

Supplementary file 3

Candida metapsilosis chromosomes graphs

For each chromosome we have plotted: i) coding genes for +/- strand (grey bars) and GC-content in 1kb windows (blue plot) in the bottom track and log₂ of observed vs expected value in 1kb windows for depth of coverage (blue) in the top fourteen tracks. In the bottom panel, the X axis reflects the genomic position given in bp (from 0 up to 3.25Mb for the longest chromosome), while the Y axis the GC% content (0-100%). In the other panels the Y axis reflect the log₂ of observed vs expected depth-of-coverage (from -4 to +4).

In addition, loss of heterozygosity (LOH) regions have been marked in grey, if the same genotype as reference was kept (hapA), and orange, if alternative genotype was kept (hapB). Four replicas (pe300, pe600, mp500 and pe400ov) were analysed for PL429.

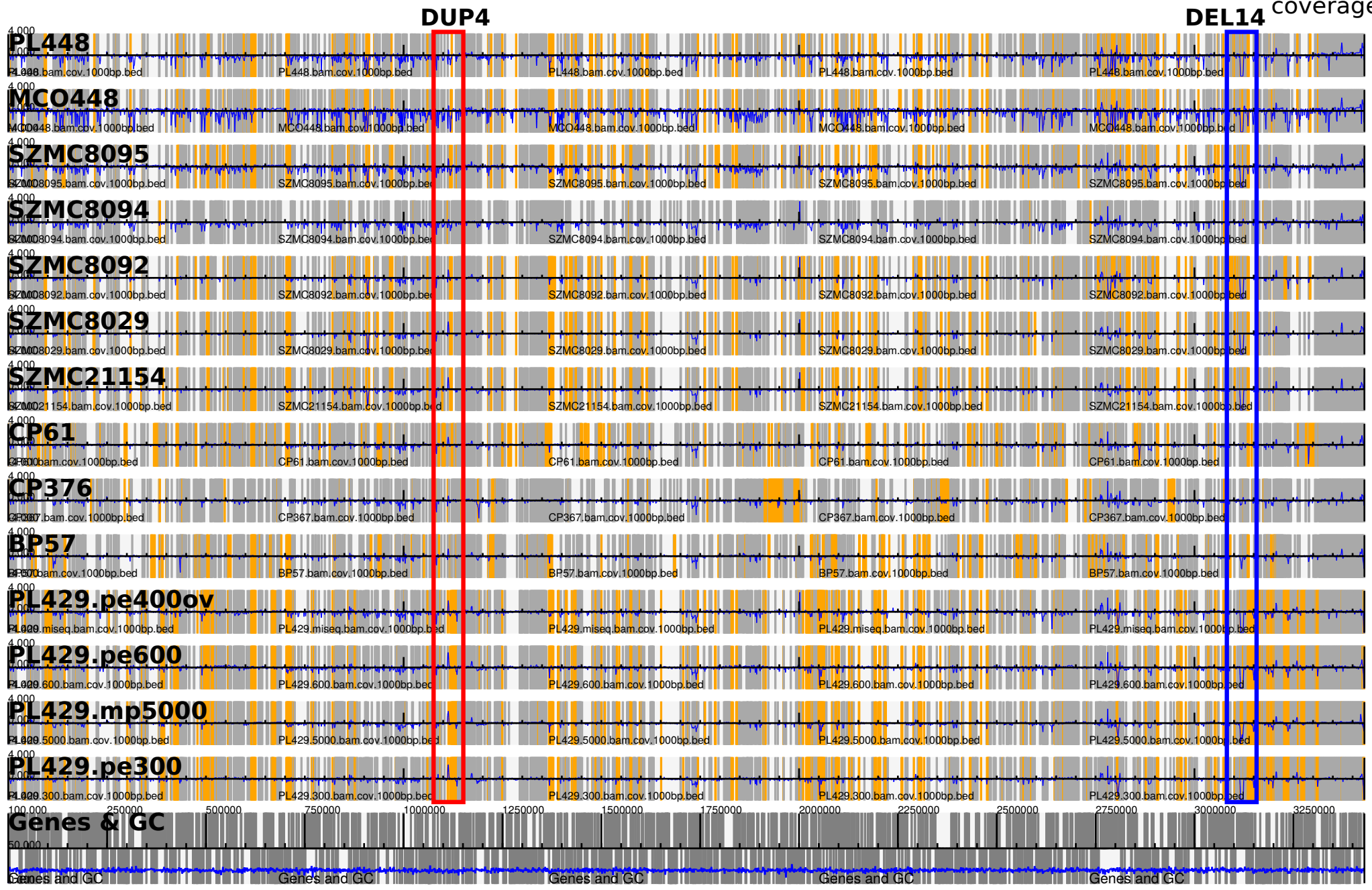
C. metapsilosis genome is a mixture of heterozygous (light grey), haplotype B (dark grey) and haplotype A (orange) regions. We suspect all analysed strains originate from single hybridisation event, as most of LOH events are shared by all strains.

