

Supplementary Figure 1: MLST results for *P. aeruginosa* isolate (extended output format).

Using the MLST web-server, a *P. aeruginosa* strain that had been sequenced on the Illumina platform, single reads, was typed. For the sake of the example, we have chosen to show the results when using short sequence reads that assemble into a draft genome with a low N50. For explanation of the table headers, see the legend of Figure 1. No perfect match was found for the *acs* locus, for which the % identity to the closets matching MLST allele is only 99.74%. This is an example of a minor mismatch. Also, no perfect match is found for the *aro* locus. The % identity of the HSP is 100%, but the length of the HSP is shorter than the length of the MLST allele. When looking at the nucleotide sequences, it can be seen that the MLST allele exceeds the length of the contig (the MLST locus is at the boundaries of a contig). This is an example of a major mismatch.