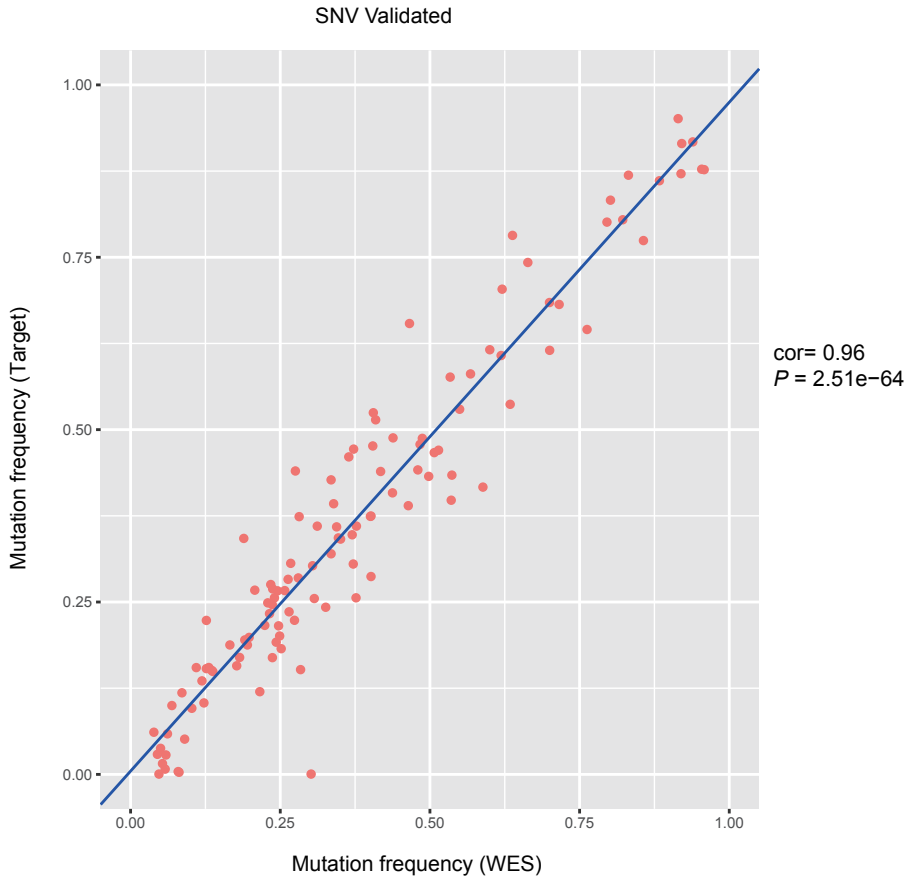
Figure S3


SNV Validated
Mutation frequency (Target)
Mutation frequency (WES)
1.00
0.75
0.50
0.25
0.00
0.00
0.25
0.50
0.75
1.00
cor= 0.96
P = 2.51e−64

Supplementary information, Figure S3 Mutation frequency validation for SNVs by ultra-deep targeted sequencing. Each dot represents a SNV. X-axis and Y-axis denote the mutation frequency of each SNVs in whole exome and ultra-deep targeted sequencing data. Mutation frequency is calculated by (supporting reads)/(total reads) in the SNV site. Pearson correlation was shown.