SUPPLEMENTARY FILE

A RENEWED MODEL OF PANCREAS CANCER EVOLUTION BASED ON GENOMIC REARRANGEMENT PATTERNS

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Supplementary Results

Tumour enrichment and overview of somatic alterations

The extreme desmoplastic response in PC (herein referring to ductal adenocarcinoma only) is due to the accumulation of stromal cell types such as fibroblasts and lymphocytes. A cohort of 107 primary, stage I/II operable tumours were subjected two enrichment methodologies based on availability of viable fresh samples or frozen tissue. A complete list of clinical features of this cohort is provided in Supplementary Table 2. Fresh tumours were subjected to a multiparameter cell-sorting scheme where tumour epithelial cells were distinguished from fibroblasts and lymphocytes using cell surface antigens. Tumour cells were identified using epithelial cell adhesion molecule (EpCAM, CD326) (Extended Data Fig. 1a). Immunohistochemical (IHC) analyses of primary tumours using the same EpCAM antibody clone used for flow sorting confirmed the high specificity of this antigen to demarcate tumour epithelium (Extended Data Fig. 1b). Fibroblasts and lymphocytes were identified using a combination of markers associated with the mesenchymal (CD90, CD140b) or the blood cell lineage (CD45) (Supplementary Fig. 5a) and were not tumour derived (Supplementary Fig. 5b). From frozen tissue, tumour material was identified morphologically and enriched using laser capture microdissection (LCM) (Extended Data Fig. 1c). We performed whole genome sequencing (WGS) of tumour-enriched samples from 107 cases at an average depth of ~50X. Based on regions of loss of heterozygosity (LOH), we estimated that the median tumour cellularity of the sample cohort was 76% (flow-sorted: 95%, n=21; LCM: 72%, n=86; total) (Extended Data Fig. 1d). The application of these techniques enabled us to perform genome analysis on a large number of PC at a resolution that has previously not been reported.

Across our cohort (n=107), we identified a total of 942,773 somatic mutations (median: 5979, range: 3082 – 90290) and a mutation burden of 1.93 per Mb (range: 0.996 – 29.17 per Mb) (Extended Data Fig. 1e). At 50X WGS, we could easily detect the classical mutations in PC at high frequencies (*KRAS* – 93%; *TP53* – 74%; *SMAD4* – 30%; *CDKN2A* – 22%; Extended Data Fig. 1e). We replicated recent finding of the phenomenon of chromosome X hypermutation[1] (Extended Data Fig. 1f). We found a total of 11,293 somatic copy number changes (median: 85, range: 24 – 349) and 10,123 structural variants (4097 deletions, 2078 duplications, 2537 inversions, 1411 translocations) in our cohort (median: 74, range: 1 – 470).

Description of CN patterns in Diploids versus Polyploids using CELLULOID

We used a new informatics tool, Celluloid, to analyze our tumour-enriched cohort and found a distinct pattern of copy number (CN)/SNP changes associated with diploid and polyploid tumours. Diploid tumours typically displayed three major CN/SNP clusters, with the largest cluster of heterozygous SNPs at CN 2 (Fig. 1a, top panel; Extended Data Fig. 2, Diploid). For example in Ashpc_0008 (Fig. 1a, top panel), there are three distinct CN states (1 through 3), and there is a large cluster of germline heterozygous SNPs that align with a CN of 2. Regions of LOH (CN=1) and gain (CN=3) correspond to the loss or the addition of one parental allele. In a diploid tumour, regions unaffected by CN change (CN=2) would remain heterozygous (50% ratio) due to the retention of both parental alleles. Similarly, regions of LOH and gain would be expected to display SNP ratios that correspond to the loss or the addition of a parental allele (0 or 100%, 33 or 66%) (Supplementary Fig. 6a). Thus, the patterns of CN changes in Ashpc_0008 are consistent with a diploid tumour. By contrast, polyploid tumours often exhibited four or more CN/SNP clusters, with a dominant cluster of heterozygous SNPs at CN 4 in tetraploids (Fig. 1a, bottom panel; Extended Data Fig. 2, polyploid). In Ashpc_0005, there are 5 major CN states, and the largest cluster of heterozygous SNPs (50%) resides at a CN of 4 (Fig. 1a, bottom panel). The rest of the CN states (5, 3, 2, 1) correspond to SNP ratios that denote the absolute number of parental alleles present at that state. In a tetraploid tumour, regions unaffected by CN change would have two copies of each parental allele (CN=4) and thus would retain heterozygosity (Supplementary Fig. 6bi). However, CN losses and gains that occurred before or after genome duplication would display a variegated pattern of SNP ratios (Supplementary Fig. 6b, bottom). These patterns of CN/SNP changes are consistent with a polyploid tumour. We validated several tumours for CN changes from ploidy call from Celluloid (Extended Data Fig. 2). By relating tumour cellularity to ploidy, we also verified that the frequency of polyploidization was not being under or overestimated (p=0.46, Kruskal-Wallis test; Extended Data Fig. 3a).

Timing of CN alterations and mutations in polyploids

We used the following approach to determine the mutational timing in polyploids. To develop the reasoning behind the approach, consider the illustrative scenario in which a single copy of DNA was lost in a tetraploid tumour prior to genome duplication (i.e. from 2 to 1); after doubling, the CN of this alteration would return to 2 but would appear to be loss of heterozygosity (LOH) because only one allele could be duplicated (Supplementary Fig. 6b-ii).

Thus, in tetraploids, we can estimate that segments at 2 copies at LOH represent losses before genome duplication, although we cannot exclude the possibility that both alleles from one parent were lost after genome duplication. On the other hand, CN losses following genome duplication would generally appear as single step changes (e.g. 4 to 3; Supplementary Fig. 6b-iii,iv). A similar set of logical deductions can also be applied to other CN changes (Methods). We also inferred the timing of mutations in polyploids. According to the principle of parsimony, mutations acquired before genome duplication would be duplicated as part of the event and would be at higher ploidy (>1). Conversely, mutations acquired after genome duplication would be present on one copy of DNA and reside at lower ploidy (≤1).

As covered in part in the main text of the paper, we used the above approach to assess the dynamics of mutation accrual in polyploids. Approximately 76% (78/102, n=5 not available) of cases were enriched for C>T transitions in context of NpCpG trinucleotides related to ageing and the spontaneous deamination of 5-methyl-cytosine (referred to as Age-related). Seventeen percent of cases (n=17/102) harboured more or less balanced distribution of all six classes of base substitutions (C>A, C>G, C>T, T>A, T>C, T>G), a signature associated with DNA double-strand break repair (referred to as DSBR) of which half possessed mutations in *BRCA1/2*. The proportion of Age-related and DSBR cases did not differ amongst polyploids and diploids (Age-related: poly vs. dip – 74% vs. 78%, p=0.19; DSBR: 17% vs. 16%, p=0.21, Fisher's exact test; Extended Data Fig. 3d). In DSBR cases, a slightly higher proportion of mutations were acquired before polyploidization (median: before - 58%, after - 47%; p=0.02, t-test; Fig. 1c). Age-related cases, which represent the bulk of this group, displayed a marked effect of accumulating most of their mutations while they were still diploid (median: before - 65%, after - 42%; $p=9.6x10^{-7}$, t-test; Fig 1b). Three of 102 cases displayed a distinct increase in C>A transversions, a signature not yet assigned to a specific aetiology (referred to as Signature 8[2]). All three cases with Signature 8 cases were polyploid and demonstrated a striking pattern of accumulating most mutations after polyploidization (median: before - 35%, after – 70%; Supplementary Fig. 7a). More studies are need on the Signature 8 cases to determine if this pattern would persist.

To determine if mutational signatures are stable in polyploids, we rederived the signatures separating the mutations that occurred before or after polyploidization. In cases where there was enough mutation data to perform this analysis, we established that most polyploids displayed a stable signature pattern in both the diploid and the non-diploid phases of tumour development (28/30; Supplementary Fig. 7d, left column), except in two cases where the attributed signature only came to dominate after polyploidization (1 DSBR and 1 Signature

8; Supplementary Figure 7d, middle and right columns). Thus, mutational signatures are largely unaffected by the genomic instability in polyploids.

Algorithm to detect chromothripsis – Chrom-AL

Chrom-AL was designed based on the four features of chromothripsis: 1) focal CN oscillations that vary between a few states, 2) random joining of DNA breakpoints from all four types of structural rearrangements (tail-to-head [TH], head-to-head [HH], tail-to-tail [TT], head-to-tail [HT]), 3) intervening segments of LOH, and 4) clustering of rearrangement breakpoints. Chrom-AL can detect chromothripsis in presence of other rearrangement phenomenon such as breakage-fusion-bridge (BFB) (see methods below and online Chrom-AL solutions). The sensitivity of Chrom-AL can be shown with its ability to resolve chromothripsis events with as few as 7-10 structural variants (SVs) (Supplementary Fig. 8). By applying Chrom-AL to acute leukaemias, where chromothripsis is rare[3,4], we verified that the algorithm does not overestimate the rate of such events. Only one of 50 acute leukemia genomes harboured such an event (Supplementary Fig. 9a).

Further details of chromothripsis in PC

Using Chrom-AL, we found the chromothripsis rate in two independent cohorts of PC to be similar (60 – 65%; ICGC cohort is shown in Supplementary Fig. 10), dramatically higher than previous reports[5]. We used CELLULOID to distinguish CN changes under lower cellularity conditions of the ICGC cohort. The increased rate of chromothripsis reported here compared to previous reports[5] is likely due to the combined effect of the increased sensitivity of detecting CN events using CELLULOID on the backdrop of tumour-enriched genomes. We found that locally rearranged and unstable subtypes identified by Waddell *et al*[5] were particularly enriched for chromothripsis (Supplementary Fig. 9b,c; Supplementary Fig. 10 and Supplementary Table 2).

In our tumour-enriched genome cohort (n=107), a total of 192 chromosome level chromothripsis events were observed (2.7 events/case, range: 1-9; n=70/107 cases). Chromothripsis events varied markedly in size ranging from a few megabases to involving several whole chromosomes (Supplementary Fig. 11a,b). Chromothripsis was frequently observed alongside other cataclysmic processes such as BFB[6], polyploidization or both (Supplementary Fig. 11c). *TP53* mutations were also associated with increased rate of chromothripsis (76% versus 36%; p=0.0002, Fisher's exact test; Extended Data Fig. 1e) as shown previously[7]. Whereas only 3% of events were localized to chr19, we observed a focal amplification effect on *PAK4* (Extended Data Fig. 4b, bottom panel, p=0.003, Wilcoxon test), a kinase predicted to be a marker of gemcitabine sensitivity[8,9]. A survey of common tumour suppressor genes revealed that several resided in regions lost due to chromothripsis (e.g. *ARID1A*, *ARID1B*, *PTEN*, *RUNX1*, *SMARCB1*, *NF2*; Supplementary Fig. 12).

Description of Extended Data Fig. 5c

We first approached this question by annotating two cases where a large number of CN alterations were observed. In Ashpc_0008, a diploid tumour, five chromosomes harboured 71% of all CN alterations (chr14, chr6, chr18, chr3, chr20; Extended Data Fig. 5c). By tracking DNA rearrangements, we found these CN alterations were a result of two chromothripsis events; one that rejoined pieces of chr14, chr6 and chr8 (Extended Data Fig. 5c, ①), and the other that reconnected pieces of chr3 and chr20 (Extended Data Fig. 5c, ②). With recent evidence that chromothripsis is sustained and resolved in a single cell division[10,11], we can infer that 71% of the CN changes in this tumour were derived from approximately two aberrant cell mitoses.

Patterns of cataclysmic events in metastatic progression (related to Extended Data Fig. 6)

To investigate cataclysmic phenomena in disease progression, we analyzed the genomes of 15 distinct metastases from six cases. Five metastases, mainly from common PC metastatic sites such as the liver and lymph nodes, from three different cases were all polyploid (Extended Data Fig. 6a; Pcsi_0380, Pcsi_0378, Pcsi_0386). In Pcsi_0380, the primary tumour was also polyploid suggesting a polyploid clone seeded both metastases (Extended Data Fig. 6a, left). In Pcsi_0407, we found the ploidy status of the two independent metastases to be discordant (Extended Data Fig. 6b). The lymph node metastasis was diploid (ploidy = 1.79), whereas the liver metastasis that was tetraploid (ploidy = 3.08). As the primary tumour was also diploid (ploidy = 1.83) in this case, we looked to the mutation data to determine if a diploid or a polyploid clone initiated the liver metastasis. We found that a subset of the diploid mutations (i.e. mutations that occurred before polyploidization) were unique to the liver metastasis suggesting that a diploid clone initially seeded the liver and accumulated mutations before undergoing polyploidization (Extended Data Fig. 6c). We cannot formally rule out that a polyploid clone from an unknown metastatic site seeded the liver; however, we believe this scenario unlikely as the liver is amongst the earliest sites to be seeded by the primary tumour.

Reconstruction of rearrangement events in Pcsi_0171

In addition to Ashpc_0005 shown in Fig. 3, we also performed a detailed reconstruction of the events in one more case. In Pcsi_0171, a diploid tumour, 43% (9/21) of all rearrangements were confined to chr9 and chr18 (Extended Data Fig. 8a). The crisscrossing rearrangements that connect the identical DNA copy state between these two chromosomes bear the hallmarks of chromothripsis. At a single time point in this tumour's development, a single copy of chr9 and chr18 were broken into tens of segments where most of chr9p and chr18q were lost. The retained pieces were repaired mostly through inversion type rearrangements. Notably, two of these inversions, one intrachromosomal denoting the left border of the event on chr9 (30.5 Mb, Extended Data Fig. 8b) and the other interchromosomal demarcating the right border on chr18 (35.3 Mb), were liable for the contemporaneous loss of *CDKN2A* and *SMAD4* (Extended Data Fig. 8c,d). This result cannot be explained under the current model of PC progression.

Evidence for allelic losses preceding mutation in key preneoplastic driver genes, *TP53* and *SMAD4*

Thirty-eight of 192 chromothripsis events occurred on chromosomes where the three key tumour suppressor genes reside (chr9: *CDKN2A*; chr17: *TP53*, chr18: *SMAD4*; Extended Data Fig. 4a). These genes are commonly inactivated in a biallelic manner by diverse mechanisms of genetic inactivation (deletions, mutations, SVs). Overall, we observed LOH at *CDKN2A* (91%; 97/107), *TP53* (91%; 97/107) and *SMAD4* (86%; 92/107) at similar rates, comparable to the frequency of *KRAS* mutations in this cohort (90%; n=96/107) (Extended Data Fig. 1e). In 75% of cases, the second copy of *CDKN2A* was inactivated mostly due to an additional deletion event (56/107 homozygous dels; 24/107 mutation; Extended Data Fig. 1e). A second hit in *TP53* and *SMAD4* was found in 77% and 48%, respectively, predominately due to somatic mutations (*TP53*: 82/107 mutations; *SMAD4* – 35/107 mutation, 16/107 homozygous dels). Importantly, mutations in these key driver genes were not observed in the absence of allelic losses implying that the latter are obligatory for transformation.

This led us to examine the relative timing of allelic losses and mutations in these key driver genes. As homozygous deletions cannot be temporally ordered relative to one another under the current experimental design, we focused on *TP53* and *SMAD4*. Biallelic inactivation of both *TP53* and *SMAD4* occurs very early in tumour progression[12]; however we reasoned that some cases in our cohort may harbour subclonal events in these genes. Among samples that had mutations in *TP53* and *SMAD4*, the corresponding allelic loss was at integer value (Supplementary Fig. 13a,c), supporting that these events are present in all cells. In 7% (n=6/82; Supplementary Fig. 13a,b) of *TP53* cases and 23% of *SMAD4* cases (n=8/35; Supplementary Fig. 13c,d), the mutation was not fully clonal, indicating that it occurred after the allelic loss. Direct evidence that mutations in *TP53* and *SMAD4* follow allelic losses in these genes comes from an analysis of a primary tumour and two matched metastases (Supplementary Fig. 14a). Here, the CN profile illustrating a single copy loss in *TP53* and *SMAD4* was constant in all sequential samples (Supplementary Fig. 14b), whereas the proportion of cells carrying *TP53* and *SMAD4* mutations was greater in the metastases than in the primary tumour (Supplementary Fig. 14c,d). This supports that the mutations transitioned to be fully clonal only in the metastases. This sample also had a chromothripsis event that deleted a copy of *CDKN2A* that was fully clonal by CN in both the primary and metastatic tumours (Supplementary Fig. 14e). Importantly, this suggests that the chromothripsis event resulting in the loss of *CDKN2A* preexisted the *TP53* or *SMAD4* mutations, and provides an alternate line of evidence that such catastrophic events occur early in tumourigenesis. These data provide evidence that allelic losses in *TP53* and *SMAD4* precede mutation in PC and corroborate the report by Luttges *et al*[13]. Generally, these findings reinforce a view that allelic losses are critical for transformation and mutations promote metastatic progression in PC[14-16].

Methods

Ethics approval and sample acquisition

A total of 107 surgically resectable cases of pancreatic ductal adenocarcinoma were obtained via informed consented under the ICGC protocol from collaborating hospitals in Canada and the United States. 84 cases were obtained from University Health Network (Toronto, Canada), 14 cases from Mayo Clinic, 3 cases from University of Nebraska as part of a rapid autopsy program, 5 cases from Sunnybrook Health Sciences Centre (Toronto, Canada), and 1 case from McGill University (Montreal, Canada). Consent for WGS was obtained locally at each institute. At the Ontario Institute for Cancer Research, approval was obtained through the University Health Network Research Ethics Board (08-0767-T) and University of Toronto Research Ethics Board (#30024). Preoperatively, blood samples were collected for germline DNA. In cases where blood was not collected, duodenal mucosa or other non-cancerous tissue was collected post-operatively for germline DNA. Tumours were sectioned to confirm diagnosis of ductal adenocarcinoma and a piece was snap frozen in liquid nitrogen, and stored at -80°C or -150°C before proceeding with laser capture microdissection (LCM). For 21 cases (17 UHN, 4 Sunnybrook), fresh tumour material was dissociated and viably sorted at -150°C (below). We obtained clinical follow-up on the majority of cases.

Tumour cell enrichment

Sample dissociation and cell sorting: Freshly resected tumours were minced into fine pieces in 10cm tissue culture dishes using a razor blade. After mechanical dissociation, 9mL of RPMI (at 1% fetal bovine serum) was added. 1ml of 10X Collagenase/hylauronidase mix (Stem cell technologies) was added to bring the volume to 10mL and the sample was placed at 37°C incubator. Every 20 mins, the tissue pieces in the culture dish were pipetted through narrowing orifices (ex 10mL then 5ml then 1mL pipet) for a total of 60 – 120 mins. The sample was then passed through a 70-150 micron nylon mesh, centrifuged and resuspended in dimethyl sulfoxide (DMSO - Sigma) based cryopreservation media (20% FBS/10% DMSO final) and placed at -150°C for long-term storage.

For cell sorting, frozen vials of viable cells were thawed via dropwise addition of RPMI solution (IMDM + 20%FCS + DNaseI). Final concentration of DNaseI (Roche Applied Science, 10104159001) in RPMI solution was 200ug/mL. Post-thaw, cells were spun at low

RPM (~1000) for 20min at 4°C. After the spin, thawing solution was removed and cells were resuspended in 100uL of PBS+5% FBS for antibody staining for cell sorting. The following antibodies were used for cell sorting: GlyA FITC (BD bioscience, clone HIR2), CD140b PE (BD bioscience, clone 28D4), CD45 PC5 (Beckman Coulter, clone IM1833), EpCAM PerCP-eFluor710 (eBioscience, clone 1B7), CD31 PC7 (eBioscience, clone WM-59), CD90 (BD Biosciences, clone 5E10), CD34 APC7 (BD bioscience, clone 581, custom conjugation). Cell sorting was performed on the BD FACSAria III using 4-laser configuration.

Laser capture microdissection: Snap frozen tumour tissue embedded in OCT was cut into 8um sections and mounted on PEN-Membrane Slides (Leica). Sections were stained with diluted hematoxylin to distinguish tumour epithelium from stroma. A staff pathologist marked tumour sections and LCM was performed according to manufacturer's protocol on the Leica LMD7000 system. Specimens were collected by gravity – contact-free and contamination-free and directly placed in DNA lysis buffer.

Library Construction and Whole Genome Sequencing

DNA from tumour enriched samples (flow sorted or LCM) was isolated according to standard protocols and quantified using Qubit Fluorometric system (Life Technologies). Genomic DNA (gDNA) from tumours that underwent cell sorting was subjected to Nextera Library Preparation (Illumina Inc) according to manufacturer's protocol. Briefly, 50ng of gDNA was resuspended in 20ul of Nuclease Free water, followed by addition of tagmentation buffer (25uL) and enzyme (5uL). The reaction was placed at 55°C for 5min. Clean-up of tagmented DNA was performed using Agencourt AMPure XP SPRI beads (Beckman Coulter). Illumina indexes and adaptors were added using limited PCR amplification (5 cycles), and followed by a second cleanup step using Agencourt AMPure XP beads (Beckman Coulter). Libraries were quantified using Qubit and analyzed using the Agilent Bioanalyzer High Sensitivity DNA Kit (Agilent Technologies, Santa Clara, CA, USA).

gDNA from tumours that underwent LCM were subjected to the KAPA Library Preparation. 50ng of Qubit (Life Technologies, Carlsbad, CA, Cat #Q32854) quantified gDNA was sheared to 300-500bp fragments using the Covaris S2 Ultra-sonicator (Covaris Inc., Woburn, MA, USA) followed by 1x volume AMPure XP SPRI bead cleanup (Beckman Coulter Genomics, Danvers, MA, USA). Libraries were constructed using enzymatic reagents from KAPA Library Preparation Kits (KAPA Biosystems, Woburn, MA USA) according to protocols as described in reference 17[17] for end repair, A-tailing, and adapter ligation. Adapter-ligated libraries were enriched using optimized PCR conditions by adding 3 μL of Ilumina paired-end enrichment primers (Integrated DNA Technologies, Coralville, Iowa, USA), 75 µL of 2x KAPA HiFi HotStart ReadyMix (KAPA Biosystems, Woburn, MA, USA) and 33 µL of nuclease-free water (Life Technologies, Carlsbad, CA, USA) to 36 µL of eluted DNA and amplified across 3 individual PCR reaction tubes. Libraries were incubated in Verti 96-well Thermal Cyclers (Life Technologies, Carlsbad, CA, USA) for 45s at 98°C and cycled 10 times for 15s at 98°C, 30s at 65°C, and 30s at 72°C. Following a 0.6x SPRI bead clean-up (Agencourt AMPure XP beads), post-PCR enriched libraries were eluted in 30uL of elution buffer (Qiagen, Hilden Germany, Cat#19086) and validated using Agilent Bioanalyzer High Sensitivity DNA Kit (Agilent Technologies, Santa Clara, CA, USA).

Prior to sequencing, both Nextera and KAPA libraries were quantified on the Illumina Eco Real-Time PCR Instrument (Illumina Inc., San Diego, CA, USA) using qPCR according to the standard manufacturer's protocol (Illumina Inc). Paired-end cluster generation and sequencing was carried out for all libraries on the Illumina HiSeq 2000/2500 platform using high-throughput (a) 2X101 cycles (Illumina Inc., San Diego, CA, USA) and (b) 2X126 cycles (Illumina Inc., San Diego, CA, USA), combined with rapid run (c) 2X101 cycles (Illumina Inc., San Diego, CA, US). Samples were sequenced with the number of lanes predicted to yield a collapsed coverage of 50x and 30x for tumour and normal samples, respectively. Post-sequencing, insert size of DNA fragments for each run was monitored to ensure that there were minimal to no differences between the two different library preparation methodologies. In our analysis, we never observed any biases in calling of somatic variants, copy number or structural variants between these methodologies.

Immunohistochemistry and Fluorescence In-Situ Hybridization

Dual-colour interphase FISH was performed on whole mount paraffin sections using in-house brewed probes for smad4 gene and commercial probes for KRAS (not shown), p53 and p16/CEP9 (not shown). Two BAC clones RP11-729G3 (starts 48,478,290 ends 48,634,496) and RP11-348N10 (48,542,628 – 48,715,868) – actual probe size 48,611,411 - that correspond to the 18q21.2 region containing *SMAD4* gene (starts 48,556,583 ends 48,611,411) were selected from the Human UCSC Genome Browser assembly (Feb.2009 CRch37/hg19) and obtained from TCAG Genome Resource Facility (Sickkids Hospital, Toronto, Canada). Nick translation kit (Abbott Laboratories, Abbott Park, Illinois, USA) was used to directly label BAC clones with SpO fluorochrome according to the manufacturer's protocol while CEP18 labeled in green (Abbott Laboratories, Abbott Park, Illinois, USA) served as an internal control. Probes were verified on normal blood metaphases to confirm their correct localization. A commercially available LSI *CDKN2A* Spectrum Orange probe with CEP9 Spectrum Green included as internal control was used to identify copy numbers of p16/CDKN2A gene (Abbott Laboratories, Abbott Park, Illinois, USA), *KRAS* labeled in red was purchased from Agilent (Agilent Technologies, Santa Clara, CA, USA) and combined with CEP12 SpG (Abbott Laboratories, Abbott Park, Illinois, USA). *TP53*-17p13 labeled in orange and copy control 17 labeled in green were bought from CymoGen DX (Biocare medical (CymoGen DX), Concord, CA, USA). FISH was performed by standard methods using the probes described above. Briefly, slides were deparaffinized in Xylen, incubated in Cytric buffer (pH=6.0) for 35 minutes at 80°C and digested with pepsin (Sigma, 75,000 U in 0.01N HCl) for 13-17 minutes at 37°C followed by codenaturation for 7 minutes at 75°C. Hybridization was conducted at 37°C for 2 days. After washings slides were counterstained with 4',6-Diamidino-2-phenylindole, dihydrochloride (DAPI). A Zeiss Imager.M1 microscope (Carl Zeiss Canada Ltd., Canada) equipped with a camera (JAI Inc., San Jose, CA, USA) and the MetaSystems Isis FISH Imaging System (MetaSystems GmbH, Altlussheim, Germany) was employed for manual signal analysis and image capturing. For *TP53/SMAD4* FISH: Two BAC clones for *SMAD4* (see above) were labeled with SpG and RP11-89D11 (7,571,720 –7,663,042) that correspond to the 17p13.1 region containing TP53 gene (starts 7,571,720 ends 7,590,868 -Human UCSC Genome Browser assembly (Feb.2009 CRch37/hg19) was labeled with SpO.

Immunohistochemistry: Paraffin sections at 4um thickness were dried in a 60°C oven overnight before staining. The immunohistochemistry (IHC) was performed according to the manufacture's guidelines using BenchMark XT-an automated slide stainer (Ventana Medical System) with standard (or mild) antigen retrieval (CC1,Tris/Borate/EDTA pH8.0, #950-124) or with protease1 (760-2018) for 4 minutes. The concentration for EpCAM (eBioscience, clone 1B7) was 1/100 for 60 minutes. Ventana Ultraview Universal DAB Detection Kit (#760-500) was utilized. The complex is then visualized with hydrogen peroxide substrate and 3, 3'-diaminobenzidine tetrahydrochloride (DAB) chromogen. The slides were counterstained with Ventana Hematoxylin II and Bluing reagent, dehydrated in graded alcohol, cleared in xylene and coverslipped in Permount.

Sequence alignment, variant calling and structural variants

The data was aligned to the GRCh37.p0 reference including random contigs using Burrows-Wheeler Aligner (BWA) v0.6.2[18]. Multiple lanes of the same sample were sorted, merged and duplicates were marked across libraries using Picard v1.90 (http://broadinstitute.github.io/picard).

Germline single nucleotide polymorphisms (SNPs) were called using the Genome Analysis Toolkit (GATK) v1.3.16 [19]. In brief, the data was locally realigned around indels and the base quality values were recalibrated prior to variant calling using the Unified Genotyper. The data was then filtered using the VariantFiltration module. Mutations with a QUAL score of greater than 50 in the normal sample were classified as germline variants. In all cases the tumour and matched normal samples were processed simultaneously. Strelka v1.0.7[20] was used to call somatic SNVs using default settings. The Tier 1 SNVs were utilized for all downstream analysis. All mutations were annotated with dbSNP v142 (http://www.ncbi.nlm.nih.gov/SNP/) and COSMIC v64 (http://cancer.sanger.ac.uk/cosmic). Protein coding consequences were predicted for each mutation using ANNOVAR v2013-06-21[21].

Structural variants (SVs) were called using both Crest vAlpha[22] and Delly v0.5.5[23]. Custom in-house scripts filtered for high confident SVs from their respective tools. The union of the high confident SVs were then utilized for all downstream analysis. In all cases default parameters were used unless otherwise specified.

Mutational Signatures

Mutation signatures were derived as previously described[2].

CELLULOID: Evaluation of tumour cellularity, tumour ploidy, and absolute copy number profiles

After alignment, reads are counted in 1 kbp bins using functions from the *R* package HMMcopy. These counts are then adjusted for the GC content of each bin using LOESS (local) regression and scaled to the mean (scaled GC-corrected read count [SRC]). Segmentation of the data in both tumour and normal tissue (say, from matched non malignant tissue or from blood) is performed using penalized least squares, as implemented in the *R* package copynumber. To each segment is assigned the mean SRC value, calculated from the bins within the segment. SRC is proportional to the mean number of chromosomes (copies), averaged over all sequenced cells.

Germline heterozygous positions are extracted in the autosome, except in regions of the genome where duplication or deletion events are observed in the normal tissues. The number of reads supporting each allele (the reference allele – the one observed on the reference human assembly – and the alternate allele) is recorded from the tumour data and the allelic ratio (AR; the proportion of reads supporting the reference allele) calculated. Each heterozygous position is also paired with the SRC value of the segment it belongs to, evaluated from the tumour data, to form pairs of values (SRC, AR). These pairs of points are represented in a three-dimensional graph as a contour (elevation) plot (Fig. 2). This figure is a visual representation of the autosomal-wide copy number profile of the tumour. Each peak (or pair of peaks since the graph is reflected around AR=0.5) corresponds to a specific copy-number state that summarizes both the total copy number (on the x-axis, once appropriately scaled) and the ratio of relative abundance of maternal and paternal copies (on the y-axis, once contamination from normal tissues – or tumour cellularity – is accounted for). The relative positions of these peaks can be mathematically derived in the following way.

Let us define the autosomal ploidy of a *sequenced sample* (that includes both tumour and possibly contamination from normal cells) as

$$P = \frac{1}{N_B} \sum_{b} c_b$$

where $c_b$represents the mean number of chromosomal copies at base *b*, averaged over all cells, and N_B is the number of autosomal bases. This can be interpreted as the relative abundance of autosomal DNA in the sequenced sample compared to a normal (reference) haploid autosomal genome. We aim to use the SRC values to estimate the ploidy. Re-writing the above as

$$P \approx K \times \frac{1}{N_{bins}} \sum_{bin} SRC_{bin}$$

(where K is a scaling constant) is not informative since the SRC values are scaled and relative, making this expression trivial. However, because SRC are scaled to the mean, bins that fall in regions of exactly P copies (averaged over all cells) are expected to display SRC values of 1. Let S be the value of SRC that would be expected in regions where all cells display 2 copies of chromosomes (such regions do not need to actually exist in the sequenced sample). Because of proportionality, we have the relationship

$$P = \frac{2}{S},$$

thus, ploidy can be evaluated by finding S.

Consider the more general case of a sequenced sample that consists of a proportion n of normal cells and t of tumour cells ($n+t=1$). Because ploidy may differ in normal and tumour cells, these percentages *are not* equivalent to percentages of reads originating from normal or tumour cells. Consider a segment in the genome that is present in 2 copies in the normal cells and an average of T copies in the tumour cells. The tumour cells can be further broken down in subclones, in proportions t_1, t_2, …($t = t_1+t_2+\ldots$), each subclone displaying a different number of copies (T_1, T_2, ...). Then, by proportionality, the SRC of bins in that segment are expected to take the value

$$\frac{S}{2}\times(2n + T_1t_1 + T_2t_2 + \cdots)$$

(Eq. 1). To determine the expected AR of heterozygous positions in that segment, the number of copies need to be further broken down into number of maternal and paternal copies: $T_i=M_i+P_i$. Normal cells are assumed to have one maternal chromosome and one paternal chromosome. In a segment that displays M_i maternal and P_i paternal copies in subclone i, the AR is expected to take the value

$$\frac{n + M_1t_1 + M_2t_2 + \cdots}{2n + T_1t_1 + T_2t_2 + \cdots}$$

(Eq. 2) if, say, the maternal chromosome carries the reference allele, and reflected around 0.5 otherwise. Let

$$EP(S, n, t, M_1, P_1, M_2, P_2, \cdots)$$

represent the (x,y) coordinates described in Eq. 1 and 2. Let $OP = \{OP_i\}$ be the set of observed contour plot peaks (or subset of peaks deemed of particular interest by the user). The algorithm used to estimate S, n and t finds parameters that minimize the total distance between the observed peaks and the EP coordinate closest to each. In other words, if

$$d_i(S, n, t) = \min_{M_1,P_1,M_2,P_2,\cdots} |OP_i - EP(S, n, t, M_1, P_1, M_2, P_2, \cdots)|,$$

then the algorithm consists on finding S, n and t that minimize

$$\sum_i d_i(S, n, t).$$

In practice, the number of expected peak locations grows exponentially with the number of subclones and the number of maternal/paternal configurations. The algorithm further depends on a set of allowed copy-number configurations (a set of M_i and P_i) that can be set by the user. For example, the user might want to ignore configurations where the number of maternal chromosomes is smaller than the number of paternal chromosomes in one subclone but higher in another; this would reduce the number of possible ARs. Other restrictions may include situations where the number of copies between different subclones cannot differ (by difference or by ratio) by more than some specified threshold.

The objective function to be minimized is not convex and multiple local minima exist. Optimization is done either by simulated annealing if a global minimum is desired (using the *R* package GenSA) or using the *R* built-in function optim with grid-defined starting points to survey and inspect a set of local minima.

Once values for S, n and t are obtained, the ploidy in the *tumour* cells (P_T) can then be calculated as

$$P_T = \frac{P - 2n}{1 - n}$$

where $P=2/S$ is the ploidy of the whole sample that was sequenced. The SRC values can be rescaled into their corresponding integer copy number in tumours using Eq. 1 above.

The above describes the current implementation of an *R* package named CELLULOID, which can be obtained from http://github.com/mathieu-lemire.

The interconnection between tumour ploidy and sample cellularity

Tumor ploidy and sample cellularity estimates are interconnected: while the ploidy of a tumor can always be doubled and still provide copy-number segments at integer levels (albeit only at even values), the estimate of cellularity would have to be decreased. Indeed, in order to maintain an allelic ratio at a given value, the proportion of tumor cells has to be reduced to compensate the higher number of copies in them (from a cellularity value t to a value $t/(2-t)$ in the case of a doubling of the ploidy). A test (e.g. Kruskal-Wallis) can thus be designed to verify that ploidy estimates have not been systematically over- or underestimated, simply by comparing the distribution of cellularity estimates stratified by ploidy.

To compare CELLULOID's calls with other software, we ran TITAN[24] on the tumors to get estimates of ploidy and cellularity. We varied the number of clonal clusters from 1 to 2, and for each, starting values for ploidy were set at 2, 3.5 and 5.5. Of the 6 possible solutions, we chose the one that was associated with the smallest validity score index. For the selected 12 tumors that were validated using FISH (Supplementary Figures 16 and 17), we present in Supplementary Figure 17 the contour plots of their copy number profiles, overlaid with expected peak locations calculated from equations presented in Methods, calculated from TITAN's estimates of tumor ploidy and tumor cellularity; the majority of the solutions based on minimum validity index alone appeared to inadequately capture the tumor copy number profiles (Supplementary Figure 17, left column). We note that for the large majority of tumors, curation of TITAN's possible solutions by inspection of the copy number profile would reveal a solution that is in close proximity to the call made by CELLULOID (Supplementary Figure 16; Supplementary Figure 17, second and third panels), with the exception of high ploidy calls and the apparent underestimation of cellularity by TITAN compared to CELLULOID.

Chrom-AL: Algorithm to detect cataclysmic genetic events

Chrom-AL is an in-house tool developed to standardize the detection of complex rearrangement patterns linked to chromothripsis[10]. Chrom-AL applies a series of statistical tests and thresholds at the level of the chromosome and also within the windows of the structural events to infer a call. We inspected 80 genomes manually and estimate that the false-positive and false-negative rate of Chrom-AL is approximately ~7% and ~8%, respectively, in our data set. The tool is designed based on the chromothripsis criteria presented by Korbel and Campbell[25]. Complex rearrangement patterns can often involve multiple distinct types of mitotic errors (ex. FoSTeS, MMBIR) including a chromothripsis event[10,11,26]. Chrom-AL is not designed to distinguish chromothripsis from other replication based mitotic errors, which can also be catastrophic occurring within one or few cell divisions. As such, we use the term chromothripsis to broadly refer to a 'one-off' mitotic catastrophe.

As chromothripsis events typically increase the number of SVs in a genome, there is a correlation between tumours with increased numbers of SVs and rate of chromothripsis[7]. Thus, proper SV calling becomes a critical parameter in implementation of any algorithm to call chromothripsis. Despite this correlation, a high rate of SVs does not necessarily imply a chromothripsis event. Thus, the false positive and false negative rates of Chrom-AL will likely vary with the overall rate of SVs that differs amongst tumour types. For this reason, visual inspection still remains a critical tool in evaluating such events. Chrom-AL does not detect chromothripsis events that are predominately driven by a single SV type. For example, on rare occasions, we observed the typically CN oscillation hallmark of chromothripsis that was connected mostly by HH or TT inversions. Whether such rearrangements were indeed accumulated over time or all at once is not known. To remain consistent with the criteria discussed below, we excluded these events from the analysis. Below, we describe the criteria and conditions used to detect cataclysmic events by Chrom-AL. Chrom-AL was implemented in *R*.

Tests for Catastrophic Events:

1) **Threshold for number of structural variants (SVs) and copy number (CN) alterations (chromosomal level)**

   Catastrophic events typically have large numbers of SVs and CNs changes. Only events with at least 7-8 SV and 8 CN segments were considered in the analysis.

2) **Clustering of breakpoints (chromosomal level)**

   Catastrophic events are typically localized to particular genomic regions that can be assessed statistically. To do this, we ordered the breakpoints sequentially and calculated the distances between each breakpoint. The distribution of distances were compared against the exponential distribution as described by Korbel and Campbell [25] using a Kolmogorov-Smirnov (KS) test and followed by Bonferroni correction. Regions with a q <= 0.1 were considered to display evidence of breakpoint clustering.

3) **Chromosomal breakpoint enrichment (chromosomal level)**

   We observed several instances where SVs comprising a catastrophic event were scattered chromosome wide and did not cluster within a particular region of a chromosome. Thus, they failed the KS test described above. To account for this shortcoming, we performed an additional test to determine if SVs were enriched on any particular chromosome than would be expected by chance. To identify chromosomes enriched for SVs, a hyper-geometric test was run on each chromosome based on all the breakpoints identified in the tumour. This was followed by a Bonferroni correction. Chromosomes with a q <= 0.1 were identified as having a high rate of breakpoints.

4) **Join Distribution (chromosomal and window level)**

In paired end sequencing, all SVs can be categorized into 4 read-pair orientations based on the direction of the + or − reads: tail-to-head [+/-, TH], head-to-head [-/-, HH], tail-to-tail [+/+, TT], head-to-tail [-/+, HT]. Pairs in standard orientation (+/-) are considered to be a deletion type SV with a TH join. Duplication type SVs are in the reverse orientation -/+ and defined by a HT join. Inversions can be both in the forward (+/+) orientation or reverse (-/-) orientation. In the forward orientation, they were defined as TT and in the reverse orientation they were defined at HH. Using read-pair information for SVs, we classified each SV based on their segment joins. In a catastrophic event, we expect SVs of all 4 types to be present. For each region we tested this hypothesis. To initially run the test, we required at least 1 type of read-pair join from each of the 4 subtypes to be present. A multinomial test, from the EMT v1.1 package, was run to test the distribution of segment joins against an equal distribution. The regions with a p-value > 0.05 were considered to show evident of equal distributions of segment joins.

5) **CN Oscillations (chromosomal and window level)**

Catastrophic events typically display oscillations in CN that vary between a few states. However, when chromothripsis is coopted with BFB cycles as part of a single catastrophic event, there will be some segments in the event that will oscillate between limited CN states versus other segments that may appear to increase in a stepwise manner. To be categorized as a bona-fide ‘one-off’ event, there must be some sequential segments that retain an oscillation pattern. We required at least 4 sequential segments in any catastrophic event must oscillate between two different states. Due to polyploidization, the amplitude of the CN step was defined to be variable (1, 2 or more).

6) **Interspersed LOH (chromosomal and window level)**

Chromothripsis drives CN losses, and thus CN oscillations should correspond to interspersed loss of heterozygosity (LOH). To test for LOH, we identified all the high confident germline heterozygous SNPs in the genome and determined the allelic ratio in the tumour sample. The distributions of allelic ratios between each sequential CN segments were compared using a t-test. A minimum of 10 positions had to be identified within each CN segment to be processed otherwise those segments were exclude from the analysis. A bonferroni correction test was run. Those segments with a q <= 0.1 were considered significantly different. To show evidence of interspersed LOH, at least 4 comparisons had to be made (thus at least 5 CN segments had to be present in the region). At least 50% of the compared segments had to show some significant difference in the distribution of allele ratio to be classified as showing interspersed LOH.

Chromosome level analysis:

Genomic regions were first evaluated at the chromosome level. For each sample, all chromosomes were independently evaluated for the above tests. For tests 2 and 3, we used CN breakpoints for segments where a matching SV could not be mapped. The importance of this point is shown in Fig. 4a (Ashpc_0008, event 2). In this case, there was a chained chromothripsis event connecting chromosomes 3 and 20. On chr 3, the left edge of at 42.8 Mb was part of the chromothripsis event but the corresponding SV to this CN loss is not mapped. This was also the case for the right edge of the chromothripsis event on chr20 (7.1Mb). In this scenario, CN breakpoint was critical to utilize in the tests to decipher whether this was indeed a chromothripsis event. If CN breakpoints are not integrated into the analysis, such events would go undetected or be misclassified. We found that including CN breakpoint was necessary to properly establish the DNA windows of chromothripsis events, especially when SVs could not be properly mapped (discussed below).

Identification of DNA rearrangement windows:

The next step was to identify the borders of the catastrophic event on each chromosome. Catastrophic events typically display overlapping SVs throughout the region of the event. To localize the chromosomal window where the catastrophic event occurred, we selected the left and right borders of overlapping SV breakpoints. SVs resulting in translocations were used to establish the rearrangement window when at least two independent translocations were detected between the same two chromosomes. In this manner, we could establish inter- and intra-chromosomal windows to facilitate the segregation of multi-chromosome events from single-chromosome events. Each window was flanked with 6kbp on either end. The windows that define each candidate catastrophic event were used for downstream analysis.

Window Level Analysis:

A window was first scored on whether there were at least 8 SVs present within the window. Each window was then evaluated for tests 4-6.

Classification of single chromosome versus multi-chromosome catastrophic event:
Single chromosome catastrophic events were classified when all SVs within a window occurred on the same chromosome. In the case of translocations, at least 2 SV had to have occurred between the same two chromosomes to be considered a multi-chromosome event. If more than 2 chromosomes were involved, each chromosome had to have SVs occurring with *n*-2 of the other chromosomes, where *n* refers to the total number of chromosomes involved, to be considered part of the chain.

Event (CR1 vs. CR2)
Each window was independently scored. If a window was classified as a catastrophic and was involved in a multi-chromosome event, both windows on either side of the translocation were considered to be catastrophic at the chromosomal level but were counted as a single catastrophic event. Through a large number of iterations where the tests described above were iteratively optimized, we established two distinct criteria maximize sensitivity and specificity of detection.

Criteria 1 (CR1)
To be classified as an event under CR1, a region had to pass at least 5 of the 6 chromosomal level tests (test 1-6). A window had to be identified with at least 8 SV and the window had to pass the segment join and the interspersed LOH test (test 4 and 6).

Criteria 2 (CR2)
To be classified as event under CR2, a region had to pass at least 5 of following test: the 6 chromosomal level tests (test 1-6), the identification of a window with at least 8 SV, the window segment join and the window interspersed LOH test (test 4 and 6). In addition to these conditions, the window had to have at least 7 SV events and had to pass window oscillation (criteria 5).

Timing of copy number and mutations in polyploid tumours

CN alterations were classified according to whether they occurred 'before' or 'after' genome duplication. Although this analysis is more accurately tetraploids (due to the number of limited paths to a give final CN state in tetraploids), we did perform analysis on hexaploids

(Supplementary Fig. 7b,c). In the case of deletions, a copy state of 0 implies an event that occurred prior to genome duplication. According to the most parsimonious interpretation, a copy state of 1 and 3 implies CN changes that occurred after genome duplication. To determine the relative timing CN alterations that resided at a state of 2, we used germline allelic ratios. A CN of 2 at LOH was considered to be a CN loss that occurred before genome duplication. However, lack of LOH was considered to be an alteration that occurred after genome duplication. For amplifications, events at even CN state were considered to be alterations that occurred before genome duplication versus those with odd CN states were considered to occur after, and consistent with criteria used previously [27].

To time somatic mutations, we looked only at the mutations that fell within regions that had a copy state of 4. At each of these positions, we calculated the number of mutated copies found in the cell using the following formula that accounts for the cellularity of the sample.

$$Somatic\ AR = \frac{t * k}{\big(t * (m + p)\big) + (n * 2)}$$

Where the t is fraction of tumour in the sample (cellularity), n is the fraction of normal in the sample, k is the number of mutated copies, m is the number of maternal copies and p is the number of paternal copies. Mutations with greater than 1 copy were deemed to occur before genome duplication because they lie on multiple copies. On the other hand, mutations that lie on 1 copy were considered to occur after genome duplication.

Statistical Analysis

To test whether any chromosomes were statistically enriched for chromothripsis events, we performed Monte Carlo sampling. The 192 detected chromothripsis events were randomly scattered across the genome using a multinomial distribution assuming an equal probability of hitting each chromosome. We did not account for chromosome size, as the recently identified mechanism of chromothripsis suggests that such events are independent of size of the chromosome as any size piece of a chromosome or whole chromosomes can get caught in micronuclei[10]. The test was iterated 100,000 times. For each chromosome, we identified the number of times a value greater than or equal the observed value was spotted for each chromosome (Fig. 3b). To infer a p-value, the fraction of the simulated observation per chromosome over the total number of tests was used. For instance, we detected 22 samples with a chromothripsis event on chr18. In only 49 replicates (p=0.00049; 49/100,000) did we observe at least one chromosome (any) displaying chromothripsis in 22 or more simulated samples, illustrating that results on chr18 are robust to multiple testing issues.

Data Availability

Raw data (fastq files) and clinical information on the patient cohort are available from the International Cancer Genome Consortium (ICGC) data portal at http://dcc.icgc.org.

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Supplementary Figure and Table Legends

Supplementary Figure 1: In Ashpc_0027, a focal set of SVs resembling a mitotic catastrophe which included cycles of BFB resulting in the concurrent loss *SMAD4* and gain in *GATA6*.

Supplementary Figure 2: Survival analysis of patient cohort used in this study. (a) Kaplan-Meier curve for overall survival for cases with (blue) and without chromothripsis (red). The poor prognosis associated with chromothripsis was maintained in multi-variable analysis including traditional prognostic factors of tumour stage and grade. The survival curves include an additional 41 cases that were sequenced during the course of our analysis (n=148; Connor et al., manuscript submitted). **(b)** The wide spectrum of chromothripsis events (from 8 SVs to 100s) prompted us to perform a basic analysis based on the median number of SV rearrangements in our tumour cohort (SV high > 70 rearrangements; SV low <= 70 rearrangements; 70 patients in each group). p values were derived using log-rank test. However, further studies with larger patient cohorts will be required to establish the prognostic value of chromothripsis in PC.

Supplementary Figure 3: The data presented here is related to the analysis presented in Fig. 3 and Extended Data Fig. 7. **(a)** Copy number profile of chr17 and chr18 from the heart (hr) metastasis (Pcsi_0410) showing that *TP53* and *SMAD4* genes are at copy number of 2 but at LOH due to a ploidy event (shown in Extended Data Fig. 7). **(b)** FISH validation for copy number of *TP53* and *SMAD4* genes in the heart metastasis and primary tumour. This confirms that the primary tumour was polyploid. FISH probes overlap *TP53* and *SMAD4* genes (shown as black line in a. **(c)** Chromosome rearrangement plot depicting an additional chromothripsis event specific to the adrenal gland (ag) metastasis in Pcsi_0410. The copy number step in the chromothripsis event is one indicating that it occurred after polyploidization event in Pcsi_0410. hr – heart.

Supplementary Figure 4: Summary of all cases where a simultaneous event affected classical driver genes in PC evolution (*KRAS, CDKN2A*, *TP53, SMAD4*). Single unbalanced translocations are included in these analyses because, by definition, such events are simultaneous similar to chromothripsis. **(a)** Ashpc_0003: *CDKN2A* and *SMAD4*. **(b)** Ashpc_0017: *TP53* and *SMAD4*. **(c)** Ashpc_0026: *TP53* and *SMAD4*. **(d)** Pcsi_0227: *TP53* and *SMAD4*. **(e)** Pcsi_0326: *TP53* and *SMAD4*. **(f)** Pcsi_0239: *CDKN2A* and *SMAD4*. **(g)** Pcsi_0297: *TP53* and *SMAD4*. **(h)** Pcsi_0492: *TP53* and *SMAD4*. **(i)** Ramp_0007: *CDKN2A* and *SMAD4*. **(j)** Pcsi_0236: *CDKN2A* and *SMAD4*. **(k)** Pcsi_0078: *KRAS* and *CDKN2A*. **(l)** Pcsi_0078: *KRAS* and *SMAD4*. **(m)** Pcsi_0294: *TP53* and *SMAD4* loss. **(n)** Pcsi_0102: *TP53* and *SMAD4* loss. **(o)** Pcsi_0312: *TP53* and *SMAD4* loss.

Supplementary Figure 5: Design of flow sorting scheme used to distinguish tumour epithelial cells from stromal cells. (a) Gating strategy to purify tumour epithelial cells (EpCAM+), lymphocytes (CD45+), endothelium (CD31+CD34+), and fibroblasts (CD90+CD140b+) from primary pancreas ductal adenocarcinoma. Viable cells were gated based on propidium iodide staining. **(b)** Whole genome sequencing was performed on lymphocytes and fibroblasts to demonstrate that these lineages are not tumour derived. Representative IGV plot of the *KRAS* mutation from purified tumour cells, lymphocytes and fibroblasts is shown.

Supplementary Figure 6: Rationale used to distinguish diploid and polyploid tumours by CELLULOID. (a) Scenarios of CN events where heterozygosity is retained (i) or lost (LOH) in a diploid tumour. **(b)** Scenarios of CN events where heterozygosity is retained (i), or lost (ii-iv) due to CN alterations that occur before or after genome duplication. Schematic plots of the consequences of these scenarios on germline allelic SNP ratios and CN are shown. 'a' and 'b' represent heterozygous germline SNP. For simplification, only deletions are depicted.

Supplementary Figure 7: **(a)** Box whisker plots of the proportion of mutations acquired before or after polyploidization event in three cases with increased C>A transversions defined as Signature 8 by Alexandrov et al[2]. **(b)** Proportion of mutations acquired before (yellow) or after (blue) polyploidization event for tumour >4N (n=6). **(c)** Proportion of genome lost and gained either before (yellow) or after (blue) for these tumours. Box whisker plots represent 10-90% quartiles. p values were derived using t-test. **(d)** In polyploid tumours, the signature of mutations that occurred before and after polyploidization was derived independently. In tetraploid tumours, 28 of 30 cases did not demonstrate a change in the mutational signature before and after polyploidization (representative case is shown on the left column – Pcsi_0388). In two cases (DSBR – middle column; Signature 8 – right column), the defining signature only appeared after polyploidization. Pure mutational signatures from the Aging, DSBR and Signature 8 phenotype are shown according to the 96 base substitution context (bottom).

Supplementary Figure 8: Representative tumours where a chromothripsis event could be distinguished with as few as 7 structural variants (SVs) (left). Cases with similar number of SVs where Chrom-AL did not call a chromothripsis event are shown on the right. All Chrom-AL solutions are shown in the supplementary text. No of SVs used to make the chromothripsis call by Chrom-AL is shown top right for each case. Importantly, the algorithm needs to be combined with a visualization step to ensure the chromothripsis events are bona fide especially in cases where few SVs are involved in the event.

Supplementary Figure 9: **(a)** Chromothripsis image in a single case of lymphoblastic leukemia. **(b)** Percentage of the four subtypes of rearrangement profiles classified by Waddell *et al.*[5] observed across our cohort. **(c)** Number of chromothripsis events per sample subcategorized according to the rearrangement subtype in b.

Supplementary Figure 10: Images depicting SVs and CN alterations for chromothripsis calls from Supplementary Table 1 (ICGC validation group).

Supplementary Figure 11: Description of chromothripsis events observed in this study. **(a)** A focal chromothripsis event spanning a 2Mb window that removed a copy of *CDKN2A*. **(b)** A representative case of a multi-chromosome chromothripsis event spanning three distinct chromosomes. **(c)** A representative cases where a chromothripsis event was coopted with cycles of BFB cycles. Foldback (FB) inversions that denote a BFB cycle are shown as black curved arrows on top of the plot.

Supplementary Figure 12: Consensus copy number plots from cases with and without chromothripsis. To facilitate comparison of CN profiles amongst all cases, polyploidy tumours were normalized according to tumour ploidy (shown as Normalized CN on the y-axis). Interquartile ranges for chromothripsis cases are indicated in pale red, and for non-chromothripsis cases in pale blue. The location of common tumour suppressor genes in cancer, obtained from Vogelstein et al[28], are shown to uncover regions whether CN changes from chromothripsis affected driver genes.

Supplementary Figure 13: Characterization of copy number and mutation events in *TP53* and *SMAD4* genes. **(a,b)** CN number of the *TP53* gene with a coinciding mutation. In **a**, cases where the mutation is present in all cells (fully clonal) is shown. In **b**, cases where the mutation is subclonal to the allelic loss are shown. Cases where the CN of the gene is above 1 are polyploidy tumours. **(c,d)** Similar to a and b for status of the *SMAD4* gene. To determine the fraction of tumour cells carrying the mutation, we used the following formula from Nik-Zainal et al.[29]: $f = \min\left(1, \frac{r}{R}\frac{pCN_T+(1-p)CN_N}{p}\right)$. r – read depth of mutant allele, R – total read depth, ρ - cellularity, CN_T – copy number of variant in tumour, CN_N – copy number in normal.

Supplementary Figure 14: Characterization of *TP53* and *SMAD4* mutational status in a case of primary tumour and matched metastases. **(a)** Schematic depiction of the case. The primary tumour (P) was in the head of the pancreas was removed by whipple resection. The two metastases appeared at the site of anastomoses (M1) and in pancreas tail (M2) one year after the surgery. All tumours had a minimum cellularity of at least 80% prior to sequencing. All three samples underwent WGS to ~45X depth with a paired normal (blood) at ~40X. **(b)** CN status of *TP53* and *SMAD4* in the primary tumour and metastases. CN for all cases for both genes resides directly at integer copy indicating that it is present in all cells. **(c)** IGV depiction of the *TP53* and *SMAD4* variant observed in these tumours. **(d)** Proportion of cells carrying the *TP53* (top) and *SMAD4* (bottom) variant in primary and metastases. **(e)** The chromothripsis event on chr9 that removed a one copy of *CDKN2A* in present in the primary tumour and metastases. * indicates region reads that mapped to repeat regions.

Supplementary Figure 15: Phylogenetic tree of metastatic progression in Pcsi_0410 (related to Figure 3). a) To derive the genetic relationship between metastases in Pcsi_0410, a neighbour-joining tree was inferred using the Euclidean distance defined by copy number profiles (encompassing structural variants) and weighted by the length of the segments. Copy number profiles of each sample are below the clustering dendrogram (log2 scale). (**b**) Genetic relationship of metastases based on somatic SNV data using neighbour joining method based on whether the SNV was present. There are a total 6,750 somatic SNVs shown in the heatmap and 4,183 that were common in all of the metastases (not present on the map).

Supplementary Figure 16: Assessment of ploidy by CELLULOID and TITAN. Comparison of **(a)** ploidy and **(b)** cellularity estimates between CELLULOID and TITAN. TITAN's solutions were inspected according to contour plots (shown in Supplementary Figure 17) and curated. The size of the points indicates the rank of TITAN's validity index measure based on 6 possible solutions.

Supplementary Figure 17: Comparison of TITAN solutions and CELLULOID solutions for FISH validated samples. Cases showing ploidy solutions for TITAN based recommended validity index (indicated to left corner, TITAN – default) versus an alternate solution (TITAN curated) that verified with FISH data (bottom left). The CELLULOID solution corresponds to revised TITAN ploidy solution.

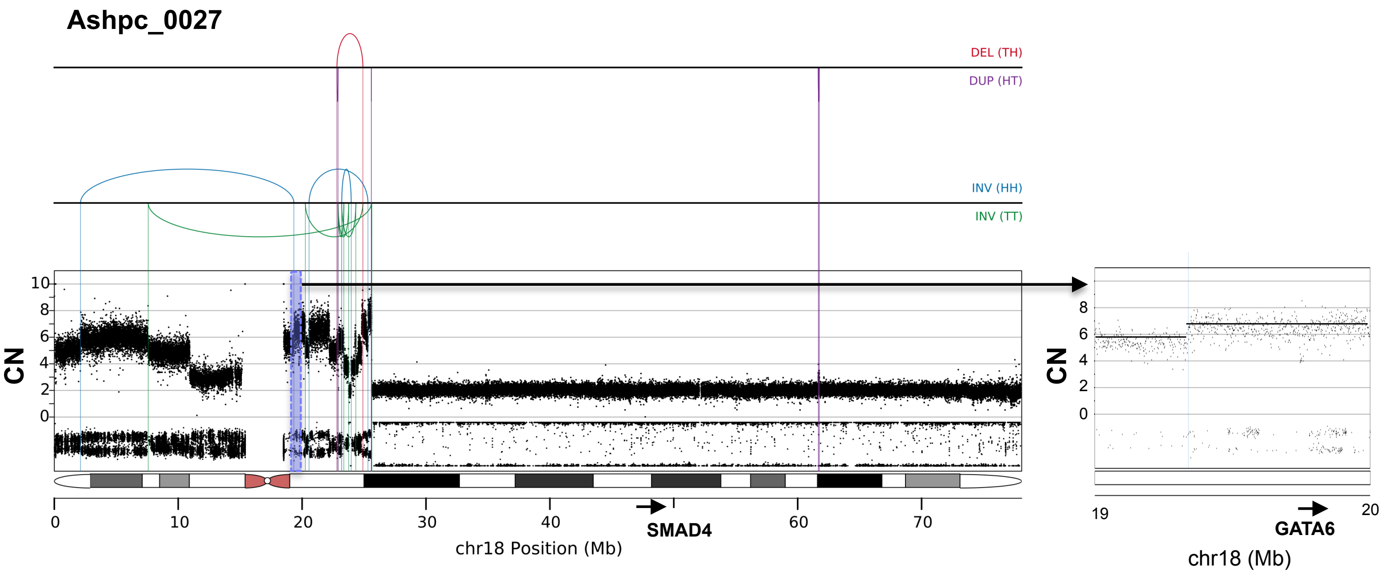
Supplementary Figure 18: Related to Extended Figure 9: **(a)** High concordance between LOH events in bulk (*) tumour versus single tumour cells. **(b)** Coverage statistics on single cells used in the analysis above.

Supplementary Table 1: Summary of pathological and clinical variable of the cases used in this study.

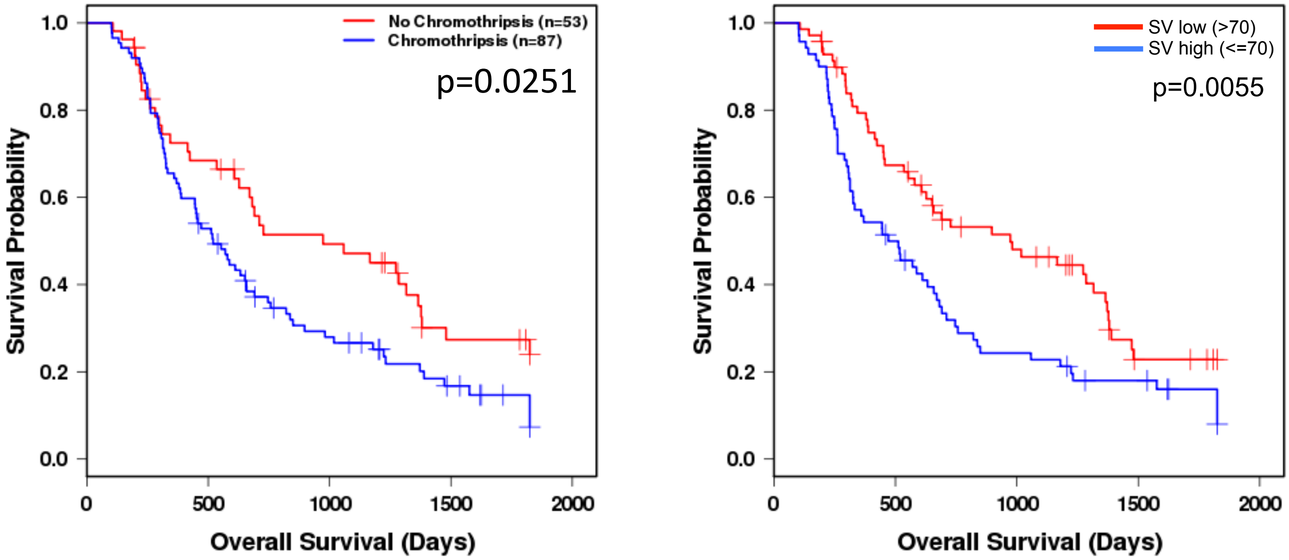
Supplementary Table 2: Summary of chromothripsis events in the validation cohort of PC genomes made available through the International Cancer Genome Consortium. Images of all events are presented in Supplementary Fig. 10.

Supplementary Figures and Tables

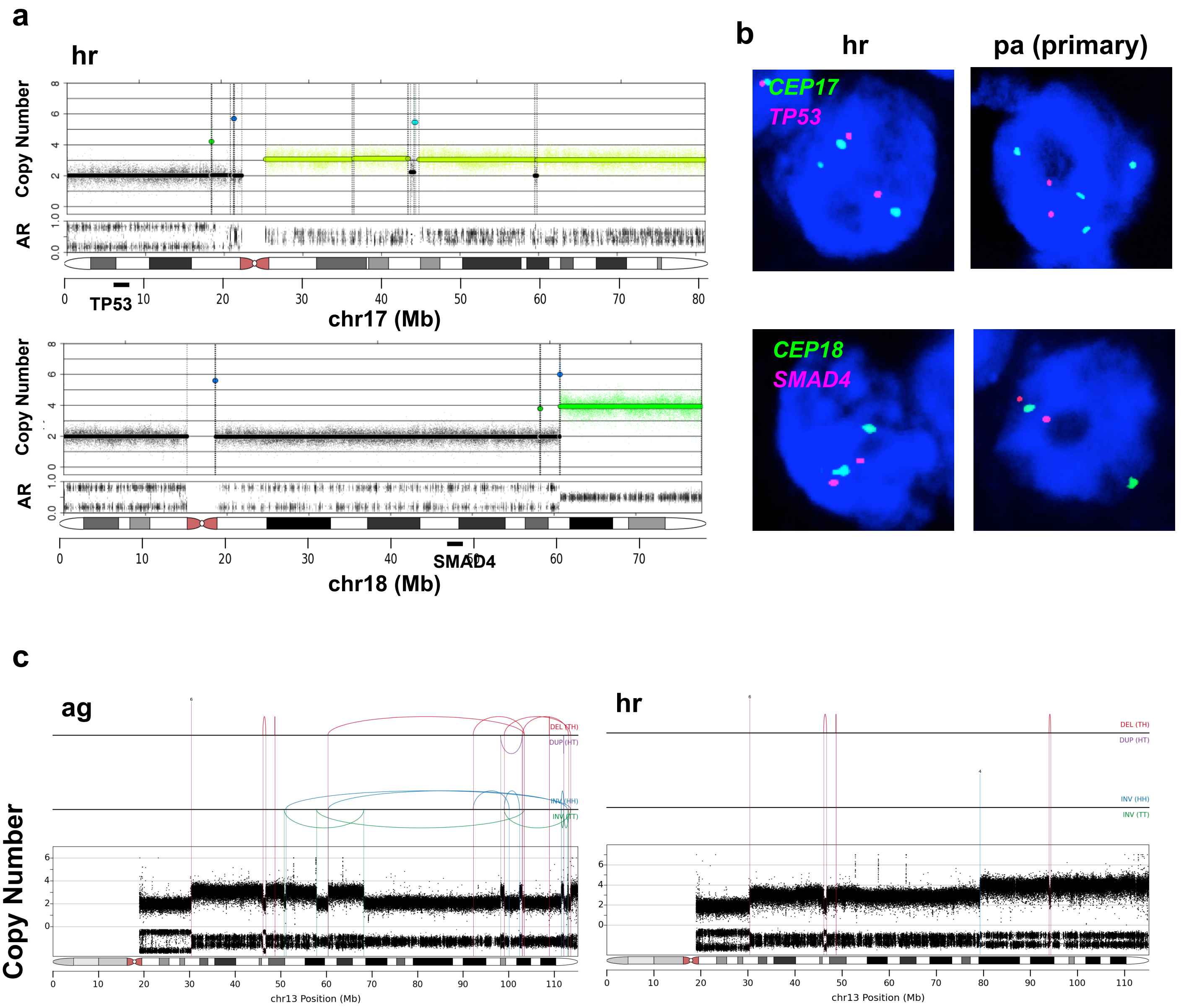
Supplementary Figure 1



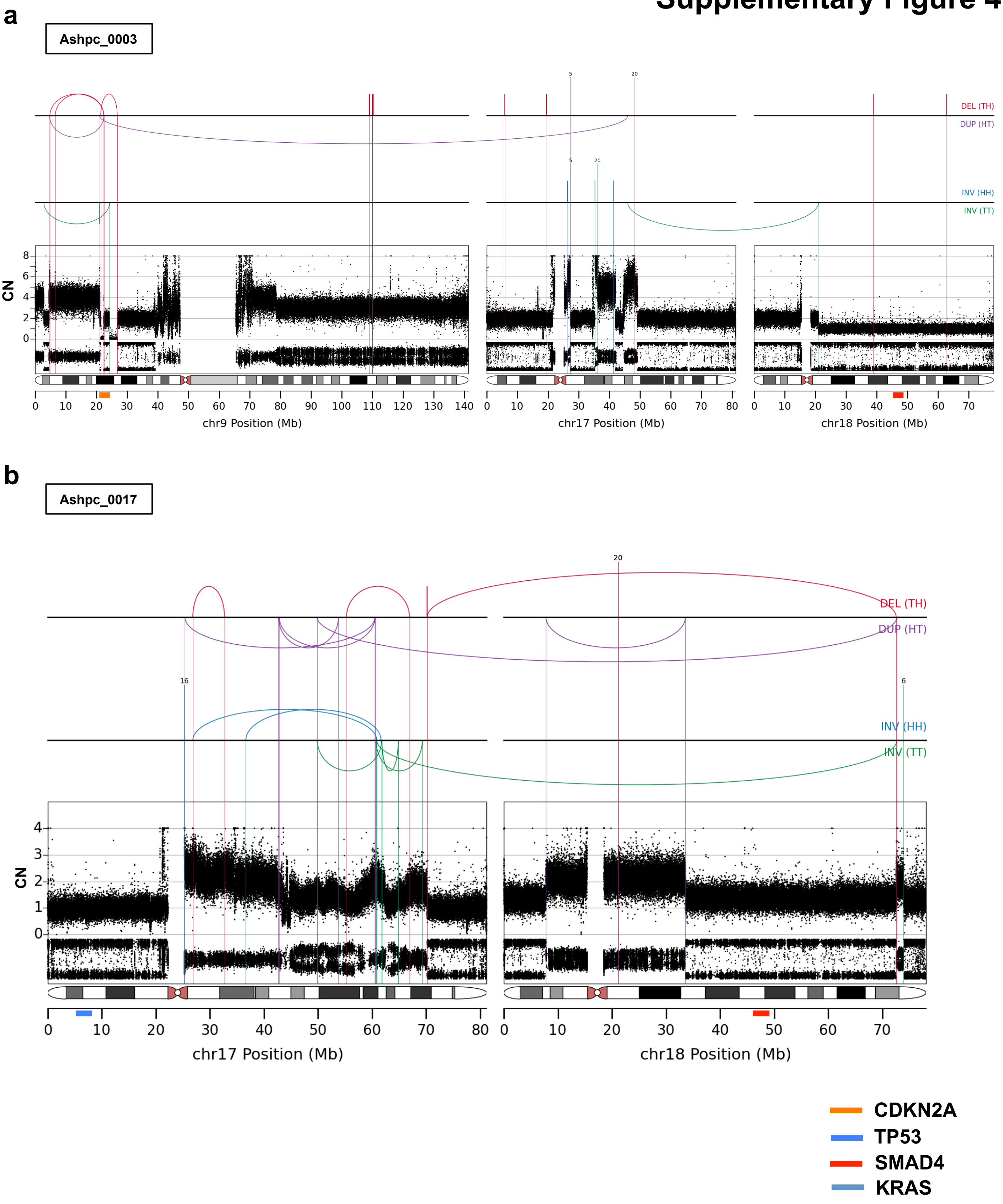
Supplementary Figure 2



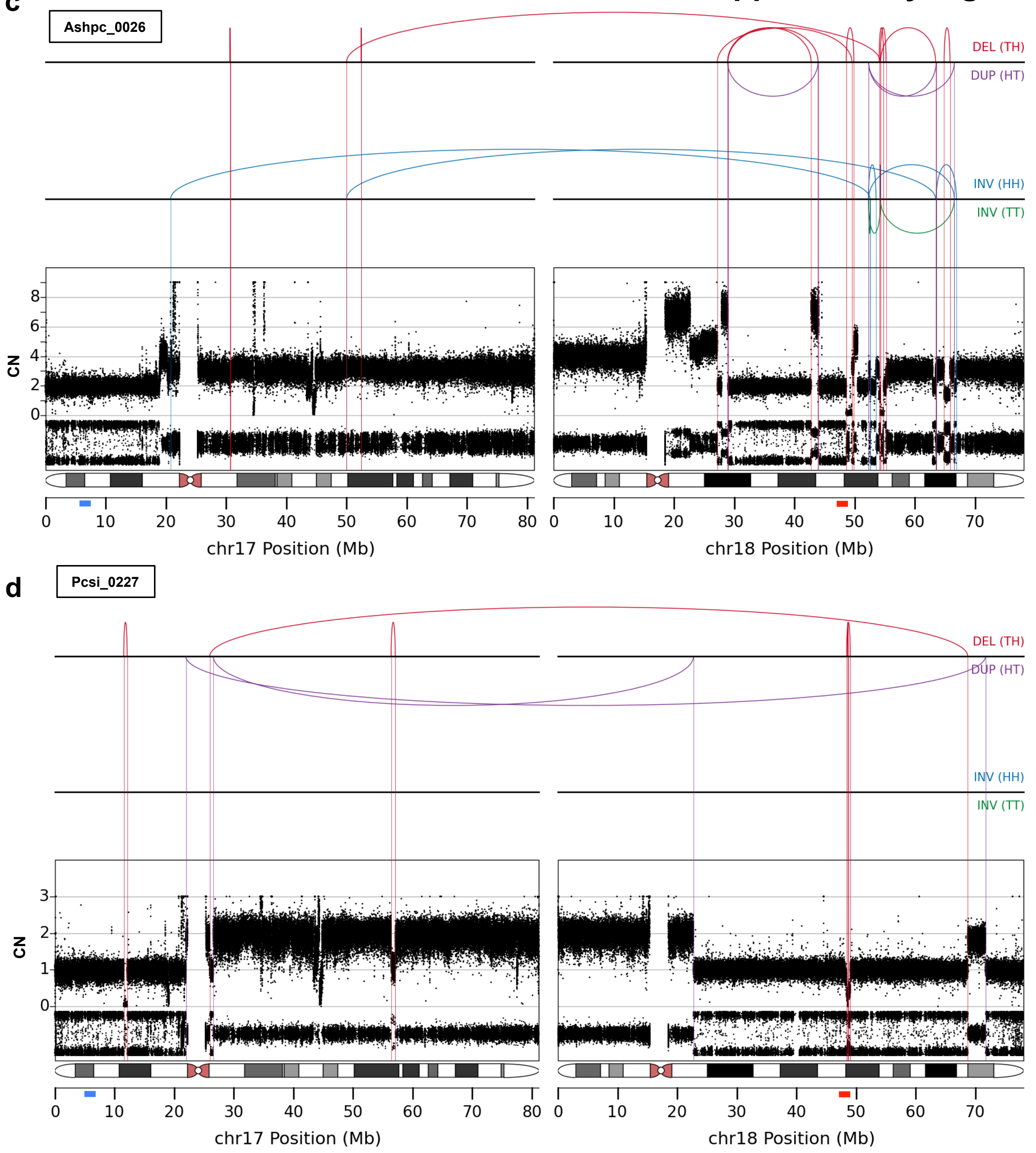
Supplementary Figure 3

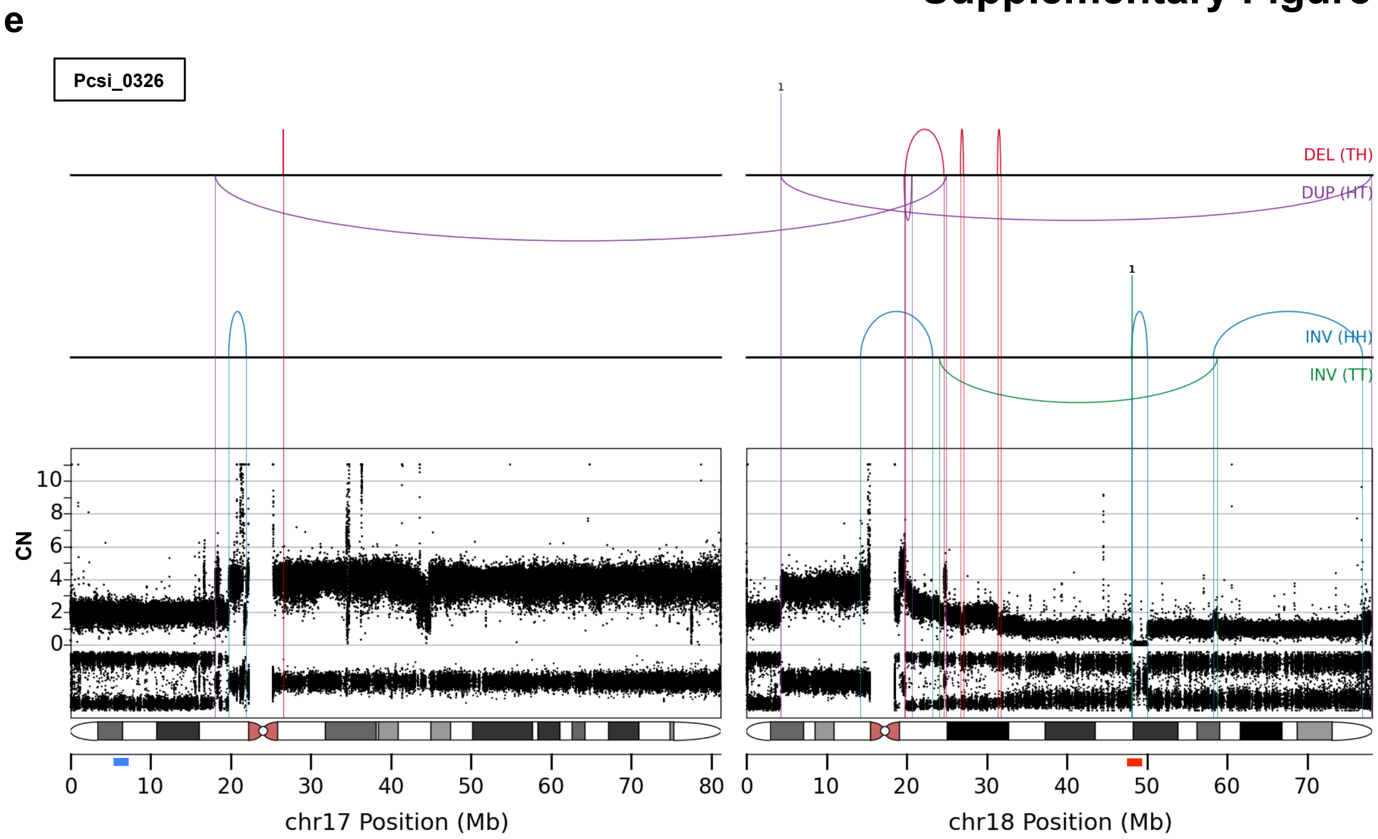


Supplementary Figure 4



Supplementary Figure 4

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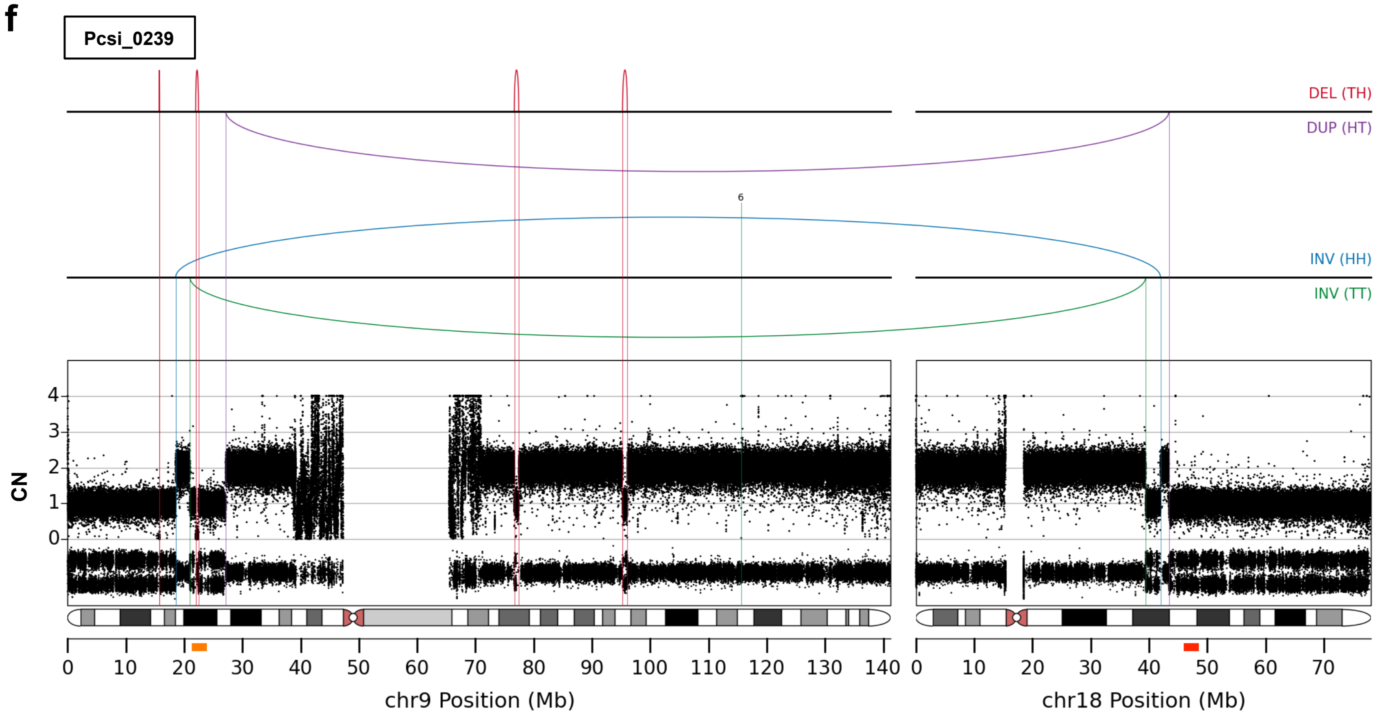
Pcsi_0326
1
1
DEL (TH)
DUP (HT)
INV (HH)
INV (TT)
CN
10
8
6
4
2
0
0 10 20 30 40 50 60 70 80
chr17 Position (Mb)
0 10 20 30 40 50 60 70
chr18 Position (Mb)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Pcsi_0239
6
DEL (TH)
DUP (HT)
INV (HH)
INV (TT)
CN
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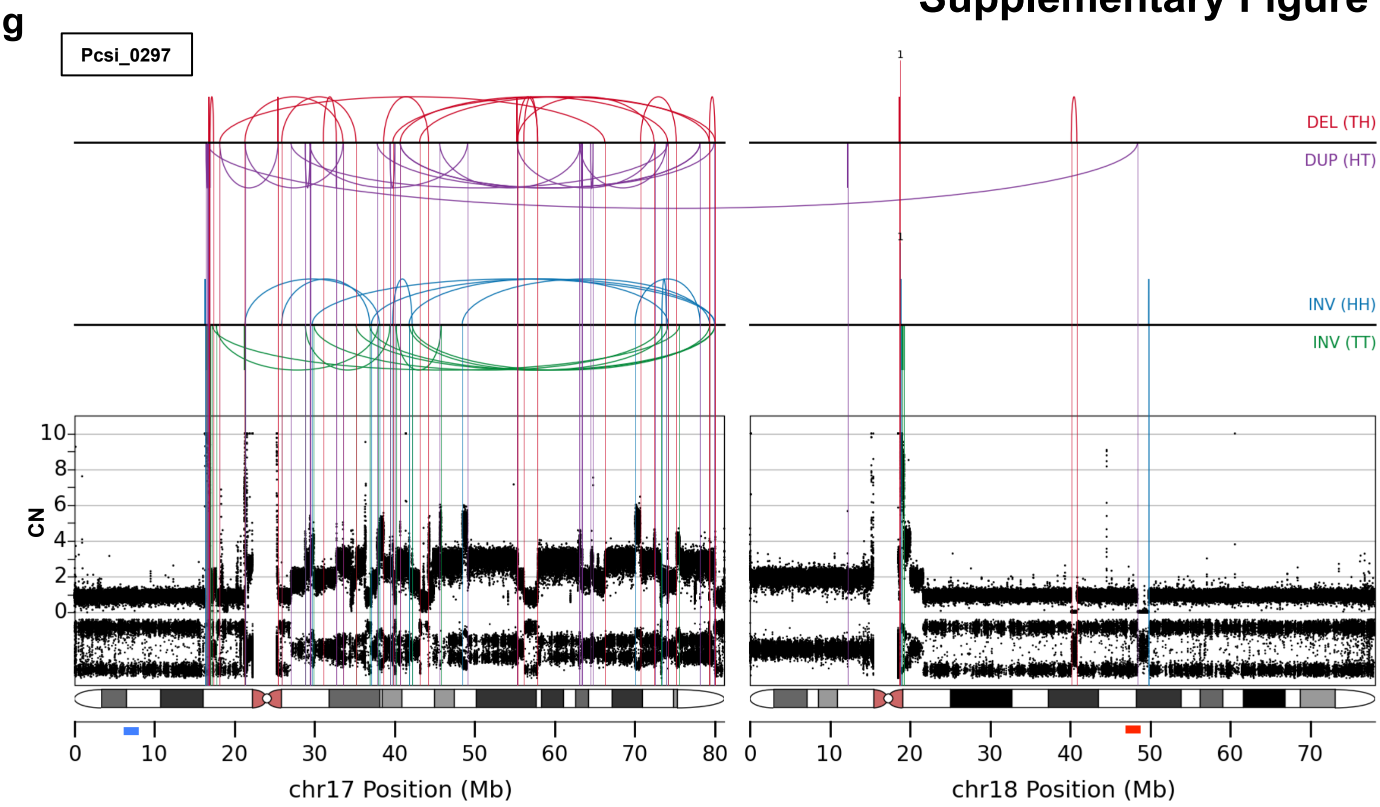
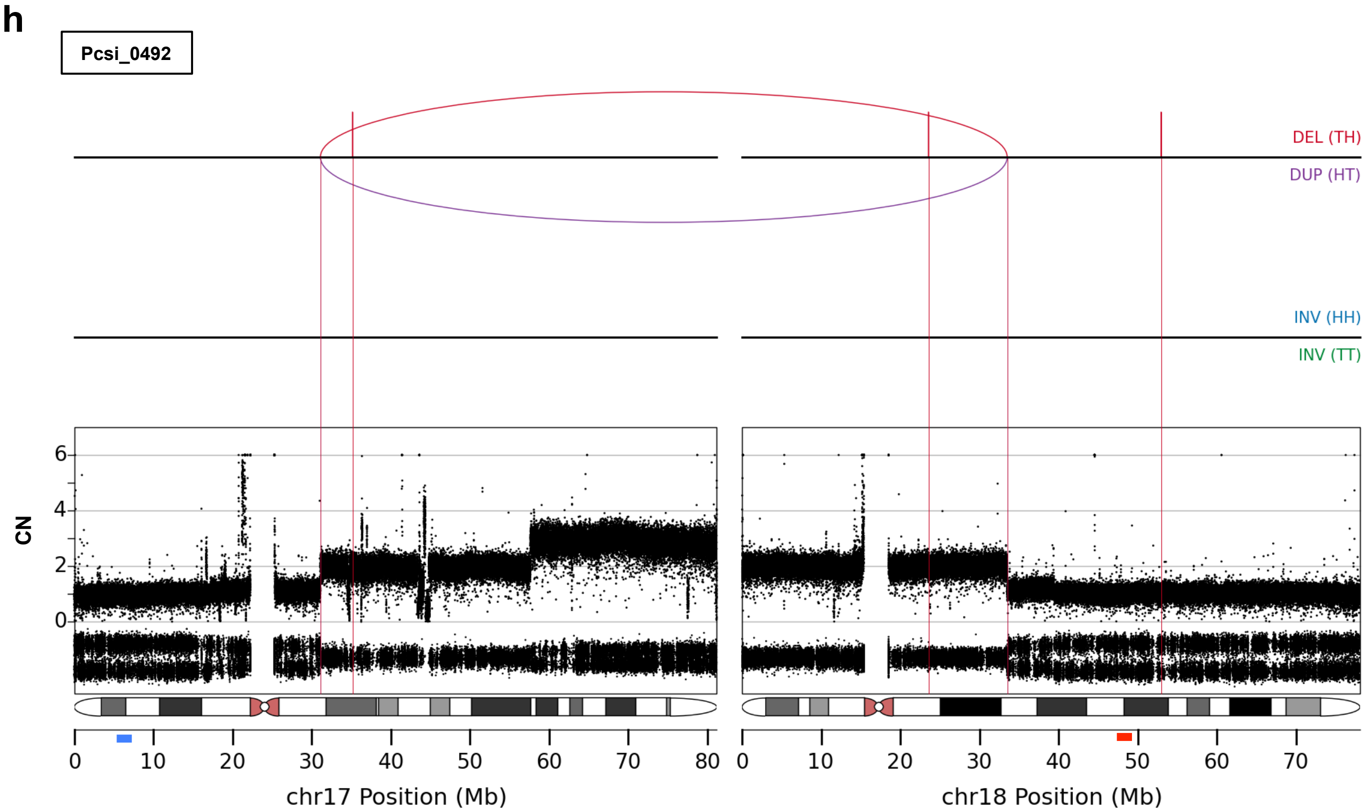
3
2
1
0
0 10 20 30 40 50 60 70 80 90 100 110 120 130 140
chr9 Position (Mb)
0 10 20 30 40 50 60 70
chr18 Position (Mb)

