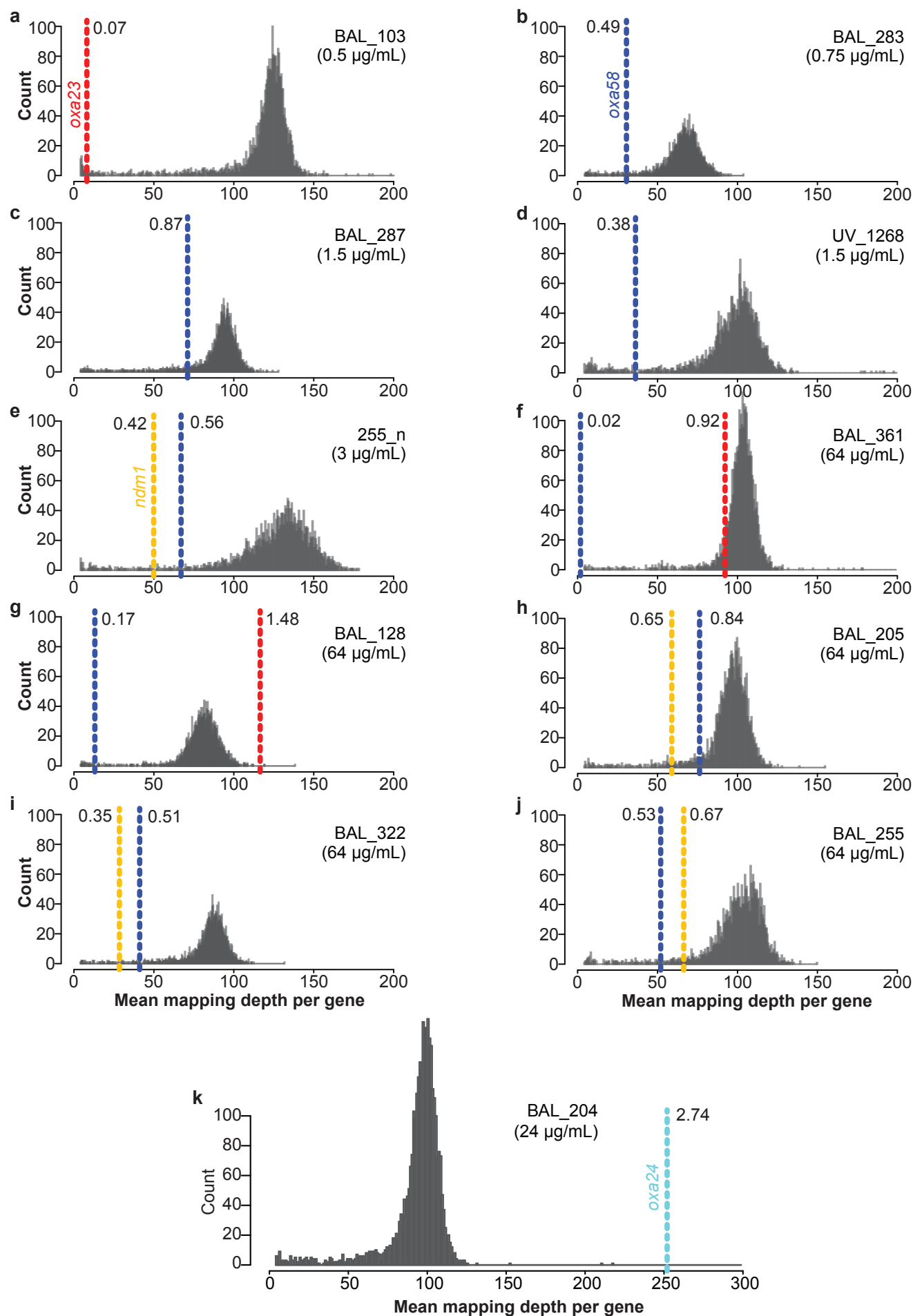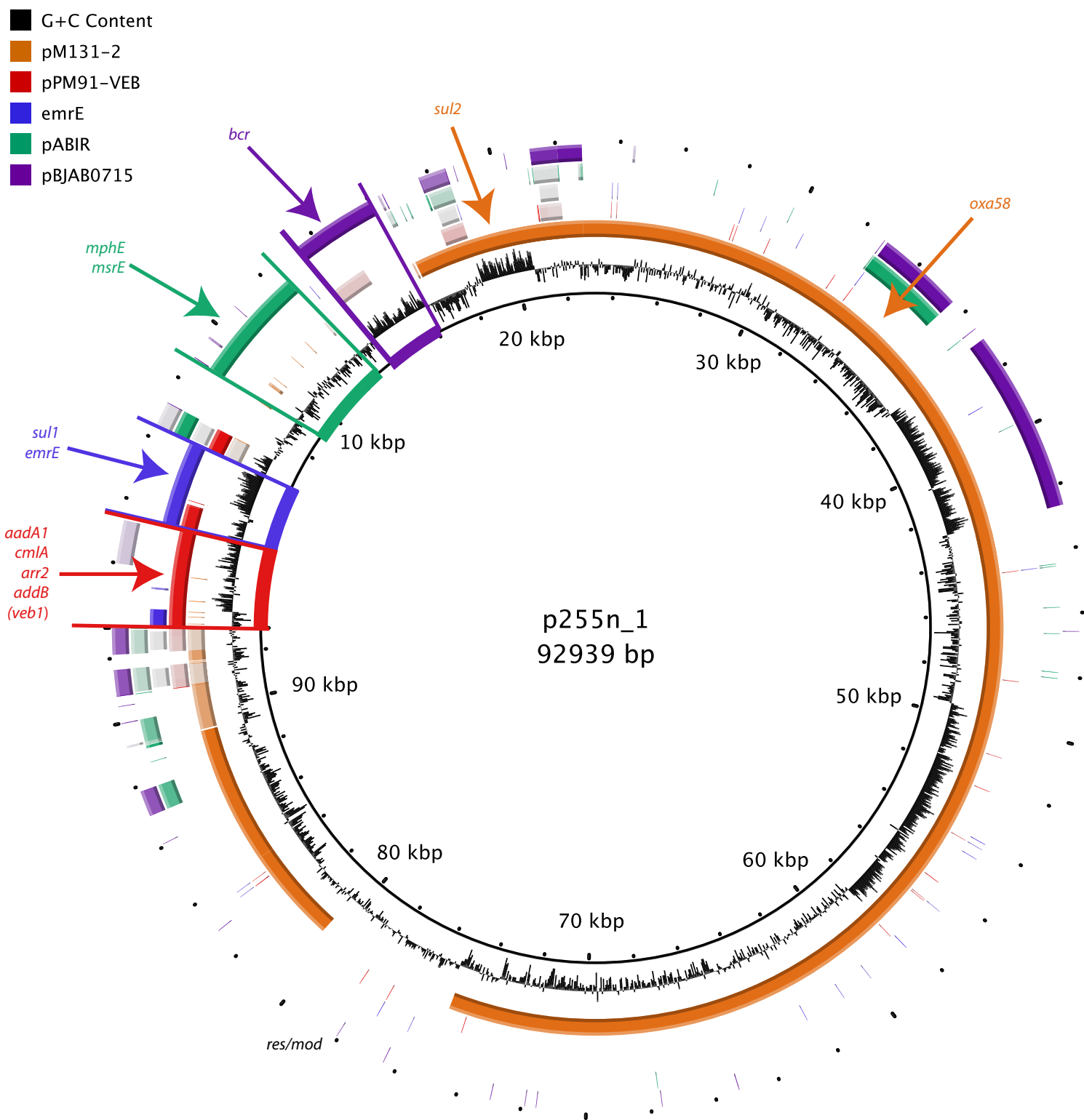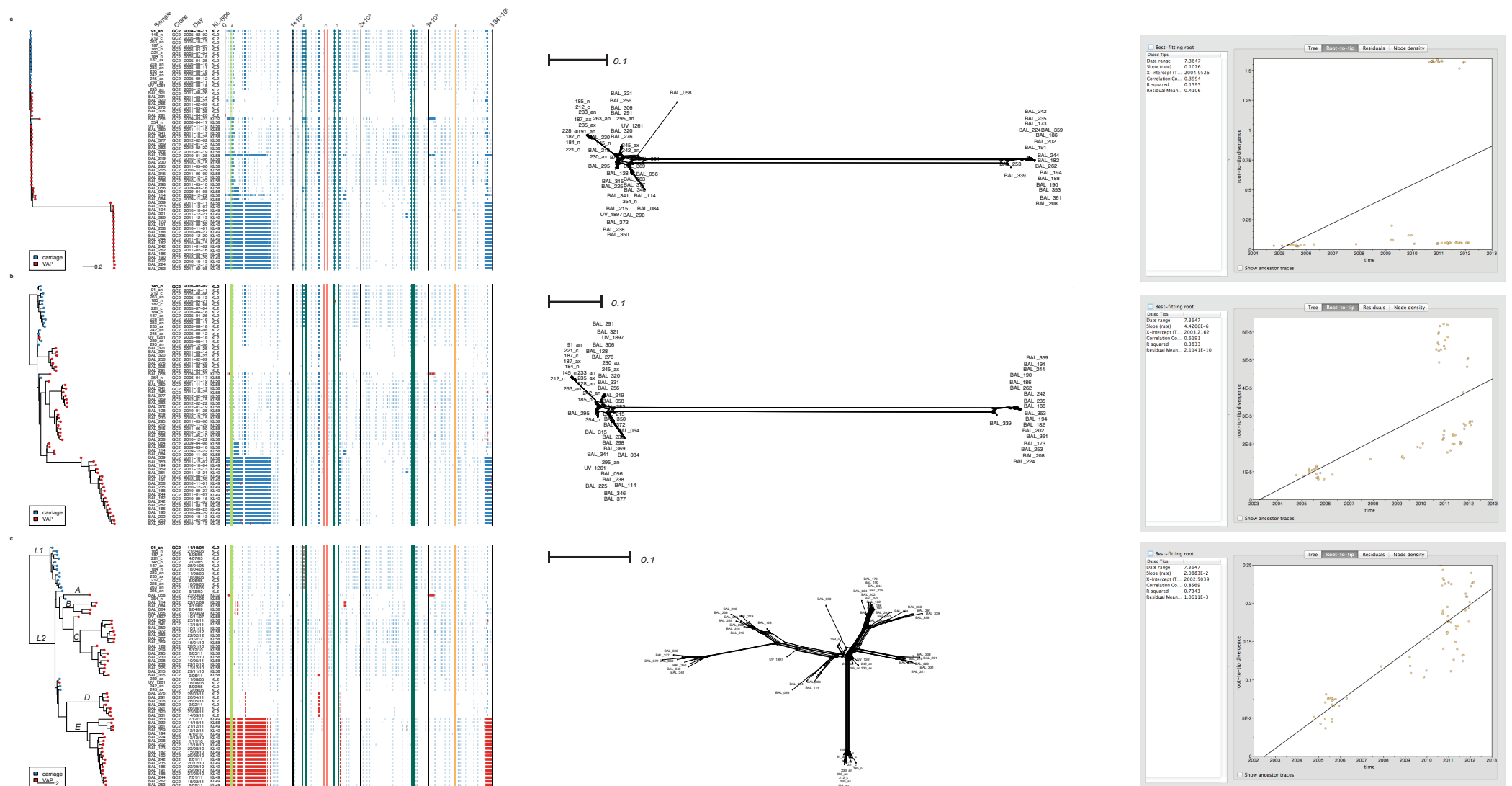Supplementary Figure 1. Inference of oxa23 copy number from read depth. Plot shows the distribution of the ratio of average read depths for oxa23 vs known chromosomal genes, smoothed using a bandwidth of 0.1, for all oxa23 containing isolates (n=56, isolates listed in Supplementary File 1). Shaded regions highlight cut-off ranges used to assign discrete copy numbers for chromosomal insertions of oxa23, which are shown in Table 1 and Figure 4. Note that for the three isolates with depth ratio <0.6, oxa23 was plasmid located and not inserted in the chromosome.
