

4-Hydroxy-3-Methyl-2-Alkenylquinoline Disrupts Temporospatial Control of Flagellar Assembly and Induces Transcriptomic Remodeling in *Bacillus subtilis* Consistent with a Short-Circuiting of the Spo0A Phosphorelay

McKinley D. Williams ^{1,2} and Leif Smith ^{1,3,*}

¹ Department of Biology, Texas A&M University, College Station, TX 77843, USA; mcdwilliams@pvamu.edu

² Department of Biology, Prairie View A&M University, Prairie View, TX 77446, USA

³ Antimicrobial Division, Sano Chemicals Inc., Bryan, TX 77808, USA

* Correspondence: jsmith@bio.tamu.edu

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Table S1: Genes involved in Flagellar Assembly with Corresponding Directional Log₂ Fold Changes

Gene Name	Log ₂ FC	P _{adj}
<i>flgB</i>	1.982845659	0.000315138
<i>flgC</i>	2.404207714	7.7262E-07
<i>flgD</i>	2.990061146	4.26914E-09
<i>flgG</i>	2.777652087	1.68713E-07
<i>flgK</i>	3.769171831	6.86873E-19
<i>flgL</i>	3.655141117	5.60284E-16
<i>flgM</i>	3.366077778	1.84773E-13
<i>flgN</i>	3.021674246	1.03179E-10
<i>flhA</i>	2.873740099	4.83738E-09
<i>flhB</i>	3.179254769	8.57329E-10
<i>flhF</i>	3.15546347	7.78558E-10
<i>flhG</i>	2.989572276	2.54744E-09
<i>flhO</i>	1.763503093	0.003584667
<i>flhP</i>	1.875815401	0.002768506
<i>fliD</i>	2.002722886	0.00034327
<i>fliE</i>	3.436857962	1.54012E-14
<i>fliF</i>	3.05292211	8.31758E-12
<i>fliG</i>	3.271738892	2.29135E-13
<i>fliH</i>	3.409249755	1.74093E-12
<i>fliI</i>	3.211380931	3.39483E-10
<i>fliJ</i>	3.545570544	9.13324E-12
<i>fliK</i>	3.270819256	4.06443E-11
<i>fliL</i>	3.164466435	2.4522E-10
<i>fliM</i>	3.102751926	7.1986E-10
<i>fliP</i>	3.596219714	1.9283E-14
<i>fliQ</i>	3.8567602	2.92119E-13
<i>fliR</i>	3.142199214	1.33274E-10
<i>fliS</i>	2.094608448	8.63808E-05
<i>fliT</i>	2.071405364	0.000127514
<i>fliW</i>	0.950473608	0.592823436
<i>fliY</i>	2.619529713	2.65013E-07
<i>fliZ</i>	3.646004338	6.71111E-14
<i>hag</i>	2.591484674	8.63914E-07

Table S2: Genes involved in Chemotaxis with Corresponding Log₂ Fold Changes

Gene Name	Log ₂ FC	P _{adj}
<i>cheA</i>	1.8922143	0.001967417
<i>cheB</i>	2.879506794	1.34366E-08
<i>cheC</i>	1.641239896	0.015478546
<i>cheD</i>	2.266132176	3.50378E-05
<i>cheR</i>	1.079215606	0.369229924
<i>cheV</i>	1.259422094	0.121799342
<i>cheW</i>	1.58071401	0.026930101
<i>cheY</i>	2.855292916	1.70186E-08
<i>motA</i>	3.055265307	1.05933E-09
<i>motB</i>	2.909372367	2.12833E-08
<i>motP</i>	1.635764883	0.068269348
<i>motS</i>	-1.415471037	0.247068394

Table S3: Genes involved in Pellicle/Biofilm Biosynthesis

Gene	Log ₂ FC	P _{adj}
<i>epsA</i>	-6.260031066	1.75248E-33
<i>epsB</i>	-5.539592651	1.14947E-25
<i>epsC</i>	-0.16716238	1
<i>epsD</i>	-2.830317544	4.68999E-07
<i>epsE</i>	-3.023276739	2.13184E-07
<i>epsF</i>	-2.943579935	4.83775E-08
<i>epsG</i>	-3.252281201	1.89643E-09
<i>epsH</i>	-3.210046772	1.29554E-07
<i>epsI</i>	-4.008552574	1.20804E-15
<i>epsJ</i>	0.168319956	1
<i>epsK</i>	-0.135224868	1
<i>epsL</i>	-3.215285224	2.44426E-08
<i>epsM</i>	-3.523544141	6.83507E-11
<i>epsN</i>	-4.442000709	1.57454E-19
<i>epsO</i>	-4.708149179	4.00433E-18
<i>sipW</i>	-9.140997883	3.75404E-54
<i>tapA</i>	-8.09438773	5.90121E-48
<i>tasA</i>	-9.771538209	2.5686E-117

