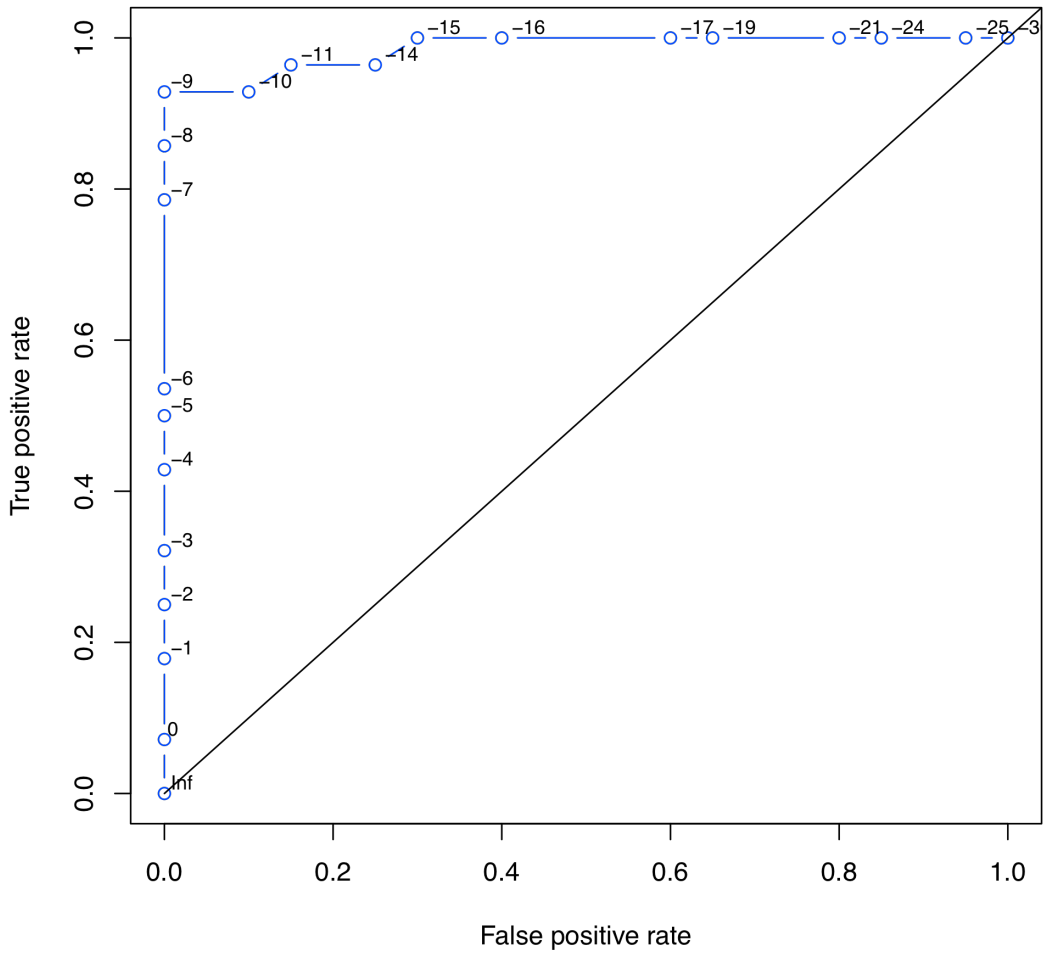
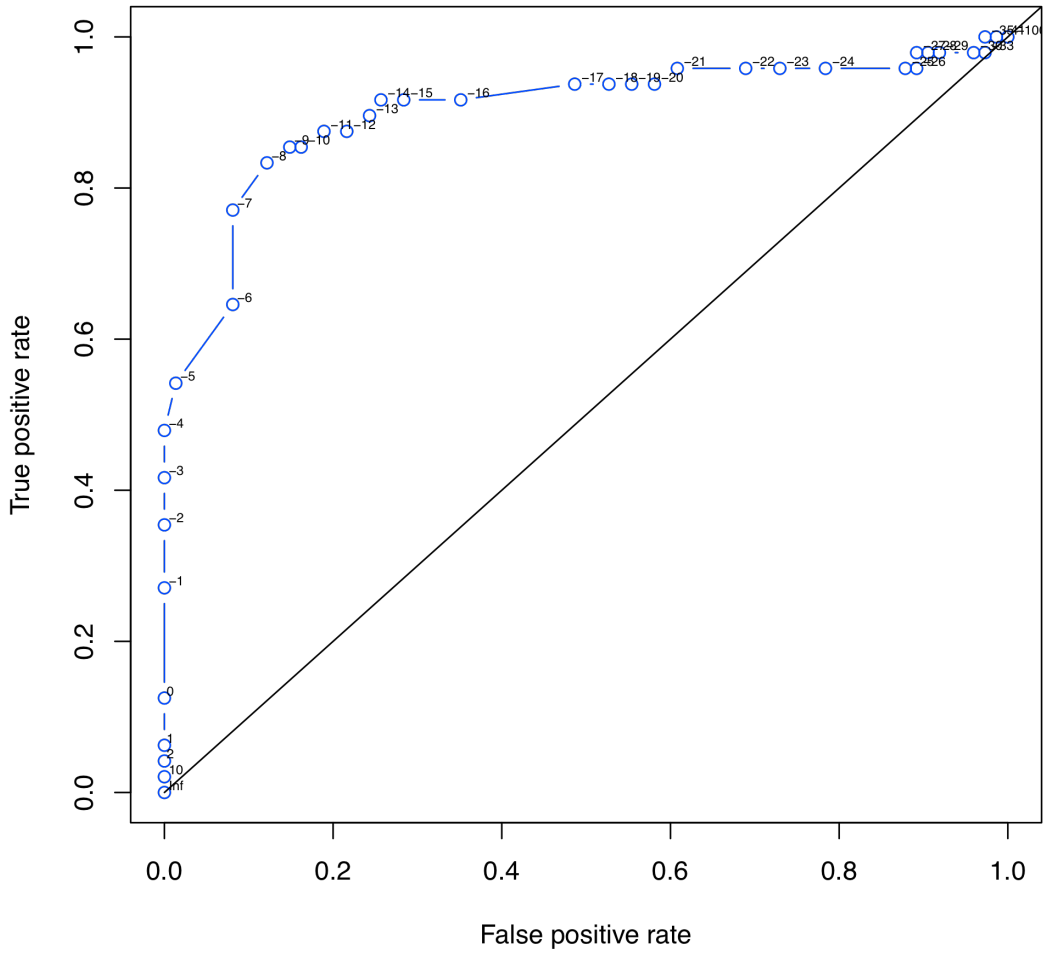
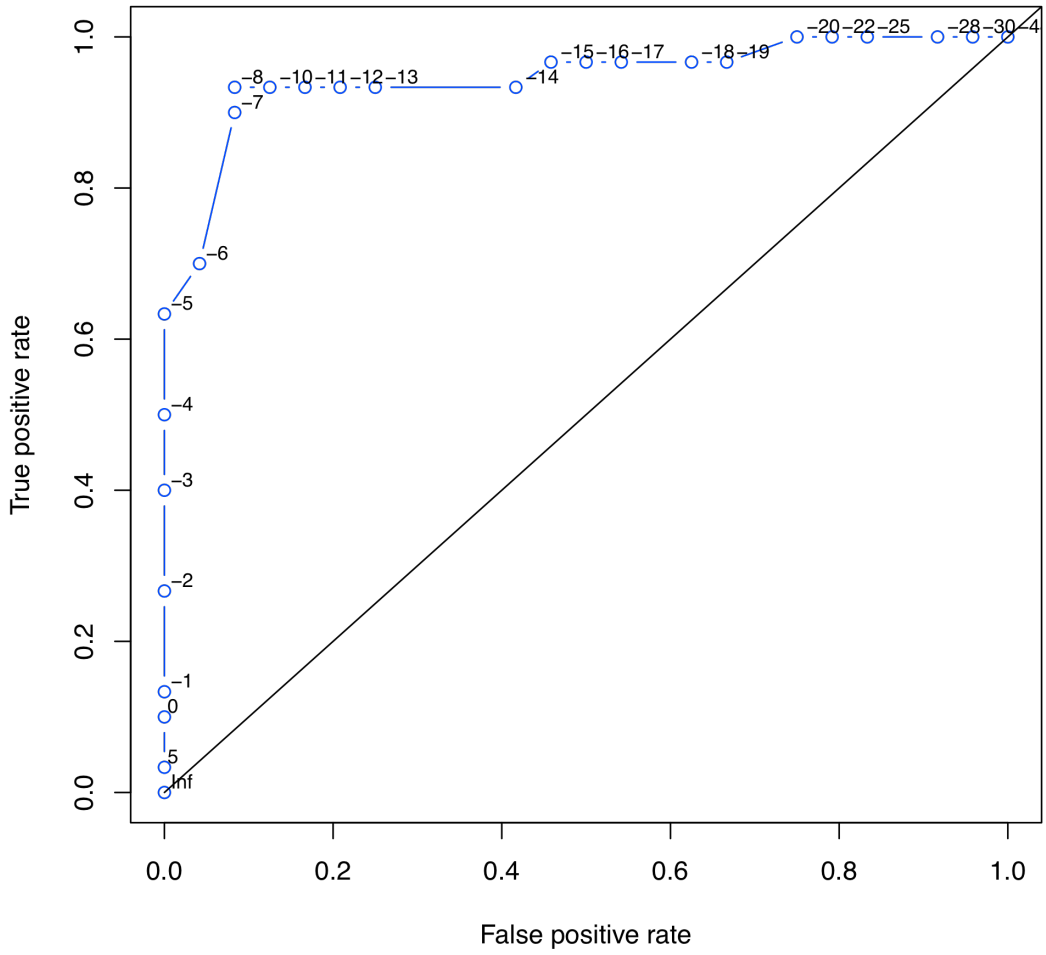
This document contains Supplementary Figures 1-11 for the Turajlic et al. manuscript "**Whole genome sequencing of a matched primary and metatstatic acral melanoma**" submitted as a Research Article to Genome Research.



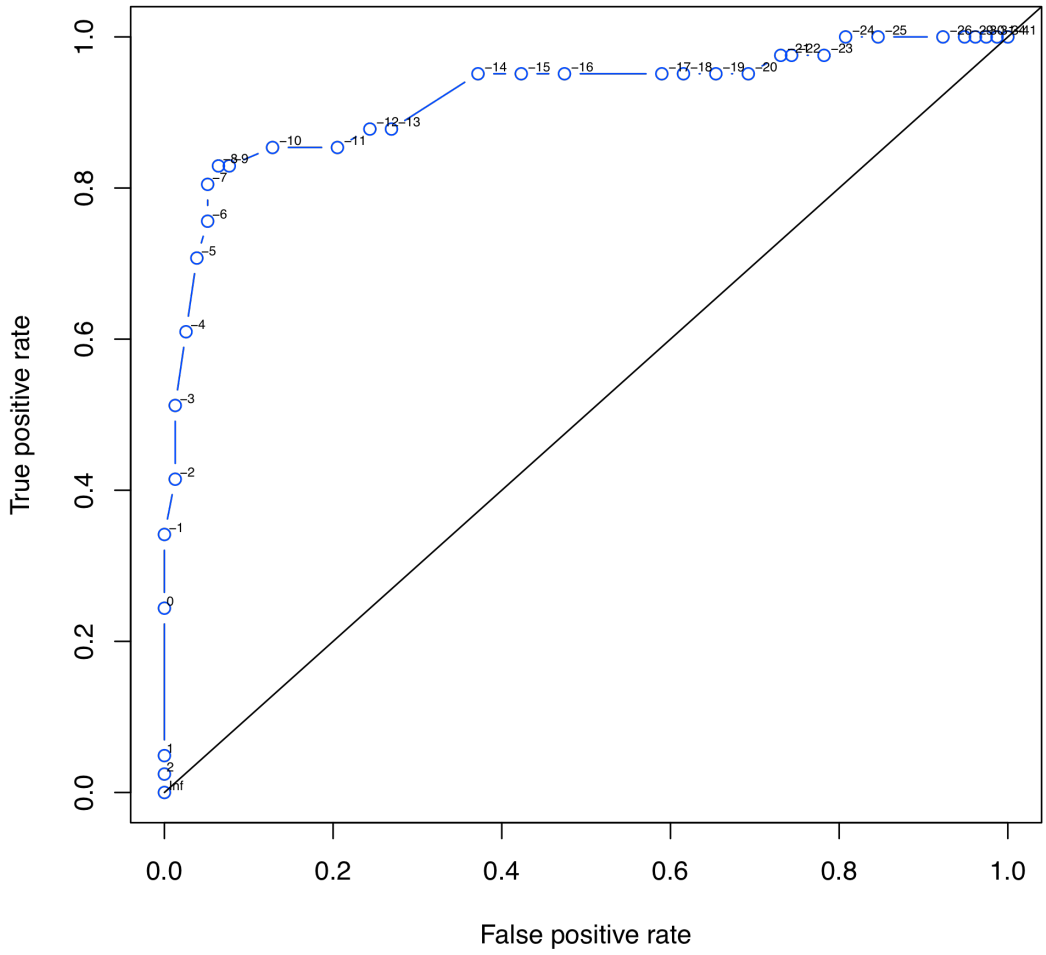
Supplementary Figure 1a. Receiver Operating Characteristic curve of random candidate somatic SNVs in primary tumour assessed by Sanger sequencing.



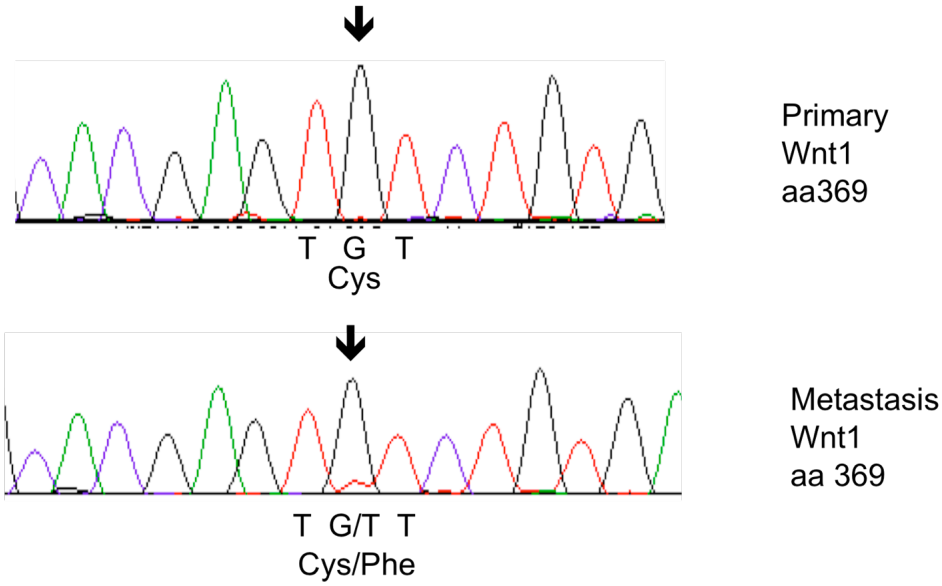
Supplementary Figure 1b. Receiver Operating Characteristic curve of random candidate somatic SNVs in primary tumour assessed by exome sequencing.



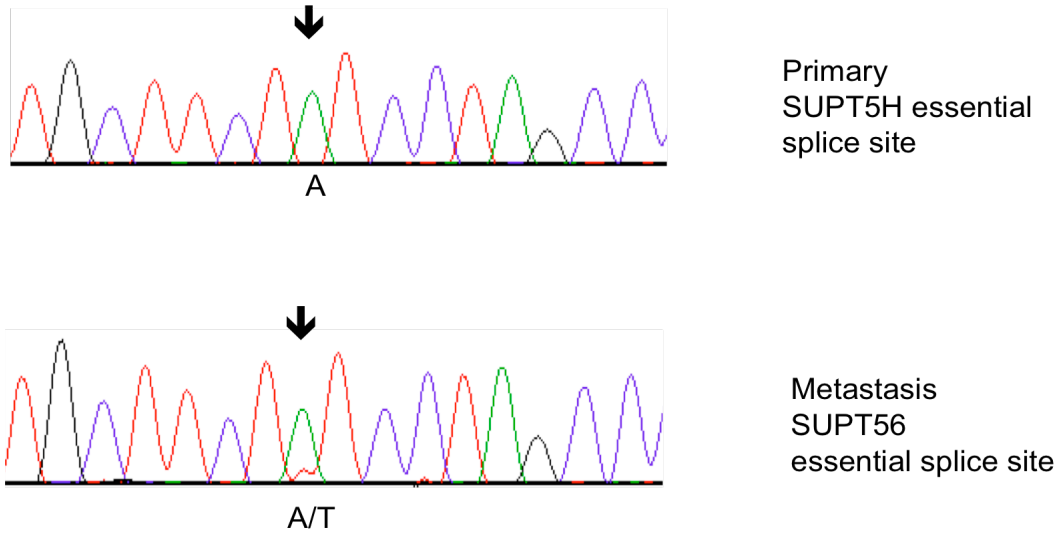
Supplementary Figure 2a. Receiver Operating Characteristic curve of random candidate somatic SNVs in metastasized tumour assessed by Sanger sequencing.



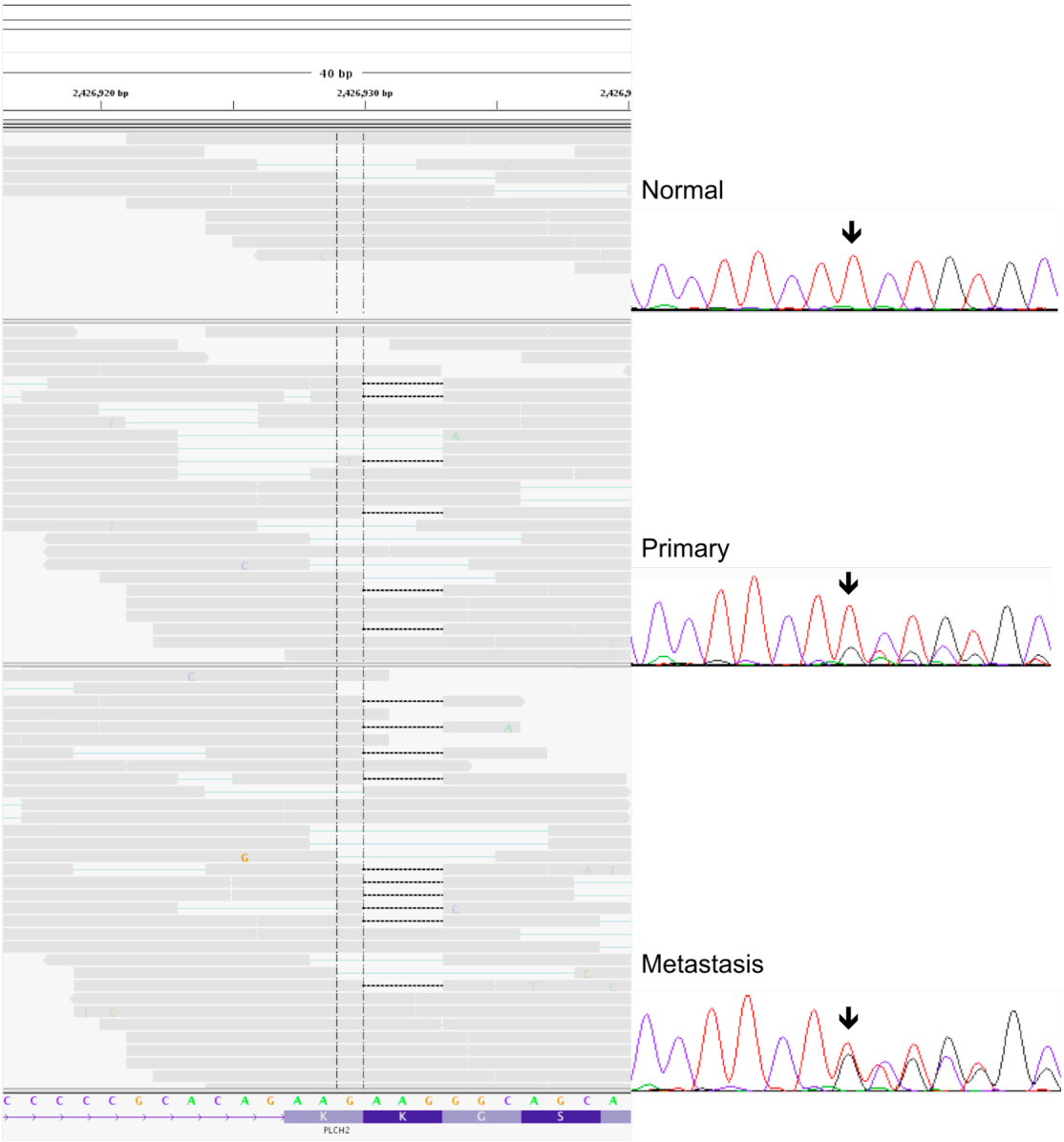
Supplementary Figure 2b. Receiver Operating Characteristic curve of random candidate somatic SNVs in metastasized tumour assessed by exome sequencing.



