

Supplementary Methods

Generation of allelic fasta records for dbSNP137 and conversion to blast database

In order to map 11 nt candidate binding sequences to SNP alleles, the optimum are sequences that have 10 nt on either flank of the allelic nucleotides, i.e. 21 nt in total for 1 nt alleles (or 20 nt for deletions); if they were any shorter, alleles mapping to the ends of the candidate would be missed, or any longer, computational effort would be unnecessarily increased due to futile mapping attempts along the flanking sequences only, i.e. where the candidate could not overlap the position of the allele. To facilitate the mapping of allelic SNP data base (or any subset thereof), chromosome-wise reference SNP (rs) fasta files for dbSNP version 137, containing the records for a total of 52,283,020 rsIDs, were downloaded on Sept 2, 2012 from ftp://ftp.ncbi.nlm.nih.gov/snp/organisms/human_9606/rs_fasta/, and processed with a custom perl script to contain, if available, 10 nt flanks on both sides of the allelic sequence. In detail, for each rsID, the nucleotide sequences for known alleles were extracted from the fasta header attribute 'alleles', and the flanking sequences were clipped to 10 nt from the provided, typically longer flanks surrounding the SNP position. Those few rsIDs that came without allele information (103,378, or 0.198 %) were not included in the final set of 105,205,157 allelic sequences for 52,179,642 rsID. Of note, a very small minority of these only has 4-9 nt flank on either side due to availability in the original rs fasta record (1782 rsIDs, or 0.0034%).

To enable efficient search for explicit 11 nt binder candidates, the above allelic fasta set (for chromosomes 1-22, X and Y) was converted to a blast source database using the program makeblastdb (NCBI blast engine version 2.2.29+) with the following essential command line arguments: `-input_type fasta -dbtype nucl`.

Supplementary Figure Legends

Figure S1. Overview of simulated structures of **(A)** Nrf2-MafG and **(B)** MafG-Nrf2 bound to DNA (5'-CAGTGACTCAGCAG-3') are shown at the time point of 10 ns together with detailed views of **(C)** Nrf2-MafG – DNA and **(D)** MafG-Nrf2 – DNA binding modes, without protein-DNA-main chain contacts. Schematic presentation of protein – DNA interactions of **(E)** Nrf2-MafG and **(F)** MafG-Nrf2 are illustrated using cyan marks for Nrf2 and green marks for MafG. Elliptical shapes stand for hydrogen bond interactions and round shaped plots for hydrophobic van der Waals' contacts.

Figure S2. C α RMSD plot illustrating the simulation stability. Nrf2-MafG-DNA is shown in blue, MafG-Nrf2-DNA in orange, Nrf2-Nrf2-DNA in grey and MafG-MafG-DNA in yellow. MafG-Nrf2-DNA and Nrf2-Nrf2-DNA compositions fluctuate more compared to the other two after 3 ns of simulation.

Figure S3. Detailed views of the **(A-B)** Nrf2-MafG – DNA (5'-CAGTGACTCAGCAG-3') and **(C-D)** MafG-Nrf2 – DNA (5'-CAGTGACTCAGCAG-3') end point structures from the 10 ns molecular dynamics simulations. Nrf2 is shown in cyan and MafG in green. Selected protein - DNA main chain interactions are also shown.

Figure S4. Image showing upper parts of helices at the time point of 10 ns for Nrf2-Nrf2 (cyan) and MafG- MafG (green). For Nrf2 homodimer, a distortion at the helical structure of subunit B occurred after 3 ns of simulation. Simulations suggest that hydrogen bonding network close to N100 is less stable for the Nrf2 homodimer than the corresponding interactions formed by N83 in the MafG homodimer.

Figure S5. Small Maf-Nrf2 heterodimer binding on single variation series. Results are depicted as measured binding relative to NQO1.ARE binding ($n=9$).

Figure S6. Pearson correlations of the predicted and measured binding strengths for i) ChIP-seq multivariate ARE sequences with new NRF2 binding model **(A)** and PWM **(B)**, ii) for position 6-8 variations with new NRF2 binding model **(C)** and PWM **(D)**, and iii) for all measured ARE sequences with NRF2 binding model **(E)** and PWM **(F)**.

Supplementary Tables

Table S1. Oligonucleotides for cloning

Table S2. Oligonucleotides for protein binding microarrays (single variations)

Table S3. Oligonucleotides for protein binding microarrays (multiple variations)

Table S4. Nrf2 binding sites in hg19: subset strong (> 0.9 relative binding strength). Locations are given in BED6 format (separate file), and can be viewed either in table format (xls) or with visualization tools, such as Integrative Genomics Viewer (IGV) (<https://www.broadinstitute.org/igv/>) or UCSC Genome Browser (<https://genome.ucsc.edu/>).

Table S5. Interactions between the protein and DNA atoms in the Nrf2-MafG – DNA and MafG-Nrf2 – DNA complexes. Interactions, excluding protein – phosphate backbone interactions, are listed for the base pairs of the GTGACTCAGCA sequence for the average structure of the last 1 ns and the end-point structure of the 10 ns MD simulation. Interactions most important for binding specificity are shown in bold.

Table S6. Single nucleotide variations

Table S7. Multivariate AREs from ChIP-seq motif detection

Table S8. Multivariate oligos for binding limit detection

Table S9. Candidate Nrf2 rSNPs. rSNPs are listed in table format (xls) on a separate file.

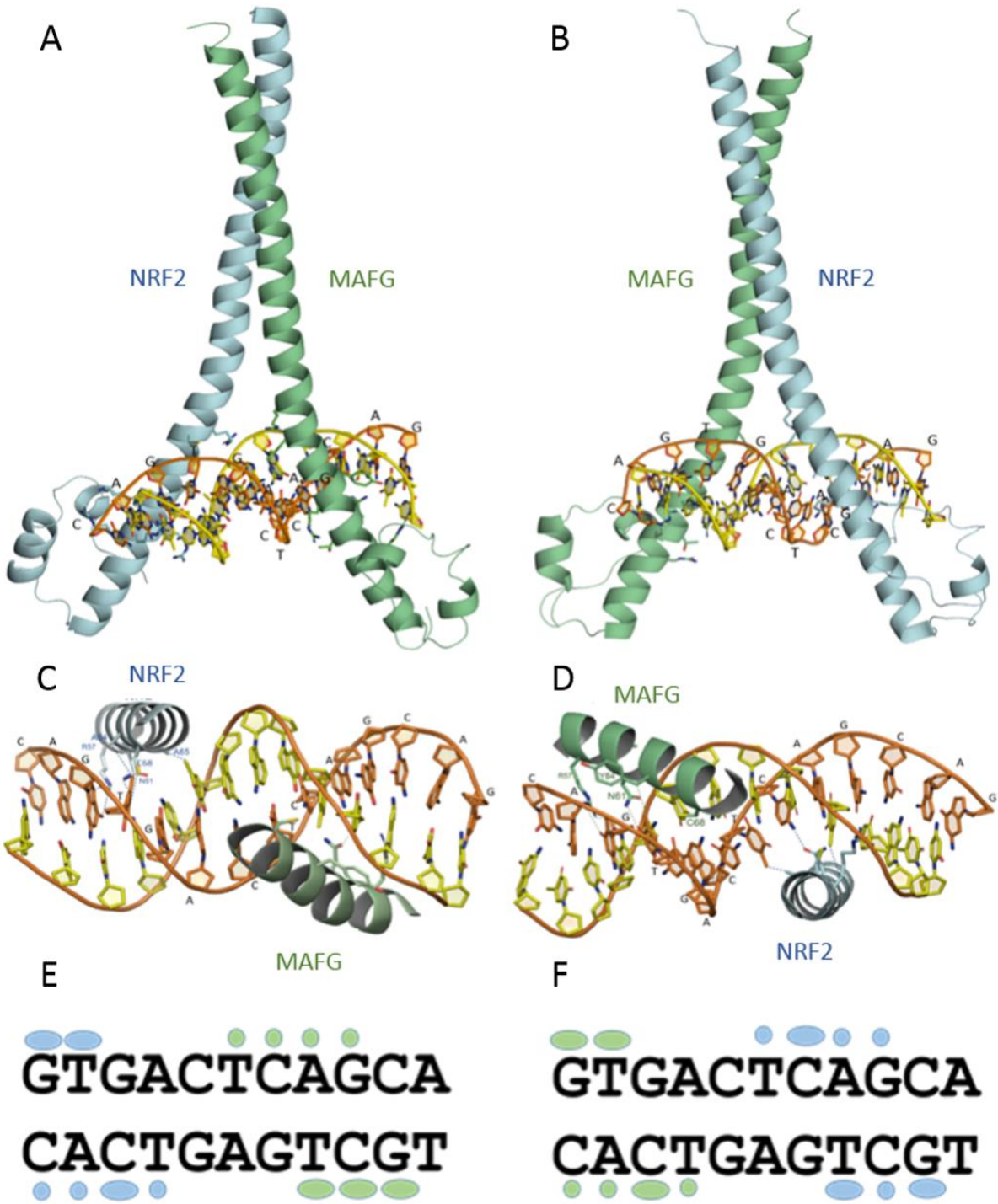


Figure S1.

