TABLE S1: SwrA/DegU ChIP-Seq WT vs *swrA* Enrichment Summary

Peak[a]	Gene[b]	WT αSwrA[c]	WT αDegU[c]	*swrA* αDegU[c]	Class[d]	Ref[e]
213927	*skfA*				1	
293411	*yczC/yccF*				1	
300782	*ycdA/ycdB*				3	(5,6,10,11)
302324	*ycdC*				1	(11)
376912	*srfAA*				1	(6,7)
478800	*ydaJ*				1	
889865	*yfjA/malA*				3	
1023281	*ctrA*				1	
1117009	*comK/yhzC*				3	
1264976	*yjcM/yjcN*				3	
1289306	*yjhA*				1	
1372068	*ykhA/ykgA*				ND	
1372668	*hmp*				ND	
1599132	*bpr*				1	(6,10,11,13)
1665617	*rnc*				ND	
1691171	*flgB* (P_{flache})				2	(1,5,6,8,10-12)
1924010	*yneI*				1	
1998239	*ppsA*				1	
2033801	*exlX*				1	
2204071	*yopS/yopR*				3	
2219547	*yonU*				1	
2272024	*yolC/yolD*				1	
2308418	*degR/ypzA*				1	
2397791	*motI*				3	
2551865	*yqhG (intragenic)*				3	
2819207	*yrvJ (intragenic)*				1	
3028129	*iscS/braB*				1	
3105979	*ytvA/ytvB*				1	(6,11)
3208278	*mcpA*				2	(6,11)
3210376	*tlpA*				2	
3244781	*maeN*				ND	
3257423	*degQ*				3	(9)
3276581	*yukE*				3	
3293560	*besA*				1	
3535733	*sacB/pbpE*				3	
3622315	*swrA*				1	(5)
3640693	*flgM*				1	(4,6,11)
3701166	*rbsR/pgsB*				ND	
3718673	*ywrE*				1	
3728282	*ywqH*				2	

3882923	*yweA*				1	
3902219	*ywdA*				1	
3923156	*slrA/ywcC*				1	
3941940	*sacX*				1	(2)
3979458	*cydA/cimH*				1	
3989186	*yxkC*				3	(6,11)
3996762	*yxjJ*				1	
4030682	*wapA*				2	(3,6,11)
4039337	*yxiB*				3	
4104395	*yxaJ/yxaI*				1	
4204590	*yaaD*				3	

[a]Peak indicates the location in base pairs of the center of the peak of ChIP-seq signal.
[b]Gene indicates the closes proximal gene to peak center. Two genes are indicated when it wasn't clear which of the two genes might be regulated by the DNA binding activity. Two peaks are intragenic and are labeled with (intragenic).
[c]Data lanes are presented with the genotype of the parent and the primary antibody (α) used for ChIP-seq analysis. Data is presented as: dark gray, indicates a major peak with over 50 input units, light gray indicates a minor peak with between 5-50 input units, and white box, indicates the absence of a peak with less than 5 input units of peak intensity.
[d]Class indicates the way in which the DegU-dependent peak intensity changed in response to various genetic backgrounds. Class 1 represents the DegU-dependent peaks that were abolished in the absence of SwrA, Class 2 represents the DegU-dependent peaks that were reduced in the absence of SwrA, and Class 3 represents the DegU-dependent peaks that did not change in intensity in the absence of SwrA. ND, indicates that we were unable to class the target with certainty often due to very low peak intensity.
[e]References indicate publications in which the target was either predicted or demonstrated.

TABLE S3: SwrA/DegU ChIP-Seq *degQ*$^{+++}$ vs *swrA degQ*$^{+++}$ Enrichment Summary

Peak[a]	**Gene**[b]	***degQ*$^{+++}$ αDegU**[a]	***swrA degQ*$^{+++}$ αDegU**[a]	**Class**[b]
45389	*abrB/metS*			1
213927	*skfA*			1
293411	*yczC/yccF*			1
300782	*ycdA/ycdB*			1
302324	*ycdC*			1
376912	*srfAA*			1
478800	*ydaJ*			1
749613	*yeeF*			1
859668	*yfkN/yfkM*			1
889865	*yfjA/malA*			1
1023281	*ctrA*			1
1056366	*yhaZ*			1
1117009	*comK/yhzC*			3
1121049	*yhjC*			1

1151193	*yisI*			1
1264976	*yjcM/yjcN*			2
1289306	*yjhA*			1
1291068	*yjiA*			1
1354187	*ykcB/mhqA*			1
1372068	*ykhA/ykgA*			3
1372668	*hmp*			3
1398916	*ykoM(intragenic)*			1
1507445	*fruR*			3
1599132	*bpr*			1
1665617	*rnc*			1
1691171	*flgB*			2
1783589	*pksC*			1
1924010	*yneI*			1
1940485	*eglS*			1
1998239	*ppsA*			1
2033801	*exlX*			1
2076944	*yobO*			1
2204071	*yopS/yopR*			1
2219547	*yonU*			1
2272024	*yolC/yolD*			1
2308418	*degR/ypzA*			3
2397791	*dgrA*			2
2551865	*yqhG(intragenic)*			2
2581676	*pstS*			1
2661024	*yqcG*			1
2773724	*cypB/yrkH*			3
2773754	*yrkH/cypB*			3
2780534	*yrhG*			1
2818395	*yrzK/yrvJ*			1
2819207	*yrvJ(intragenic)*			1
3028129	*iscS/braB*			1
3105979	*ytvA/ytvB*			1
3208278	*mcpA*			2
3210376	*tlpA*			1
3239698	*yufN*			1
3244781	*maeN*			1
3257423	*degQ*			2
3276581	*yukE*			2
3293560	*besA*			1
3535733	*sacB/pbpE*			3
3615618	*yvkC/csbA*			1
3622315	*swrA*			1

3640693	*flgM*			1
3701166	*rbsR/pgsB*			1
3718673	*ywrE*			1
3728282	*ywqH*			2
3775553	*ywmD*			1
3882923	*yweA*			1
3902219	*ywdA*			1
3907807	*vpr*			1
3923156	*slrA/ywcC*			1
3941940	*sacX*			1
3979458	*cydA/cimH*			1
3989186	*yxkC*			3
3996762	*yxjJ*			1
4014576	*yxiP/yxiO*			1
4030682	*wapA*			3
4035905	*bglP*			1
4039337	*yxiB*			3
4104395	*yxaJ/yxaI*			1
4204590	*yaaD*			3

[a]Data lanes are presented with the genotype of the parent and the primary antibody (α) used for ChIP-seq analysis. Data is presented as: dark gray, indicates a major peak with over 50 input units, light gray, indicates a minor peak with between 5-50 input units, and open box indicates the absence of a peak with less than 5 input units of peak intensity.

[b]Class indicates the way in which the DegU-dependent peak intensity changed in response to various genetic backgrounds. Class 1 represents the DegU-dependent peaks that were abolished in the absence of SwrA, Class 2 represents the DegU-dependent peaks that were reduced in the absence of SwrA, and Class 3 represents the DegU-dependent peaks that did not change in intensity in the absence of SwrA. ND, indicates that we were unable to class the target with certainty often due to very low peak intensity.

