Supplementary Table 4

| ID | Genes in dataset |
|---|---|
| ENSMUSG00000067931 | Zfp948 |
| ENSMUSG00000044786 | ZFP36 |
| ENSMUSG00000034640 | TIPARP |
| ENSMUSG00000049516 | SPTY2D1 |
| ENSMUSG00000024042 | Sik1 |
| ENSMUSG00000019970 | SGK1 |
| ENSMUSG00000025283 | SAT1 |
| ENSMUSG00000040511 | Pvr |
| ENSMUSG00000031538 | PLAT |
| ENSMUSG00000035828 | PIM3 |
| ENSMUSG00000020893 | PER1 |
| ENSMUSG00000049612 | OMG |
| ENSMUSG00000028341 | NR4A3 |
| ENSMUSG00000023034 | NR4A1 |
| ENSMUSG00000045903 | NPAS4 |
| ENSMUSG00000025402 | NAB2 |
| ENSMUSG00000020190 | MKNK2 |
| ENSMUSG00000035621 | MIDN |
| ENSMUSG00000038612 | MCL1 |
| ENSMUSG00000053907 | MAT2A |
| ENSMUSG00000026822 | LCN2 |
| ENSMUSG00000052837 | JUNB |
| ENSMUSG00000052684 | JUN |
| ENSMUSG00000026864 | HSPA5 |
| ENSMUSG00000007617 | HOMER1 |
| ENSMUSG00000031770 | HERPUD1 |
| ENSMUSG00000028214 | GEM |
| ENSMUSG00000003545 | FOSB |
| ENSMUSG00000021250 | FOS |
| ENSMUSG00000032265 | FAM46A |
| ENSMUSG00000028967 | ERRFI1 |
| ENSMUSG00000071341 | EGR4 |
| ENSMUSG00000037868 | EGR2 |
| ENSMUSG00000038418 | EGR1 |
| ENSMUSG00000018648 | DUSP14 |
| ENSMUSG00000024190 | DUSP1 |
| ENSMUSG00000007682 | DIO2 |

Supplementary Table 4

| | |
|---|---|
| ENSMUSG00000028195 | CYR61 |
| ENSMUSG00000001467 | CYP51A1 |
| ENSMUSG00000029380 | CXCL2 |
| ENSMUSG00000032515 | CSRNP1 |
| ENSMUSG00000063889 | CREM |
| ENSMUSG00000050370 | CH25H |
| ENSMUSG00000023067 | CDKN1A |
| ENSMUSG00000020423 | BTG2 |
| ENSMUSG00000026628 | ATF3 |
| ENSMUSG00000022602 | ARC |
| ENSMUSG00000090698 | APOLD1 |

**Supplementary Table 4. IPA associations of CREB and pink module genes.** IPA-annotated associations between CREB and genes within the pink module used to designate CREB as an upstream regulator.

