Supplementary Datasets, Tables & Figures

Supplementary datasets:

Supplementary dataset S1. List of essential genes in liquid medium. The essential genome of *Bv* and *Pk* was estimated through the EL-ARTIST pipeline and predicts whether a gene is essential, non-essential or domain-essential for the survival in LBm medium.

Supplementary dataset S2. List of core genes. The core-genome shared between *Bv* and *Pk* was calculated using homology constraints set at minLrap ≥ 0.8 and identity ≥ 50%.

Supplementary dataset S3. Detailed list of colonization depleted and enriched genes. Shortlist of the genes of interest detailed throughout the manuscript which were identified to be involved in rice colonization.

Supplementary dataset S4. Detailed list of cultivar-specific colonization depleted and enriched genes. Shortlist of the genes of interest detailed throughout the manuscript which were identified to be specifically involved in the colonization of either IR64 or Nipponbare rice cultivars.

Supplementary dataset S5. List of *Pk* genes detected by multiple approaches. Cross-comparison of the dataset generated in the present study and the transcriptomic dataset from Coutinho et al., 2015 (14) obtained through the stimulation of *Pk* with root exudates.

Supplementary dataset S6: TA sites counts of transposon insertion in each gene for each condition.

Supplementary Tables:

Supplementary Table S1. Primers used to generate the gene fragments for targeted gene disruption.

Supplementary Figure:

Supplementary Figure S1. Genomic context of *cobW*, *edd* and *pdeR* genes, including fold change scores between rich medium and root conditions

Supplementary Table S1. Primers used to generate the gene fragments for targeted gene disruption.

Construction	Forward primer	Reverse primer
B. vietnamiensis LMG10929 Ω*cobW*	GTCACGATCGTCACTCGAGTTCTCGG	GATGGTCGTCTAGATGAACGCCTG
P. kururiensis M130 Ω*cobW*	CTGGGCTCGAGCAAAACCACGCTGCTC	GACTTCTCTAGAGTCGAGCTGGTGG
P. kururiensis M130 Ω*pdeR*	CGACAGCAACGCTCGAGAGCTCACG	CGAATCTCTAGAGGCGAGTTCGGTGAG
B. vietnamiensis LMG10929 Ω*pdeR*	GTAGCGACAGCAATCTCGAGGAACTG	CAGCACTCTAGAATTCGCGAGCTCG
B. vietnamiensis LMG10929 Ω*edd*	CAATCGACCCGTCTCGAGTATCTGCAG	CATCAGCTCTAGAAGCATCTGGTTGCTGTTC
P. kururiensis M130 Ω*edd*	GAGTCGTATCTCGCGCCTCGAGAGGCAG	CATCACTTCTAGAAGCATCTGGTTGCTGTTC

Supplementary Figure 1: Genomic context of *cobW*, *edd* and *pdeR* genes, including gene fold change scores between rich medium and root mutant libraries

- Supp. Figure S1A: Genomic context of *cobW* in Pk
- Supp. Figure S1B: Genomic context of *cobW* in Bv
- Supp. Figure S1C: Genomic context of *edd* in Pk
- Supp. Figure S1D: Genomic context of *edd* in Bv
- Supp. Figure S1E: Genomic context of *pedR* in Pk
- Supp. Figure S1F: Genomic context of *pedR* in Bv

