

Supplementary Table 1. Variants numbers in different QC stages

MAF Internal	S1		S2
	No#	Freq%	
0	126400	0.221892582	
0-0.001	99512	0.174691255	84360
0.001-0.005	24629	0.043235699	18428
0.005-0.01	7717	0.013547034	5023
0.01-0.05	22547	0.039580792	8102
>0.05	259296	0.455188758	13643
	413701		129556 P=0.22

S1: SNP-set after genotyping rate, missing rate in samples and monopolymorphism removing.

S2: remove non-loss-of-functional related SNPs from S1 dataset.