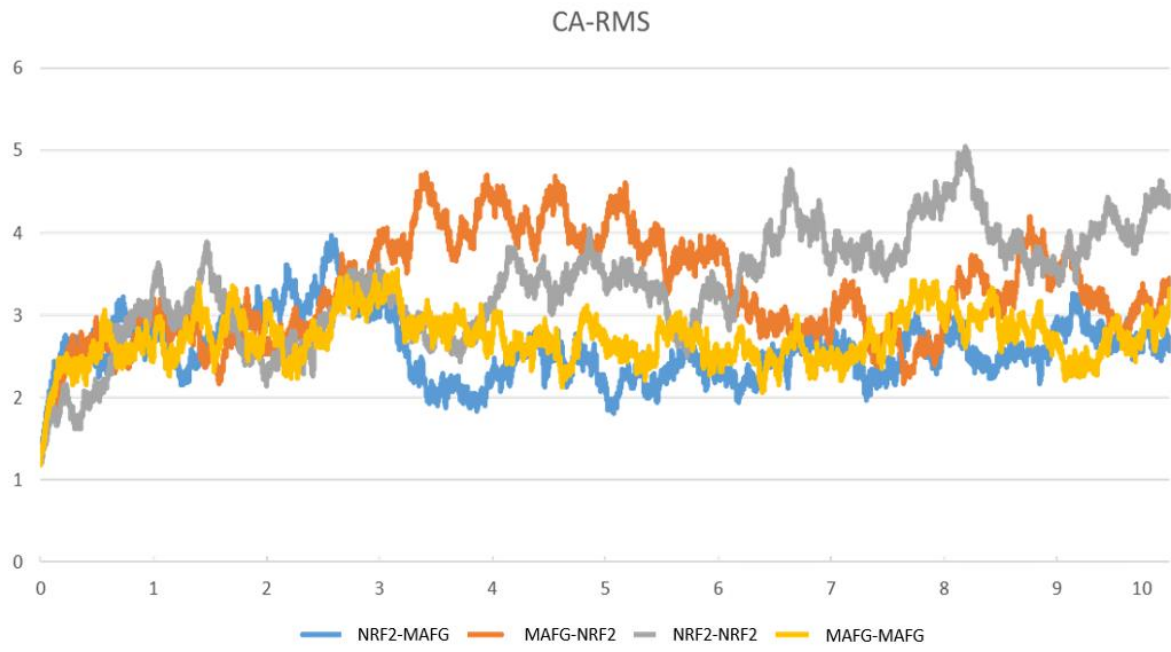


Figure S2.

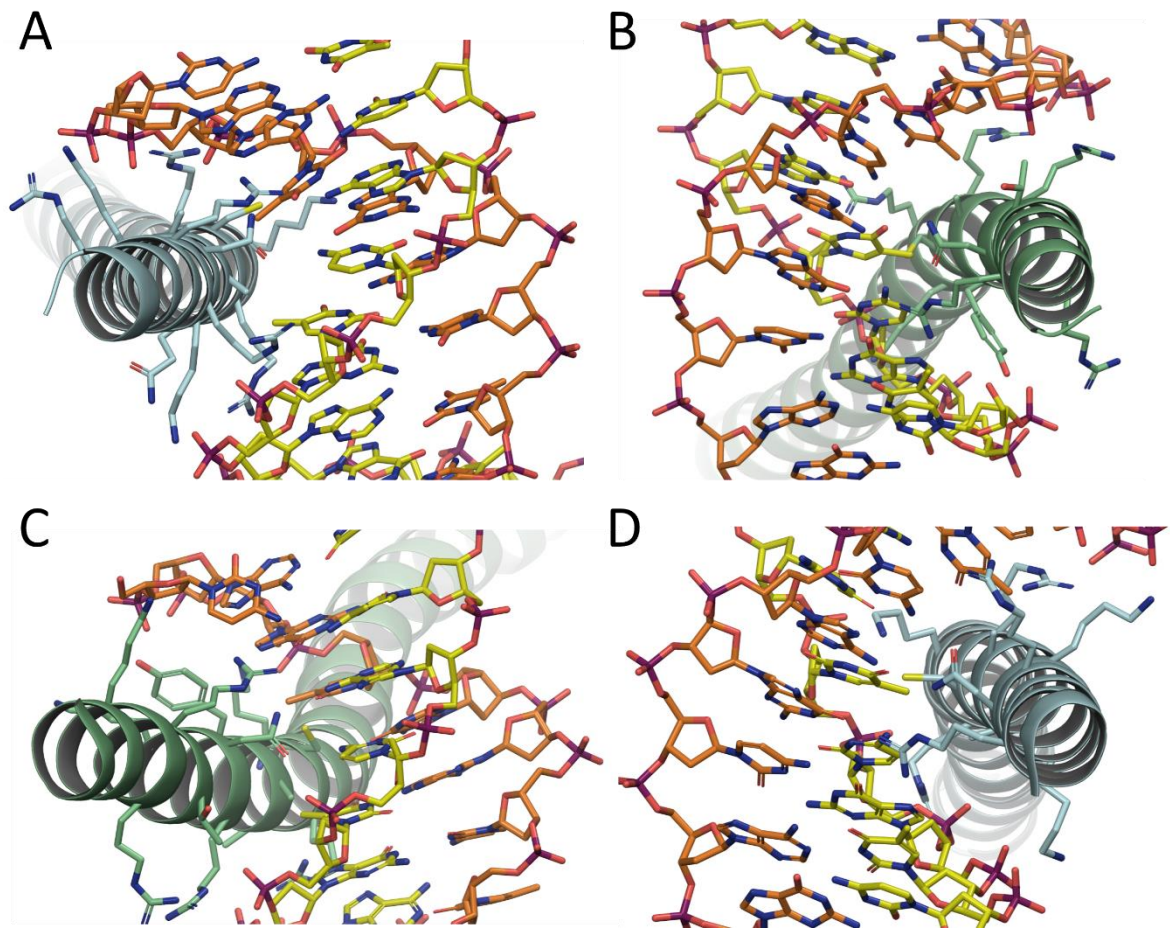


Figure S3.

