Supplementary tables and figures
„Detecting adaptive changes in gene copy number distribution accompanying the human out-of-Africa expansion“ by Otto et al.

Suppl. 1:

Table S1: List of gene families from Brahmachary *et al.* (2014) and description of filtering procedure. After filtering, 42 gene families were chosen for further analysis

Suppl. 2:

Table S2: Positions in genome assembly hg38 of gene copies from 33 MANE (Morales *et al.* 2022) selected gene families. Note: this is a subset of the 42 gene families which remained after filtering (Table S1).

Suppl. 3:

Tajima’s *D* profiles.
Tajima’s *D* was calculated in a 1 Mb region centered in the respective gene family (positions from Suppl. Table S2) in sliding windows of size 10 kb and based on SNPs from the 1k human genomes project phase III (http://ftp.1000genomes.ebi.ac.uk/vol1/ftp/release/20130502/)

(Raw data shown in separate file "TajD-raw.pdf")

Suppl. 4 and 5:

Introgression profiles for (a) individual gene families and (b) summed over all gene families. Introgression in gene families was calculated as the total number of introgressed SNPs in a 10Mb window centered in the respective gene family and in sliding windows of size 100 kb. Introgression data from Browning et al. (2018).

(Raw data shown in separate file "introgression-raw.pdf")

Table S1 List of all gene families from Brahmachary *et al.* (2014). We applied three levels of filtering: first (comment in gray), we excluded microsatellites and all genes which are sex-chromosome linked. Second (comment in orange), we excluded gene families which displayed either very little variation (mean copy number in YRI is less than 5 copies; one or more individuals in CEU or CHB have only one copy; coefficient of variation smaller than 0.004) or which are extremely large (mean copy number in YRI larger than 60). Third (comment in red), gene families were excluded for which neither the t-test nor the F-test between YRI and CEU or CHB turned out to be significant ('homogeneous'). The remaining families (green checkmark) were investigated further.

Gene Name	Filtering	Gene Name	Filtering	Gene Name	Filtering
AMY1A	✓	GSTM	<5 copies	NXF2	sex-linked
ANAPC11	min copies <2	GSTT2	min copies <2	OPN1MW	sex-linked
ANKRD20A3	✓	GTF2H2C	<5 copies	ORM1	<5 copies
ANXA8L1	<5 copies	GTPBP6	sex-linked	P4HB	min copies <2
AREG	min copies <2	GUSBP1	✓	PCYT2	min copies <2
ARL17B	<5 copies	H2AFB1	sex-linked	PGA3	✓
ATG4B	min copies <2	HGD	min copies <2	PGAM4	sex-linked
AURKAIP1	min copies <2	HIST2	✓	PLGLB2	low CV
BOLA2B	✓	HP	min copies <2	PPIAP21	✓
BPY2	sex-linked	HRNR	min copies <2	PRAMEF14	✓
BTNL8	min copies <2	HSFY2	sex-linked	PRAMEF20	✓
C16orf54	min copies <2	KIF22	min copies <2	PRAMEF5	✓
C4B	<5 copies	KIR2DL2	homogeneous	PRAMEF8	✓
C6orf124	min copies <2	KIR2DL4	min copies <2	PRR11	✓
CBWD3	✓	KIR2DL5A	homogeneous	PRR20A	✓
CCL3	min copies <2	KIR2DS2	homogeneous	PRR20A (probe2)	excluded (duplicate)
CCL4	min copies <2	KIR3DP1	min copies <2	PRY2	sex-linked
CCR2	min copies <2	KLRC2	<5 copies	PSG11	sex-linked
CCR5	min copies <2	KPNA2	<5 copies	PSG3	✓
CCRL2	min copies <2	KRT39	min copies <2	PTPN20A	<5 copies
CDC37P1	✓	KRT40	min copies <2	PYCR1	min copies <2
CDY1B	sex-linked	KRTAP1-1	min copies <2	RBMY1E	sex-linked
CFC1	<5 copies	KRTAP2-1	min copies <2	REXO1L1	>60 copies
CKMT1A	<5 copies	KRTAP3-1	min copies <2	REXO1L1 (probe2)	>60 copies
CLEC18A	✓	KRTAP4-1	min copies <2	RGPD1	✓
CR1	<5 copies	KRTAP5-1	min copies <2	RGPD6	low CV
CRLF2	sex-linked	KRTAP7-1	min copies <2	RHOXF2	sex-linked
CSAG2	sex-linked	KRTAP8-1	min copies <2	RPS17	<5 copies
CSH	✓	KRTAP9-1	<5 copies	RSPH10B	<5 copies
CT45	sex-linked	LCE2	<5 copies	SCRT1	min copies <2
CT47 (probe 1)	sex-linked	LIMS3	✓	SCXB	min copies <2
CT47 (probe 2)	sex-linked	LOC100506776	min copies <2	SERF1B	min copies <2
CTAG1B	sex-linked	LOC23117	✓	SFTPA1	<5 copies
D2HGDH	min copies <2	LOC389852	sex-linked	SIRT7	min copies <2
DAZ1	sex-linked	LOC653606	✓	SLX1B	homogeneous
DEFA1	✓	LOC727800	min copies <2	SMN2	min copies <2
DEFB103A	min copies <2	LOC728932	<5 copies	SNAR-A1	homogeneous
DEFB104A	<5 copies	LPA	<5 copies	SPAG11	min copies <2
DEFB105A	min copies <2	MAFG	<5 copies	SPANXA1	sex-linked
DEFB106A	min copies <2	MAGEA2	sex-linked	SPDYE3	✓
DEFB107A	min copies <2	MAGEA9	sex-linked	SSX4	sex-linked
DEFB130	✓	MGC59937	min copies <2	SULT1A1	min copies <2
DGAT1	min copies <2	MRC1	min copies <2	SULT1A3	✓
DHRS4	<5 copies	MSat1	microsatellite	TAF9B	sex-linked
DMRTC1	sex-linked	MSat10	microsatellite	TAS1R3	min copies <2
DTYMK	min copies <2	MSat11	microsatellite	TBC1D3	✓
DUX4	>60 copies	MSat12	microsatellite	TBC1D3 (probe2)	excluded (duplicate)
EIF3C	<5 copies	MSat13	microsatellite	TCEB3C	✓
ELA	<5 copies	MSat14	microsatellite	THAP4	min copies <2
F8A2	sex-linked	MSat15	microsatellite	TMEM106A	min copies <2
FAM156A	sex-linked	MSat2	microsatellite	TMEM167B	min copies <2
FAM203A	min copies <2	MSat5	microsatellite	TMPRSS11E	min copies <2
FAM21B	<5 copies	MSat6	microsatellite	TP53TG3	✓
FAM23A	min copies <2	MSat7	microsatellite	TRIM49L1	✓
FAM72A	✓	MSat8	microsatellite	TSPY4	sex-linked
FAM75A1	✓	MSat9	microsatellite	UGT2B15	min copies <2
FAM75A5	✓	MUC12	✓	USP17	>60 copies
FAM90A	>60 copies	MUC5AC	min copies <2	XAGE1	sex-linked
FCGBP	✓	NBPF10	>60 copies	XAGE2	sex-linked
FCGR	min copies <2	NBPF11	✓	XKRY2	sex-linked
FOXD4L2	✓	NBPF16	✓	ZFP62	min copies <2
FUSIP1	<5 copies	NDUFB4	min copies <2	ZG16	min copies <2
GAGE6	sex-linked	NEB	min copies <2	ZNF658B	✓
GOLGA6L9	✓	NPB	min copies <2		
GOLGA8G	✓	NPIP	✓		

Table S2: Positions of genes in hg38

Gene	Chromosome	Start	End
AMY1A	chr1	103655519	103664554
BOLA2B	chr16	29453588	29454964
BOLA2B	chr16	30192932	30193666
CBWD3	chr9	65666374	65734041
CBWD3	chr9	68241866	68300035
CLEC18A	chr16	69950232	69968478
CSH	chr7	123763708	123877481
CSH	chr16	81081945	81096395
CSH	chr17	18327873	18363560
CSH	chr17	63872012	63873729
CSH	chr17	63894918	63896574
CSH	chr17	63909602	63911280
CSH	chr19	11435290	11450968
CSH	chr19	58498333	58512028
DEFA1	chr8	6977649	6980120
DEFA1	chr8	6996766	6999198
DEFB130	chr8	12064389	12071747
DEFB130	chr8	12310962	12318316
FAM72A	chr1	206186179	206205773
FAM75A1	chr9	39355667	39361962
FAM75A5	chr9	60914372	60920653
FOXD4L2	chr9	65737146	65738396
FOXD4L2	chr9	68302867	68305084
GOLGA6L9	chr15	82429363	82439153
GOLGA8G	chr15	28519611	28533014
HIST2	chr1	143902386	143905977
HIST2	chr1	149782689	149812370
HIST2	chr1	149813225	149813693
HIST2	chr1	149832657	149833052
HIST2	chr1	149840687	149841208
HIST2	chr1	149842218	149842750
HIST2	chr1	149851061	149851594
HIST2	chr1	149852608	149853125
HIST2	chr1	149853262	149861159
HIST2	chr1	149884459	149886682
HIST2	chr1	149886918	149887411
HIST2	chr1	149887469	149887965

LIMS3	chr2	109898688	109925625
LIMS3	chr2	110386341	110473075
MUC12	chr7	100969565	101018936
NBPF11	chr1	148102151	148152281
NBPF16	chr1	144421390	144461669
NPIP	chr1	44221070	44355298
NPIP	chr16	11927263	11976643
NPIP	chr16	14703411	14726342
NPIP	chr16	14742533	14765462
NPIP	chr16	14937443	14952056
NPIP	chr16	15363613	15381467
NPIP	chr16	16379140	16393972
NPIP	chr16	18317919	18336736
NPIP	chr16	21834568	21857756
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NPIP	chr16	29381310	29406711
NPIP	chr16	30222897	30248479
NPIP	chr16	74374986	74392115
PGA3	chr11	61203515	61213098
PRAMEF14	chr1	13341892	13347134
PRAMEF20	chr1	13410450	13421328
PRAMEF5	chr1	13254198	13263435
PRAMEF8	chr1	13281223	13285137
PRR11	chr17	59155355	59206709
PRR20A	chr13	57140918	57143939
PRR20A	chr13	57147488	57150509
PRR20A	chr13	57154061	57157082
PRR20A	chr13	57160632	57163653
PRR20A	chr13	57167197	57170218
PSG3	chr19	42721642	42740486
RGPD1	chr2	86913577	87013976
SPDYE3	chr7	100306798	100322196
SULT1A3	chr16	30199255	30204310
TBC1D3	chr6	121079494	121335384
TBC1D3	chr8	123041961	123165173
TBC1D3	chr12	64759484	64881033
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TBC1D3	chr17	37923805	37935371
TBC1D3	chr17	37978155	37989060
TBC1D3	chr17	38003976	38014908
TBC1D3	chr17	38057693	38068634
TBC1D3	chr17	38118408	38138868
TBC1D3	chr17	38181659	38192555
TP53TG3	chr16	32251603	32255928
TP53TG3	chr16	32673528	32676165
TP53TG3	chr16	33191770	33196858
TP53TG3	chr16	33301850	33306945
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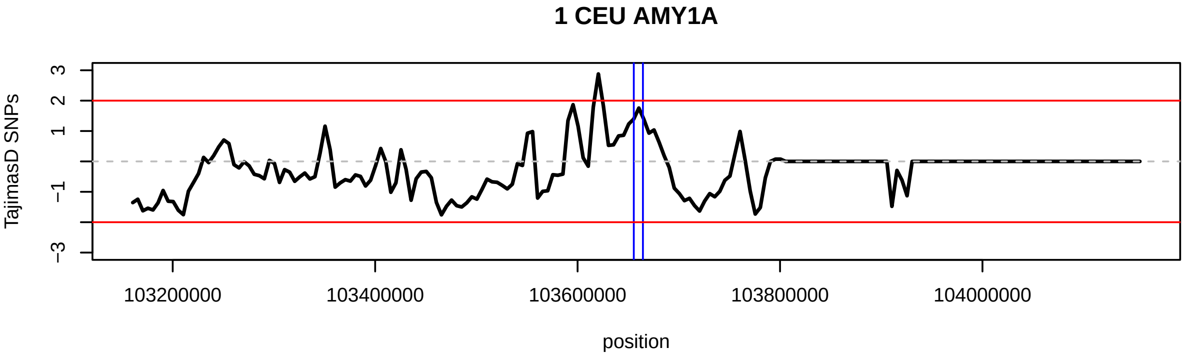
TRIM49L1	chr11	89924064	89933063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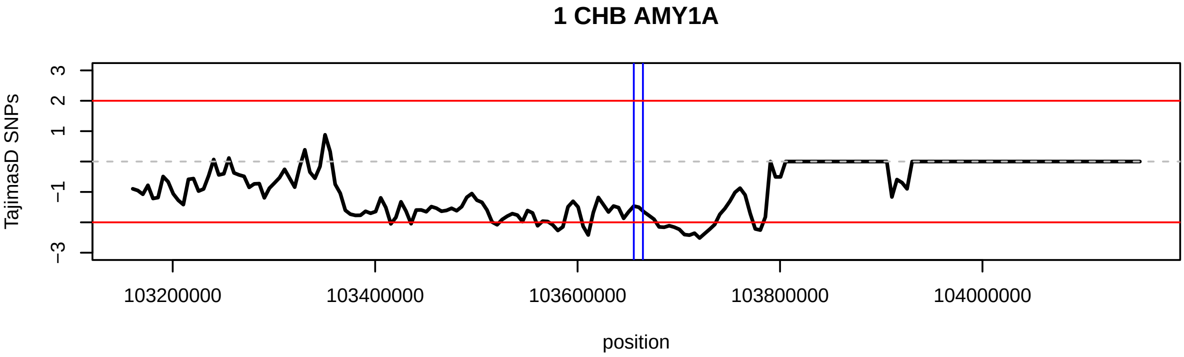
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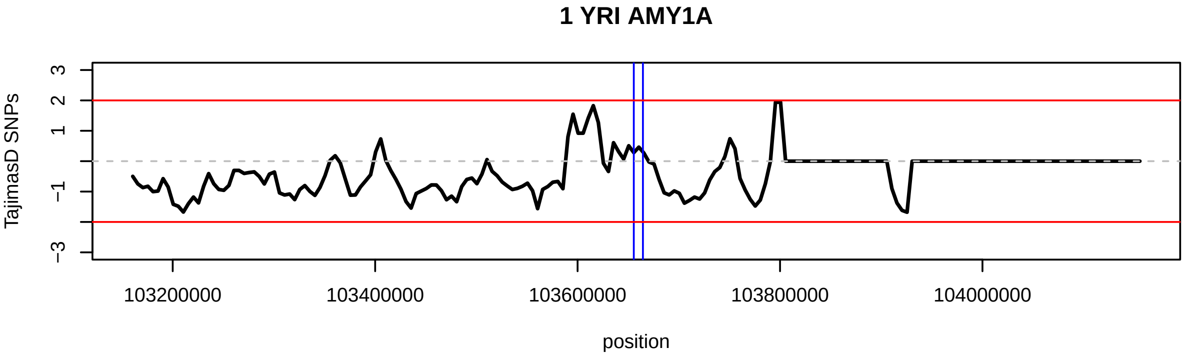
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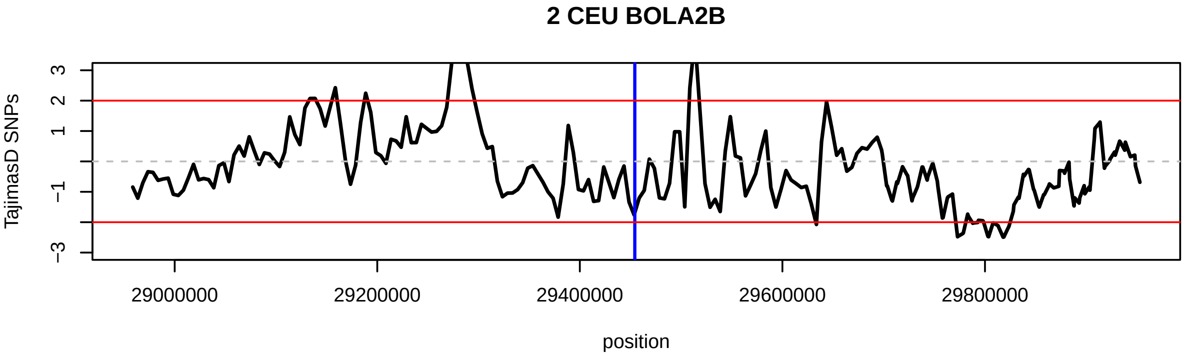
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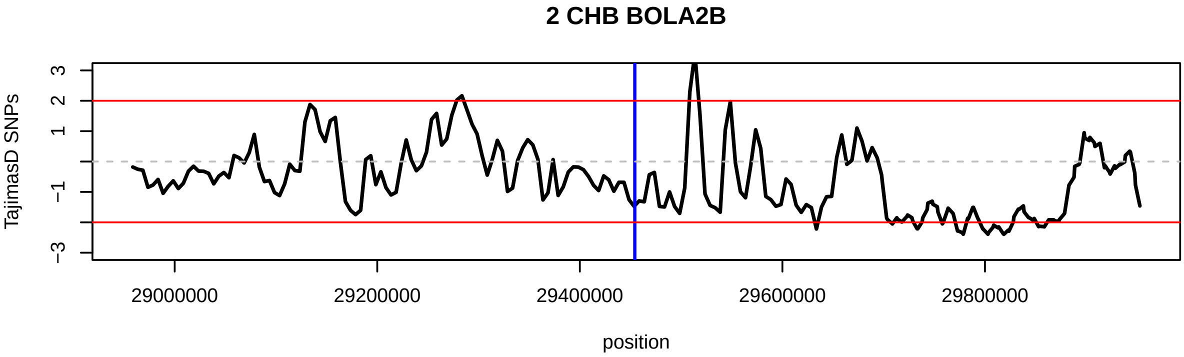
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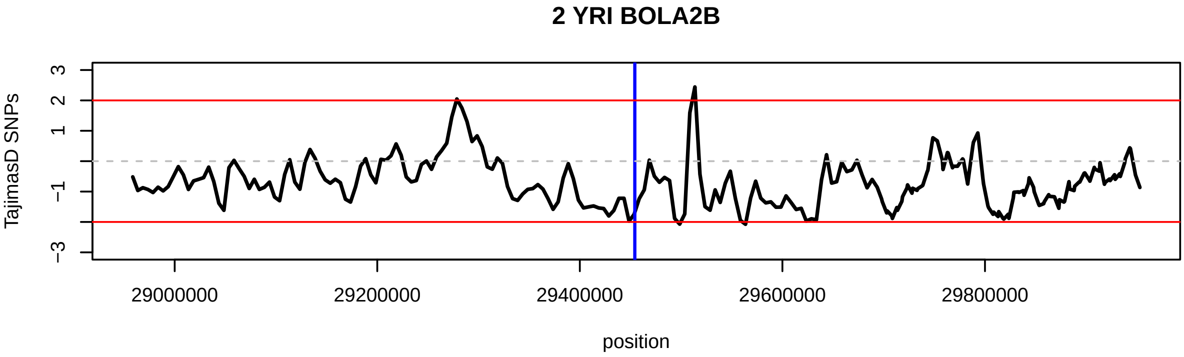
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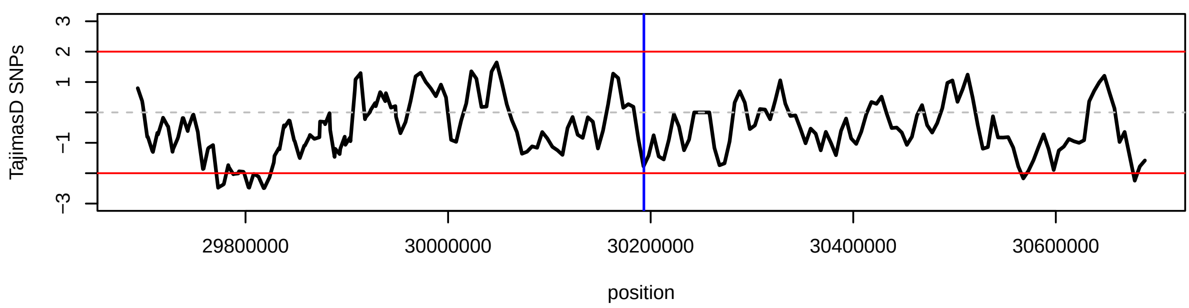
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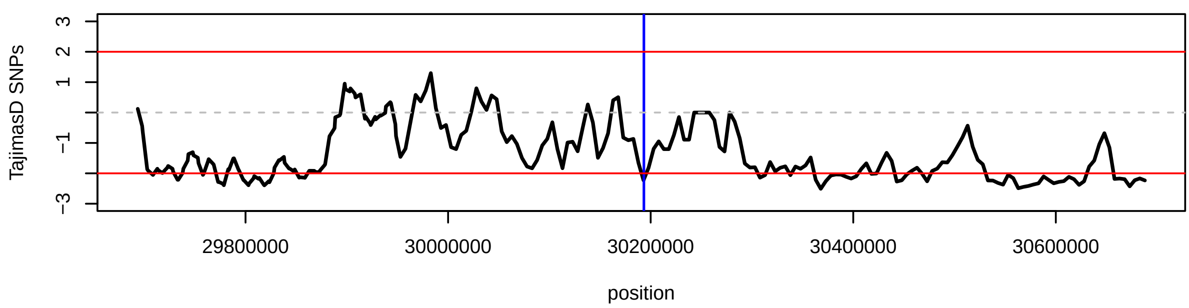
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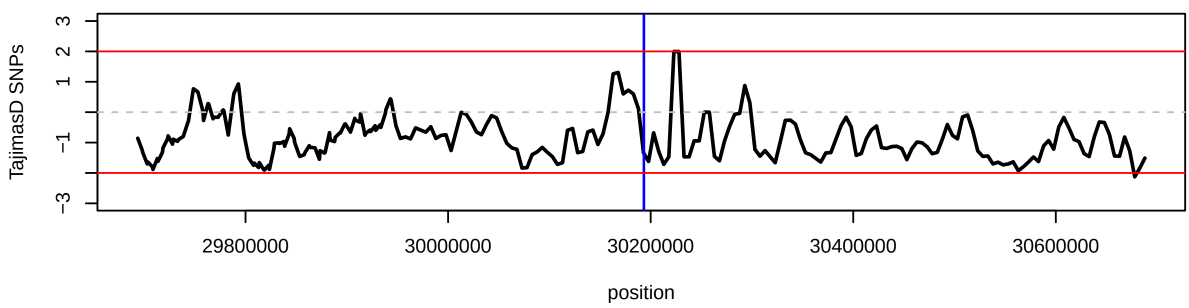
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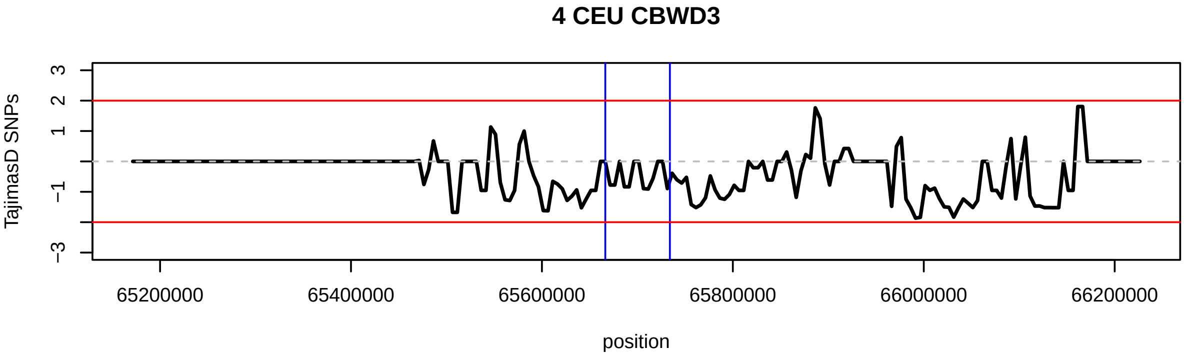
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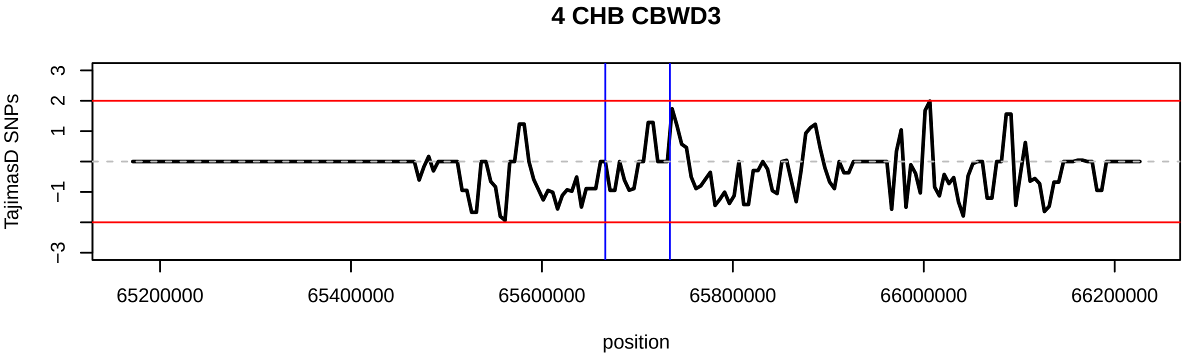
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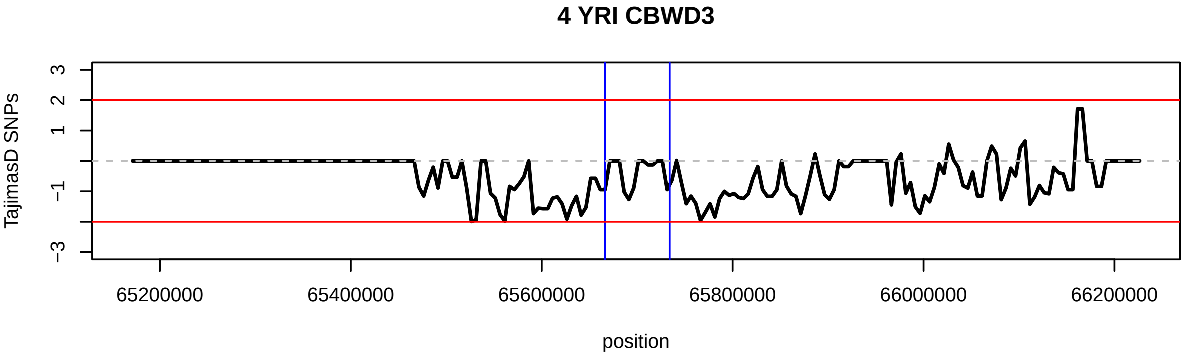
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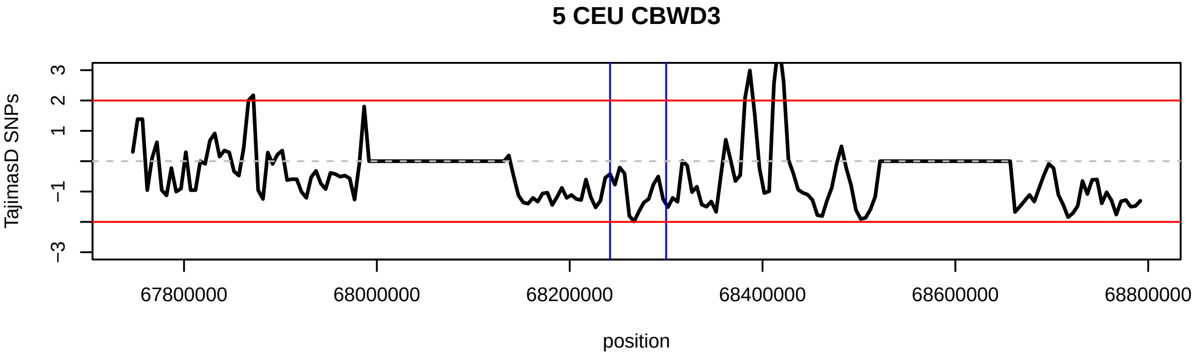

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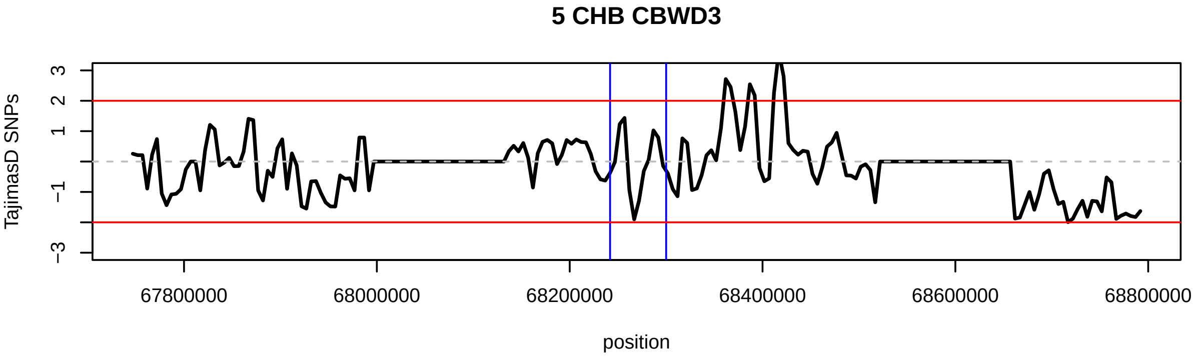

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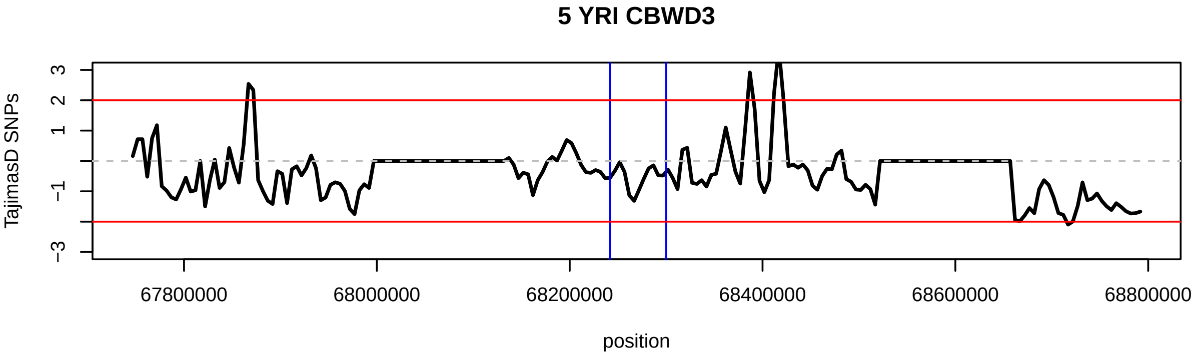

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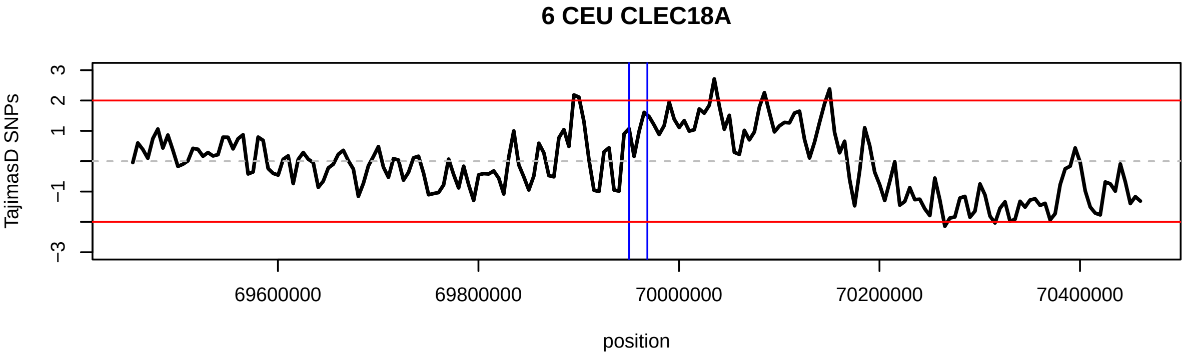
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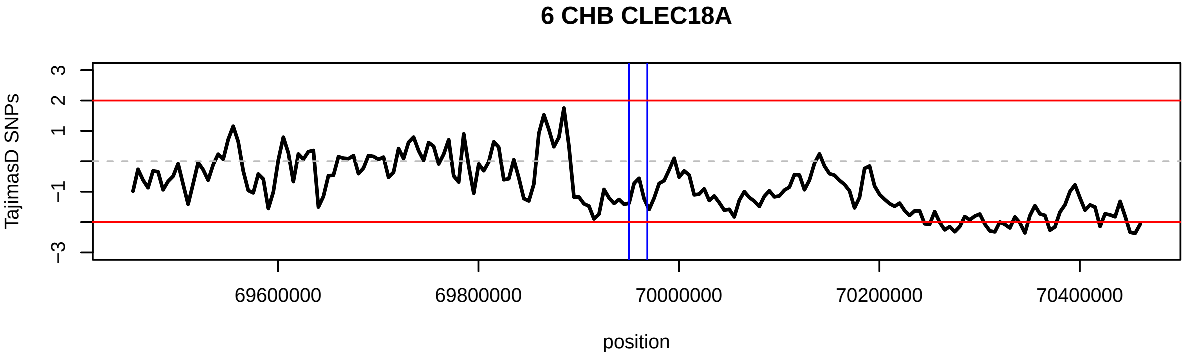
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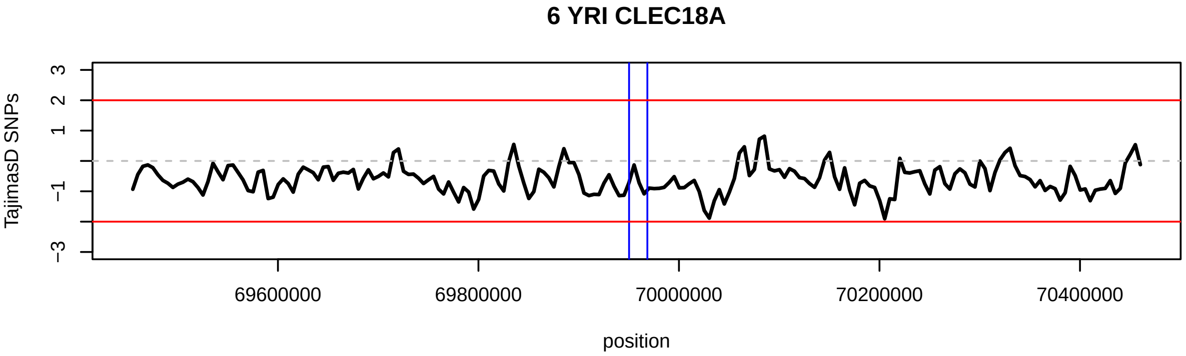
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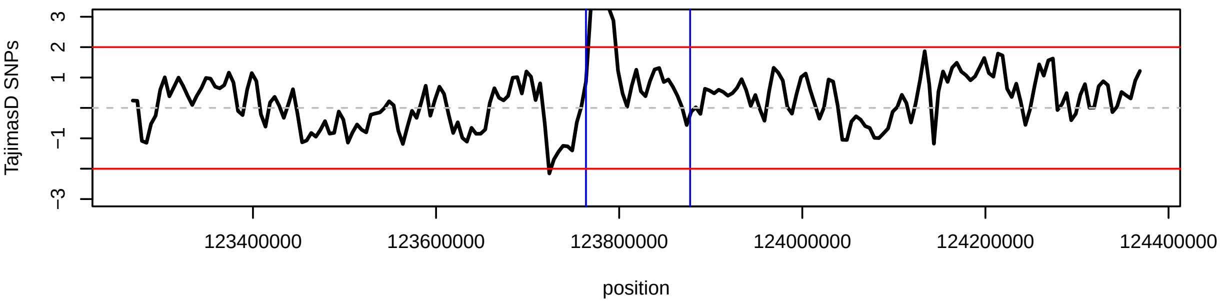

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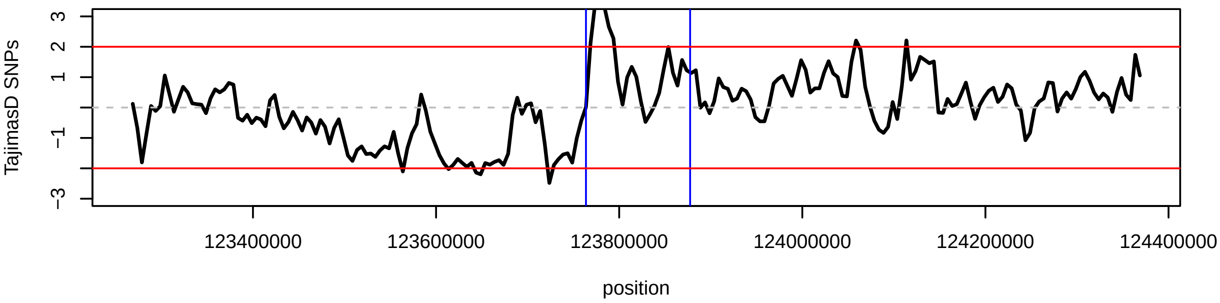

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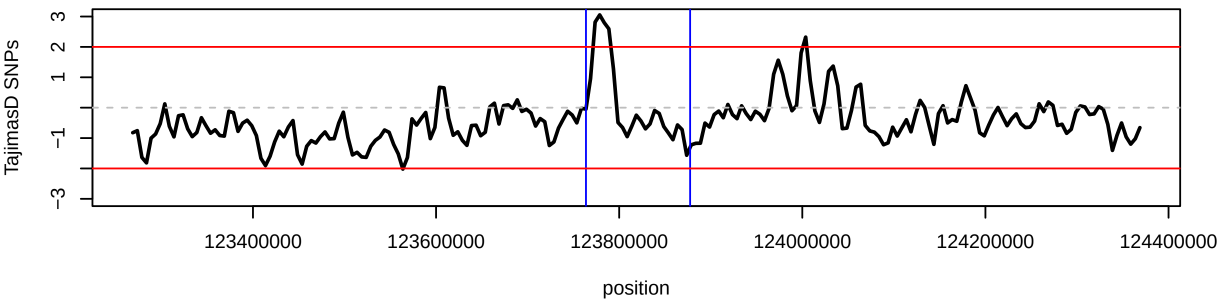

