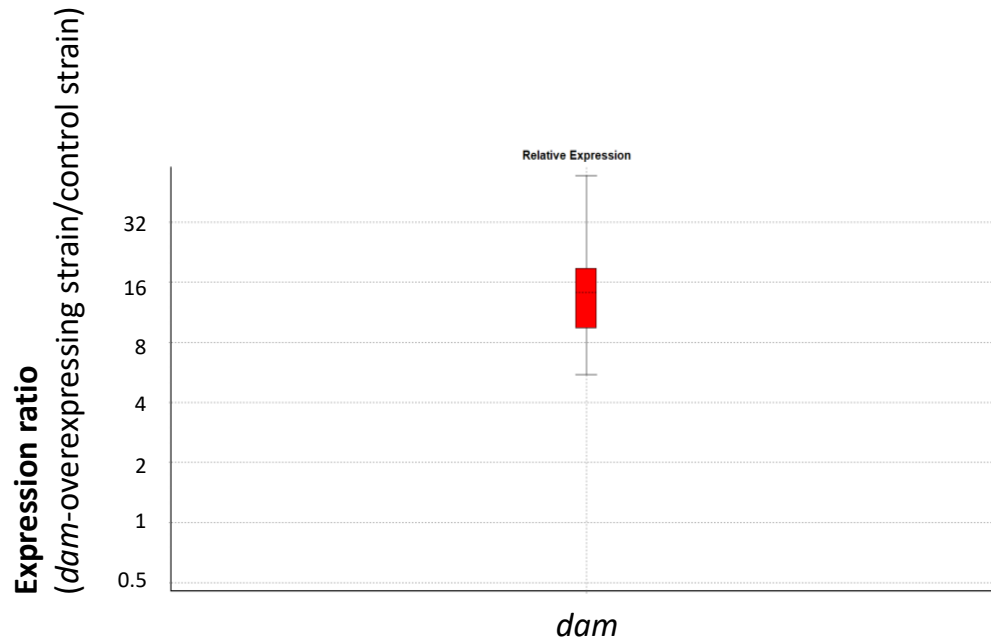


Fig. S1



Relative Expression Results

| Parameter | Value |
|------------|-------|
| Iterations | 2000 |

| Gene | Type | Reaction Efficiency | Expression | Std. Error | 95% C.I. | P(H1) | Result |
|------|------|---------------------|------------|----------------|----------------|-------|--------|
| GyrB | REF | 0,7929 | 1,157 | | | | |
| Dam | TRG | 1,1132 | 14,217 | 8,224 - 23,010 | 5,785 - 41,381 | 0,000 | UP |
| fis | REF | 0,7791 | 0,864 | | | | |

Interpretation

Dam is UP-regulated in sample group (in comparison to control group) by a mean factor of 14,217 (S.E. range is 8,224 - 23,010).

Dam sample group is different to control group. P(H1)=0,000

Figure S1. Relative expression of the *dam* gene in the *P. luminescens* *dam*-overexpressing strain.

qRT-PCR was carried out with total RNA extracted from 3 independent samples of exponentially growing cells of the *dam*-overexpressing strain and of the control strain. Left panel, Box-plot representing the expression ratio between the two strains is represented for the *dam* gene. Right panel, detailed report of the REST-analysis using with *gyrB* and *fis* used as control genes (see Materials & Methods section for details). The level of expression between the 2 strains was different at $p < 0.001$.