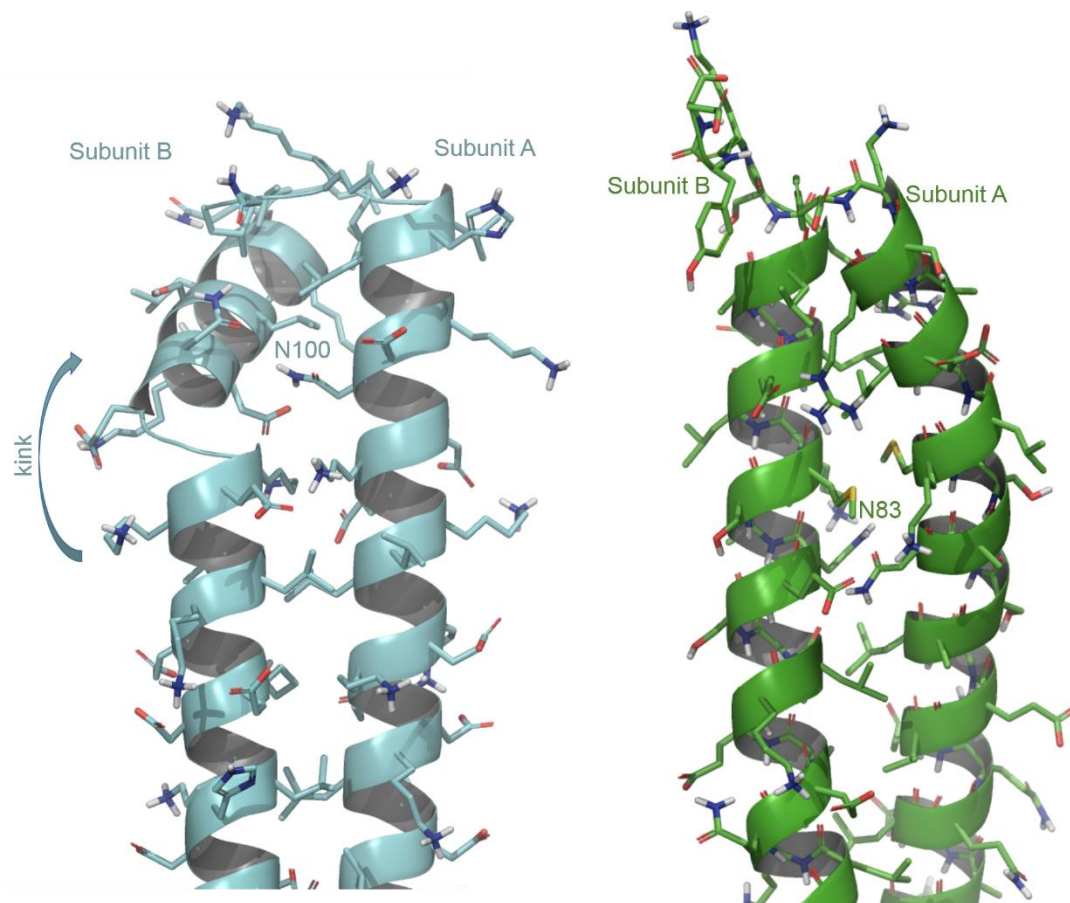


Figure S4.

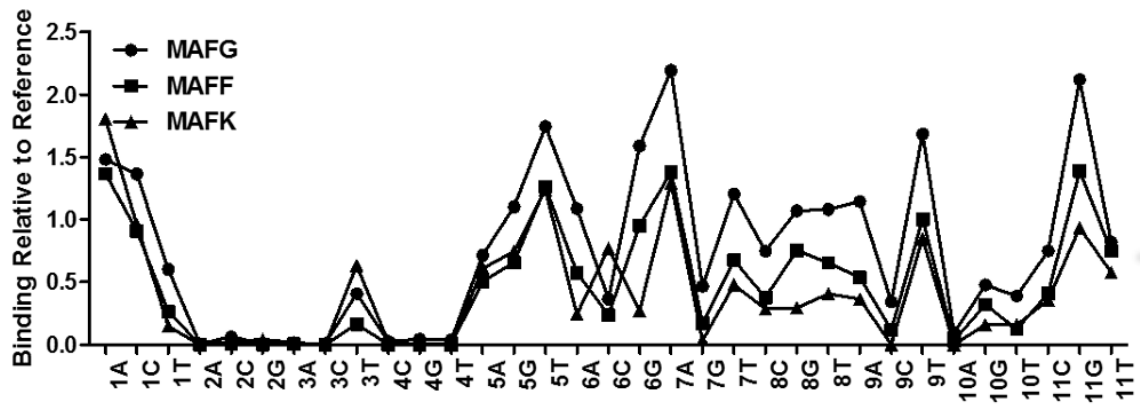


Figure S5.

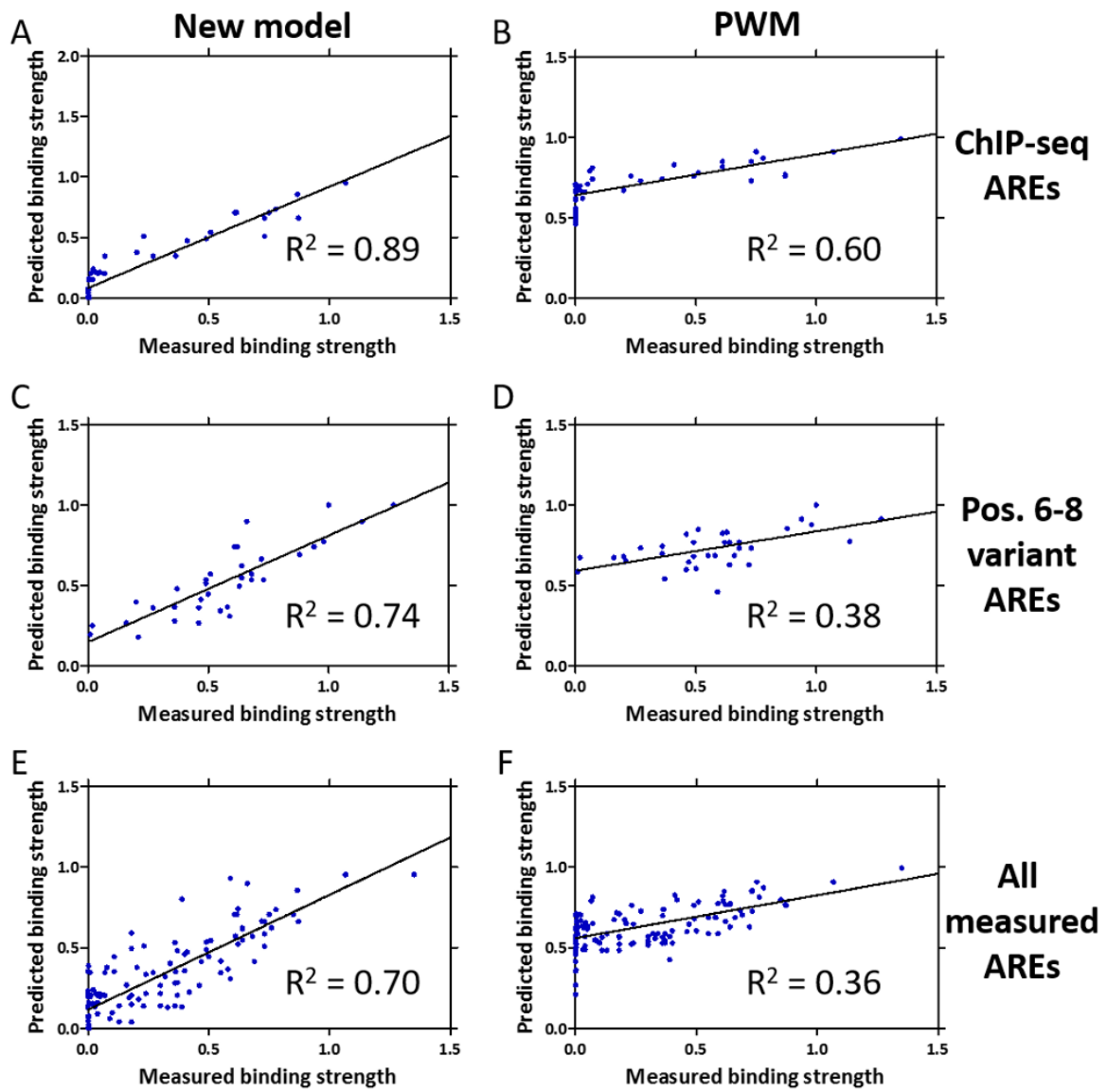


Figure S6.

Table S1.

Primer	Sequence
MAF F sense	5'-AATAAGCTTGCCACCATGTCTGTGGATCCCCTATCC-3'
MAF F antisense	5'-AAAGAATTCAGTAGGAGCAGGAGGCCG-3'
MAF K sense	5'-AATAAGCTTGCCACCATGACGACTAATCCCAAACCG-3'
MAF K antisense	5'-AAAGAATTCCTAGGATGCAGCCGAGAAGG-3'
SNP A forward	5' CTCAGCATGACTCAGCAGTCGCGAGCT 3'
SNP A reverse	5' CGCGACTGCTGAGTCATGCTGAGGTAC 3'
SNP C forward	5' CTCAGCATGCCTCAGCAGTCGCGAGCT 3'
SNP C reverse	5' CGCGACTGCTGAGGCATGCTGAGGTAC 3'

Table S2.

