PP1
5′-CGGAATTCTA CGAATTTTTC TTTTGTTTAT TTCCTTTCGC TTTGCTTCTC TTCCCTTCGT TCTGTTCCGT TTTACCTTGT
CTTGCCTTAT CTTACTTTA-3′

PP2
5′-TATCTTACTT TAGTTTCATT TAATTGTGTT GTACTCTCCT CTGCGTTCAC TTAGCTTAAC TTGGTTTGGC TTGATTTGAC
TTCAGTTGCG CTCTATTCTA-3′

PP3
5′-CGCTCTATTC TACTGTCCTG TGCATTCAAT CGTTGAGTTC GATCTAGTCT CGTCTAACCC TCCCCTGCTC CGCTGGTCTG
GCCTCGCCTA TCCTACCCAT-3′

PP4
5′-TATCCTACCC ATTGGGCTCA TCTGATCCAT CCGGTCCCGT CCACTCGGCT ATGTTATGCT GTATTGCAGT CGTGTCGCGT
CGAGCTGCCC TAATCCCACC-3′

PP5
C5′-CTAATCCCA CCTAGCGTAT CGGGTCATGT AGTGCTACGT TACGGCCCCCG CCCGGCATCA TATTATATCA CCCCAGTGTA
ATGTGGTGTG AGGTTGGAG-3′

PP6