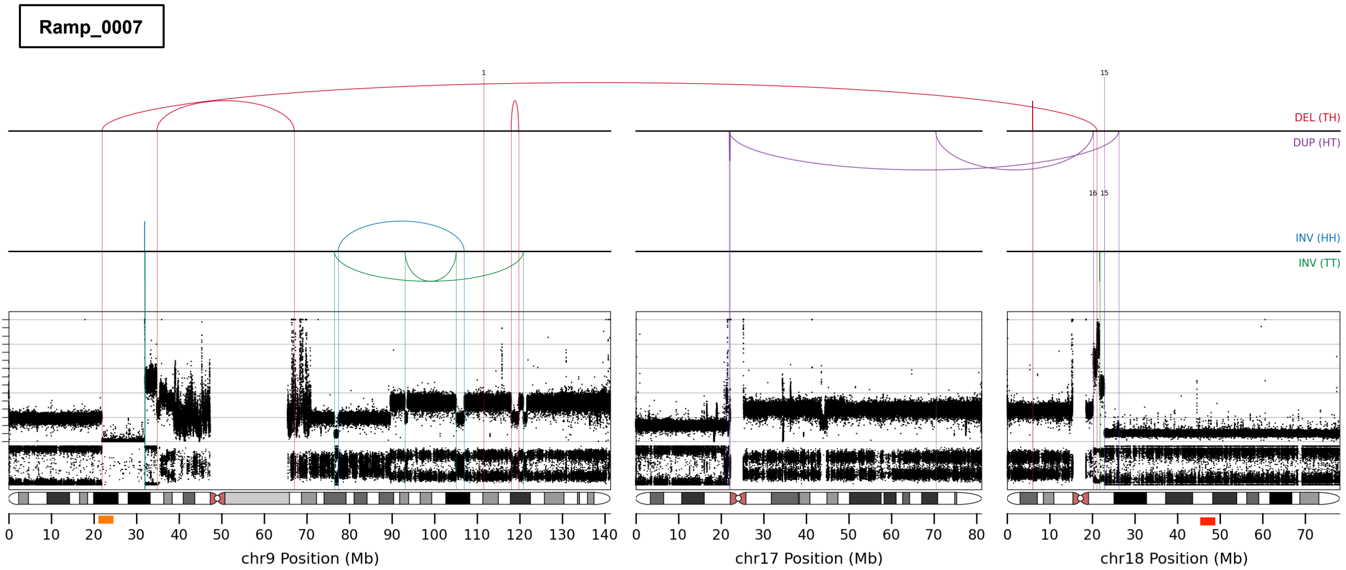
Supplementary Figure 4





Supplementary Figure 4

i



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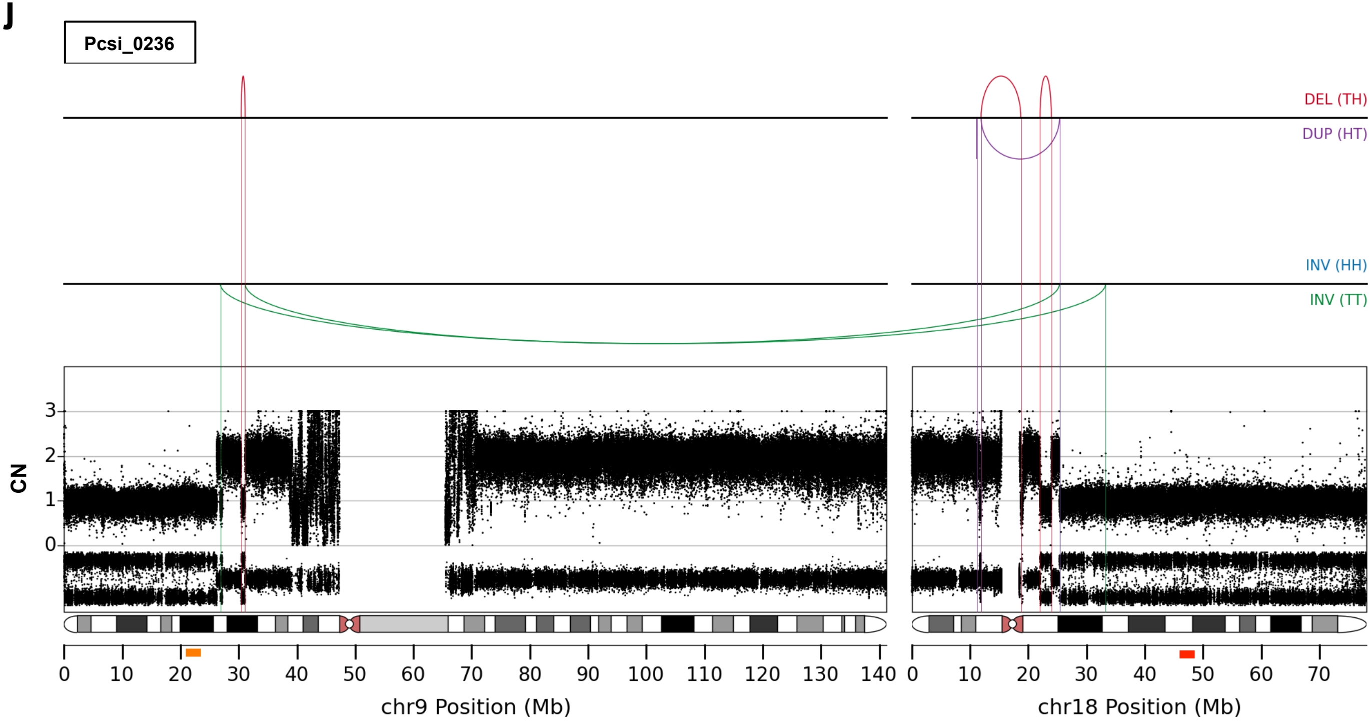
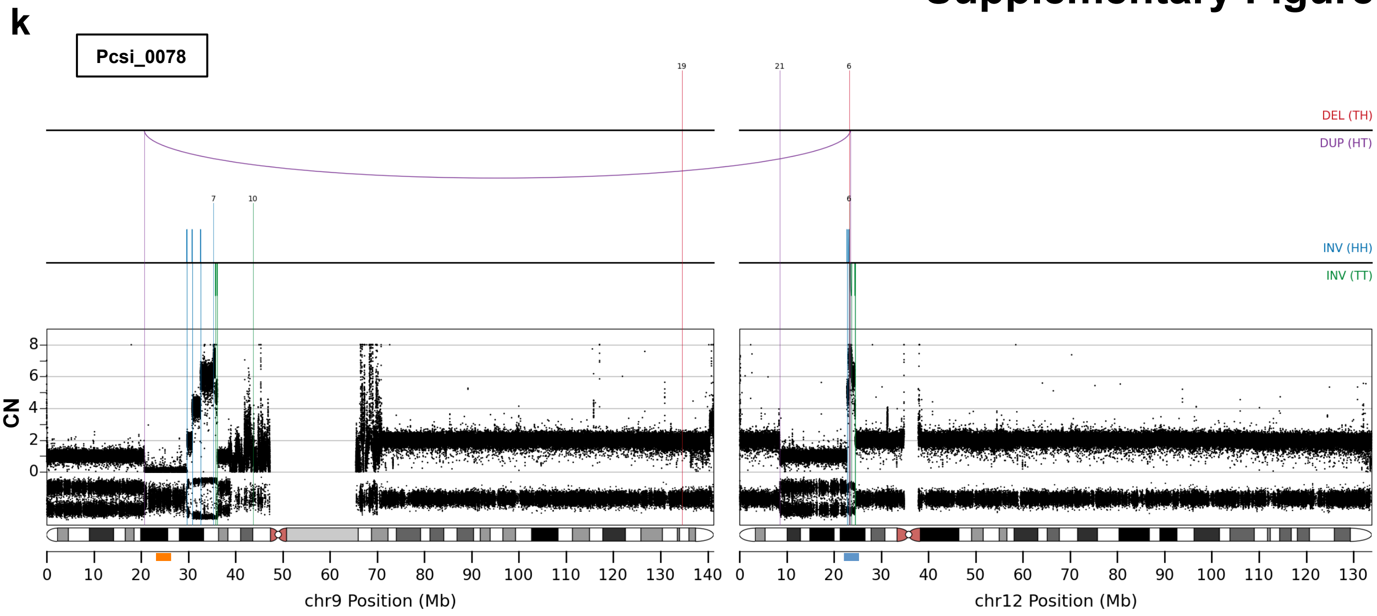
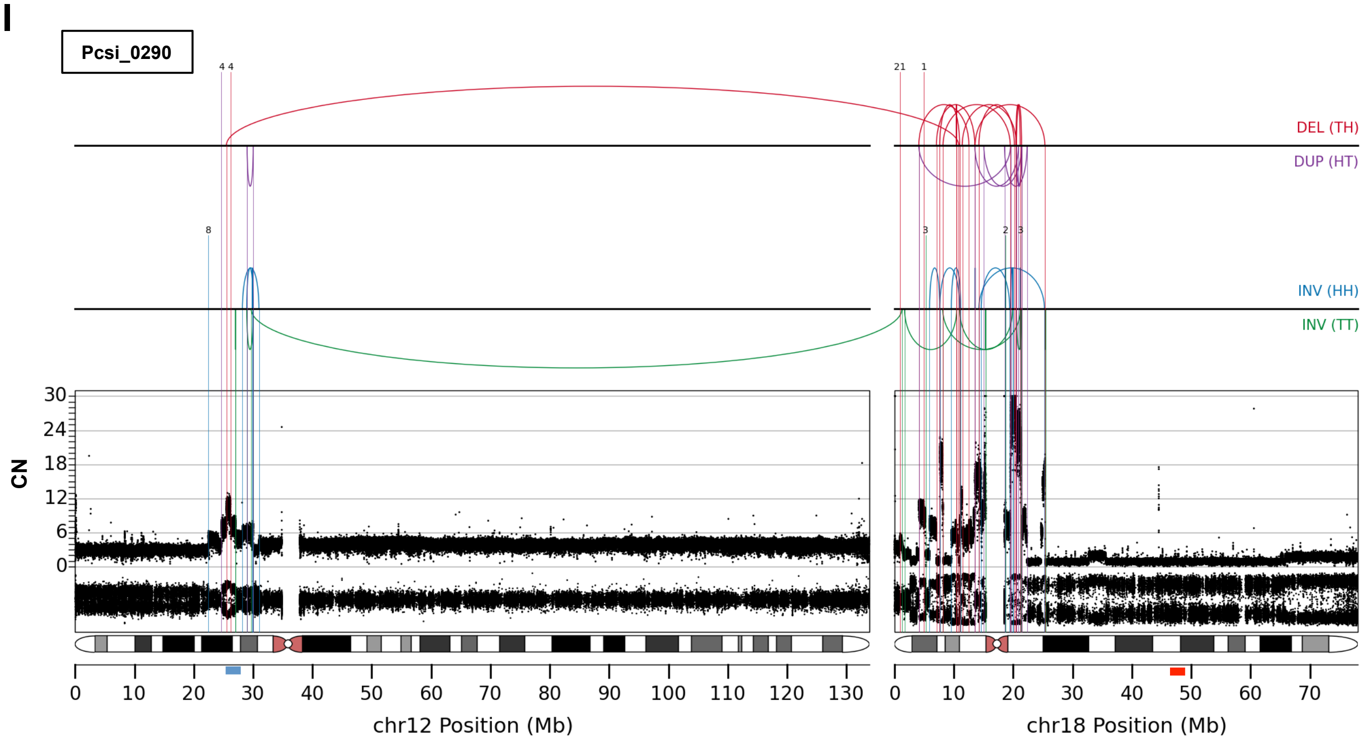


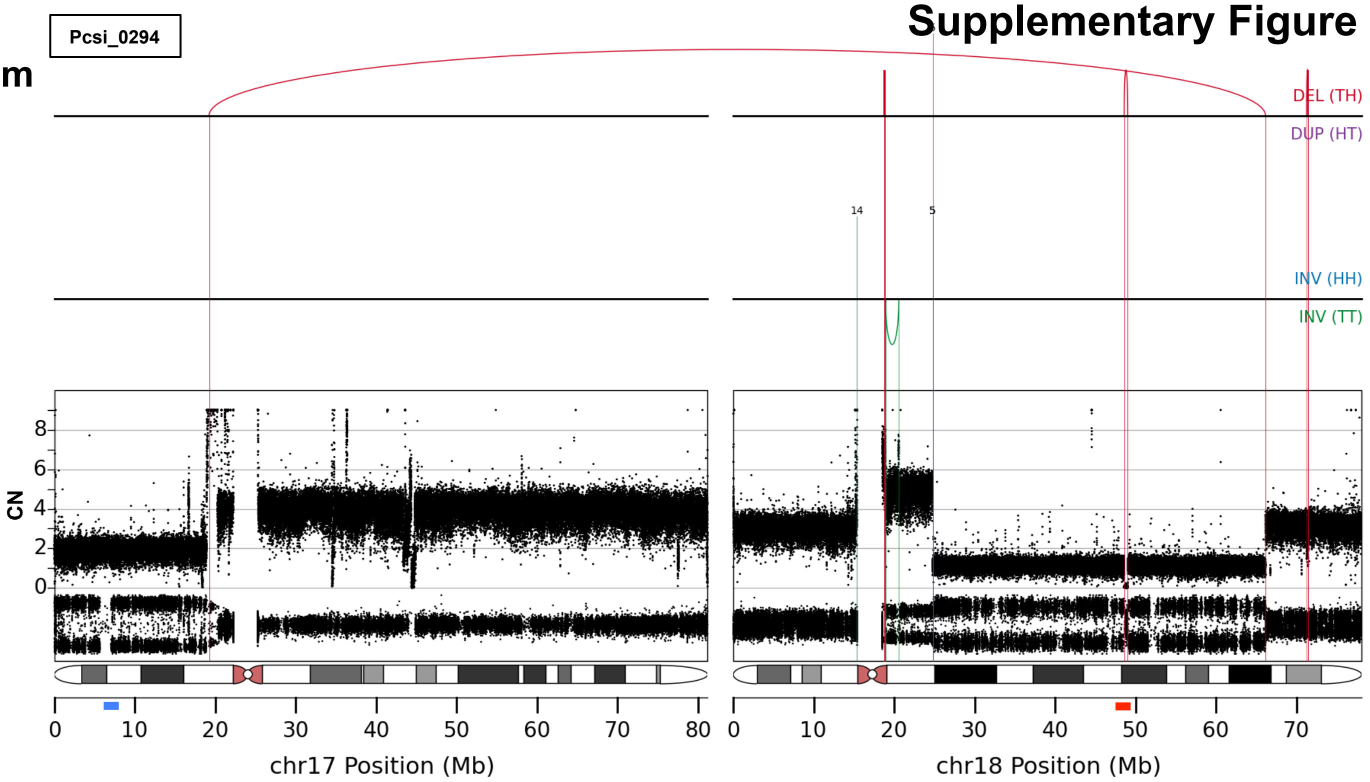
Supplementary Figure 4





Supplementary Figure 4

m



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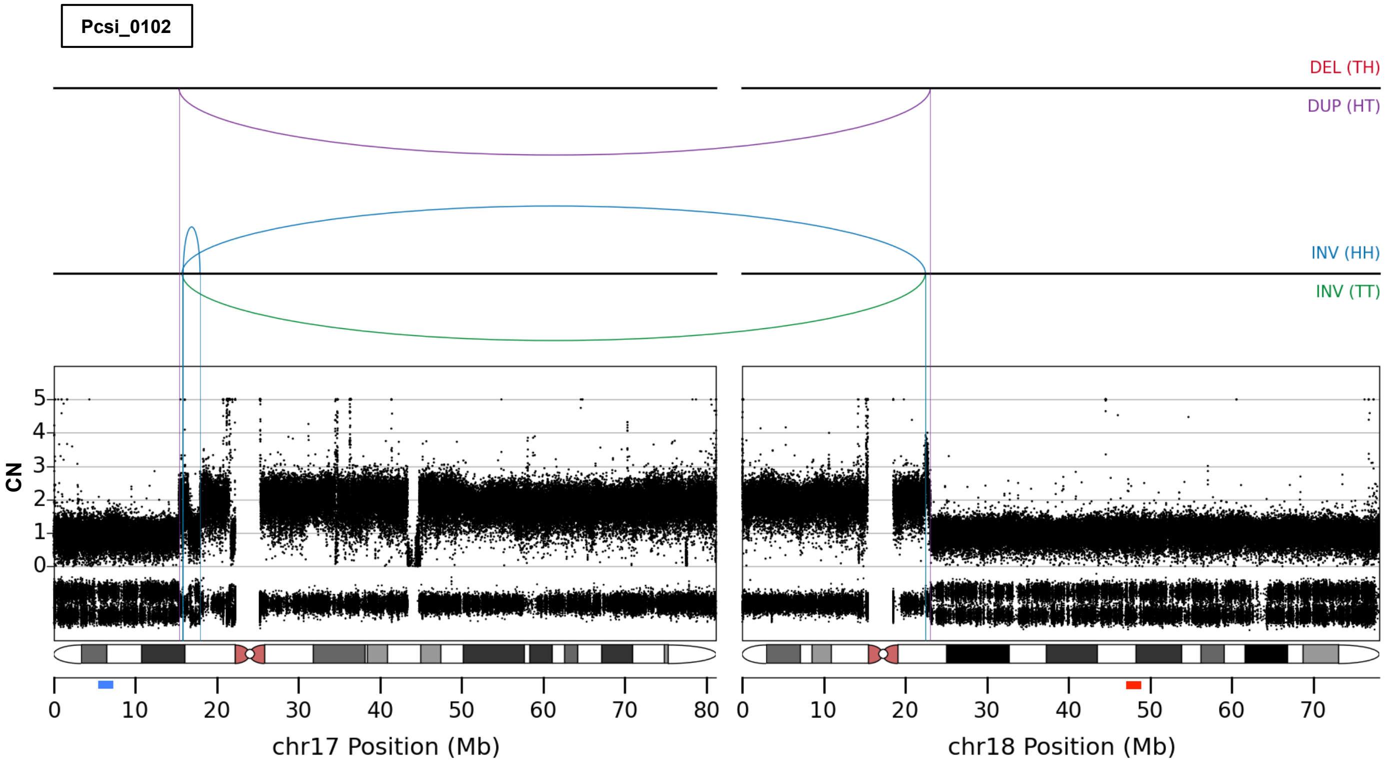
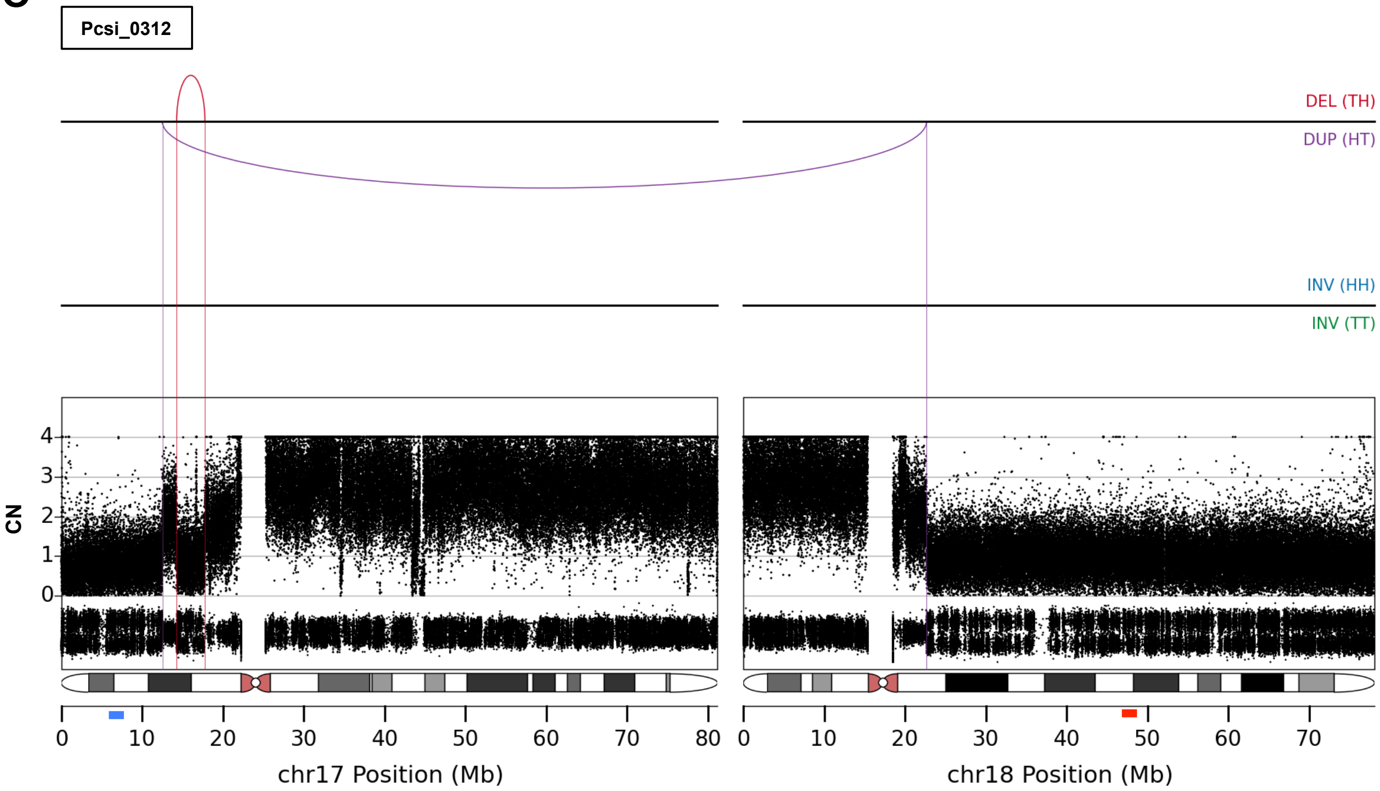
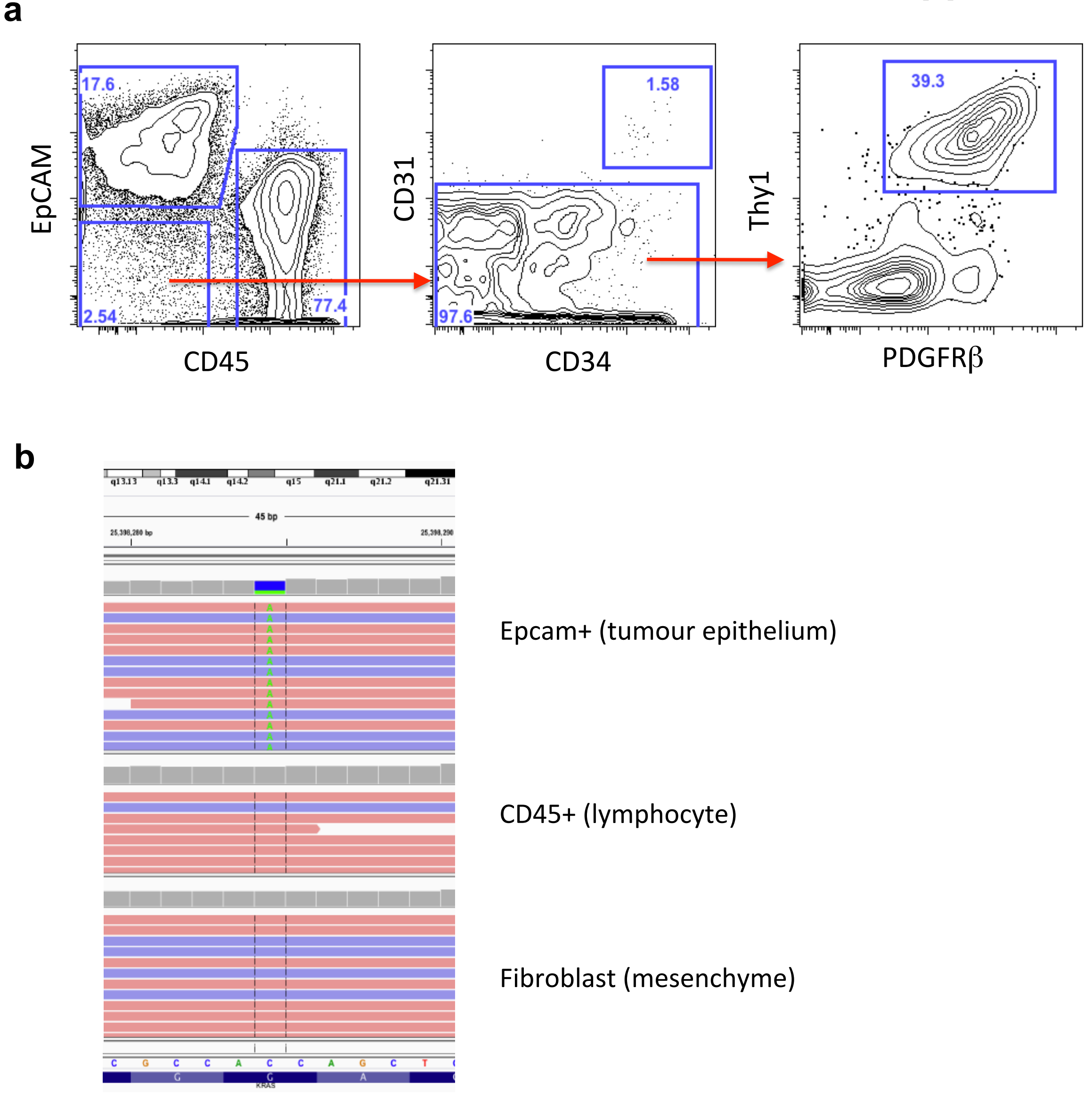


Supplementary Figure 4

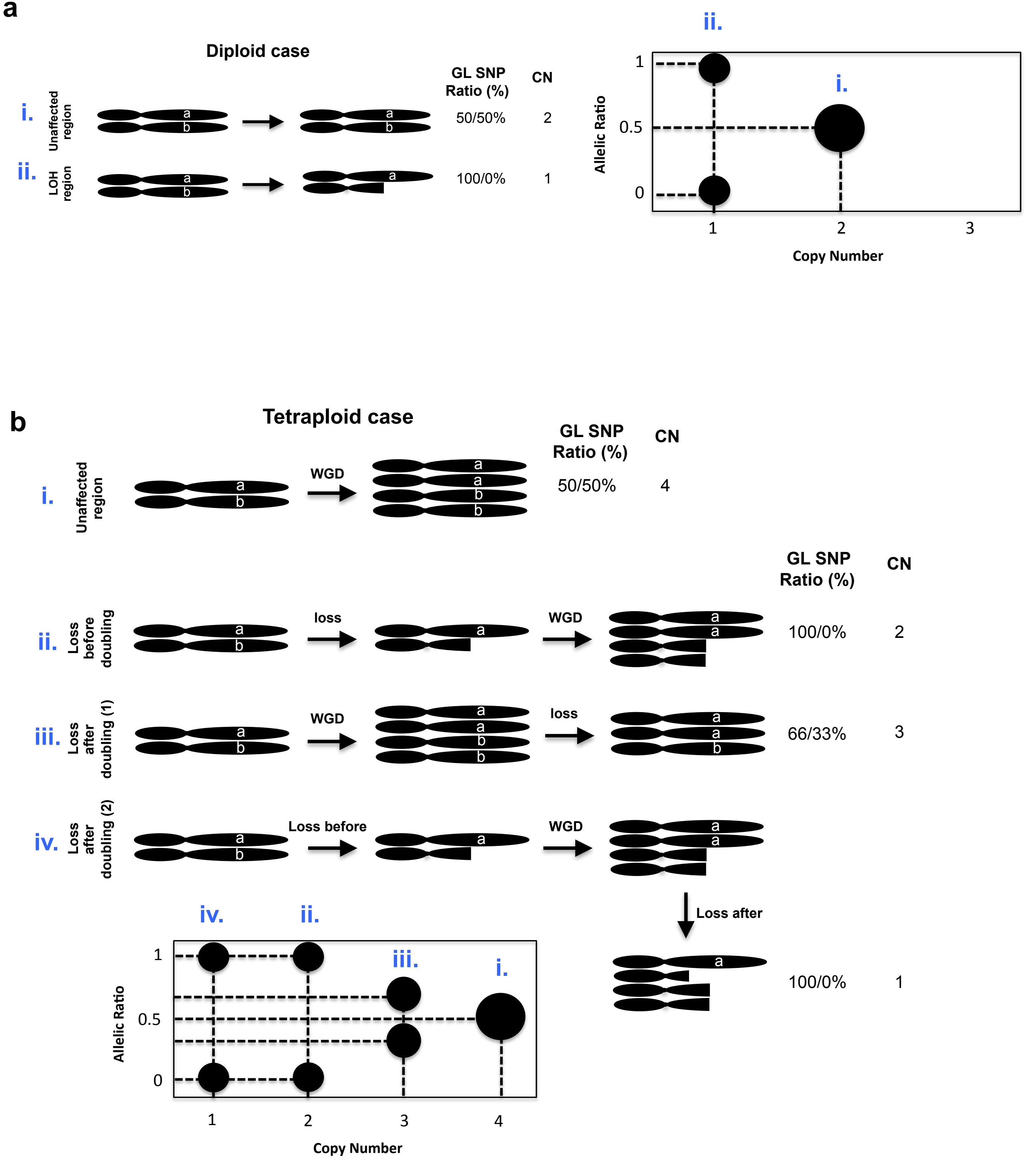
O



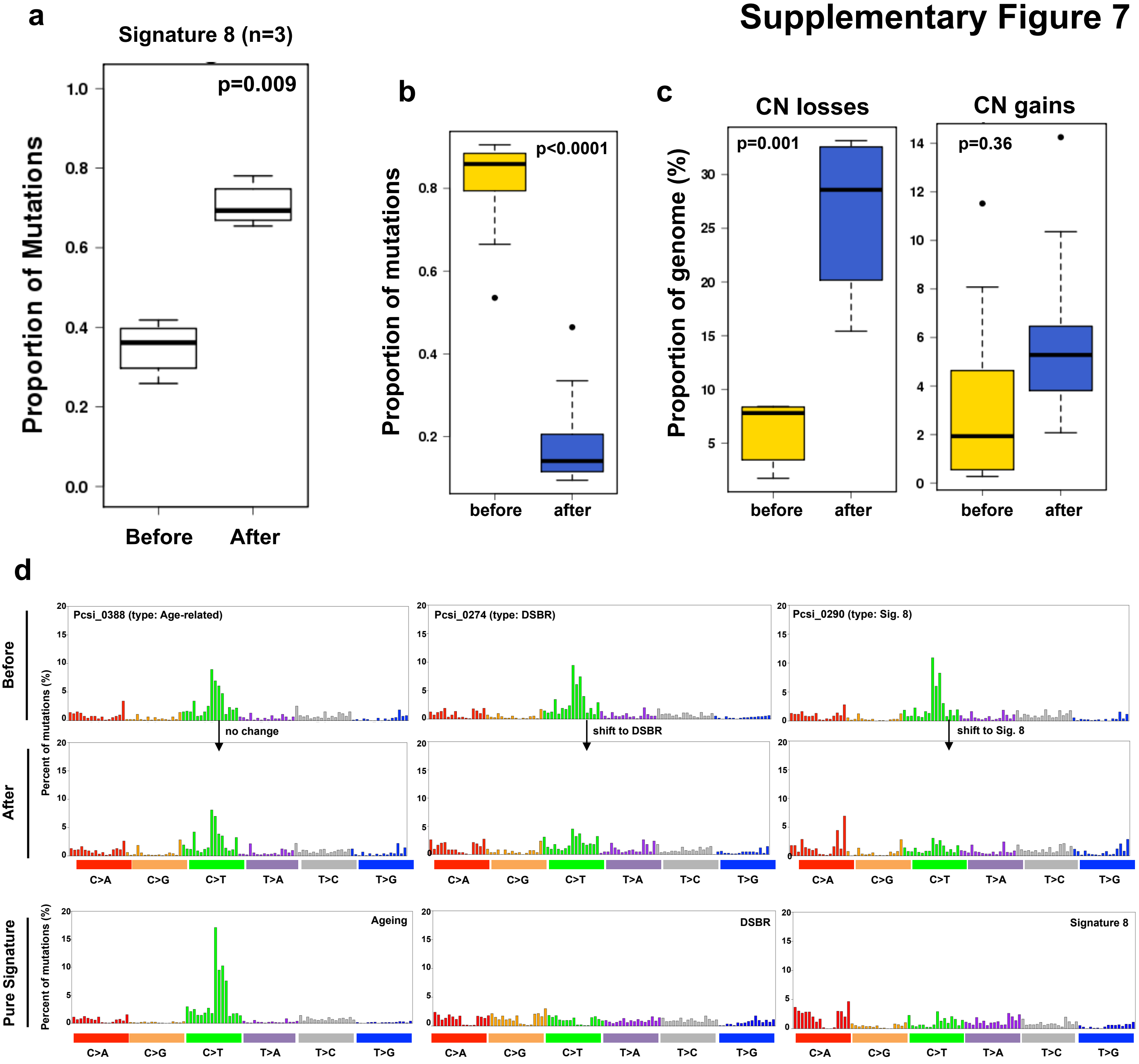
Supplementary Figure 5



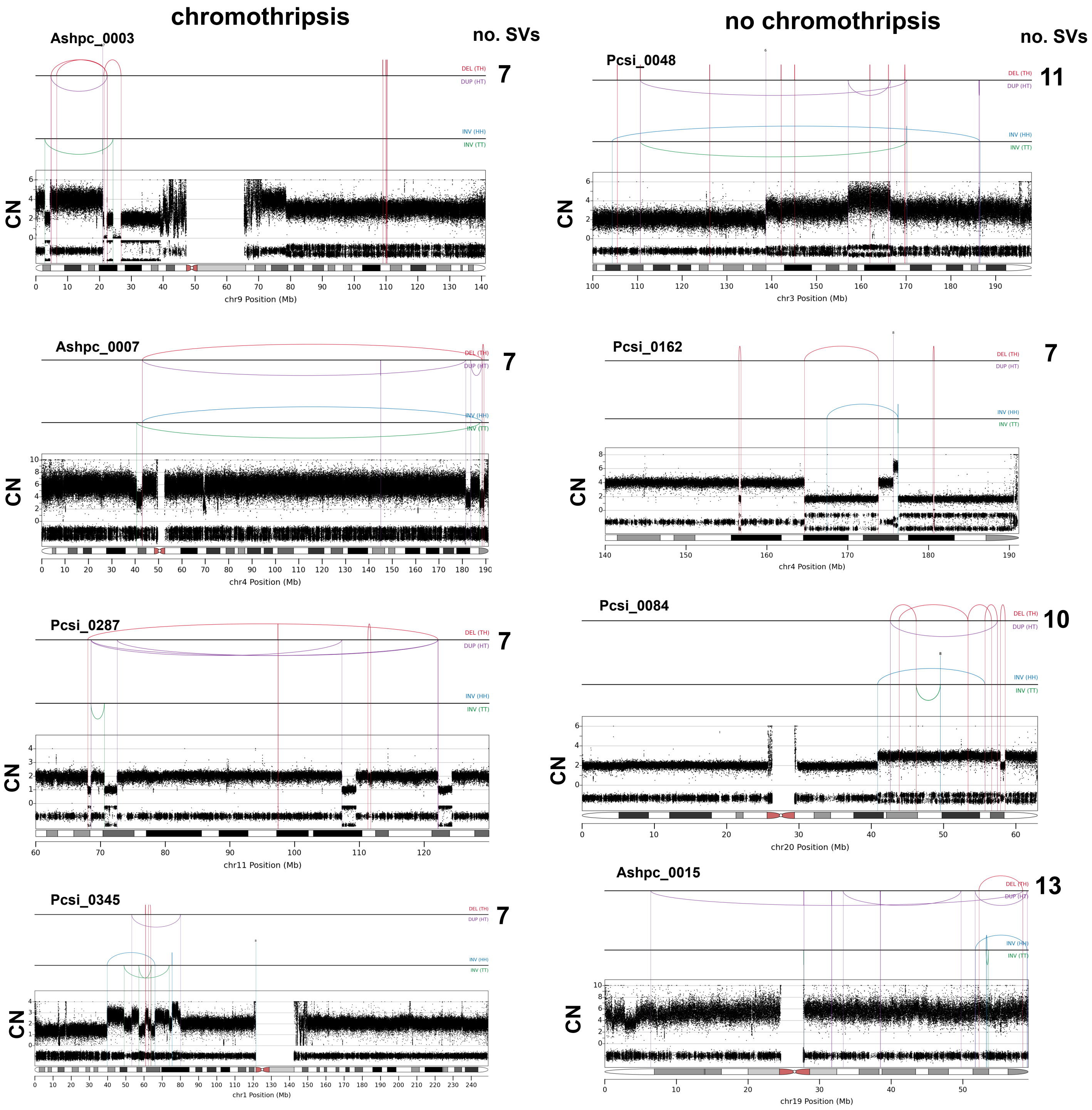
Supplementary Figure 6



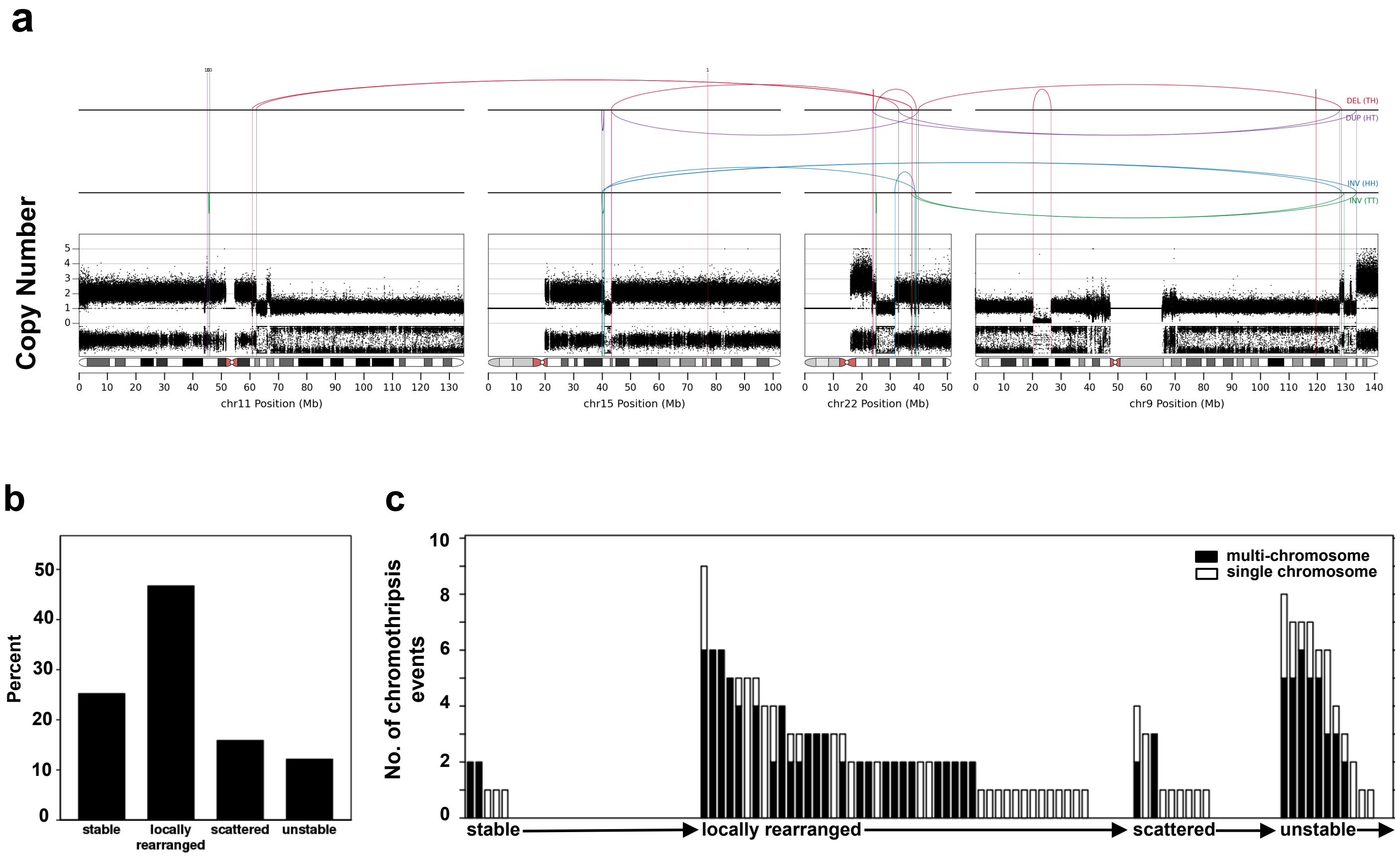
Supplementary Figure 7



Supplementary Figure 8



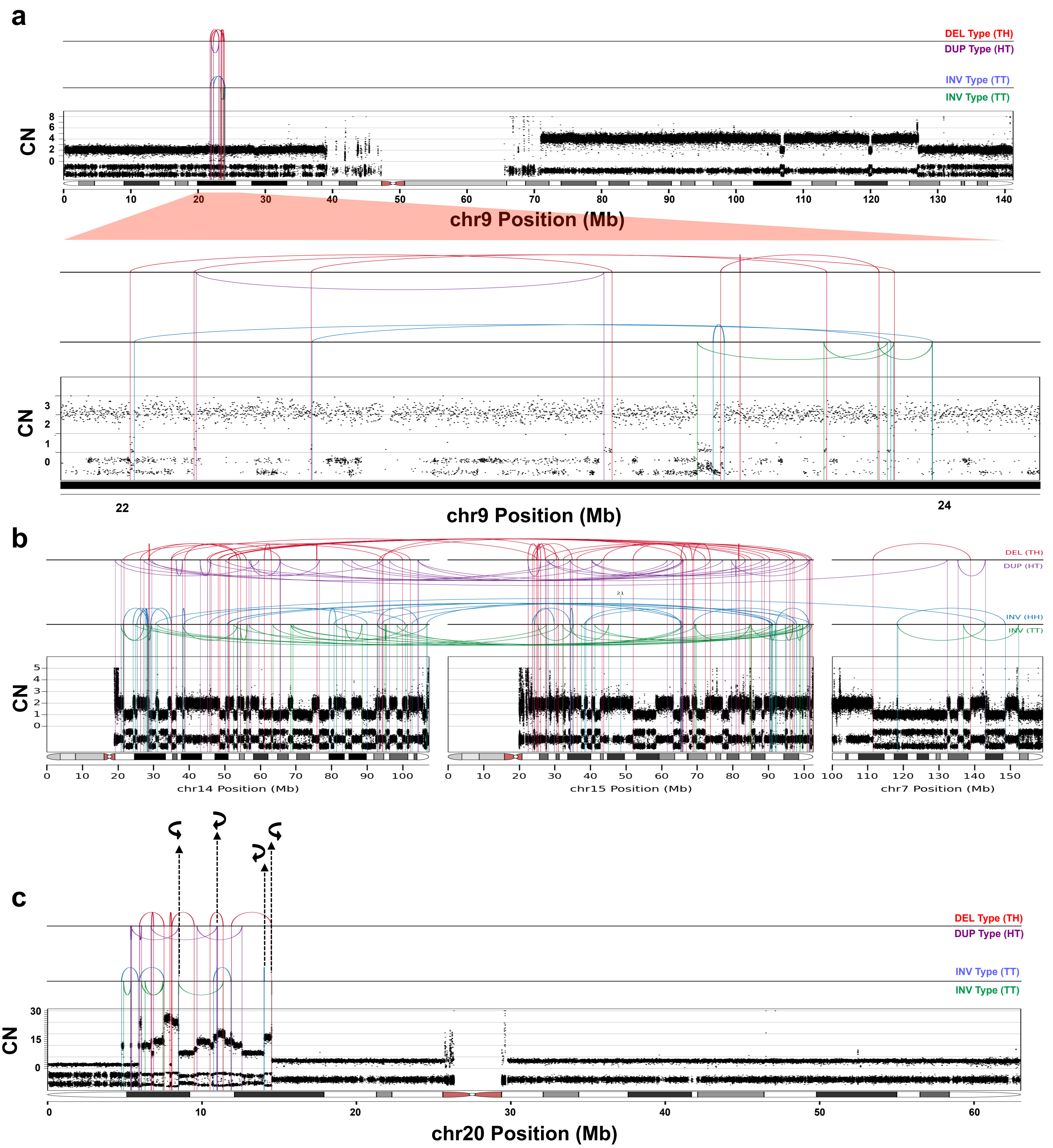
Supplementary Figure 9



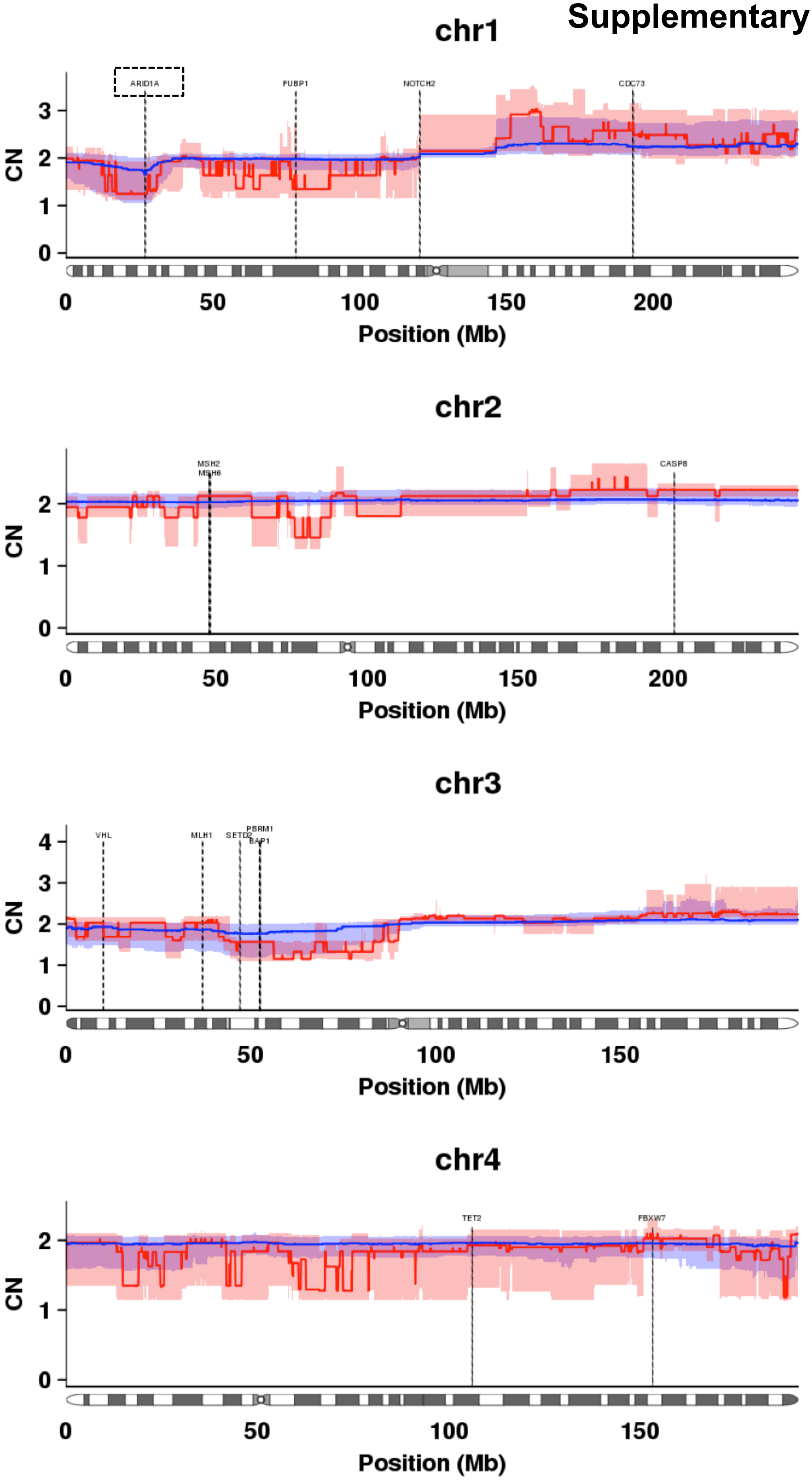
Supplementary Figure 10

Supplementary Figure 10

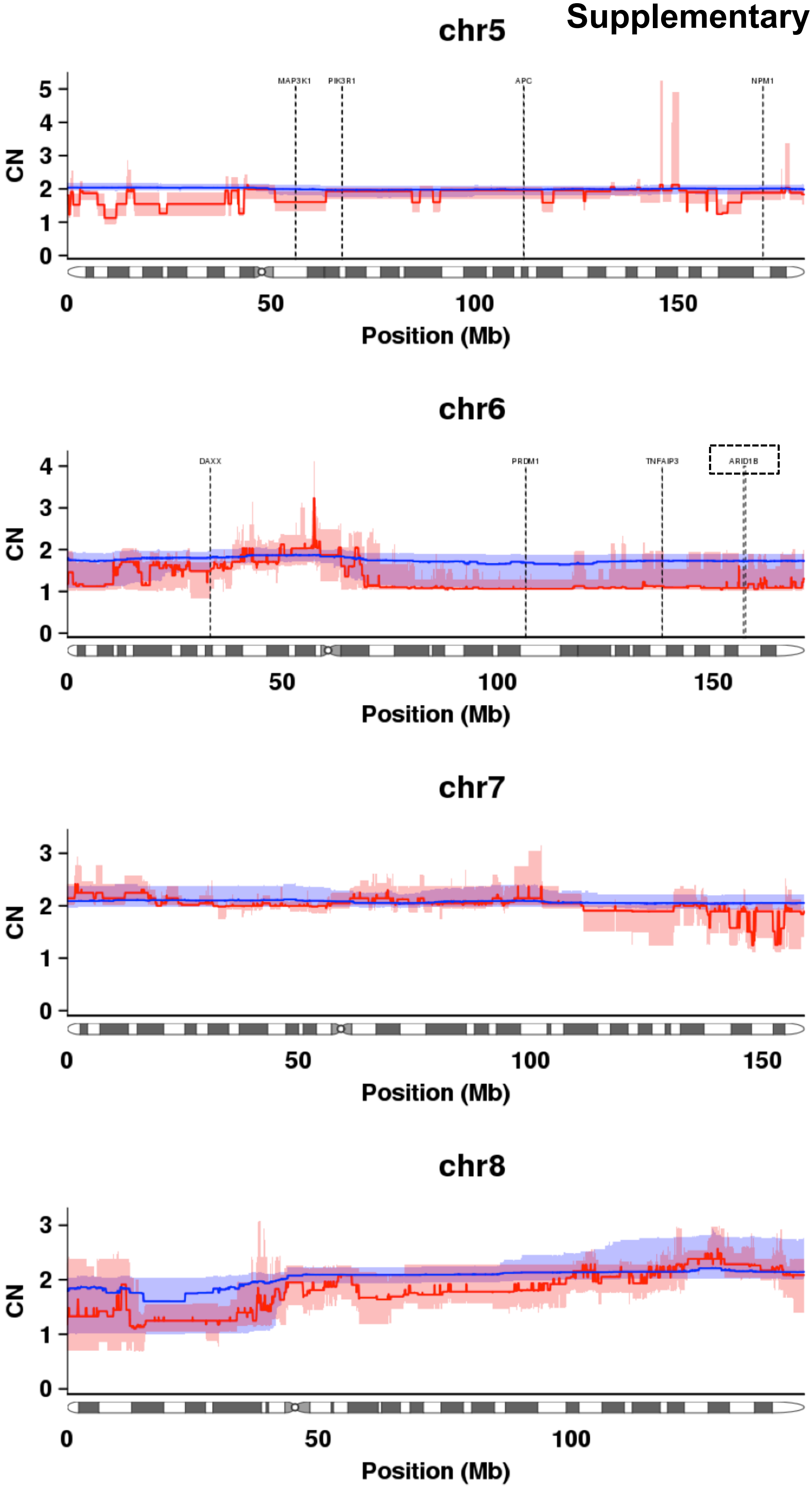
Supplementary Figure 11



Supplementary Figure 12



Supplementary Figure 12



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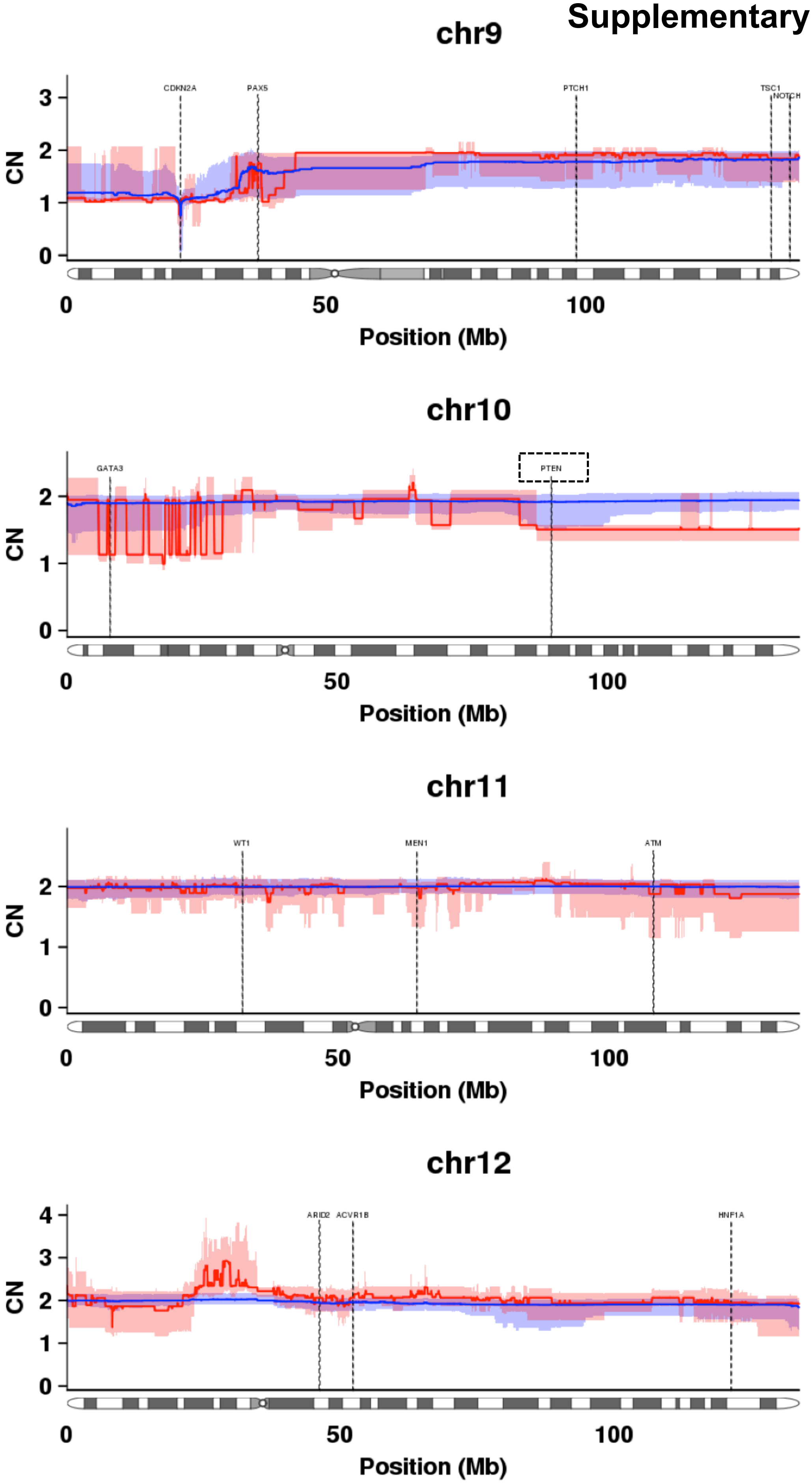
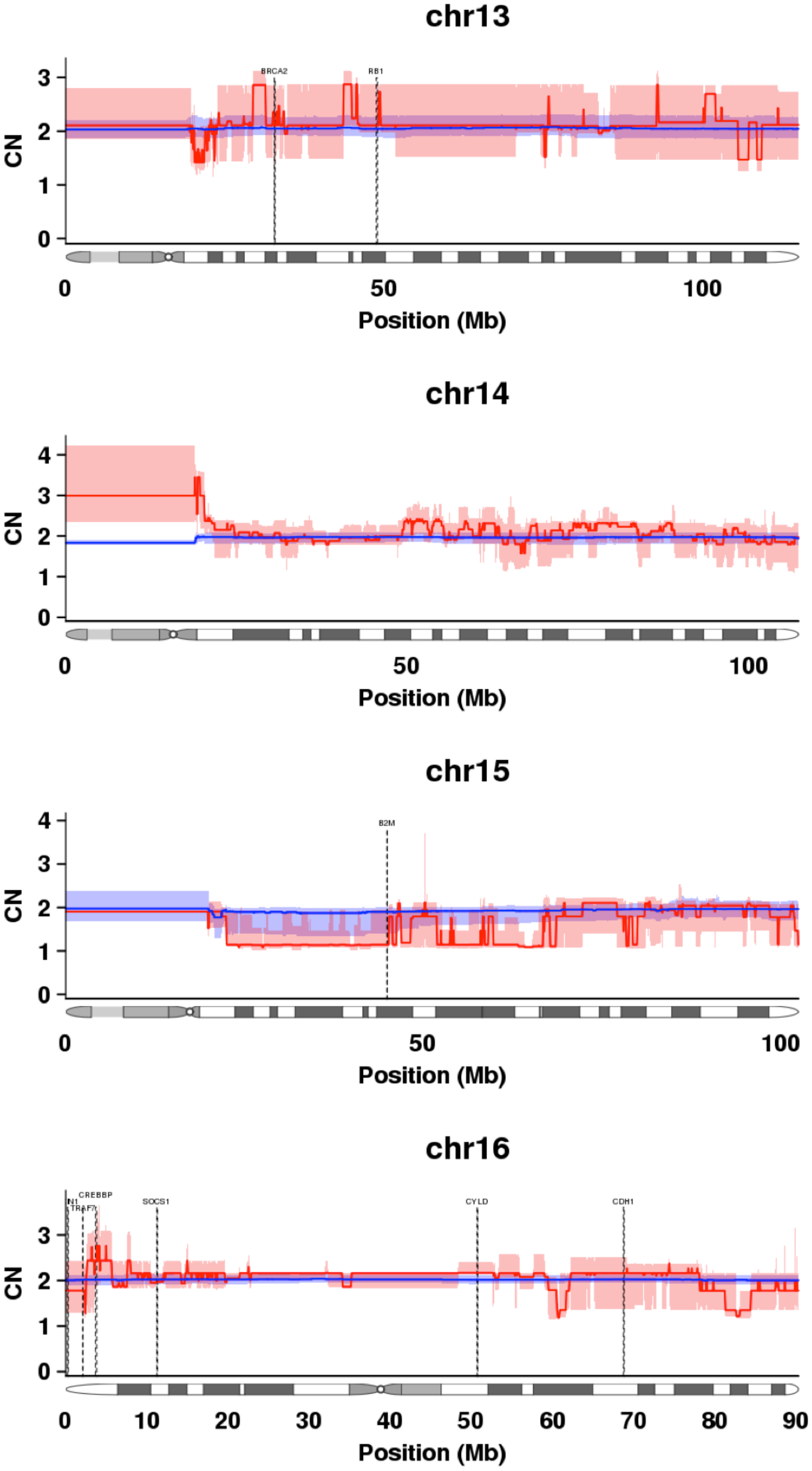

chr9

chr10

chr11

chr12

Supplementary Figure 12



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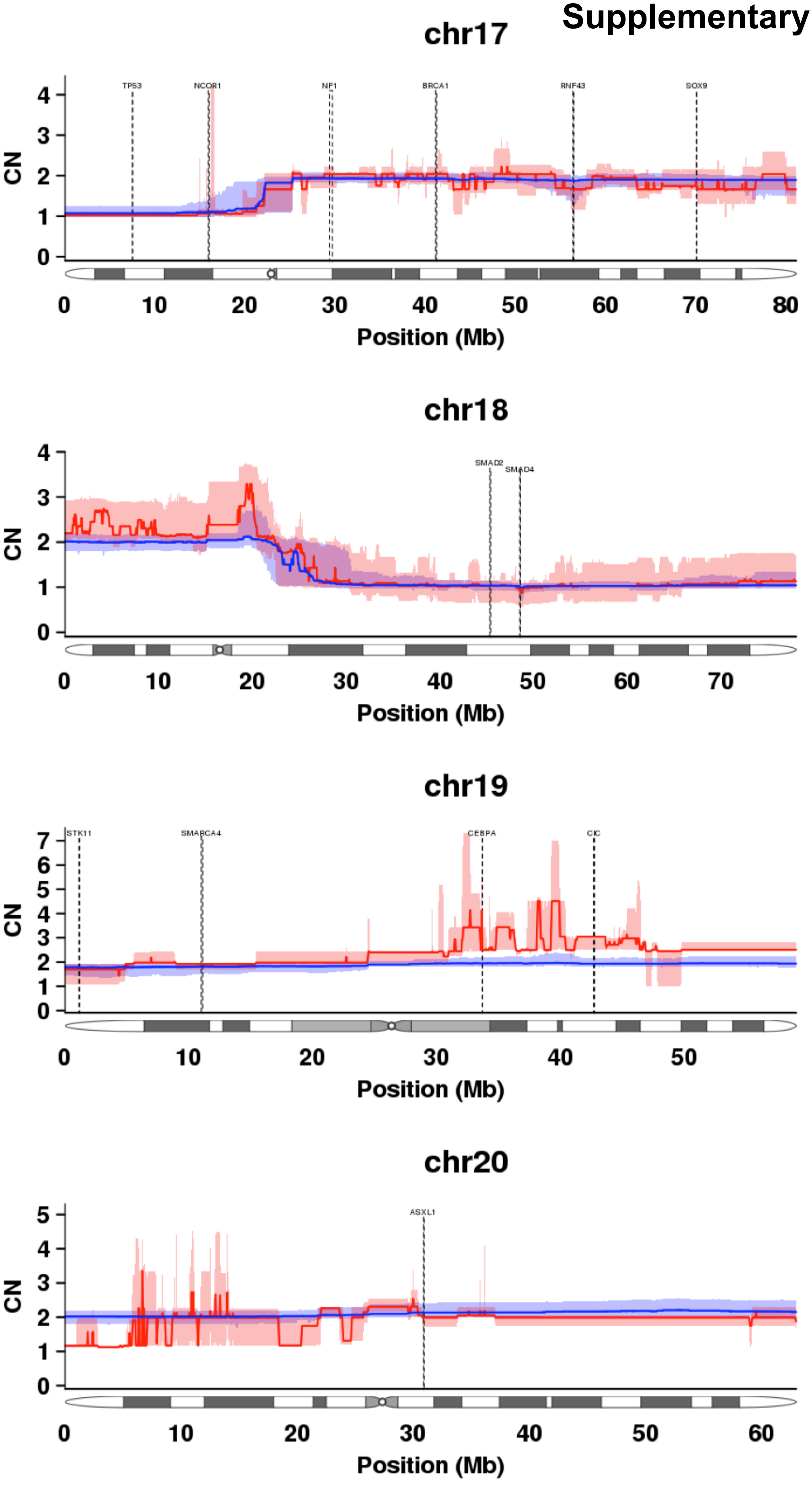

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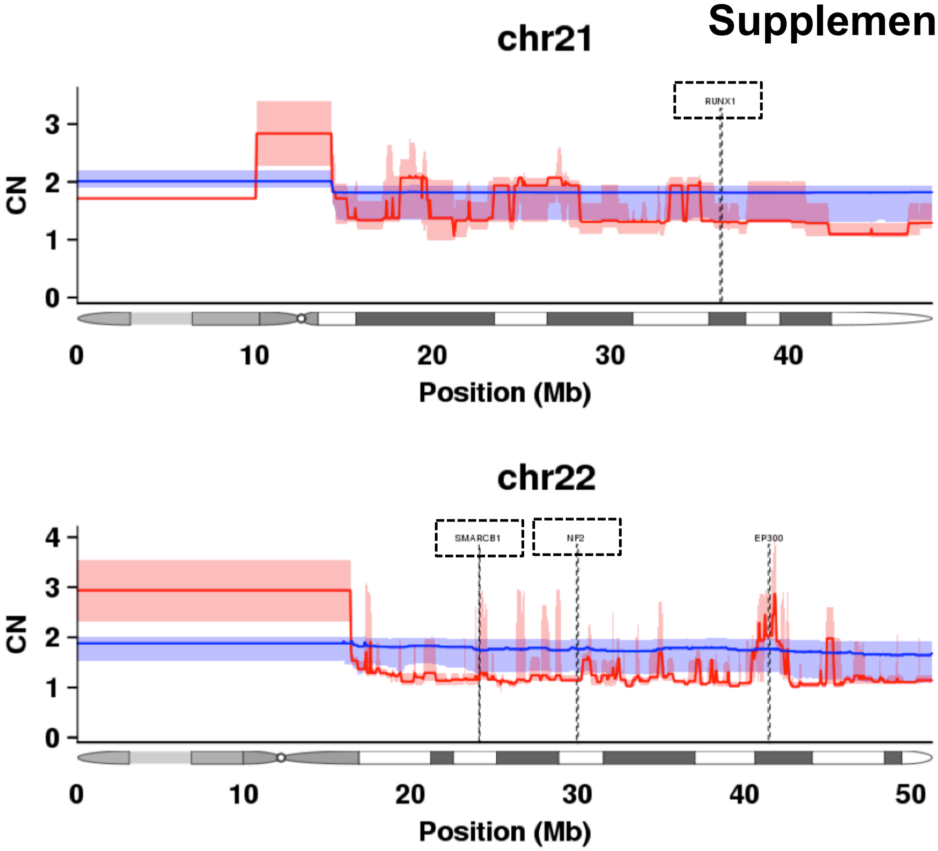

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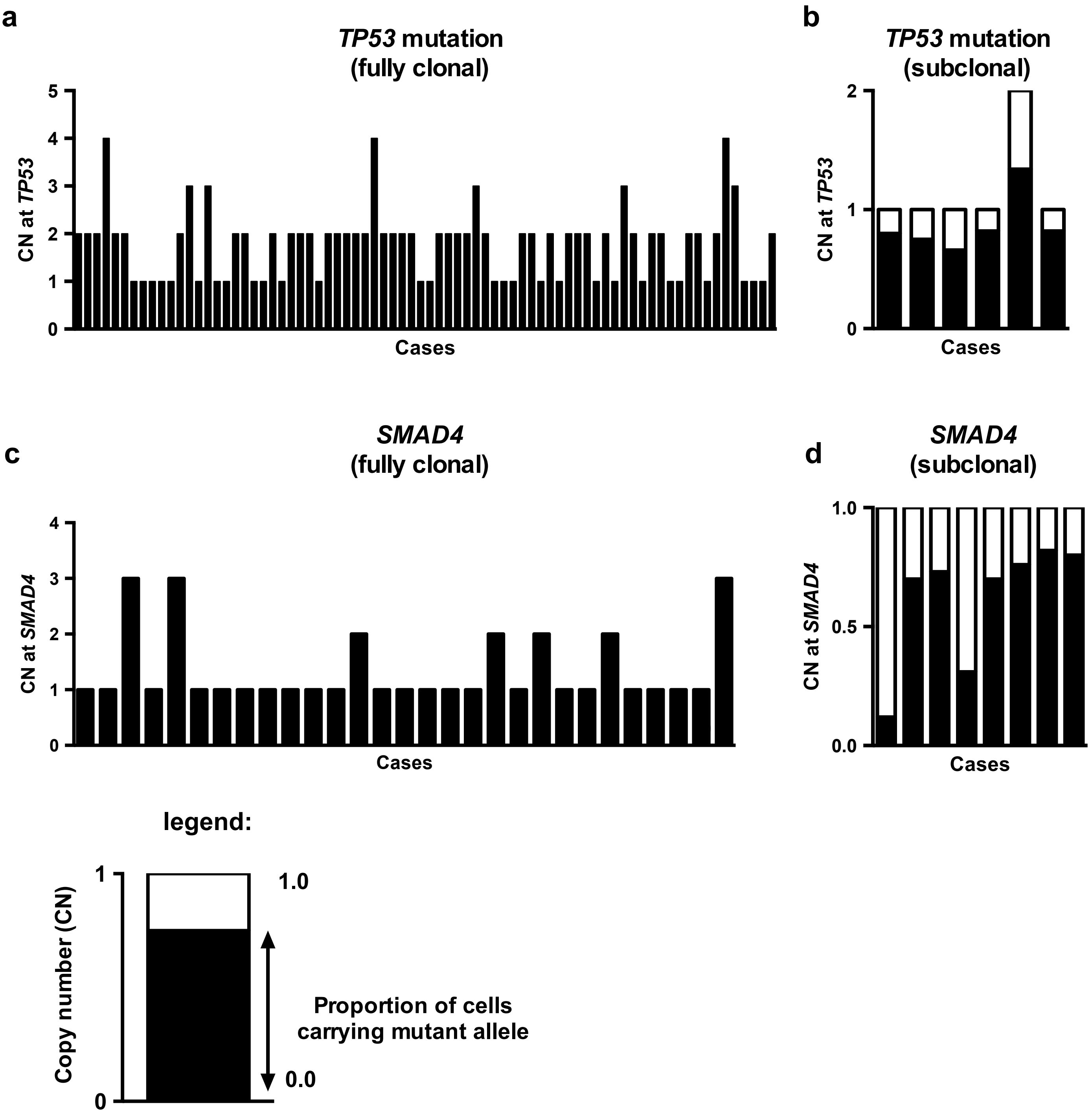

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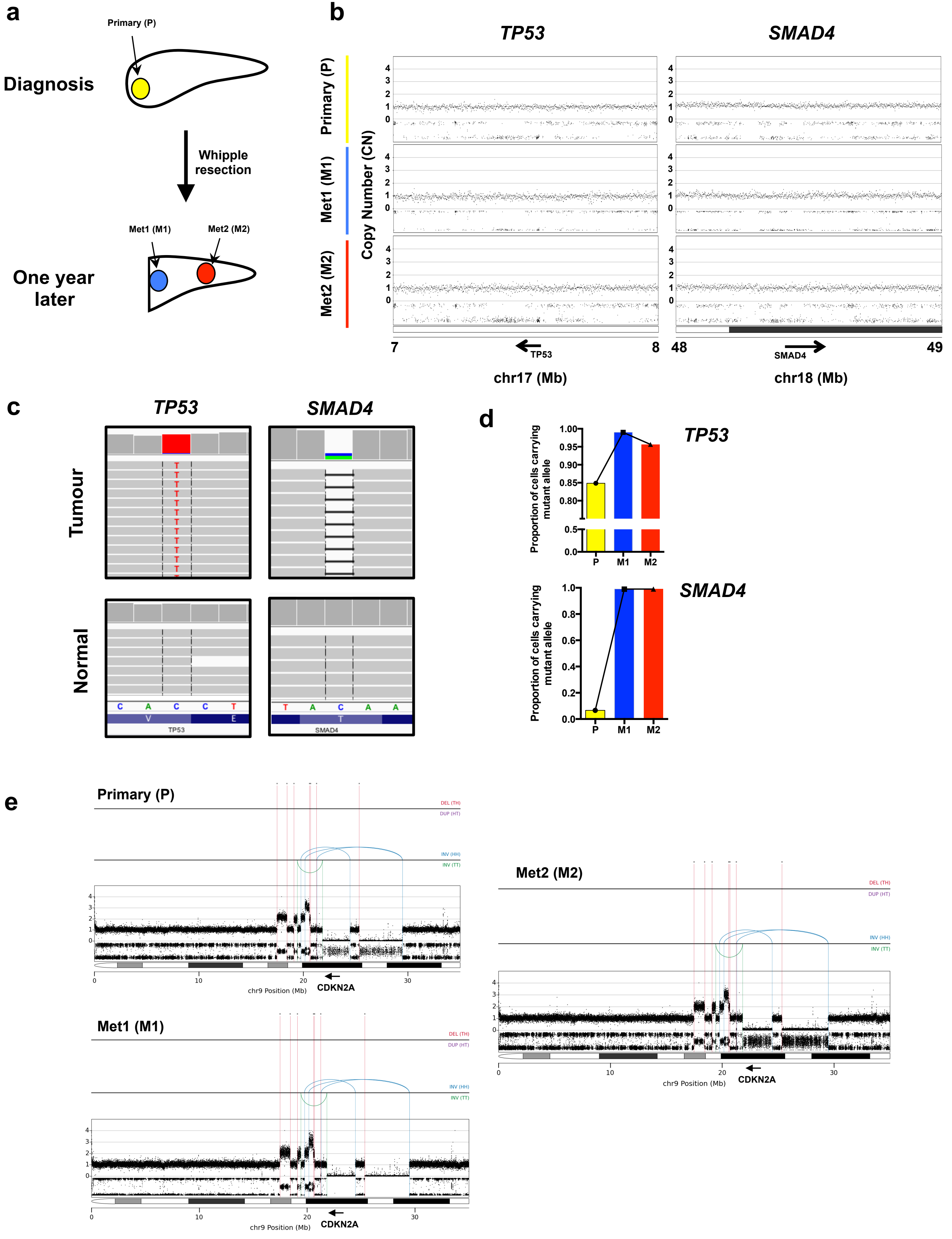
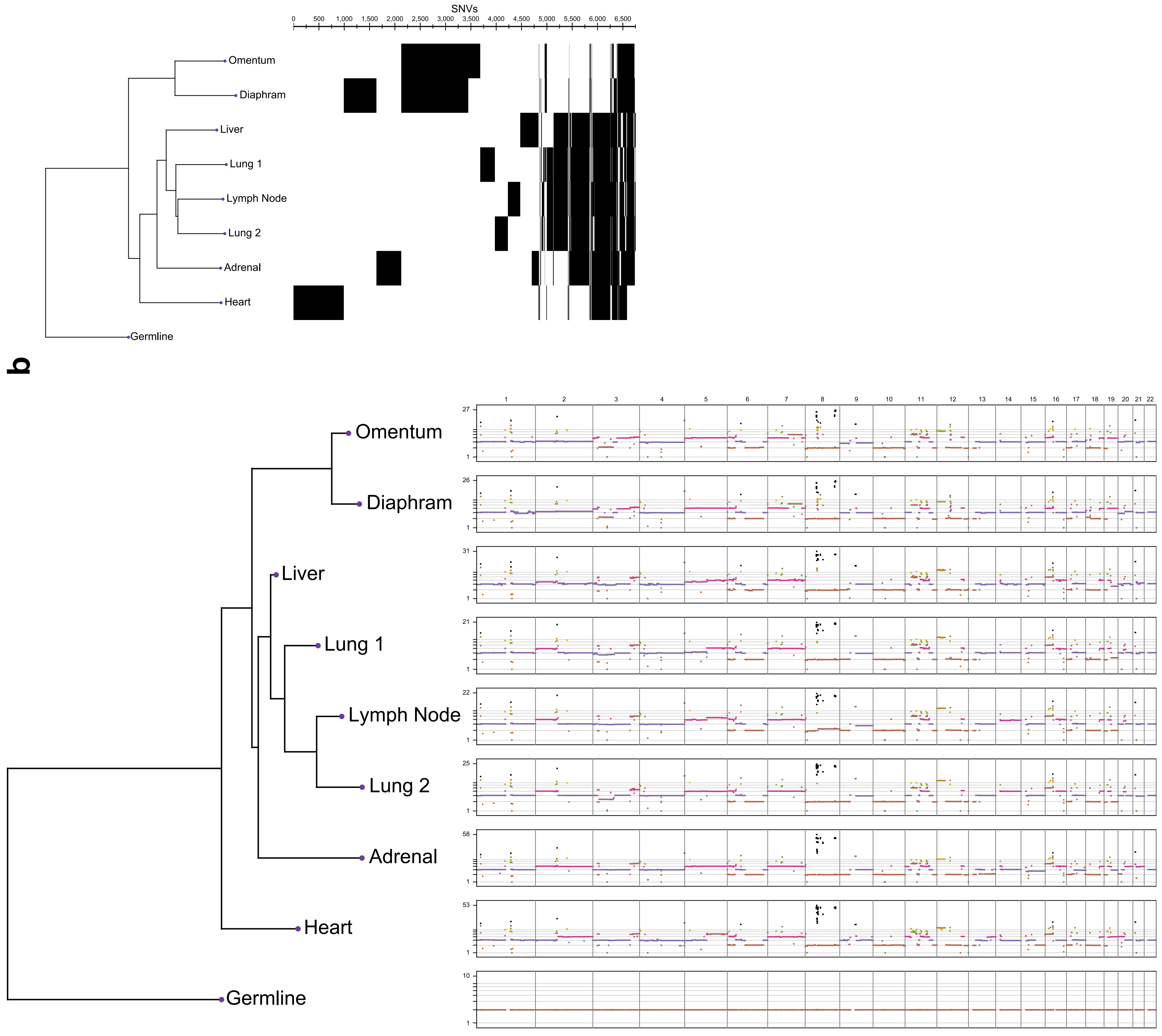
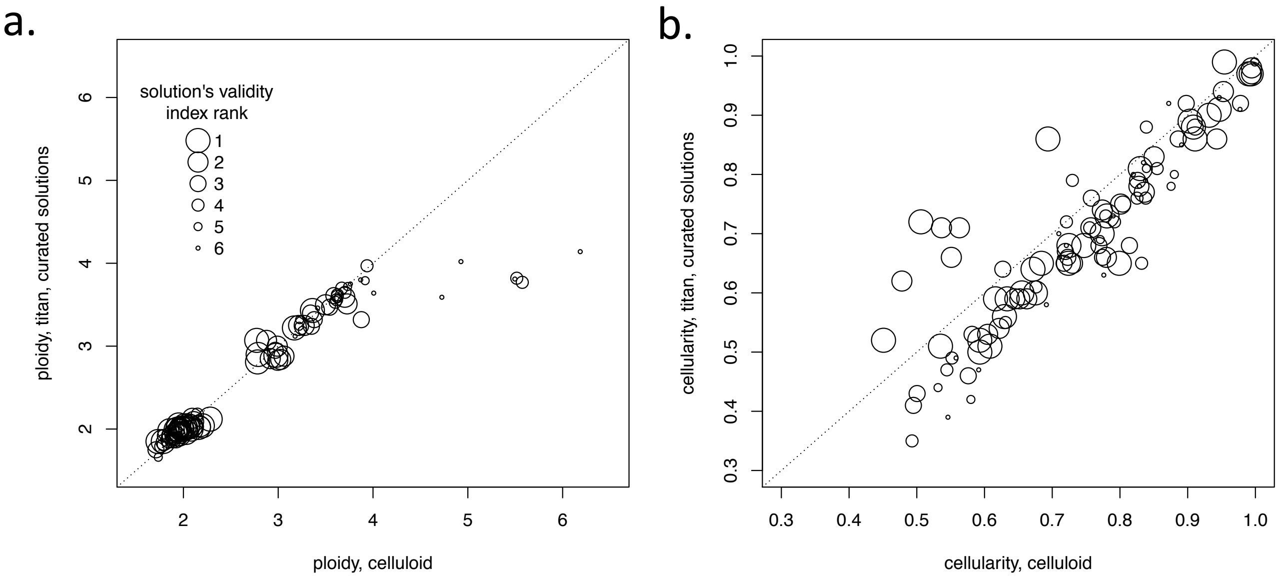


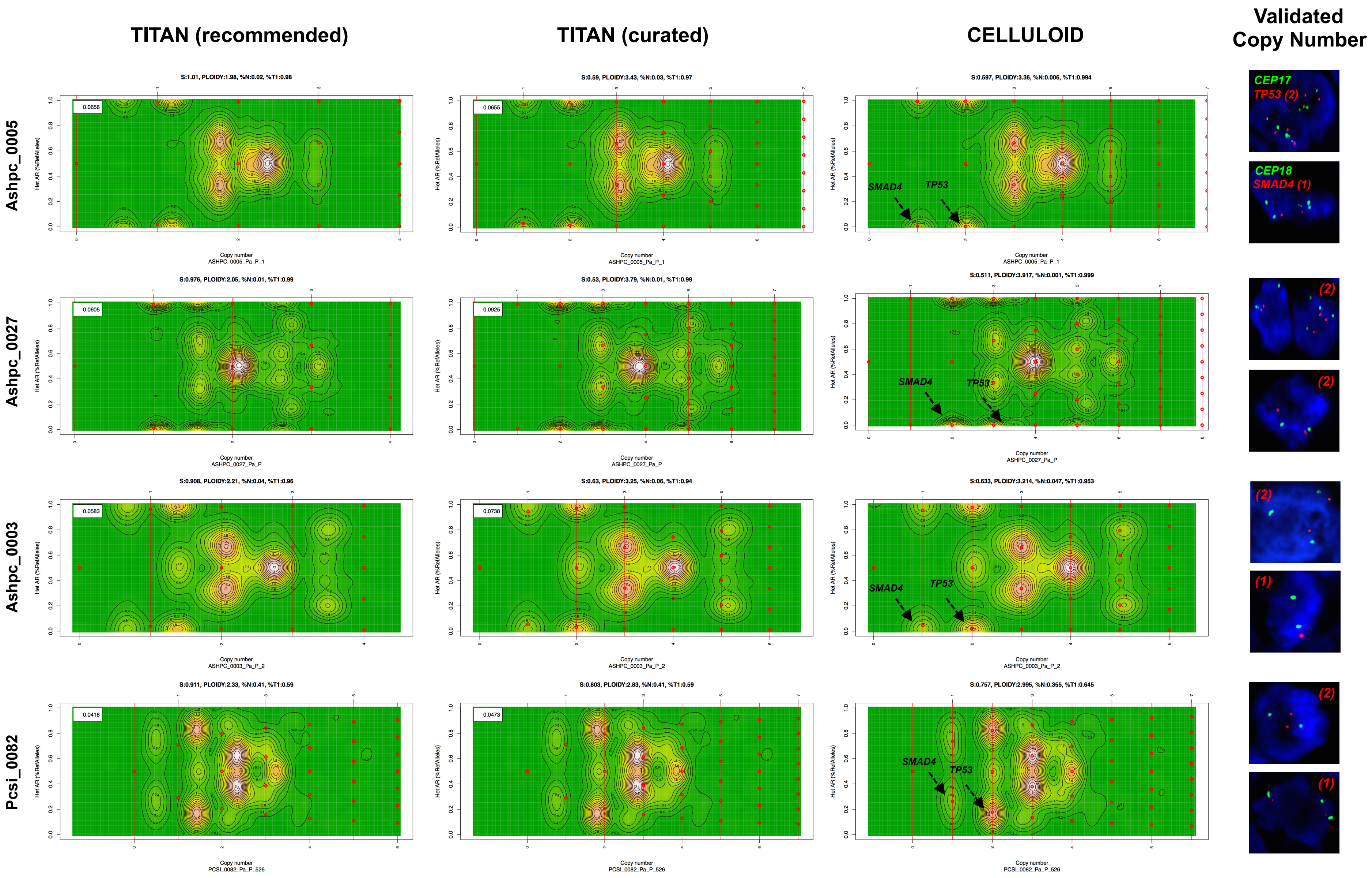
Supplementary Figure 15



Supplementary Figure 16



Supplementary Figure 17



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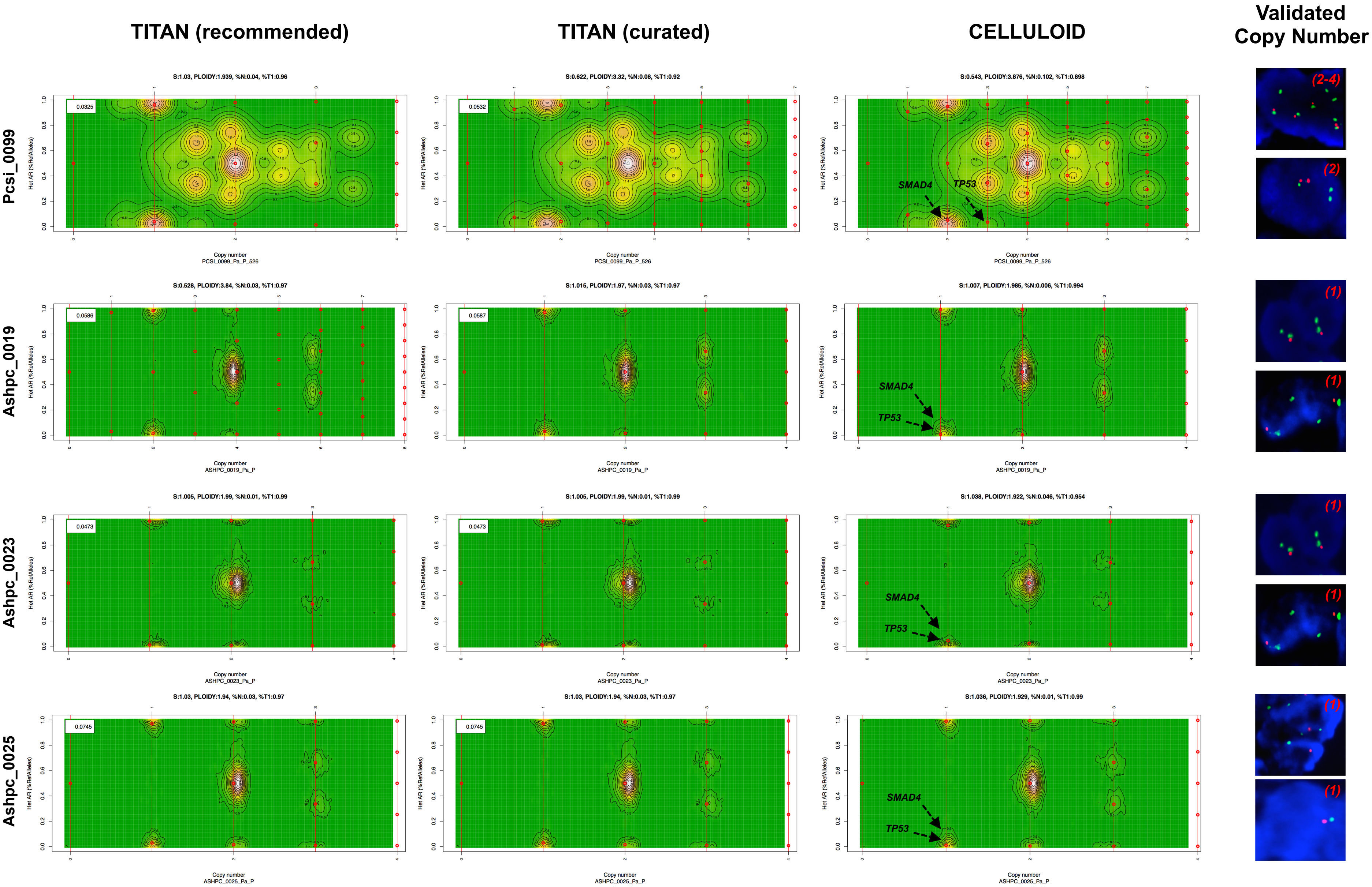

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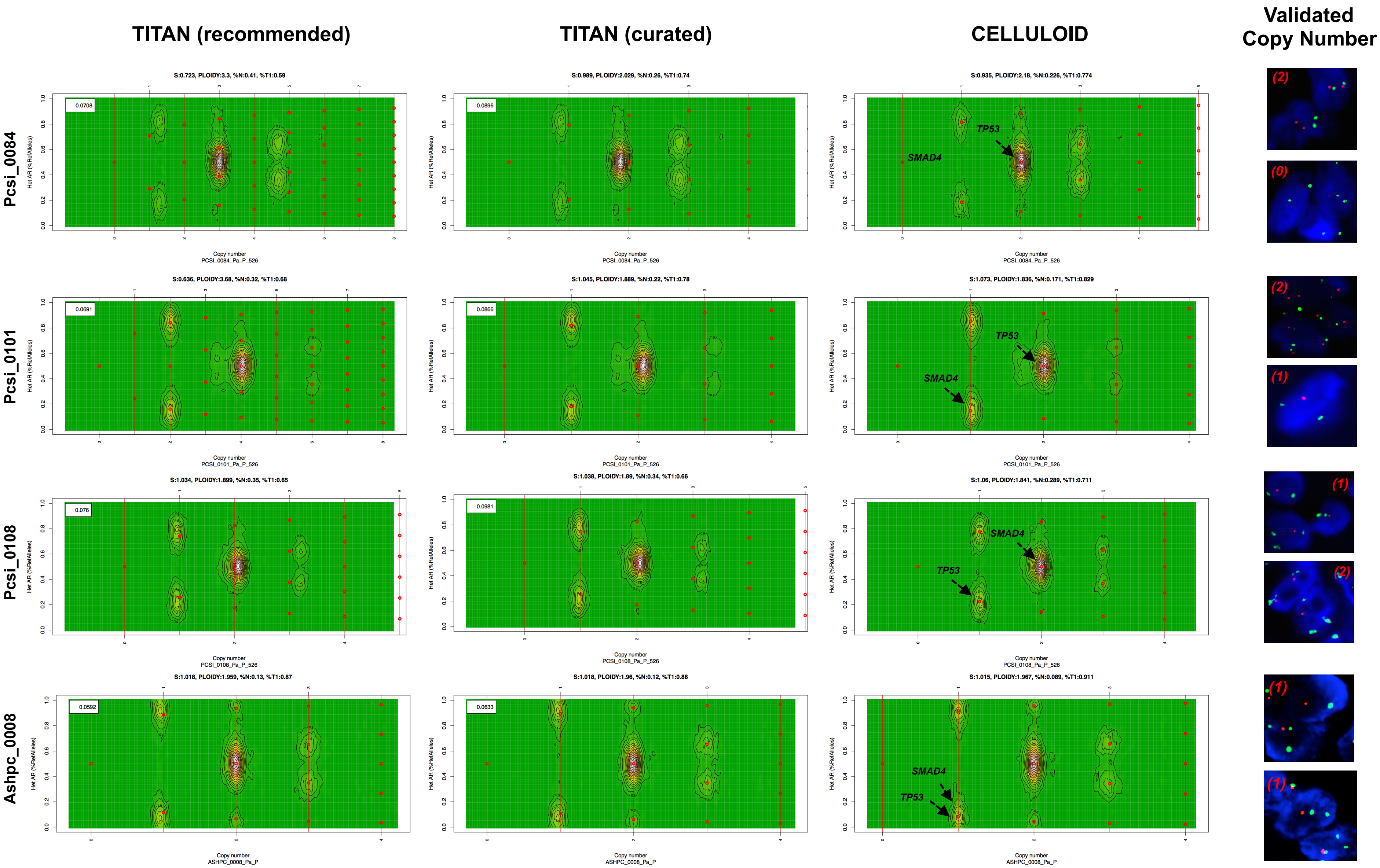
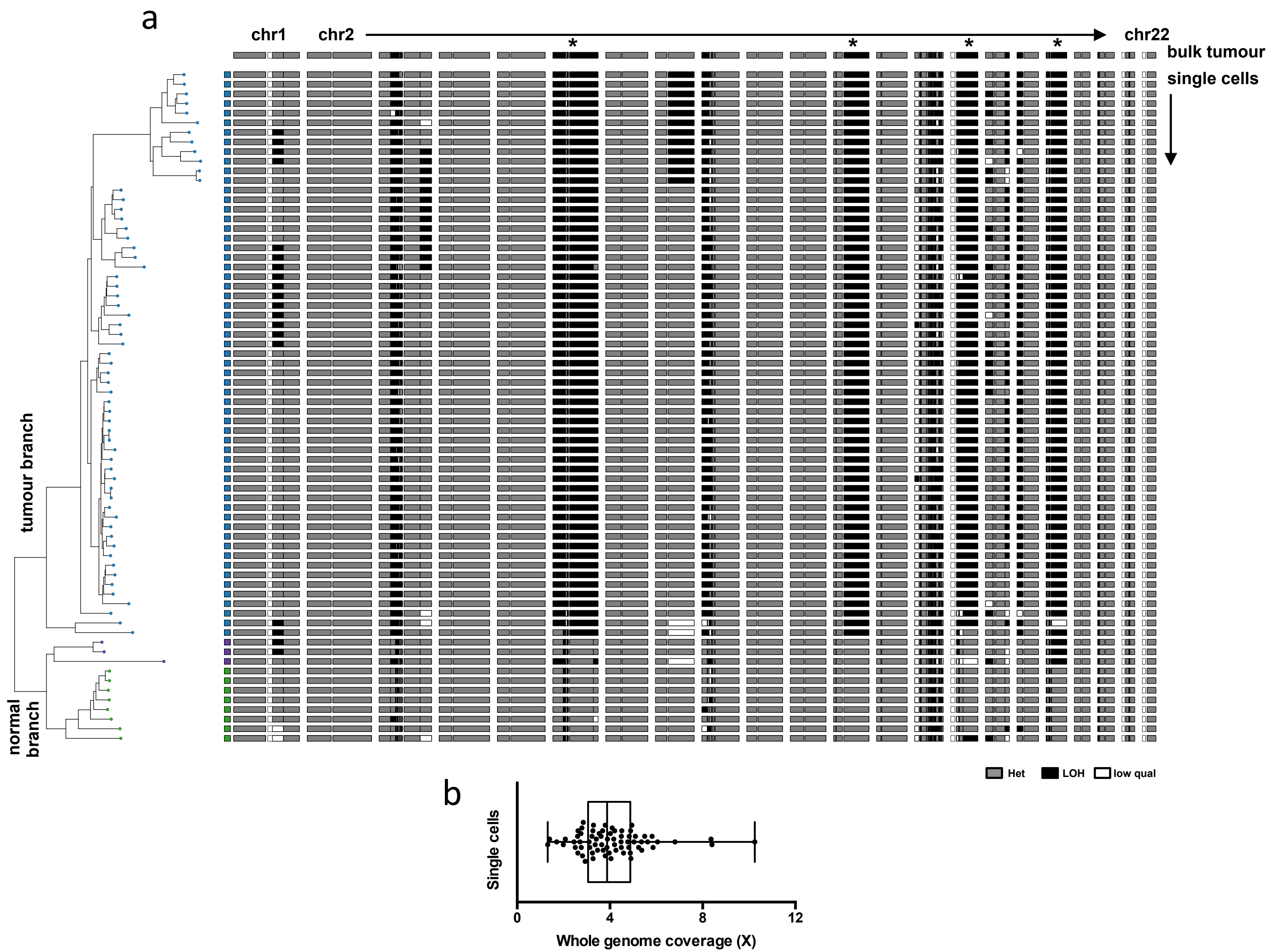


Supplementary Figure 18



Supplementary Table 1

Variables	n=107 (100%)
Gender	
Male	52 (49%)
Female	55 (51%)
Age (years)	
Mean	65.7
Median	67
Range	41.0 - 87.0
Histological Subtype	
Ductual Adenocarcinoma	98 (92%)
Ductual Adenocarcinoma with IPMN	7 (7%)
Mucinous Adenocarcinoma	2 (1%)
Histological Grade (differentiation)	
Well	17 (16%)
Moderate	50 (47%)
Poor	35 (33%)
Undifferentiated	4 (4%)
NA	1 (<1%)
T Stage	
TI	2 (2%)
T2	11 (10%)
T3	90 (84%)
T4	2 (2%)
NA	2 (2%)
N Stage	
N0	24 (22%)
N1	80 (75%)
NA	3 (3%)

Supplementary Table 2: (images for events below are provided in Supplementary Figure 12)

