Table S2. Identification of high-confidence common and rare variants

Variant Type	Total High Confidence	Common High Confidence	Rare High Confidence
Total SNVs	45,058	42,291	2,767
Total gene-associated SNVs	45,020	42,253	2,767
Total coding	21,587	20,688	899
Missense: benign	8,476	8,097	379
Missense: deleterious (LOF)	2,124	1,918	206
Nonsense (LOF)	105	96	9
Synonymous	10,882	10,577	305
5′UTR	1,169	1,091	78
3′UTR	1,882	1,788	94
Intron	19,324	17,957	1,367
Ts/Tv	2.61	—	—