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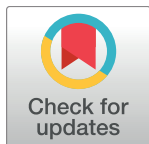
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CORRECTION

Correction: Functional Constraint Profiling of a Viral Protein Reveals Discordance of Evolutionary Conservation and Functionality

Nicholas C. Wu, C. Anders Olson, Yushen Du, Shuai Le, Kevin Tran, Roland Remenyi, Danyang Gong, Laith Q. Al-Mawsawi, Hangfei Qi, Ting-Ting Wu, Ren Sun

There is a labelling error in Panel C of [Fig 2](#). The labels 'PA N-terminal Domain' and 'PA C-terminal Domain' are swapped. The left label should be 'PA N-terminal Domain', and the right label should be 'PA C-terminal Domain'. The authors have provided the correct version of [Fig 2](#) which can be viewed below.



OPEN ACCESS

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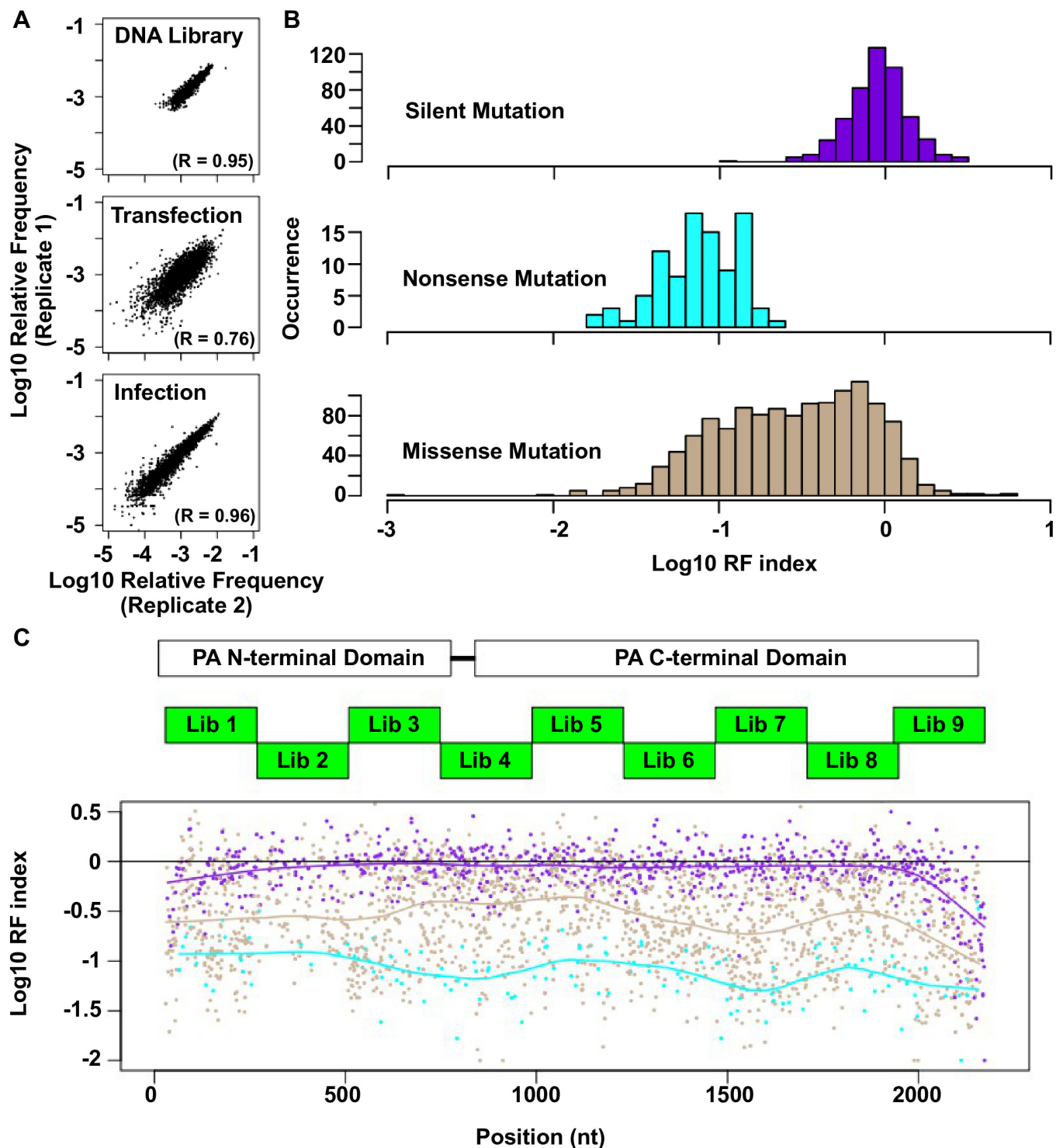


Fig 2. Fitness profiling of PA influenza virus polymerase subunit. (A) Correlations of log₁₀ relative frequency of individual point mutations between replicates are shown. Relative frequency_{mutation i} = (Occurrence frequency_{mutation i}) / (Occurrence frequency_{WT}) (B) Log₁₀ RF indices for silent mutations, nonsense mutations, and missense mutations are shown as histograms. Point mutations located at the 5 terminal 400 bp and 3 terminal 400 bp regions are not included in this analysis to avoid complication by the vRNA packaging signal [93, 94]. (C) The locations of the PA C-terminal domain and the PA N-terminal domain are shown as white boxes. The locations of the mutated regions in each mutant library are shown as green boxes. Log₁₀ RF indices for individual point mutations are plotted across the PA gene. Each point mutation is colored coded as in panel B. Purple: silent mutations; Cyan: nonsense mutations; Brown: missense mutations. A smooth curve was fitted by loess and plotted for each point mutation type.

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Reference

1. Wu NC, Olson CA, Du Y, Le S, Tran K, Remenyi R, et al. (2015) Functional Constraint Profiling of a Viral Protein Reveals Discordance of Evolutionary Conservation and Functionality. PLoS Genet 11(7): e1005310. <https://doi.org/10.1371/journal.pgen.1005310> PMID: 26132554