Sample	Chromothripsis	Number of Events	Event(CR1) Reactions	Event(CR2) Reactions
ICGC_0006_Pa_P_8031121	yes	2	chr4:119141674-190583192, chr11:3857001-42860000	-
ICGC_0007_Pa_P_8012199	yes	2	chr1:38807432-49403757, chr20:1220916-53876562	-
ICGC_0009_Pa_P_8012321	yes	1	chr10:81878711-132340500	-
ICGC_0020_Pa_P_8067541	yes	1	chr11:19382658-73704272 + chr18:23746770-70216075 + chr6:14869820-98354849	-
ICGC_0021_Pa_P_8015109	yes	2	chr18:388221-19388487, chr19:28272240-58070000	-
ICGC_0025_Pa_P_8012211	yes	2	-	chr1:152793001-227435776, chr11:19268841-82026000 + chr2:194317737-200534000 + chr4:54977001-178340245
ICGC_0026_Pa_P_8014825	no	0	-	-
ICGC_0031_Pa_P_8014807	yes	1	chr3:20313547-191370000 + chr7:90171001-147405313	-
ICGC_0037_Pa_P_8015259	yes	1	chr13:22601936-91517618 + chr5:27822135-101940729 + chr8:31057842-33184912 + chr9:10485425-84628448	-
ICGC_0051_Pa_P_8015277	no	0	-	-
ICGC_0052_Pa_P_8015858	no	0	-	-
ICGC_0053_Pa_P_8064559	yes	1	chr6:12284188-65918328 + chr7:61963702-138259000	-
ICGC_0054_Pa_P_8016486	no	0	-	-
ICGC_0055_Pa_P_8016498	no	0	-	-
ICGC_0059_Pa_P_8030340	yes	1	chr3:78125968-190531000	-
ICGC_0061_Pa_P_8030032	no	0	-	-
ICGC_0063_Pa_P_8030353	yes	1	chr1:44735953-91085000	-
ICGC_0066_Pa_P_8031681	yes	1	chr15:23935953-39587428	-
ICGC_0069_Pa_P_8053200	yes	1	chr15:62553001-96296030	-
ICGC_0075_Pa_P_8014187	no	0	-	-
ICGC_0087_Pa_P_8033523	yes	2	chr7:17118521-62393134 + chrX:150743716-150756151	chr10:60719577-84096607
ICGC_0088_Pa_P_8032817	yes	1	chr17:11412234-61138000 + chr18:22984960-59090269	-
ICGC_0099_Pa_P_8067507	no	0	-	-
ICGC_0103_Pa_P_8031073	no	0	-	-
ICGC_0105_Pa_P_8031085	no	0	-	-
ICGC_0108_Pa_P_8029781	yes	3	chr19:787019-40699181, chr10:64265789-78493082 + chr18:4869120-22568155 + chr20:11625346-12862531	chr16:2038476-21189028 + chr8:130576805-136046121
ICGC_0109_Pa_P_8031146	yes	1	chr21:42789811-43243876 + chr5:55531001-177534040	-
ICGC_0114_Pa_P_8044091	yes	3	chr1:32132001-65797000, chr6:92940001-139752552	chr2:12368001-45055653
ICGC_0115_Pa_P_8031668	yes	1	-	chr13:70447001-94109000
ICGC_0124_Pa_P_8068548	no	0	-	-
ICGC_0134_Pa_P_8034252	no	0	-	-
ICGC_0135_Pa_P_8034278	no	0	-	-
ICGC_0140_Pa_P_8035555	no	0	-	-

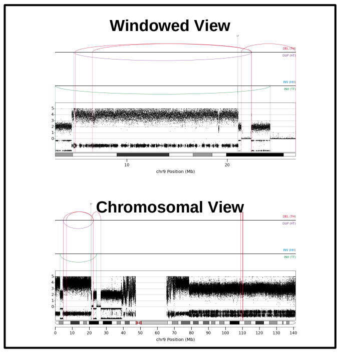
Sample	Chromothripsis	Number of Events	Event(CR1) Reactions	Event(CR2) Reactions
ICGC_0141_Pa_P_8043971	no	0	-	-
ICGC_0144_Pa_P_8035693	no	0	-	-
ICGC_0146_Pa_P_8043983	yes	2	chr10:3245988-120473283 + chr3:23871307-74921000 + chr5:10334406-14659841, chr11:44267469-122915221 + chr5:65165957-65213263	-
ICGC_0150_Pa_P_8066037	yes	1	chr19:14991001-24027955 + chrY:7917901-8070966	-
ICGC_0169_Pa_P_8044594	yes	1	chr14:44497557-78996543	-
ICGC_0185_Pa_P_8057676	no	0	-	-
ICGC_0188_Pa_P_8044983	no	0	-	-
ICGC_0192_Pa_P_8068554	no	0	-	-
ICGC_0199_Pa_P_8057479	yes	1	chr2:109779001-139791000	-
ICGC_0201_Pa_P_8057482	yes	1	chr21:14704472-41675000 + chr8:18756001-25760000	-
ICGC_0206_Pa_P_8031544	yes	1	-	chr18:20981938-27796673
ICGC_0207_Pa_P_8031704	yes	1	-	chr7:121028865-151116416
ICGC_0212_Pa_P_8035633	no	0	-	-
ICGC_0214_Pa_P_8051974	yes	4	chr1:196993875-239103445, chr1:33852332-33865200 + chr2:1473001-230678821 + chr4:27184750-162020226 + chr6:16963400-24709000	chrX:98097871-154472372, chr8:298610-1625901 + chr9:18780346-36541180
ICGC_0215_Pa_P_8052570	no	0	-	-
ICGC_0217_Pa_P_8065126	yes	1	-	chrX:136982418-147033291
ICGC_0223_Pa_P_8057484	no	0	-	-
ICGC_0224_Pa_P_8057490	no	0	-	-
ICGC_0230_Pa_P_8068563	no	0	-	-
ICGC_0235_Pa_P_8050939	yes	1	chr11:9746226-73065000 + chr12:40995001-116758747 + chr1:168543716-169262776	-
ICGC_0295_Pa_P_8058336	no	0	-	-
ICGC_0296_Pa_P_8057714	yes	1	chr18:2188460-21883265 + chr7:70084135-72295679	-
ICGC_0300_Pa_P_8058344	yes	2	chr1:31664933-242106869, chr13:27869960-52828178 + chr9:20973001-68222000	-
ICGC_0301_Pa_P_8068579	yes	1	chr18:25566441-75681666	-
ICGC_0303_Pa_P_8058184	yes	1	chr17:28709866-50798662	-
ICGC_0304_Pa_P_8058330	yes	1	chr18:1484781-31587000	-
ICGC_0309_Pa_P_8058339	yes	1	chr17:11446622-56223367 + chr3:65172798-101912639 + chrX:23483143-23579966	-
ICGC_0312_Pa_P_8058333	no	0	-	-
ICGC_0315_Pa_P_8049223	no	0	-	-
ICGC_0321_Pa_P_8061178	no	0	-	-
ICGC_0326_Pa_P_8061105	yes	2	chr12:73739582-128134138 + chr15:86999782-87157000, chr18:20632703-75024999 + chr20:2720376-15316884	-
ICGC_0338_Pa_P_8064632	no	0	-	-
ICGC_0391_Pa_P_8067175	no	0	-	-
ICGC_0392_Pa_P_8067180	yes	2	chr6:26366154-56659000 + chr8:24080552-130012489, chr12:12083354-58332929 + chr17:19426001-76916717 + chr7:89474527-92364151	-

Sample	Chromothripsis	Number of Events	Event(CR1) Reactions	Event(CR2) Reactions
ICGC_0393_Pa_P_8067182	yes	2	chr13:24905001-114487669 + chr22:19442148-51029010	chr3:118842791-159597000
ICGC_0395_Pa_P_8066852	yes	1	chr7:86035902-153368549	-
ICGC_0406_Pa_P_8067211	no	0	-	-
ICGC_0412_Pa_P_8067226	yes	1	chr18:3346945-25568170	-
ICGC_0415_Pa_P_8067232	yes	2	chr9:10009001-21759698, chr17:26762993-79337786 + chr18:1927686-31124924	-
ICGC_0419_Pa_P_8067242	yes	2	chr2:33805559-80731252, chr21:16555068-46488206	-
ICGC_0420_Pa_P_8067246	yes	1	chr12:27339001-85853159	-
ICGC_0486_Pa_P_8068564	yes	3	chr2:95882001-200539577, chr10:907872-92767218 + chr21:10861001-35164441 + chr4:65693783-160611077 + chr6:43279902-138568410	chr18:28018001-35175000
ICGC_0502_Pa_P_8068976	yes	1	chr5:23463169-45911622	-
ICGC_0503_Pa_P_8069319	no	0	-	-
ICGC_0507_Pa_P_8069060	no	0	-	-
ICGC_0518_Pa_P_8069120	yes	1	-	chr12:16384995-42011319 + chr8:42534001-96221000
ICGC_0521_Pa_P_8069443	yes	2	chr4:131679252-183296000, chr17:21737346-25340558 + chr9:85192726-125508753	-
ICGC_0526_Pa_P_8069453	yes	3	chr6:11430001-53080081, chr16:4622923-69128190, chr12:77168515-81380773 + chr13:42394145-51286894	-
ICGC_0533_Pa_P_8070181	no	0	-	-
ICGC_0535_Pa_P_8070213	yes	2	chr18:890528-21111000	chr12:80584438-121394005
ICGC_0543_Pa_P_8070199	yes	2	chr20:15750001-41058204, chr7:94685001-95587605 + chr9:181480-137306520	-

ASHPC_0003_Pa_P_2

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	1	FAIL	NA	NA	NA	NA	NA	NA
chr2	1	FAIL	NA	NA	NA	NA	NA	NA
chr3	1	FAIL	NA	NA	NA	NA	NA	NA
chr4	5	FAIL	NA	NA	NA	NA	NA	NA
chr5	1	FAIL	NA	NA	NA	NA	NA	NA
chr6	1	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9:2858001−26808000	5	FAIL	FAIL	FAIL	PASS	inter	NA	Event(CR2)
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12:60911525−61100331	4	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17:27299750−27317398	5	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr17:36126715−48291000	5	FAIL	PASS	PASS	FAIL	chain	chr17:36126715−48291000, chr20:22654370−41679000	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19:11480890−21893138	0	FAIL	FAIL	FAIL	FAIL	chain	chr19:11480890−21893138, chr20:8080720−8554165	NA
chr20:8080720−8554165	4	FAIL	PASS	FAIL	FAIL	chain	chr19:11480890−21893138, chr20:8080720−8554165	NA
chr20:22654370−41679000	4	FAIL	PASS	FAIL	FAIL	chain	chr17:36126715−48291000, chr20:22654370−41679000	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

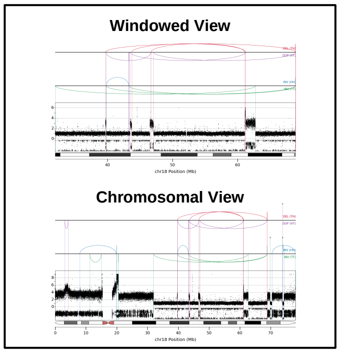
ASHPC_0003_Pa_P_2

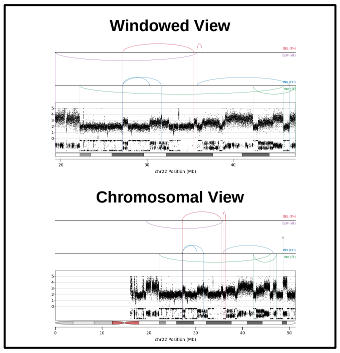


ASHPC_0005_Pa_P_1

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9:2627754−21822941	6	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr9:29098519−29904903	6	FAIL	FAIL	FAIL	FAIL	chain	chr18:69813001−78009123, chr9:29098519−29904903	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17:16787919−21320992	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr18:8016920−19845686	6	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr18:31950001−68900000	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr18:69813001−78009123	6	FAIL	FAIL	FAIL	FAIL	chain	chr18:69813001−78009123, chr9:29098519−29904903	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22:19340885−47240370	5	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

ASHPC_0005_Pa_P_1

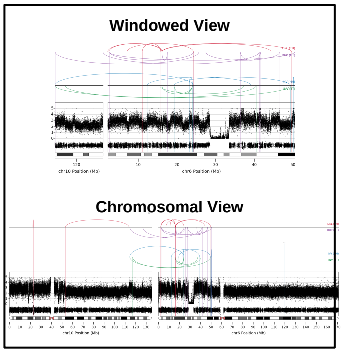




ASHPC_0006_Pa_P

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	1	FAIL	NA	NA	NA	NA	NA	NA
chr3	3	FAIL	NA	NA	NA	NA	NA	NA
chr4:27963243−28246286	6	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr4:89636001−180440000	6	PASS	FAIL	PASS	PASS	NA	NA	NA
chr5	1	FAIL	NA	NA	NA	NA	NA	NA
chr6:2111001−50491114	6	PASS	PASS	PASS	PASS	chain	chr10:114374890−126834137, chr6:2111001−50491114	Event(CR1)
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10:114374890−126834137	5	FAIL	FAIL	PASS	PASS	chain	chr10:114374890−126834137, chr6:2111001−50491114	Event(CR1)
chr11	2	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	1	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16:84256414−85724416	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	1	FAIL	NA	NA	NA	NA	NA	NA
chrX	1	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

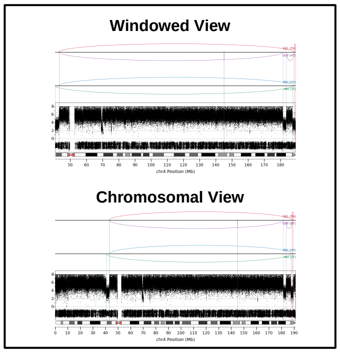
ASHPC_0006_Pa_P



ASHPC_0007_Pa_P

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	1	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4:40668001−189310000	4	FAIL	PASS	PASS	PASS	inter	NA	Event(CR2)
chr5	2	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7:5464001−11249295	4	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9:19995001−25945117	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr9:26174973−29143000	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11:118670624−119396074	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18:5451001−14575136	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	1	FAIL	NA	NA	NA	NA	NA	NA
chrX:121613891−130860896	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chrX:134315021−134465374	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

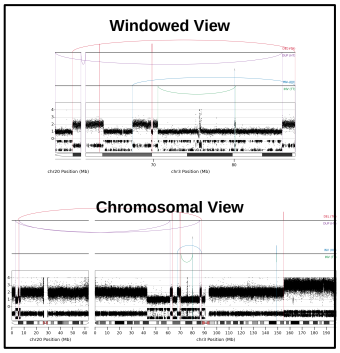
ASHPC_0007_Pa_P



ASHPC_0008_Pa_P

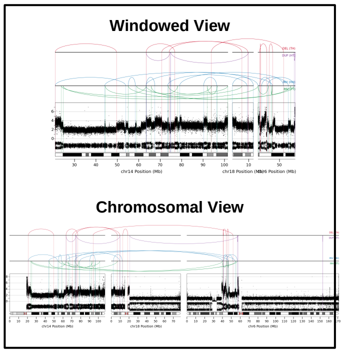
	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	2	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3:61609001−87574000	6	PASS	PASS	PASS	PASS	chain	chr20:2913001−6118000, chr3:61609001−87574000	Event(CR1)
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6:40005980−57333811	5	PASS	PASS	PASS	FAIL	chain	chr14:20953001−101625000, chr18:2451001−12237273, chr6:40005980−57333811	Event(CR1)
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	3	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	1	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14:20953001−101625000	6	PASS	PASS	PASS	PASS	chain	chr14:20953001−101625000, chr18:2451001−12237273, chr6:40005980−57333811	Event(CR1)
chr15	1	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18:2451001−12237273	6	FAIL	PASS	PASS	FAIL	chain	chr14:20953001−101625000, chr18:2451001−12237273, chr6:40005980−57333811	Event(CR1)
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20:2913001−6118000	1	FAIL	FAIL	FAIL	FAIL	chain	chr20:2913001−6118000, chr3:61609001−87574000	Event(CR1)
chr21:26011547−29983023	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

ASHPC_0008_Pa_P



Windowed View

Chromosomal View



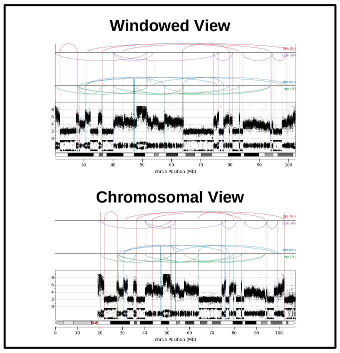
Windowed View

Chromosomal View

ASHPC_0009_Pa_P

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6:41383818−53480855	5	FAIL	FAIL	PASS	FAIL	inter	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14:20253865−102381471	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr15:82459322−84717397	5	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	5	FAIL	NA	NA	NA	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

ASHPC_0009_Pa_P



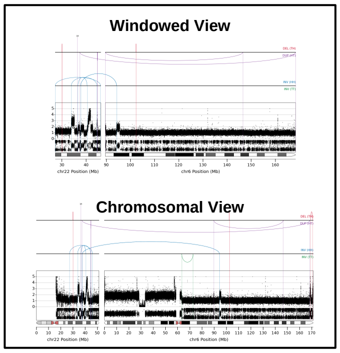
Windowed View

Chromosomal View

ASHPC_0010_Pa_P

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	5	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6:89620678−168374137	3	FAIL	FAIL	FAIL	FAIL	chain	chr22:27232901−46027000, chr6:89620678−168374137	Event(CR2)
chr7	1	FAIL	NA	NA	NA	NA	NA	NA
chr8	2	FAIL	NA	NA	NA	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	1	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18:4121001−73582992	3	FAIL	PASS	FAIL	FAIL	inter	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22:27232901−46027000	4	FAIL	FAIL	PASS	PASS	chain	chr22:27232901−46027000, chr6:89620678−168374137	Event(CR2)
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

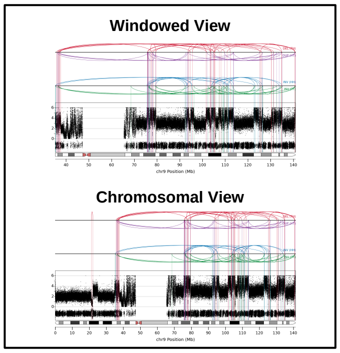
ASHPC_0010_Pa_P

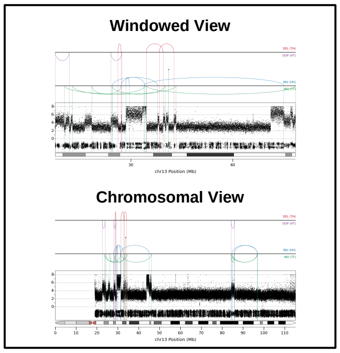


ASHPC_0016_Pa_P

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1:14759444−31722000	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	2	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	2	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8:36048001−43191000	2	FAIL	FAIL	PASS	FAIL	chain	chr20:20185692−20225981, chr8:36048001−43191000	NA
chr9:35216985−140949599	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13:22553635−46181129	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr13:84334001−96923988	6	FAIL	FAIL	FAIL	FAIL	inter	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20:20185692−20225981	0	FAIL	FAIL	FAIL	FAIL	chain	chr20:20185692−20225981, chr8:36048001−43191000	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

ASHPC_0016_Pa_P

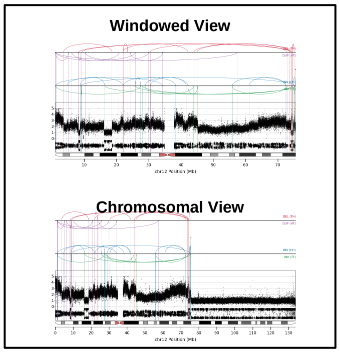




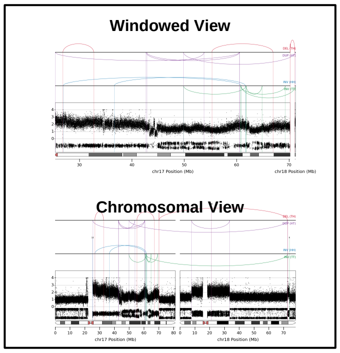
ASHPC_0017_Pa_P

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	1	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12:1002500−75488000	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17:25361904−70203528	5	PASS	PASS	PASS	FAIL	chain	chr17:25361904−70203528, chr18:72561937−72701616	Event(CR1)
chr18:21073333−21085337	1	FAIL	FAIL	FAIL	FAIL	chain	chr18:21073333−21085337, chr20:47937001−59966136	NA
chr18:72561937−72701616	1	FAIL	FAIL	FAIL	FAIL	chain	chr17:25361904−70203528, chr18:72561937−72701616	Event(CR1)
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20:47937001−59966136	0	FAIL	FAIL	FAIL	FAIL	chain	chr18:21073333−21085337, chr20:47937001−59966136	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

ASHPC_0017_Pa_P


Windowed View

Chromosomal View

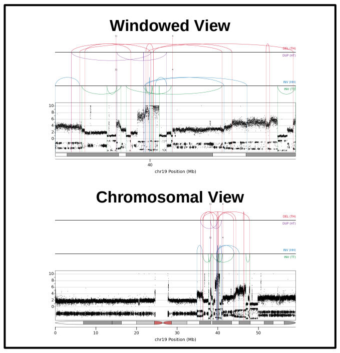

Windowed View

Chromosomal View

ASHPC_0022_Pa_P

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3:184641589−185313600	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr4	1	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	5	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	1	FAIL	NA	NA	NA	NA	NA	NA
chr18	1	FAIL	NA	NA	NA	NA	NA	NA
chr19:34861316−47890217	5	PASS	PASS	PASS	FAIL	inter	NA	Event(CR1)
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX:9528067−137731601	2	FAIL	PASS	FAIL	FAIL	inter	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

ASHPC_0022_Pa_P

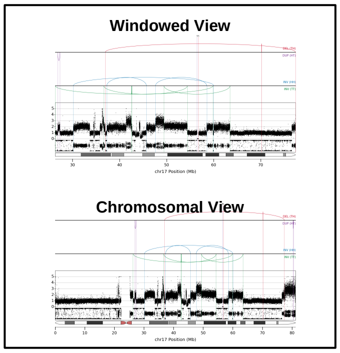

Windowed View

Chromosomal View

ASHPC_0025_Pa_P

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	1	FAIL	NA	NA	NA	NA	NA	NA
chr2	1	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	1	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6:120211595−120461595	2	FAIL	PASS	FAIL	FAIL	NA	NA	NA
chr7	1	FAIL	NA	NA	NA	NA	NA	NA
chr8	1	FAIL	NA	NA	NA	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	1	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12:31001001−32959000	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	2	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17:26315719−77395420	5	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	1	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

ASHPC_0025_Pa_P

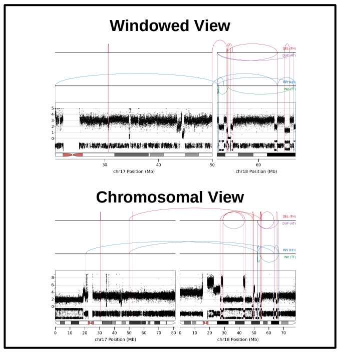

Windowed View

Chromosomal View

ASHPC_0026_Pa_P

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	1	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3:9782837−85004366	4	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr4	3	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	1	FAIL	NA	NA	NA	NA	NA	NA
chr7:1993736−24244676	3	FAIL	FAIL	FAIL	FAIL	inter	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	1	FAIL	NA	NA	NA	NA	NA	NA
chr10:50401001−52139100	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	1	FAIL	NA	NA	NA	NA	NA	NA
chr13	1	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17:20767312−50004922	0	FAIL	FAIL	FAIL	FAIL	chain	chr17:20767312−50004922, chr18:52273997−66884000	Event(CR1)
chr18:27205001−49868000	6	FAIL	FAIL	PASS	PASS	NA	NA	NA
chr18:52273997−66884000	6	PASS	PASS	PASS	PASS	chain	chr17:20767312−50004922, chr18:52273997−66884000	Event(CR1)
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

ASHPC_0026_Pa_P

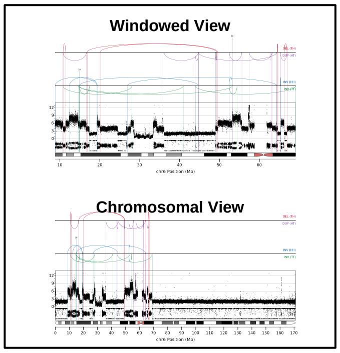

Windowed View

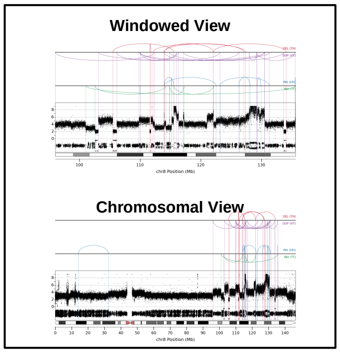
Chromosomal View

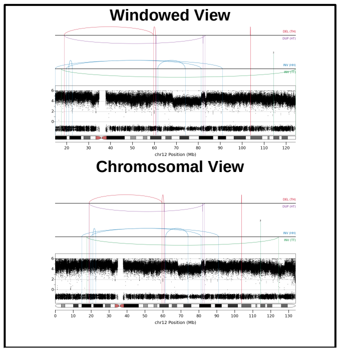
ASHPC_0027_Pa_P

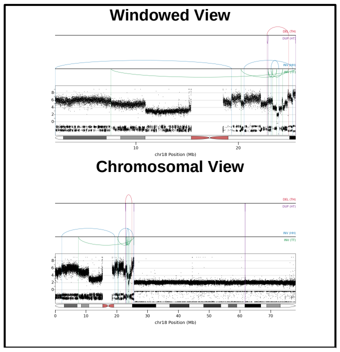
	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	1	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6:8838001−69083000	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8:95993001−135627433	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr9	2	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12:14783594−124335905	5	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	1	FAIL	NA	NA	NA	NA	NA	NA
chr18:2114001−25595735	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

ASHPC_0027_Pa_P





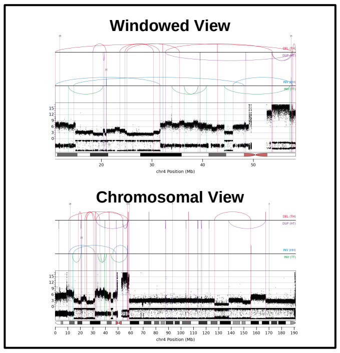


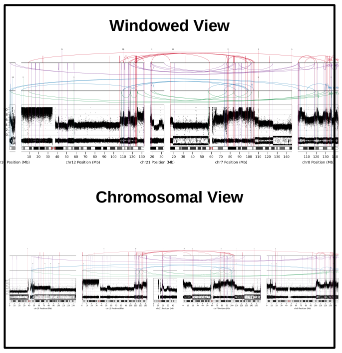


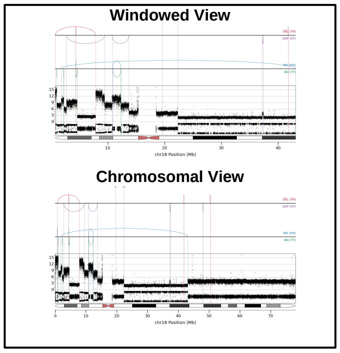
PCSI_0015_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	4	FAIL	NA	NA	NA	NA	NA	NA
chr2	4	FAIL	NA	NA	NA	NA	NA	NA
chr3:147818562−164045445	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr4:10887125−58346424	5	PASS	PASS	PASS	FAIL	inter	NA	Event(CR1)
chr4:126720001−167337152	5	FAIL	FAIL	PASS	FAIL	NA	NA	NA
chr5	3	FAIL	NA	NA	NA	NA	NA	NA
chr6	3	FAIL	NA	NA	NA	NA	NA	NA
chr7:16202363−145704711	5	PASS	FAIL	PASS	PASS	chain	chr10:43756294−49739037, chr12:1756415−132638651, chr21:18184001−32820000, chr7:16202363−145704711, chr8:100543001−143454000	Event(CR1)
chr7:158468001−158938016	5	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr8:100543001−143454000	5	PASS	PASS	PASS	PASS	chain	chr10:43756294−49739037, chr12:1756415−132638651, chr21:18184001−32820000, chr7:16202363−145704711, chr8:100543001−143454000	Event(CR1)
chr9	1	FAIL	NA	NA	NA	NA	NA	NA
chr10:43756294−49739037	2	FAIL	FAIL	FAIL	FAIL	chain	chr10:43756294−49739037, chr12:1756415−132638651, chr21:18184001−32820000, chr7:16202363−145704711, chr8:100543001−143454000	Event(CR1)
chr10:72533335−83774753	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr11	4	FAIL	NA	NA	NA	NA	NA	NA
chr12:1756415−132638651	5	PASS	FAIL	PASS	PASS	chain	chr10:43756294−49739037, chr12:1756415−132638651, chr21:18184001−32820000, chr7:16202363−145704711, chr8:100543001−143454000	Event(CR1)
chr13	3	FAIL	NA	NA	NA	NA	NA	NA
chr14	2	FAIL	NA	NA	NA	NA	NA	NA
chr15	3	FAIL	NA	NA	NA	NA	NA	NA
chr16:12049001−62561271	2	FAIL	PASS	FAIL	FAIL	NA	NA	NA
chr17:41262409−41275447	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr17:57910039−58382562	2	FAIL	FAIL	FAIL	FAIL	inter	NA	NA
chr18:745559−43072000	5	PASS	PASS	PASS	FAIL	inter	NA	Event(CR1)
chr19:43521001−48948000	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr20	5	FAIL	NA	NA	NA	NA	NA	NA
chr21:18184001−32820000	4	FAIL	PASS	PASS	FAIL	chain	chr10:43756294−49739037, chr12:1756415−132638651, chr21:18184001−32820000, chr7:16202363−145704711, chr8:100543001−143454000	Event(CR1)
chr22	2	FAIL	NA	NA	NA	NA	NA	NA
chrX:154198126−154505533	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0015_Pa_P_526



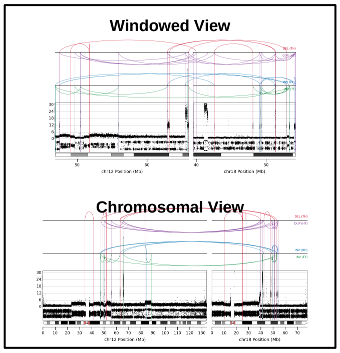




PCSI_0044_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6:890641−68031073	5	PASS	PASS	PASS	FAIL	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8:1611741−120526101	3	FAIL	FAIL	PASS	FAIL	inter	NA	NA
chr9	2	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12:46842760−65974409	6	PASS	PASS	PASS	FAIL	chain	chr12:46842760−65974409, chr18:39585517−54213000	Event(CR1)
chr12:83504072−88612346	6	FAIL	FAIL	FAIL	PASS	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18:39585517−54213000	5	PASS	PASS	PASS	FAIL	chain	chr12:46842760−65974409, chr18:39585517−54213000	Event(CR1)
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

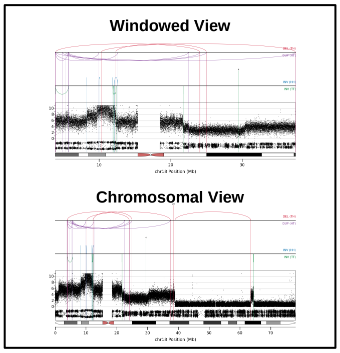
PCSI_0044_Pa_P_526



PCSI_0072_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2:35940001−46192000	4	FAIL	FAIL	FAIL	PASS	NA	NA	NA
chr2:233584806−233997267	4	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr3	2	FAIL	NA	NA	NA	NA	NA	NA
chr4:38366−4371687	6	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr4:5558001−8275056	6	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr4:121062400−135810076	6	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6:108190661−116861507	5	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	2	FAIL	NA	NA	NA	NA	NA	NA
chr11:10000001−32484000	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18:3854803−37442167	5	PASS	PASS	PASS	FAIL	inter	NA	Event(CR1)
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

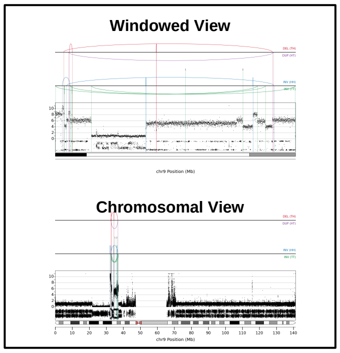
PCSI_0072_Pa_P_526



PCSI_0077_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3:159437814−190405423	1	FAIL	PASS	FAIL	FAIL	NA	NA	NA
chr4	2	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	5	FAIL	NA	NA	NA	NA	NA	NA
chr9:32604603−37179322	5	PASS	PASS	PASS	FAIL	inter	NA	Event(CR1)
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16:75923001−77705044	2	FAIL	FAIL	FAIL	FAIL	inter	NA	NA
chr17	6	FAIL	NA	NA	NA	NA	NA	NA
chr18:6797844−24209011	4	FAIL	PASS	PASS	FAIL	inter	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

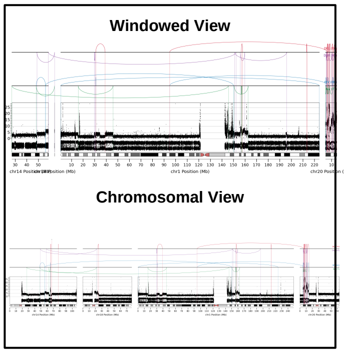
PCSI_0077_Pa_P_526

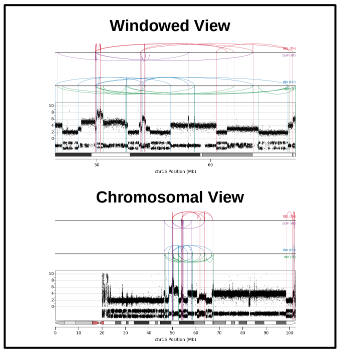


PCSI_0080_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1:711405−224208132	5	PASS	PASS	PASS	PASS	chain	chr14:27047001−58675000, chr18:21810227−21837269, chr1:711405−224208132, chr20:4783983−14509733	Event(CR1)
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	3	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	1	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14:27047001−58675000	6	FAIL	FAIL	PASS	PASS	chain	chr14:27047001−58675000, chr18:21810227−21837269, chr1:711405−224208132, chr20:4783983−14509733	Event(CR1)
chr14:62902779−65183427	6	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr15:46323001−67509081	5	PASS	PASS	PASS	FAIL	inter	NA	Event(CR1)
chr15:101373220−102124843	5	PASS	PASS	FAIL	FAIL	inter	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18:21810227−21837269	2	FAIL	FAIL	FAIL	FAIL	chain	chr14:27047001−58675000, chr18:21810227−21837269, chr1:711405−224208132, chr20:4783983−14509733	Event(CR1)
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20:4783983−14509733	6	PASS	PASS	PASS	PASS	chain	chr14:27047001−58675000, chr18:21810227−21837269, chr1:711405−224208132, chr20:4783983−14509733	Event(CR1)
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0080_Pa_P_526

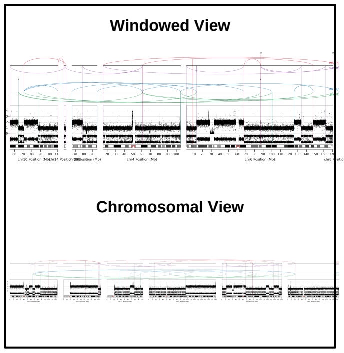


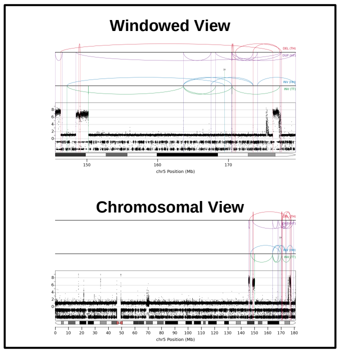


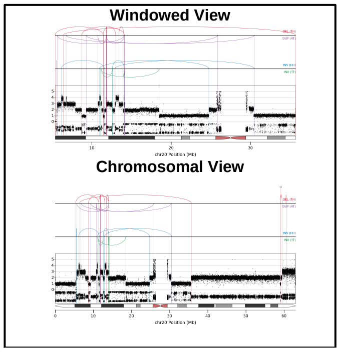
PCSI_0081_Pa_P_526

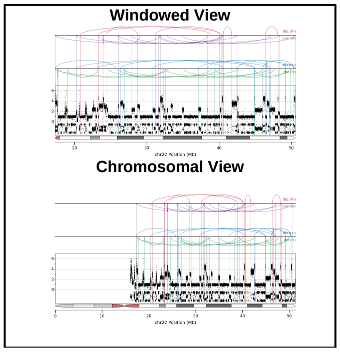
	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	1	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	1	FAIL	NA	NA	NA	NA	NA	NA
chr4:15427510−104890034	2	FAIL	PASS	FAIL	FAIL	chain	chr10:54785001−110315622, chr14:100993565−103488000, chr15:66229865−95222000, chr4:15427510−104890034, chr6:1401274−170855263, chr8:21289267−21308632	Event(CR1)
chr5:145519001−179497755	5	PASS	PASS	PASS	FAIL	inter	NA	Event(CR1)
chr6:1401274−170855263	5	PASS	PASS	PASS	PASS	chain	chr10:54785001−110315622, chr14:100993565−103488000, chr15:66229865−95222000, chr4:15427510−104890034, chr6:1401274−170855263, chr8:21289267−21308632	Event(CR1)
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8:21289267−21308632	2	FAIL	PASS	FAIL	FAIL	chain	chr10:54785001−110315622, chr14:100993565−103488000, chr15:66229865−95222000, chr4:15427510−104890034, chr6:1401274−170855263, chr8:21289267−21308632	Event(CR1)
chr9	3	FAIL	NA	NA	NA	NA	NA	NA
chr10:54785001−110315622	5	PASS	PASS	FAIL	PASS	chain	chr10:54785001−110315622, chr14:100993565−103488000, chr15:66229865−95222000, chr4:15427510−104890034, chr6:1401274−170855263, chr8:21289267−21308632	Event(CR1)
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14:100993565−103488000	2	FAIL	FAIL	FAIL	FAIL	chain	chr10:54785001−110315622, chr14:100993565−103488000, chr15:66229865−95222000, chr4:15427510−104890034, chr6:1401274−170855263, chr8:21289267−21308632	Event(CR1)
chr15:66229865−95222000	2	FAIL	FAIL	FAIL	FAIL	chain	chr10:54785001−110315622, chr14:100993565−103488000, chr15:66229865−95222000, chr4:15427510−104890034, chr6:1401274−170855263, chr8:21289267−21308632	Event(CR1)
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	1	FAIL	NA	NA	NA	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19	4	FAIL	NA	NA	NA	NA	NA	NA
chr20:5377001−35686173	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr20:58984795−59518218	6	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22:17333870−50567698	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0081_Pa_P_526





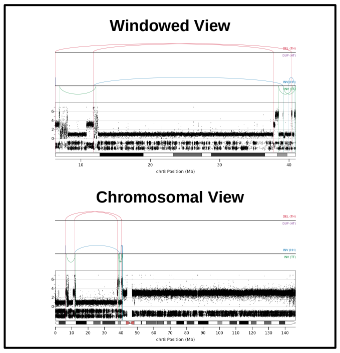


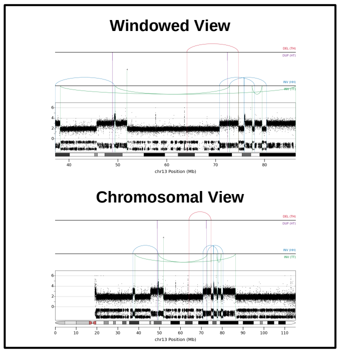


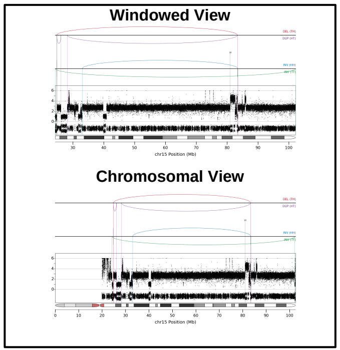
PCSI_0082_Pa_P_526

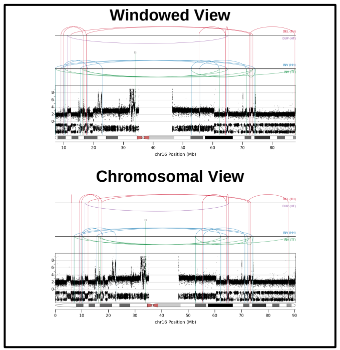
	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	2	FAIL	NA	NA	NA	NA	NA	NA
chr3:155271694−185042636	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr4	2	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	1	FAIL	NA	NA	NA	NA	NA	NA
chr7	4	FAIL	NA	NA	NA	NA	NA	NA
chr8:6292001−40943002	4	FAIL	FAIL	PASS	PASS	inter	NA	Event(CR2)
chr9:9213001−9327154	4	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr9:21798582−22202000	4	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr10	1	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12:9066621−9082264	5	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr12:14530415−29964205	5	FAIL	FAIL	PASS	FAIL	NA	NA	NA
chr13:37169764−86359000	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15:24255590−102194000	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr16:7089949−87860085	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18:1710535−32015792	5	PASS	PASS	PASS	FAIL	inter	NA	Event(CR1)
chr19	1	FAIL	NA	NA	NA	NA	NA	NA
chr20:14702166−15026000	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

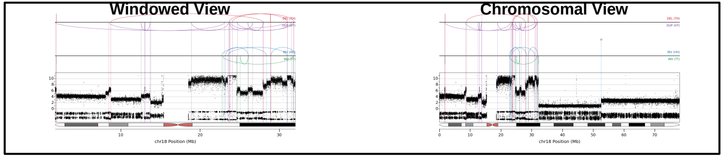
PCSI_0082_Pa_P_526







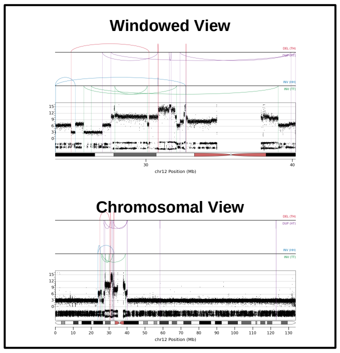




PCSI_0085_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1:2693988−162765916	3	FAIL	FAIL	PASS	FAIL	chain	chr1:2693988−162765916, chr8:2693001−12884000	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	3	FAIL	NA	NA	NA	NA	NA	NA
chr4:190642229−190661741	1	FAIL	FAIL	FAIL	FAIL	chain	chr4:190642229−190661741, chr6:3702001−25410670	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6:3702001−25410670	3	FAIL	FAIL	FAIL	FAIL	chain	chr4:190642229−190661741, chr6:3702001−25410670	NA
chr7:77579968−90060000	0	FAIL	FAIL	FAIL	FAIL	chain	chr16:46785092−58628765, chr7:77579968−90060000	NA
chr8:2693001−12884000	3	FAIL	FAIL	PASS	FAIL	chain	chr1:2693988−162765916, chr8:2693001−12884000	NA
chr9:17391699−138137000	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12:23800056−40219628	5	PASS	PASS	PASS	FAIL	inter	NA	Event(CR1)
chr13:21670949−25919260	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16:46785092−58628765	5	FAIL	FAIL	FAIL	FAIL	chain	chr16:46785092−58628765, chr7:77579968−90060000	NA
chr17:29719331−33178119	4	FAIL	PASS	FAIL	FAIL	inter	NA	NA
chr18	1	FAIL	NA	NA	NA	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0085_Pa_P_526

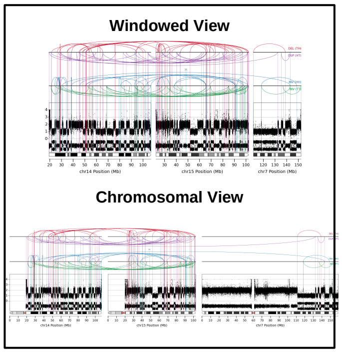

Windowed View

Chromosomal View

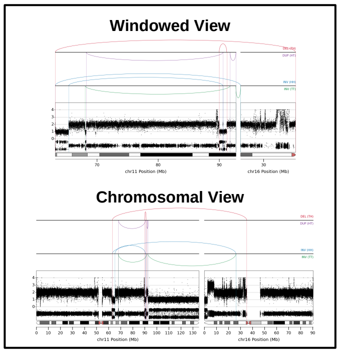
PCSI_0101_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	2	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6:34740001−46936000	3	FAIL	FAIL	PASS	FAIL	NA	NA	NA
chr7:111507715−152374000	4	FAIL	PASS	PASS	PASS	chain	chr14:19250282−106848507, chr15:22466221−102201721, chr7:111507715−152374000	Event(CR1)
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9:25821478−32071665	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11:63150797−92717000	5	PASS	PASS	PASS	PASS	chain	chr11:63150797−92717000, chr16:26231184−35220572	Event(CR1)
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14:19250282−106848507	6	PASS	PASS	PASS	PASS	chain	chr14:19250282−106848507, chr15:22466221−102201721, chr7:111507715−152374000	Event(CR1)
chr15:22466221−102201721	6	PASS	PASS	PASS	PASS	chain	chr14:19250282−106848507, chr15:22466221−102201721, chr7:111507715−152374000	Event(CR1)
chr16:26231184−35220572	0	FAIL	FAIL	FAIL	FAIL	chain	chr11:63150797−92717000, chr16:26231184−35220572	Event(CR1)
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22:16648392−43453432	5	PASS	FAIL	PASS	PASS	inter	NA	Event(CR2)
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

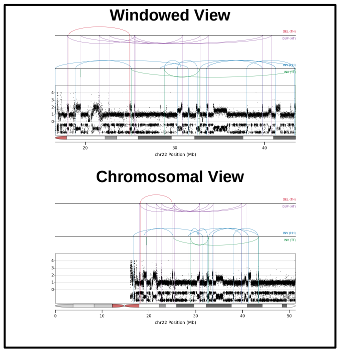
PCSI_0101_Pa_P_526


Windowed View

Chromosomal View


Windowed View

Chromosomal View


Windowed View

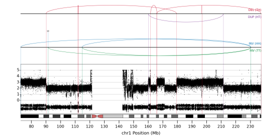
Chromosomal View

PCSI_0104_Pa_P_526

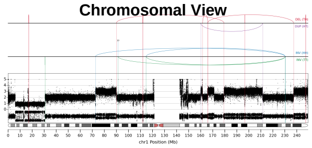
	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1:72688825−237339437	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr2:184422297−206560000	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	1	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6:21289001−53533834	4	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8:113147192−113491121	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr9:21823001−22415270	4	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	2	FAIL	NA	NA	NA	NA	NA	NA
chr12	1	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	3	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	1	FAIL	NA	NA	NA	NA	NA	NA
chr17	1	FAIL	NA	NA	NA	NA	NA	NA
chr18:26919802−66027547	4	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr19	2	FAIL	NA	NA	NA	NA	NA	NA
chr20:3722001−19787293	3	FAIL	FAIL	FAIL	PASS	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX:64063463−64461151	2	FAIL	PASS	FAIL	FAIL	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0104_Pa_P_526

Windowed View



Chromosomal View

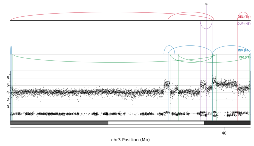


PCSI_0105_Pa_P_526

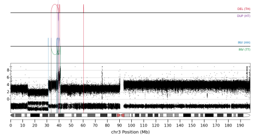
	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	1	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3:33550196−40793000	5	PASS	PASS	PASS	FAIL	inter	NA	Event(CR1)
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6:48514390−49152864	2	FAIL	FAIL	FAIL	FAIL	chain	chr11:24949001−25248000, chr6:48514390−49152864	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8:32293001−43493440	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11:24949001−25248000	2	FAIL	FAIL	FAIL	FAIL	chain	chr11:24949001−25248000, chr6:48514390−49152864	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13:35860923−109420000	6	PASS	PASS	PASS	PASS	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	2	FAIL	NA	NA	NA	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19	4	FAIL	NA	NA	NA	NA	NA	NA
chr20:22650867−62656813	5	FAIL	PASS	PASS	FAIL	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0105_Pa_P_526

Windowed View



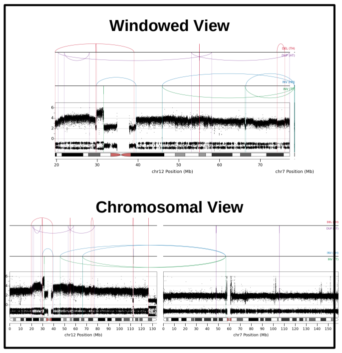
Chromosomal View



PCSI_0109_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	1	FAIL	NA	NA	NA	NA	NA	NA
chr6	1	FAIL	NA	NA	NA	NA	NA	NA
chr7:56717499−56814099	0	FAIL	FAIL	FAIL	FAIL	chain	chr12:19633912−77195612, chr7:56717499−56814099	Event(CR1)
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	1	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	1	FAIL	NA	NA	NA	NA	NA	NA
chr12:19633912−77195612	5	PASS	PASS	PASS	FAIL	chain	chr12:19633912−77195612, chr7:56717499−56814099	Event(CR1)
chr12:111912962−112643161	5	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr13	2	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18:20482001−25466361	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20:37732001−51506950	5	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22:29757845−29927000	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

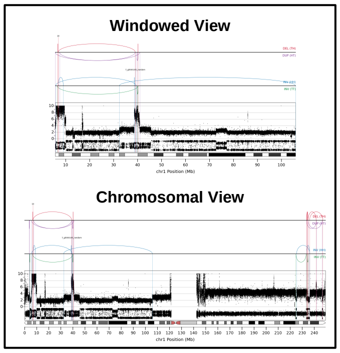
PCSI_0109_Pa_P_526

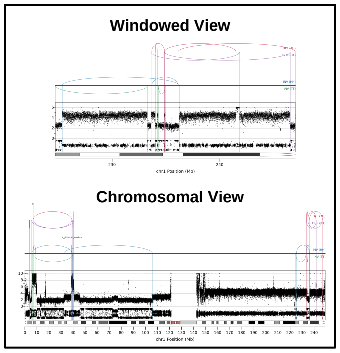


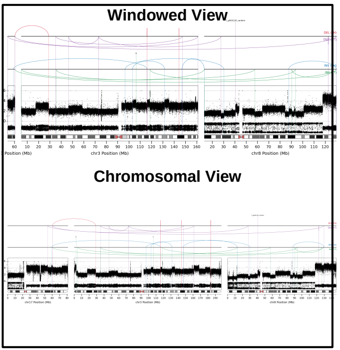
PCSI_0111_Pa_P_526

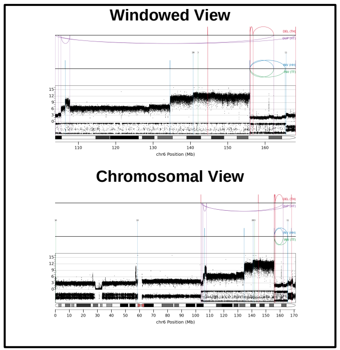
	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1:5645001−105889022	6	PASS	PASS	PASS	FAIL	inter	NA	Event(CR1)
chr1:224730777−247029065	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr2:137920001−146682453	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr3:4690049−161090000	4	FAIL	PASS	PASS	PASS	chain	chr17:53978341−60459185, chr3:4690049−161090000, chr8:12945001−129797000	Event(CR2)
chr4:1403211−46042043	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr5:11033718−40766702	5	FAIL	PASS	PASS	PASS	NA	NA	NA
chr6:103782441−168186007	5	PASS	PASS	PASS	FAIL	inter	NA	Event(CR1)
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8:12945001−129797000	3	FAIL	FAIL	PASS	PASS	chain	chr17:53978341−60459185, chr3:4690049−161090000, chr8:12945001−129797000	Event(CR2)
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10:5513832−45337780	5	PASS	PASS	PASS	FAIL	NA	NA	NA
chr11:65994746−116844000	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr12:57182013−66051807	6	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17:53978341−60459185	2	FAIL	PASS	FAIL	FAIL	chain	chr17:53978341−60459185, chr3:4690049−161090000, chr8:12945001−129797000	Event(CR2)
chr18:5882001−19800442	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr19	2	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

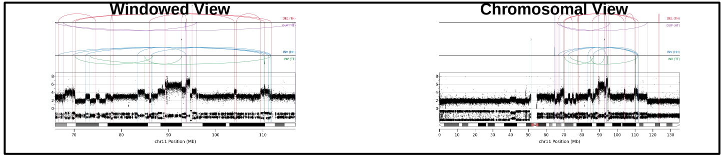
PCSI_0111_Pa_P_526







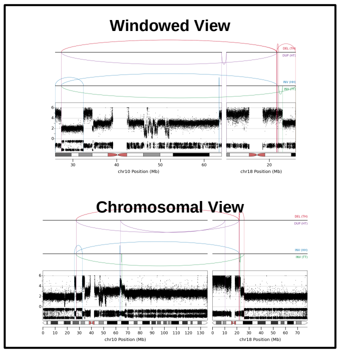


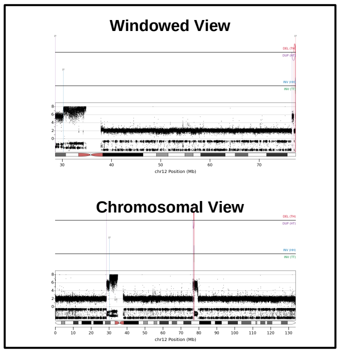


PCSI_0132_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10:25942001−64013019	6	PASS	PASS	PASS	PASS	chain	chr10:25942001−64013019, chr18:10191618−26009000	Event(CR1)
chr11:23837769−76341155	5	PASS	PASS	PASS	FAIL	NA	NA	NA
chr12:28578001−77383370	6	PASS	PASS	FAIL	PASS	inter	NA	Event(CR2)
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14:54443557−54457039	5	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	1	FAIL	NA	NA	NA	NA	NA	NA
chr18:10191618−26009000	3	FAIL	PASS	FAIL	FAIL	chain	chr10:25942001−64013019, chr18:10191618−26009000	Event(CR1)
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0132_Pa_P_526

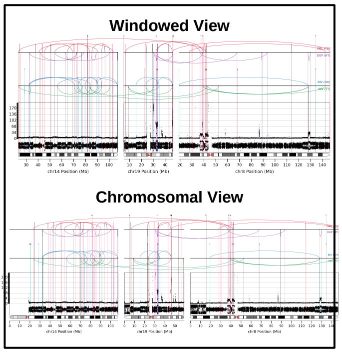


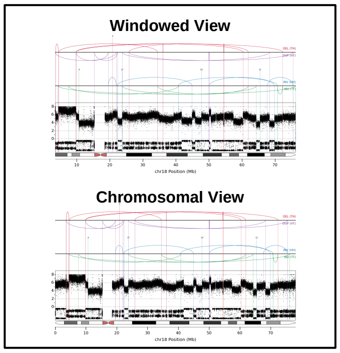


PCSI_0145_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	3	FAIL	NA	NA	NA	NA	NA	NA
chr2	3	FAIL	NA	NA	NA	NA	NA	NA
chr3	3	FAIL	NA	NA	NA	NA	NA	NA
chr4:91318816−92063535	4	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr4:106860903−108184000	4	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr5:58375267−116054236	4	FAIL	FAIL	PASS	FAIL	NA	NA	NA
chr6:1950845−2233304	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr7	3	FAIL	NA	NA	NA	NA	NA	NA
chr8:19052905−146296559	5	PASS	PASS	PASS	PASS	chain	chr14:23421680−107122709, chr19:5064997−46549000, chr8:19052905−146296559	Event(CR1)
chr9	3	FAIL	NA	NA	NA	NA	NA	NA
chr10	2	FAIL	NA	NA	NA	NA	NA	NA
chr11	3	FAIL	NA	NA	NA	NA	NA	NA
chr12	4	FAIL	NA	NA	NA	NA	NA	NA
chr13	3	FAIL	NA	NA	NA	NA	NA	NA
chr14:20383487−20514081	6	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr14:23421680−107122709	6	PASS	PASS	PASS	PASS	chain	chr14:23421680−107122709, chr19:5064997−46549000, chr8:19052905−146296559	Event(CR1)
chr15:56314808−65046981	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr16:47966726−71056398	4	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr17	1	FAIL	NA	NA	NA	NA	NA	NA
chr18:3500001−76204610	5	PASS	PASS	PASS	FAIL	inter	NA	Event(CR1)
chr19:5064997−46549000	5	PASS	PASS	PASS	FAIL	chain	chr14:23421680−107122709, chr19:5064997−46549000, chr8:19052905−146296559	Event(CR1)
chr20:18846509−25900818	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr21	2	FAIL	NA	NA	NA	NA	NA	NA
chr22:49523942−51054000	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chrX	1	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0145_Pa_P_526

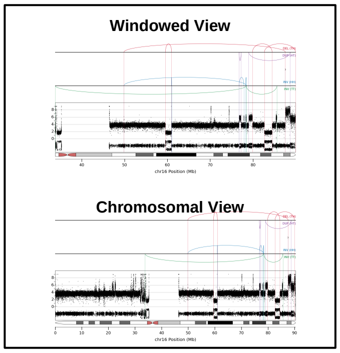




PCSI_0162_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2:58641001−63191747	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr3	1	FAIL	NA	NA	NA	NA	NA	NA
chr4:91606712−91974284	6	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr4:164651947−176242000	6	FAIL	PASS	FAIL	FAIL	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	3	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16:33785523−89933000	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18:1465450−21963017	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	1	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0162_Pa_P_526

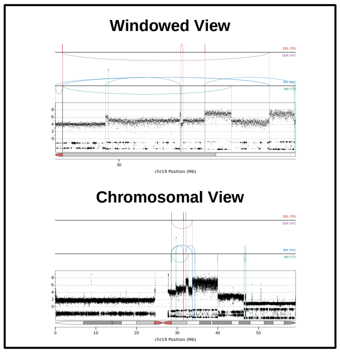

Windowed View

Chromosomal View

PCSI_0170_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5:10806091−11072115	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8:36422294−40949000	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	1	FAIL	NA	NA	NA	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19:28420607−34376000	6	PASS	PASS	PASS	FAIL	inter	NA	Event(CR1)
chr19:46412611−46922000	6	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0170_Pa_P_526

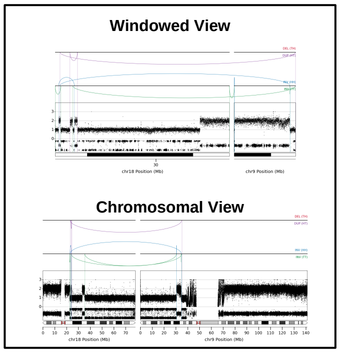

Windowed View

Chromosomal View

PCSI_0171_Pa_P_526

PCSI_0171_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6:41379001−81982000	3	FAIL	PASS	FAIL	FAIL	inter	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9:30530921−35000887	1	FAIL	FAIL	FAIL	FAIL	chain	chr18:22673001−35355700, chr9:30530921−35000887	Event(CR2)
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13:74288459−115111854	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18:22673001−35355700	5	FAIL	FAIL	PASS	PASS	chain	chr18:22673001−35355700, chr9:30530921−35000887	Event(CR2)
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

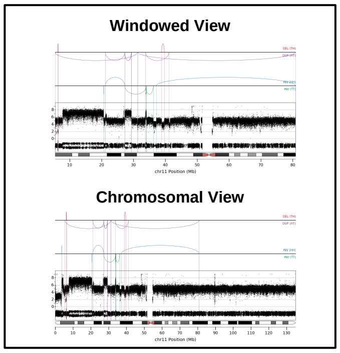

Windowed View

Chromosomal View

PCSI_0174_Pa_P_526

PCSI_0174_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1:40488001−40731122	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr2:115155981−153721549	2	FAIL	FAIL	PASS	FAIL	NA	NA	NA
chr3	3	FAIL	NA	NA	NA	NA	NA	NA
chr4:55698656−55812027	2	FAIL	FAIL	FAIL	FAIL	chain	chr4:55698656−55812027, chr9:37796037−37820662	NA
chr4:153342748−163556153	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr5:130769001−169835490	3	FAIL	FAIL	PASS	FAIL	NA	NA	NA
chr6	3	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8:86022587−141819757	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr9:37796037−37820662	2	FAIL	FAIL	FAIL	FAIL	chain	chr4:55698656−55812027, chr9:37796037−37820662	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11:5430001−80867710	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr12	1	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14:55091211−87318000	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	3	FAIL	NA	NA	NA	NA	NA	NA
chr17:18900244−30708066	4	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr18	1	FAIL	NA	NA	NA	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22:19885702−50341000	1	FAIL	FAIL	PASS	FAIL	NA	NA	NA
chrX:14214952−14352349	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

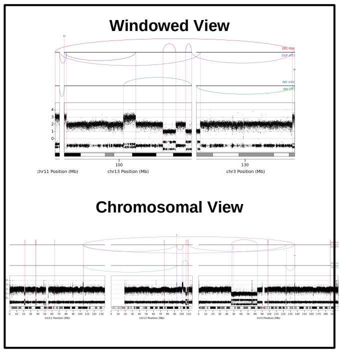

Windowed View

Chromosomal View

PCSI_0175_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1:75556988−215134804	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3:46122724−83085000	5	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr3:123687001−136429461	5	FAIL	PASS	FAIL	FAIL	chain	chr11:104027413−104618080, chr13:92886051−109392801, chr3:123687001−136429461	Event(CR1)
chr4	2	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7:122806920−123004554	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11:104027413−104618080	3	FAIL	FAIL	FAIL	FAIL	chain	chr11:104027413−104618080, chr13:92886051−109392801, chr3:123687001−136429461	Event(CR1)
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13:92886051−109392801	6	PASS	PASS	PASS	PASS	chain	chr11:104027413−104618080, chr13:92886051−109392801, chr3:123687001−136429461	Event(CR1)
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	1	FAIL	NA	NA	NA	NA	NA	NA
chr18:39501001−74069611	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0175_Pa_P_526

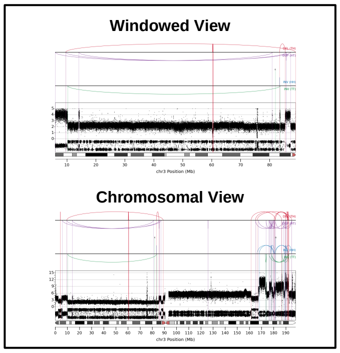

Windowed View

Chromosomal View

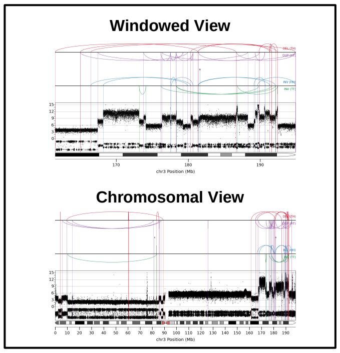
PCSI_0210_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3:5942001−88961651	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr3:161515001−194901662	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	4	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8:33785126−43504000	5	PASS	PASS	PASS	FAIL	chain	chr18:12829001−19910168, chr8:33785126−43504000	Event(CR1)
chr8:53095222−73186182	5	PASS	PASS	FAIL	FAIL	inter	NA	NA
chr9:16027001−38057393	3	FAIL	FAIL	PASS	PASS	NA	NA	NA
chr10:74911274−110823000	3	FAIL	FAIL	PASS	PASS	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12:33984229−61255159	5	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr12:61591001−61922727	5	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17:14778233−25306237	5	PASS	PASS	PASS	FAIL	inter	NA	Event(CR1)
chr18:12829001−19910168	2	FAIL	FAIL	FAIL	FAIL	chain	chr18:12829001−19910168, chr8:33785126−43504000	Event(CR1)
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX:25108062−56603146	2	FAIL	PASS	FAIL	FAIL	inter	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

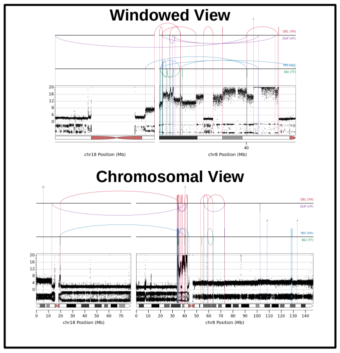
PCSI_0210_Pa_P_526


Windowed View

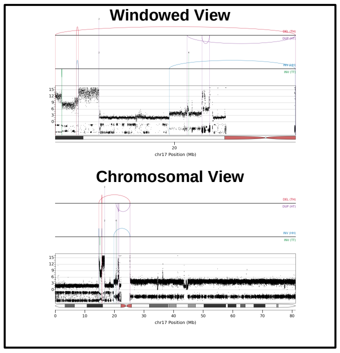
Chromosomal View


Windowed View

Chromosomal View


Windowed View

Chromosomal View

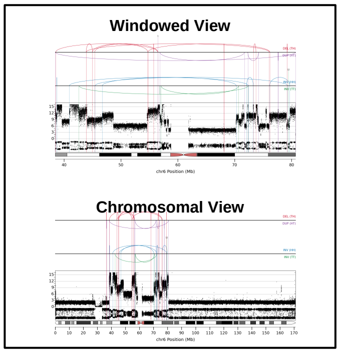

Windowed View

Chromosomal View

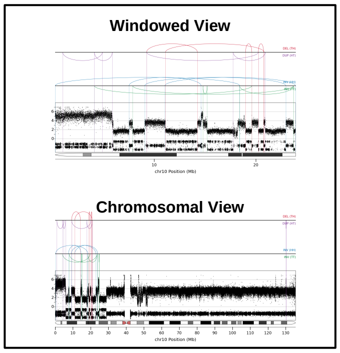
PCSI_0217_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1:191310974−191337927	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr2:120512266−120731274	4	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr3	4	FAIL	NA	NA	NA	NA	NA	NA
chr4:45527001−64603651	4	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr5	1	FAIL	NA	NA	NA	NA	NA	NA
chr6:36457001−36705057	6	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr6:38429850−80706255	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr7:7848747−17934717	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr7:61963118−149787391	3	FAIL	FAIL	PASS	PASS	NA	NA	NA
chr8:37384914−37511000	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr8:55498001−108314521	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr9:74291116−74473491	5	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr10:260001−23904132	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr11	2	FAIL	NA	NA	NA	NA	NA	NA
chr12:54064384−121402908	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr13	1	FAIL	NA	NA	NA	NA	NA	NA
chr14	1	FAIL	NA	NA	NA	NA	NA	NA
chr15:66920001−67142503	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr16:78651755−78968340	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20:30889230−31039813	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr21:44946406−45433443	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

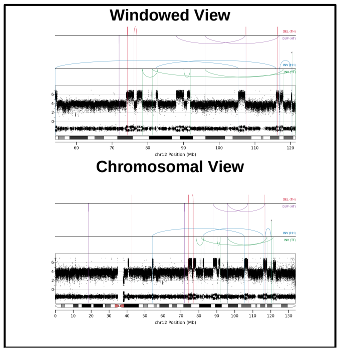
PCSI_0217_Pa_P_526


Windowed View

Chromosomal View


Windowed View

Chromosomal View

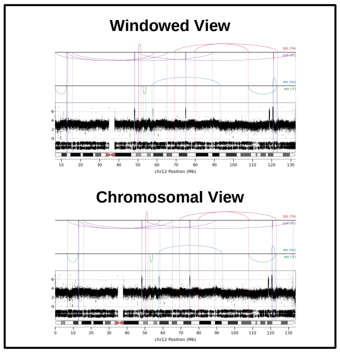

Windowed View

Chromosomal View

PCSI_0226_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	3	FAIL	NA	NA	NA	NA	NA	NA
chr2:141635001−142150000	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr3	3	FAIL	NA	NA	NA	NA	NA	NA
chr4:124701341−124878976	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	2	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8:98700862−98888000	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr9	1	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11:65141122−65366000	1	FAIL	FAIL	FAIL	FAIL	inter	NA	NA
chr12:6787814−132455367	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr13:48852855−96438919	2	FAIL	PASS	FAIL	FAIL	chain	chr13:48852855−96438919, chr14:65671940−100468137	NA
chr14:65671940−100468137	2	FAIL	PASS	FAIL	FAIL	chain	chr13:48852855−96438919, chr14:65671940−100468137	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	1	FAIL	NA	NA	NA	NA	NA	NA
chr17	1	FAIL	NA	NA	NA	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19:54029751−57771486	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	2	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0226_Pa_P_526

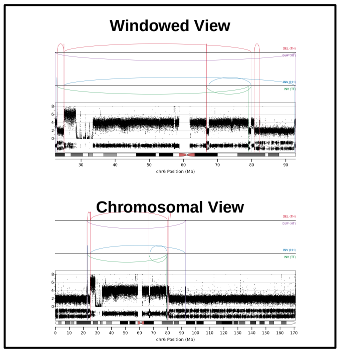

Windowed View

Chromosomal View

PCSI_0228_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6:22425001−92870609	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19:7096101−27775515	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

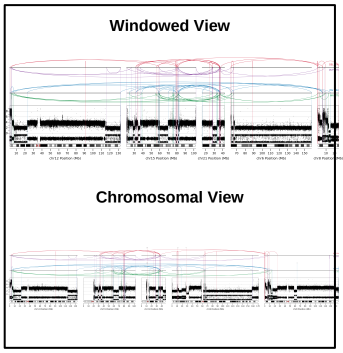
PCSI_0228_Pa_P_526

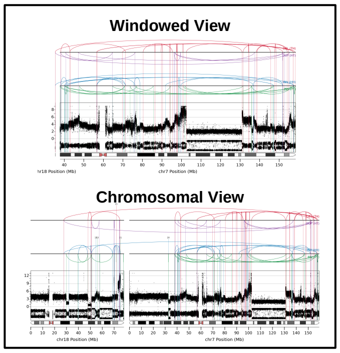


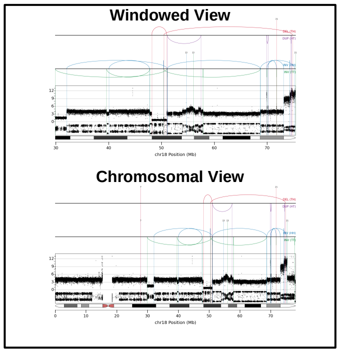
PCSI_0230_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	2	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6:63093814−158127040	6	PASS	PASS	PASS	PASS	chain	chr12:2049001−132452607, chr15:20937454−102512224, chr21:15645666−42300116, chr6:63093814−158127040, chr8:153382−24991000	Event(CR1)
chr7:32686530−32696000	6	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr7:37823001−158416032	6	PASS	PASS	PASS	PASS	chain	chr18:27756642−27775389, chr7:37823001−158416032	Event(CR1)
chr8:153382−24991000	4	FAIL	PASS	PASS	FAIL	chain	chr12:2049001−132452607, chr15:20937454−102512224, chr21:15645666−42300116, chr6:63093814−158127040, chr8:153382−24991000	Event(CR1)
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12:2049001−132452607	5	PASS	PASS	PASS	PASS	chain	chr12:2049001−132452607, chr15:20937454−102512224, chr21:15645666−42300116, chr6:63093814−158127040, chr8:153382−24991000	Event(CR1)
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15:20937454−102512224	6	PASS	PASS	PASS	PASS	chain	chr12:2049001−132452607, chr15:20937454−102512224, chr21:15645666−42300116, chr6:63093814−158127040, chr8:153382−24991000	Event(CR1)
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	2	FAIL	NA	NA	NA	NA	NA	NA
chr18:27756642−27775389	6	FAIL	FAIL	FAIL	FAIL	chain	chr18:27756642−27775389, chr7:37823001−158416032	Event(CR1)
chr18:29879708−75377000	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21:15645666−42300116	5	PASS	PASS	PASS	FAIL	chain	chr12:2049001−132452607, chr15:20937454−102512224, chr21:15645666−42300116, chr6:63093814−158127040, chr8:153382−24991000	Event(CR1)
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0230_Pa_P_526



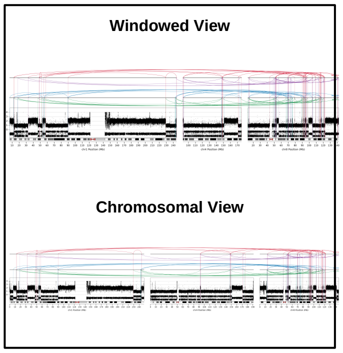




PCSI_0236_Pa_P_526

PCSI_0236_Pa_P_526

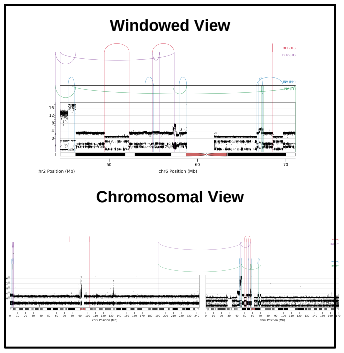
	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1:6585984−244736597	6	PASS	PASS	PASS	PASS	chain	chr1:6585984−244736597, chr4:92173684−175718413, chr8:12443819−142219000	Event(CR1)
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3:29119145−156171063	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr4:92173684−175718413	5	PASS	PASS	PASS	PASS	chain	chr1:6585984−244736597, chr4:92173684−175718413, chr8:12443819−142219000	Event(CR1)
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8:12443819−142219000	6	PASS	PASS	PASS	PASS	chain	chr1:6585984−244736597, chr4:92173684−175718413, chr8:12443819−142219000	Event(CR1)
chr9:26831539−31102000	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	1	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18:11882405−25374000	3	FAIL	FAIL	PASS	PASS	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	1	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

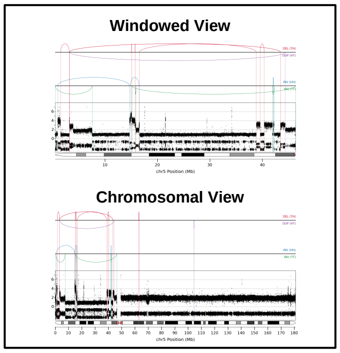


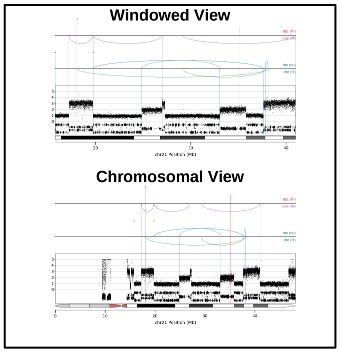
PCSI_0237_Pa_P_526

PCSI_0237_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2:1819709−4528064	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr2:190434582−190446738	2	FAIL	FAIL	FAIL	FAIL	chain	chr2:190434582−190446738, chr6:44454055−71075000	Event(CR1)
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5:491001−46343941	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr6:44454055−71075000	6	PASS	PASS	PASS	PASS	chain	chr2:190434582−190446738, chr6:44454055−71075000	Event(CR1)
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	2	FAIL	NA	NA	NA	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11:27234966−27505000	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17:15906810−60766474	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21:15773949−41006313	5	PASS	PASS	PASS	FAIL	chain	chr21:15773949−41006313, chrX:63926388−154855088	Event(CR1)
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX:63926388−154855088	0	FAIL	FAIL	FAIL	FAIL	chain	chr21:15773949−41006313, chrX:63926388−154855088	Event(CR1)
chrY	0	FAIL	NA	NA	NA	NA	NA	NA



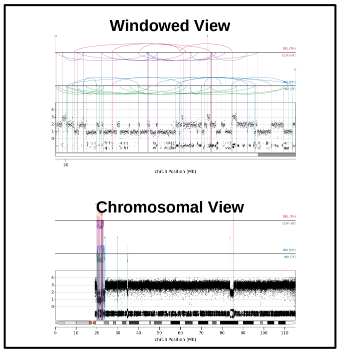




PCSI_0239_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	2	FAIL	NA	NA	NA	NA	NA	NA
chr2:198475911−199273179	5	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr3:15327330−15422111	4	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr3:22359792−31869610	4	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr4	4	FAIL	NA	NA	NA	NA	NA	NA
chr5:79030001−99583241	3	FAIL	PASS	FAIL	FAIL	NA	NA	NA
chr6	2	FAIL	NA	NA	NA	NA	NA	NA
chr7	1	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9:18559001−27143000	4	FAIL	PASS	FAIL	FAIL	chain	chr18:39432001−43433270, chr9:18559001−27143000	NA
chr10	1	FAIL	NA	NA	NA	NA	NA	NA
chr11	2	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13:19818766−23944483	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr13:34485466−34921013	6	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18:39432001−43433270	0	FAIL	FAIL	FAIL	FAIL	chain	chr18:39432001−43433270, chr9:18559001−27143000	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

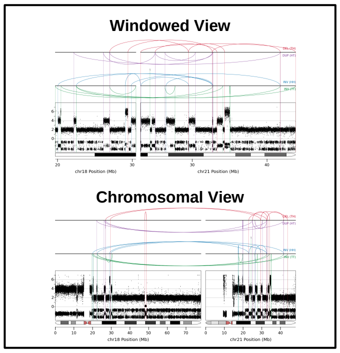
PCSI_0239_Pa_P_526



PCSI_0240_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	3	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	3	FAIL	NA	NA	NA	NA	NA	NA
chr18:19689856−30495013	6	PASS	PASS	PASS	PASS	chain	chr18:19689856−30495013, chr21:23068555−43836118	Event(CR1)
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21:17418001−19954876	6	FAIL	FAIL	FAIL	PASS	NA	NA	NA
chr21:23068555−43836118	6	PASS	PASS	PASS	PASS	chain	chr18:19689856−30495013, chr21:23068555−43836118	Event(CR1)
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

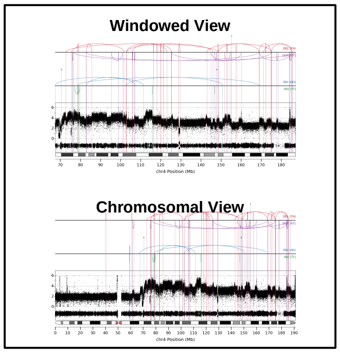
PCSI_0240_Pa_P_526



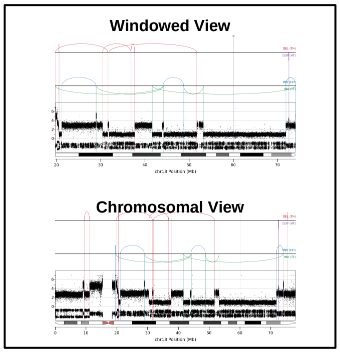
PCSI_0261_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	3	FAIL	NA	NA	NA	NA	NA	NA
chr2:108043951−124391011	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr2:142658470−231054641	3	FAIL	PASS	FAIL	FAIL	inter	NA	NA
chr3:112287797−112300804	3	FAIL	FAIL	FAIL	FAIL	chain	chr11:127710316−131214077, chr3:112287797−112300804	NA
chr4:59121561−59386000	5	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr4:67443001−187141000	5	PASS	FAIL	PASS	PASS	inter	NA	Event(CR2)
chr5:2309912−23420023	4	FAIL	PASS	FAIL	FAIL	NA	NA	NA
chr5:55812123−78866929	4	FAIL	FAIL	PASS	FAIL	inter	NA	NA
chr6	5	FAIL	NA	NA	NA	NA	NA	NA
chr7:129397032−129633634	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr7:156071107−157576329	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr8:130752639−130767164	2	FAIL	FAIL	FAIL	FAIL	chain	chr12:34053222−90714380, chr8:130752639−130767164	NA
chr9	3	FAIL	NA	NA	NA	NA	NA	NA
chr10	2	FAIL	NA	NA	NA	NA	NA	NA
chr11:37127426−41223136	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr11:127710316−131214077	3	FAIL	FAIL	FAIL	FAIL	chain	chr11:127710316−131214077, chr3:112287797−112300804	NA
chr12:34053222−90714380	2	FAIL	PASS	FAIL	FAIL	chain	chr12:34053222−90714380, chr8:130752639−130767164	NA
chr13:86970001−91883087	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15:84172692−84283076	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr16	3	FAIL	NA	NA	NA	NA	NA	NA
chr17:47068795−67727021	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr18:19709355−74084000	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0261_Pa_P_526


Windowed View

Chromosomal View

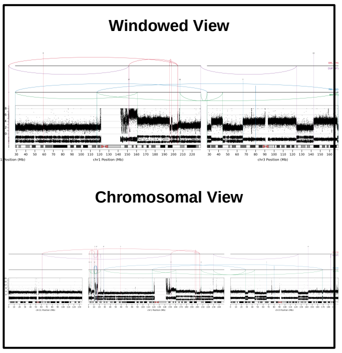

Windowed View

Chromosomal View

PCSI_0268_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1:28699267−229430158	6	PASS	PASS	PASS	FAIL	chain	chr11:61364001−61635890, chr1:28699267−229430158, chr3:27598784−169520086	Event(CR1)
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3:27598784−169520086	3	FAIL	FAIL	PASS	PASS	chain	chr11:61364001−61635890, chr1:28699267−229430158, chr3:27598784−169520086	Event(CR1)
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	1	FAIL	NA	NA	NA	NA	NA	NA
chr9	2	FAIL	NA	NA	NA	NA	NA	NA
chr10:126845447−127083177	3	FAIL	PASS	FAIL	FAIL	inter	NA	NA
chr11:61364001−61635890	0	FAIL	FAIL	FAIL	FAIL	chain	chr11:61364001−61635890, chr1:28699267−229430158, chr3:27598784−169520086	Event(CR1)
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18:12570001−14837210	5	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr18:21926931−22135000	5	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0268_Pa_P_526

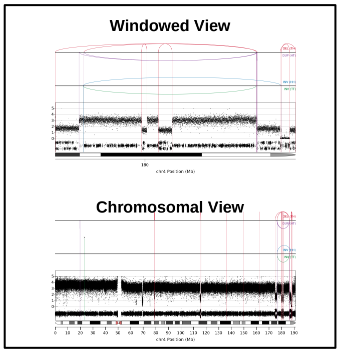

Windowed View

Chromosomal View

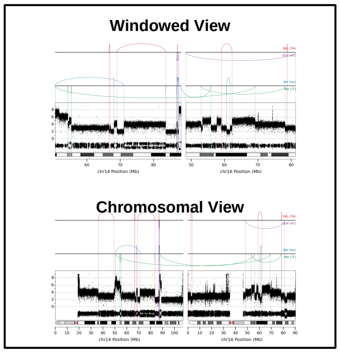
PCSI_0274_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	3	FAIL	NA	NA	NA	NA	NA	NA
chr2	3	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4:174928558−188505000	5	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	4	FAIL	NA	NA	NA	NA	NA	NA
chr7:111066314−111739458	5	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr8	1	FAIL	NA	NA	NA	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10:965893−36433000	5	FAIL	FAIL	FAIL	PASS	chain	chr10:965893−36433000, chr17:15180001−21908000	NA
chr10:71072854−102132000	5	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr11	3	FAIL	NA	NA	NA	NA	NA	NA
chr12:53377001−63829533	5	PASS	PASS	PASS	FAIL	NA	NA	NA
chr12:79750745−80599600	5	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr13:104383001−108106703	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr14:50495917−88279000	6	PASS	PASS	PASS	PASS	chain	chr14:50495917−88279000, chr16:48397966−81330000	Event(CR1)
chr15	1	FAIL	NA	NA	NA	NA	NA	NA
chr16:48397966−81330000	5	PASS	PASS	PASS	PASS	chain	chr14:50495917−88279000, chr16:48397966−81330000	Event(CR1)
chr17:15180001−21908000	5	FAIL	PASS	PASS	FAIL	chain	chr10:965893−36433000, chr17:15180001−21908000	NA
chr18:24495617−64320000	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr19	1	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX:11381212−13301142	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chrX:49636025−93389108	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

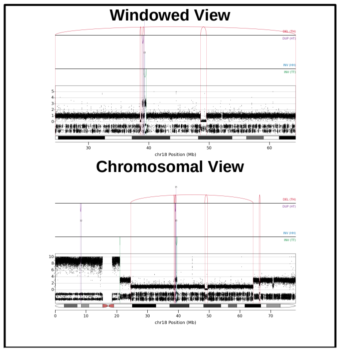
PCSI_0274_Pa_P_526


Windowed View

Chromosomal View


Windowed View

Chromosomal View

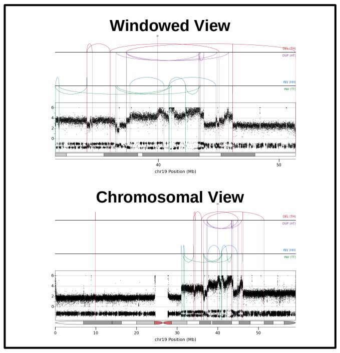

Windowed View

Chromosomal View

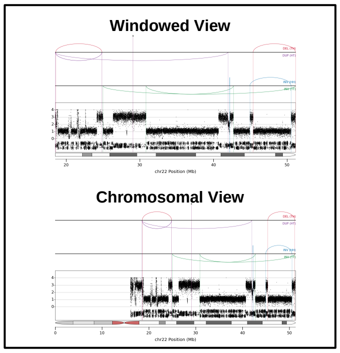
PCSI_0279_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	2	FAIL	NA	NA	NA	NA	NA	NA
chr16:27585469−80620710	3	FAIL	FAIL	PASS	PASS	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18	2	FAIL	NA	NA	NA	NA	NA	NA
chr19:31466617−51372172	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22:18515809−51142114	5	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0279_Pa_P_526


Windowed View

Chromosomal View

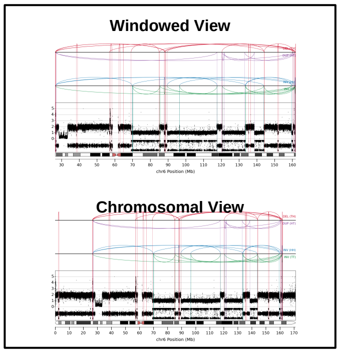

Windowed View

Chromosomal View

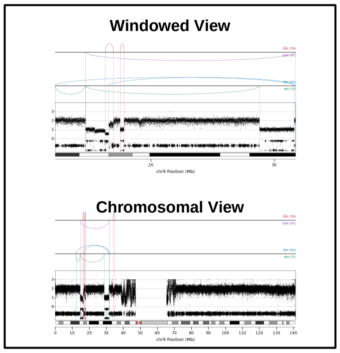
PCSI_0287_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1:1574755−35959936	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr2	3	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	3	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6:26439448−161801680	5	PASS	FAIL	PASS	PASS	inter	NA	Event(CR2)
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9:12257448−31725169	5	FAIL	PASS	PASS	PASS	inter	NA	Event(CR2)
chr10	3	FAIL	NA	NA	NA	NA	NA	NA
chr11:31038155−45142757	6	PASS	PASS	FAIL	FAIL	inter	NA	NA
chr11:68056001−122175186	6	FAIL	FAIL	PASS	PASS	inter	NA	Event(CR2)
chr12	2	FAIL	NA	NA	NA	NA	NA	NA
chr13:32380051−34992381	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	3	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17:7471759−8159870	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr17:56151806−57435286	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

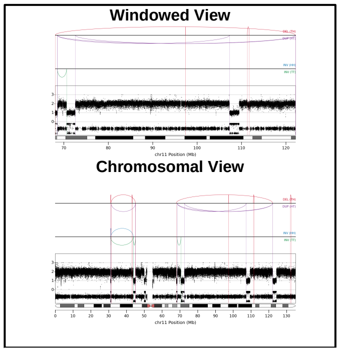
PCSI_0287_Pa_P_526


Windowed View

Chromosomal View


Windowed View

Chromosomal View

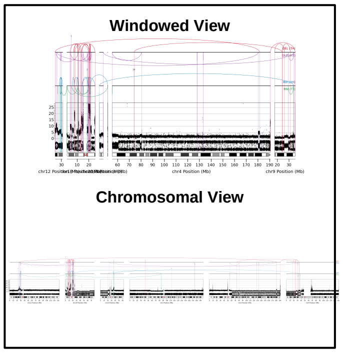

Windowed View

Chromosomal View

PCSI_0290_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3:84718681−84838371	1	FAIL	FAIL	FAIL	FAIL	chain	chr12:24656584−30991444, chr18:1270001−25347900, chr20:20406001−23707633, chr3:84718681−84838371, chr4:55397892−190660873, chr9:17800782−35220174	Event(CR1)
chr4:55397892−190660873	2	FAIL	PASS	PASS	FAIL	chain	chr12:24656584−30991444, chr18:1270001−25347900, chr20:20406001−23707633, chr3:84718681−84838371, chr4:55397892−190660873, chr9:17800782−35220174	Event(CR1)
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8:42310317−144319337	6	PASS	FAIL	PASS	PASS	NA	NA	NA
chr9:17800782−35220174	5	PASS	PASS	PASS	PASS	chain	chr12:24656584−30991444, chr18:1270001−25347900, chr20:20406001−23707633, chr3:84718681−84838371, chr4:55397892−190660873, chr9:17800782−35220174	Event(CR1)
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	4	FAIL	NA	NA	NA	NA	NA	NA
chr12:24656584−30991444	4	FAIL	PASS	PASS	FAIL	chain	chr12:24656584−30991444, chr18:1270001−25347900, chr20:20406001−23707633, chr3:84718681−84838371, chr4:55397892−190660873, chr9:17800782−35220174	Event(CR1)
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18:1270001−25347900	5	PASS	PASS	PASS	FAIL	chain	chr12:24656584−30991444, chr18:1270001−25347900, chr20:20406001−23707633, chr3:84718681−84838371, chr4:55397892−190660873, chr9:17800782−35220174	Event(CR1)
chr19	4	FAIL	NA	NA	NA	NA	NA	NA
chr20:20406001−23707633	5	FAIL	FAIL	FAIL	FAIL	chain	chr12:24656584−30991444, chr18:1270001−25347900, chr20:20406001−23707633, chr3:84718681−84838371, chr4:55397892−190660873, chr9:17800782−35220174	Event(CR1)
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0290_Pa_P_526

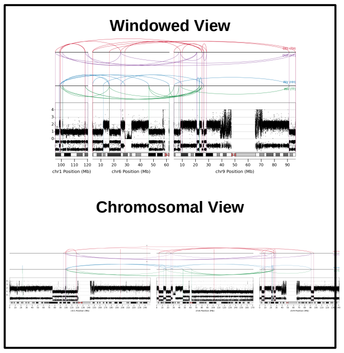

Windowed View

Chromosomal View

PCSI_0297_Pa_P_526

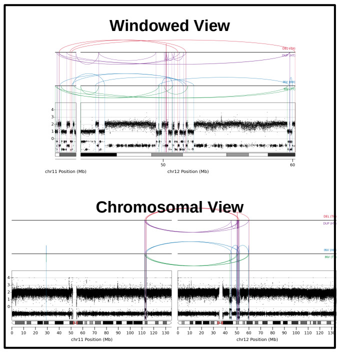
	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1:95390001−120227000	5	PASS	PASS	PASS	PASS	chain	chr1:95390001−120227000, chr6:3708179−62124252, chr9:3583986−96148287	Event(CR1)
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	2	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6:3708179−62124252	4	FAIL	PASS	PASS	PASS	chain	chr1:95390001−120227000, chr6:3708179−62124252, chr9:3583986−96148287	Event(CR1)
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8:47532303−48640488	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr9:3583986−96148287	6	PASS	PASS	PASS	PASS	chain	chr1:95390001−120227000, chr6:3708179−62124252, chr9:3583986−96148287	Event(CR1)
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11:112157676−113770443	5	PASS	PASS	PASS	PASS	chain	chr11:112157676−113770443, chr12:43625536−60197672	Event(CR1)
chr12:43625536−60197672	6	PASS	PASS	PASS	PASS	chain	chr11:112157676−113770443, chr12:43625536−60197672	Event(CR1)
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15:45286001−98711755	5	FAIL	PASS	PASS	PASS	inter	NA	Event(CR2)
chr16	1	FAIL	NA	NA	NA	NA	NA	NA
chr17:16432475−80056000	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr18:18772660−18785600	6	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	1	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0297_Pa_P_526