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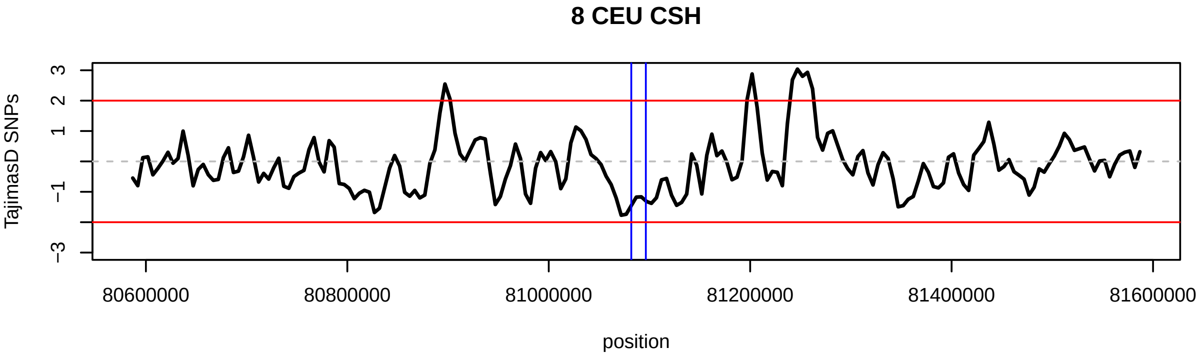

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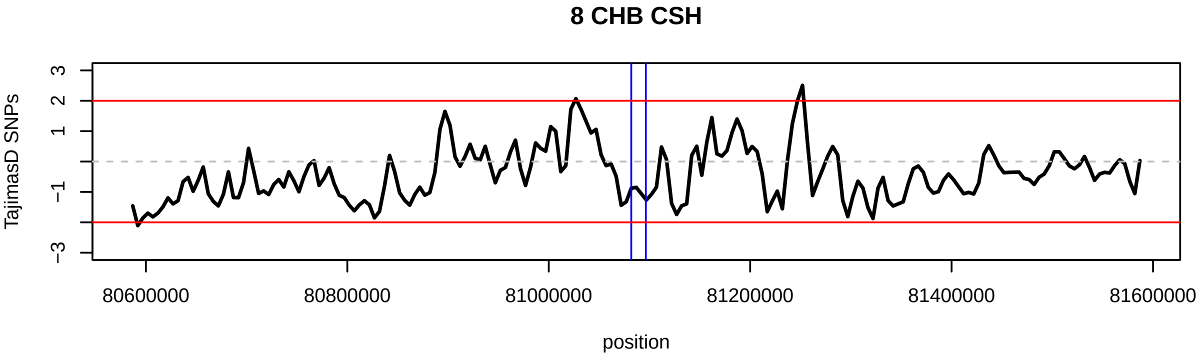

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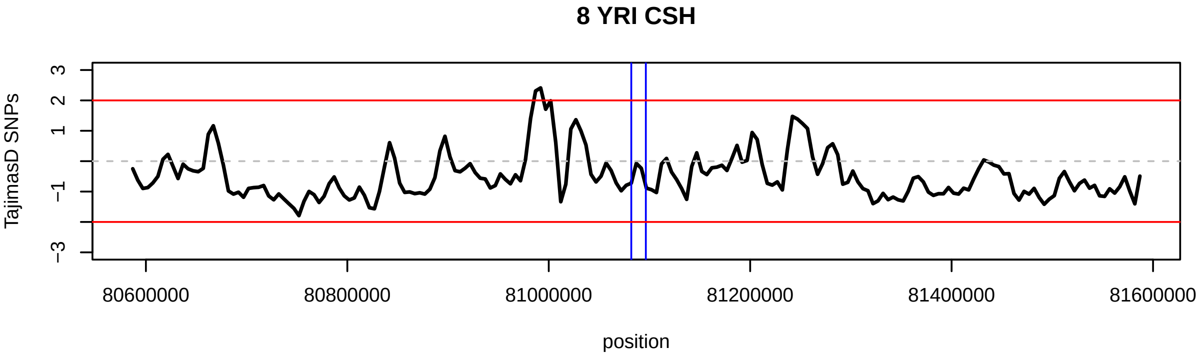

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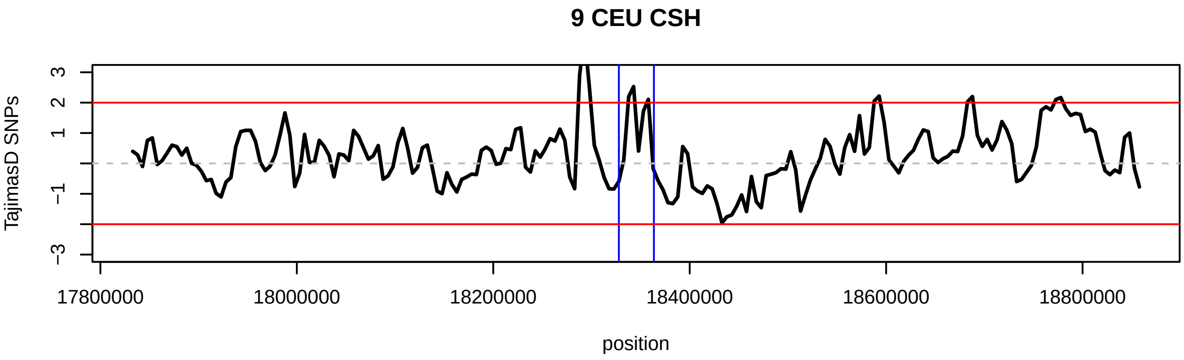
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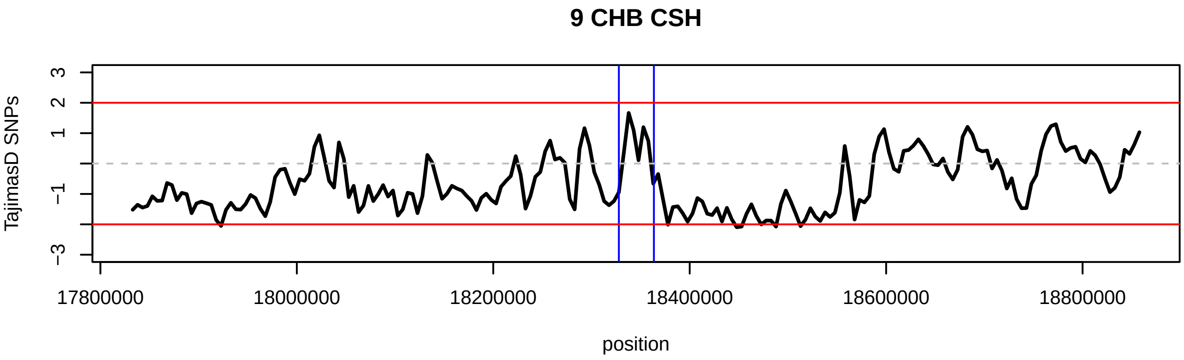
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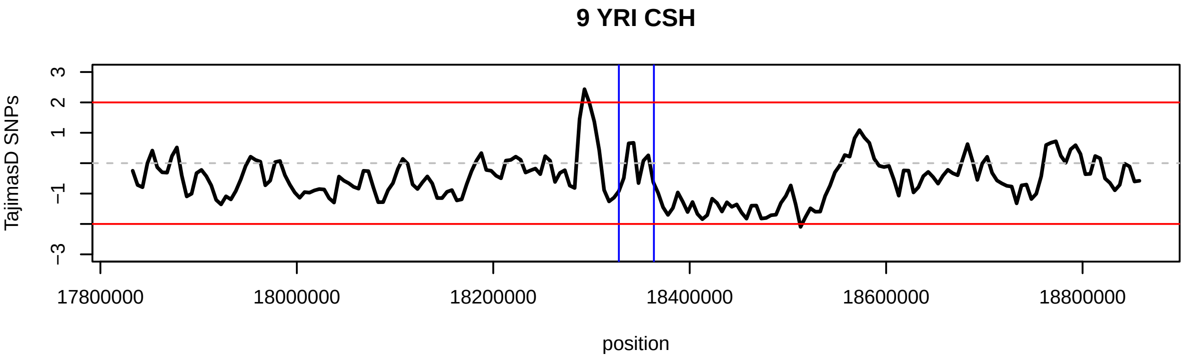
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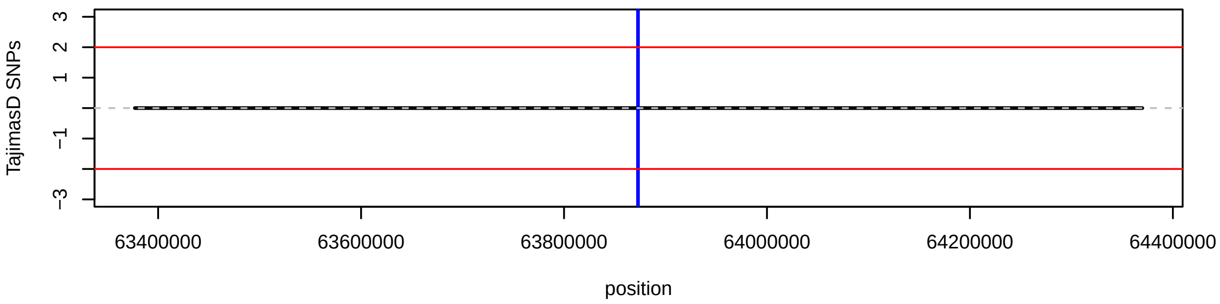

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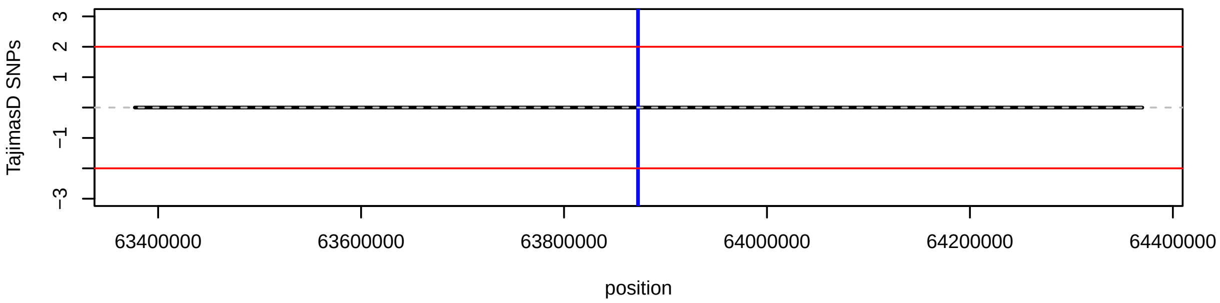

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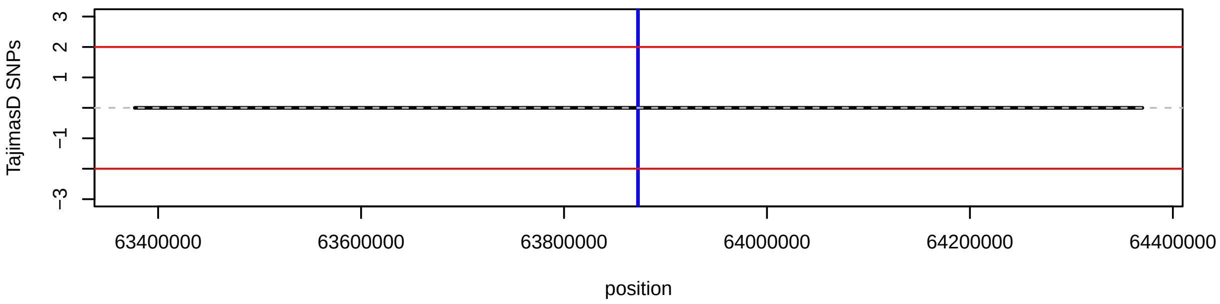

10 YRI CSH

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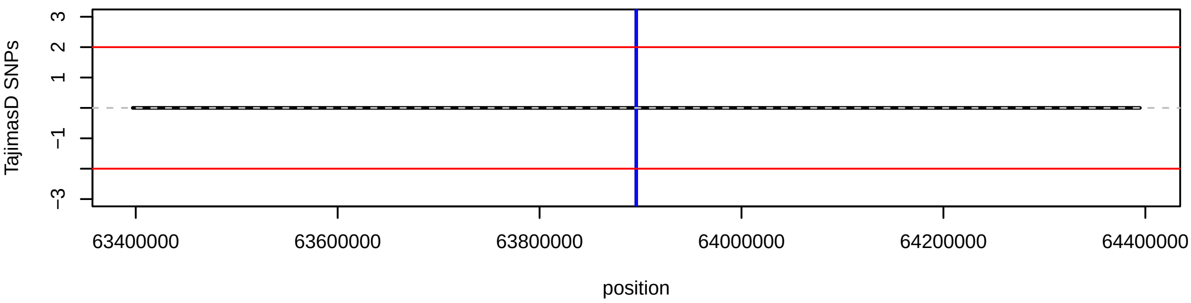
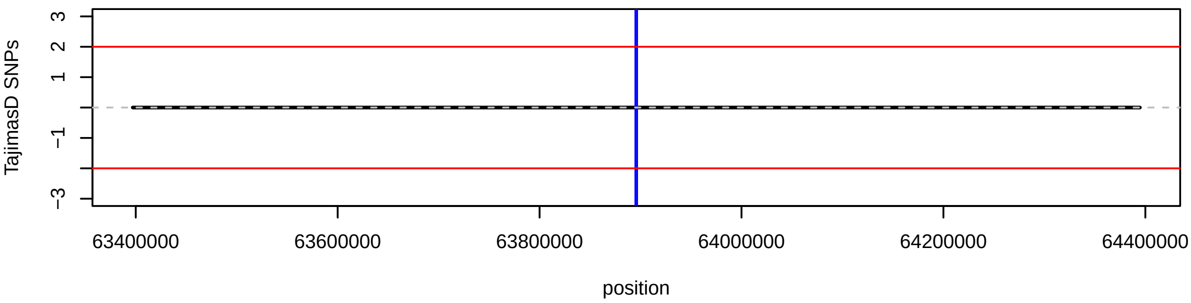


11 CHB CSH



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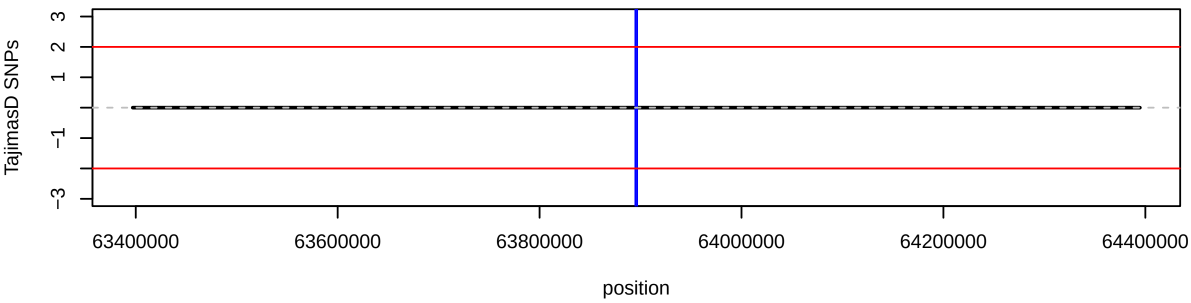

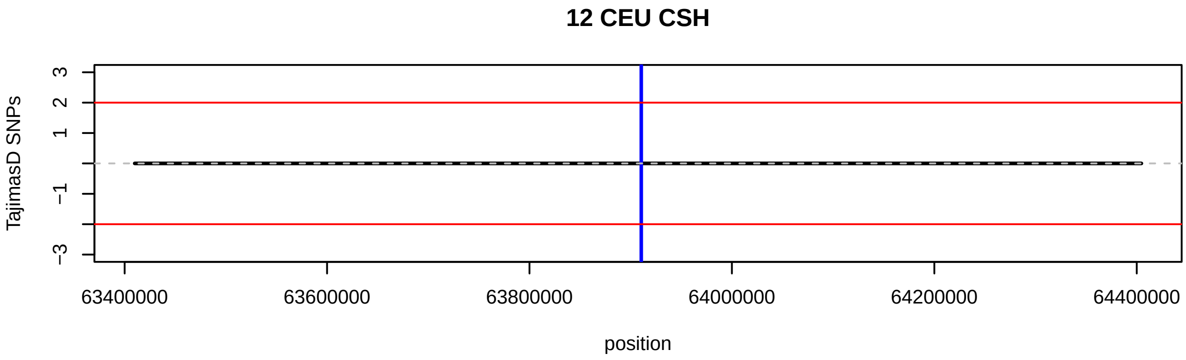
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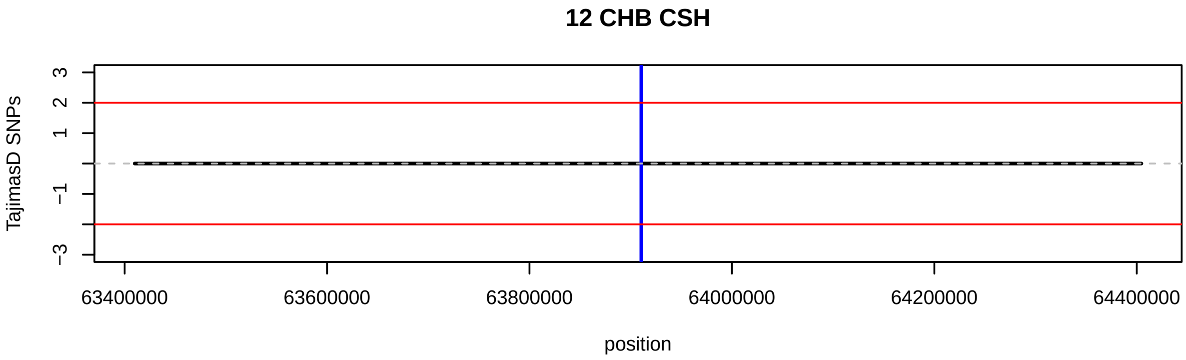
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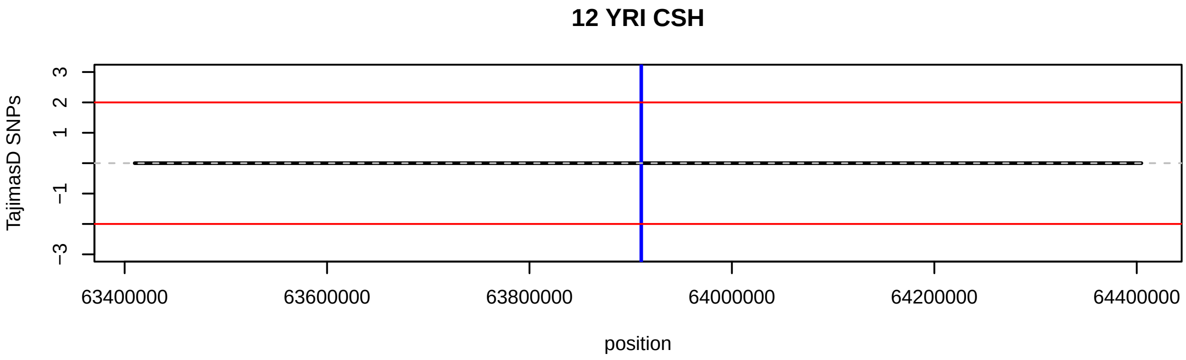
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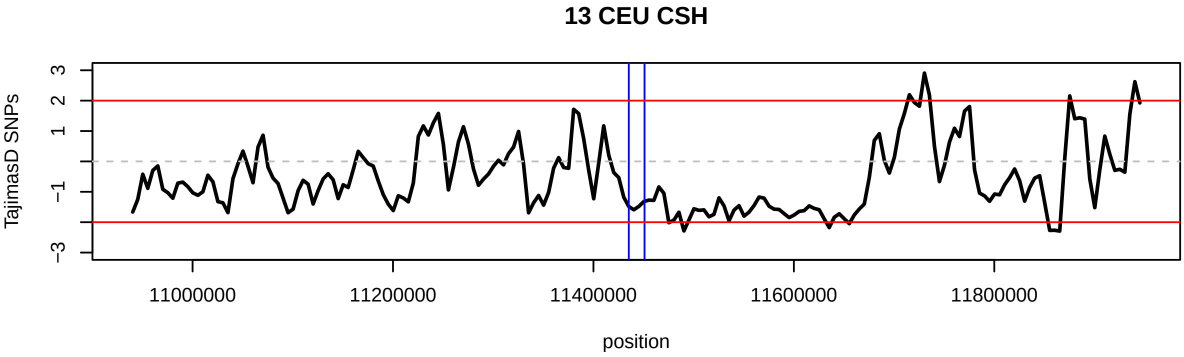
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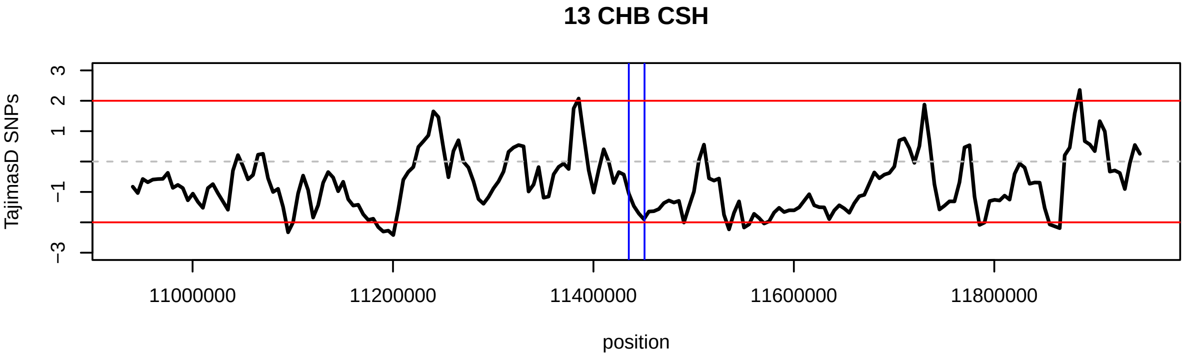
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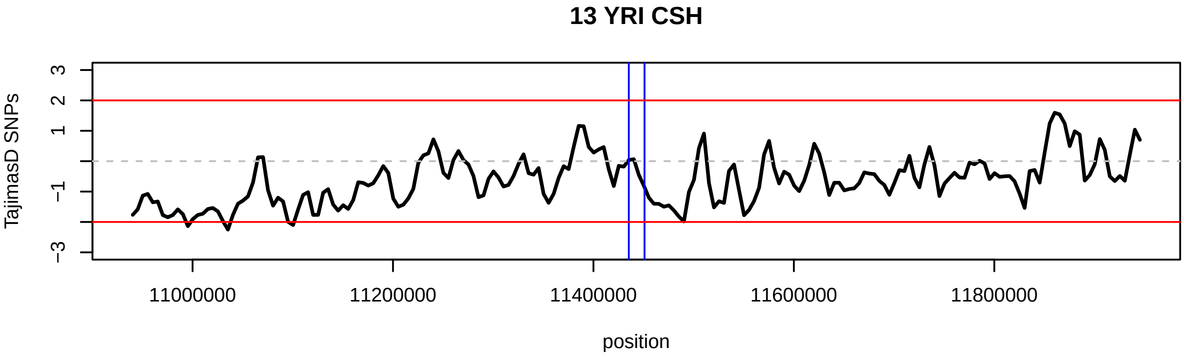
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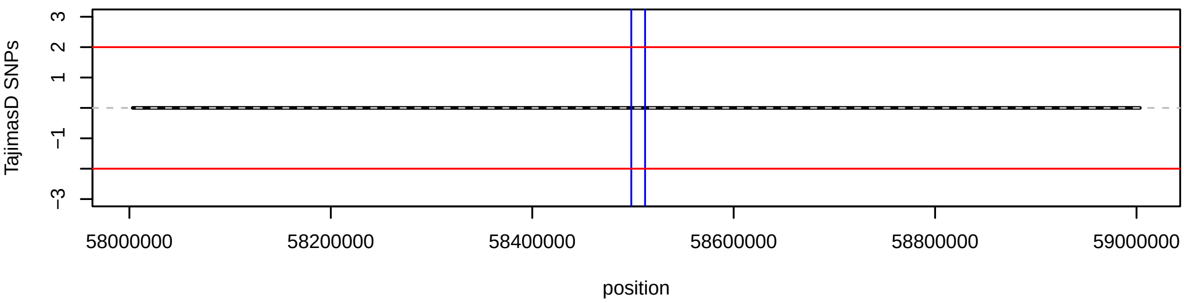
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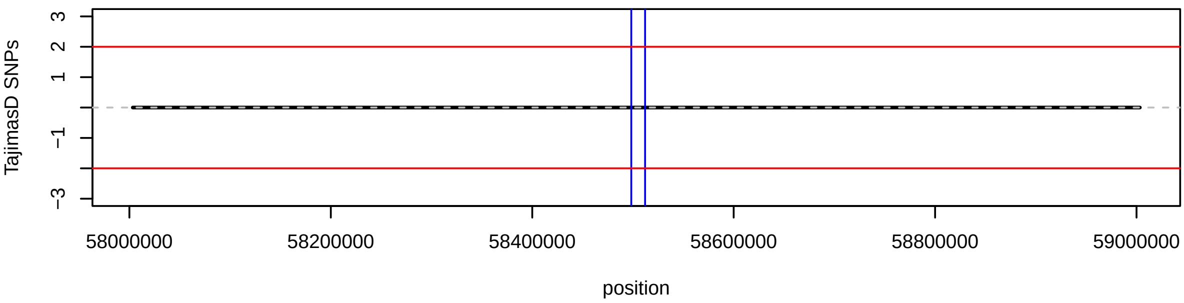
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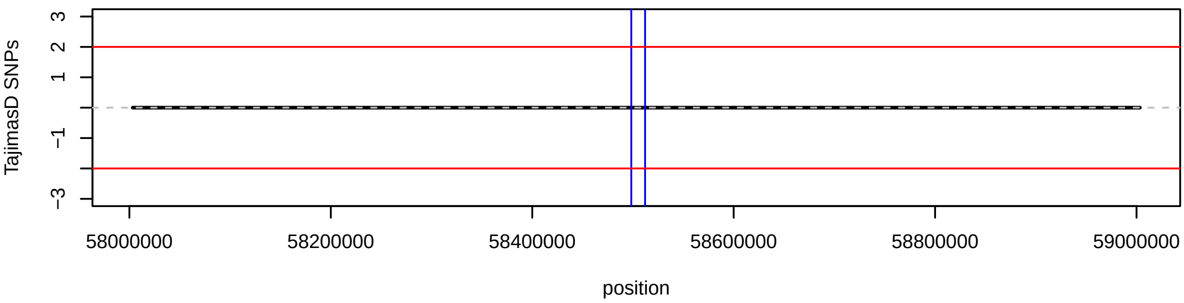
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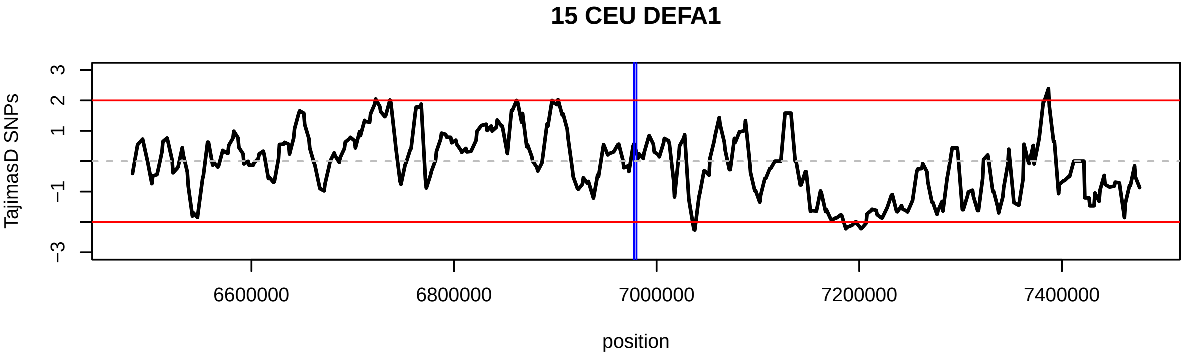

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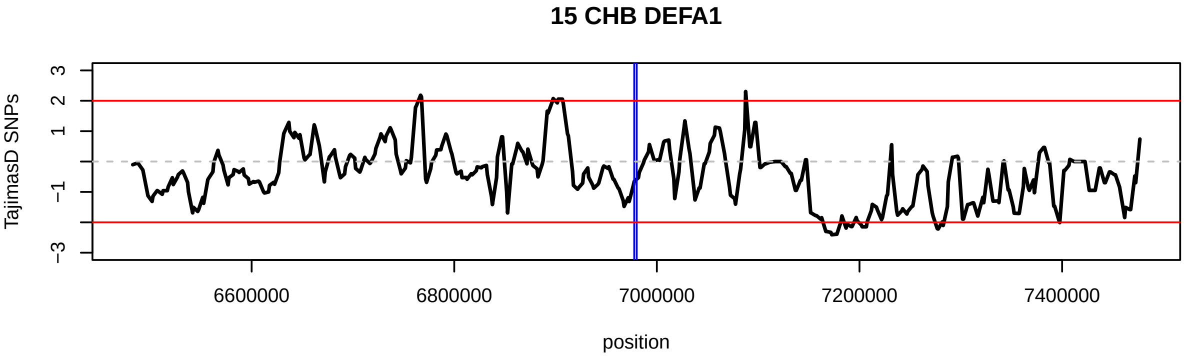

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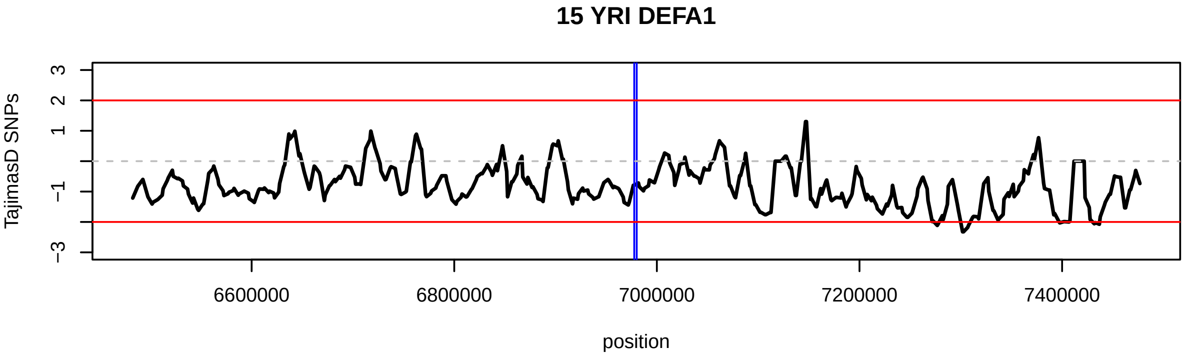

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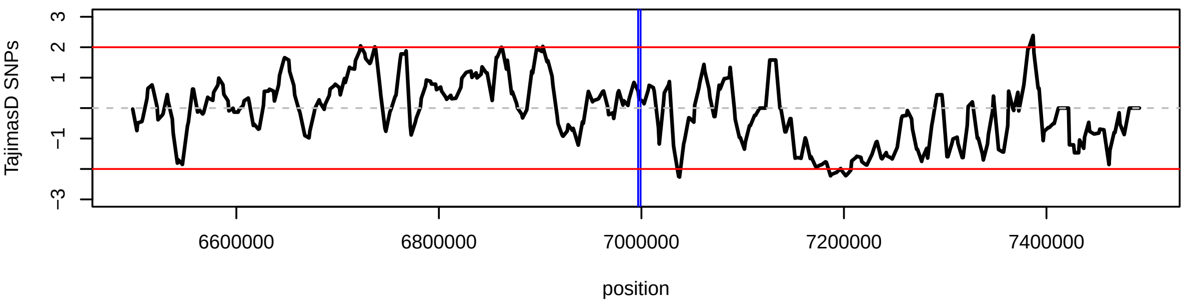
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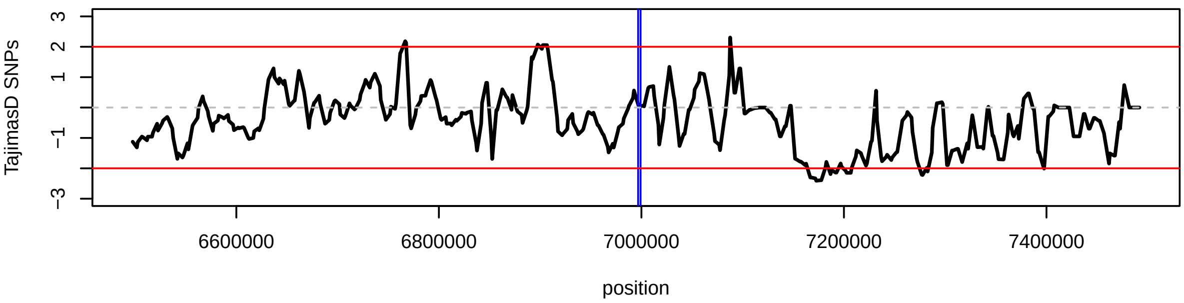
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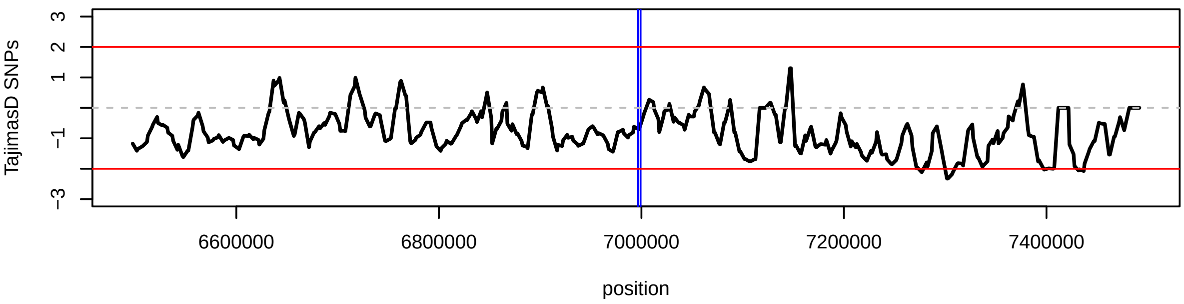
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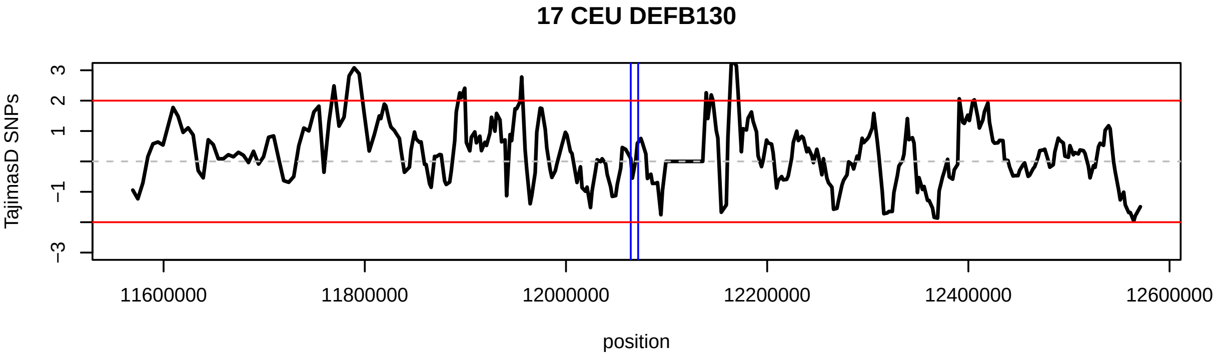

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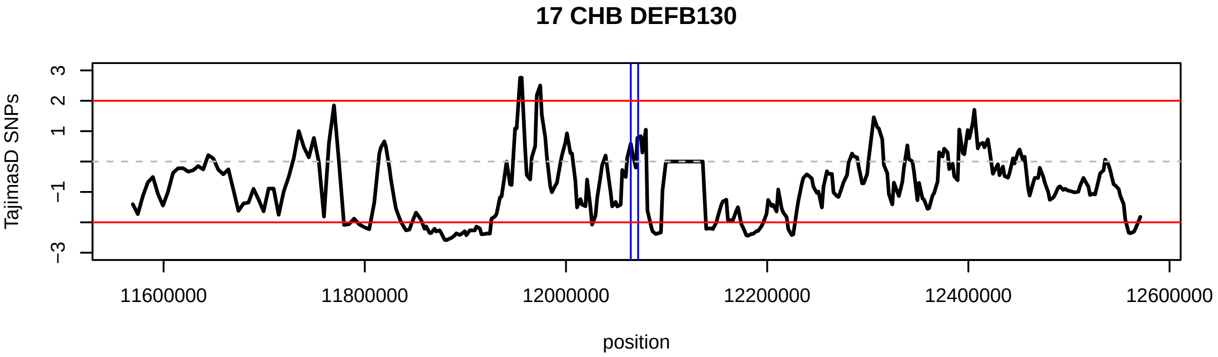

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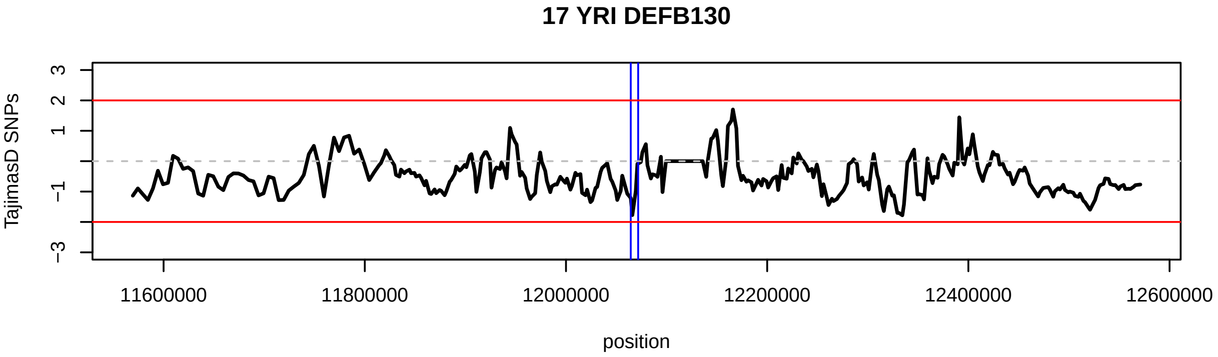

