Supplementary table 1 The sequences of shRNA construction

| **Gene** | | **Sequences (5’-3’)** |
|---|---|---|
| GINS2-shRNA | Sense | 5’-CCGGGCGATTAACCTGAAACAAAGACTCGAGTCTTTGTTTCAGGTTAATCGCTTTTTG-3’ |
| | Antisense | 5’-AATTCAAAAAGCGATTAACCTGAAACAAAGACTCGAGTCTTTGTTTCAGGTTAATCGC-3’ |
| Scramble-shRNA | Sense | 5’-GATCCGTGGCATGCGTAGAAGGCAACTCGAGATTGCCTTCTACGCATGCCATTTTTC-3 |
| | Antisense | 5’-TCGAGAAAAAGTGGCATGCGTAGAAGGCAACTCGAGATTGCCTTCTACGCATGCCAG-3 |

Supplementary table 2 The sequences of qRT-PCR primers

| Gene | Forward | Reverse | Products (bp) |
|---|---|---|---|
| GAPDH | TGACTTCAACAGCGACACCCA | CACCCTGTTGCTGTAGCCAAA | 121 |
| GINS2 | CAGAAATGTCGCCTGCTCC | GGATTTCGTCTGCCTTCG | 153 |
| GADD45A | GAGAGCAGAAGACCGAAAGG | CAGCAGGCACAACACCAC | 152 |
| BRCA2 | CACCCACCCTTAGTTCTACTGT | CCAATGTGGTCTTTGCAGCTAT | 250 |
| IL1A | AGATGCCTGAGATACCCAAAACC | CCAAGCACACCCAGTAGTCT | 147 |
| TNFAIP3 | CCACGATGCTCAGGTTTG | TCCCTTTCTCAGCCAAGAC | 222 |
| IFIT1 | GCGCTGGGTATGCGATCTC | CAGCCTGCCTTAGGGGAAG | 96 |
| IFIT3 | AAAAGCCCAACAACCCAGAAT | CGTATTGGTTATCAGGACTCAGC | 132 |
| E2F8 | AAGTACGCCGAGCAGATTATG | ATGTCTGGGTGTCCATTTGGG | 128 |
| FGFR2 | GGTGGCTGAAAAACGGGAAG | AGATGGGACCACACTTTCCATA | 104 |
| IFITM1 | TCCGTGAAGTCTAGGGACAG | GTCACAGAGCCGAATACCAG | 152 |
| STAT2 | GGTTTGATTTGGGACTTTGGT | CTGCTGGTTCTGAAGGTTTGG | 267 |
| BMPR2 | ACGGGTATCTTTTGTTGGTGT | TGTCAGCTTTCATAGTGGCATC | 213 |
| PRKACB | GATTGGTGGGCATTAGGAGTG | TCTGAACTGAAGTGGGATGGG | 134 |
| IFI35 | TGAGCAGGTGCTGCAACAAAAG | CCACTCCATCCCTAGCAAACCC | 299 |
| IFITM2 | ATGAACCACATTGTGCAAACC | CATAGCCACTTCCTGCTCCTC | 90 |
| TNIP1 | CCTCTTCCATCTGCCGGAAT | TCTCATCCAGCTGAGGCTCT | 258 |
| NFKBIE | TTACCCATGTTGGGTCAGCC | AACGGTGTTTCAGGGTCCTC | 140 |
| IFI6 | CTCGCTGATGAGCTGGTCT | GATACTTGTGGGTGGCGTAG | 149 |
| ISG15 | CAGCTCCATGTCGGTGTCA | AGGTTCGTCGCATTTGTCC | 184 |
| MX1 | GGTCAGTTACCAGGACTACGAG | GGTTATGCCAGGAAGGTCTATT | 181 |

| | | | |
|---|---|---|---|
| NTRK3 | AAGCCCACCCACTACAACAAT | TGGGACTCACTTCGTCAAACA | 148 |
| FANCD2 | CACTGACCAGGCATACTTT | TCTAGGAGCGGCATACATT | 268 |
| RELB | CAGCCTCGTGGGGAAAGAC | CCAGCGTTGTAGGGGTCAA | 171 |
| RAP1A | TTGAGGCGGTCTAACTACCC | CAACGAACATACATCATCCC | 300 |
| FANCB | CAACTTATGGATTCAGGTGGAG | TTTCCCATTTAGCAGCAACC | 109 |
| IL1R2 | CCTGGAAGATGCTGGCTATTAC | CGGTTCCCAGAAACACCTTAC | 200 |
| IRF1 | GATGCTTCCACCTCTCACC | TGCTCCACCTCCAAGTCC | 201 |
| STAT1 | GGCACCAGAACGAATGAGG | CCACAACGGGCAGAGAGG | 124 |
| KRAS | GGAGGGCTTTCTTTGTGTATTTG | TGTCTTGTCTTTGCTGATGTTTC | 225 |
| IFITM3 | TCGTCTGGTCCCTGTTCAA | CCAACCATCTTCCTGTCCC | 100 |
| IRF9 | CAGTAGTTGTCCGTGATAATCG | GTGCTTGGCTTTAGAGTTGG | 205 |