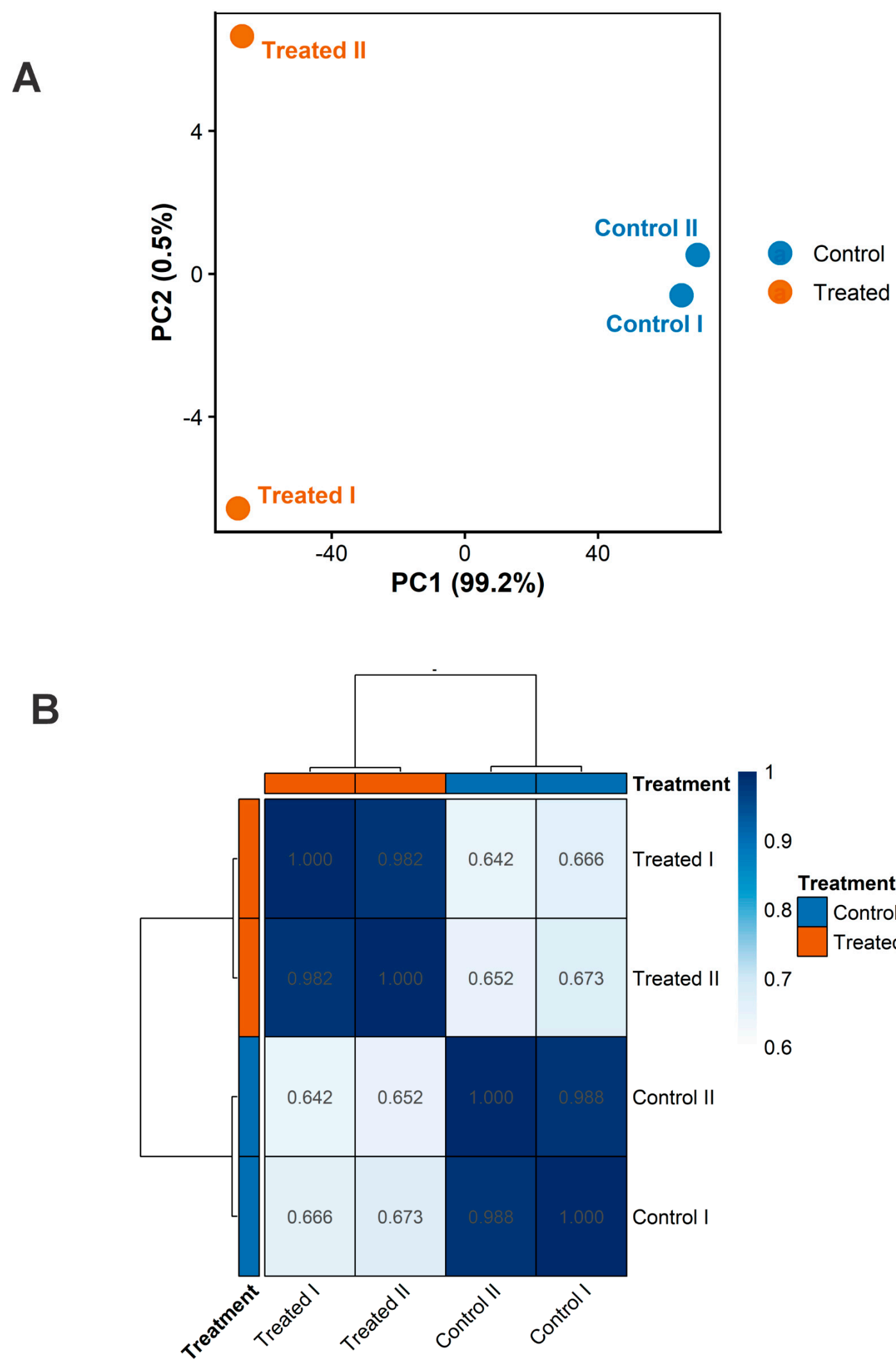


Figure S1: Exposure to HMAQ-7 induces a distinct transcriptional adaptation in treated cells when compared to control. A.) PCA plot of treated and control *B. subtilis* cultures. B.) Corresponding Pearson Correlation HeatMap

