

Supplemental Figure: ENR sequences selected for this study were from *Arabidopsis thaliana* (AtENR, GenBank accession number: NM_126612), *Brassica napus* (BnENR, GenBank accession number: P80030), *Olea europaea* (OeENR, GenBank accession number: AY083164), *Nicotiana tabacum* enr-T2 (NtENR, GenBank accession number: Y13861), *Petunia x hybrida* (PhENR, GenBank accession number: CAA05879), *Oryza sativa* (OsENR, GenBank accession number: XM_481639), *Zea mays* (ZmENR, GenBank accession number: AY106087), *Bigeloviella natans* (BinENR, GenBank accession number: AY267627), *Plasmodium falciparum* (PfENR, GenBank accession number: AF338731), *Plasmodium vivax* (PvENR, GenBank accession number: AY423071), *Toxoplasma gondii* (TgENR, GenBank accession number: AY372520), *Chlamydomonas reinhardtii* (CcENR, GenBank accession number: AAP05135), *Chlamydia muridarum* Nigg (CmENR, GenBank accession number: AAF39238), *Synechococcus elongatus* PCC 6301 (SeENR, GenBank accession number: BAD79568), *Thermus thermophilus* HB8 (TtENR, GenBank accession number: BAD70127), *Campylobacter jejuni* RM1221 (CjENR, GenBank accession number: AAW36020), *Staphylococcus aureus* (SaENR, GenBank accession number: AAF05840), *Salmonella typhimurium* (StENR, GenBank accession number: P16657), *Bacillus cereus* (BcENR, GenBank accession number: AAS40268) and *Escherichia coli* (EcENR, GenBank accession number: AAN80225). Protein sequences were aligned by using ClustalW program (Thompson et al., 1994) running under the software Lasergene, Version 6 (DNASTAR, Madison, WI) with default parameters (gap penalty 10, gap length penalty 0.2). Identical amino acids are shaded with black and similar amino acids are in gray.

Thompson JD, Higgins DG, Gibson TJ. CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. *Nucleic Acids Res.* 1994 Nov 11;22(22):4673-80.