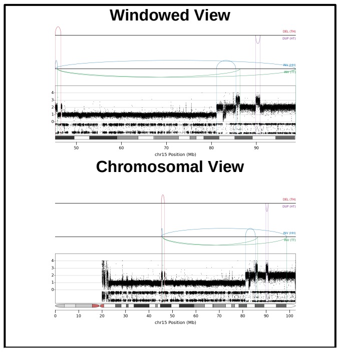
Windowed View

Chromosomal View



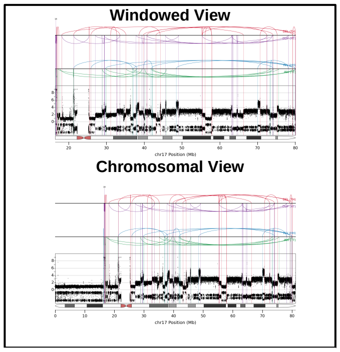
Windowed View

Chromosomal View



Windowed View

Chromosomal View



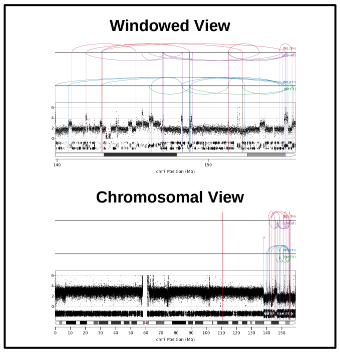
Windowed View

Chromosomal View

PCSI_0300_Pa_P_526

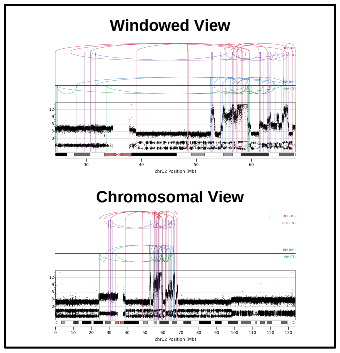
	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	3	FAIL	NA	NA	NA	NA	NA	NA
chr3	1	FAIL	NA	NA	NA	NA	NA	NA
chr4	2	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7:139879932−155779000	5	PASS	PASS	PASS	FAIL	inter	NA	Event(CR1)
chr8	1	FAIL	NA	NA	NA	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	1	FAIL	NA	NA	NA	NA	NA	NA
chr12:24377749−67988000	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17:18008968−20336938	3	FAIL	PASS	FAIL	FAIL	chain	chr17:18008968−20336938, chr19:29264988−41804580	NA
chr18:913001−22133486	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr19:29264988−41804580	6	PASS	FAIL	PASS	FAIL	chain	chr17:18008968−20336938, chr19:29264988−41804580	NA
chr19:44444753−48824000	6	FAIL	FAIL	PASS	PASS	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	1	FAIL	NA	NA	NA	NA	NA	NA
chrX:116533581−125907838	2	FAIL	PASS	FAIL	FAIL	NA	NA	NA
chrX:150625299−151575031	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0300_Pa_P_526



Windowed View

Chromosomal View



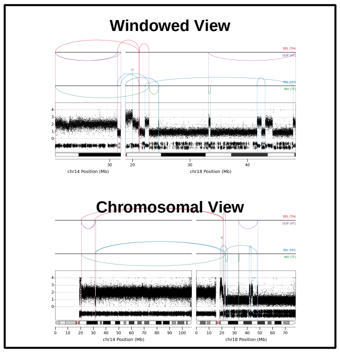
Windowed View

Chromosomal View

PCSI_0303_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7:88372476−88468200	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14:20525777−31919665	3	FAIL	PASS	FAIL	FAIL	chain	chr14:20525777−31919665, chr18:18787459−48367189	Event(CR1)
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18:18787459−48367189	6	PASS	PASS	PASS	PASS	chain	chr14:20525777−31919665, chr18:18787459−48367189	Event(CR1)
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0303_Pa_P_526

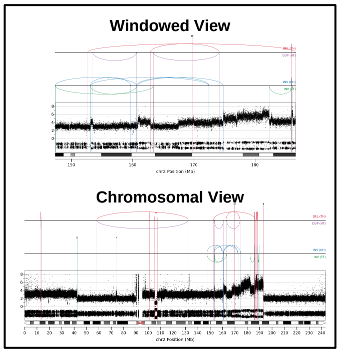

Windowed View

Chromosomal View

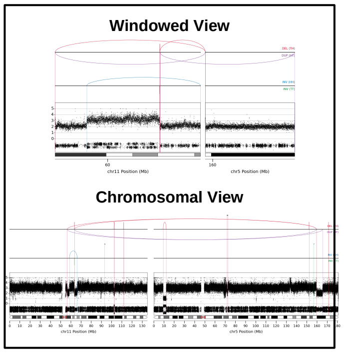
PCSI_0305_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	3	FAIL	NA	NA	NA	NA	NA	NA
chr2:58380309−132236909	6	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr2:147364933−186606238	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4:15026733−15039031	6	FAIL	FAIL	FAIL	FAIL	chain	chr10:92740641−135327144, chr4:15026733−15039031	NA
chr4:39012639−39900000	6	FAIL	FAIL	FAIL	FAIL	chain	chr4:39012639−39900000, chr9:116421601−117281000	NA
chr4:56502355−59734502	6	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr4:60397607−71613334	6	FAIL	FAIL	FAIL	FAIL	inter	NA	NA
chr5:159495084−165558328	2	FAIL	FAIL	FAIL	FAIL	chain	chr11:56440058−66297000, chr5:159495084−165558328	Event(CR2)
chr6	3	FAIL	NA	NA	NA	NA	NA	NA
chr7	1	FAIL	NA	NA	NA	NA	NA	NA
chr8:57199635−57213805	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr9:116421601−117281000	4	FAIL	FAIL	FAIL	FAIL	chain	chr4:39012639−39900000, chr9:116421601−117281000	NA
chr10:21748001−22149128	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr10:92740641−135327144	2	FAIL	FAIL	FAIL	FAIL	chain	chr10:92740641−135327144, chr4:15026733−15039031	NA
chr11:56440058−66297000	4	FAIL	PASS	FAIL	PASS	chain	chr11:56440058−66297000, chr5:159495084−165558328	Event(CR2)
chr12:9771311−95710764	6	PASS	PASS	FAIL	FAIL	chain	chr12:9771311−95710764, chr13:40562144−41486110, chr20:10655296−11661636, chr21:37963001−38451019	NA
chr13:40562144−41486110	4	FAIL	PASS	FAIL	FAIL	chain	chr12:9771311−95710764, chr13:40562144−41486110, chr20:10655296−11661636, chr21:37963001−38451019	NA
chr14	2	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	2	FAIL	NA	NA	NA	NA	NA	NA
chr18	2	FAIL	NA	NA	NA	NA	NA	NA
chr19	4	FAIL	NA	NA	NA	NA	NA	NA
chr20:6680751−7720000	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr20:10655296−11661636	1	FAIL	FAIL	FAIL	FAIL	chain	chr12:9771311−95710764, chr13:40562144−41486110, chr20:10655296−11661636, chr21:37963001−38451019	NA
chr21:18404157−19330000	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr21:37963001−38451019	2	FAIL	FAIL	FAIL	FAIL	chain	chr12:9771311−95710764, chr13:40562144−41486110, chr20:10655296−11661636, chr21:37963001−38451019	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX:107830861−119281432	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0305_Pa_P_526


Windowed View

Chromosomal View

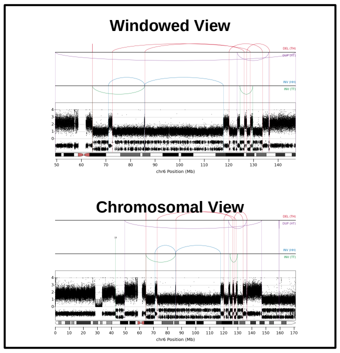

Windowed View

Chromosomal View

PCSI_0307_Pa_P_526

PCSI_0307_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1:40259001−59848000	5	FAIL	FAIL	PASS	PASS	inter	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6:49402001−147104000	5	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8:34754543−38754977	0	FAIL	FAIL	FAIL	FAIL	chain	chr8:34754543−38754977, chr9:31280815−35408637	NA
chr9:18384809−22859000	6	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr9:31280815−35408637	6	FAIL	FAIL	FAIL	PASS	chain	chr8:34754543−38754977, chr9:31280815−35408637	NA
chr10	2	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	1	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA



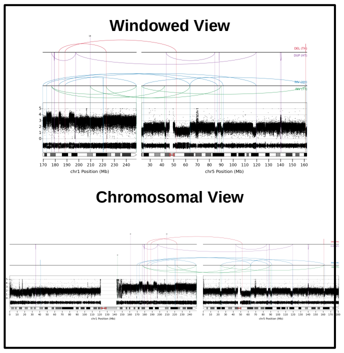
Windowed View

Chromosomal View

PCSI_0324_Pa_P_526

PCSI_0324_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1:169681439−248445801	5	PASS	PASS	PASS	PASS	chain	chr1:169681439−248445801, chr5:22796001−162205117	Event(CR1)
chr2	1	FAIL	NA	NA	NA	NA	NA	NA
chr3:87024011−137447708	5	PASS	PASS	PASS	FAIL	NA	NA	NA
chr4	3	FAIL	NA	NA	NA	NA	NA	NA
chr5:22796001−162205117	6	PASS	PASS	PASS	PASS	chain	chr1:169681439−248445801, chr5:22796001−162205117	Event(CR1)
chr6	2	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8:78094001−138925287	2	FAIL	PASS	PASS	FAIL	NA	NA	NA
chr9:3130712−21110320	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	1	FAIL	NA	NA	NA	NA	NA	NA
chr16	1	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18	5	FAIL	NA	NA	NA	NA	NA	NA
chr19:35029365−40521791	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr20	1	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX:148170983−150326006	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA



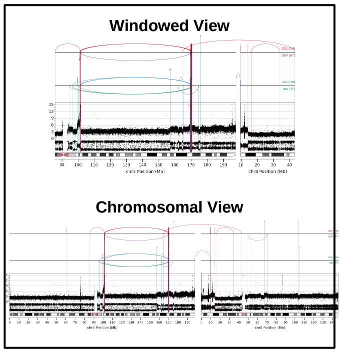
Windowed View

Chromosomal View

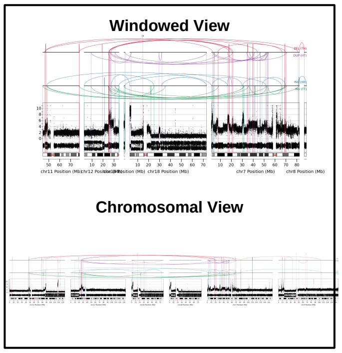
PCSI_0325_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3:85725613−197664349	6	PASS	PASS	PASS	PASS	chain	chr3:85725613−197664349, chr8:9607687−43205301	Event(CR1)
chr4	1	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6:19692214−20462558	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr7:1713824−82399406	6	PASS	PASS	PASS	PASS	chain	chr11:44565819−78023545, chr12:2802174−34727000, chr18:1144001−2144162, chr18:2708927−73038519, chr7:1713824−82399406, chr8:103419668−105411372	Event(CR1)
chr8:9607687−43205301	3	FAIL	FAIL	FAIL	FAIL	chain	chr3:85725613−197664349, chr8:9607687−43205301	Event(CR1)
chr8:49601753−70634000	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr8:103419668−105411372	3	FAIL	FAIL	FAIL	FAIL	chain	chr11:44565819−78023545, chr12:2802174−34727000, chr18:1144001−2144162, chr18:2708927−73038519, chr7:1713824−82399406, chr8:103419668−105411372	Event(CR1)
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11:44565819−78023545	5	PASS	FAIL	PASS	FAIL	chain	chr11:44565819−78023545, chr12:2802174−34727000, chr18:1144001−2144162, chr18:2708927−73038519, chr7:1713824−82399406, chr8:103419668−105411372	Event(CR1)
chr11:89041662−123121855	5	FAIL	PASS	FAIL	FAIL	NA	NA	NA
chr12:2802174−34727000	6	PASS	PASS	PASS	PASS	chain	chr11:44565819−78023545, chr12:2802174−34727000, chr18:1144001−2144162, chr18:2708927−73038519, chr7:1713824−82399406, chr8:103419668−105411372	Event(CR1)
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	1	FAIL	NA	NA	NA	NA	NA	NA
chr18:1144001−2144162	4	FAIL	FAIL	FAIL	FAIL	chain	chr11:44565819−78023545, chr12:2802174−34727000, chr18:1144001−2144162, chr18:2708927−73038519, chr7:1713824−82399406, chr8:103419668−105411372	Event(CR1)
chr18:2708927−73038519	4	FAIL	PASS	PASS	FAIL	chain	chr11:44565819−78023545, chr12:2802174−34727000, chr18:1144001−2144162, chr18:2708927−73038519, chr7:1713824−82399406, chr8:103419668−105411372	Event(CR1)
chr19	1	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0325_Pa_P_526


Windowed View

Chromosomal View

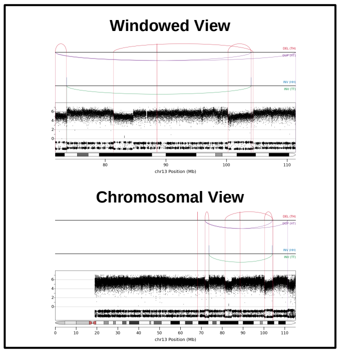

Windowed View

Chromosomal View

PCSI_0326_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1:211067001−214131084	5	FAIL	PASS	FAIL	FAIL	chain	chr18:4251854−77944211, chr1:211067001−214131084, chr2:204186569−204198757	NA
chr2:204186569−204198757	0	FAIL	FAIL	FAIL	FAIL	chain	chr18:4251854−77944211, chr1:211067001−214131084, chr2:204186569−204198757	NA
chr3:48432001−50521014	1	FAIL	FAIL	FAIL	FAIL	chain	chr3:48432001−50521014, chrX:82597806−83952059	NA
chr4:85476001−117536000	2	FAIL	FAIL	PASS	PASS	chain	chr4:85476001−117536000, chrX:106946387−107421642	NA
chr5	1	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7:138233528−141334359	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13:71759273−111390184	5	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	1	FAIL	NA	NA	NA	NA	NA	NA
chr18:4251854−77944211	4	FAIL	PASS	PASS	FAIL	chain	chr18:4251854−77944211, chr1:211067001−214131084, chr2:204186569−204198757	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX:82597806−83952059	1	FAIL	FAIL	FAIL	FAIL	chain	chr3:48432001−50521014, chrX:82597806−83952059	NA
chrX:106946387−107421642	1	FAIL	FAIL	FAIL	FAIL	chain	chr4:85476001−117536000, chrX:106946387−107421642	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0326_Pa_P_526

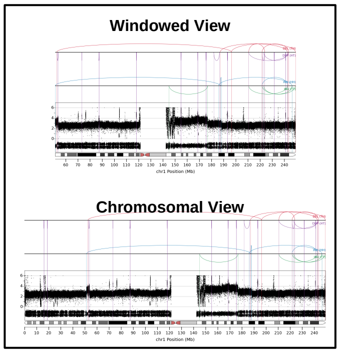

Windowed View

Chromosomal View

PCSI_0338_Pa_P_526

PCSI_0338_Pa_P_526

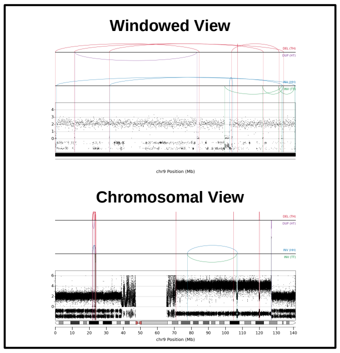
	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1:51302307−249198720	5	PASS	FAIL	PASS	PASS	inter	NA	Event(CR2)
chr2	4	FAIL	NA	NA	NA	NA	NA	NA
chr3:39966001−56638553	4	FAIL	FAIL	FAIL	PASS	NA	NA	NA
chr3:152752420−153113262	4	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr4:80349001−80506372	4	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr5:139022001−160537509	4	FAIL	PASS	PASS	FAIL	NA	NA	NA
chr5:161123756−161226000	4	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr6:64151458−67347000	5	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr7:36808670−37240284	4	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr7:100677643−101034723	4	FAIL	FAIL	FAIL	FAIL	chain	chr7:100677643−101034723, chr8:66877001−67110580	NA
chr8:36061564−48163700	4	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr8:66877001−67110580	4	FAIL	FAIL	FAIL	FAIL	chain	chr7:100677643−101034723, chr8:66877001−67110580	NA
chr9	5	FAIL	NA	NA	NA	NA	NA	NA
chr10	3	FAIL	NA	NA	NA	NA	NA	NA
chr11	4	FAIL	NA	NA	NA	NA	NA	NA
chr12	4	FAIL	NA	NA	NA	NA	NA	NA
chr13:106984582−107335557	4	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr14	2	FAIL	NA	NA	NA	NA	NA	NA
chr15	3	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	2	FAIL	NA	NA	NA	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19	2	FAIL	NA	NA	NA	NA	NA	NA
chr20:46491001−49832547	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr21	2	FAIL	NA	NA	NA	NA	NA	NA
chr22	2	FAIL	NA	NA	NA	NA	NA	NA
chrX:147559184−147894020	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA



PCSI_0341_Pa_P_526

PCSI_0341_Pa_P_526

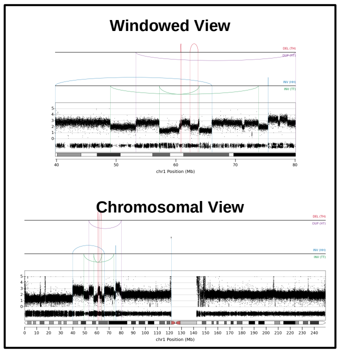
	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	3	FAIL	NA	NA	NA	NA	NA	NA
chr2:137719824−143469895	5	PASS	PASS	FAIL	FAIL	inter	NA	NA
chr2:172978226−187328630	5	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4:15572992−19091000	4	FAIL	FAIL	PASS	PASS	NA	NA	NA
chr5:129755279−141675356	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr6:17051806−89561000	4	FAIL	FAIL	PASS	FAIL	NA	NA	NA
chr6:97380303−98080147	4	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr7:82693651−83281000	4	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr8:102609180−104847969	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr9:21791001−24009472	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr9:77624870−107179654	6	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr9:126906549−127134255	6	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr10	2	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12:108063408−108472453	5	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr13	1	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16:65871828−65915828	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr17:62259677−62402000	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr18:48599001−51118000	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr19	2	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA



PCSI_0345_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1:39773751−80101792	6	FAIL	PASS	PASS	PASS	inter	NA	Event(CR2)
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8:48335608−138820342	3	FAIL	PASS	FAIL	FAIL	chain	chr19:18873975−52443284, chr8:48335608−138820342	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	1	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18:24292322−24305354	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr19:18873975−52443284	3	FAIL	FAIL	PASS	FAIL	chain	chr19:18873975−52443284, chr8:48335608−138820342	NA
chr19:54477606−56800596	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0345_Pa_P_526

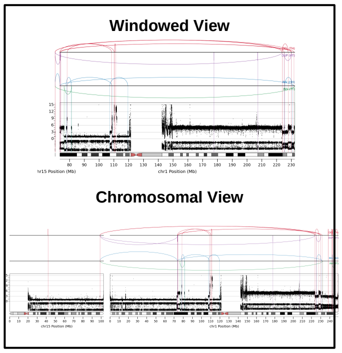

Windowed View

Chromosomal View

PCSI_0347_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1:73460809−232273199	5	PASS	PASS	PASS	PASS	chain	chr15:98556222−98598061, chr1:73460809−232273199	Event(CR1)
chr1:242666001−245595000	5	FAIL	FAIL	FAIL	PASS	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4:68457085−75664682	1	FAIL	PASS	FAIL	FAIL	chain	chr4:68457085−75664682, chr6:116921601−117653161	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6:116921601−117653161	2	FAIL	PASS	FAIL	FAIL	chain	chr4:68457085−75664682, chr6:116921601−117653161	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8:32194001−32581222	3	FAIL	PASS	FAIL	FAIL	chain	chr11:55409115−55704014, chr8:32194001−32581222	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11:55409115−55704014	0	FAIL	FAIL	FAIL	FAIL	chain	chr11:55409115−55704014, chr8:32194001−32581222	NA
chr12:43757906−74671000	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15:98556222−98598061	2	FAIL	PASS	FAIL	FAIL	chain	chr15:98556222−98598061, chr1:73460809−232273199	Event(CR1)
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0347_Pa_P_526

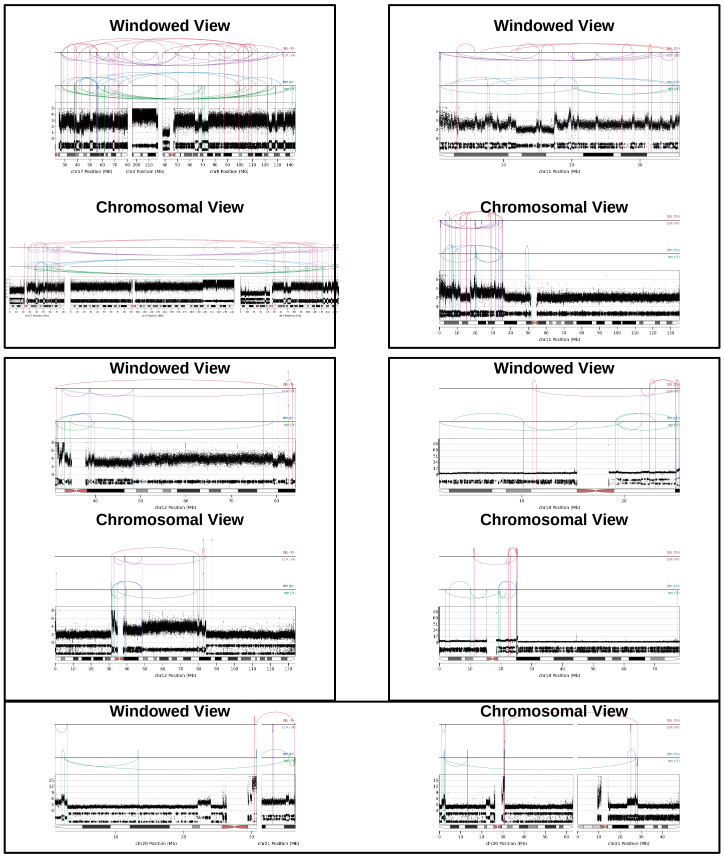

Windowed View

Chromosomal View

PCSI_0356_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2:196607224−217222000	1	FAIL	FAIL	FAIL	FAIL	chain	chr17:22218711−80138542, chr2:196607224−217222000, chr8:38113754−144229000	Event(CR1)
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6:52960075−53171041	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8:38113754−144229000	6	PASS	PASS	PASS	PASS	chain	chr17:22218711−80138542, chr2:196607224−217222000, chr8:38113754−144229000	Event(CR1)
chr9	1	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11:609292−35813000	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr12:31159318−84140077	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17:22218711−80138542	6	PASS	PASS	PASS	PASS	chain	chr17:22218711−80138542, chr2:196607224−217222000, chr8:38113754−144229000	Event(CR1)
chr18:1941225−25433313	5	PASS	PASS	PASS	FAIL	inter	NA	Event(CR1)
chr19	1	FAIL	NA	NA	NA	NA	NA	NA
chr20:1085001−30782148	5	PASS	PASS	PASS	FAIL	chain	chr20:1085001−30782148, chr21:23450001−28404816	Event(CR1)
chr21:23450001−28404816	3	FAIL	PASS	PASS	FAIL	chain	chr20:1085001−30782148, chr21:23450001−28404816	Event(CR1)
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX:100871747−100883885	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

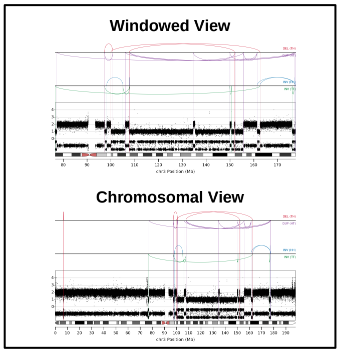
PCSI_0356_Pa_P_526



PCSI_0467_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3:76615001−177579163	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9:13293001−24336000	6	FAIL	FAIL	FAIL	PASS	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	1	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16:11069001−11632000	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr17:18551356−18821120	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr18:20437643−20912000	1	FAIL	FAIL	FAIL	FAIL	chain	chr18:20437643−20912000, chr21:14614168−20675153	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21:14614168−20675153	2	FAIL	FAIL	FAIL	FAIL	chain	chr18:20437643−20912000, chr21:14614168−20675153	NA
chr22:26201479−46445513	4	FAIL	PASS	PASS	FAIL	inter	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

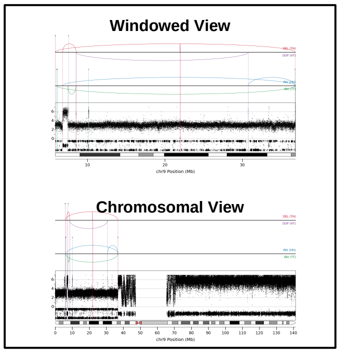
PCSI_0467_Pa_P_526



PCSI_0468_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	1	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	2	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	4	FAIL	NA	NA	NA	NA	NA	NA
chr9:5829446−36871593	5	PASS	PASS	PASS	FAIL	chain	chr9:5829446−36871593, chrY:5964707−7152459	Event(CR1)
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11:50463829−50477052	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17:41481001−42624631	5	FAIL	PASS	FAIL	FAIL	NA	NA	NA
chr17:43133716−48320000	5	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr18:18684332−27596000	4	FAIL	PASS	FAIL	FAIL	inter	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	1	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY:5964707−7152459	1	FAIL	PASS	FAIL	FAIL	chain	chr9:5829446−36871593, chrY:5964707−7152459	Event(CR1)

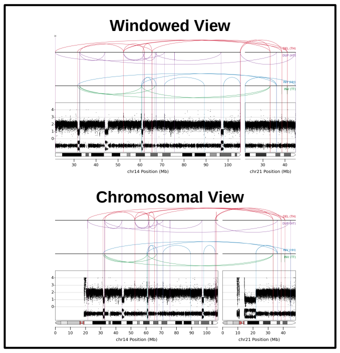
PCSI_0468_Pa_P_526



PCSI_0469_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7:99434749−103133163	4	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10:85219786−87399031	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14:21416378−105660885	5	PASS	PASS	PASS	FAIL	chain	chr14:21416378−105660885, chr21:21937611−44860077	Event(CR1)
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21:21937611−44860077	3	FAIL	PASS	FAIL	FAIL	chain	chr14:21416378−105660885, chr21:21937611−44860077	Event(CR1)
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

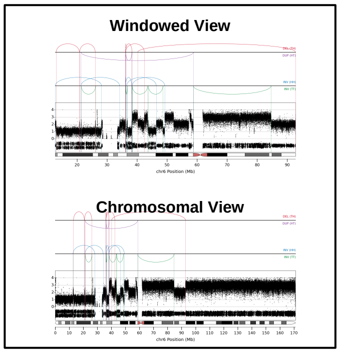
PCSI_0469_Pa_P_526



PCSI_0473_Pa_P_526

PCSI_0473_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3:87979008−90293128	0	FAIL	FAIL	FAIL	FAIL	chain	chr3:87979008−90293128, chrX:67514117−68859055	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6:12719001−92777454	6	PASS	PASS	PASS	PASS	inter	NA	Event(CR1)
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16:4864099−22303037	3	FAIL	FAIL	PASS	FAIL	inter	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18:18671973−28949847	5	FAIL	PASS	PASS	PASS	chain	chr18:18671973−28949847, chr19:55976863−57693531	NA
chr19:55976863−57693531	4	FAIL	FAIL	FAIL	FAIL	chain	chr18:18671973−28949847, chr19:55976863−57693531	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX:67514117−68859055	0	FAIL	FAIL	FAIL	FAIL	chain	chr3:87979008−90293128, chrX:67514117−68859055	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

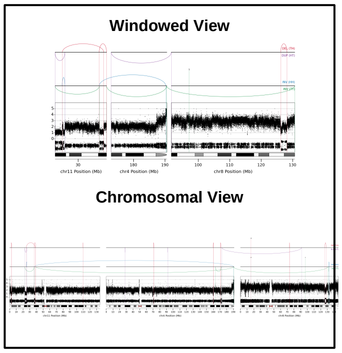

Windowed View

Chromosomal View

PCSI_0504_Pa_P_526

PCSI_0504_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1:213207691−213955670	2	FAIL	FAIL	FAIL	FAIL	chain	chr19:37007892−37279000, chr1:213207691−213955670	NA
chr2	2	FAIL	NA	NA	NA	NA	NA	NA
chr3	2	FAIL	NA	NA	NA	NA	NA	NA
chr4:163371078−171983568	4	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr4:172916001−190563794	4	FAIL	FAIL	FAIL	FAIL	chain	chr11:22650591−39031524, chr4:172916001−190563794, chr8:91456279−130665095	Event(CR2)
chr5:163352841−163546999	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8:91456279−130665095	1	FAIL	FAIL	FAIL	FAIL	chain	chr11:22650591−39031524, chr4:172916001−190563794, chr8:91456279−130665095	Event(CR2)
chr9	1	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11:22650591−39031524	5	FAIL	PASS	PASS	PASS	chain	chr11:22650591−39031524, chr4:172916001−190563794, chr8:91456279−130665095	Event(CR2)
chr12	2	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15:86478889−87068583	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr15:91849856−102426272	3	FAIL	PASS	FAIL	FAIL	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18	4	FAIL	NA	NA	NA	NA	NA	NA
chr19:30007505−30154161	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr19:37007892−37279000	1	FAIL	FAIL	FAIL	FAIL	chain	chr19:37007892−37279000, chr1:213207691−213955670	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

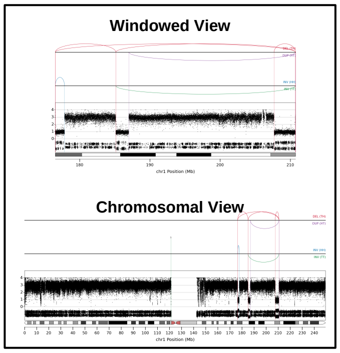

Windowed View

Chromosomal View

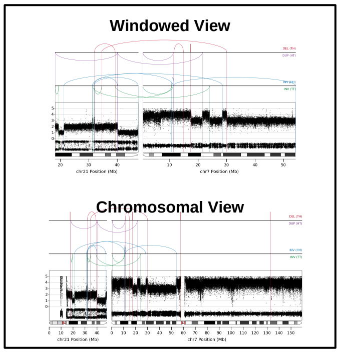
PCSI_0549_Pa_P_5266

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1:176524929−210742679	4	FAIL	PASS	PASS	PASS	inter	NA	Event(CR2)
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7:631233−54238000	5	PASS	PASS	PASS	PASS	chain	chr21:18230493−47379696, chr7:631233−54238000	Event(CR1)
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11:2206807−3920423	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr12:7108001−58029482	5	PASS	PASS	PASS	FAIL	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14:47103448−77034705	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20:16602001−23005338	4	FAIL	FAIL	FAIL	PASS	NA	NA	NA
chr21:18230493−47379696	5	PASS	PASS	PASS	PASS	chain	chr21:18230493−47379696, chr7:631233−54238000	Event(CR1)
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0549_Pa_P_5266


Windowed View

Chromosomal View

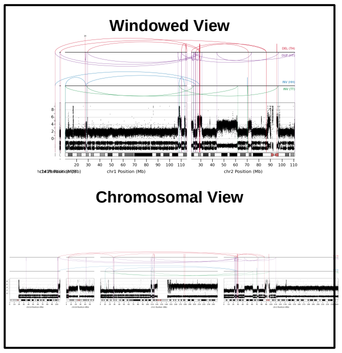

Windowed View

Chromosomal View

PCSI_0572_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1:10146742−114793741	5	PASS	PASS	PASS	FAIL	chain	chr14:103400154−103424480, chr19:4006241−4925261, chr1:10146742−114793741, chr2:21945001−110881941	Event(CR1)
chr2:21945001−110881941	6	PASS	PASS	PASS	PASS	chain	chr14:103400154−103424480, chr19:4006241−4925261, chr1:10146742−114793741, chr2:21945001−110881941	Event(CR1)
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14:102327001−102567606	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr14:103400154−103424480	1	FAIL	FAIL	FAIL	FAIL	chain	chr14:103400154−103424480, chr19:4006241−4925261, chr1:10146742−114793741, chr2:21945001−110881941	Event(CR1)
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19:4006241−4925261	0	FAIL	FAIL	FAIL	FAIL	chain	chr14:103400154−103424480, chr19:4006241−4925261, chr1:10146742−114793741, chr2:21945001−110881941	Event(CR1)
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22:38067441−38705578	3	FAIL	PASS	FAIL	FAIL	inter	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0572_Pa_P_526

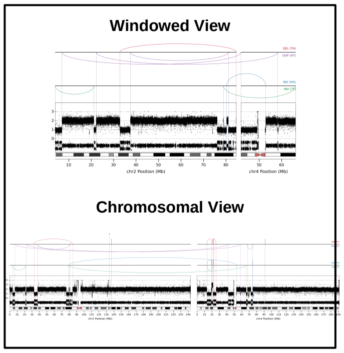

Windowed View

Chromosomal View

RAMP_0003_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2:4002001−84635426	5	FAIL	PASS	PASS	PASS	chain	chr2:4002001−84635426, chr4:41895636−66184137	Event(CR2)
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4:13306001−25693000	6	PASS	FAIL	FAIL	FAIL	inter	NA	NA
chr4:41895636−66184137	6	FAIL	FAIL	FAIL	PASS	chain	chr2:4002001−84635426, chr4:41895636−66184137	Event(CR2)
chr4:67721001−74846653	6	FAIL	FAIL	FAIL	PASS	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6:46086001−69047000	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	1	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	1	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

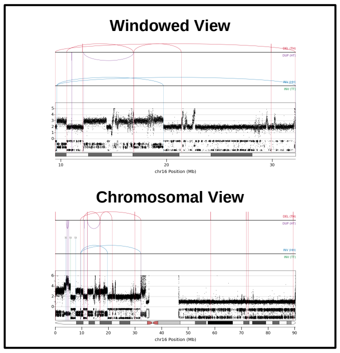
RAMP_0003_Pa_P_526



Windowed View

Chromosomal View

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	3	FAIL	NA	NA	NA	NA	NA	NA
chr2	4	FAIL	NA	NA	NA	NA	NA	NA
chr3	2	FAIL	NA	NA	NA	NA	NA	NA
chr4	1	FAIL	NA	NA	NA	NA	NA	NA
chr5	4	FAIL	NA	NA	NA	NA	NA	NA
chr6	4	FAIL	NA	NA	NA	NA	NA	NA
chr7	2	FAIL	NA	NA	NA	NA	NA	NA
chr8	1	FAIL	NA	NA	NA	NA	NA	NA
chr9	1	FAIL	NA	NA	NA	NA	NA	NA
chr10	1	FAIL	NA	NA	NA	NA	NA	NA
chr11:60495001−66071000	3	FAIL	FAIL	FAIL	FAIL	chain	chr11:60495001−66071000, chr16:3985652−7659000	NA
chr12	1	FAIL	NA	NA	NA	NA	NA	NA
chr13	1	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	1	FAIL	NA	NA	NA	NA	NA	NA
chr16:3985652−7659000	5	FAIL	FAIL	PASS	PASS	chain	chr11:60495001−66071000, chr16:3985652−7659000	NA
chr16:9464851−32208716	5	PASS	FAIL	PASS	PASS	inter	NA	Event(CR2)
chr17	3	FAIL	NA	NA	NA	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19:12012001−21352145	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr20	1	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX:29381465−29393480	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA



Windowed View

Chromosomal View

ASHPC_0001_Pa_P_2

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14:62224704−100790416	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18:1402001−25760642	3	FAIL	FAIL	PASS	FAIL	NA	NA	NA
chr18:26249932−47705000	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr19	1	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

ASHPC_0011_Pa_P

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1:31302012−50493696	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3:43186935−65136472	6	FAIL	FAIL	PASS	PASS	inter	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8:41517313−41530153	0	FAIL	FAIL	FAIL	FAIL	chain	chr18:20973927−20988324, chr8:41517313−41530153	NA
chr9	2	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18:20973927−20988324	2	FAIL	FAIL	FAIL	FAIL	chain	chr18:20973927−20988324, chr8:41517313−41530153	NA
chr19	1	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	3	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX:74922541−74962043	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

ASHPC_0013_Pa_P

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6:48535589−125747591	3	FAIL	FAIL	PASS	FAIL	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	1	FAIL	NA	NA	NA	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	1	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	2	FAIL	NA	NA	NA	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

ASHPC_0015_Pa_P

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9:20406142−22225000	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19:6421936−58980326	3	FAIL	PASS	FAIL	FAIL	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

ASHPC_0019_Pa_P

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6:18731223−66148378	5	FAIL	FAIL	PASS	PASS	inter	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9:19426001−29485589	5	FAIL	FAIL	PASS	PASS	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18	1	FAIL	NA	NA	NA	NA	NA	NA
chr19:39612200−39625632	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr19:56397879−56494445	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

ASHPC_0023_Pa_P

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7:42408186−65232070	0	FAIL	FAIL	FAIL	FAIL	chain	chr7:42408186−65232070, chr9:25243001−115566359	NA
chr8:47668760−136147805	4	FAIL	PASS	FAIL	FAIL	chain	chr22:29059555−29071915, chr8:47668760−136147805	NA
chr9:25243001−115566359	5	PASS	PASS	FAIL	FAIL	chain	chr7:42408186−65232070, chr9:25243001−115566359	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17:40742985−70942000	3	FAIL	FAIL	PASS	FAIL	inter	NA	NA
chr18:99466−22579055	4	FAIL	PASS	PASS	FAIL	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22:29059555−29071915	0	FAIL	FAIL	FAIL	FAIL	chain	chr22:29059555−29071915, chr8:47668760−136147805	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

ASHPC_0028_Pa_P

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5:109052663−117362607	4	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10:35299826−36172890	3	FAIL	PASS	FAIL	FAIL	chain	chr10:35299826−36172890, chr15:85931493−98439225	NA
chr11	1	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15:85931493−98439225	3	FAIL	PASS	FAIL	FAIL	chain	chr10:35299826−36172890, chr15:85931493−98439225	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18:39178001−48581914	4	FAIL	PASS	FAIL	PASS	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

ASHPC_0029_Pa_P

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	5	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9:19451547−22103260	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18	2	FAIL	NA	NA	NA	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0019_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	1	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	1	FAIL	NA	NA	NA	NA	NA	NA
chr18:9203001−12579000	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0046_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	1	FAIL	NA	NA	NA	NA	NA	NA
chr3:166316471−181958222	3	FAIL	FAIL	FAIL	FAIL	inter	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	1	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7:25190319−34959000	4	FAIL	FAIL	PASS	FAIL	NA	NA	NA
chr8	2	FAIL	NA	NA	NA	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	5	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	2	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	1	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0048_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1:149720950−229843311	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr2	3	FAIL	NA	NA	NA	NA	NA	NA
chr3:3114898−83852277	5	FAIL	PASS	PASS	FAIL	inter	NA	NA
chr4	1	FAIL	NA	NA	NA	NA	NA	NA
chr5:141600602−171739097	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr6	1	FAIL	NA	NA	NA	NA	NA	NA
chr7	2	FAIL	NA	NA	NA	NA	NA	NA
chr8	1	FAIL	NA	NA	NA	NA	NA	NA
chr9:34275068−91905224	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11:85318593−134008564	2	FAIL	FAIL	FAIL	FAIL	inter	NA	NA
chr12:72177001−94422198	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	1	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0073_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1:77716560−77728589	1	FAIL	FAIL	FAIL	FAIL	chain	chr18:35303112−35855245, chr1:77716560−77728589	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11:24813830−24827809	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18:35303112−35855245	3	FAIL	PASS	FAIL	FAIL	chain	chr18:35303112−35855245, chr1:77716560−77728589	NA
chr19	2	FAIL	NA	NA	NA	NA	NA	NA
chr20:9021884−20915000	6	FAIL	FAIL	PASS	PASS	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0078_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	2	FAIL	NA	NA	NA	NA	NA	NA
chr8	1	FAIL	NA	NA	NA	NA	NA	NA
chr9	4	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12:23101173−23265140	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	3	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	1	FAIL	NA	NA	NA	NA	NA	NA
chr18:76933401−77328000	5	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr19:29861299−31233513	4	FAIL	PASS	FAIL	FAIL	inter	NA	NA
chr19:38628955−38787797	4	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	2	FAIL	NA	NA	NA	NA	NA	NA
chr22	1	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0084_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	1	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8:106844374−106856374	0	FAIL	FAIL	FAIL	FAIL	chain	chr20:40900299−57468011, chr8:106844374−106856374	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	1	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20:40900299−57468011	3	FAIL	PASS	FAIL	FAIL	chain	chr20:40900299−57468011, chr8:106844374−106856374	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0096_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	2	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12:114529663−128417358	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0099_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	1	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	1	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5:54615001−62660000	3	FAIL	FAIL	FAIL	PASS	NA	NA	NA
chr6:47673256−48136309	3	FAIL	PASS	FAIL	FAIL	NA	NA	NA
chr7	4	FAIL	NA	NA	NA	NA	NA	NA
chr8	1	FAIL	NA	NA	NA	NA	NA	NA
chr9:33061830−36356025	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	3	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0102_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3:39117323−86416000	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17:15334477−15743376	4	FAIL	FAIL	FAIL	FAIL	chain	chr17:15334477−15743376, chr18:22445001−23059000	NA
chr18:22445001−23059000	0	FAIL	FAIL	FAIL	FAIL	chain	chr17:15334477−15743376, chr18:22445001−23059000	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX:122876058−123041937	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0103_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0108_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4:1683659−1776353	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX:129111024−129180372	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0146_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	2	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8:104070061−104180047	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr9:21791001−33139155	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	1	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0161_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	2	FAIL	NA	NA	NA	NA	NA	NA
chr2	4	FAIL	NA	NA	NA	NA	NA	NA
chr3	5	FAIL	NA	NA	NA	NA	NA	NA
chr4	2	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6:57977460−62517020	5	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr7	1	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9:9045173−9817351	4	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr10	2	FAIL	NA	NA	NA	NA	NA	NA
chr11	4	FAIL	NA	NA	NA	NA	NA	NA
chr12	5	FAIL	NA	NA	NA	NA	NA	NA
chr13	3	FAIL	NA	NA	NA	NA	NA	NA
chr14	2	FAIL	NA	NA	NA	NA	NA	NA
chr15	1	FAIL	NA	NA	NA	NA	NA	NA
chr16:78585001−78893000	5	FAIL	FAIL	FAIL	PASS	NA	NA	NA
chr17	2	FAIL	NA	NA	NA	NA	NA	NA
chr18	1	FAIL	NA	NA	NA	NA	NA	NA
chr19:5145980−6164000	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr20	1	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	1	FAIL	NA	NA	NA	NA	NA	NA
chrX:5327741−5429856	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chrX:6007762−6081902	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chrX:9969439−10013720	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chrX:119846237−119910037	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0164_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	2	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0218_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	3	FAIL	NA	NA	NA	NA	NA	NA
chr2:63172857−72099683	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr3	2	FAIL	NA	NA	NA	NA	NA	NA
chr4:100941380−108888000	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr5:59991562−105532439	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr6	1	FAIL	NA	NA	NA	NA	NA	NA
chr7:33875149−136458590	1	FAIL	FAIL	FAIL	FAIL	inter	NA	NA
chr8	2	FAIL	NA	NA	NA	NA	NA	NA
chr9:36387423−137861371	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr10:31030912−55837000	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr11:41947195−97467037	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr12:75685389−90439318	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr13:30751725−30764958	2	FAIL	FAIL	FAIL	FAIL	chain	chr13:30751725−30764958, chr16:7205775−7218220	NA
chr13:46539001−102069000	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15:76933873−76946840	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr16:7205775−7218220	0	FAIL	FAIL	FAIL	FAIL	chain	chr13:30751725−30764958, chr16:7205775−7218220	NA
chr17	1	FAIL	NA	NA	NA	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0227_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	2	FAIL	NA	NA	NA	NA	NA	NA
chr2:23708603−234411307	0	FAIL	FAIL	FAIL	FAIL	inter	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6:48762914−98653504	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr6:130205062−132271653	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9:20305001−27310000	4	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	1	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17:21960458−26570072	2	FAIL	FAIL	FAIL	FAIL	chain	chr17:21960458−26570072, chr18:22715768−71713195	NA
chr18:22715768−71713195	1	FAIL	FAIL	PASS	FAIL	chain	chr17:21960458−26570072, chr18:22715768−71713195	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0264_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2:65236001−81409000	2	FAIL	FAIL	FAIL	FAIL	chain	chr2:65236001−81409000, chr3:4067421−74942000	NA
chr3:4067421−74942000	5	PASS	FAIL	PASS	FAIL	chain	chr2:65236001−81409000, chr3:4067421−74942000	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	5	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15:20106623−102045624	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18:28016599−28029332	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX:63028017−126568220	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chrX:140224516−150435658	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0269_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	2	FAIL	NA	NA	NA	NA	NA	NA
chr2	1	FAIL	NA	NA	NA	NA	NA	NA
chr3:86258639−172815066	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5:52986042−84562289	1	FAIL	FAIL	FAIL	FAIL	chain	chr21:20385537−24988220, chr5:52986042−84562289	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	2	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17:46341115−47113000	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21:20385537−24988220	2	FAIL	FAIL	FAIL	FAIL	chain	chr21:20385537−24988220, chr5:52986042−84562289	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0292_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1:92759615−118700152	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr2	1	FAIL	NA	NA	NA	NA	NA	NA
chr3	3	FAIL	NA	NA	NA	NA	NA	NA
chr4	1	FAIL	NA	NA	NA	NA	NA	NA
chr5:57359001−83127060	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr6	1	FAIL	NA	NA	NA	NA	NA	NA
chr7:79415678−115982431	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr8	2	FAIL	NA	NA	NA	NA	NA	NA
chr9	3	FAIL	NA	NA	NA	NA	NA	NA
chr10	4	FAIL	NA	NA	NA	NA	NA	NA
chr11:79190816−126602773	4	FAIL	PASS	PASS	FAIL	inter	NA	NA
chr12	1	FAIL	NA	NA	NA	NA	NA	NA
chr13	1	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18:31054680−64639000	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	1	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0294_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	1	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5:127802118−127814452	0	FAIL	FAIL	FAIL	FAIL	chain	chr18:24774001−24781473, chr5:127802118−127814452	NA
chr6	1	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8:34588001−35185405	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18:24774001−24781473	4	FAIL	FAIL	FAIL	FAIL	chain	chr18:24774001−24781473, chr5:127802118−127814452	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0310_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	2	FAIL	NA	NA	NA	NA	NA	NA
chr2	1	FAIL	NA	NA	NA	NA	NA	NA
chr3	2	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5:50378882−121945000	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr6	1	FAIL	NA	NA	NA	NA	NA	NA
chr7	3	FAIL	NA	NA	NA	NA	NA	NA
chr8	2	FAIL	NA	NA	NA	NA	NA	NA
chr9	1	FAIL	NA	NA	NA	NA	NA	NA
chr10	1	FAIL	NA	NA	NA	NA	NA	NA
chr11	2	FAIL	NA	NA	NA	NA	NA	NA
chr12	1	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	1	FAIL	NA	NA	NA	NA	NA	NA
chr17:31305525−43847205	3	FAIL	FAIL	PASS	FAIL	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22:27086872−27100217	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chrX:17604025−17630853	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0312_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9:8692374−30515171	3	FAIL	FAIL	PASS	FAIL	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	1	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	2	FAIL	NA	NA	NA	NA	NA	NA
chr18	1	FAIL	NA	NA	NA	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0329_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5:178817607−179832210	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	1	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15:28264230−87789199	2	FAIL	FAIL	PASS	FAIL	chain	chr15:28264230−87789199, chr22:29534957−30134090	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20:60370014−60388248	4	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22:29534957−30134090	2	FAIL	FAIL	FAIL	FAIL	chain	chr15:28264230−87789199, chr22:29534957−30134090	NA
chrX:8608047−9996024	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chrX:13880513−39211380	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0344_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7:78166001−81085251	6	FAIL	FAIL	FAIL	PASS	NA	NA	NA
chr7:82205001−101583125	6	FAIL	FAIL	PASS	FAIL	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	2	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	3	FAIL	NA	NA	NA	NA	NA	NA
chr12	1	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	1	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0465_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10:52732988−53032137	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18:2115199−5556802	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0466_Pa_P_526

	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3	0	FAIL	NA	NA	NA	NA	NA	NA
chr4:160108471−178301083	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	2	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9:35806799−104263432	5	PASS	PASS	FAIL	FAIL	NA	NA	NA
chr10	3	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	1	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18:1123606−21490773	6	FAIL	PASS	PASS	FAIL	inter	NA	NA
chr19:41577001−41694000	4	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX:37682056−88480181	2	FAIL	PASS	FAIL	FAIL	inter	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

PCSI_0492_Pa_P_526

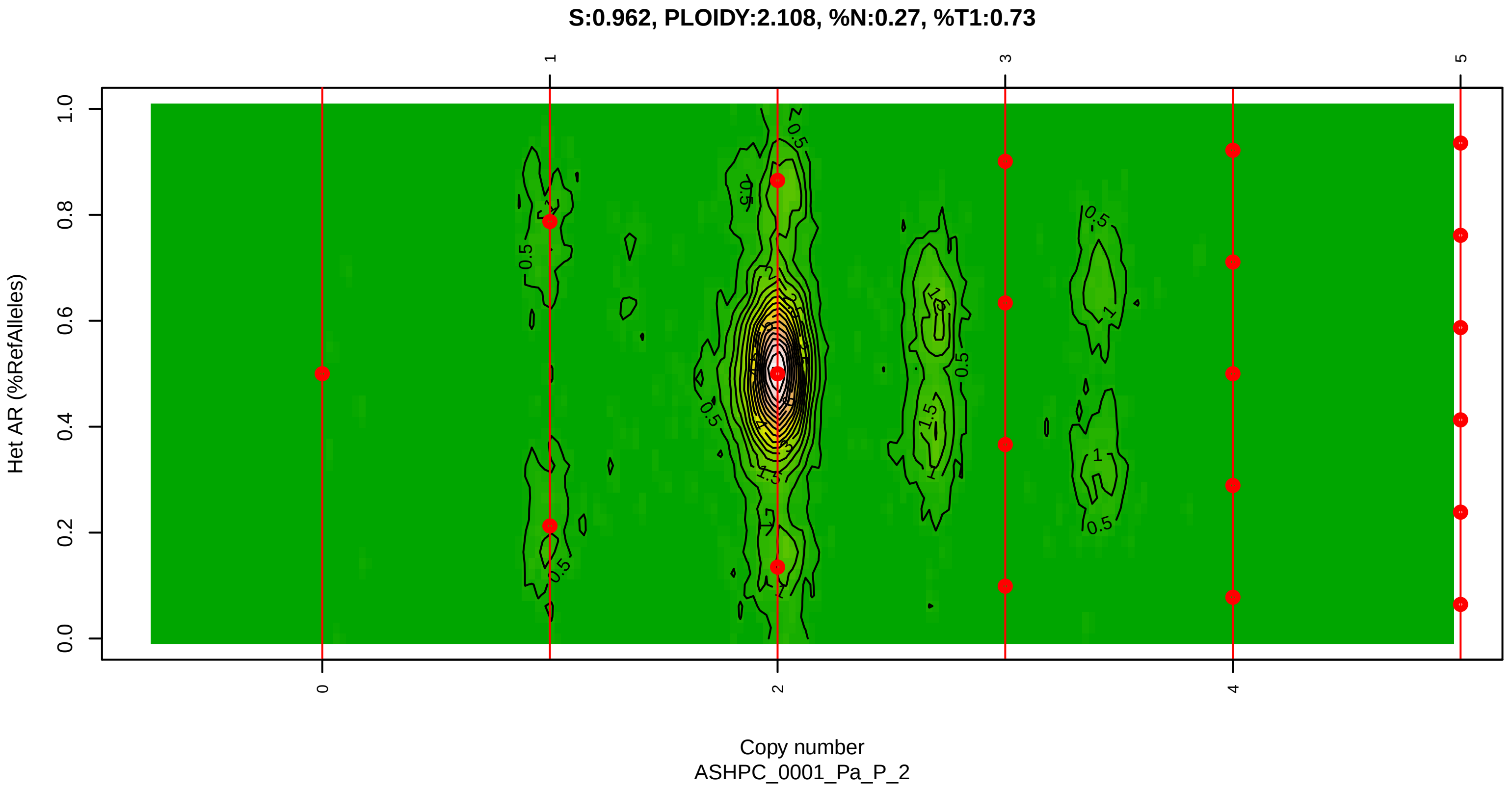
	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	1	FAIL	NA	NA	NA	NA	NA	NA
chr2	2	FAIL	NA	NA	NA	NA	NA	NA
chr3	1	FAIL	NA	NA	NA	NA	NA	NA
chr4:10891627−30046000	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	1	FAIL	NA	NA	NA	NA	NA	NA
chr8	0	FAIL	NA	NA	NA	NA	NA	NA
chr9	0	FAIL	NA	NA	NA	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13:19797155−27142000	4	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	1	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18	0	FAIL	NA	NA	NA	NA	NA	NA
chr19	0	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	1	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

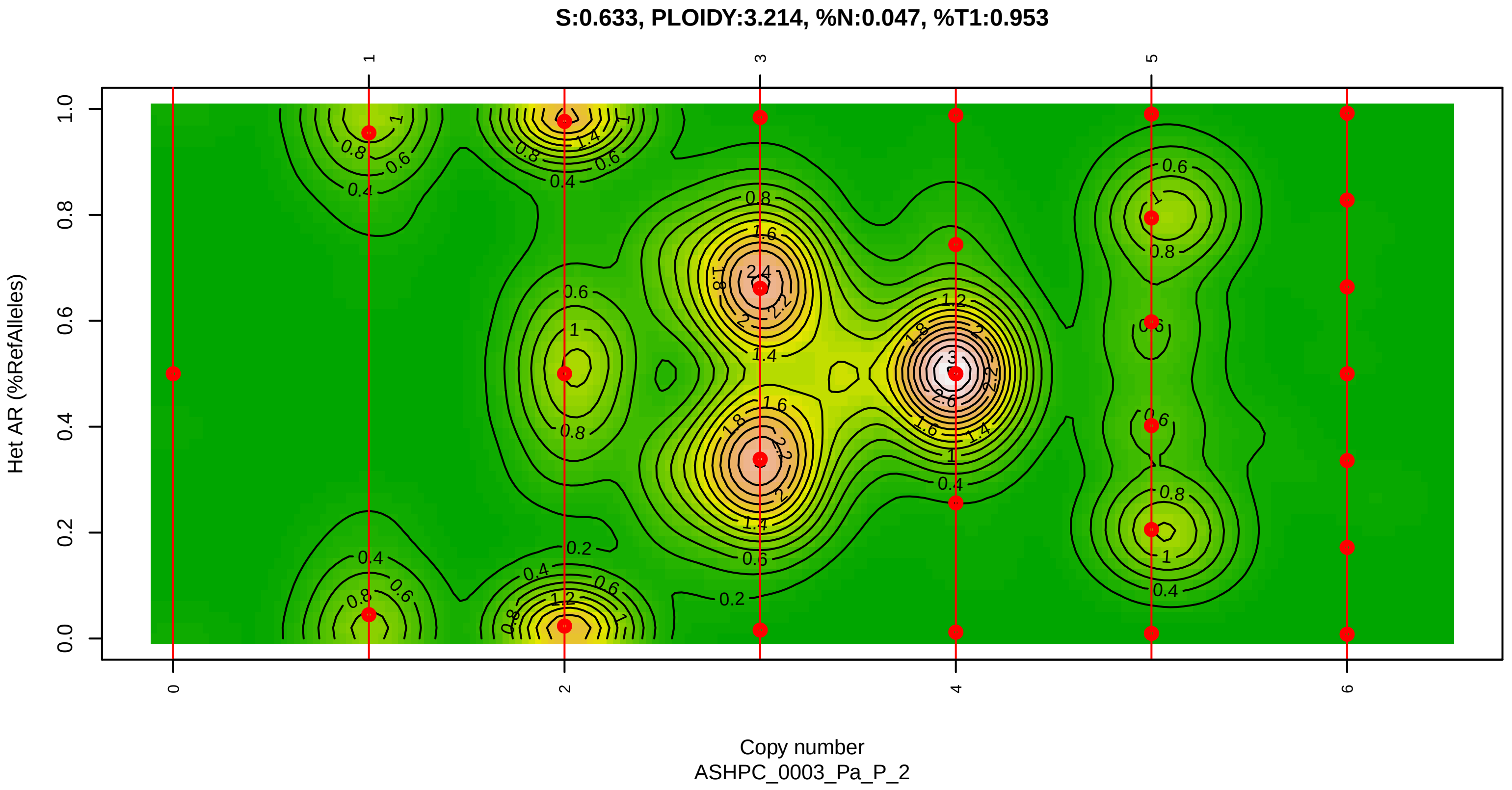
PCSI_0547_Pa_P_526

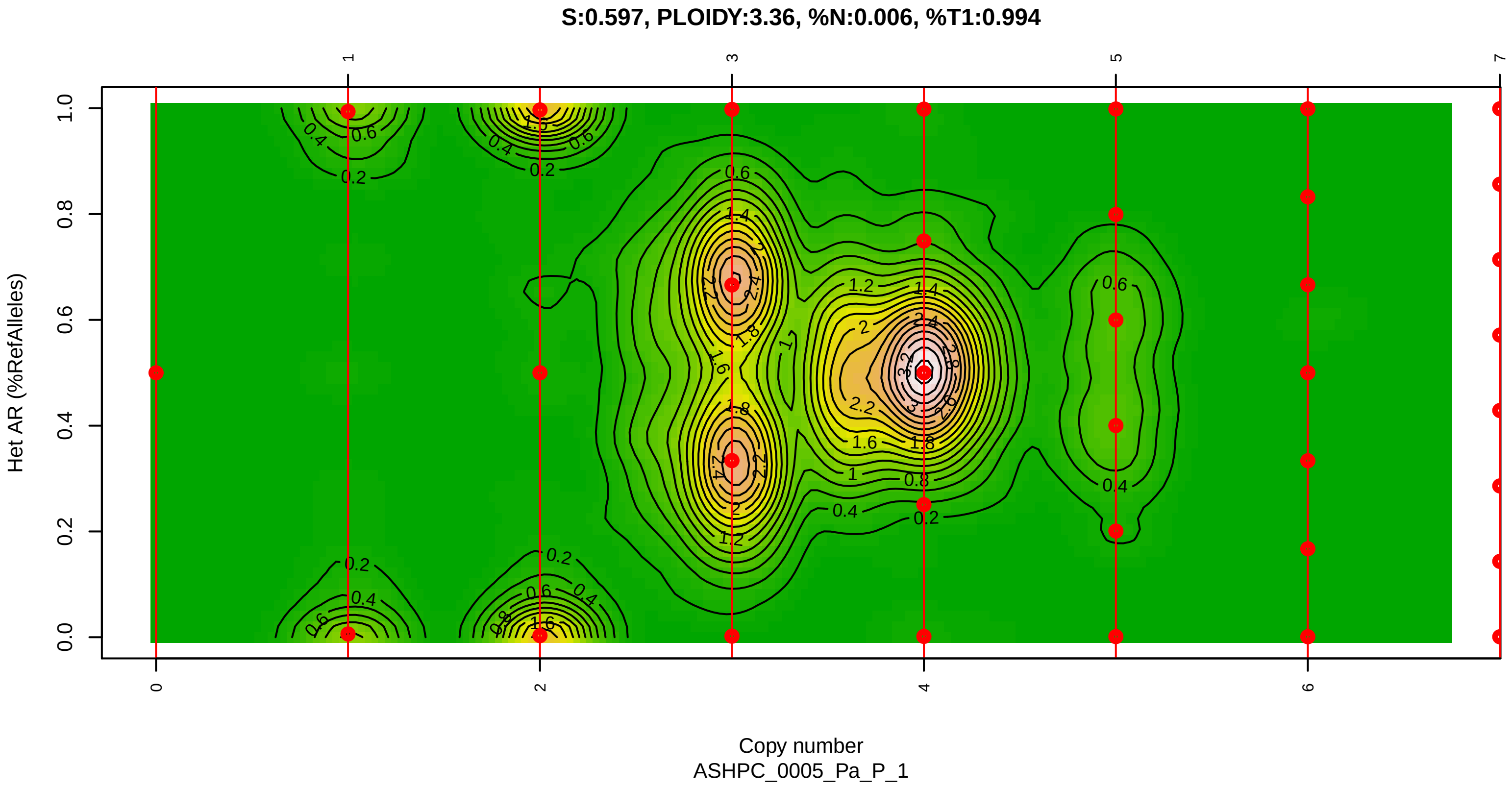
	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	3	FAIL	NA	NA	NA	NA	NA	NA
chr2:115527233−184857983	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr3	3	FAIL	NA	NA	NA	NA	NA	NA
chr4:107269496−123280135	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr5:39462795−63247693	1	FAIL	FAIL	FAIL	FAIL	inter	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	1	FAIL	NA	NA	NA	NA	NA	NA
chr8	1	FAIL	NA	NA	NA	NA	NA	NA
chr9	1	FAIL	NA	NA	NA	NA	NA	NA
chr10:25407823−102981000	1	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr11	1	FAIL	NA	NA	NA	NA	NA	NA
chr12	1	FAIL	NA	NA	NA	NA	NA	NA
chr13	1	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15:94880001−101086521	3	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17	0	FAIL	NA	NA	NA	NA	NA	NA
chr18:30580938−63595000	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr19	1	FAIL	NA	NA	NA	NA	NA	NA
chr20	0	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22:25069016−46026945	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

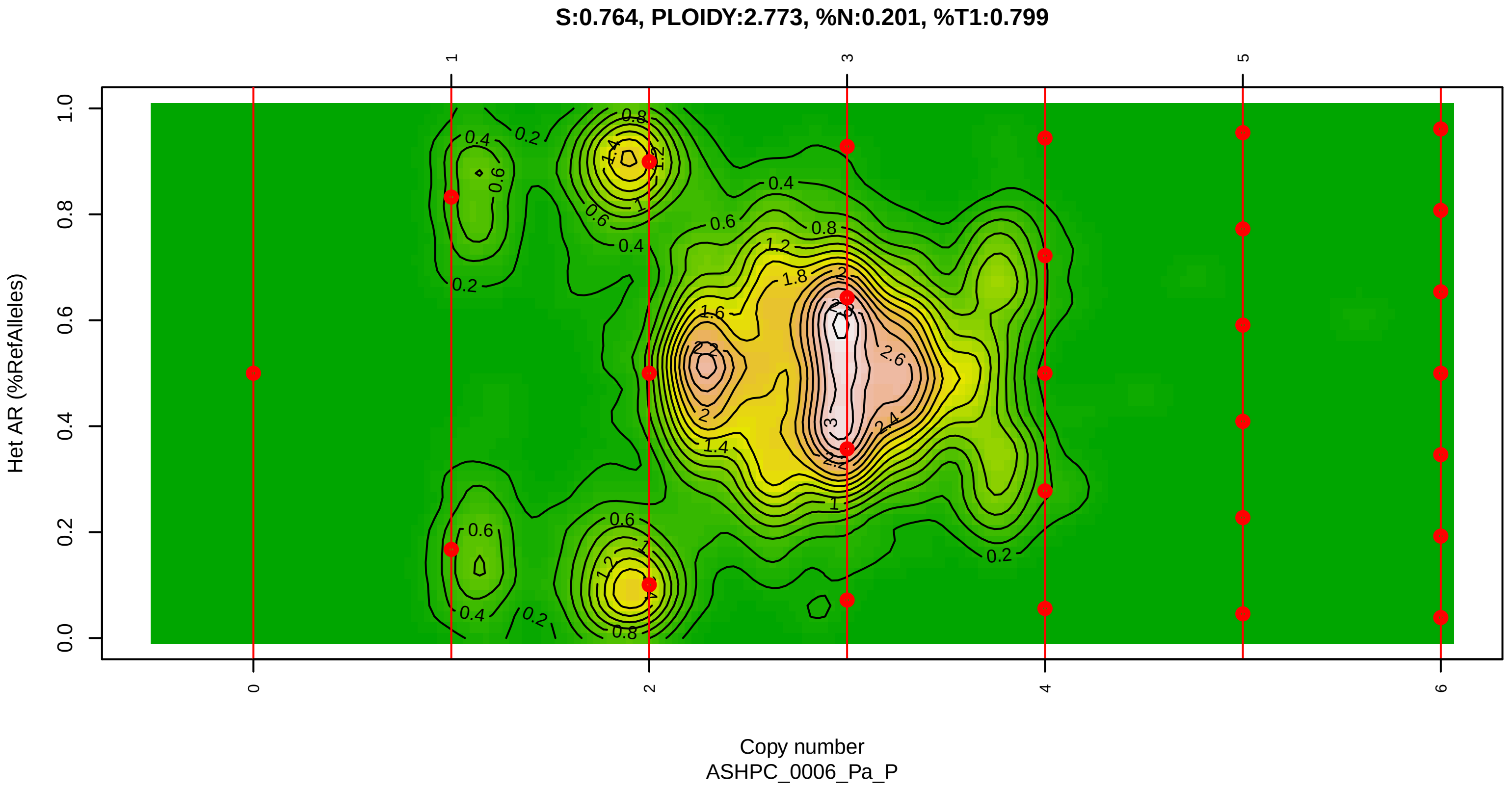
RAMP_0007_Pa_P_526

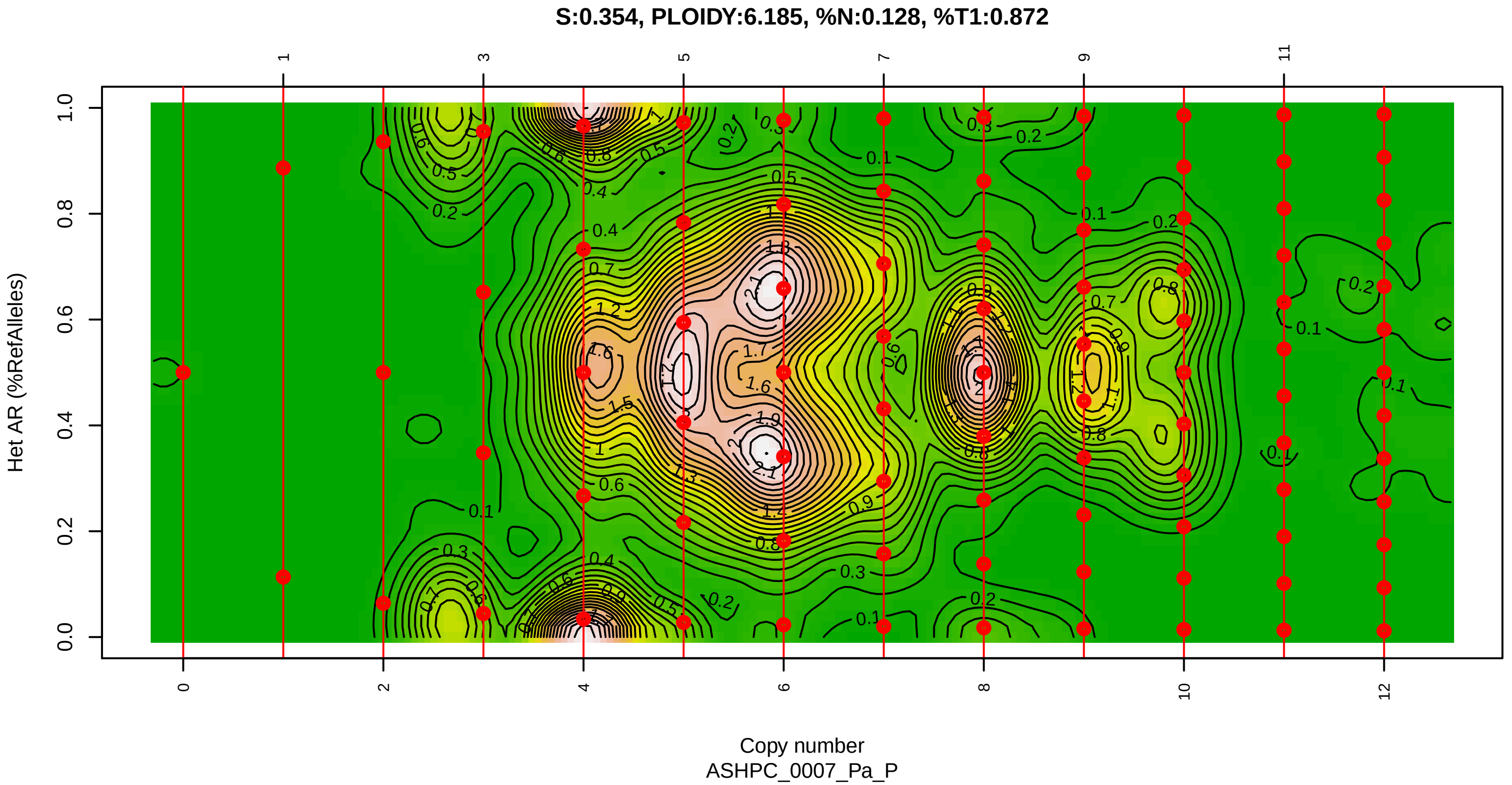
	Total Pass: Chromosome(/6)	Window ID with >= 8 SV	Window Join	Window AR	Window Osciallation	Window Type	Window Chain	Overall
chr1	0	FAIL	NA	NA	NA	NA	NA	NA
chr2	0	FAIL	NA	NA	NA	NA	NA	NA
chr3:1626776−123596752	0	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr4	0	FAIL	NA	NA	NA	NA	NA	NA
chr5	0	FAIL	NA	NA	NA	NA	NA	NA
chr6	0	FAIL	NA	NA	NA	NA	NA	NA
chr7	0	FAIL	NA	NA	NA	NA	NA	NA
chr8	1	FAIL	NA	NA	NA	NA	NA	NA
chr9:76461001−120839000	3	FAIL	FAIL	PASS	FAIL	NA	NA	NA
chr10	0	FAIL	NA	NA	NA	NA	NA	NA
chr11	0	FAIL	NA	NA	NA	NA	NA	NA
chr12	0	FAIL	NA	NA	NA	NA	NA	NA
chr13	0	FAIL	NA	NA	NA	NA	NA	NA
chr14	0	FAIL	NA	NA	NA	NA	NA	NA
chr15	0	FAIL	NA	NA	NA	NA	NA	NA
chr16	0	FAIL	NA	NA	NA	NA	NA	NA
chr17:21954561−70441215	0	FAIL	FAIL	FAIL	FAIL	chain	chr17:21954561−70441215, chr18:20210001−26215405	NA
chr18:20210001−26215405	5	FAIL	PASS	PASS	FAIL	chain	chr17:21954561−70441215, chr18:20210001−26215405	NA
chr19:14010844−14057552	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr19:14992992−19710000	2	FAIL	FAIL	FAIL	FAIL	NA	NA	NA
chr20	1	FAIL	NA	NA	NA	NA	NA	NA
chr21	0	FAIL	NA	NA	NA	NA	NA	NA
chr22	0	FAIL	NA	NA	NA	NA	NA	NA
chrX	0	FAIL	NA	NA	NA	NA	NA	NA
chrY	0	FAIL	NA	NA	NA	NA	NA	NA

