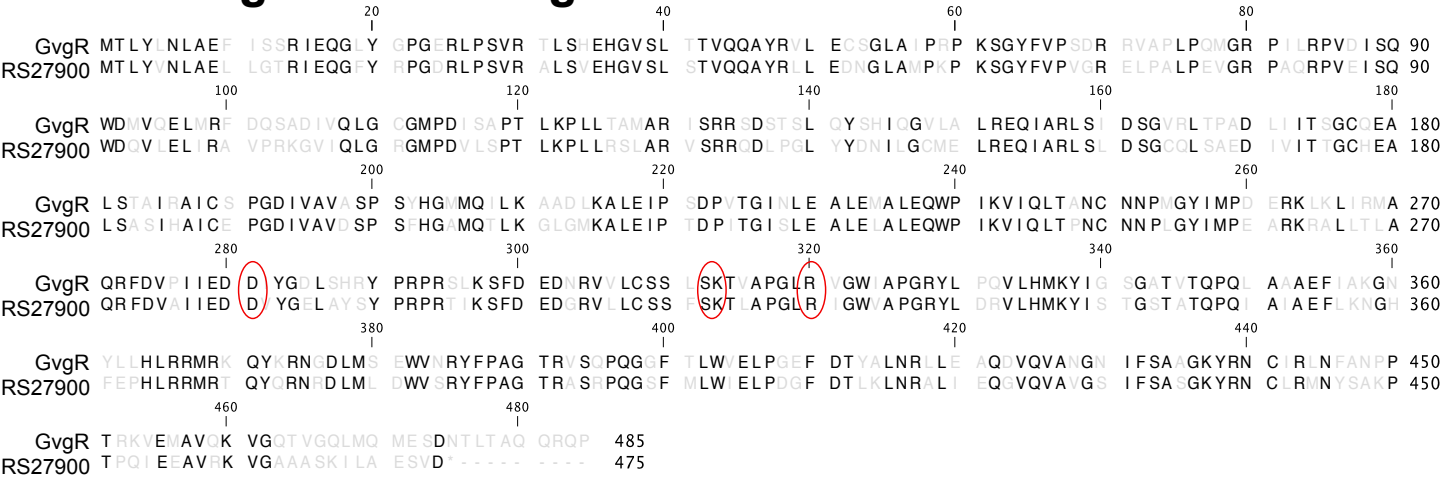


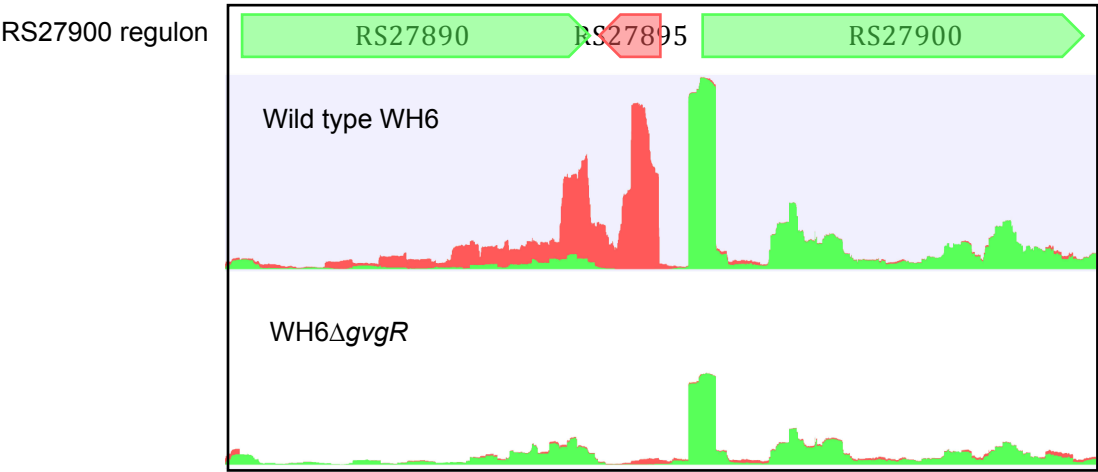
A. Amino acid comparison of MocR TFs in WH6

Amino Acid Percent Identity														
WH6 locus		1	2	3	4	5	6	7	8	9	10	11	12	13
GvgR	1		63.92	35.80	36.81	21.83	20.75	24.51	21.34	20.15	17.51	19.31	18.43	16.18
RS27900	2	175		39.29	39.50	22.27	21.78	25.60	23.82	21.90	17.01	17.50	18.22	16.12
RS12370	3	312	289		39.92	23.65	22.55	21.04	19.66	19.61	16.60	19.81	19.96	15.29
RS21500	4	309	291	289		22.42	23.32	20.75	19.77	20.81	17.70	20.31	18.15	15.77
RS08645	5	394	391	381	391		32.51	20.19	19.52	16.38	16.76	17.97	19.61	15.66
RS12515	6	401	395	388	388	328		18.52	18.44	17.56	18.80	19.06	19.13	15.61
RS15445	7	388	375	394	401	411	418		35.70	29.07	17.46	17.59	15.99	14.66
RS28335	8	424	403	421	426	433	438	335		34.98	16.76	18.68	15.78	15.17
RS19630	9	420	403	410	411	439	432	366	342		17.01	14.53	13.99	14.26
RS21270	10	438	439	437	437	432	419	435	452	444		35.61	19.96	19.57
RS21540	11	422	429	413	416	420	412	431	444	459	311		20.93	18.77
RS13985	12	425	422	409	424	410	410	436	459	461	405	389		13.18
RS15350	13	435	432	432	438	431	438	454	464	457	415	411	448	
Amino Acid Differences														

B. Protein alignment of GvgR and RS27900



C. Mapping of reads from WT and $\Delta gvgR$ strains to the RS27900 regulon



Supplemental Figure 1. Comparison of GvgR and the MocR RS27900. (A) Amino acid comparison between MocR's in WH6. (B) Protein alignment of the two most similar MocR's GvgR and RS27900. Black residues are identical. Amino acids circled in red are conserved PLP-binding residues. (C) Mapping of sequencing reads from wild type WH6 and $\Delta gvgR$ strains to the RS27900 regulon. Arrowheads on the genes point to direction of transcription. Green = reads map to sense strand and red = reads map to anti-sense strand. From CLC Genomics Workbench.