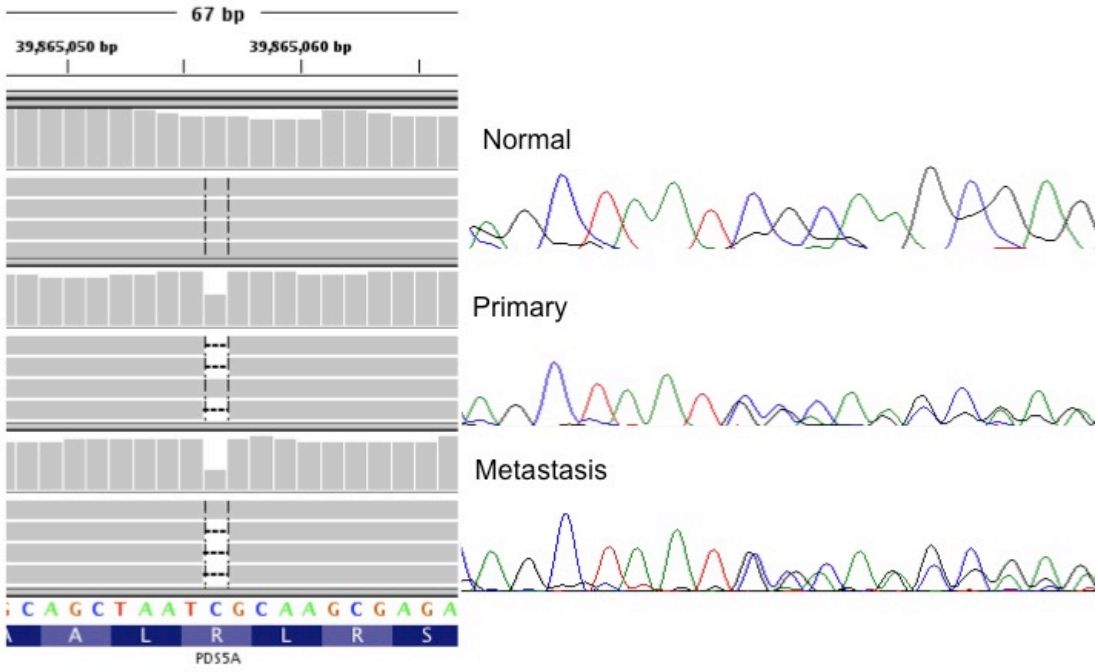
Supplementary Figure 3a. Sanger sequencing traces representing the non-synonymous coding mutation (C369F) detected in the metastasis but not in the primary.



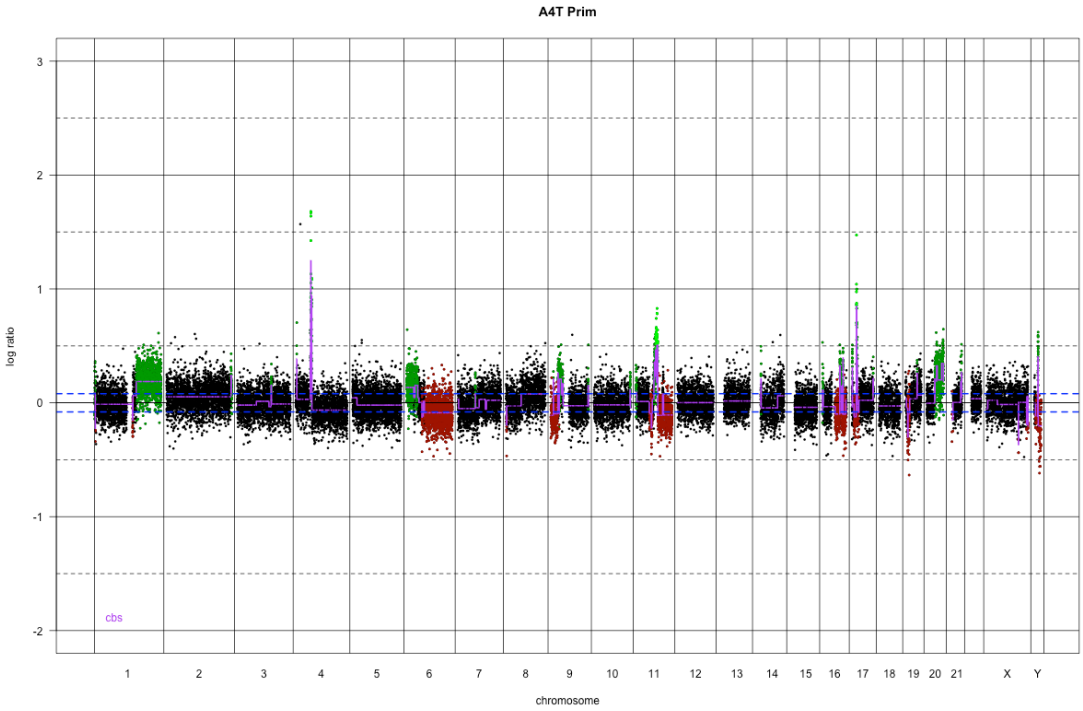
Supplementary Figure 3b. Sanger sequencing traces representing the essential splice site variant in *SUPT5H* present in the metastasis bit not in the primary.



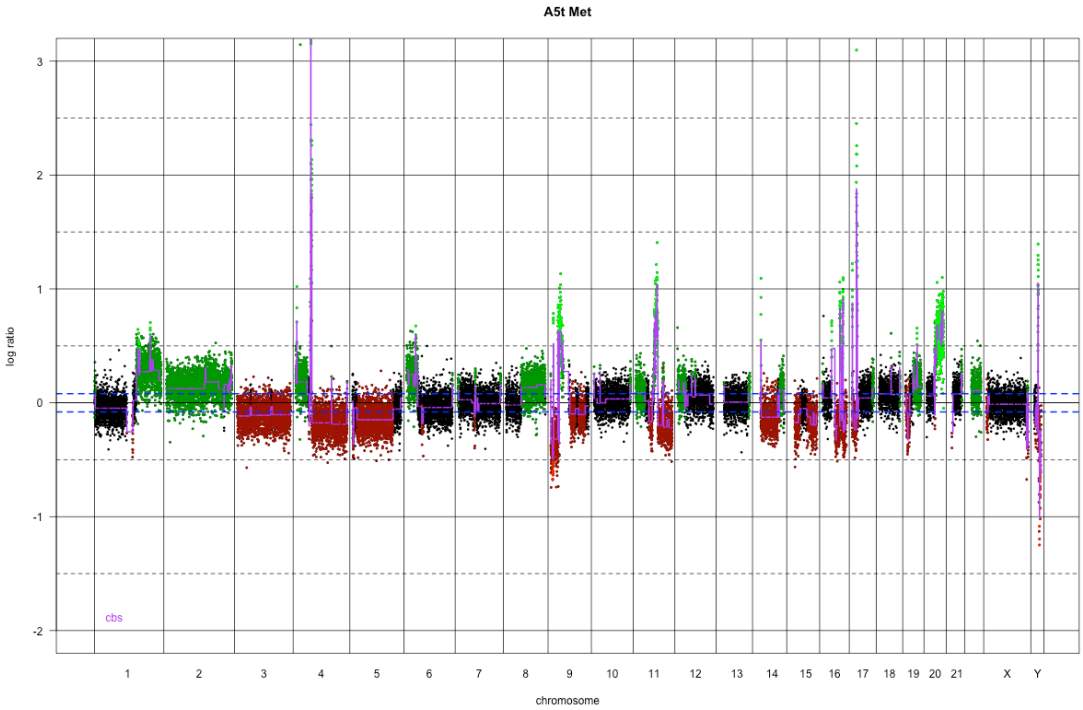
Supplementary figure 4a: IGV browser representation of the reads mapping to chr1 2426929. 3 bp deletion in *PLCH2* is validated as a somatic variant by Sanger sequencing. The arrow indicates the deletion locus K585_586del.



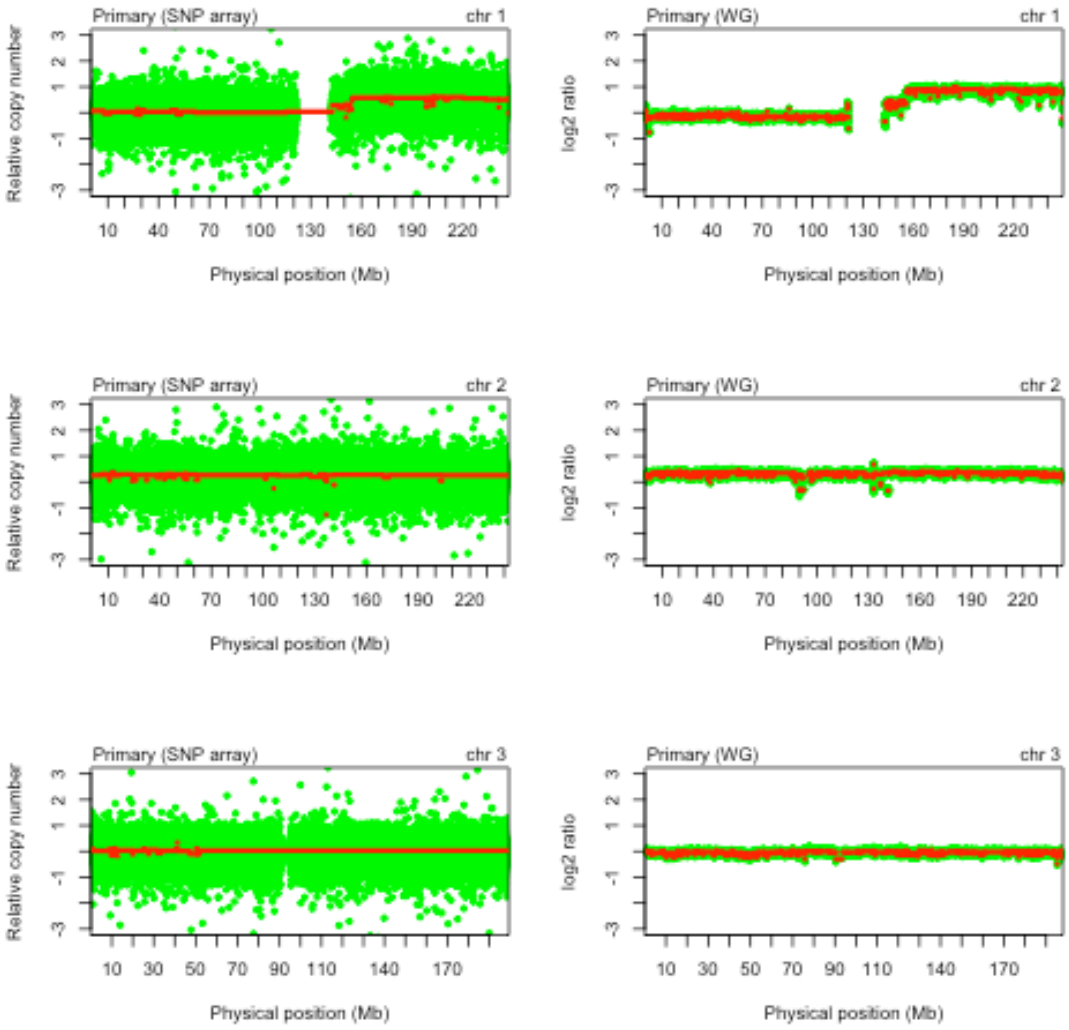
Supplementary figure 4b: IGV browser representation of the reads mapping around the 1 bp deletion in *PDS5A* is validated as a somatic variant by Sanger sequencing.



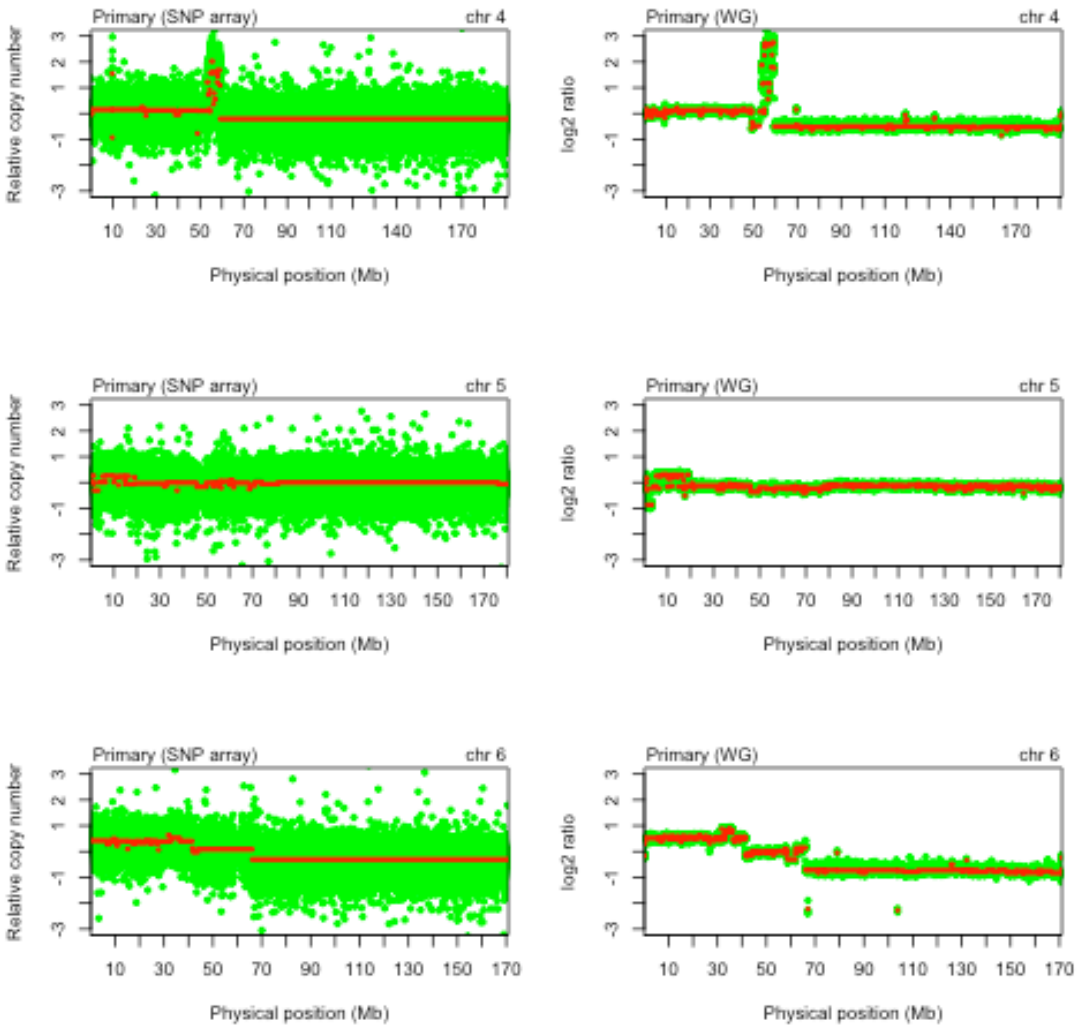
Supplementary Figure 5a. Array CGH of primary tumour sample.



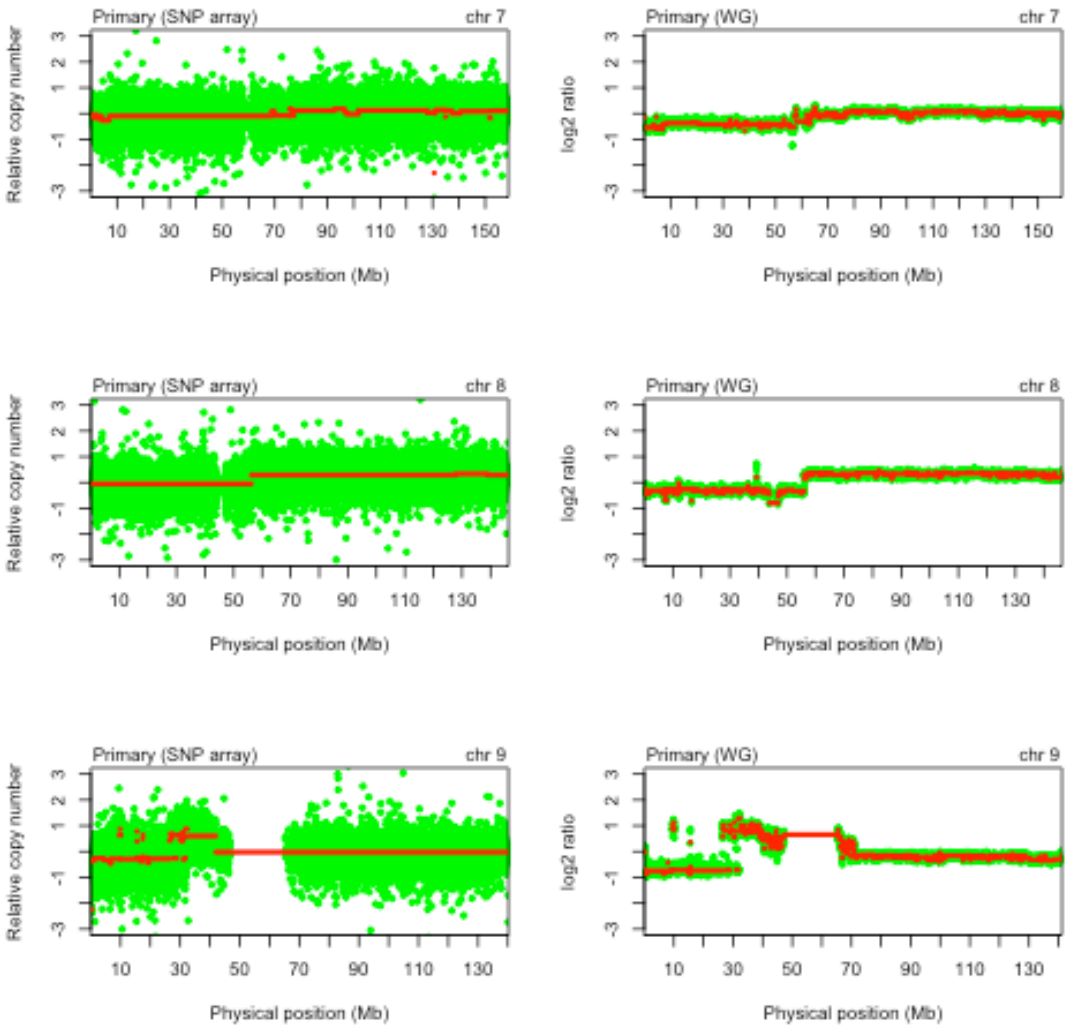
Supplementary Figure 5b. Array CGH of metastatic tumour sample.