TABLE S4: SwrA/DegU ChIP-Seq *degU*$^{hy32+++}$ vs *swrA degU*$^{hy32+++}$ Enrichment Summary

Peak[a]	Gene[b]	*degU*$^{hy32+++}$ αDegU[a]	*swrA degU*$^{hy32+++}$ αDegU[a]	Class
45389	*abrB/metS*			1
1105819	*aprE*			3
3293560	*besA*			1
4035905	*bglP*			1
1599132	*bpr*			1
3253560	*comA*			3
1117009	*comK/yhzC*			3
3256928	*comQ*			1
3716154	*cotB*			1
1023281	*ctrA*			1
3979458	*cydA/cimH*			1
2773724	*cypB/yrkH*			3
3257423	*degQ*			2
2308418	*degR/ypzA*			2
3645362	*degU*			3
2397791	*dgrA*			2
1940485	*eglS*			1
2033801	*exlX*			2
1691171	*flgB*			2
3640693	*flgM*			1
1507445	*fruR*			3
266397	*glnJ(intragenic)*			3
1372668	*hmp*			3
3028129	*iscS/braB*			1
1387091	*ispA/rsbRB*			3
2765963	*levR*			2
1018839	*lytE/phoA*			3
3244781	*maeN*			1
3208278	*mcpA*			2
449657	*mtlA/ycnL*			3
828536	*pel*			3
1783589	*pksC*			3
1998239	*ppsA*			2
2581676	*psts*			1
3701166	*rbsR/capB*			1
1665617	*rnc*			1
3535733	*sacB/pbpE*			3
3941940	*sacX*			2
3464400	*sdpA/sdpB*			1

3971006	*sigY/yxlA*			3
213927	*skfA*			1
3923156	*slrA/ywcC*			1
376912	*srfAA*			1
3622315	*swrA*			1
3210376	*tlpA*			2
3907807	*vpr*			1
4030682	*wapA*			3
4204590	*yaaD*			3
48076	*yabD*			1
185198	*ybbB*			2
190271	*ybbF(intragenic)*			3
193600	*ybbJ*			2
300782	*ycdA/ycdB*			3
302324	*ycdC*			2
293411	*yczC/yccF*			3
478800	*ydaJ*			1
548818	*yddM*			1
594245	*ydfK*			1
743573	*yeeB(intragneic)*			1
744752	*yeeC*			1
749613	*yeeF*			2
889865	*yfjA/malA*			3
859668	*yfkN/yfkM*			1
821653	*yfmG*			1
1056366	*yhaZ*			1
1121049	*yhjC*			1
1151193	*yisI*			1
1264976	*yjcM/yjcN*			2
1289306	*yjhA*			1
1291068	*yjiA*			1
1354187	*ykcB/mhqA*			1
1372068	*ykhA/ykgA*			2
1398916	*ykoM(intragenic)*			1
1410764	*ykoY(intragenic)*			1
1476554	*ykuD*			1
1442885	*ykvO/ykvN*			2
1473462	*ykzT/cheV*			2
1552212	*ylaN*			3
1781134	*ymzD*			1
1924010	*yneI*			1
2069142	*yobI*			1
2073577	*yobL(intragenic)*			1

2076944	*yobO(intragenic)*			1
2114594	*yojN*			1
2272024	*yolC/yolD*			1
2221441	*yonR*			2
2219547	*yonU*			1
2204071	*yopS/yopR*			2
2700775	*yqaB/yqaC*			2
2661024	*yqcG*			1
2698615	*yqdA*			1
2551865	*yqhG(intragenic)*			2
2841492	*yrbD*			1
2780534	*yrhG*			1
2773754	*yrkH/cypB*			3
2802030	*yrrI(intragenic)*			3
2819207	*yrvJ(intragenic)*			1
2818395	*yrzK/yrvJ*			1
3105979	*ytvA/ytvB*			1
3190799	*yubF*			1
3239698	*yufN*			2
3276581	*yukE*			2
3615618	*yvkC/csbA*			1
3902219	*ywdA*			1
3882923	*yweA*			2
3874914	*ywfA*			2
3775553	*ywmD*			1
3756632	*ywoB/amtB*			3
3728282	*ywqH*			2
3718673	*ywrE*			1
4104395	*yxaJ/yxaI*			1
4039337	*yxiB*			3
4014576	*yxiP/yxiO*			1
3996762	*yxjJ*			2
3989186	*yxkC*			3
4194290	*yyaK/yyaJ*			1
4176028	*yybJ(intragenic)*			1
4175313	*yybK(intragenic)*			1
4174633	*yybK/yybL*			1
4173156	*yybN*			1
4133714	*yydB/yydC*			1
4132875	*yydC*			1
4127781	*yydF*			1

[a]Data lanes are presented with the genotype of the parent and the primary antibody (α) used for ChIP-seq analysis. Data is presented as: dark gray, indicates a major peak with over 50 input units, light gray,

indicates a minor peak with between 5-50 input units, and open box indicates the absence of a peak with less than 5 input units of peak intensity.

[b]Class indicates the way in which the DegU-dependent peak intensity changed in response to various genetic backgrounds. Class 1 represents the DegU-dependent peaks that were abolished in the absence of SwrA, Class 2 represents the DegU-dependent peaks that were reduced in the absence of SwrA, and Class 3 represents the DegU-dependent peaks that did not change in intensity in the absence of SwrA. ND, indicates that we were unable to class the target with certainty often due to very low peak intensity.

TABLE S5a: Expression of reporters in Figure 2A and 2B (Miller units)[a]

reporters	*wt*	*ΔswrA*	*swrA*$^{+++}$	*ΔdegU*	*ΔdegU swrA*$^{+++}$
flache	142 ± 7	46 ± 3	307 ± 19	48 ± 4	41 ± 5
flgM	17 ± 1	6 ± 1	29 ± 1	4 ± 1	4 ± 1
swrA	27 ± 8	15 ± 4	54 ± 10	12 ± 1	12 ± 5
yxjJ	31 ± 0	10 ± 5	78 ± 8	10 ± 1	5 ± 3
mcpA	20 ± 5	2 ± 1	51 ± 8	8 ± 1	10 ± 2
yneI	16 ± 1	16 ± 1	13 ± 4	20 ± 1	18 ± 2
ytvA	12 ± 1	15 ± 3	13 ± 1	13 ± 1	18 ± 2
ydaJ	4 ± 1	6 ± 1	5 ± 2	3 ± 0	4 ± 1
ywdA	6 ± 1	8 ± 2	9 ± 2	5 ± 1	5 ± 0
yweA	53 ± 4	23 ± 5	41 ± 6	45 ± 1	47 ± 10

[a]± is the standard deviation of three replicates.

TABLE S5b: Expression of reporters in Figure 2C (Miller units)[a]

reporters	*wt*	*swrA*	*swrA degU*
flache	230±8	100±10	91±8
flgM	7±2	4±1	2±0.5
swrA	19±0.5	10±0	6±1
yxjJ	10±3	3±5	3±0.6
mcpA	21±7	3±1	3±0

[a]± is the standard deviation of three replicates.

TABLE S5c: Expression of various *flache* reporters in Figure 2D (Miller units)[a]

reporters	*wt*	*swrA*	*swrA*$^{+++}$
wt	230±8	100±10	458±21
site1+2	90±3	80±21	109±11
+20	35±8	17±2	52±1
-35-+1	10±0.08	9±0.4	9±1
UAS^{r}	34±2	23±1	48±2

[a]± is the standard deviation of three replicates.

TABLE S5d: Expression of P_{flache} in Figure S11 (Miller units)[a]

Strain	Miller units
wt	119±4
degUhy32^{++}	90±19
swrA degUhy32^{++}	31±1

[a]± is the standard deviation of three replicates.

