

1 **Supplemental Material**

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3 **Table S1.** Gene expression changes in different growth phases as determined by microarray  
 4 analysis. Relative changes (log<sub>2</sub> ratios) were calculated in comparison to exponential phase.  
 5 The dataset contains columns with following information from left to right: Gene Annotation  
 6 (RSP), COG cluster, Gene Name, Description, 28 h after inoculation (early stationary phase)  
 7 and the following outgrowth, 72 h after inoculation (late stationary phase) and the following  
 8 outgrowth, 72 h after inoculation (late stationary phase) and the following outgrowth in strain  
 9 *ΔrpoHI*, and RpoH dependency as identified elsewhere (1-3).

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11 **Table S2.** Strains and oligonucleotides used throughout this study.

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Strain	Relevant features	Reference
<i>Rhodobacter sphaeroides</i> 2.4.1	Wild type	(4)
2.4.1 $\Delta$ <i>rpoHI</i>	Km <sup>r</sup> , <i>rpoHI</i> deletion strain	(2)
2.4.1 $\Delta$ <i>rpoHII</i>	Sp <sup>r</sup> , <i>rpoHII</i> deletion strain	(1)
2.4.1 $\Delta$ <i>rpoHI</i> / $\Delta$ <i>rpoHII</i>	Sp <sup>r</sup> , Km <sup>r</sup> , <i>rpoHI/II</i> double deletion strain	(2)
2.4.1 $\Delta$ <i>rpoHI</i> (pRK2.4.1 <i>rpoHI</i> )	Km <sup>r</sup> , Tc <sup>r</sup> , complementation of <i>rpoHI</i> deletion strain	(2)

Oligonucleotide	Sequence	Efficiency	Reference
<i>rpoHI</i> _RT-A	5'-GATCGCCAAGGATCT-3'		(1)
<i>rpoHI</i> _RT-B	5'-CTGGTCGCTGTCTTCA-3'	1.82	(1)
<i>rpoHII</i> _RT-A	5'-GCCGATGAACGACCTGAT-3'		(1)
<i>rpoHII</i> _RT-B	5'-AAGAACAGCGCCTTCTGG-3'	1.93	(1)

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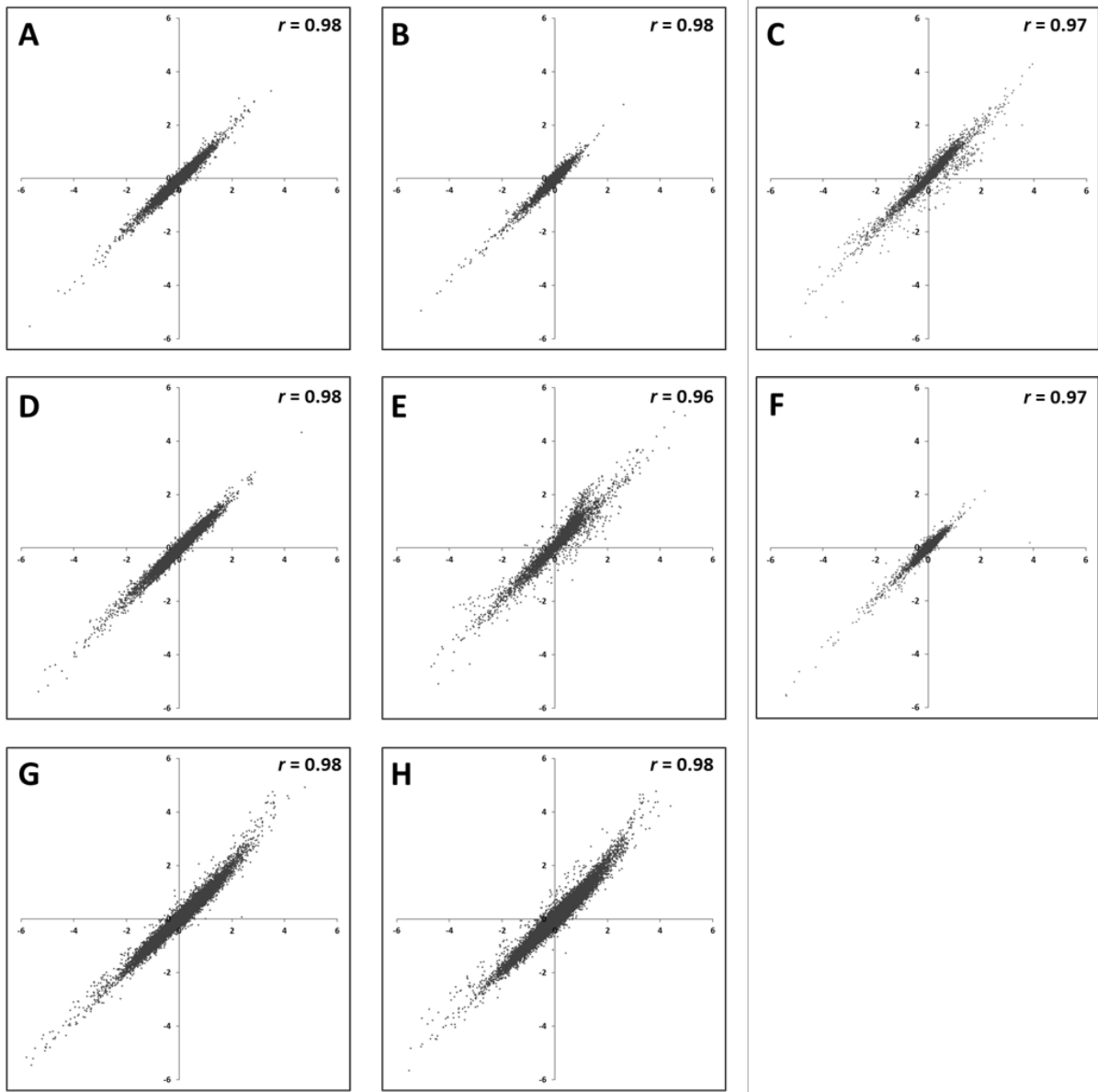
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22 **Table S3.** Mapping of RNA sequencing reads to the genome of *R. sphaeroides*.