Supp. Figure S1A   Cobalamin biosynthesis operon in *P. kururiensis* M130, with fold change from Tn-seq data (enrichment in green/depletion in red) of mutants in root versus rich medium)
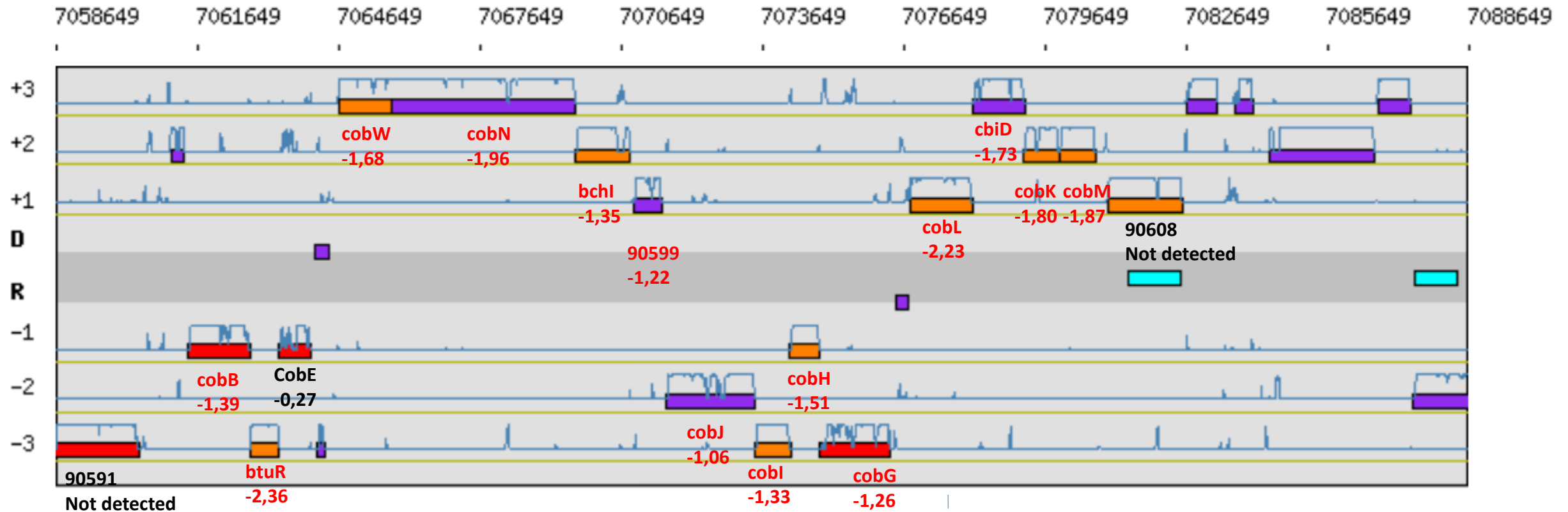
Score in Tnseq analysis on log2
ND= not detected as up or down in Tn-seq datasets
Negative fold change (in red) indicates mutants are depleted in root TN-seq libraries (so genes are important for root colonization)
Positive fold change (in green) indicates mutants are enriched in root TN-seq libraries (so these genes negatively impact root colonization)