Name	Sequence	Name	Sequence
ARE	5'- CCGCAGTCACAGTGA CTCAGCAG AATCTGAGCC-3'	ARE_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGAGT CACTGTGACTGCGG-3'
1A	5'- CCGCAGTCACAATGA CTCAGCAGA ATCTGAGCC-3'	1A_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGAGT CATTGTGACTGCGG-3'
1C	5'- CCGCAGTCACACTGA CTCAGCAGA ATCTGAGCC-3'	1C_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGAGT CAGTGTGACTGCGG-3'
1T	5'- CCGCAGTCACATTGA CTCAGCAGA ATCTGAGCC-3'	1T_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGAGT CAATGTGACTGCGG-3'
2A	5'- CCGCAGTCACAGAGA CTCAGCAG AATCTGAGCC-3'	2A_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGAGT CTCTGTGACTGCGG-3'
2C	5'- CCGCAGTCACAGCGA CTCAGCAG AATCTGAGCC-3'	2C_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGAGT CGCTGTGACTGCGG-3'
2G	5'- CCGCAGTCACAGGGG CTCAGCAG AATCTGAGCC-3'	2G_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGAGT CCCTGTGACTGCGG-3'
3A	5'- CCGCAGTCACAGTAA CTCAGCAGA ATCTGAGCC-3'	3A_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGAGT TACTGTGACTGCGG-3'
3C	5'- CCGCAGTCACAGTCA CTCAGCAGA ATCTGAGCC-3'	3C_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGAGT GACTGTGACTGCGG-3'
3T	5'- CCGCAGTCACAGTTA CTCAGCAGA ATCTGAGCC-3'	3T_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGAGT AACTGTGACTGCGG-3'
4C	5'- CCGCAGTCACAGTGC CTCAGCAGA ATCTGAGCC-3'	4C_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGAGG CACTGTGACTGCGG-3'
4G	5'- CCGCAGTCACAGTGG CTCAGCAG AATCTGAGCC-3'	4G_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGAGC CACTGTGACTGCGG-3'
4T	5'- CCGCAGTCACAGTGT CTCAGCAGA ATCTGAGCC-3'	4T_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGAGA CACTGTGACTGCGG-3'
5A	5'- CCGCAGTCACAGTGA ATCAGCAG AATCTGAGCC-3'	5A_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGATT CACTGTGACTGCGG-3'
5G	5'- CCGCAGTCACAGTGA GTCAGCAG AATCTGAGCC-3'	5G_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGACT CACTGTGACTGCGG-3'
5T	5'- CCGCAGTCACAGTGA TTCAGCAGA ATCTGAGCC-3'	5T_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGAAT CACTGTGACTGCGG-3'

6A	5'- CCGCAGTCACAGTGACACAGCAG AATCTGAGCC-3'	6A_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGTGT CACTGTGACTGCGG-3'
6C	5'- CCGCAGTCACAGTGACCCAGCAG AATCTGAGCC-3'	6C_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGGGT CACTGTGACTGCGG-3'
6G	5'- CCGCAGTCACAGTGACGCAGCAG AATCTGAGCC-3'	6G_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGCGT CACTGTGACTGCGG-3'
7A	5'- CCGCAGTCACAGTGACTAAGCAG AATCTGAGCC-3'	7A_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTTAGT CACTGTGACTGCGG-3'
7G	5'- CCGCAGTCACAGTGACTGAGCAG AATCTGAGCC-3'	7G_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTCAGT CACTGTGACTGCGG-3'
7T	5'- CCGCAGTCACAGTGACTTAGCAGA ATCTGAGCC-3'	7T_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTAAGT CACTGTGACTGCGG-3'
8C	5'- CCGCAGTCACAGTGACTCCGCAGA ATCTGAGCC-3'	8C_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCGGAGT CACTGTGACTGCGG-3'
8G	5'- CCGCAGTCACAGTGACTCGGCAG AATCTGAGCC-3'	8G_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCCGAGT CACTGTGACTGCGG-3'
8T	5'- CCGCAGTCACAGTGACTCTGCAGA ATCTGAGCC-3'	8T_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCAGAGT CACTGTGACTGCGG-3'
9A	5'- CCGCAGTCACAGTGACTCAACAGA ATCTGAGCC-3'	9A_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGTTGAGT CACTGTGACTGCGG-3'
9C	5'- CCGCAGTCACAGTGACTCACCAGA ATCTGAGCC-3'	9C_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGGTGAGT CACTGTGACTGCGG-3'
9T	5'- CCGCAGTCACAGTGACTCATCAGA ATCTGAGCC-3'	9T_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGATGAGT CACTGTGACTGCGG-3'
10A	5'- CCGCAGTCACAGTGACTCAGAAG AATCTGAGCC-3'	10A_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTTCTGAGT CACTGTGACTGCGG-3'
10G	5'- CCGCAGTCACAGTGACTCAGGAG AATCTGAGCC-3'	10G_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTCCTGAGT CACTGTGACTGCGG-3'
10T	5'- CCGCAGTCACAGTGACTCAGTAGA ATCTGAGCC-3'	10T_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTACTGAGT CACTGTGACTGCGG-3'
11C	5'- CCGCAGTCACAGTGACTCAGCCGA ATCTGAGCC-3'	11C_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCGGCTGAGT CACTGTGACTGCGG-3'
11G	5'- CCGCAGTCACAGTGACTCAGCGG AATCTGAGCC-3'	11G_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCGGCTGAGT CACTGTGACTGCGG-3'

11T	5'- CCGCAGTCACAGTGA CTCAGCTGATCTGAGCC-3'	11T_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCAGCTGAGT CACTGTGACTGCGG-3'
Primer	5'-ACCCAACCGCCCAACTT-Biotin- 3'		

Table S3.

Name	Sequence	Name	Sequence
mv1	5'- CCGCAGTCACAAGGACTCAGCAG AATCTGAGCC-3'	mv1_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGAG TCCTTGTGACTGCGG-3'
mv2	5'- CCGCAGTCACAAGGACTAAGCAG AATCTGAGCC-3'	mv2_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTTAG TCCTTGTGACTGCGG-3'
mv3	5'- CCGCAGTCACAATCACACAGCAG AATCTGAGCC-3'	mv3_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGTG TGATTGTGACTGCGG-3'
mv4	5'- CCGCAGTCACAATCACTAAGCAG AATCTGAGCC-3'	mv4_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTTAG TGATTGTGACTGCGG-3'
mv5	5'- CCGCAGTCACAATCACTCAGCAGA ATCTGAGCC-3'	mv5_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGAG TGATTGTGACTGCGG-3'
mv6	5'- CCGCAGTCACAATCACTCCGCAGA ATCTGAGCC-3'	mv6_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCGGAG TGATTGTGACTGCGG-3'
mv7	5'- CCGCAGTCACAATGACAAAGCAG AATCTGAGCC-3'	mv7_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTTTG TCATTGTGACTGCGG-3'
mv8	5'- CCGCAGTCACAATGACACAGCAG AATCTGAGCC-3'	mv8_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGTG TCATTGTGACTGCGG-3'
mv9	5'- CCGCAGTCACAATGACACCGCAG AATCTGAGCC-3'	mv9_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCGGTG TCATTGTGACTGCGG-3'
mv10	5'- CCGCAGTCACAATGACACGGCAG AATCTGAGCC-3'	mv10_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCCGTG TCATTGTGACTGCGG-3'
mv11	5'- CCGCAGTCACAATGACAGAGCAG AATCTGAGCC-3'	mv11_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTCTG TCATTGTGACTGCGG-3'
mv12	5'- CCGCAGTCACAATGACATAGCAG AATCTGAGCC-3'	mv12_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTATG TCATTGTGACTGCGG-3'
mv13	5'- CCGCAGTCACAATGACCAAGCAG AATCTGAGCC-3'	mv13_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTTGG TCATTGTGACTGCGG-3'
mv14	5'- CCGCAGTCACAATGACCCAGCAG AATCTGAGCC-3'	mv14_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGGG TCATTGTGACTGCGG-3'
mv15	5'- CCGCAGTCACAATGACCCGGCAG AATCTGAGCC-3'	mv15_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCCGGG TCATTGTGACTGCGG-3'
mv16	5'- CCGCAGTCACAATGACGCAGCAG AATCTGAGCC-3'	mv16_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGCG TCATTGTGACTGCGG-3'

