Common *cis*-regulatory variation modifies the penetrance of pathogenic *SHROOM3* variants in craniofacial microsomia

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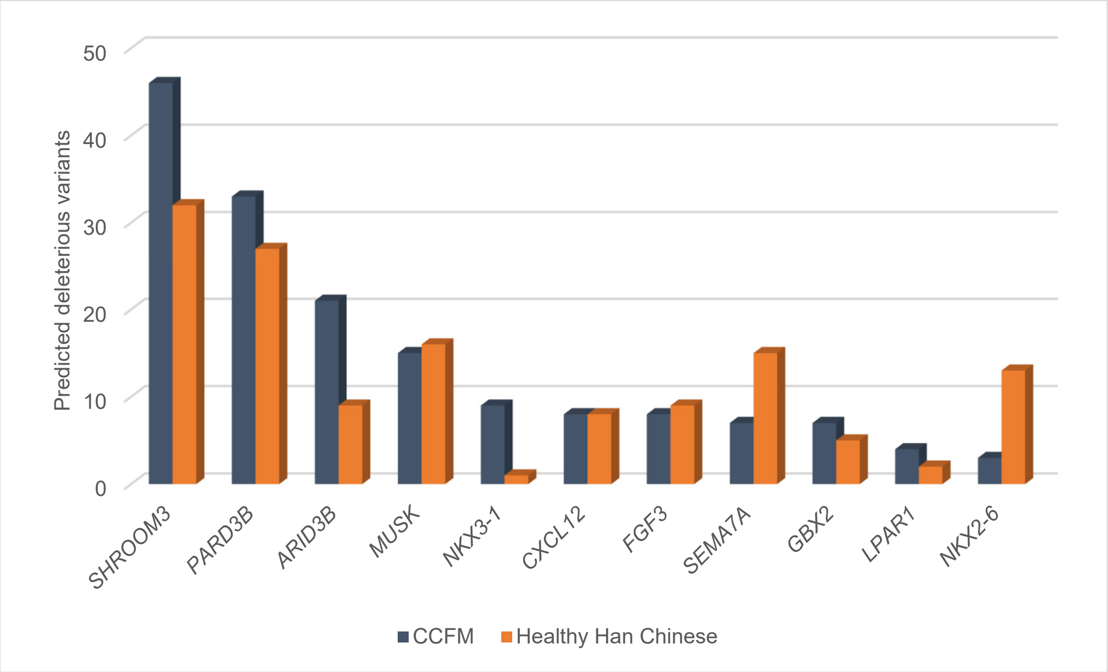

Supplementary Figure 1. Quantification of predicted deleterious variants in CFM risk genes in 2,009 Chinese CFM patients and 2,625 Han Chinese from the SG10K project. This figure presents a quantitative analysis of deleterious variants found within CFM risk genes as identified through Genome-Wide Association Studies (GWAS)[8,9]. For the purpose of this study, only those risk genes directly encompassed by GWAS signals were considered. Genes proximal to, but not directly within, GWAS signals were excluded from this analysis. CCFM represents Chinese Craniofacial Microsomia.