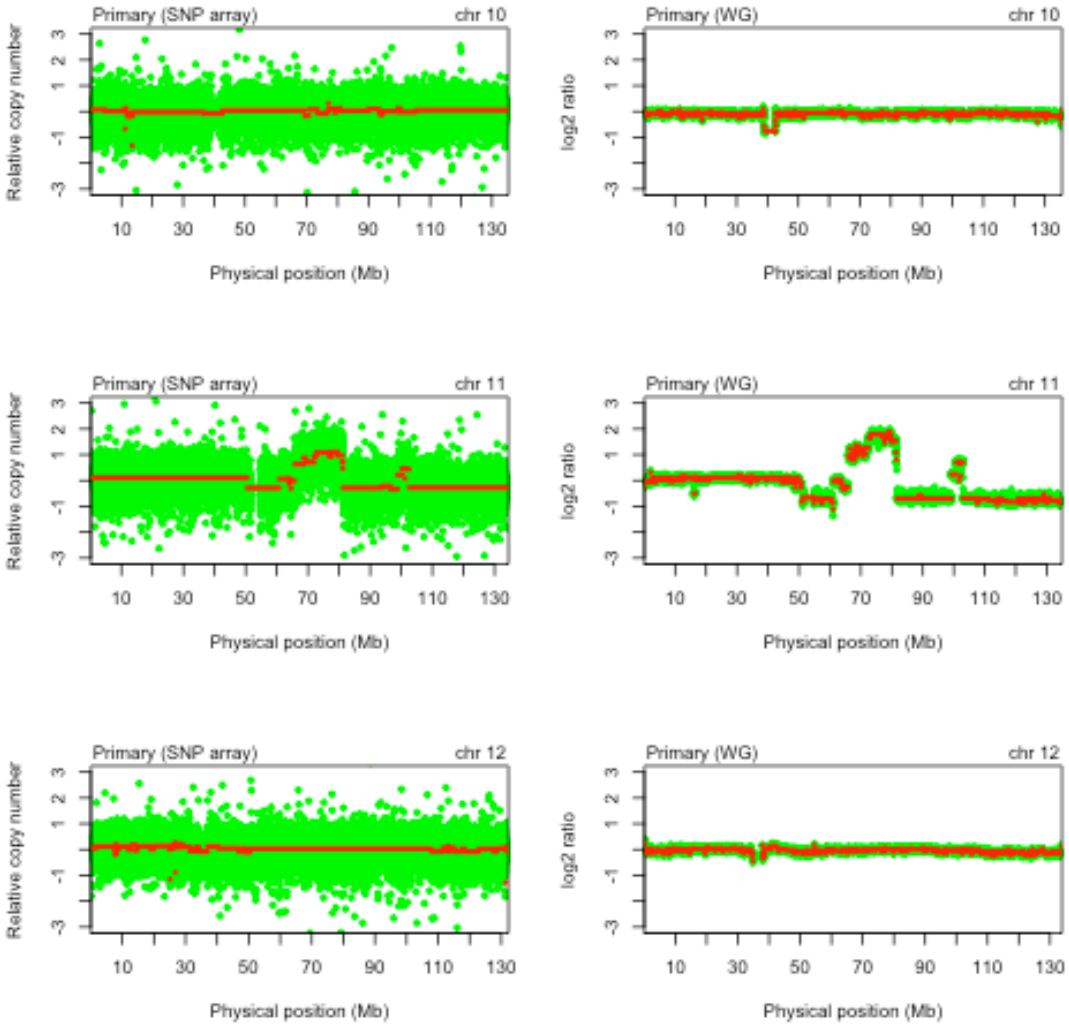
Supplementary Figure 6a. Somatic copy number alteration (CNA) in the primary tumour detected by genome-wide SNP arrays (left column) and whole-genome (WG) sequencing normalized read-depth per 10 kb (right column) for chromosomes 1-3.



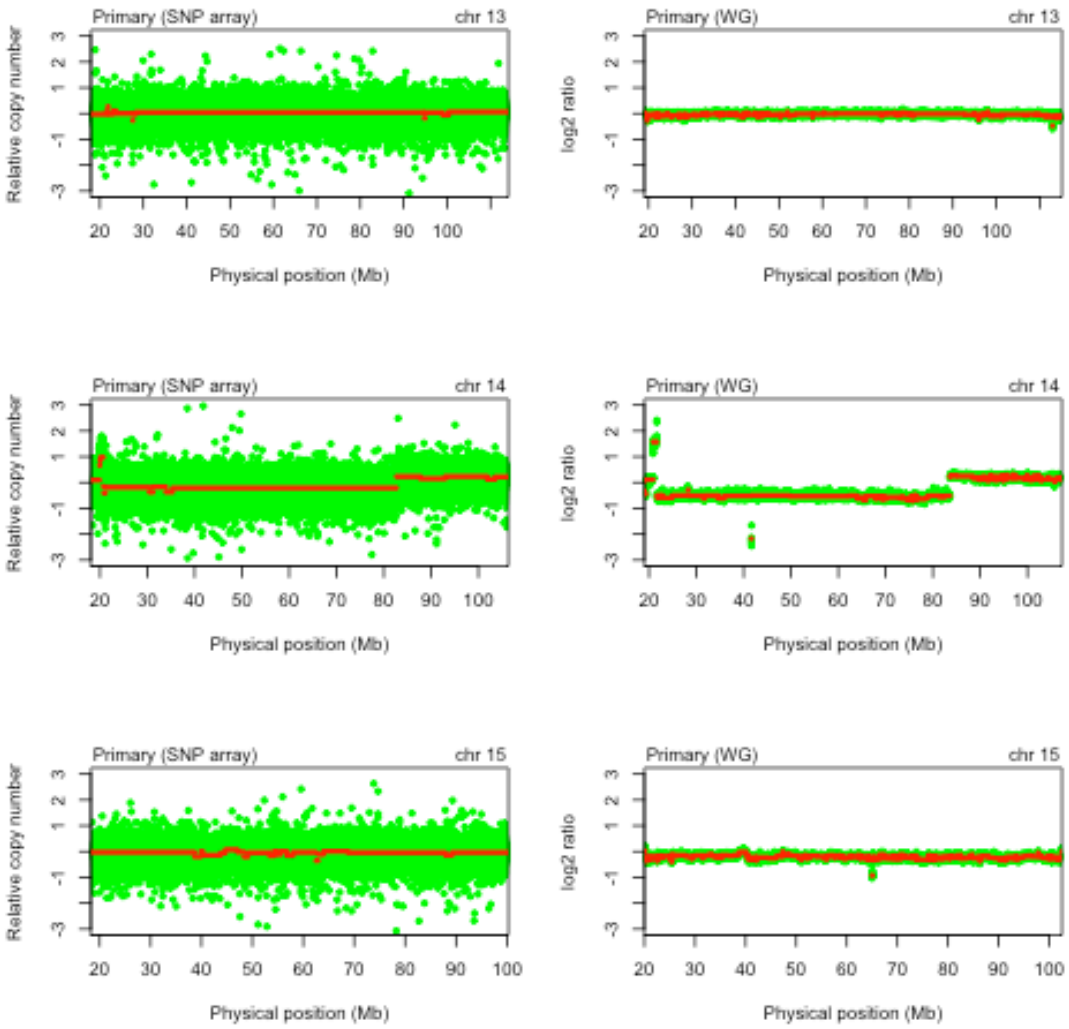
Supplementary Figure 6b. Somatic copy number alteration (CNA) in the primary tumour detected by genome-wide SNP arrays (left column) and whole-genome (WG) sequencing normalized read-depth per 10 kb (right column) for chromosomes 4-6.



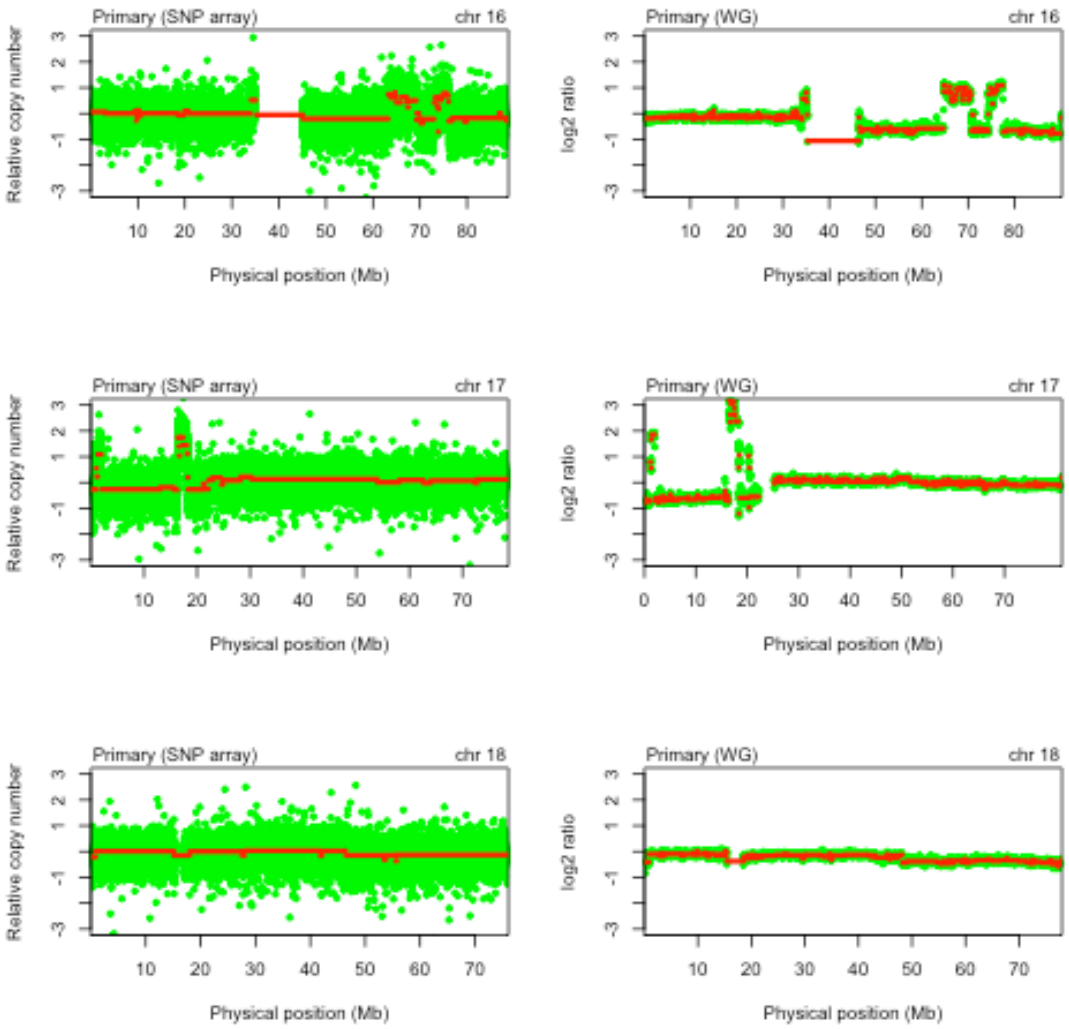
Supplementary Figure 6c. Somatic copy number alteration (CNA) in the primary tumour detected by genome-wide SNP arrays (left column) and whole-genome (WG) sequencing normalized read-depth per 10 kb (right column) for chromosomes 7-9.



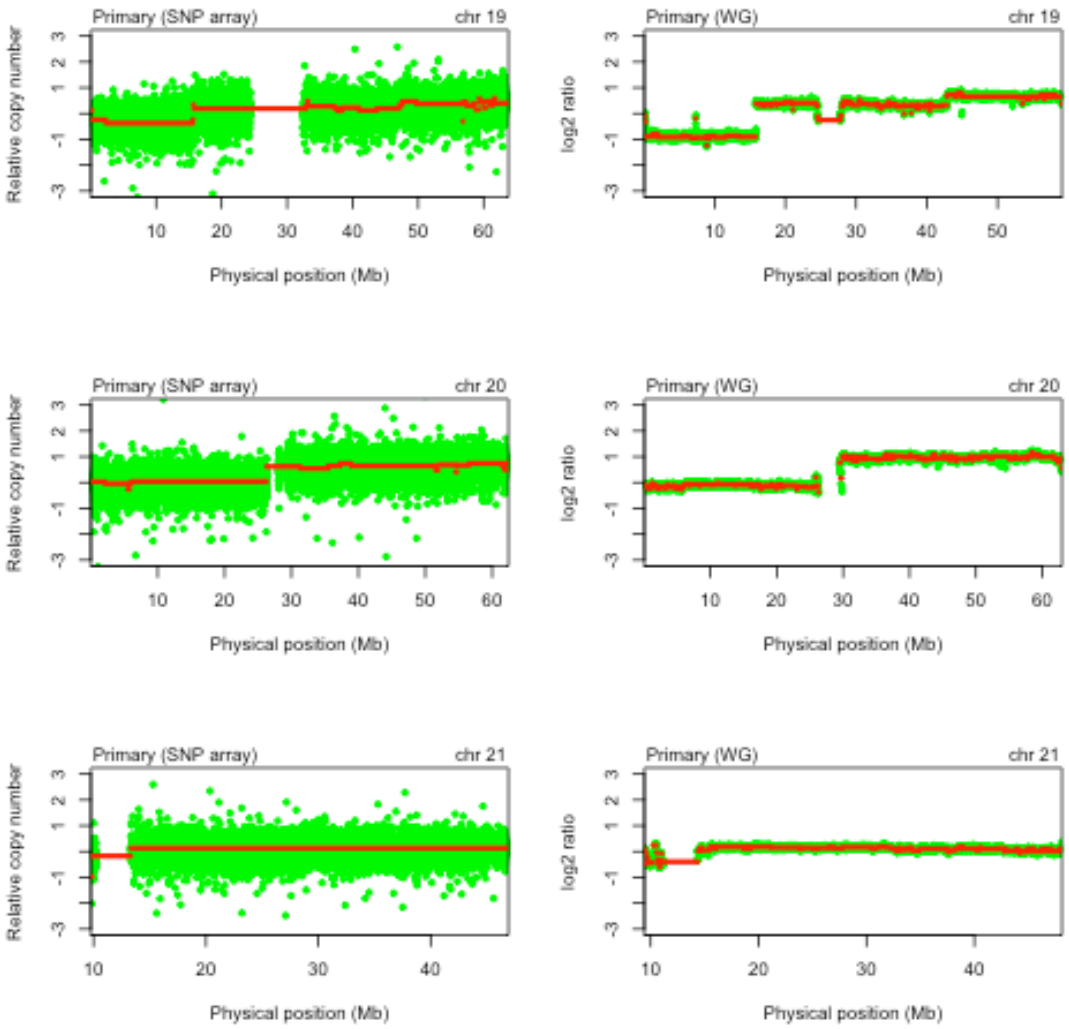
Supplementary Figure 6d. Somatic copy number alteration (CNA) in the primary tumour detected by genome-wide SNP arrays (left column) and whole-genome (WG) sequencing normalized read-depth per 10 kb (right column) for chromosomes 10-12.



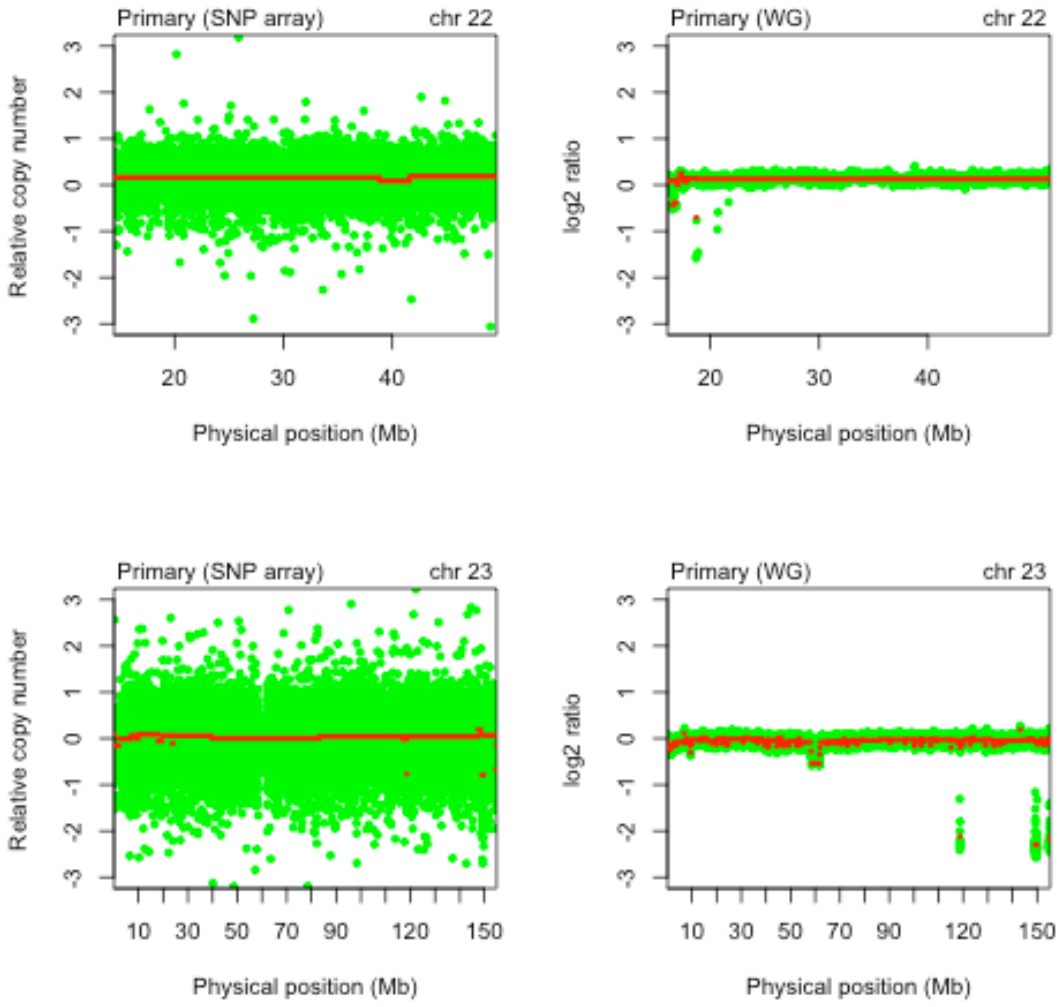
Supplementary Figure 6e. Somatic copy number alteration (CNA) in the primary tumour detected by genome-wide SNP arrays (left column) and whole-genome (WG) sequencing normalized read-depth per 10 kb (right column) for chromosomes 13-15.