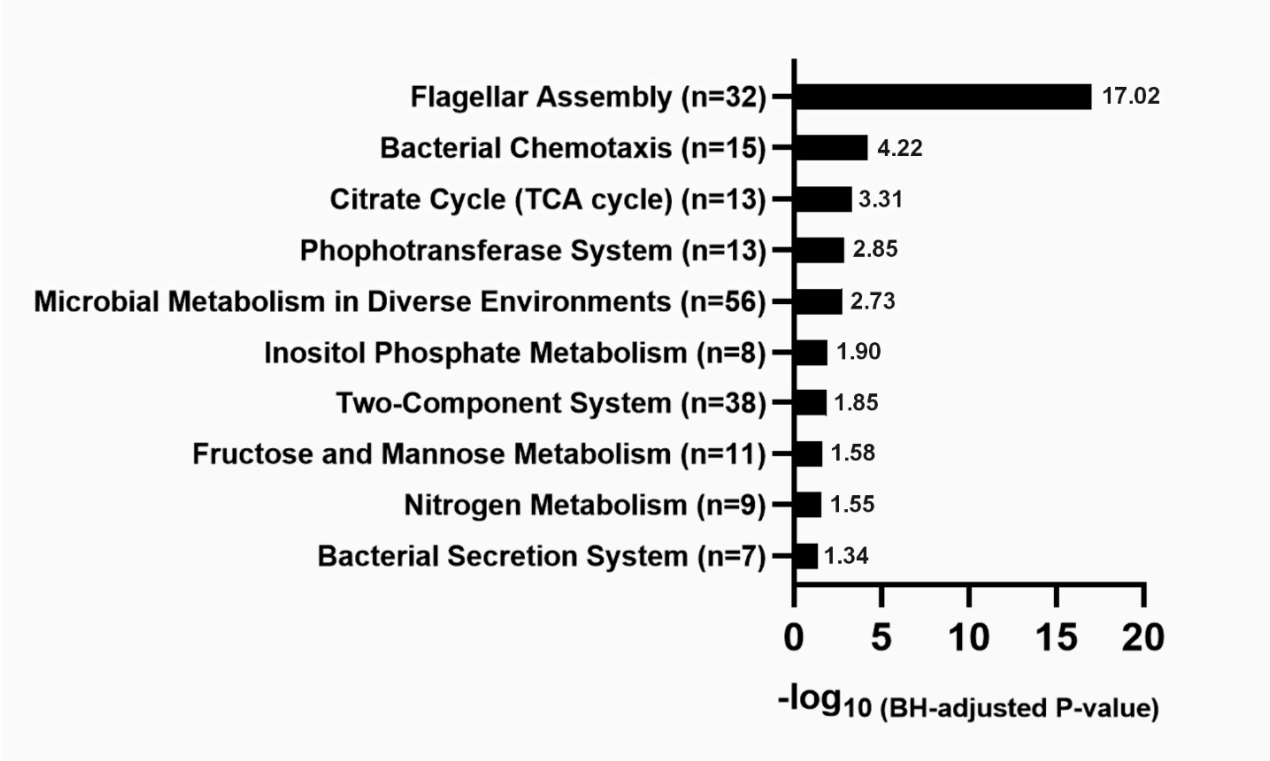


Figure S2: KEGG Enrichment. HMAQ-7 promotes several pathways involved in motility, cellular metabolism, and flagellar assembly in *B. subtilis*. KEGG analysis identifies a number of pathways, shown in order of enrichment, associated with significant ($p < 0.05$) upregulation. The “n” next to each pathway denotes the number of genes therein.

