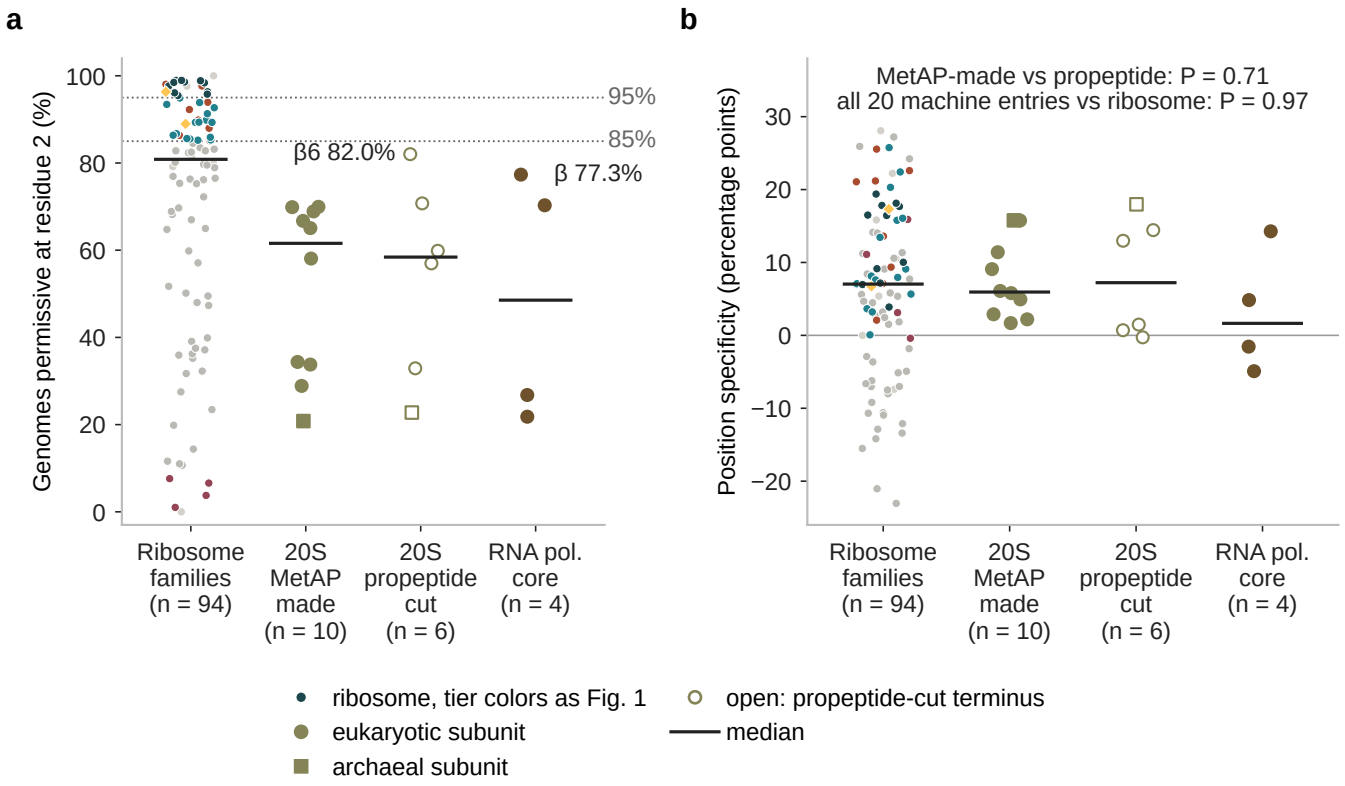