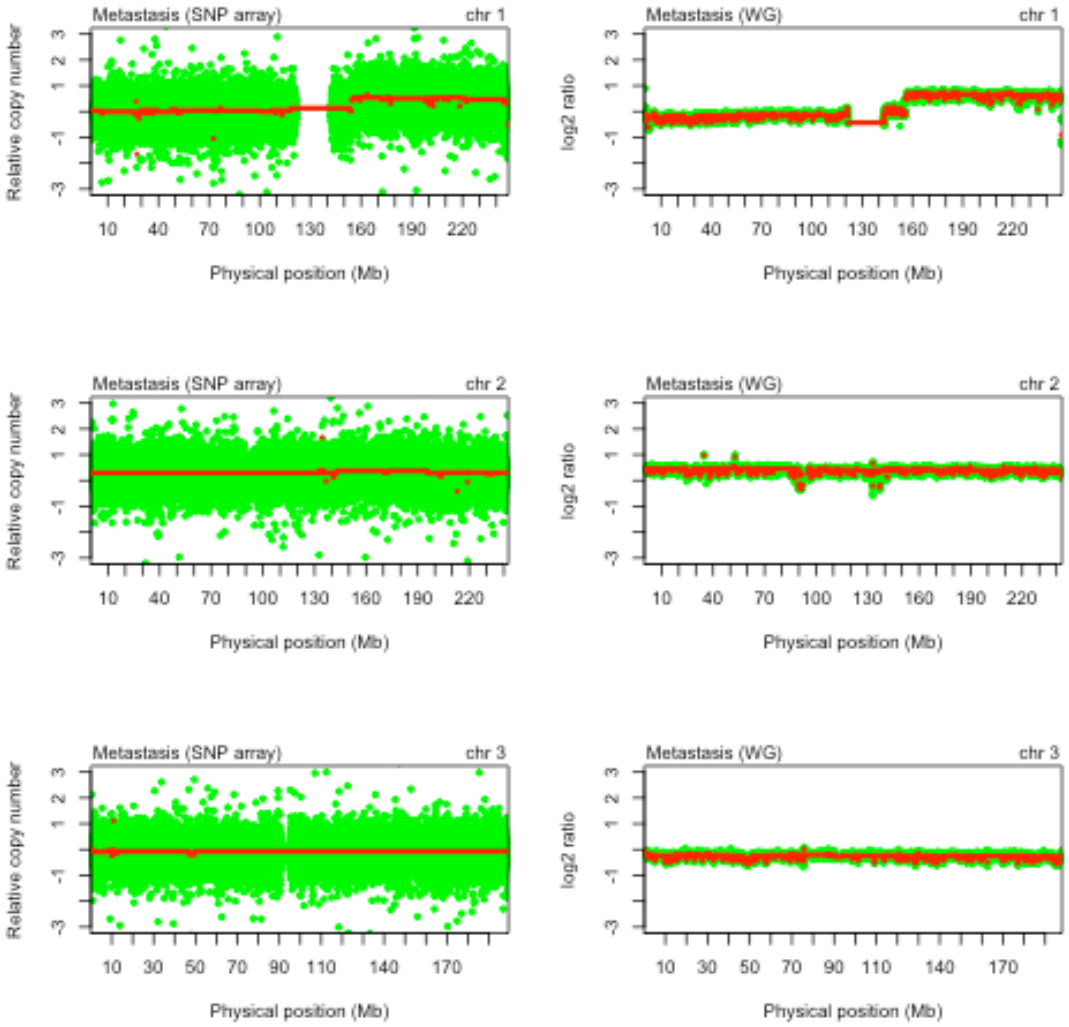
Supplementary Figure 6f. Somatic copy number alteration (CNA) in the primary tumour detected by genome-wide SNP arrays (left column) and whole-genome (WG) sequencing normalized read-depth per 10 kb (right column) for chromosomes 16-18.



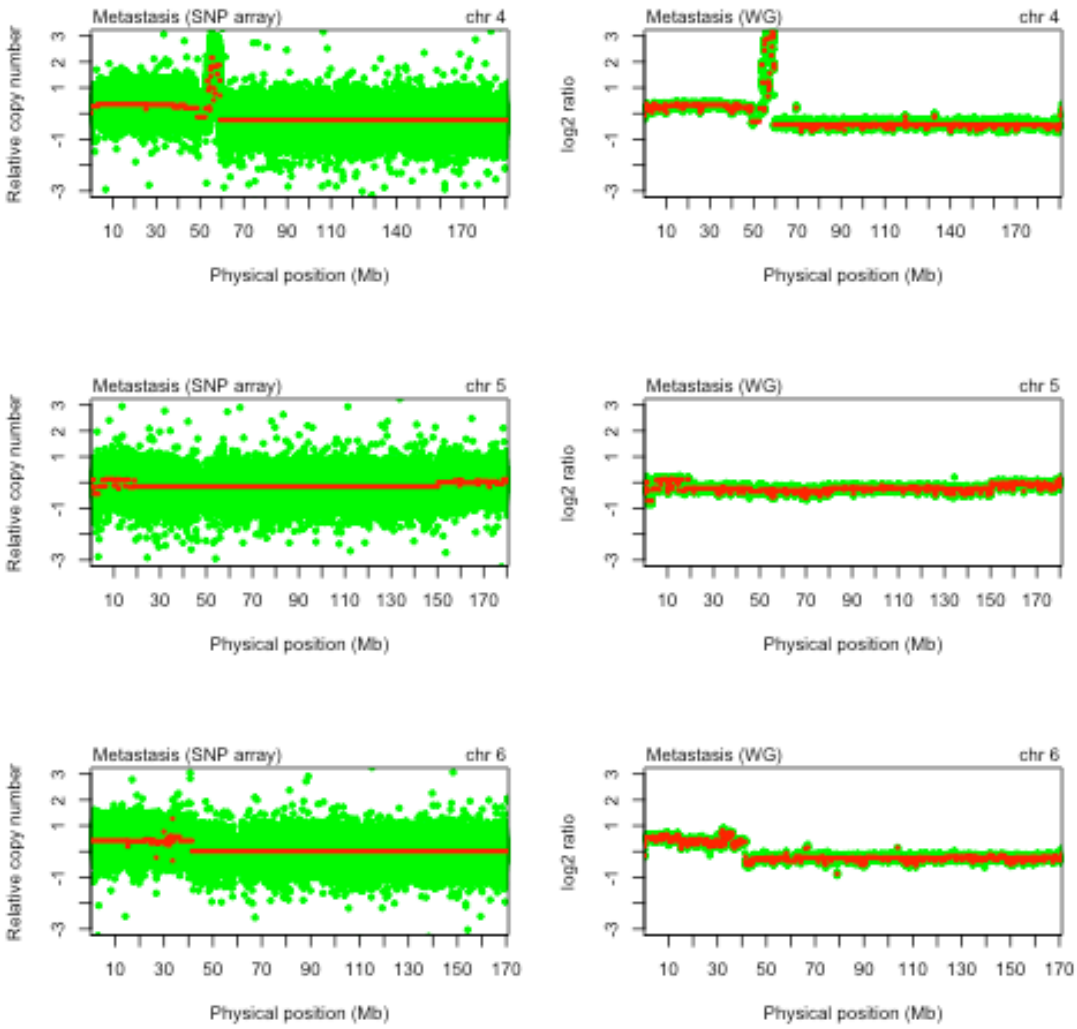
Supplementary Figure 6g. Somatic copy number alteration (CNA) in the primary tumour detected by genome-wide SNP arrays (left column) and whole-genome (WG) sequencing normalized read-depth per 10 kb (right column) for chromosomes 19-21.



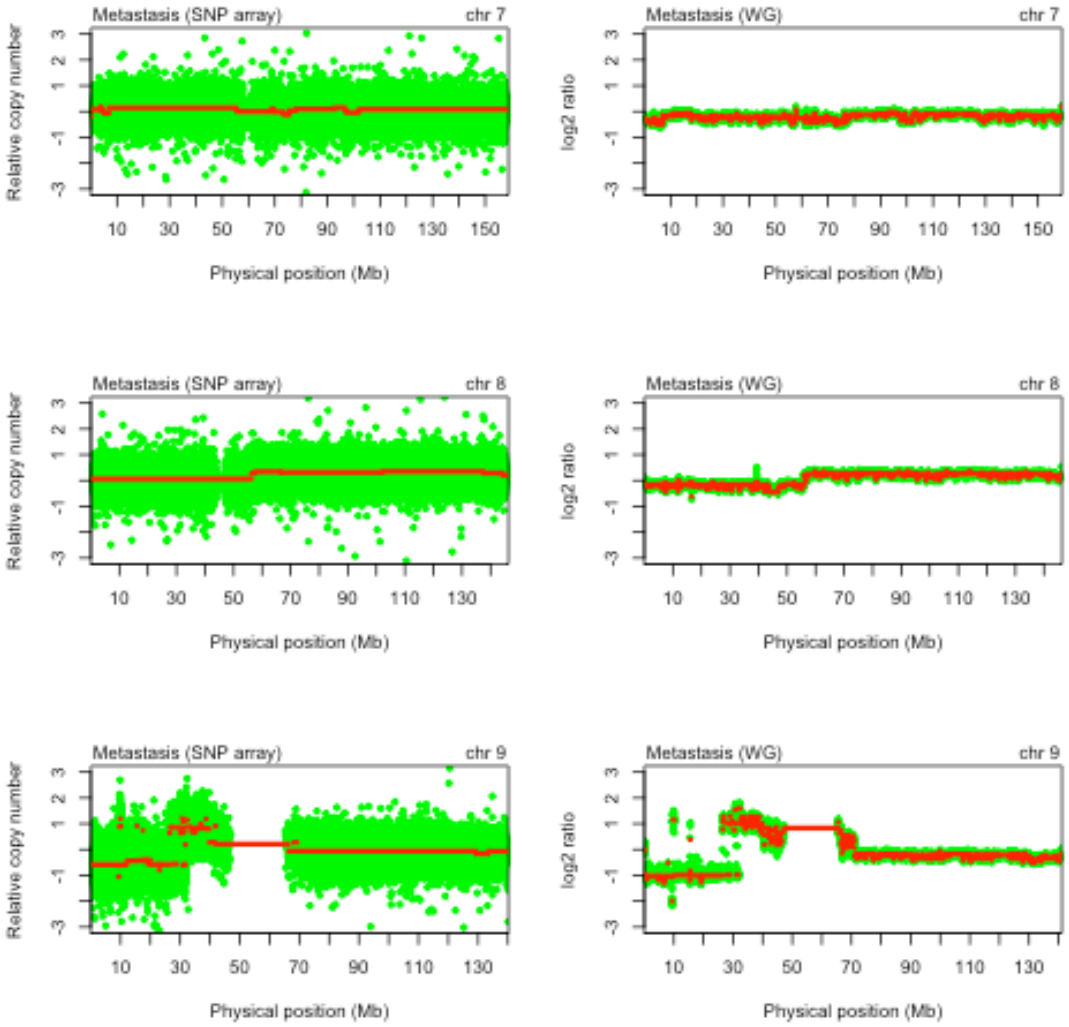
Supplementary Figure 6h. Somatic copy number alteration (CNA) in the primary tumour detected by genome-wide SNP arrays (left column) and whole-genome (WG) sequencing normalized read-depth per 10 kb (right column) for chromosomes 22-23.



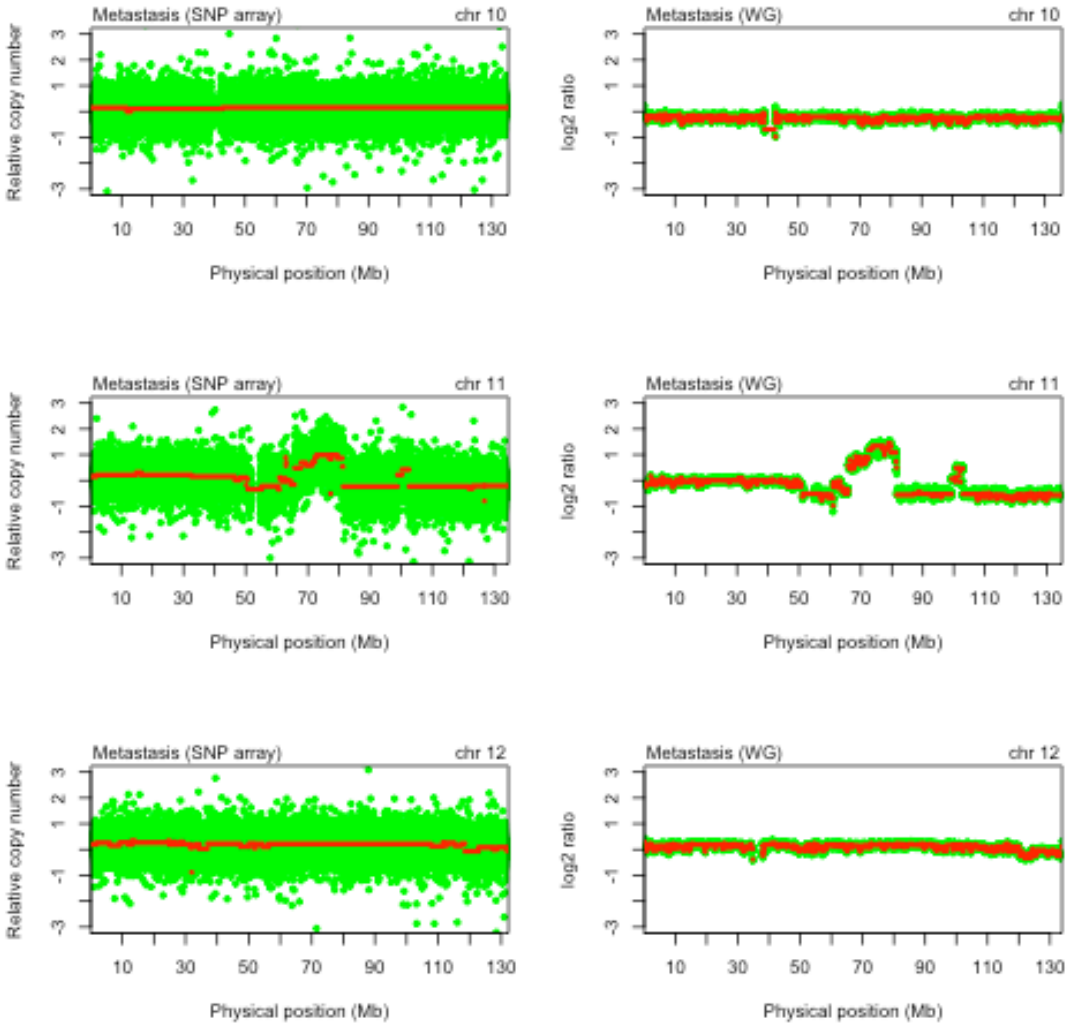
Supplementary Figure 7a. Somatic copy number alteration (CNA) in the metastatic tumour detected by genome-wide SNP arrays (left column) and whole-genome (WG) sequencing normalized read-depth per 10 kb (right column) for chromosomes 1-3.



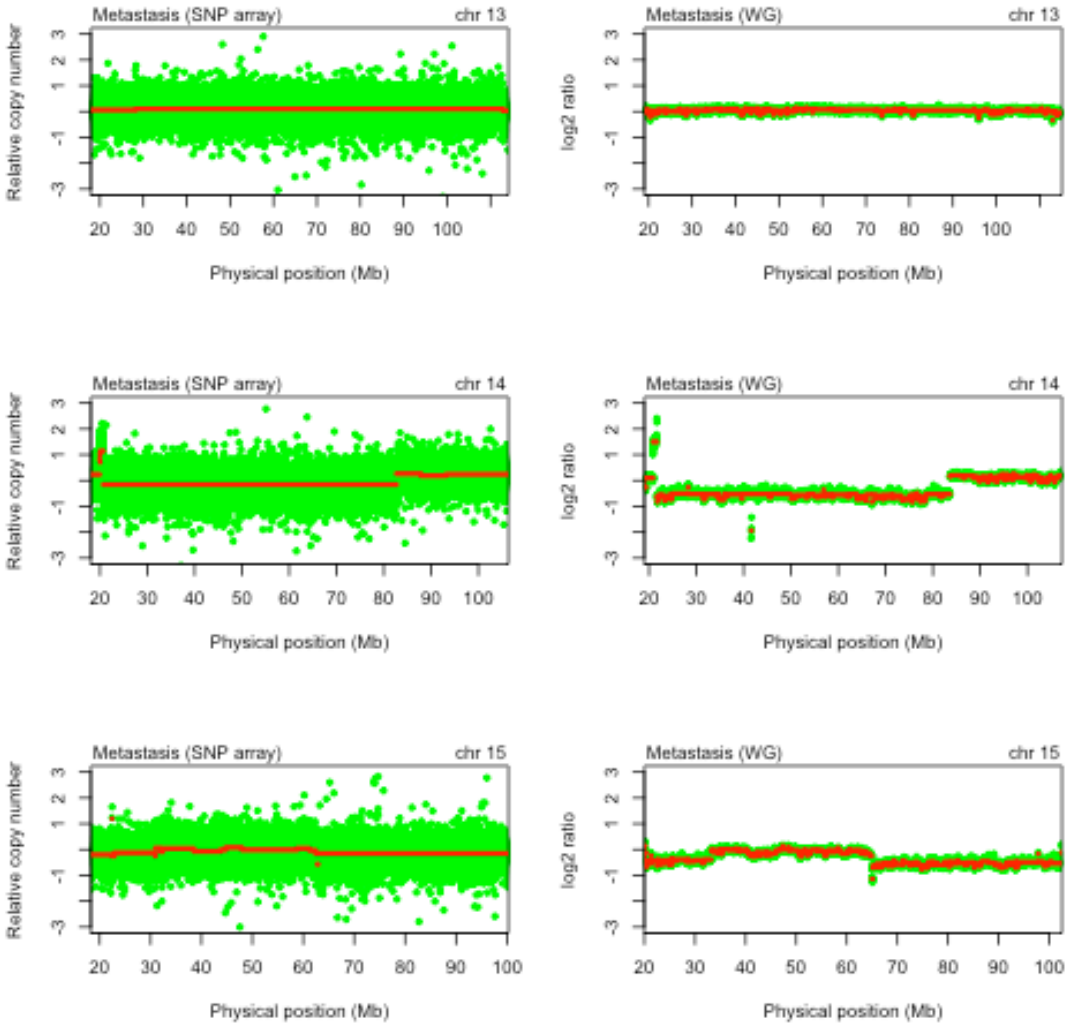
Supplementary Figure 7b. Somatic copy number alteration (CNA) in the metastatic tumour detected by genome-wide SNP arrays (left column) and whole-genome (WG) sequencing normalized read-depth per 10 kb (right column) for chromosomes 4-6.