5′-GTGAGGTTGG AGTCCGACCT GGAATCTCAG CCTGACGTGC CATGCGGTGC GATGTCACGC CGCGCCACGG TATAGTATGG
TACGGGATCC CG-3′

PP7
5′-TAAAGTAAGA TAAGGCAAGA CAAGGTAAAA CGGAACAGAA CCGAAGGGAA GAGAAGCAAA GCGAAAGGAA ATAAACAAAA
GAAAAATTCG TAGAATTCCG-3′

PP8
5′-TAGAATAGAG CGCAACTGAA GTCAAATCAA GCCAAACCAA GTTAAGCTAA GTGAACGCAG AGGAGAGTAC AACACAATTA
AATGAAACTA AAGTAAGATA-3′

PP9
5′-ATGGGTAGGA TAGGCGAGGC CAGACCAGCG GAGCAGGGGAG GGTTAGACGA GACTAGATCG AACTCAACGA TTGAATGCAC
AGGACAGTAG AATAGAGCG-3′

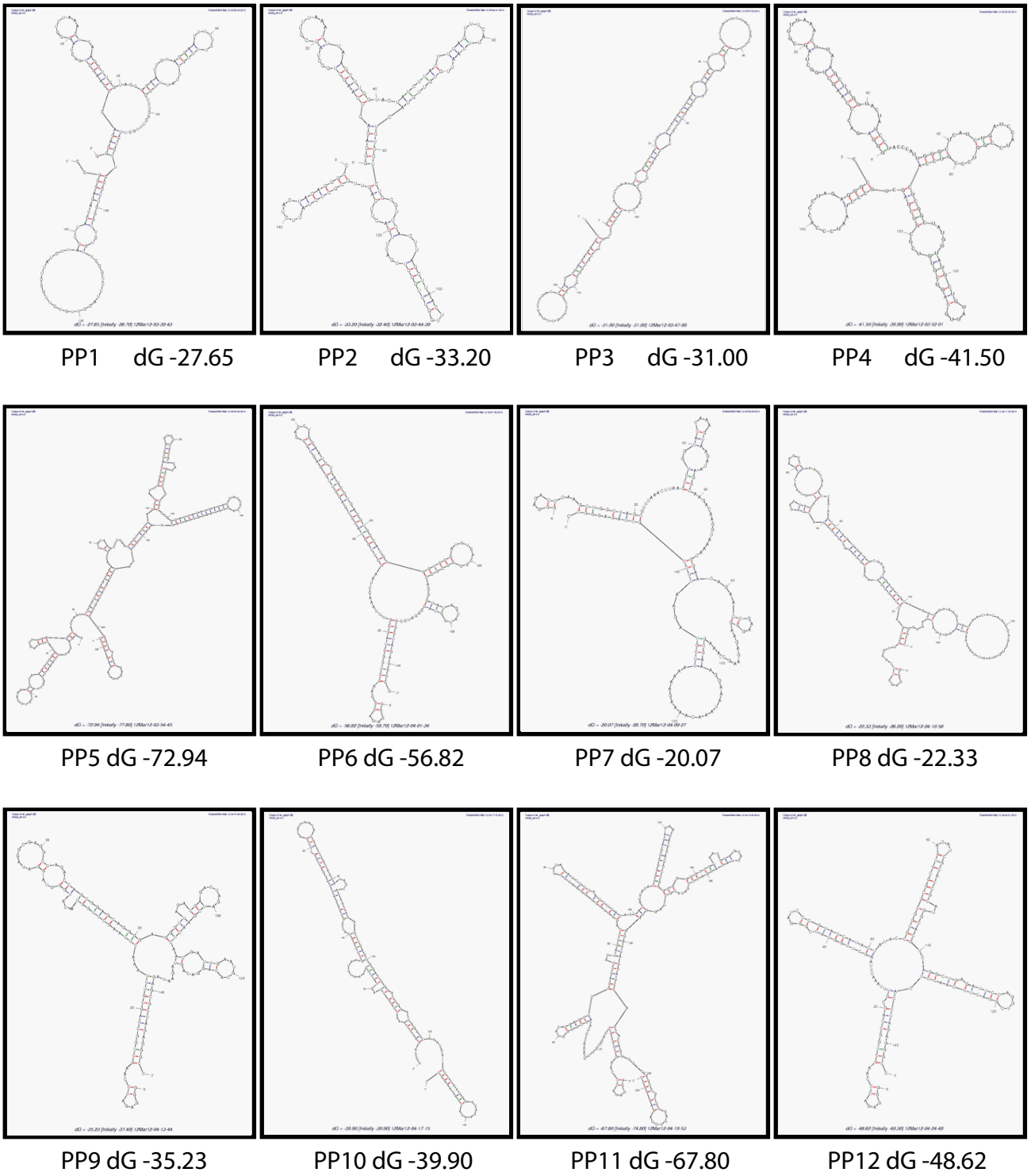
PP10
5′-GGTGGGATTA GGGCAGCTCG ACGCGACACG ACTGCAATAC AGCATAACAT AGCCGAGTGG ACGGGACCGG ATGGATCAGA
TGAGCCCAAT GGGTAGGATA-3′