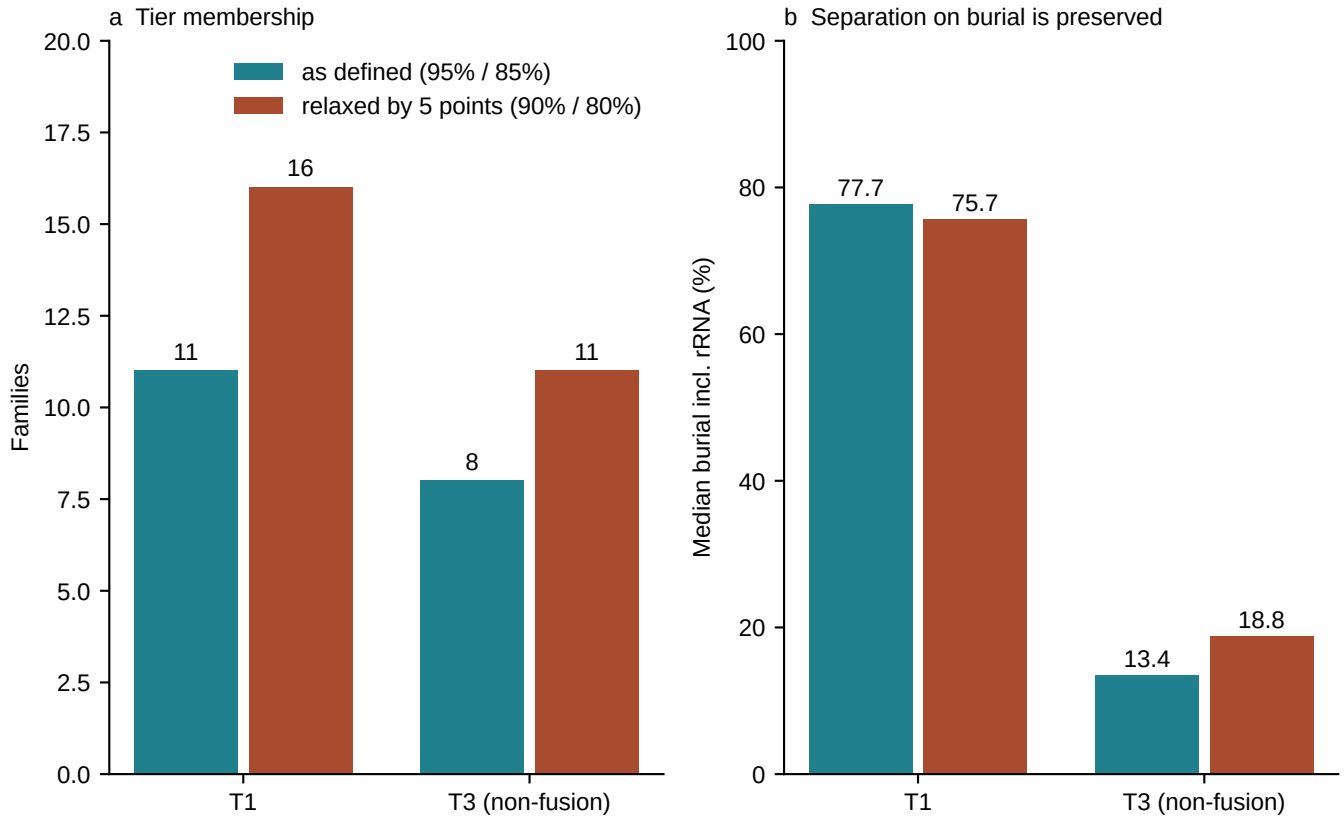


