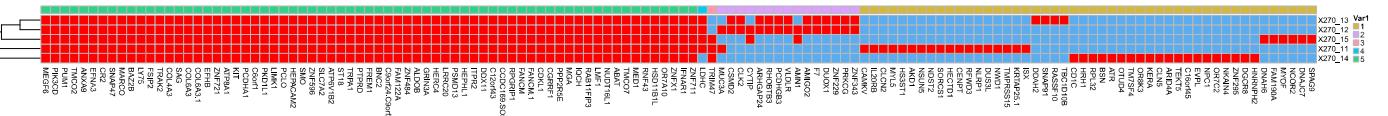


Figure S1. Mutation frequency of stopgains and synonymous SNVs across samples, and verification of 27 trunk mutations.

(A) Mutation frequency of stopgains. (B) Mutation frequency of synonymous SNVs. The colorramp shows the range of mutation frequency.

n&Var1: the number of samples involved in each mutation. (C) Verification of 27 nonsynonymous trunk mutations by PCR amplification and sequencing.

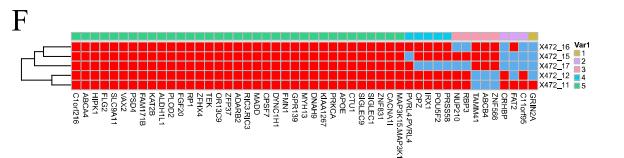
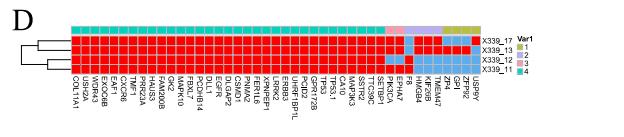
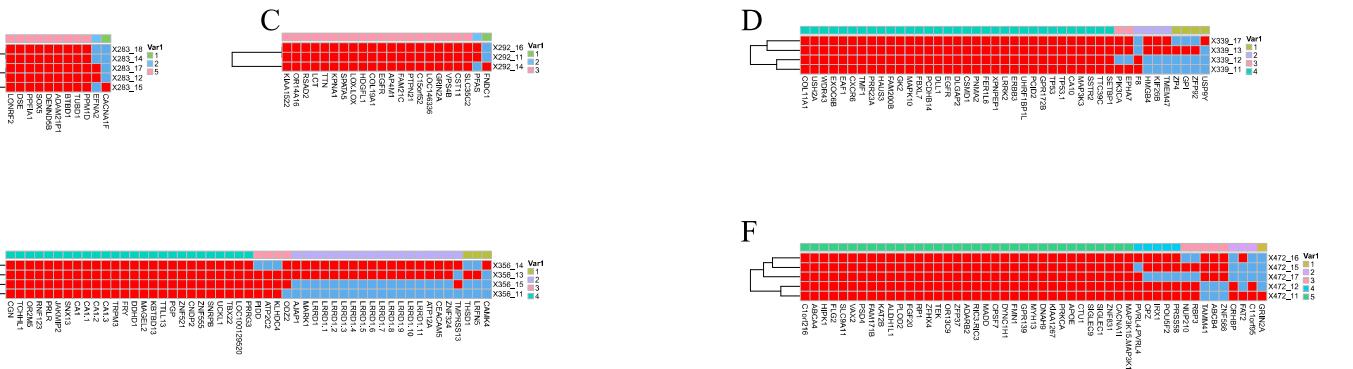
A



