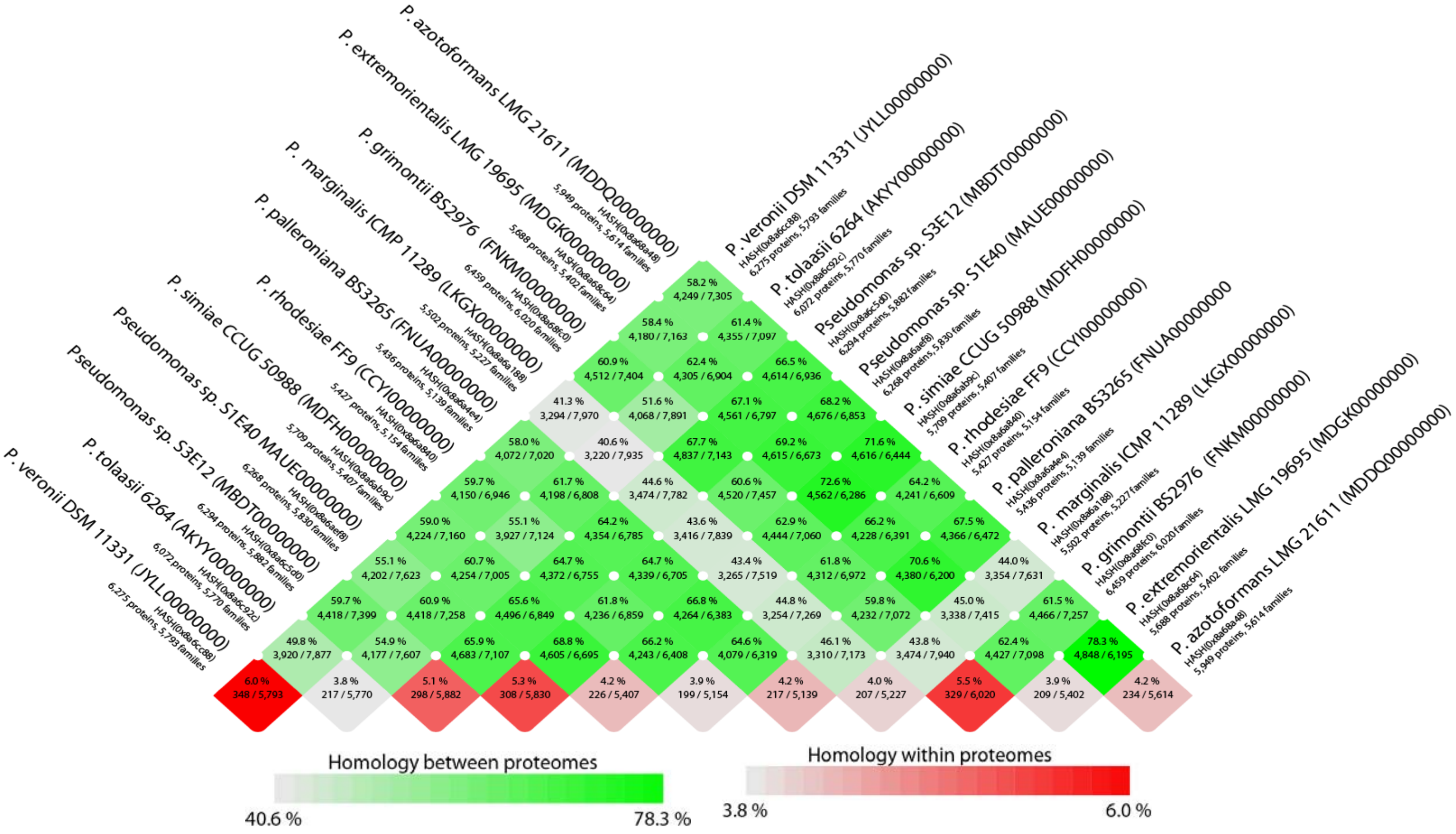

Figure S2. BLAST matrix of proteomes of the two new *Pseudomonas sp.* strains (S1E40 and S3E12) and their close lineages based on all against all protein comparison to define homologs. A hit is considered significant if 50%/50% (identity/length coverage) requirement between-proteomes is met. Paralogs (internal homology) are proteins within a genome matching the same 50–50 rule. BLAST matrix was performed using CMG-Biotools (Vesth *et al*., 2013).