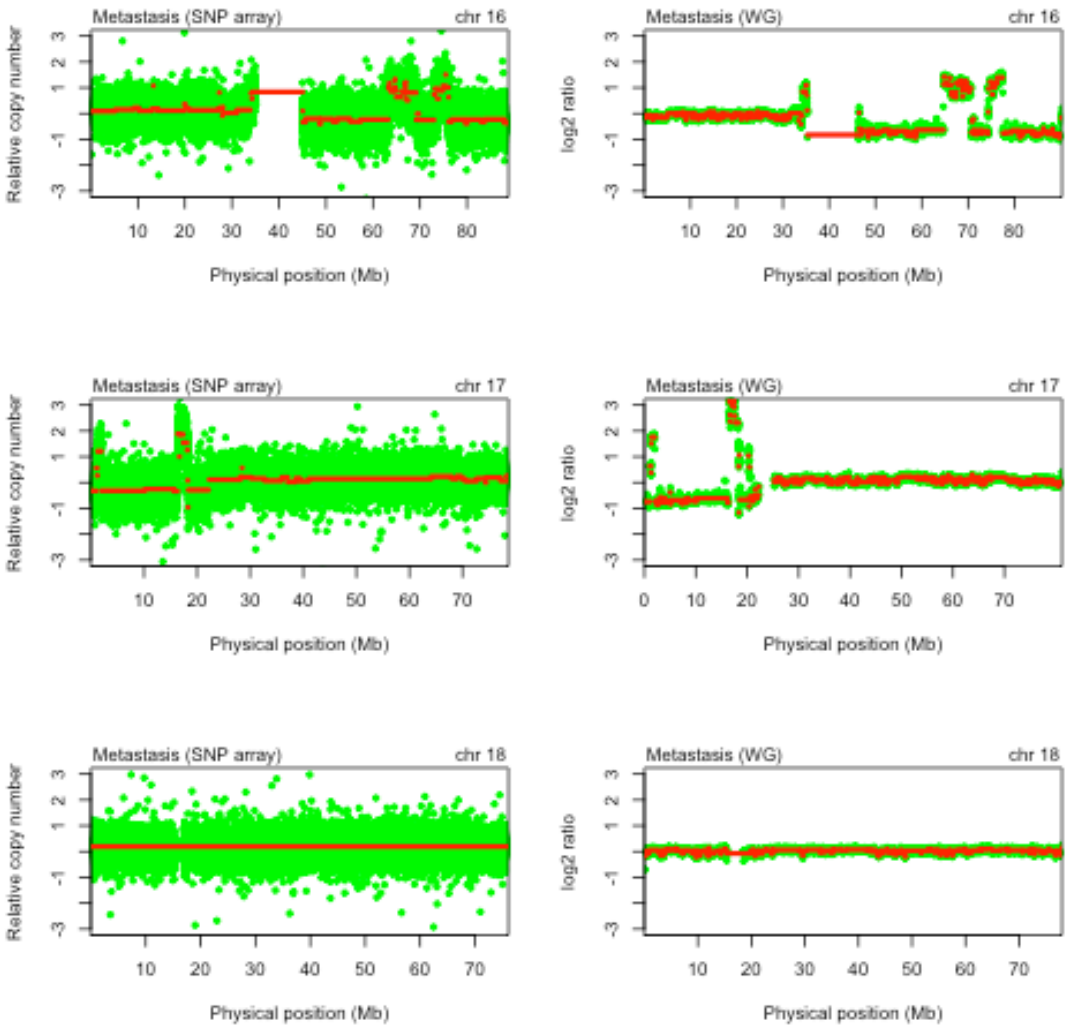
Supplementary Figure 7c. Somatic copy number alteration (CNA) in the metastatic tumour detected by genome-wide SNP arrays (left column) and whole-genome (WG) sequencing normalized read-depth per 10 kb (right column) for chromosomes 7-9.



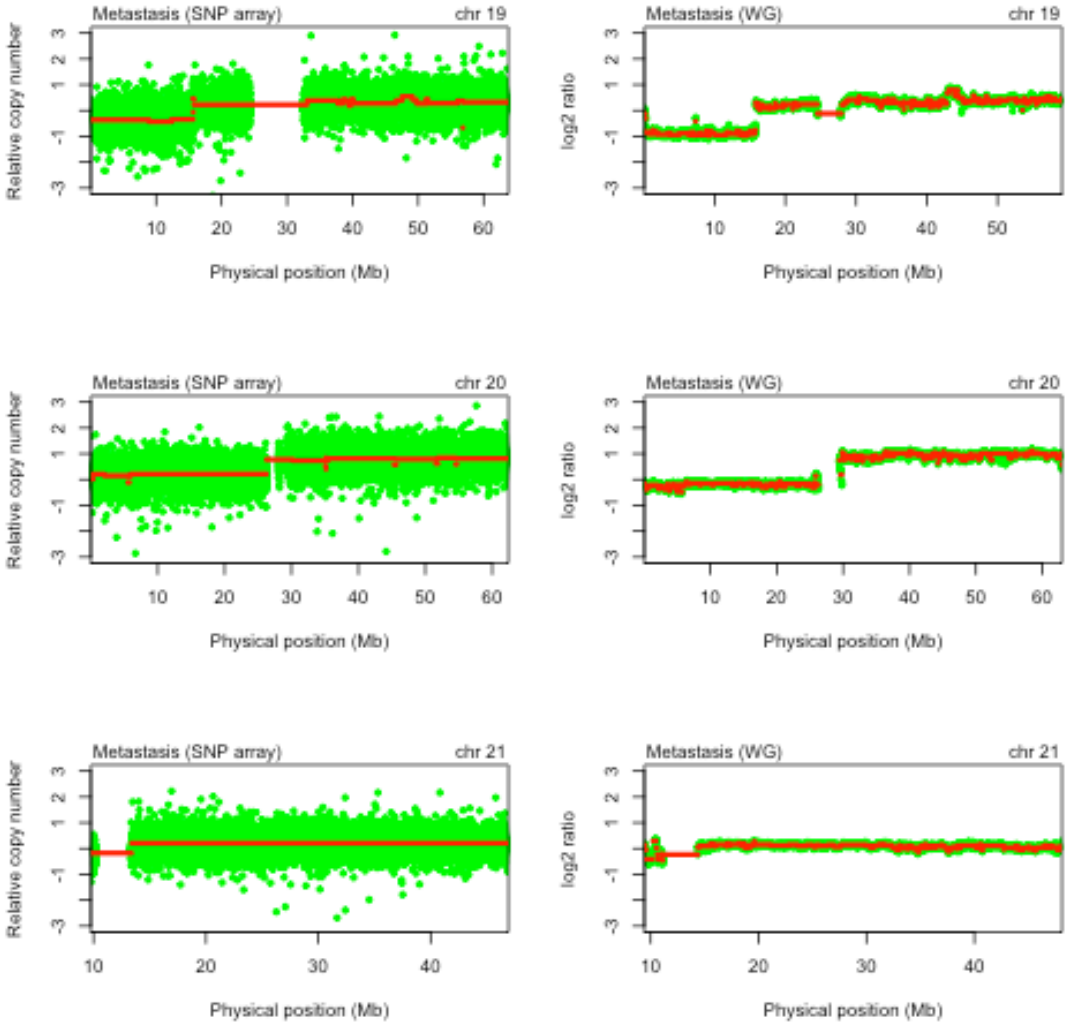
Supplementary Figure 7d. Somatic copy number alteration (CNA) in the metastatic tumour detected by genome-wide SNP arrays (left column) and whole-genome (WG) sequencing normalized read-depth per 10 kb (right column) for chromosomes 10-12.



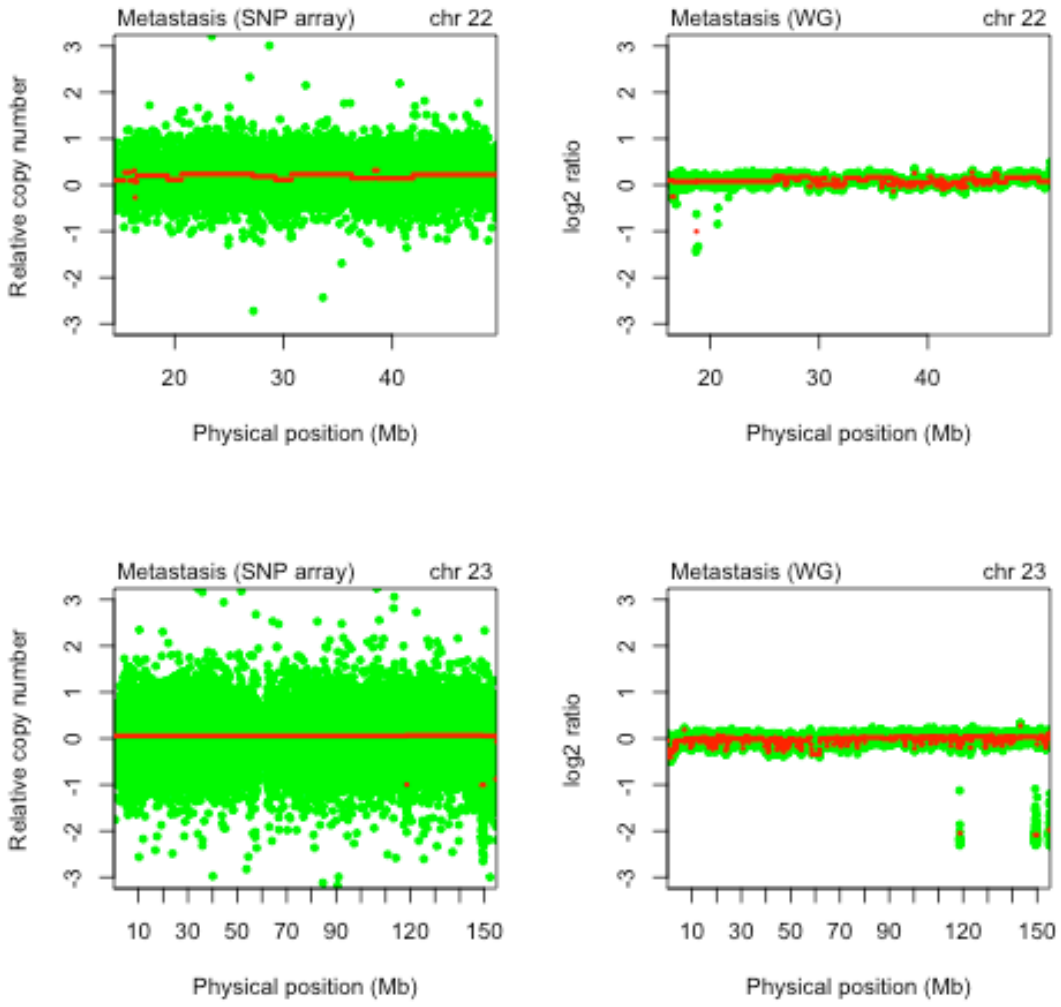
Supplementary Figure 7e. Somatic copy number alteration (CNA) in the metastatic tumour detected by genome-wide SNP arrays (left column) and whole-genome (WG) sequencing normalized read-depth per 10 kb (right column) for chromosomes 13-15.



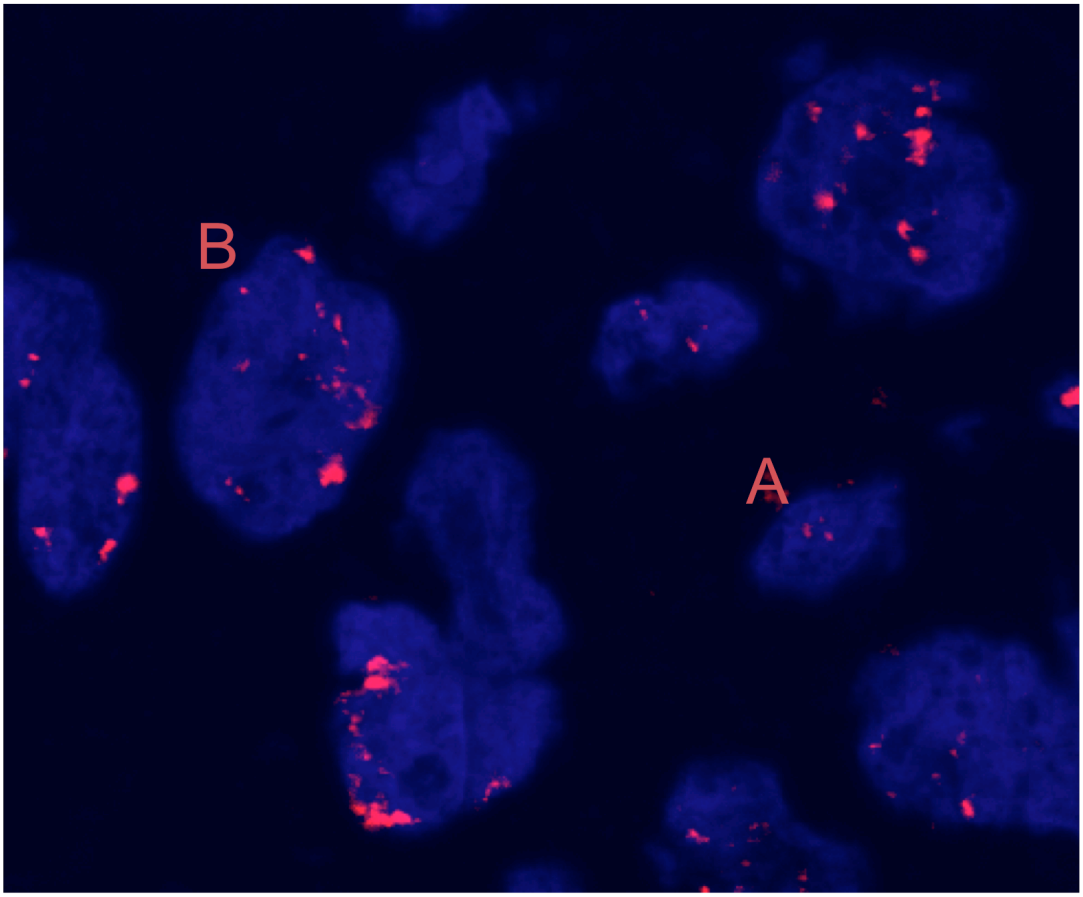
Supplementary Figure 7f. Somatic copy number alteration (CNA) in the metastatic tumour detected by genome-wide SNP arrays (left column) and whole-genome (WG) sequencing normalized read-depth per 10 kb (right column) for chromosomes 16-18.



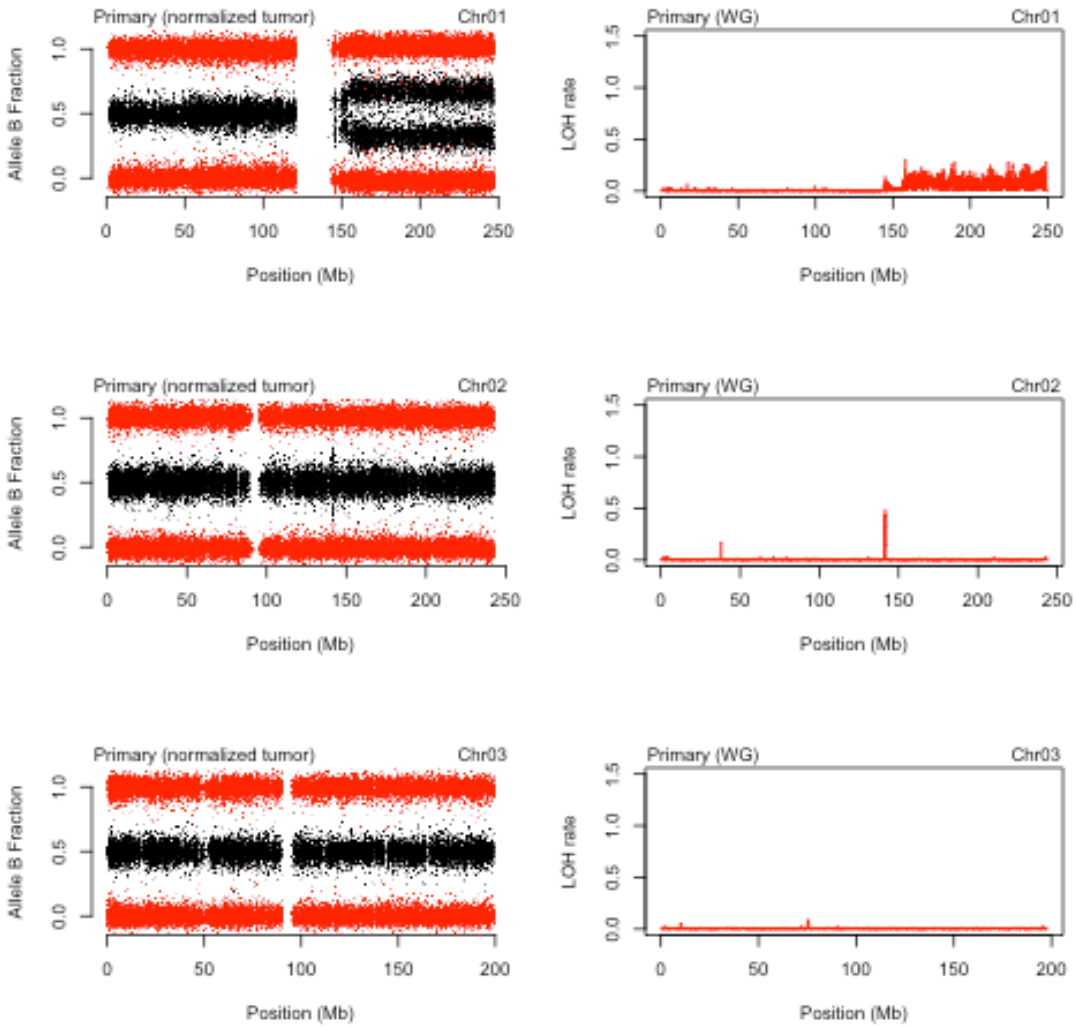
Supplementary Figure 7g. Somatic copy number alteration (CNA) in the metastatic tumour detected by genome-wide SNP arrays (left column) and whole-genome (WG) sequencing normalized read-depth per 10 kb (right column) for chromosomes 19-21.