Supp. Figure S1B Cobalamin biosynthesis operon in *B. vietnamiensis* LMG10929, with fold change from Tn-seq data (enrichment in green/depletion in red) of mutants in root versus rich medium
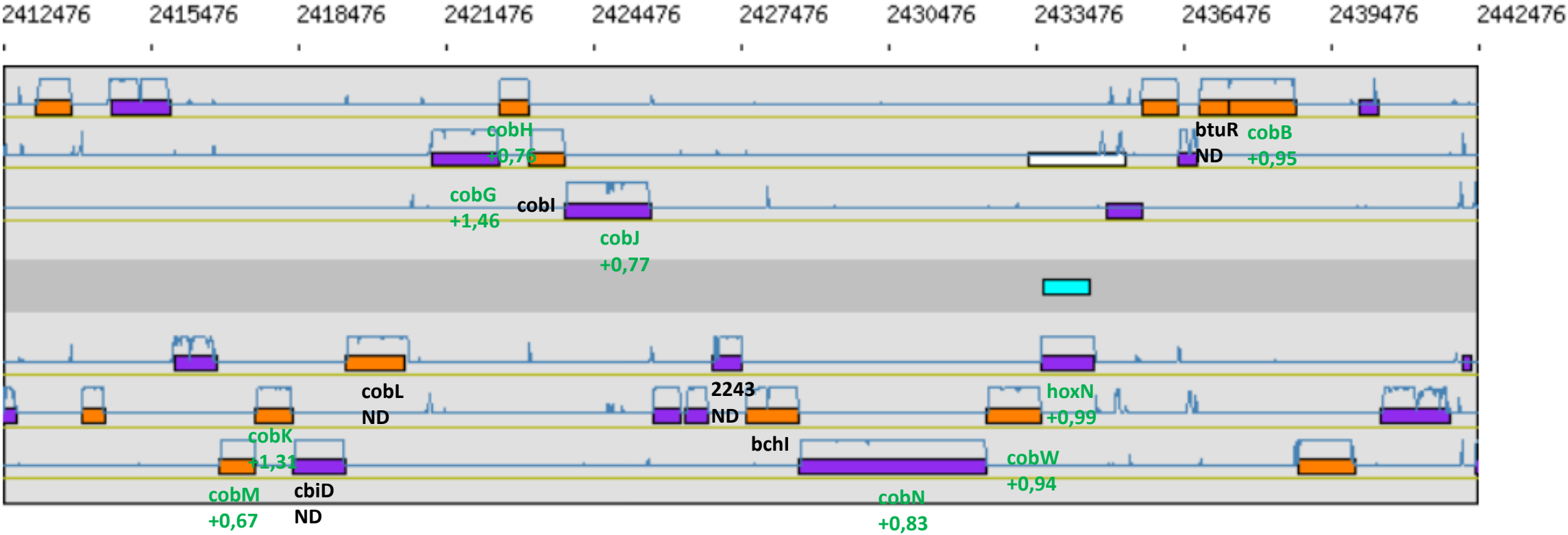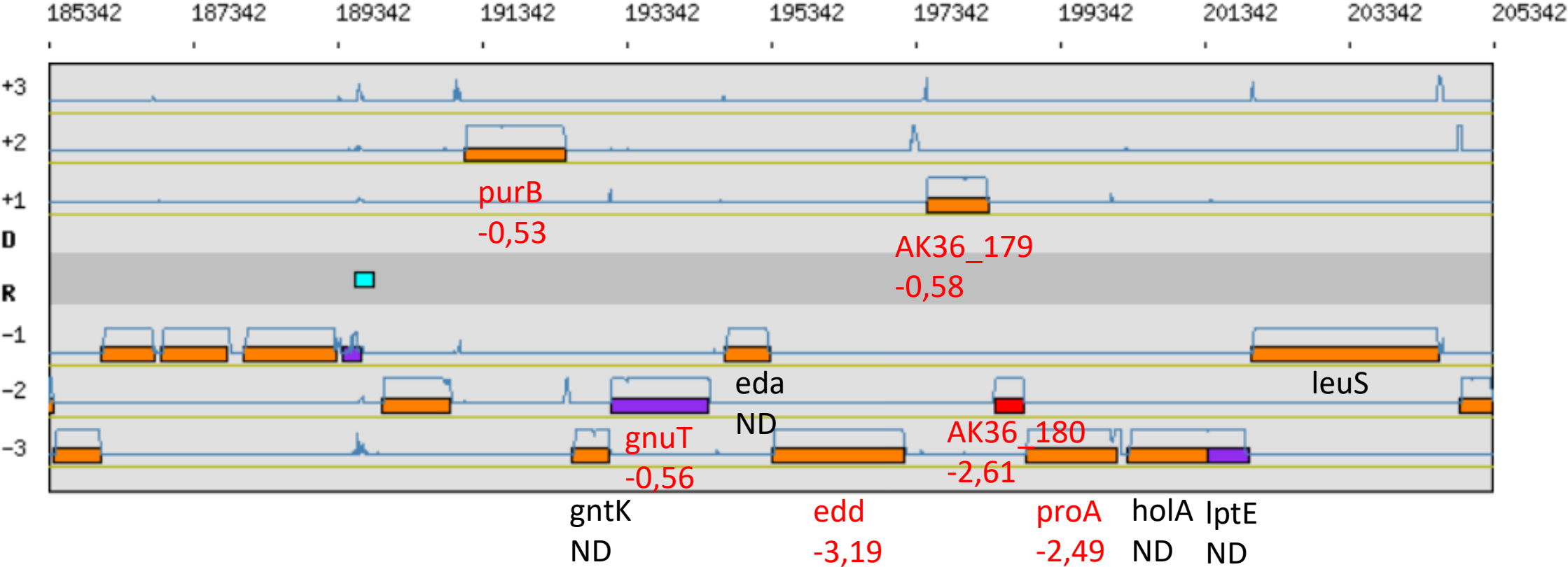
ND: not differentially detected

