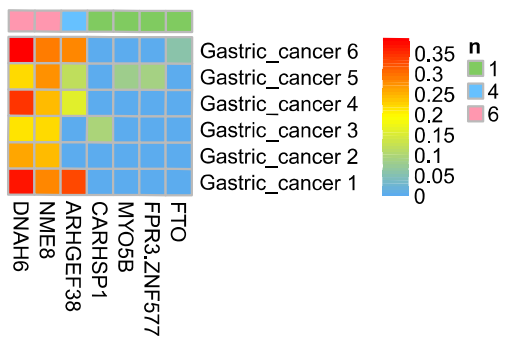
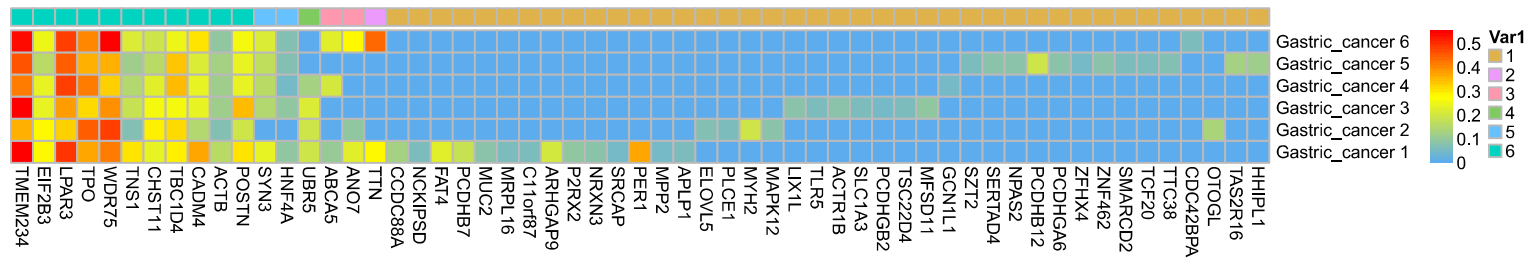


