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Table 2. Common high-probability LoF variants in OMIM genes

Gene	rsID	Consequence	Global allele Frequency (GnomAD)	% of homozygous individuals per population (GnomAD)
<i>CLDN16</i>	rs760754693	Frameshift	0.194	AFR (0.68%) AMR (1.50%) EAS (0.05%) EUR (6.07%) SAS (3.18%)
<i>GUF1</i>	rs141526764	Splice Donor Variant	0.015	AFR (0.00%) AMR (1.35%) EAS (0.00%) EUR (0.00%) SAS (0.00%)
<i>TMEM216</i>	rs10897158	Splice Acceptor Variant	0.830	AFR (12.83%) AMR (74.35%) EAS (92.64%) EUR (72.84%) SAS (70.05%)