

Table S1. Sequence coverage of WT SAGA complex.

SAGA subunit	Sequence coverage [%]					
	a	b	c	d	2mM	5mM
Gcn5	81.8	81.8	81.8	81.5	34.4	21.9
Ada2	77.6	77.6	77.6	77.4	26.3	24.4
Ada3	77.6	78.8	74.9	78.8	48.3	31.6
Sgf29	81.9	81.9	78.8	81.9	53.3	49
Ubp8	82	82.8	80.7	82.8	29.9	16.6
Sgf11	77.8	77.8	77.8	77.8	0	0
Sgf73	50.5	50.5	50.5	50.5	27.7	22.2
Sus1	85.4	85.4	85.4	85.4	21.9	0
Spt7	84.2	86.9	85.7	86.4	40.9	33.1
Spt8	77.1	77.1	77.1	77.1	44	35
Spt20	73.8	74	73.8	73.7	47	45.2
Spt3	62.9	62.9	62.9	62.9	27.3	27
Ada1	72.1	74.2	74.2	71.9	24.4	24.4
Tra1	77.8	78	78.6	79.6	26.1	21.9
Taf10	64.1	67.5	67.5	67.5	35.4	24.3
Taf12	72	75.3	67.5	82.4	33.6	31.9
Taf9	77.7	79	79	79	52.2	52.9
Taf6	68.4	68.6	68.6	68.6	46.3	39.1
Taf5	71.9	73.9	79.9	79.9	45.4	48.1
Chd1	0	0	0.8	0.7	0	0