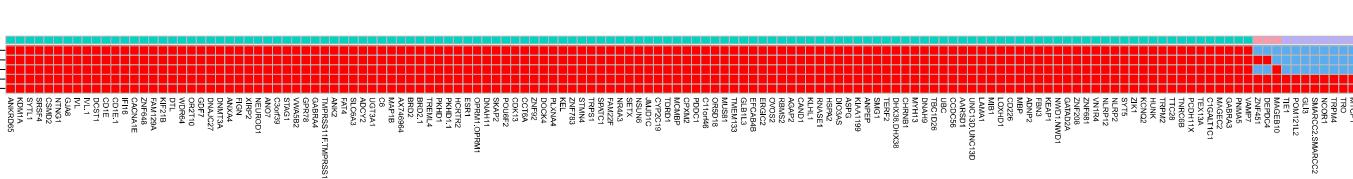
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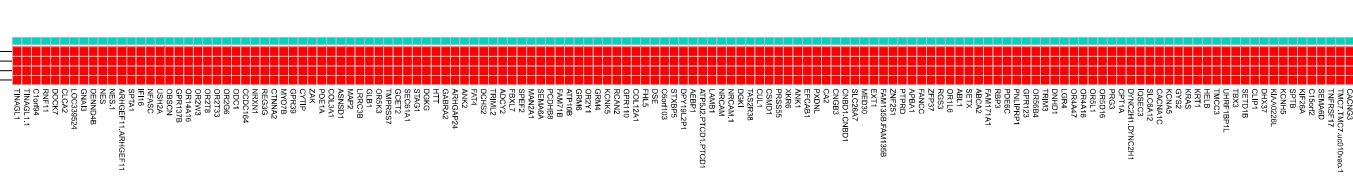
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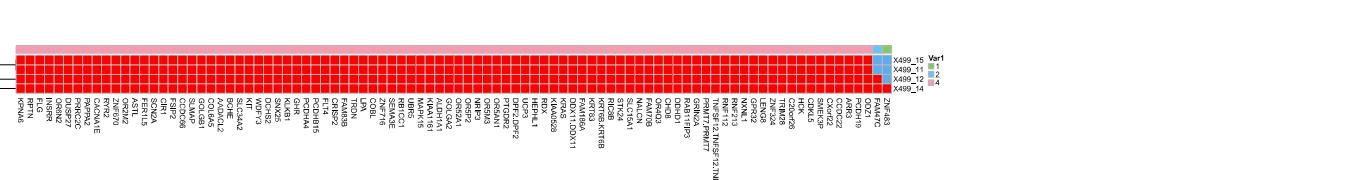
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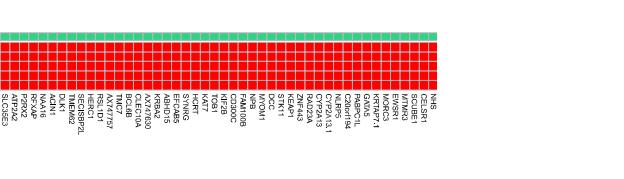
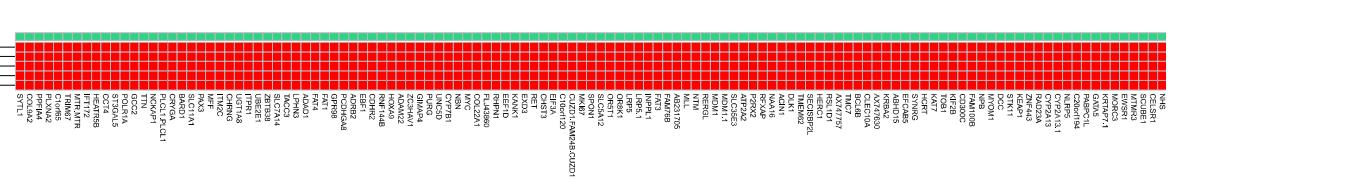
H