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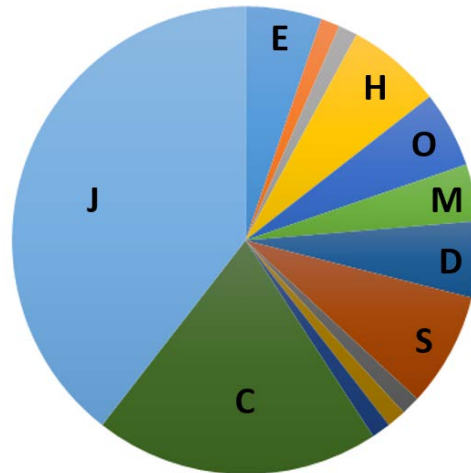


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25 **Figure S1.** The scatter plots showing the comparison between two biological replicates of the  
26 log<sub>2</sub> expression value. **(A)** wild type early stationary phase (28 h); **(B)** wild type outgrowth 20  
27 min after dilution from early stationary phase; **(C)** wild type outgrowth 90 min after dilution  
28 from early stationary phase; **(D)** wild type late stationary phase (72 h); **(E)** wild type outgrowth  
29 20 min after dilution from late stationary phase; **(F)** wild type outgrowth 90 min after dilution  
30 from late stationary phase; **(G)**  $\Delta rpoHI$  late stationary phase (72 h); **(H)**  $\Delta rpoHI$  outgrowth 20

31 min after dilution from late stationary phase. Pearson correlation ( $r$ ) is indicated. For a complete  
32 list of genes and information on their functions, see Table S1.

