

*Supplementary Table 1. Summary of primers used in this study*

| Primer           | Sequence (5'-3')                              |
|------------------|-----------------------------------------------|
| <i>NK-M1</i>     | 5'-CGGAATTCGGAGAGGGTAAAGAATGAGAAG-3'          |
| <i>NK-M2</i>     | 5'-CGGGATCC AAGCAGGTATGGAGGAACC-3'            |
| <i>LHA-U</i>     | 5'- CCGCTCGAGTGCCTCATCAAATGTTATT-3'           |
| <i>LHA-D</i>     | 5'- GTTGGTTCATGATCCTATTCTTTTTAAGCTCATC-3'     |
| <i>RHA-U</i>     | 5'-ATGATTAAAGATAAGAACATTACCACAATCGAAAC-3'     |
| <i>RHA-D</i>     | 5'-CCTGATCATTAAATCTAATGGAAAAATAT-3'           |
| <i>U6-U</i>      | 5'-AGCTTAAAAAGAATAGGATCATGAACCAACGGC-3'       |
| <i>U6-D</i>      | 5'-ATTTTT TGCTTCTCATCACACAAGCGACAGCGCGC-3'    |
| <i>T-U</i>       | 5'-AGCAGCTGCACAATAAATATGAAGATGAAGATGAA-3'     |
| <i>T-D</i>       | 5'-CGATTGTGTAATGTTCTTATCTTTAATCATATTC-3'      |
| <i>NK-U</i>      | 5'-GCGCGCTGTCGCTTGTGTGATGAGAAGCAAAAATTGTG-3'  |
| <i>NK-D</i>      | 5'-TTCATCTTCATCTTCATATTTATTGTGCAGCTGCTTGTA-3' |
| <i>pZHY988-U</i> | 5'-GGTGGAGTAAAGAAGGAGTGC-3'                   |
| <i>pZHY988-D</i> | 5'-GGTGGAGTAAAGAAGGAGTGC-3'                   |
| <i>pX6-U</i>     | 5'-TGGTGGTTGGTGTAAGGAGATGG-3'                 |
| <i>pX6-D</i>     | 5'-CTCGCAGTAATGCCAACTTTGT-3'                  |

Supplementary Table 2. Design of sgRNA target BT gene using BiooTools

| Number | Start | End | Protospacer_sequence+PAM (5'-3')        | Length (nt) | GC%    |
|--------|-------|-----|-----------------------------------------|-------------|--------|
| 1      | 152   | 174 | 5'-AGCCAAAAAAGGTCGTCGG <u>CGG</u> -3'   | 23          | 50.00% |
| 2      | 171   | 193 | 5'-GCGGAAGTCCCCGAACACTT <u>CGG</u> -3'  | 23          | 60.00% |
| 3      | 183   | 205 | 5'-GAACACTTCGGCCGATATTG <u>AGG</u> -3'  | 23          | 50.00% |
| 4      | 254   | 276 | 5'-GAGATGTTGAACGCCAAAGA <u>AGG</u> -3'  | 23          | 45.00% |
| 5      | 300   | 322 | 5'-CGCTCTTCGCTCACTTCTCC <u>CGG</u> -3'  | 23          | 60.00% |
| 6      | 303   | 325 | 5'-TCTTCGCTCACTTCTCCCGG <u>TGG</u> -3'  | 23          | 60.00% |
| 7      | 315   | 337 | 5'-TCTCCCGGTGGAATATCTCA <u>AGG</u> -3'  | 23          | 50.00% |
| 8      | 679   | 701 | 5'-TTGAAGATGGTGAGGATTCC <u>AGG</u> -3'  | 23          | 45.00% |
| 9      | 750   | 772 | 5'-CTAGTGATGCCAAGATCATGT <u>TGG</u> -3' | 23          | 45.00% |
| 10     | 753   | 775 | 5'-GTGATGCCAAGATCATGTGG <u>AGG</u> -3'  | 23          | 50.00% |
| 11     | 790   | 812 | 5'-TAGACACAGCTACACACCAT <u>AGG</u> -3'  | 23          | 45.00% |
| 12     | 874   | 896 | 5'-ATTCTACTAGGAAGAACGAC <u>AGG</u> -3'  | 23          | 40.00% |

Note: The underlined part is the PAM sequence.