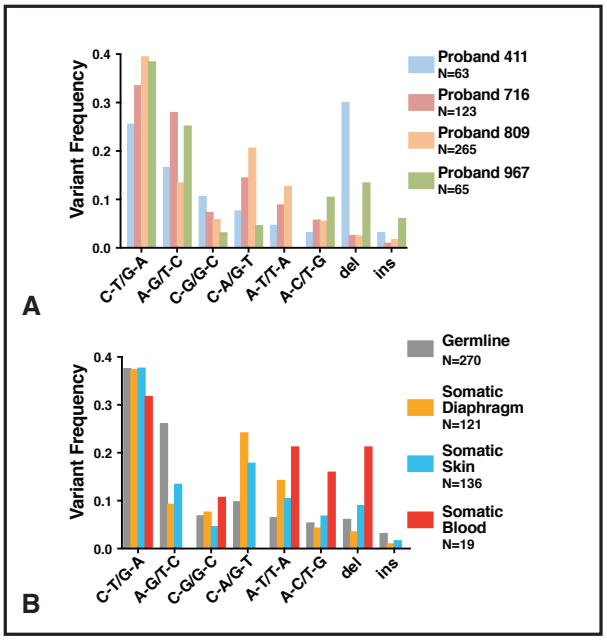

Figure S2: The spectrum of *de novo* variants varies between the different CDH probands (A), but does not vary widely between the three tissues sampled from the probands (B).