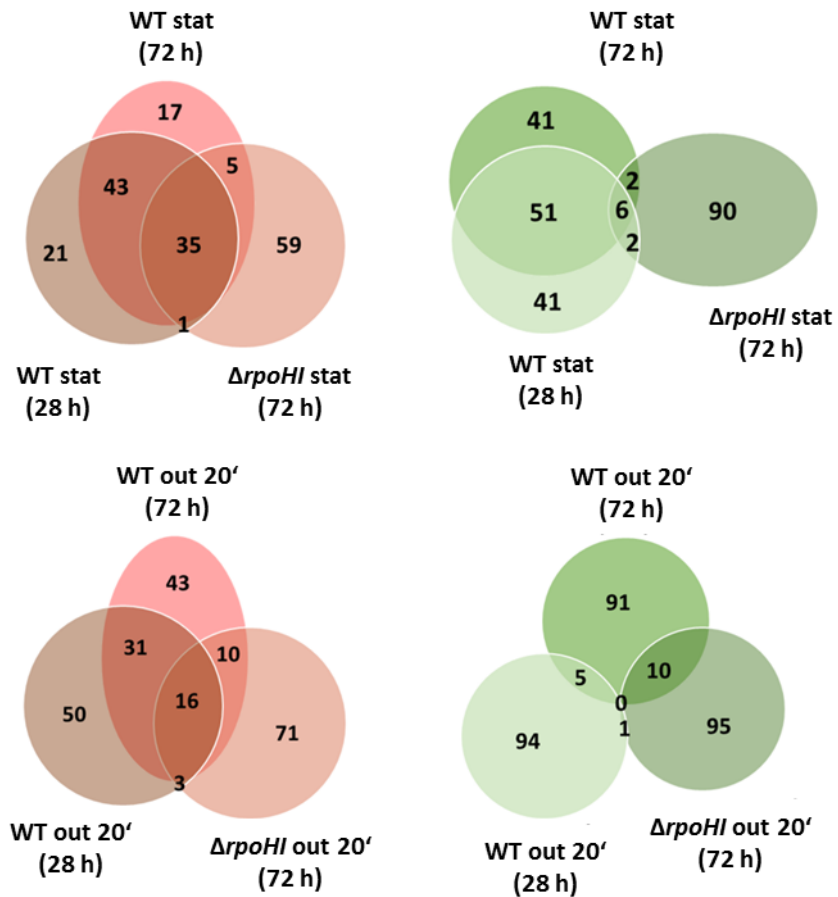
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35 **Figure S2.** Classification of genes with decreased transcript levels (fold change < -1.6) in early  
36 stationary phase based on designation of COG. C - Energy production and conversion; D - Cell  
37 cycle control; E - Amino Acid metabolism and transport; H - Coenzyme metabolism; J-  
38 Translation; M - Cell wall/membrane/envelop biogenesis; O - Post-translational modification;  
39 S - Function Unknown.

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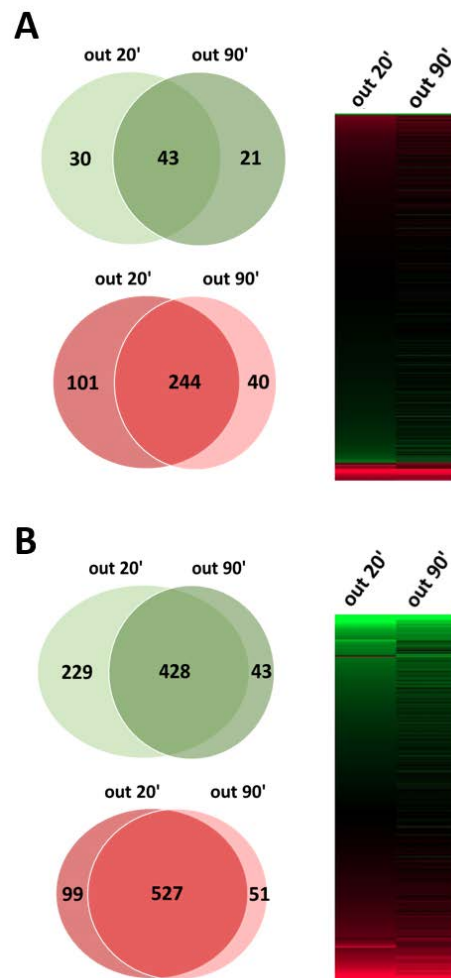


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42 **Figure S3.** Venn diagram of the 100 strongest regulated genes in the respective growth phase.

43 Genes, which decreased (red) or increased transcript levels (green) in early stationary phase (28

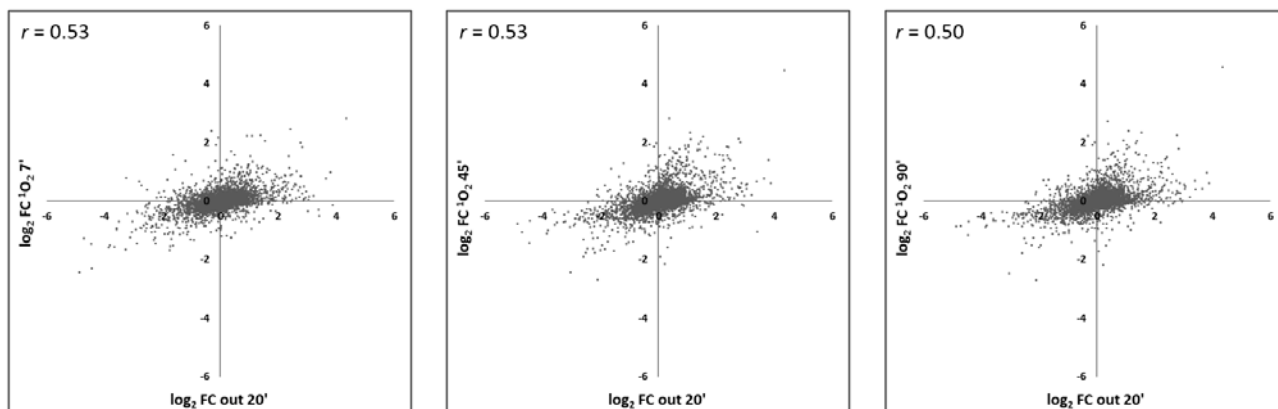
44 h), late stationary phase (72 h) or 20 minutes of outgrowth (out 20').