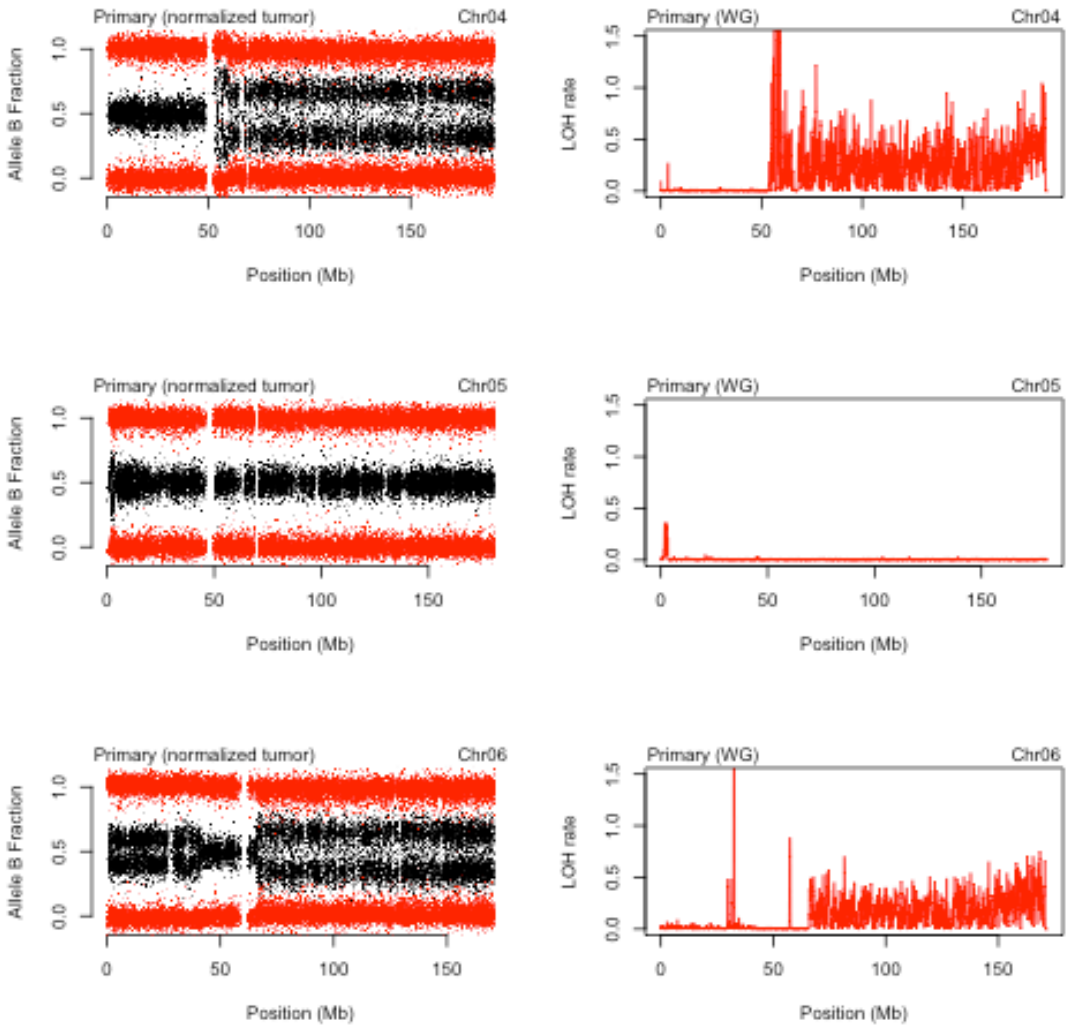
Supplementary Figure 7h. Somatic copy number alteration (CNA) in the metastatic tumour detected by genome-wide SNP arrays (left column) and whole-genome (WG) sequencing normalized read-depth per 10 kb (right column) for chromosomes 22-23.



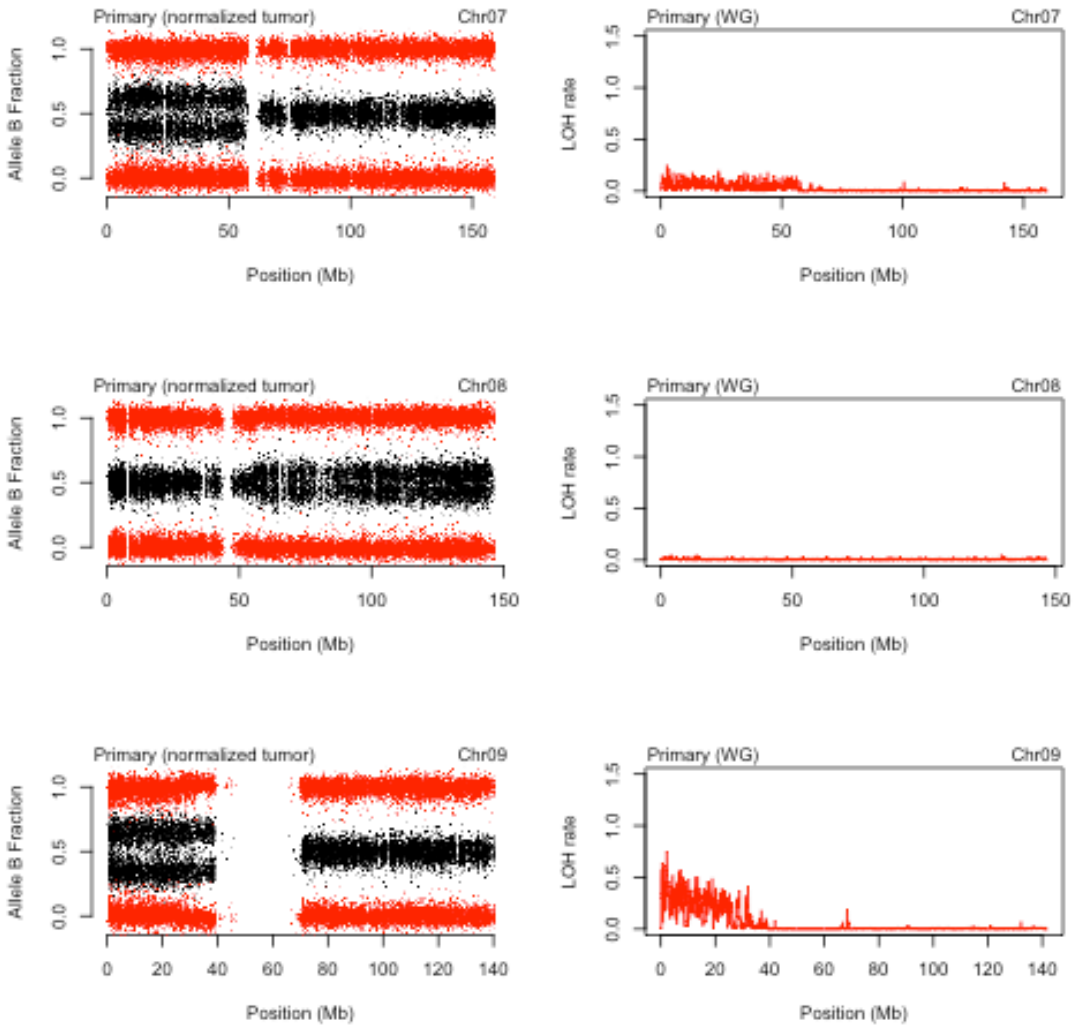
Supplementary Figure 8. Photomicrograph of representative c-KIT FISH results from the primary tumour. A: normal cells within tumour stroma with two copies of c-KIT gene (red signal); B: high level amplification of c-KITgene (red signal)



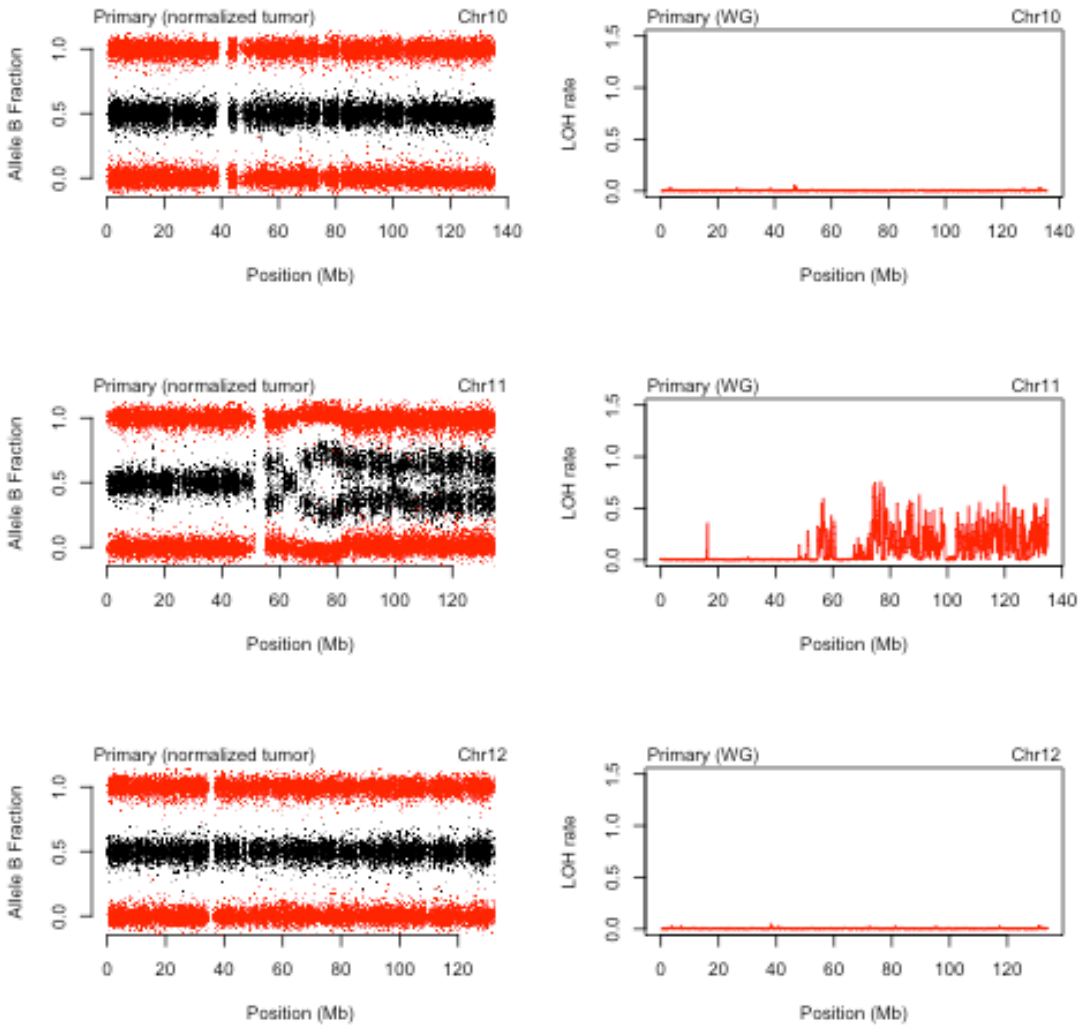
Supplementary Figure 9a. Loss of heterozygosity (LOH) in the primary tumour as detected by Allele B frequency from SNP array (left column) and whole-genome sequencing LOH rate (right column) in 100 Kb windows for chromosomes 1-3.



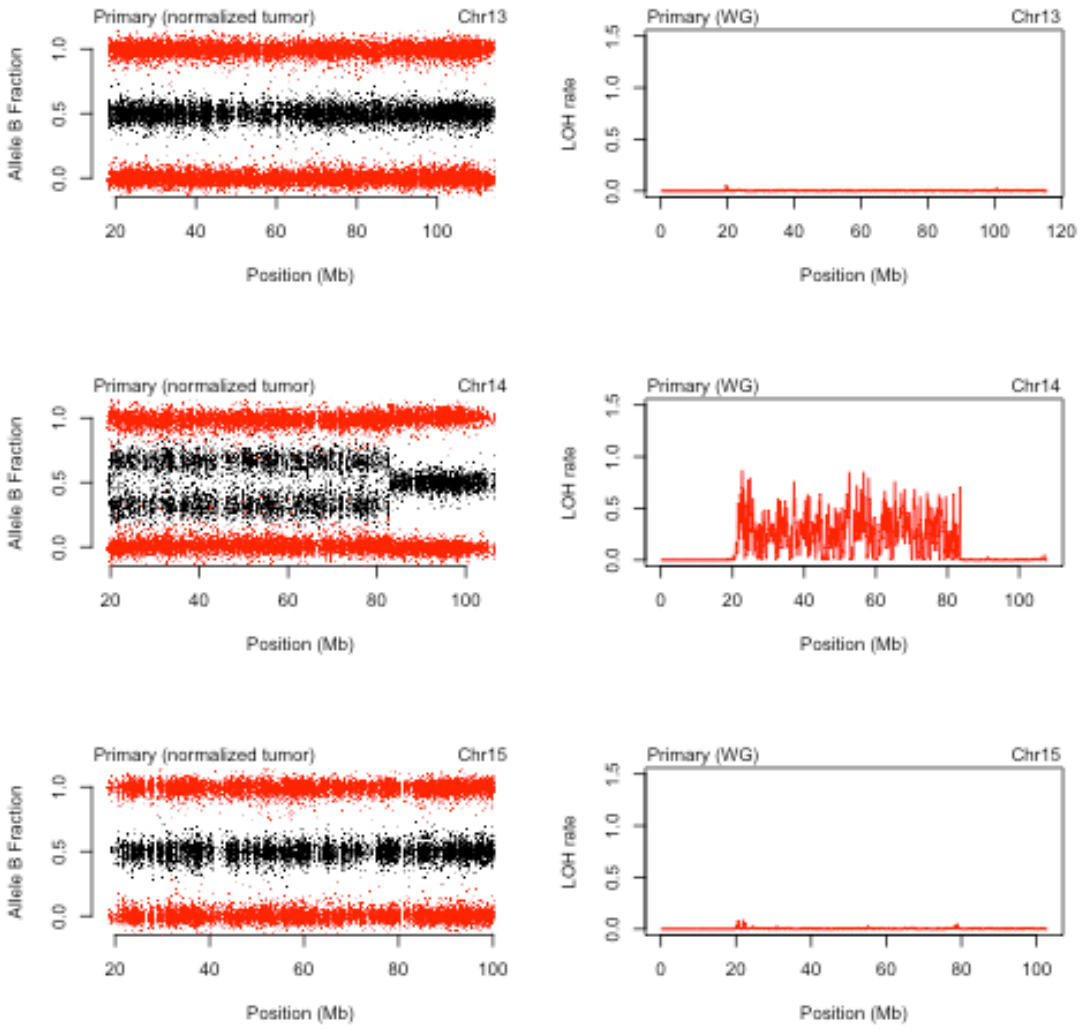
Supplementary Figure 9b. Loss of heterozygosity (LOH) in the primary tumour as detected by Allele B frequency from SNP array (left column) and whole-genome sequencing LOH rate (right column) in 100 Kb windows for chromosomes 4-6.



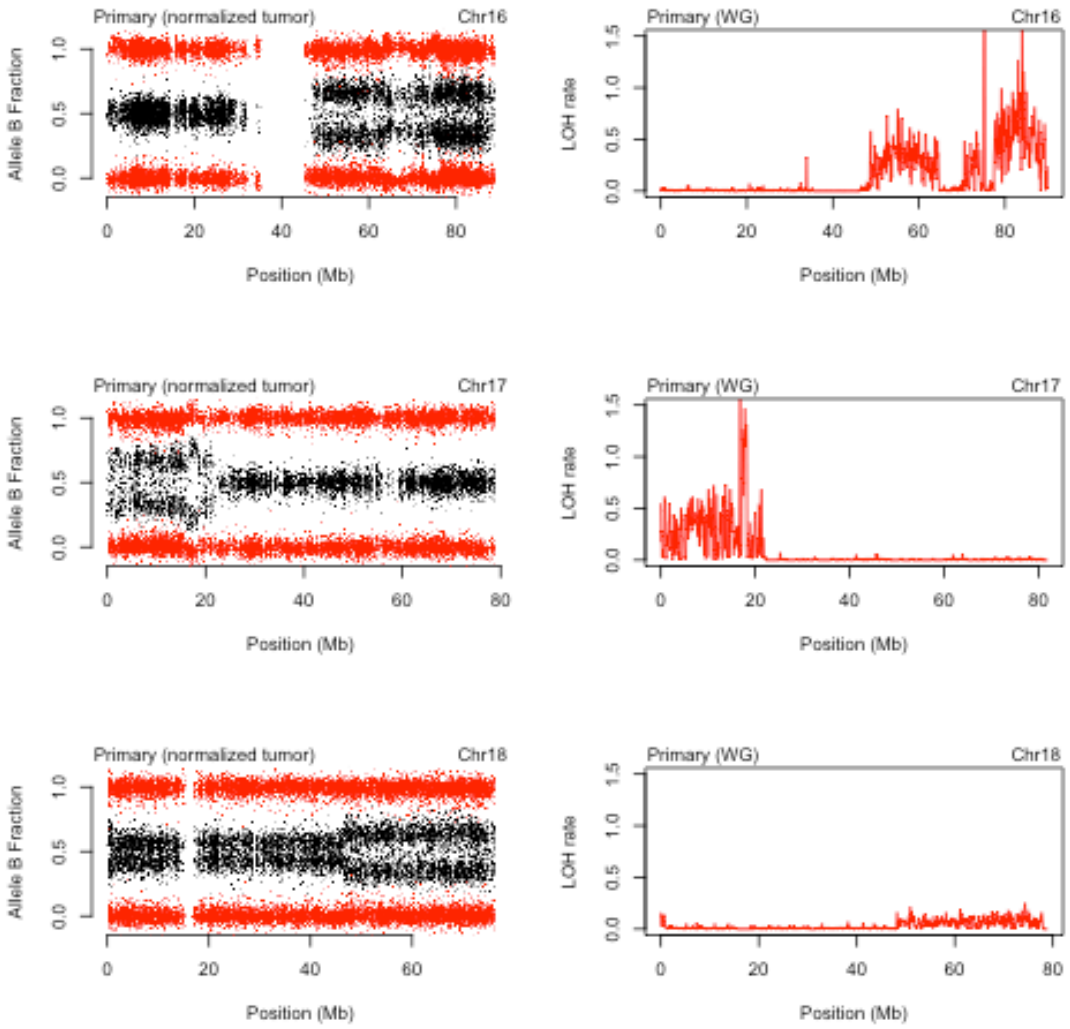
Supplementary Figure 9c. Loss of heterozygosity (LOH) in the primary tumour as detected by Allele B frequency from SNP array (left column) and whole-genome sequencing LOH rate (right column) in 100 Kb windows for chromosomes 7-9.



