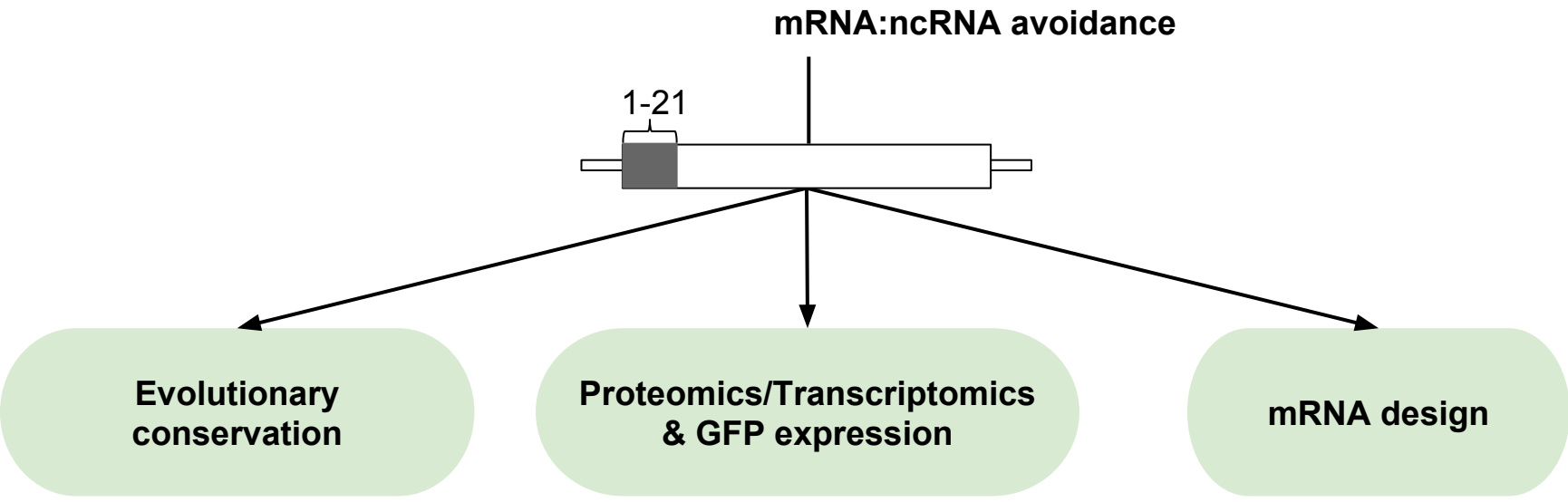

Evolutionary conservation	Proteomics/Transcriptomics & GFP expression	mRNA design
1,582 bacterial & 118 archaeal genomes 189,074 core mRNAs 110,085 core ncRNAs	2 species (*E. coli* & *P. aeruginosa*) 10,317 mRNA & protein measurements 14,388 GFP expression data points	13 synthetic GFP mRNAs sampled from high/low codon usage, 5' end internal secondary structure and avoidance using 52 biological replicates
97% of bacteria & archaea show signatures of avoidance (extrinsic or intrinsic). Sliding window analysis of *T. thermophilus* ribosomal RNA shows regions of avoidance distributed on SSU ribosomal RNA but less than expected in protein binding regions (P = 9.3×10^{-15}).	Avoidance significantly correlates with protein/mRNA ratios and GFP expression values in 100% of these datasets (R_s are between 0.10-0.65). Sliding window analysis of GFP expression data shows 5` end of mRNAs influence avoidance more than other regions.	Codon usage (R_s =0.29) Secondary structure (R_s =0.34) Avoidance (R_s =0.56) Avoidance explains more variance than other measures. The mRNA with high CAI, low internal secondary structure and high avoidance has maximal expression.