mv17	5'- CCGCAGTCACAATGACTAAGCAG AATCTGAGCC-3'	mv17_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTTAG TCATTGTGACTGCGG-3'
mv18	5'- CCGCAGTCACAATGACTAGGCAG AATCTGAGCC-3'	mv18_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCCTAG TCATTGTGACTGCGG-3'
mv19	5'- CCGCAGTCACAATGACTCAGCAG AATCTGAGCC-3'	mv19_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGAG TCATTGTGACTGCGG-3'
mv20	5'- CCGCAGTCACAATGACTCCGCAG AATCTGAGCC-3'	mv20_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCGGAG TCATTGTGACTGCGG-3'
mv21	5'- CCGCAGTCACAATGACTCGGCAG AATCTGAGCC-3'	mv21_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCCGAG TCATTGTGACTGCGG-3'
mv22	5'- CCGCAGTCACAATGACTCTGCAG AATCTGAGCC-3'	mv22_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCAGAG TCATTGTGACTGCGG-3'
mv23	5'- CCGCAGTCACAATGACTGAGCAG AATCTGAGCC-3'	mv23_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTCAG TCATTGTGACTGCGG-3'
mv24	5'- CCGCAGTCACAATGACTTAGCAG AATCTGAGCC-3'	mv24_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTAAG TCATTGTGACTGCGG-3'
mv25	5'- CCGCAGTCACAATGACTTGGCAG AATCTGAGCC-3'	mv25_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCCAAG TCATTGTGACTGCGG-3'
mv26	5'- CCGCAGTCACAATGCCACAGCAG AATCTGAGCC-3'	mv26_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGTG GCATTGTGACTGCGG-3'
mv27	5'- CCGCAGTCACAATGCCCCAGCAG AATCTGAGCC-3'	mv27_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGGG GCATTGTGACTGCGG-3'
mv28	5'- CCGCAGTCACAATGCCTCAGCAG AATCTGAGCC-3'	mv28_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGAG GCATTGTGACTGCGG-3'
mv29	5'- CCGCAGTCACAATGGCTAAGCAG AATCTGAGCC-3'	mv29_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTTAG CCATTGTGACTGCGG-3'
mv30	5'- CCGCAGTCACAATGGCTCAGCAG AATCTGAGCC-3'	mv30_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGAG CCATTGTGACTGCGG-3'
mv31	5'- CCGCAGTCACAATGTCACAGCAG AATCTGAGCC-3'	mv31_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGTG ACATTGTGACTGCGG-3'
mv32	5'- CCGCAGTCACAATGTCTAAGCAG AATCTGAGCC-3'	mv32_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTTAG ACATTGTGACTGCGG-3'
mv33	5'- CCGCAGTCACAATGTCTCAGCAG AATCTGAGCC-3'	mv33_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGAG ACATTGTGACTGCGG-3'

mv34	5'- CCGCAGTCACAATTACACAGCAG AATCTGAGCC-3'	mv34_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGTG TAATTGTGACTGCGG-3'
mv35	5'- CCGCAGTCACAATTACCCAGCAGA ATCTGAGCC-3'	mv35_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGGG TAATTGTGACTGCGG-3'
mv36	5'- CCGCAGTCACAATTACTAAGCAGA ATCTGAGCC-3'	mv36_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTTAG TAATTGTGACTGCGG-3'
mv37	5'- CCGCAGTCACAATTACTCAGCAGA ATCTGAGCC-3'	mv37_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGAG TAATTGTGACTGCGG-3'
mv38	5'- CCGCAGTCACAATTACTTAGCAGA ATCTGAGCC-3'	mv38_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTAAG TAATTGTGACTGCGG-3'
mv39	5'- CCGCAGTCACAATTTCTCAGCAGA ATCTGAGCC-3'	mv39_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGAG AAATTGTGACTGCGG-3'
mv40	5'- CCGCAGTCACAATCACTCAGGAG AATCTGAGCC-3'	mv40_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTCCTGAG TGATTGTGACTGCGG-3'
mv41	5'- CCGCAGTCACAATGACACAGGAG AATCTGAGCC-3'	mv41_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTCCTGTG TCATTGTGACTGCGG-3'
mv42	5'- CCGCAGTCACAATGACCCAGGAG AATCTGAGCC-3'	mv42_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTCCTGGG TCATTGTGACTGCGG-3'
mv43	5'- CCGCAGTCACAATGACTAAGTAG AATCTGAGCC-3'	mv43_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTACTTAG TCATTGTGACTGCGG-3'
mv44	5'- CCGCAGTCACAATGACTAAGGAG AATCTGAGCC-3'	mv44_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTCCTTAG TCATTGTGACTGCGG-3'
mv45	5'- CCGCAGTCACAATGACTCAGTAG AATCTGAGCC-3'	mv45_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTACTGAG TCATTGTGACTGCGG-3'
mv46	5'- CCGCAGTCACAATGACTCAGGAG AATCTGAGCC-3'	mv46_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTCCTGAG TCATTGTGACTGCGG-3'
mv47	5'- CCGCAGTCACAATTACTCAGGAG AATCTGAGCC-3'	mv47_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTCCTGAG TAATTGTGACTGCGG-3'
mv48	5'- CCGCAGTCACACTTACTCAGCAGA ATCTGAGCC-3'	mv48_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGAG TAAGTGTGACTGCGG-3'
mv49	5'- CCGCAGTCACATTTACTCAGCAGA ATCTGAGCC-3'	mv49_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGAG TAAATGTGACTGCGG-3'
mv50	5'- CCGCAGTCACAGTGACTCAGGCG AATCTGAGCC-3'	mv50_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTGCCTGAG TCACTGTGACTGCGG-3'

mv51	5'- CCGCAGTCACAGTGACTCAGGTG AATCTGAGCC-3'	mv51_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCACCTGAG TCACTGTGACTGCGG-3'
mv52	5'- CCGCAGTCACAGTGACTCAGGGG AATCTGAGCC-3'	mv52_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCCTGAG TCACTGTGACTGCGG-3'
mv53	5'- CCGCAGTCACAGTGACTCAGTCG AATCTGAGCC-3'	mv53_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCGACTGAG TCACTGTGACTGCGG-3'
mv54	5'- CCGCAGTCACAGTGACTCAGTTG AATCTGAGCC-3'	mv54_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCAACTGAG TCACTGTGACTGCGG-3'
mv55	5'- CCGCAGTCACAGTGACTCAGTGG AATCTGAGCC-3'	mv55_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCCTGAG TCACTGTGACTGCGG-3'
mv56	5'- CCGCAGTCACAGTGACTCATCCGA ATCTGAGCC-3'	mv56_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCGGATGAG TCACTGTGACTGCGG-3'
mv57	5'- CCGCAGTCACAGTGACTCATCTGA ATCTGAGCC-3'	mv57_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCAGATGAG TCACTGTGACTGCGG-3'
mv58	5'- CCGCAGTCACAGTGACTCATCGG AATCTGAGCC-3'	mv58_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCAGATGAG TCACTGTGACTGCGG-3'
mv59	5'- CCGCAGTCACAATGACTCATCAGA ATCTGAGCC-3'	mv59_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCATGATGAG TCACTGTGACTGCGG-3'
mv60	5'- CCGCAGTCACAGTGACTCAGAGG AATCTGAGCC-3'	mv60_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCCTCTGAG TCACTGTGACTGCGG-3'
mv61	5'- CCGCAGTCACAGTGACTCAGACG AATCTGAGCC-3'	mv61_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCGTCTGAG TCACTGTGACTGCGG-3'
mv62	5'- CCGCAGTCACAGTGACTCAGATG AATCTGAGCC-3'	mv62_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCATCTGAG TCACTGTGACTGCGG-3'
mv63	5'- CCGCAGTCACAGTGACTCAACGG AATCTGAGCC-3'	mv63_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCAGTTGAG TCACTGTGACTGCGG-3'
mv64	5'- CCGCAGTCACAGTGACTCAACCG AATCTGAGCC-3'	mv64_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCAGTTGAG TCACTGTGACTGCGG-3'
mv65	5'- CCGCAGTCACAGTGACTCAACTG AATCTGAGCC-3'	mv65_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCAGTTGAG TCACTGTGACTGCGG-3'
mv66	5'- CCGCAGTCACAGTGACTCACCGG AATCTGAGCC-3'	mv66_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCAGTTGAG TCACTGTGACTGCGG-3'
mv67	5'- CCGCAGTCACAGTGACTCACCCG AATCTGAGCC-3'	mv67_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCAGTTGAG TCACTGTGACTGCGG-3'

