Supplementary File 1. Genomes sampled via the Metropolis-Hastings algorithm with the motif entropy replacing the energy function. The table summarizes the sequence of the genome, its characteristic length scales L_E and L_U, as well as the motif entropy on all length scales of interest. The keyword "bias" is used to distinguish two different sampling procedures: Weakly biased genomes are designed to obey the desired length scales L_E and L_U while retaining a close-to-uniform motif distribution for subsequences of length $L_E < L < L_U$, whereas the motif distribution is far from uniform for strongly biased genomes.

L_G	L_E	L_U	bias	entropy S	genome	L_G	L_E	L_U	bias	entropy S	genome
64	3	4	none	$S(1) = 1.0$ $S(2) = 2.0$ $S(3) = 3.0$ $S(\geq 4) = 3.5$	CUUUCGUGCCAUCUAC GCCCCUCGGUCUCACU GAACAGGUUACUUAUU GGAUUUGUCCGCUAUG	64	2	4	weak	$S(1) = 1.0$ $S(2) = 2.0$ $S(3) = 2.961$ $S(\geq 4) = 3.5$	UUAGGGUAGUAAUGGC GACUUUCUCACGAGCA CCUGUGUAUUCAUCUU GCCGUCCCAGCGGAUU
64	3	6	weak	$S(1) = 1.0$ $S(2) = 2.0$ $S(3) = 3.0$ $S(4) = 3.469$ $S(5) = 3.484$ $S(\geq 6) = 3.5$	ACUGCUACAUAAUCUC ACACCCUGGAACGAAA GCGAGUAUCCGUCUUG CCGCCAAUGACCCUAA	64	2	6	weak	$S(1) = 1.0$ $S(2) = 2.0$ $S(3) = 2.961$ $S(4) = 3.469$ $S(5) = 3.484$ $S(\geq 6) = 3.5$	GCUGUCUCCUCUAUUC ACGAUAAAGGGAAAUG GUAAGAUGCCGCCACC GUUGUAGCGUUGACCU
64	3	8	weak	$S(1) = 1.0$ $S(2) = 2.0$ $S(3) = 3.0$ $S(4) = 3.438$ $S(5) = 3.453$ $S(6) = 3.469$ $S(7) = 3.484$ $S(\geq 8) = 3.5$	UUUGAACCCCAUUACA GGCUCGUCCUCCGCCA CCGAUAACUUUGAUGC UAUUCUGCGUAGACAC	64	2	8	weak	$S(1) = 1.0$ $S(2) = 2.0$ $S(3) = 2.961$ $S(4) = 3.438$ $S(5) = 3.453$ $S(6) = 3.469$ $S(7) = 3.484$ $S(\geq 8) = 3.5$	AAGAUUGUAUGCCGUC UAAUAGGGUGAAAAGC CUCUGUUACGCUCCUG GUUCACCCGAUGUCGC
64	3	10	weak	$S(1) = 1.0$ $S(2) = 2.0$ $S(3) = 3.0$ $S(4) = 3.406$ $S(5) = 3.422$ $S(6) = 3.438$ $S(7) = 3.453$ $S(8) = 3.469$ $S(9) = 3.484$ $S(\geq 10) = 3.5$	CCUCCGCCAUUACAGG CUAUGCUCGUCCCACU UUGAUUCUGCGUAGAC CGAACACUUUGAUAAC	64	2	10	weak	$S(1) = 1.0$ $S(2) = 2.0$ $S(3) = 2.961$ $S(4) = 3.406$ $S(5) = 3.422$ $S(6) = 3.438$ $S(7) = 3.453$ $S(8) = 3.469$ $S(9) = 3.484$ $S(\geq 10) = 3.5$	CCCAUUGGACUUAGUG GUUGCUCUGUAUGCGG GAACGACCGUGCUCUG UAAAAGGAUAGAUUCG
64	3	4	none	$S(1) = 1.0$ $S(2) = 2.0$ $S(3) = 3.0$ $S(\geq 4) = 3.5$	CUUUCGUGCCAUCUAC GCCCCUCGGUCUCACU GAACAGGUUACUUAUU GGAUUUGUCCGCUAUG	64	2	4	strong	$S(1) = 1.0$ $S(2) = 2.0$ $S(3) = 2.824$ $S(\geq 4) = 3.5$	UACUGUCCGAGCCUCA UUGUUUUGACUCCCGU CGUAGGAUGUAUUAGC GUUGCCCCUGCUGAUU
64	3	6	strong	$S(1) = 1.0$ $S(2) = 2.0$ $S(3) = 3.0$ $S(4) = 3.172$ $S(5) = 3.344$ $S(\geq 6) = 3.5$	AAACCCUGCUUAUUCA AGCAUCUCCAGGGCGU CGGCGUACACUCCAUC UAGUGUCGGUUUAUUG	64	2	6	strong	$S(1) = 1.0$ $S(2) = 2.0$ $S(3) = 2.437$ $S(4) = 2.863$ $S(5) = 3.266$ $S(\geq 6) = 3.5$	GCGCUAAAUUAAAUGG UCAUUUUAGUCAGUCC GGUCCAGUCAUGGACU AGCUGACCGCUGGUCC
64	3	8	strong	$S(1) = 1.0$ $S(2) = 2.0$ $S(3) = 3.0$ $S(4) = 3.125$ $S(5) = 3.219$ $S(6) = 3.313$ $S(7) = 3.406$ $S(\geq 8) = 3.5$	GGCAUCGCUCUGACAC UAAGGAUGCCCAAUAC UGACACCAAUACCGUU UCCUUAGAGCGAAACG	64	2	8	strong	$S(1) = 1.0$ $S(2) = 2.0$ $S(3) = 2.358$ $S(4) = 2.65$ $S(5) = 2.94$ $S(6) = 3.176$ $S(7) = 3.359$ $S(\geq 8) = 3.5$	CUACCAUUCGCUAGGU UCAUUCAUGGUUCGCG CUGAACCUGAACCAUU CAGGUAGCGAACCUAC
64	3	10	strong	$S(1) = 1.0$ $S(2) = 2.0$ $S(3) = 3.0$ $S(4) = 3.078$ $S(5) = 3.156$ $S(6) = 3.227$ $S(7) = 3.297$ $S(8) = 3.367$ $S(9) = 3.438$ $S(\geq 10) = 3.5$	GAGCGUAUCGAAACCC UGCCGGCAUUGUGGAG CGUAUCUUAGUCAGGG UUUCCACAAUGACUAA	64	2	10	strong	$S(1) = 1.0$ $S(2) = 2.0$ $S(3) = 2.27$ $S(4) = 2.502$ $S(5) = 2.72$ $S(6) = 2.931$ $S(7) = 3.136$ $S(8) = 3.314$ $S(9) = 3.438$ $S(\geq 10) = 3.5$	UGACAGCUGUUUCCGG AACCGGUUUCCGGAUA UAUAUACAGCUGUUCA GCUGUUCCGGUUCAGC