Table S1 Doubling times, budding pattern quantifications, and length-to-width ratios

Histone target	genotype	*SSN8*	doubling time (h)	Budding pattern			length to width ratio		
				% Bipolar	% Unipolar	% Random	25%	median	75%
	wt	+	1.5 ± 0.2	83	14	3	1.05	1.19	1.39
		Δ	1.6 ± 0.1	43	52	5	1.09	1.18	1.30
		ssn3Δ	2.3 ± 0.5	68	30	2	1.15	1.32	1.56
H3 Lys4	*set1Δ*	+	1.7 ± 0.1	11	62	27	1.08	1.18	1.35
		Δ	1.7 ± 0.3	15	83	2	1.11	1.27	1.50
		ssn3Δ	2.1 ± 0.3	77	20	3	1.13	1.24	1.38
	jhd2Δ	+	1.7 ± 0.2	49	47	4	1.10	1.31	1.58
		Δ	1.9 ± 0.6	9	90	1	1.23	1.53	1.87
		ssn3Δ	2.5 ± 0.1	13	82	5	1.16	1.40	1.69
H3 Lys36	*set2Δ*	+	1.9 ± 0.5	61	38	1	1.24	1.43	1.77
		Δ	1.5 ± 0.2	89	9	2	1.16	1.38	1.62
	jhd1Δ	+	1.6 ± 0.2	78	17	5	1.10	1.21	1.41
		Δ	2.1 ± 0.9	83	14	3	1.14	1.30	1.55
	rph1Δ	+	1.7 ± 0.1	53	44	3	1.14	1.34	1.57
		Δ	1.7 ± 0.1	60	35	5	1.10	1.24	1.41
	gis1Δ	+	2.0 ± 0.2	58	40	2	1.14	1.37	1.64
		Δ	1.8 ± 0.5	17	82	1	1.10	1.25	1.54
H3 Lys79	*dot1Δ*	+	1.7 ± 0.1	59	40	1	1.13	1.29	1.59
		Δ	1.5 ± 0.3	71	27	2	1.14	1.24	1.44
H4 Lys5, 8, 12	*set5Δ*	+	1.6 ± 0.1	84	13	3	1.12	1.22	1.39
		Δ	1.9 ± 0.1	60	38	2	1.18	1.36	1.61

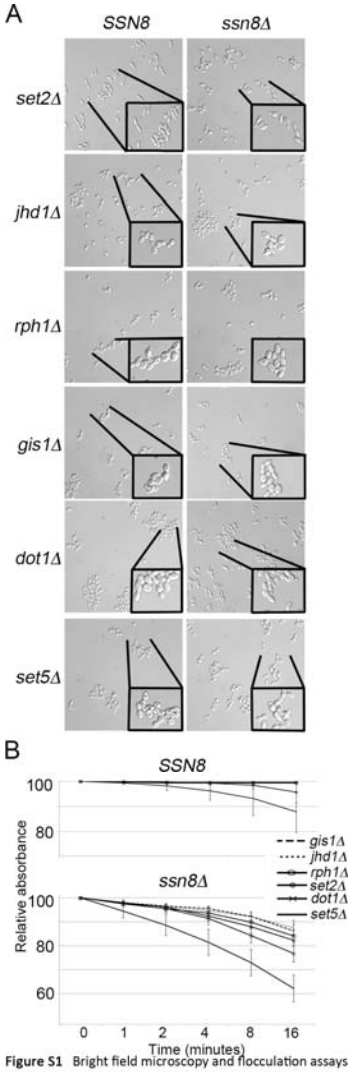

Figure S1 Bright field microscopy and flocculation assays of histone methylation and *SSN8* yeast mutants (A) Bright field microscopy of yeast harboring the indicated mutations grown to mid-logarithmic phase in rich media. (B) Flocculation time course of yeast mutants with the indicated genotypes as described in Figure 1.

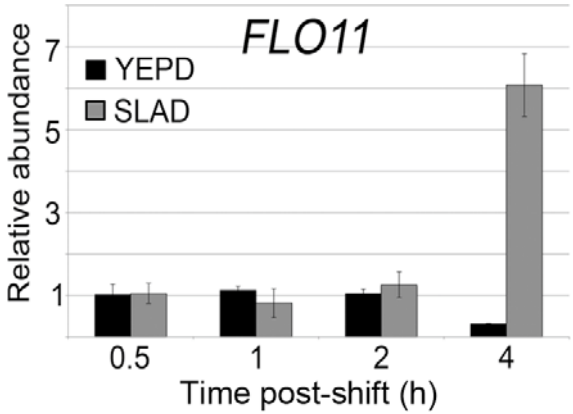

Figure S2 *FLO11* SLAD time course optimization. *FLO11* mRNA was measured using RT-qPCR in a time course experiment. Wild type yeast cultured to mid-logarithmic phase in lowe peptone YEPD were harvested, washed, and shifted into either YEPD or SLAD media to monitor *FLO11* transcription kinetics. Results are from three independent biological replicates and error bars show SEM.