S13 Fig. Variants in amiA2 and era associated with bedaquiline MIC. Manhattan plots showing the association results for the amiA2/era coding region for the A oligopeptides and B oligonucleotides, and oligonucleotide alignment plots showing close ups of the significant region in amiA2/era in the correct reading frame for C amiA2 and D era. The black dashed lines indicate the Bonferroni-corrected significance thresholds. In the Manhattan plots, oligopeptides are coloured by the reading frame that they align to, black for the correct reading frame for amiA2. Oligo-peptides and nucleotides assigned to the region but did not align using BLAST are shown in grey on the right hand side of the plots. In the oligonucleotide alignment plots, the H37Rv reference alleles are shown at the bottom of the figure, grey for an invariant site, coloured at variant site positions. The oligonucleotides that aligned to the region are plotted from least significant at the bottom to most significant at the top. The background colour of the oligonucleotides represents the direction of the β estimate, light grey when β < 0 (associated with lower MIC), dark grey when β > 0 (associated with higher MIC). Oligonucleotides are coloured by their allele at all variant positions. Oligonucleotides below the MAF threshold and not included in the analysis, but visualised here for signal interpretation, are marked by *s.