Supplemental Materials

Supplemental figures

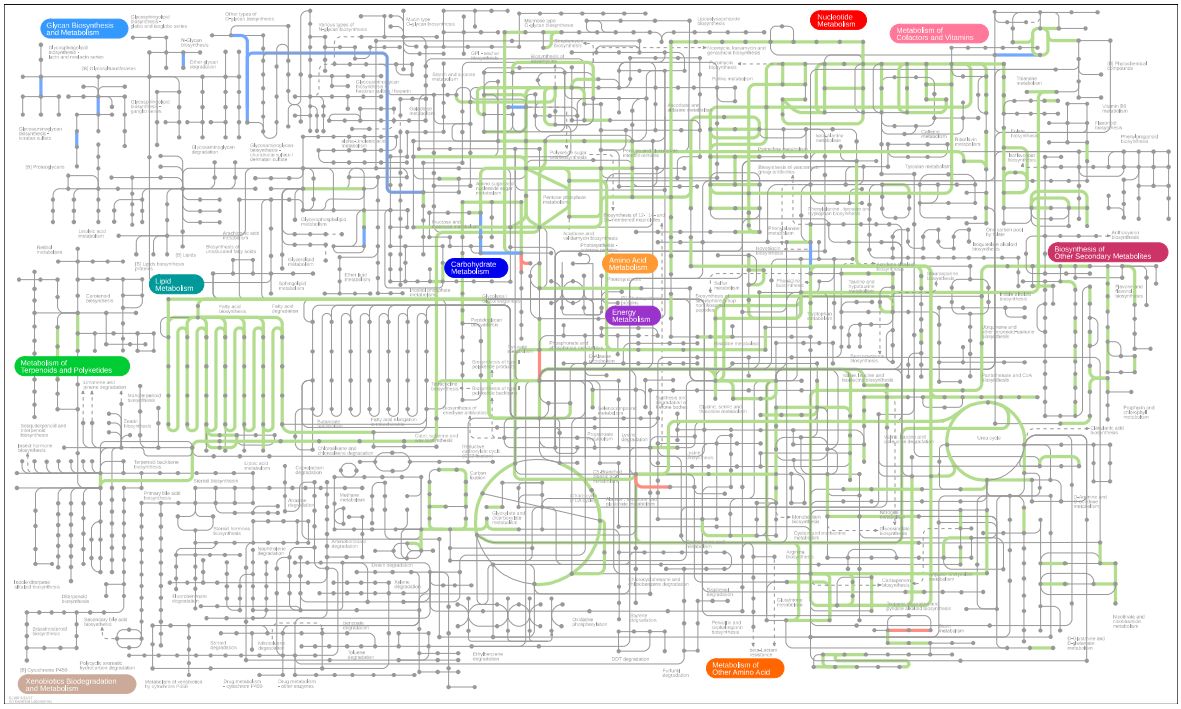

Figure S1. Metabolic pathways representation for MED4 and NATL1A using iPath3 showing common and unique pathways for MED4 and NATL1A. Blue and red links represent unique pathways for MED4 and NATL1A, respectively, while green links represent the shared pathways among the two strains.

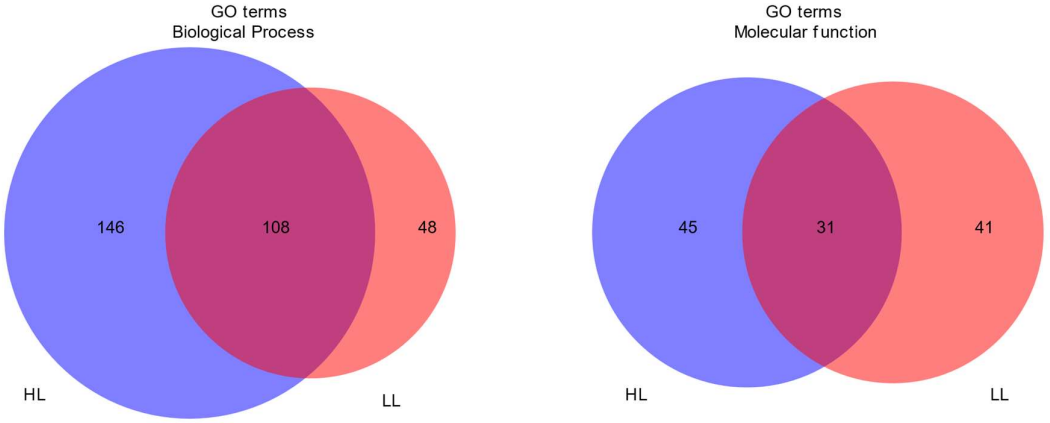

Figure S2. GO-term enrichment analysis comparing Pfams distinguishing high- and low-light P. marinus strains. Venn diagrams representing enrichment for biological processes and molecular functions GO-terms are shown in the left and right panels, respectively. High-light (HL) and low-light (LL) are highlighted in the blue and orange circles, respectively.