TABLE S6: Primers

Number	Primer sequence
353	TTGCGGAATTCTTGTCAATTAAAGGAGATGGTATTTCA
354	TTGCGGGATCCCACGCACAATACTTGCCCTCTTC
1782	CTATATGCTTATTGTAAGAAATAACAGG
1921	AGGAGGAATTCAGGTACTTATATCAAGGTACTAAACAA
3042	CTGCTGAATTCAGCTCTTGTCGTATCCATATTTGCT
5116	AGGAGGAATTCTGCTTATTATTTTGTTCGGTTTC
5117	CTCCTGGATCCCAATCGATTTCCACAGATAATAG
5118	AGGAGGAATTCGTGAGAAAGCTCGCGGTAC
5119	CTCCTGGATCCCTTTTTTATGCTACCCTTCATATC
5120	AGGAGGAATTCCATAACGCCAAAAGCCAGTCC
5121	CTCCTGGATCCCCAAAAAAAGTTTTGGTACTCTC
6064	AGGAGGGATCCGCTGAAGAAAAGTCGGCTTG
6069	AGGAGAAGCTTATCCGCTCAGTCTGCAGTG
6481	AGGAGGAATTCCGGCAAATTGAAATCGGCTGT
6482	AGGAGGGATCCGAAGCAAATCAGACGCTCAC
6483	AGGAGGAATTCGCCTGAGCTAAAAGCCATGC
6484	AGGAGGGATCCCAGAAAAAAATAGTAGGTTATCG
6487	AGGAGCAATTGGCTTCGTCATTCTGGGCTTC
6488	AGGAGGGATCCAGGCCGTCAGCTTGCTATG
6489	AGGAGCAATTGGATCTTCGAGAGGATTCAAAG
6490	AGGAGGGATCCAATTGATTGTTGAAATTTGGCCA
7227	AGGGAATTCCACGAACTTCATAGACTTTATG
7228	AGGGGATCCTCAGTTTTTTTCACCCTCAATATC
7229	AAAGAATCCCCCCAATGCCT
7230	CGTCTGTTTTCTGACTCATATT
7231	CAAAAAGTTTCAAAAATGCCGAA
7459	GACATCGATTAGAGAAGGCAA
7460	CGTTGCAGTCTTTAAACAATCT
7461	TGATTTGCAGCTTCAAACAGC
7462	ATGCATATTAACTCGTTAGAAAG
7463	TGTGTTCAATTCCGCAAAATAG
7464	ACAGTATTACCTGATGACCTG
7465	GTCAGATCTTTTTGGAGGCTT
7466	GCCTGCGATTATGTAATTTGC
7548	/56-FAM/TTCCTGGGTTGAAAGTCTTTC
7549	/5HEX/ATAAGCTCAAATCCACTTACCT
7550	/56-FAM/TCAGATCACTCATCTTCCTAAT
7551	/5HEX/ACGGATTGTGTTCCAAATTGAT
7554	TGCACTGACGCTTGAAAGAAT
7555	GCTTCCGTGTAATTGATCTTTG
7562	/56-FAM/CTAAATACAATCCGTATTCACC
7563	/5HEX/TCTATTGTACGGATAAAATGCC

7564	/56-FAM/TGATTTGCAGCTTCAAACAGC
7565	/5HEX/ACAATACTTGCCCTCTTCAATT
7566	/56-FAM/TATCGCCGCTTCAGCTGAG
7567	/5HEX/CAATATGACAACCGGTATGATG
7568	/56-FAM/CATTATGAAAGCTGGTGGCG
7569	/5HEX/ATATCCATTGTCACAAGGTCC
7597	TAACCGTGCAGCAGCGTTAT
7598	CCTGAATATGTTGTTAAGGCAC
7817	AGGAGGAATTCAGGAGGATTATTTATCATGGCT
7818	AGGAGGTCGACGCATTAATCACATTCATTCACC
7819	TAGTTCTAACAATCTAGGACTTTTTTCCTAGTTGCAAAATAGATAA
7820	TTATCTATTTTGCAACTAGGAAAAAAGTCCTAGATTGTTAGAACTA
7821	TAGTTCTAACAATCTAGGACAAAAAACCTAGTTGCAAAATAGATAA
7822	TTATCTATTTTGCAACTAGGTTTTTTGTCCTAGATTGTTAGAACTA
7823	AATGTAGTTCTAACAATCTAATACTTTATACCTAGTTGCAAA
7824	TTTGCAACTAGGTATAAAGTATTAGATTGTTAGAACTACATT
7825	TTTGCAACTAGGTATAAAGTATTAGATTGTTAGAACTACATT
7826	AATTATCTATTTTGCAACTAATTATAAAGTCCTAGATTGTTA
7827	AATGTAGTTCTAACAATCTAATACTTTATAATTAGTTGCAAA
7828	TTTGCAACTAATTATAAAGTATTAGATTGTTAGAACTACATT
7869	TAGTTCTAACAATCTAGGACGGGGGGCCTAGTTGCAAAATAGATAA
7870	TTATCTATTTTGCAACTAGGCCCCCCGTCCTAGATTGTTAGAACTA
7871	TAGTTCTAACAATCTAGGACCCCCCCCCTAGTTGCAAAATAGATAA
7872	TTATCTATTTTGCAACTAGGGGGGGGGTCCTAGATTGTTAGAACTA
7885	AGGAGGTCGACTGCATTAATCACATTCATTCACC
7886	ATCTAGGACTTTATACCTAGTTTAATTGTGAGGACATTTTTTTA
7887	TAAAAAAATGTCCTCACAATTAAACTAGGTATAAAGTCCTAGAT
7888	ATCTAGGACTTTATACCTAGTTTACACGAACTTCATAGACTTTATG
7889	CATAAAGTCTATGAAGTTCGTGTAAACTAGGTATAAAGTCCTAGAT
7979	ATCTAGGACTTTATACCTAGTTGACATTTTTTTACACGAACTTC
7980	GAAGTTCGTGTAAAAAAATGTCAACTAGGTATAAAGTCCTAGAT
7981	TTATACCTAGTTTAAGCTCGTAGCAAAATAGATAATTGTGAGGA
7982	TATCTATTTTGCTACGAGCTTAAACTAGGTATAAAGTCCTAGAT
7983	TAAGCTCGTACTTGACTGAAGCAAAATAGATAATTGTGAGGA
7984	TTCAGTCAAGTACGAGCTTAAACTAGGTATAAAGTCCTAGAT
8005	ATCTAGGACTTTATACCTAGTTTACACGAACTTCATAGACTTTATG
8006	CATAAAGTCTATGAAGTTCGTGTAAACTAGGTATAAAGTCCTAGAT
8007	CTCCTGGATCCTCAGTTTTTTTCACCCTCAATATCCT
8008	AGGAGGAATTCCGTTCTGTTATTGTGAACGCA
8205	AGGAGGAATTCCTCCATGCTGCAAGCTGCGGC
8206	CTCCTGCTAGCATCGCTTATACCGCAACTAGGTATAAAGTCCTAGATTG
8207	AGGAGGCTAGCACTCTGCTGCACTAAGAACTTCATAGACTTTATGCCTGTTATTTC
8208	CTCCTGGATCCGAAATTGCATTAATCACATTCATTCAC

TABLE S7: Plasmids

Plasmid	Genotype	Reference
pAM01	*amyE::P_{sacX}-lacZ cat amp*	
pAM08	*amyE::P_{ydaJ}-lacZ cat amp*	
pAM09	*amyE::P_{ywdA}-lacZ cat amp*	
pAM11	*amyE::P_{ytvA}-lacZ cat amp*	
pAM12	*amyE::P_{yweA}-lacZ cat amp*	
pAM19	*amyE::P_{ycdC}-lacZ cat amp*	
pAM27	*amyE::$P_{flache(-35-+1)}$-lacZ cat amp*	
pAM39	*ΩP_{flache} DegUBS(6T) oriBsTs mls amp*	
pAM40	*ΩP_{flache} DegUBS(6A) oriBsTs mls amp*	
pAM41	*ΩP_{flache} DegUBS(site1) oriBsTs mls amp*	
pAM42	*ΩP_{flache} DegUBS(site2) oriBsTs mls amp*	
pAM43	*ΩP_{flache} DegUBS(site1+2)oriBsTs mls amp*	
pAM48	*ΩP_{flache} DegUBS(6G) oriBsTs mls amp*	
pAM49	*ΩP_{flache} DegUBS(6C) oriBsTs mls amp*	
pAM56	*ΩP_{flache} DegUBS(+10) oriBsTs mls amp*	
pAM67	*ΩP_{flache} DegUBS(+20) oriBsTs mls amp*	
pAM68	*ΩP_{flache} DegUBS(-10) oriBsTs mls amp*	
pAM69	*ΩP_{flache} DegUBS(-20) oriBsTs mls amp*	
pAM72	*amyE:: P_{flache} DegUBS(site1+2)-lacZ cat amp*	
pAM77	*amyE:: P_{flache} DegUBS(+20)-lacZ cat amp*	
pDG268	*amyE::lacZ cat amp*	(18)
pDP139	*amyE::P_{flache}-lacZ cat amp*	(14)
pDP144	*amyE::P_{swrA}-lacZ cat amp*	
pDP145	*amyE::P_{flgM}-lacZ cat amp*	(14)
pDP155	*amyE::P_{hag}-GFP cat amp*	(14)
pDP462	*amyE::P_{yneI}-lacZ cat amp*	
pDP463	*amyE::P_{mcpA}-lacZ cat amp*	
pDP464	*amyE::P_{yxjJ}-lacZ cat amp*	
pDP521	*amyE::P_{sinI}-lacZ cat amp*	
pDP522	*amyE::P_{tlpA}-lacZ cat amp*	
pDP616	*ΩP_{flache}RANDO-UAS oriBsTs mls amp*	
pDP617	*amyE:: $P_{flacheRANDO-UAS}$-lacZ cat amp*	
pEC20	*amyE::$P_{hyspank}$-degQ spec amp*	(15)
pminiMAD	*oriBsTs mls amp*	(19)
pNW43	*pT7 DegU-His6 amp*	(16)
pSM94	*pT7-GST-SwrA amp*	(17)
pYH8	*pT7 DegS-His6 kan*	(4)

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SUPPLEMENTAL FIGURE LEGENDS

Figure legend S1: SwrA does not bind to DNA directly. Electrophoretic mobility shift assays (EMSA) with the indicated radiolabeled promoter fragments (classes in parentheses) and μM of protein, either GST-SwrA (left), unphosphorylated DegU-His_6 (center) or DegU-P-His_6 phosphorylated by DegS-His_6 and ATP (right). Ø indicates that no protein was added.

