

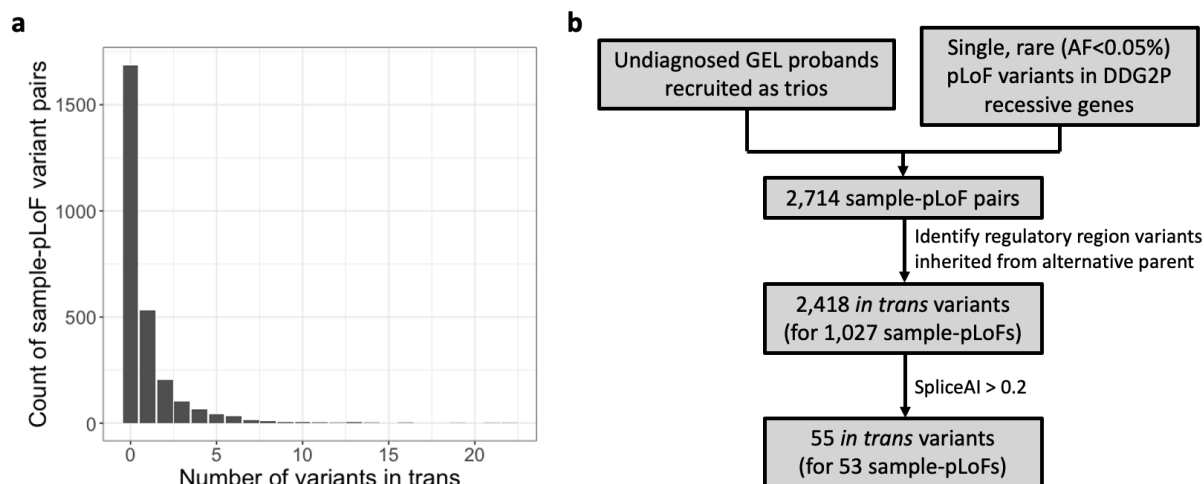


Fig S1: Identifying regulatory variants *in trans* with pLoF variants in GEL. (a) The number of variants identified in trans per sample-pLoF pair. One or more *in trans* variants were found for 37.8% of pLoF variants. (b) A flow diagram of the approach.