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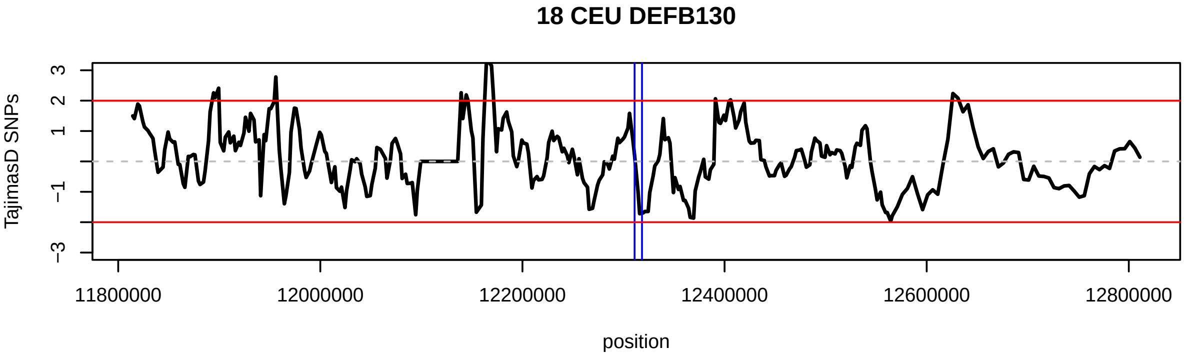
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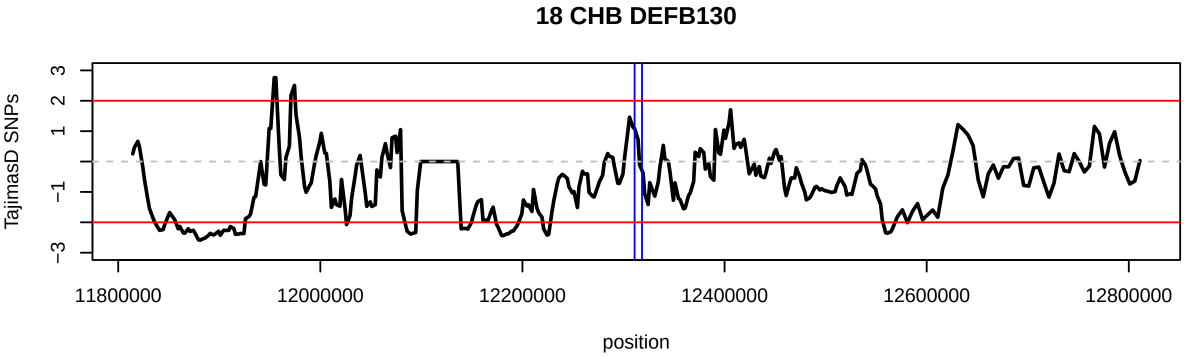
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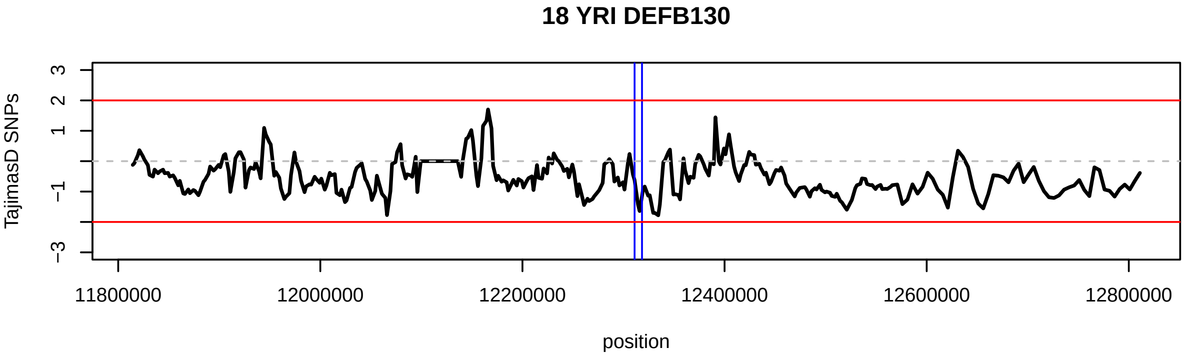
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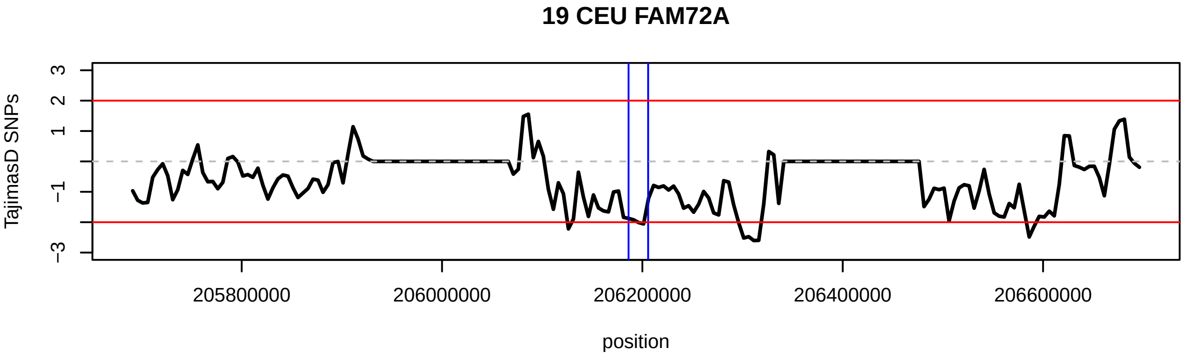
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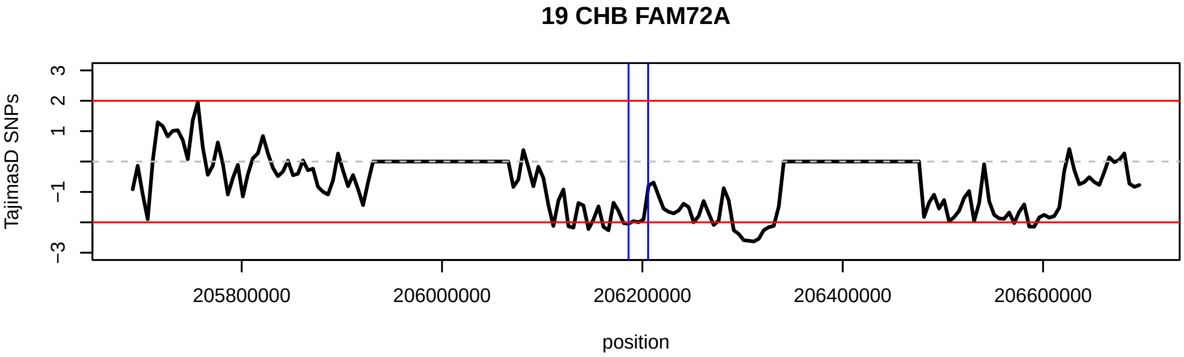
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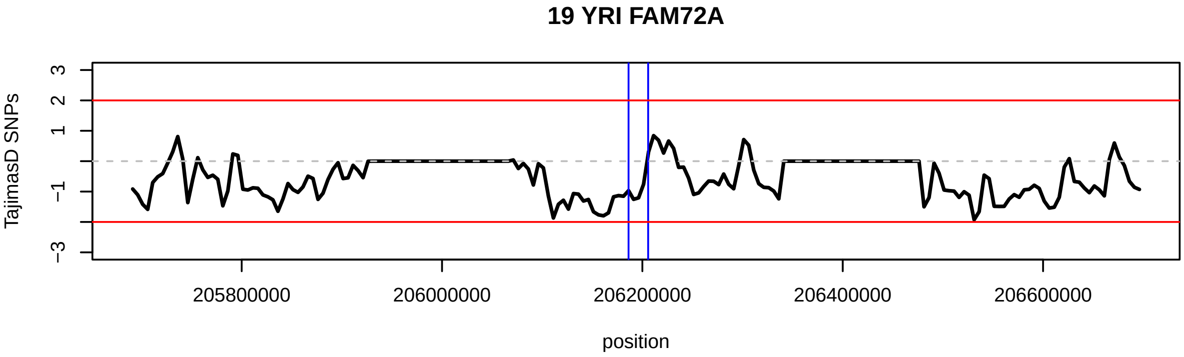
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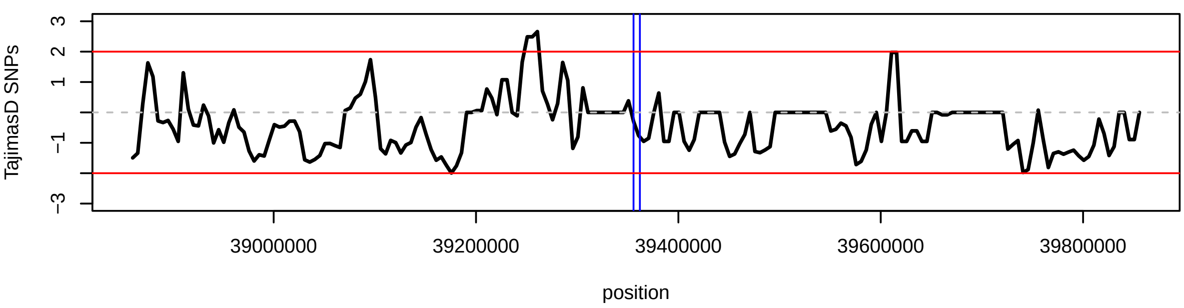

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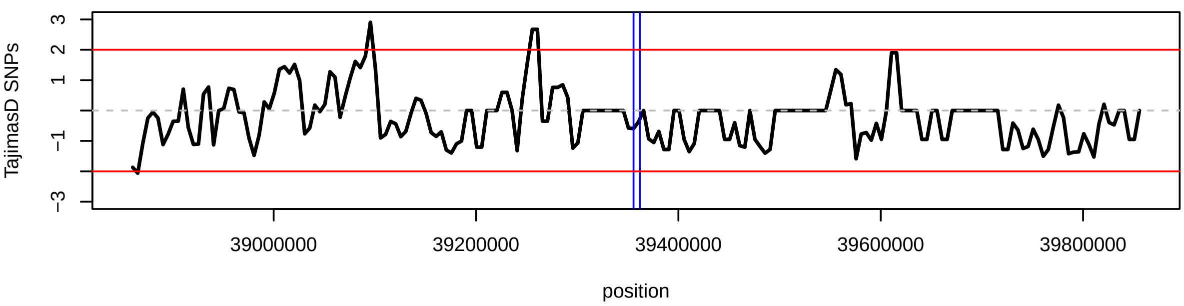

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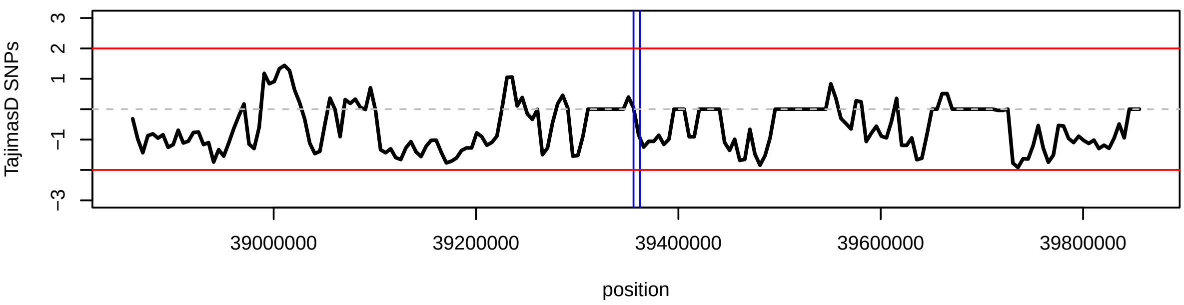

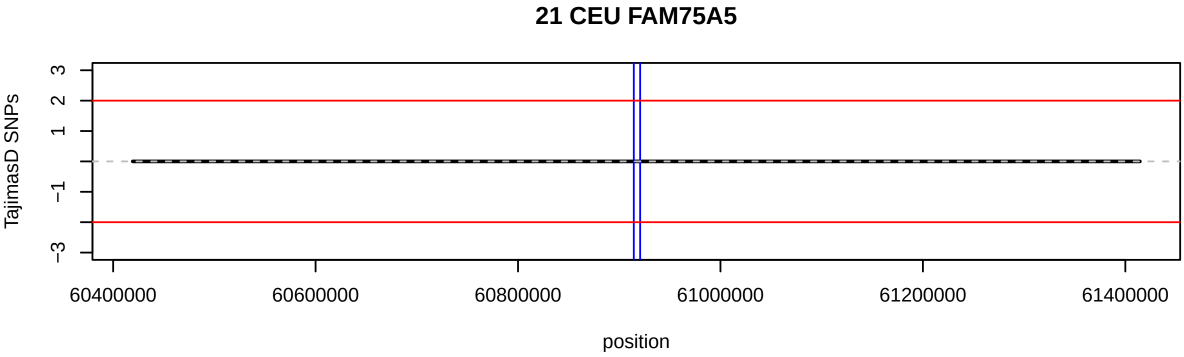
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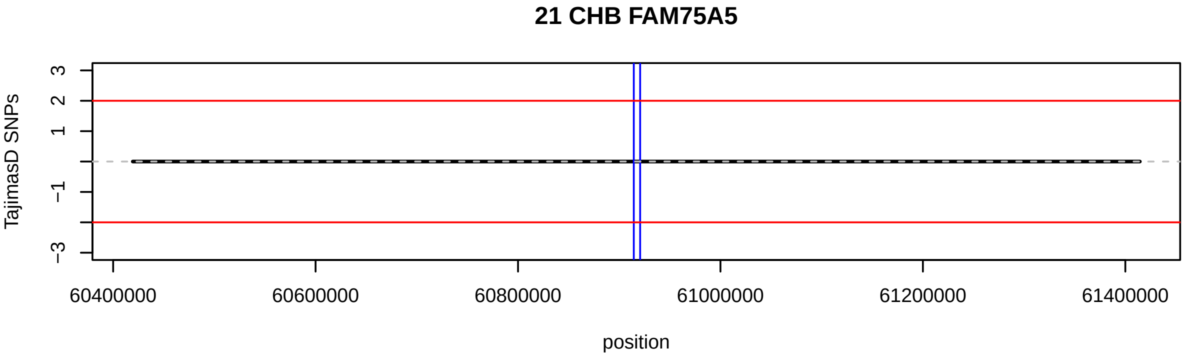
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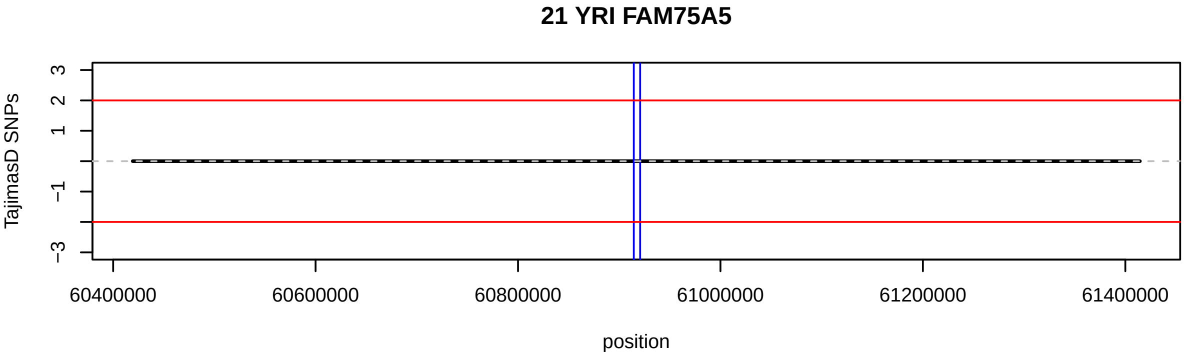
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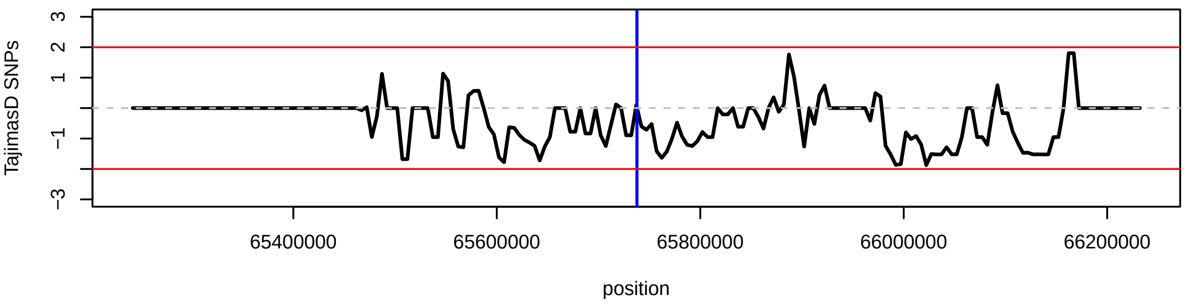

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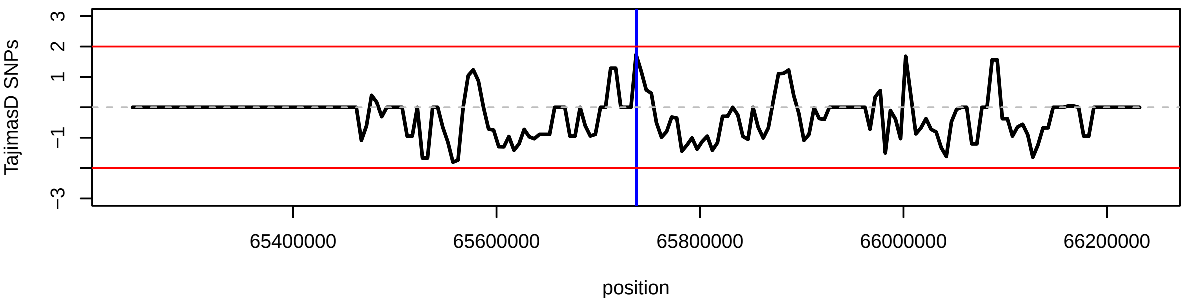

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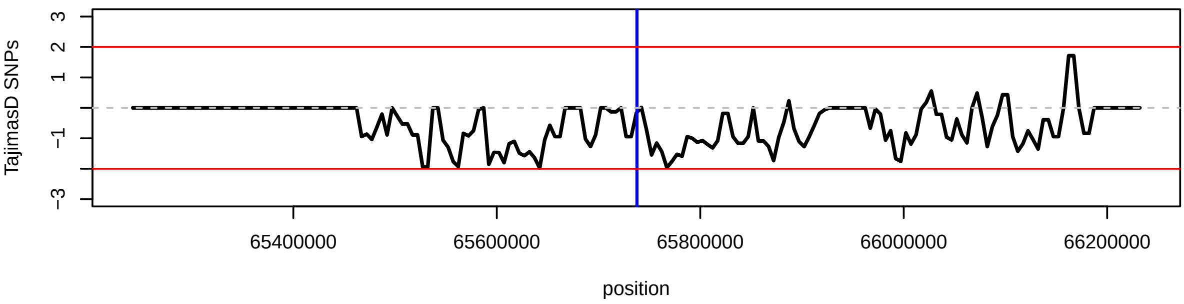

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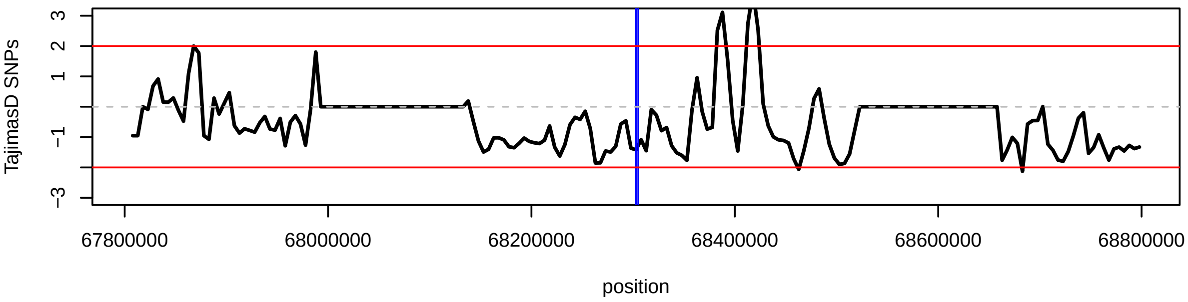
23 CEU FOXD4L2



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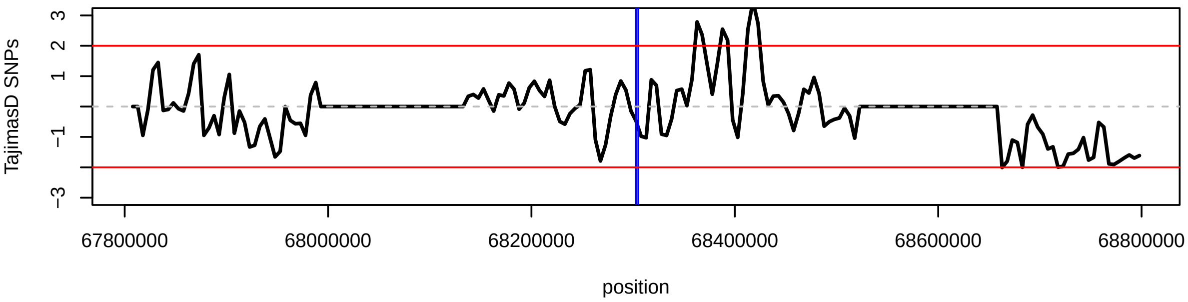

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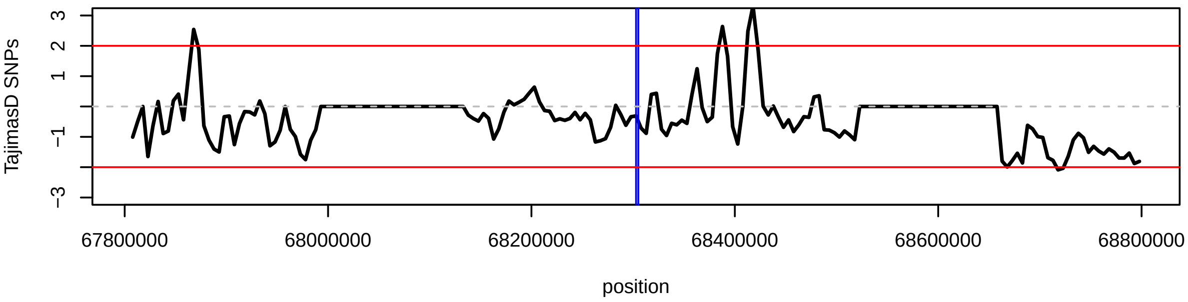

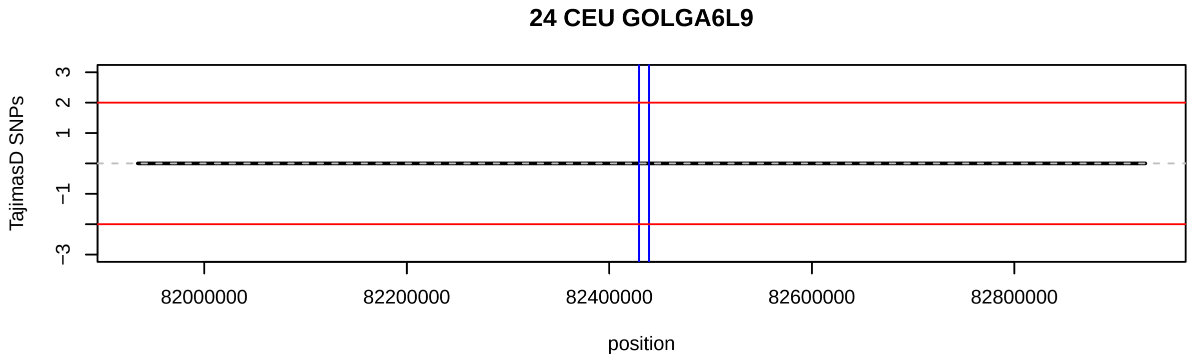
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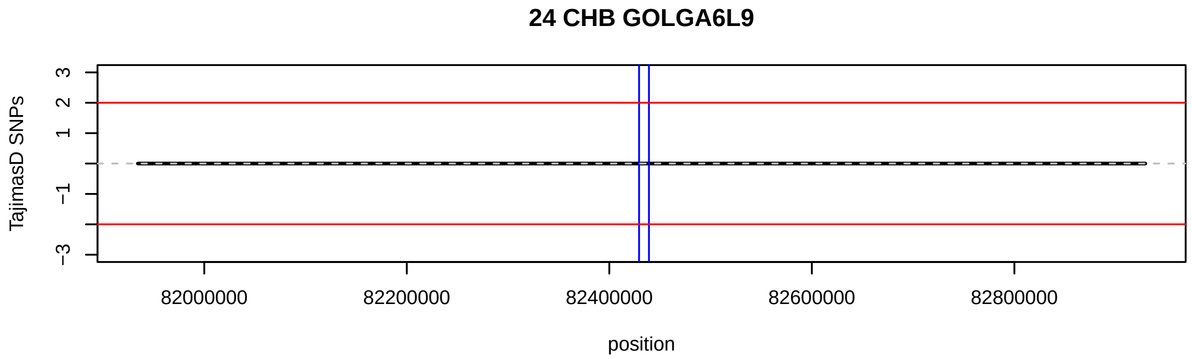
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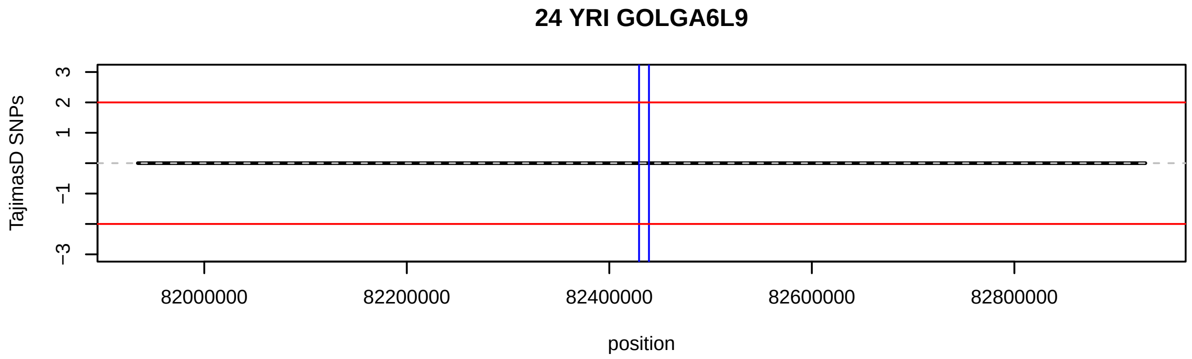
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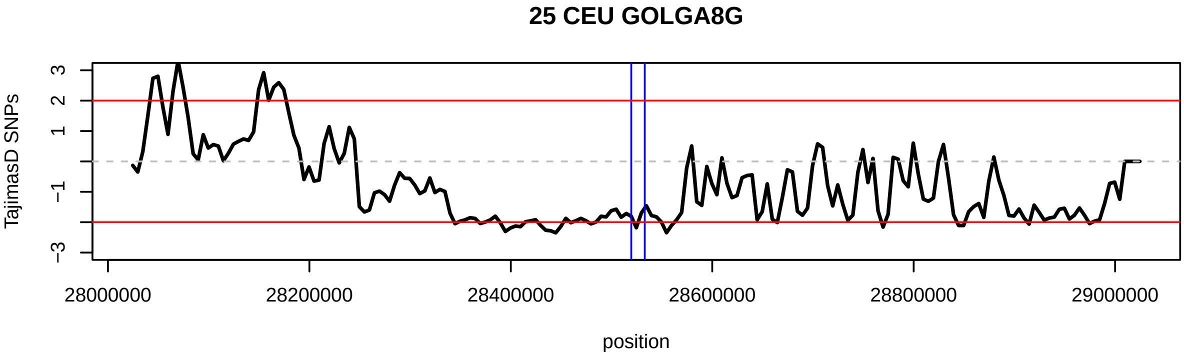
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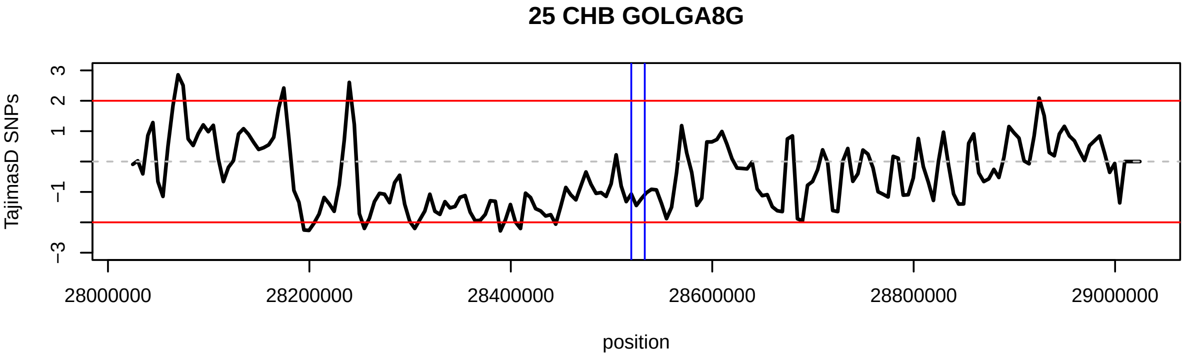
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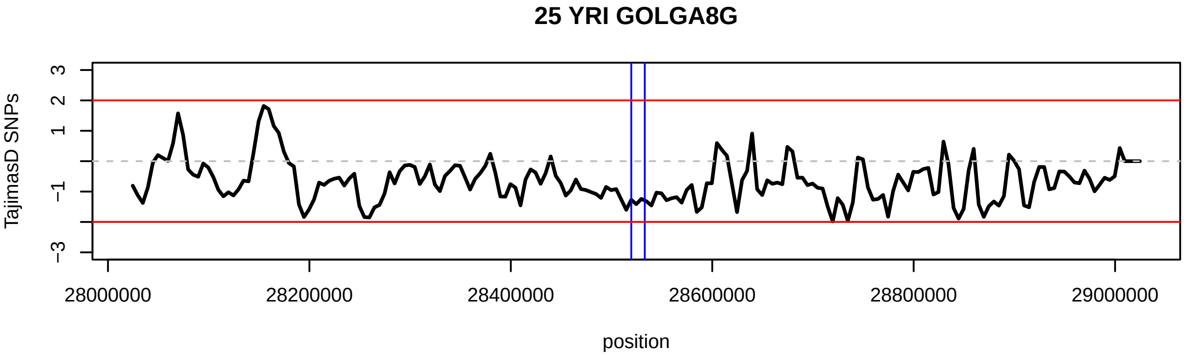
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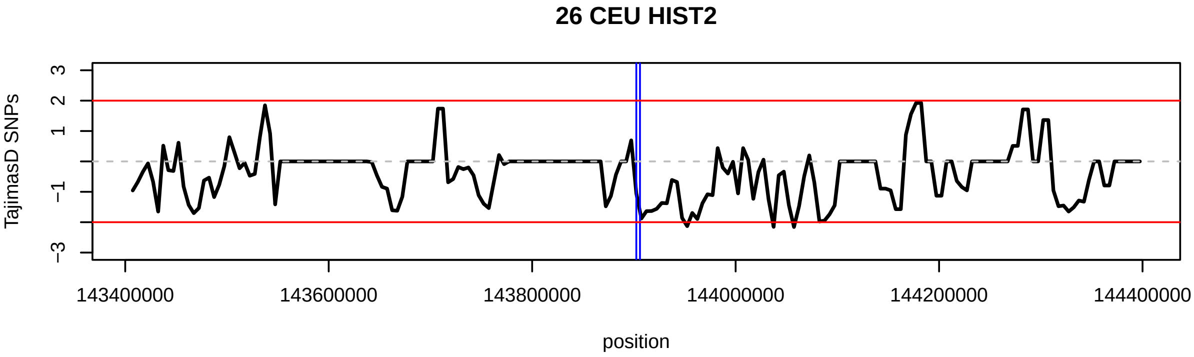
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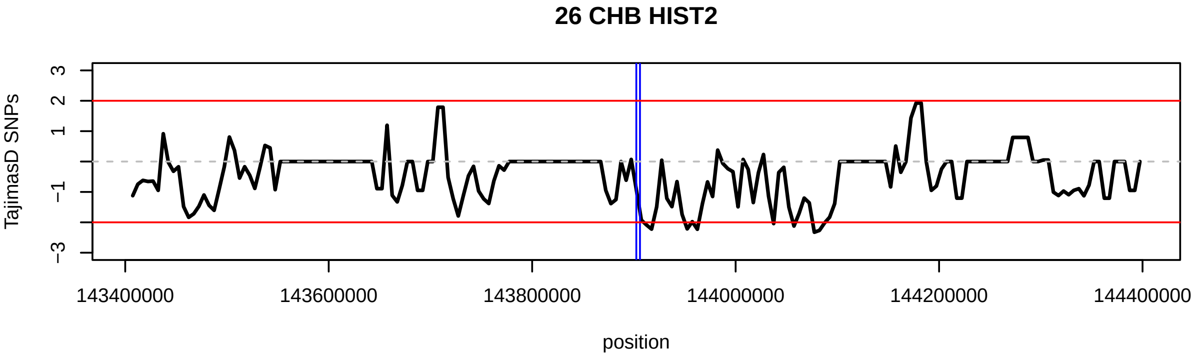
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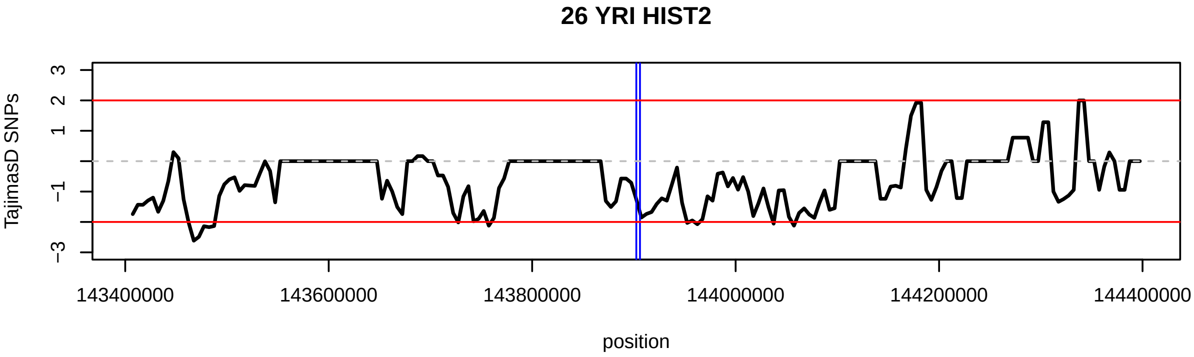
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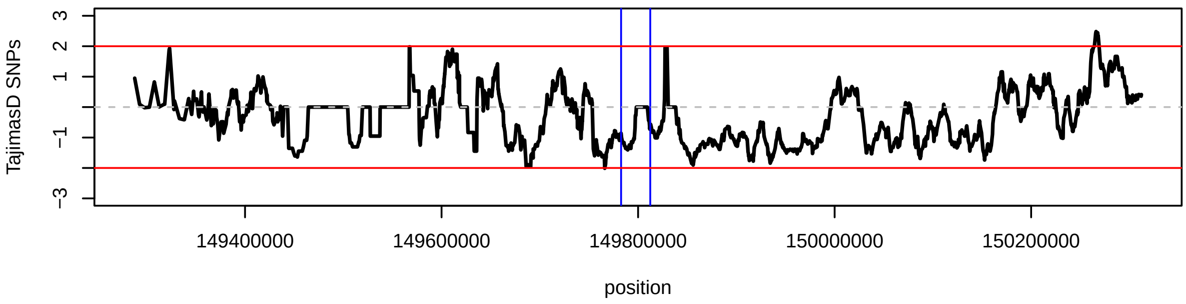
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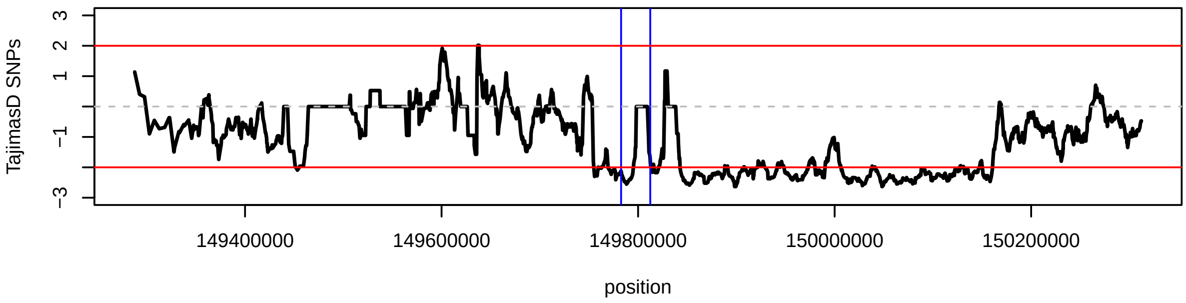
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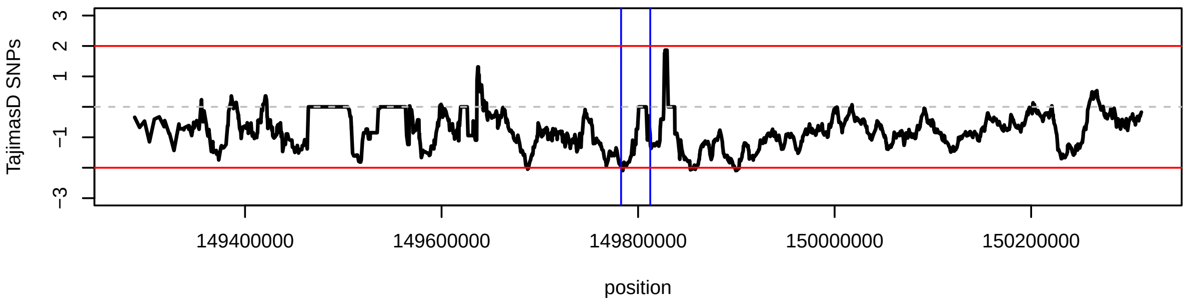
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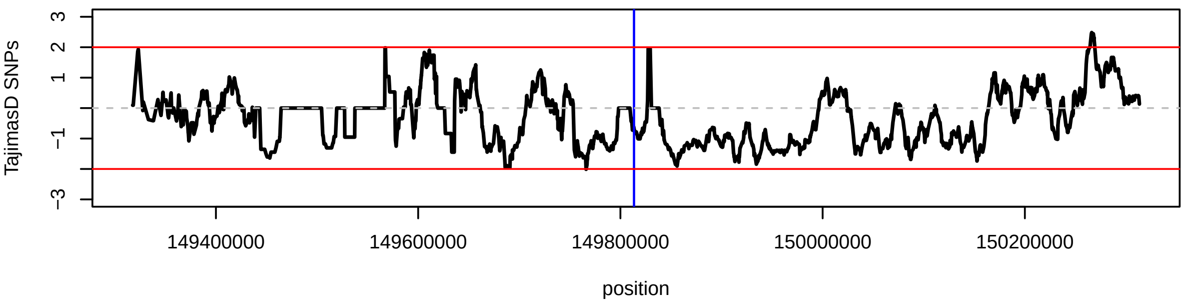