mv68	5'- CCGCAGTCACAGTGA CTCACCTGA ATCTGAGCC-3'	mv68_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCAGGTGAG TCACTGTGACTGCGG-3'
mv69	5'- CCGCAGTCACAGTGACCCCGCAG AATCTGAGCC-3'	mv69_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCGGGG TCACTGTGACTGCGG-3'
mv70	5'- CCGCAGTCACAGTGACGGGGCAG AATCTGAGCC-3'	mv70_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCCCG TCACTGTGACTGCGG-3'
mv71	5'- CCGCAGTCACAGTGA CTTTGCAG AATCTGAGCC-3'	mv71_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCAAAG TCACTGTGACTGCGG-3'
mv72	5'- CCGCAGTCACAGTGACACTGCAG AATCTGAGCC-3'	mv72_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCAGTG TCACTGTGACTGCGG-3'
mv73	5'- CCGCAGTCACAGTGACCTAGCAG AATCTGAGCC-3'	mv73_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTAGG TCACTGTGACTGCGG-3'
mv74	5'- CCGCAGTCACAGTGACCGAGCAG AATCTGAGCC-3'	mv74_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTCGG TCACTGTGACTGCGG-3'
mv75	5'- CCGCAGTCACAGTGACCCTGCAG AATCTGAGCC-3'	mv75_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCAGGG TCACTGTGACTGCGG-3'
mv76	5'- CCGCAGTCACAGTGACGGAGCAG AATCTGAGCC-3'	mv76_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTCCG TCACTGTGACTGCGG-3'
mv77	5'- CCGCAGTCACAGTGACGAAGCAG AATCTGAGCC-3'	mv77_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTTCG TCACTGTGACTGCGG-3'
mv78	5'- CCGCAGTCACAGTGACGTAGCAG AATCTGAGCC-3'	mv78_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTACG TCACTGTGACTGCGG-3'
mv79	5'- CCGCAGTCACAGTGACGCCGCAG AATCTGAGCC-3'	mv79_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCGGCC TCACTGTGACTGCGG-3'
mv80	5'- CCGCAGTCACAGTGACGCGGCAG AATCTGAGCC-3'	mv80_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCCCG TCACTGTGACTGCGG-3'
mv81	5'- CCGCAGTCACAGTGACGCTGCAG AATCTGAGCC-3'	mv81_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCAGCG TCACTGTGACTGCGG-3'
mv82	5'- CCGCAGTCACAGTGA CTACGCAG AATCTGAGCC-3'	mv82_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCGTAG TCACTGTGACTGCGG-3'
mv83	5'- CCGCAGTCACAGTGA CTATGCAG AATCTGAGCC-3'	mv83_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCATAG TCACTGTGACTGCGG-3'
mv84	5'- CCGCAGTCACAGTGA CTGCGCAG AATCTGAGCC-3'	mv84_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCGCAG TCACTGTGACTGCGG-3'

mv85	5'- CCGCAGTCACAGTGACTGGGCAG AATCTGAGCC-3'	mv85_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCCAG TCACTGTGACTGCGG-3'
mv86	5'- CCGCAGTCACAGTGACTGTGCAG AATCTGAGCC-3'	mv86_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCACAG TCACTGTGACTGCGG-3'
mv87	5'- CCGCAGTCACAGTGACTTCGCAG AATCTGAGCC-3'	mv87_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCGAAG TCACTGTGACTGCGG-3'
mv88	5'- CCGCAGTCACAGTGACTTGGCAG AATCTGAGCC-3'	mv88_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCCAAG TCACTGTGACTGCGG-3'
mv89	5'- CCGCAGTCACAATGATTCAGCAG AATCTGAGCC-3'	mv89_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGAA TCATTGTGACTGCGG-3'
mv90	5'- CCGCAGTCACAATGAGTCAGCAG AATCTGAGCC-3'	mv90_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGAC TCATTGTGACTGCGG-3'
mv91	5'- CCGCAGTCACAATGAATCAGCAG AATCTGAGCC-3'	mv91_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTGAT TCATTGTGACTGCGG-3'
mv92	5'- CCGCAGTCACAATGACTCAGCGG AATCTGAGCC-3'	mv92_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCCGCTGAG TCATTGTGACTGCGG-3'
mv93	5'- CCGCAGTCACAATGACTCAGCCG AATCTGAGCC-3'	mv93_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCCGCTGAG TCATTGTGACTGCGG-3'
mv94	5'- CCGCAGTCACAATGACTCAGCTG AATCTGAGCC-3'	mv94_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCCAGCTGAG TCATTGTGACTGCGG-3'
mv95	5'- CCGCAGTCACAATGATATAGCAG AATCTGAGCC-3'	mv95_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTATA TCATTGTGACTGCGG-3'
mv96	5'- CCGCAGTCACAATGAGATAGCAG AATCTGAGCC-3'	mv96_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTATC TCATTGTGACTGCGG-3'
mv97	5'- CCGCAGTCACAATGAAATAGCAG AATCTGAGCC-3'	mv97_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTATTT CATTGTGACTGCGG-3'
mv98	5'- CCGCAGTCACAATGACATAGCGG AATCTGAGCC-3'	mv98_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCCGCTATG TCATTGTGACTGCGG-3'
mv99	5'- CCGCAGTCACAATGACATAGCCG AATCTGAGCC-3'	mv99_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCCGCTATG TCATTGTGACTGCGG-3'
mv100	5'- CCGCAGTCACAATGACATAGCTG AATCTGAGCC-3'	mv100_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCCAGCTATG TCATTGTGACTGCGG-3'
mv101	5'- CCGCAGTCACAATGATTCAGTAG AATCTGAGCC-3'	mv101_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTACTGAA TCATTGTGACTGCGG-3'

mv102	5'- CCGCAGTCACAATGAGTCAGTAG AATCTGAGCC	mv102_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTACTGAC TCATTGTGACTGCGG-3'
mv103	5'- CCGCAGTCACAATGAATCAGTAG AATCTGAGCC-3'	mv103_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTACTGAT TCATTGTGACTGCGG-3'
mv104	5'- CCGCAGTCACAATGACTCAGTGG AATCTGAGCC-3'	mv104_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCCACTGAG TCATTGTGACTGCGG-3'
mv105	5'- CCGCAGTCACAATGACTCAGTCG AATCTGAGCC-3'	mv105_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTGACTGAG TCATTGTGACTGCGG-3'
mv106	5'- CCGCAGTCACAATGACTCAGTTGA ATCTGAGCC-3'	mv106_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCAACTGAG TCATTGTGACTGCGG-3'
mv107	5'- CCGCAGTCACAATGAATAAGCGG AATCTGAGCC-3'	mv107_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCCGCTTAT TCATTGTGACTGCGG-3'
mv108	5'- CCGCAGTCACAATGATTAAGCCG AATCTGAGCC-3'	mv108_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCCGCTTAA TCATTGTGACTGCGG-3'
mv109	5'- CCGCAGTCACAATGAGTAAGCTG AATCTGAGCC-3'	mv109_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTGAGCTTAC TCATTGTGACTGCGG-3'
mv110	5'- CCGCAGTCACAATGAGACGGCGG AATCTGAGCC-3'	mv110_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCCGCCGTC TCATTGTGACTGCGG-3'
mv111	5'- CCGCAGTCACAATGAAACGGCCG AATCTGAGCC-3'	mv111_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCCGCCGTT TCATTGTGACTGCGG-3'
mv112	5'- CCGCAGTCACAATGATACGGCTG AATCTGAGCC-3'	mv112_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTGAGCCGTA TCATTGTGACTGCGG-3'
mv113	5'- CCGCAGTCACAATGATTAAGGGG AATCTGAGCC-3'	mv113_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCCCCTTAA TCATTGTGACTGCGG-3'
mv114	5'- CCGCAGTCACAATGAGTAAGGCG AATCTGAGCC-3'	mv114_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTGCGCTTAC TCATTGTGACTGCGG-3'
mv115	5'- CCGCAGTCACAATGAATAAGGTG AATCTGAGCC-3'	mv115_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCACCTTATT CATTGTGACTGCGG-3'
mv116	5'- CCGCAGTCACAATGATGCAGCGG AATCTGAGCC-3'	mv116_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCCGCTGCA TCATTGTGACTGCGG-3'
mv117	5'- CCGCAGTCACACTGAGGCAGCCG AATCTGAGCC-3'	mv117_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCCGCTGCC TCAGTGTGACTGCGG-3'
mv118	5'- CCGCAGTCACAGTACTCAGTAG AATCTGAGCC-3'	mv118_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTACTGAG TCATTGTGACTGCGG-3'

mv119	5'- CCGCAGTCACACTGACTCAGTAG AATCTGAGCC-3'	mv119_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTACTGAG TCAGTGTGACTGCGG-3'
mv120	5'- CCGCAGTCACATTGACTCAGTAGA ATCTGAGCC-3'	mv120_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTACTGAG TCAATGTGACTGCGG-3'
mv121	5'- CCGCAGTCACAGTGACATAGCAG AATCTGAGCC-3'	mv121_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTATG TCACTGTGACTGCGG-3'
mv122	5'- CCGCAGTCACACTGACATAGCAG AATCTGAGCC-3'	mv122_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTATG TCAGTGTGACTGCGG-3'
mv123	5'- CCGCAGTCACATTGACATAGCAG AATCTGAGCC-3'	mv123_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCTGCTATG TCAATGTGACTGCGG-3'
mv124	5'- CCGCAGTCACATTGAAGCAGCTG AATCTGAGCC-3'	mv124_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCAGCTGCT TCAATGTGACTGCGG-3'
mv125	5'- CCGCAGTCACAATGATTGAGCGG AATCTGAGCC-3'	mv125_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCGGCTCAA TCATTGTGACTGCGG-3'
mv126	5'- CCGCAGTCACACTGAGTGAGCCG AATCTGAGCC-3'	mv126_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCGGCTCAC TCAGTGTGACTGCGG-3'
mv127	5'- CCGCAGTCACATTGAATGAGCTG AATCTGAGCC-3'	mv127_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCAGCTCAT TCAATGTGACTGCGG-3'
mv128	5'- CCGCAGTCACAATGATTAAGTGG AATCTGAGCC-3'	mv128_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCCAATTAA TCATTGTGACTGCGG-3'
mv129	5'- CCGCAGTCACACTGAGTAAGTCG AATCTGAGCC-3'	mv129_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCGACTTAC TCAGTGTGACTGCGG-3'
mv130	5'- CCGCAGTCACATTGAATAAGTTGA ATCTGAGCC-3'	mv130_L	5'- AAGTTGGGCGGTTGGGTGGCTCAGATTCAACTTAT TCAATGTGACTGCGG-3'
Primer	5'-ACCCAACCGCCCAACTT-Biotin- 3'		

Table S5.

