**Supplemental Table S3.** Statistical analysis of the quantification of nuclear speckle patterns.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| siRNA LB1 [pmol]siRNA scr.I-Hg [60 µM] | --- | 30-- | 60-- | -+- | --+ | 30-+ | 60-+ | -++ |
| **average speckle # per cell** | --- |  |  |  |  |  |  |  |  |
| 30-- | 0.01502 |  |  |  |  |  |  |  |
| 60-- | 0.00309 | 0.98980 |  |  |  |  |  |  |
| -+- | 0.99400 | 0.00354 | 0.00075 |  |  |  |  |  |
| --+ | 0.94720 | 0.11816 | 0.02631 | 0.60268 |  |  |  |  |
| 30-+ | 0.00574 | 0.99954 | 0.99997 | 0.00137 | 0.04826 |  |  |  |
| 60-+ | 0.00266 | 0.98300 | 1.00000 | 0.00065 | 0.02271 | 1.00000 |  |  |
| -++ | 0.78001 | 0.24056 | 0.05948 | 0.36230 | 0.99981 | 0.10600 | 0.05158 |  |
| **average speckle size** | --- |  |  |  |  |  |  |  |  |
| 30-- | 0.22816 |  |  |  |  |  |  |  |
| 60-- | 0.10789 | 0.99975 |  |  |  |  |  |  |
| -+- | 0.97452 | 0.72515 | 0.46345 |  |  |  |  |  |
| --+ | 0.14871 | 0.00109 | 0.00047 | 0.02577 |  |  |  |  |
| 30-+ | 0.84285 | 0.92451 | 0.72421 | 0.99976 | 0.01082 |  |  |  |
| 60-+ | 0.41660 | 0.99983 | 0.98481 | 0.91676 | 0.00245 | 0.99281 |  |  |
| -++ | 0.58055 | 0.00713 | 0.00298 | 0.15277 | 0.97216 | 0.06940 | 0.01623 |  |
| **average speckle shape factor** | --- |  |  |  |  |  |  |  |  |
| 30-- | 0.16127 |  |  |  |  |  |  |  |
| 60-- | 0.11366 | 1.00000 |  |  |  |  |  |  |
| -+- | 0.99978 | 0.31986 | 0.23601 |  |  |  |  |  |
| --+ | 0.23073 | 0.00121 | 0.00082 | 0.11079 |  |  |  |  |
| 30-+ | 0.84983 | 0.83690 | 0.73206 | 0.97584 | 0.01887 |  |  |  |
| 60-+ | 0.29536 | 0.99991 | 0.99853 | 0.52286 | 0.00254 | 0.96215 |  |  |
| -++ | 0.79693 | 0.00986 | 0.00662 | 0.54508 | 0.95140 | 0.14024 | 0.02088 |  |
|  | siRNA LB1 [pmol]siRNA scr.I-Hg [60 µM] |  |  |  |  |  |  |  |  |