

Table S3: Sequences of MPRA Controls

Gene	Type	Sequence
PKRRE	Ref	AGGAAATGCCAGGAGATGAGGGCAGAGAGCAGGCCGTTCTGGGGGAGGGATTCTGTGGGGACAGGGTGGCCTACTGG GTGTGCCCCCTTTTCTCTTCTCTGTCTCCCTTAGATAAGACCAGCAGTTTTGTCATCCTCTCCCTCTCATTCCA
PKRRE	Mut	AGGAAATGCCAGGAGATGAGGGCAGAGAGCAGGCCGTTCTGGGGGAGGGATTCTGTGGGGACAGGGTGGCCTACTGG GTGTGCCCCCTTTTCTCTTATCTGTCTCCCTTAGATAAGACCAGCAGTTTTGTCATCCTCTCCCTCTCATTCCA
PKRRE	Ref	AGGAAATGCCAGGAGATGAGGGCAGAGAGCAGGCCGTTCTGGGGGAGGGATTCTGTGGGGACAGGGTGGCCTACTGG GTGTGCCCCCTTTTCTCTTCTCTGTCTCCCTTAGATAAGACCAGCAGTTTTGTCATCCTCTCCCTCTCATTCCA
PKRRE	Mut	AGGAAATGCCAGGAGATGAGGGCAGAGAGCAGGCCGTTCTGGGGGAGGGATTCTGTGGGGACAGGGTGGCCTACTGG GTGTGCCCCCTTTTCTCTTCGCTGTCTCCCTTAGATAAGACCAGCAGTTTTGTCATCCTCTCCCTCTCATTCCA
PKRRE	Ref	AGGAAATGCCAGGAGATGAGGGCAGAGAGCAGGCCGTTCTGGGGGAGGGATTCTGTGGGGACAGGGTGGCCTACTGG GTGTGCCCCCTTTTCTCTTCTCTGTCTCCCTTAGATAAGACCAGCAGTTTTGTCATCCTCTCCCTCTCATTCCA
PKRRE	Mut	AGGAAATGCCAGGAGATGAGGGCAGAGAGCAGGCCGTTCTGGGGGAGGGATTCTGTGGGGACAGGGTGGCCTACTGG GTGTGCCCCCTTTTCTCTTCTATGTCTCCCTTAGATAAGACCAGCAGTTTTGTCATCCTCTCCCTCTCATTCCA
PKRRE	Ref	AGGAAATGCCAGGAGATGAGGGCAGAGAGCAGGCCGTTCTGGGGGAGGGATTCTGTGGGGACAGGGTGGCCTACTGG GTGTGCCCCCTTTTCTCTTCTCTGTCTCCCTTAGATAAGACCAGCAGTTTTGTCATCCTCTCCCTCTCATTCCA
PKRRE	Mut	AGGAAATGCCAGGAGATGAGGGCAGAGAGCAGGCCGTTCTGGGGGAGGGATTCTGTGGGGACAGGGTGGCCTACTGG GTGTGCCCCCTTTTCTCTTCTCGGTCTCCCTTAGATAAGACCAGCAGTTTTGTCATCCTCTCCCTCTCATTCCA
PKRRE	Ref	AGGAAATGCCAGGAGATGAGGGCAGAGAGCAGGCCGTTCTGGGGGAGGGATTCTGTGGGGACAGGGTGGCCTACTGG GTGTGCCCCCTTTTCTCTTCTCTGTCTCCCTTAGATAAGACCAGCAGTTTTGTCATCCTCTCCCTCTCATTCCA
PKRRE	Mut	AGGAAATGCCAGGAGATGAGGGCAGAGAGCAGGCCGTTCTGGGGGAGGGATTCTGTGGGGACAGGGTGGCCTACTGG GTGTGCCCCCTTTTCTCTTCTCTCTCTCCCTTAGATAAGACCAGCAGTTTTGTCATCCTCTCCCTCTCATTCCA
ALAS2	Ref	CTGGAGATATGTGTTTCCCTTCCCCTGCCTGCTTGTGAAAGCTAAAGCACTTGGGGCTGAGCCTGCAGACCACAGATAA AGTTGCCAGAGTTTATCGCCATTGGGGTCTGACCACTCCCCAAGCTGAGACCAGGGCGTGGGAGAGAAGAG
ALAS2	Mut	CTGGAGATATGTGTTTCCCTTCCCCTGCCTGCTTGTGAAAGCTAAAGCACTTGGGGCTGAGCCTGCAGACCACACATAA AGTTGCCAGAGTTTATCGCCATTGGGGTCTGACCACTCCCCAAGCTGAGACCAGGGCGTGGGAGAGAAGAG
ALAS2	Ref	TGGAGATATGTGTTTCCCTTCCCCTGCCTGCTTGTGAAAGCTAAAGCACTTGGGGCTGAGCCTGCAGACCACAGATAAA GTTGCCAGAGTTTATCGCCATTGGGGTCTGACCACTCCCCAAGCTGAGACCAGGGCGTGGGAGAGAAGAGG
ALAS2	Mut	TGGAGATATGTGTTTCCCTTCCCCTGCCTGCTTGTGAAAGCTAAAGCACTTGGGGCTGAGCCTGCAGACCACAGGTA GTTGCCAGAGTTTATCGCCATTGGGGTCTGACCACTCCCCAAGCTGAGACCAGGGCGTGGGAGAGAAGAGG
ALAS2	Ref	GGAGATATGTGTTTCCCTTCCCCTGCCTGCTTGTGAAAGCTAAAGCACTTGGGGCTGAGCCTGCAGACCACAGATAAAG TTGCCAGAGTTTATCGCCATTGGGGTCTGACCACTCCCCAAGCTGAGACCAGGGCGTGGGAGAGAAGAGGA
ALAS2	Mut	GGAGATATGTGTTTCCCTTCCCCTGCCTGCTTGTGAAAGCTAAAGCACTTGGGGCTGAGCCTGCAGACCACAGACAAAG TTGCCAGAGTTTATCGCCATTGGGGTCTGACCACTCCCCAAGCTGAGACCAGGGCGTGGGAGAGAAGAGGA
UROS	Ref	TGGAAGAGACCTATCCCTCCTACACCATGACTTAGCACTAATGGGCTTGTCTTTTCTGAAGACCCCTGTCACTGATAAGG CCAAGAAAGAGCATGTTAGCAGTTGATATCACTTGGAAAGACAGATGAAACCATTAGTGAAGCCAAGTG