A



B



C

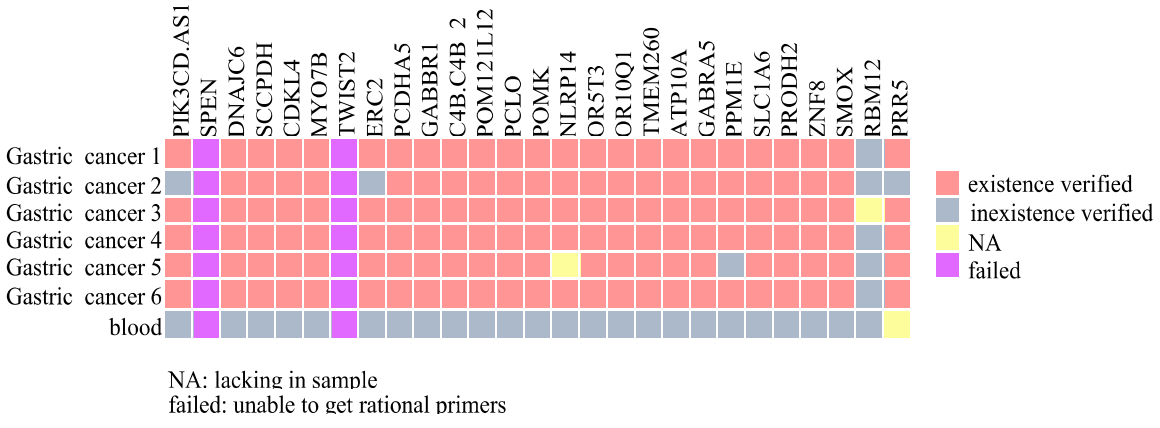
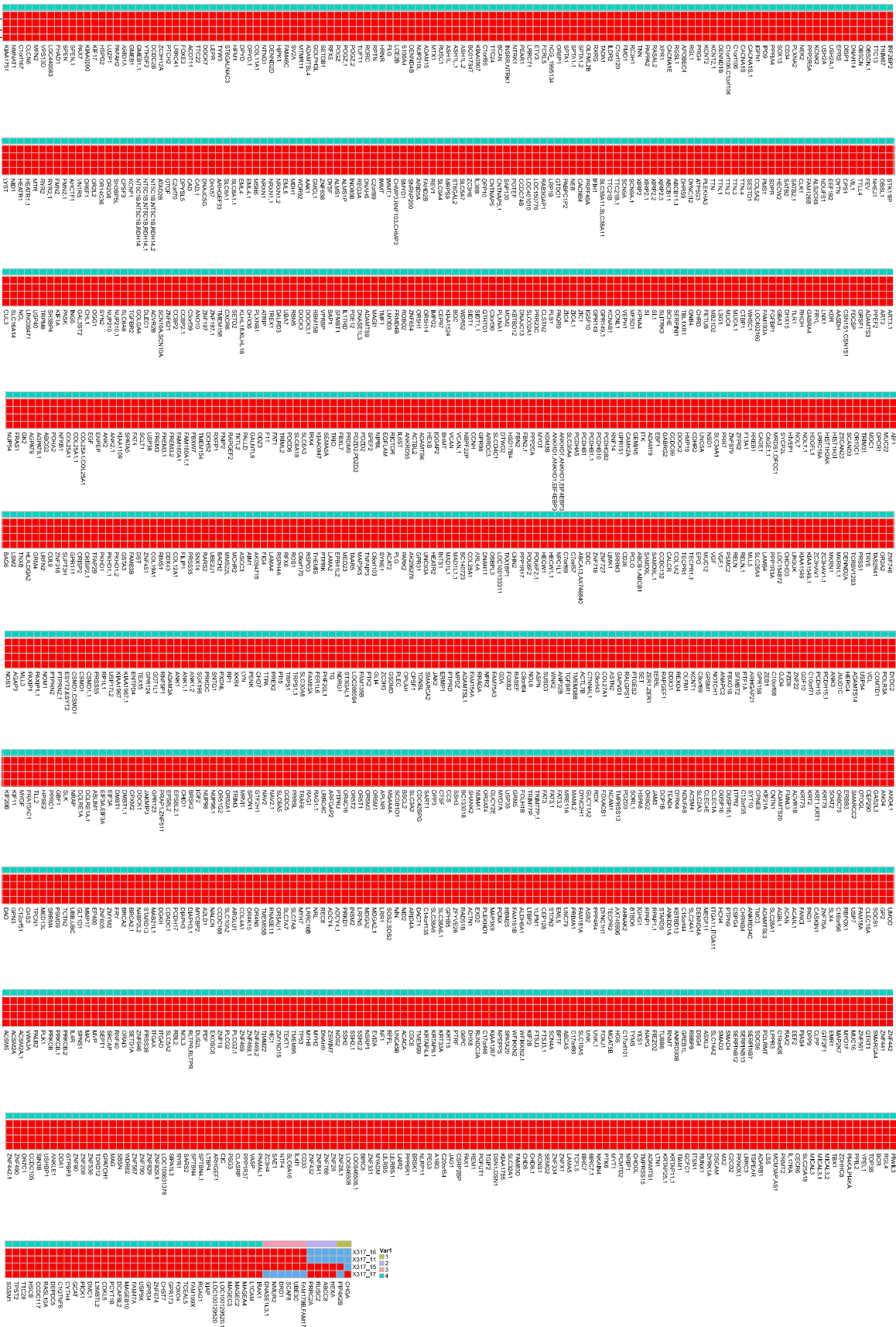


Figure S1. Mutation frequency of stopgains and synonymous SNVs across samples, and verification of 27 trunk mutations.
 (A) Mutation frequency of stopgains. (B) Mutation frequency of synonymous SNVs. The color ramp shows the range of mutation frequency.
 n & Var1: the number of samples involved in each mutation. (C) Verification of 27 nonsynonymous trunk mutations by PCR amplification and sequencing.