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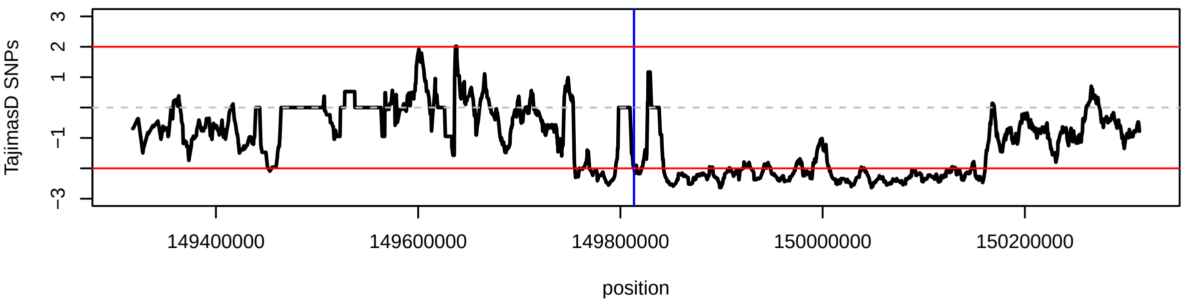

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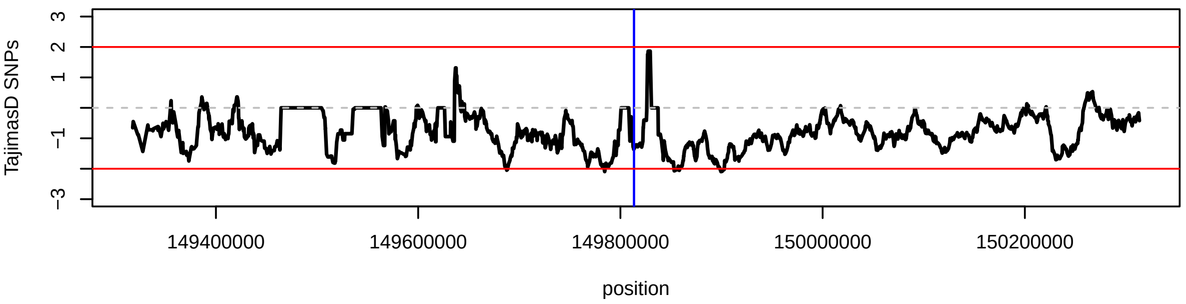

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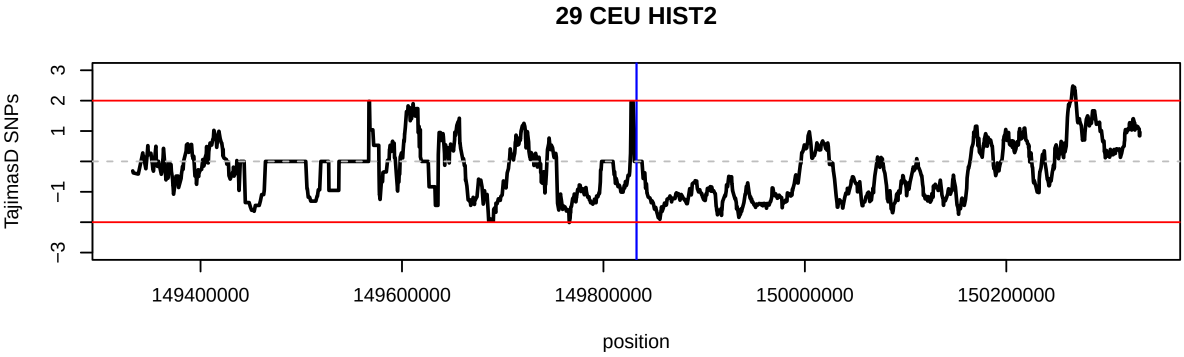
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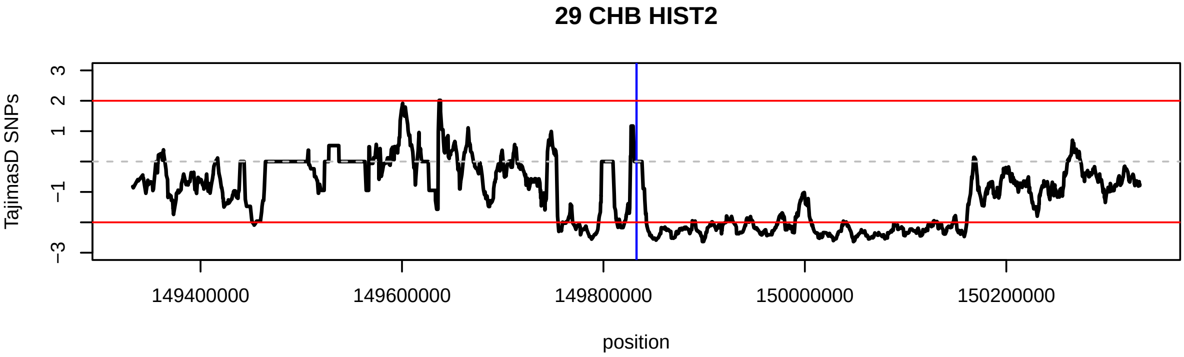
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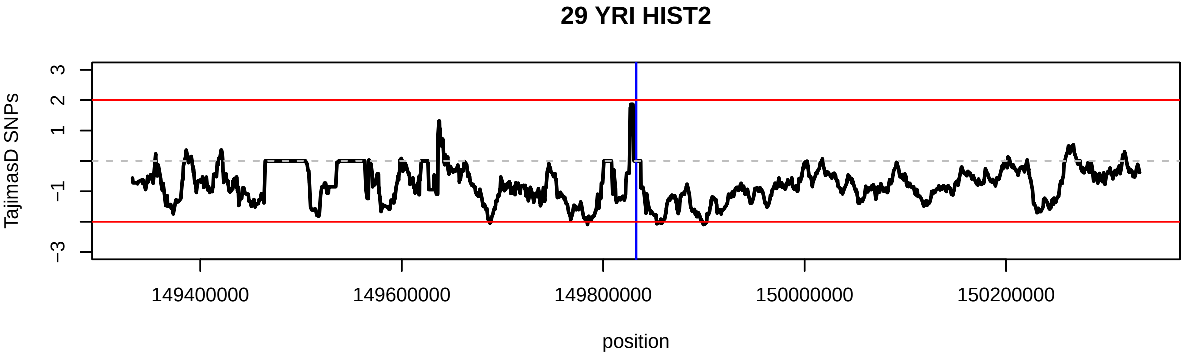
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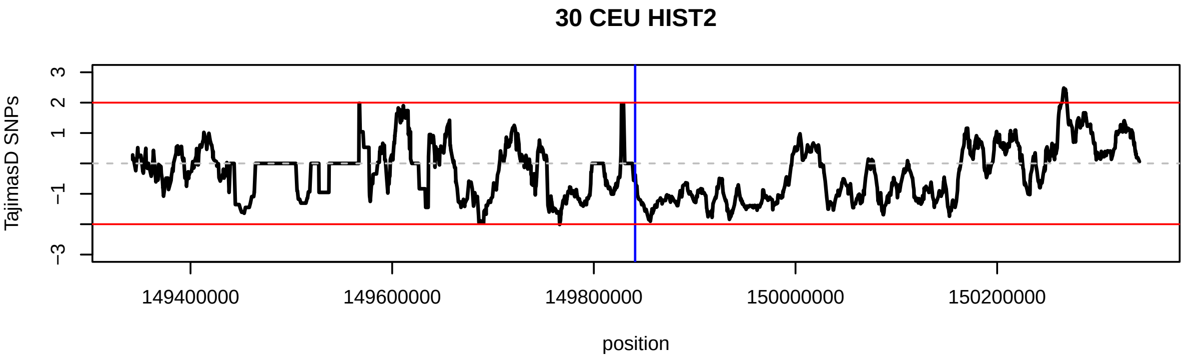
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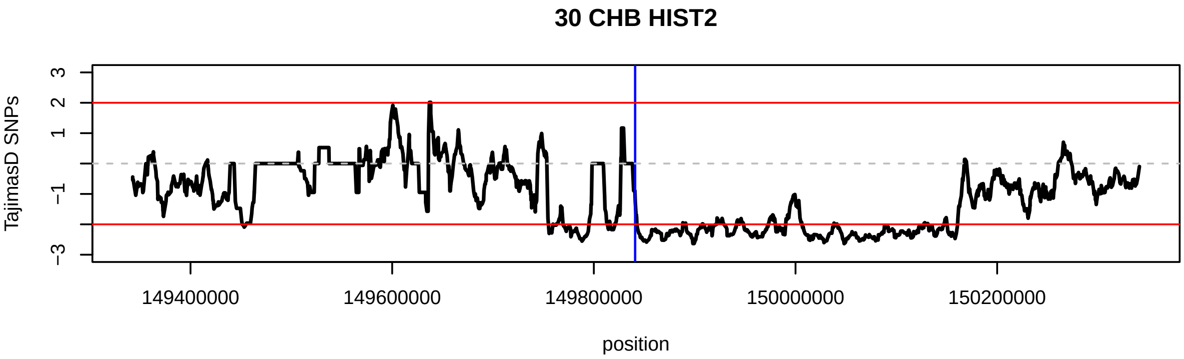
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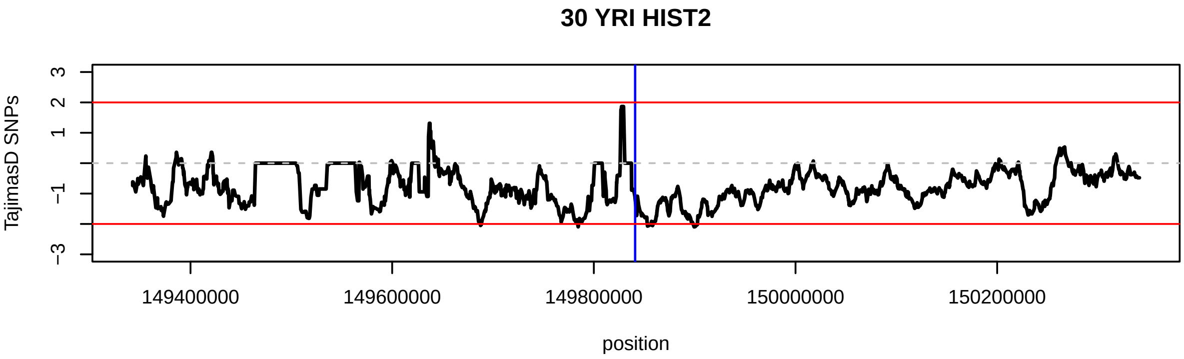
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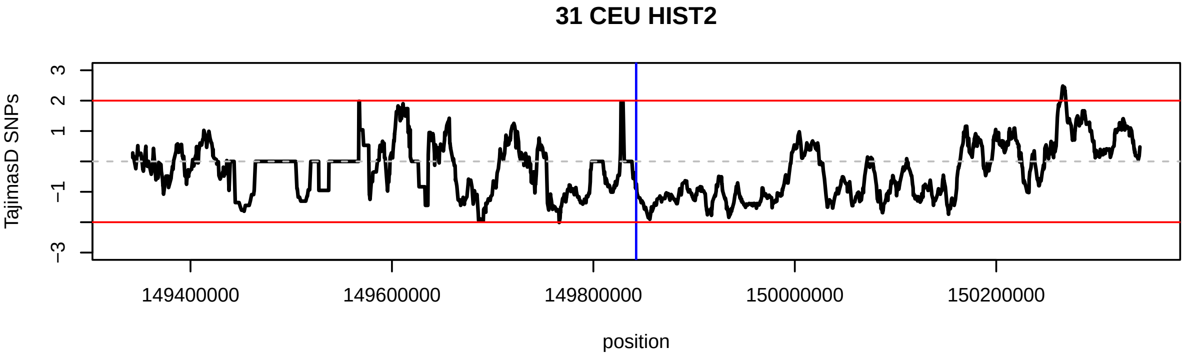
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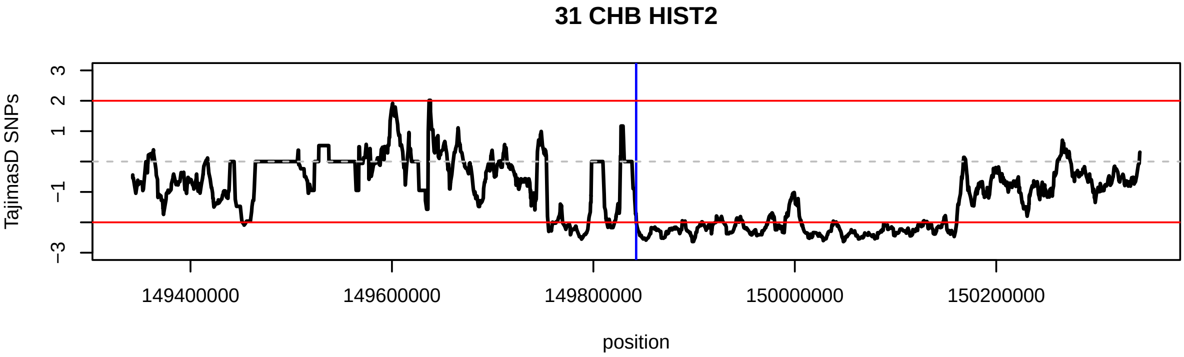
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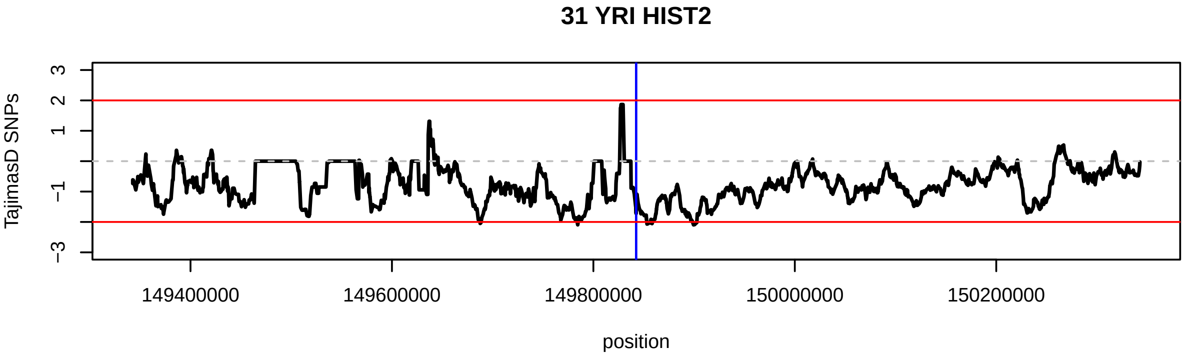
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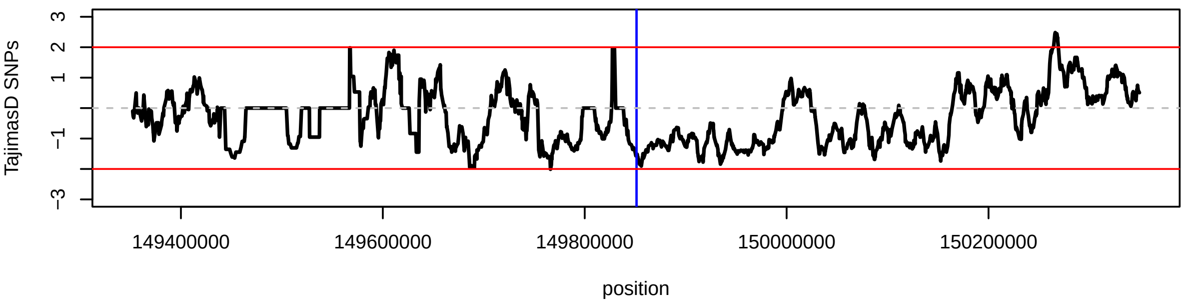
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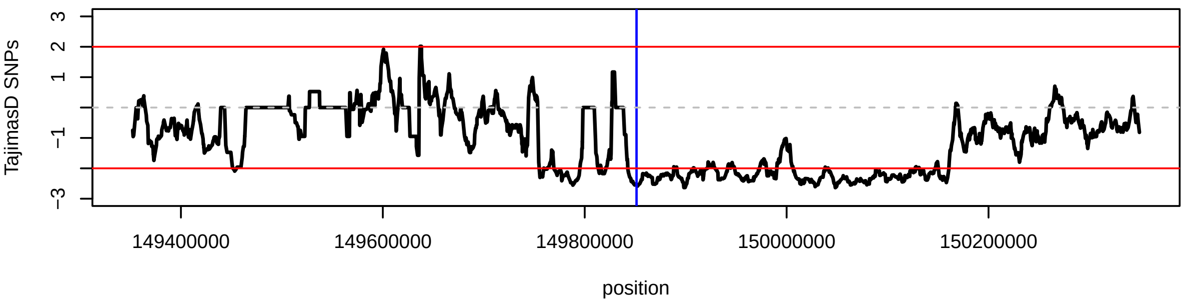
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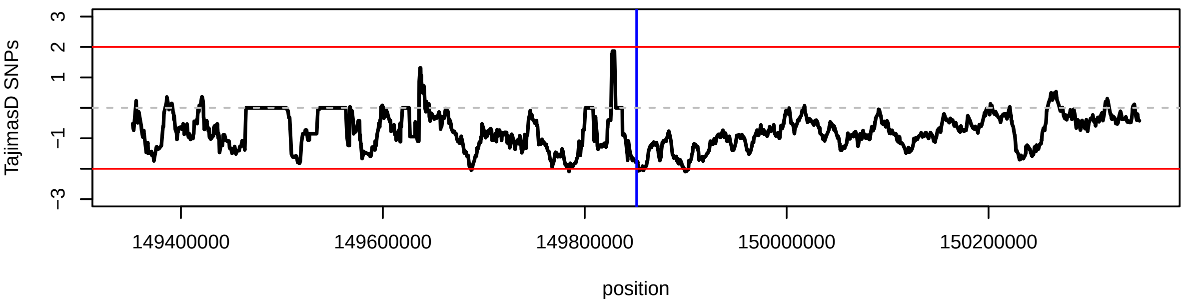
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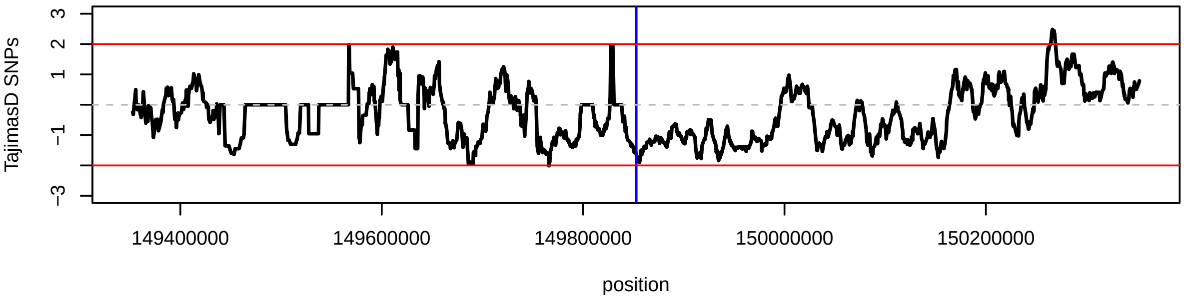
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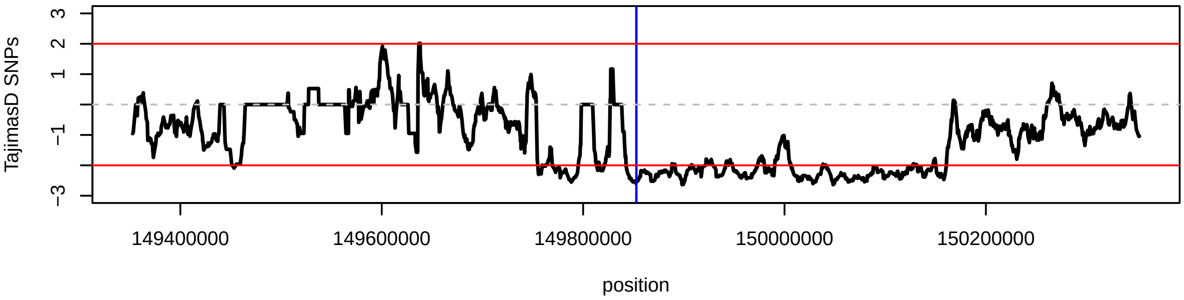
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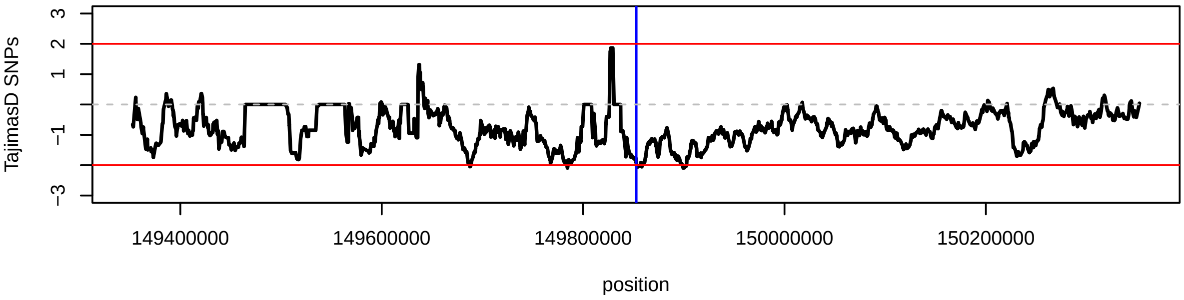
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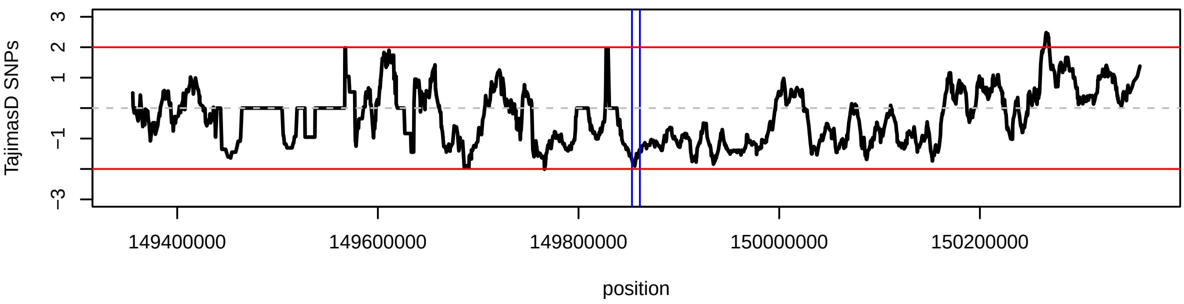
34 CEU HIST2



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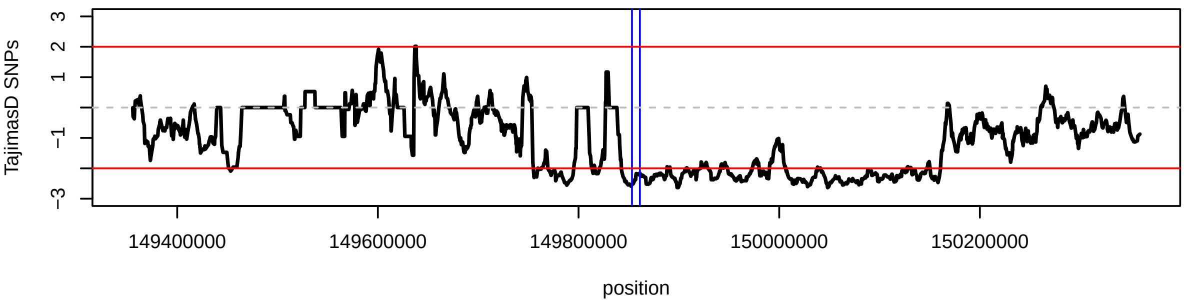

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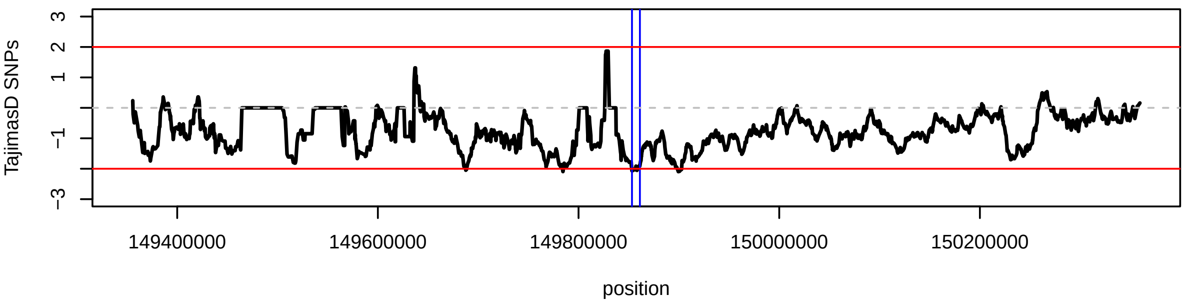

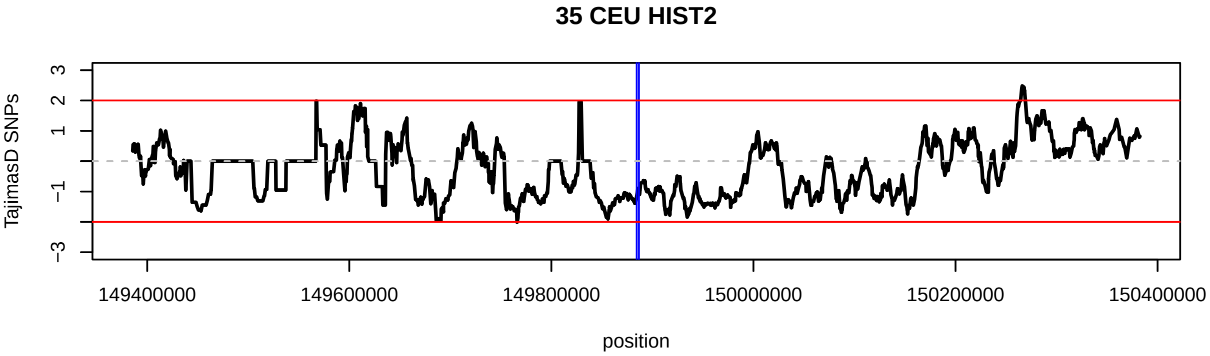
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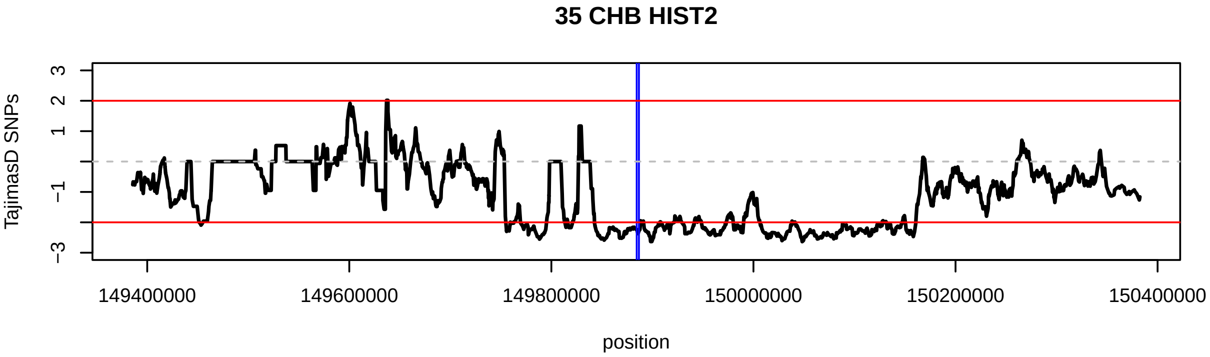
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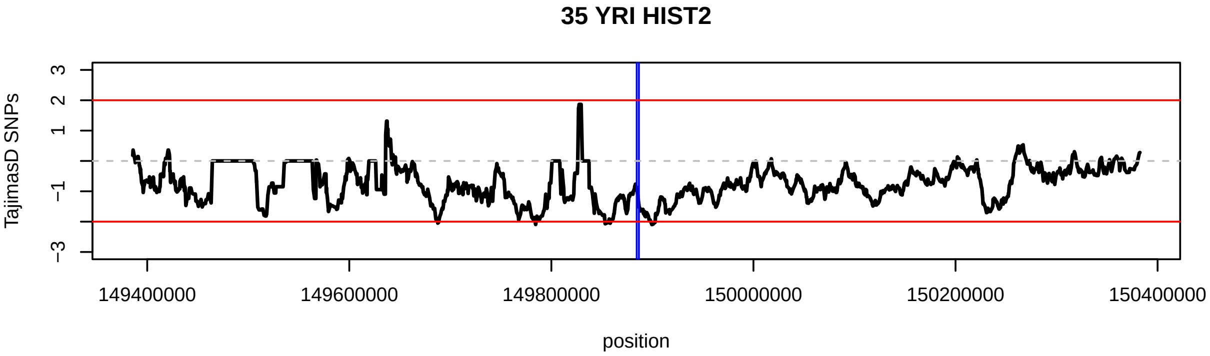
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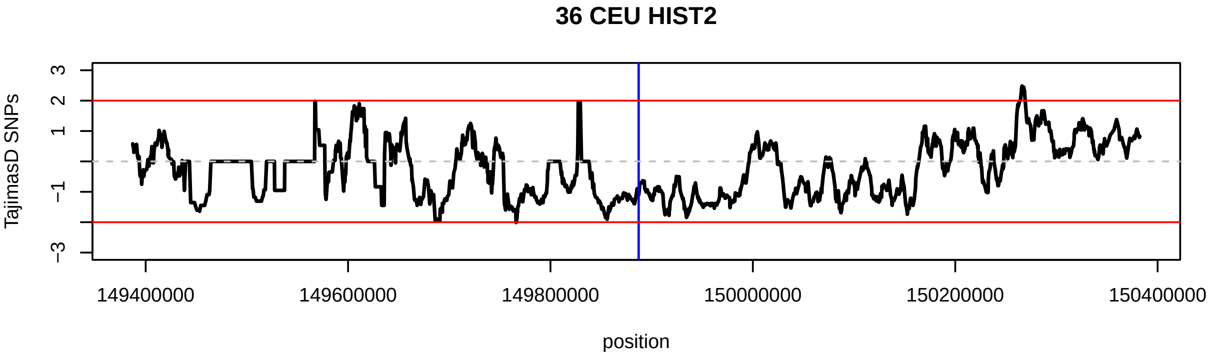
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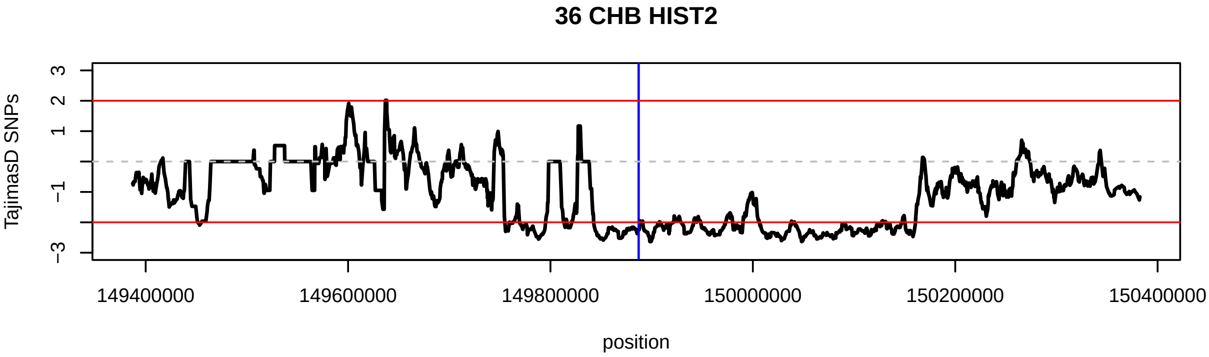
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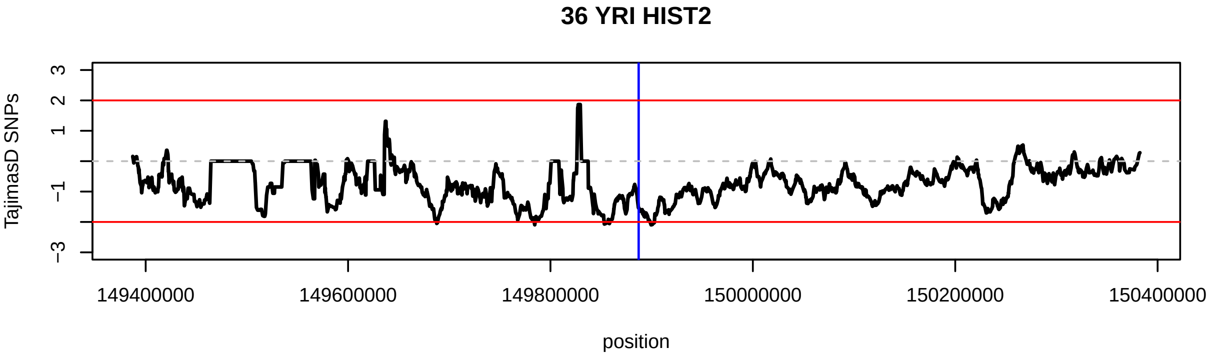
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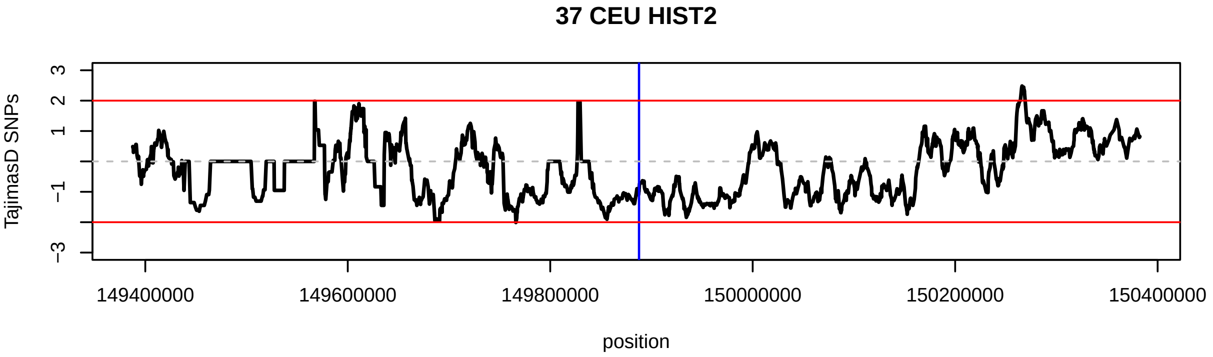
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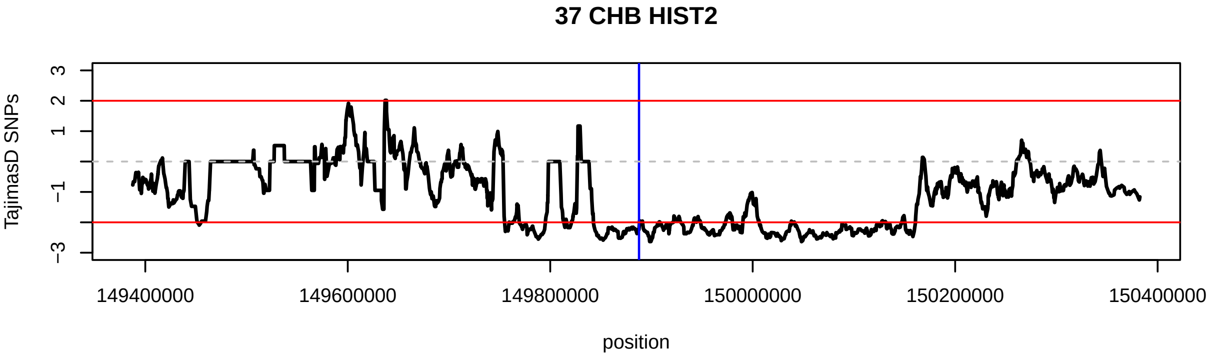
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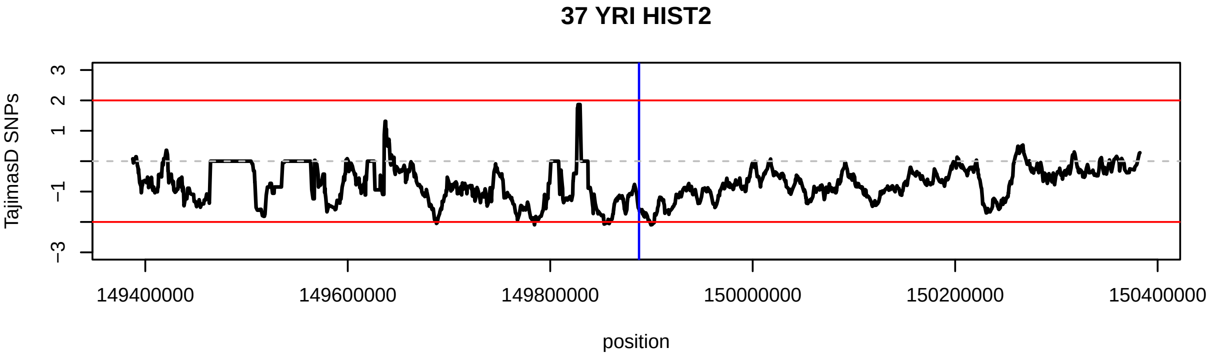
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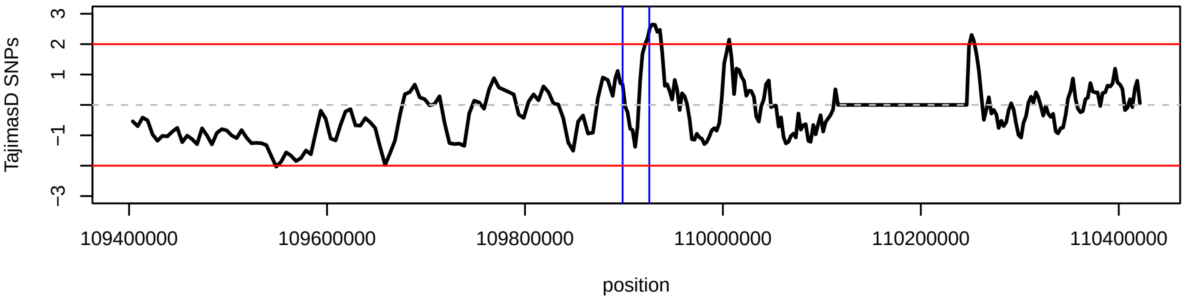