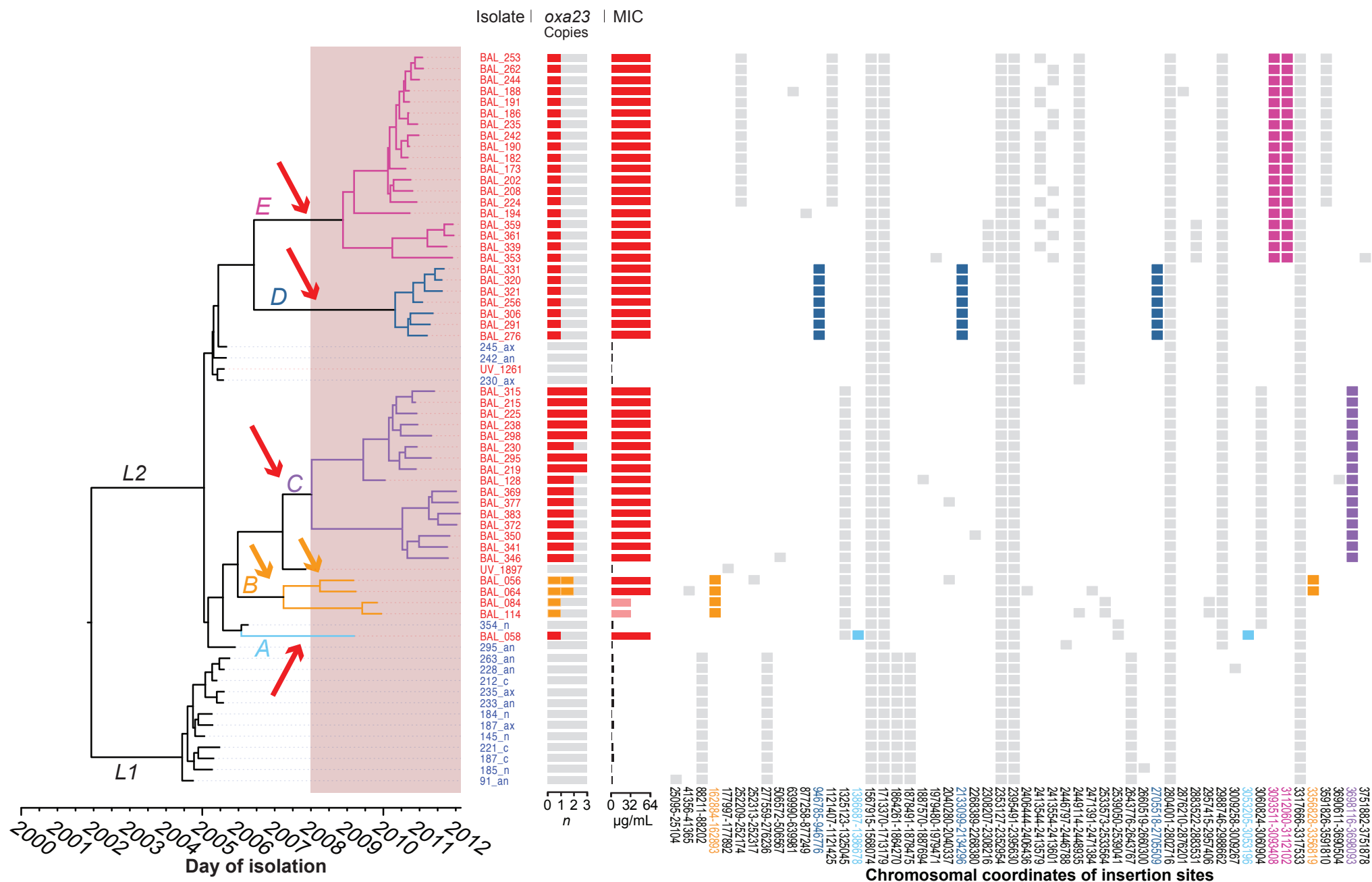
Supplementary Figure 2. Read depth distributions for selected isolates with carbapenemase sequences detected. Histograms indicate distribution of mean read depths for 3,716 chromosomal genes, inferred by mapping of reads to the reference genome. Lines indicate the mean read depth for carbapenemase genes (yellow, ndm1; red, oxa23; light-blue, oxa24; blue, oxa58), these are labelled with the ratio of average read depths for the carbapanemase vs the mean depth of the 3,716 chromosomal genes. Panels are labelled with the isolate name, MIC for imipenem is shown in brackets.