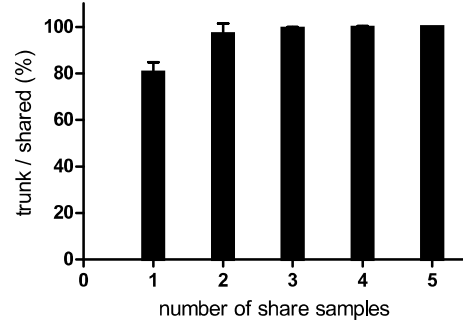
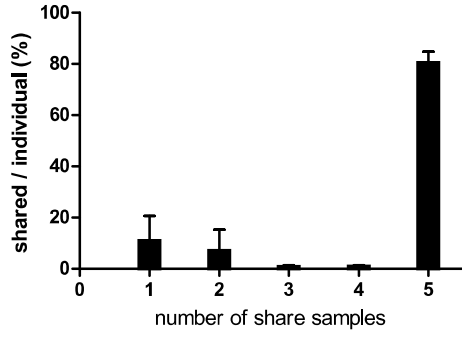
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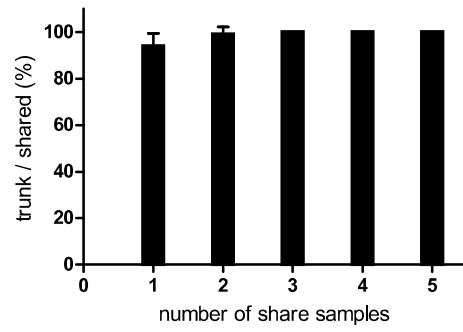
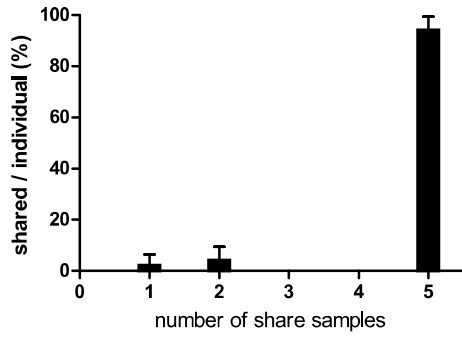
A

