Table S1: Fluorescently labelled DNA. *denotes the label (X = fluorescein, Y = Alexa488), *P* if a p53RE (bold letters) is present, *n* the spacer length, and *K* if a Klf4RE (italic letters) is present. Non-canonical three quarter-sites are highlighted in green for the constructs *108K and *47K. The affinity-defining bases C4, G7, C14 and G17 are underlined and changes to the canonical bases indicated in red.

*P	Y**GGACATGTCCGGACATGTCC**
*PK	Y**GGACATGTCCGGACATGTCC***AGGGTGTGGCCCGC*
*P5K	Y**GGACATGTCCGGACATGTCC**AGCTC*AGGGTGTGGCCCGC*
*P10K	Y**GGACATGTCCGGACATGTCC**AGCTCTGGC*AAGGGTGTGGCCCGC*
*P30K	Y**GGACATGTCCGGACATGTCC**AGCTCTGGCATAGAAGAGGCTGGTGGCTAT*AGGGTGTGGCCCGC*
*P88K	Y**GGACATGTCCGGACATGTCC**AGCTCTGGCATAGAAGAGGCTGGTGGCTATTTTGTCCTTGGGCTGCCTG TTTTCAGGTGAGGAAGGGGATGGTAGGAGACAGGAGACC*AGGGTGTGGCCCGC*
*P185K	Y**GGACATGTCCGGACATGTCC**AGCTCTGGCATAGAAGAGGCTGGTGGCTATTTTGTCCTTGGGCTGCCTG TTTTCAGGTGAGGAAGGGGATGGTAGGAGACAGGAGACCTCTAAAGACCCCAGGTAAACCTTAGCCTGT TACTCTGAACAGGGTATGTGATCTGCCAGCAGATCCTTGCGACAGGG*AGGGTGTGGCCCGC*
*P1000K	Y**GGACATGTCCGGACATGTCC**AGCTCTGGCATAGAAGAGGCTGGTGGCTATTTTGTCCTTGGGCTGCCTG TTTTCAGGTGAGGAAGGGGATGGTAGGAGACAGGAGACCTCTAAAGACCCCAGGTAAACCTTAGCCTGT TACTCTGAACAGGGTATGTGATCTGCCAGCAGATCCTTGCGACAGGGCTGGGATCTGATGCATGCGTGCT TGTGTGAGTGTGTGCTGGGAGTCAGATTCTGTGTGTGACTTTTAACAGCCTGCTCCCTTGCCTTCTTCAGG GCAGAAGTCCTCCCTTAGAGTGTGTCTGGGAACACATTCAAGTGCATGGTTGCAAACTTTTTTTTTTAAAG CACTGAATAGTACTAGACACTTAGTAGGTACTTAAGAAATATTGAATGTCGTGGTGGTGGTGAGCAAGGG TGGGCGCGCCGACCCAGCTTTCTTGTACAAAGTTGGCATTATAAGAAAGCATTGCTTATCAATTTGTTGCA ACGAACAGGTCACTATCAGTCAAAATAAAATCATTATTTGCCATCCAGCTGATATCCCCTATAGTGAGTCG TATTACATGGTCATAGCTGTTTCCTGCATATGAATTCGAAGCTTGATCCGGCTGCTAACAAAGCCCGAAAG GAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATAACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCT TGAGGGGTTTTTTGCTGAAAGGAGGAACTATATCCGGATCTGGCGTAATAGCGAAGAGGCCCGCACCGA TCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGGACGCGCCCTGTAGCGGCGCATTAAGCGCG GCGGGTGTGGTGGTTACGCGCAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTT CTTCCCTTCCTTTCTCGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTT CCGATTTAGAGCTTTACGGCACCTCGACCGCAAAA*AGGGTGTGGCCCGC*
*K-1	X*AGGGTGTGGCCCGC*
*47K	XATCCCAGGTCACCCTGACCTAGCTCTGGCATAGAAGAGGCTGGTGGCTAT*AGGGTGTGGCCCGC*
*K-2	X*GGGCCACCCCGCC*
*108K	XGAAGATCTCCCAAGATCTTGAGCTCTGGCATAGAAGAGGCTGGTGGCTATTTTGTCCTTGGGCTGCCTGT TTTCAGGTGAGGAAGGGGATGGTAGGAGACAGGAGACC*AGGGTGTGGCCCGC*