**Table S4:** All log2-fold changes in gene expression determined by qPCR.

| | | BrrF overexpression in iron-replete condition | | Iron depletion | | BrrF overexpression under iron depletion | | |
|---|---|---|---|---|---|---|---|---|
| Background strain | | WT | Δ*brrF* | WT | Δ*brrF* | Δ*brrF* | Δ*brrF* | Δ*brrF* |
| Gene | Locus tag | WT-pBrrF-d1 / WT-VC | Δ*brrF*-pBrrF-d1 / Δ*brrF*-VC | 200 µM dipyridyl / no dipyridyl | | Δ*brrF*-pBrrF-d1 / Δ*brrF*-VC | Δ*brrF*-pBrrF-d2 / Δ*brrF*-VC | Δ*brrF*-pBrrF-d3 / Δ*brrF*-VC |
| *sdhC* | BCAM0967 | -0.36 (0.093) | -0.40 (0.059) | **-1.28** (0) | -0.29 (0.241) | **-1.41** (0.023) | **-1.62** (0.011) | **-1.34** (0.03) |
| *sdhA* | BCAM0969 | -0.13 (0.597) | -0.10 (0.766) | **-2.25** (0) | 0.24 (0.479) | **-2.28** (0.008) | **-2.48** (0.005) | **-2.24** (0.009) |
| *acnA* | BCAM0961 | **-0.76** (0.028) | -0.30 (0.522) | **-4.22** (0) | -0.52 (0.401) | **-3.53** (0) | **-3.19** (0) | -0.47 (0.178) |
| *acnM* | BCAM2701 | -0.46 (0.189) | -0.17 (0.829) | **-2.00** (0) | 0.42 (0.568) | 1.05 (0.812) | 2.22 (0.309) | 2.28 (0.289) |
| *fumC* | BCAL2908 | **1.13** (0.003) | **1.00** (0.007) | **1.76** (0) | **0.42** (0.006) | **1.61** (0.036) | 0.96 (0.248) | -0.69 (0.498) |
| *fumA* | BCAL2287 | **-1.39** (0.020) | -0.69 (0.301) | **-5.38** (0) | **-1.09** (0) | **-5.11** (0) | **-3.59** (0) | -0.76 (0.08) |
| *sodB* | BCAL2757 | **-1.22** (0.010) | -0.64 (0.174) | **-2.34** (0) | **0.75** (0.001) | **-4.31** (0) | **-3.49** (0) | **-1.32** (0.006) |
| *katB* | BCAL3299 | -0.23 (0.864) | 0.01 (1.0) | **-1.72** (0) | **0.98** (0.001) | **-2.01** (0.039) | -1.88 (0.053) | -0.54 (0.803) |
| catalase | BCAM0931 | -0.25 (0.519) | 0.04 (0.995) | **-0.83** (0) | **-0.18** (0.032) | -0.93 (0.072) | -0.82 (0.120) | -0.33 (0.73) |
| *nuoB* | BCAL2343 | 0.11 (0.875) | -0.07 (0.968) | **-1.20** (0) | -0.07 (0.951) | -0.58 (0.364) | -0.68 (0.252) | -0.58 (0.369) |
| *edd* | BCAL3367 | -0.32 (0.740) | 0.23 (0.885) | **-3.60** (0) | **-1.54** (0.001) | **-2.06** (0.001) | **-1.92** (0.002) | **-1.67** (0.005) |
| *cyoB* | BCAL2143 | 0.03 (0.602) | n.d. | -0.52 (0.372) | -0.19 (0.916) | n.d. | n.d. | n.d. |
| *sodC* | BCAL2643 | 0.04 (0.586) | n.d. | 0.21 (0.300) | **0.74** (0.001) | n.d. | n.d. | n.d. |
| *icd* | BCAL2735 | 0.04 (0.682) | n.d. | -0.42 (0.078) | -0.00 (1.000) | n.d. | n.d. | n.d. |
| *mdh* | BCAM0965 | 0.02 (0.837) | n.d. | -0.15 (0.489) | **-0.41** (0.017) | n.d. | n.d. | n.d. |
| *gltA* | BCAM0971 | -0.12 (0.198) | n.d. | **-0.75** (0) | -0.25 (0.134) | n.d. | n.d. | n.d. |
| *acnB* | BCAM1833 | -0.17 (0.218) | n.d. | 0.03 (0.993) | **0.44** (0.026) | n.d. | n.d. | n.d. |
| *katA* | BCAM2107 | -0.02 (0.637) | n.d. | -0.57 (0.156) | 0.15 (0.921) | n.d. | n.d. | n.d. |

In brackets: p-values after Tukey's post-hoc test of ANOVA, 0 denotes p-value < 0.001, fold changes with p ≤ 0.05 are in bold, n.d. not determined.