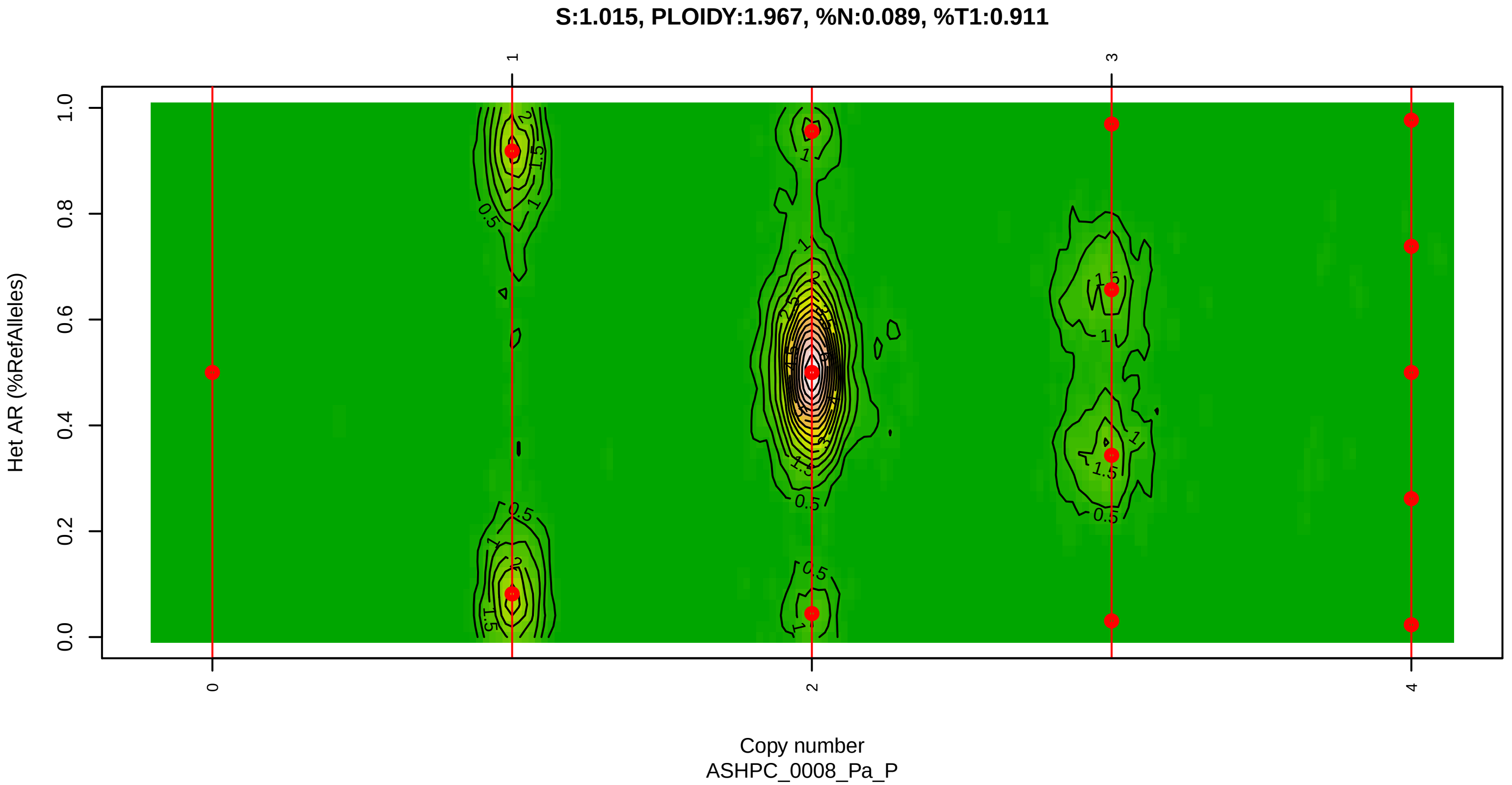

S:0.962, PLOIDY:2.108, %N:0.27, %T1:0.73


S:0.633, PLOIDY:3.214, %N:0.047, %T1:0.953

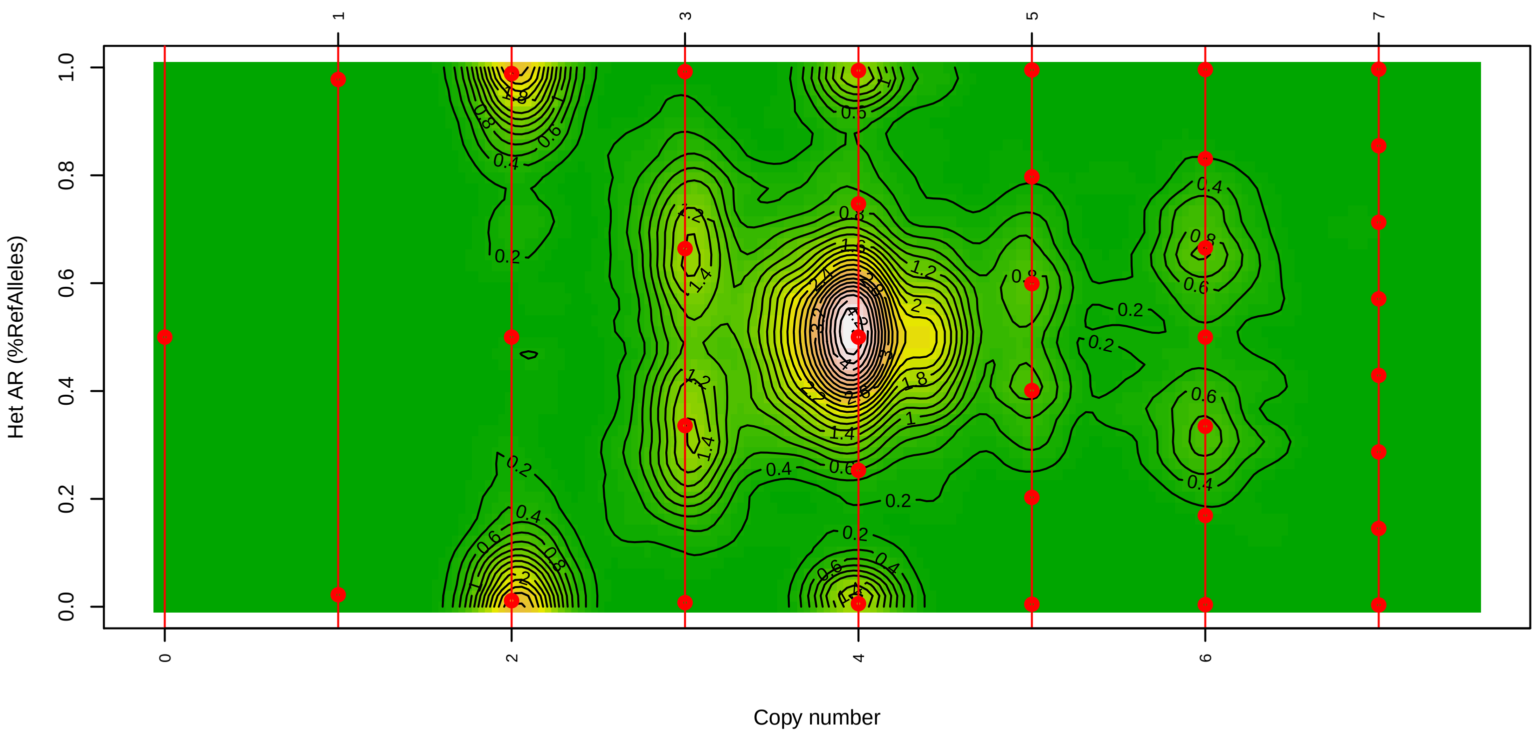

S:0.597, PLOIDY:3.36, %N:0.006, %T1:0.994


S:0.764, PLOIDY:2.773, %N:0.201, %T1:0.799


S:0.354, PLOIDY:6.185, %N:0.128, %T1:0.872

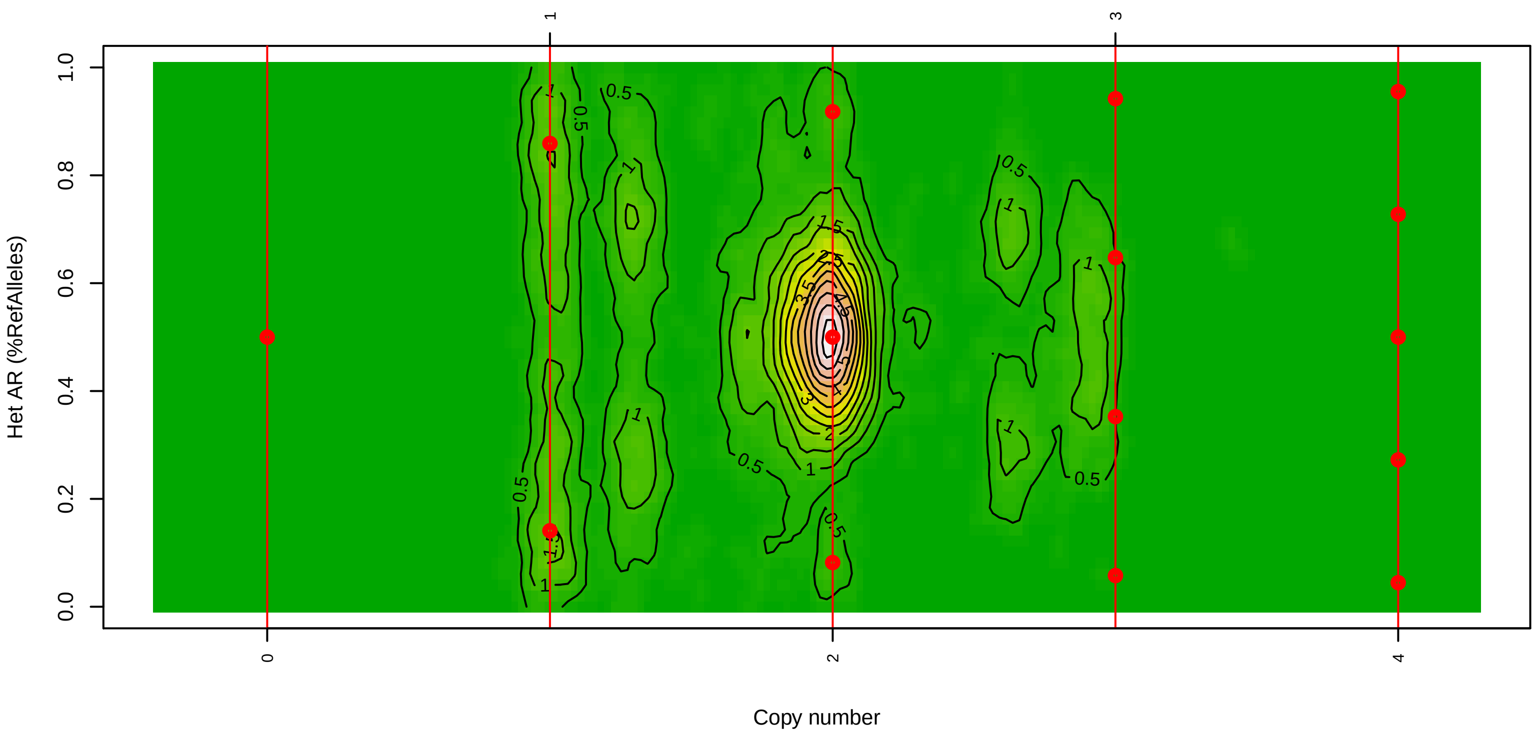

S:1.015, PLOIDY:1.967, %N:0.089, %T1:0.911

S:0.537, PLOIDY:3.761, %N:0.023, %T1:0.977



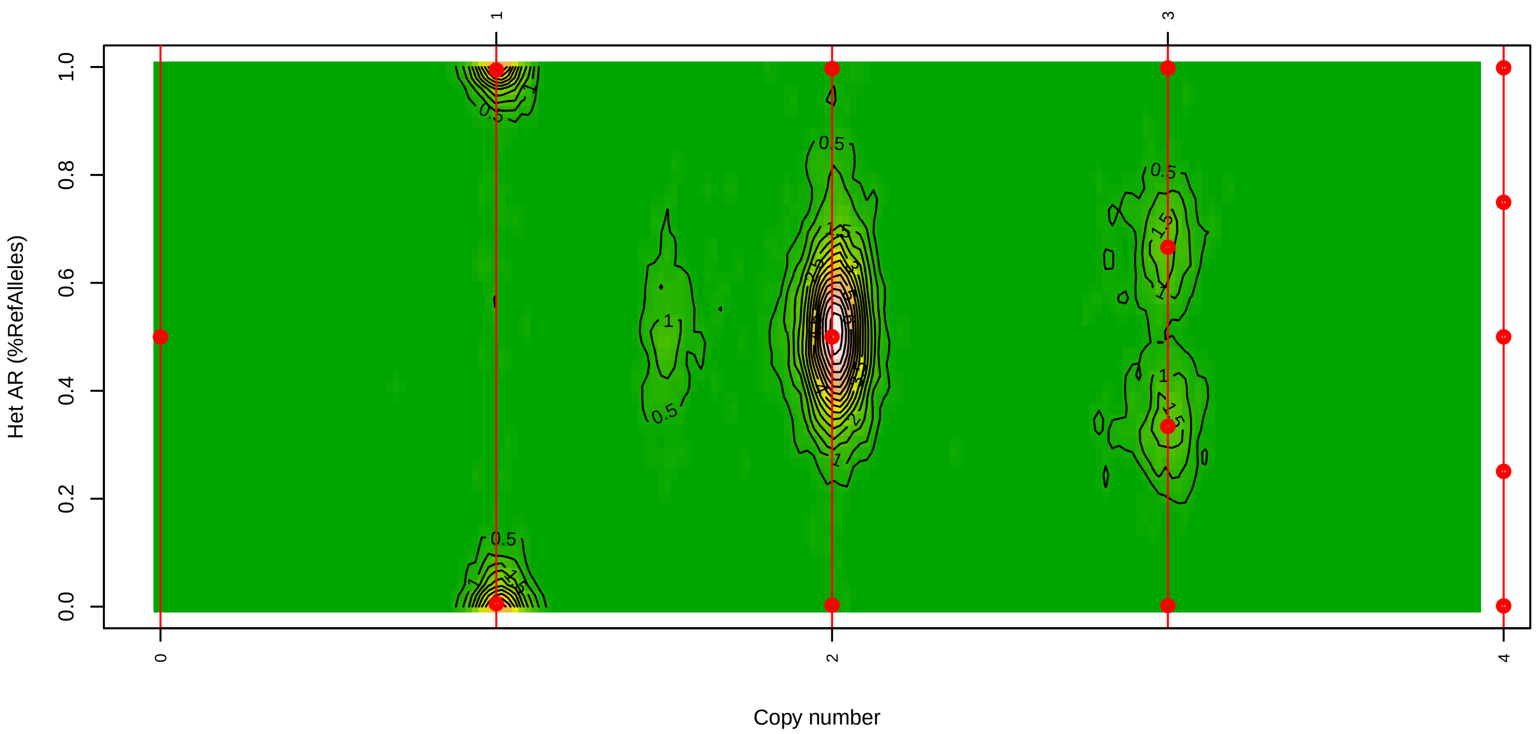
ASHPC_0009_Pa_P

S:1.024, PLOIDY:1.943, %N:0.164, %T1:0.836



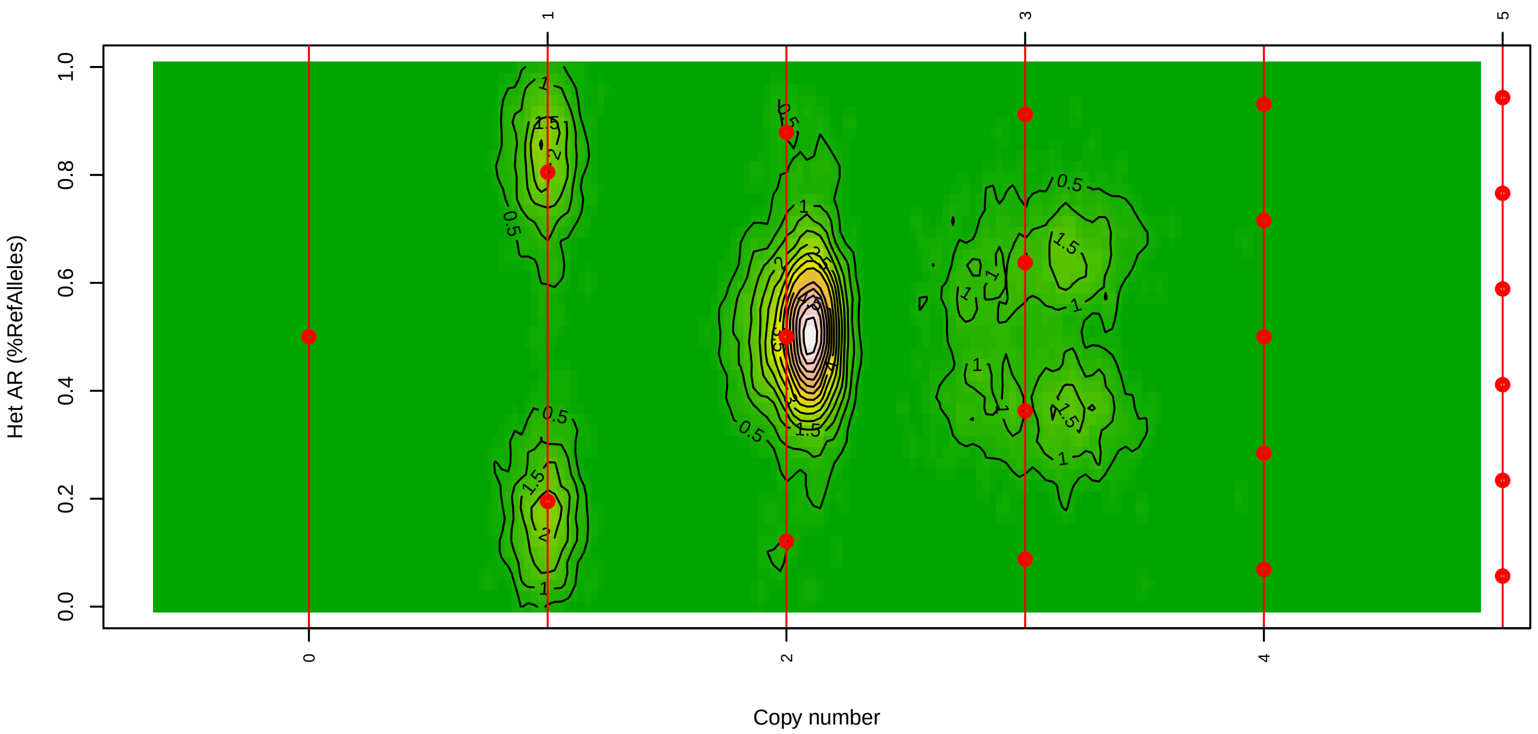
ASHPC_0010_Pa_P

S:1.023, PLOIDY:1.955, %N:0.006, %T1:0.994



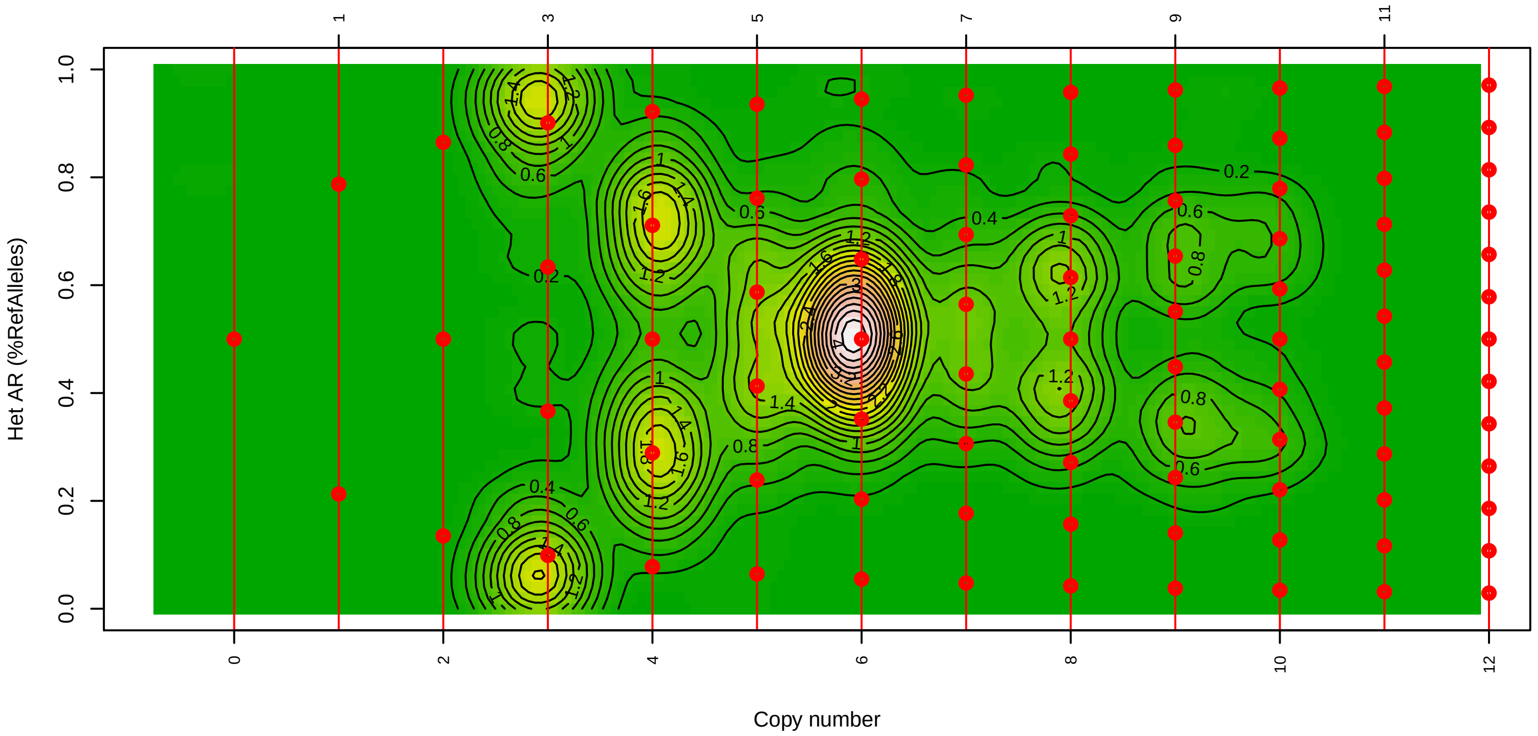
ASHPC_0011_Pa_P

S:0.954, PLOIDY:2.127, %N:0.242, %T1:0.758



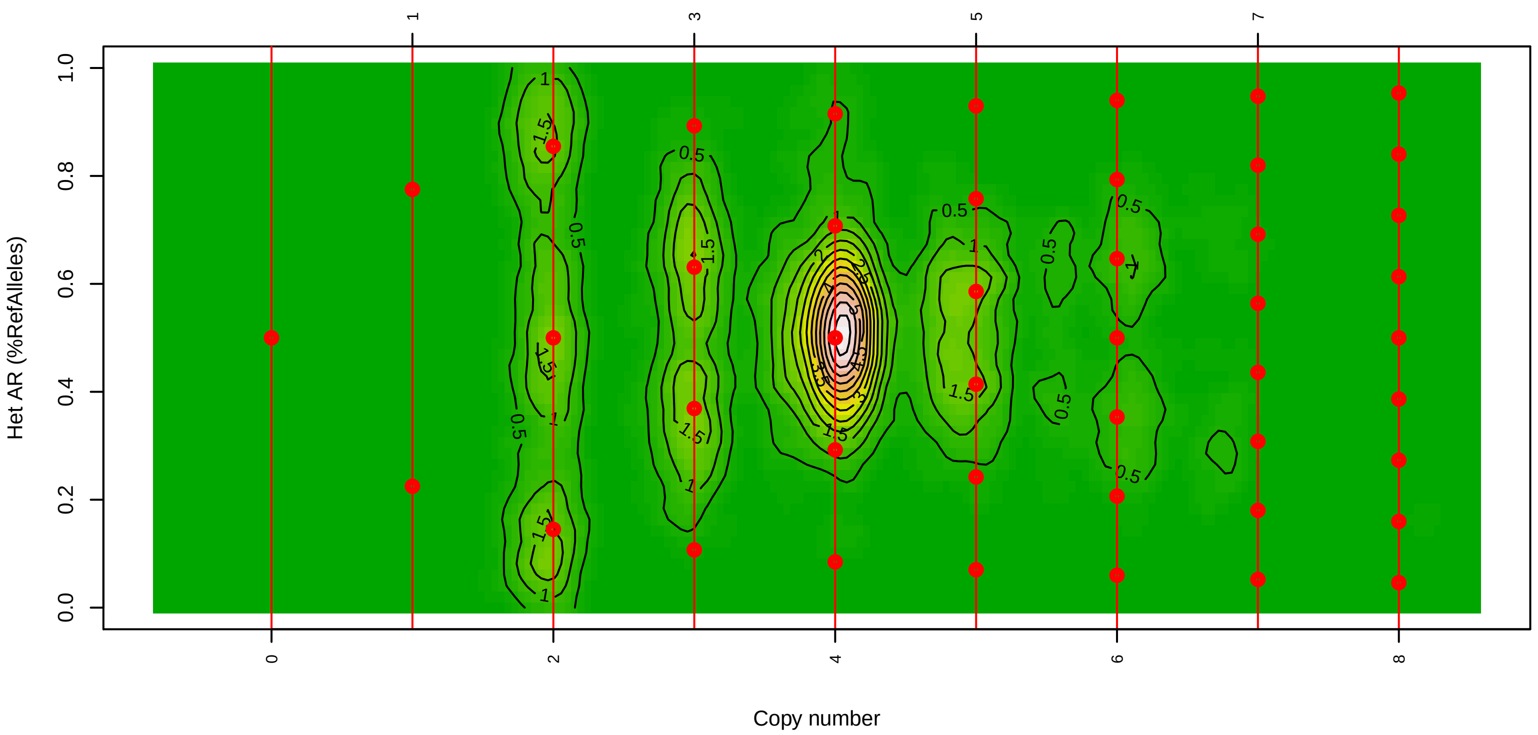
ASHPC_0013_Pa_P

S:0.434, PLOIDY:5.573, %N:0.27, %T1:0.73

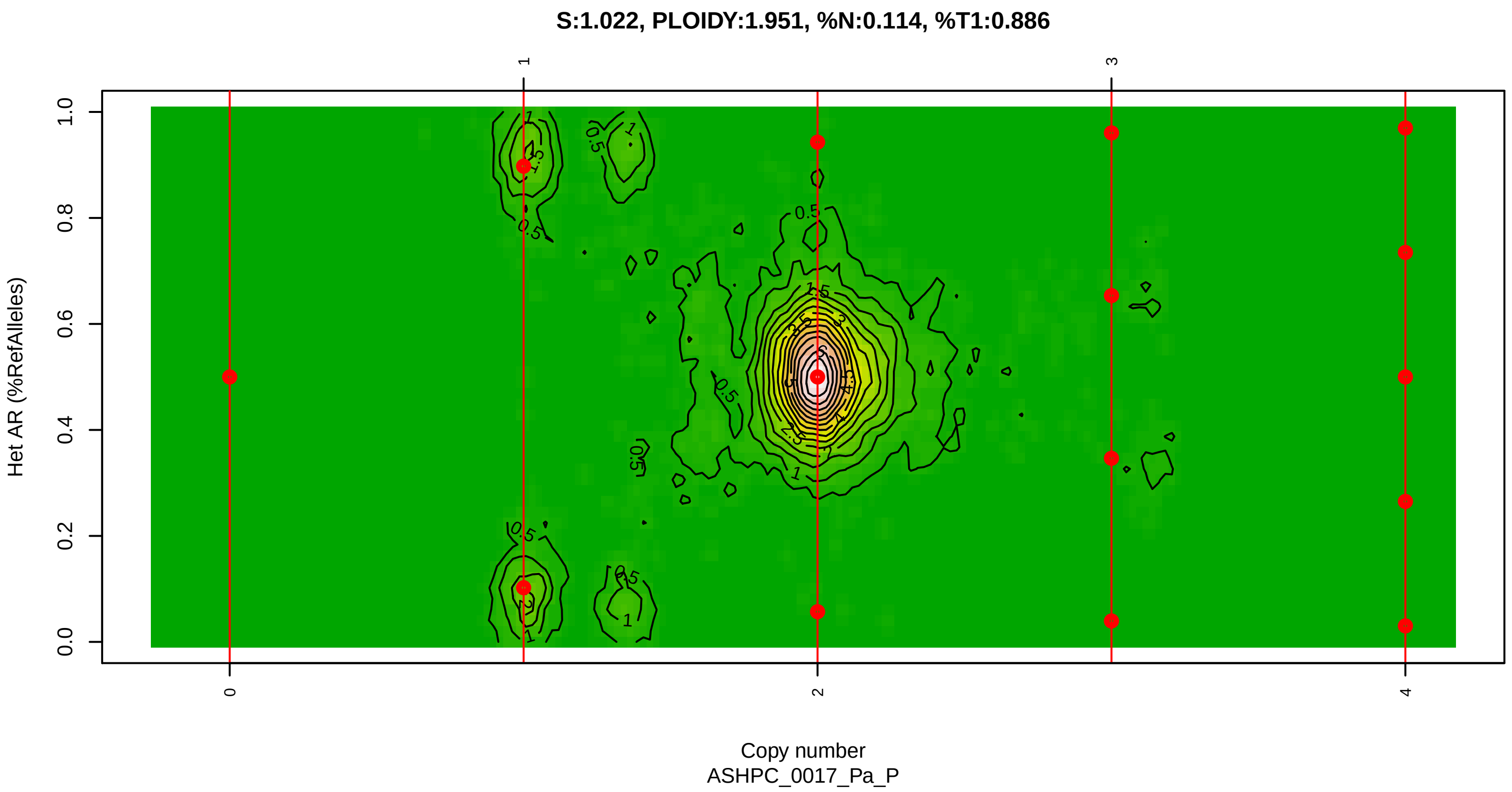


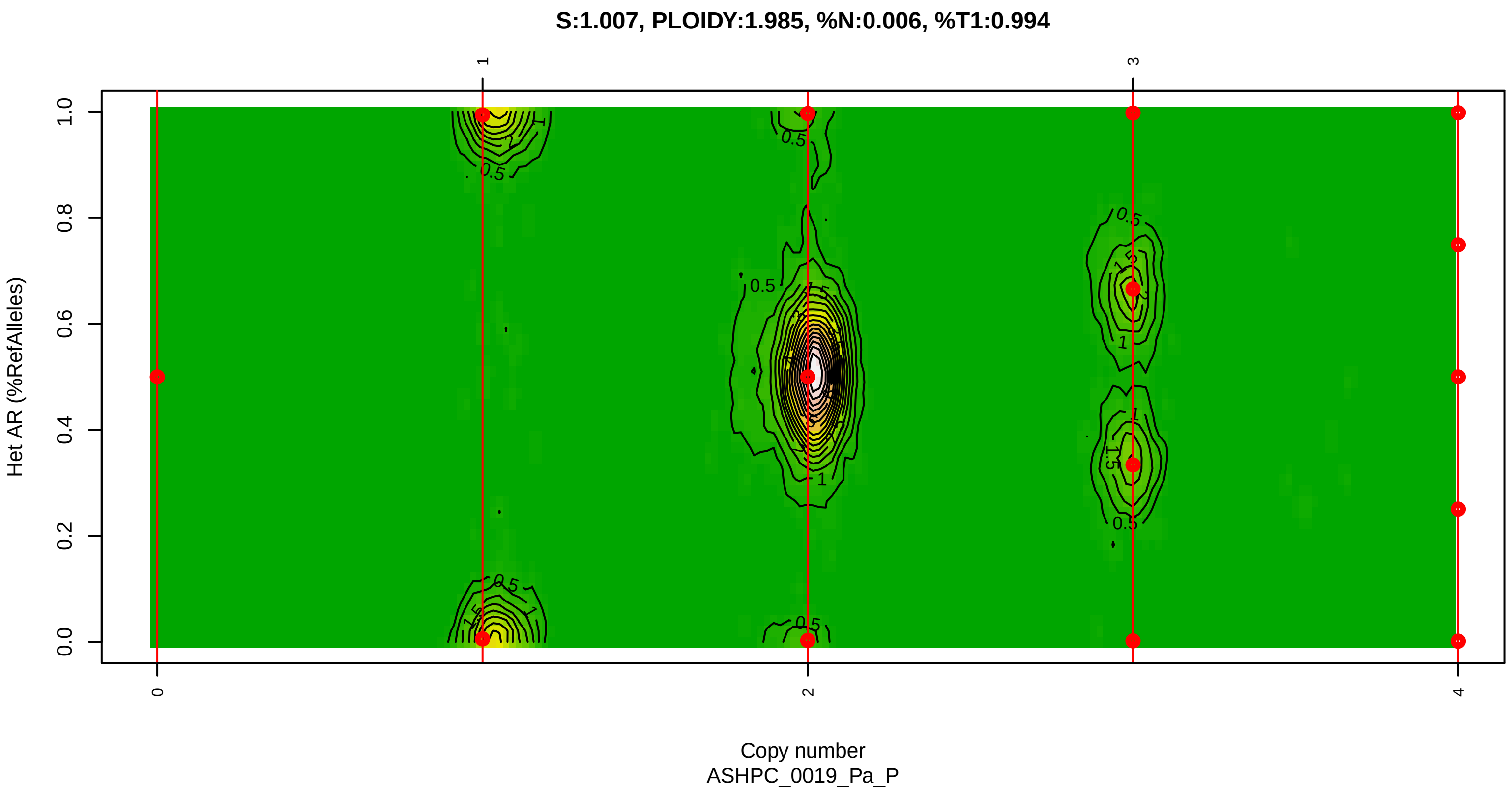
ASHPC_0015_Pa_P

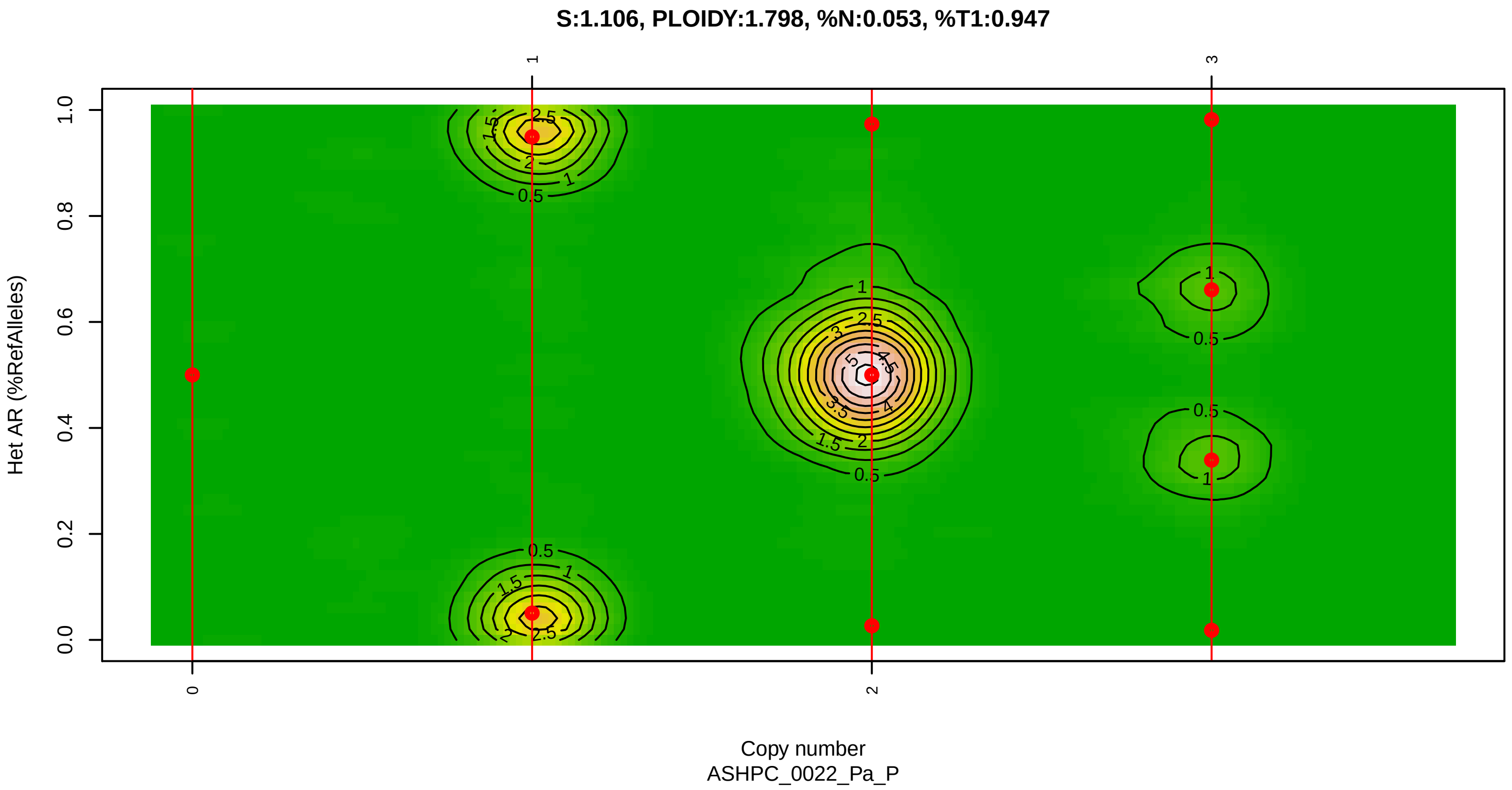
S:0.601, PLOIDY:3.869, %N:0.29, %T1:0.71

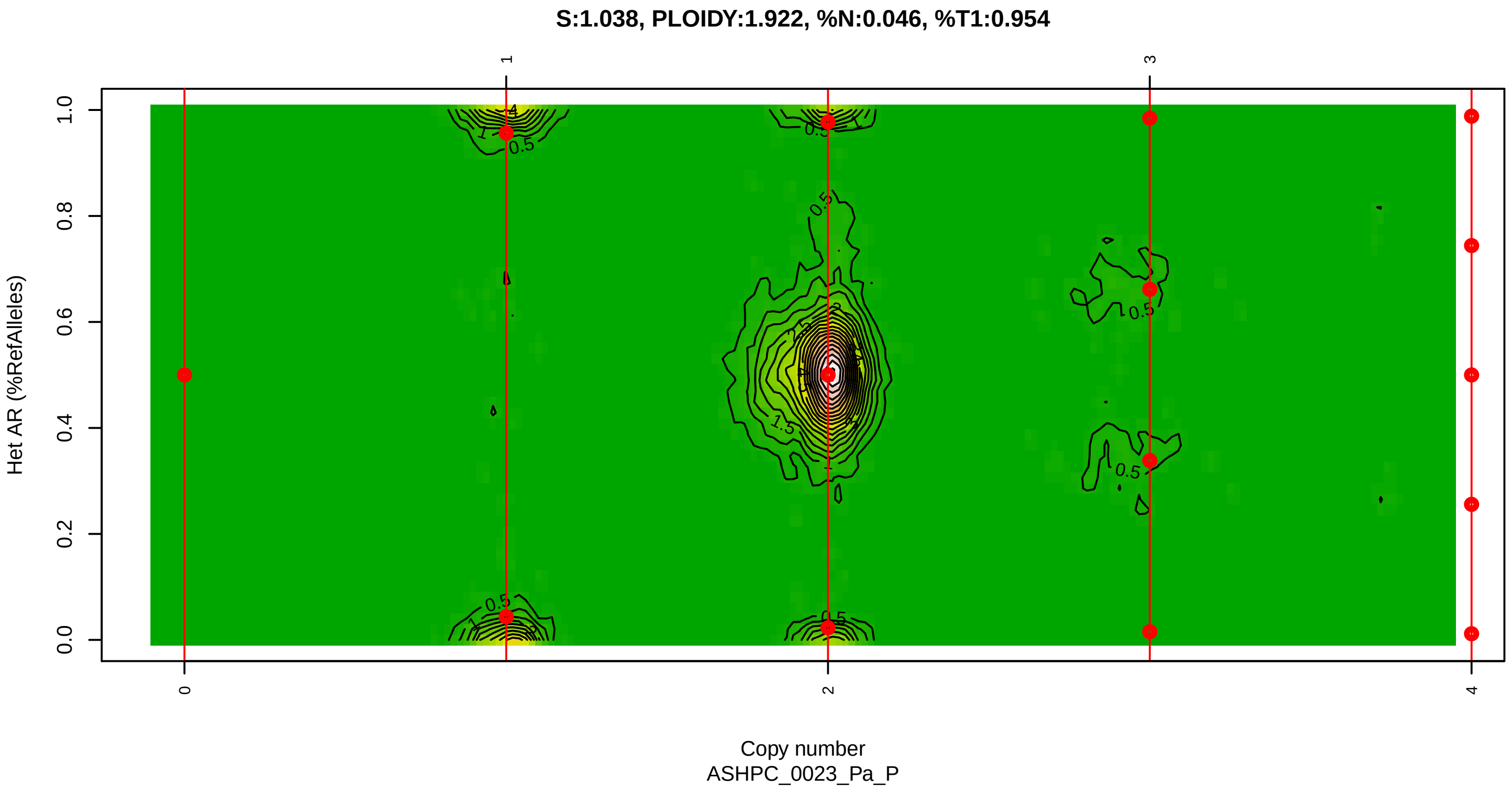


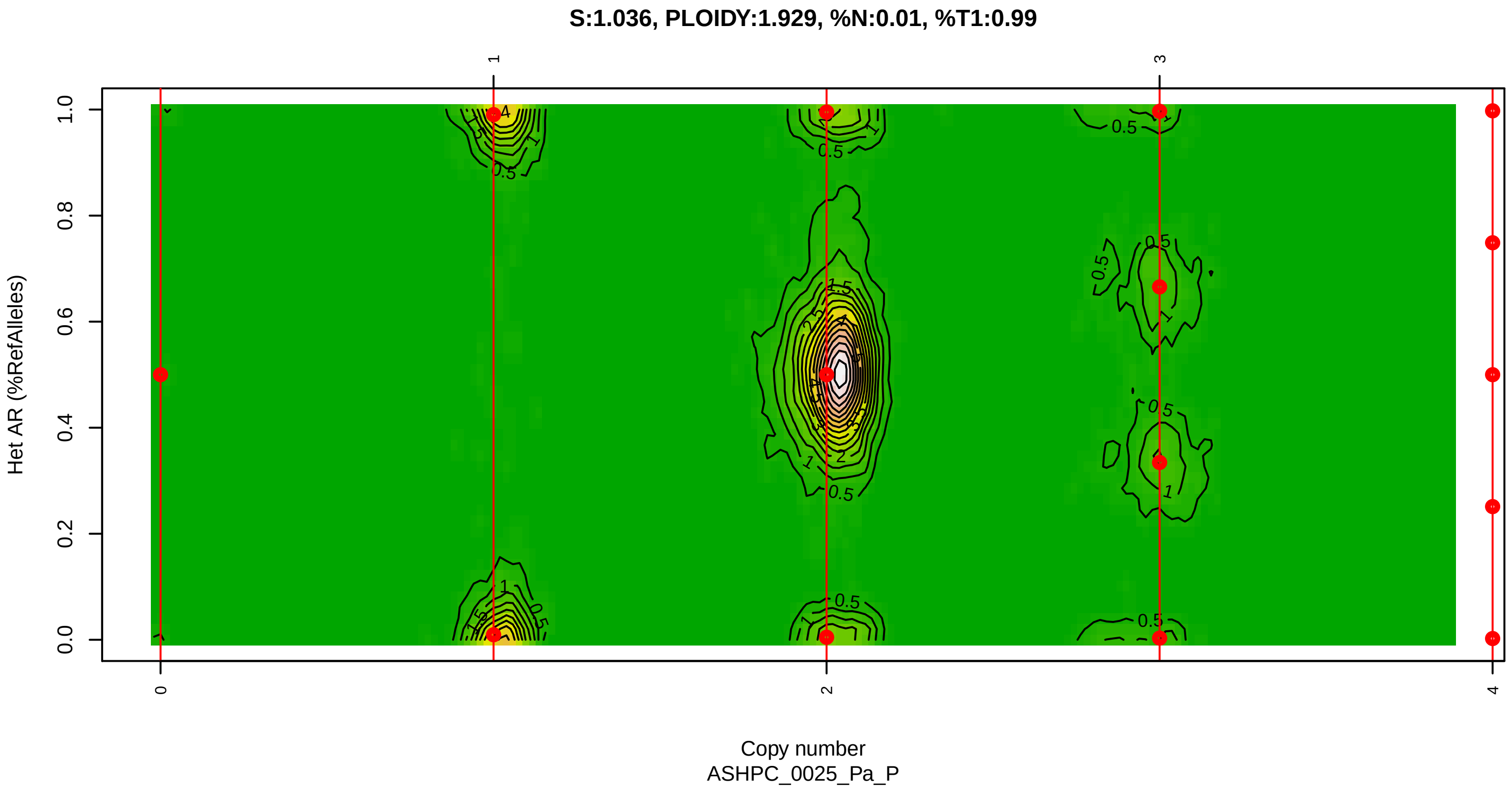
ASHPC_0016_Pa_P

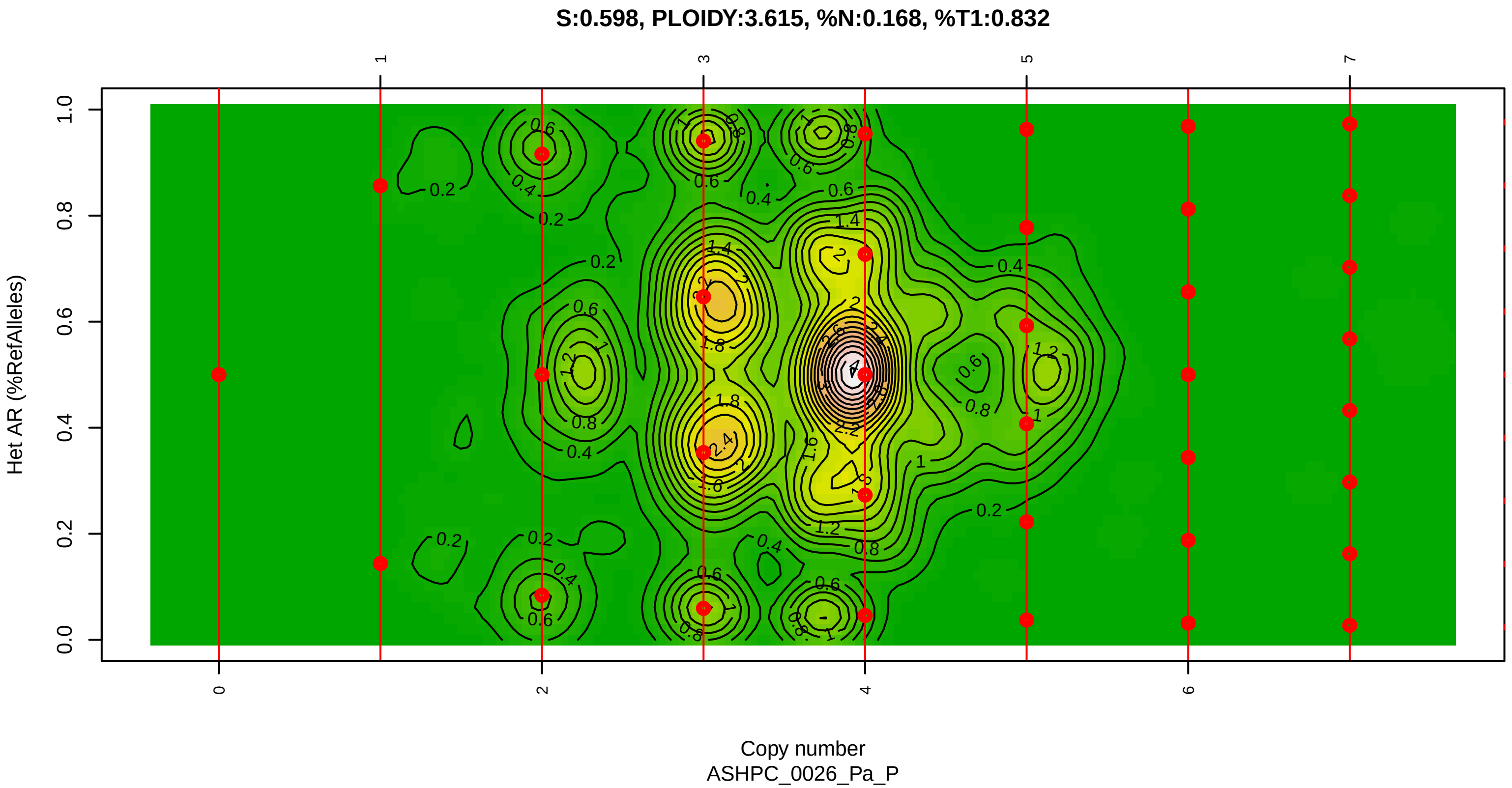

S:1.022, PLOIDY:1.951, %N:0.114, %T1:0.886

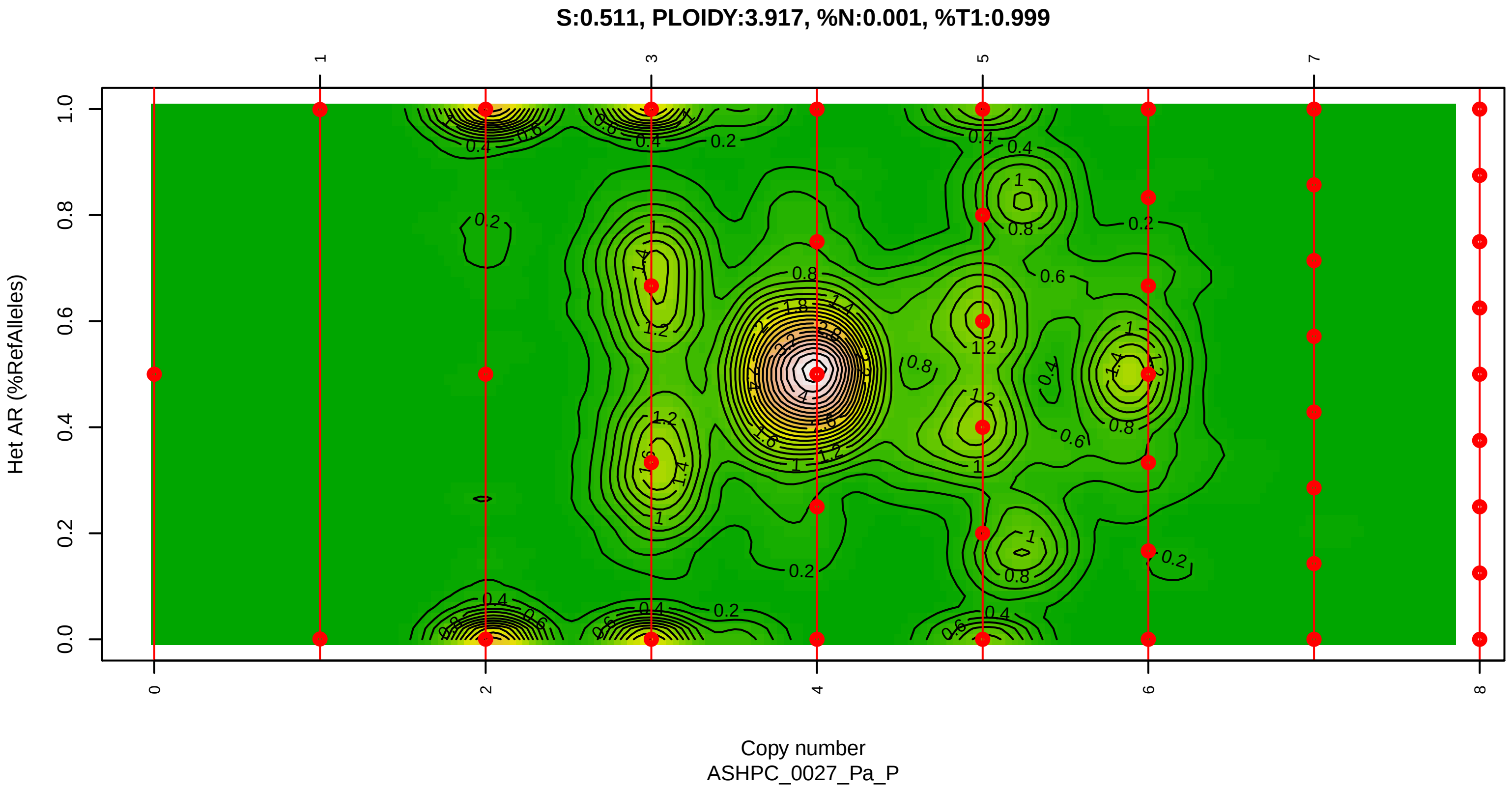

S:1.007, PLOIDY:1.985, %N:0.006, %T1:0.994


S:1.106, PLOIDY:1.798, %N:0.053, %T1:0.947


S:1.038, PLOIDY:1.922, %N:0.046, %T1:0.954


S:1.036, PLOIDY:1.929, %N:0.01, %T1:0.99


S:0.598, PLOIDY:3.615, %N:0.168, %T1:0.832


S:0.511, PLOIDY:3.917, %N:0.001, %T1:0.999
Het AR (%RefAlleles)
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0.2
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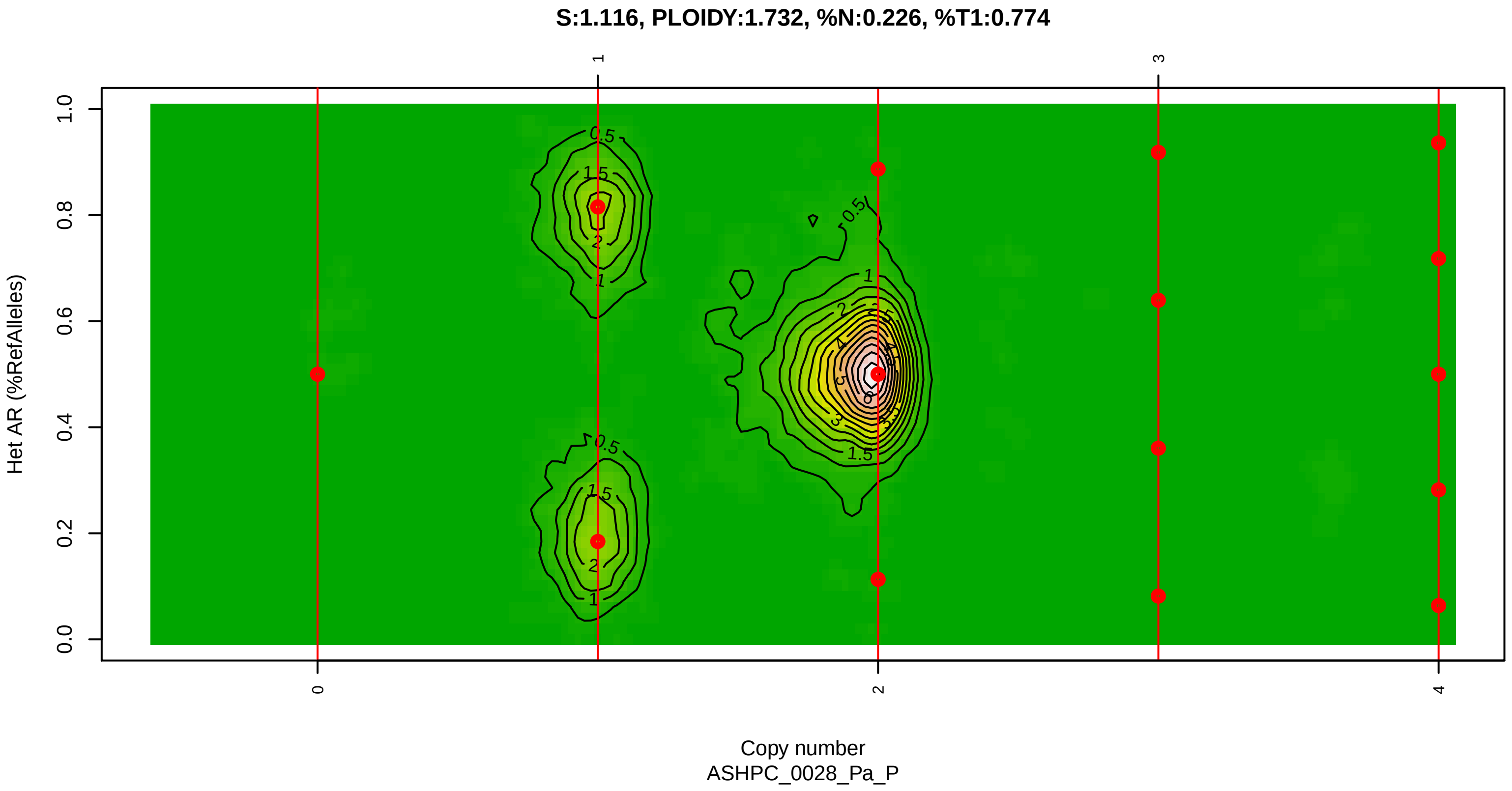
0.6
0.8
1.0
1
3
5
7
0
2
4
6
8
Copy number
ASHPC_0027_Pa_P


S:1.116, PLOIDY:1.732, %N:0.226, %T1:0.774
Het AR (%RefAlleles)
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0.4
0.6
0.8
1.0
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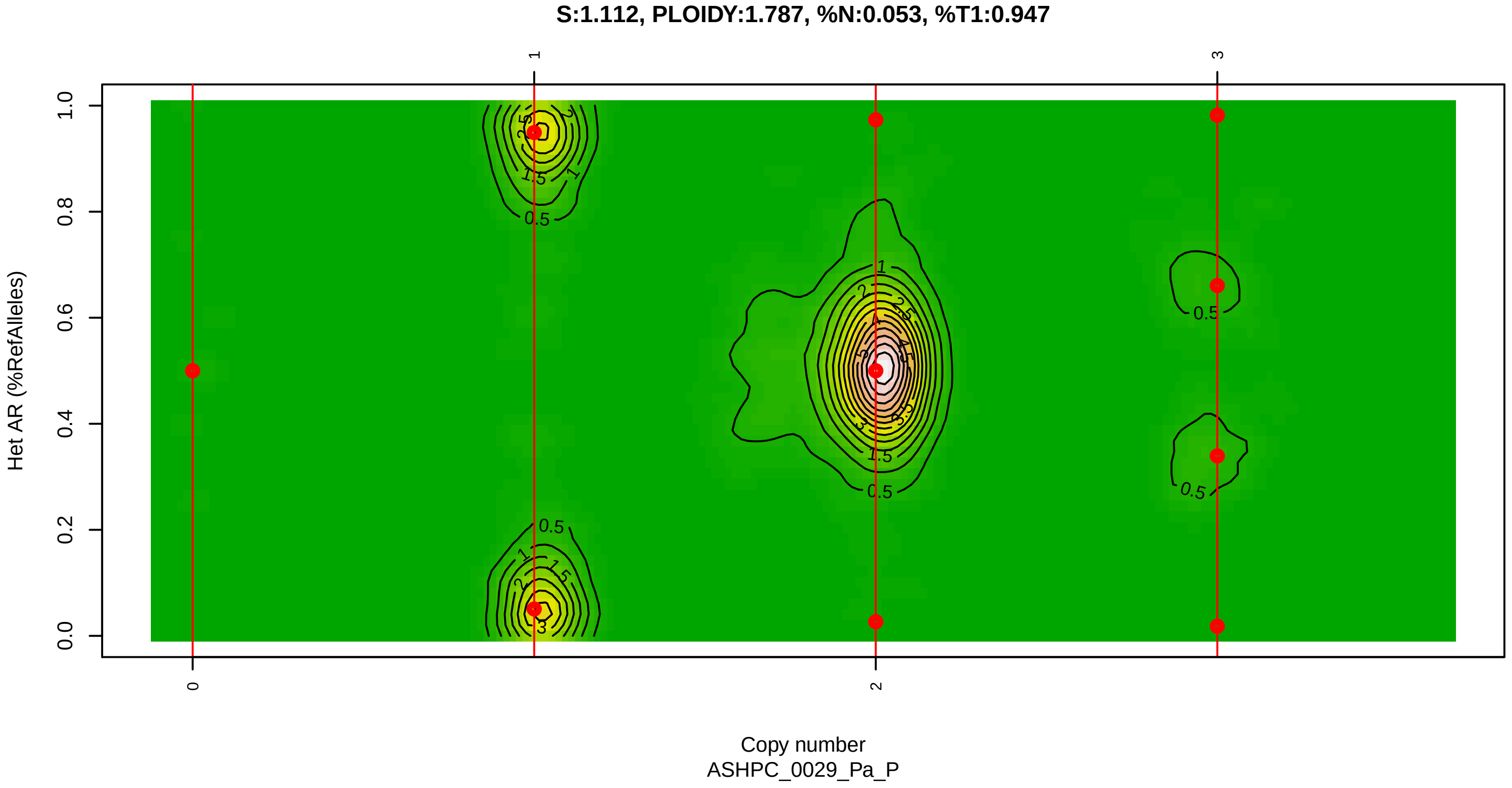
0
2
4
Copy number
ASHPC_0028_Pa_P


S:1.112, PLOIDY:1.787, %N:0.053, %T1:0.947
Het AR (%RefAlleles)
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0.8
1.0
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3
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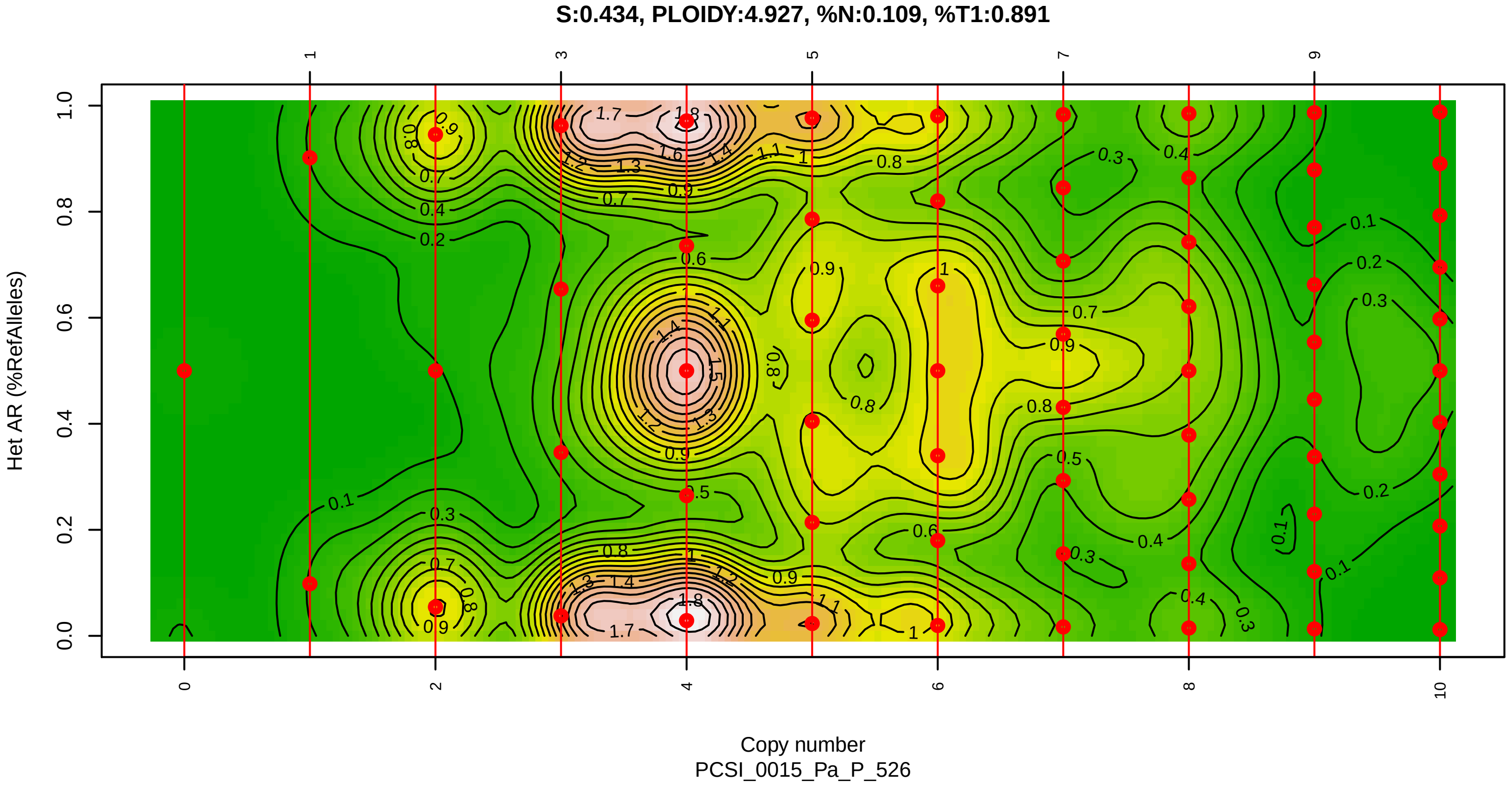
Copy number
ASHPC_0029_Pa_P


S:0.434, PLOIDY:4.927, %N:0.109, %T1:0.891
Het AR (%RefAlleles)
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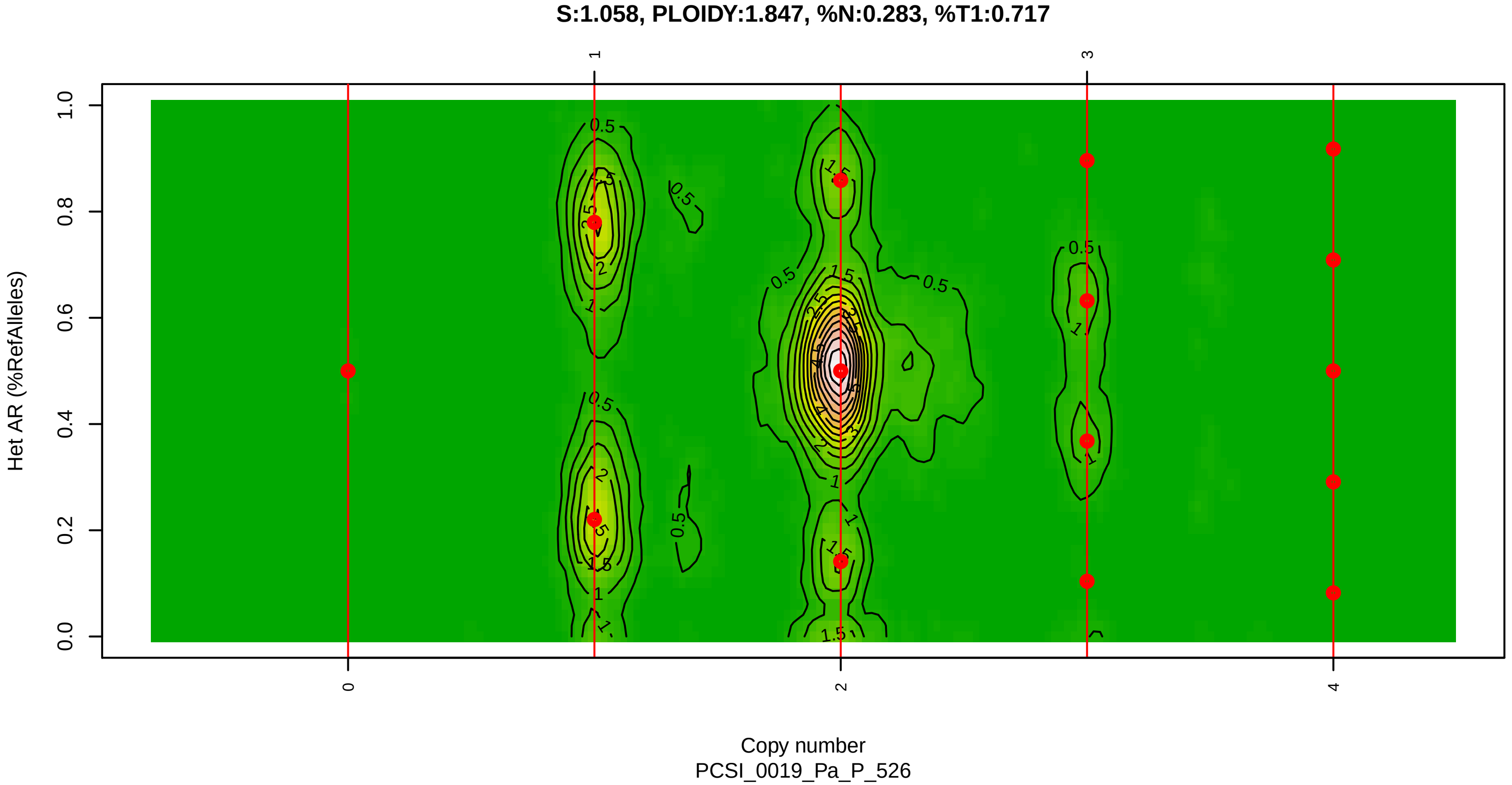
0.2
0.4
0.6
0.8
1.0
1
3
5
7
9
0
2
4
6
8
10
Copy number
PCSI_0015_Pa_P_526


S:1.058, PLOIDY:1.847, %N:0.283, %T1:0.717
Het AR (%RefAlleles)
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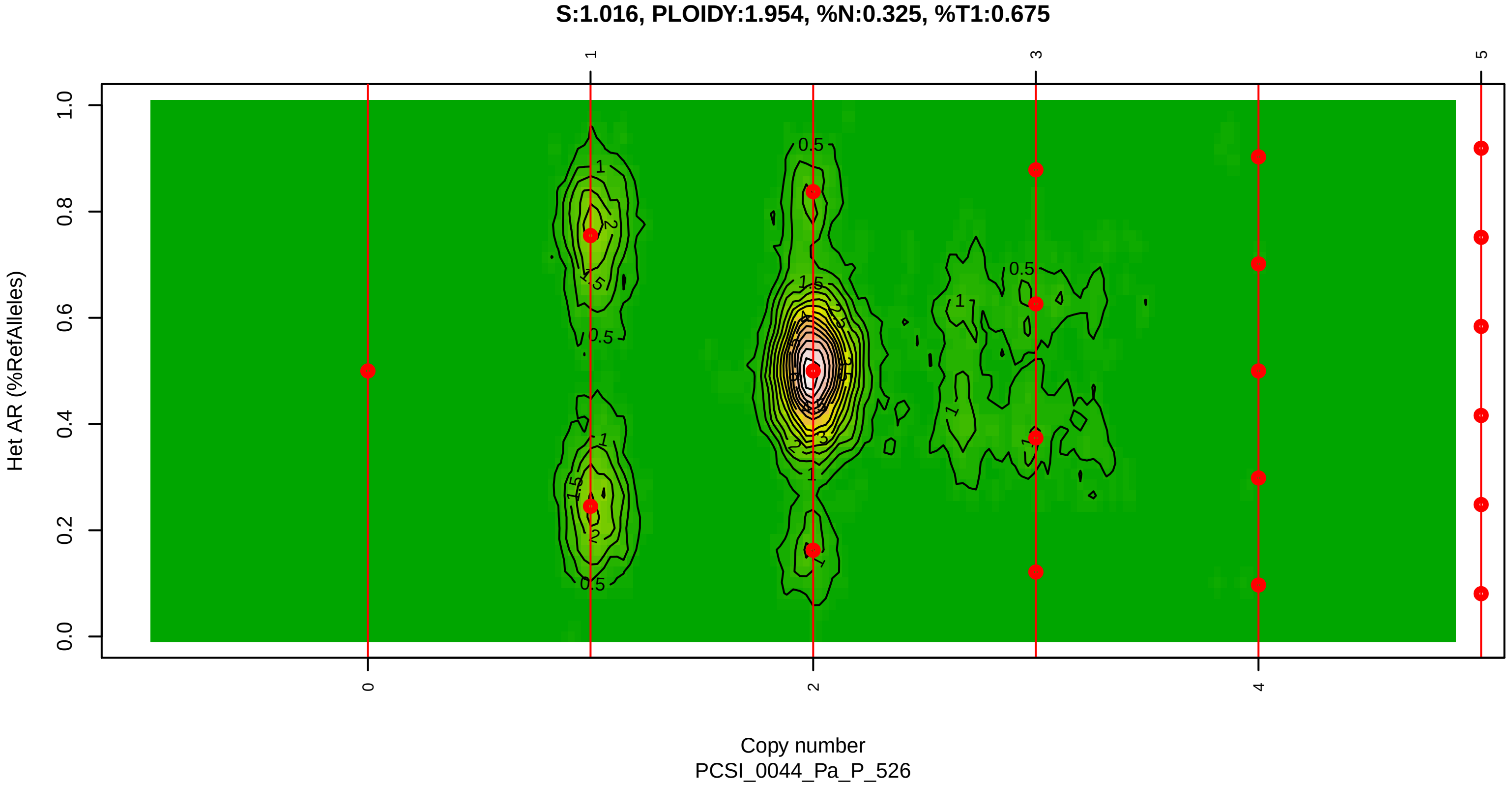
0.6
0.8
1.0
1
3
0
2
4
Copy number
PCSI_0019_Pa_P_526


S:1.016, PLOIDY:1.954, %N:0.325, %T1:0.675
Het AR (%RefAlleles)
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1.0
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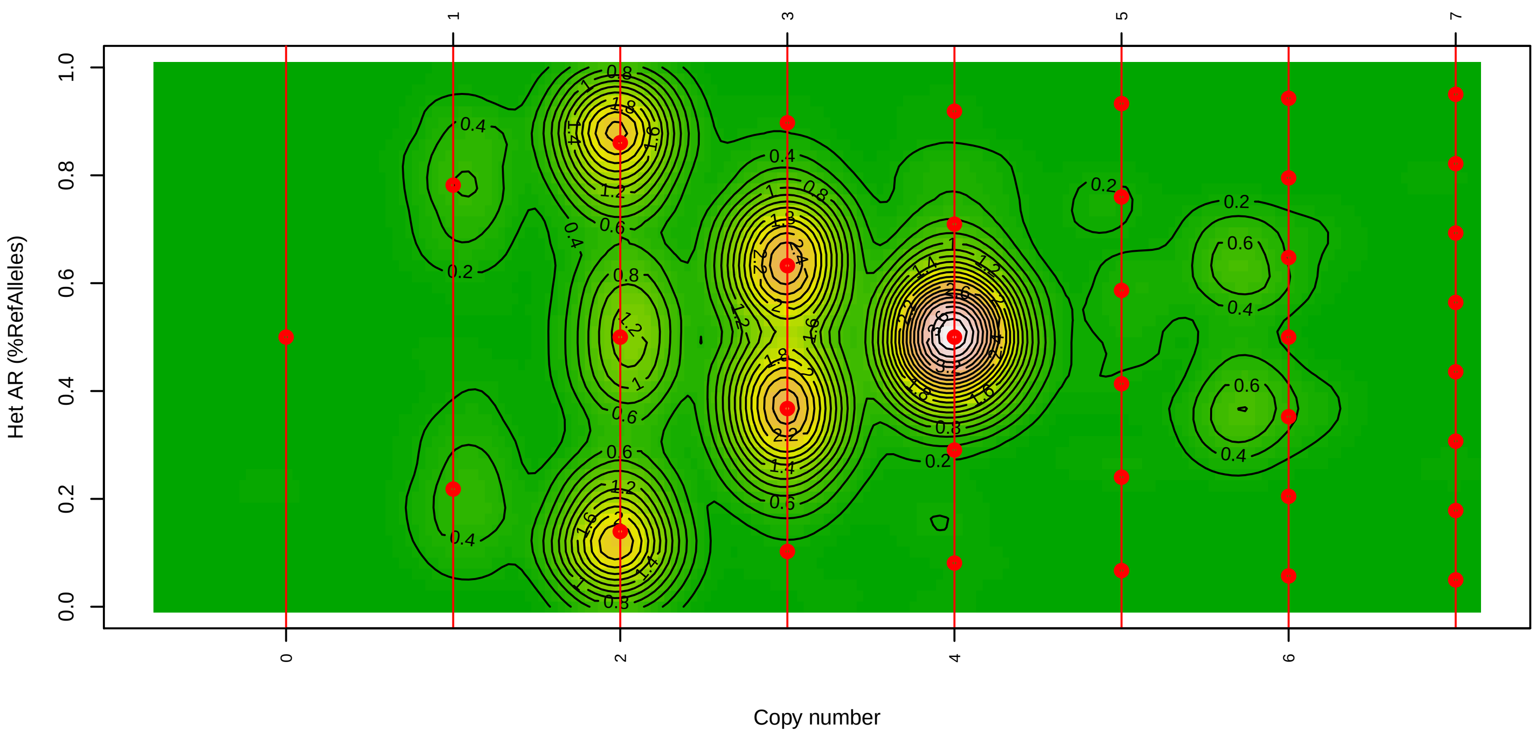
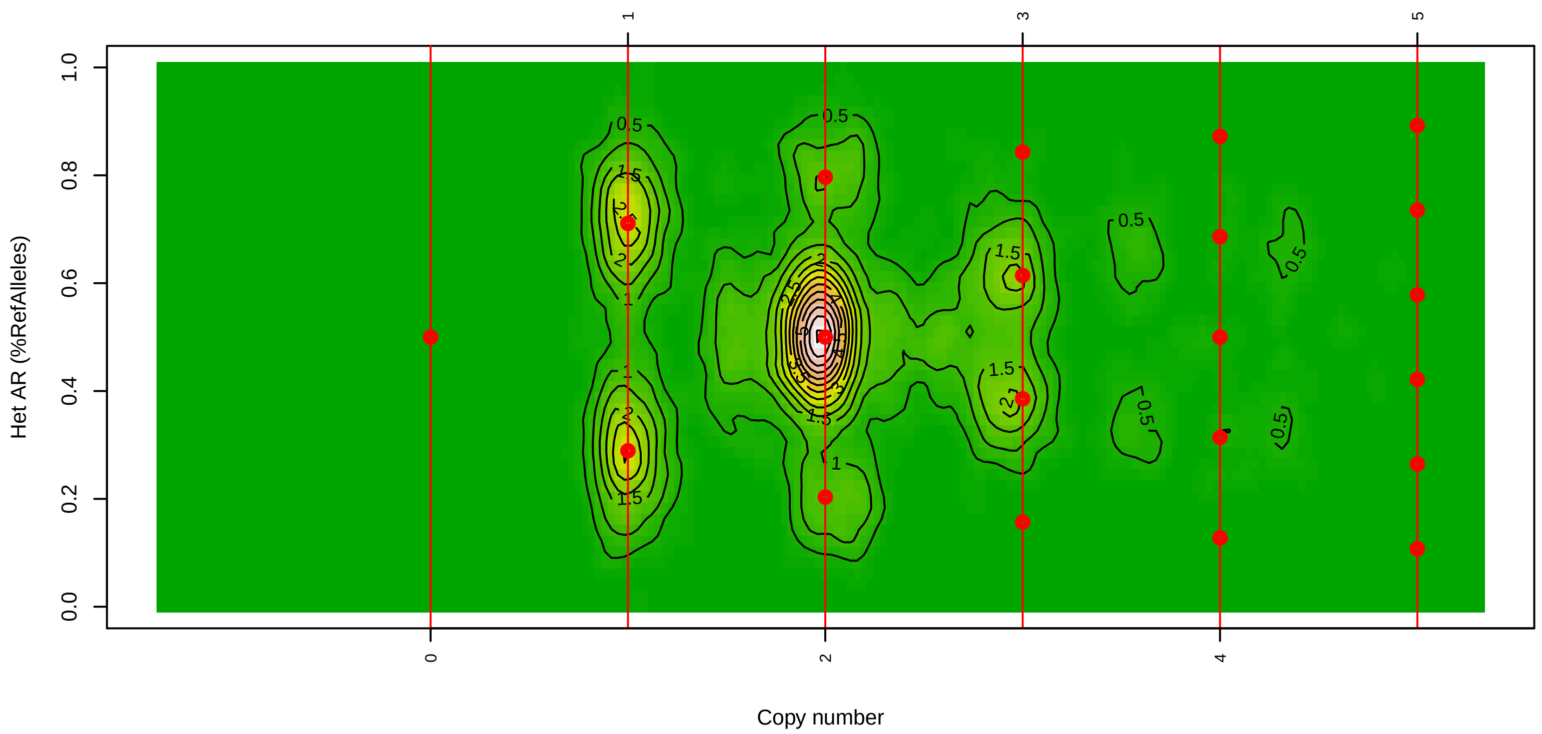
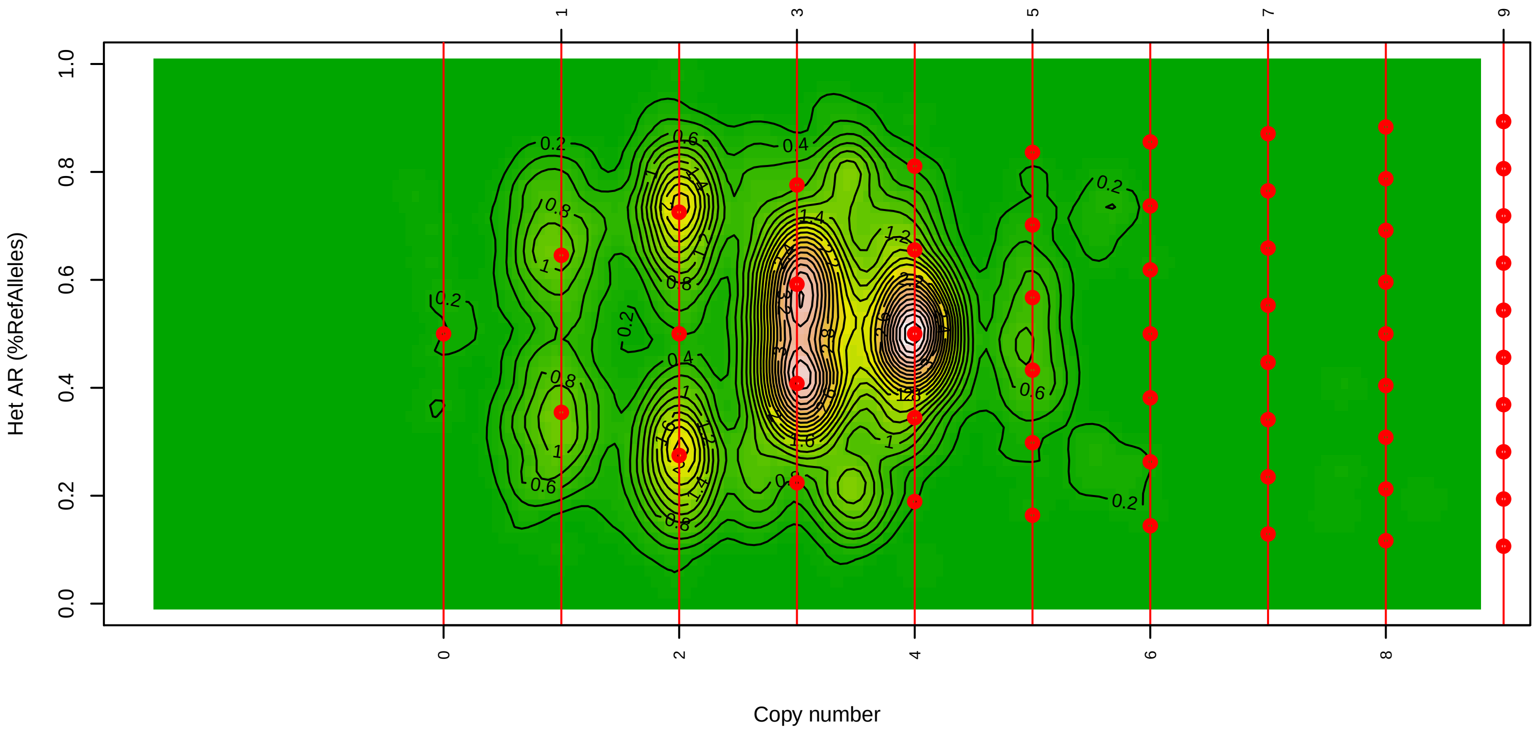
0
2
4
Copy number
PCSI_0044_Pa_P_526


S:0.702, PLOIDY:3.177, %N:0.279, %T1:0.721

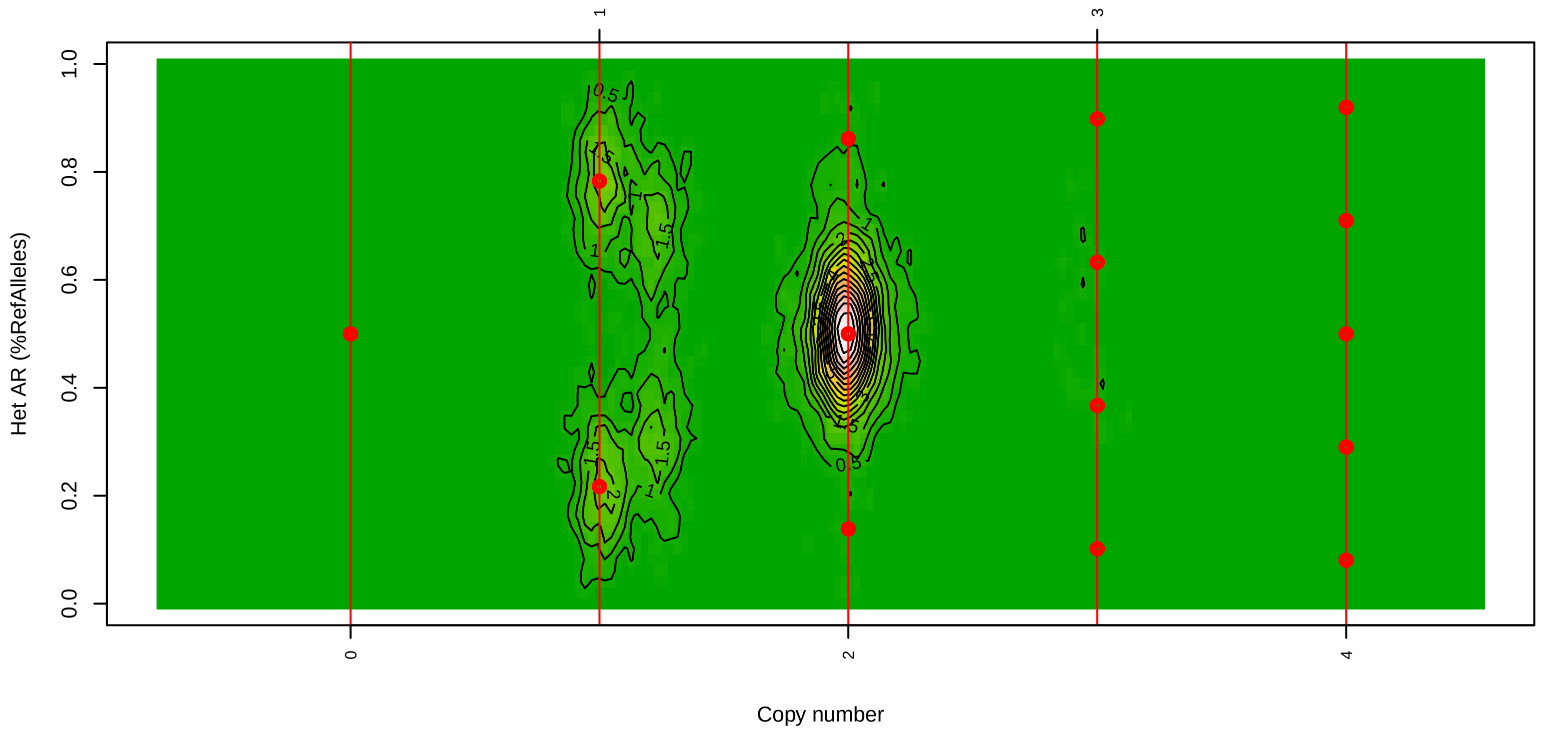
PCSI_0046_Pa_P_526


S:1.007, PLOIDY:1.976, %N:0.407, %T1:0.593

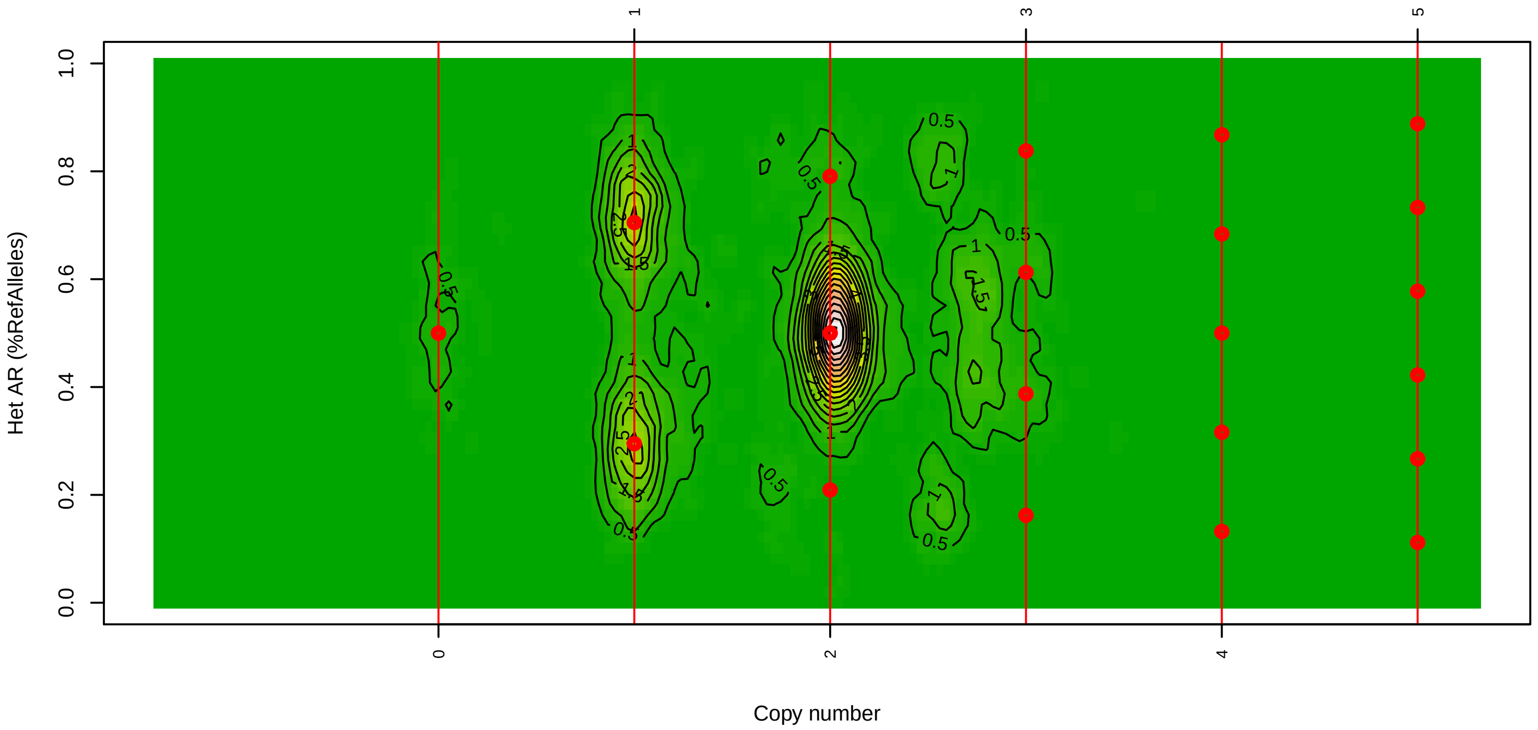
PCSI_0048_Pa_P_526


S:0.791, PLOIDY:3.17, %N:0.549, %T1:0.451

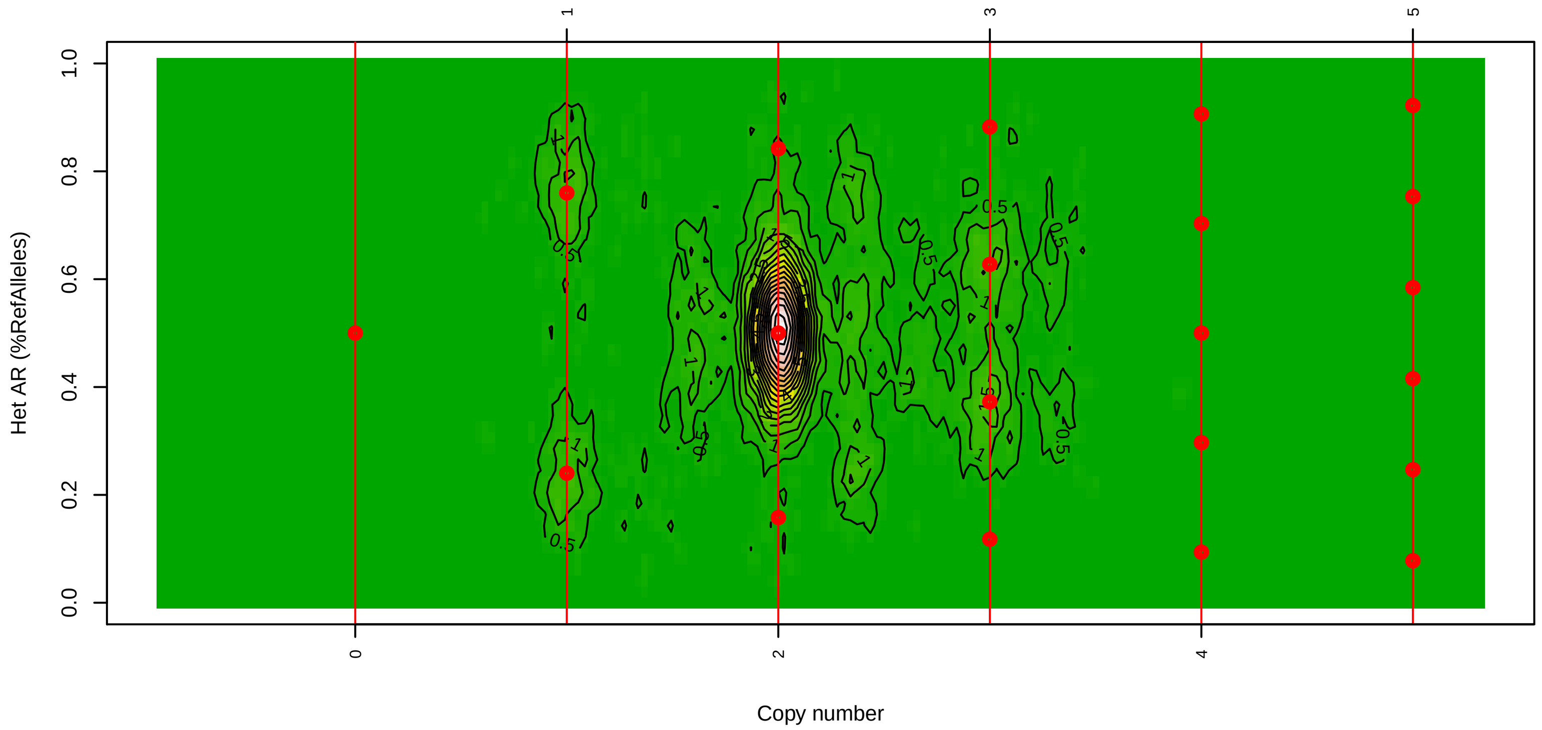
PCSI_0072_Pa_P_526


S:1.042, PLOIDY:1.888, %N:0.277, %T1:0.723

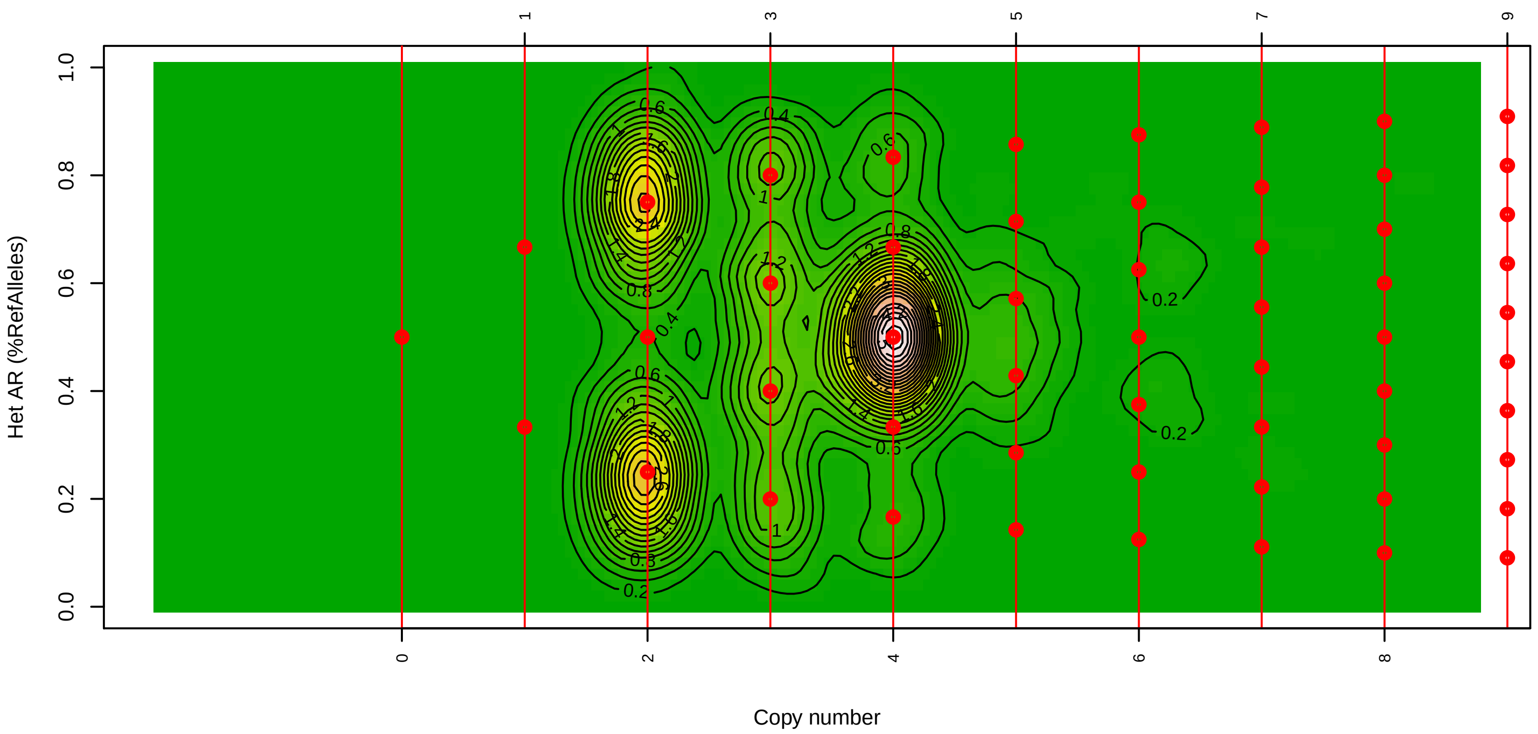
PCSI_0073_Pa_P_526


S:1.02, PLOIDY:1.933, %N:0.418, %T1:0.582

PCSI_0077_Pa_P_526

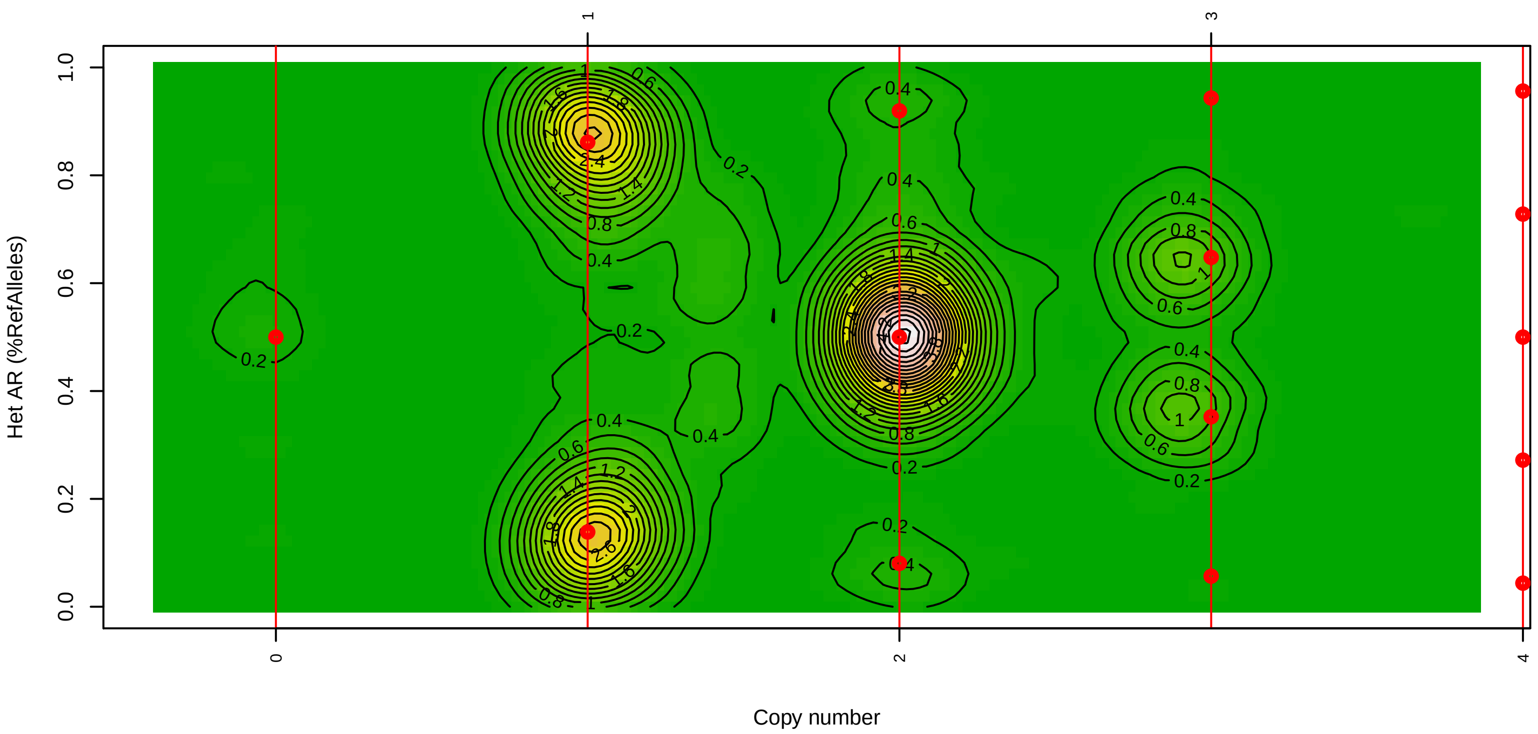

S:0.936, PLOIDY:2.199, %N:0.316, %T1:0.684

PCSI_0078_Pa_P_526



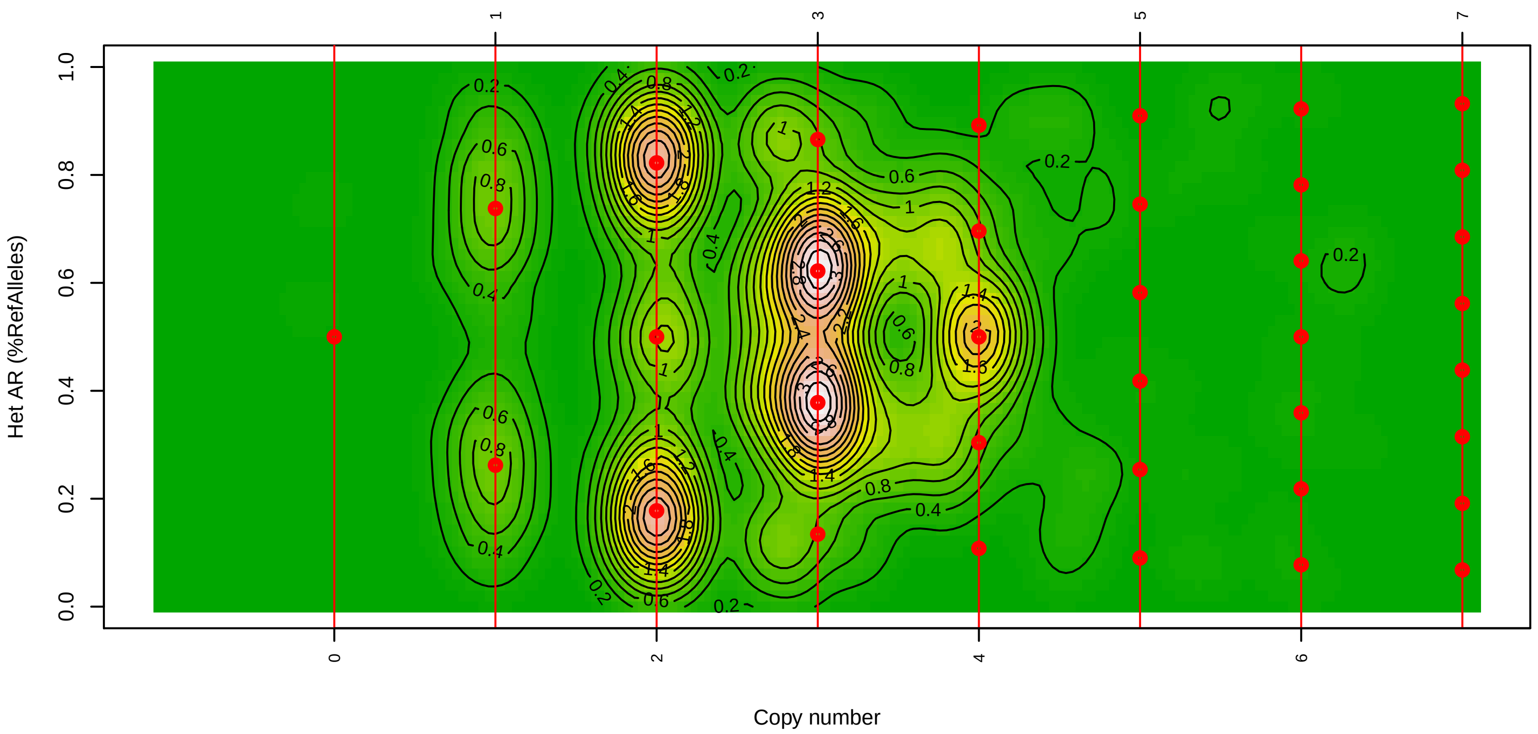
S:0.743, PLOIDY:3.381, %N:0.5, %T1:0.5

PCSI_0080_Pa_P_526



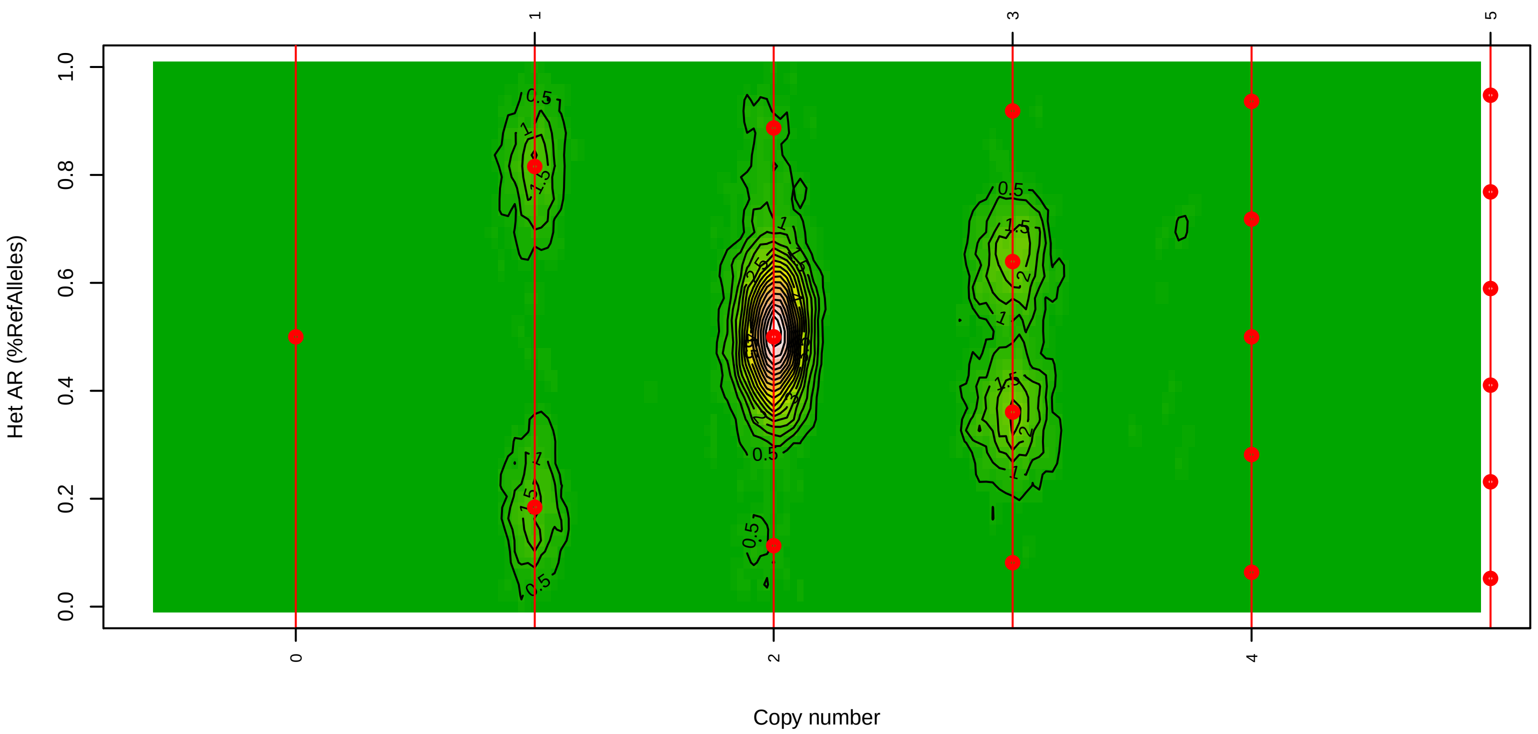
S:1.125, PLOIDY:1.735, %N:0.161, %T1:0.839