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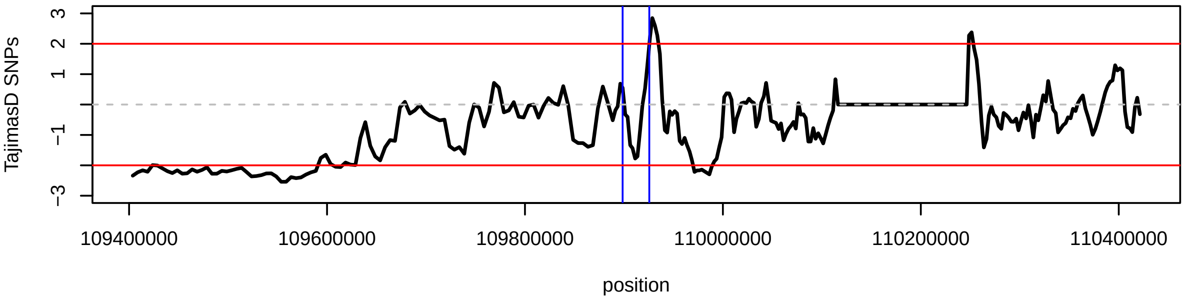

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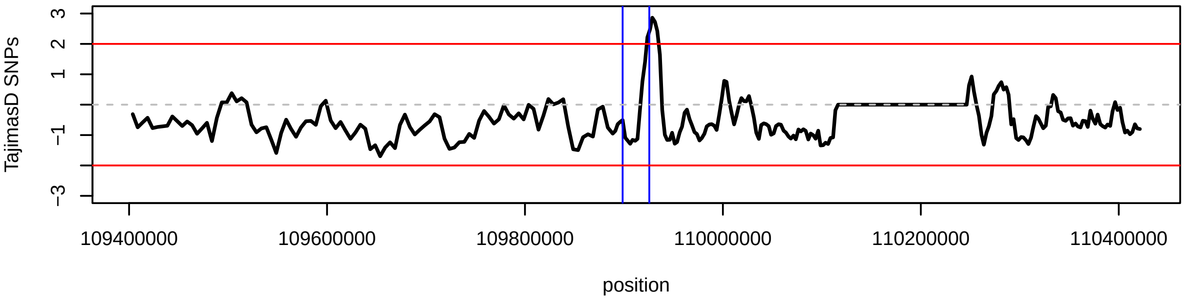

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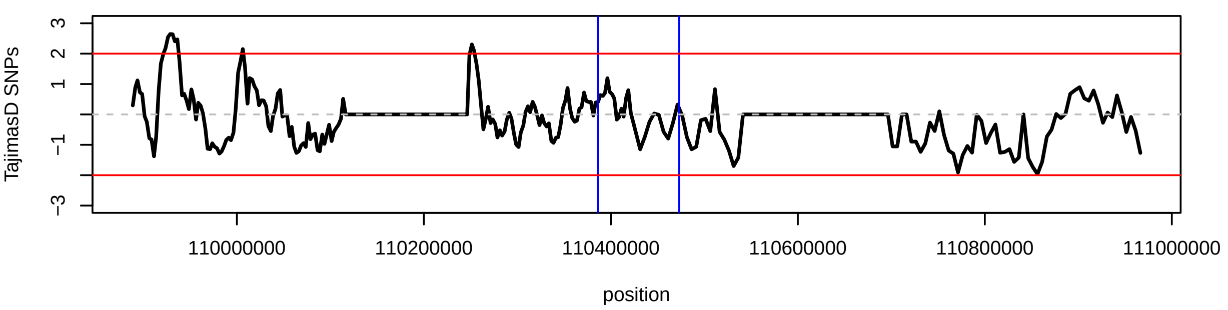

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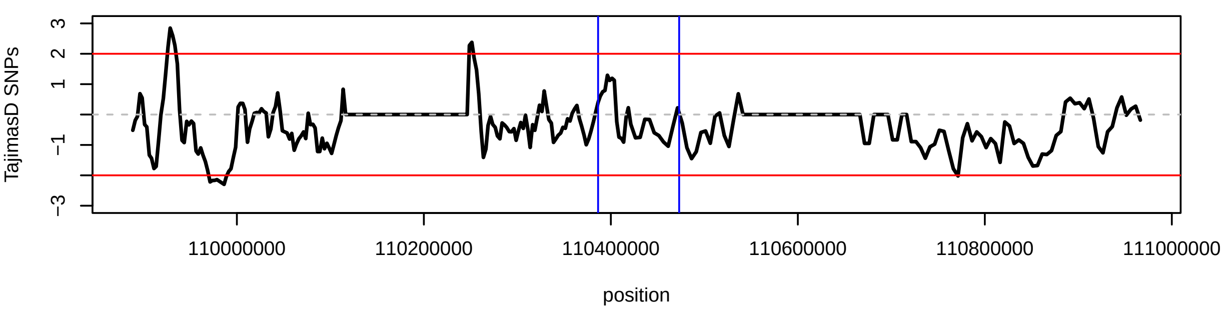

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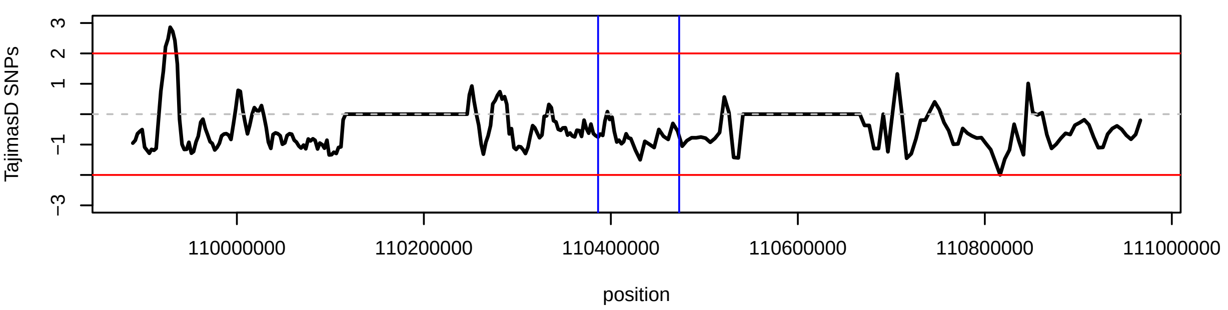

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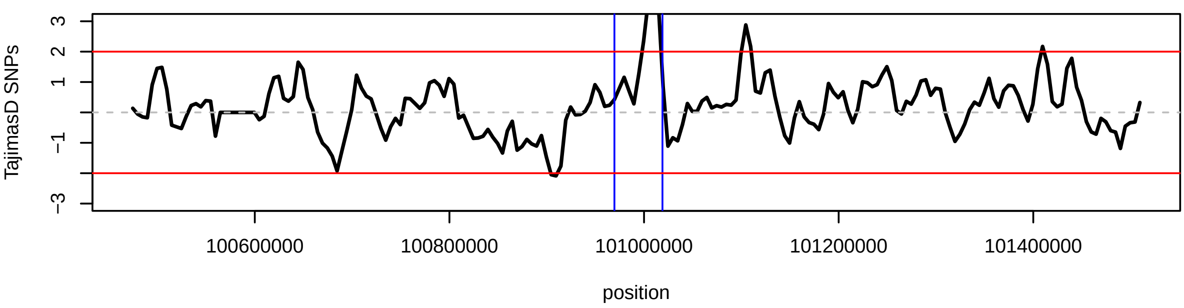
40 CEU MUC12



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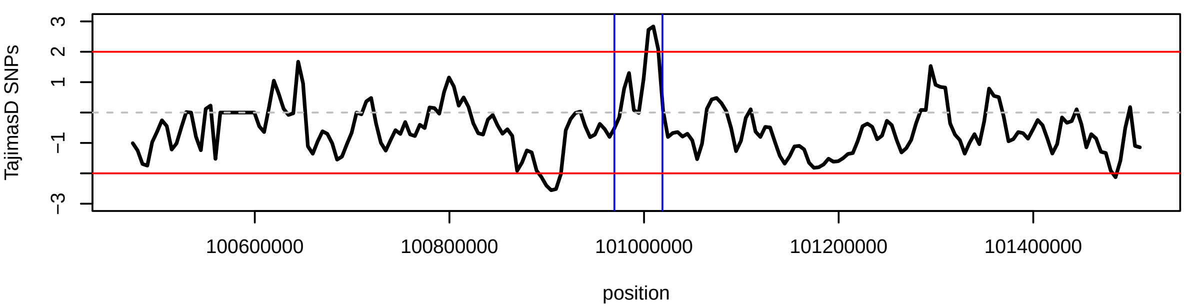

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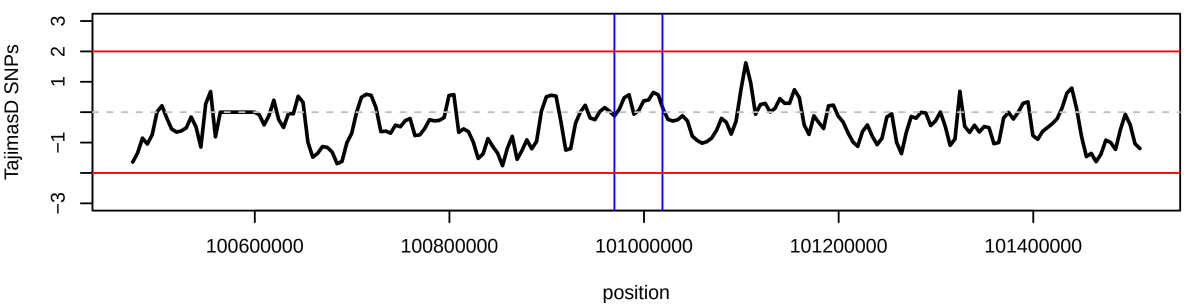

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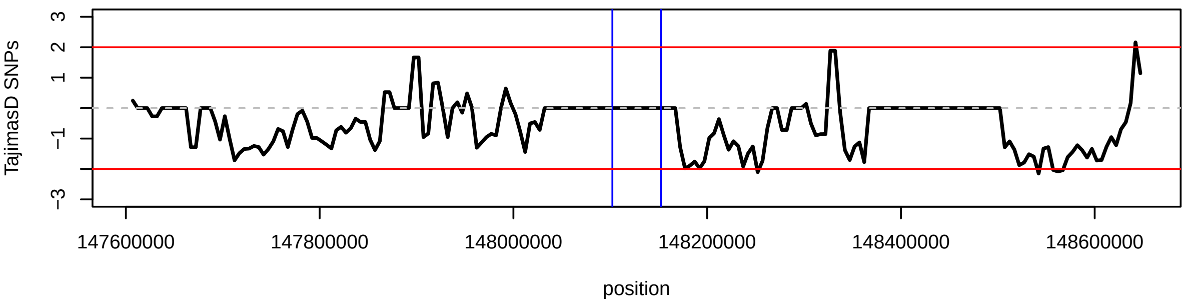

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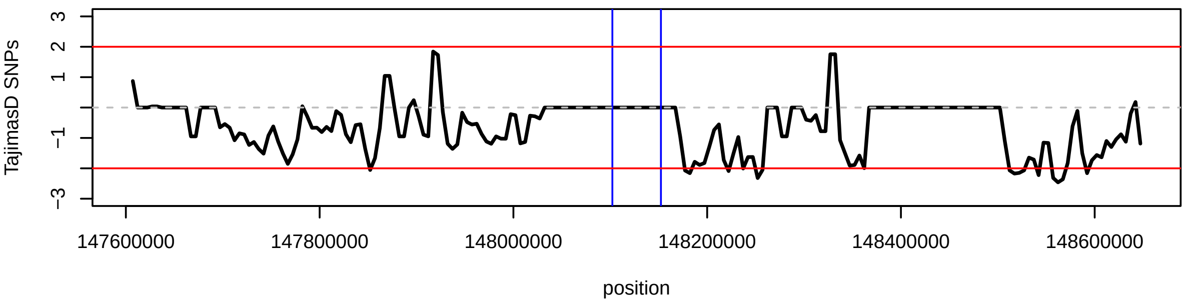

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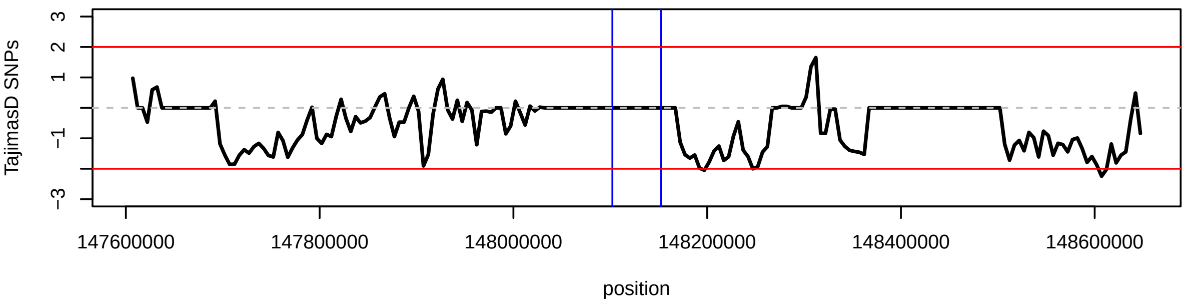

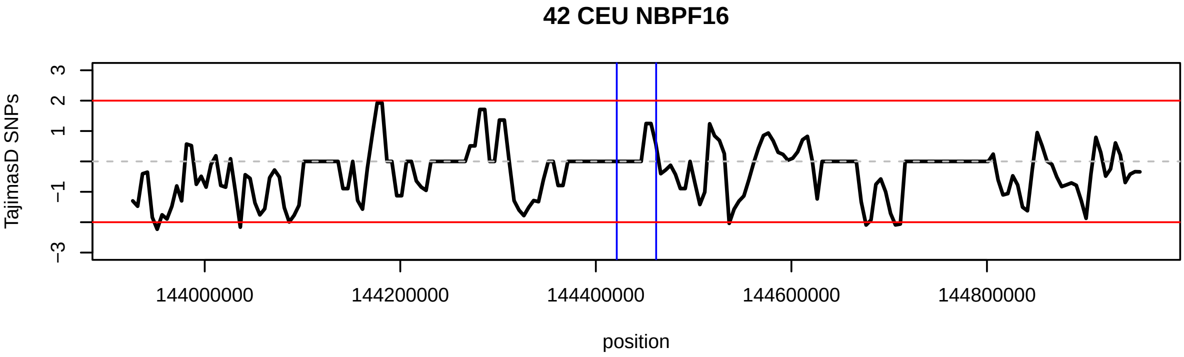
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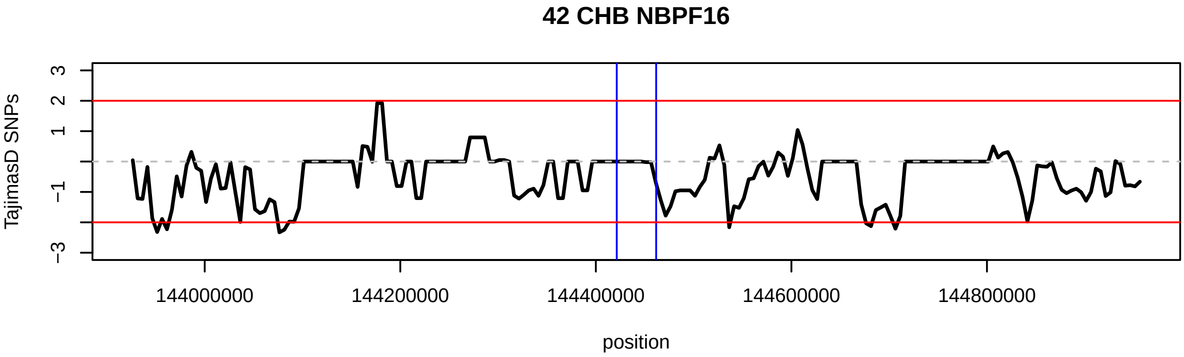
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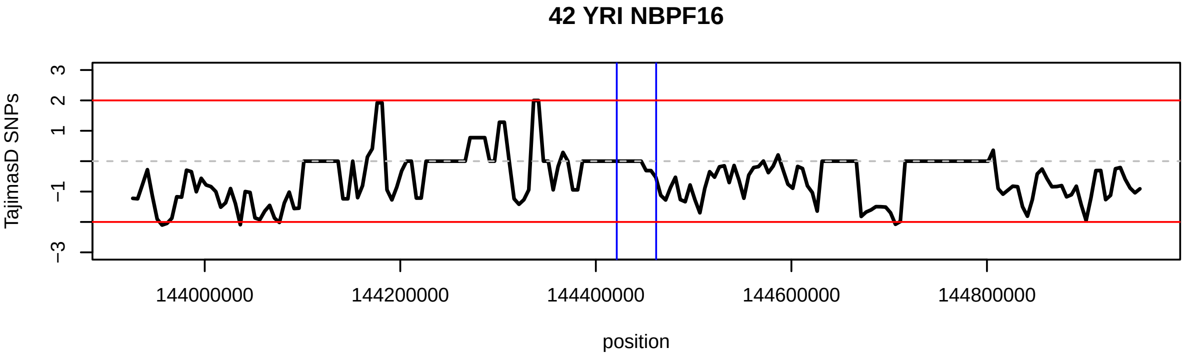
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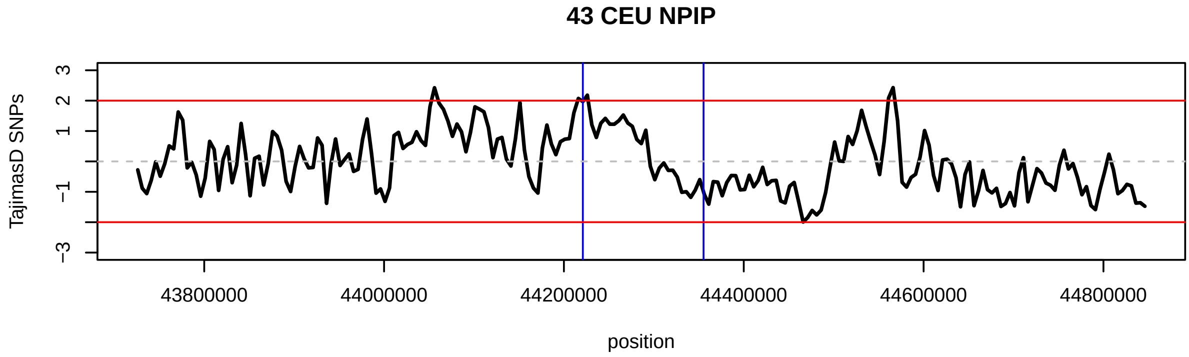
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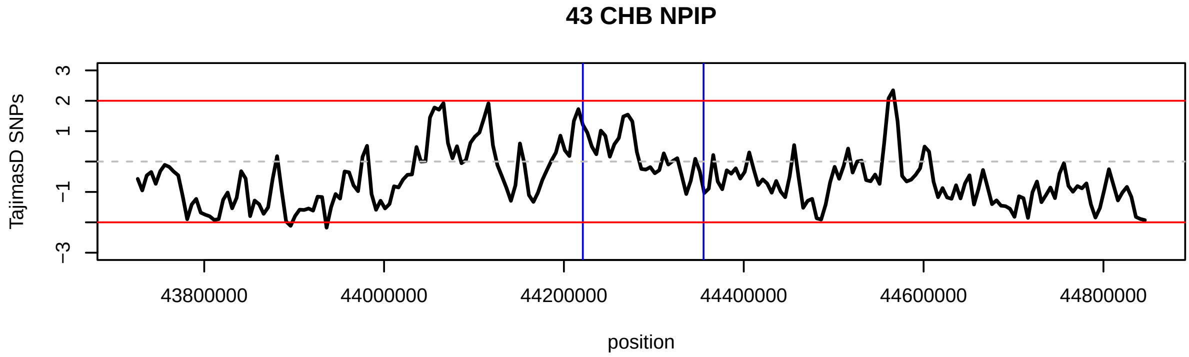
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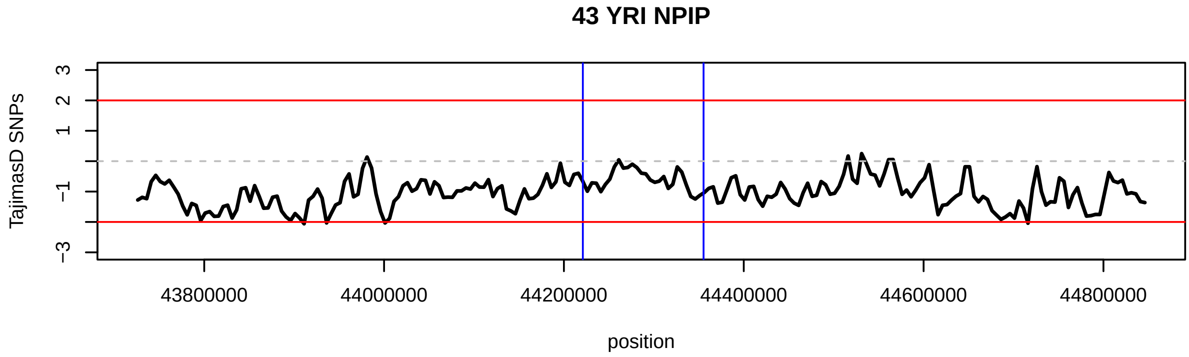
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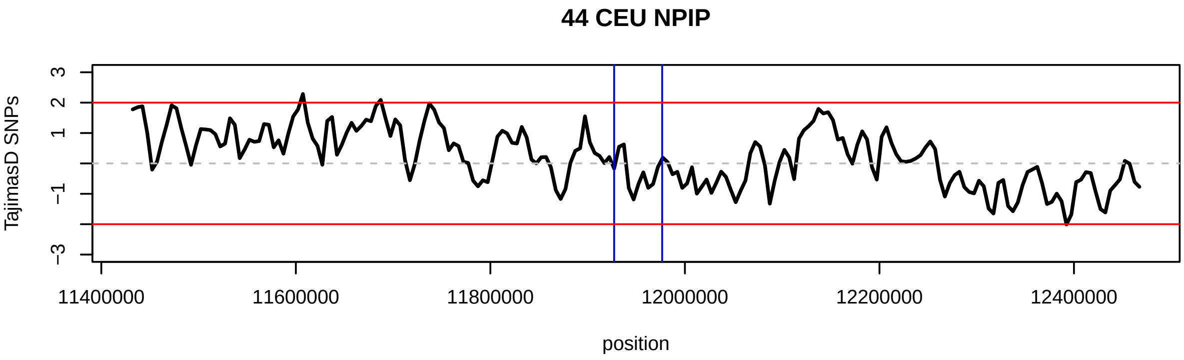
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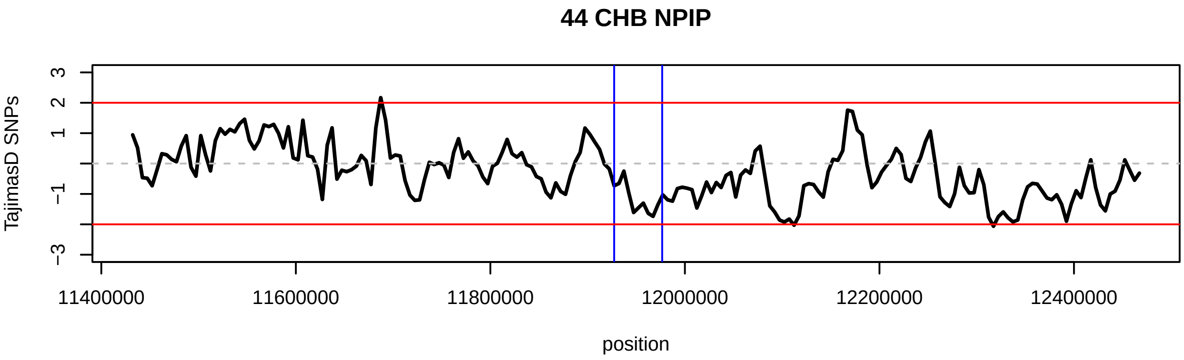
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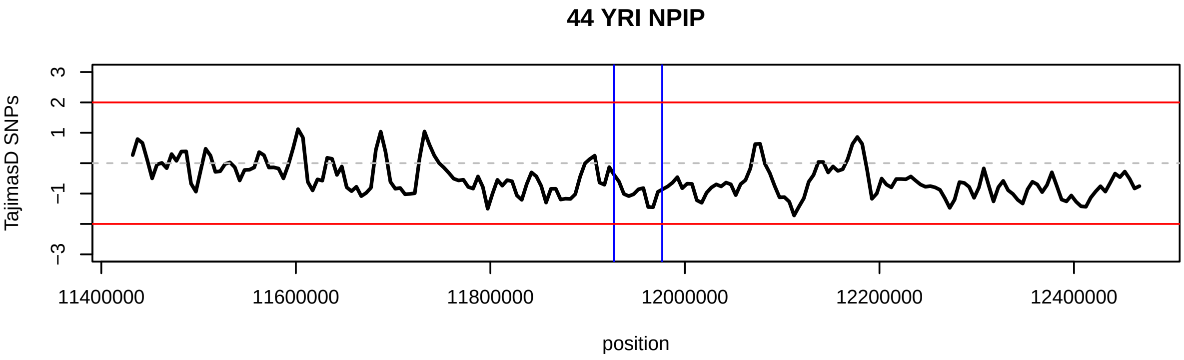
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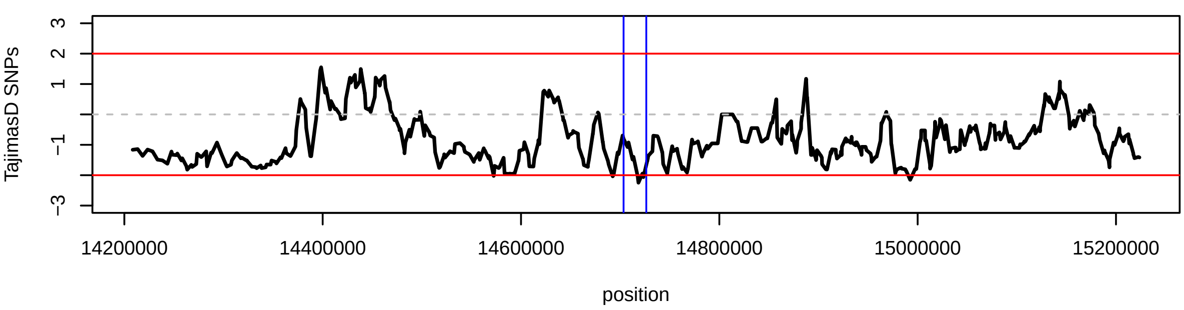

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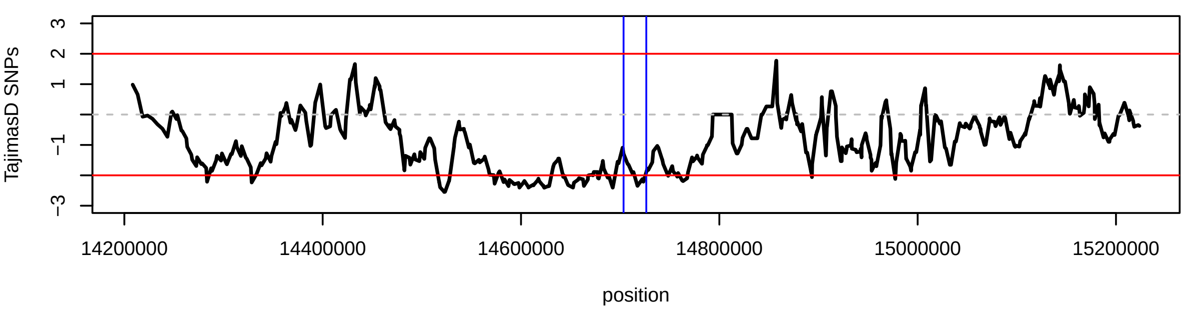

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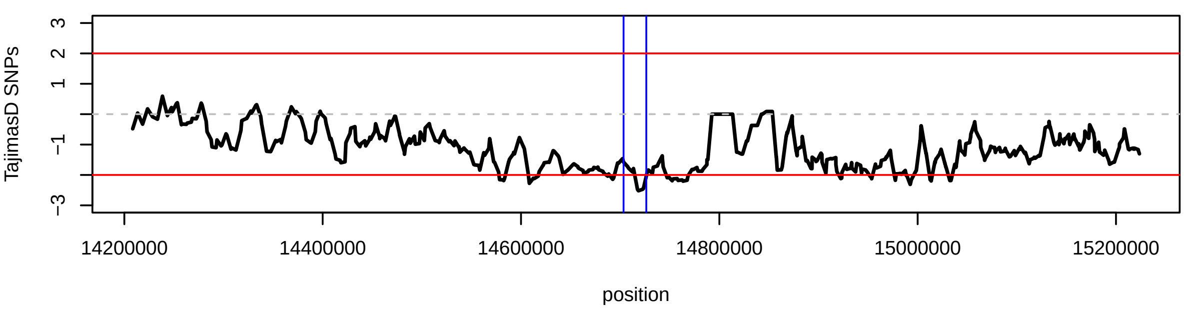

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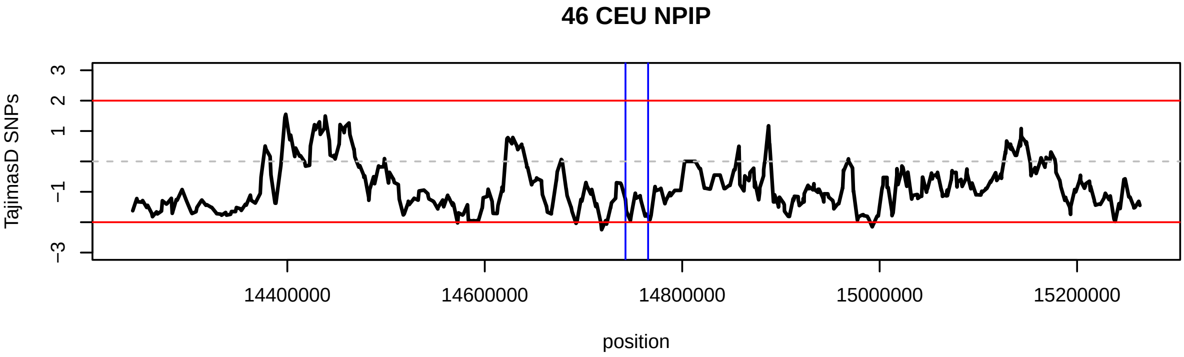
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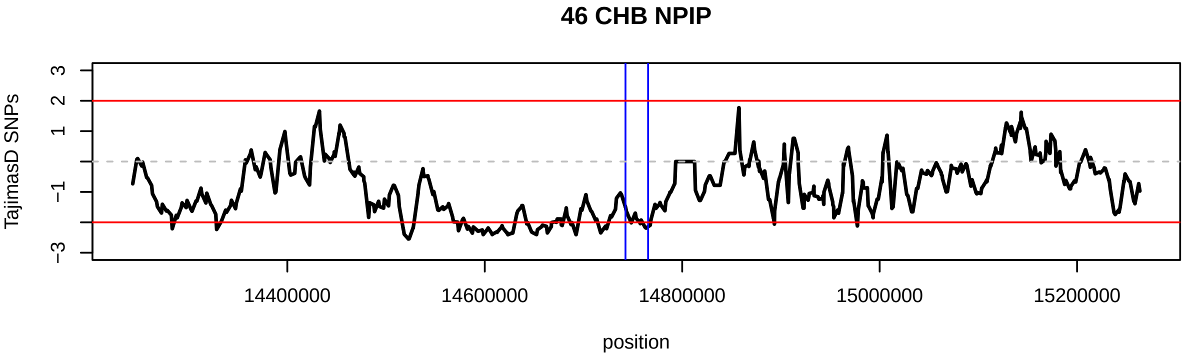
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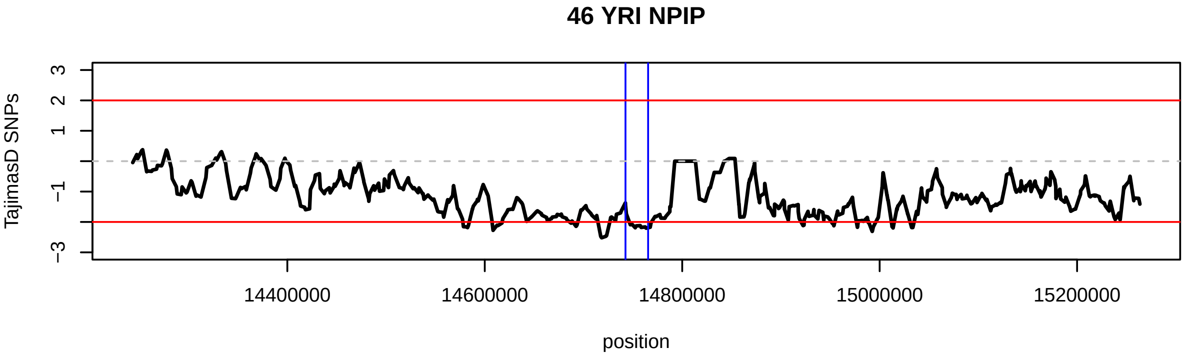
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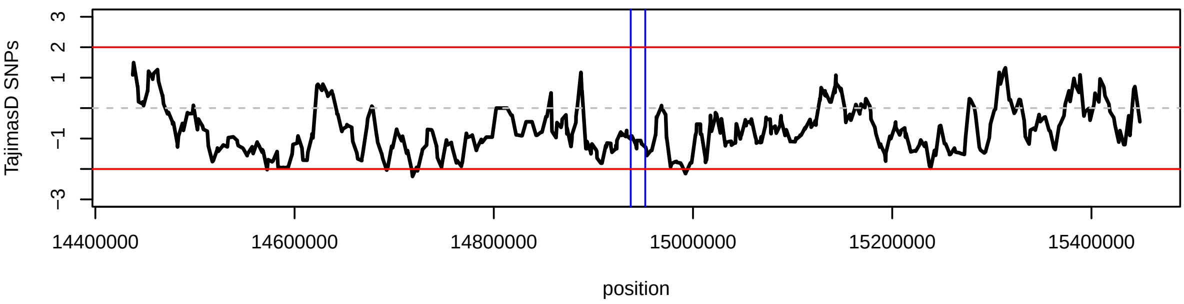
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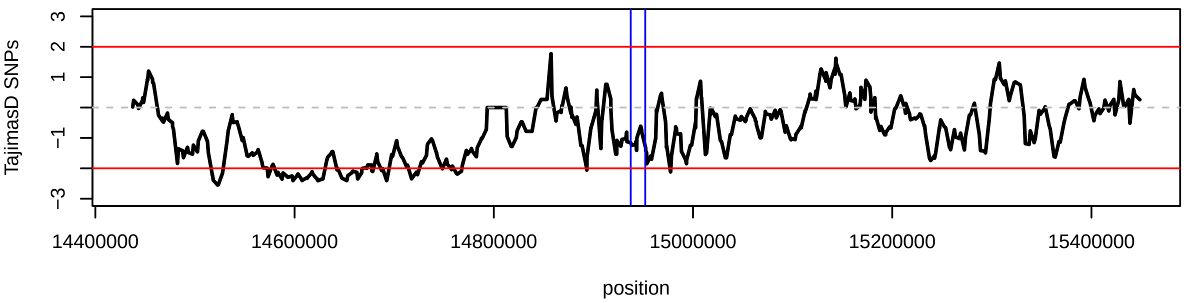
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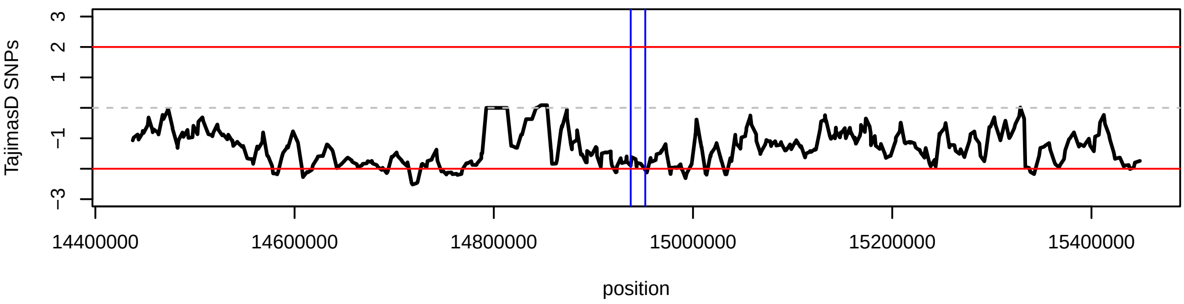
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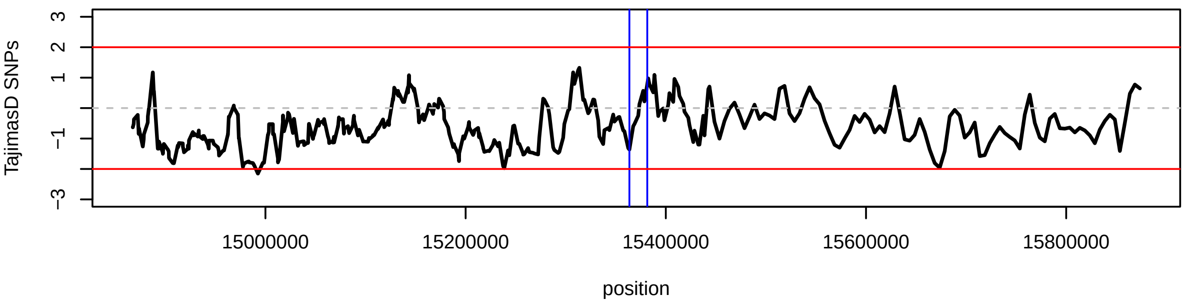