UROS	Mut	TGGAAGAGACCTATCCCTCCTACACCATGACTTAGCACTAATGGGCTTGTTCTTTCTGAAGACCCCTGTCACTGGTAAGG CCAAGAAAGAGCATGTTAGCAGTTGATATCACTTGAAAGACAGATGAAACCATTAGTGAAAGCCAAGTG
SPI1	Ref	GTTGTTTAAAATTTTCTCTGAGACACGACGTTCTCCTACCTAACTCTTATTGAAATGAACAAAAACCCTCCTCCAATTACC CACCTCCCCACTCTCCCCTCTAGACTAAATGTATGCCTGAACTCTGAGGGTTCGGTCATGGGGCCCA
SPI1	Mut	GTTGTTTAAAATTTTCTCTGAGACACGACGTTCTCCTACCTAACTCTTATTGAAATGAACAAAAACCCTCCTCTAATTACC CACCTCCCCACTCTCCCCTCTAGACTAAATGTATGCCTGAACTCTGAGGGTTCGGTCATGGGGCCCA
HBG2	Ref	TAAACATTAATCTATTCCTGCACTGAACTGTTGCTTTATAGGATTTTTCACTACACTAATGAGAACTTAAGAGATAATGGCC TAAAACACAGAGAGTATATTCAAAGATAAGTATAGCACTTCTTATTTGGAAACCAATGCTTACTAAA
HBG2	Mut	TAAACATTAATCTATTCCTGCACTGAACTGTTGCTTTATAGGATTTTTCACTACACTAATGAGAACTTAAGAGAGAATGGC CTAAAACACAGAGAGTATATTCAAAGATAAGTATAGCACTTCTTATTTGGAAACCAATGCTTACTAAA