I



J



K

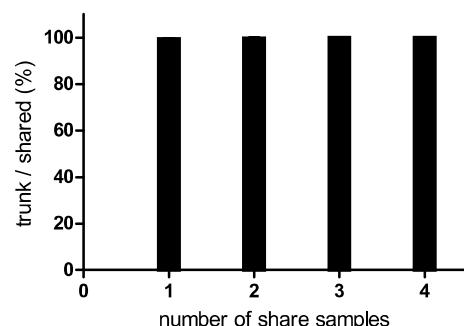
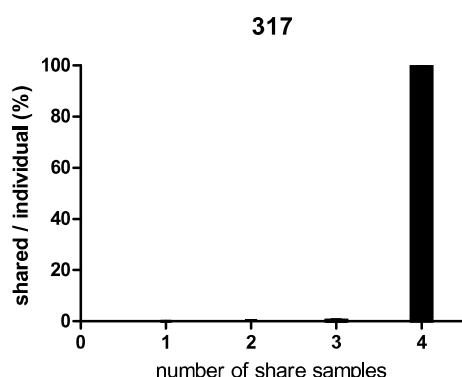
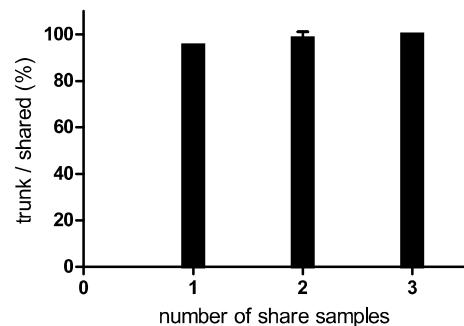
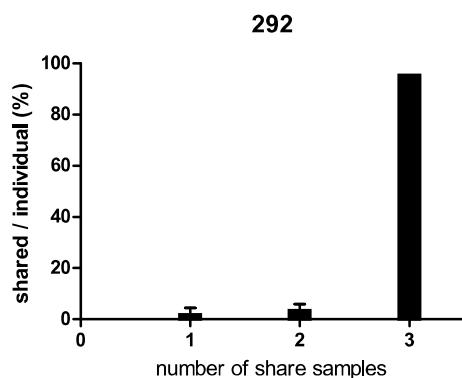
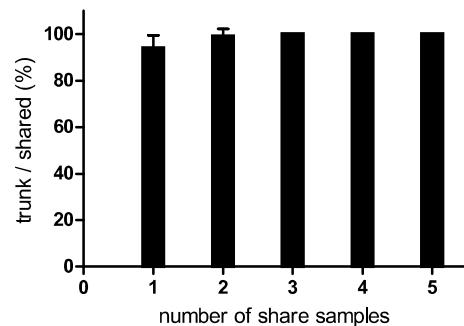
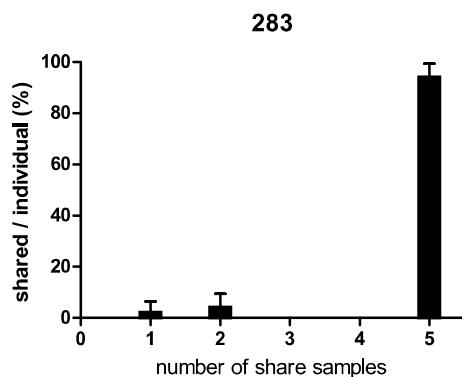
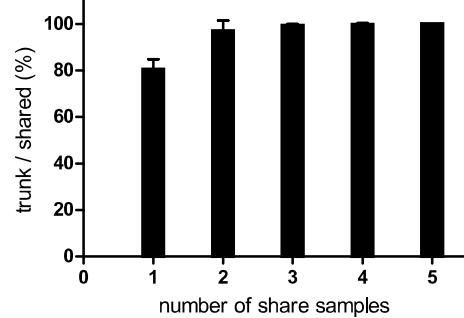
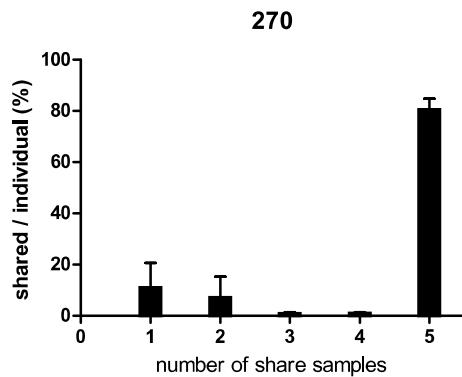


