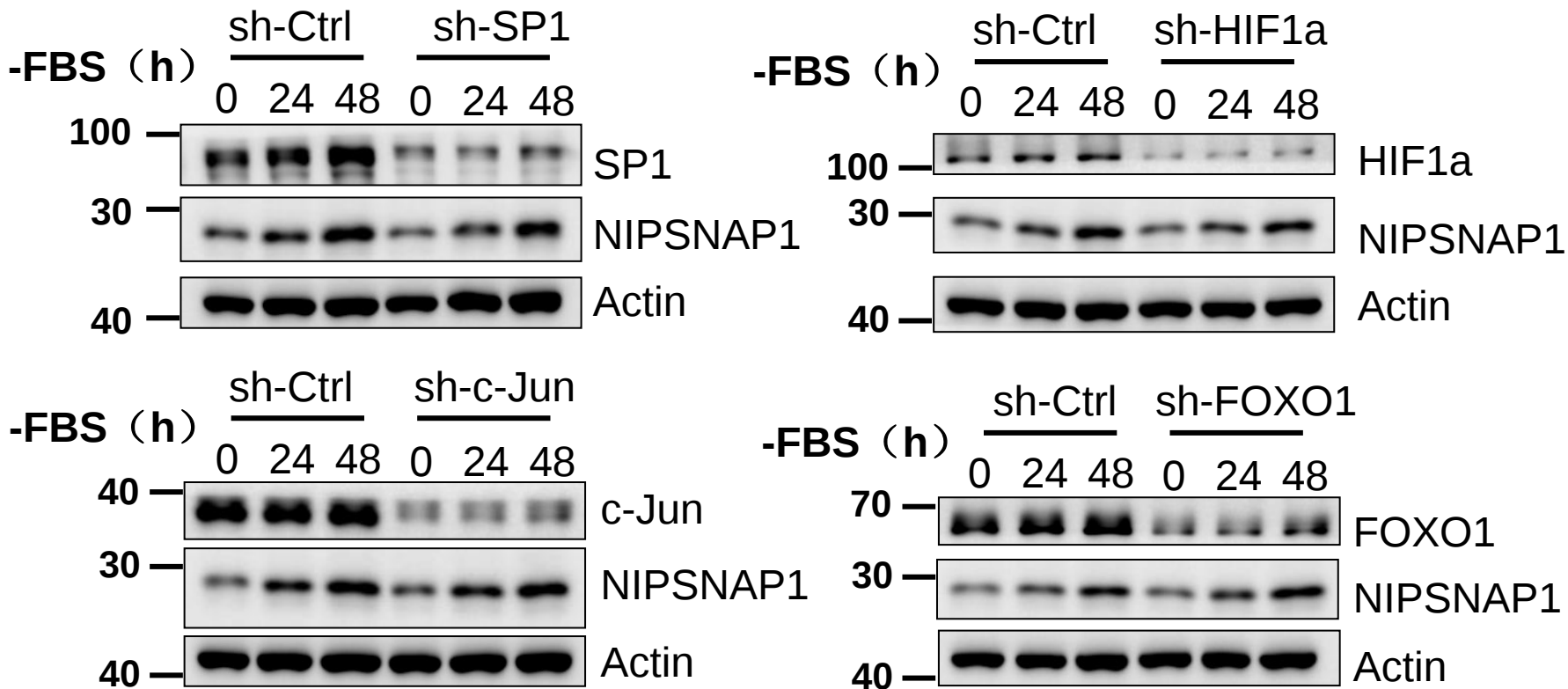


A

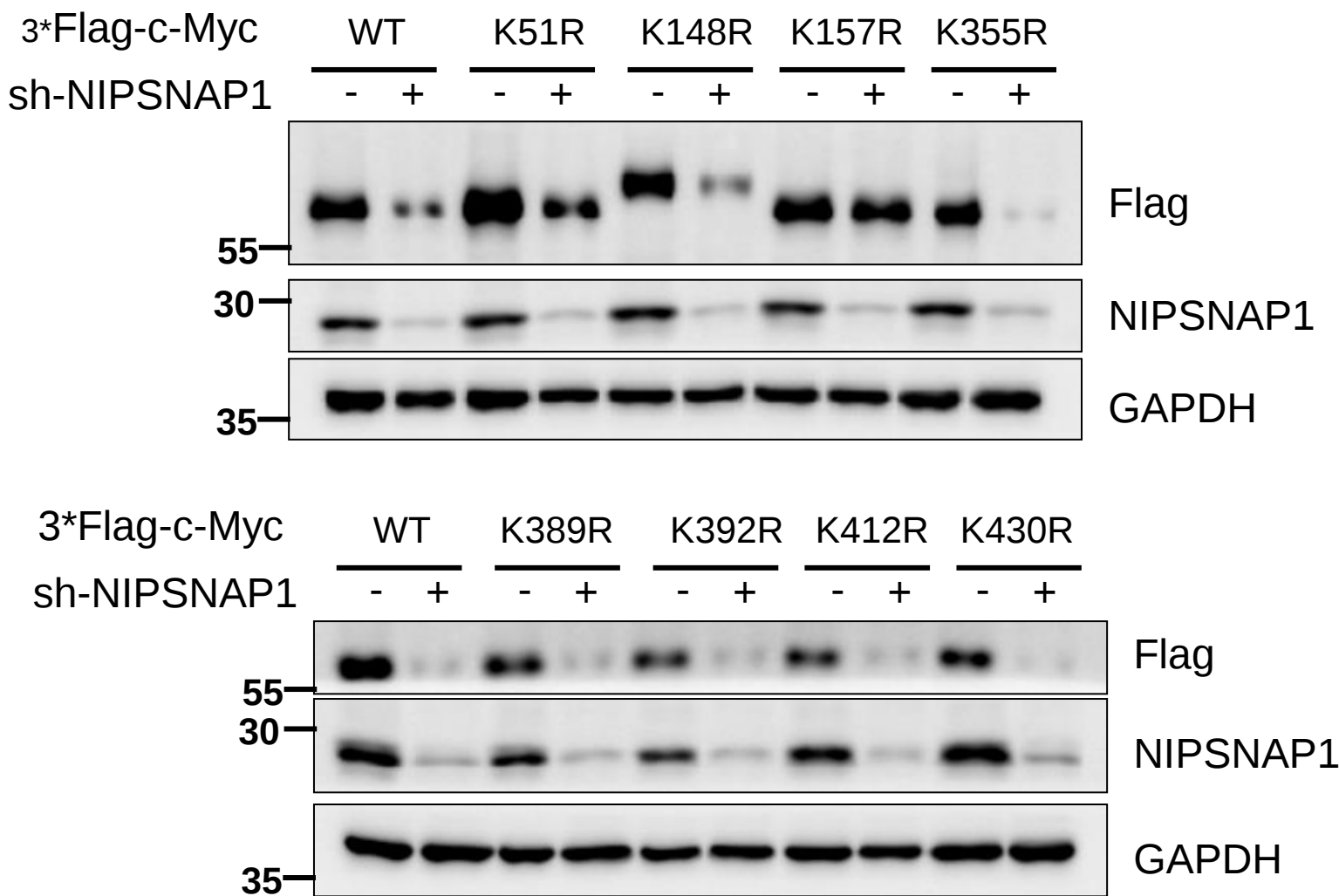
|          | Factor name | Score     | Start | End   | Strand | predicted site sequence |
|----------|-------------|-----------|-------|-------|--------|-------------------------|
| MA0079.3 | SP1         | 13.924208 | -117  | -107  | -1     | GCTCCGCCTCC             |
| MA0079.2 | SP1         | 12.262342 | -1729 | -1720 | 1      | CCCTGCCCCC              |
| MA0104.4 | c-Myc       | 11.641556 | -1929 | -1921 | 1      | CACGTGGTC               |
| MA1106.1 | HIF1a       | 11.2201   | -1429 | -1420 | -1     | TTACGTGCTC              |
| MA0059.1 | c-Myc       | 10.470099 | -279  | -272  | 1      | CACGAGGC                |
| MA0480.1 | FOXO1       | 8.845745  | -1224 | -1214 | 1      | TC TTGTTGCC C           |
| MA0099.2 | c-Jun       | 8.680231  | -502  | -496  | -1     | TTACTCA                 |

