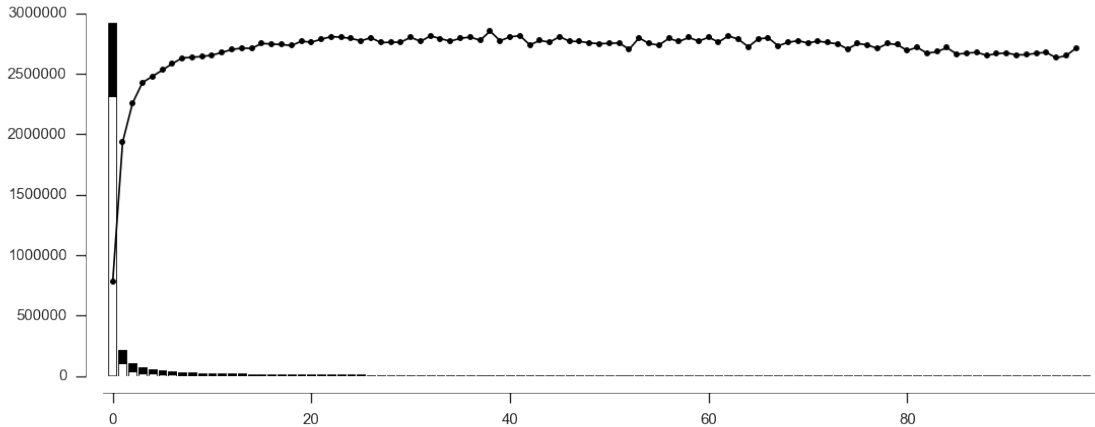


No. variants



No. samples with no coverage

Percent variants with Mendelian errors