

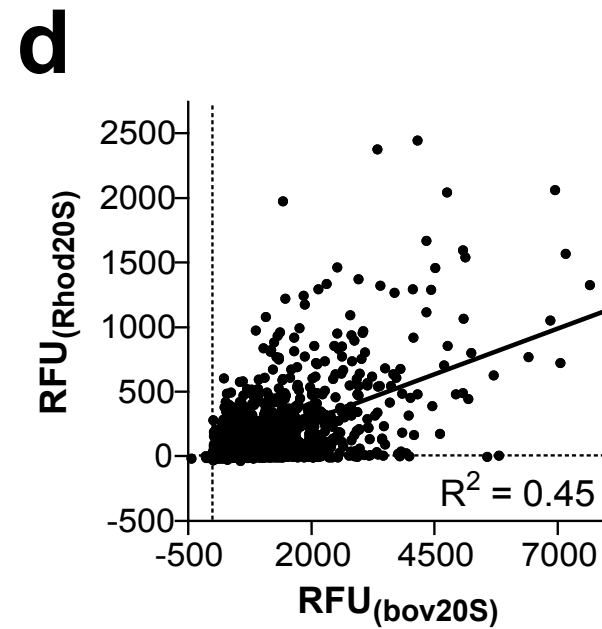
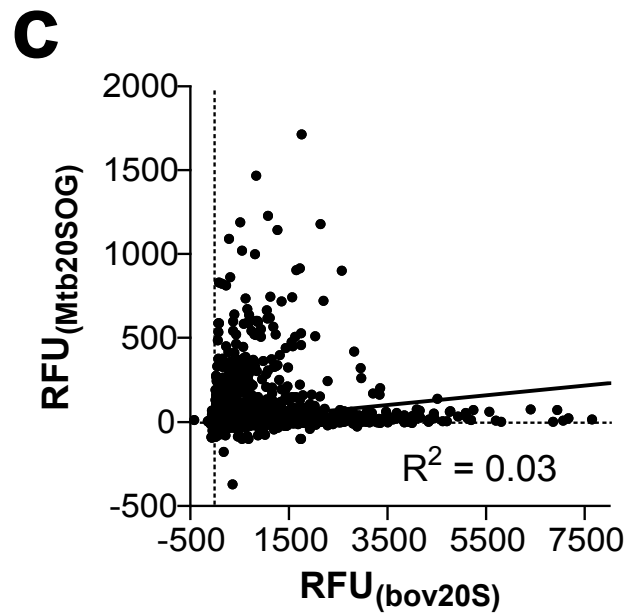
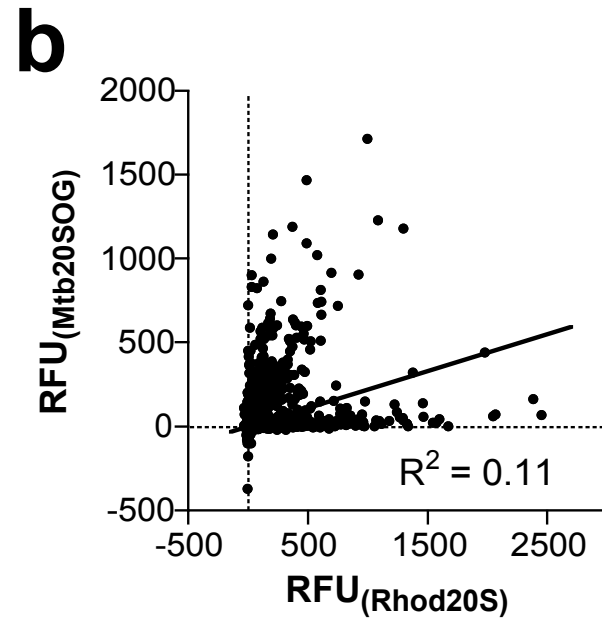
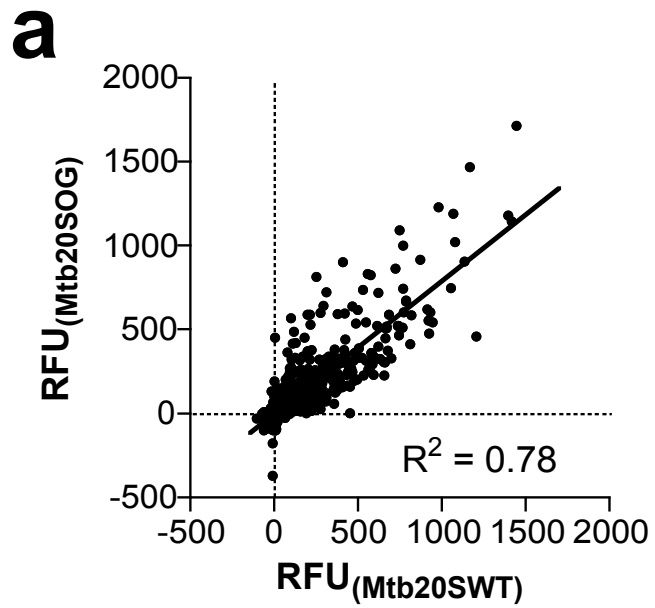
## Supplemental information

**Fig. S1** Correlation between peptidolytic activities of different proteasome preparations from different organisms. Each dot represents results for one of the 5920 peptides tested. (a) Mtb20SOG vs Mtb20SWT WT proteasomes; (b) Mtb20SOG vs Rhod20S; (c) Mtb20SOG vs bov20S; (d) Rhod20S vs bov20S. RFU, relative fluorescence units. The plots were generated with Prism (GraphPad Software, Inc. San Diego, CA).