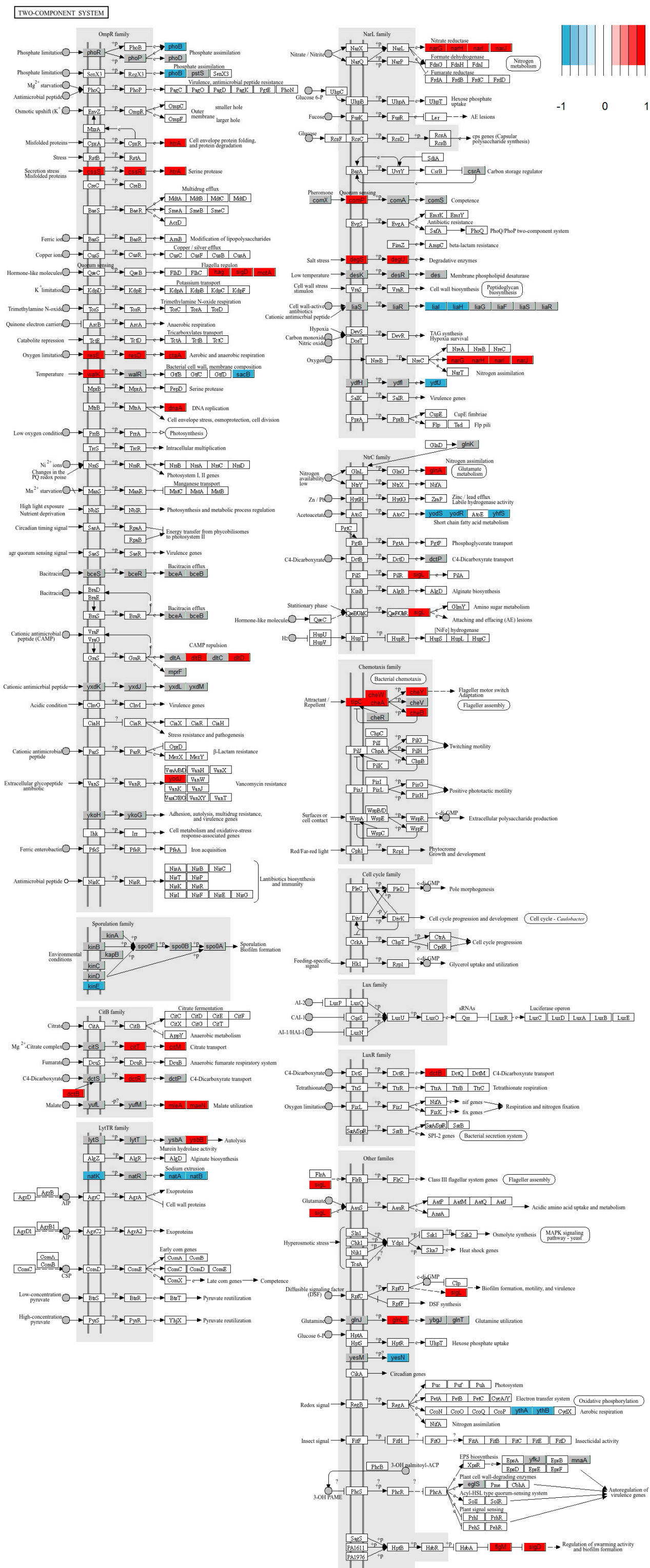


Figure S4: Two-component systems in *B. subtilis*. HMAQ-7 modulates several genes associated with two-component systems in *B. subtilis* including systems tied to sporulation/biofilm, phosphate assimilation, competence, and aerobic respiration. Data on KEGG graph and rendered by Pathview.

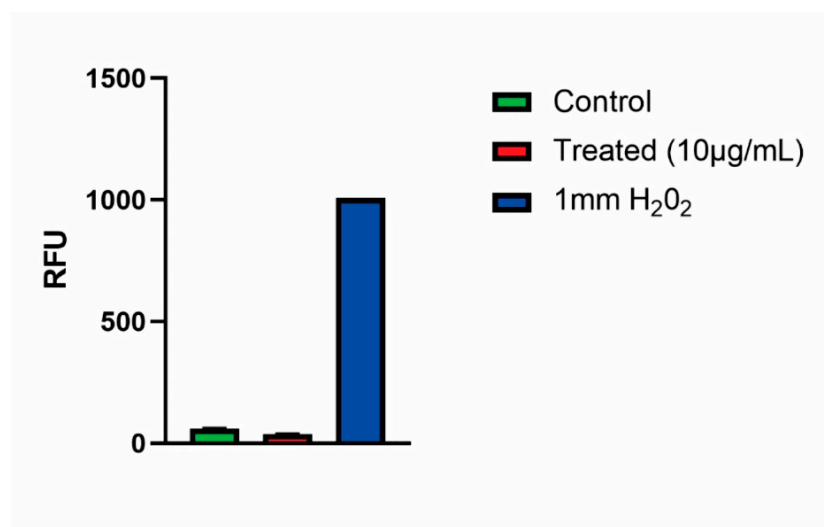


Figure S5: Induction of ROS in *B. subtilis*. Unlike similar compounds, HMAQ-7 does not induce ROS production in *B. subtilis*.

24hrs incubation with HMAQ-7 results in significantly lower level of ROS compared to control.