

SUPPLEMENTARY TABLE

Supplementary Table 1. Primer and siRNA sequences used in experiments.

| Target primer and siRNA | Sequence 5' → 3' | Position in sequence |
|--|-------------------------|----------------------|
| qRT-PCR primers | | |
| STAT1 | | |
| Forward | TCCGTTTTTCATGACCTCCTG | nt 10179-10198 |
| Reverse | TGAATATTCCTCCGACTGAGC | nt 18088-18107 |
| GAPDH | | |
| Forward | GCACCGTCAAGGCTGAGAAC | nt 249 to 268 |
| Reverse | TGGTGAAGACGCCAGTGGA | nt 368 to 386 |
| siRNA | | |
| STAT1-siRNA | | |
| Sense | GCGUAAUCUUCAGGAUAAUtt | nt 649 to 667 |
| Antisense | AUUAUCCUGAAGAUUACGctt | |
| Control-siRNA | | |
| Sense | UUCUCCGAACGUGUCACGUtt | Scramble |
| Antisense | ACGUGACACGUUCGGAGAAtt | |
| MSP and Sanger sequencing primers | | |
| Fragment A | | |
| Forward | GAGGTAGGAAAAAGTAAGAAGG | nt 4542-4563 |
| Reverse | CTAAATAAACTACAACCCAATCC | nt 4874-4896 |
| Fragment B | | |
| Forward | GGATTGGGTTGTAGTTTATTTAG | nt 4874-4896 |
| Reverse | CAACCAAACCCCTCCACAAACTC | nt 5098-5120 |
| Fragment C | | |
| Forward | GAGTTTGTGGAGGGGTTTGGTTG | nt 5098-5120 |
| Reverse | CTCAAACACATTCTTCCTC | nt 5356-5375 |

The sequence position of STAT1 and GAPDH primers is indicated based on the sequences in the GenBank with accession # NG_008294.1 and # NM_002046, respectively. MSP, methylation-specific polymerase chain reaction; nt, nucleotide.