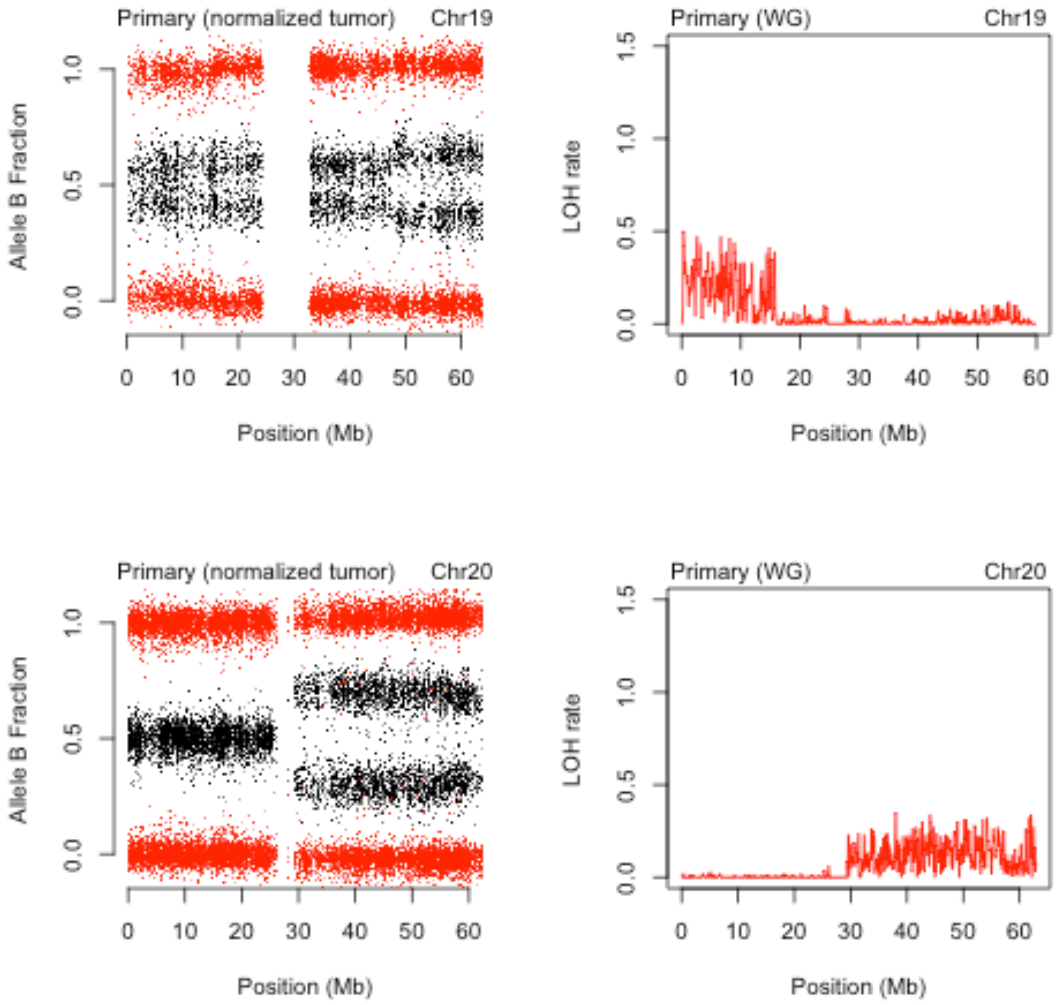
Supplementary Figure 9d. Loss of heterozygosity (LOH) in the primary tumour as detected by Allele B frequency from SNP array (left column) and whole-genome sequencing LOH rate (right column) in 100 Kb windows for chromosomes 10-12.



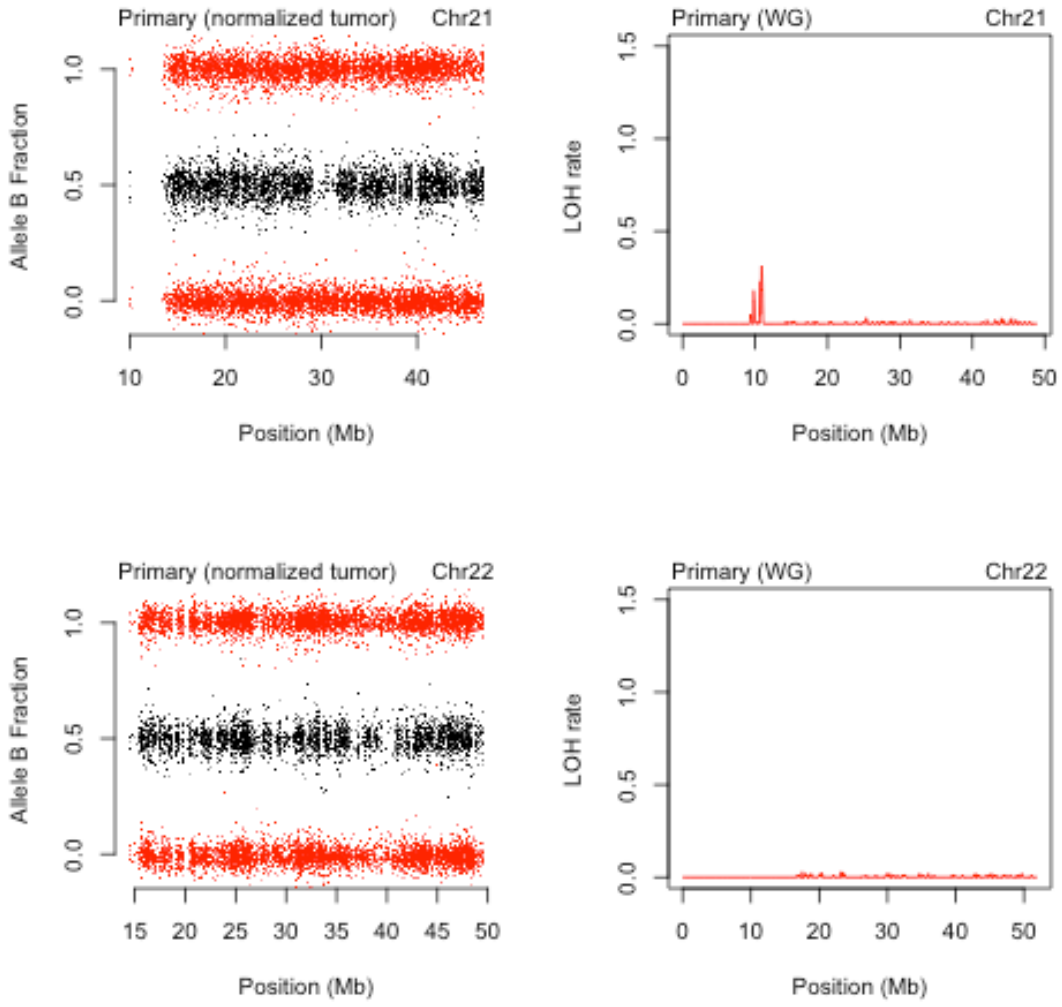
Supplementary Figure 9e. Loss of heterozygosity (LOH) in the primary tumour as detected by Allele B frequency from SNP array (left column) and whole-genome sequencing LOH rate (right column) in 100 Kb windows for chromosomes 13-15.



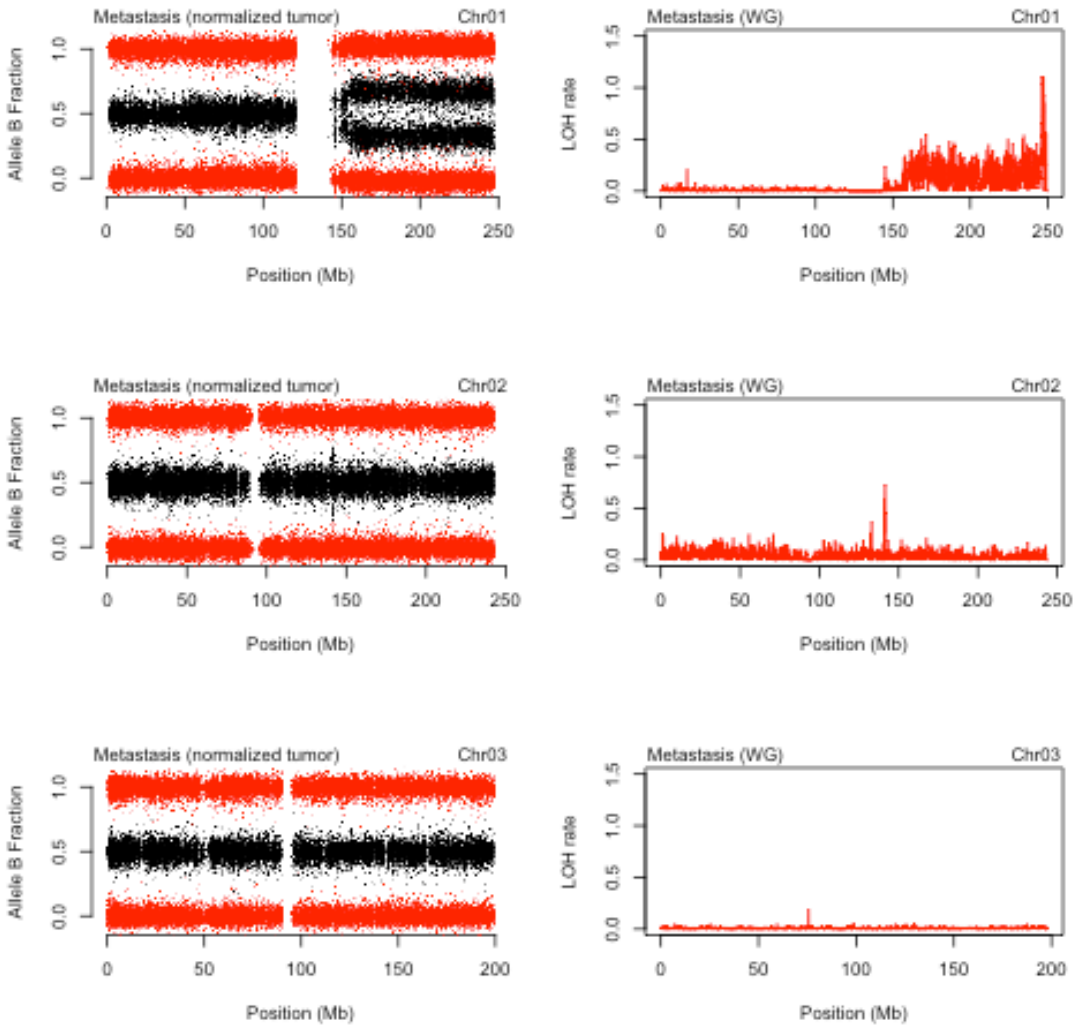
Supplementary Figure 9f. Loss of heterozygosity (LOH) in the primary tumour as detected by Allele B frequency from SNP array (left column) and whole-genome sequencing LOH rate (right column) in 100 Kb windows for chromosomes 16-18.



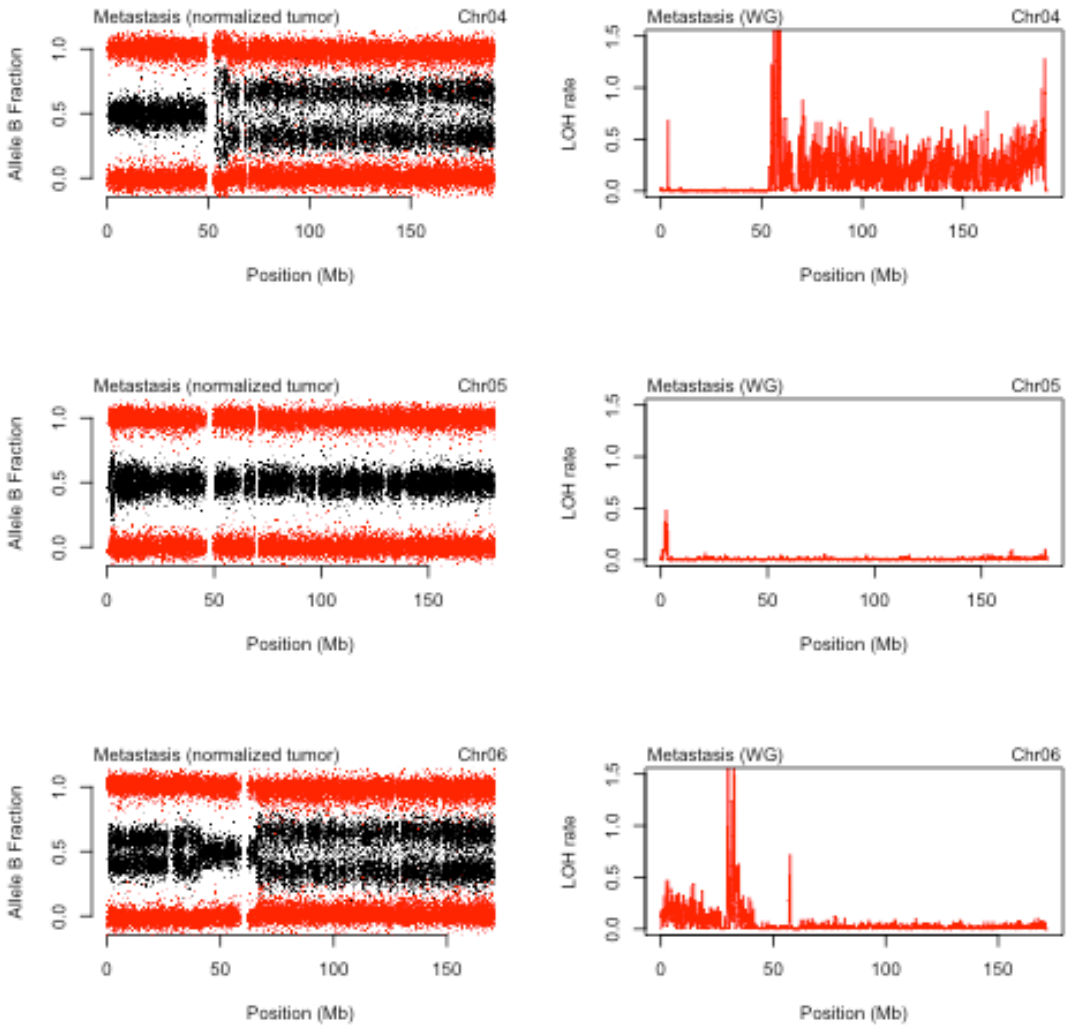
Supplementary Figure 9g. Loss of heterozygosity (LOH) in the primary tumour as detected by Allele B frequency from SNP array (left column) and whole-genome sequencing LOH rate (right column) in 100 Kb windows for chromosomes 19-20.



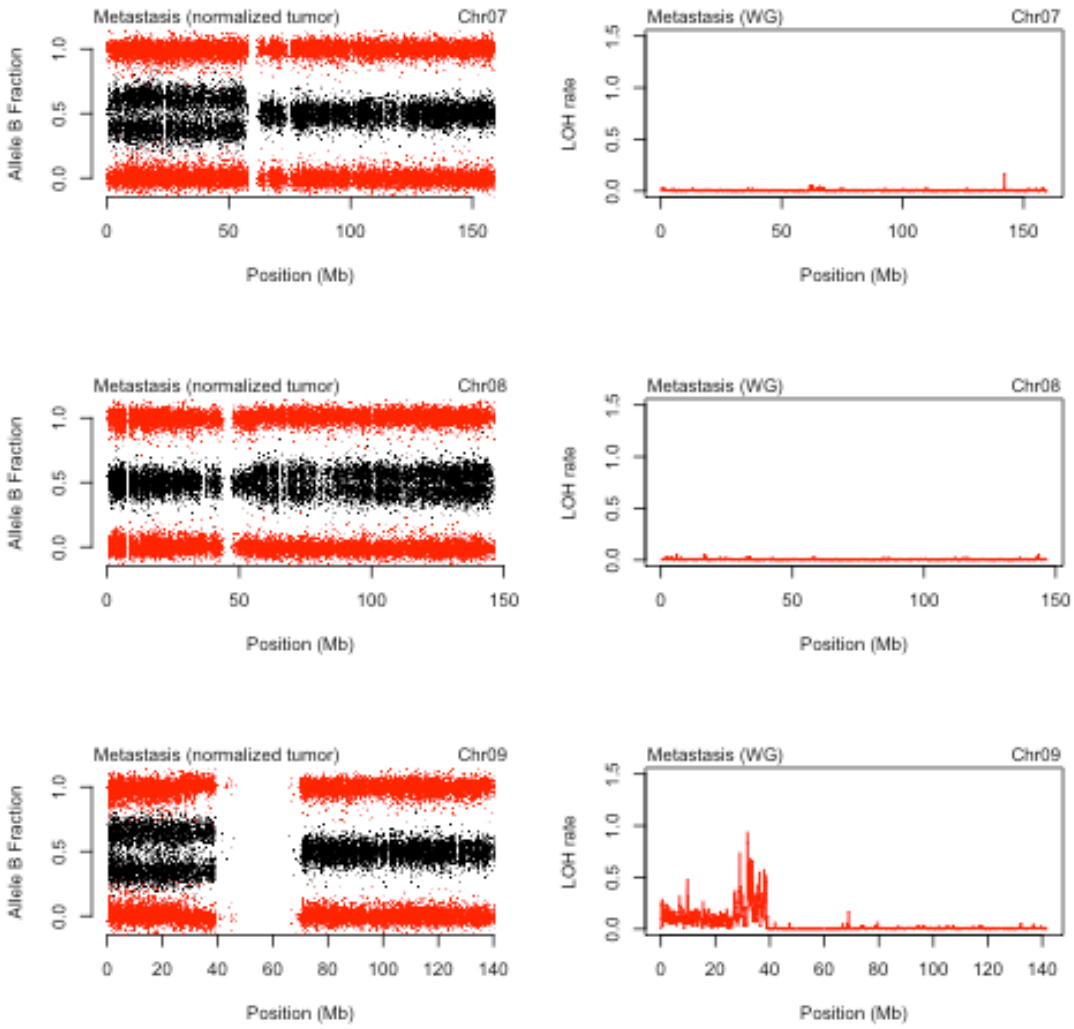
Supplementary Figure 9h. Loss of heterozygosity (LOH) in the primary tumour as detected by Allele B frequency from SNP array (left column) and whole-genome sequencing LOH rate (right column) in 100 Kb windows for chromosomes 21-22.



