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Supplementary information

Semantic design of functional de novo genes from a genomic language model

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Semantic design of functional *de novo* genes from a genomic language model

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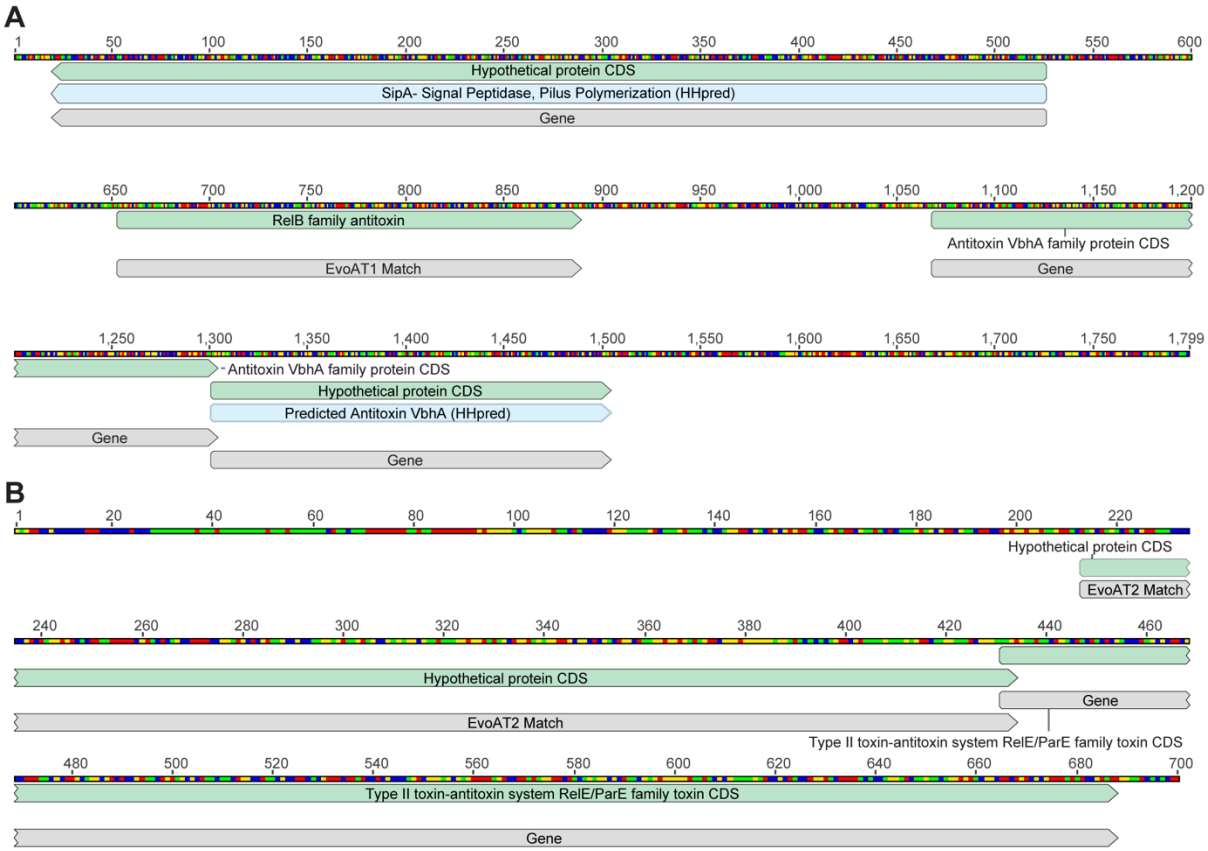
Supplementary information