NRF2-MAFG														
Nucleotide	Atom	Residue/ NRF2	Residue/ MAFG	Atom	Distance ^a (Å)	Distance ^b (Å)	Nucleotide	Atom	Residue/ NRF2	Residue/ MAFG	Atom	Distance ^a (Å)	Distance ^b (Å)	
1G	O6	R57		NH2	2,76	2,96	11C	N4	R57		NH2	3,87	4,30	
	N7	R57		NH1	3,07	2,89								
2T	O4	N61		ND2	2,8	2,76	10A	N6	R57		NH2	3,58	3,36	
	C7	A64		CB	4,20	3,96			N6	N61		ND2	4,13	4,16
	C7	A65		CB	4,54	4,23								
3G							9C	N4	N61		OD1	2,97	3,12	
4A							8T	C7	A65		CB	3,88	3,40	
5C							7G							
6T							6A							
7C	N4		N61	ND2	3,64	4,04	5G							
8A	N6		N61	ND2	3,56	3,90	4T	O4		N61	ND2	3,03	3,04	
9G	O6	R57	NH2	2,89	3,19	C7			C68	SG	4,00	3,87		
						C7			Y64	CB	4,26	3,7		
10C						3C	N4		N61	OD1	2,86	2,98		
11A							2G	N7		R57	NH1	3,03	2,95	
								O6		R57	NH2	2,78	2,85	

MAFG-NRF2														
Nucleotide	Atom	Residue/M AFG	Residue/ NRF2	Atom	Distance ^a (Å)	Distance ^b (Å)	Nucleotide	Atom	Residue/ MAFG	Residue/ NRF2	Atom	Distance ^a (Å)	Distance ^b (Å)	
1G	O6	R57		NH2	2,71	2,63	11C	N4	R57		NH2	3,78	3,59	
	N7	R57		NH1	4,26	4,07								
2T	O4	N61		ND2	2,92	2,78	10A	N6	R57		NH2	4,07	3,10	
	C7	Y64		CB	3,66	3,50			N6	N61		ND2	3,98	3,30
	C6	C68		SG	4,00	3,73								
3G							9C	N4	N61		OD1	2,99	3,02	
4A							8T	C7	A65		CB	3,64	3,82	
								C7	R62		CA	3,88	4,03	
5C							7G	N7	R69		NH1	3,26	4,00	
6T	C7		A65	CB	3,89	4,00	6A							
	C7		K62	CA	4,09	3,98								
7C	N4		N61	OD1	3,03	3,19	5G							
8A	N6		N61	ND2	3,31	3,44	4T	O4		N61	ND2	2,92	3,04	
9G	O6	R57	NH2	3,24	2,78	C7			C68	CB	4,00	4,40		
						C7			A64	CB	4,32	4,14		
10C						3C	N4		N61	ND2	3,58	3,43		
11A							2G	O6		R57	NH1	3,41	2,84	
								O6		R57	NH2	2,89	2,98	
								N7		R57	NH1	2,97	3,53	

Table S6.

1	2	3	4	5	6	7	8	9	10	11	Name	Measured binding
A	T	G	A	C	T	C	A	G	C	A	1A	1.21
C	T	G	A	C	T	C	A	G	C	A	1C	1.10
T	T	G	A	C	T	C	A	G	C	A	1T	0.77
G	A	G	A	C	T	C	A	G	C	A	2A	0.00
G	C	G	A	C	T	C	A	G	C	A	2C	0.15
G	G	G	A	C	T	C	A	G	C	A	2G	0.00
G	T	A	A	C	T	C	A	G	C	A	3A	0.01
G	T	C	A	C	T	C	A	G	C	A	3C	0.00
G	T	T	A	C	T	C	A	G	C	A	3T	0.55
G	T	G	C	C	T	C	A	G	C	A	4C	0.01
G	T	G	G	C	T	C	A	G	C	A	4G	0.05
G	T	G	T	C	T	C	A	G	C	A	4T	0.01
G	T	G	A	A	T	C	A	G	C	A	5A	0.82
G	T	G	A	G	T	C	A	G	C	A	5G	0.94
G	T	G	A	T	T	C	A	G	C	A	5T	1.24
G	T	G	A	C	A	C	A	G	C	A	6A	0.94
G	T	G	A	C	C	C	A	G	C	A	6C	0.46
G	T	G	A	C	G	C	A	G	C	A	6G	1.14
G	T	G	A	C	T	A	A	G	C	A	7A	1.27
G	T	G	A	C	T	G	A	G	C	A	7G	0.63
G	T	G	A	C	T	T	A	G	C	A	7T	0.98
G	T	G	A	C	T	C	C	G	C	A	8C	0.68
G	T	G	A	C	T	C	G	G	C	A	8G	0.88
G	T	G	A	C	T	C	T	G	C	A	8T	0.94
G	T	G	A	C	T	C	A	A	C	A	9A	0.84
G	T	G	A	C	T	C	A	C	C	A	9C	0.37
G	T	G	A	C	T	C	A	T	C	A	9T	1.10
G	T	G	A	C	T	C	A	G	A	A	10A	0.16
G	T	G	A	C	T	C	A	G	G	A	10G	0.54
G	T	G	A	C	T	C	A	G	T	A	10T	0.57
G	T	G	A	C	T	C	A	G	C	C	11C	0.78
G	T	G	A	C	T	C	A	G	C	G	11G	1.22
G	T	G	A	C	T	C	A	G	C	T	11T	0.83

Table S7.

1	2	3	4	5	6	7	8	9	10	11	Name	Measured binding
A	G	G	A	C	T	C	A	G	C	A	1A2G	0.01
A	G	G	A	C	T	A	A	G	C	A	1A2G7A	0.00
A	T	C	A	C	A	C	A	G	C	A	1A3C6A	0.00
A	T	C	A	C	T	A	A	G	C	A	1A3C7A	0.00
A	T	C	A	C	T	C	A	G	C	A	1A3C	0.00
A	T	C	A	C	T	C	A	G	G	A	1A3C10G	0.00
A	T	C	A	C	T	C	C	G	C	A	1A3C8C	0.00
A	T	G	A	C	A	A	A	G	C	A	1A6A7A	0.61
A	T	G	A	C	A	C	A	G	C	A	1A6A	0.75
A	T	G	A	C	A	C	A	G	G	A	1A6A10G	0.00
A	T	G	A	C	A	C	C	G	C	A	1A6A8C	0.20
A	T	G	A	C	A	C	G	G	C	A	1A6A8G	0.49
A	T	G	A	C	A	G	A	G	C	A	1A6A7G	0.36
A	T	G	A	C	A	T	A	G	C	A	1A6A7T	0.51
A	T	G	A	C	C	A	A	G	C	A	1A6C7A	0.27
A	T	G	A	C	C	C	A	G	C	A	1A6C	0.07
A	T	G	A	C	C	C	A	G	G	A	1A6C10G	0.00
A	T	G	A	C	C	C	G	G	C	A	1A6C8G	0.02
A	T	G	A	C	G	C	A	G	C	A	1A6G	0.87
A	T	G	A	C	T	A	A	G	C	A	1A7A	1.07
A	T	G	A	C	T	A	A	G	T	A	1A7A10T	0.03
A	T	G	A	C	T	A	A	G	G	A	1A7A10G	0.04
A	T	G	A	C	T	A	G	G	C	A	1A7A8G	0.87
A	T	G	A	C	T	C	A	G	C	A	1A	1.35
A	T	G	A	C	T	C	A	G	T	A	1A10T	0.05
A	T	G	A	C	T	C	A	G	G	A	1A10G	0.07
A	T	G	A	C	T	C	C	G	C	A	1A8C	0.23
A	T	G	A	C	T	C	G	G	C	A	1A8G	0.73
A	T	G	A	C	T	C	T	G	C	A	1A8T	0.61
A	T	G	A	C	T	G	A	G	C	A	1A7G	0.41
A	T	G	A	C	T	T	A	G	C	A	1A7T	0.78
A	T	G	A	C	T	T	G	G	C	A	1A7T8G	0.73
A	T	G	C	C	A	C	A	G	C	A	1A4C6A	0.00
A	T	G	C	C	C	C	A	G	C	A	1A4C6C	0.00
A	T	G	C	C	T	C	A	G	C	A	1A4C	0.00
A	T	G	G	C	T	A	A	G	C	A	1A4G7A	0.00
A	T	G	G	C	T	C	A	G	C	A	1A4G	0.00
A	T	G	T	C	A	C	A	G	C	A	1A4T6A	0.00
A	T	G	T	C	T	A	A	G	C	A	1A4T7A	0.00
A	T	G	T	C	T	C	A	G	C	A	1A4T	0.00
A	T	T	A	C	A	C	A	G	C	A	1A3T6A	0.02
A	T	T	A	C	C	C	A	G	C	A	1A3T6C	0.00
A	T	T	A	C	T	A	A	G	C	A	1A3T7A	0.01
A	T	T	A	C	T	C	A	G	C	A	1A3T	0.06
A	T	T	A	C	T	C	A	G	G	A	1A3T10G	0.00
A	T	T	A	C	T	T	A	G	C	A	1A3T7T	0.00
A	T	T	T	C	T	C	A	G	C	A	1A3T4T	0.00