Supp. Figure S1C Gene *edd* genomic context in *P. kururiensis* M130, , with fold change from Tn-seq data (enrichment in green/depletion in red) of mutants in root versus rich medium)
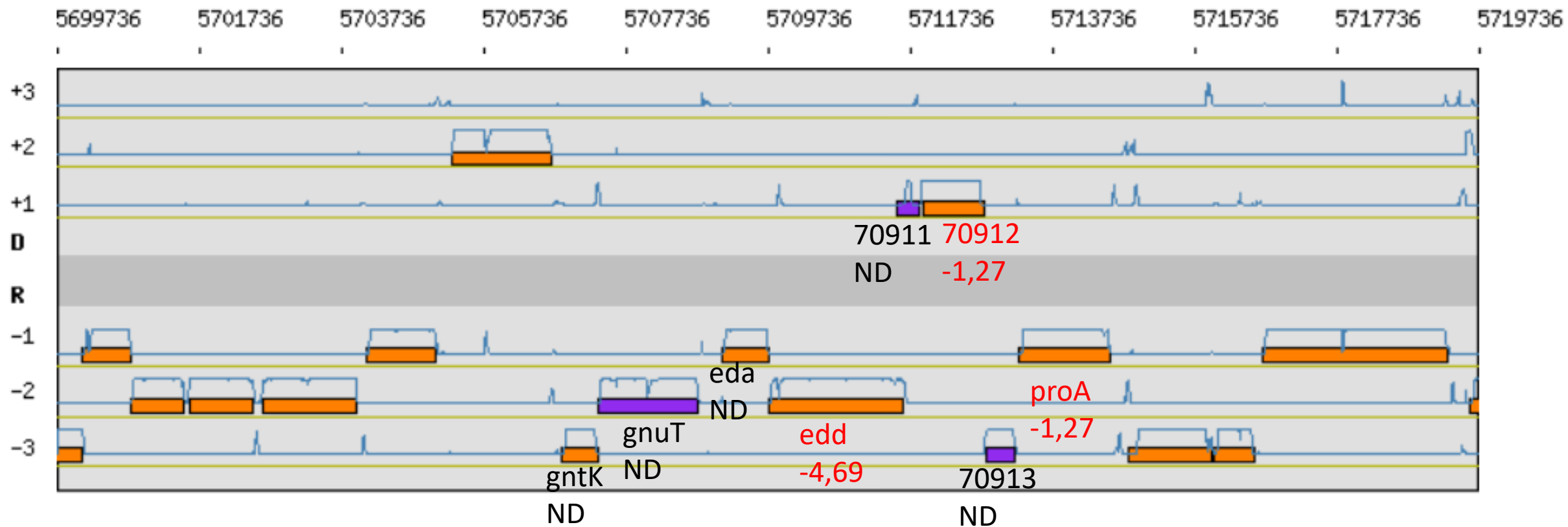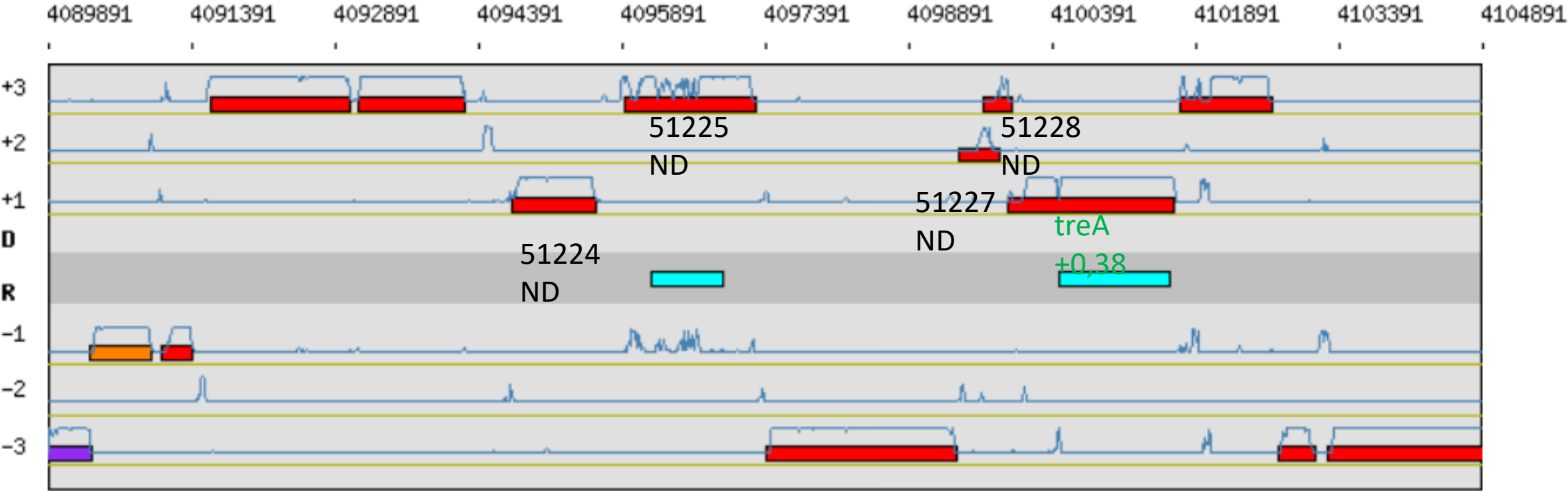
ND: not differentially detected