B

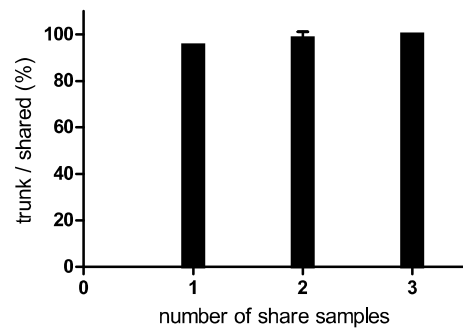
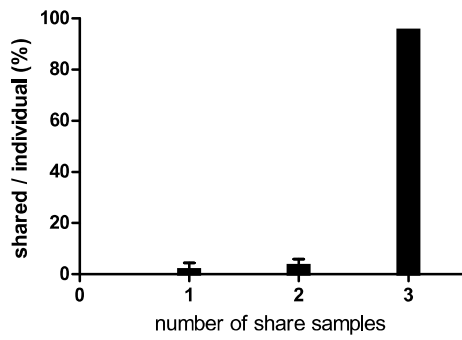
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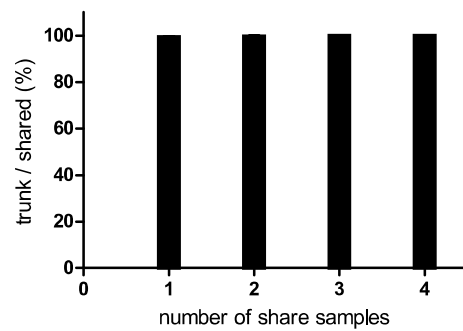
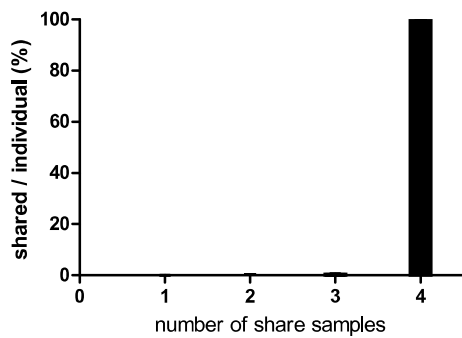
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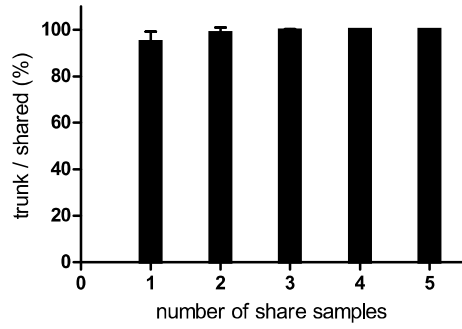
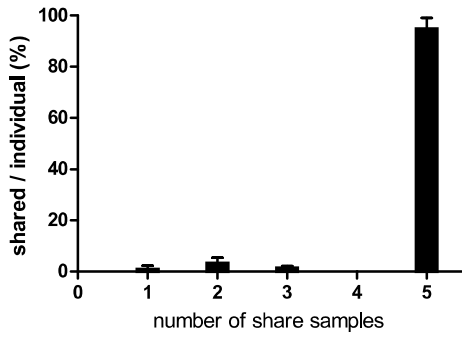
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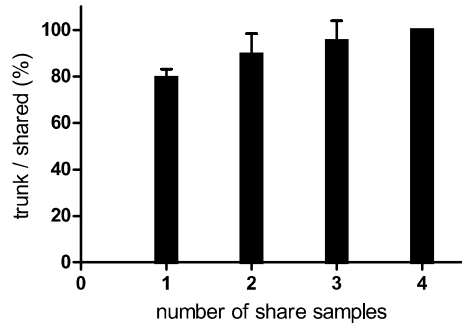
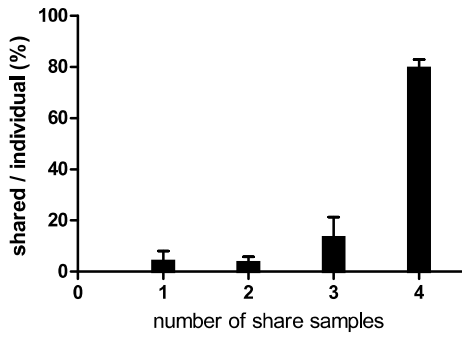
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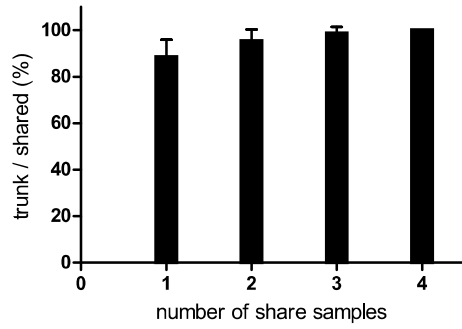
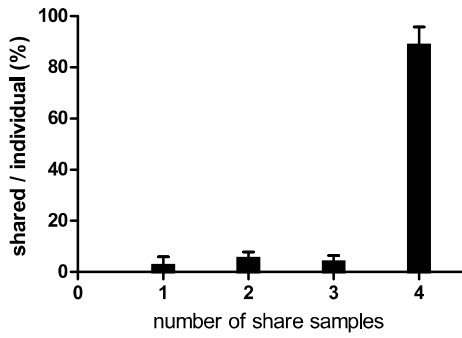
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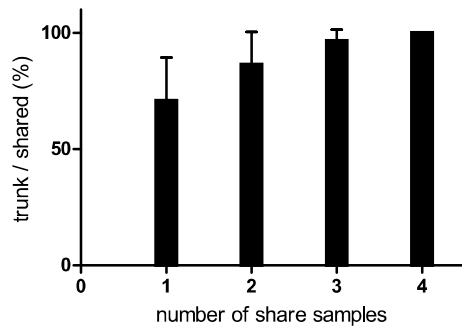
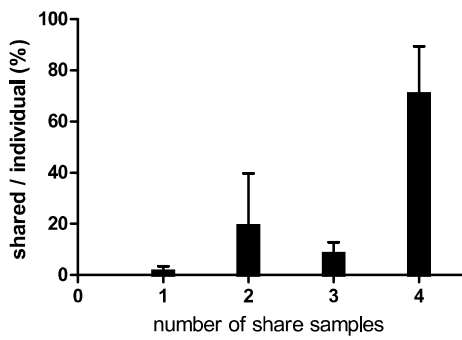
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339