Examples of large LOH, duplications and deletions have been annotated ie. rDNA cluster (scaffold5), scaffold5 triploidy in PL448, partial scaffold2 triploidy in SZMC21154 and PL448, and complete LOH in scaffold6 in PL448. For the sake of simplicity, only some selected duplications and deletions among those longer than 5Kb are represented (annotated as such in Supplementary table S4).

rDNA cluster is found on the edge of the largest LOH (over 350kb, scaffold5). Interestingly, we have also found rDNA cluster in long (200kb) LOH track in *C. orthopsilosis* MCO448 ([PMID: 24747362](https://pubmed.ncbi.nlm.nih.gov/24747362/)).

scaffold1

LOH hapA —
LOH hapB —
coverage —



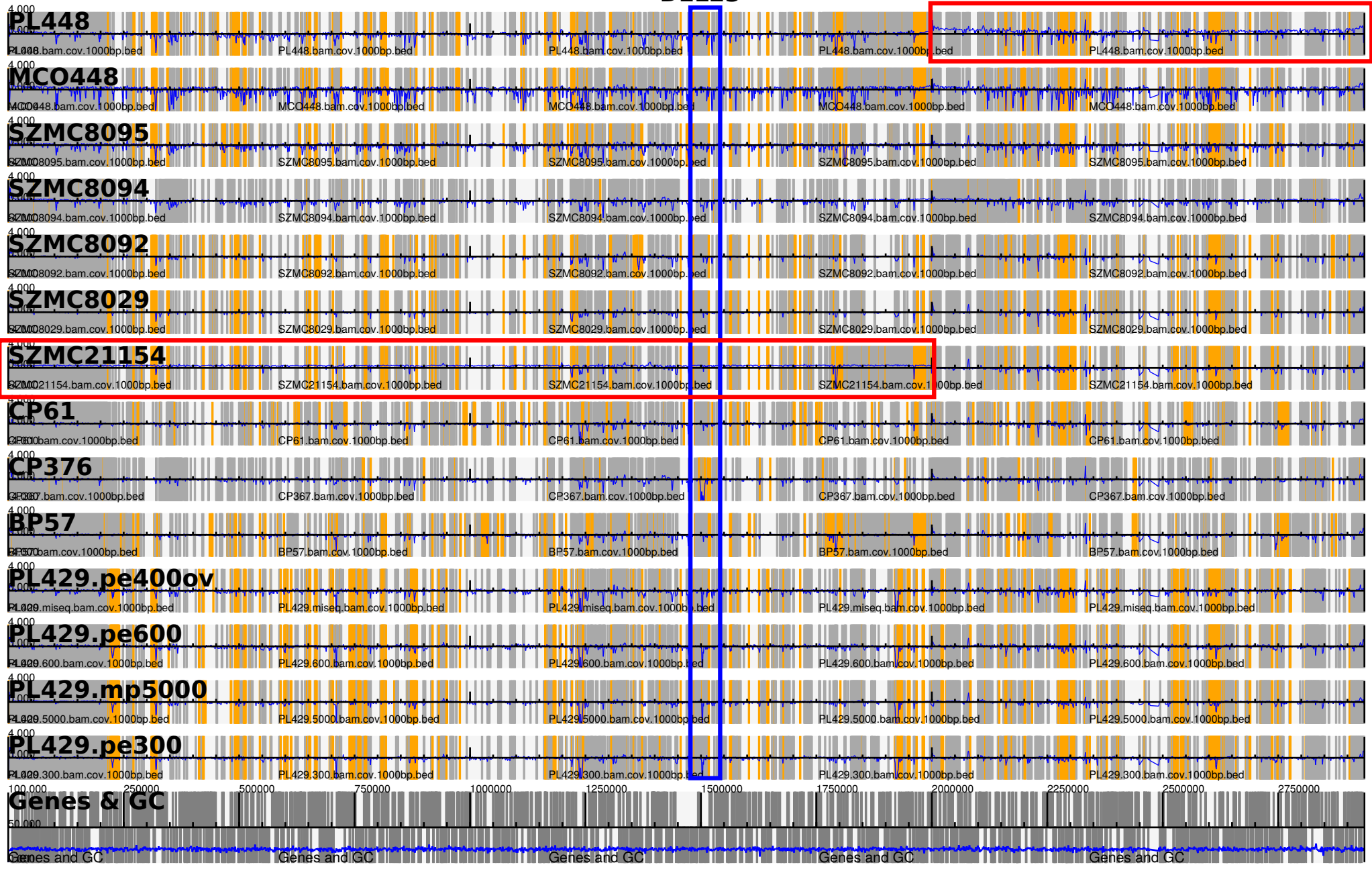
scaffold2

LOH hapA —
LOH hapB —
coverage —

DEL23

DUP

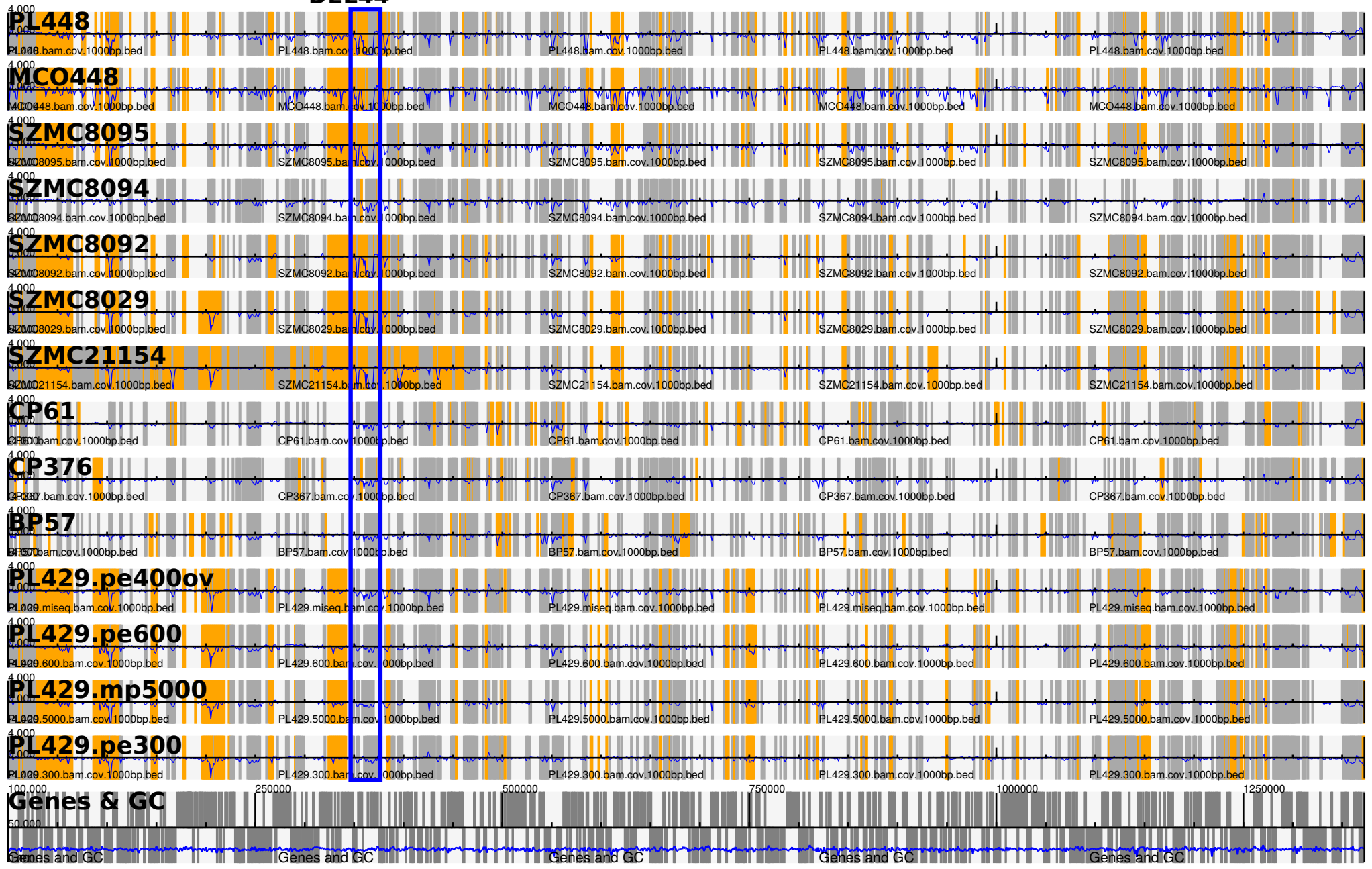
DUP



scaffold3

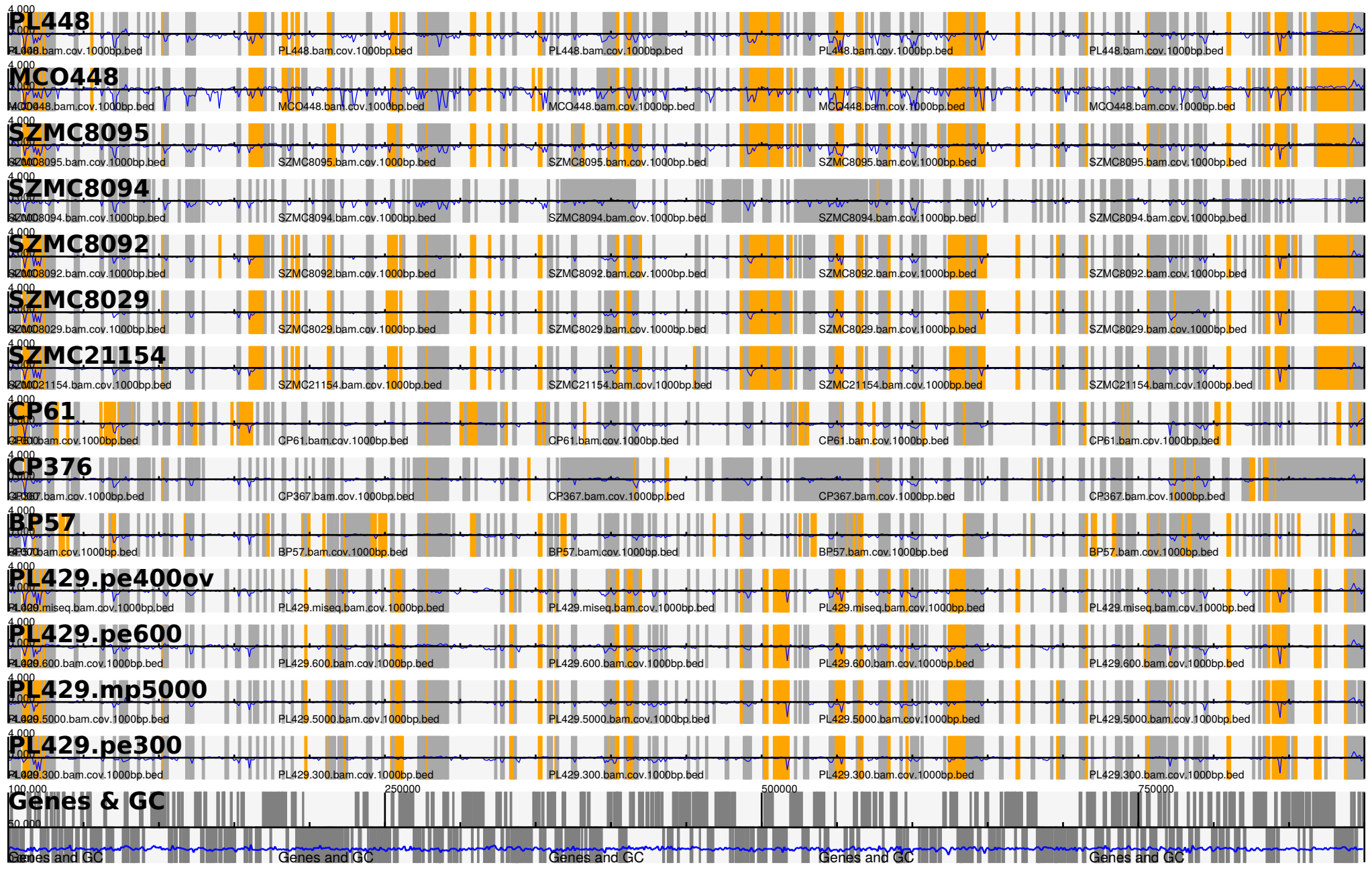