Figure legend S2: SwrA and DegU are mutually required for swarming. Quantitative swarm expansion assays of the following strains: gray circles, WT (3610), open circles, *swrA* (DS2415), closed circles, *swrA*$^{+++}$ induced with 1 mM IPTG (DS8094), open squares, *degU* (DS3649), closed squares, *degU*$^{+++}$ induced with 1 mM IPTG (DS3534), open triangles, *swrA degU*$^{+++}$ induced with 1 mM IPTG (DS8111), closed triangles, *degU swrA*$^{+++}$ induced with 1 mM IPTG (DS8259) and closed diamonds, *degU swrA* (DS6262). Each data point is the average of three replicates. Wildtype was included as a control while gathering the data displayed.

Figure legend S3: Enlarged peaks from ChIP-seq experiments. Each panel indicates a 4 kb window corresponding to the promoter region of the likely gene indicated in the upper left. The class of binding from table 1 is indicated as I, II, or III in upper left parenthetical. Green trace, SwrA ChIP-seq from wild type cells; blue trace, DegU ChIP-seq from wild type cells; magenta trace, DegU ChIP-seq from *swrA* mutant cells. X-axis is genome position in kb.

Figure legend S4: MEME analysis of DegU binding sites. 200bp sequence surrounding ChIP-seq peaks were grouped as indicated in the upper left and run through the MEME suite to predict a putative inverted repeat to which SwrA and/or DegU might bind. Note that MEME analysis of the class II sites looks particularly strong but relatively few sites are in this class. Sequences used to generate this figure are presented in **Table S2**.

Figure legend S5: DegU ChIP sequencing in strains overexpressing DegQ and DegU^{hy32}. A) ChIP-Seq analysis using a primary antibody to DegU (αDegU) in wild type (top) and *swrA* mutant (bottom) in which DegQ had been artificially overexpressed by growth in the presence of 1 mM IPTG. The *pgsB* gene necessary for poly-glutamate production was also mutated due to the extreme mucoidy resulting from DegQ overexpression. Data is presented as number of sequences reads per kilobase (kb) pair position in the chromosome such that SwrA-enriched sequences appear as peaks. The following strains were used to generate this panel: *degQ*$^{+++}$(DK9504) and *ΔswrA degQ*$^{+++}$ (DK9525). B) ChIP-Seq analysis using a primary antibody to DegU (αDegU) in *ΔdegU* (top) and *ΔdegU swrA* mutant (bottom) in which the hyperactive DegU^{hy32} allele had been artificially overexpressed by growth in the presence of 1 mM IPTG. The *pgsB* gene necessary for poly-glutamate production was also mutated due to the extreme mucoidy resulting from DegU^{hy32} overexpression. Data is presented as number of sequence reads per kilobase (kb) pair position in the chromosome such that SwrA-enriched sequences appear as peaks. The following strains were used to generate this panel: *ΔdegU degUhy32*$^{+++}$ (DK9523), *ΔswrA ΔdegU degUhy32*$^{+++}$(DK9524). C) Each panel indicates a 4 kb window corresponding to the promoter region of the likely gene indicated in the upper left. Blue trace, DegU ChIP-seq from wild type cells in which DegQ was overexpressed; red trace, DegU ChIP-seq from *swrA* mutant cells in which DegQ was overexpressed. D) Each panel indicates a 4 kb window corresponding to the promoter region of the likely gene indicated in the upper left. Purple trace, DegU ChIP-seq from *degU* mutant cells in which DegU^{hy32} was artificially overexpressed; red trace, *degU swrA* mutant cells in which DegU^{hy32} was artificially overexpressed.

Figure legend S6: DegU-P protects DNA in additional target promoter regions only the presence of SwrA. DNaseI sequencing footprint analysis of the A) P_{flgM} B) P_{mcpA} C) P_{swrA} and D) P_{ynel} . 300-400 bp fragments of dsDNA were fluorescently labeled on the forward strand, the

indicated protein was added, followed by partial digestion with DNase I and sequencing of the digested fragments. Top panel, 1 uM BSA added; middle panel 3 μM of DegU-P-His_6 added; bottom panel 3 μM of DegU-P-His_6 and 1μ M of GST-SwrA added. Orange bars indicate the region of protection in the presence of SwrA/DegU-P. Peaks indicate the number of sequences reads terminating at that location on one strand.

Figure legend S7: Sequence alignment of sequence immediately upstream of that shown in Figure 5C. This alignment is included to show that sequence conservation upstream of the P_{flache} promoter breaks down farther upstream of the DegU binding site, UP element and promoter boxes.

Figure legend S8. Neither SwrA nor DegU act like repressors in a strain in which the DegU binding site was moved 20 base pairs closer to the P_{flache} promoter. Fluorescence micrographs of strains in which the DegU binding site was moved 20 base pairs closer to the P_{flache} promoter in strains mutated for *swrA* (top, DB613) and *degU* (bottom, DB795). Membrane, false colored red; P_{hag}-GFP expression, false colored green. Scale bar is 8 μm. Note, no P_{hag}-GFP expression was detected above background in either strain.

Figure legend S9. Suppressors of P_{flache} *site1+2* and P_{flache} UAS^r mutant restore swarming motility. Quantitative swarm expansion assays of the following strains: A) gray circles, suppressors of P_{flache} *site1+2* mutant and B) black circles, suppressors of P_{flache} *(*UAS^r*)* mutant**.** Each data point is the average of three replicates. Wildtype, P_{flache} *site1+2* and P_{flache} UAS^r were included as controls while gathering the data displayed. Details of strains used to generate this figure are mentioned in **Table1**.

Figure legend S10. Predicted aligned error matrices of DegU-DegU and DegU-DegU-SwrA-SwrA complexes.

Figure legend S11. DegUhy32 does represses motility downstream of P_{flache}. A) β-galactosidase activity of P_{flache} fused to the *lacZ* gene. *degUhy32* was artificially overexpressed by growth in the presence of 1 mM IPTG. Error bars are the standard deviation of three replicates. The following strains were used to generate this panel: *wildtype* (DB643), *degUhy32*$^{+++}$(DB1159) and *swrA degUhy32*$^{+++}$ (DB1160). Average miller units are presented in **Table S5d.** B) Fluorescence micrographs of wildtype (DB456), *degUhy32*$^{+++}$(DB1161) and *swrA degUhy32*$^{+++}$ (DB1162). *degUhy32* was artificially overexpressed by growth in the presence of 1 mM IPTG. Membrane, false colored red; P_{hag}-GFP expression, false colored green. Scale bar is 8μm. Note, no P_{hag}-GFP expression was detected above background in *degUhy32*$^{+++}$ and *swrA degUhy32*$^{+++}$.

Figure legend S12. EMSAs for the densitometry analysis in Figure 4. Electrophoretic mobility shift assays (EMSA) with the indicated radiolabeled promoter fragment and protein. Ø indicates that no protein was added. Left panels, an increasing about of SwrA was added to a constant 0.3 μM of DegU. Right panels, an increasing amount of SwrA was added to a constant 0.3μM of DegU-P phosphorylated by DegS and ATP. Gray carets indicate the position of DNA shifted by the presence of either DegU or DegU-P alone. Black carets indicated the position of DNA supershifted by the presence of either DegU or DegU-P and SwrA. * Indicates aggregation.