Supplementary Table 5

| sequence | score | mismatches | region | locus |
|---|---|---|---|---|
| GTGTCTCTAGTAGCAAGAAGGAG | 1.3 | 3MMs [8:9:10] | Intronic | chr13:58,017,033-58,017,052 |
| TTCTCTTGGATAGCAAGAAGAGG | 0.9 | 4MMs [1:3:7:10] | Exonic | chr10:120,862,516-120,862,538 |
| GAGGCTAGGCTAGCAAGAAGCAG | 0.9 | 4MMs [2:4:7:10] | Intronic | chr17:66,912,485-66,912,507 |
| TGGTCTCATTTAGCAAGAAGGAG | 0.9 | 4MMs [1:2:8:9] | Intronic | chr1:54,726,324-54,726,346 |
| TTGTTTCAGTGAGCAAGAAGAAG | 0.8 | 4MMs [1:5:8:11] | Intronic | chr8:106,647,508-106,647,530 |
| GAGACTCGGGCAGCAAGAAGCAG | 0.7 | 4MMs [2:4:10:11] | Exonic | chr11:4,620,726-4,620,748 |
| ATGTATCTGTTGGCAAGAAGGGG | 0.7 | 4MMs [1:5:8:12] | Intergenic | chr10:98,263,028-98,263,047 |
| GTGTCTAGGCTAGCAATAAGAAG | 0.7 | 3MMs [7:10:17] | Intronic | chrX:59,487,863-59,487,885 |
| GTGTCTCATTTAGCAAAAAGCGG | 0.6 | 3MMs [8:9:17] | Intronic | chr6:39,880,798-39,880,817 |
| TTGTATCTGTTACCAAGAAGGAG | 0.6 | 4MMs [1:5:8:13] | Intergenic | chr7:76,226,866-76,226,888 |
| GTCTATTGCTTAGCAAGAAGCAG | 0.6 | 4MMs [3:5:7:9] | Intergenic | chr3:141,217,776-141,217,795 |
| GTGTATATTTTAGCAAGAAGAAG | 0.6 | 4MMs [5:7:8:9] | Intergenic | chr3:-140880732 |
| TTGTCTGTGTGAGCAAGAAGTGG | 0.6 | 4MMs [1:7:8:11] | Intronic | chr15:60,923,593-60,923,615 |
| CTGACTAGGTGAGCAAGAAGAGG | 0.6 | 4MMs [1:4:7:11] | Intronic | chr9:77,780,867-77,780,889 |
| ATGTCTTTGTCAGCAAGAAGTGG | 0.6 | 4MMs [1:7:8:11] | Intergenic | chr17:78,503,795-78,503,814 |
| GCTTCCGGGTTAGCAAGAAGGGG | 0.5 | 4MMs [2:3:6:7] | Intergenic | chrX:140,519,228-140,519,247 |
| GTTTTGTGGTTAGCAAGAAGTGG | 0.5 | 4MMs [3:5:6:7] | Intergenic | chr15:46,795,651-46,795,670 |
| GATTCTAGGTCAGCAAGAAGTGG | 0.5 | 4MMs [2:3:7:11] | Intergenic | chr7:115,388,496-115,388,518 |
| GTTCCTGGGTGAGCAAGAAGGGG | 0.5 | 4MMs [3:4:7:11] | Intergenic | chr1:156,308,549-156,308,568 |
| GGGTCTTGGAAAGCAAGAAGCAG | 0.5 | 4MMs [2:7:10:11] | Intronic | chr10:119,120,732-119,120,754 |
| GTGTAACCTTTAGCAAGAAGTAG | 0.5 | 4MMs [5:6:8:9] | Exonic | chrX:46,329,695-46,329,717 |
| GGCTCTCGATCAGCAAGAAGAAG | 0.5 | 4MMs [2:3:9:11] | Intronic | chr10:39,308,257-39,308,279 |
| GAGTCTCAGATAGCAAGATGGAG | 0.5 | 4MMs [2:8:10:19] | Intronic | chr5:124,012,822-124,012,842 |
| GTTTCACTGTGAGCAAGAAGGGG | 0.5 | 4MMs [3:6:8:11] | Intronic | chr3:138,425,682-138,425,701 |
| GTGTGTCCATCAGCAAGAAGGGG | 0.5 | 4MMs [5:8:9:11] | Intronic | chr15:6,381,046-6,381,068 |
| GTGACTCAGGTAGCAAGAGGGGG | 0.5 | 4MMs [4:8:10:19] | Intronic | chr2:27,686,048-27,686,067 |
| GTGTTACTGTGAGCAAGAAGAAG | 0.5 | 4MMs [5:6:8:11] | Intronic | chr15:54,416,659-54,416,681 |
| CTGTCTTGGCTTGCAAGAAGAGG | 0.5 | 4MMs [1:7:10:12] | Intergenic | chrX:134,612,978-134,612,997 |
| ATGTCTCAATTAGCAAGAATTAG | 0.4 | 4MMs [1:8:9:20] | Intergenic | chr16:74,573,254-74,573,273 |
| CTGTGGCGGTTAGCAAGAATTGG | 0.4 | 4MMs [1:5:6:20] | Intergenic | chr13:57,310,961-57,310,980 |
| AAGTCTCAGTTAGCCAGAAGAGG | 0.4 | 4MMs [1:2:8:15] | Intronic | chr5:129,000,768-129,000,787 |
| GGGACTCTGTTAGCTAGAAGGAG | 0.4 | 4MMs [2:4:8:15] | Intergenic | chr17:14,766,129-14,766,151 |
| GAGTCTCGGGTAGGAAGAAGTGG | 0.4 | 3MMs [2:10:14] | Intronic | chr4:104,584,561-104,584,583 |

Supplementary Table 5

| | | | | |
|---|---|---|---|---|
| TTGTCTCAGTGAGCAAGAACAAG | 0.4 | 4MMs [1:8:11:20] | Intergenic | chr9:104,001,895-104,001,917 |
| GCGTCTGGGATACCAAGAAGGAG | 0.4 | 4MMs [2:7:10:13] | Intronic | chr1:74,035,356-74,035,378 |
| CTGTCTCTGTTGGCAAGAATAGG | 0.3 | 4MMs [1:8:12:20] | Intergenic | chr1:122,025,746-122,025,765 |
| GTGACCAGTTTAGCAAGAAGTAG | 0.3 | 4MMs [4:6:7:9] | Intronic | chr2:37,847,382-37,847,401 |
| GATTCTCGGTTTGCAAGAAAAAG | 0.3 | 4MMs [2:3:12:20] | Intergenic | chr6:138,762,486-138,762,508 |
| CTGACTCCGTTAGCAAGCAGAGG | 0.3 | 4MMs [1:4:8:18] | Intergenic | chr8:10,706,481-10,706,503 |
| ATGACTCAGTTAGCAAGCAGGAG | 0.3 | 4MMs [1:4:8:18] | Intergenic | chr7:13,526,174-13,526,196 |
| TTGTCTGGCTTAGCAAGAATAGG | 0.3 | 4MMs [1:7:9:20] | Intronic | chr13:66,959,308-66,959,327 |
| CTGTCTCTGATAGCAAGCAGAAG | 0.3 | 4MMs [1:8:10:18] | Intronic | chr5:148,115,931-148,115,950 |
| CTGTCCAGGTTAGCAAGAAAAAG | 0.3 | 4MMs [1:6:7:20] | Intergenic | chr17:52,061,997-52,062,016 |
| GTTTCTTGATTTGCAAGAAGTGG | 0.3 | 4MMs [3:7:9:12] | Intergenic | chr5:18,717,619-18,717,641 |
| GTGTCTGGCACAGCAAGAAGTGG | 0.3 | 4MMs [7:9:10:11] | Intronic | chr2:64,072,392-64,072,411 |
| GAGTCTCGTTTAGGAAGAAGCAG | 0.3 | 3MMs [2:9:14] | Intronic | chr11:119,674,065-119,674,087 |
| GAGTCTCTGTTAGCAACAAAGGG | 0.3 | 4MMs [2:8:17:20] | Intergenic | chr19:55,008,407-55,008,429 |
| GTGTCTTACTTAGCAAGAATGAG | 0.3 | 4MMs [7:8:9:20] | Intronic | chr1:51,068,885-51,068,907 |
| TTGTGTCGGTTTGCAAGAGGGGG | 0.3 | 4MMs [1:5:12:19] | Intronic | chr18:21,959,602-21,959,624 |

