**Table S1. *upSET* gRNA oligos and HRMA Primers**

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| **Name** | **Sequence** | **Description** |
| **Crispr\_upSET\_1F** | gttcgAACCGAGTCGTGACTGGACA | 3L:14000954..14000976 (-strand) CRISPR seq: AACCGAGTCGTGACTGGACATGG; remove NGG add BbsI cloning site fragments to generate oligos at left; no off targets, efficiency score = 3.96; 4bp downstream from ATG |
| **Crispr\_upSET\_1R** | aaacTGTCCAGTCACGACTCGGTTc |
| **Crispr\_upSET\_3F** | gttcgAGGCGCGATGCCGTCTGATT | 3L:14010960..14010982 (+ strand) CRISPR seq: AGGCGCGATGCCGTCTGATTAGG; remove NGG add BbsI cloning site fragments to generate oligos at left; no off targets, efficiency score = 7.71; at stop codon |
| **Crispr\_upSET\_3R** | aaacAATCAGACGGCATCGCGCCTc |
| **Crispr\_upSET\_5F** | gttcgTGGCCAGGCGCAGTAGTAAT | 3L:13995983..13996005 (+ strand) CRISPR seq: TGGCCAGGCGCAGTAGTAATAGG; remove NGG add BbsI cloning site fragments to generate oligos at left; no off targets, efficiency score = 7.08; 5'UTR, ~5kb upstream of ATG |
| **Crispr\_upSET\_5R** | aaacATTACTACTGCGCCTGGCCAc |
| **Crispr\_upSET\_7F** | gttcgACAGCAGATCAGCCTACCGC | 3L:14002035..14002057 (+ strand) CRISPR seq: ACAGCAGATCAGCCTACCGCAGG; remove NGG add BbsI cloning site fragments to generate oligos at left; no off targets, efficiency score = 6.55; exon 1, ~1kb downstream from start |
| **Crispr\_upSET\_7R** | aaacGCGGTAGGCTGATCTGCTGTc |
| **KAM187** | ccactgggagtttcagcttc | ~250bp left of Crispr\_upSET\_1 target; HRMA primer set step 1 |
| **KAM188** | gcgactgattgatcgactga | ~250bp right of Crispr\_upSET\_1; HRMA primer set step 1 |
| **KAM201** | gctgcacatgtttgatgataagc | ~250bp left of Crispr\_upSET\_3; HRMA primer set step 1 |
| **KAM202** | gtgcaagctcatactttatgcgc | ~250bp right of Crispr\_upSET\_3; HRMA primer set step 1 |
| **KAM203** | gcactcttcggcagtatggt | ~250bp left of Crispr\_upSET\_5; HRMA primer set step 1 |
| **KAM204** | cgtatggcacaagaagcaga | ~250bp right of Crispr\_upSET\_5; HRMA primer set step 1 |
| **KAM205** | ccttccctgtaaacacacgtc | ~50bp left of Crispr\_upSET\_1 target; HRMA primer set step 2 |
| **KAM206** | cgatgcgatttatgctgctgg | ~50bp right of Crispr\_upSET\_1; HRMA primer set step 2 |
| **KAM209** | ggtcatcgagcgattggg | ~50bp left of Crispr\_upSET\_3; HRMA primer set step 2 |
| **KAM210** | ggattgaaaggcattcaattaagac | ~50bp right of Crispr\_upSET\_3; HRMA primer set step 2 |
| **KAM211** | cgaataggcggaaaggcg | ~50bp left of Crispr\_upSET\_5; HRMA primer set step 2 |
| **KAM212** | gccctgcttcttcttcttgg | ~50bp right of Crispr\_upSET\_5; HRMA primer set step 2 |
| **KAM236** | cagcagcagcaactactacag | ~250bp left of Crispr\_upSET\_7 target; HRMA primer set step 1 |
| **KAM237** | ggttatcagtgaggagttcgc | ~250bp right of Crispr\_upSET\_7; HRMA primer set step 1 |
| **KAM250** | caatggtcaccacgtcgac | ~50bp left of Crispr\_upSET\_7 target; HRMA primer set step 2 |
| **KAM251** | gagactgctgcagaagatatcc | ~50bp right of Crispr\_upSET\_7; HRMA primer set step 2 |

Oligonucleotide pairs for cloning of *upSET*-targeted gRNA constructs into pL018 and a description of the CRISPR sequence location are listed. Primers used for HRMA assays to identify potential mutant cell lines and subsequent sequence verification of mutations are also listed. All sequences are written from 5’ to 3’.