|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **HSV1-GFP** | **siRNA #**  **(QIAGEN)** | **siRNA sequence** | **# of wells** | **# of exp.** | **GFP [%]** | **GFPcorr [%]** | **DAPI [%]** | **GFPcorr/ DAPI** | **av. x**  **[%]** | **relative rank** |
| **no HSV1** | N.A. | negative control for infection | 48 | 12 | 0 | 0 | 100 | 0 | 0 | **N.A.** |
| **random** | scr | positive control for infection | 48 | 12 | 100 | 100 | 100 | 1 | 100 | **N.A.** |
| **GFP** | GFP | positive control for RNAi | 48 | 12 | 19 | 19 | 96 | 0.21 | 21 | **N.A.** |
| **ND** | N.A. | without microtubules | 20 | 5 | 21 | 21 | 97 | 0.22 | 22 | **N.A.** |
| **Imp β1**  **KPNB1** | KPNB1\_6 | CTGGAATCGTCCAGGGATTAA | 12 | 3 | 3 | 3 | 34 | 0.08 | 14 | **1** |
| KPNB1\_3 | AAGGGCGGAGATCGAAGACTA | 12 | 3 | 3 | 3 | 27 | 0.11 |
| KPNB1\_1 | TCGGTTATATTTGCCAAGATA | 12 | 3 | 5 | 5 | 42 | 0.16 |
| KPNB1\_2 | CAAGAACTCTTTGACATCTAA | 12 | 3 | 7 | 7 | 35 | 0.20 |
| **Imp α1**  **hKPNA2** | KPNA2\_5 | ACGAATTGGCATGGTGGTGAA | 16 | 4 | 4 | 4 | 24 | 0.14 | 46 | **2** |
| KPNA2\_2 | ACCAGTGGTGGAACAGTTGAA | 16 | 4 | 37 | 37 | 78 | 0.49 |
| KPNA2\_6 | CCGGGCTGGTTTGATTCCGAA | 8 | 2 | 65 | 65 | 90 | 0.75 |
| **Imp α6**  **hKPNA5** | KPNA5\_2 | CACAATGATTATAAAGTTGTA | 16 | 4 | 12 | 12 | 65 | 0.18 | 63 | **3** |
| KPNA5\_4 | CTCAAATTTATGTAGAGGCAA | 16 | 4 | 31 | 31 | 67 | 0.46 |
| KPNA5\_1 | ATGGATGGATTTCAACTTTAA | 16 | 4 | 24 | 24 | 46 | 0.59 |
| KPNA5\_3 | TAGAGTTATTAACAAATTCAA | 16 | 4 | 127 | 127 | 99 | 1.29 |
| **TNPO1**  **(KPNB2)** | TNP01\_6 | CAGCATGTTAAGCCTTGTATA | 8 | 2 | 49 | 49 | 94 | 0.53 | 68 | **4** |
| TNP01\_7 | CAGAATTGGCCTGACCTCTTA | 16 | 4 | 23 | 23 | 49 | 0.57 |
| TNP01\_2 | CTGGAACAACTTAATCAGTAT | 8 | 2 | 53 | 53 | 80 | 0.73 |
| TNP01\_8 | ATGCCGTTGCATCATGGATTA | 8 | 2 | 69 | 69 | 80 | 0.90 |
| **Imp α7**  **hKPNA6** | KPNA6\_5 | AACCATTCTCTTACAGTTTAA | 8 | 2 | 50 | 50 | 72 | 0.65 | 86 | **5** |
| KPNA6\_3 | CAGGTACTTATTATTGGCCAT | 8 | 2 | 58 | 58 | 69 | 0.82 |
| KPNA6\_1 | CTGGGTGGATTACATATGATA | 8 | 2 | 77 | 77 | 89 | 0.90 |
| KPNA6\_6 | TTGCCGAGATTACGTCTTGAA | 8 | 2 | 56 | 56 | 55 | 1.07 |
| **IPO4** | IPO4\_5 | TACAGCCTATTTGCAGCCTTA | 8 | 2 | 45 | 45 | 80 | 0.57 | 90 | **6** |
| IPO4\_1 | CTGCCTGGAGGTAGCTAGAAA | 8 | 2 | 59 | 59 | 78 | 0.76 |
| IPO4\_6 | CCCAAGCATTTCGCTGTACAA | 8 | 2 | 80 | 80 | 63 | 1.36 |
| **Imp α3**  **hKPNA4** | KPNA4\_3 | CAGCACTGAGATATATATATA | 16 | 4 | 39 | 39 | 71 | 0.60 | 90 | **7** |
| KPNA4\_1 | CAGGTTCATCTTTGAAATCTA | 16 | 4 | 50 | 50 | 74 | 0.84 |
| KPNA4\_4 | CACCATTAGCATCTATATCTA | 16 | 4 | 88 | 88 | 96 | 1.02 |
| KPNA4\_2 | CTCGATGGACTAAGTAATATA | 16 | 4 | 87 | 87 | 79 | 1.15 |
| **IPO7** | IPO7\_2 | CAGAAGAAGATCGCCATTGTA | 20 | 5 | 32 | 32 | 63 | 0.51 | 93 | **8** |
| IPO7\_5 | CACCTACTACTCAATACCTTA | 20 | 5 | 119 | 119 | 90 | 1.35 |
| **Imp α4**  **hKPNA3** | KPNA3\_1 | CAGCATCTTTCCCACATTCAA | 16 | 4 | 16 | 16 | 49 | 0.39 | 95 | **9** |
| KPNA3\_2 | AAGCGTATGTTTAAACTGCAA | 12 | 3 | 93 | 93 | 92 | 0.99 |