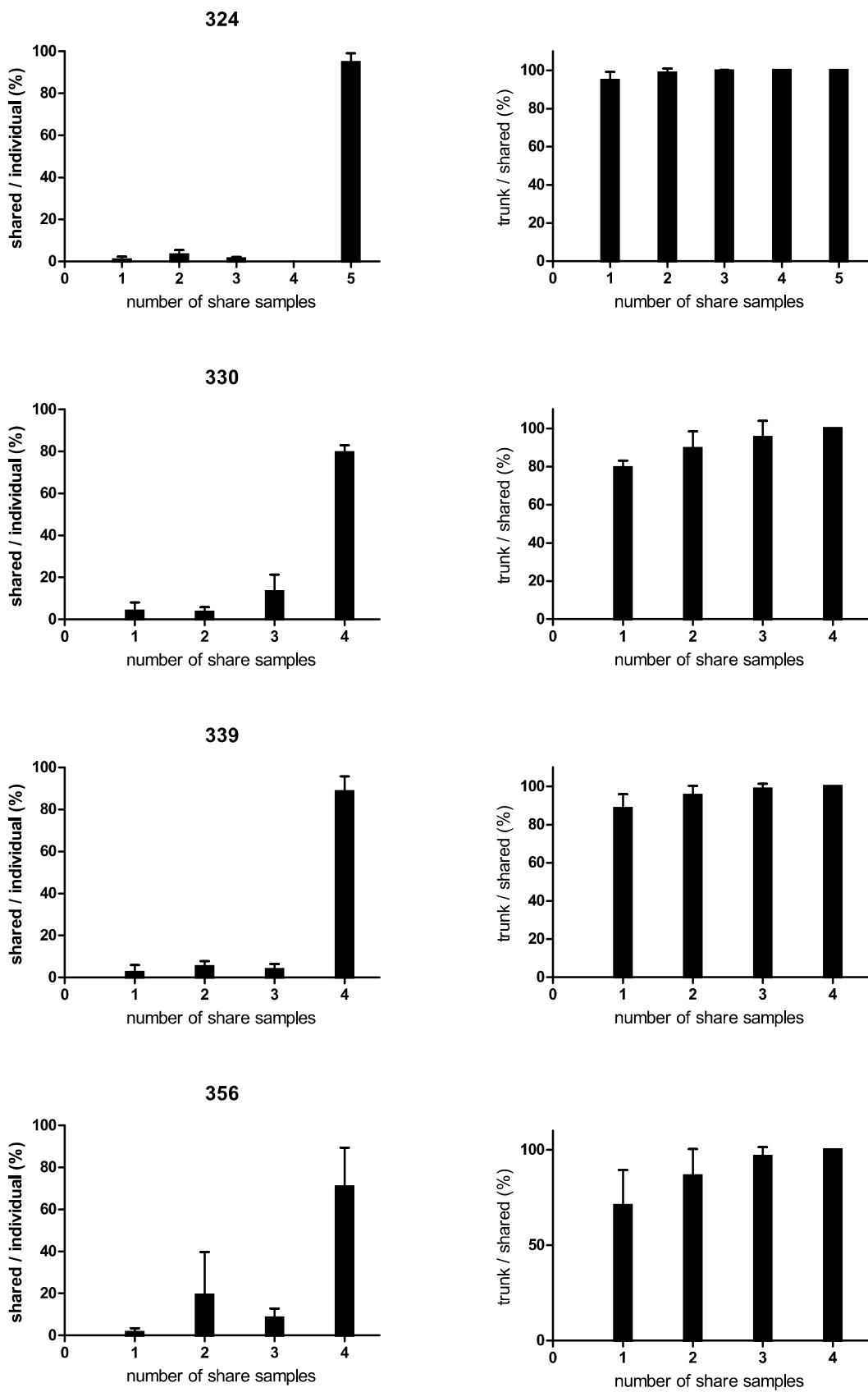
Figure S2. Distribution of exonic nonsynonymous SNVs of 11 lung adenocarcinomas across samples.

A-K: Distribution of mutations across samples from 11 lung adenocarcinomas, x(n)_(_n): sample id_region id, var1: the number of samples involved in each mutation. Samples were clustered in each tumor.