Figure S1

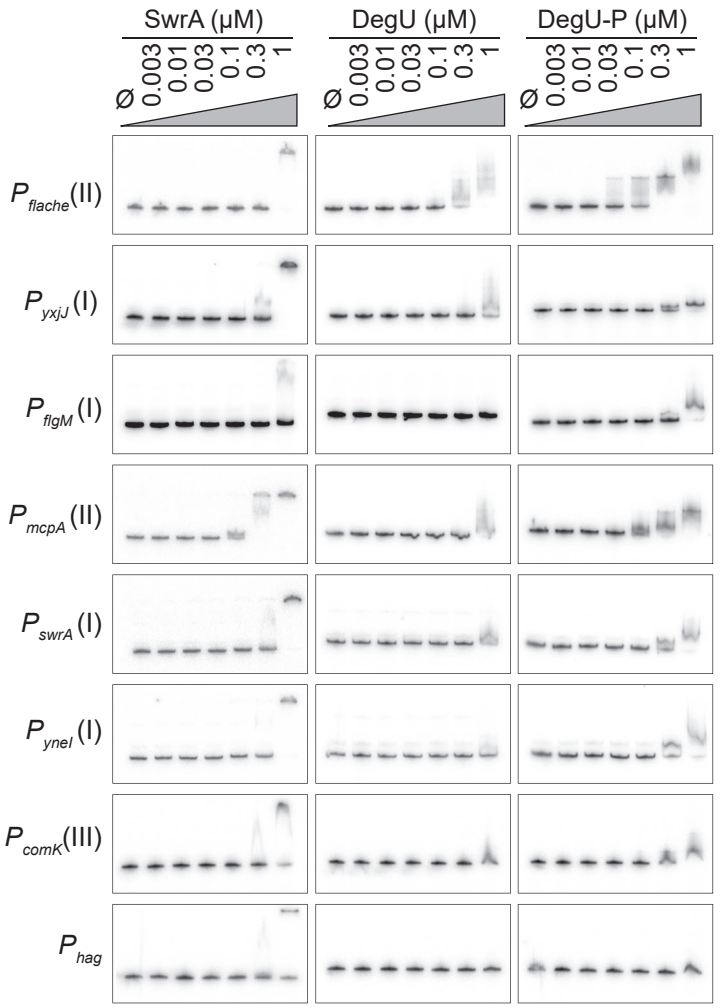
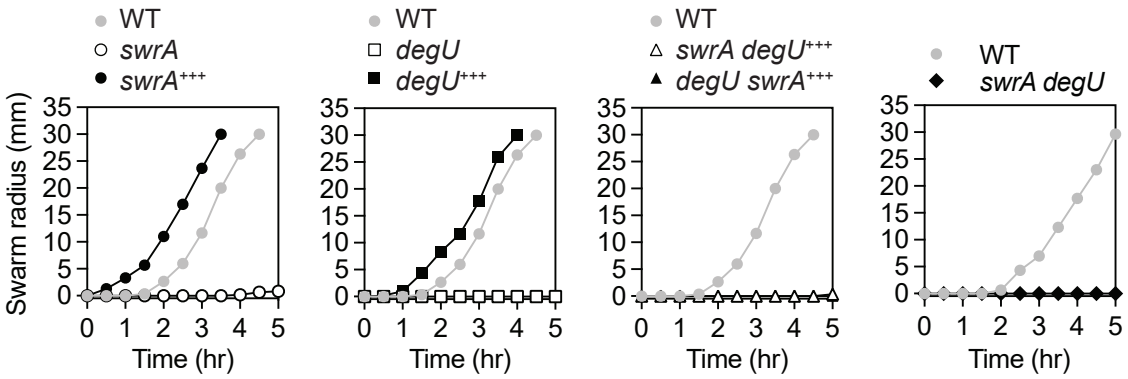

SwrA (μM)
DegU (μM)
DegU-P (μM)
Ø 0.003 0.01 0.03 0.1 0.3 1
P_{flache}(II)
P_{yxjJ}(I)
P_{flgM}(I)
P_{mcpA}(II)
P_{swrA}(I)
P_{ynel}(I)
P_{comK}(III)
P_{hag}

Figure S2


WT
swrA
swrA+++
WT
degU
degU+++
WT
swrA degU+++
degU swrA+++
WT
swrA degU
Swarm radius (mm)
0 5 10 15 20 25 30 35
0 1 2 3 4 5
Time (hr)

A
WT-αSwrA
WT-αDegU
swrA-αDegU
Figure S3
ChIP/Input
genome position
sfkA (I)
yczC/F (I)
ycdC (I)
srfAA (I)
yjhA (I)
bpr (I)
ppsA (I)
yonU (I)
yrvJ (I)
iscS/braB (I)
ywrE (I)
slrA (I)
sacX (I)
cydA/cimH (I)
tlpA (II)
wapA (II)
ycdA/B (III)
comK (III)
yjcN (III)
yopS (III)
motI (III)
yqhG (III)
degQ (III)
yxkC/D (III)
yxiB (III)
yaaD/C (III)
B
aprE
pgsB
aprE
yfhO
pgsB
19350
rbsR

Figure S4

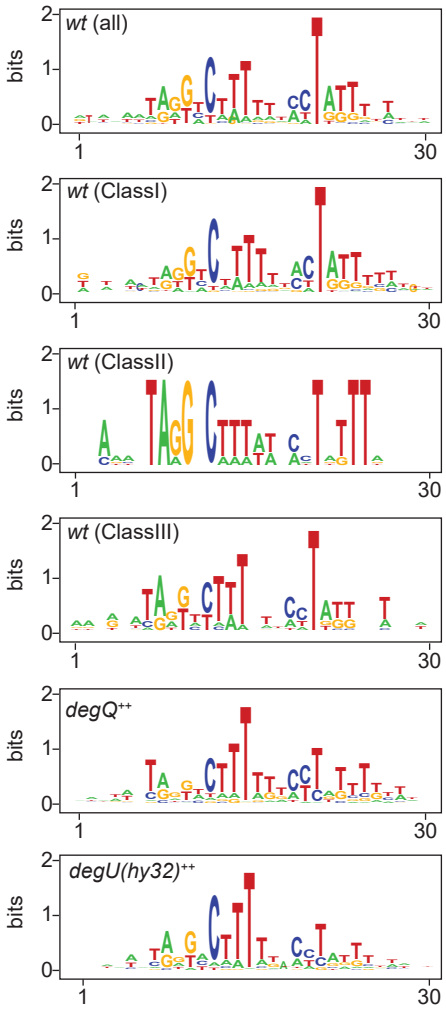

wt (all)
wt (ClassI)
wt (ClassII)
wt (ClassIII)
degQ++
degU(hy32)++
bits
2
1
0
1
30