| KPNA3\_4 | CAGGTGTGCATTCATTACAAA | 16 | 4 | 103 | 103 | 84 | 1.16 |
| KPNA3\_3 | CTGGATTAATTCCTATGATAA | 16 | 4 | 107 | 107 | 95 | 1.25 |
| **Imp α5**  **hKPNA1** | KPNA1\_3 | CAGGTTTGTGGAGTTCCTCAA | 12 | 3 | 70 | 70 | 74 | 0.91 | 95 | **10** |
| KPNA1\_4 | AAACCATATCCTGTAATTTAA | 12 | 3 | 77 | 77 | 101 | 0.92 |
| KPNA1\_2 | AAAGATGAGACTAAATCTTTA | 12 | 3 | 75 | 75 | 98 | 0.93 |
| KPNA1\_1 | ATGGGAATATACACATATTAA | 12 | 3 | 112 | 112 | 104 | 1.05 |
| **TNPO2** | TNPO2\_2 | CCCGAGCATCTCTCTCTGTAA | 16 | 4 | 61 | 61 | 67 | 0.90 | 102 | **11** |
| TNPO2\_5 | AAAGATCAGTTTCTTGTGAAA | 12 | 3 | 94 | 94 | 98 | 0.92 |
| TNPO2\_4 | CAGGAGTGTCTCAACAACATT | 12 | 3 | 100 | 100 | 89 | 0.96 |
| TNPO2\_3 | ATCGTGCAGGATAAACTCAAA | 12 | 3 | 110 | 110 | 79 | 1.32 |
| **RANBP5** | RANBP5\_6 | CAG GTC GAA GAG TCA CTA CAA | 12 | 3 | 27 | 27 | 46 | 0.58 | 103 | **12** |
| RANBP5\_3 | CCCGACAATGTGGTCCGGAAA | 12 | 3 | 84 | 84 | 88 | 1.02 |
| RANBP5\_2 | CAGGATACTTGCGGCACTCAA | 12 | 3 | 71 | 71 | 79 | 1.04 |
| RANBP5\_1 | CACGAGGCAATTAAACATGAA | 12 | 3 | 119 | 119 | 86 | 1.47 |
| **IPO13** | IPO13\_1 | CAGGATGATATTCTATCCTTT | 12 | 3 | 74 | 74 | 89 | 0.83 | 128 | **13** |
| IPO13\_5 | CTGACCAGTATGAAAGCCTAA | 12 | 3 | 68 | 42 | 43 | 0.94 |
| IPO13\_3 | CATCATGAGGATGATCATGAA | 12 | 3 | 124 | 124 | 101 | 1.16 |
| IPO13\_4 | CCCACGGATCAGCATCAGCAA | 12 | 3 | 106 | 106 | 58 | 2.18 |
| **IPO11** | IPO11\_1 | CAGCTACAACTTTGAAGTTAA | 12 | 3 | 130 | 130 | 101 | 1.26 | 156 | **14** |
| IPO11\_3 | CTGGAATGCAGTAGAAGTATA | 12 | 3 | 115 | 115 | 87 | 1.31 |
| IPO11\_2 | GAGGAGATTCTTGGAAATATA | 12 | 3 | 131 | 131 | 96 | 1.44 |
| IPO11\_4 | AACGGTTTCCATGGATCTCAA | 12 | 3 | 119 | 119 | 80 | 2.23 |
| **IPO8** | IPO8\_3 | ATGCAATTAATTGATAATCAT | 16 | 4 | 71 | 71 | 94 | 0.81 | 167 | **15** |
| IPO8\_1 | AAGAGCCTGATTGAAGATAAA | 16 | 4 | 74 | 74 | 76 | 0.92 |
| IPO8\_2 | CCCAGTTTACTTCGGATTATA | 16 | 4 | 133 | 133 | 92 | 1.42 |
| IPO8\_4 | CAGGTCTGTGCTACTAGACAA | 16 | 4 | 194 | 194 | 56 | 3.53 |
| **TNPO3** | TNPO3\_1 | ACCGAATGTCTTAGTGAACTA | 12 | 3 | 26 | 26 | 87 | 0.30 | 179 | **16** |
| TNPO3\_5 | CTGGGAGATCATGCAGGTTGA | 12 | 3 | 89 | 89 | 92 | 0.92 |
| TNPO3\_4 | CAAGTGGTCATCCCTATCTTA | 12 | 3 | 99 | 99 | 93 | 1.20 |
| TNPO3\_2 | CTGGAGATCCTTACAGTGTTA | 12 | 3 | 85 | 218 | 45 | 4.73 |
| **IPO9** | IPO9\_2 | ATCAGTCATCTTGAAACAATA | 12 | 3 | 120 | 120 | 97 | 1.24 | 206 | **17** |
| IPO9\_3 | CACAGCAAGCATGGAAAGCAA | 12 | 3 | 89 | 89 | 61 | 1.33 |
| IPO9\_1 | CTGAATTGATTTATTATATTA | 12 | 3 | 99 | 192 | 100 | 2.28 |
| IPO9\_4 | ATGGGTTGAGAGAATCGATAA | 12 | 3 | 89 | 235 | 82 | 3.39 |

**Supplement Table 1: Specific nuclear transport factors are required for HSV1 early gene expression.**

Targeted siRNA screen (QIAGEN) in HeLa cells for HSV1 gene expression; plate reader.

Franceschini et al. (2014) correction and Bonferroni correction; GFP/DAPI ratio

http://www.bioconductor.org/packages/release/bioc/manuals/scsR/man/scsR.pdf, page 26