PCSI_0081_Pa_P_526



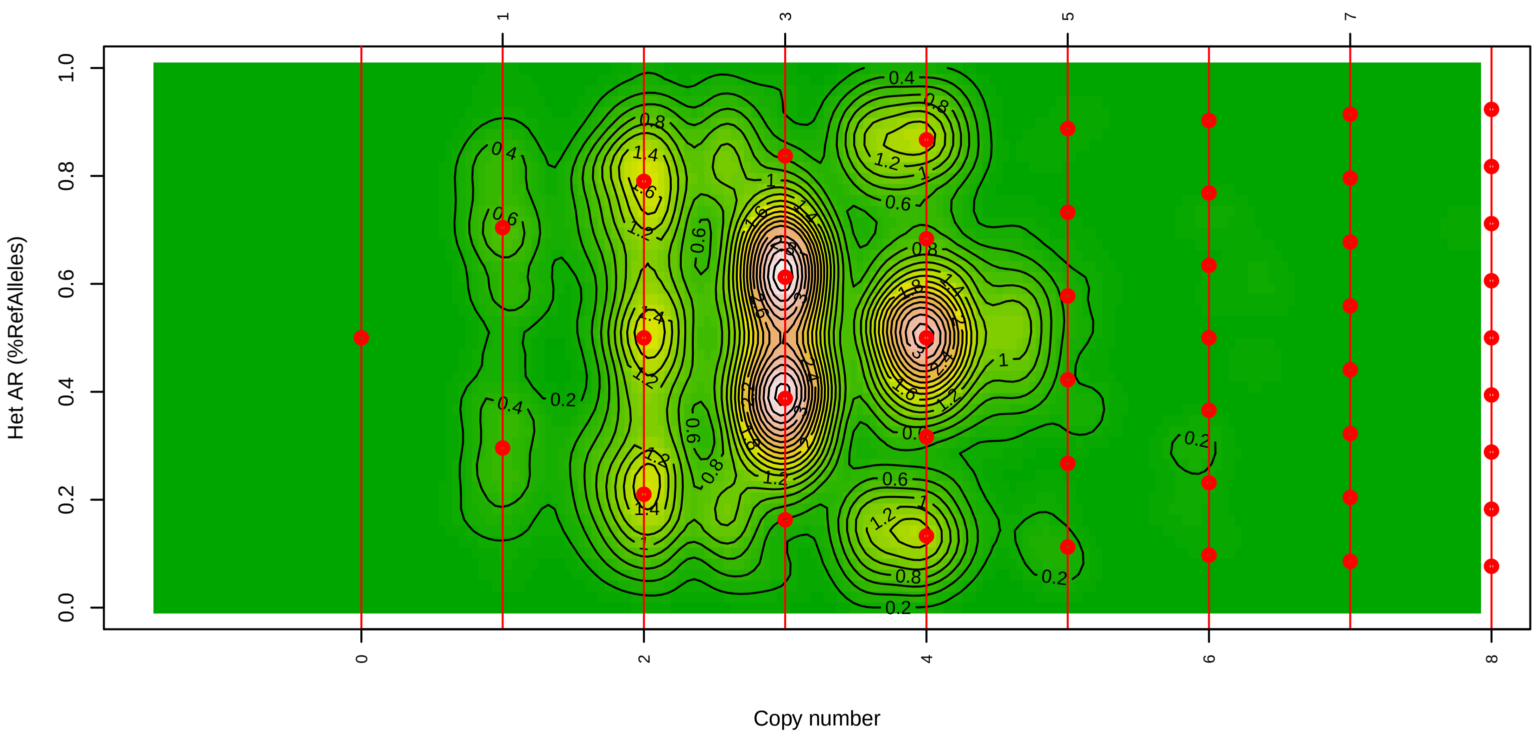
S:0.757, PLOIDY:2.995, %N:0.355, %T1:0.645

PCSI_0082_Pa_P_526



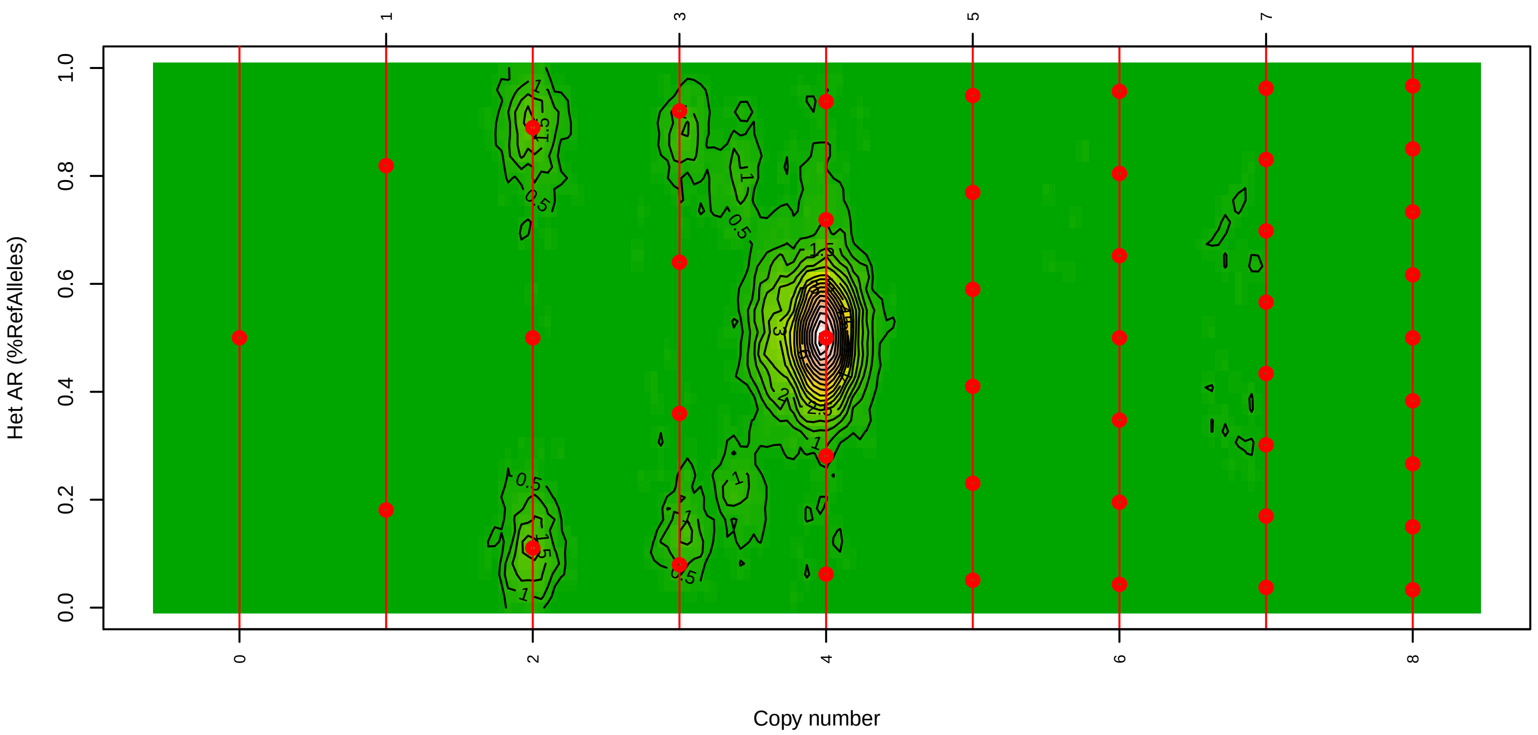
S:0.935, PLOIDY:2.18, %N:0.226, %T1:0.774

PCSI_0084_Pa_P_526



S:0.738, PLOIDY:3.225, %N:0.42, %T1:0.58

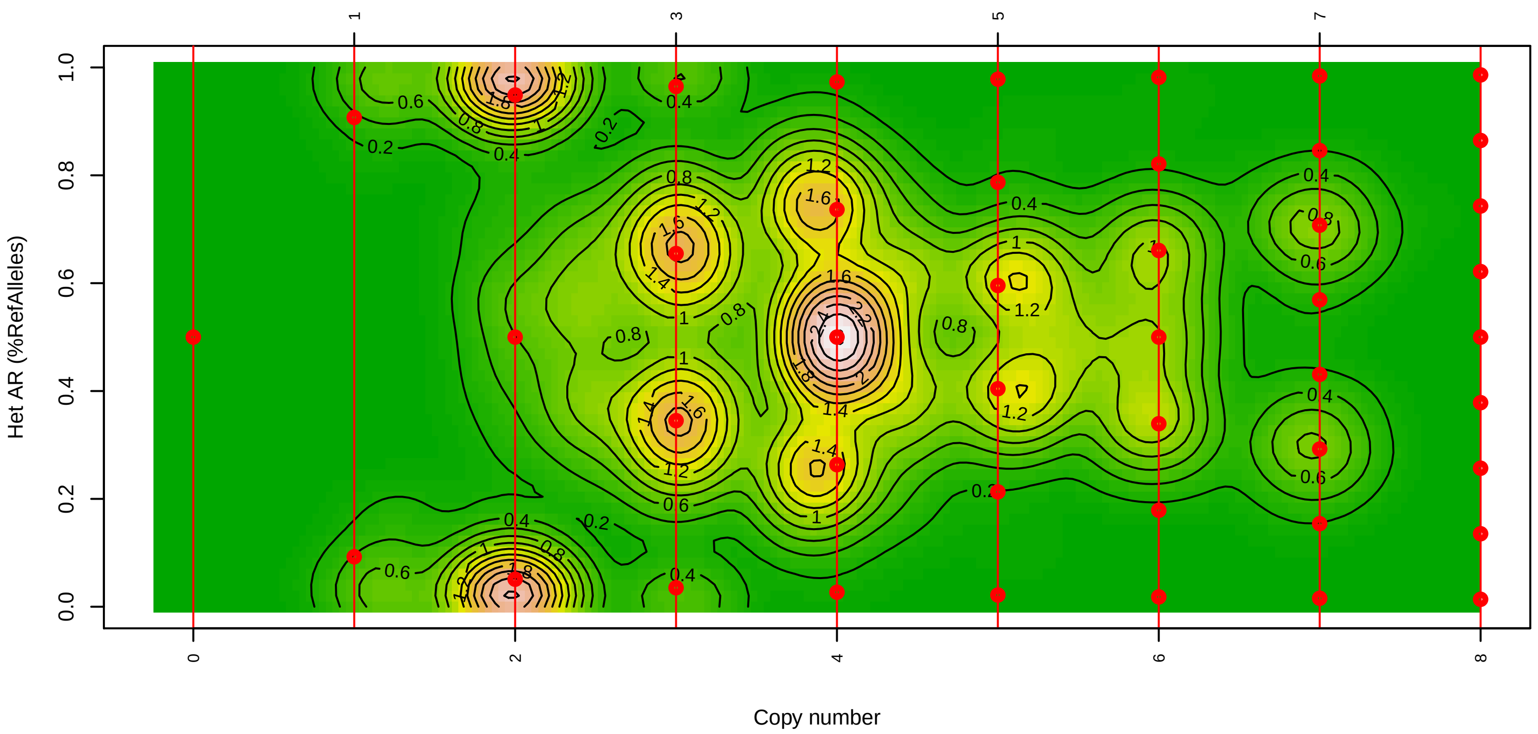
PCSI_0085_Pa_P_526



S:0.57, PLOIDY:3.936, %N:0.221, %T1:0.779

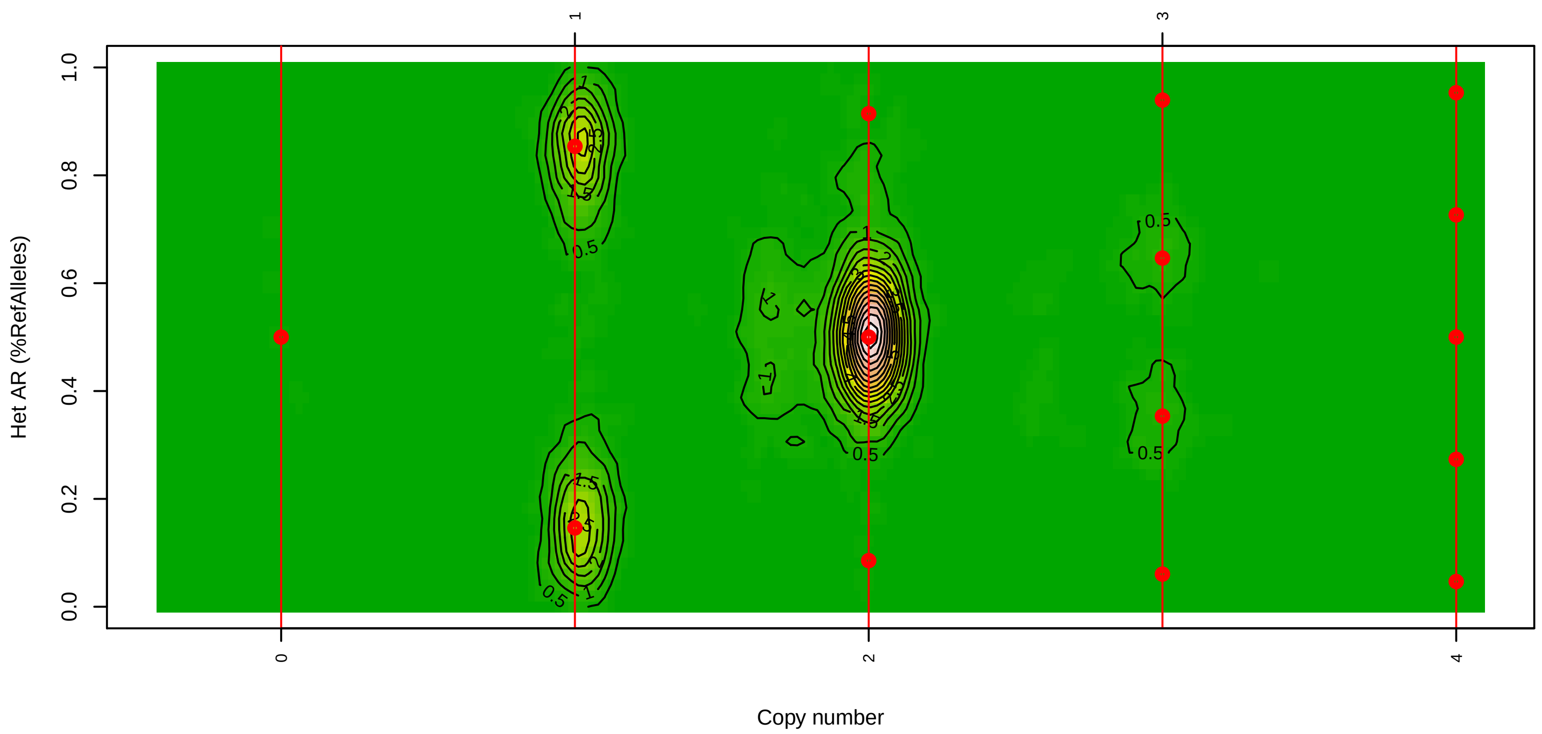
PCSI_0096_Pa_P_526

S:0.543, PLOIDY:3.876, %N:0.102, %T1:0.898



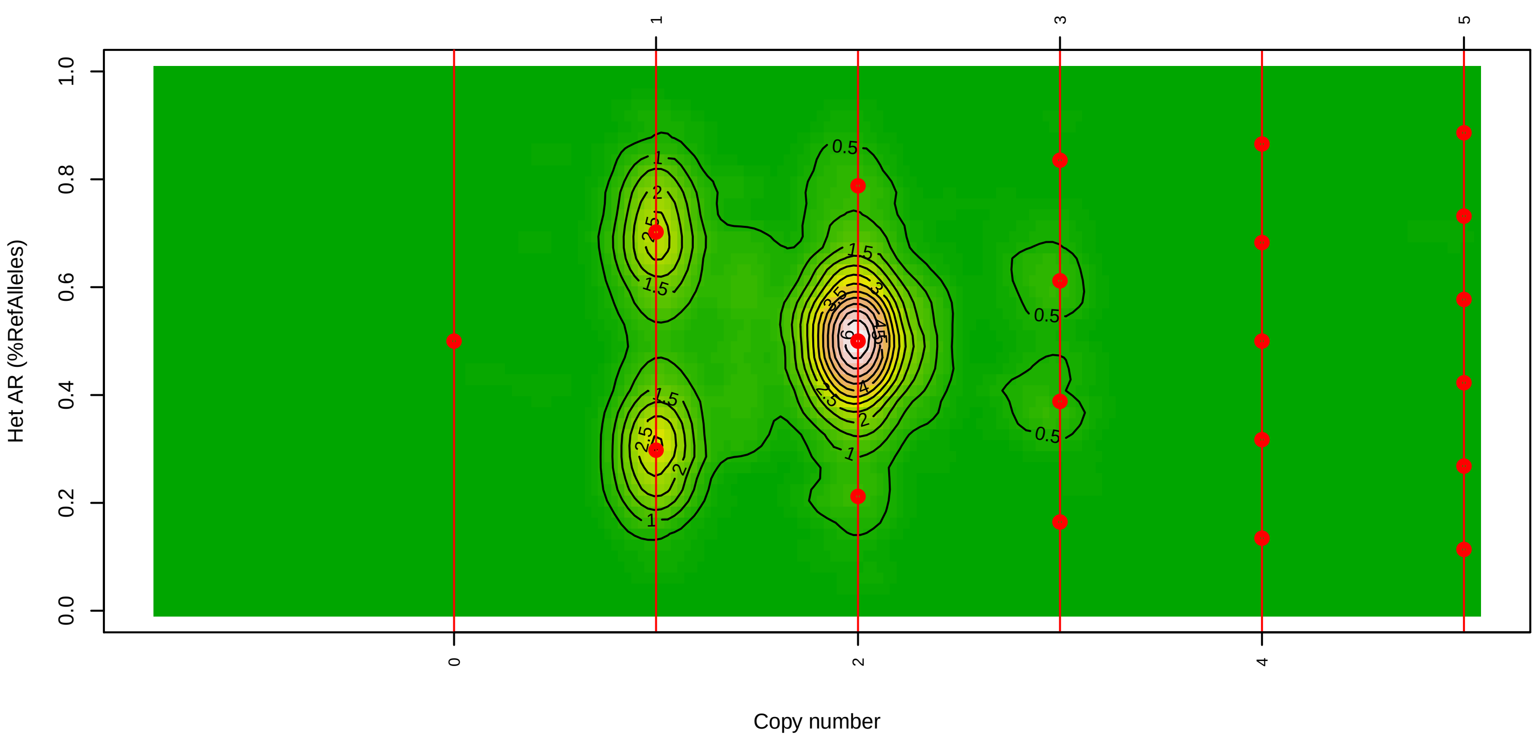
PCSI_0099_Pa_P_526

S:1.073, PLOIDY:1.836, %N:0.171, %T1:0.829



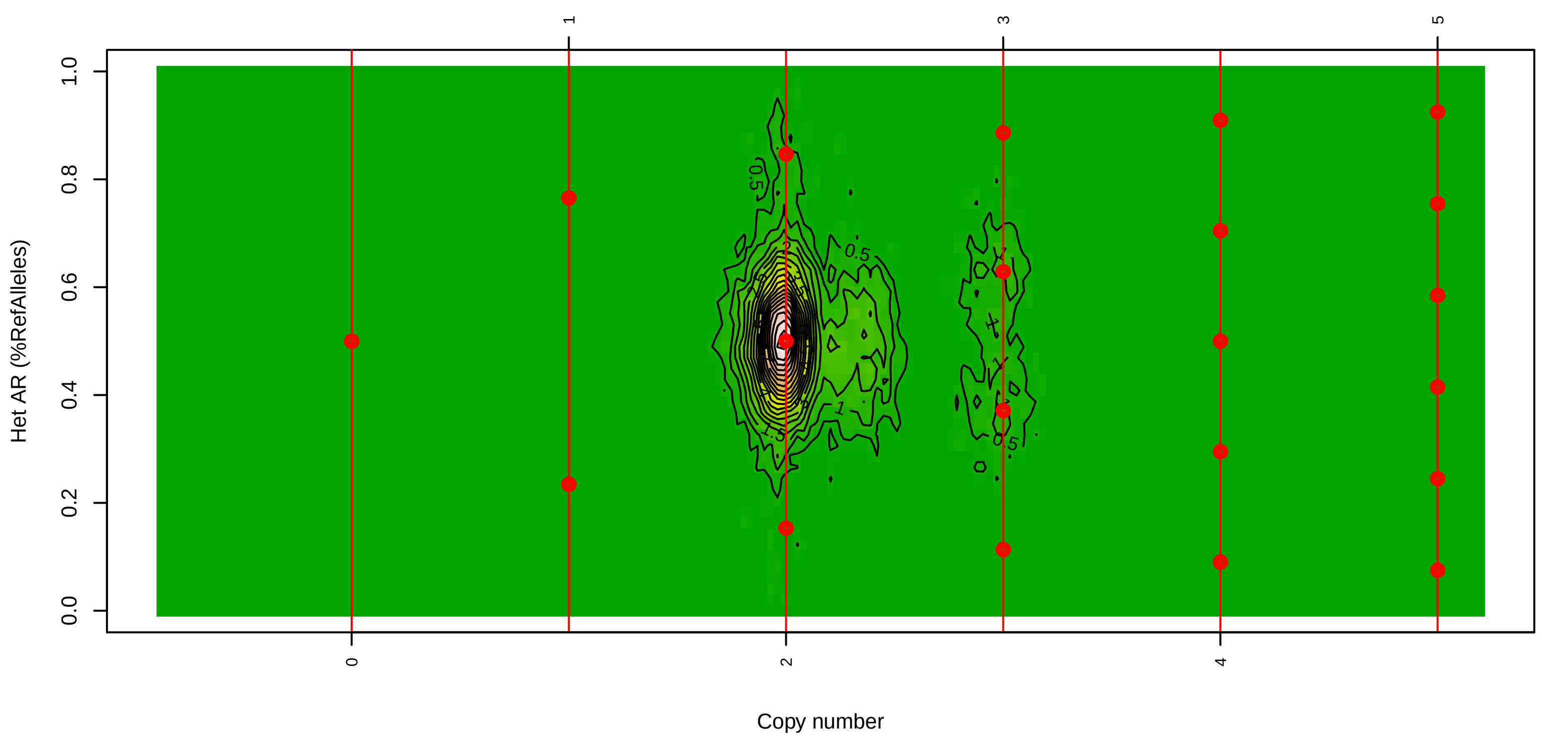
PCSI_0101_Pa_P_526

S:1.062, PLOIDY:1.797, %N:0.424, %T1:0.576



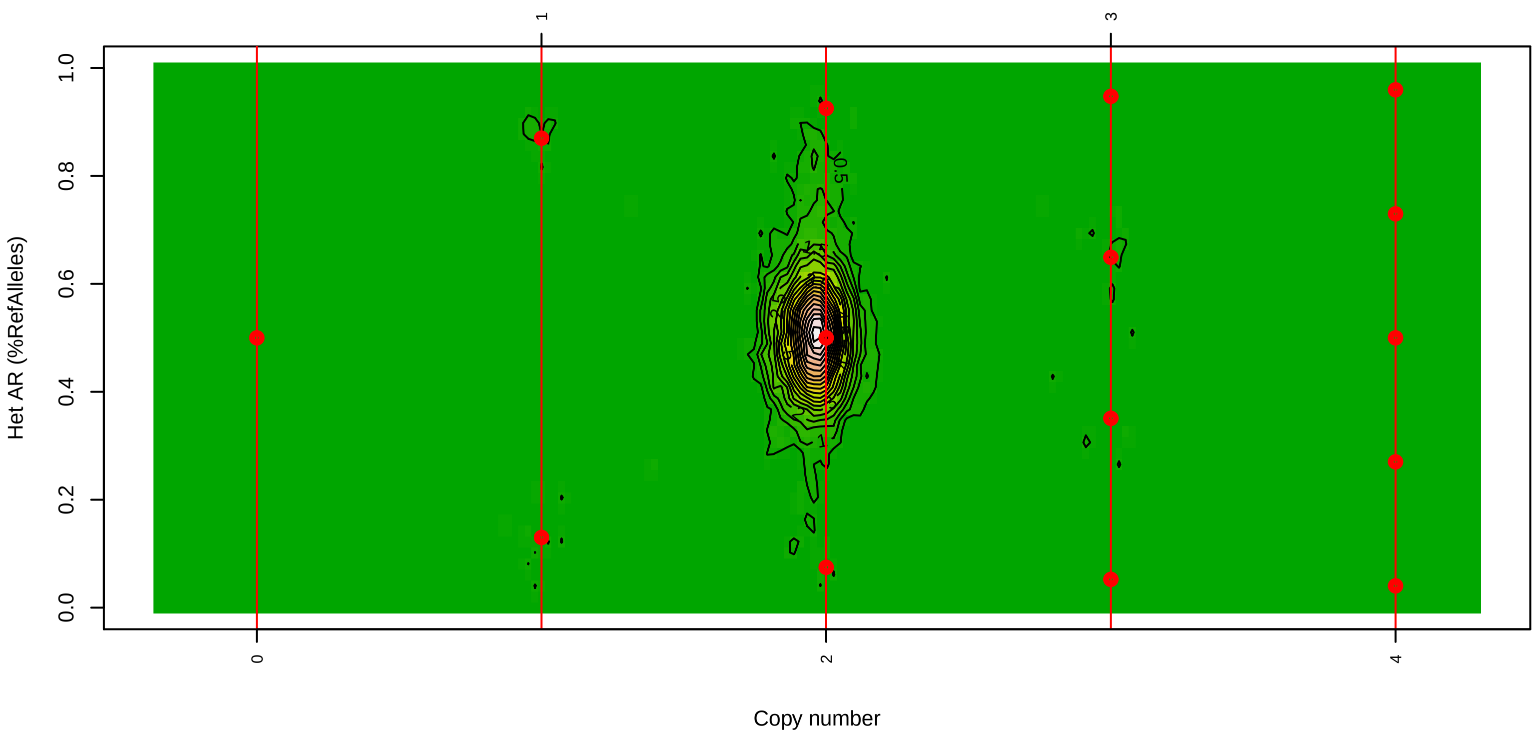
PCSI_0102_Pa_P_526

S:0.948, PLOIDY:2.159, %N:0.306, %T1:0.694



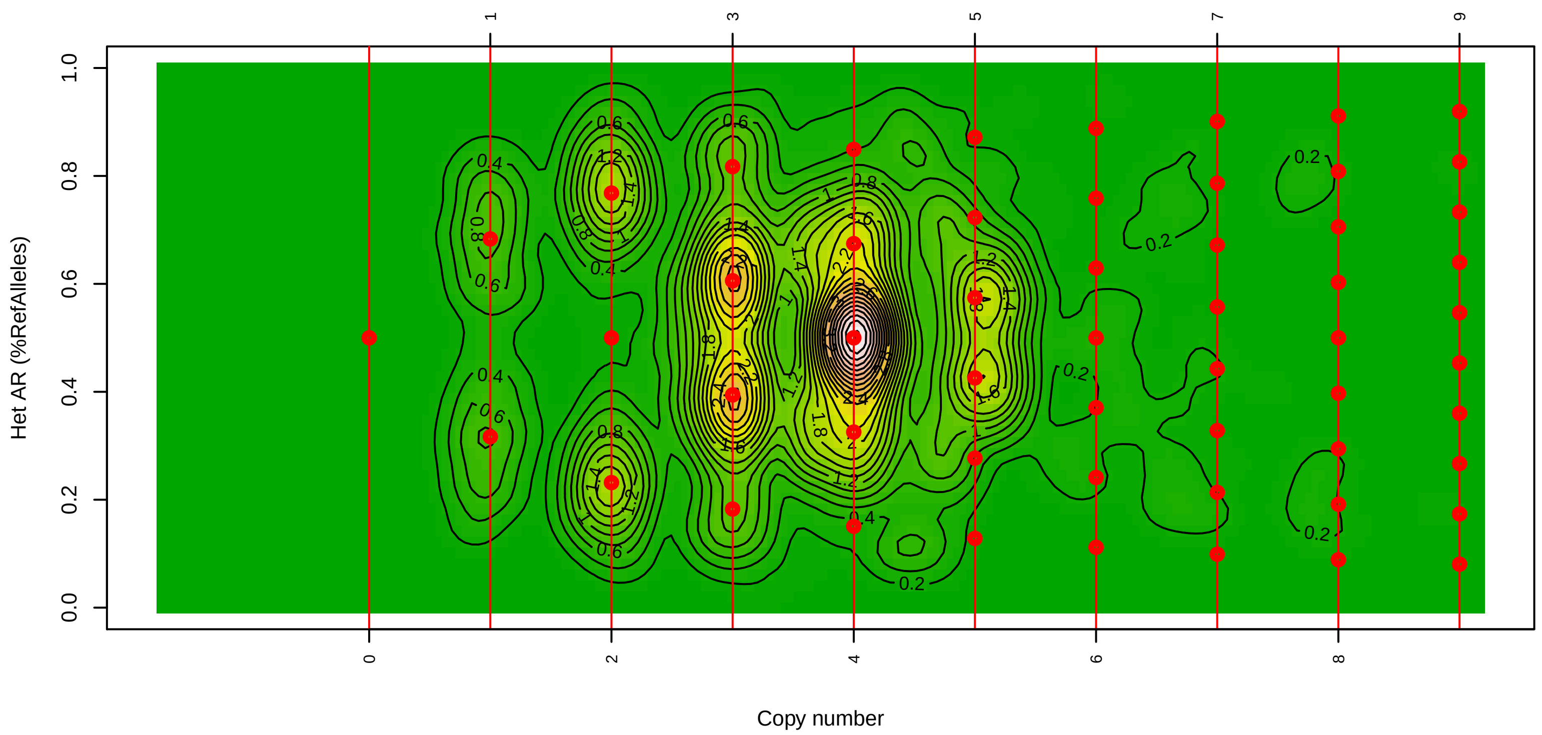
PCSI_0103_Pa_P_526

S:1.014, PLOIDY:1.967, %N:0.15, %T1:0.85



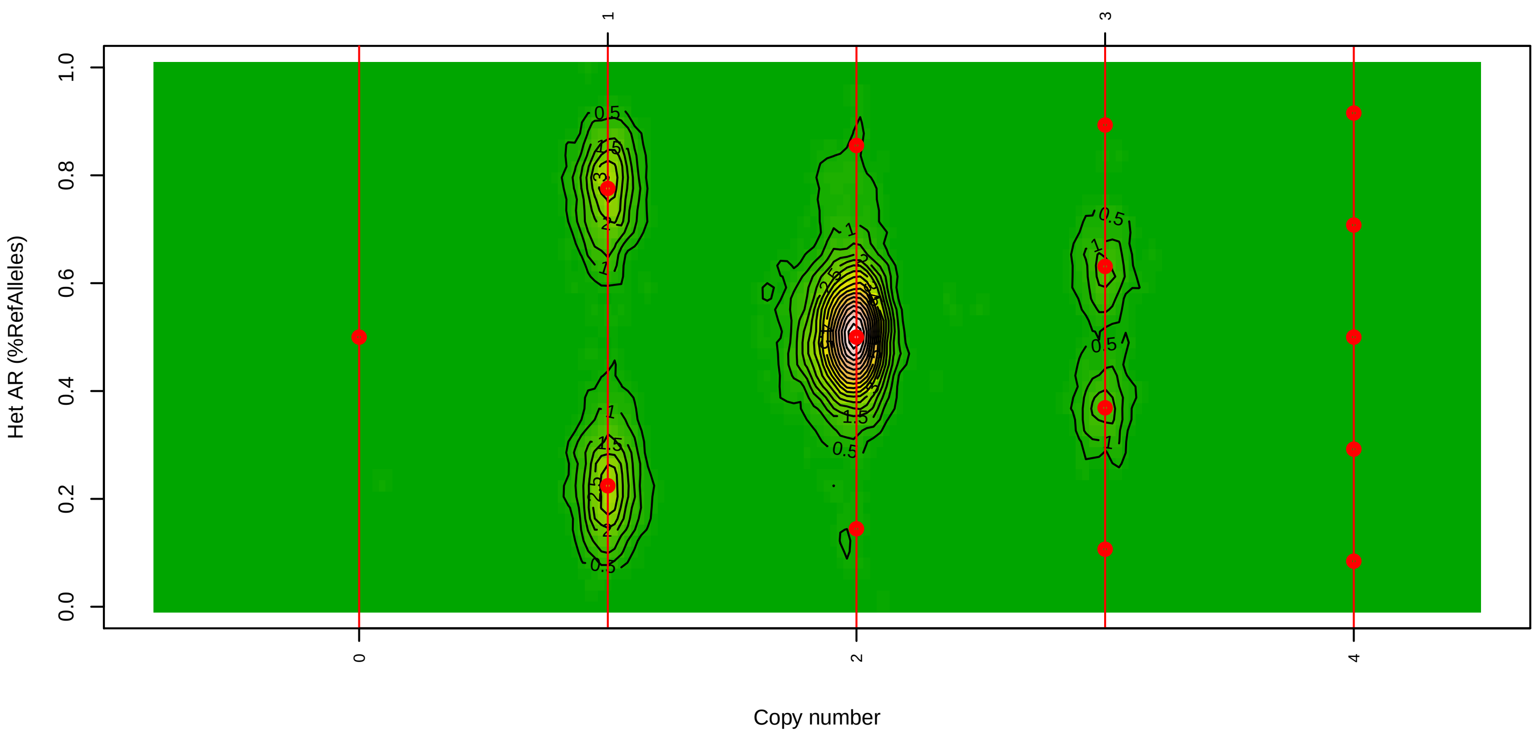
PCSI_0104_Pa_P_526

S:0.683, PLOIDY:3.727, %N:0.464, %T1:0.536



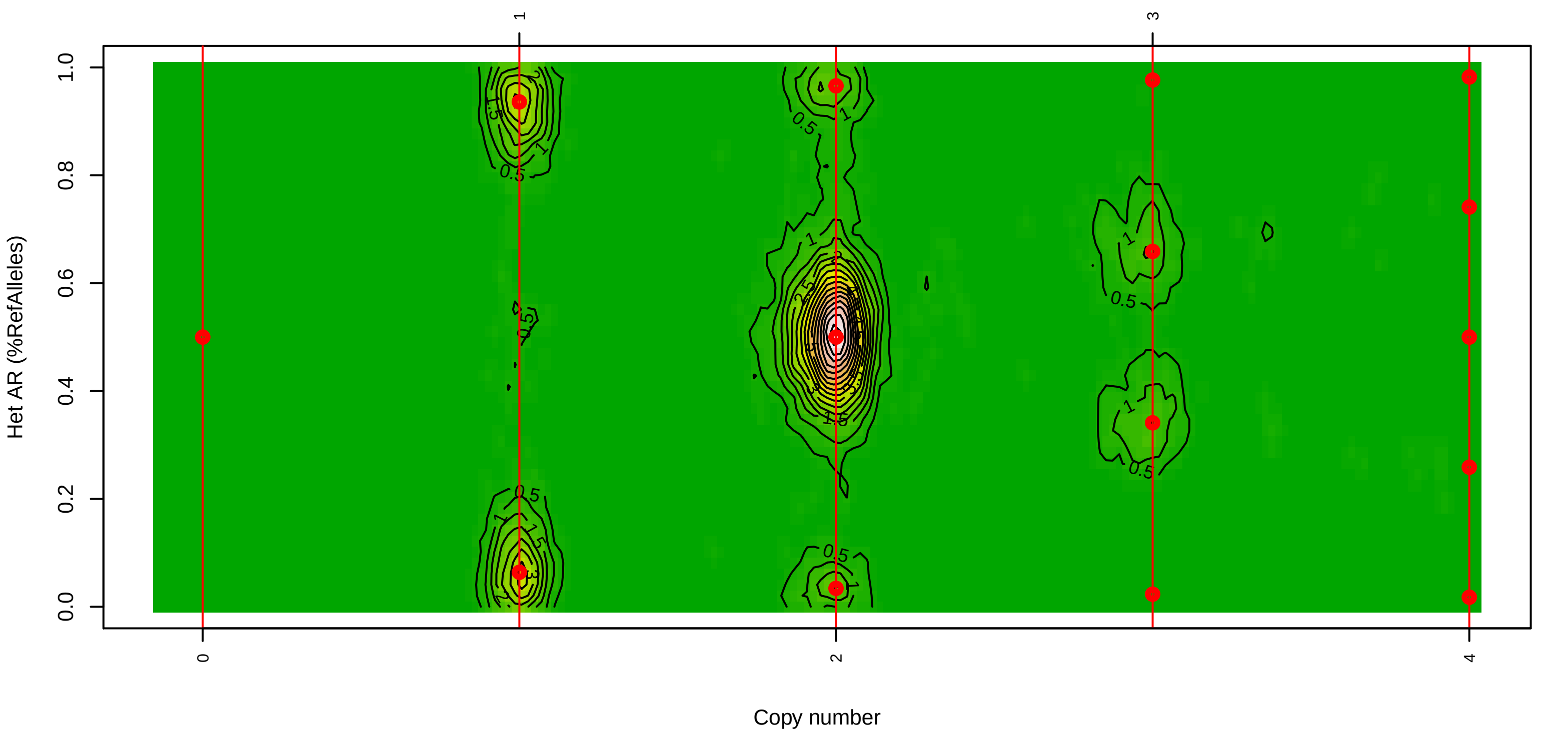
PCSI_0105_Pa_P_526

S:1.06, PLOIDY:1.841, %N:0.289, %T1:0.711



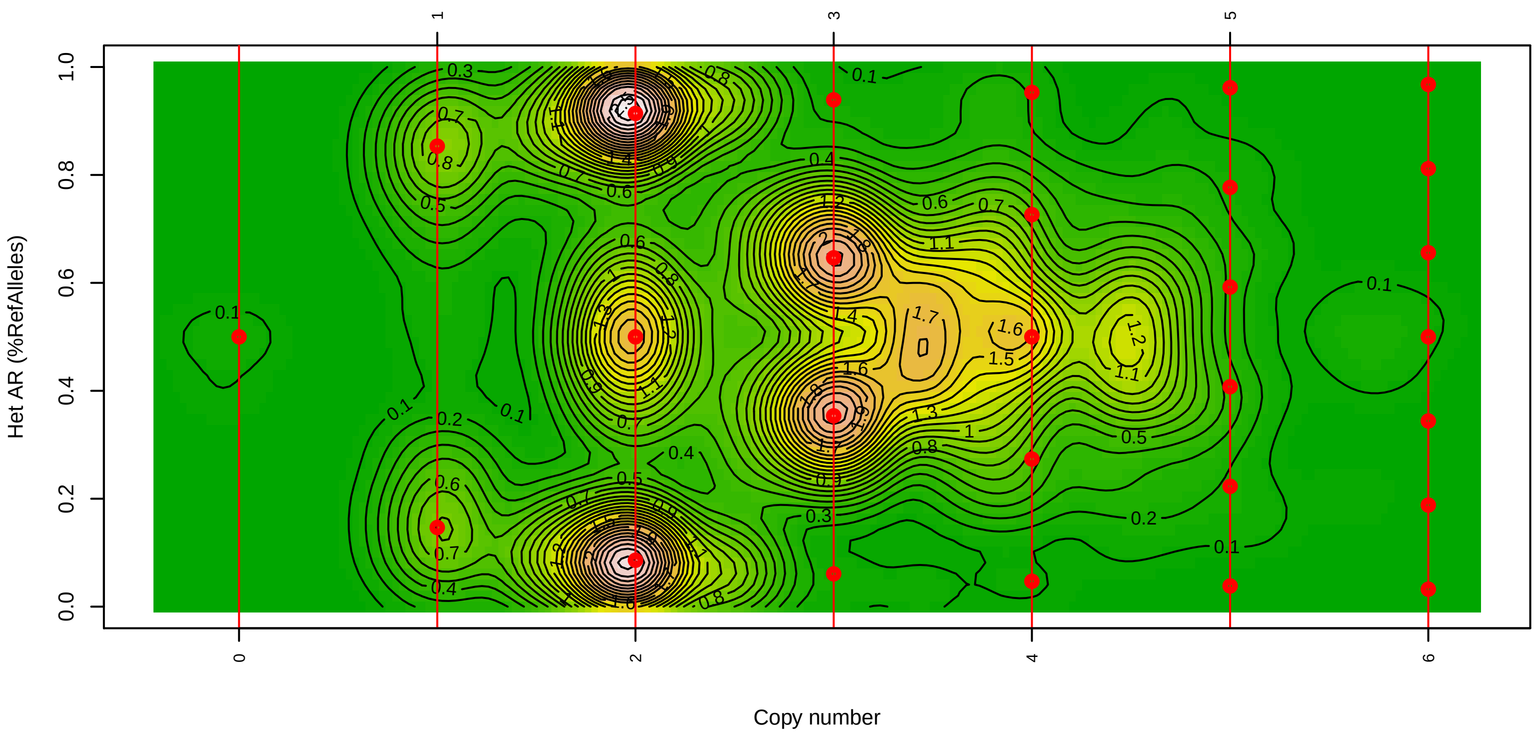
PCSI_0108_Pa_P_526

S:1.029, PLOIDY:1.94, %N:0.068, %T1:0.932



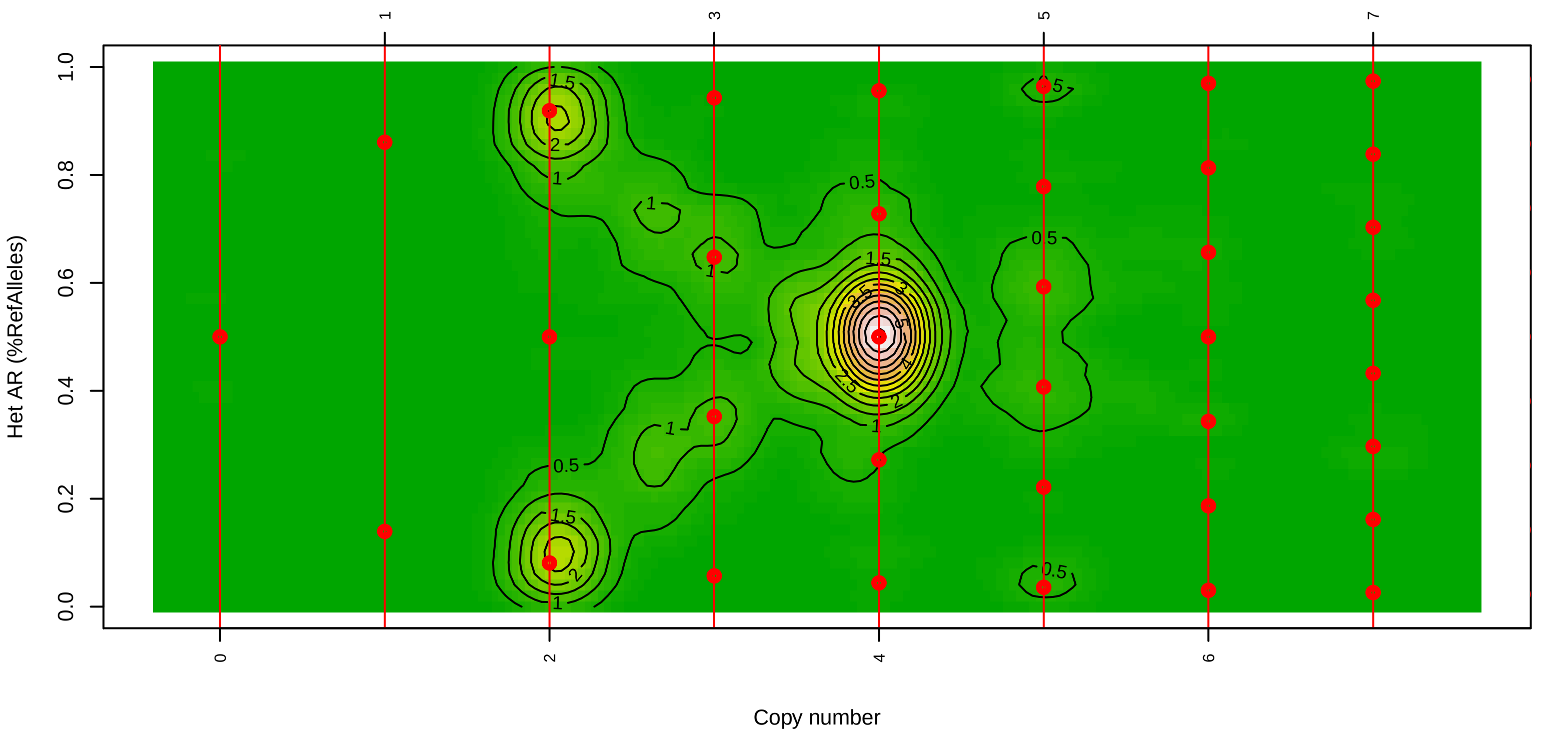
PCSI_0109_Pa_P_526

S:0.725, PLOIDY:2.916, %N:0.172, %T1:0.828



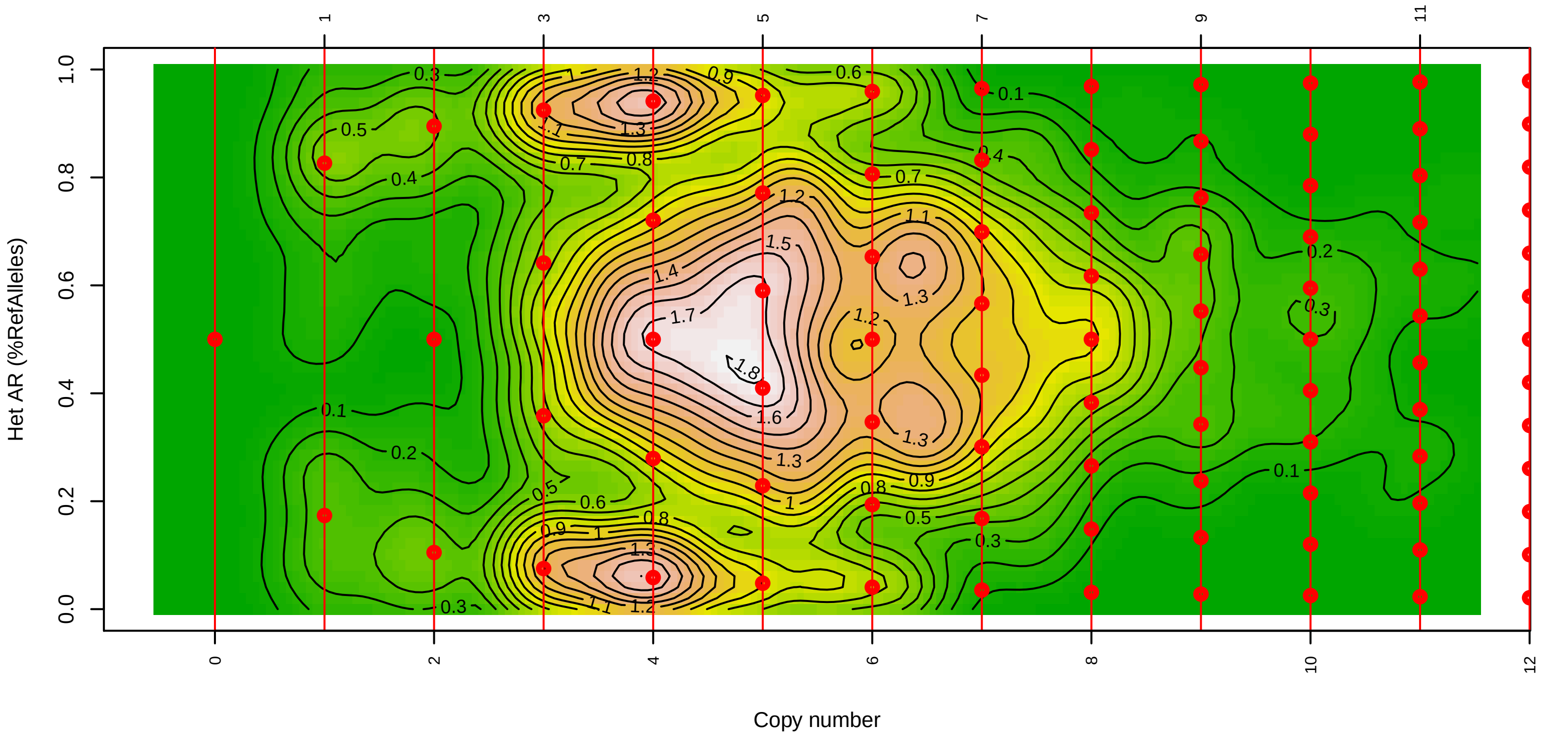
PCSI_0111_Pa_P_526

S:0.595, PLOIDY:3.624, %N:0.162, %T1:0.838



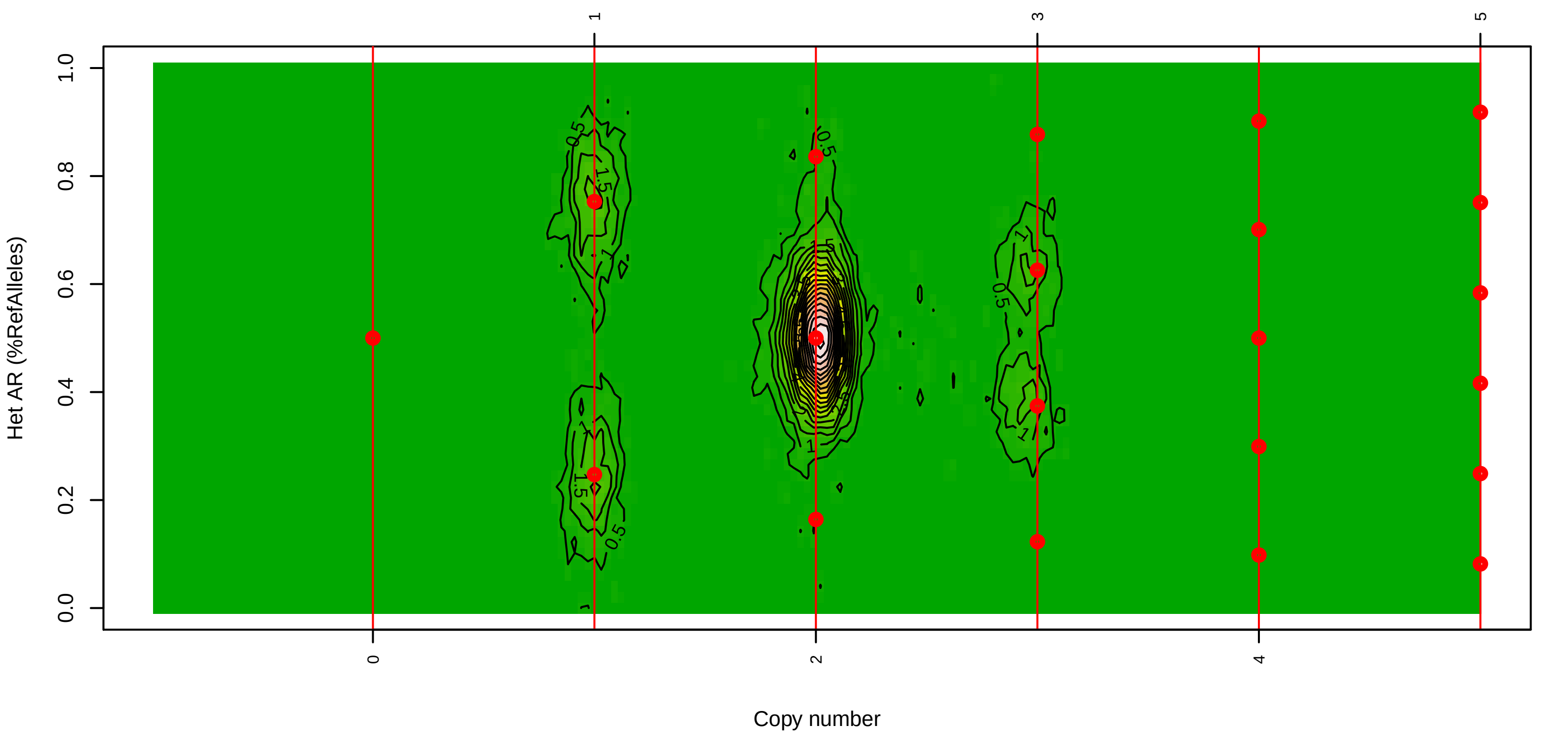
PCSI_0132_Pa_P_526

S:0.42, PLOIDY:5.496, %N:0.21, %T1:0.79

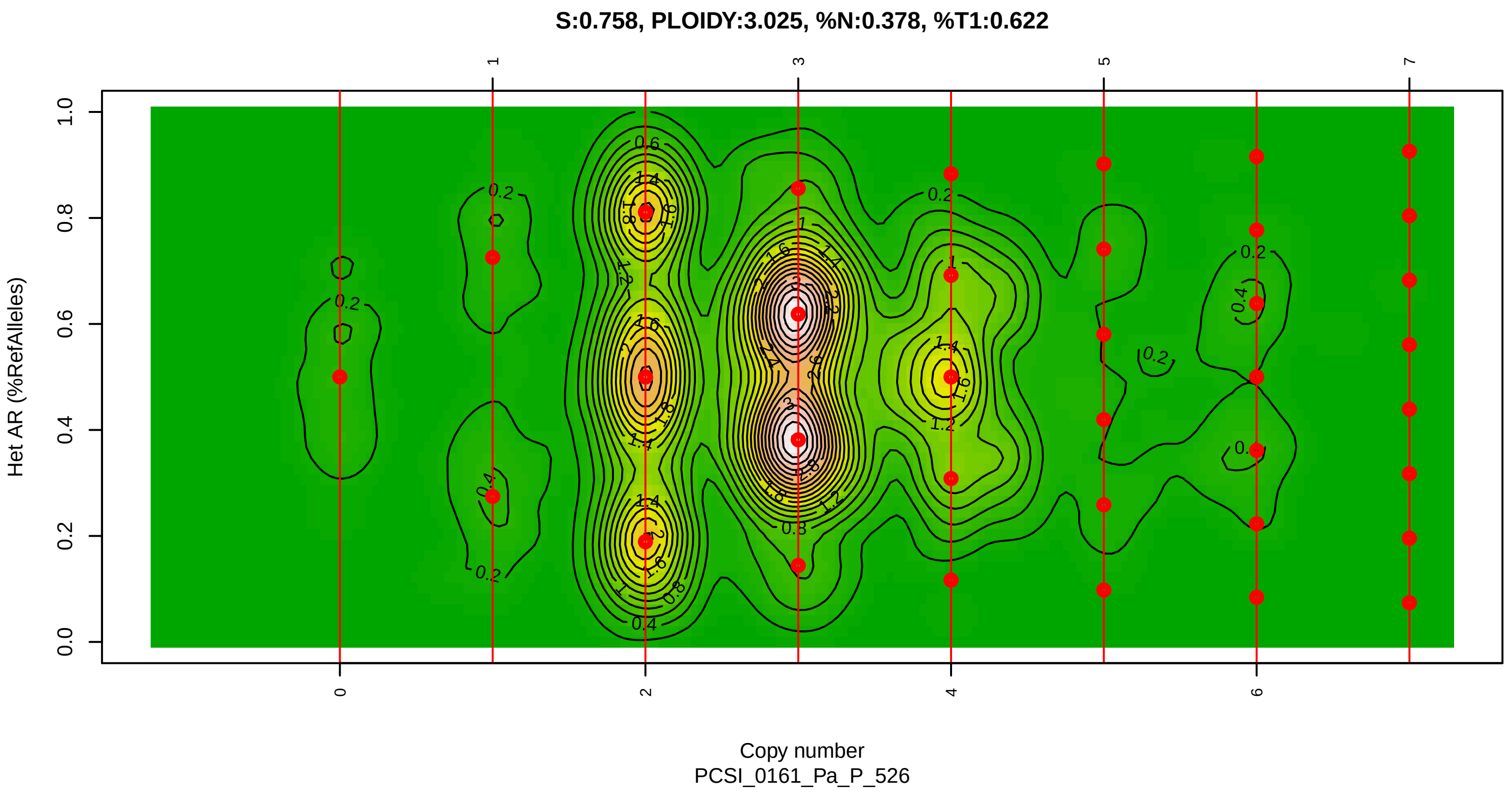


PCSI_0145_Pa_P_526

S:0.998, PLOIDY:2.005, %N:0.328, %T1:0.672



PCSI_0146_Pa_P_526


S:0.758, PLOIDY:3.025, %N:0.378, %T1:0.622
Het AR (%RefAlleles)
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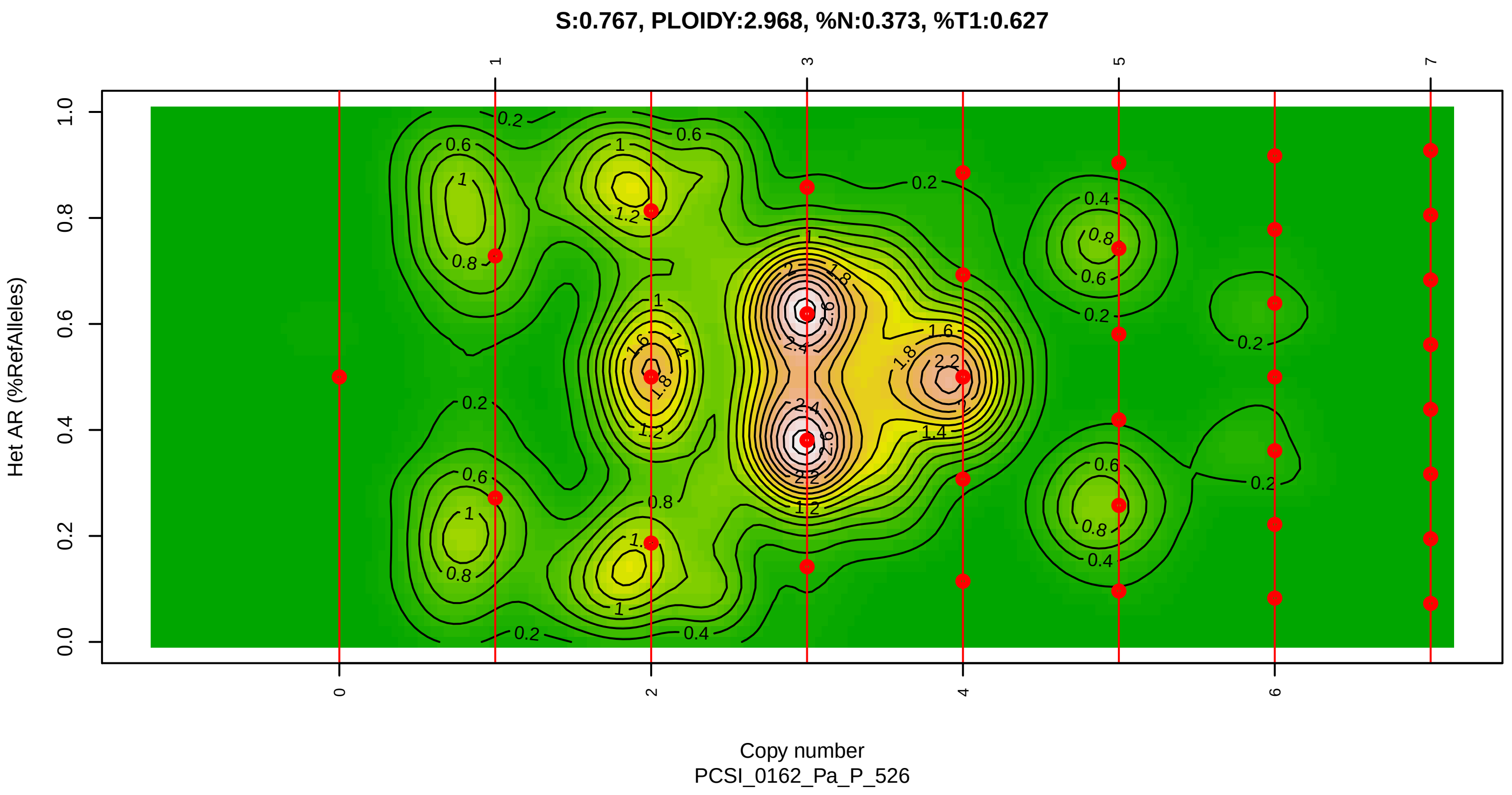
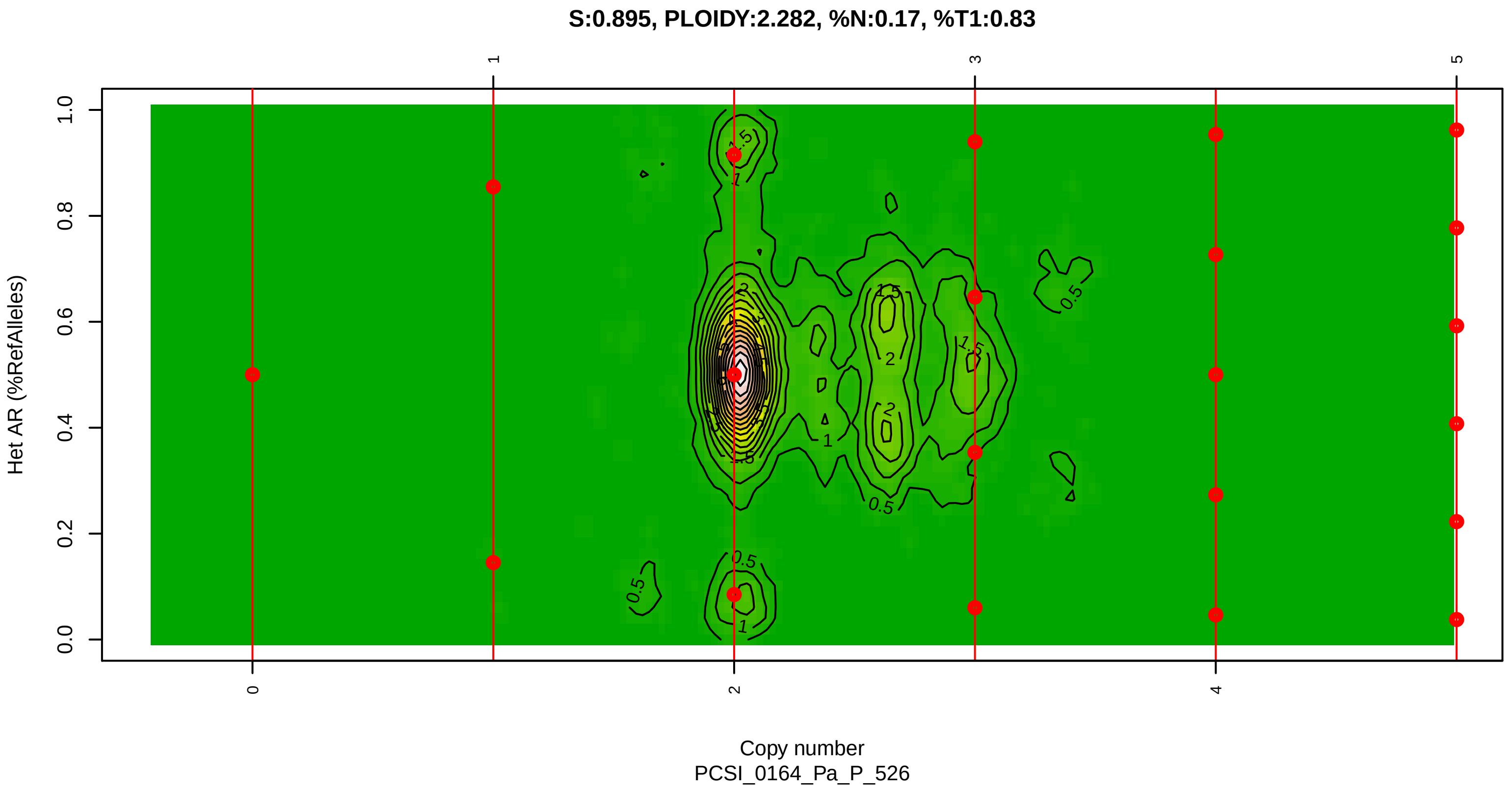
0.6
0.8
1.0
0
1
2
3
4
5
6
7
Copy number
PCSI_0161_Pa_P_526


S:0.767, PLOIDY:2.968, %N:0.373, %T1:0.627
Het AR (%RefAlleles)
0.0
0.2
0.4
0.6
0.8
1.0
0
1
2
3
4
5
6
7
Copy number
PCSI_0162_Pa_P_526


S:0.895, PLOIDY:2.282, %N:0.17, %T1:0.83
Het AR (%RefAlleles)
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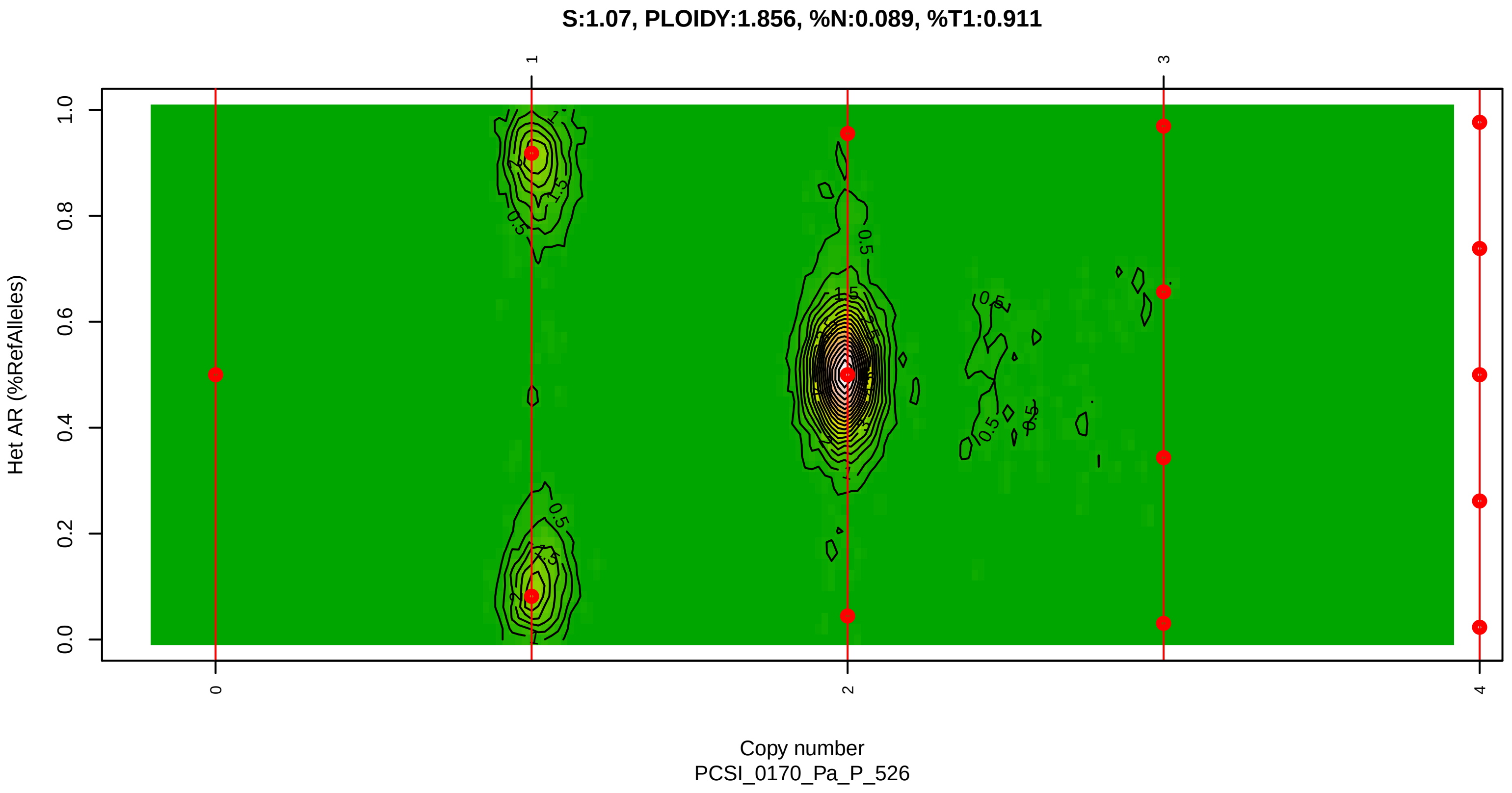
0.4
0.6
0.8
1.0
0
1
2
3
4
5
Copy number
PCSI_0164_Pa_P_526


S:1.07, PLOIDY:1.856, %N:0.089, %T1:0.911
Het AR (%RefAlleles)
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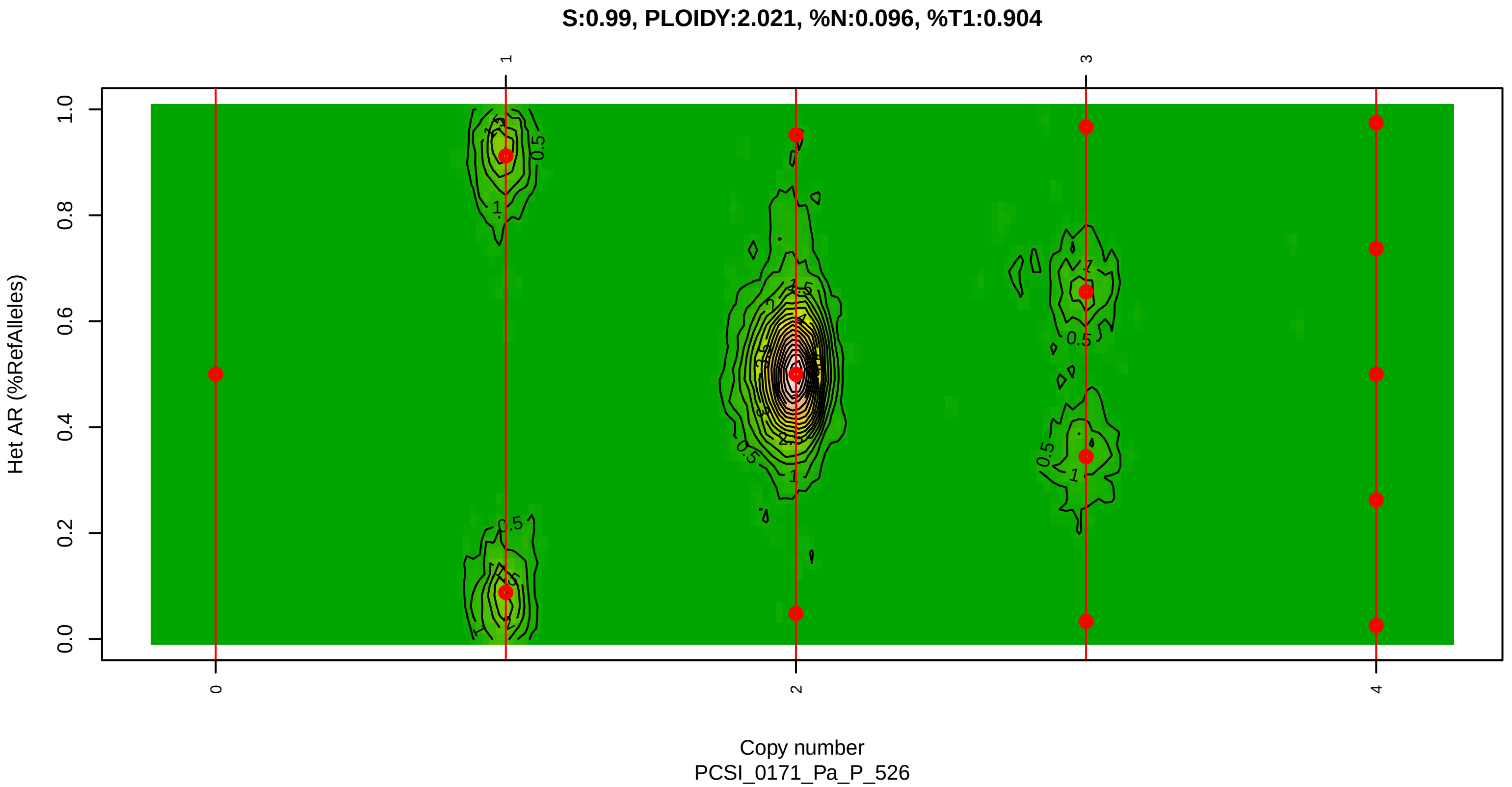
0.2
0.4
0.6
0.8
1.0
0
1
2
3
4
Copy number
PCSI_0170_Pa_P_526


S:0.99, PLOIDY:2.021, %N:0.096, %T1:0.904
Het AR (%RefAlleles)
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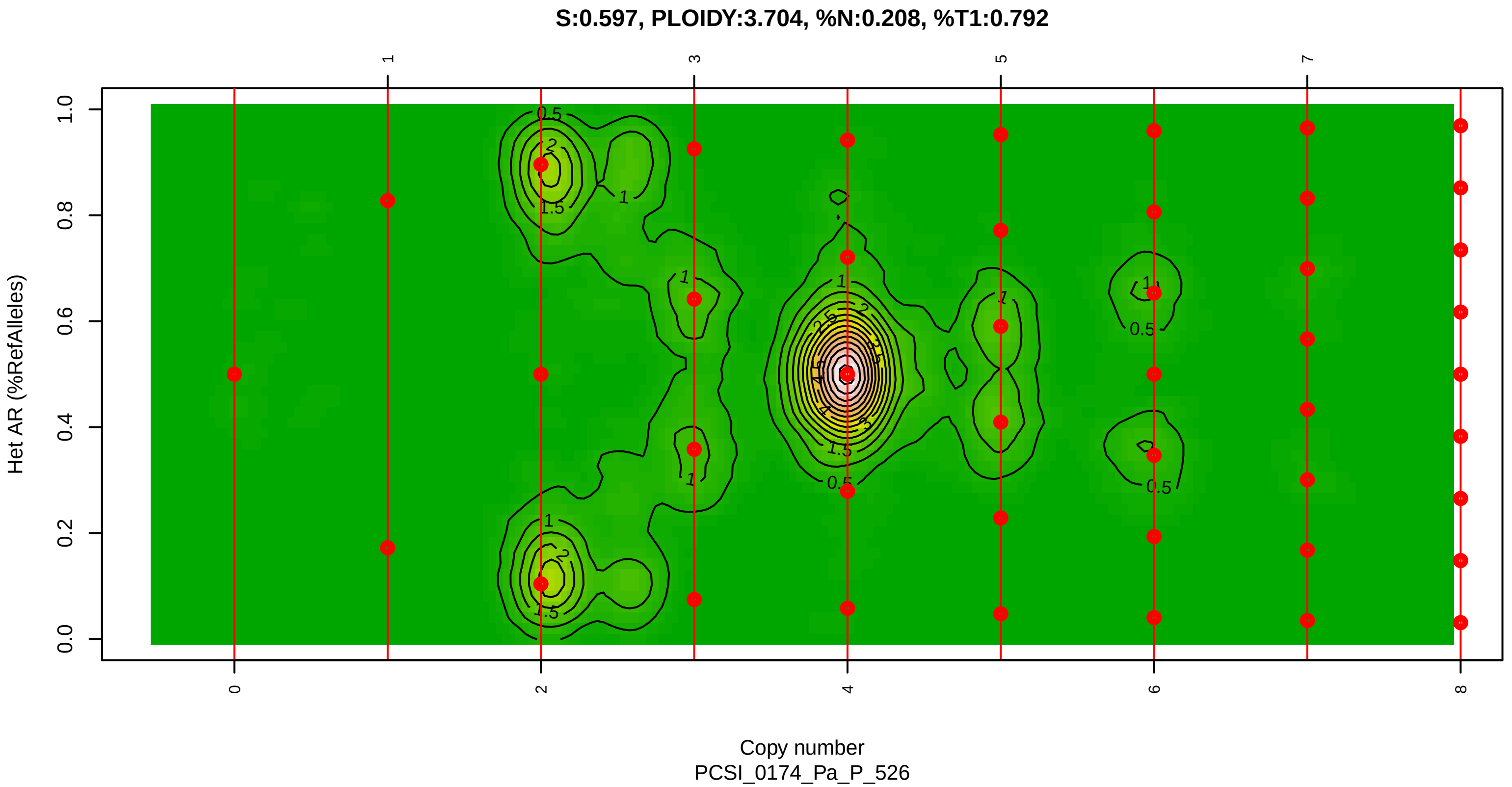
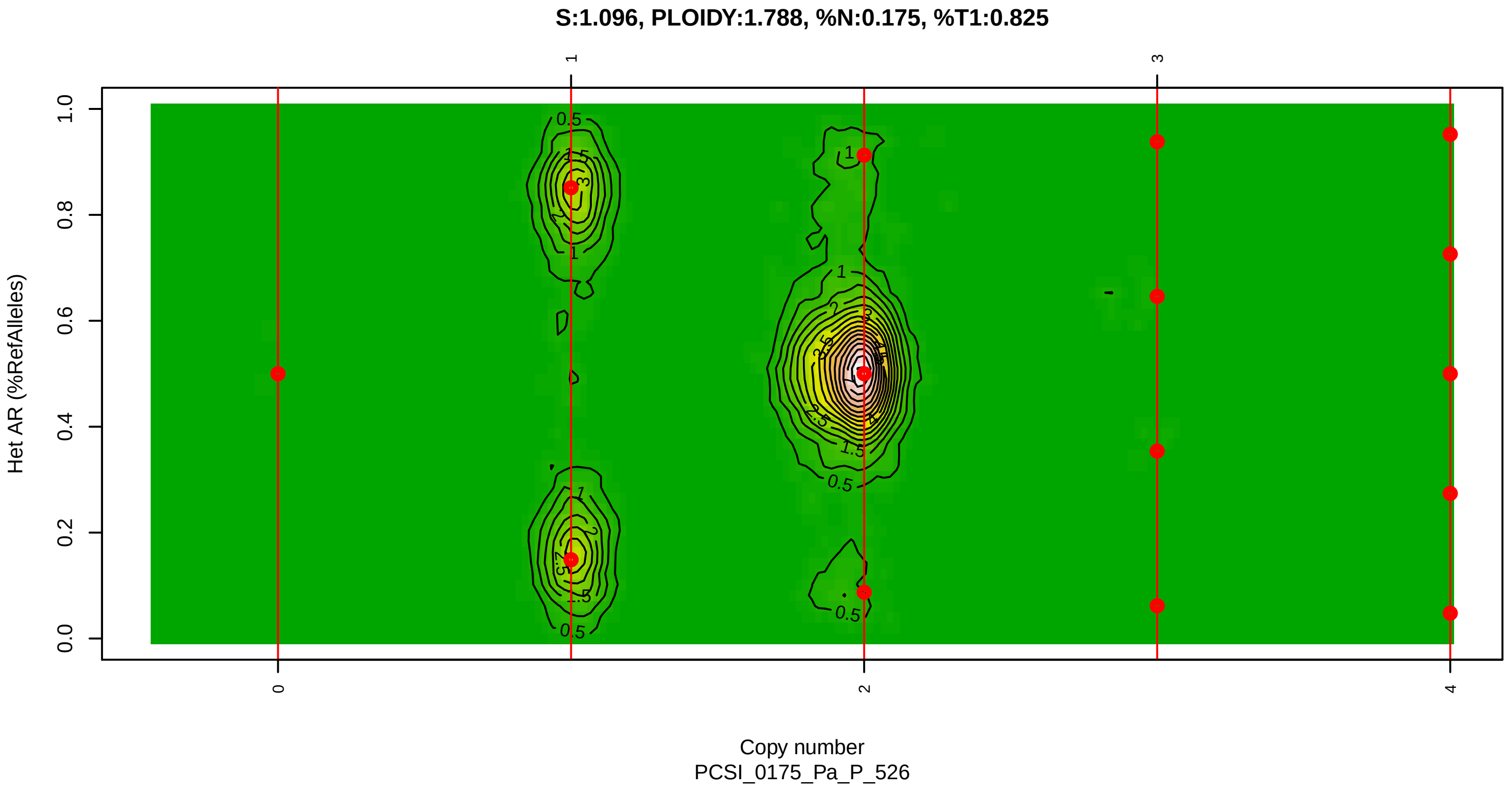
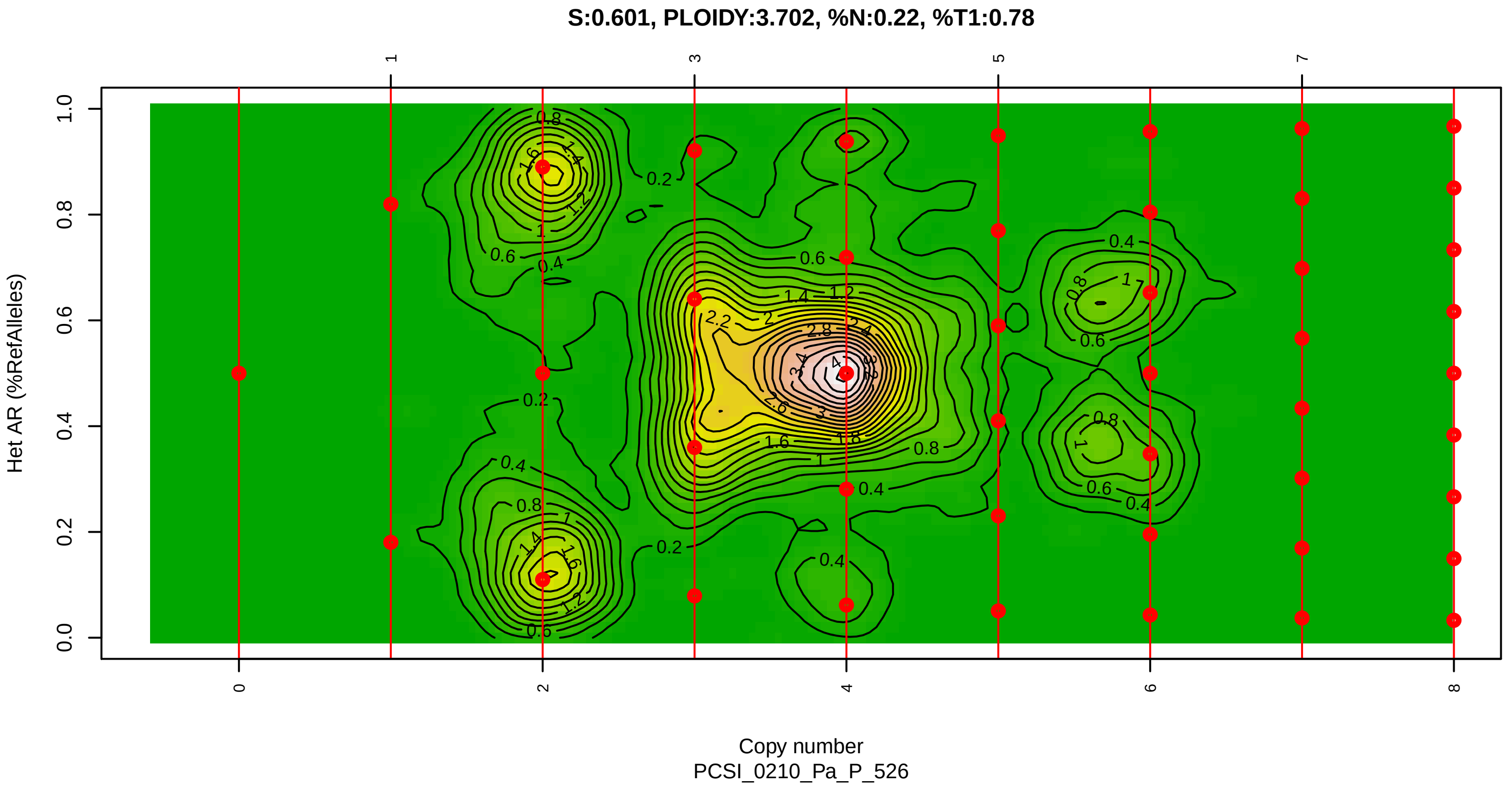
0.2
0.4
0.6
0.8
1.0
0
1
2
3
4
Copy number
PCSI_0171_Pa_P_526

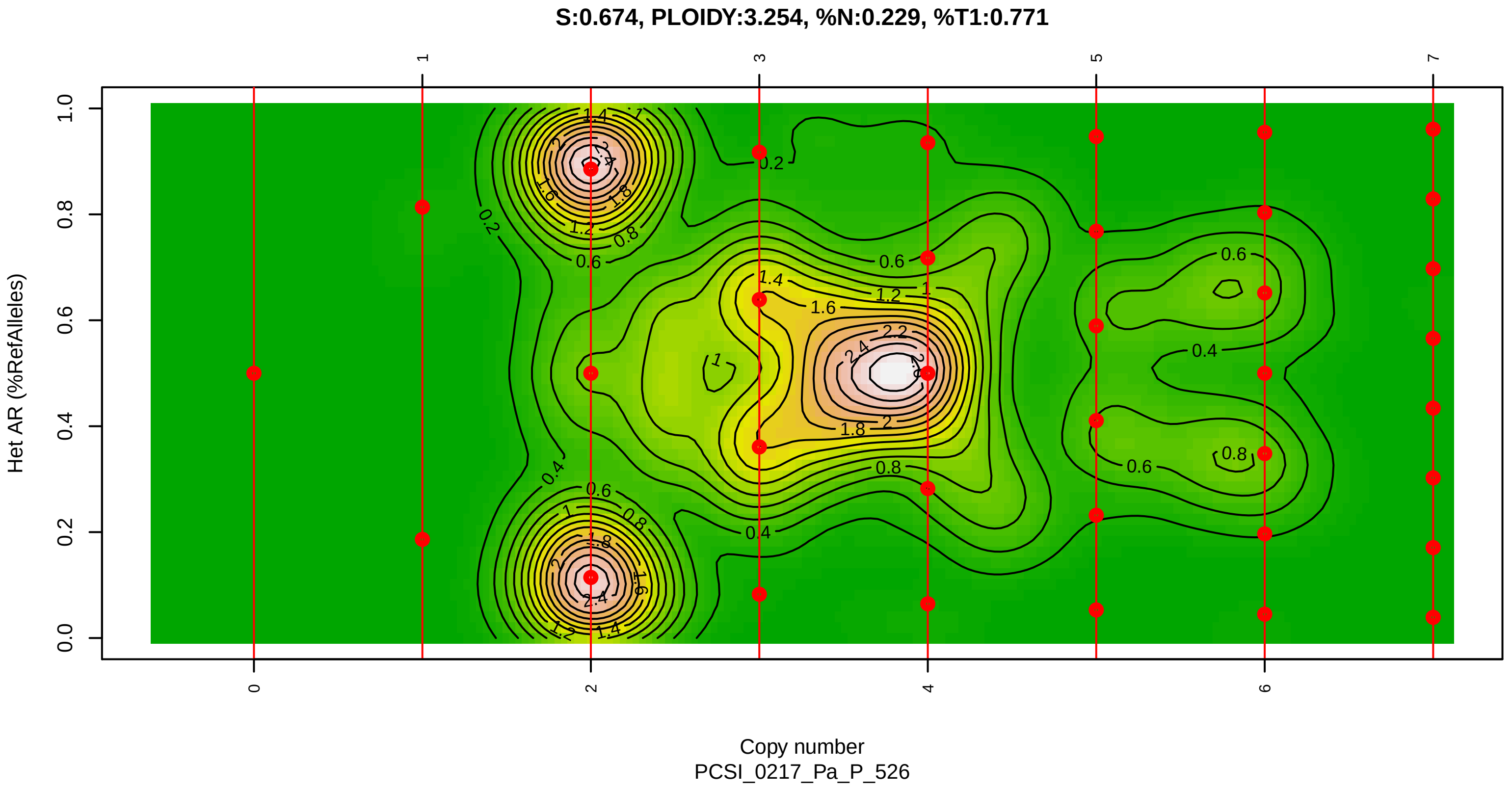

S:0.597, PLOIDY:3.704, %N:0.208, %T1:0.792
Het AR (%RefAlleles)
0.0
0.2
0.4
0.6
0.8
1.0
0
1
2
3
4
5
6
7
8
Copy number
PCSI_0174_Pa_P_526