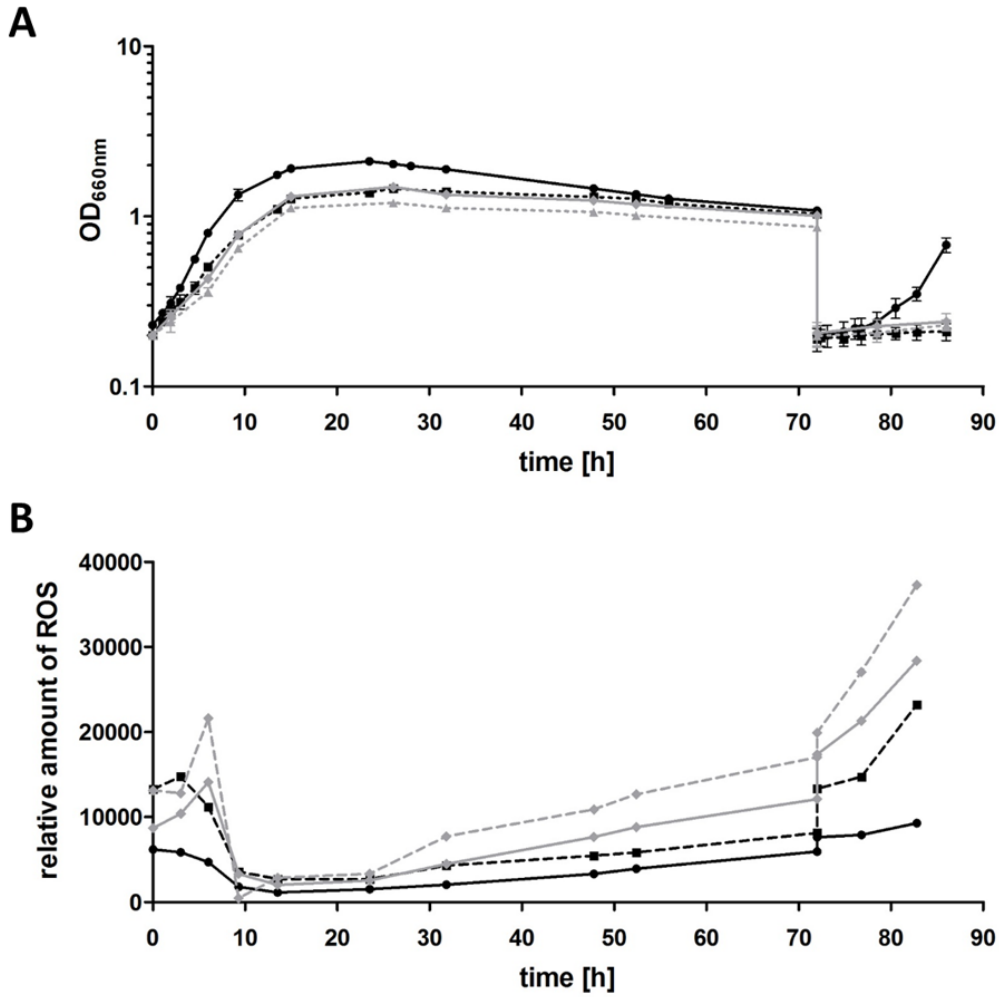
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46 **Figure S4.** Distribution and expression kinetics of the whole transcriptome in the outgrowth  
 47 phase of wild type cells. Cells were cultivated for 28 h (**A**) or 72 h (**B**), respectively. Relative  
 48 changes of RNA levels in different growth phase were monitored by microarray analysis of  
 49 total RNA and compared to exponential phase. Changes were illustrated as heat-maps with a  
 50 color code ranging from  $-2$  (red) to  $2$  (green)  $\log_2$  ratio. Venn Diagram of induced genes ( $\log_2$   
 51  $FC > 0.65$ ) are shown in green, repressed genes ( $\log_2 FC < -0.65$ ) shown in red.

