### Table S3a. The potential off-targets accessed using the Cas-OFFinder off-target searching tool

| sgRNA    | Target Sequence       | Bulge Type | Bulge Size | Mismatch | Number of Found Targets |
|----------|-----------------------|------------|------------|----------|------------------------|
| sgRNA-1  | CACCACAAATCGCCAAACTCTGTRG | X          | 0          | 2        | 1                      |
| sgRNA-1  | CACCACAAATCGCCAAACTCTGTRG | X          | 0          | 4        | 5                      |
| sgRNA-1  | CACCACAAATCGCCAAACTCTGTRG | X          | 0          | 5        | 26                     |
| sgRNA-1  | CACCACAAATCGCCAAACTCTGTRG | X          | 0          | 6        | 321                    |
| sgRNA-1  | CACCACAAATCGCCAAACTCTGTRG | X          | 0          | 7        | 2624                   |
| sgRNA-1  | CACCACAAATCGCCAAACTCTGTRG | X          | 0          | 8        | 16176                  |
| sgRNA-1  | CACCACAAATCGCCAAACTCTGTRG | X          | 0          | 9        | 83760                  |
| sgRNA-2  | CACCCTCATCTTTCTCAATATAAAG | X          | 0          | 3        | 1                      |
| sgRNA-2  | CACCCTCATCTTTCTCAATATAAAG | X          | 0          | 4        | 9                      |
| sgRNA-2  | CACCCTCATCTTTCTCAATATAAAG | X          | 0          | 5        | 127                    |
| sgRNA-2  | CACCCTCATCTTTCTCAATATAAAG | X          | 0          | 6        | 794                    |
| sgRNA-2  | CACCCTCATCTTTCTCAATATAAAG | X          | 0          | 7        | 4868                   |
| sgRNA-2  | CACCCTCATCTTTCTCAATATAAAG | X          | 0          | 8        | 26948                  |
| sgRNA-2  | CACCCTCATCTTTCTCAATATAAAG | X          | 0          | 9        | 120873                 |

### Table S3b. The potential mismatch ≤4 off-target regions accessed using the Cas-OFFinder off-target searching tool

| Target DNA sequence | Chromosome | Position | Location         | Direction | Mismatches | Nearby Gene | Position to Gene |
|---------------------|------------|----------|------------------|-----------|------------|-------------|------------------|
| aAgCACAAATCGCCAAACTCTGTTGG | chr6 | 134979327 | chr:134,979,127-134,979,527 | - | 2 | HBST1L | Intron 14-15 |
| CACCCTCATCTTTCTCAATATAAAG | chr14 | 75029254 | chr:75029054-75029454 | + | 3 | MLH3 | Intron 9-10 |
| CACCCTCATCTCTCTGATCGTAG | chr3 | 2319531 | chr:231931-231971 | - | 4 | CNTN4 | Intron 1-2 |
| CACCCTCATCTCTCTGATCGTAG | chr6 | 65029636 | chr:65029436-65029836 | - | 4 | EYS | Intron 13-14 |
| CACCACAcGCCAAACTCTGTTGG | chr15 | 26660595 | chr:26660395-26660795 | + | 4 | GABRB3 | Intron 3-4 |
| actCTCATCTCTTCTCATATAG | chr6 | 134979362 | chr:134,979,162-134,979,562 | + | 4 | HBST1L | Intron 13-14 |
| CACCACAAATCGCCAAACTCTGTTGG | chr2 | 12481111 | chr:12480911-12481311 | + | 4 | MIR3881HG | Intron 4-5 |
| CACCCTCATCTTTCTCAATATAAAG | chr20 | 4630067 | chr:4630046-46300867 | - | 4 | RPS4XP2 | Intron 1-2 |
| CACCCTCATCTCTCTGATCGTAG | chr20 | 10241310 | chr:10241110-10241510 | + | 4 | SNAP25 | Intron 1-2 |
| CACCCTCATCTCTCTGATCGTAG | chr5 | 35769486 | chr:35,769,286-35,769,886 | - | 4 | SPEF2 | Intron 26-27 |
| CACCACAAATCGCCAAACTCTGTTGG | chr9 | 11309958 | chr:113,099,368-113,099,768 | + | 4 | amorph | |
| CACCACAAATCGCCAAACTCTGTTGG | chr10 | 3671670 | chr:3671650-3671710 | + | 4 | amorph | |
| CAGCAATCGCCAAACTCTGTTGG | chr18 | 24354628 | chr:24,354,428-24,354,828 | + | 4 | amorph | |
| CACCCTCATCTCTCTGATCGTAG | chr7 | 88690588 | chr:88690388-88690788 | - | 4 | amorph | |
| CACCCTCATCTCTCTGATCGTAG | chr2 | 161620915 | chr:161620715-161621115 | - | 4 | amorph | |
| CATTCCATCTCTCTGATCGTAG | chr14 | 26367404 | chr:26367204-26367604 | - | 4 | amorph | |