**Fig. S2** Most and least active substrates for bov20S proteasomes attributable to (a)  $\beta$  5, (b)  $\beta$  1, and (c)  $\beta$  2 subunits. For  $\beta$  5, the P1 amino acids appeared to be a most important determinant than the P3 amino acids, and the P2 amino acids the least important, as the hydrophobic L is the most favored with P3 aromatic amino acids Y/W/F, whereas the hydrophilic P1 N is the least favored. For  $\beta$  1, P2 amino acids appeared to be a more important determinant than P3, as the P2 aromatic F/Y/W are the most favored, whereas the P2 basic R and small hydrophobic amino acids are the least favored. For  $\beta$  2, the P3 amino acids appeared to be a more important determinant than the P2 amino acids, as the basic R/K are most favored, whereas the acidic E/D are the least favored. X-axis, Acetyl-P3P2P1-AMC; Y-axis, RFU.

**Fig. S3** Correlation between  $k_{cat}/K_M$  values of Mtb20SOG and Mtb20SWT for individual substrates. The  $R^2$  0.82 matches the  $R^2$  0.78 of the correlation of substrate high throughput screening results between Mtb20SOG and Mtb20SWT.

Figure S1



**Fig. S2**

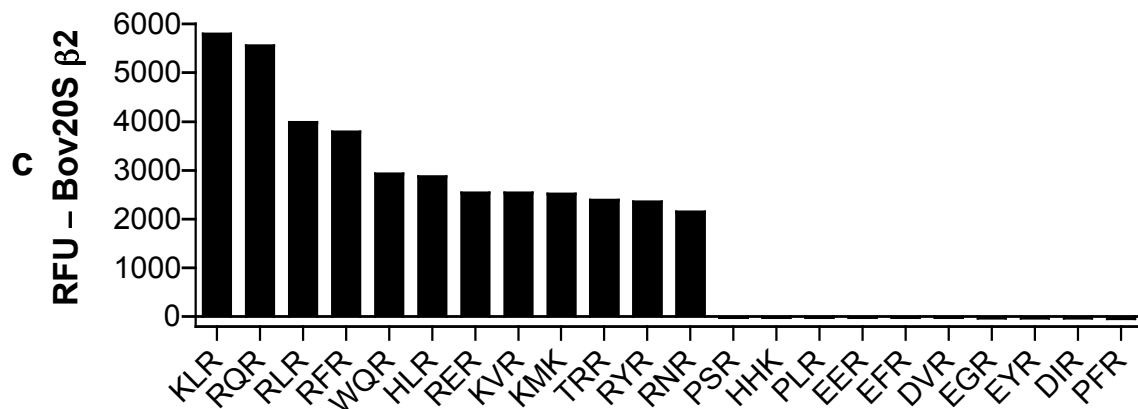
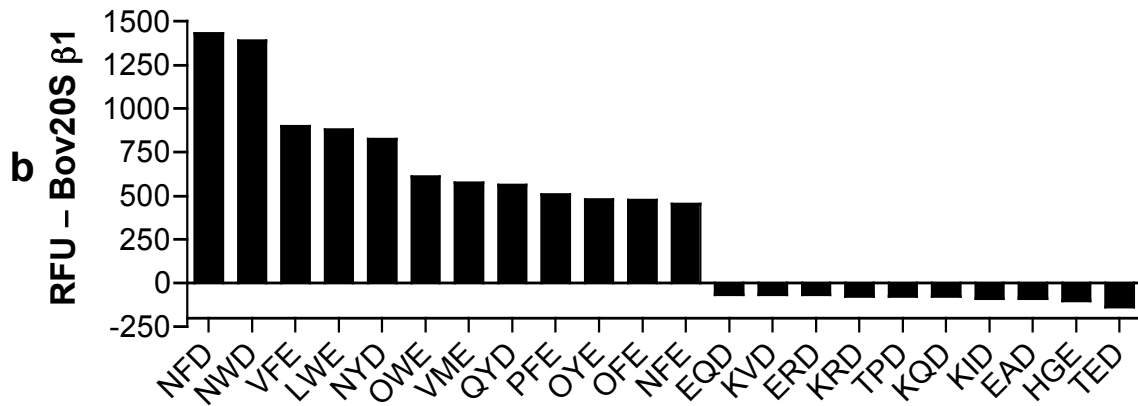
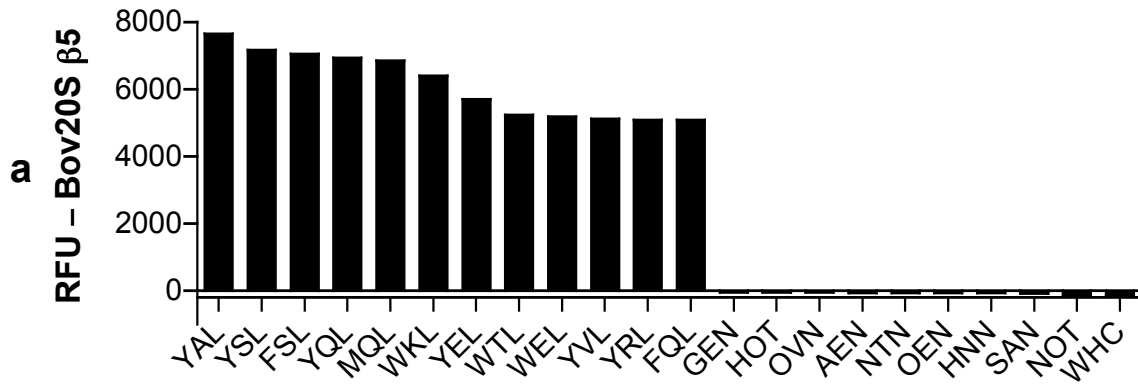


Fig. S3

