

**Supplementary Figure.1:** (A) Reference-based genome mapping of the transcriptome of *R. alkalitolerans* to *Blastochloris viridis*, *R. azotoformans*, *R. sphaeroides*. (B) Principal component analysis of replicates of samples (1) 30 µmol photons m-2s-1 npH (3) 500 µmol photons m-2s-1 npH (4) 30 µmol photons m-2s-1 hpH (6) 500 µmol photons m-2s-1 hpH. (C) Correlation matrix analysis of replicates within and between the samples. (D) Differential expression statistics of transcripts showing the total number of transcripts, significantly expressed, upregulated, and downregulated genes.



**Supplementary Figure. 2:** Heat map analysis of comparative pairs of (A) 30 µmol photons m-2s-1 npH (1) vs 30 µmol photons m-2s-1 hpH (4), (B) 30 µmol photons m-2s-1 npH (1) vs 500 µmol photons m-2s-1 npH (3), (C) 30 µmol photons m-2s-1 hpH (4) vs 500 µmol photons m-2s-1 hpH (6), (D) 500 µmol photons m-2s-1 npH (3) vs 500 µmol photons m-2s-1 hpH.



**Supplementary Figure. 3:** Volcano plot showing the differentially upregulated and downregulated genes in comparative pairs of (A) 30 µmol photons m-2s-1 npH vs 30 µmol photons m-2s-1 hpH, (B) 30 µmol photons m-2s-1 npH vs 500 µmol photons m-2s-1 npH (3), 30 µmol photons m-2s-1 hpH vs 500 µmol photons m-2s-1 hpH, (D) 500 µmol photons m-2s-1 npH vs 500 µmol photons m-2s-1 hpH. Black indicates log2 fold change≥1 and p value≤0.05. “Red” dots indicate absolute log2 fold change≥1 and FDR/adjusted p value≤0.05.



**Supplementary Figure. F4:** Principal component analysis of the (PCA plot) of replicates obtained from GC-MS. (A) 30 npH VS 250 npH (B) 30 npH VS 500 npH (C) 30 hpH VS 250 hpH (D) 30 hpH VS 500 hpH. Principal component (PC) 1 is given on the x-axis, while PC2 is given on the y-axis of each plot. The per cent of variance explained by each PC is given below each PCA plot. 30 and 500 represent the culture growth light intensity in µmol photons m -2s-1.