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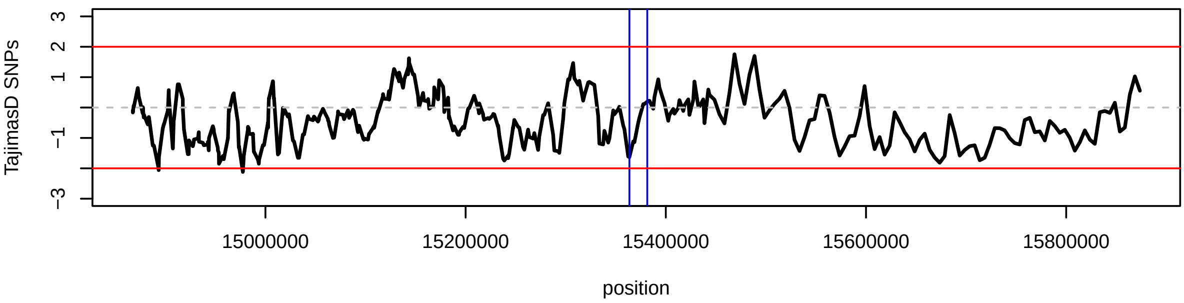

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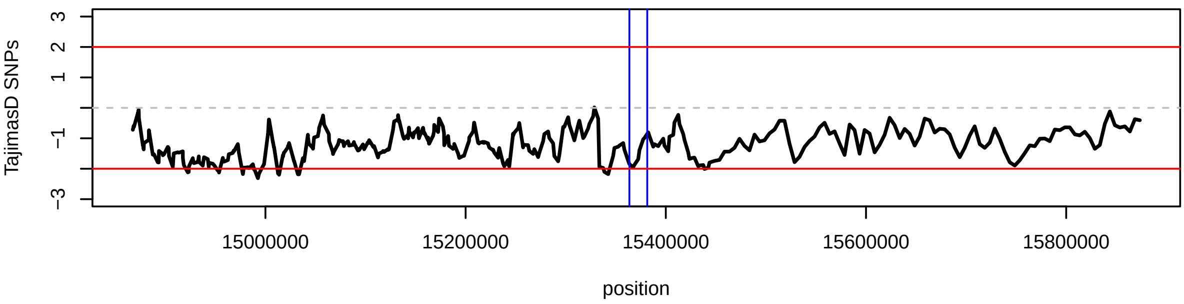

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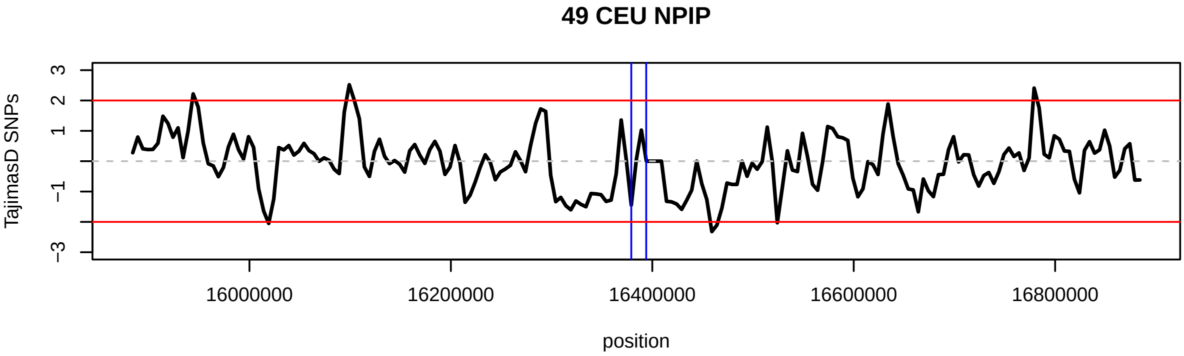
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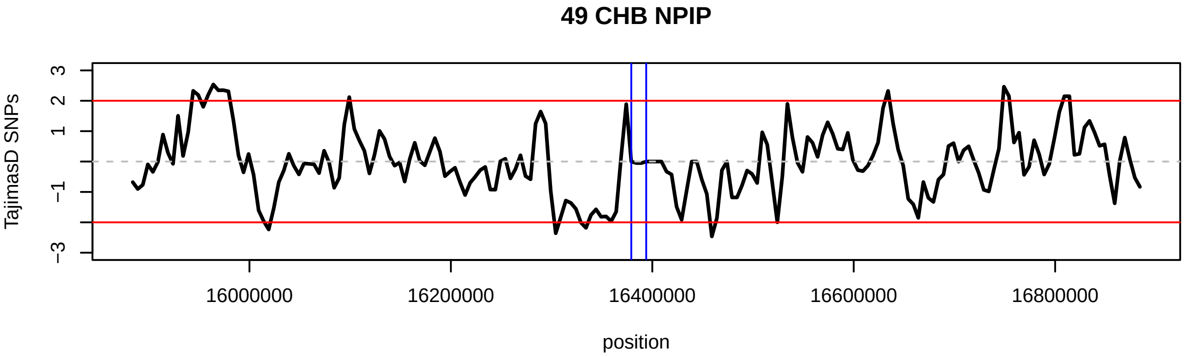
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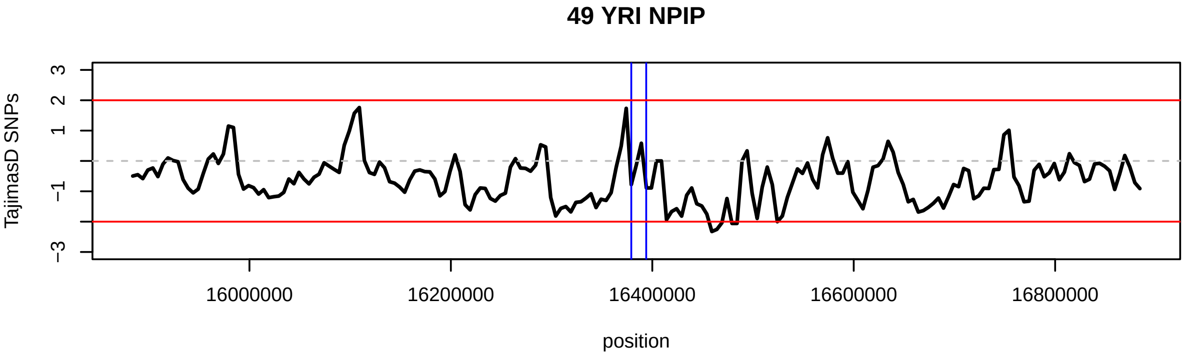
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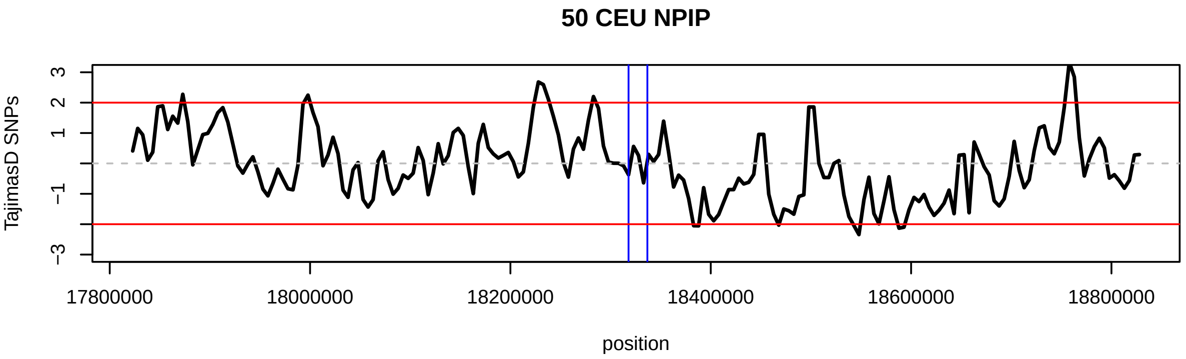
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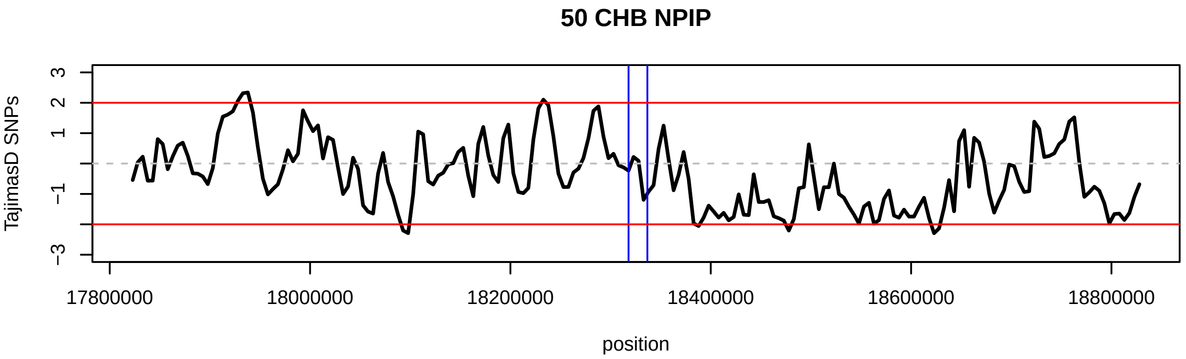
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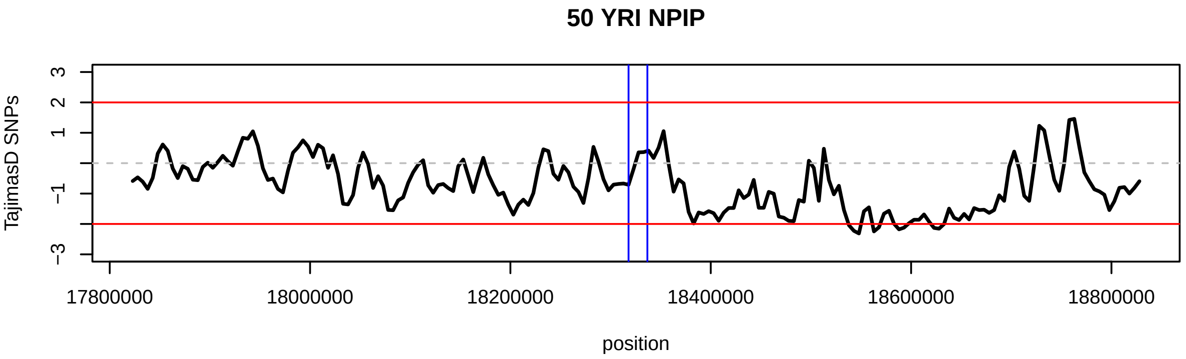
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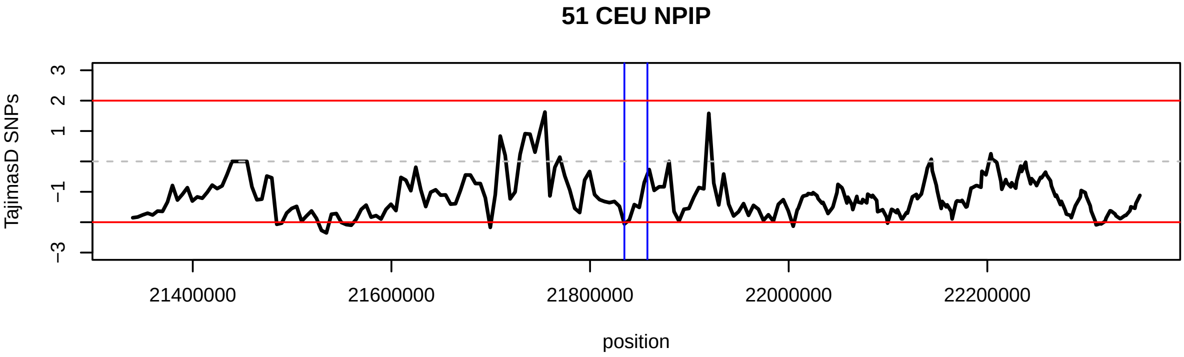
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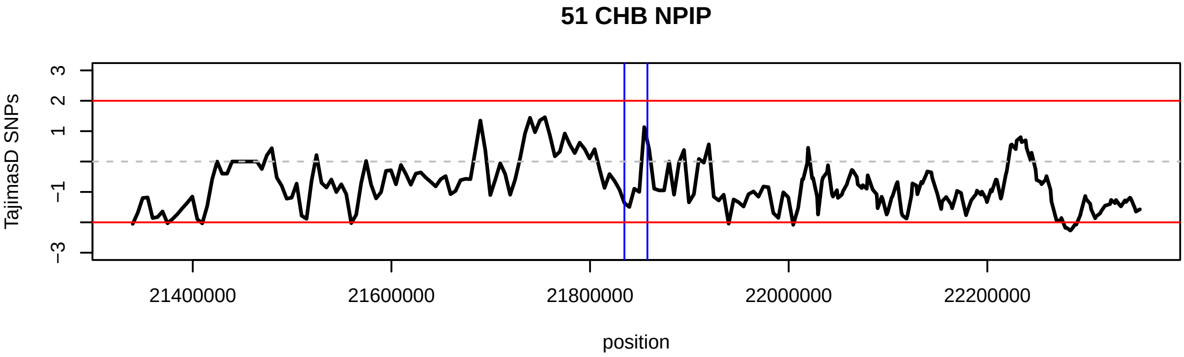
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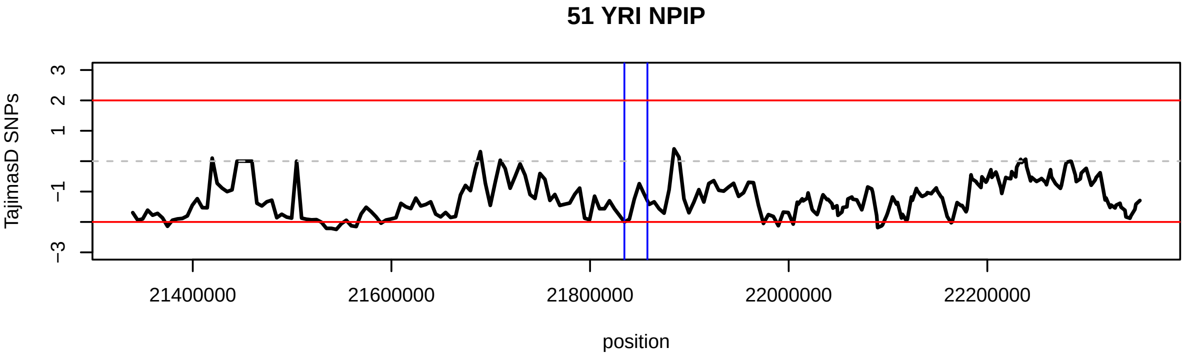
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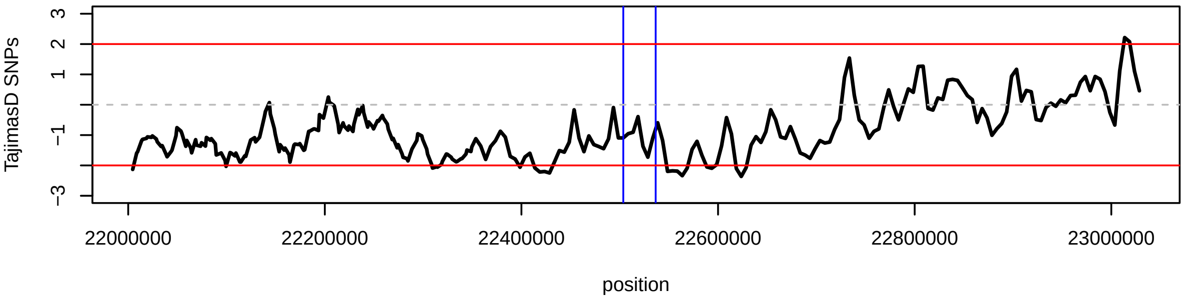

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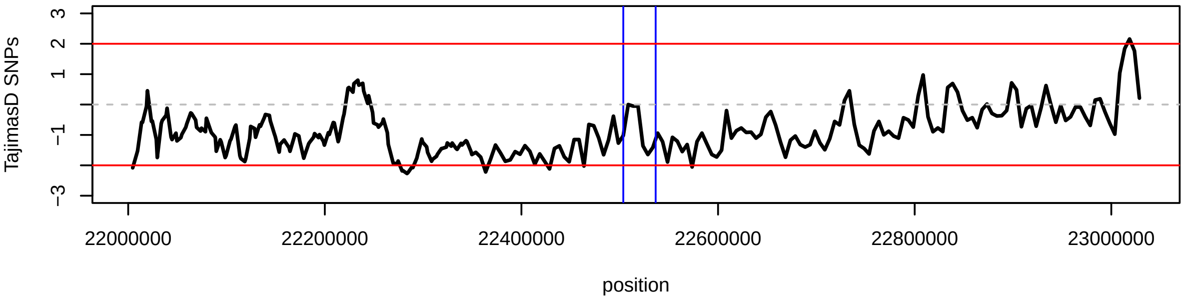

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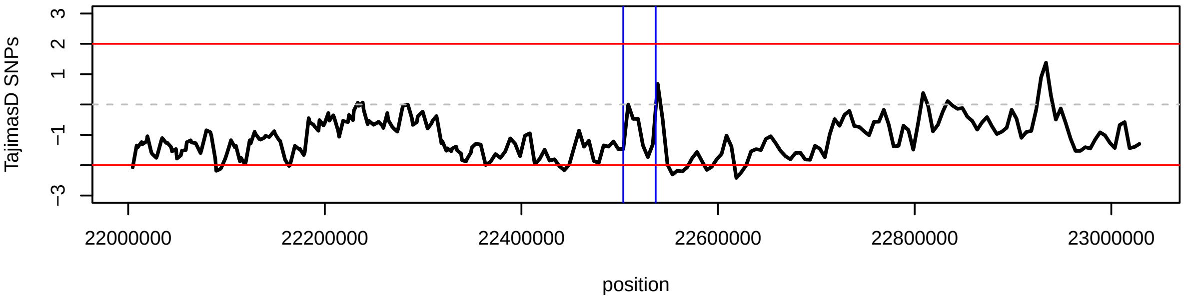

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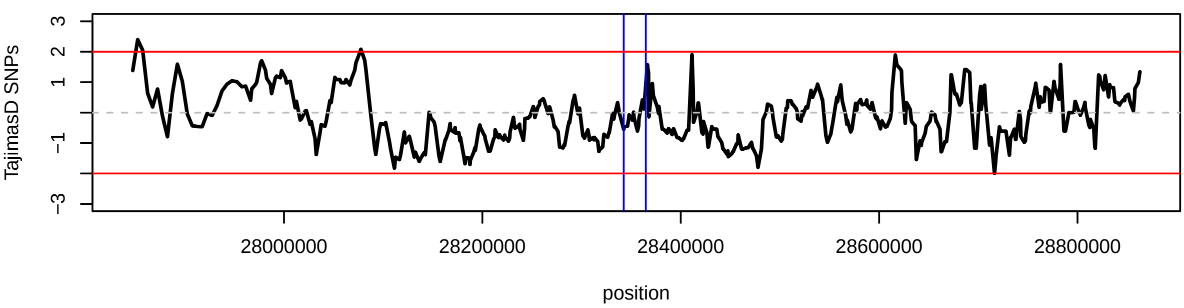

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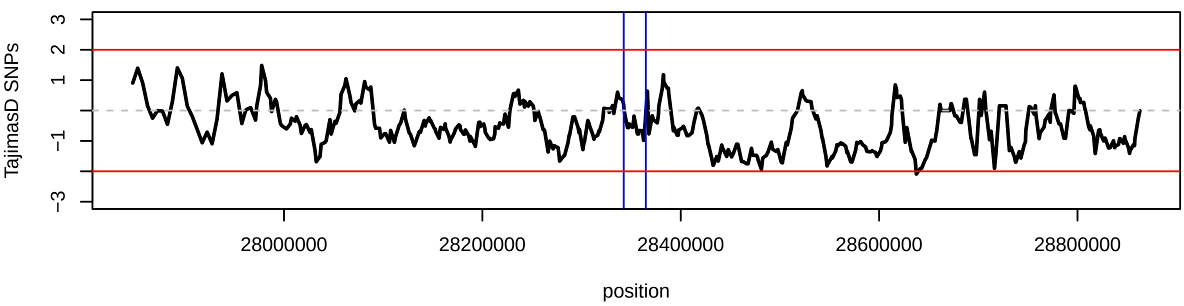

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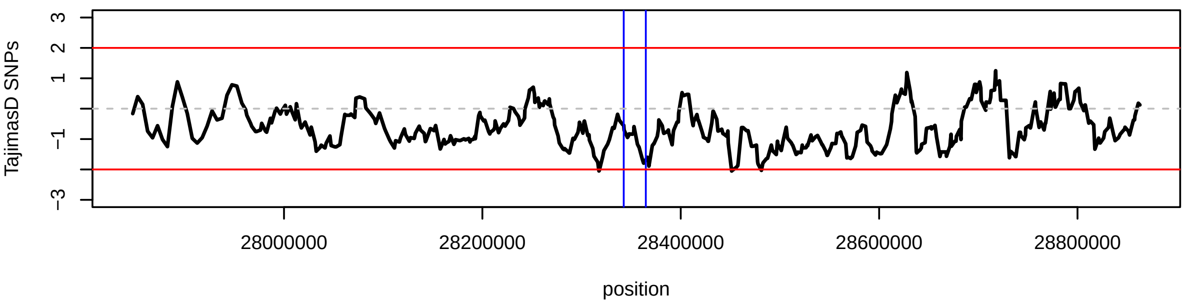

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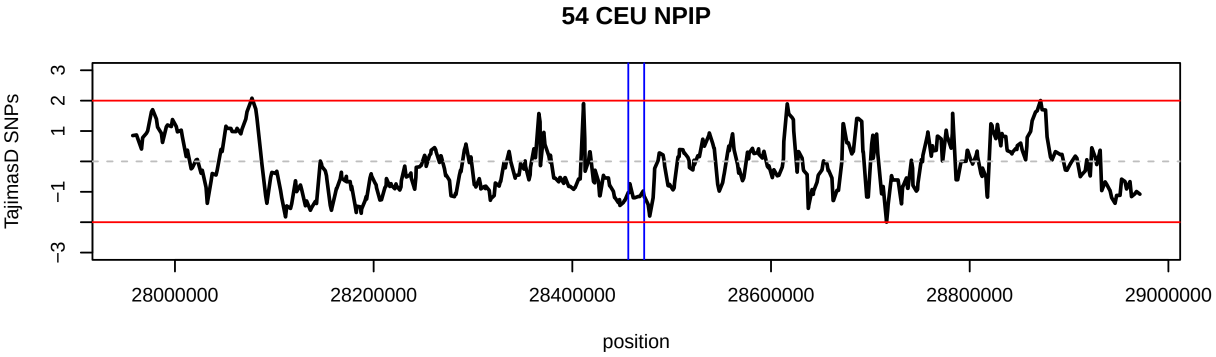
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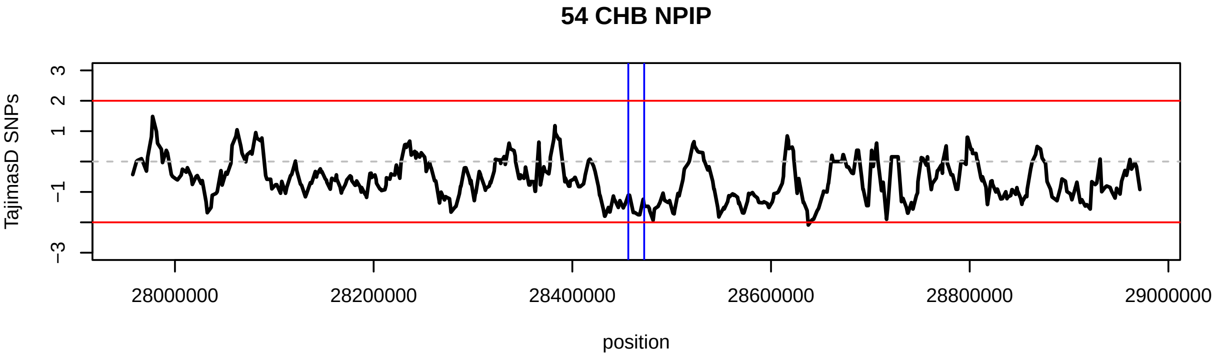
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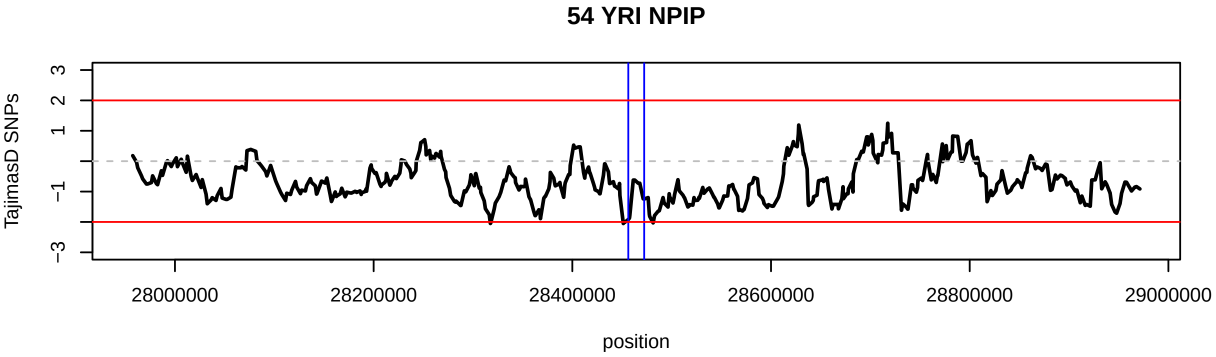
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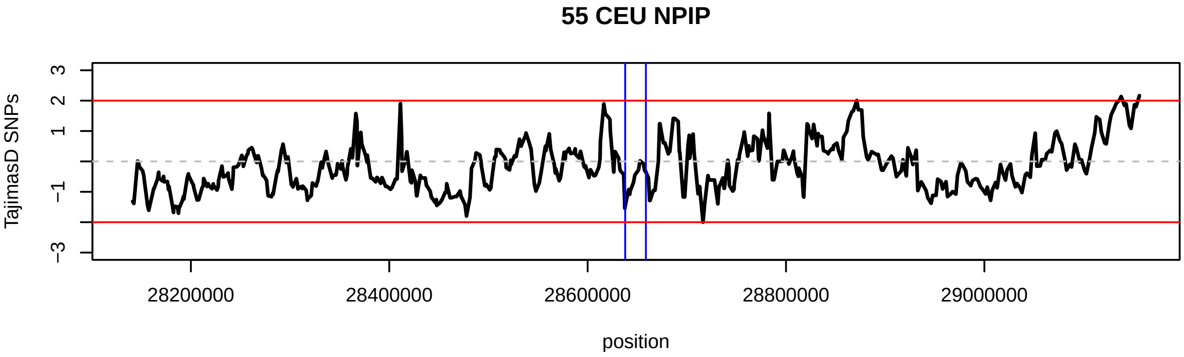
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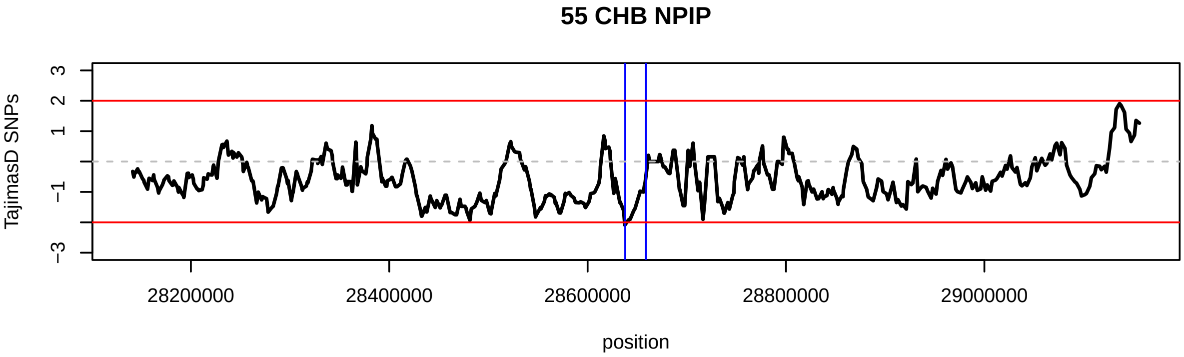
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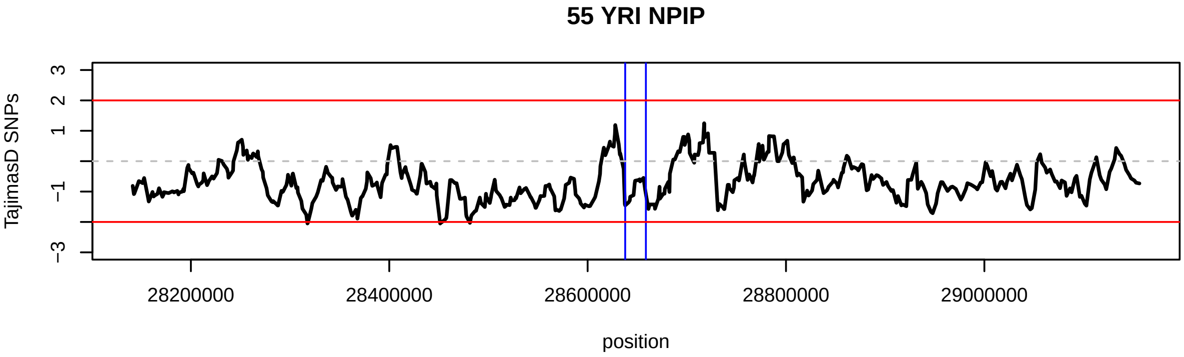
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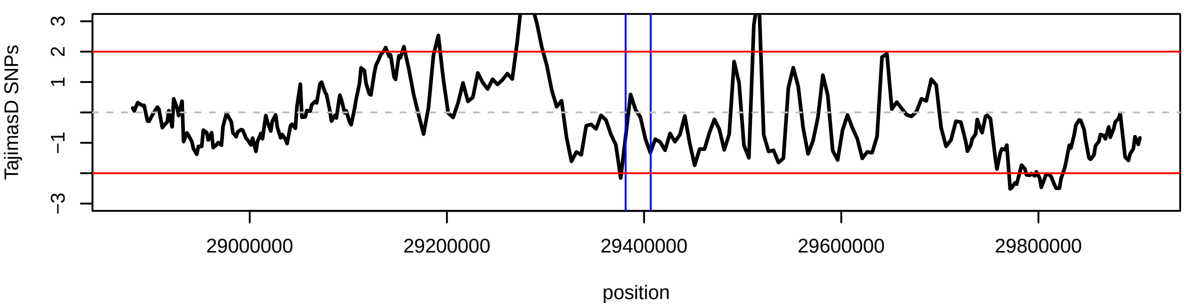

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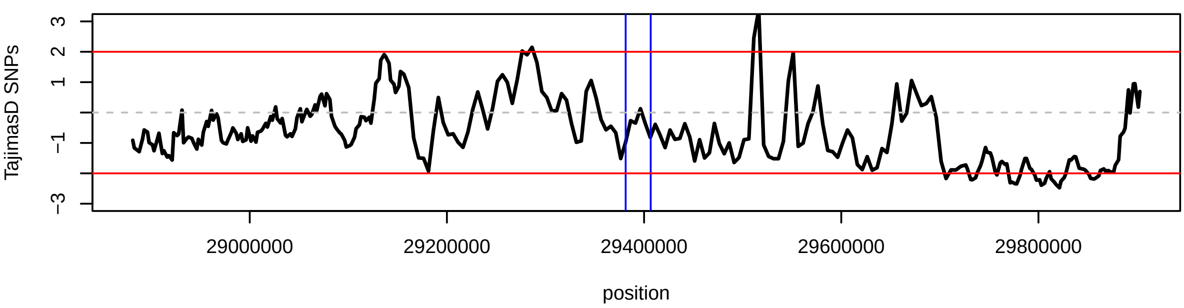

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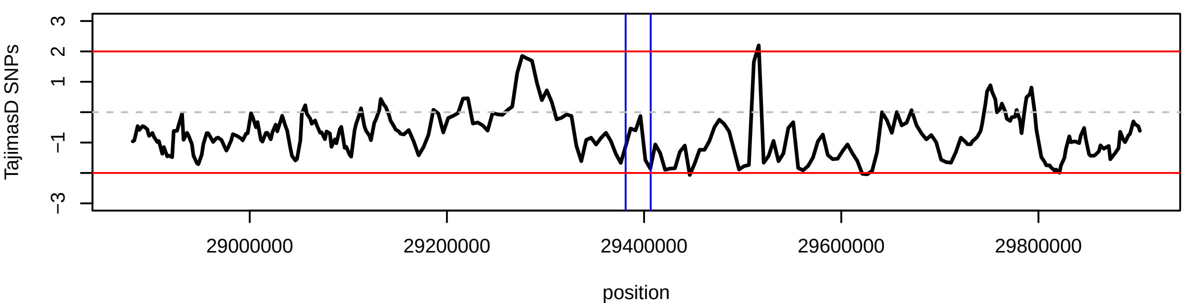