A

B





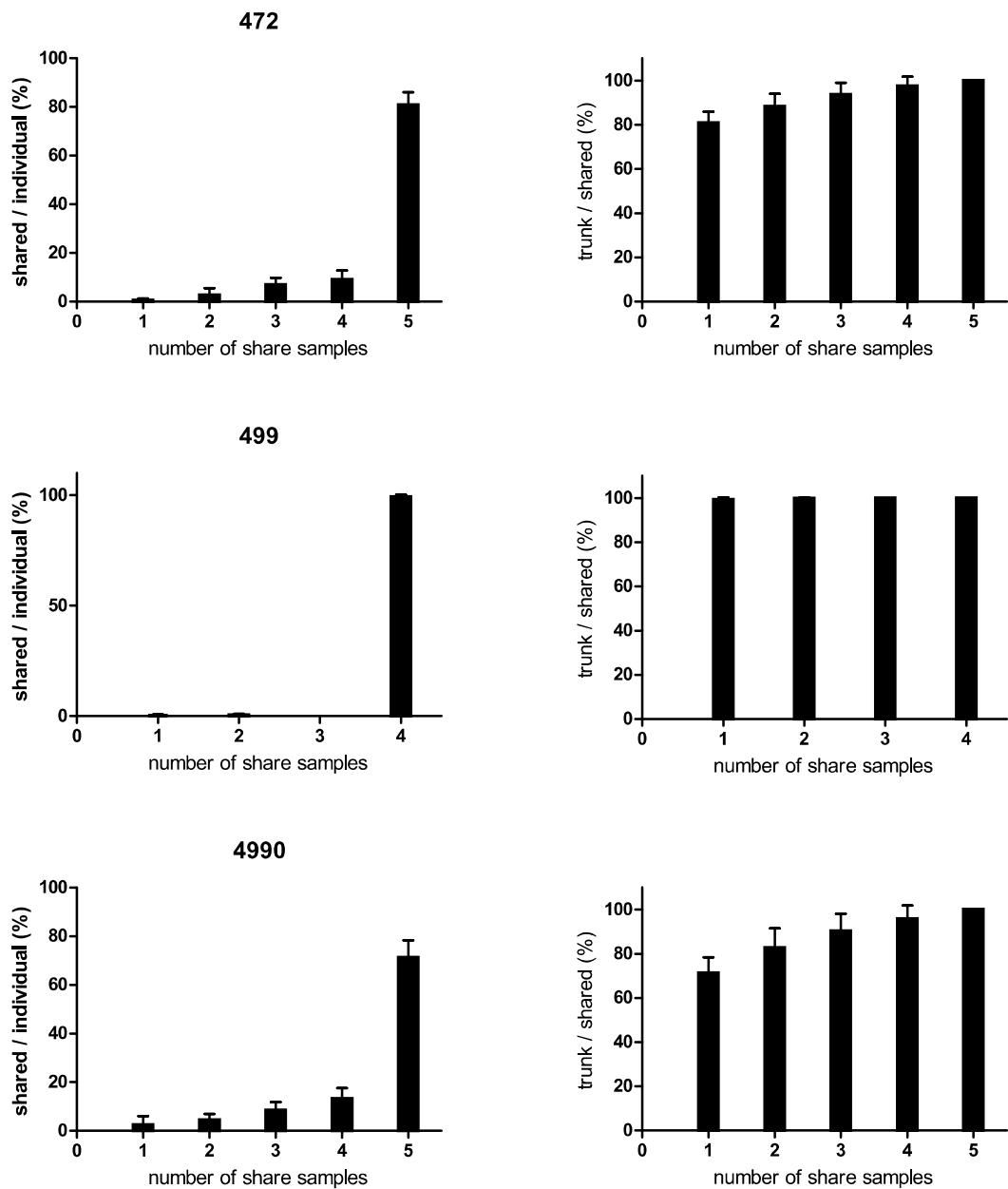


Figure S3. Mutation proportions of lung adenocarcinomas across samples.

Panel A shows the proportion of shared nonsynonymous mutations of any one to maximum volume of samples in respective samples, panel B shows the proportion of trunk mutations in shared mutations of any one to maximum volume of samples from each tumor. The x-axis indicate the volume of samples to give shared mutations.