**Supplementary File 2. Substantive changes in steady-state protein levels in cell envelope of Lpp+21**

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| **Cellular process** | **Increased** | **Function** |
| Peptidoglycan maturation, turnover, remodelling | AmiC | Amidase, cleaves peptide side-chains that link the glycan strands of PG  |
| Oligopeptide transport  | OppD, OppF, OppC, OppB | PG peptide transmembrane transport (ATP-binding subunit) |
| Ferrous Iron Uptake/transport  | FeoAB | Ferrous iron import across the inner membrane  |
| FhuE, | Feric-coprogen transport, across the OM |
| Stress response | ZraP | Response to cell envelope stress |
| YfcG | Response to oxidative stress (has disulphide oxidoreductase activity) |
| IM Protease  | RseP/YaeL | Proteolytic cleavage of the anti-sigma factor RseA; Degradation of remnant signal peptides that are left in the inner membrane |
| Protein export  | TatA | Twin arginine translocation (Tat) complex |
| c-di-GMP  | DgcM/YdaM | c-di-GMP diguanylate cyclase; curli related |
| Other/Unknown | FrdABC | Fumarate reductase complex, in the IM |
| DmsB | DMSO reductase, in the IM |
| YnfF | Unknown, predicted as a periplasmic protein |
| HiuH/YedX | Unknown, predicted as a periplasmic protein |
| **Cellular process** | **Decreased**  | **Function** |
| PG-OM bridging | Lpp  |  |
| Amino acid transport | DcuA | L-aspartate uptake |
| AroP | general aromatic amino acid uptake |
| Carbohydrate transport  | GatABCD | Transport and metabolism of Galactitol and DHAP  |
| SrlE | Transport of sorbitol / mannitol  |
| MglB | Periplasmic binding protein of a D-galactose/ methyl-D-galactoside ABC transport system |
| Stress response | OsmY | Response to hyperosmotic stress |
| OM integrity | YhdP | Maintaining the outer membrane permeability barrier; interaction with cyclic enterobacterial common antigen |
| AI-2 transport | LsrB | Putative Autoinducer-2 ABC transporter periplasmic binding protein |
| Lipoproteins  | BamE | Protein assembly into the outer membrane |
| YgdI | Unknown function |
| YgeR | Has a LysM domain involved in PG binding; implicated in cell division |
| Lipid  | LpxB | lipid A disaccharide synthase, in IM |
| GlpQ | Glycerophosphoryl diester phosphodiesterase involved in the utilization of the glycerol moiety of membrane phospholipids |
| Other/Unknown | NuoK | component of NADH dehydrogenase I, in IM |
| UbiA | ubiquinone biosynthesis, in IM |
| YjiN | Unknown |
| YfdI | Unknown  |
| YfaZ | Unknown, predicted OM Beta barrel |
| YahO | Unknown, predicted periplasmic protein |
| YdeN | Unknown, predicted periplasmic sulfatase |
| YdcS | Unknown, predicted periplasmic binding protein for uncharacterized ABC transporter |