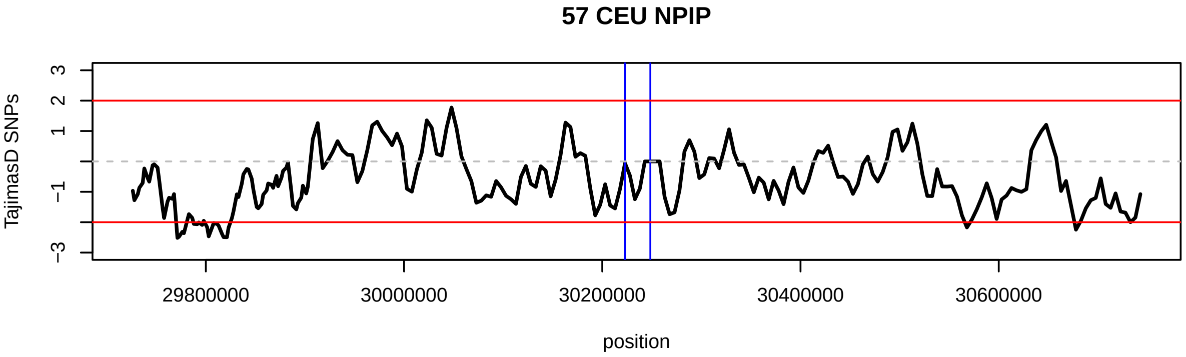
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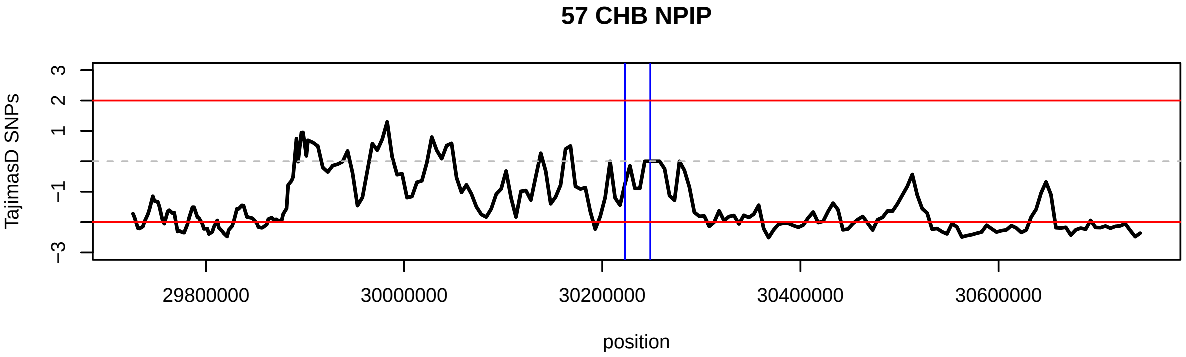
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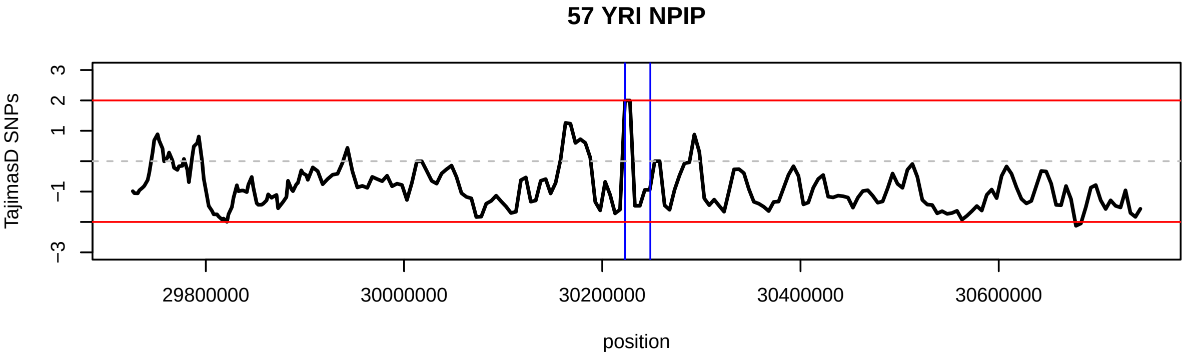
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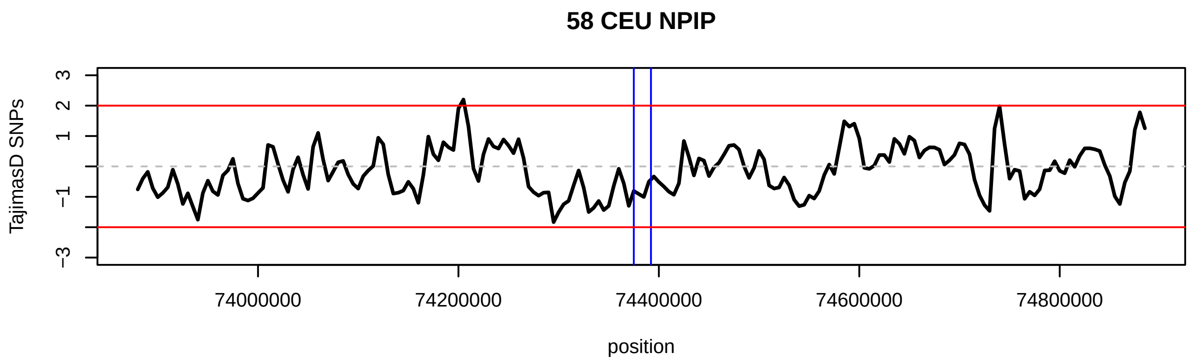
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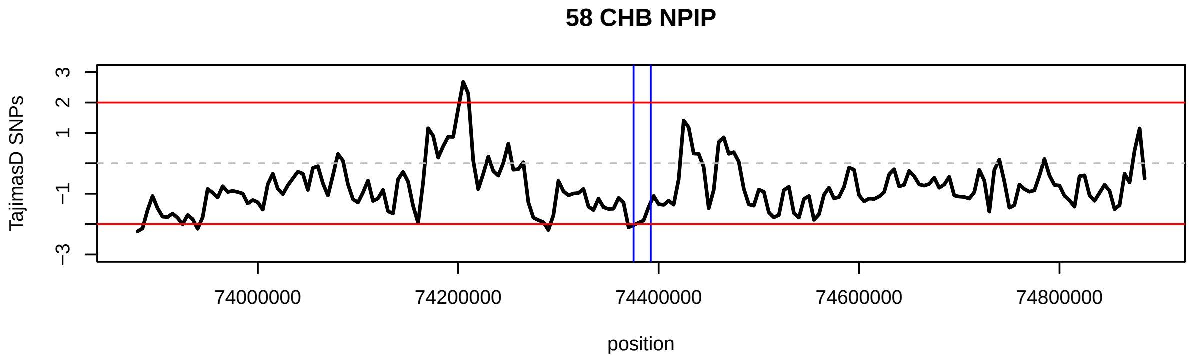
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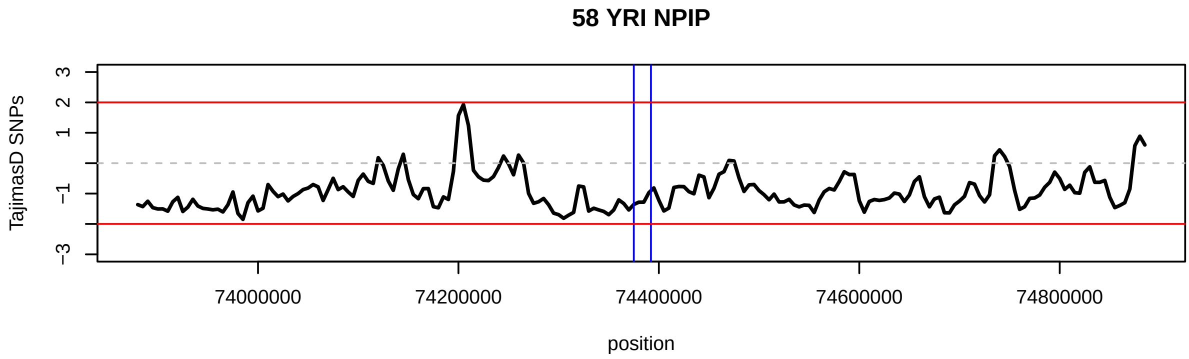
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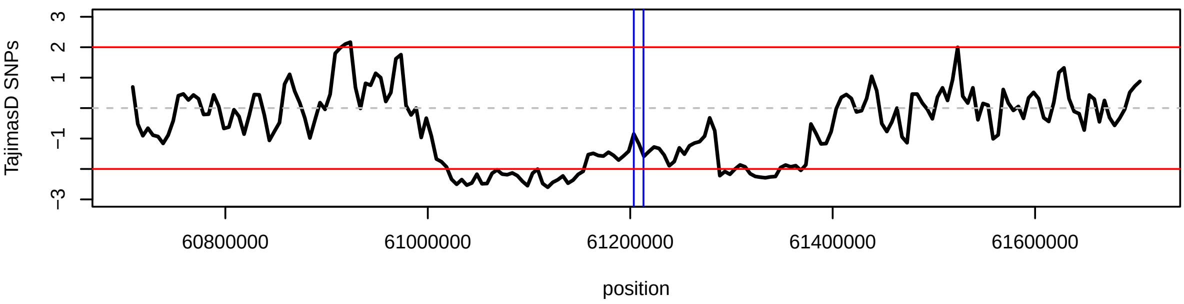
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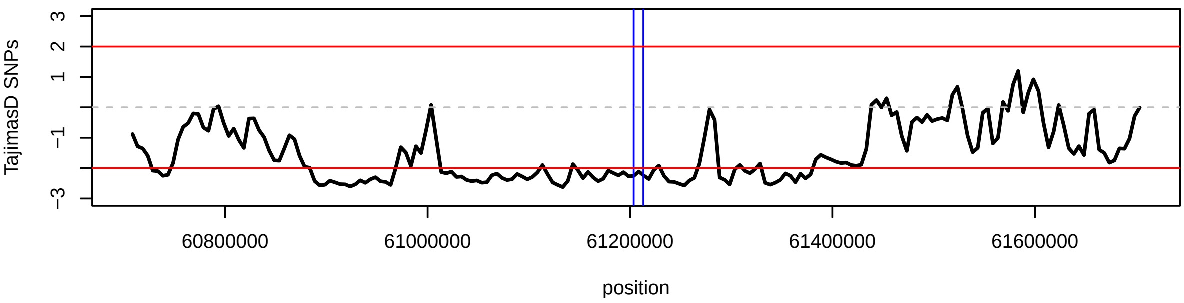
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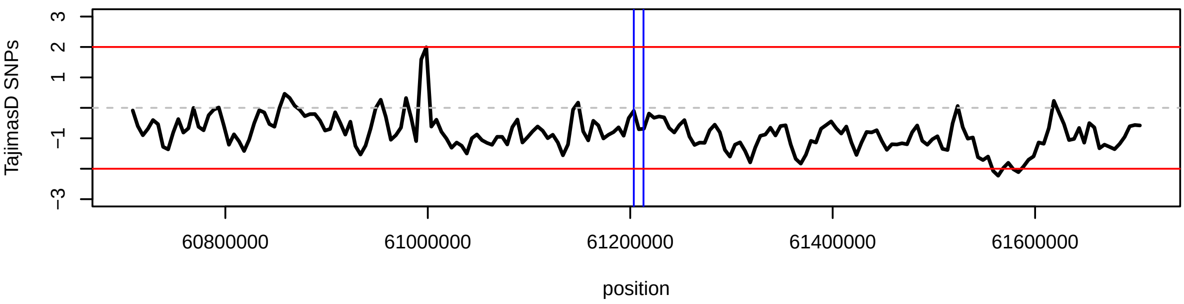
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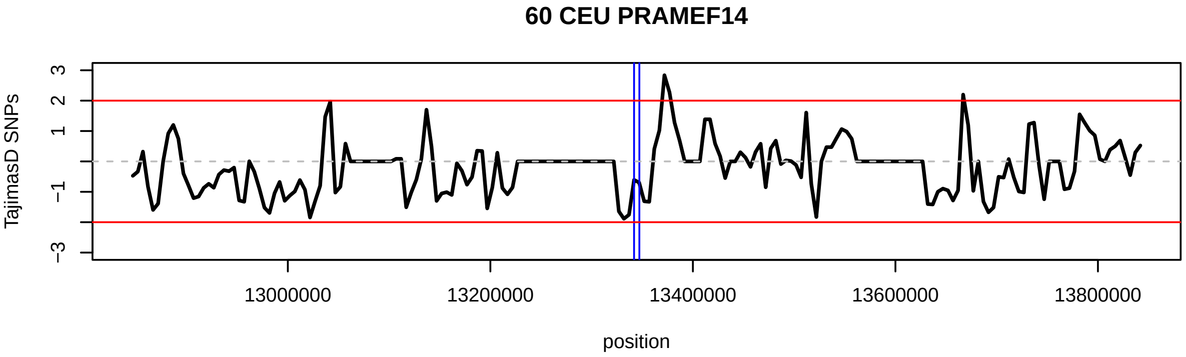
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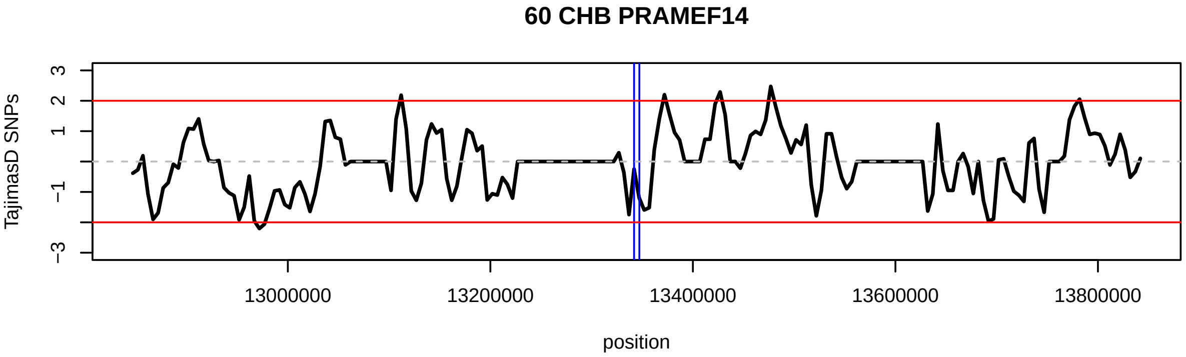
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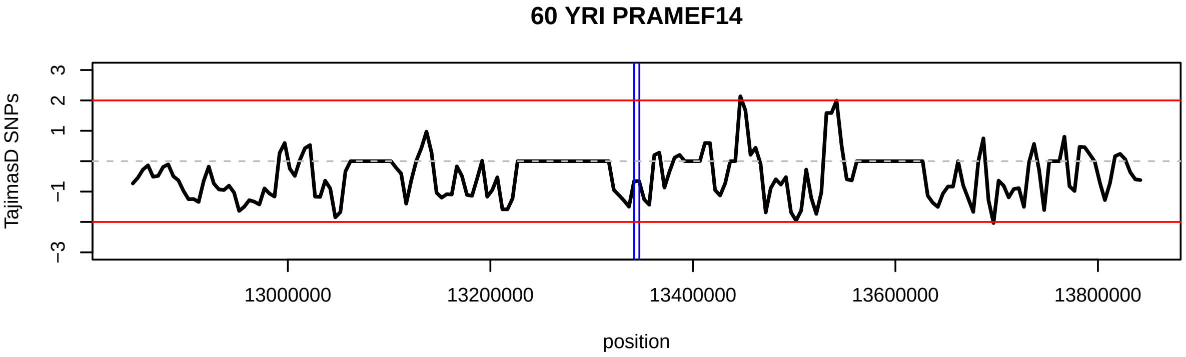
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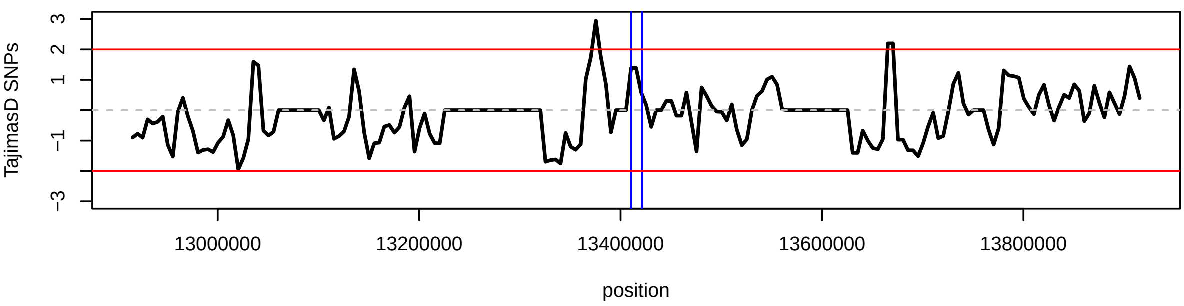

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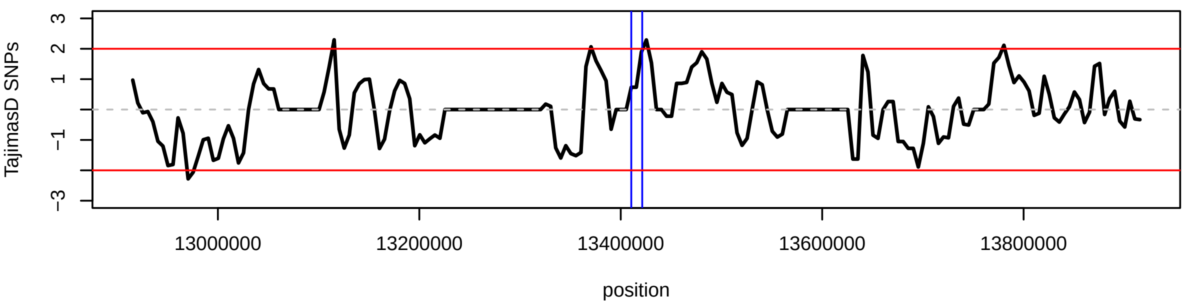

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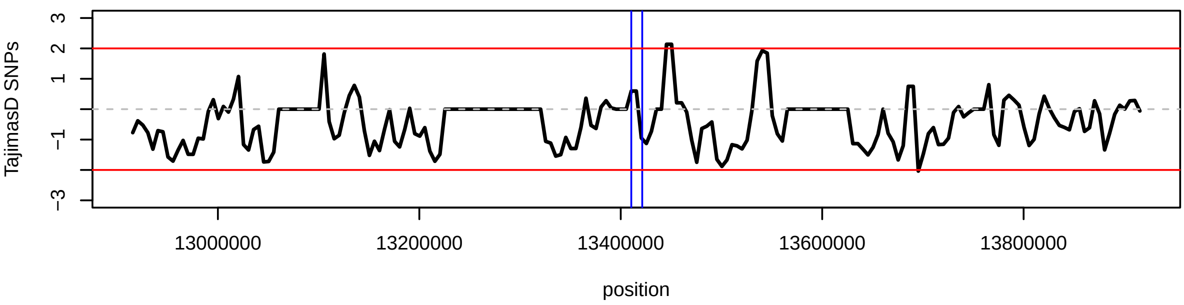

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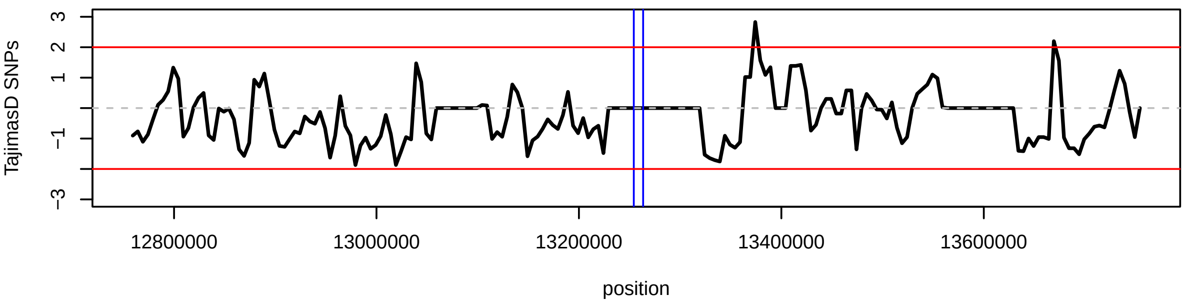

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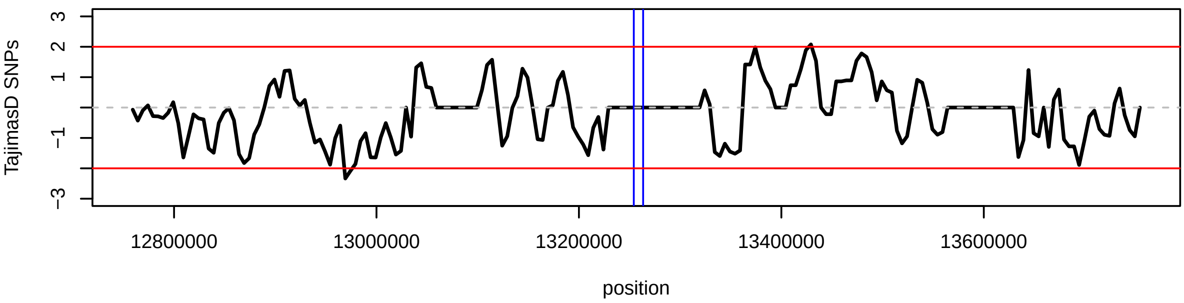

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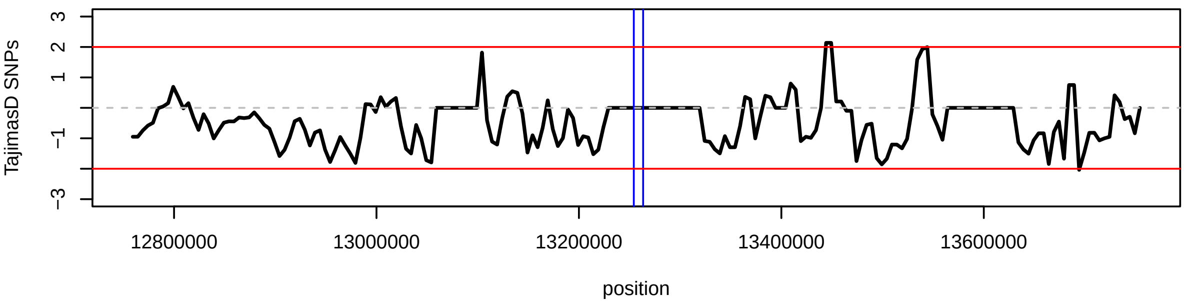

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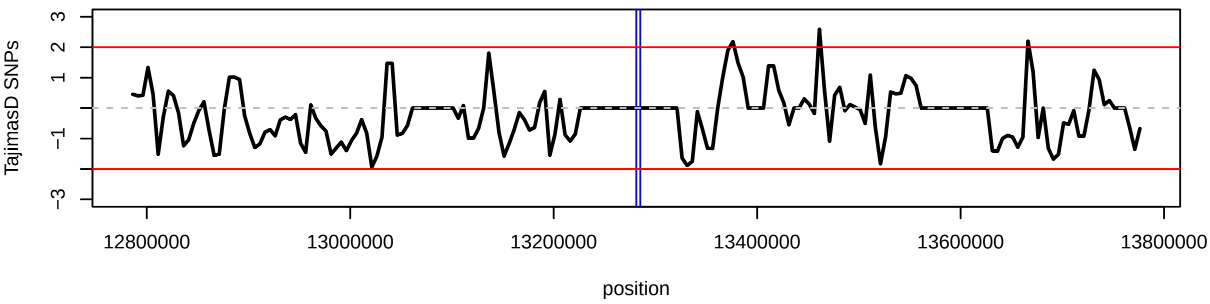

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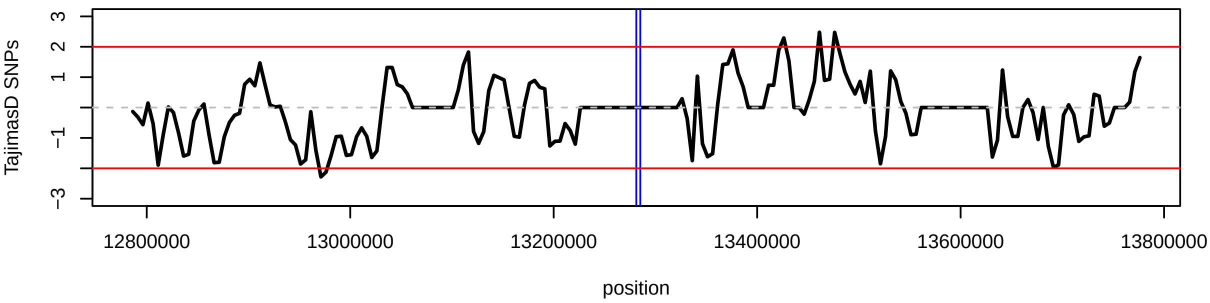

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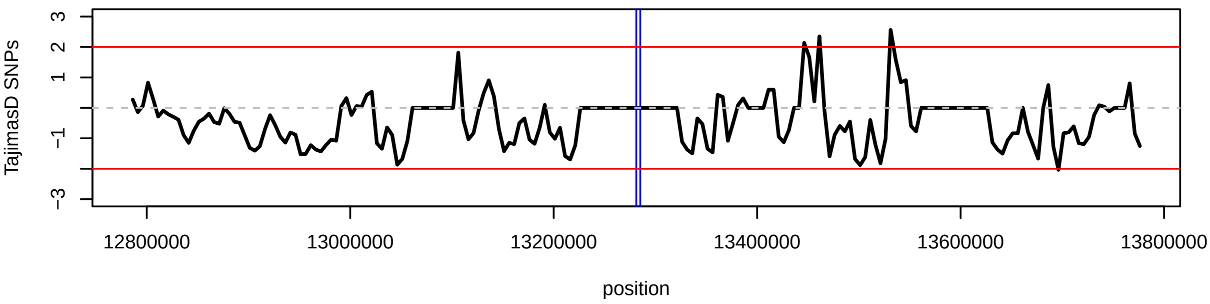

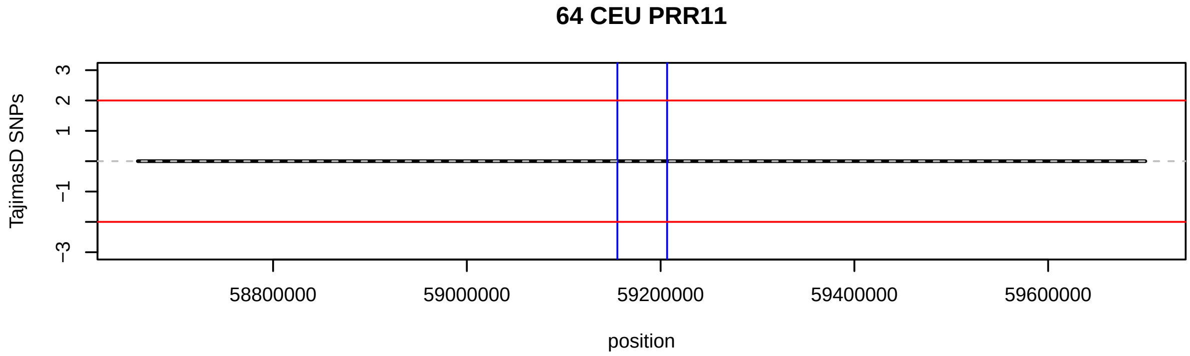
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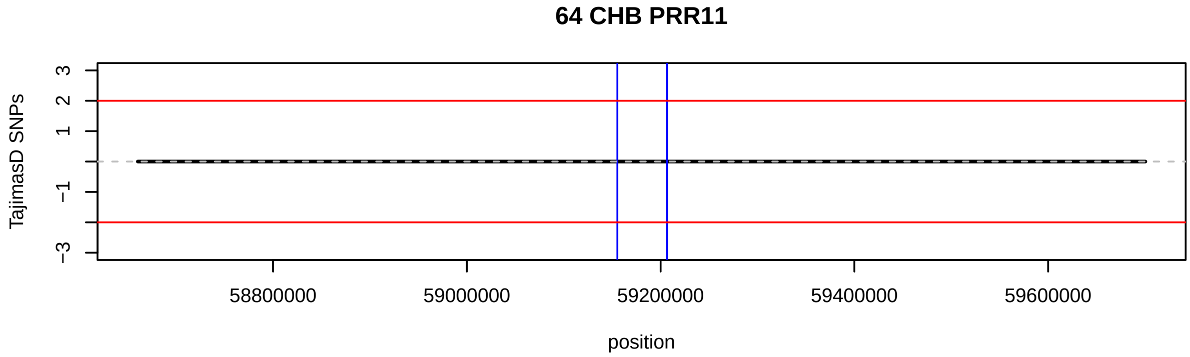
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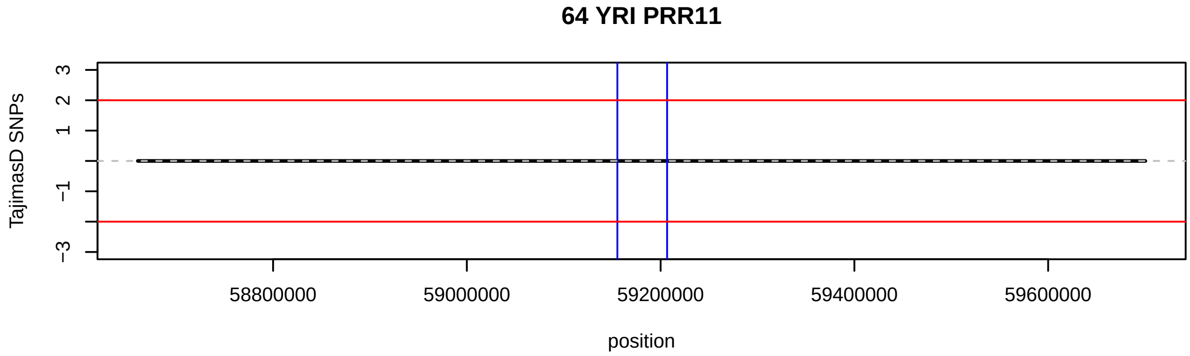
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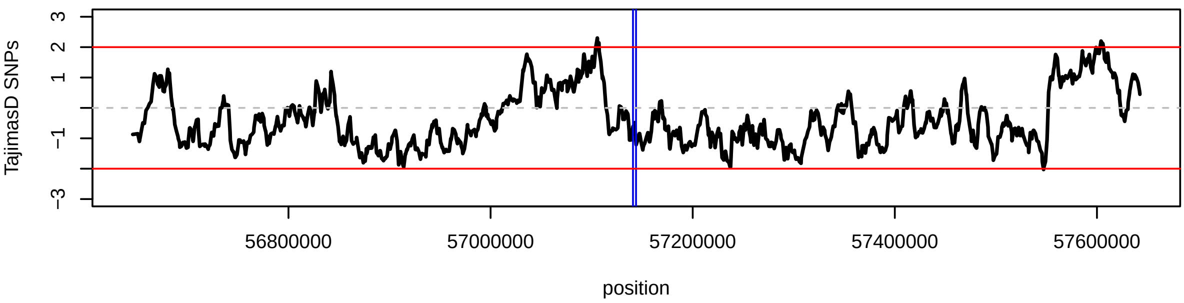
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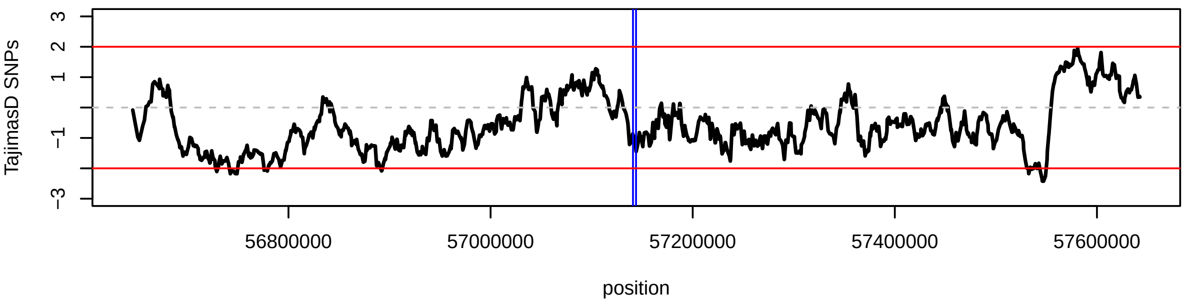
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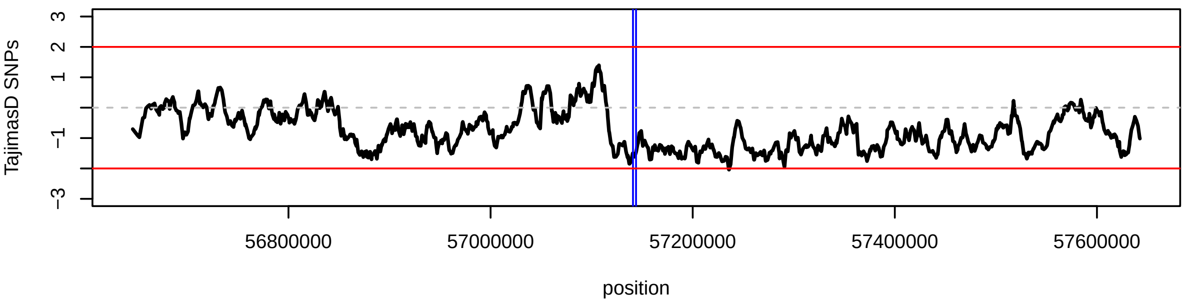
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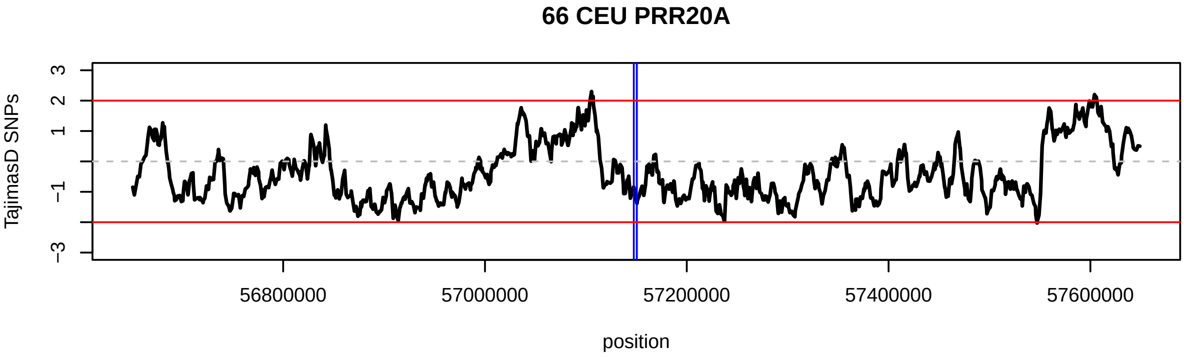

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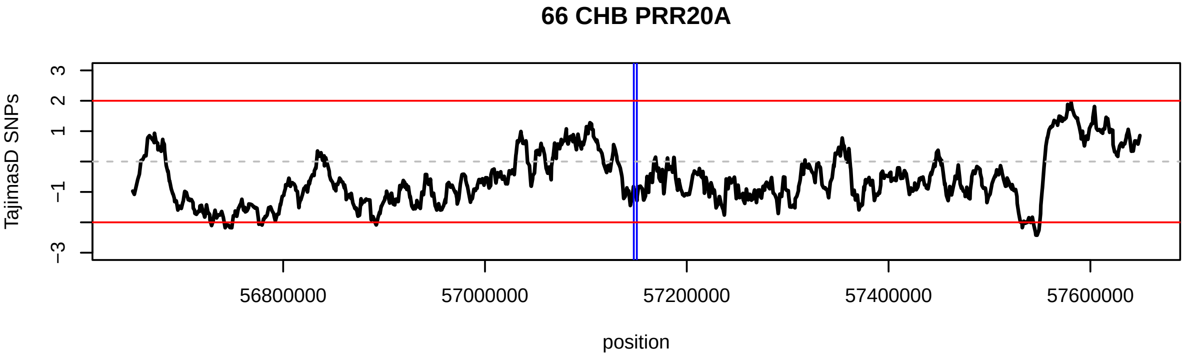

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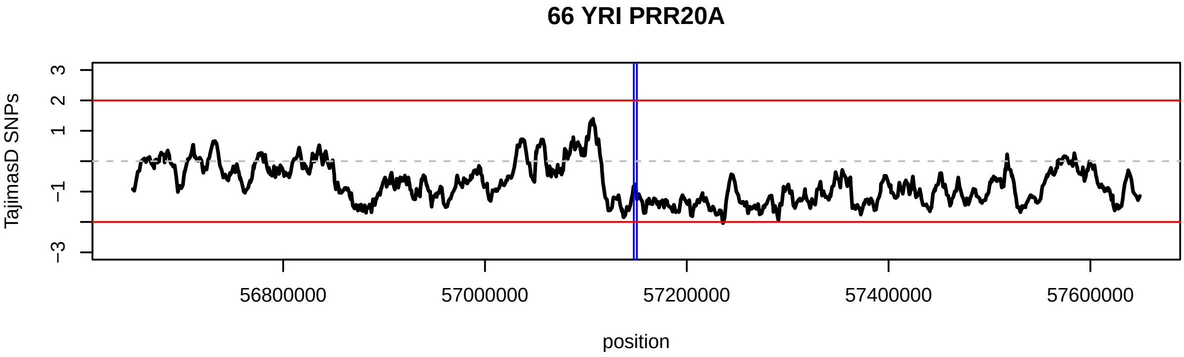

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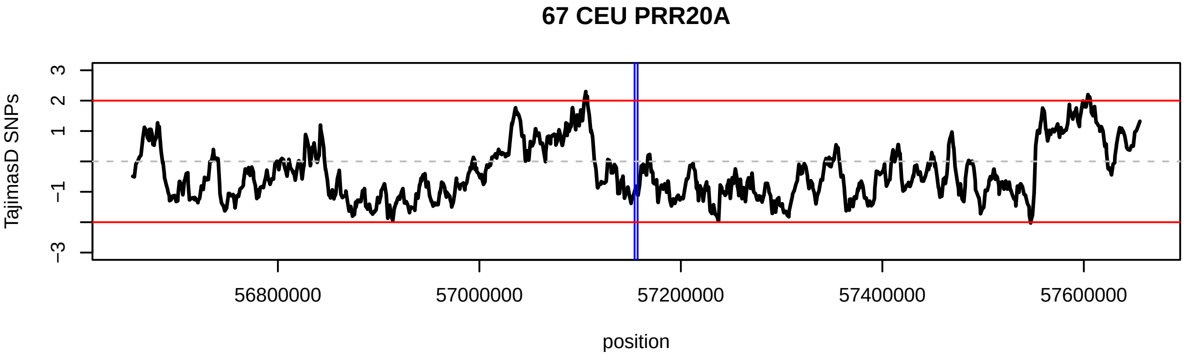

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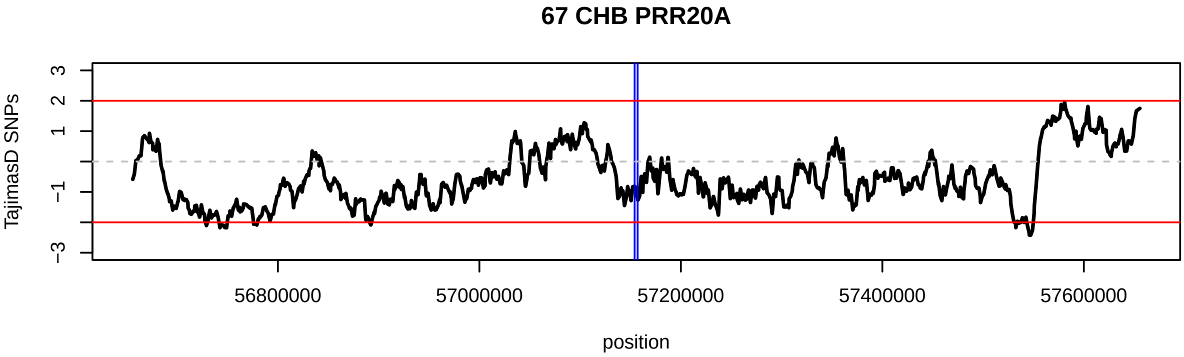

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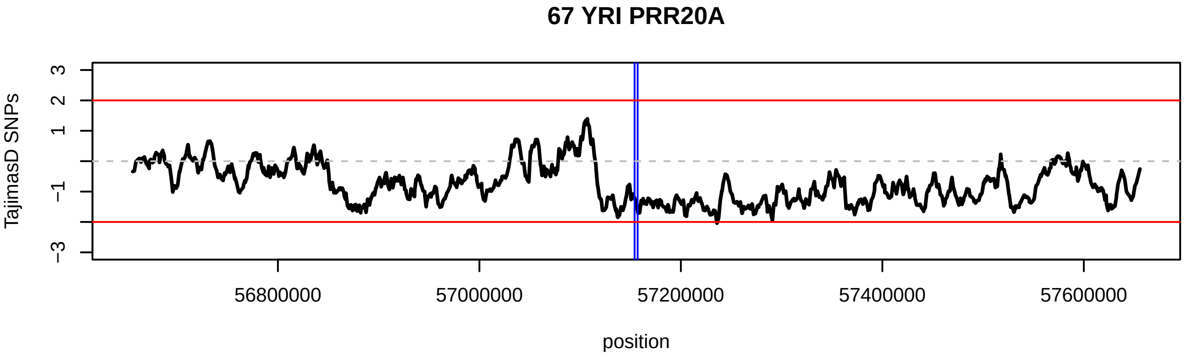