**Supplementary Table 5. *Zfp189*-targeting sgRNA predicted binding sites throughout *Mus musculus* genome.**

Except for at the targeted *Zfp189* locus, there are no high-affinity binding sites for our *Zfp189*-targeting sgRNA across the entire mouse genome. Of the 141 predicted off-targets, the top sites with “scores”>0.3 are represented here. “Score” ranges from 0-100 and denotes the predicted on-target faithfulness of our synthesized sgRNA acting at the mismatched locus. The closest “matches” exhibit >3 mismatched nucleotides.

Supplementary Table 6

| **sequence** | **score** | **mismatches** | **region** | **locus** |
|---|---|---|---|---|
| **GCCAGGTCTTTGGCTCCGCTGAG** | 0.4 | 4MMs [3:8:11:20] | Exonic | chr11:36,051,900-36,051,922 |
| **GCGAAACATTCGGCTCCGCCCAG** | 0.3 | 4MMs [5:6:7:20] | Exonic | chr1:34,169,207-34,169,226 |
| **GCGGGGTACTGGGCTCCGCATGG** | 0.2 | 4MMs [4:9:11:20] | Intergenic | chr11:117,647,952-117,647,974 |
| **GCGAGGTTATAGGCTCCGCTGAG** | 0.2 | 4MMs [8:9:11:20] | Intergenic | chrX:38,991,559-38,991,581 |
| **GCCAGGGATTGGCCTCCGCGTAG** | 0.2 | 4MMs [3:7:11:13] | Exonic | chr7:97,580,195-97,580,217 |
| **GGGAGGTAGTGGGCTCCGTGTGG** | 0.2 | 4MMs [2:9:11:19] | Intronic | chr11:109,664,427-109,664,449 |
| **AGGAGGTATTCGCCTTCGCGGAG** | 0.1 | 4MMs [1:2:13:16] | Exonic | chr9:72,891,855-72,891,877 |
| **GCGAGGTCCTCGGCGCGGCGAGG** | 0.1 | 4MMs [8:9:15:17] | Intergenic | chr5:35,399,703-35,399,722 |
| **GCTAGGTCTTCGGGTCTGCGAAG** | 0.1 | 4MMs [3:8:14:17] | Intergenic | chr10:117,568,810-117,568,832 |
| **GCAAGGTCTTCGGCTACCCGAAG** | 0.1 | 4MMs [3:8:16:18] | Exonic | chr7:5,030,840-5,030,862 |
| **GCGAGGTACGCGGTTCCGCTGAG** | 0.1 | 4MMs [9:10:14:20] | Intronic | chr1:77,513,423-77,513,445 |
| **GCGAGGGATTGGGCTCCCCTTAG** | 0.0 | 4MMs [7:11:18:20] | Intronic | chr7:45,529,474-45,529,496 |
| **GCGAGGTACTTGGCTGTGCGCAG** | 0.0 | 4MMs [9:11:16:17] | Intronic | chr6:33,395,524-33,395,543 |
| **GCGAGGTATTCGCTTACGCGTAG** | 0.0 | 3MMs [13:14:16] | Intronic | chr19:8,741,684-8,741,706 |
| **GCCAGGTATTCGGTTATGCGAGG** | 0.0 | 4MMs [3:14:16:17] | Intergenic | chr1:30,181,618-30,181,640 |

**Supplementary Table 6. Non-targeting sgRNA protospacer predicted binding sites throughout *Mus musculus* genome.**

There are no high-affinity binding sites for our NT-sgRNA across the entire mouse genome. All of the 15 total low-probability sites and “scores” are presented above. “Score” ranges from 0-100 and denotes the predicted on-target faithfulness of our synthesized sgRNA acting at the mismatched locus.