Supplemental Figures

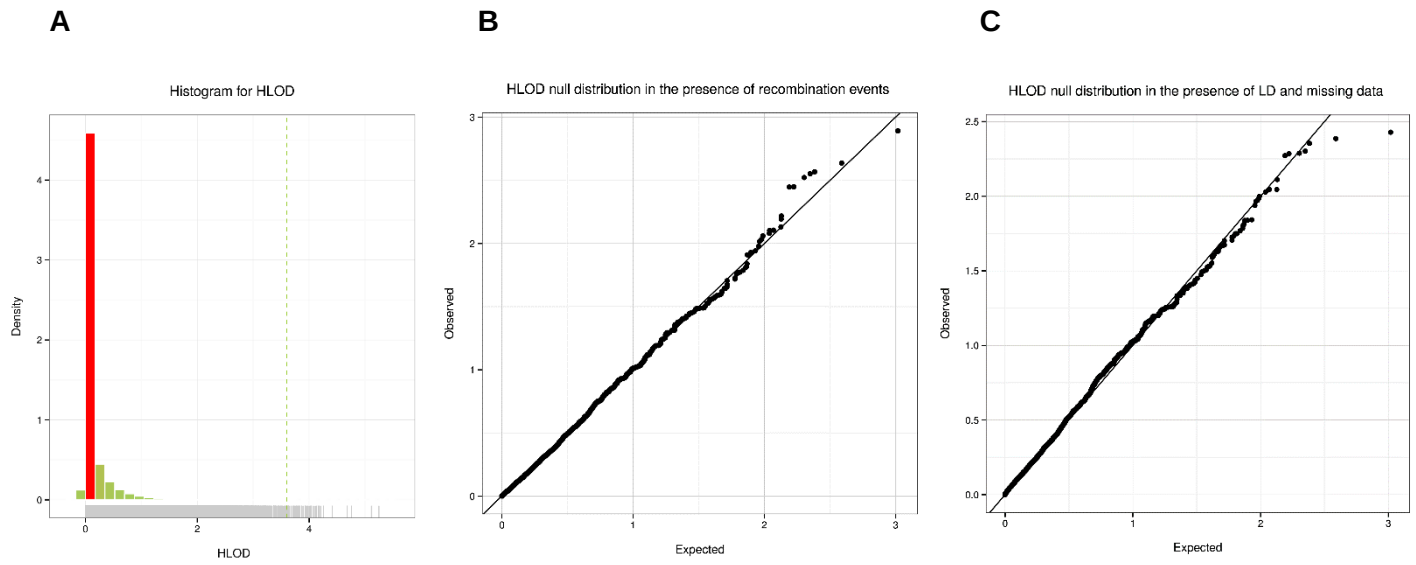

Figure S1. Distribution of CHP HLOD statistic under the null. CHP statistics are generated for gene *SLC26A4* for 20 families under compound recessive model. (A) Distribution of the HLOD statistic. The vertical dashed line represents the genome-wide significance threshold for HLOD (3.6). 56 out of the 2,000,000 HLOD statistics generated under the null exceed this threshold, leading to a numerical estimate of type I error $\hat{\alpha} = 2.8 \times 10^{-5}$. (B) Quantile-Quantile (QQ) plot for 20,000 HLOD statistics under the null, in the presence of recombination events. (C) QQ plot for 20,000 HLOD statistics under the null, in the presence of linkage disequilibrium and one parent missing genotype data in each family.

Supplemental Tables

Table S1. Power comparisons between two-point (single marker) linkage (SNV), multipoint linkage (MP) and CHP method, under compound recessive model for gene *SLC26A4*, for 20 families with different locus heterogeneity rates (see Methods of the main text).

	0%	10%	20%	30%	40%	50%	60%	70%	80%	90%	100%
SNV	0.0	0.0	0.0	0.002	0.02	0.05	0.14	0.25	0.42	0.56	0.73
MP	0.0	0.02	0.20	0.46	0.72	0.85	0.96	0.99	1.0	1.0	1.0
CHP	0.0	0.07	0.23	0.60	0.81	0.96	1.0	1.0	1.0	1.0	1.0

Web Resources

Exome Variant Server (EVS), http://evs.gs.washington.edu/EVS

Deafness Variation Database (DVD), http://deafnessvariationdatabase.com

NCBI ClinVar, https://www.ncbi.nlm.nih.gov/clinvar