Table S8.

1	2	3	4	5	6	7	8	9	10	11	Name	Measured binding
C	T	T	A	C	T	C	A	G	C	A	1C3T	0.17
T	T	T	A	C	T	C	A	G	C	A	1T3T	0.03
G	T	G	A	C	T	C	A	G	G	C	10G11C	0.33
G	T	G	A	C	T	C	A	G	G	T	10G11T	0.30
G	T	G	A	C	T	C	A	G	G	G	10G11G	0.00
G	T	G	A	C	T	C	A	G	T	C	10T11C	0.23
G	T	G	A	C	T	C	A	G	T	T	10T11T	0.18
G	T	G	A	C	T	C	A	G	T	G	10T11G	0.30
G	T	G	A	C	T	C	A	T	C	C	9T11C	0.30
G	T	G	A	C	T	C	A	T	C	T	9T11T	0.37
G	T	G	A	C	T	C	A	T	C	G	9T11G	0.55
A	T	G	A	C	T	C	A	T	C	A	1A9T	0.69
G	T	G	A	C	T	C	A	G	A	G	10A11G	0.09
G	T	G	A	C	T	C	A	G	A	C	10A11C	0.18
G	T	G	A	C	T	C	A	G	A	T	10A11T	0.13
G	T	G	A	C	T	C	A	A	C	G	9A11G	0.32
G	T	G	A	C	T	C	A	A	C	C	9A11C	0.18
G	T	G	A	C	T	C	A	A	C	T	9A11T	0.24
G	T	G	A	C	T	C	A	C	C	G	9C11G	0.13
G	T	G	A	C	T	C	A	C	C	C	9C11C	0.04
G	T	G	A	C	T	C	A	C	C	T	9C11T	0.10
G	T	G	A	C	C	C	C	G	C	A	6C8C	0.01
G	T	G	A	C	G	G	G	G	C	A	6G7G8G	0.59
G	T	G	A	C	T	T	T	G	C	A	7T8T	0.68
G	T	G	A	C	A	C	T	G	C	A	6A8T	0.64
G	T	G	A	C	C	T	A	G	C	A	6C7T	0.36
G	T	G	A	C	C	G	A	G	C	A	6C7G	0.21
G	T	G	A	C	C	C	T	G	C	A	6C7C8T	0.16
G	T	G	A	C	G	G	A	G	C	A	6G7G	0.50
G	T	G	A	C	G	A	A	G	C	A	6G7A	0.66
G	T	G	A	C	G	T	A	G	C	A	6G7T	0.01
G	T	G	A	C	G	C	C	G	C	A	6G8C	0.37
G	T	G	A	C	G	C	G	G	C	A	6G8G	0.64
G	T	G	A	C	G	C	T	G	C	A	6G8T	0.72
G	T	G	A	C	T	A	C	G	C	A	7A8C	0.49
G	T	G	A	C	T	A	T	G	C	A	7A8T	0.62
G	T	G	A	C	T	G	C	G	C	A	7G8C	0.46
G	T	G	A	C	T	G	G	G	C	A	7G8G	0.55
G	T	G	A	C	T	G	T	G	C	A	7G8T	0.58
G	T	G	A	C	T	T	C	G	C	A	7T8C	0.47
G	T	G	A	C	T	T	G	G	C	A	7T8G	0.01
A	T	G	A	T	T	C	A	G	C	A	1A5T	0.59
A	T	G	A	G	T	C	A	G	C	A	1A5G	0.85
A	T	G	A	A	T	C	A	G	C	A	1A5A	0.64
A	T	G	A	C	T	C	A	G	C	G	1A11G	0.00
A	T	G	A	C	T	C	A	G	C	C	1A11C	0.73
A	T	G	A	C	T	C	A	G	C	T	1A11T	0.76

A	T	G	A	T	A	T	A	G	C	A	1A5T6A7T	0.36
A	T	G	A	G	A	T	A	G	C	A	1A5G6A7T	0.34
A	T	G	A	A	A	T	A	G	C	A	1A5A6A7T	0.11
A	T	G	A	C	A	T	A	G	C	G	1A6A7T11G	0.62
A	T	G	A	C	A	T	A	G	C	C	1A6A7T11C	0.24
A	T	G	A	C	A	T	A	G	C	T	1A6A7T11T	0.40
A	T	G	A	T	T	C	A	G	T	A	1A5T10T	0.04
A	T	G	A	G	T	C	A	G	T	A	1A5G10T	0.04
A	T	G	A	A	T	C	A	G	T	A	1A5A10T	0.03
A	T	G	A	C	T	C	A	G	T	G	1A10T11G	0.37
A	T	G	A	C	T	C	A	G	T	C	1A10T11C	0.39
A	T	G	A	C	T	C	A	G	T	T	1A10T11T	0.36
A	T	G	A	A	T	A	A	G	C	G	1A5A7A11G	0.18
A	T	G	A	T	T	A	A	G	C	C	1A5T7A11C	0.08
A	T	G	A	G	T	A	A	G	C	T	1A5G7A11T	0.40
A	T	G	A	G	A	C	G	G	C	G	1A5G6A8G11G	0.06
A	T	G	A	A	A	C	G	G	C	C	1A5A6A8G11C	0.00
A	T	G	A	T	A	C	G	G	C	T	1A5T6A8G11T	0.02
A	T	G	A	T	T	A	A	G	G	G	1A5T7A10G11G	0.14
A	T	G	A	G	T	A	A	G	G	C	1A5G7A10G11C	0.16
A	T	G	A	A	T	A	A	G	G	T	1A5A7A10G11T	0.01
A	T	G	A	T	G	C	A	G	C	G	1A5T6G11G	0.39
C	T	G	A	G	G	C	A	G	C	C	1C5G6G11C	0.00
C	T	G	A	C	T	C	A	G	T	A	1C10T	0.05
T	T	G	A	C	T	C	A	G	T	A	1T10T	0.00
G	T	G	A	C	A	T	A	G	C	A	6A7T	0.61
C	T	G	A	C	A	T	A	G	C	A	1C6A7T	0.18
T	T	G	A	C	A	T	A	G	C	A	1T6A7T	0.01
T	T	G	A	A	G	C	A	G	C	T	1T5A6G11T	0.00
A	T	G	A	T	T	G	A	G	C	G	1A5T7G11G	0.11
C	T	G	A	G	T	G	A	G	C	C	1C5G7G11C	0.00
T	T	G	A	A	T	G	A	G	C	T	1T5A7G11T	0.00
A	T	G	A	T	T	A	A	G	T	G	1A5T7A10T11G	0.00
C	T	G	A	G	T	A	A	G	T	C	1C5G7A10T11C	0.00
T	T	G	A	A	T	A	A	G	T	T	1T5A7A10T11T	0.01