Figure S5

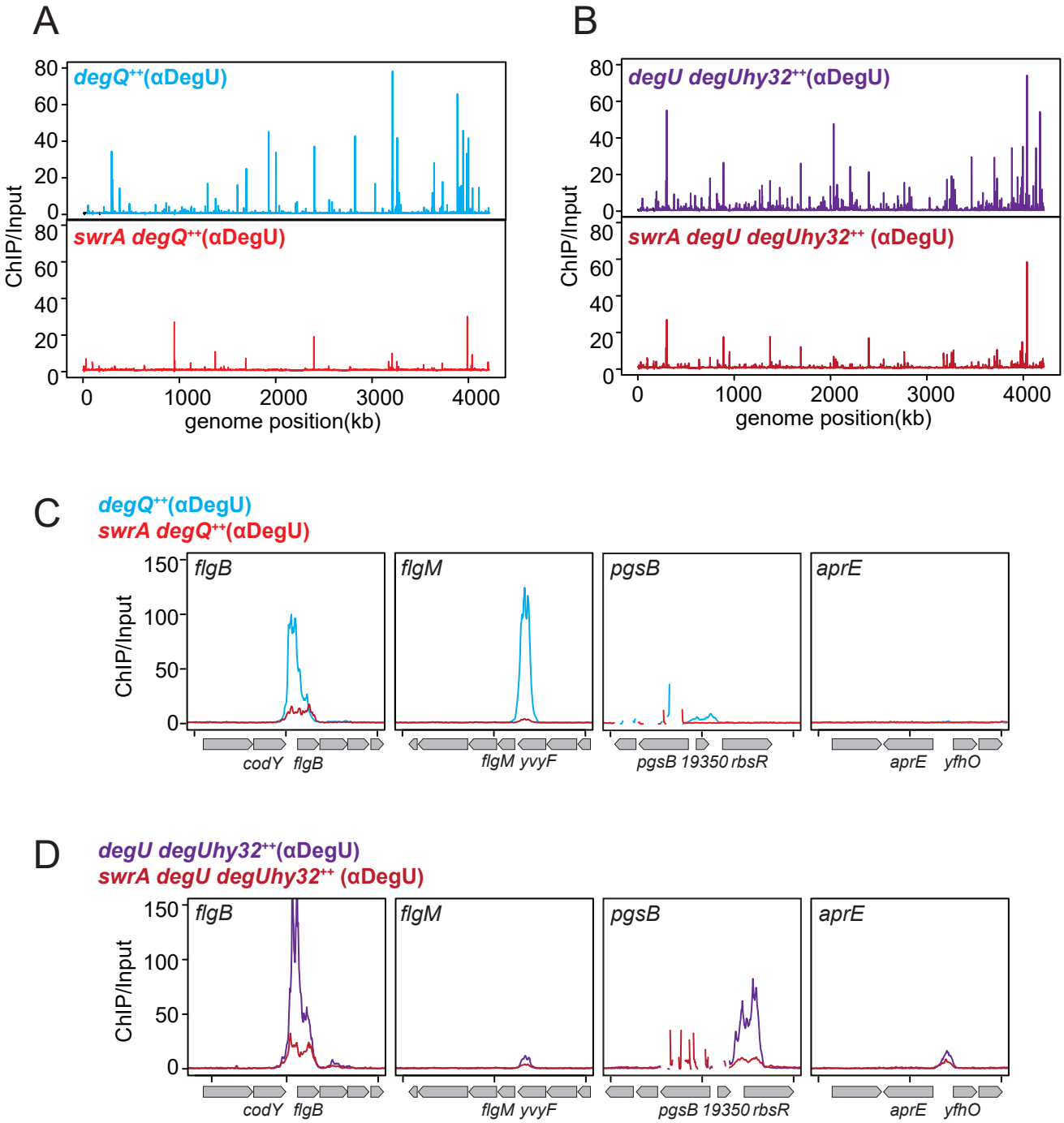

A
degQ++(αDegU)
swrA degQ++(αDegU)
ChIP/Input
genome position(kb)
B
degU degUhy32++(αDegU)
swrA degU degUhy32++ (αDegU)
ChIP/Input
genome position(kb)
C
degQ++(αDegU)
swrA degQ++(αDegU)
flgB
flgM
pgsB
aprE
ChIP/Input
codY flgB
flgM yvyF
pgsB 19350 rbsR
aprE yfhO
D
degU degUhy32++(αDegU)
swrA degU degUhy32++ (αDegU)
flgB
flgM
pgsB
aprE
ChIP/Input
codY flgB
flgM yvyF
pgsB 19350 rbsR
aprE yfhO

Figure S6

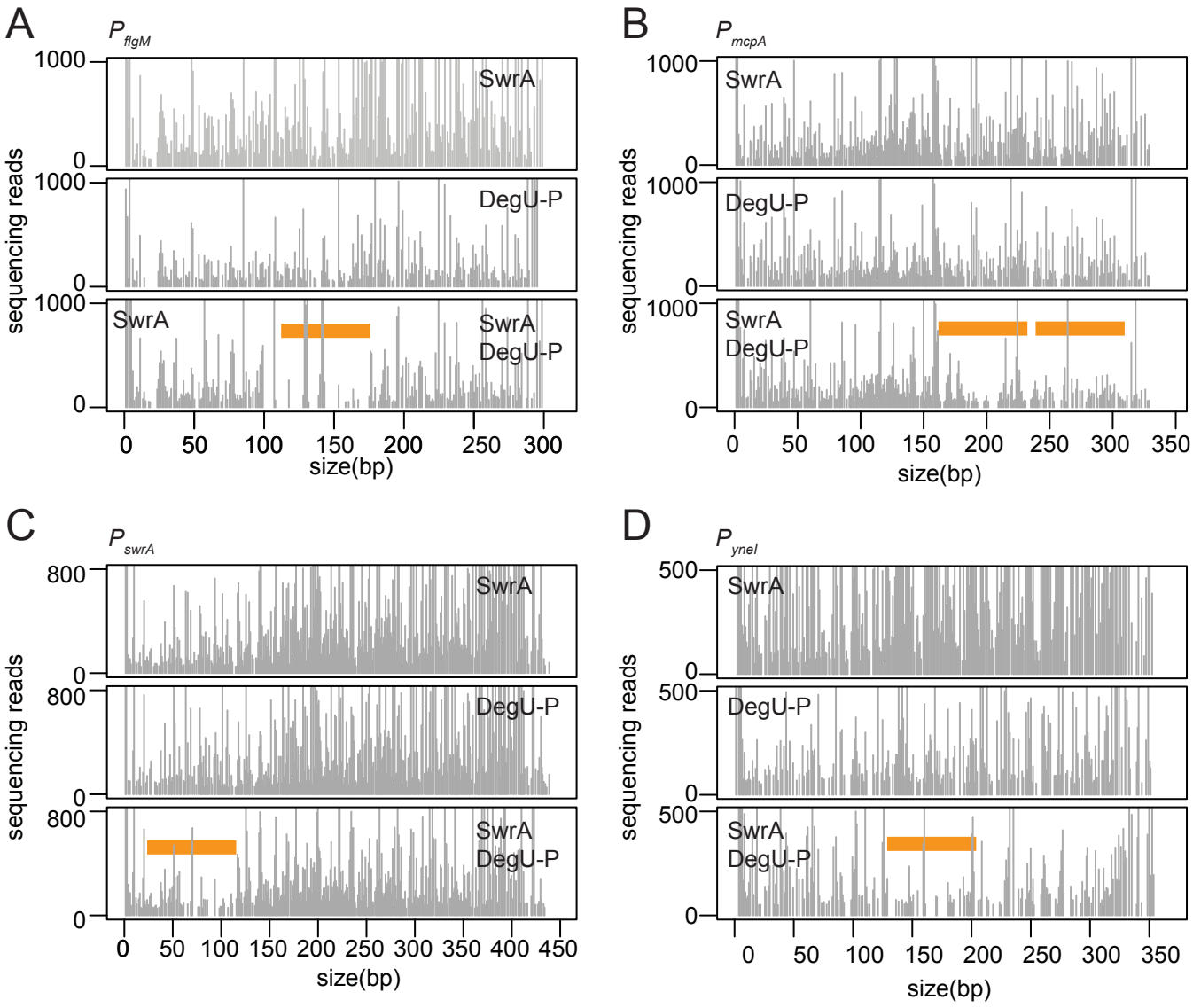

A
P_{flgM}
1000
0
SwrA
DegU-P
SwrA
SwrA
DegU-P
sequencing reads
0 50 100 150 200 250 300
size(bp)
B
P_{mcpA}
SwrA
DegU-P
SwrA
DegU-P
0 50 100 150 200 250 300 350
size(bp)
C
P_{swrA}
800
0
SwrA
DegU-P
SwrA
DegU-P
0 50 100 150 200 250 300 350 400 450
size(bp)
D
P_{ynel}
500
0
SwrA
DegU-P
SwrA
DegU-P
0 50 100 150 200 250 300 350
size(bp)

