Table S2. Ana2 phospho-sites identified by MS/MS in this study

| Sample | Peptide Sequence | Phospho Localization Probability | Ascore | Phospho Residue | Peptide Score | Sequon: Peptide Rank | Sequon: Peptide Score | Scaffold: Peptide Probability | Actual Mass | Observed Mass | Charge | Delta AMU | Delta PPM | Spectrum Counts |
|--------|-----------------|----------------------------------|--------|---------------|---------------|---------------------|---------------------|-------------------------------|-------------|--------------|--------|------------|-----------|----------------|
| + Sas4 VS OE | S38 | PSAAVpGHTNEIGPTVPVLGF | 100% | 40.54 | 152.97 | 177.3 | 1 | 0.1097 | 4.945 | 0.992 | 2671.307883 | 891.443269 | 3 | 0.0108 | 4.03 | 5/98, (5%) |
| | S63 | GQPQPDPoGPQGPPhHDESipR | 99% | 18.44 | 118.89 | 151.4 | 1 | 0.008173 | 4.681 | 0.9885 | 2814.197457 | 704.5566402 | 4 | 0.00914 | 1.47 | 21/341, (15%) |
| | S150 | LQSSSNADVL | 98% | 20.98 | 79.5 | 300.6 | 1 | 0.3128 | 1.839 | 1 | 1071.448216 | 536.751384 | 2 | 0.000787 | -0.266 | 17/55, (31%) |
| + Sas4 RNAi | S38 | (Phospho modification not detected) | | | | | | | | | | | | |
| | S63 | (Phospho modification not detected) | | | | | | | | | | | | |
| | S510 | RLGSSNADVL | 33% | 0 | 175.17 | 604.2 | 1 | 0.4541 | 3.384 | 1 | 1277.550877 | 614.7827145 | 2 | 0.001238 | 1.04 | 2/27, (7%) |
| SECTON B | | | | | | | | | | | | | | |
| + P14 KD | Lower Region | S38 | (Phospho modification not detected) | | | | | | | | | | | |
| | Upper Region | S38 | (Phospho modification not detected) | | | | | | | | | | | |
| + P14 ND | Lower Region | S38 | (Phospho modification not detected) | | | | | | | | | | | |
| | Upper Region | S38 | PSAAVpGHTNEIGPTVPVLGF | 100% | 101.45 | 211.15 | 241 | 1 | 0.1556 | 4.72 | 0.9994 | 2671.3207 | 891.447103 | 3 | 0.0236 | 8.83 | 5/8, (38%) |

*Number of phospho spectra/number of total spectra (in percent).*