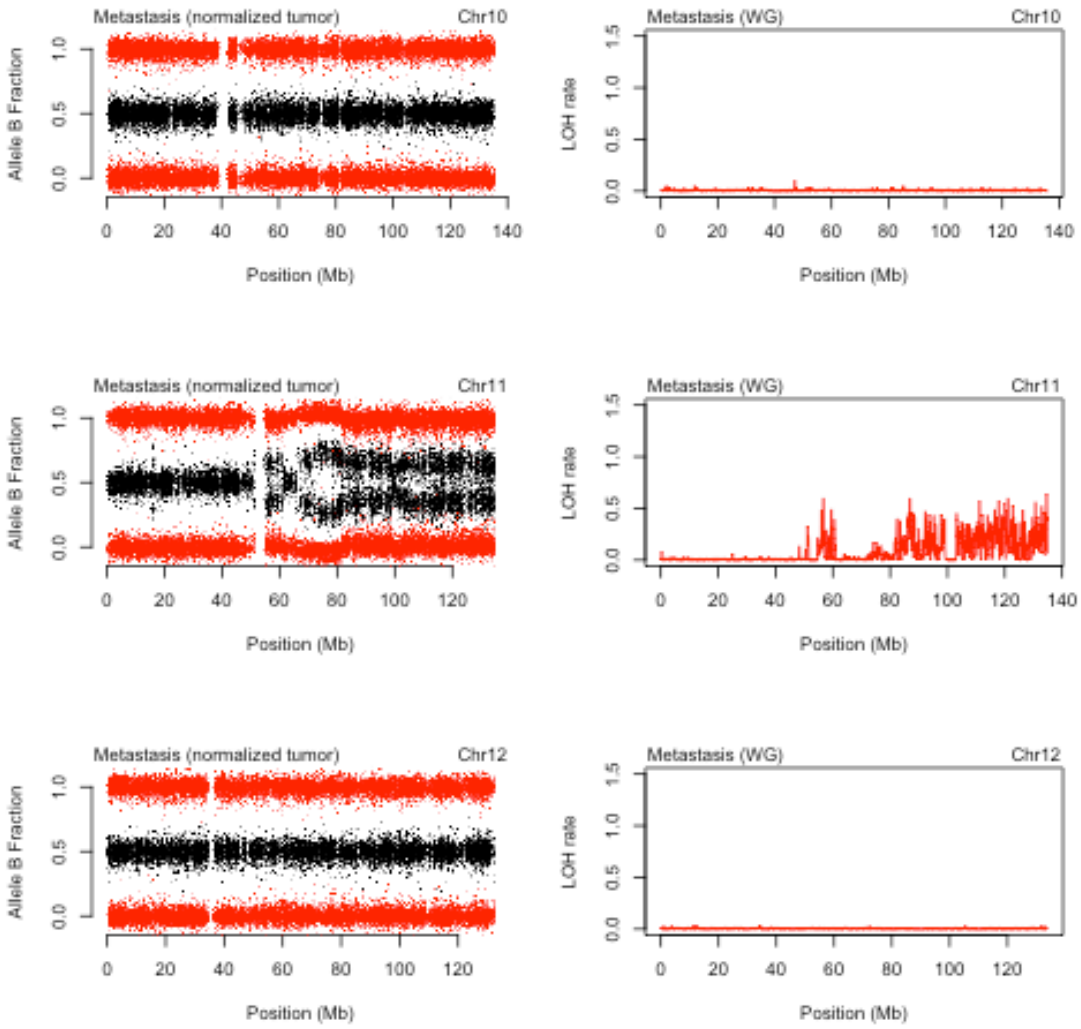
Supplementary Figure 10a. Loss of heterozygosity (LOH) in the metastatic tumour as detected by Allele B frequency from SNP array (left column) and whole-genome sequencing LOH rate (right column) in 100 Kb windows for chromosomes 1-3.



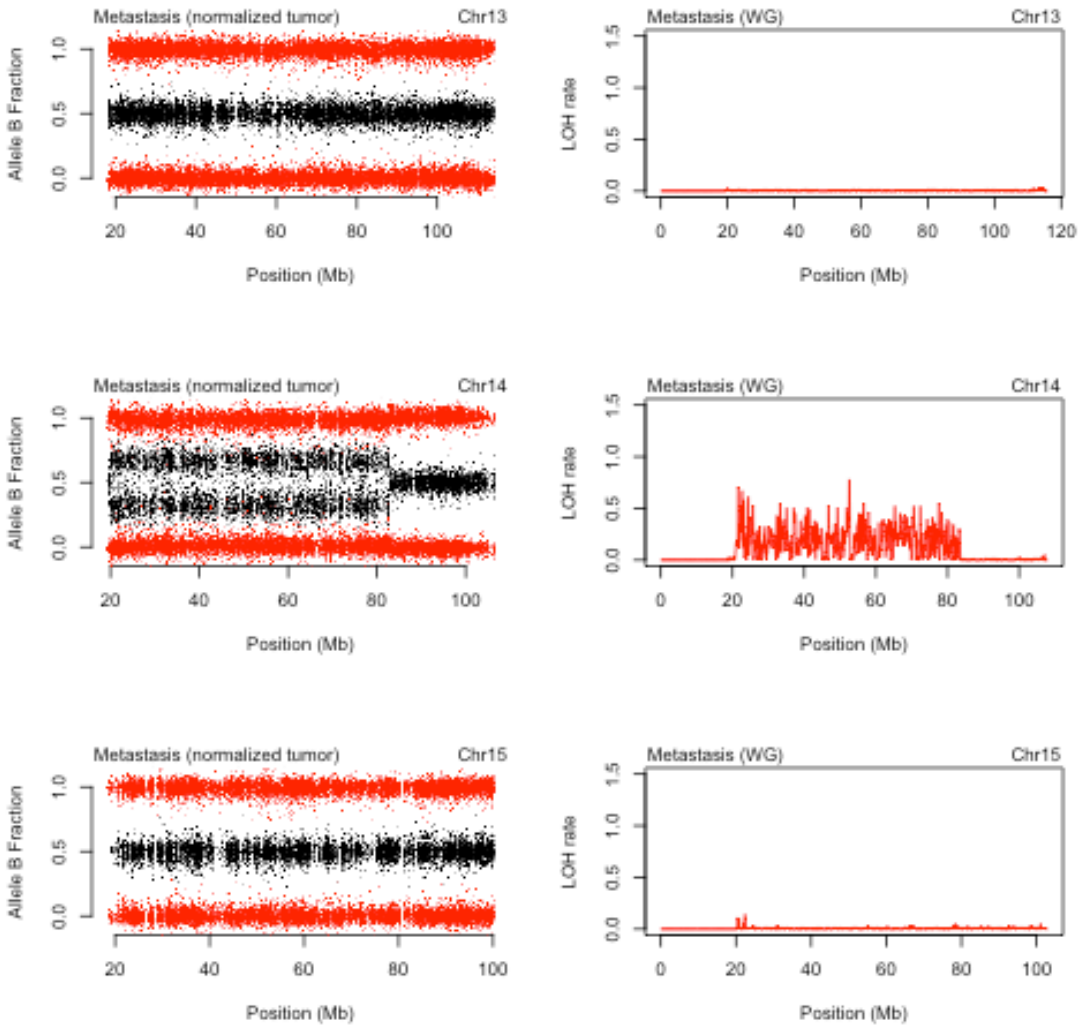
Supplementary Figure 10b. Loss of heterozygosity (LOH) in the metastatic tumour as detected by Allele B frequency from SNP array (left column) and whole-genome sequencing LOH rate (right column) in 100 Kb windows for chromosomes 4-6.



Supplementary Figure 10c. Loss of heterozygosity (LOH) in the metastatic tumour as detected by Allele B frequency from SNP array (left column) and whole-genome sequencing LOH rate (right column) in 100 Kb windows for chromosomes 7-9.



Supplementary Figure 10d. Loss of heterozygosity (LOH) in the metastatic tumour as detected by Allele B frequency from SNP array (left column) and whole-genome sequencing LOH rate (right column) in 100 Kb windows for chromosomes 10-12.



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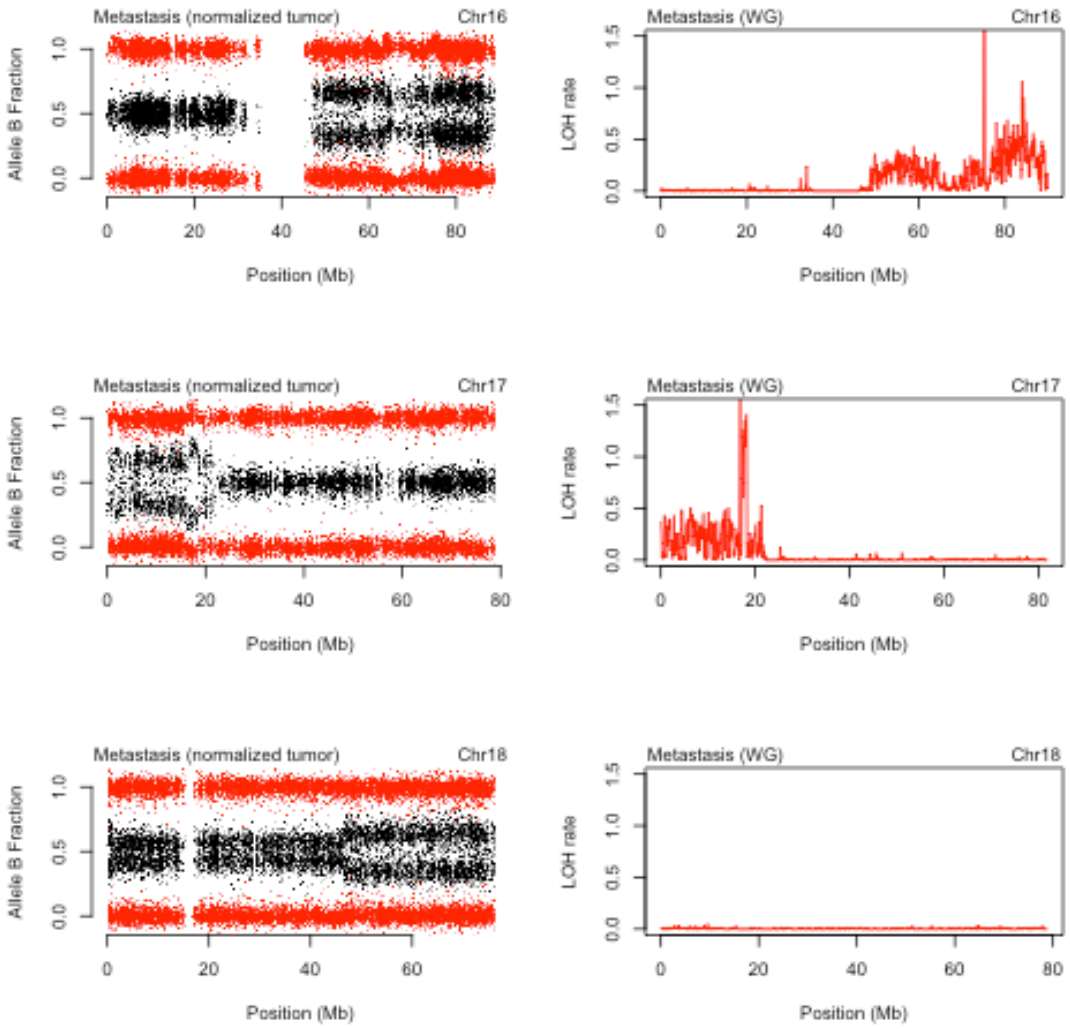
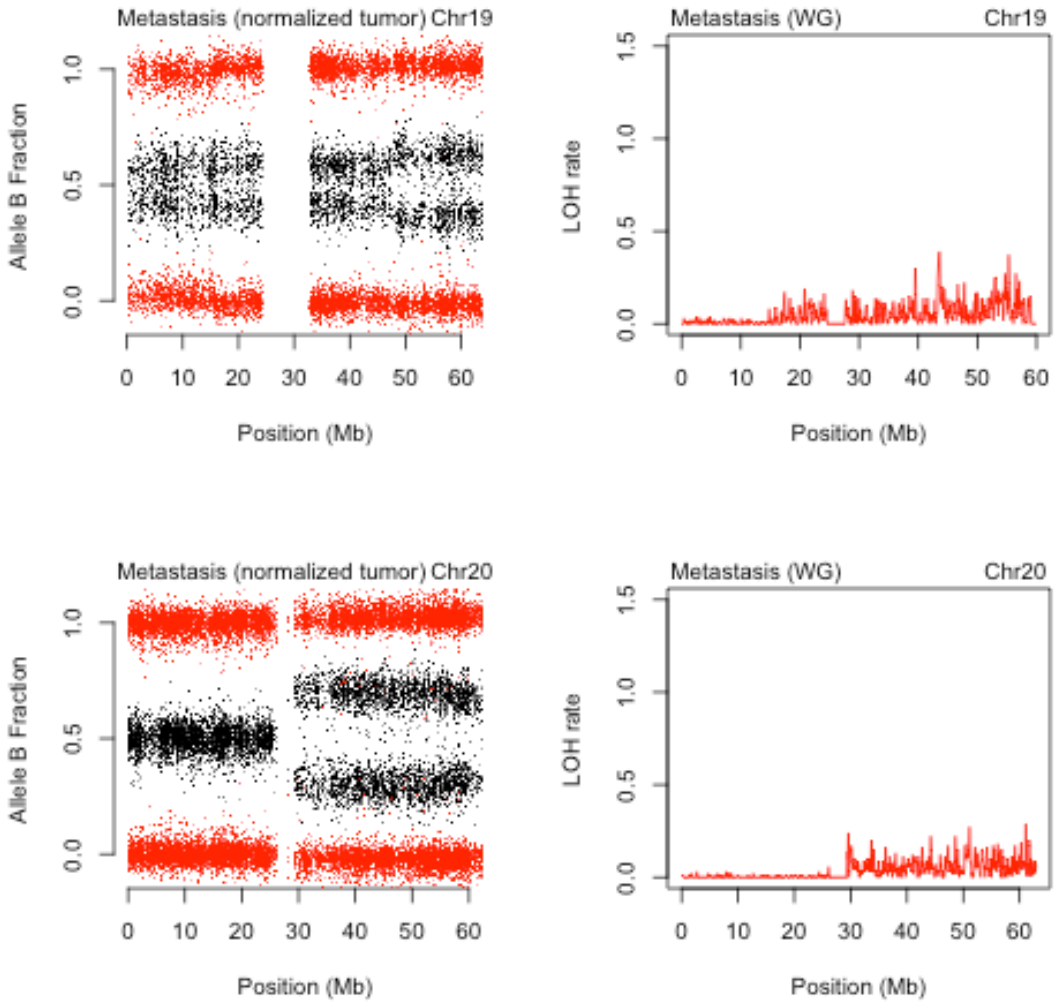
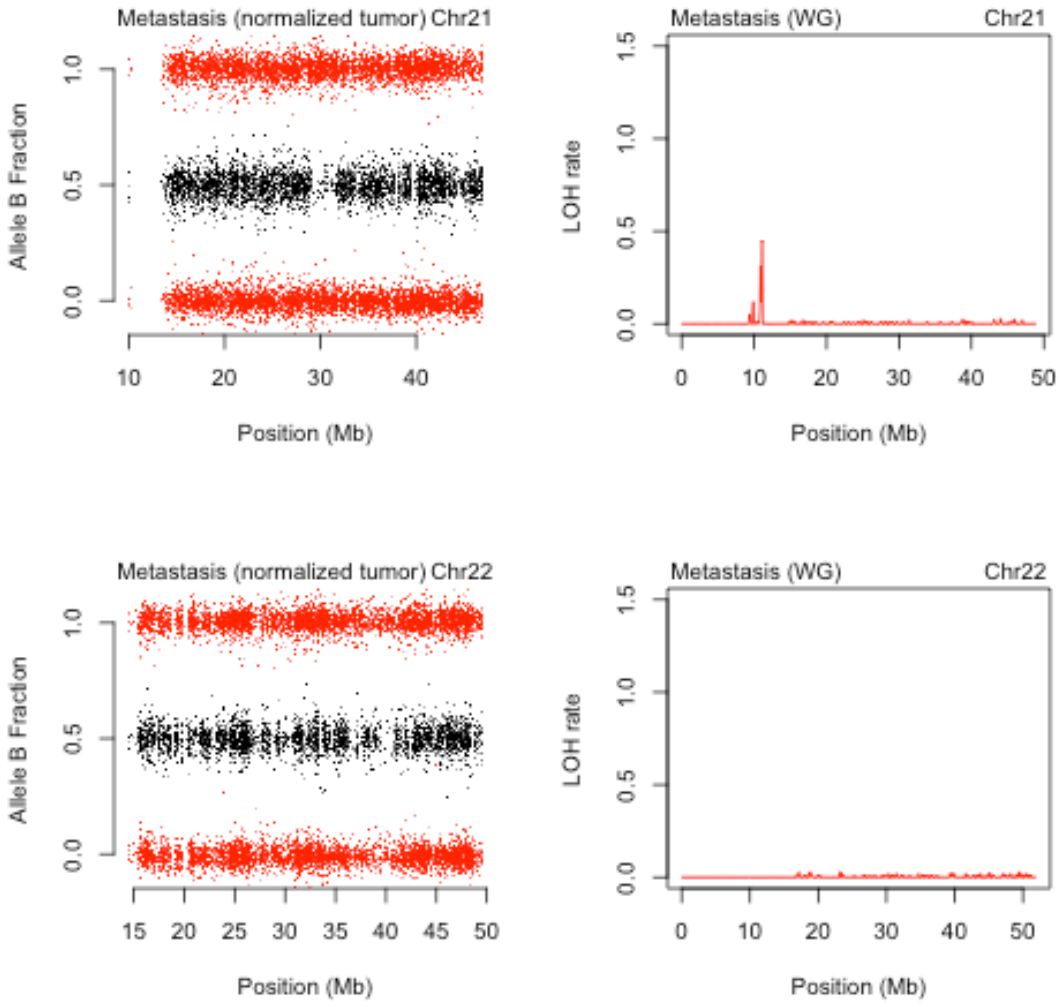


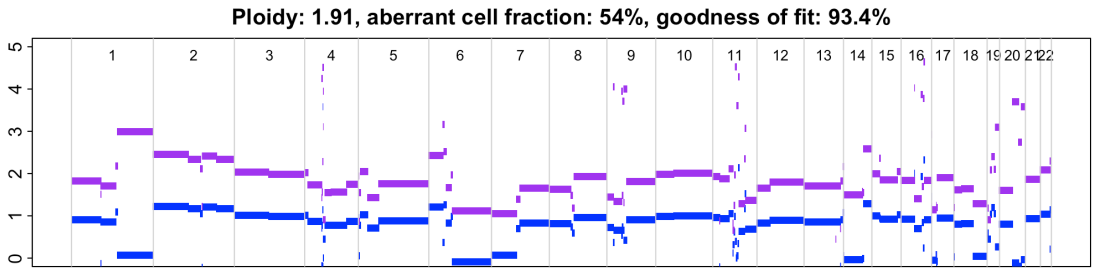
Supplementary Figure 10f. Loss of heterozygosity (LOH) in the metastatic tumour as detected by Allele B frequency from SNP array (left column) and whole-genome sequencing LOH rate (right column) in 100 Kb windows for chromosomes 16-18.



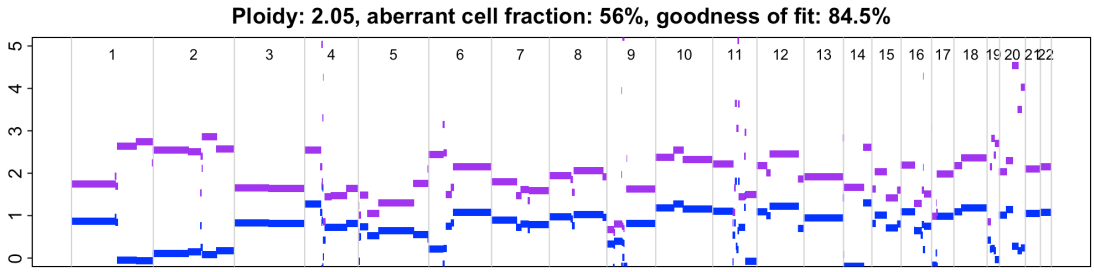
Supplementary Figure 10g. Loss of heterozygosity (LOH) in the metastatic tumour as detected by Allele B frequency from SNP array (left column) and whole-genome sequencing LOH rate (right column) in 100 Kb windows for chromosomes 19-20.



Supplementary Figure 10h. Loss of heterozygosity (LOH) in the metastatic tumour as detected by Allele B frequency from SNP array (left column) and whole-genome sequencing LOH rate (right column) in 100 Kb windows for chromosomes 21-22.



Supplementary Figure 11a. ASCAT analysis of primary tumour SNP array data.



Supplementary Figure 11b. ASCAT analysis of metastatic tumour SNP array data.