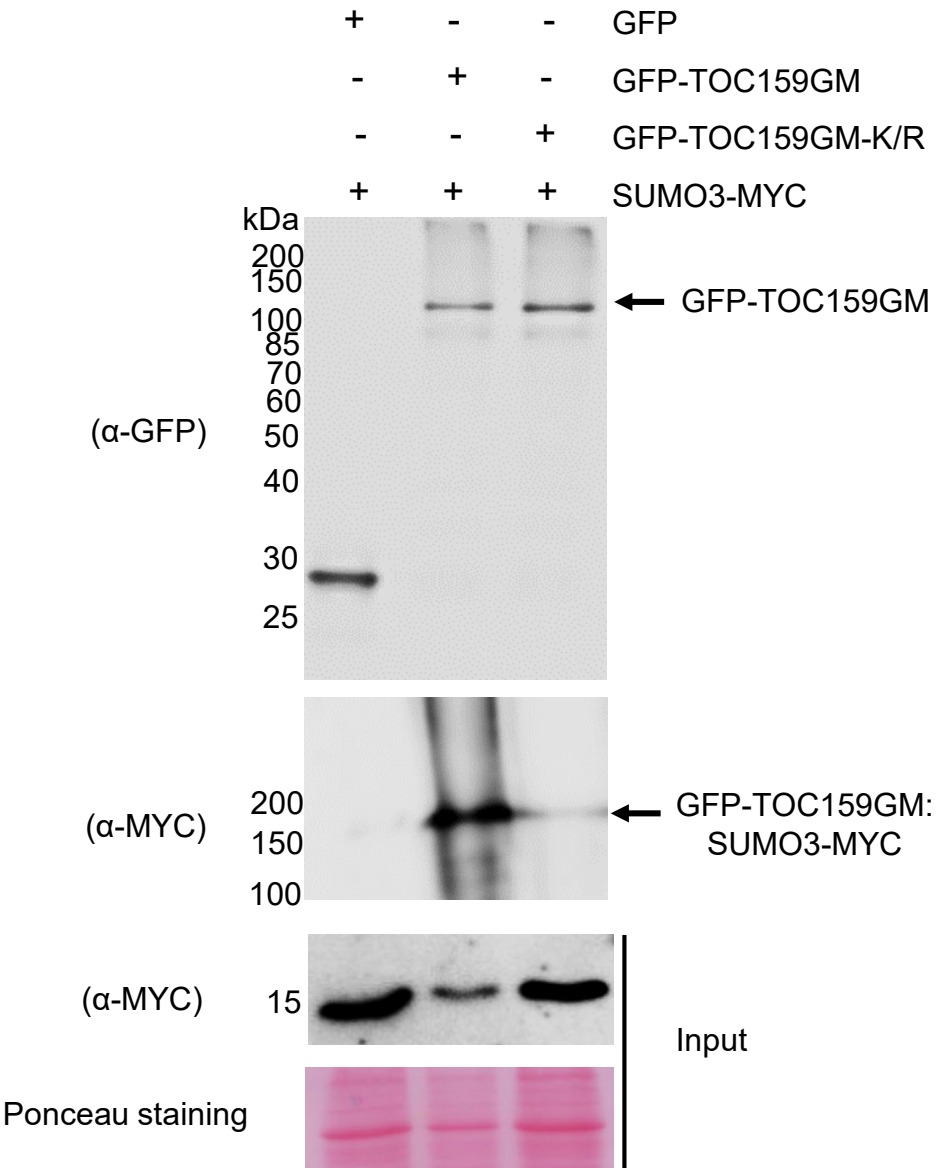


**A**

| Position | Peptide         | Score  | Cutoff | P- value | Type                     |
|----------|-----------------|--------|--------|----------|--------------------------|
| 1300     | TVQVTKDKKEFNIHL | 6.009  | 4.866  | 0.049    | Sumoylation Nonconcensus |
| 1370     | ENIATGVKLEDQIAL | 11.573 | 3.24   | 0.01     | Sumoylation Concensus    |

**B**



**Fig. S1.2**