Supp. Figure S1D   Gene *edd* genomic context in *B. vietnamiensis* LMG10929 , with fold change from Tn-seq data (enrichment in green/depletion in red) of mutants in root versus rich medium)

ND: not differentially detected

Supp. Figure S1E — *pdeR* genomic context *in P. kururiensis* M130, with fold change from Tn-seq data (enrichment in green/depletion in red) of mutants in root versus rich medium)
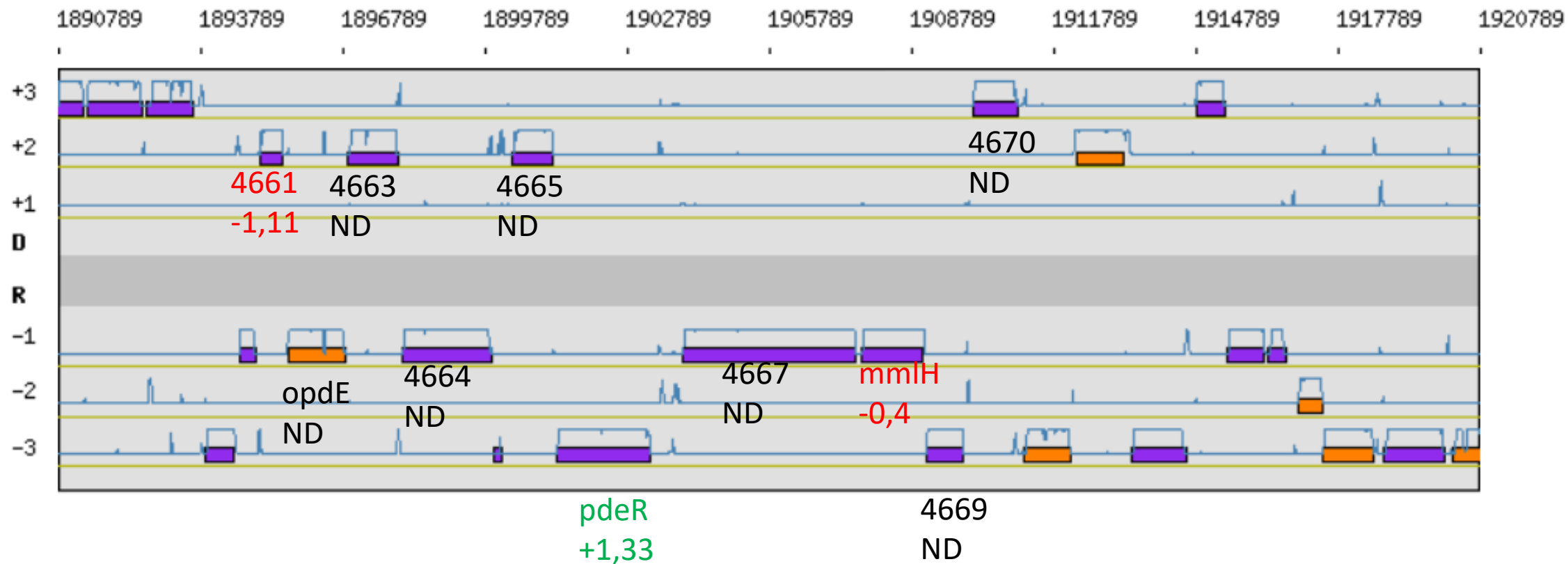
ND: not differentially detected

Supp. Figure S1F — *pdeR* genomic context *in B. vietnamiensis* LMG10929, with fold change from Tn-seq data (enrichment in green/depletion in red) of mutants in root versus rich medium)

ND: not differentially detected