Supplementary Materials

Kozak sequence libraries for characterizing transgenes across expression levels

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Supplementary Tables

Supplementary Table 1. List of primers and associated sequences for library generation, library amplification, and subsequent high throughput sequencing.

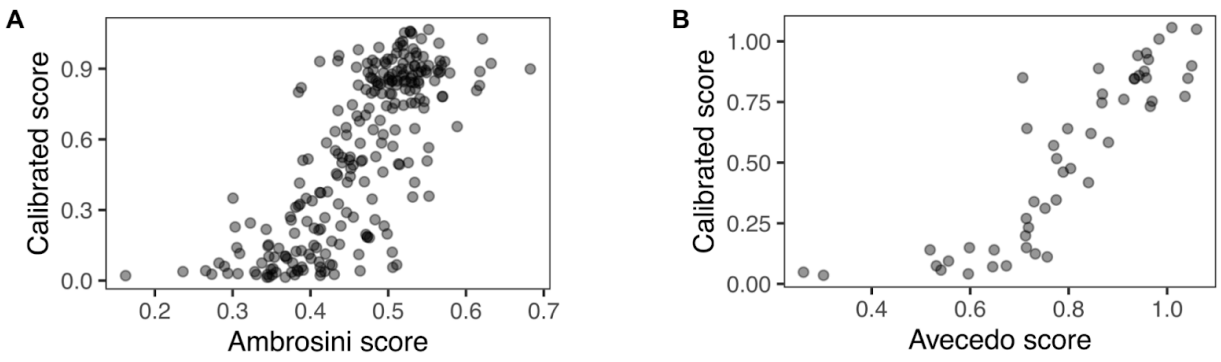
Supplementary Table 2. Table of Kozak variant ClinVar entries and their predicted impacts to protein expression.

Supplementary Table 3. List of high-throughput sequencing fastq files deposited and analyzed in this work.

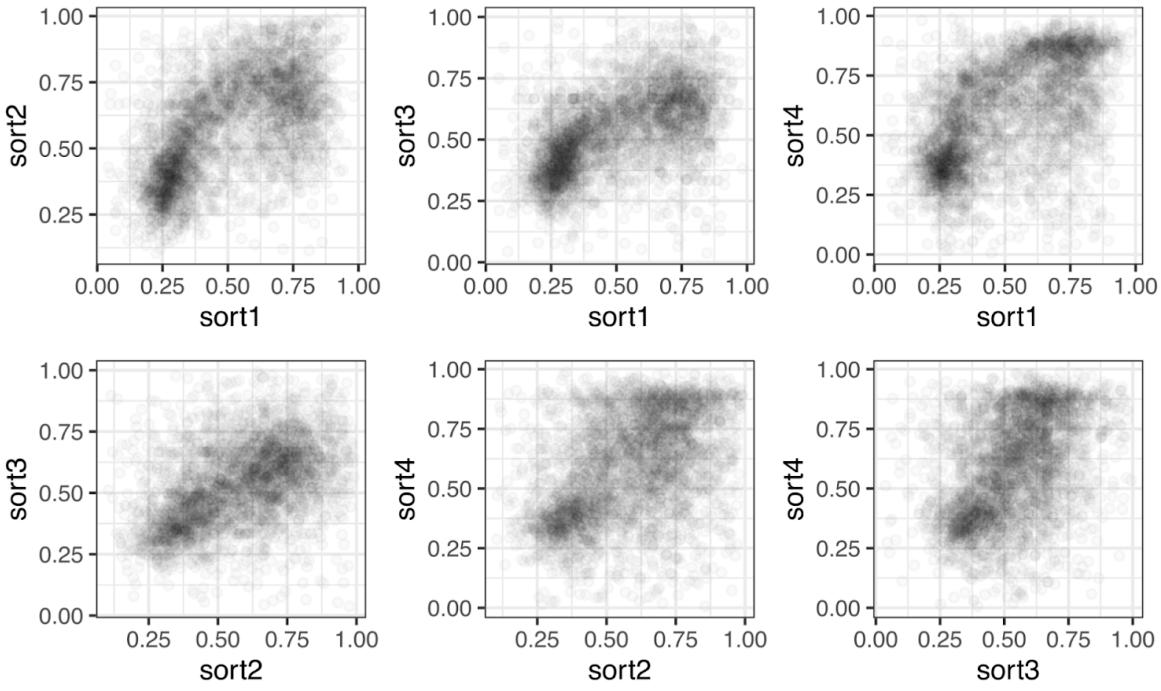
Supplementary Table 4. Table of sort-seq weighted averages, calibrated scores, random-forest imputed scores, and enrichment values following selection for cells infected with pseudotyped lentivector particles. Individual infection values and assessed mean-fluorescent intensities of control constructs are incorporated into the table.

Supplementary Table 5. Table of infection values for Kozak libraries of WT, I21N, and D355N ACE2, when mixed with VSV-G, SARS-CoV spike, and SARS-CoV-2 spike pseudotyped lentivector particles.

Supplementary Figures



Supplementary Fig 1. Comparison of calibrated scores with scores calculated in diverse model systems. Comparison with A) scores calculated by Ambrosini *et al*, with lentivirally transduced HEK 293T cells, and B) scores calculated by Avecedo *et al*, tested in Drosophila Kc167 cells.



Supplementary Fig 2. Pairwise comparison of variant-specific weighted average values for each sort-seq replicate.