Supplementary Figure 3. Mosaic structure of the novel circular plasmid p255n_1, bearing oxa58, detected in CC10 and CC16 isolates. Inner circle plot indicates G+C content of the plasmid, labelled with plasmid coordinates. Coloured rings show regions of homology to other plasmids: pM131-2, Acinetobacter sp. M131 plasmid pM131-2, JX101647.1; pPM91-VEB, Proteus mirabilis strain EYG91 plasmid pPM91-VEB (NG_041554.1); emrE, Acinetobacter genomosp. 3 strain 3/TCVGH/19991022 (NG_036847.1); pABIR, Acinetobacter baumannii plasmid pABIR (EU294228.1); pBJAB0715, Acinetobacter baumannii BJAB0715 plasmid pBJAB0715 (CP003848.1). The annotated sequence of p255n_1 was submitted to GenBank under accession KT852971.

Supplementary Figure 4. Analyses of whole genome SNP alignments for GC2: (a) all SNPs, (b) excluding recombinant SNPs identified by ClonalFrameML, (c) excluding recombinant SNPs identified by Gubbins. In each panel, the ML phylogenetic tree is plotted next to a representation of the alignment from which it was inferred; red tree tips, infection isolates; blue tree tips, carriage isolates. In the alignment, SNPs included in the phylogenetic analysis are marked in blue, whilst recombinant SNPs excluded from the analysis are marked in red. SNP coordinates relative to the GC2 reference genome (CP001921.1) are indicated along the top of the alignment in panel (a); in each alignment, known horizontally transferred regions are indicated with vertical lines: A, capsule biosynthesis locus (K locus); B-E, prophage sequences; F outer core locus (OCL). To the right of each alignment is a split network inferred from the alignment, followed by Path-O-Gen analysis of the ML tree (indicating linear relationships between ML root-to-tip branch lengths (y-axis) and date of isolation (in days, x-axis).

Supplementary Figure 5. Schematic representation of ISAba1 insertion events in GC2. Left, BEAST tree reproduced from Figure 4, branches coloured to highlight sub-clades carrying oxa23 within a transposon involving ISAba1. Right, ISAba1 insertion sites identified using ISMapper (coordinates are relative to the reference genome accession CP001921.1); insertion events unique to sub-clades are highlighted to match the subclade in the tree.

Supplementary Figure 6. Ancestral state probabilities of the K locus for nodes in the GC2 tree. Panels show the posterior probability distributions (plots) and mean values (inset tables) for each GC2 KL type at seven key nodes (including the root). Tree shown is the BEAST for GC2, with the seven key nodes labelled; tree branches are coloured by inferred capsule type transitions; sub-clades A-E are labelled with red and yellow arrows indicating bla_{OXA-23} transposon events as in Figure 4.