356



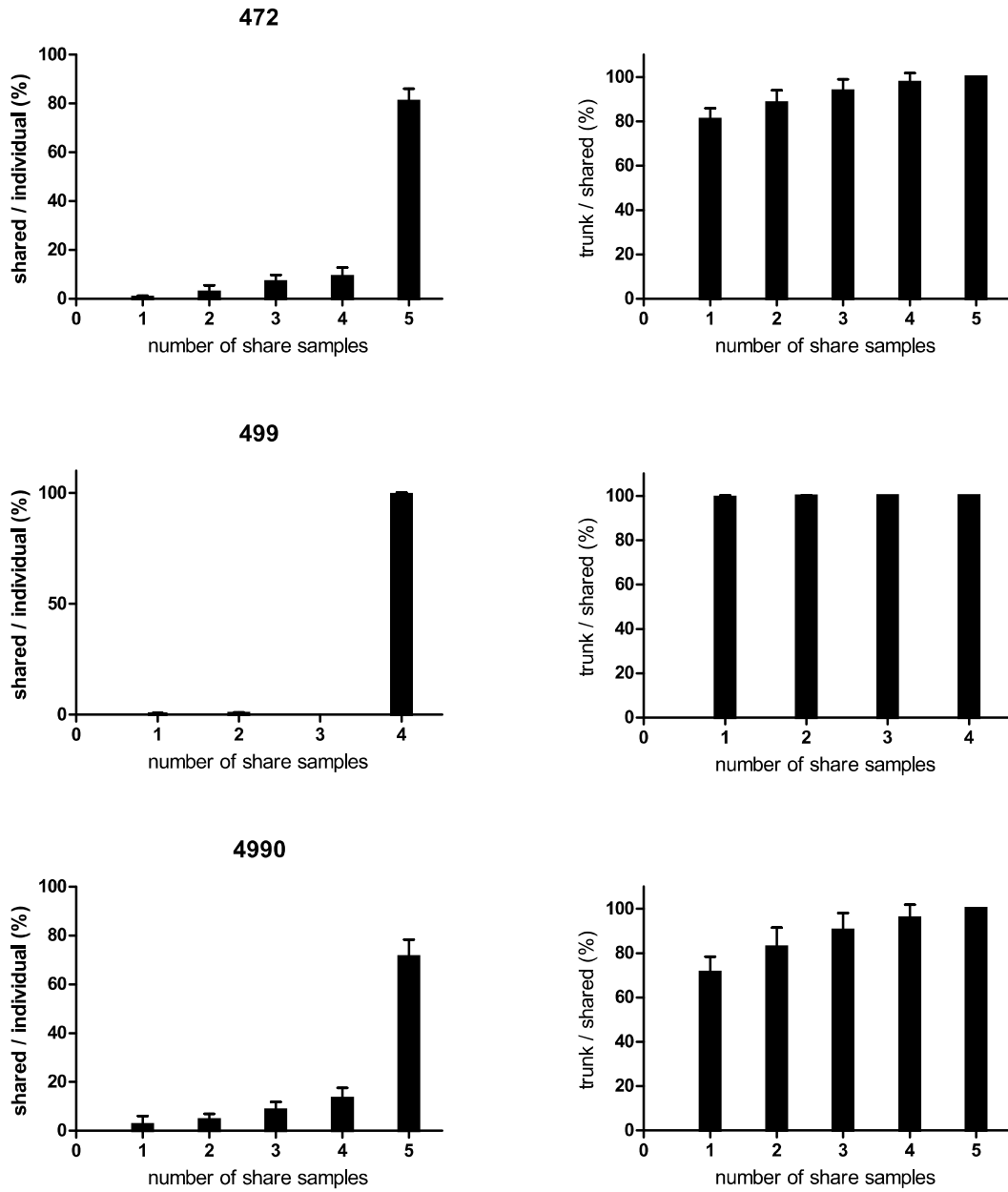


Figure S3. Mutation proportions of lung adenocarcinomas across samples.

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