Figure S7

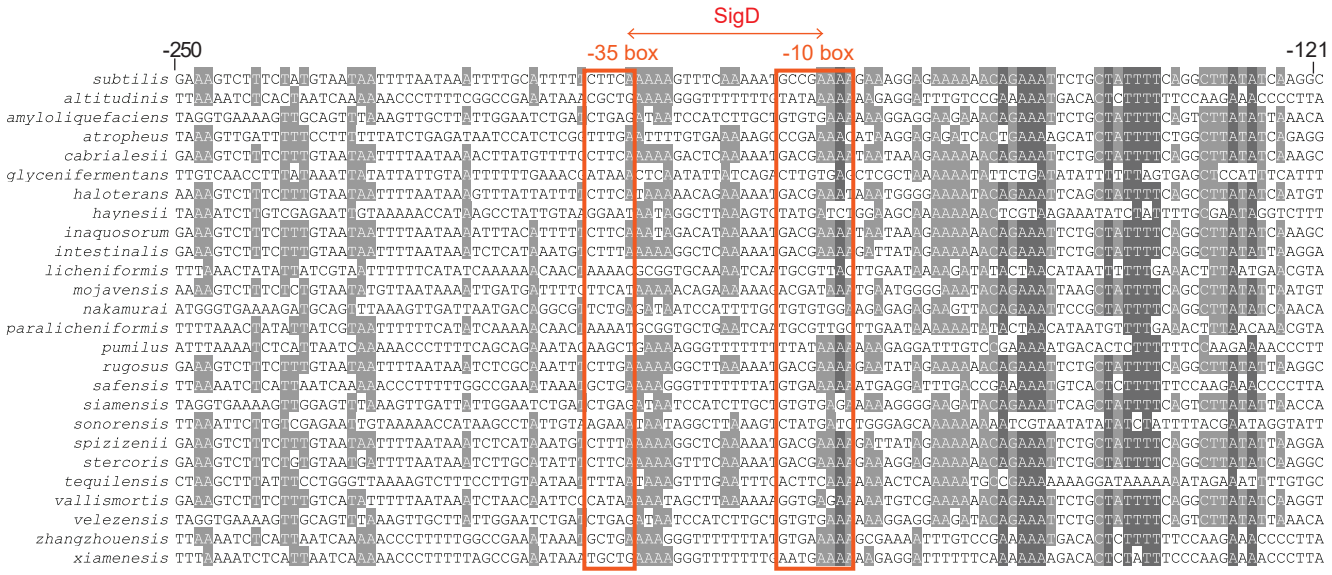

SigD
-250
-35 box
-10 box
-121
subtilis
altitudinis
amyloliquefaciens
atropheus
cabrialesii
glyceniferm entans
haloterans
haynesii
inaquosorum
intestinalis
licheniformis
mojavensis
nakamurai
paralicheniformis
pumilus
rugosus
safensis
siamensis
sonorensis
spizizenii
stercoris
tequilensis
vallismortis
velezensis
zhangzhouensis
xiamenesis

Figure S8

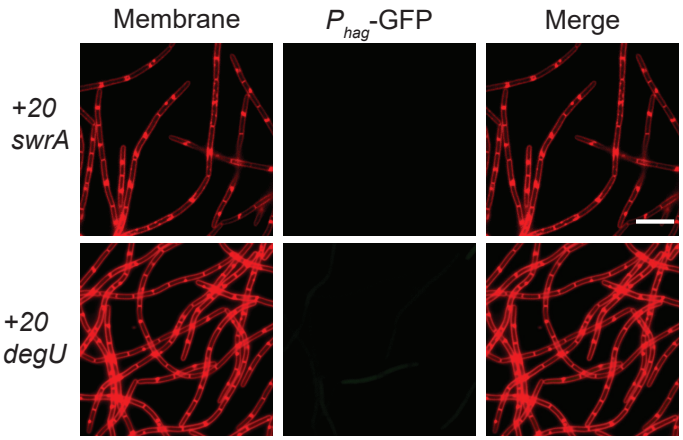


Figure S9

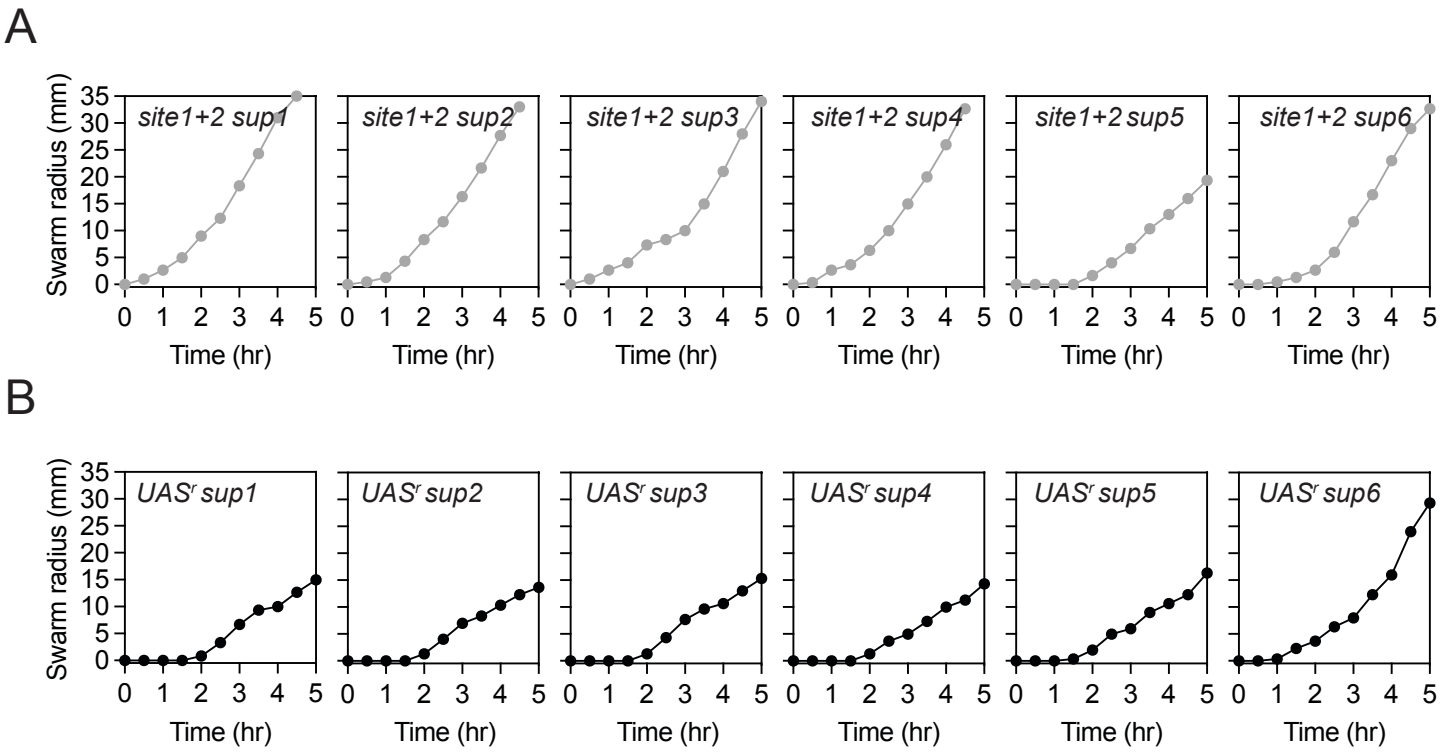
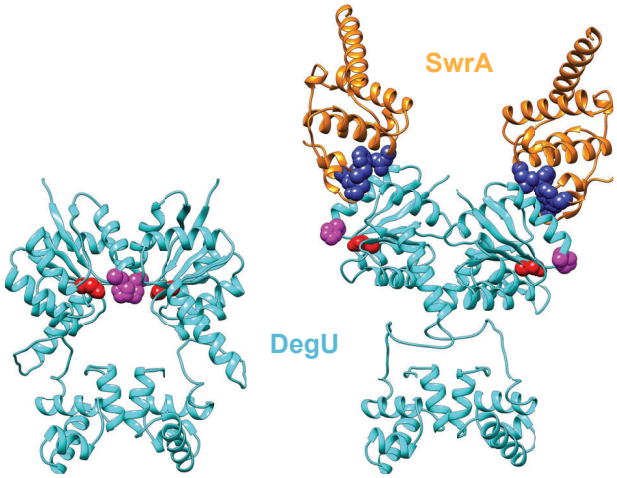