B



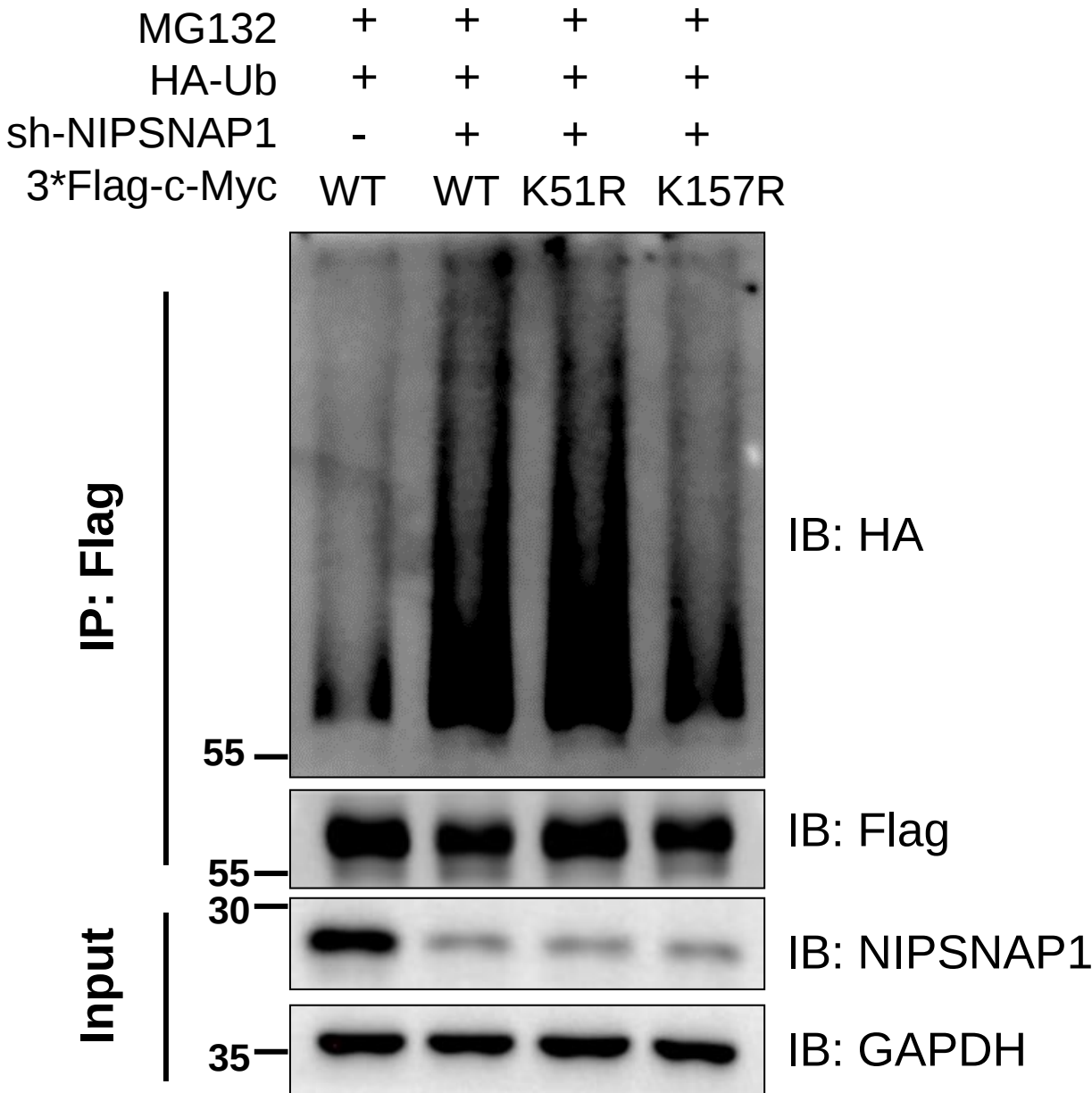
HCT116

C



HCT116

D



HCT116

Figure S2.