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53 **Figure S5.** Correlation between outgrowth phase and photooxidative stress. Scatter-plots  
 54 represent pairwise comparisons of log<sub>2</sub> ratios between cells from the outgrowth phase from  
 55 late stationary phase and cells grown under photooxidative stress conditions (aerobically  
 56 grown cultures were treated with 0.2 μM methylene blue in the presence of 800 Wm<sup>-2</sup> white  
 57 light) for 7 min, 45 min, or 90 min (5). Pearson correlation ( $r$ ) is given for every comparison.  
 58 For a complete list of genes and information on their functions, see Table S1.  
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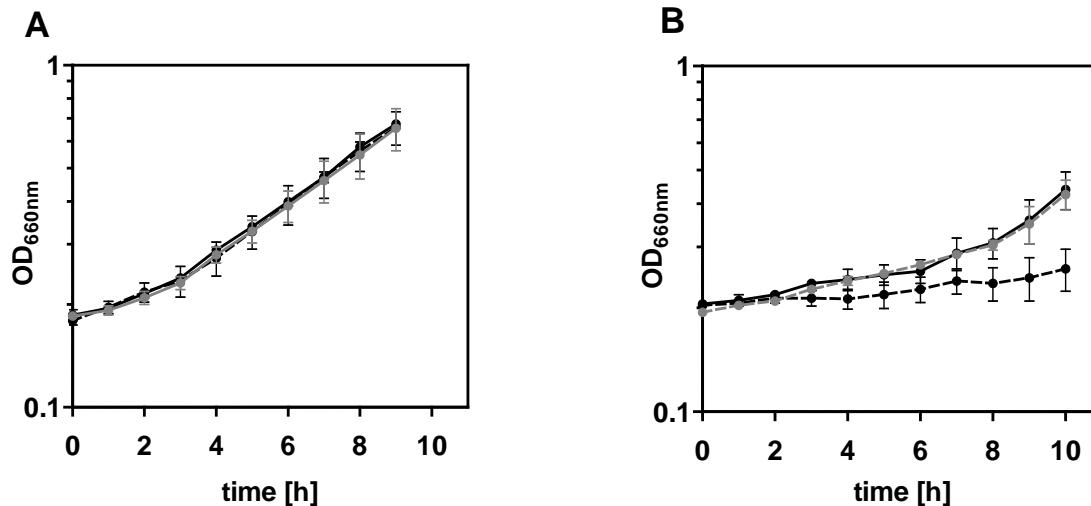


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61 **Figure S6.** Growth curves and ROS measurements for *R. sphaeroides* wild type 2.4.1  
 62 (continuous black line), 2.4.1Δ*rpoHI* (dashed black line), 2.4.1Δ*rpoHII* (continuous grey line),  
 63 and 2.4.1Δ*rpoHI/rpoHII* (dashed grey line). Cells were grown for 72 h and thereupon diluted  
 64 into fresh medium to an OD of 0.2. **(A)** The optical density at 660 nm (OD<sub>660</sub>) was determined  
 65 over time. **(B)** ROS levels were measured over time and normalized to the respective OD.

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69 **Figure S7.** Outgrowth 28 h and 48 h after inoculation (A) Growth curves of *R. sphaeroides*  
 70 wild type 2.4.1 (continuous black line), 2.4.1  $\Delta rpoHI$  (dashed black line), and 2.4.1 $\Delta rpoHII$   
 71 (grey line). Cells were grown for 28 h and thereupon diluted into fresh medium to an OD of  
 72 0.2. The optical density at 660 nm (OD<sub>660</sub>) was determined over time. (B) Growth curves of *R.*  
 73 *sphaeroides* wild type 2.4.1 (continuous black line), 2.4.1  $\Delta rpoHI$  (dashed black line), and  
 74 2.4.1 $\Delta rpoHI$ (pRK2.4.1*rpoHI*) (dashed grey line). Cells were grown for 48 h and thereupon  
 75 diluted into fresh medium to an OD of 0.2. The optical density at 660 nm (OD<sub>660</sub>) was  
 76 determined over time.

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 80 systems and is controlled by RpoE in the singlet oxygen-dependent response in  
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 91 Klug G. 2013. Integrative "omics"-approach discovers dynamic and regulatory features  
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