**Supplementary table 2.** HDX-MS data collection and validation statistics

**(related to main figure 4)**

|  |  |  |
| --- | --- | --- |
| Data set | p110γ unphosphorylated  | p110γ phosphorylated  |
| HDX reaction details | %D2O=75.5%pH(read)=7.5Temp=4ºC, 20ºC | %D2O=75.5%pH(read)=7.5Temp=4ºC, 20ºC |
| HDX time course (seconds) | 3s at 4ºC, 3s, 30s, 300s, 3000s at 20 ºC | 3s at 4ºC, 3s, 30s, 300s, 3000s at 20 ºC |
| HDX controls | N/A | N/A |
| Back-exchange | No correction, deuterium levels are relative | No correction, deuterium levels are relative |
| Number of peptides | 244 | 244 |
| Sequence coverage | 98.4% | 98.4% |
| Average peptide/redundancy | Length= 15.2Redundancy= 3.3  | Length= 15.2Redundancy= 3.3 |
| Replicates | 3  | 3 |
| Repeatability | Average StDev=0.53% | Average StDev=0.57% |
| Significant differences in HDX | >5% and >0.4 Da and unpaired t-test ≤0.01 | >5% and >0.4 Da and unpaired t-test ≤0.01 |