| Target sequence                      | bp No. | Cas9 cut | GC % | 5' Nt | PAM   | Location   | Strand | Sense sequence                  | sgRNA score | Restriction sites |
|-------------------------------------|--------|----------|------|-------|-------|------------|--------|---------------------------------|-------------|-------------------|
| GCCTCGAGTGAGAAGTCACCG               | 41     | 44       | 0.4  | G     | TGG   | Intron1    | -      | CGGTGACTTCTATCTCGAGGC          | 0.890       | HphI              |
| GCTCATTGCAAGGATTCAAG                | 915    | 932      | 0.45 | G     | CCG   | Exon3      | +      | GCTCATTGCAAGGATTCAAG           | 0.839       |                   |
| GTCGTAATCAAGTGATTGCCG               | 158    | 175      | 0.4  | G     | GGG   | Exon2      | +      | GTCGTAATCAAGTGATTGCCG          | 0.791       | HpaII             |
| GTGGGGGTGAGATGGAAAGAG               | 755    | 772      | 0.4  | G     | AGG   | Exon3      | +      | GTGGGGGTGAGATGGAAAGAG          | 0.790       |                   |
| GACTATTGACTGTTACCAAC                | 1659   | 1676     | 0.55 | G     | CCG   | Exon3      | +      | GACTATTGACTGTTACCAAC           | 0.773       |                   |
| GCATCATATTCACATGACCA                | 1380   | 1383     | 0.3  | G     | GGG   | Exon3      | -      | TGGTCATGTGGAATGATGC            | 0.692       |                   |
| GTGACTTTGGTAATCTTGGG                | 676    | 693      | 0.35 | G     | CCG   | Exon3      | +      | GTGACTTTGGTAATCTTGG            | 0.683       |                   |
| GTAGCCGATGGAGATCGTGG                | 739    | 756      | 0.6  | G     | GGG   | Exon3      | +      | GTAGCCGATGGAGATCGTGG           | 0.653       |                   |
| GATTAAAGTGTGTTCCGTGG                | 319    | 336      | 0.45 | G     | TGG   | Exon2      | +      | GATTAAAGTGTGTTCCGTGG           | 0.648       |                   |
| GGATGGGACCAAGTGTTGGA                | 225    | 242      | 0.45 | G     | CCG   | Exon2      | +      | GGATGGGACCAAGTGTTGGA           | 0.600       |                   |
| GAGAGGTCTACTCTCGTACG                | 2048   | 2065     | 0.35 | G     | TGG   | Exon4      | +      | GAGAGGTCTACTCTCGTACG           | 0.563       | Maell Csp6I SplII |
| GGAGTCATCTCAATGGTTGG                | 1306   | 1323     | 0.4  | G     | AGG   | Exon3      | +      | GGAGTCATCTCAATGGTTGG           | 0.534       |                   |
| GGTCGAATGATCTCTAGGGGA               | 246    | 263      | 0.65 | G     | GGG   | Exon2      | +      | GGTCGAATGATCTCTAGGGGA          | 0.533       |                   |
| GGTAATCCGGGATACAAATGAA              | 1138   | 1155     | 0.5  | G     | TGG   | Exon3      | +      | GGTAATCCGGGATACAAATGAA         | 0.502       | TspDTI            |
| GTTTCGGATCTAATGTCCAT                | 121    | 138      | 0.55 | G     | CCG   | Exon2      | +      | GTTTCGGATCTAATGTCCAT           | 0.500       | Bccl              |
| GAATGGATGGATCAAGTGCG                | 1905   | 1908     | 0.55 | G     | TGG   | Exon4      | -      | CCACCTTATGATCCTACCCATTC       | 0.485       |                   |
| GATTGTACCAGGTCAAGTGA                | 411    | 428      | 0.4  | G     | TGG   | Intron2    | +      | GATTGTACCAGGTCAAGTGA           | 0.481       |                   |
| GGAGATAGACCTATCTCAAGT               | 529    | 546      | 0.5  | G     | TGG   | Exon3      | +      | GGAGATAGACCTATCTCAAGT          | 0.479       |                   |
| GCAACTACTGATGAATGTGC                | 1198   | 1215     | 0.5  | G     | GGG   | Exon3      | +      | GCAACTACTGATGAATGTGC          | 0.478       | MluCI             |
| GATGGATATCGGAGAACGAGT               | 2467   | 2484     | 0.45 | G     | GGG   | Exon4      | +      | GATGGATATCGGAGAACGAGT          | 0.477       |                   |
| GCAGTAGCCTGGGCTCAGAT                | 2317   | 2334     | 0.5  | G     | GGG   | Exon4      | +      | GCAGTAGCCTGGGCTCAGAT          | 0.476       | Bccl BseMII       |
| GTGGAGGGCGACATTTCGCCA               | 208    | 225      | 0.4  | G     | TGG   | Exon2      | +      | GTGGAGGGCGACATTTCGCCA          | 0.465       | BseGI HpaII BspMII |

Figure S1