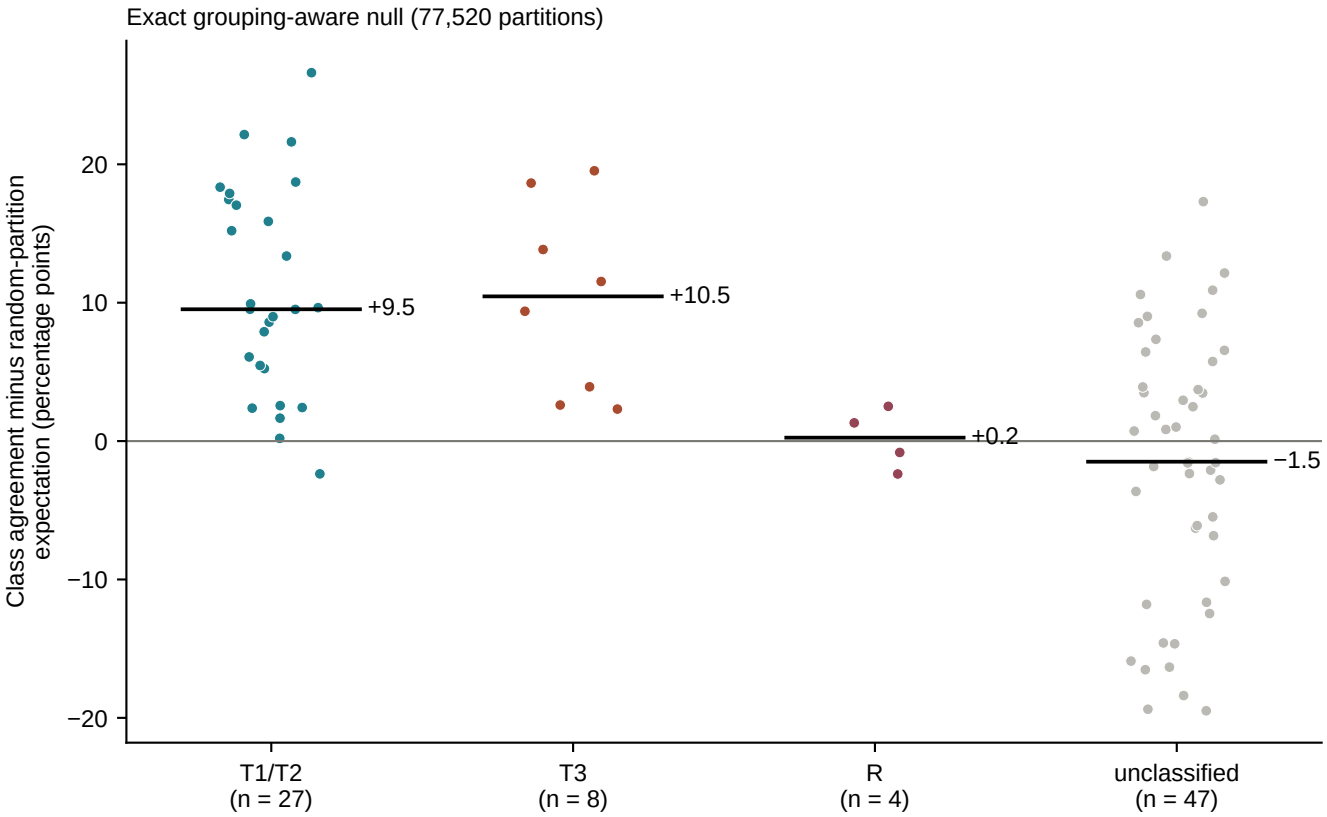
Supplementary Figure S1. The genome-scale layer in two other macromolecular machines. (a) Percentage of reference proteomes with a MetAP-permissive residue 2 for the 94 ribosomal families (colored by tier as in Figure 1), the ten 20S proteasome ring positions whose mature terminus is made by MetAP, the six whose terminus is made by propeptide cleavage, and the four bacterial RNA polymerase core subunits; squares are the archaeal α and β subunits, open symbols propeptide-cut termini, and dotted lines the 85% and 95% tier thresholds. No proteasome or polymerase entry reaches 85%; the highest are proteasome β6 (82.0%) and RNA polymerase β (77.3%). (b) Position specificity for the same entries; horizontal bars are medians. Two-sided Mann-Whitney P values compare MetAP-made with propeptide-cut proteasome positions (P = 0.71) and all 20 machine entries with the 94 ribosomal families (P = 0.97).

