

CNV Mendelian Precision Report

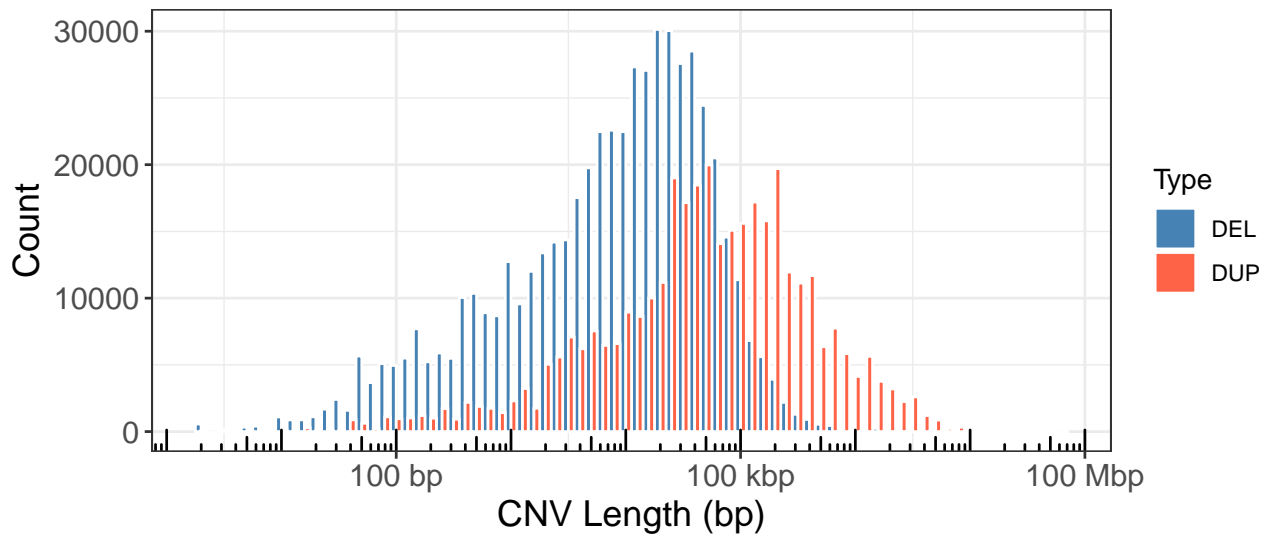
Jacquemont Lab

Dataset: SPARK_Array_GRCh37 QuantiSNP Unfilter

Date: 08/09/2025

Number of Trios or Children analyzed: 16472

CNV Length Distribution Across Samples



##	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
##	2	3916	19922	119941	64384	70336896

Distribution of CNVs by Copy Number State

##	0	1	2	3	4	5
##	7816	536145	18966	262099	78338	262

Summary of CNV Counts per Individual

##	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
##	5.00	21.00	31.00	54.86	66.00	3896.00

Mendelian precision across CNV length bins: assessing dataset quality (proportion of child CNVs observed in parents with $\geq 50\%$ reciprocal overlap) across multiple metrics.

Note: bins with fewer than 1000 CNVs were excluded from the analysis.