S:1.096, PLOIDY:1.788, %N:0.175, %T1:0.825

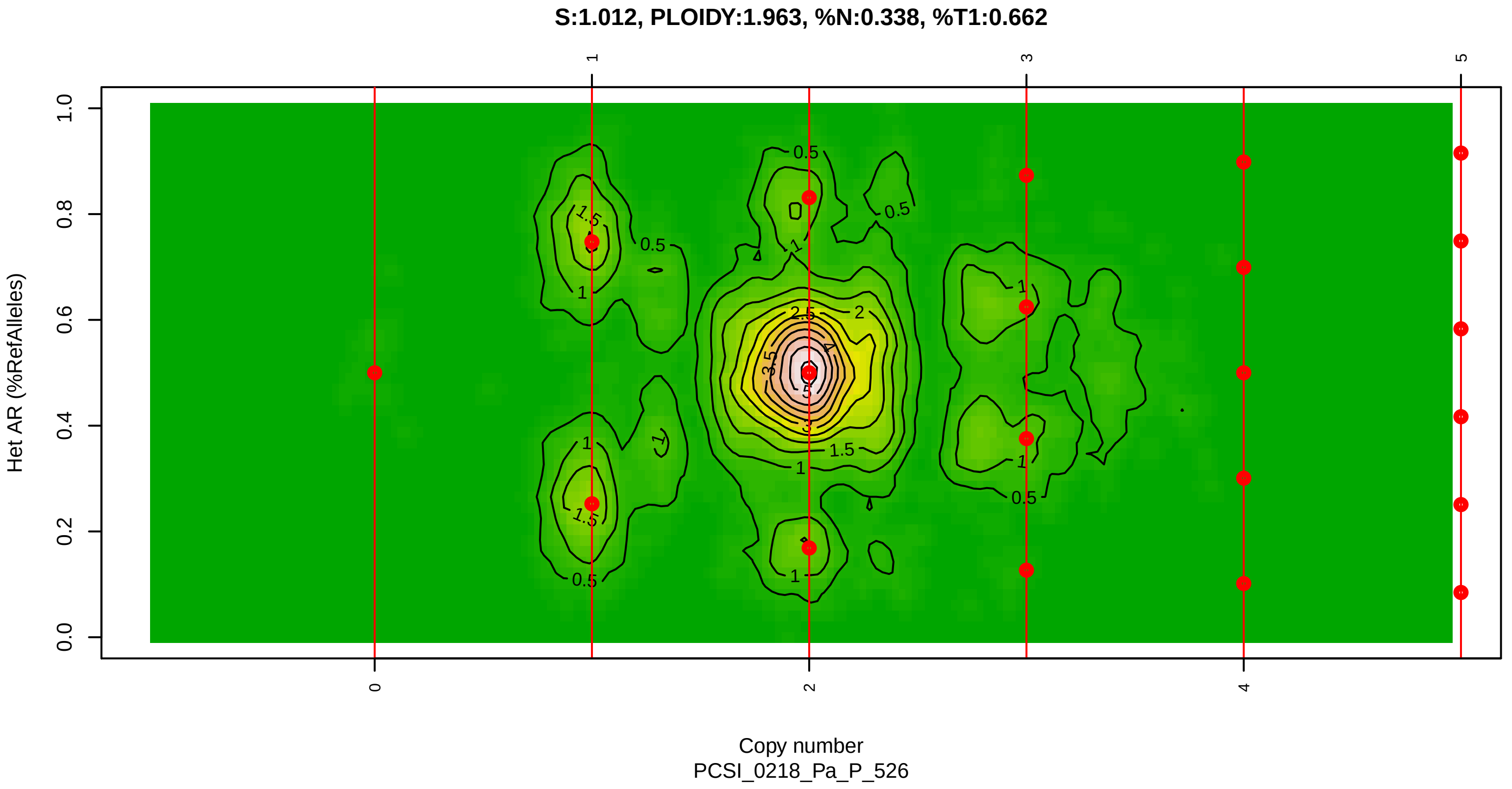
PCSI_0175_Pa_P_526


S:0.601, PLOIDY:3.702, %N:0.22, %T1:0.78

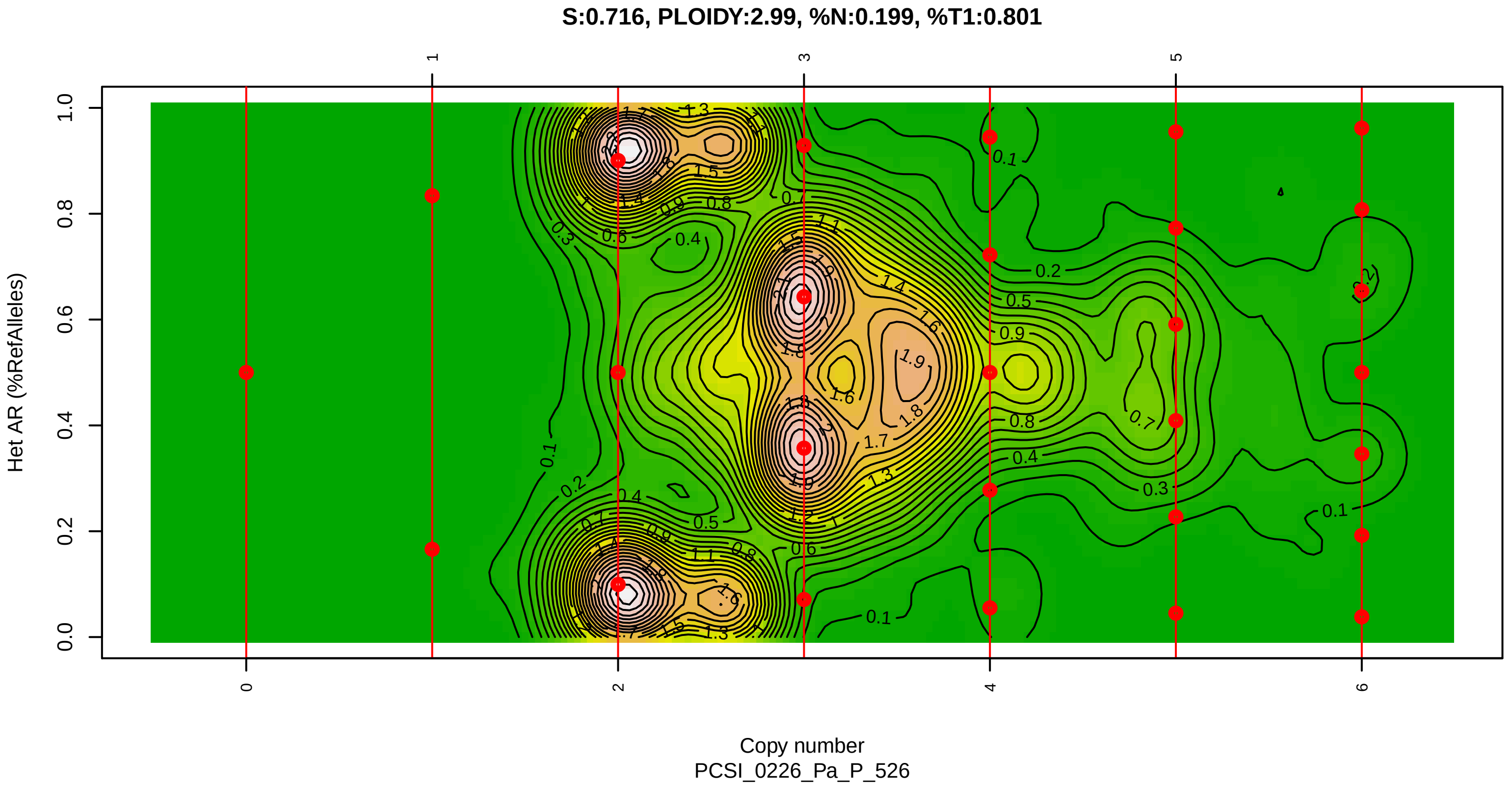
PCSI_0210_Pa_P_526


S:0.674, PLOIDY:3.254, %N:0.229, %T1:0.771

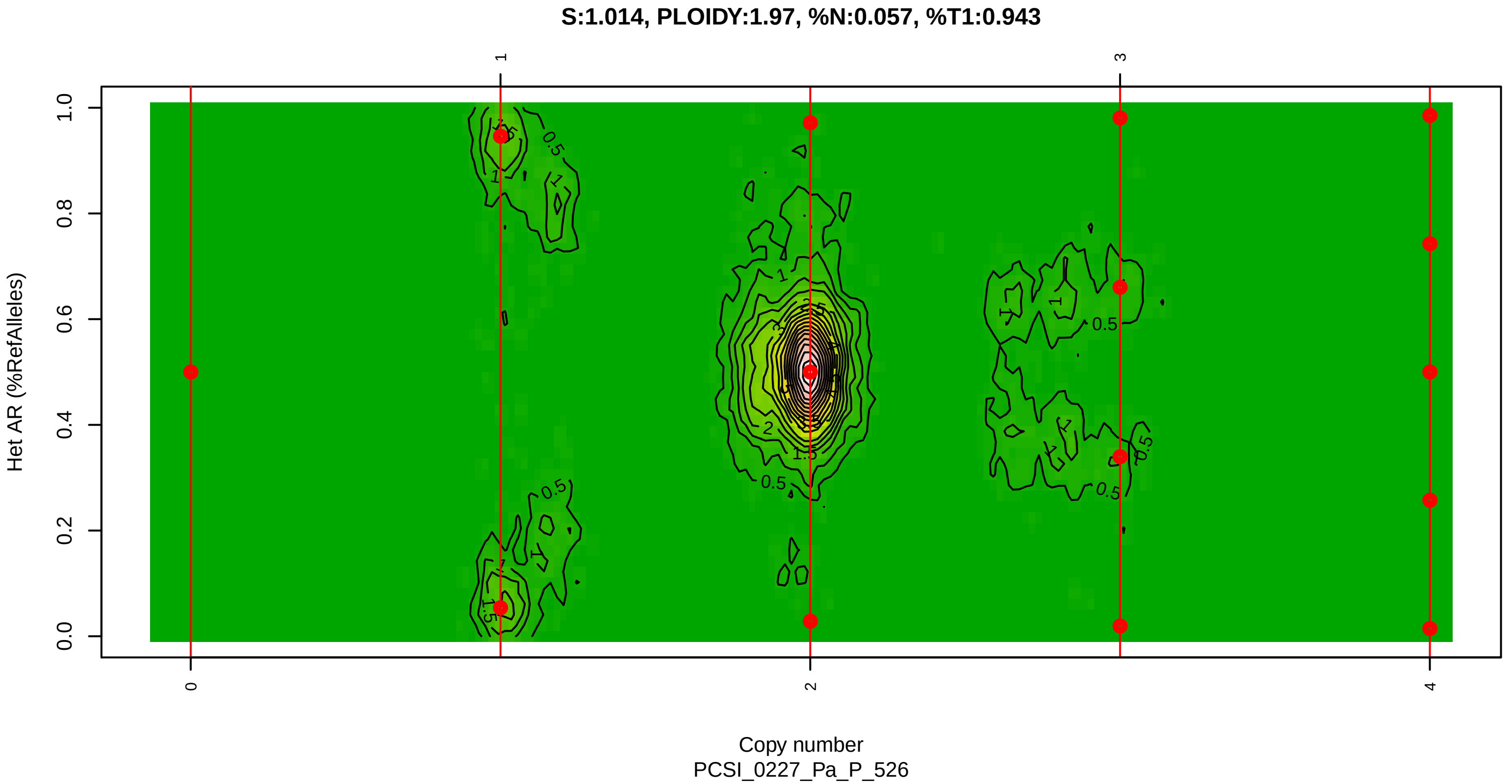
PCSI_0217_Pa_P_526


S:1.012, PLOIDY:1.963, %N:0.338, %T1:0.662

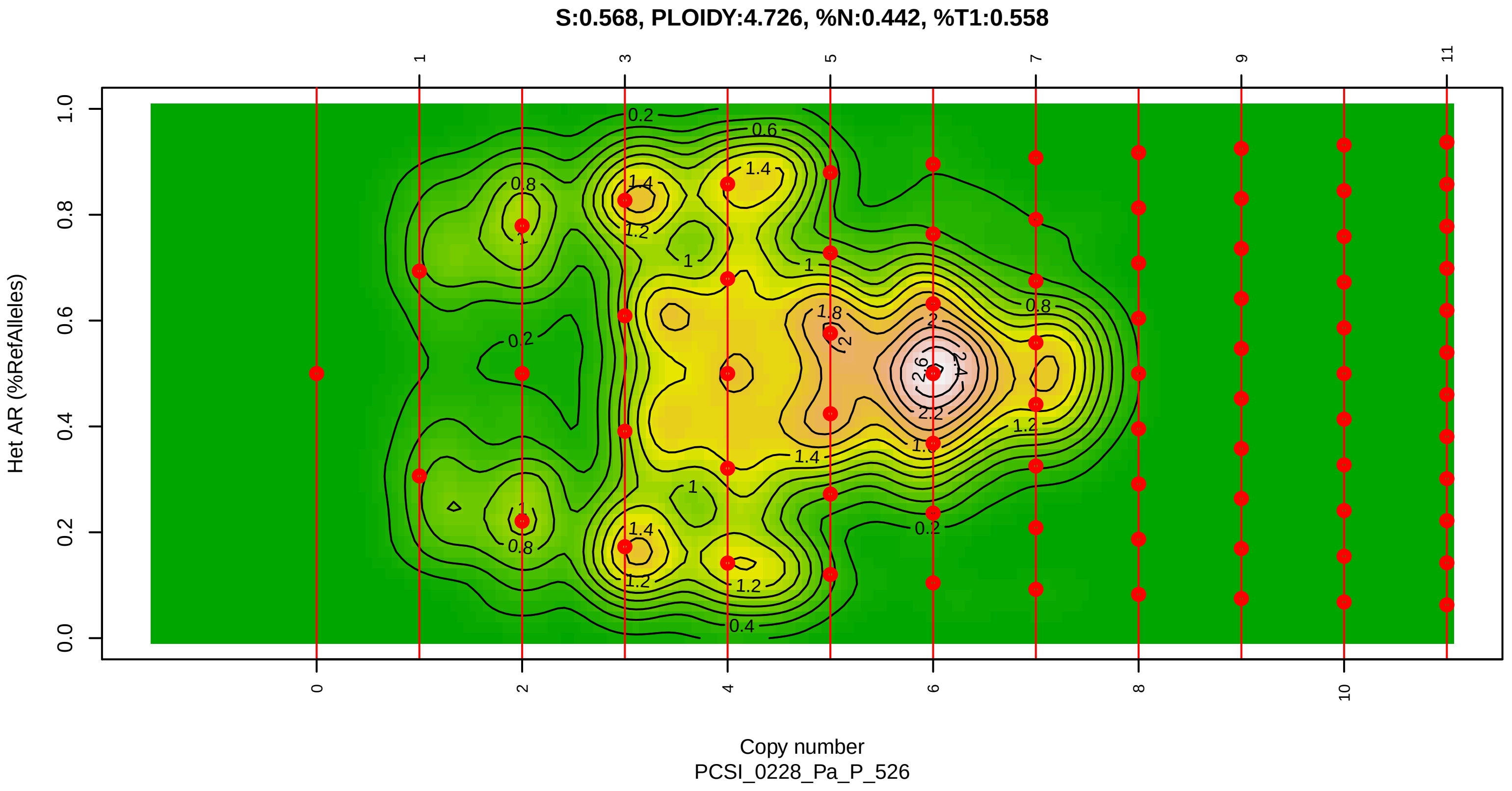
PCSI_0218_Pa_P_526


S:0.716, PLOIDY:2.99, %N:0.199, %T1:0.801

PCSI_0226_Pa_P_526


S:1.014, PLOIDY:1.97, %N:0.057, %T1:0.943

PCSI_0227_Pa_P_526


S:0.568, PLOIDY:4.726, %N:0.442, %T1:0.558
Het AR (%RefAlleles)
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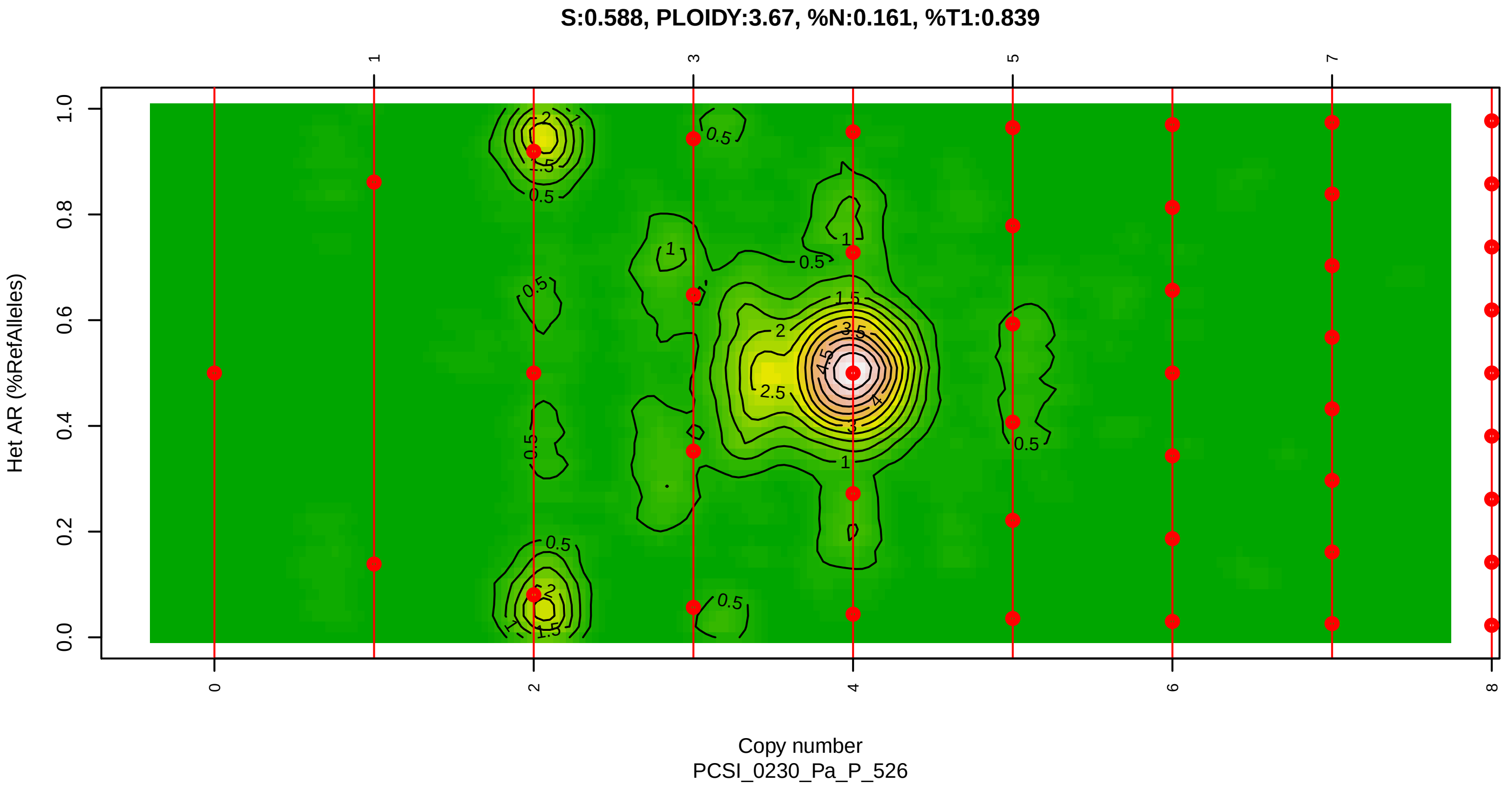
0.2
0.4
0.6
0.8
1.0
0
2
4
6
8
10
1
3
5
7
9
11
Copy number
PCSI_0228_Pa_P_526


S:0.588, PLOIDY:3.67, %N:0.161, %T1:0.839
Het AR (%RefAlleles)
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0.2
0.4
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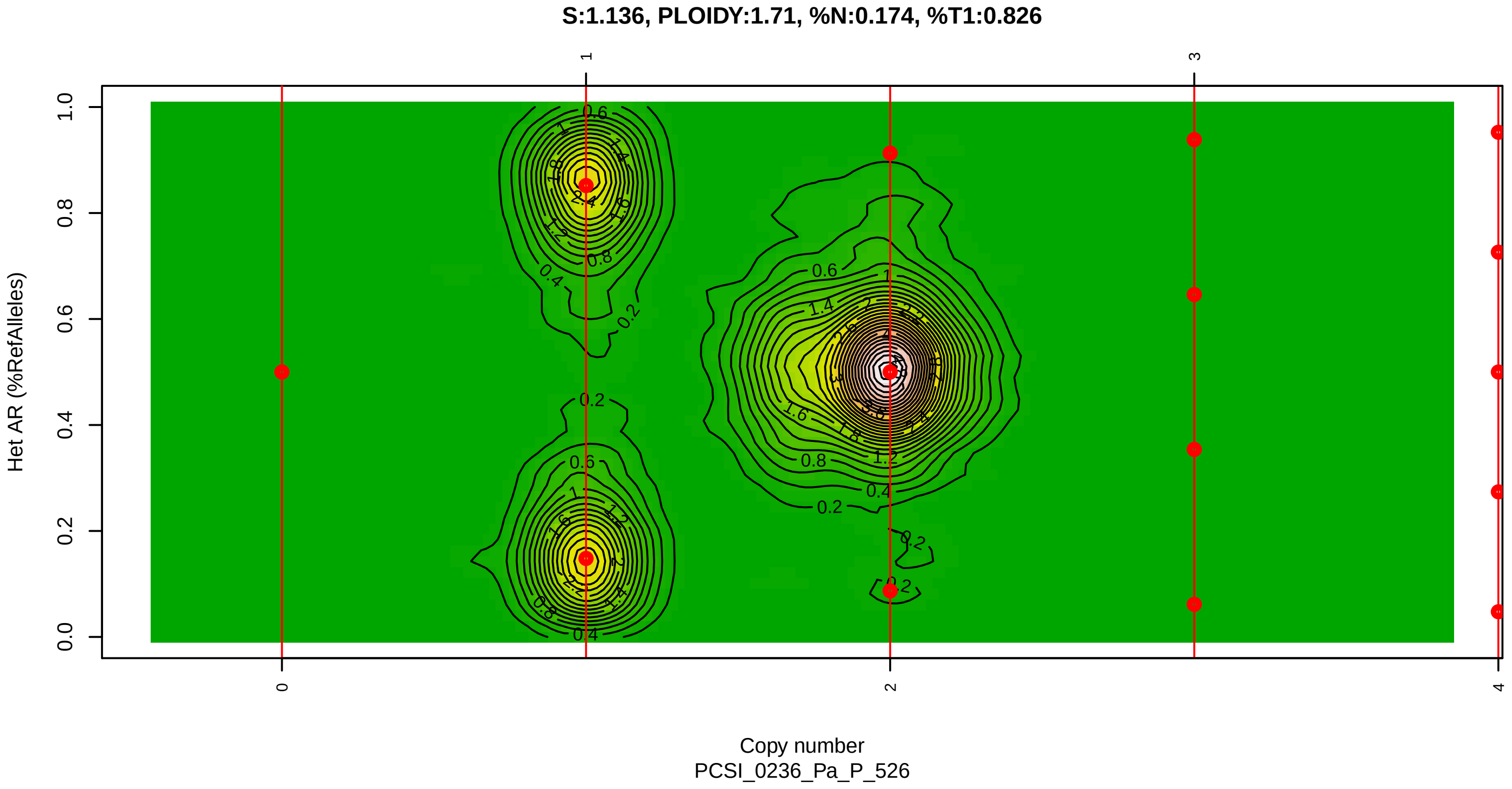
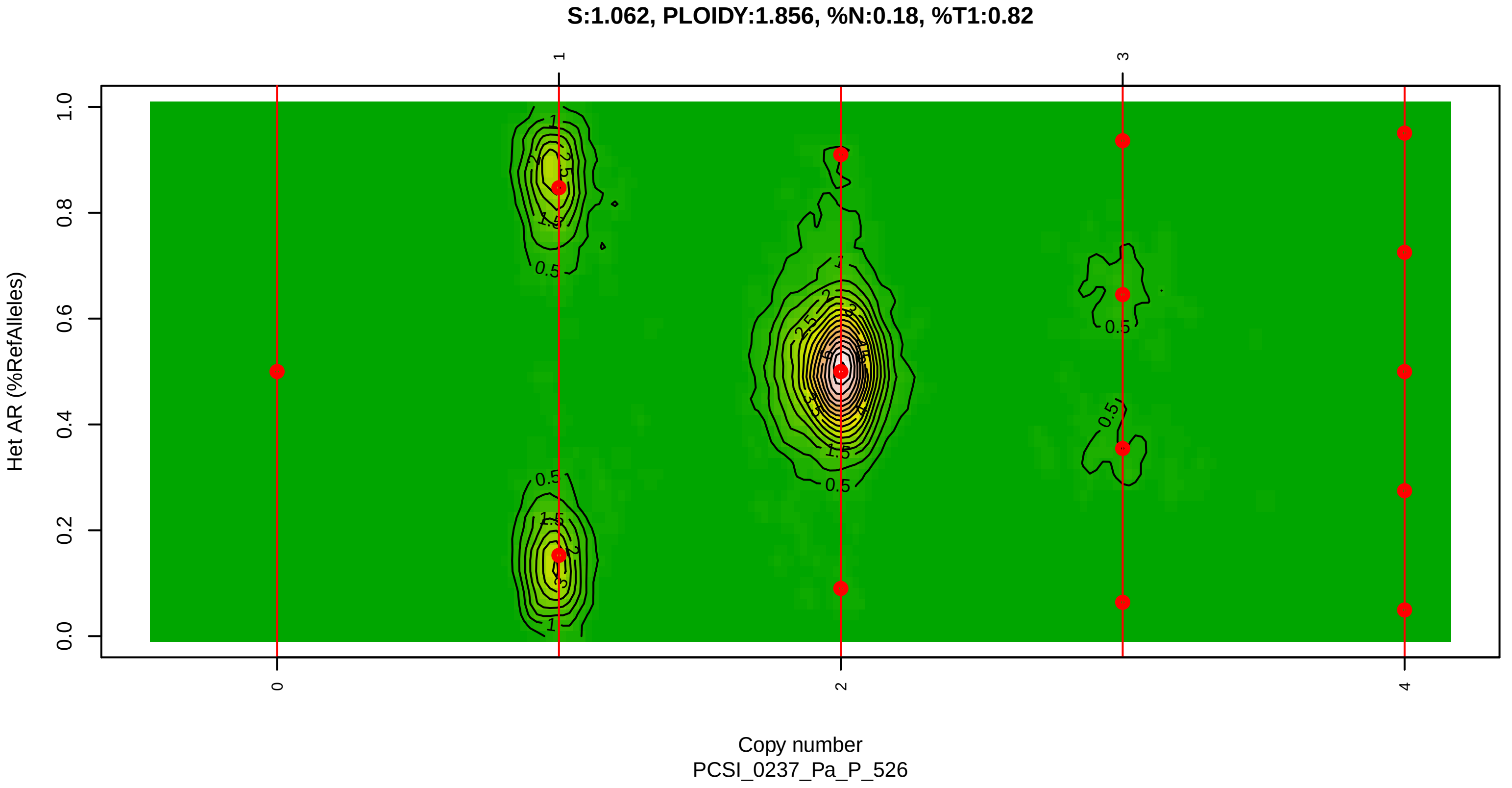
1.0
0
2
4
6
8
1
3
5
7
Copy number
PCSI_0230_Pa_P_526


S:1.136, PLOIDY:1.71, %N:0.174, %T1:0.826
Het AR (%RefAlleles)
0.0
0.2
0.4
0.6
0.8
1.0
0
2
4
1
3
Copy number
PCSI_0236_Pa_P_526


S:1.062, PLOIDY:1.856, %N:0.18, %T1:0.82
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1.0
0
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4
1
3
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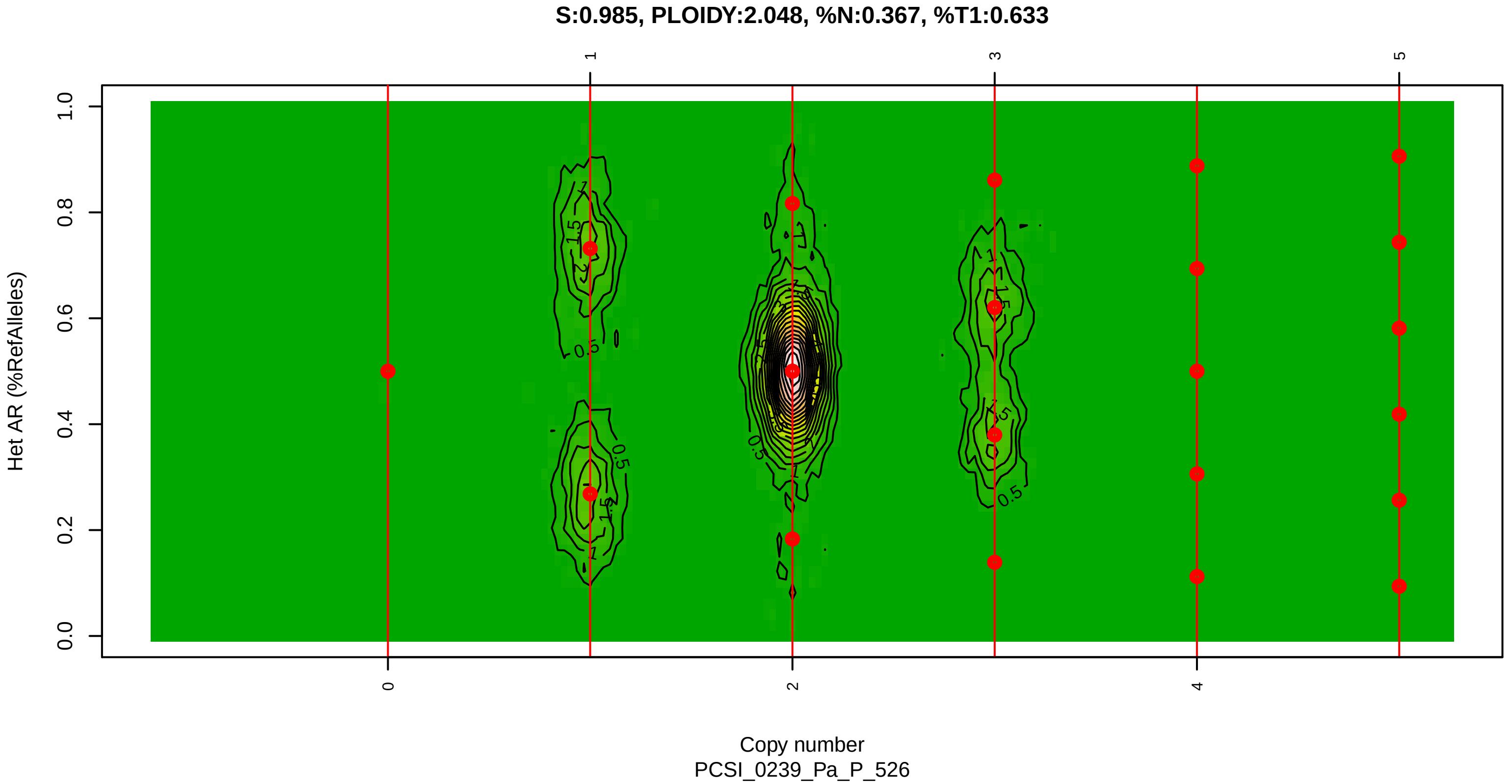
PCSI_0237_Pa_P_526


S:0.985, PLOIDY:2.048, %N:0.367, %T1:0.633
Het AR (%RefAlleles)
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5
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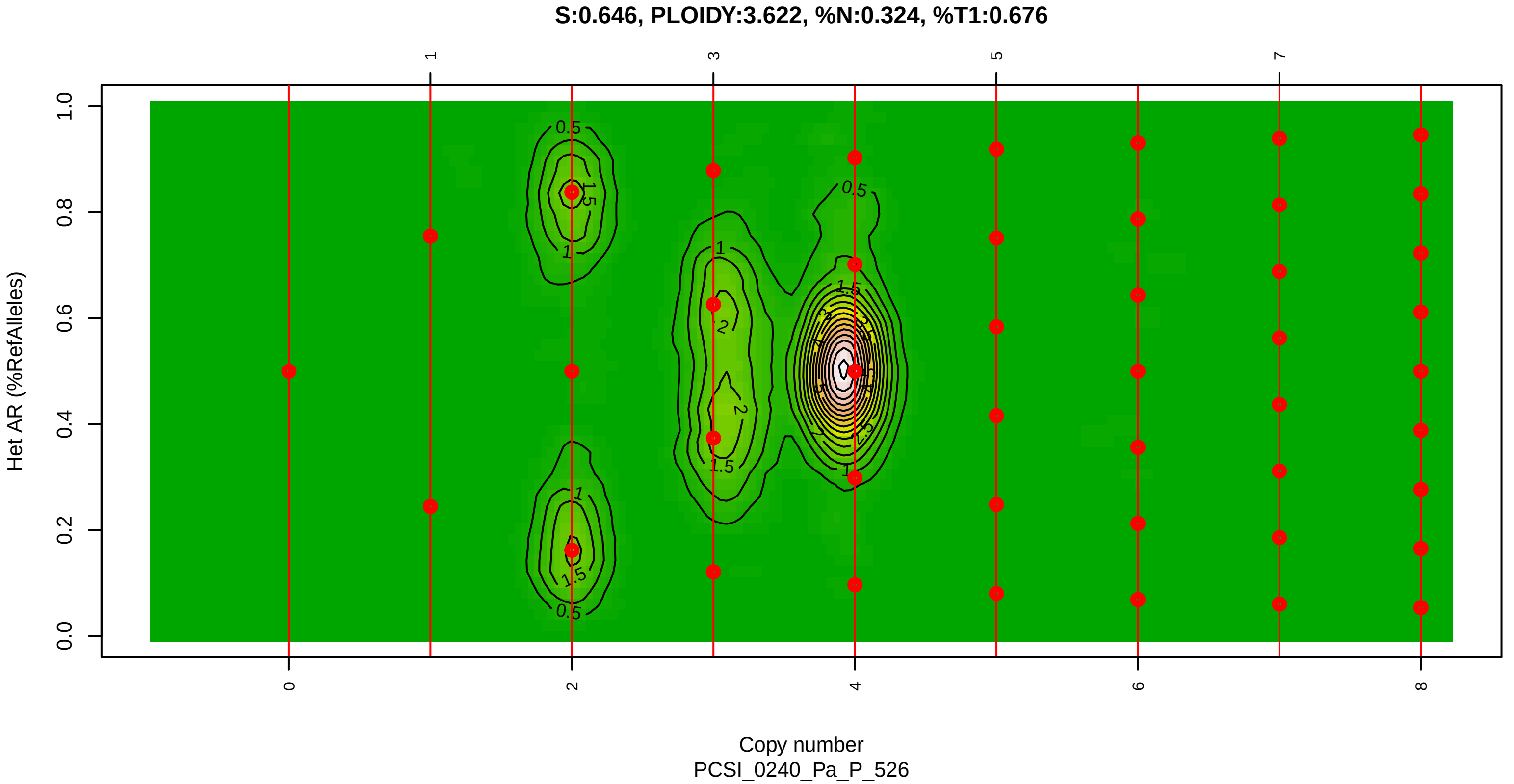
PCSI_0239_Pa_P_526


S:0.646, PLOIDY:3.622, %N:0.324, %T1:0.676
Het AR (%RefAlleles)
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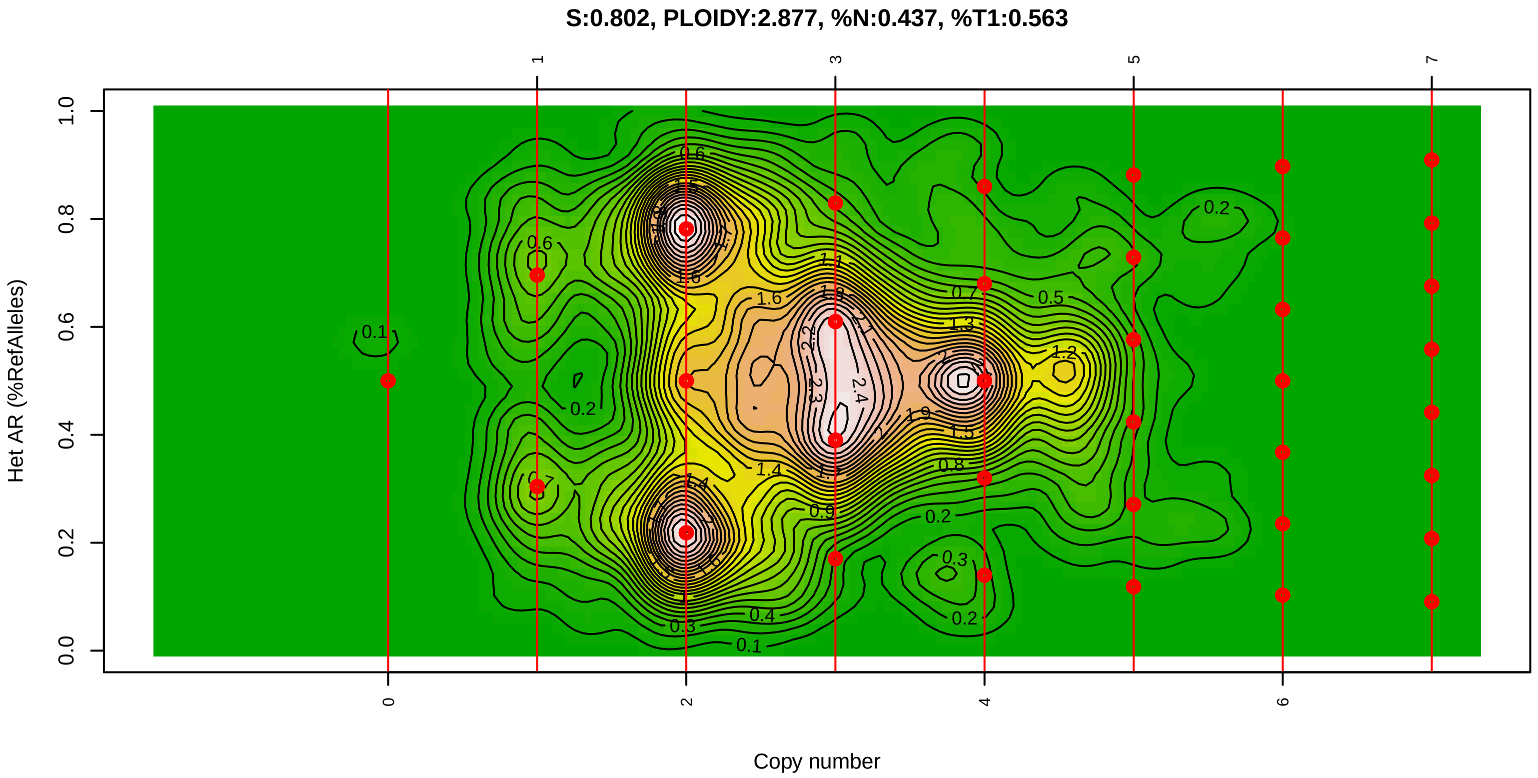
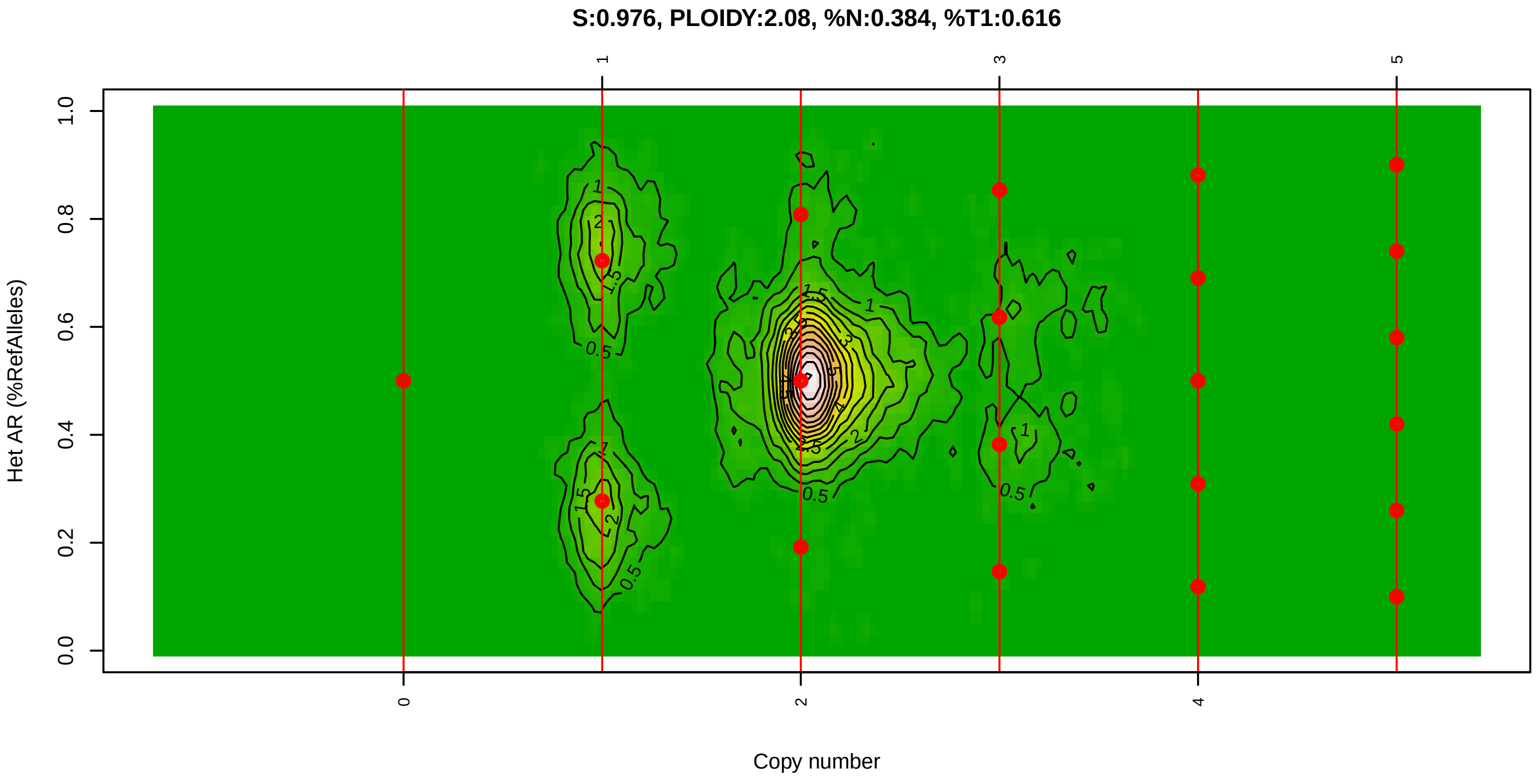
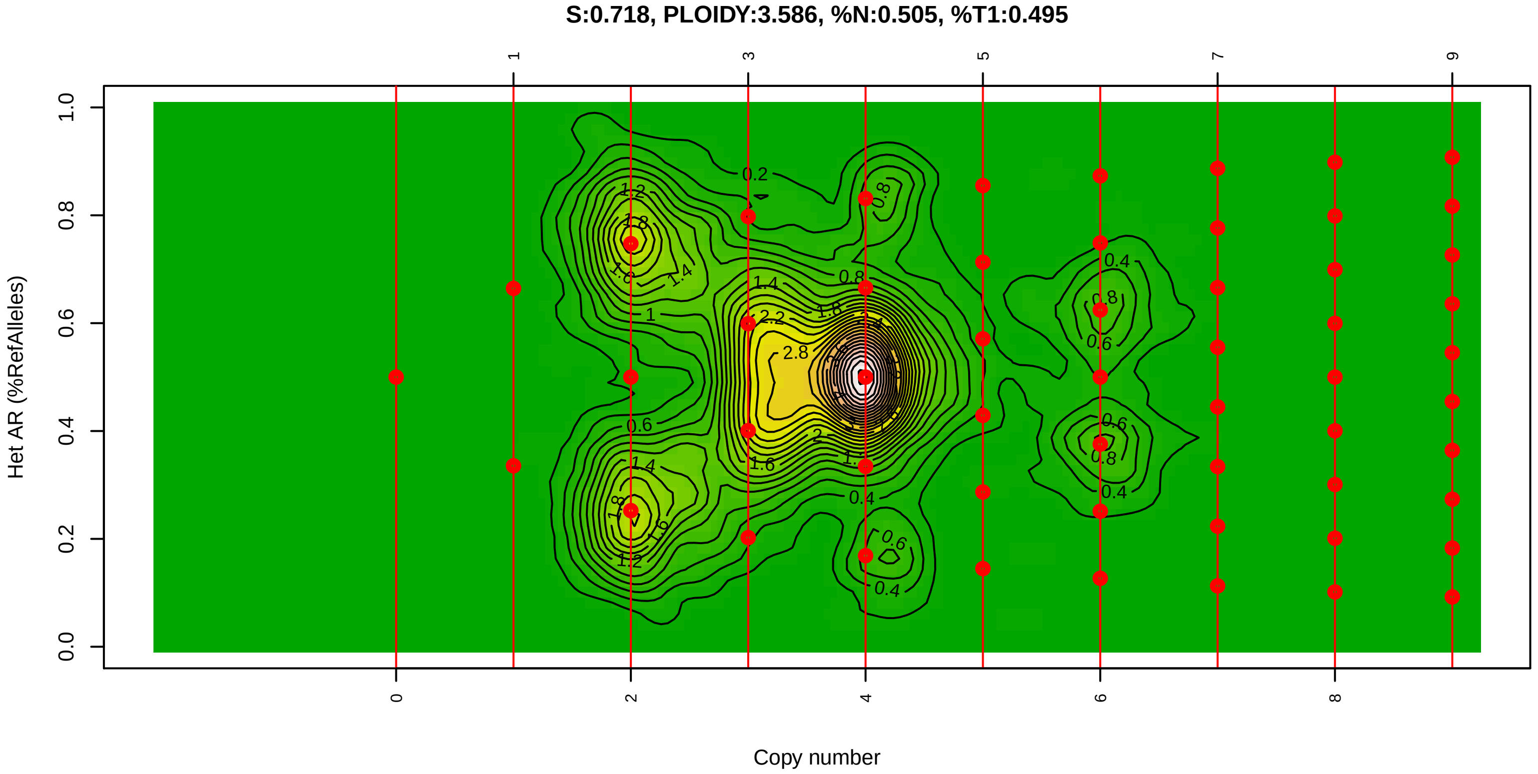
PCSI_0240_Pa_P_526



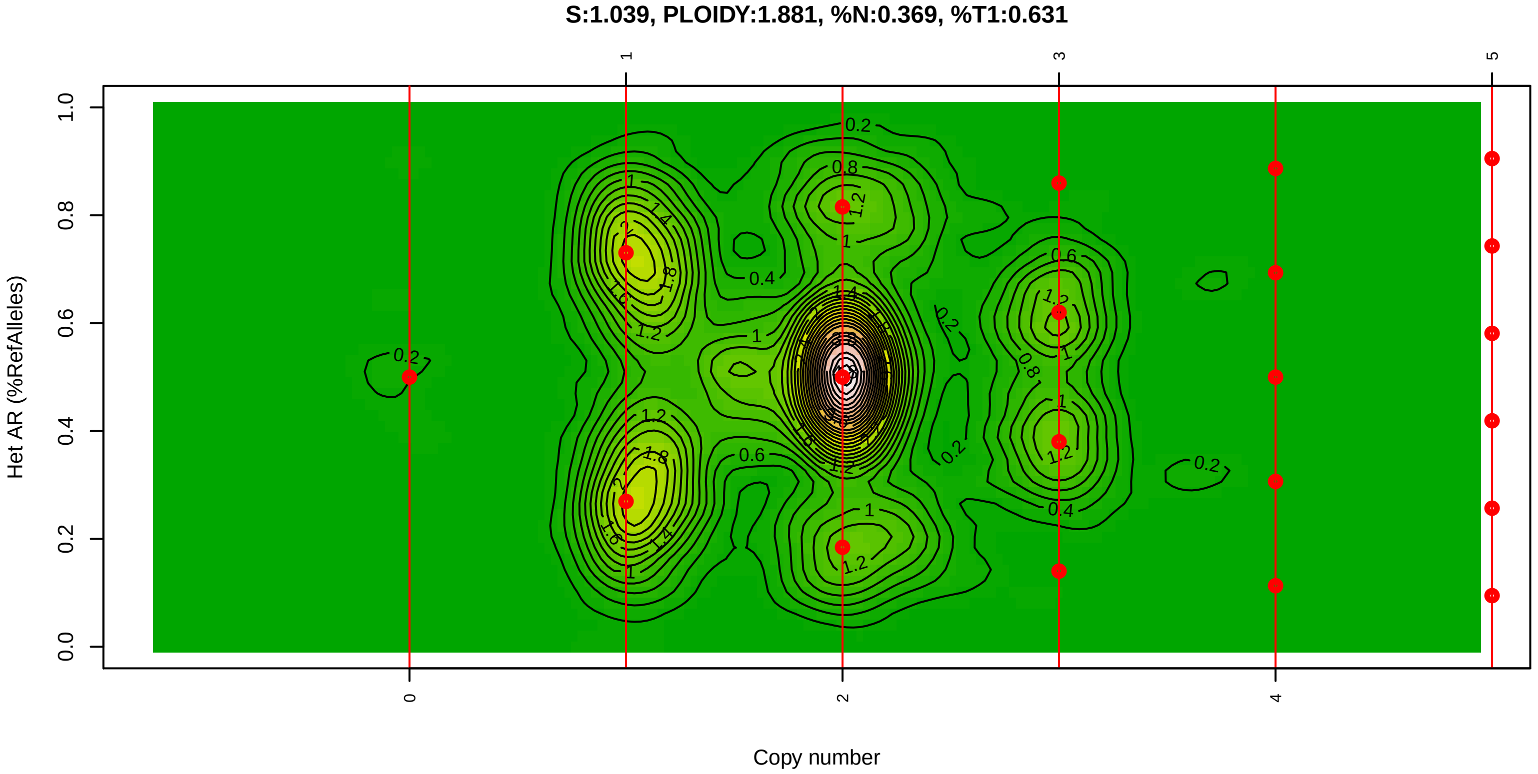
PCSI_0261_Pa_P_526



PCSI_0264_Pa_P_526



PCSI_0268_Pa_P_526



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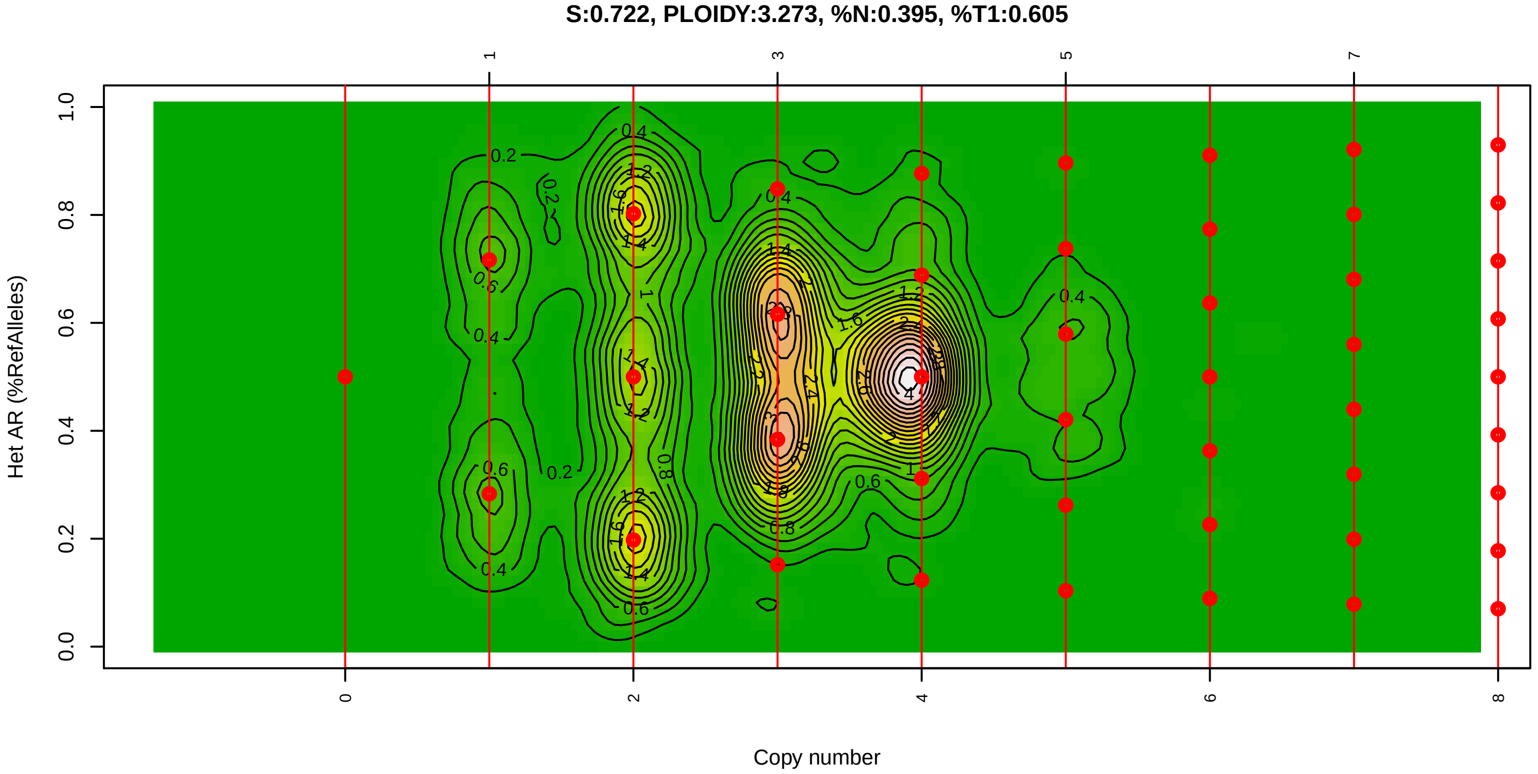
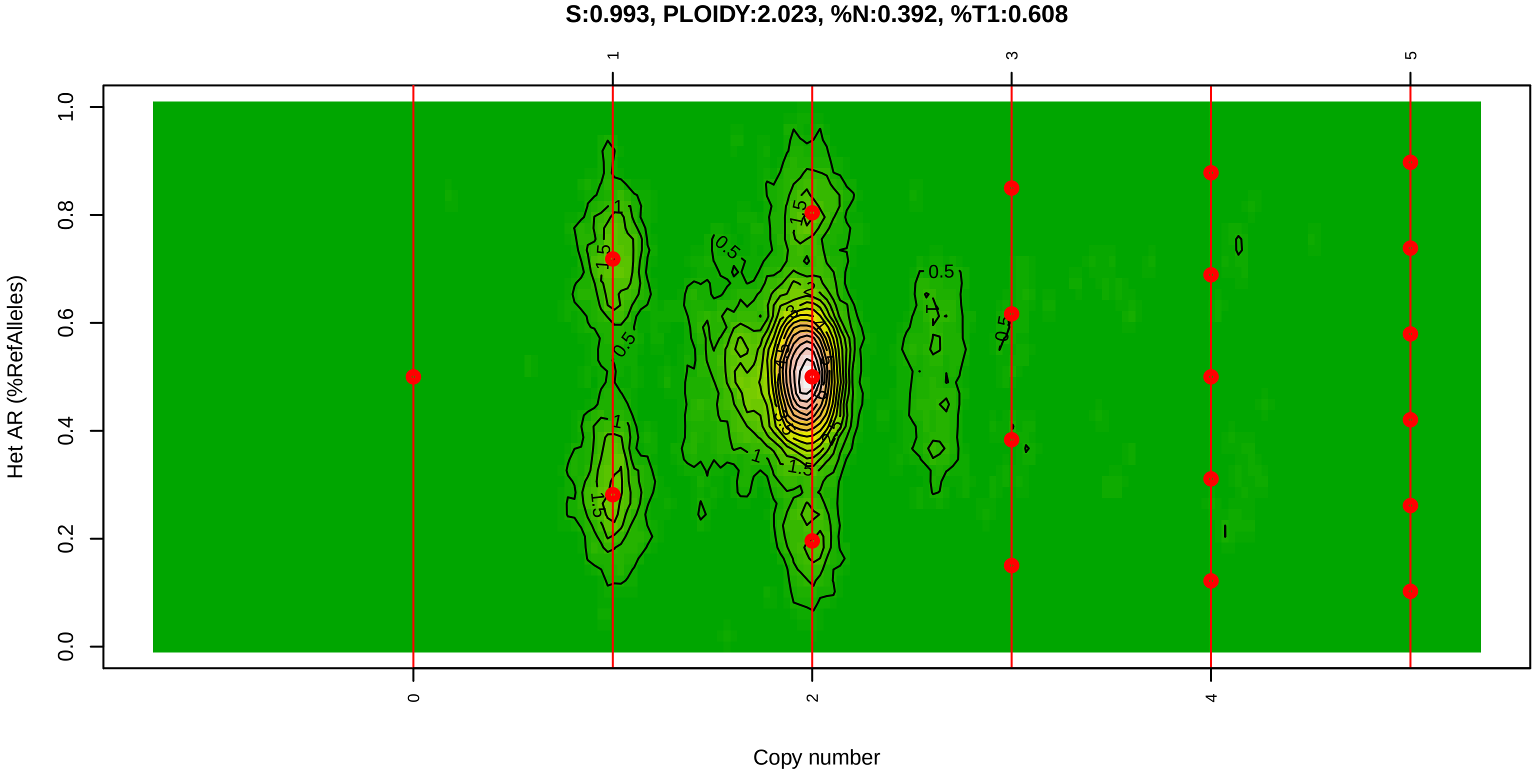
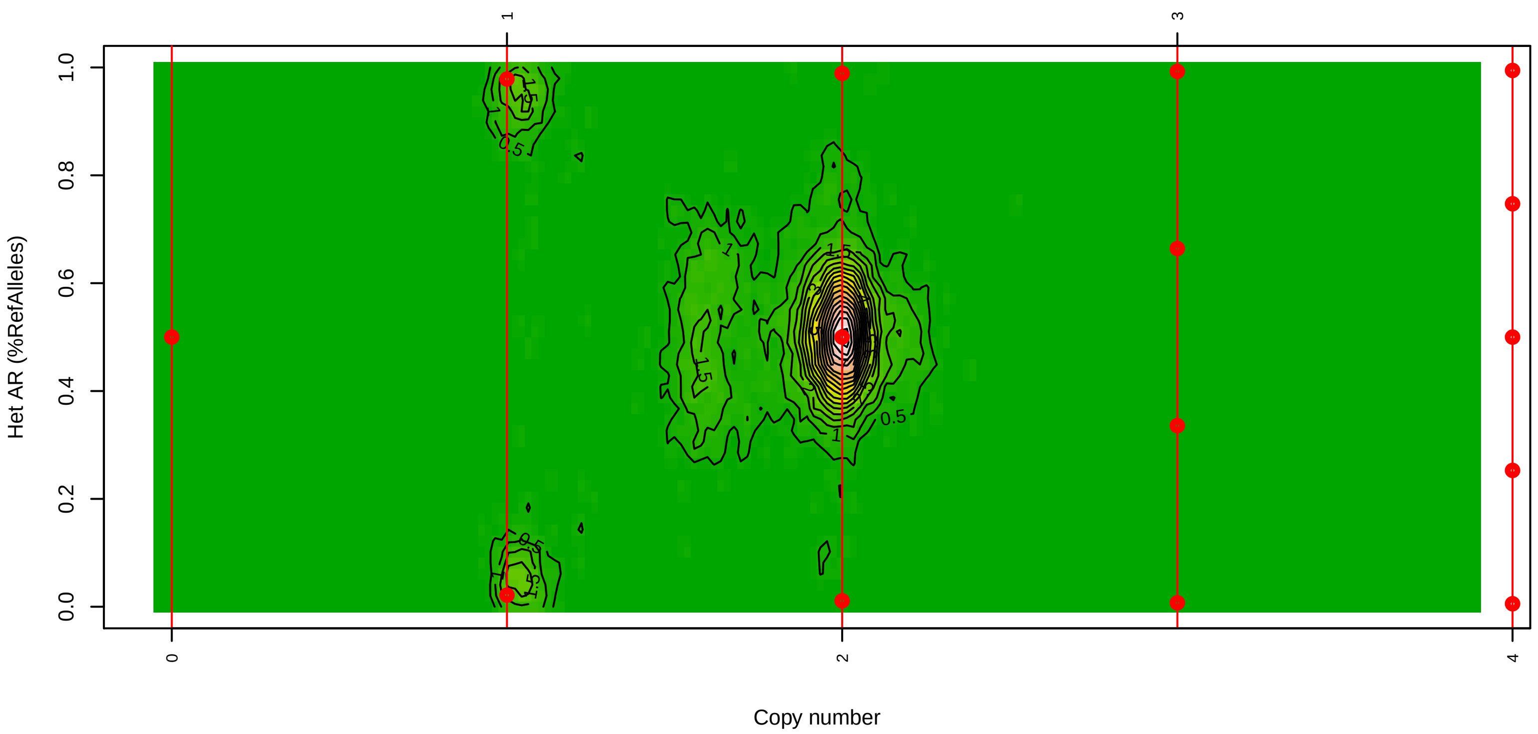