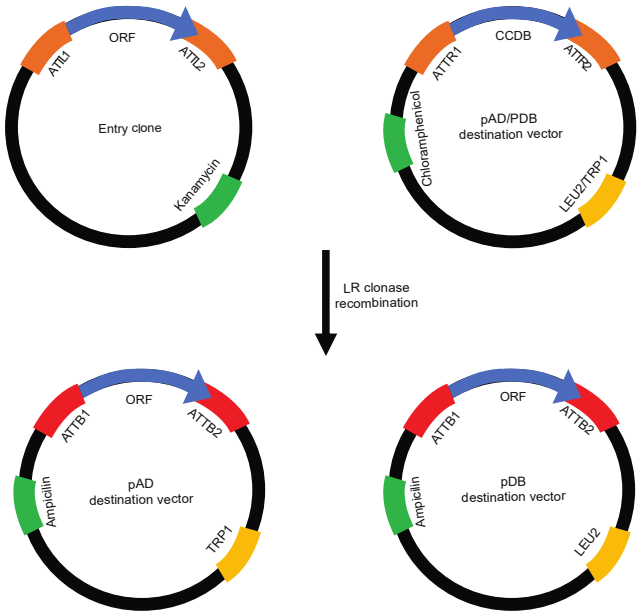

Figure S3. Schematic representation of ORFs entry clones and cloning into Y2H expression vectors. MED4 and NATL1A ORFs were synthesized in entry vectors, flanked with ATTL sites compatible with Gateway recombinational cloning. An example of LR Clonase recombination reaction with Y2H pAD and pDB destination vectors is represented. ATT sites, and antibiotic resistance are represented for each vector. In addition, pAD and pDB selectable markers are indicated, where TRP1 and LEU2 enable the growth of specific yeast strains in media lacking tryptophane and leucine, respectively.

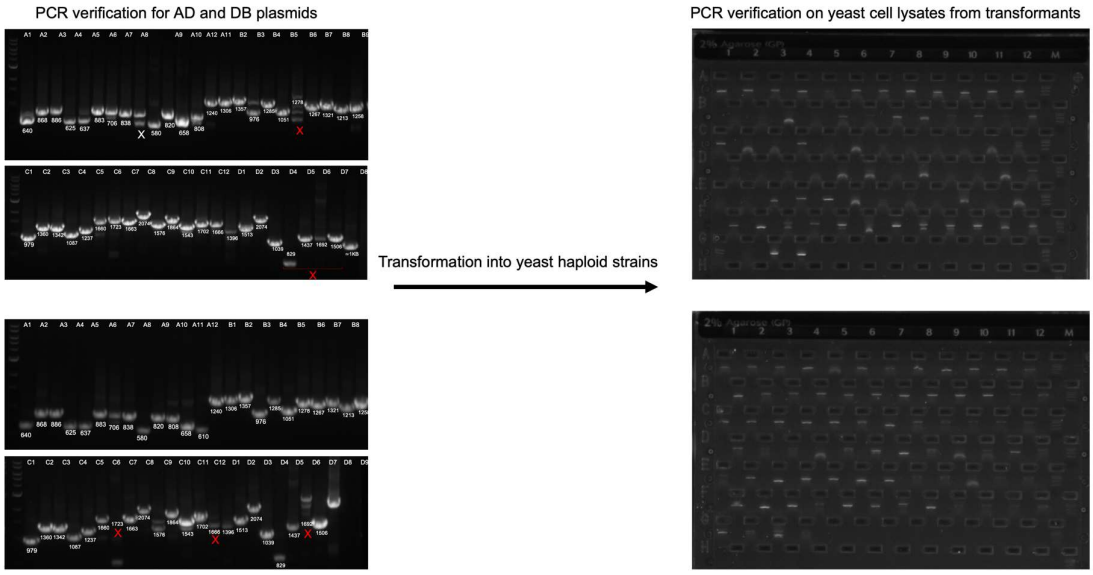

Figure S4. Cloning and transformation of a selected set of ORFs for MED4 strains. A set of 70 ORFs were cloned into pAD and pDB yeast expression vectors and validated with PCR with 85% cloning success rate. Fragments ranging from 302bp to 3030bp for MED4 strain. Expression vectors were transformed into yeast haploid cells and verified with a PCR on transformant yeast colonies.