LOH hapA —
LOH hapB —
coverage —

DEL44



scaffold4

LOH hapA —
LOH hapB —
coverage —



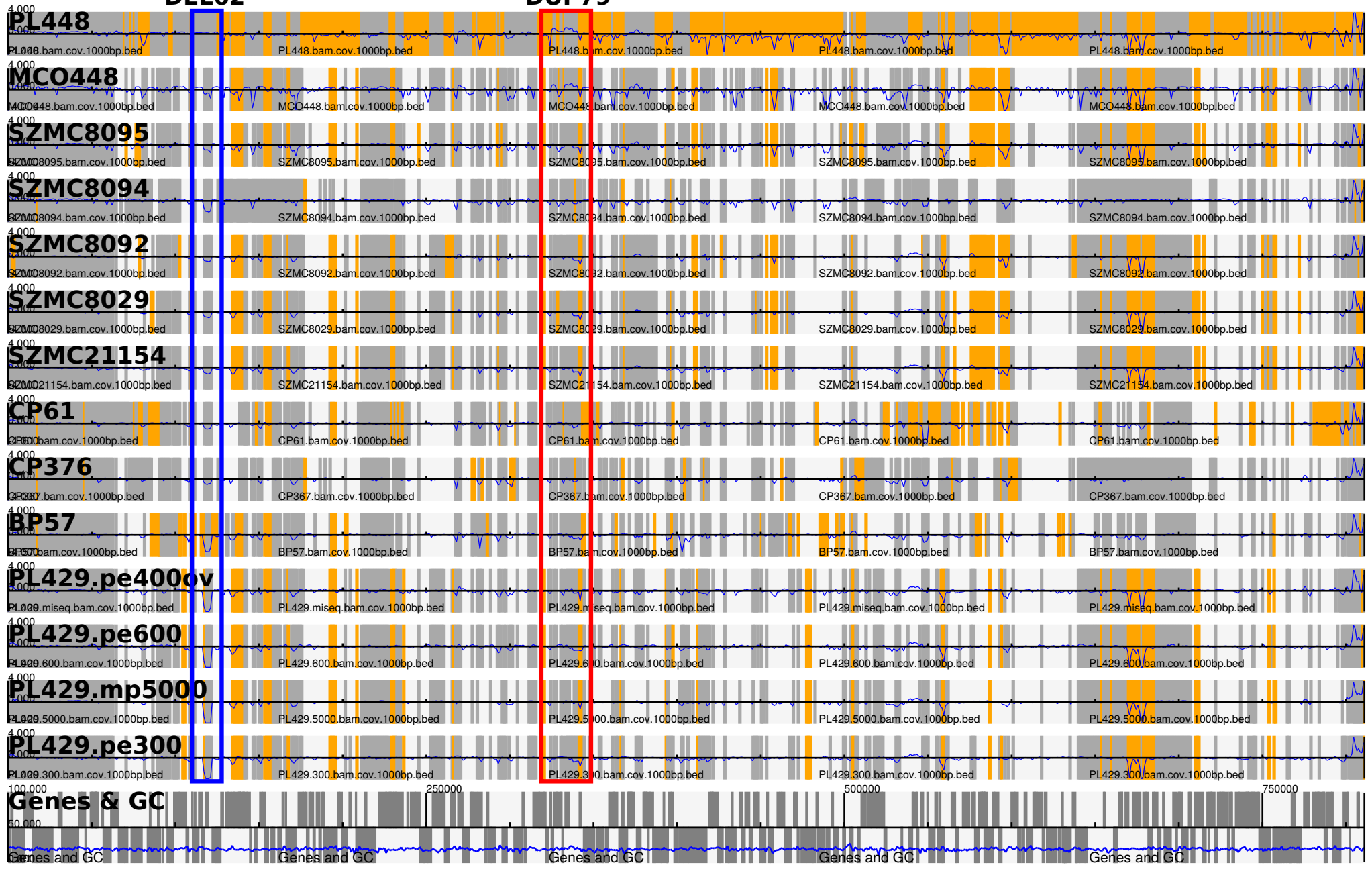
scaffold6

LOH hapA —
LOH hapB —
coverage —

DEL62