A
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600
Hypothetical protein CDS
SipA- Signal Peptidase, Pilus Polymerization (HHpred)
Gene
650
700
750
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850
900
950
1,000
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RelB family antitoxin
Antitoxin VbhA family protein CDS
EvoAT1 Match
Gene
1,250
1,300
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1,750
1,799
Antitoxin VbhA family protein CDS
Hypothetical protein CDS
Predicted Antitoxin VbhA (HHpred)
Gene
Gene
B
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180
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Hypothetical protein CDS
EvoAT2 Match
240
260
280
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320
340
360
380
400
420
440
460
Hypothetical protein CDS
Gene
EvoAT2 Match
Type II toxin-antitoxin system RelE/ParE family toxin CDS
480
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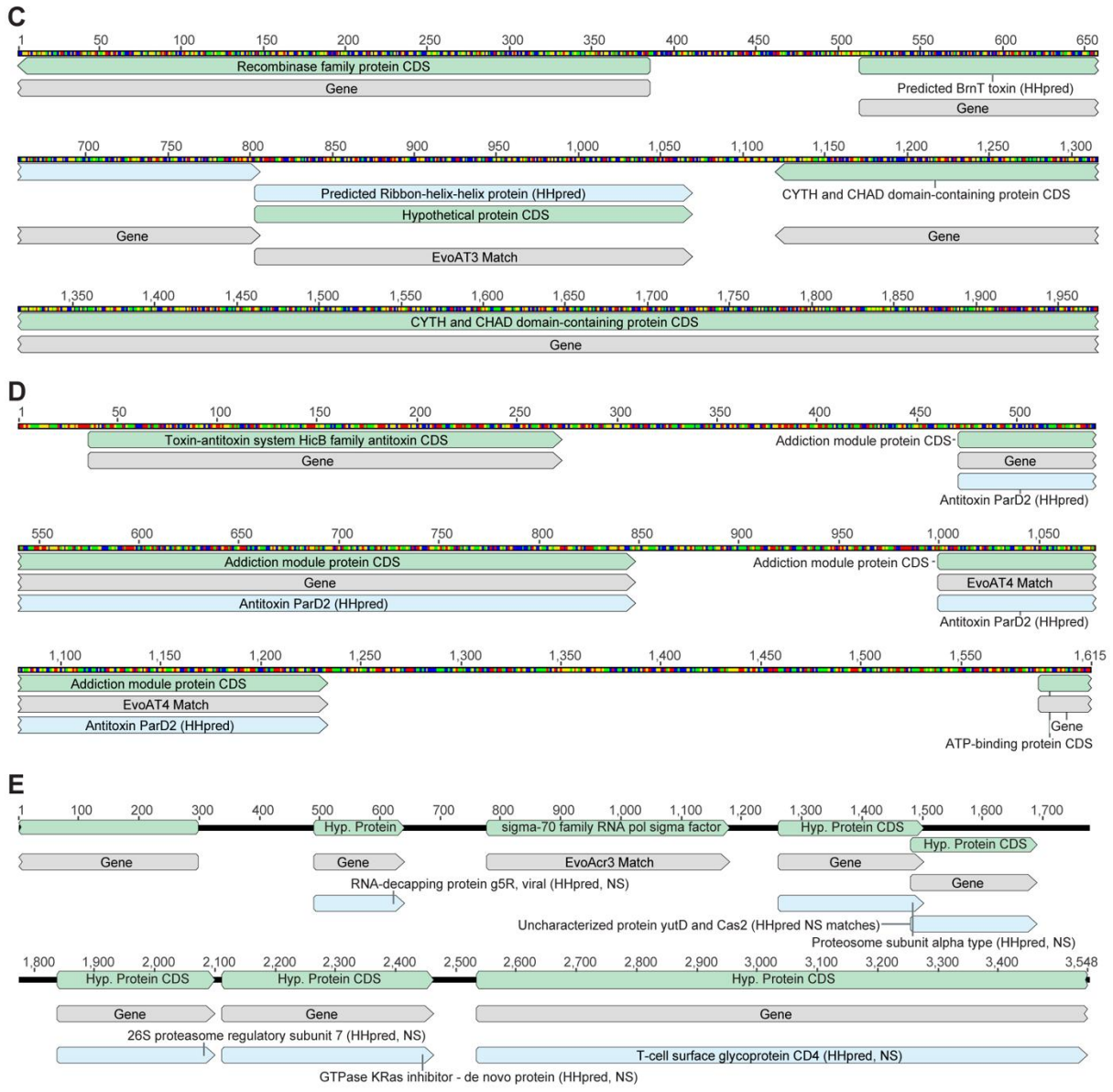
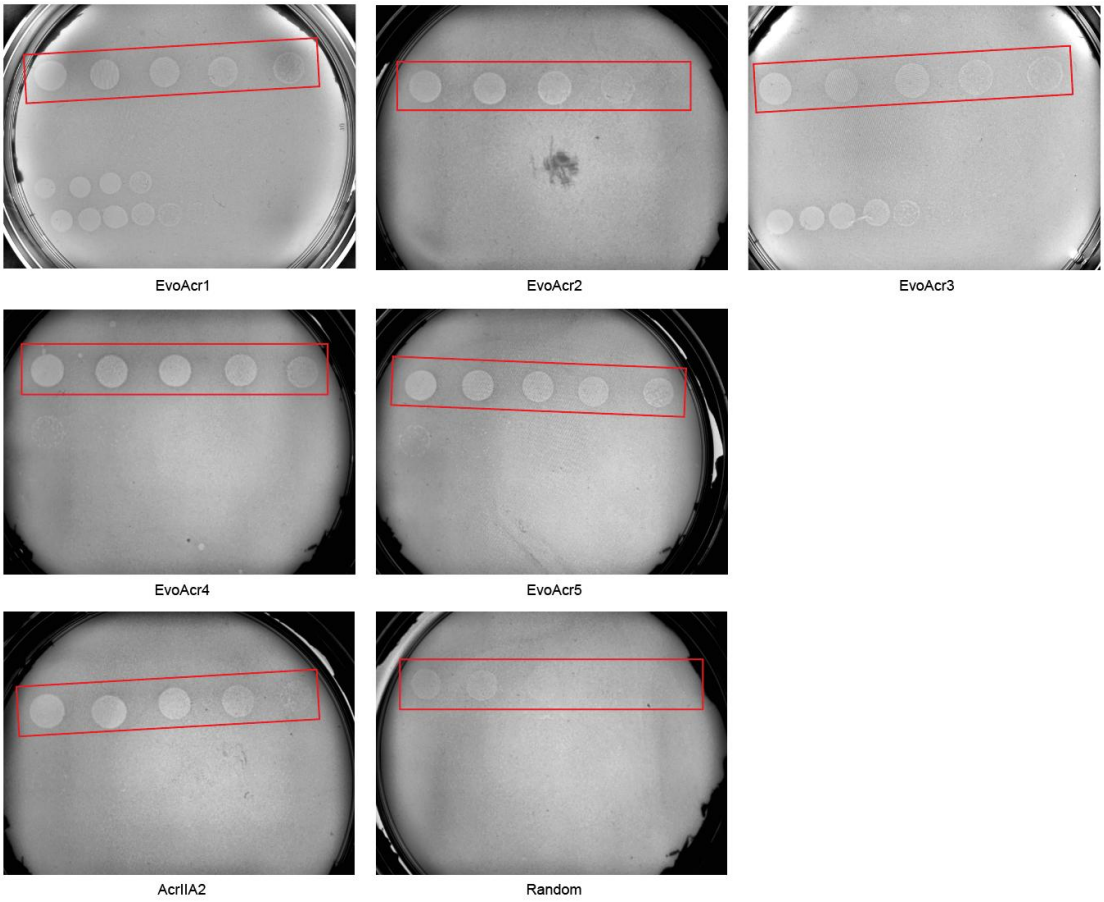
700
Type II toxin-antitoxin system RelE/ParE family toxin CDS
Gene



Supplementary Figure 1: Genomic context of closest sequence matches of EvoAT1-4 and EvoAcr3. (A-D) Genes known and predicted to be related to toxin-antitoxin systems can be found in the immediate vicinity of the closest sequence identity matches for EvoAT1-4. **(E)** The closest sequence match for EvoAcr3, a sigma-70 RNA pol sigma factor, is surrounded by primarily uncharacterized proteins that are not known to be anti-CRISPRs. NS, non-significant.



Supplementary Figure 2. Uncropped phage plaque images for Acr protection assay. Uncropped phage plaque images depicting formation of plaques in response to EvoAcr1-5, AcrIIA2, and a random sequence.