PP11
5′-CTCCAACCTC ACACCACATT ACACTGGGGT GATATAATAT GATGCCGGGC GGGGGCCGTA ACGTAGCACT ACATGACCCG
ATACGCTAGG TGGGATTAGG-3′

PP12
5′CGGGATCCCG TACCATACTA TACCGTGGCG CGGCGTGACA TCGCACCGCA TGGCACGTCA GGCTGAGATT CCAGGTCGGA
CTCCAACCTCAC-3′

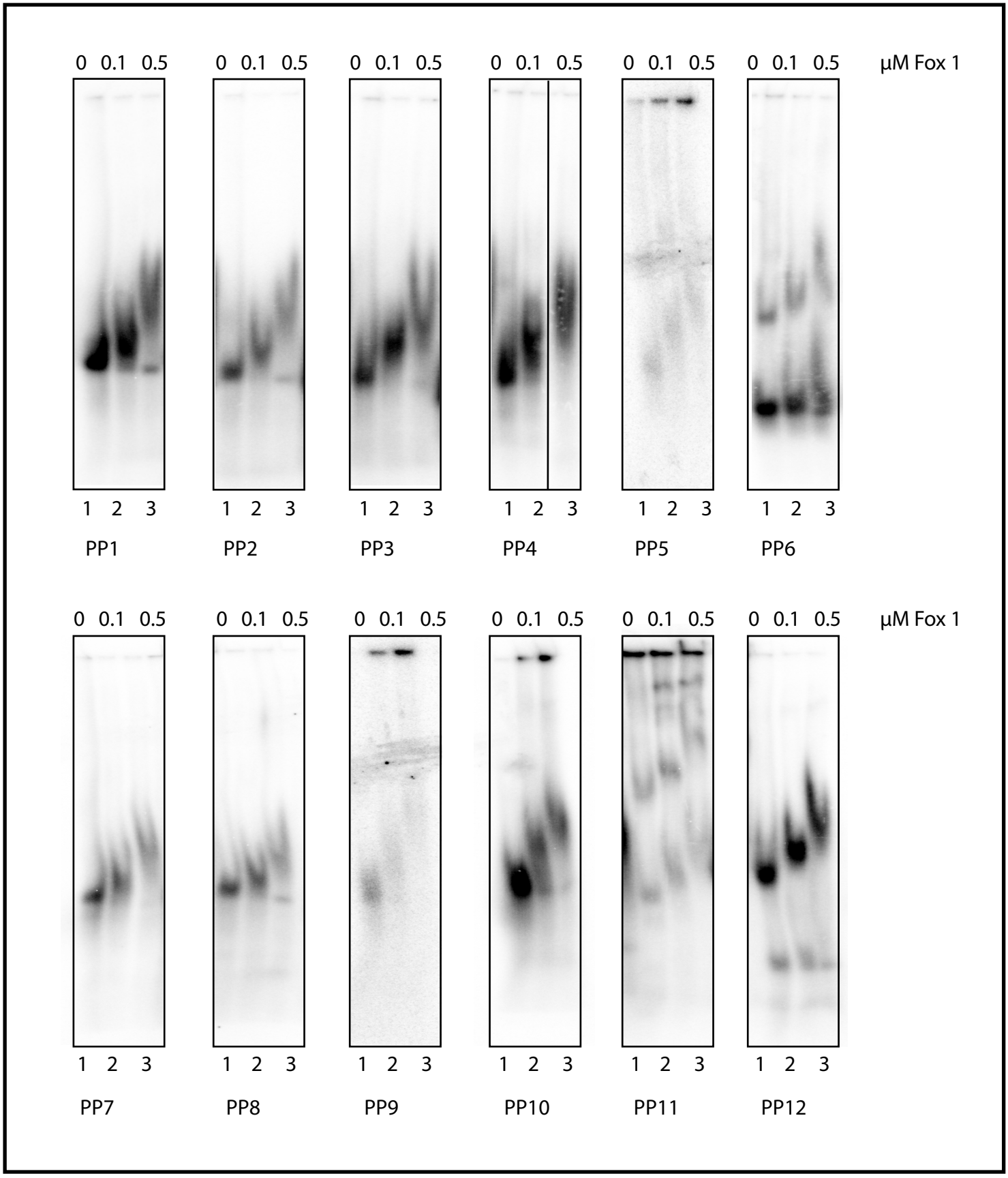
Supplementary Figure S1. List of Pentaprobe sequences encoding every possible 5 nt long motif

DNA versions of all synthetic, single stranded Pentaprobes, which together encode every possible 5 nt sequence. PP1 is reverse complementary to PP7, PP2 to PP8, and so forth, which enables production of dsDNA sequences.



Supplementary Figure S2. Secondary structure of RNA pentaprobes predicted by the Mfold web server

Each pentaprobe is represented as one secondary structure, predicted by Mfold web server, and the according free energy is indicated below each structure. In each case we show the structure with the lowest free energy, any other structure observed is energetically less favourable.



Supplementary Figure S3. Fox 1 binding to each of the Pentaprobe sequences

Each Pentaprobe is shown bound to Fox 1. Lane 1 represents the probe alone, lane2 and 3 show 0.1 and 0.5 µM protein, respectively.