PCSI_0274_Pa_P_526



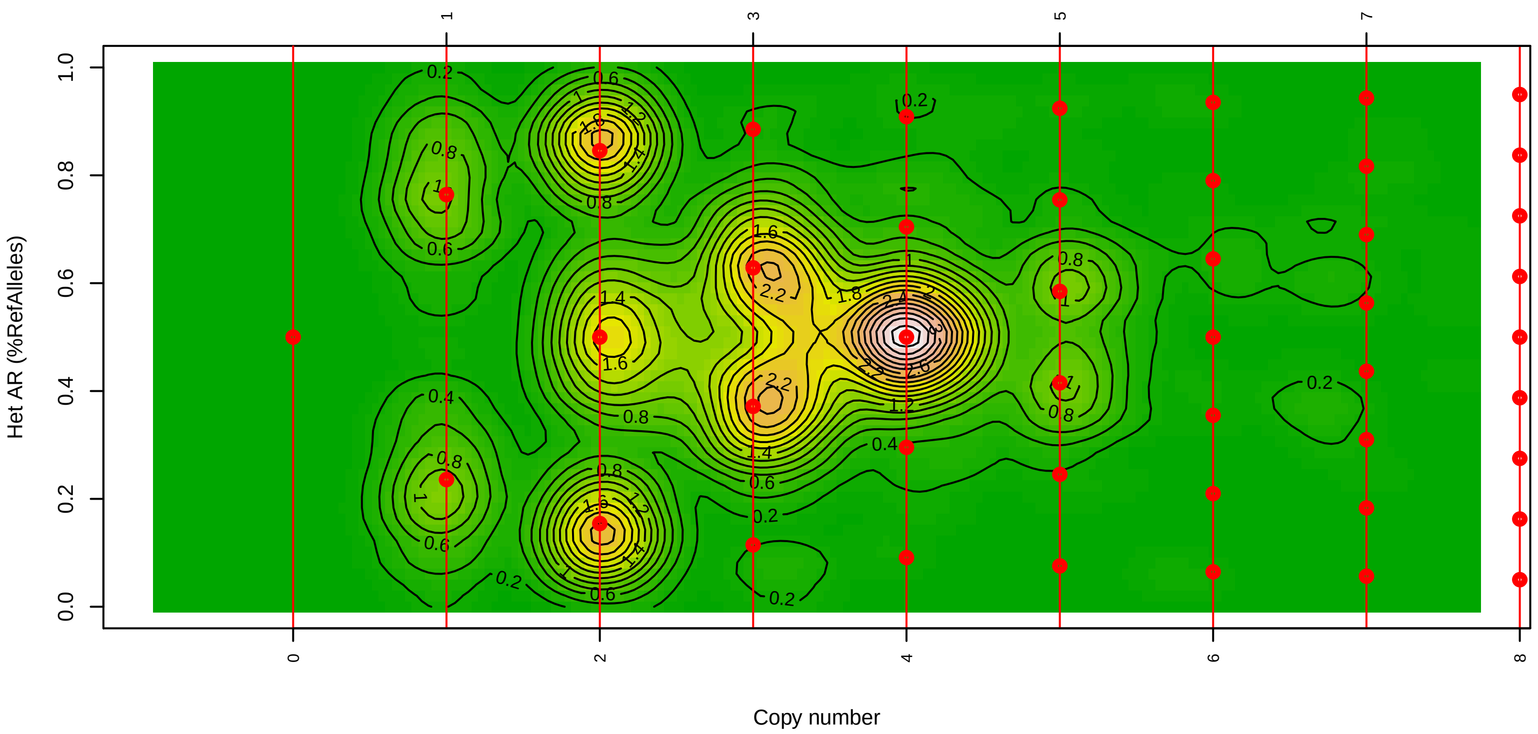
PCSI_0279_Pa_P_526

S:1.038, PLOIDY:1.925, %N:0.022, %T1:0.978



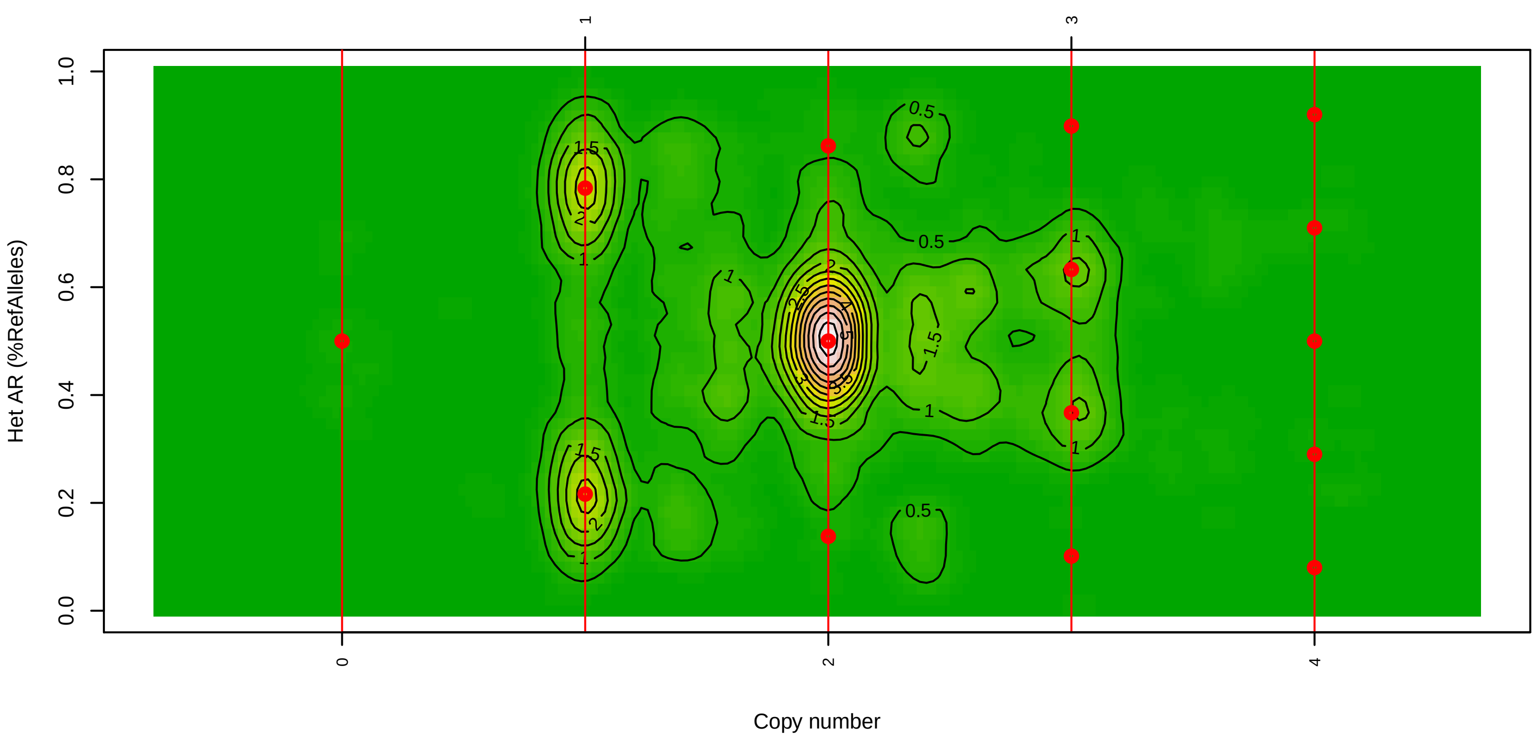
PCSI_0287_Pa_P_526

S:0.671, PLOIDY:3.416, %N:0.309, %T1:0.691



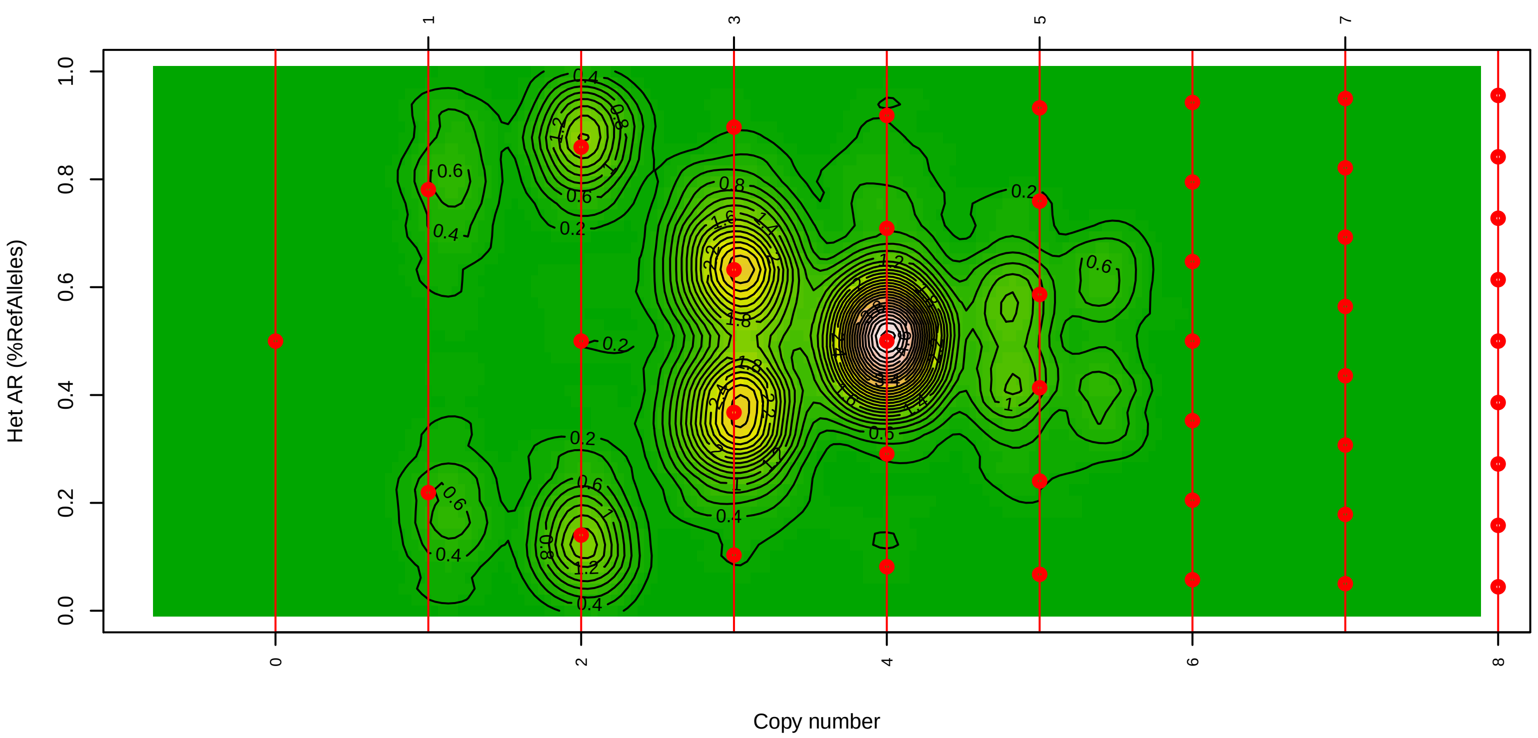
PCSI_0290_Pa_P_526

S:1.017, PLOIDY:1.953, %N:0.276, %T1:0.724



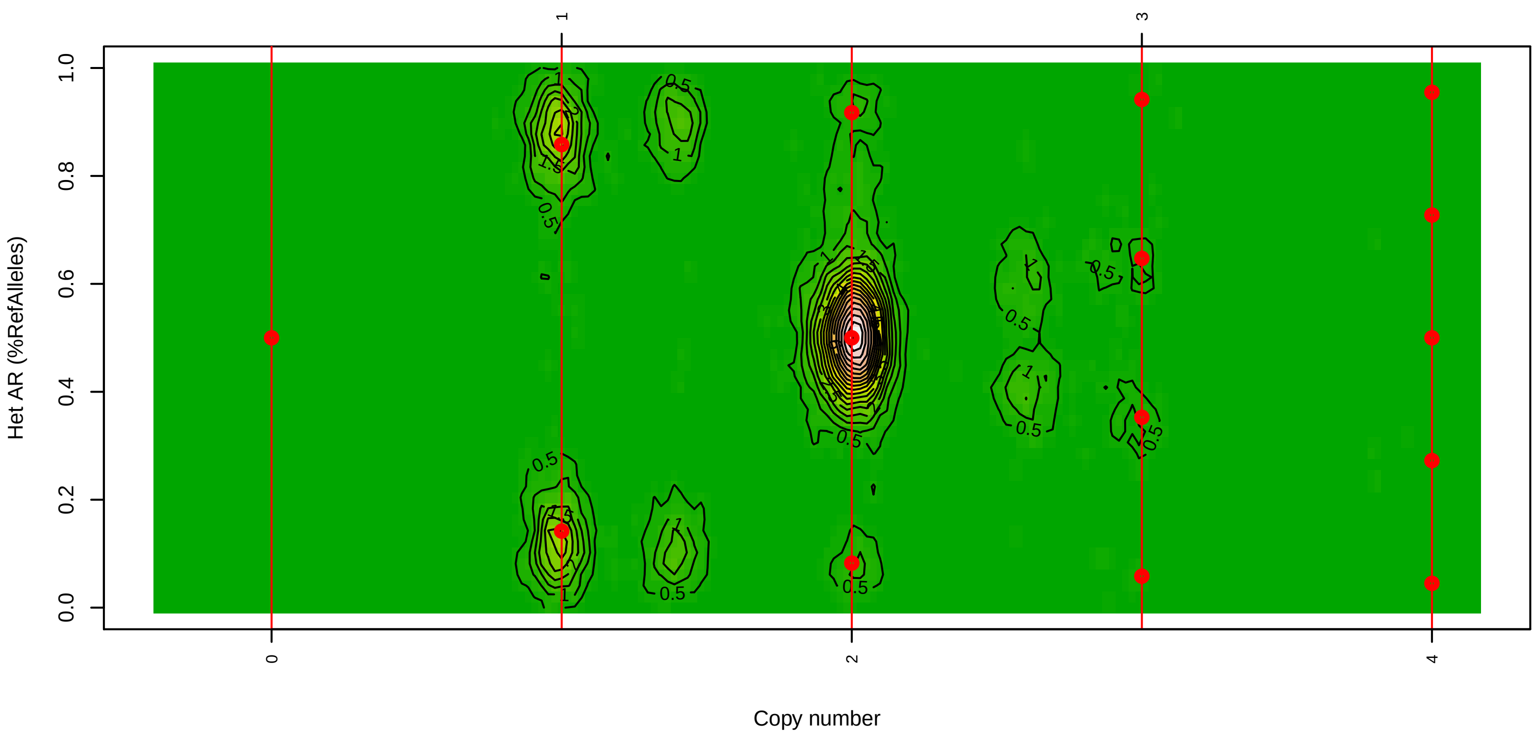
PCSI_0292_Pa_P_526

S:0.643, PLOIDY:3.542, %N:0.281, %T1:0.719



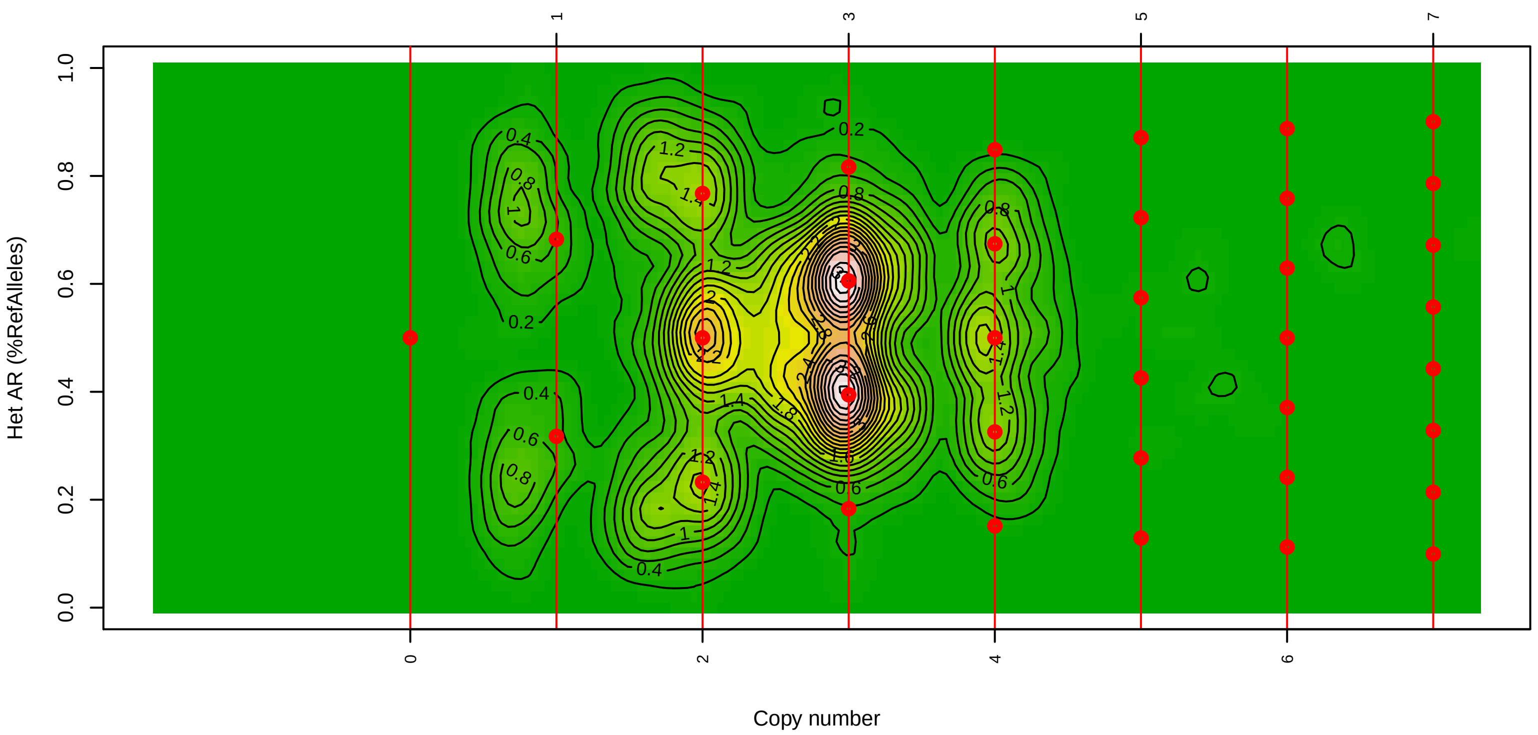
PCSI_0294_Pa_P_526

S:1.053, PLOIDY:1.88, %N:0.165, %T1:0.835



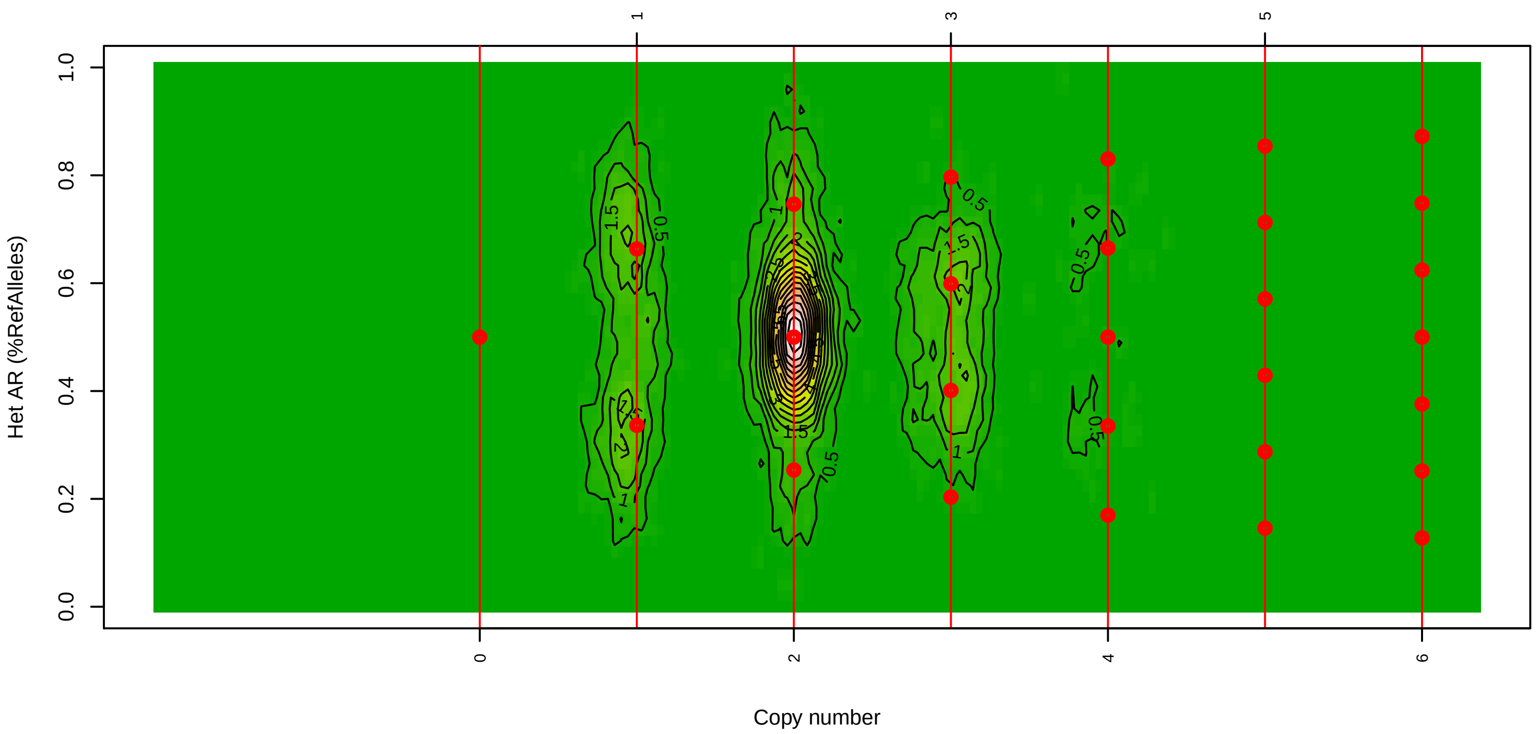
PCSI_0297_Pa_P_526

S:0.827, PLOIDY:2.782, %N:0.465, %T1:0.535



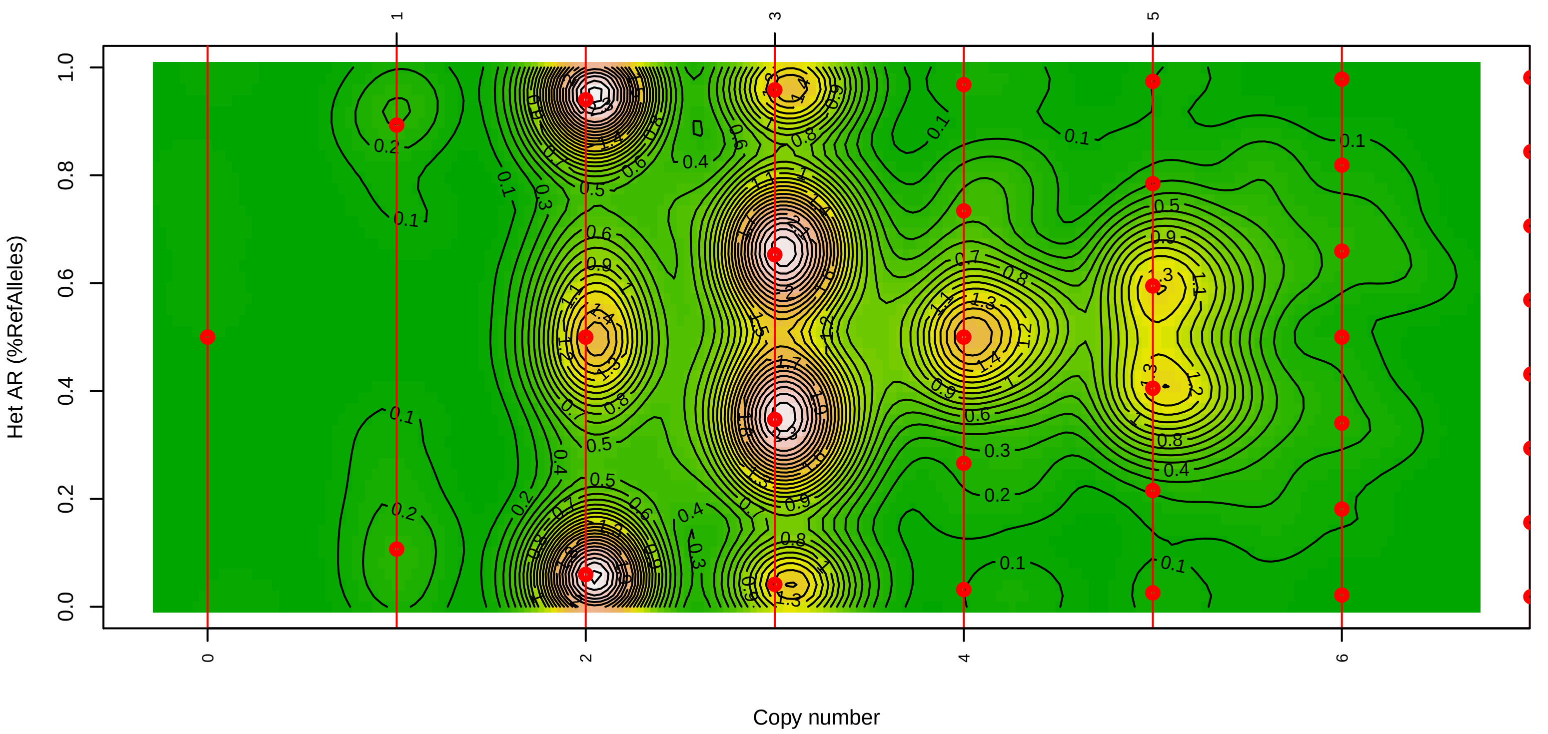
PCSI_0300_Pa_P_526

S:0.965, PLOIDY:2.147, %N:0.507, %T1:0.493



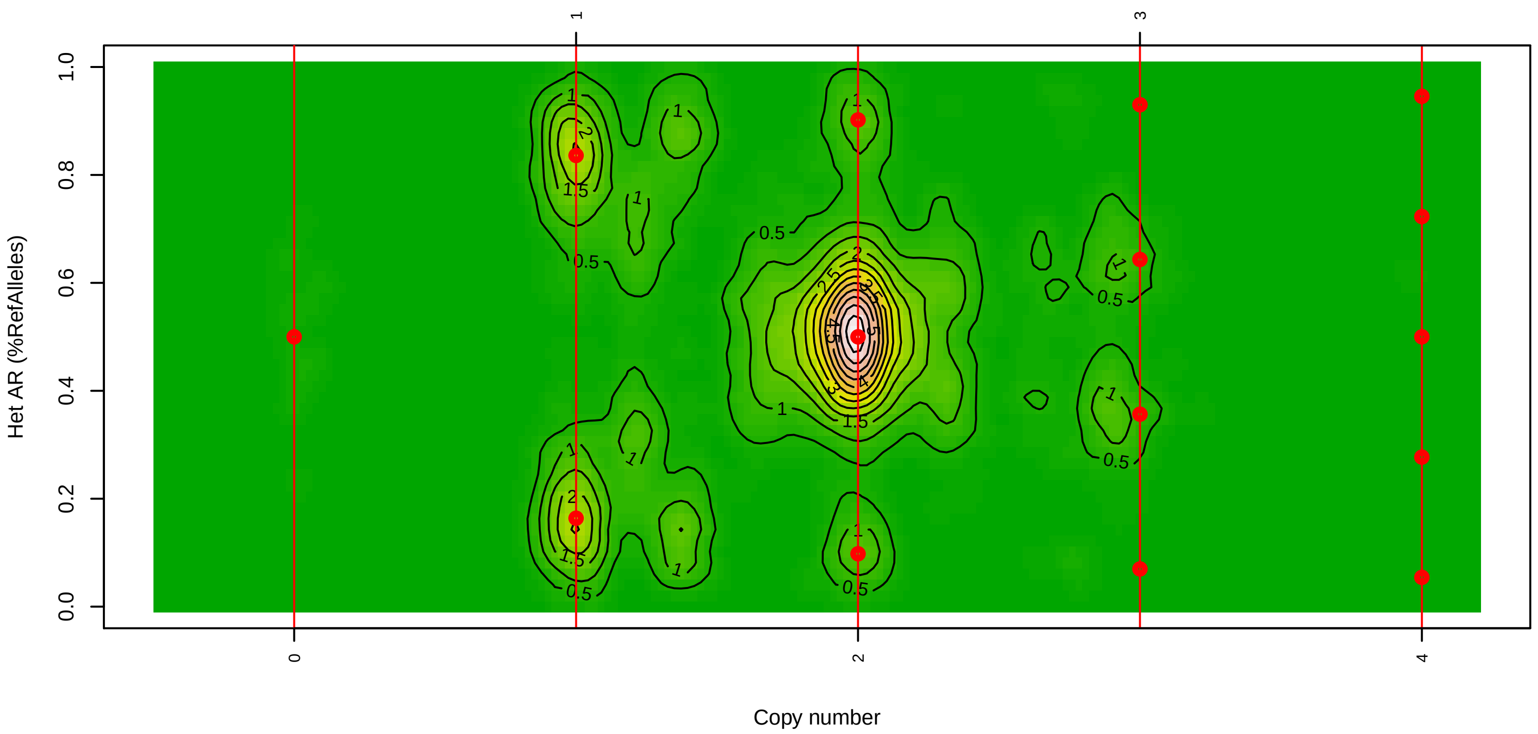
PCSI_0303_Pa_P_526

S:0.65, PLOIDY:3.221, %N:0.12, %T1:0.88



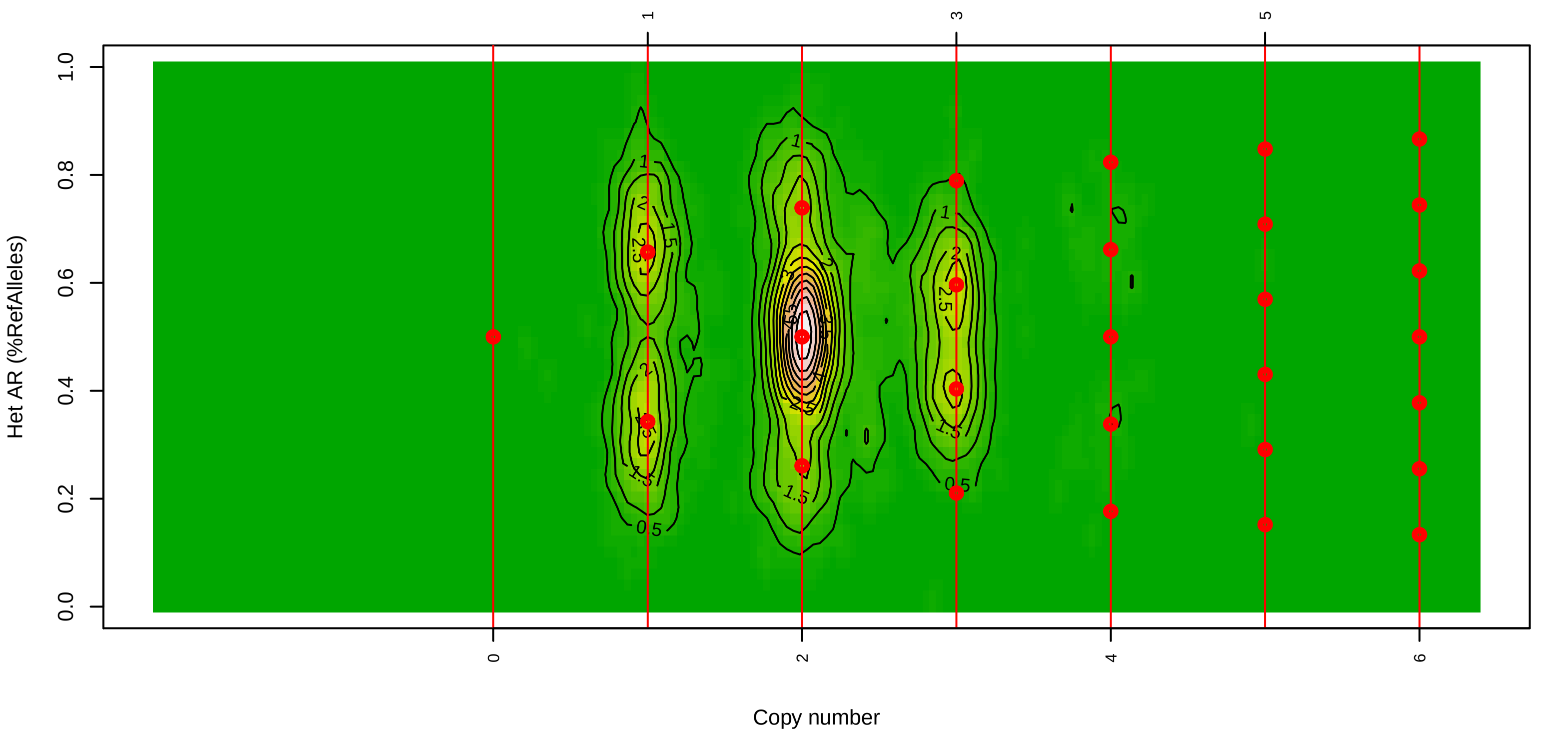
PCSI_0305_Pa_P_526

S:1.062, PLOIDY:1.854, %N:0.196, %T1:0.804



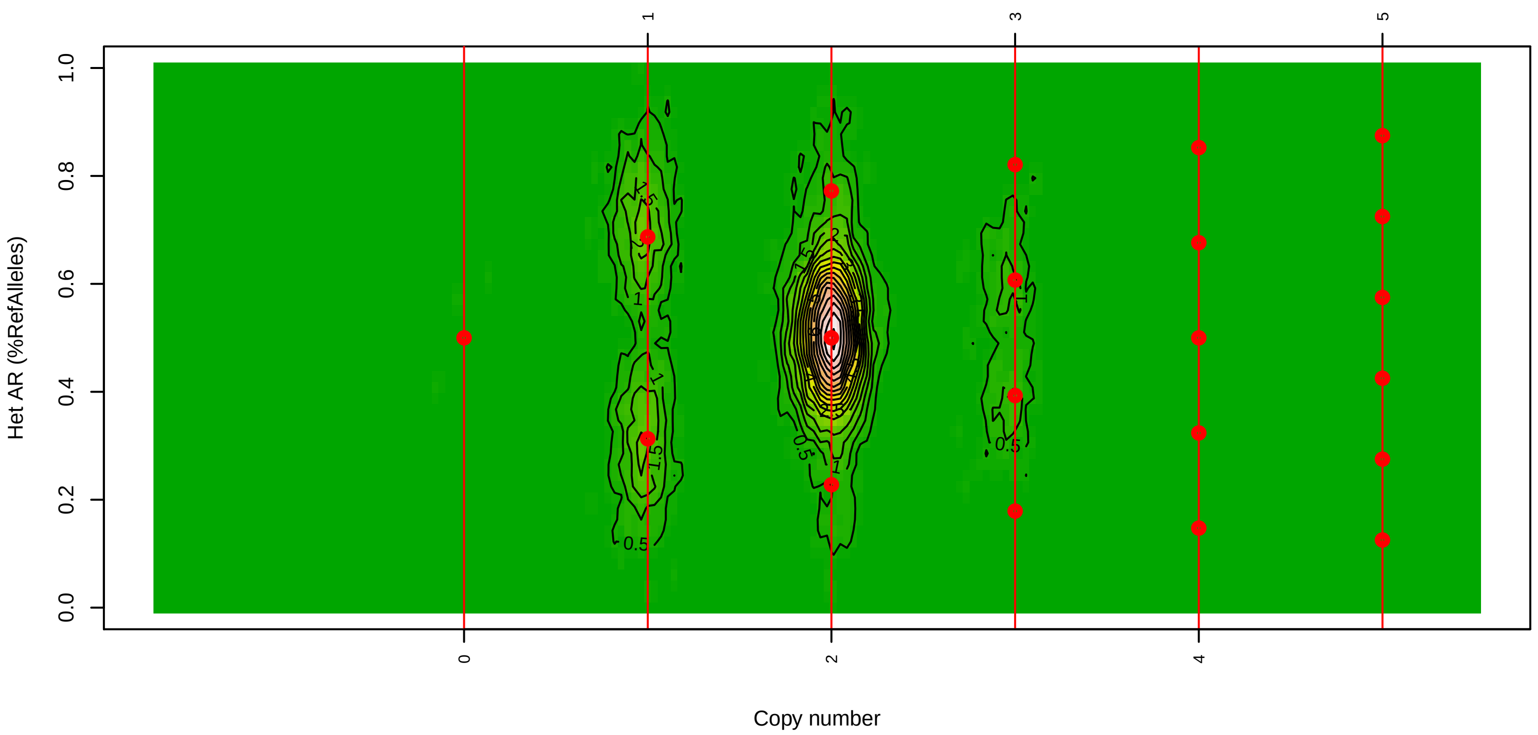
PCSI_0307_Pa_P_526

S:0.978, PLOIDY:2.094, %N:0.522, %T1:0.478



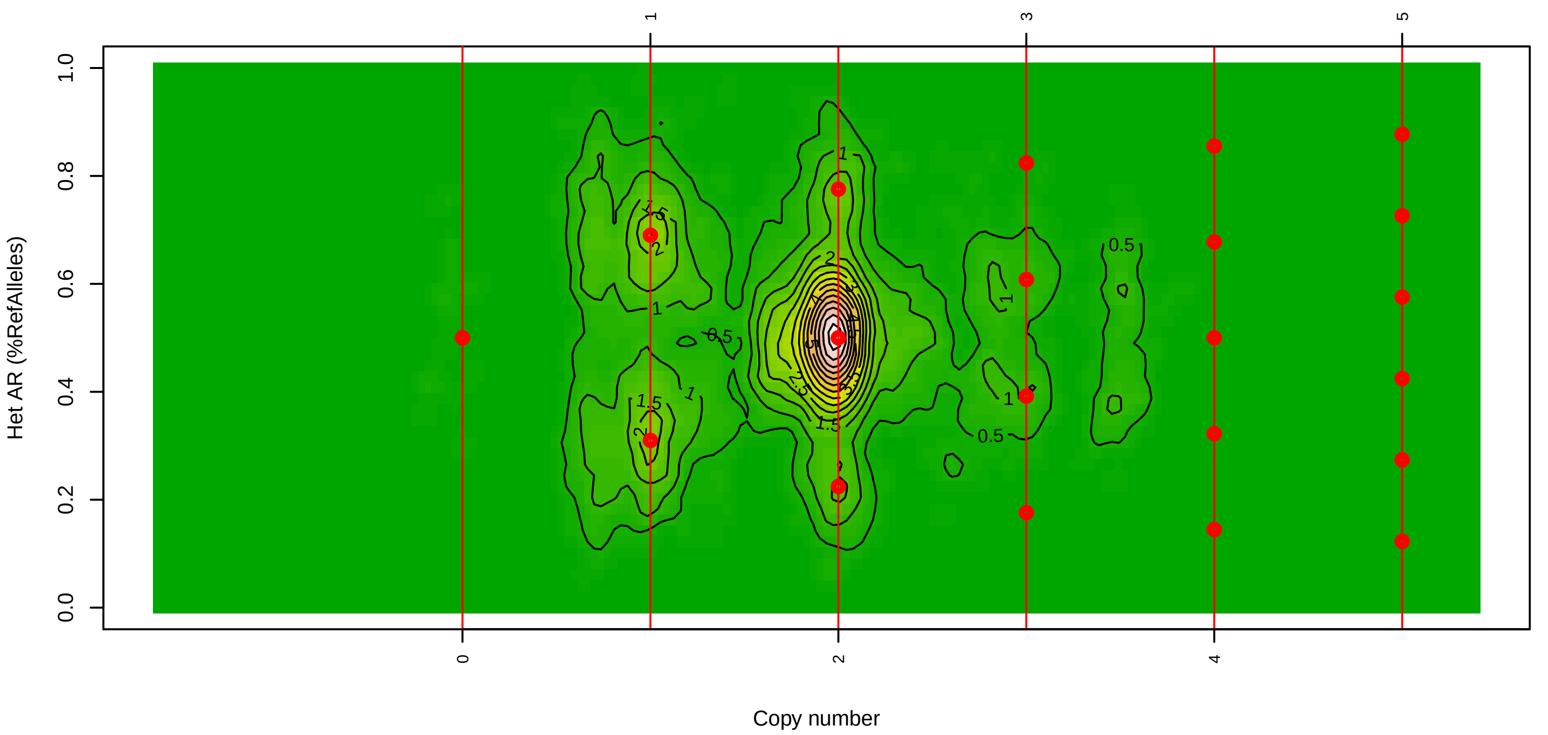
PCSI_0310_Pa_P_526

S:1.022, PLOIDY:1.921, %N:0.456, %T1:0.544



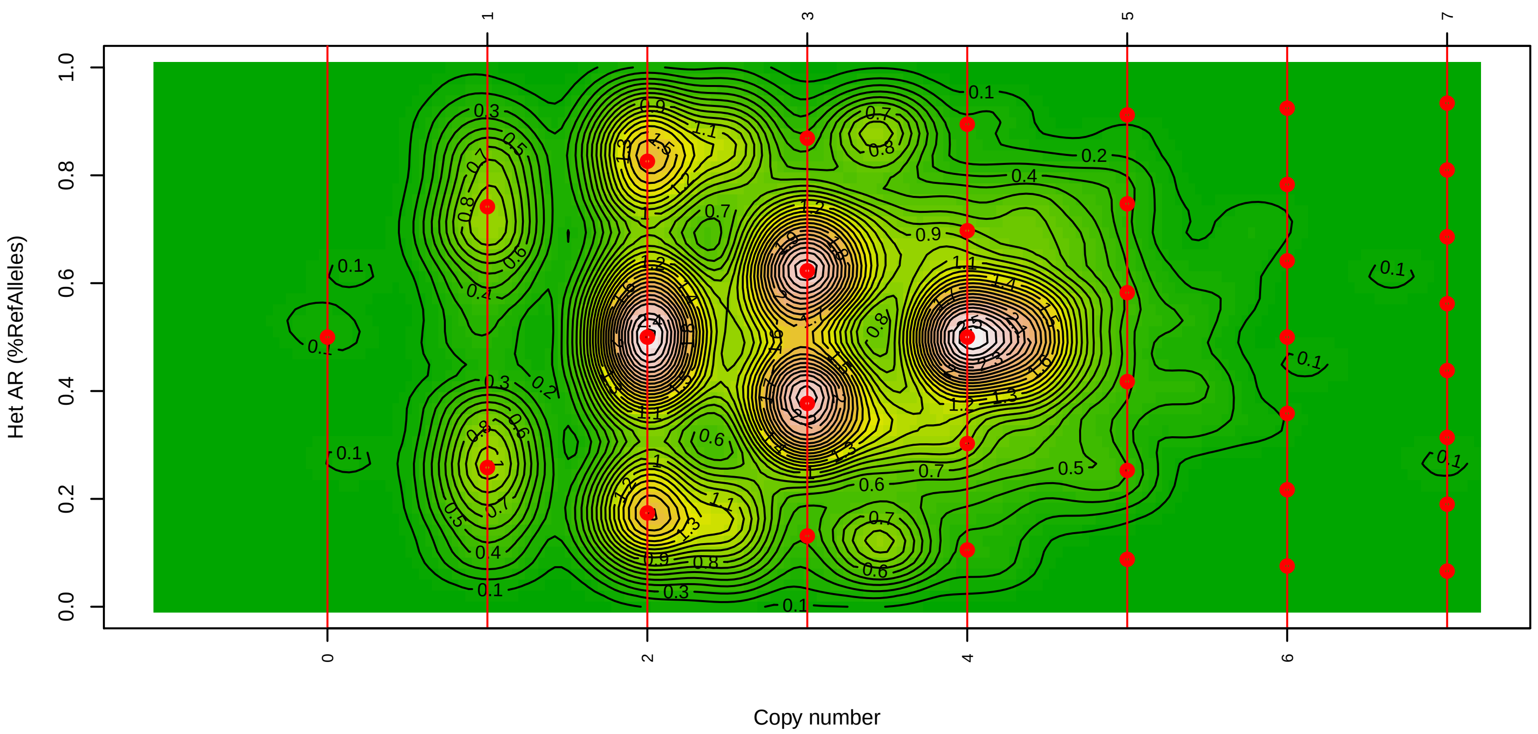
PCSI_0312_Pa_P_526

S:1.033, PLOIDY:1.884, %N:0.449, %T1:0.551



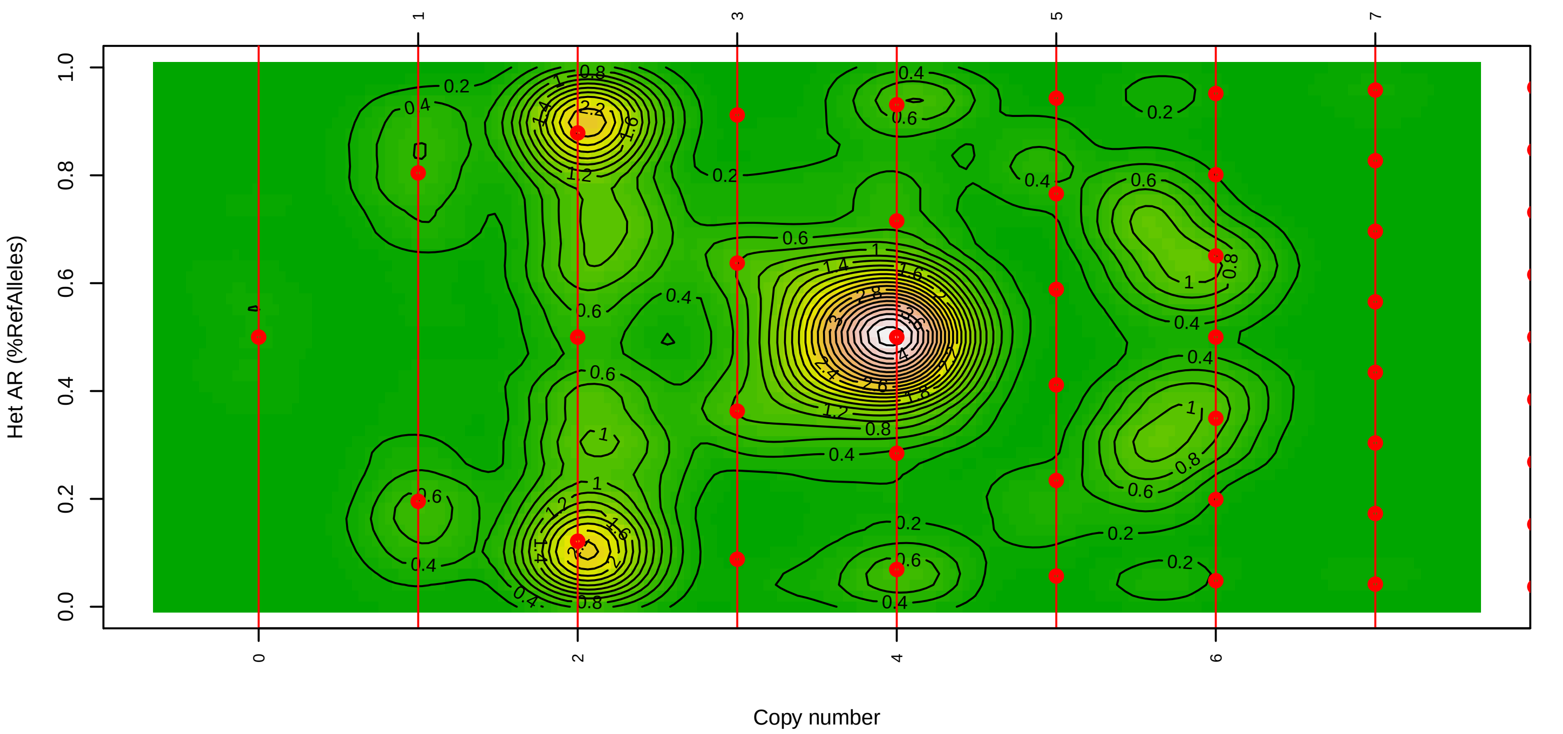
PCSI_0324_Pa_P_526

S:0.743, PLOIDY:3.061, %N:0.348, %T1:0.652



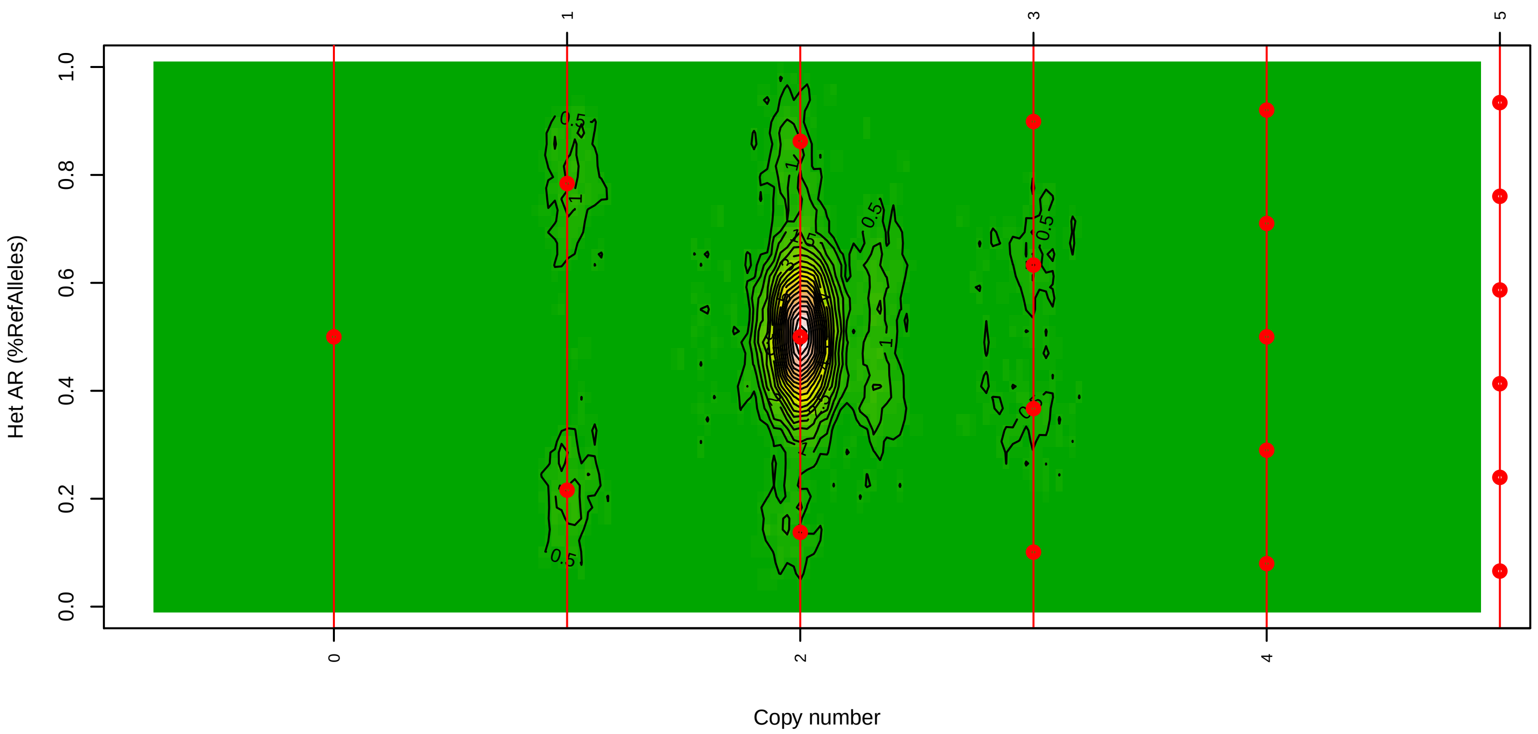
PCSI_0325_Pa_P_526

S:0.638, PLOIDY:3.499, %N:0.243, %T1:0.757



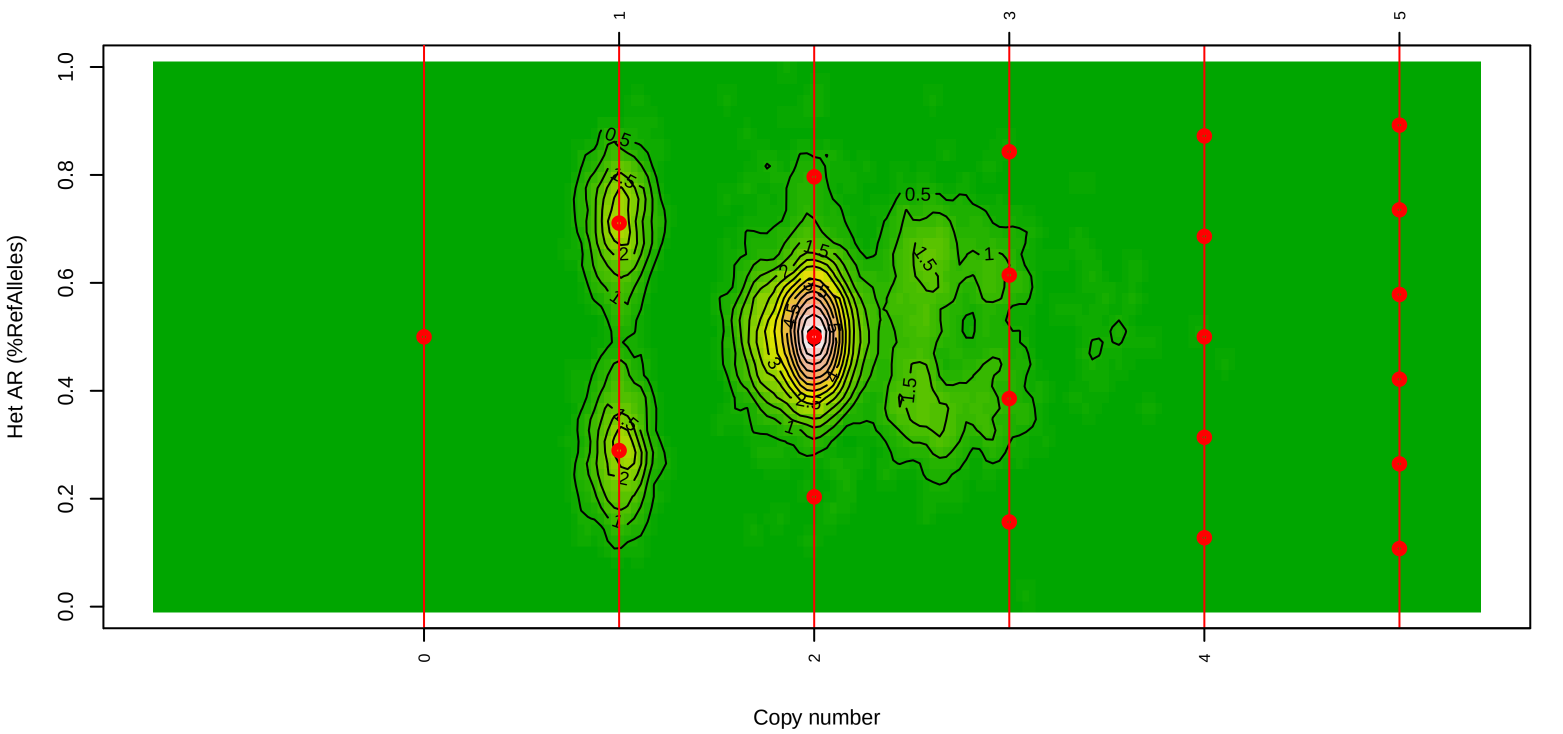
PCSI_0326_Pa_P_526

S:0.975, PLOIDY:2.071, %N:0.275, %T1:0.725



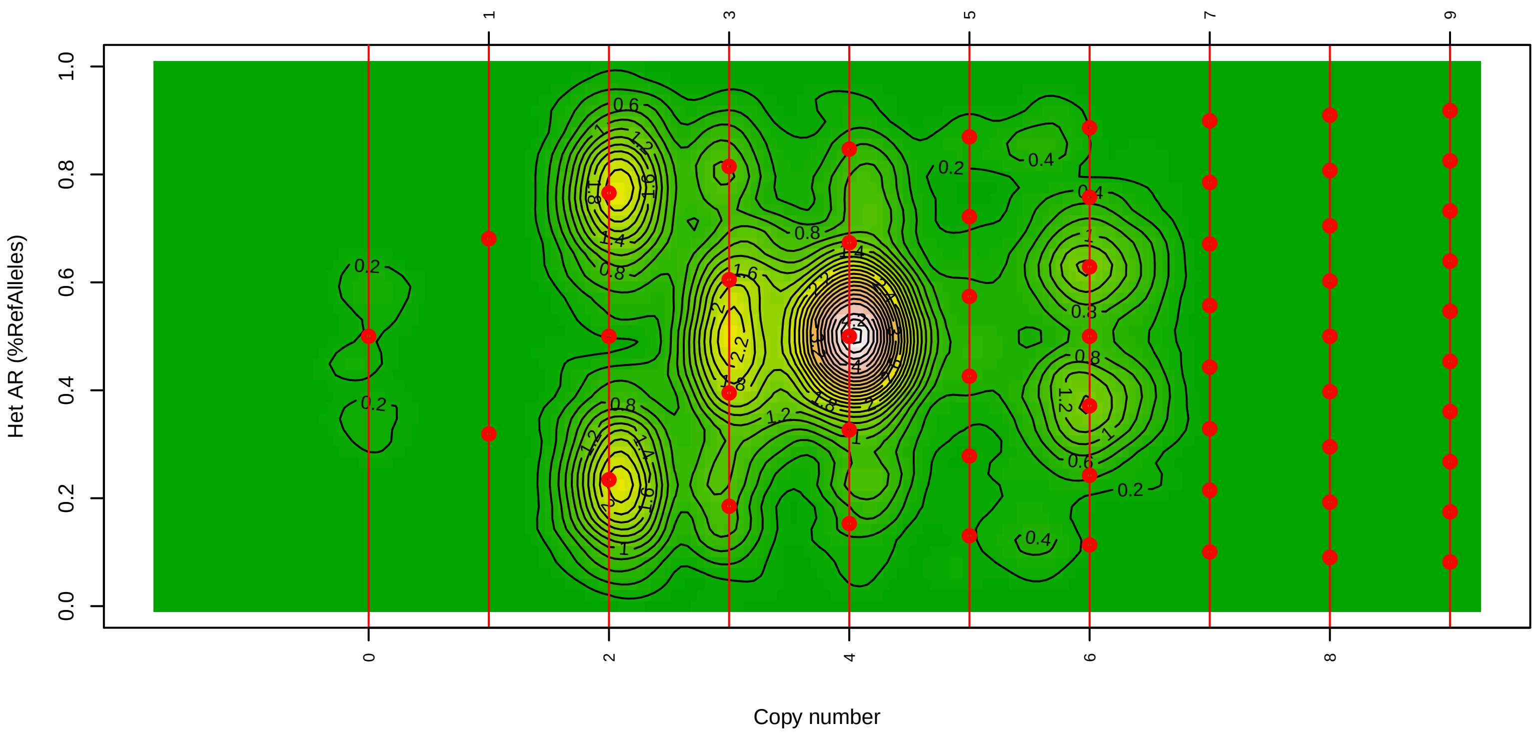
PCSI_0329_Pa_P_526

S:0.996, PLOIDY:2.013, %N:0.407, %T1:0.593



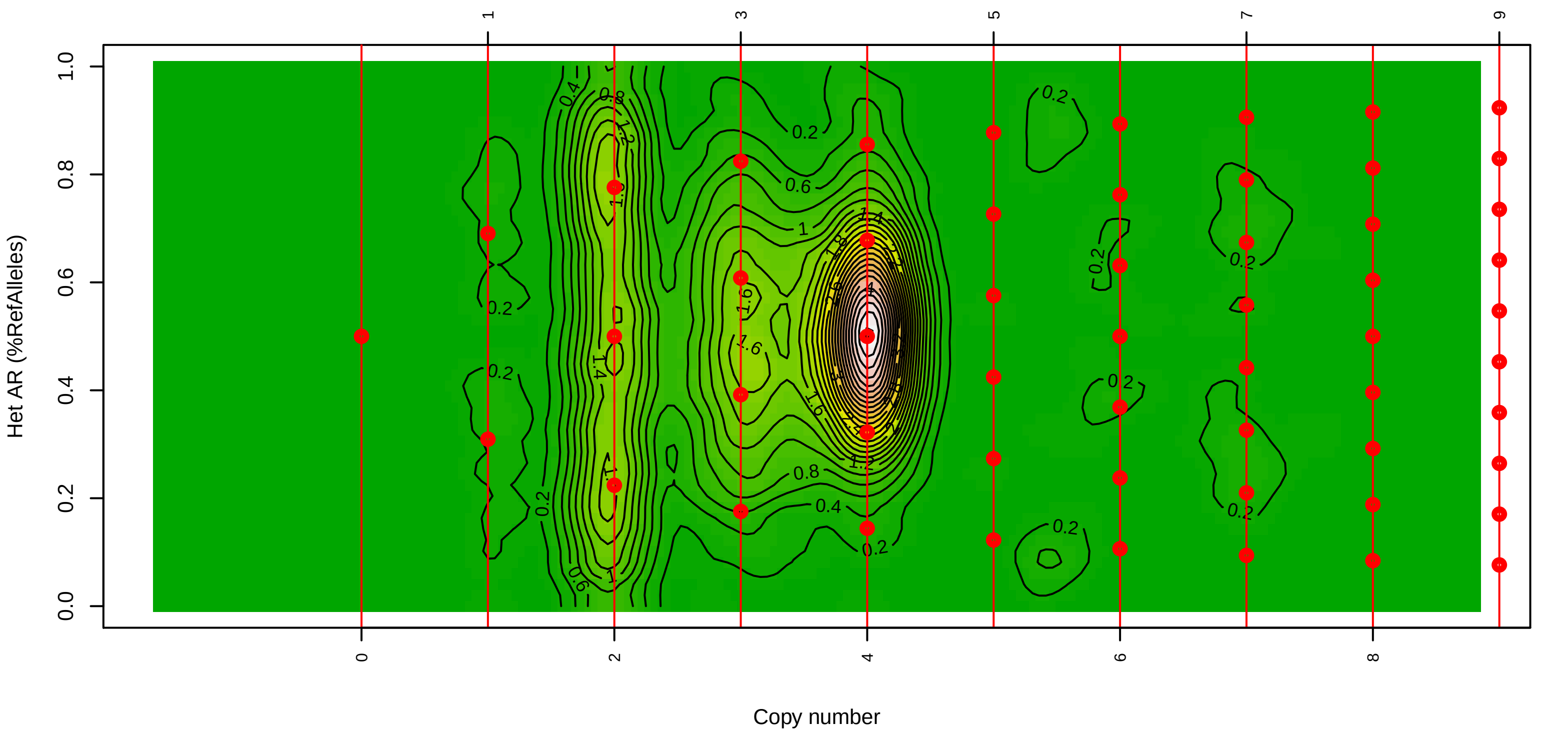
PCSI_0338_Pa_P_526

S:0.685, PLOIDY:3.733, %N:0.469, %T1:0.531

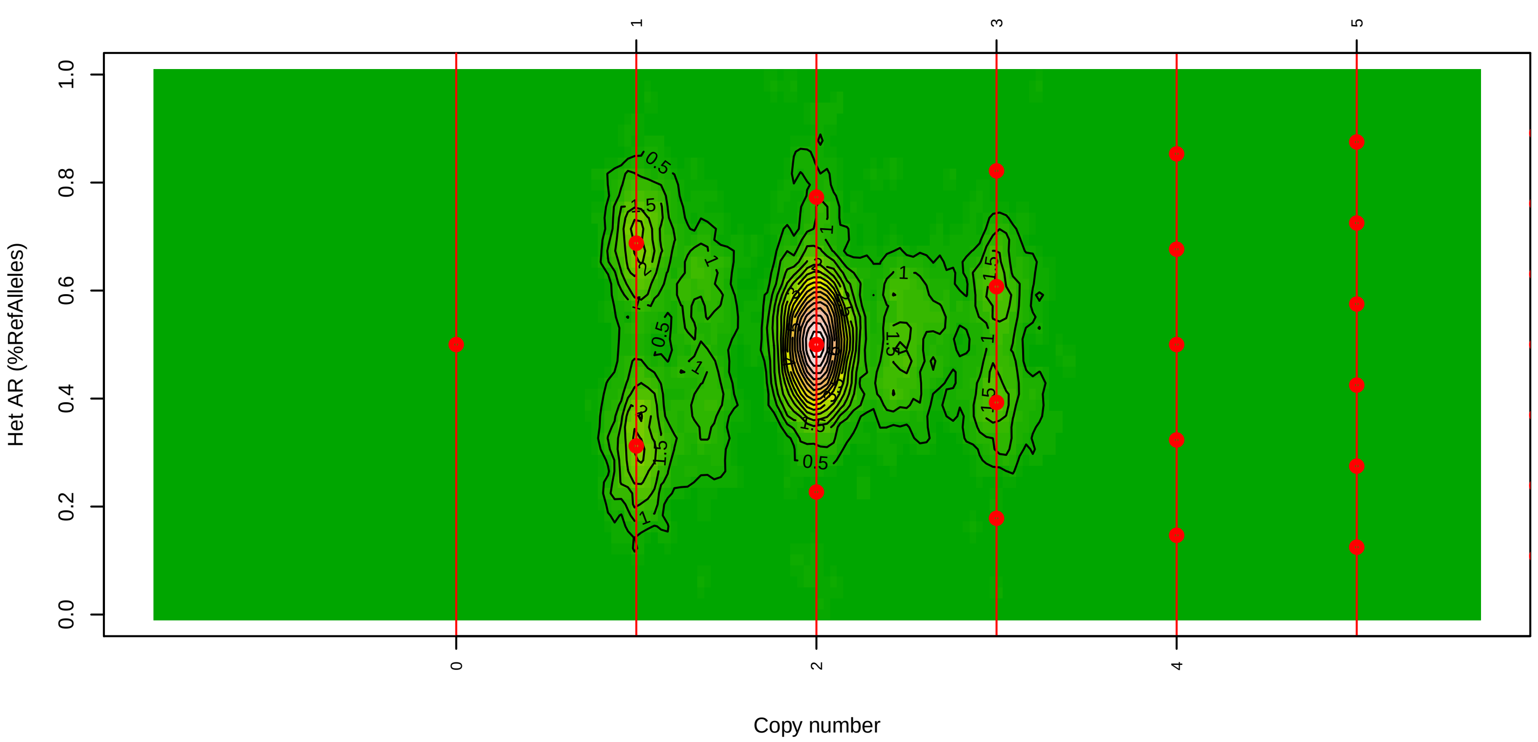


PCSI_0341_Pa_P_526

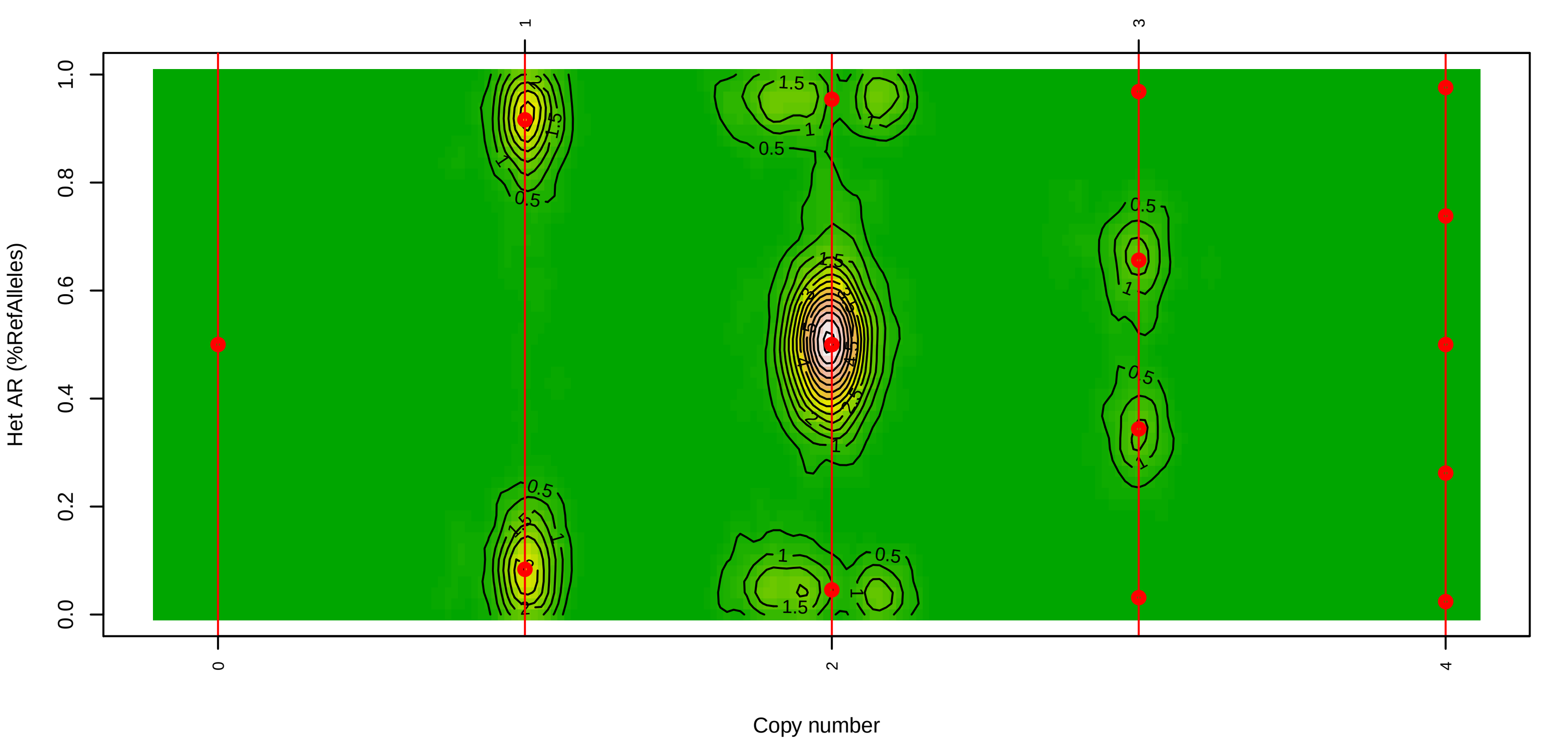
S:0.693, PLOIDY:3.601, %N:0.448, %T1:0.552



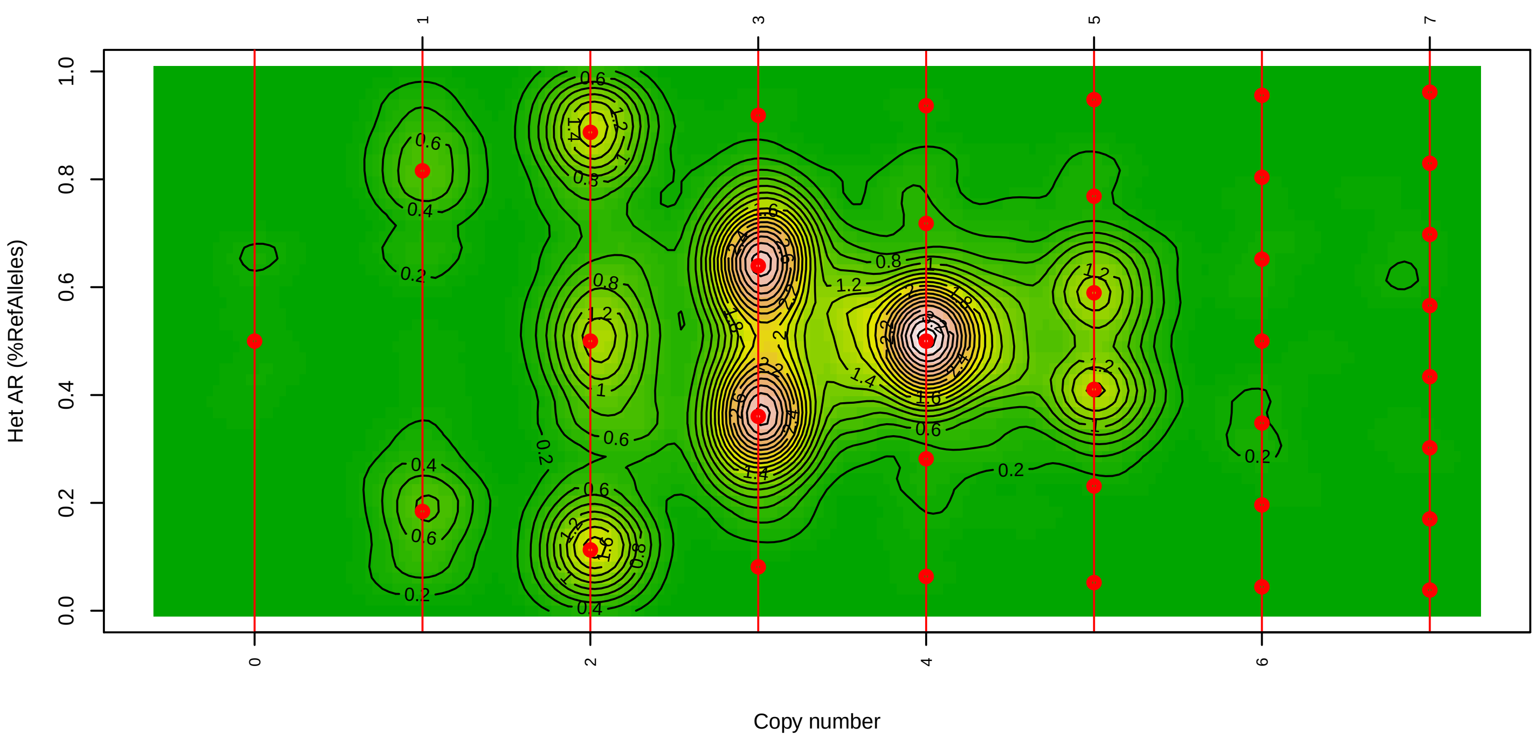
PCSI_0344_Pa_P_526


S:0.999, PLOIDY:2.003, %N:0.454, %T1:0.546

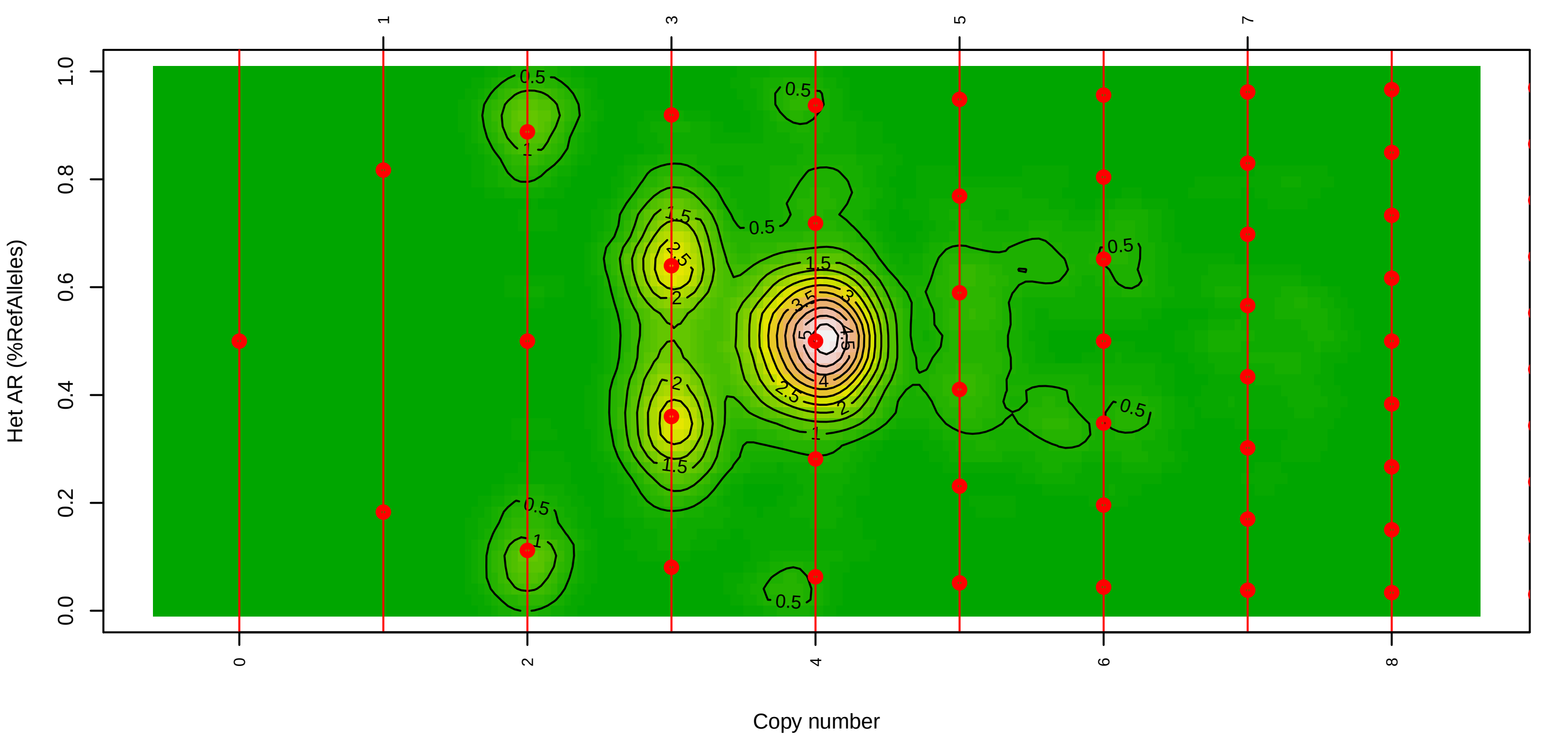
PCSI_0345_Pa_P_526


S:1.023, PLOIDY:1.95, %N:0.091, %T1:0.909

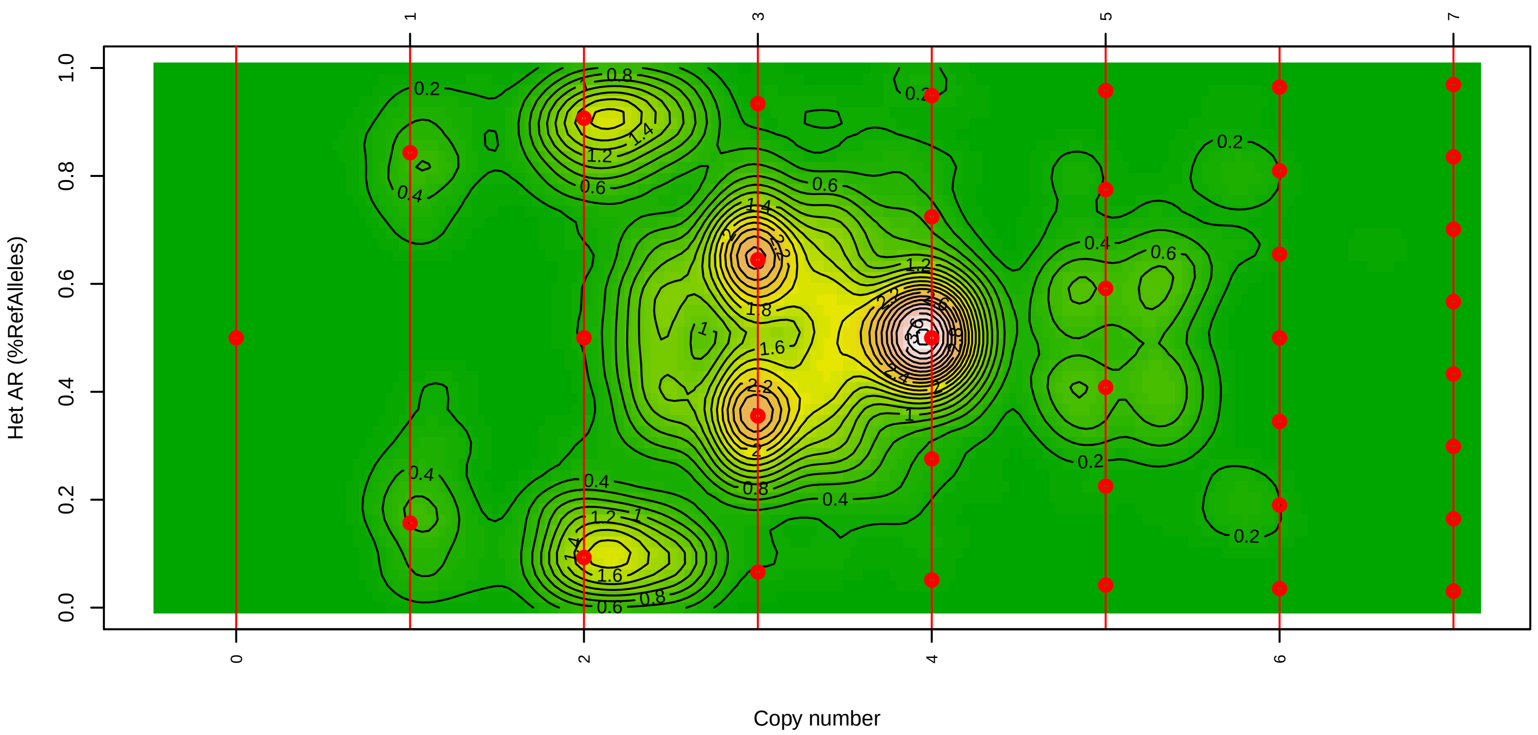
PCSI_0347_Pa_P_526


S:0.657, PLOIDY:3.35, %N:0.226, %T1:0.774

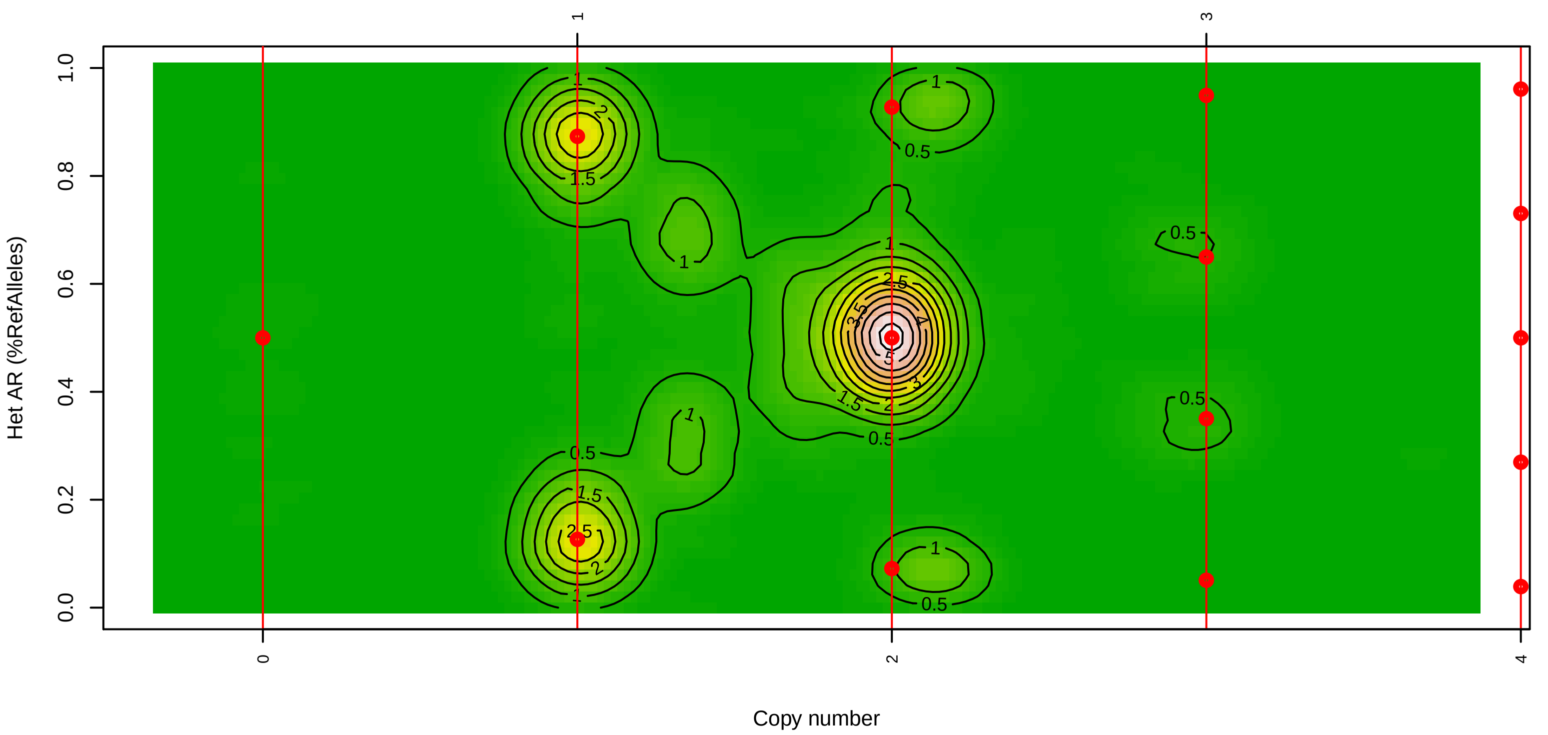
PCSI_0356_Pa_P_526


S:0.562, PLOIDY:4.007, %N:0.224, %T1:0.776

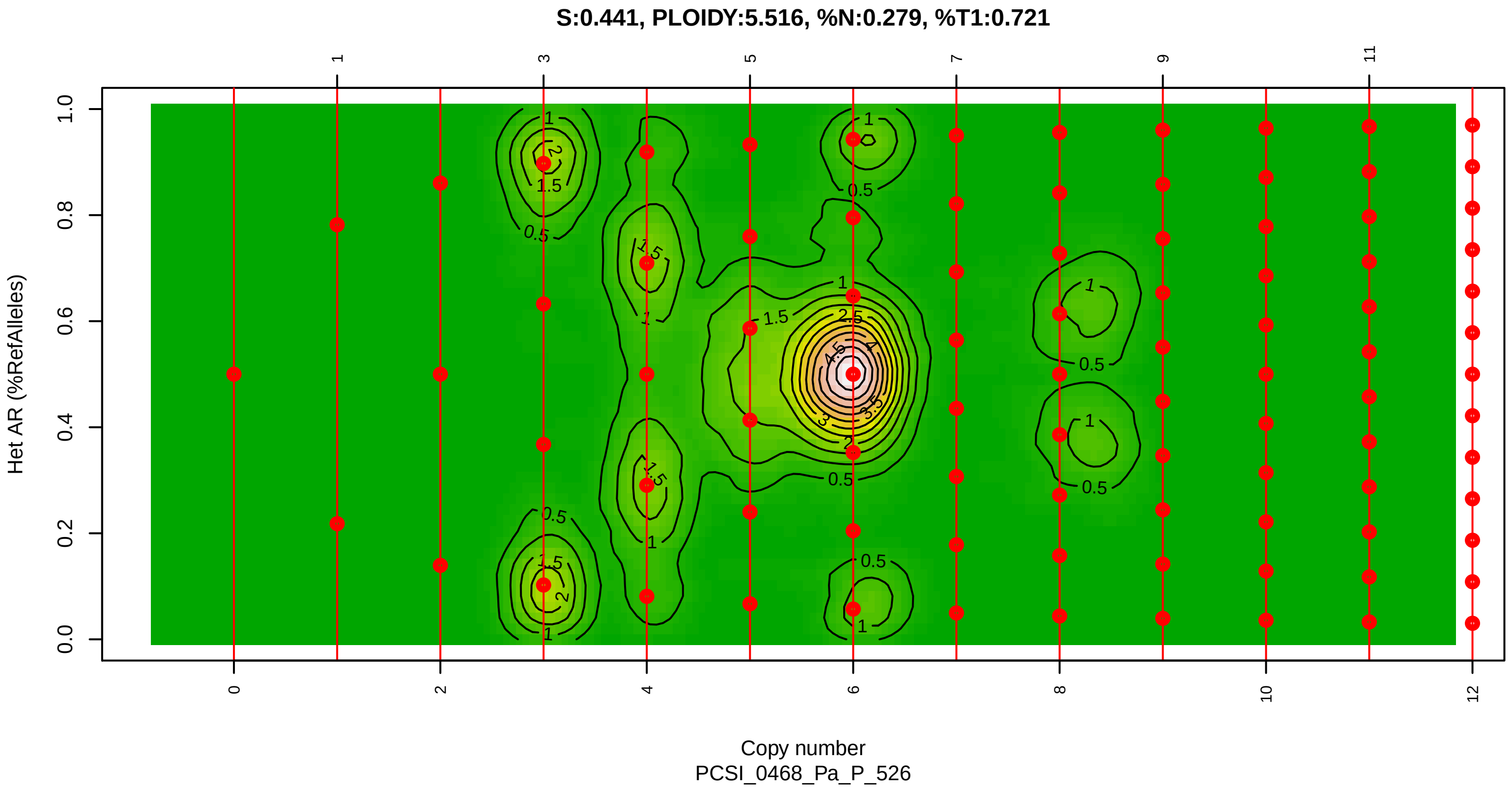
PCSI_0465_Pa_P_526


S:0.647, PLOIDY:3.34, %N:0.186, %T1:0.814

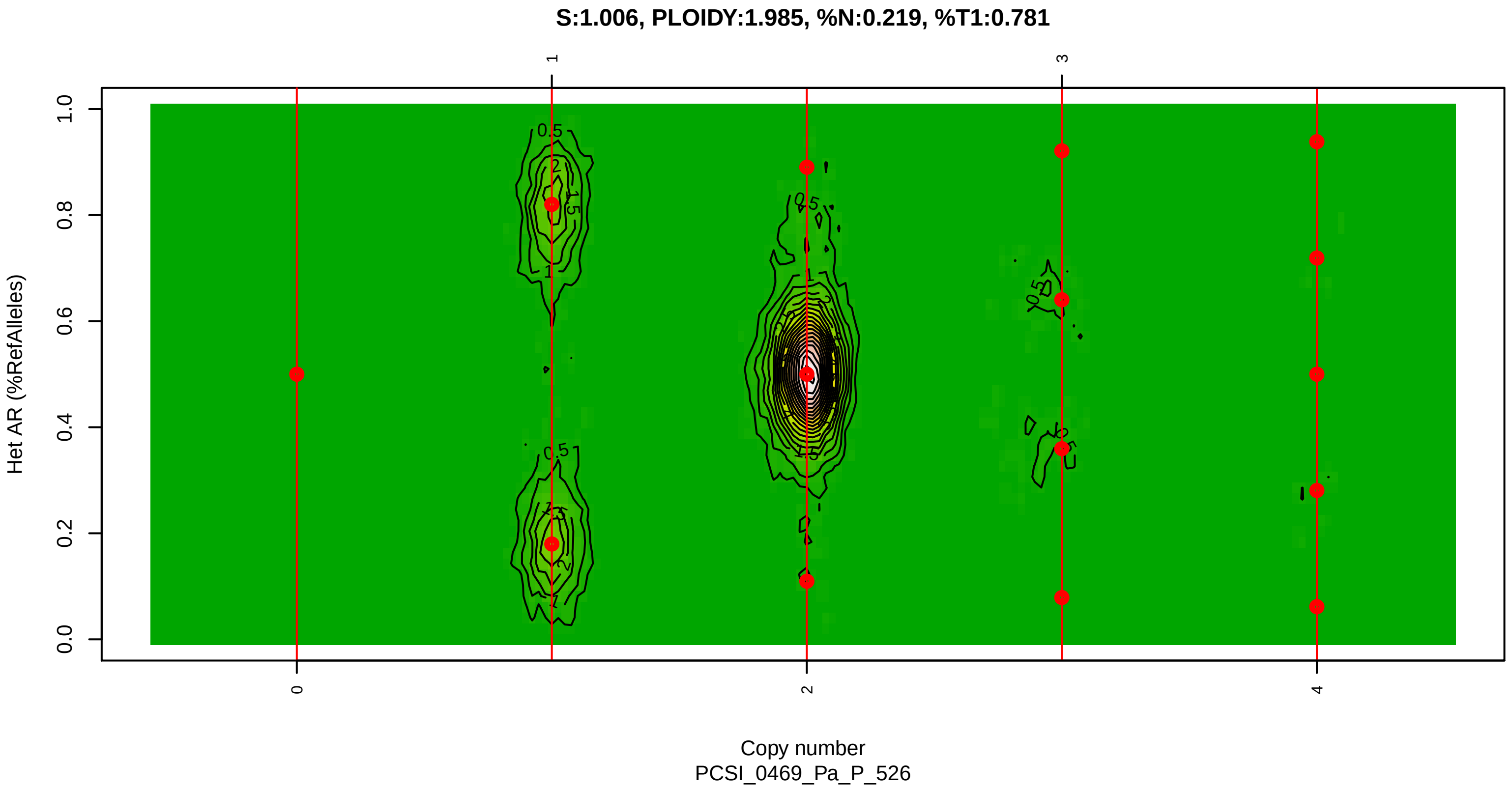
PCSI_0466_Pa_P_526


S:1.114, PLOIDY:1.76, %N:0.145, %T1:0.855

PCSI_0467_Pa_P_526


S:0.441, PLOIDY:5.516, %N:0.279, %T1:0.721

PCSI_0468_Pa_P_526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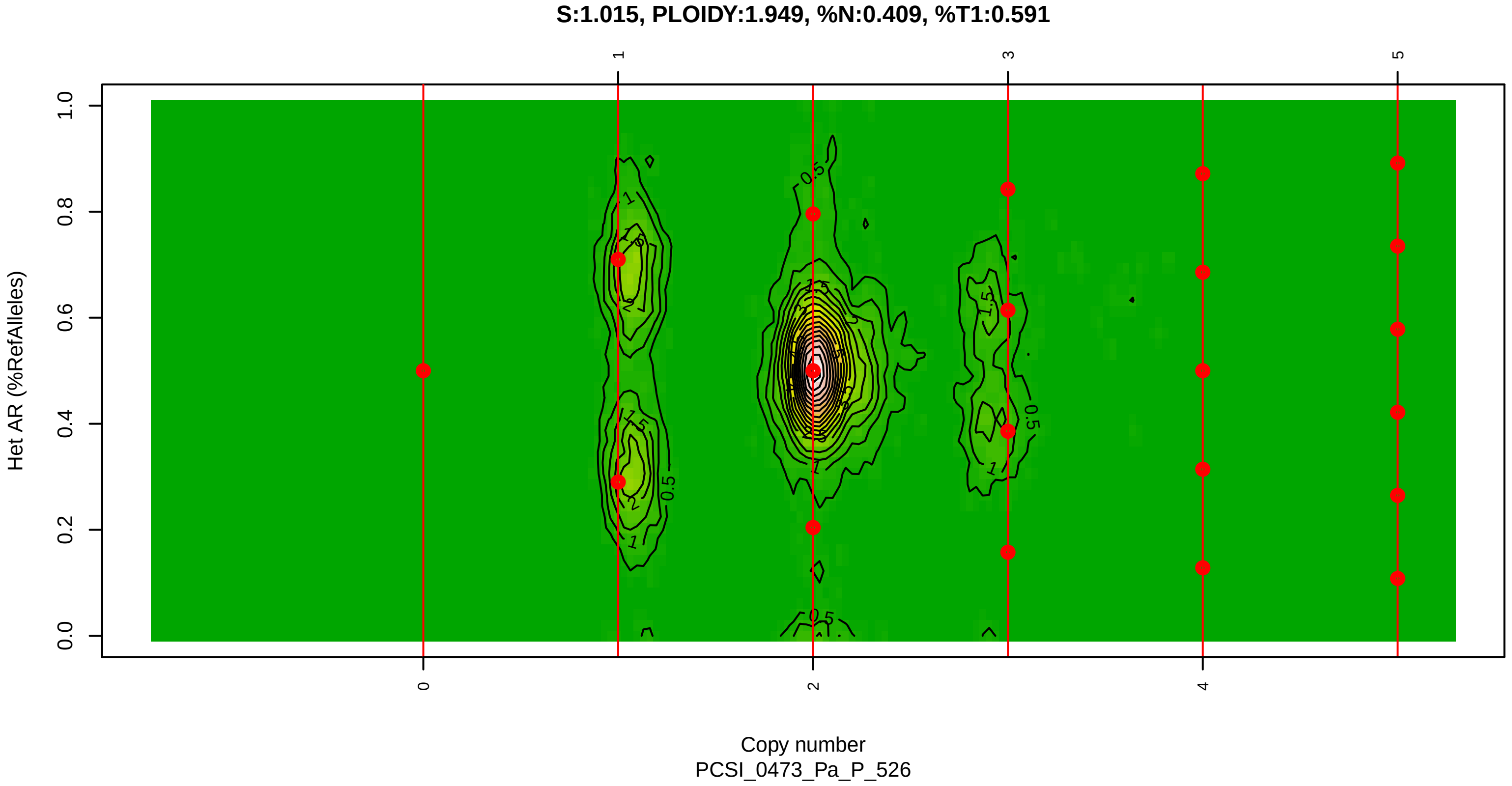
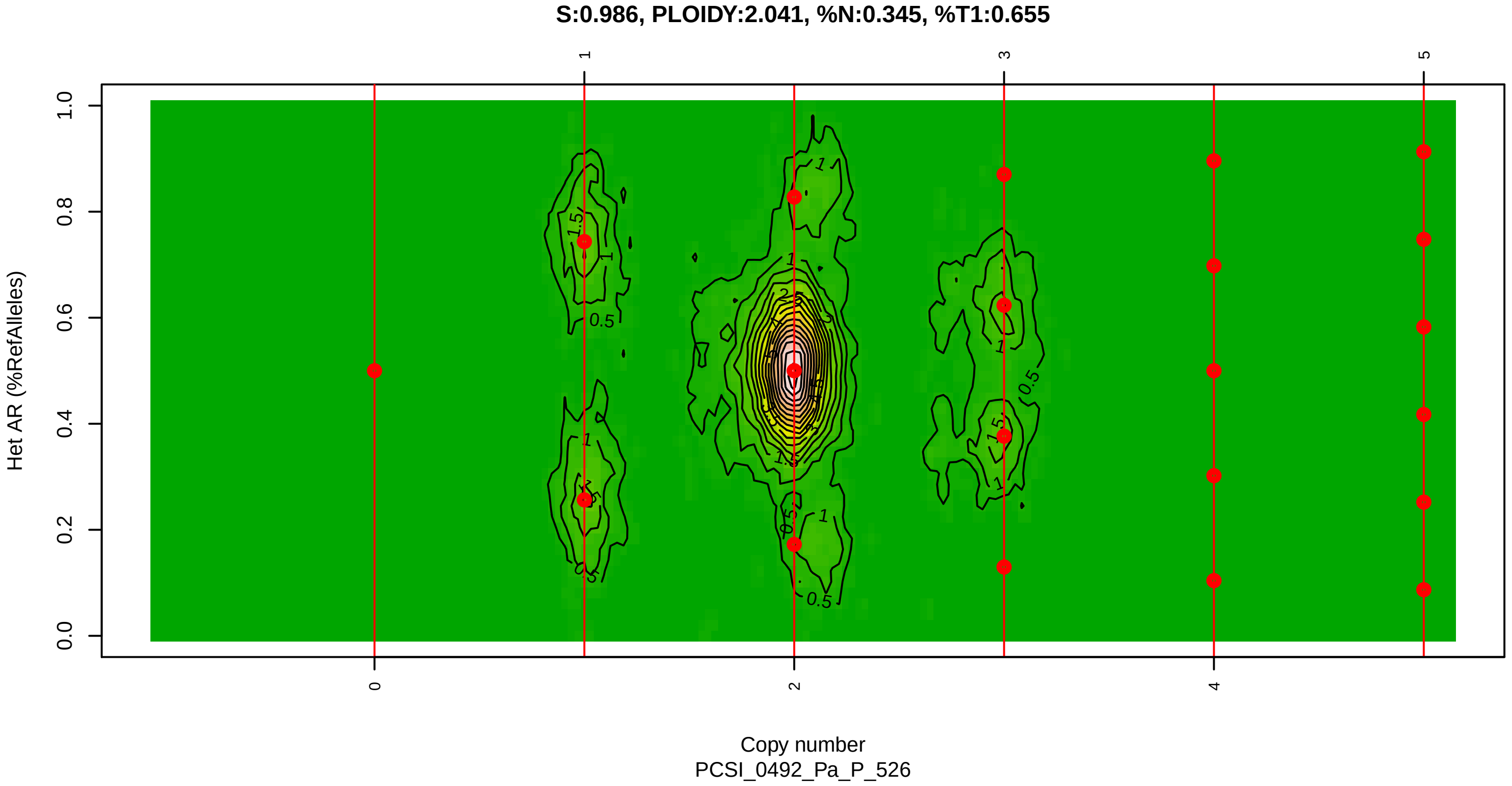
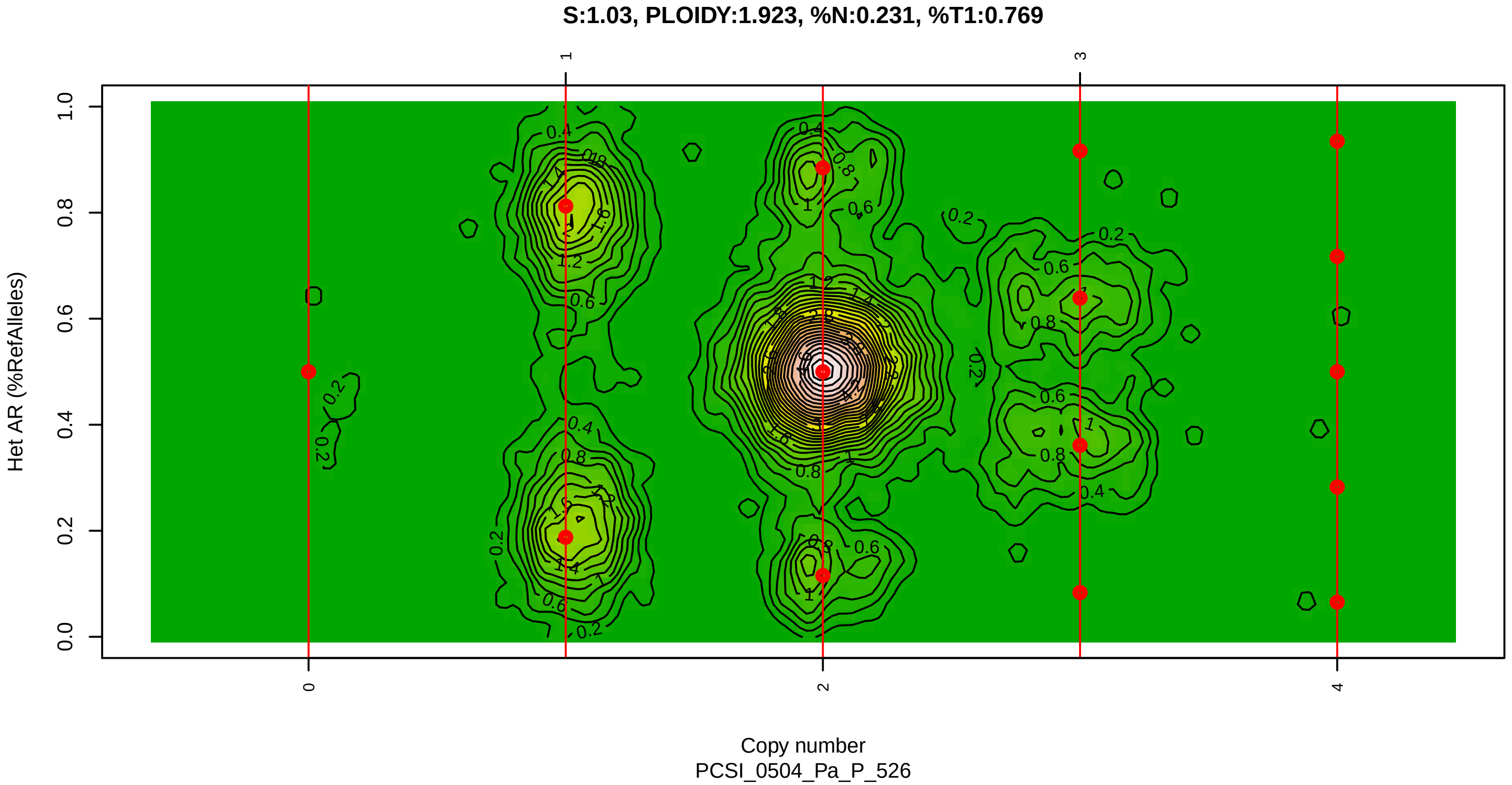
PCSI_0469_Pa_P_526


S:1.015, PLOIDY:1.949, %N:0.409, %T1:0.591

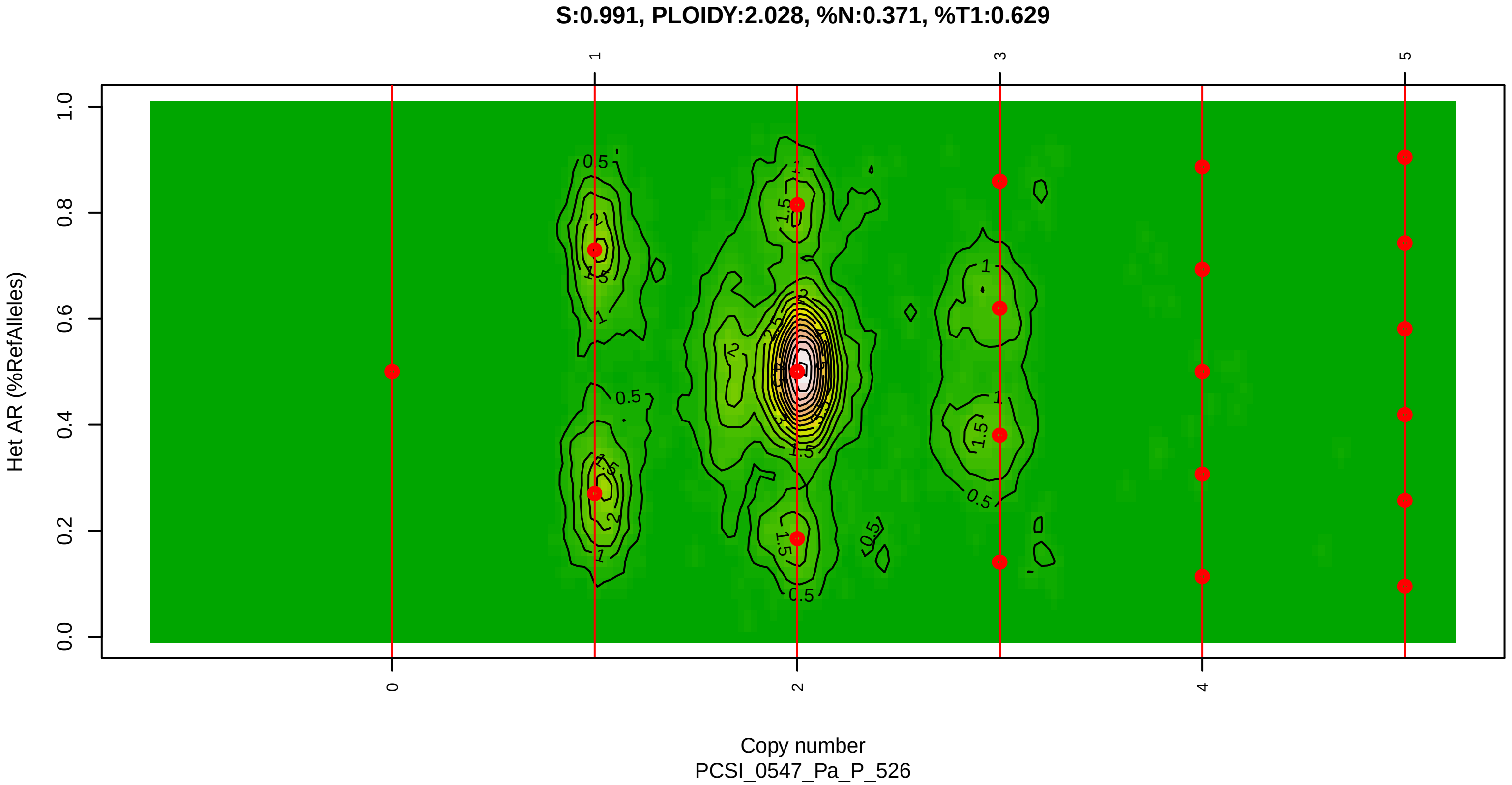
PCSI_0473_Pa_P_526


S:0.986, PLOIDY:2.041, %N:0.345, %T1:0.655

PCSI_0492_Pa_P_526

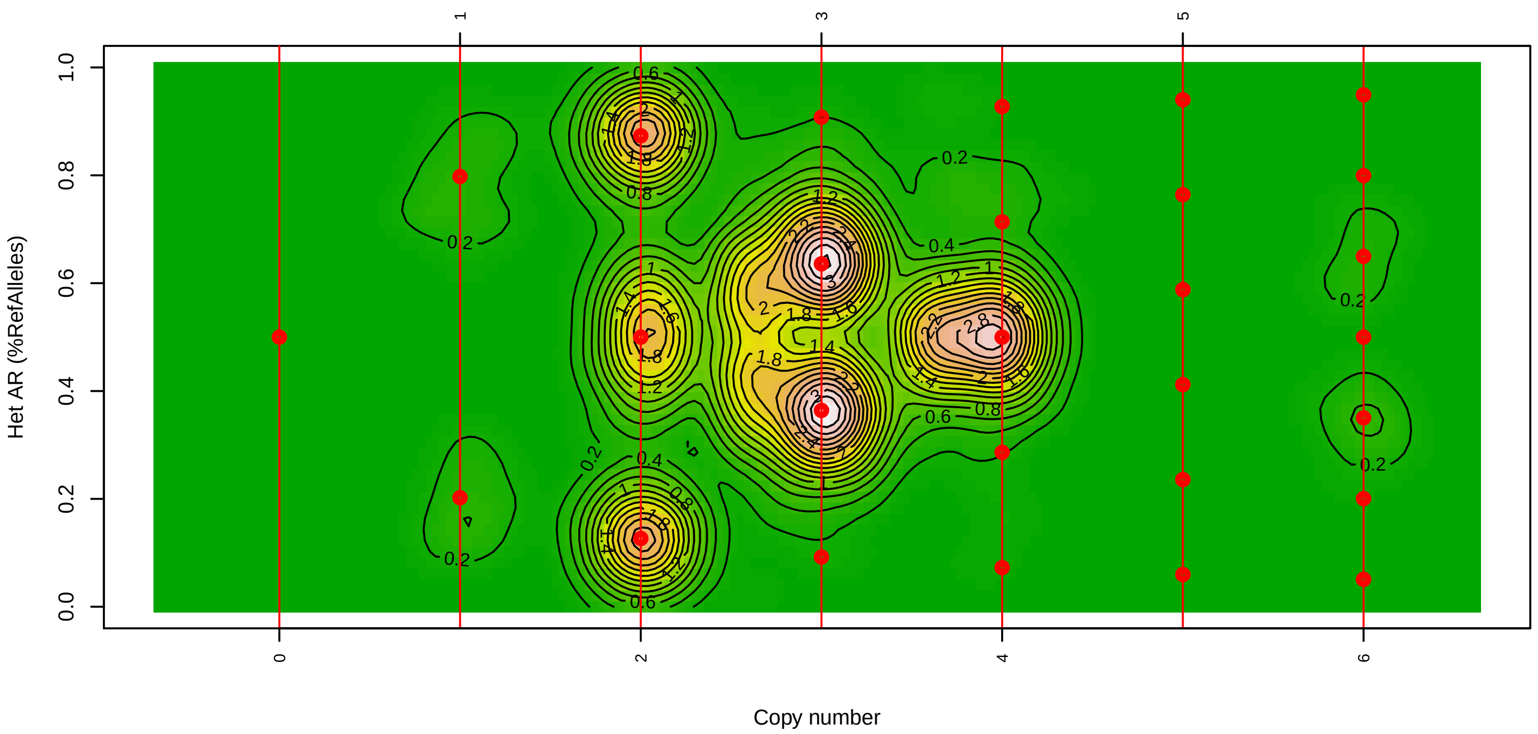

S:1.03, PLOIDY:1.923, %N:0.231, %T1:0.769

PCSI_0504_Pa_P_526


S:0.991, PLOIDY:2.028, %N:0.371, %T1:0.629

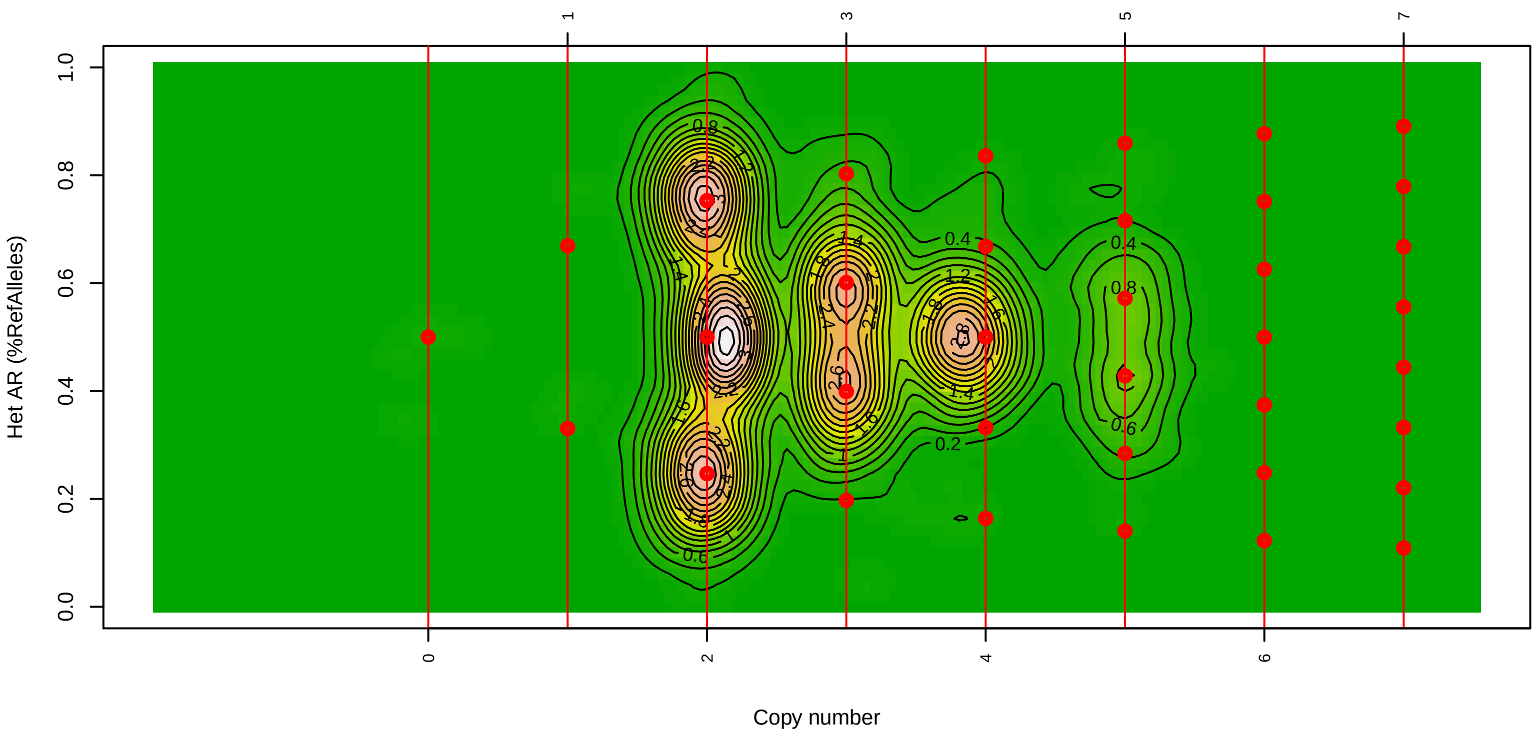
PCSI_0547_Pa_P_526

S:0.733, PLOIDY:2.975, %N:0.253, %T1:0.747



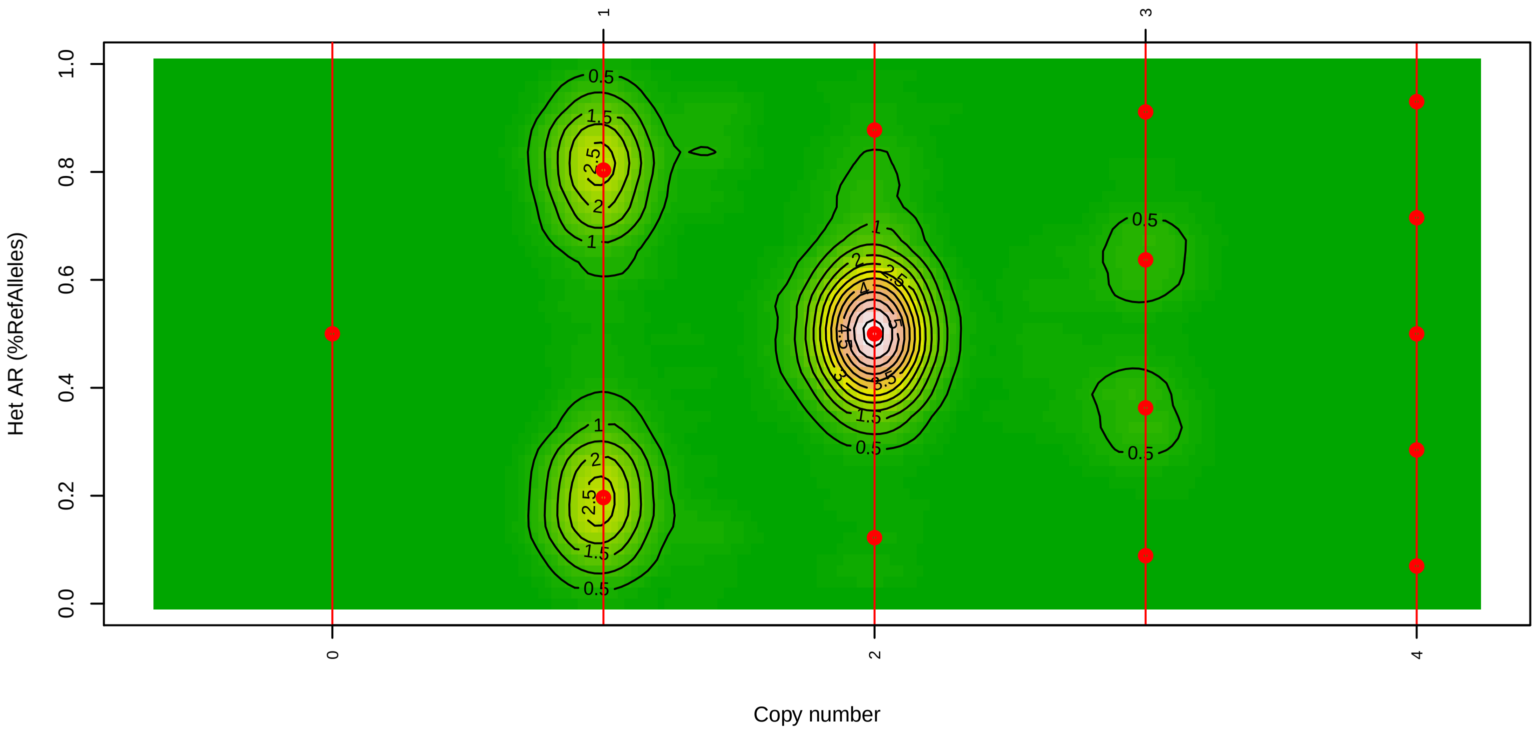
PCSI_0549_Pa_P_5266

S:0.834, PLOIDY:2.788, %N:0.494, %T1:0.506



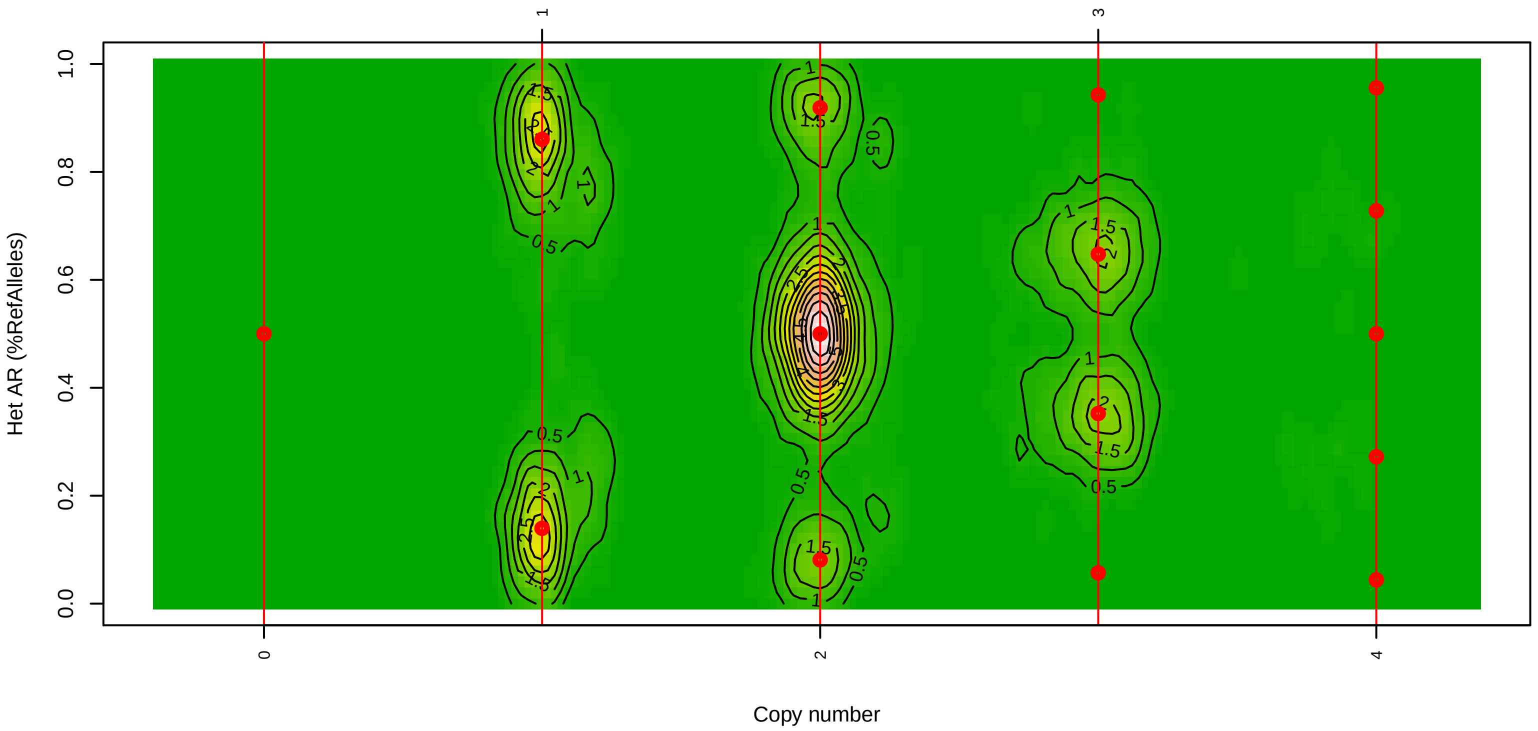
PCSI_0572_Pa_P_526

S:1.087, PLOIDY:1.787, %N:0.245, %T1:0.755



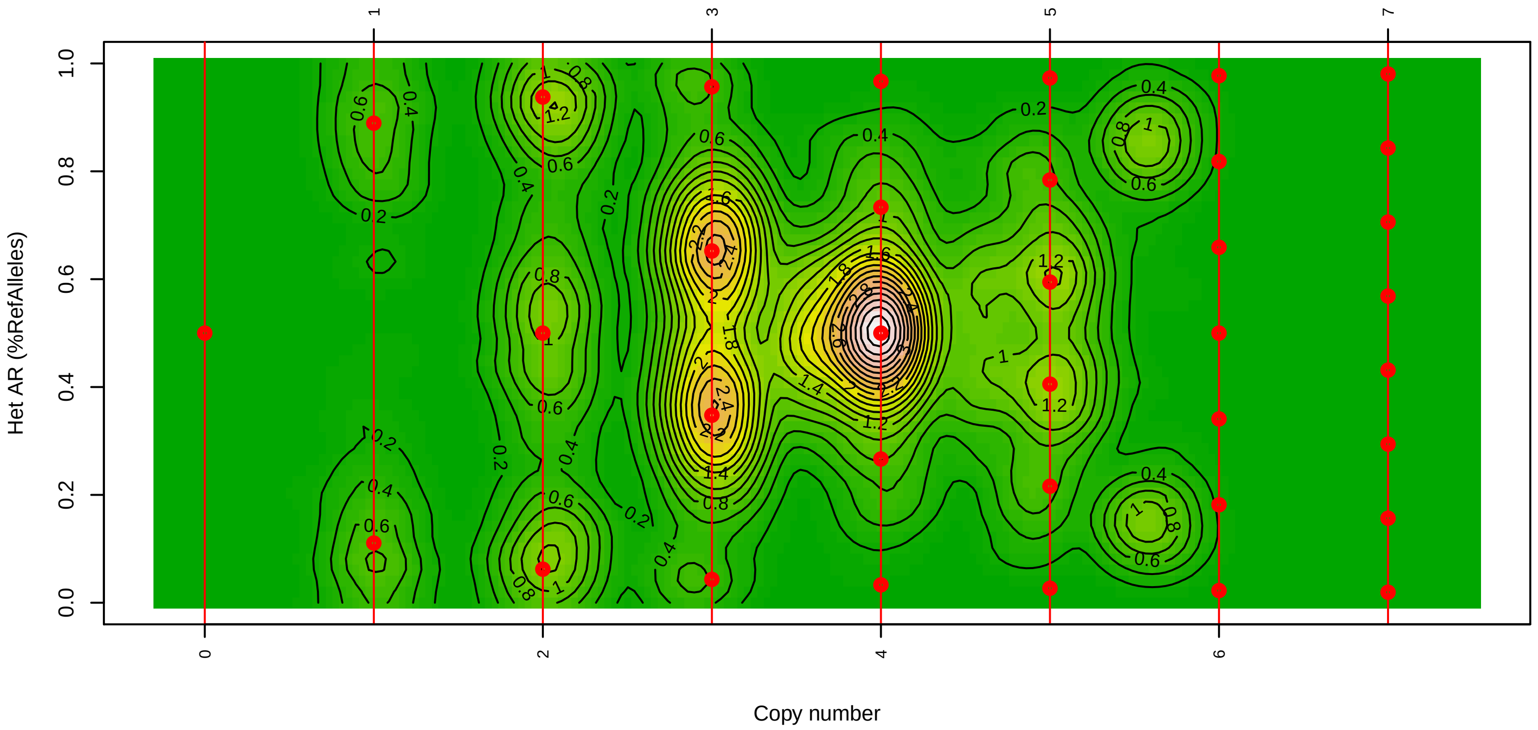
RAMP_0003_Pa_P_526

S:1.005, PLOIDY:1.988, %N:0.162, %T1:0.838



RAMP_0006_Pa_P_526

S:0.585, PLOIDY:3.623, %N:0.125, %T1:0.875



RAMP_0007_Pa_P_526