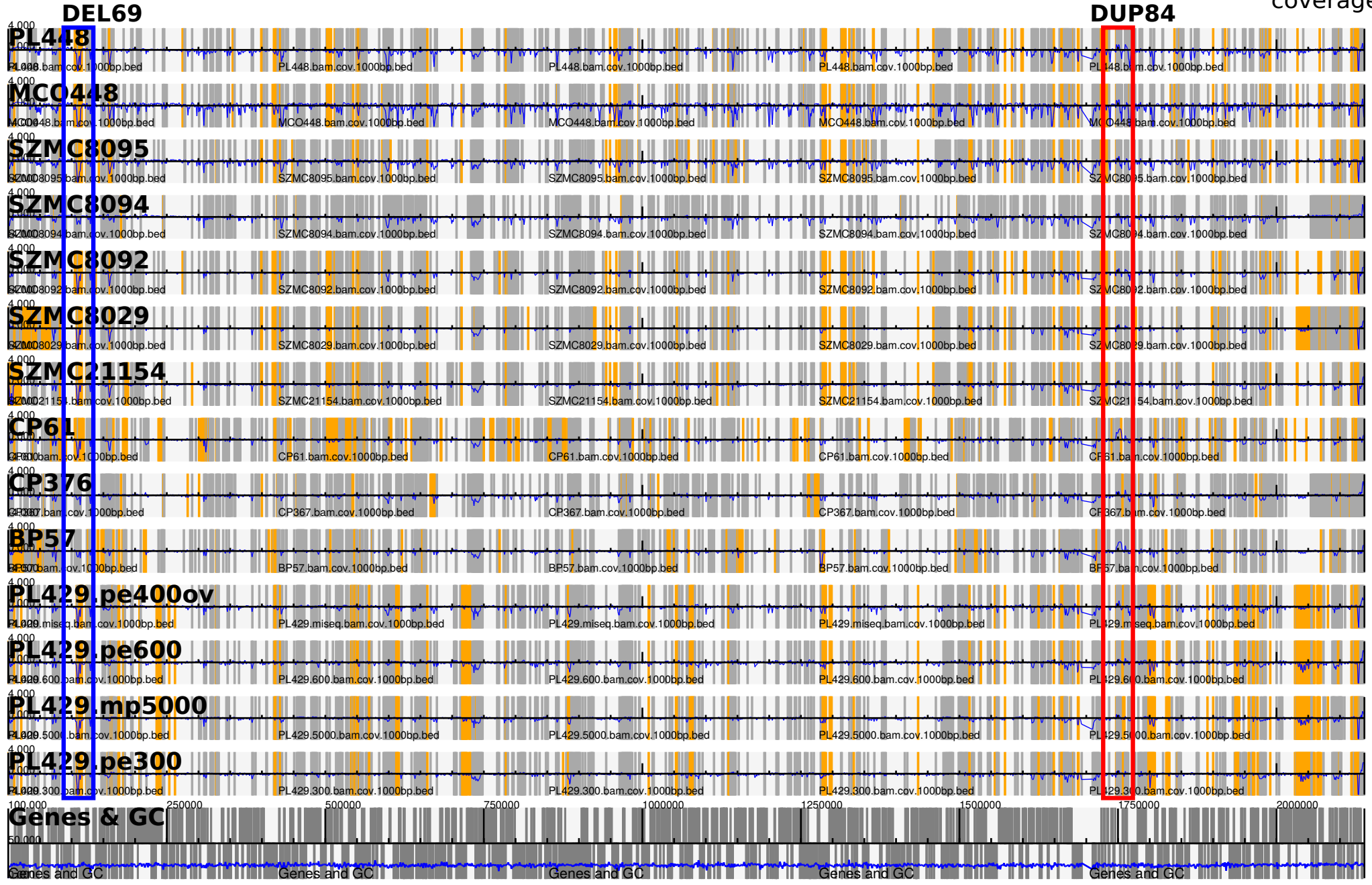
DUP79

LOH



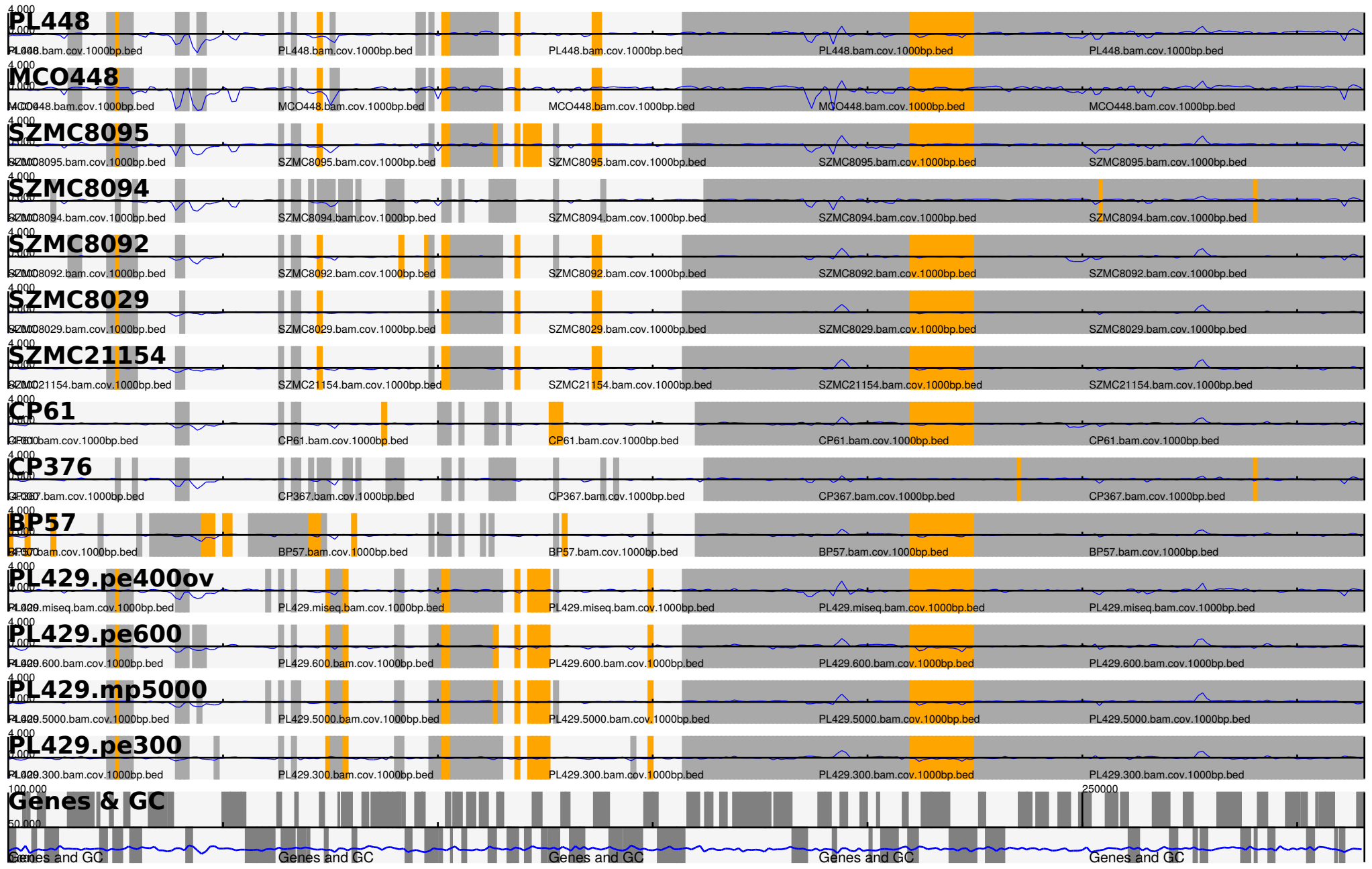
scaffold7

LOH hapA —
LOH hapB —
coverage —



scaffold8

LOH hapA —
LOH hapB —
coverage —



scaffold9

LOH hapA —
LOH hapB —
coverage —

