**Table S2. Fold-changes of the average inhibition percentages between the kinase groups in the MDA-MB-231 siRNA screen.**

|  |  |  |  |
| --- | --- | --- | --- |
|  | **Kinome-wide** | **Single** | **High** |
| **Single** | 1.22 (1.000) |  |  |
| **High** | 1.80 (<10-15) | 1.48 (0.013) |  |
| **Low** | 1.47 (3.4e-07) | 1.28 (0.707) | 1.23 (0.031) |

Kinome-wide, single kinases in the kinome-wide background; Single, single targets selected by TIMMA; High/Low, target pairs in the TIMMA selection with predicted efficacies above/below 0.6. P-values after Bonferroni adjustment are reported in the parentheses.