



Figure S7 Relative conditional substitution rates at seven *B. cenocepacia* loci (*atpD*, *gltB*, *gyrB*, *lepA*, *phaC*, *recA*, and *trpB*). Relative conditional substitution rates are estimated by assuming that the most common nucleotide at each site is ancestral and any deviation from that nucleotide is caused by a single mutation. Substitution rates were calibrated to the nucleotide content at polymorphic sites for each gene, whereby only covered sites capable of producing a given substitution are used in the denominator of each calculation.