AI-assisted code was used for reproducible rendering from the frozen source tables.



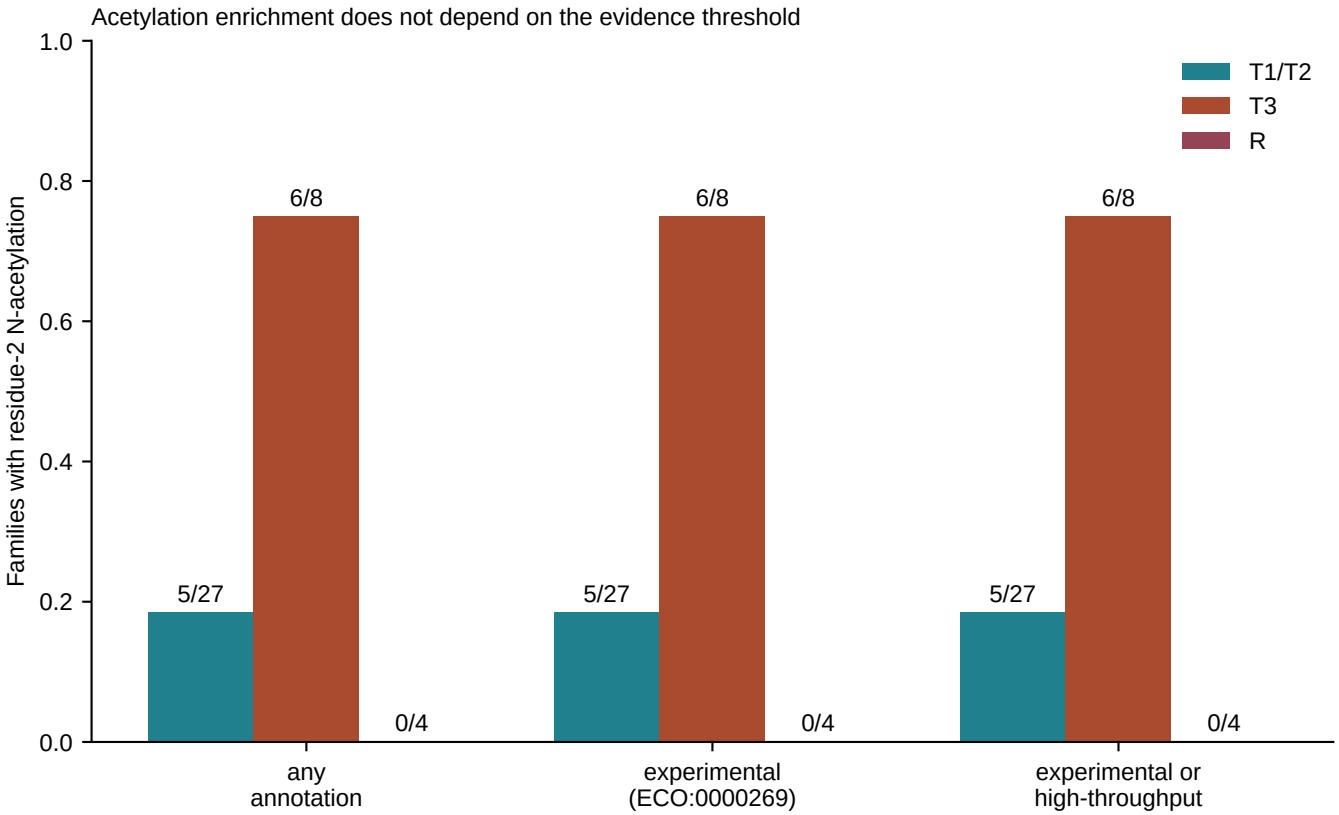
Supplementary Figure S2. Sensitivity of tier membership and of the burial separation to a five-point relaxation of both genome-scale thresholds.

AI-assisted code was used for reproducible rendering from the frozen source tables.



Supplementary Figure S3. Exact grouping-aware null for residue-2 class agreement, by tier: observed class agreement minus the mean over all 77,520 seven-versus-thirteen partitions of the twenty residues, for the 86 tiered and unclassified non-fusion families with at least 50 single-copy records (the three remaining families, which have genome evidence only, enter the overall median but are not shown); bars are medians.

AI-assisted code was used for reproducible rendering from the frozen source tables.



Supplementary Figure S4. Residue-2 acetylation by tier under three evidence thresholds.

AI-assisted code was used for reproducible rendering from the frozen source tables.