A
B
Swarm radius (mm)
Time (hr)
site1+2 sup1
site1+2 sup2
site1+2 sup3
site1+2 sup4
site1+2 sup5
site1+2 sup6
UAS^r sup1
UAS^r sup2
UAS^r sup3
UAS^r sup4
UAS^r sup5
UAS^r sup6

Figure S10



Predicted aligned error matrices

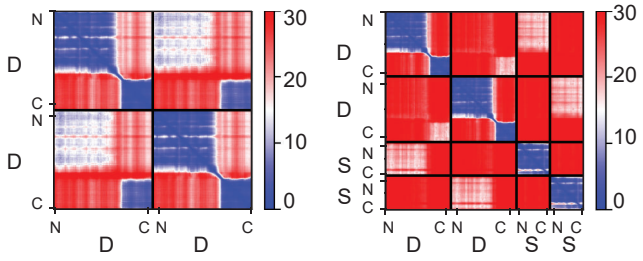
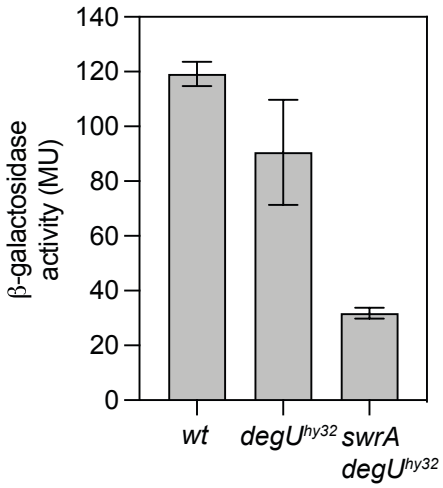


Figure S11

A



B

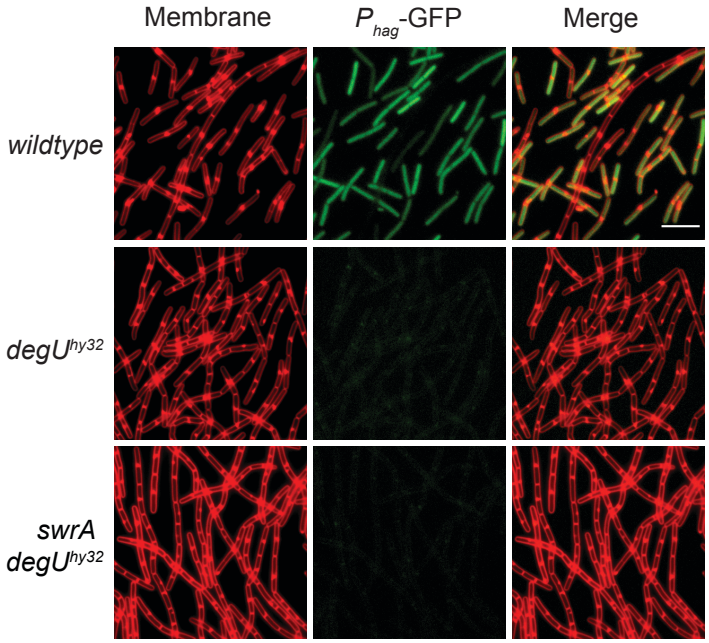
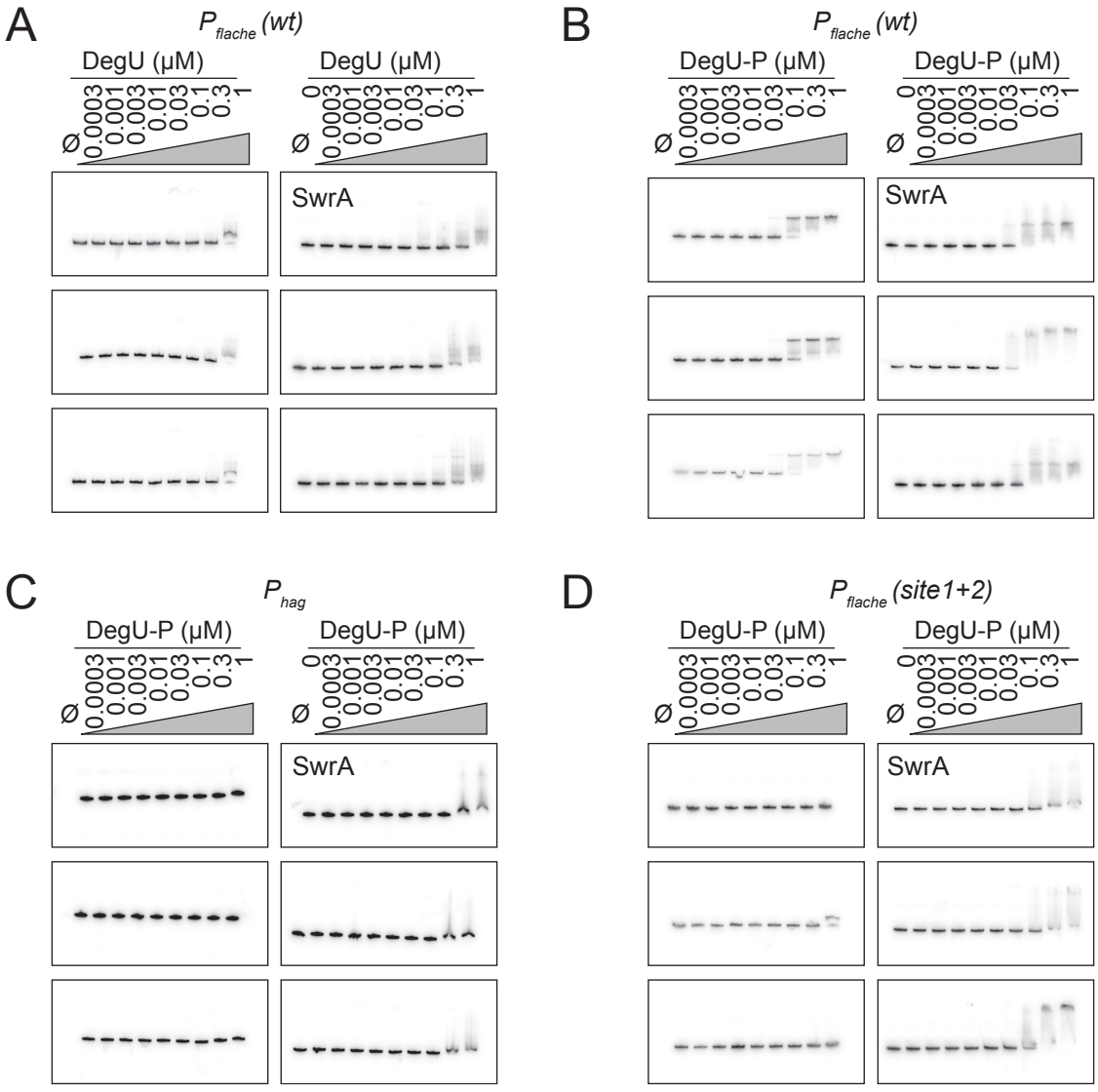


Figure S12


A
P flache (wt)
DegU (μM)
Ø 0.0003 0.0001 0.003 0.01 0.03 0.1 0.3 1
DegU (μM)
Ø 0 0.0003 0.0001 0.003 0.01 0.03 0.1 0.3 1
SwrA
B
P flache (wt)
DegU-P (μM)
Ø 0.0003 0.0001 0.003 0.01 0.03 0.1 0.3 1
DegU-P (μM)
Ø 0 0.0003 0.0001 0.003 0.01 0.03 0.1 0.3 1
SwrA
C
P hag
DegU-P (μM)
Ø 0.0003 0.0001 0.003 0.01 0.03 0.1 0.3 1
DegU-P (μM)
Ø 0 0.0003 0.0001 0.003 0.01 0.03 0.1 0.3 1
SwrA
D
P flache (site1+2)
DegU-P (μM)
Ø 0.0003 0.0001 0.003 0.01 0.03 0.1 0.3 1
DegU-P (μM)
Ø 0 0.0003 0.0001 0.003 0.01 0.03 0.1 0.3 1
SwrA