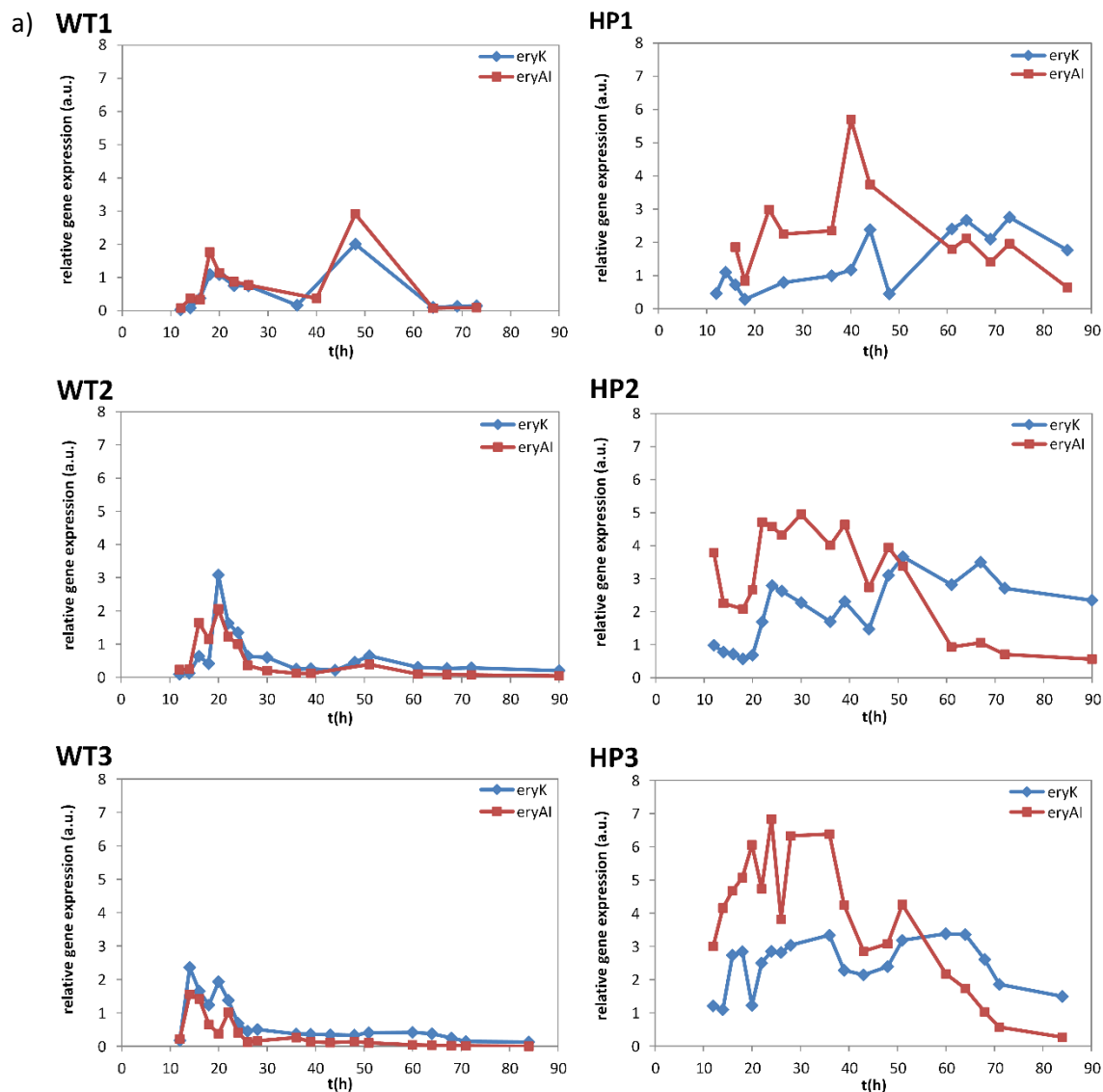


Additional file 3: a) Relative gene expression of erythromycin biosynthesis genes *eryK* and *eryAI* (normalized to the expression of 16S rRNA; arbitrary units) in 6 individual fermentations of wild type (WT1-3, left) and high producer (HP1-3, right) strain of *S. erythraea*, analysed by qPCR. b) Experimental time points from individual fermentations shown in a) chosen for transcriptome and proteome sampling (t1-t4) on the basis of gene expression and bioprocess parameters.



b)

fermentation/time (h)	t1	t2	t3	t4
WT1	18	26	48	73
WT2	20	26	51	72
WT3	20	24	51	71
HP1	36	40	44	85
HP2	24	29	51	90
HP3	24	26	51	84