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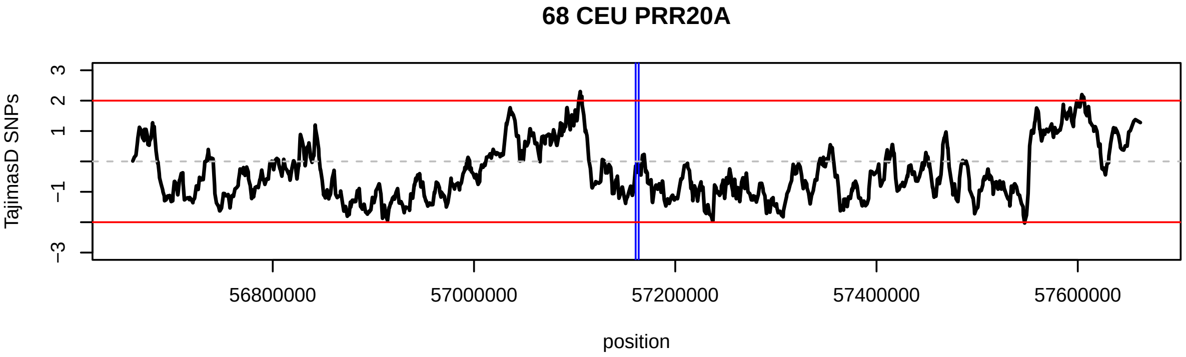
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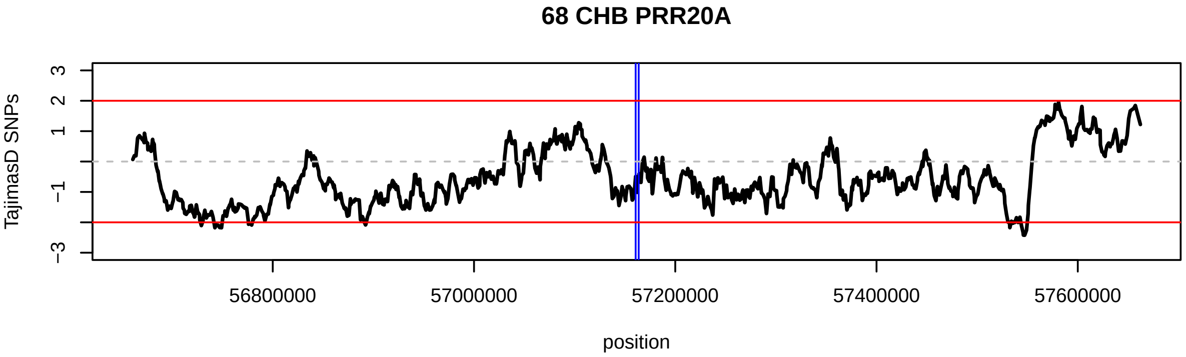
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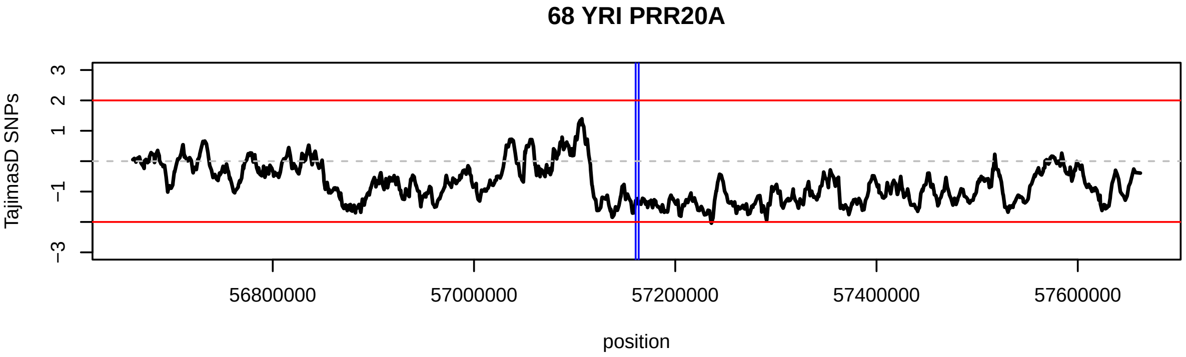
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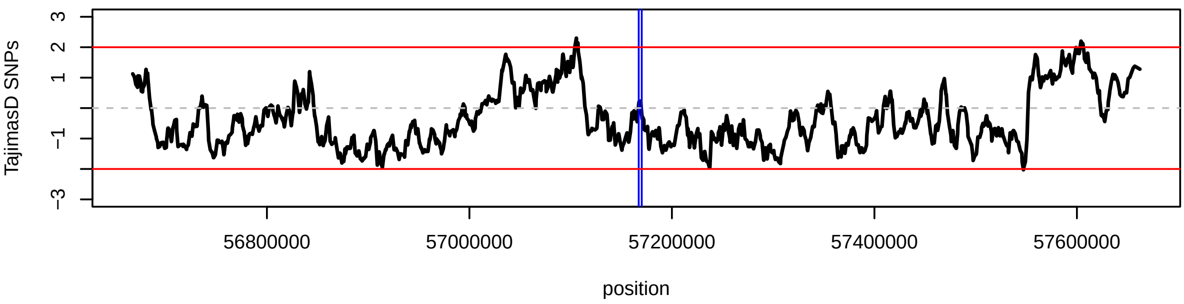

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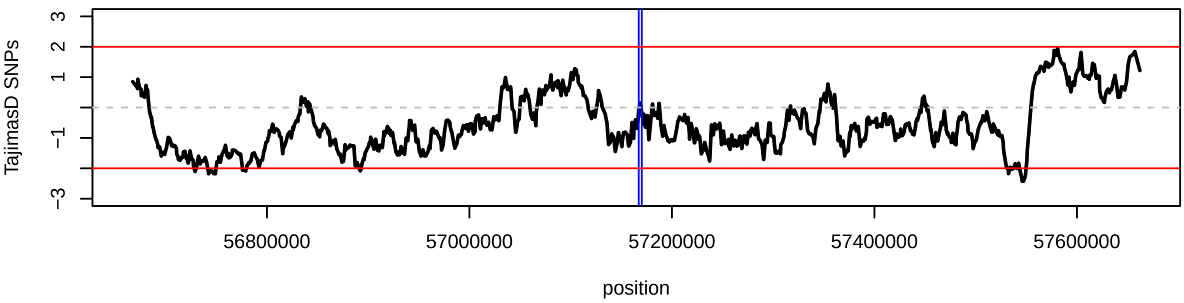

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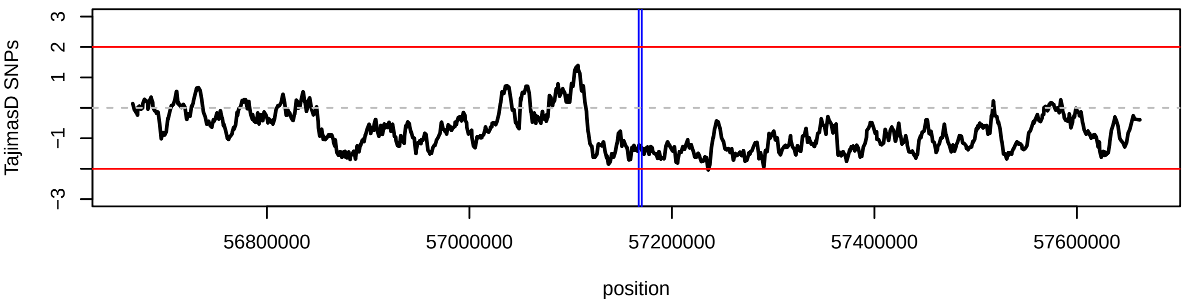

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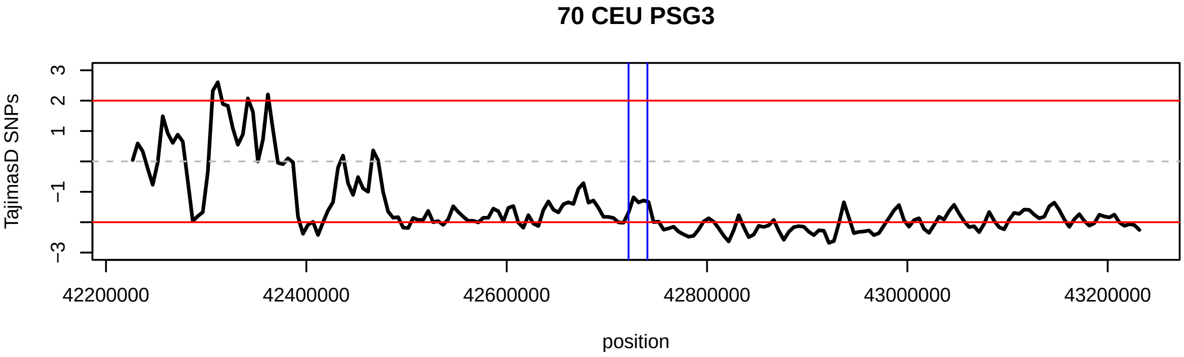
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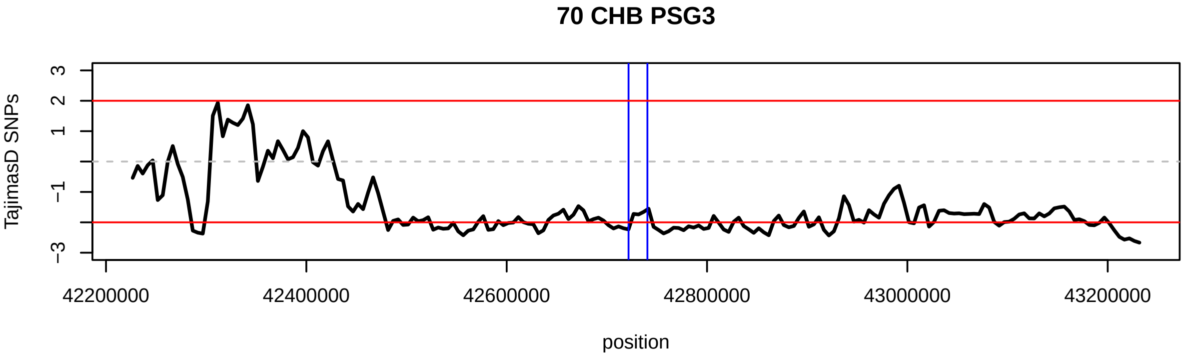
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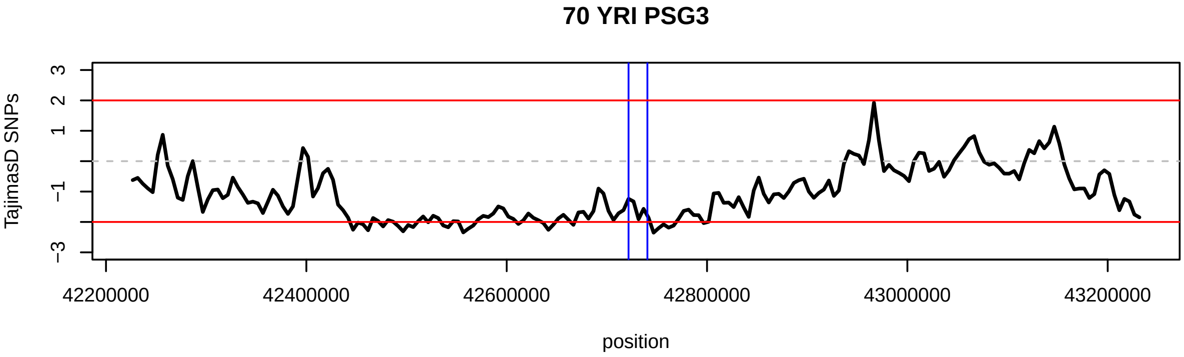
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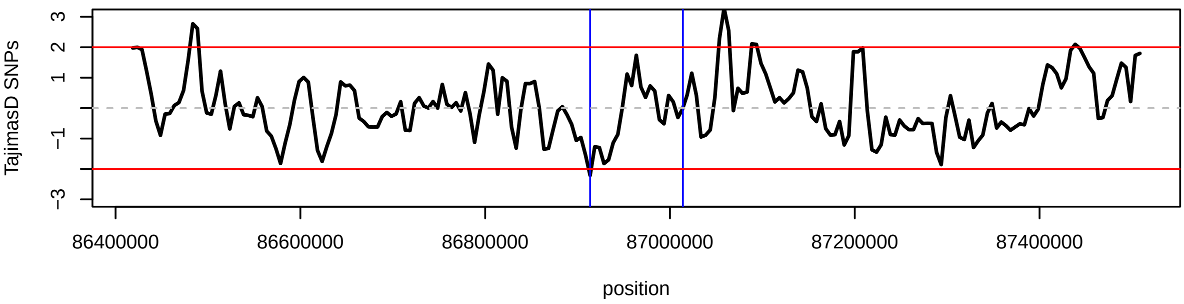

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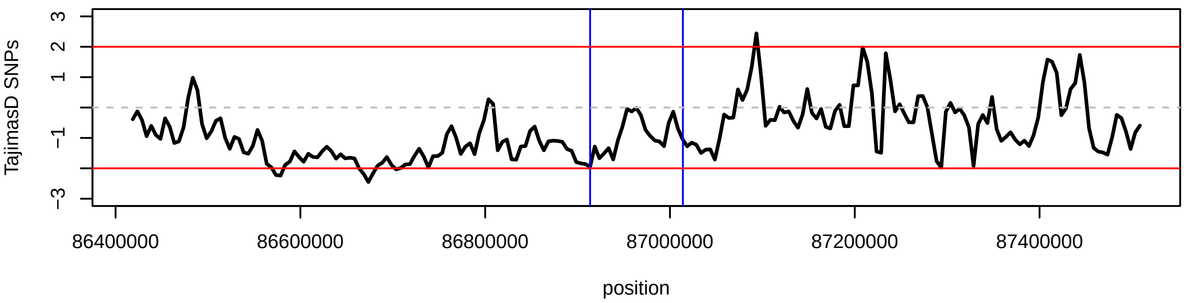

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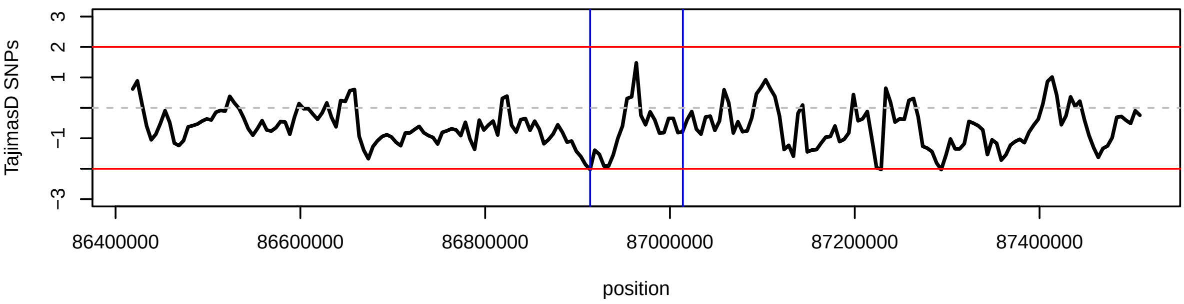

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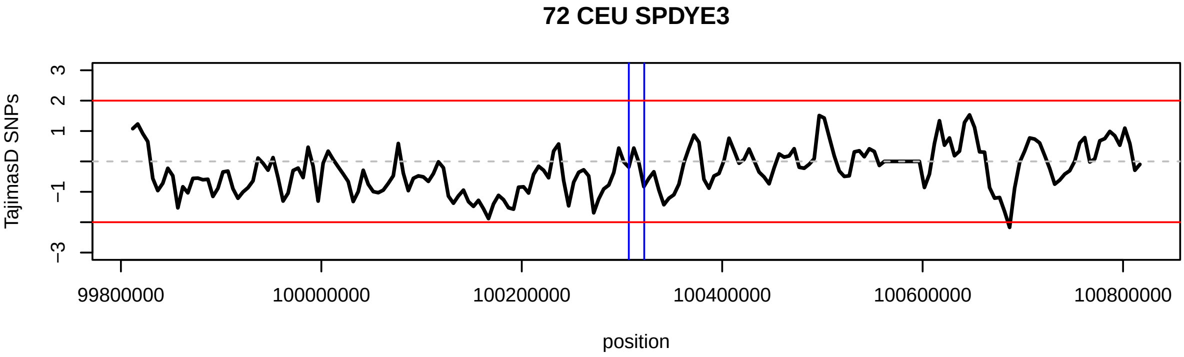
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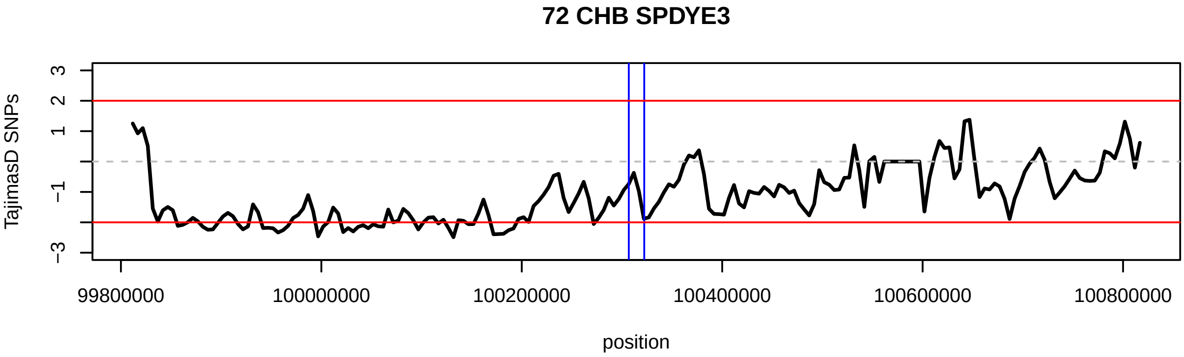
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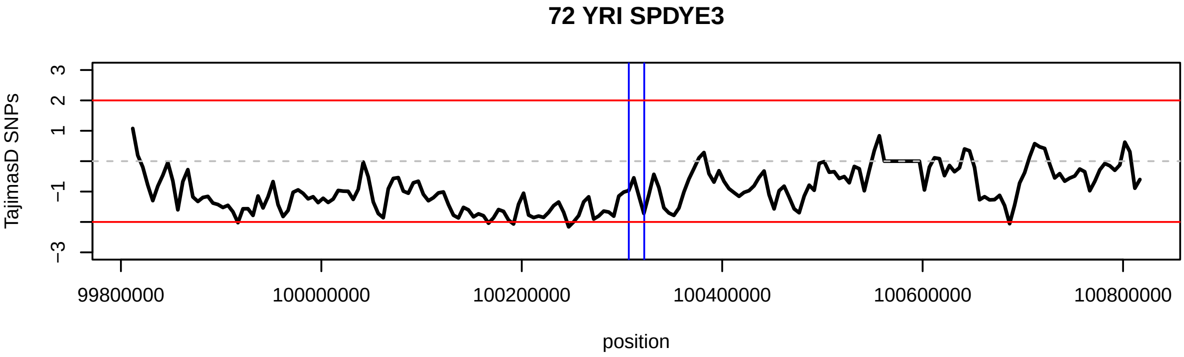
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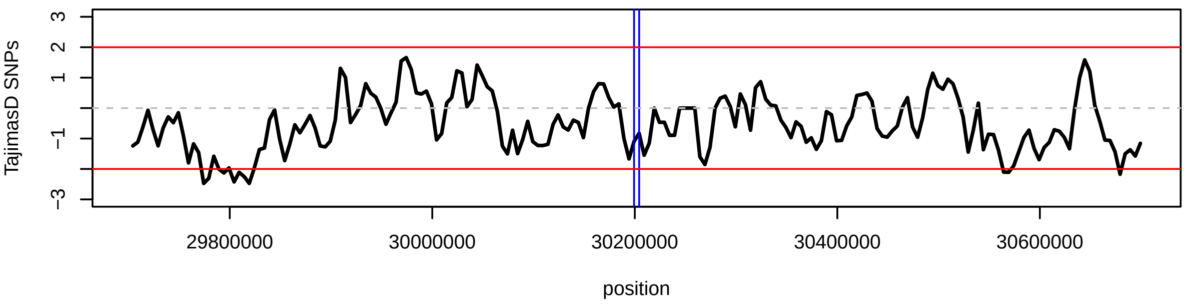

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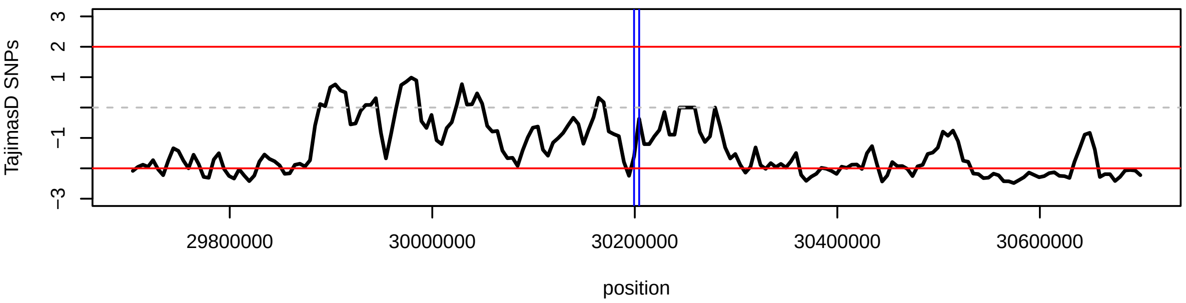

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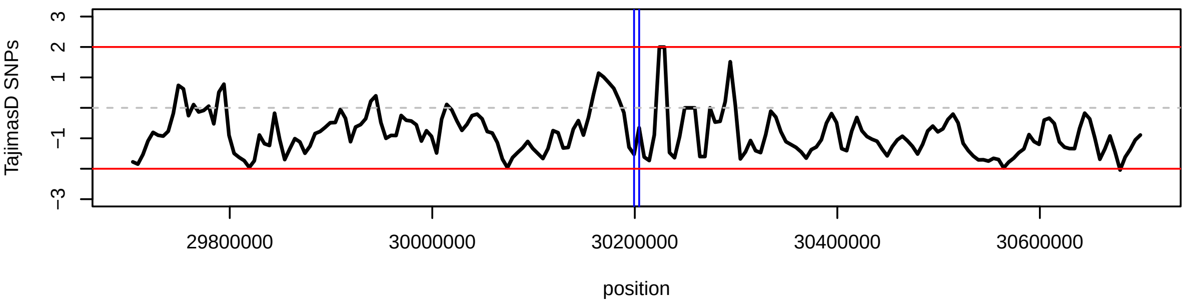

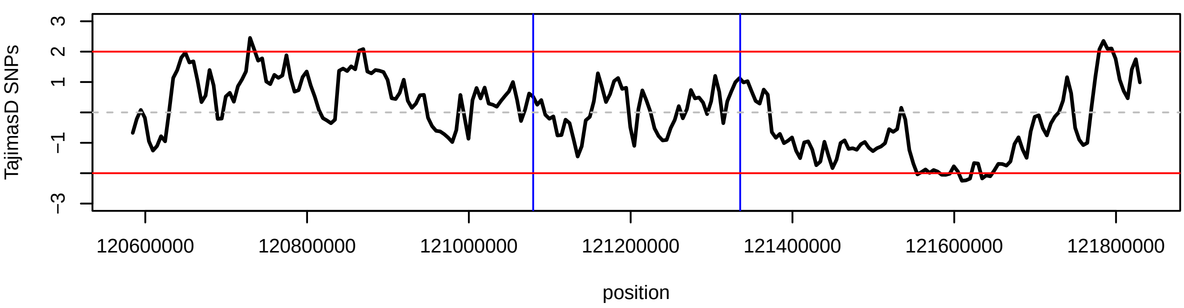
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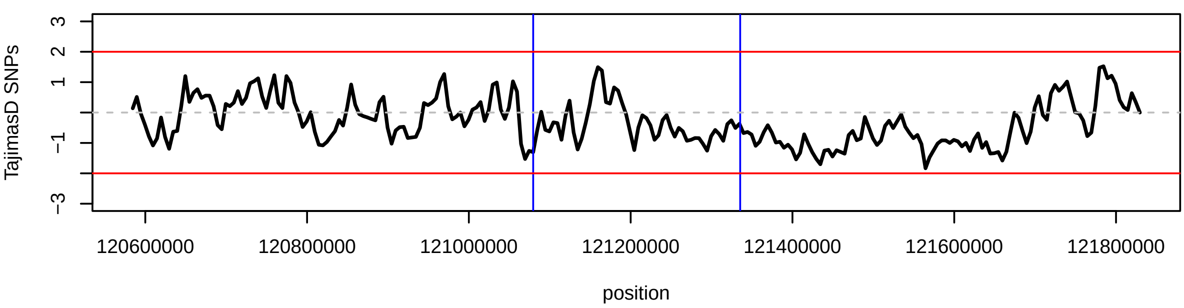
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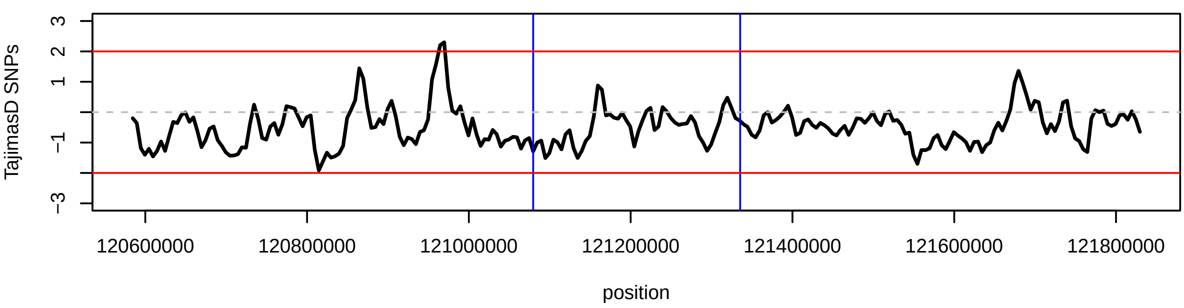
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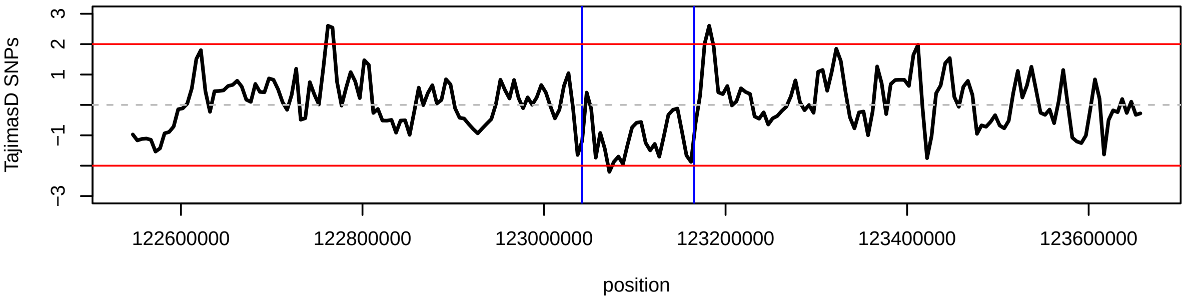

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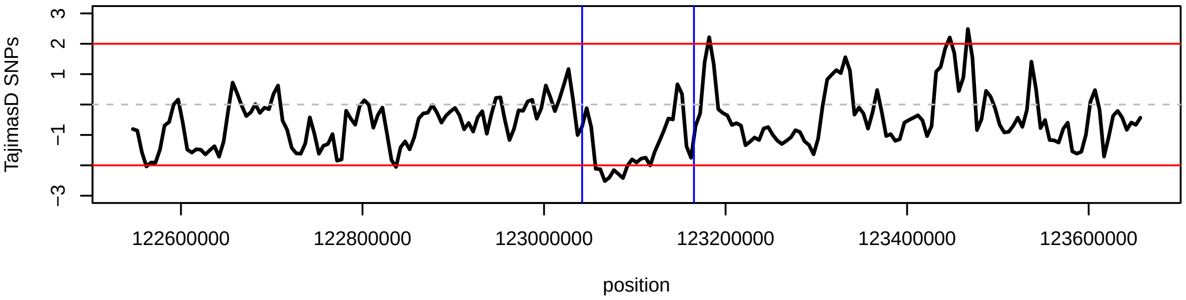

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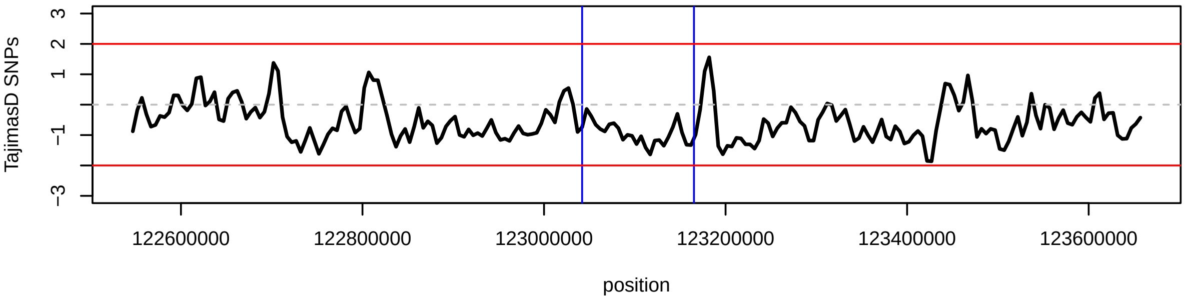

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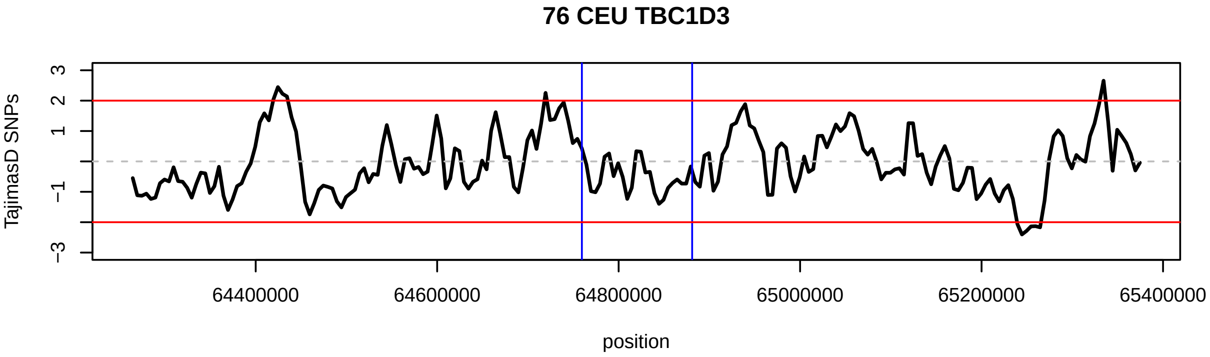
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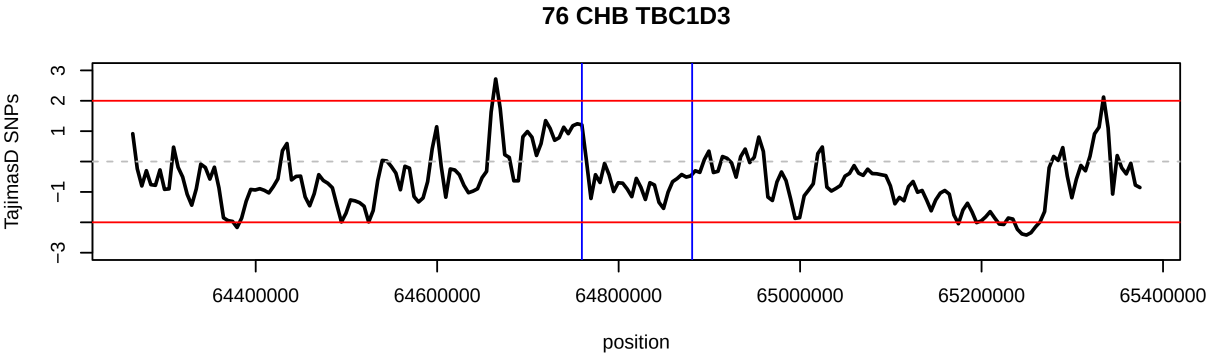
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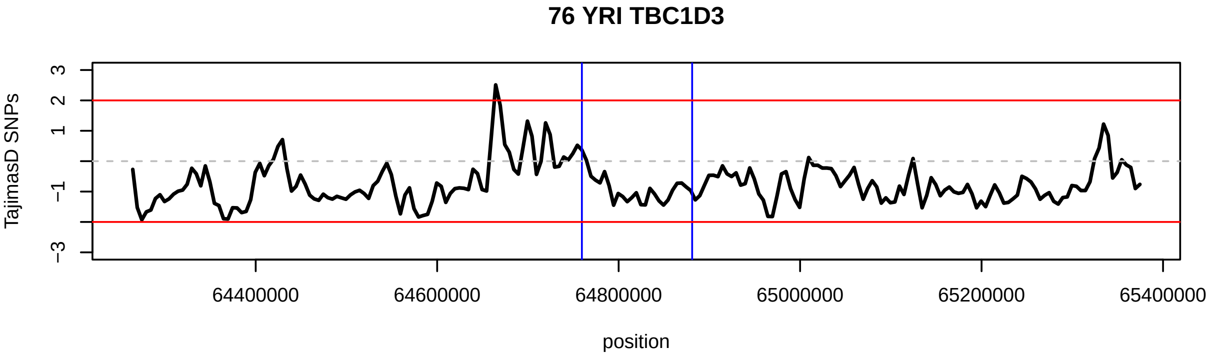
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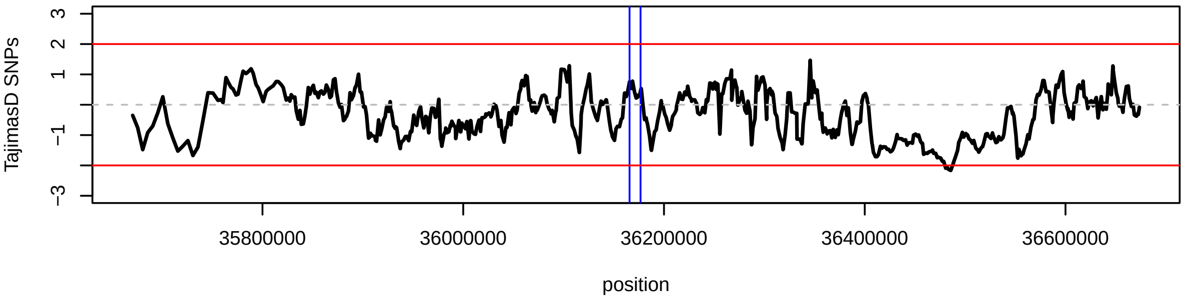

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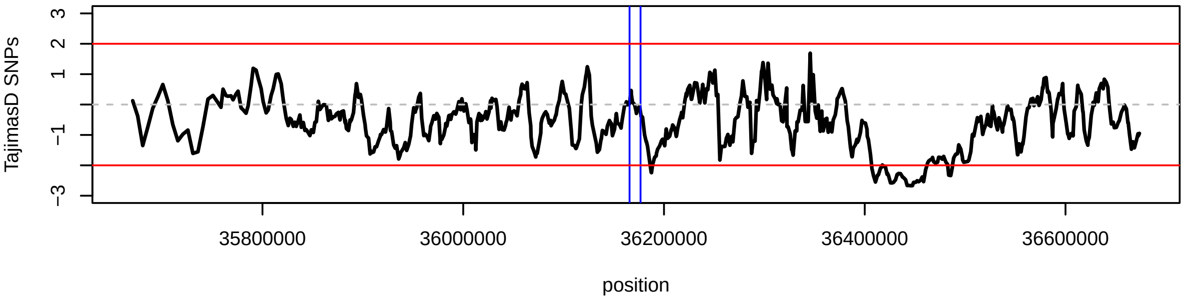

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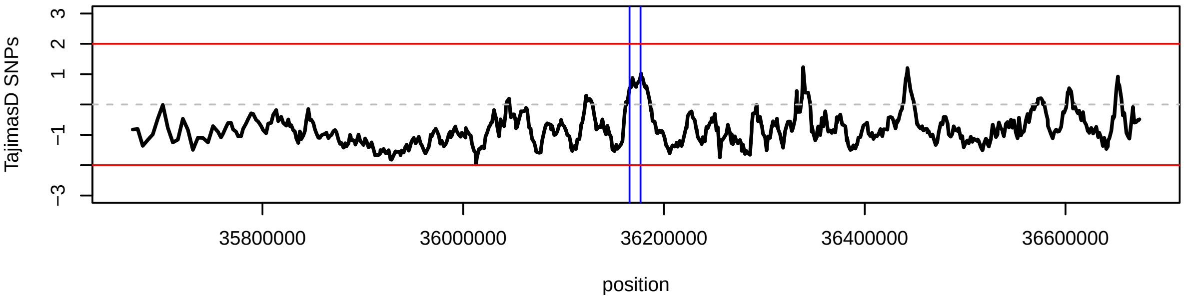

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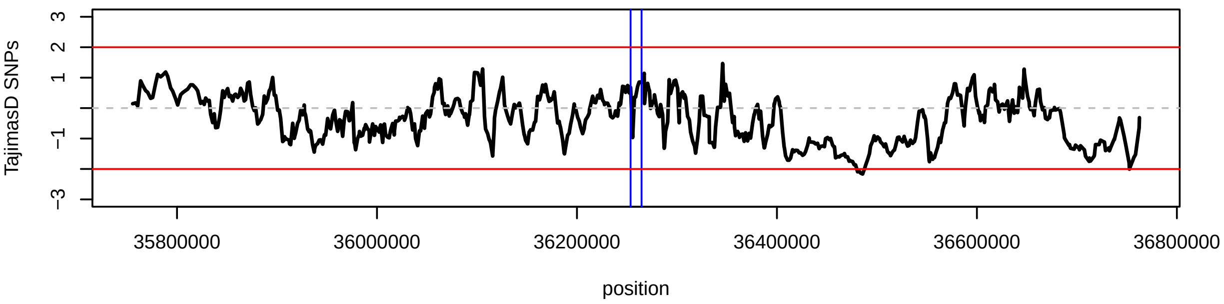

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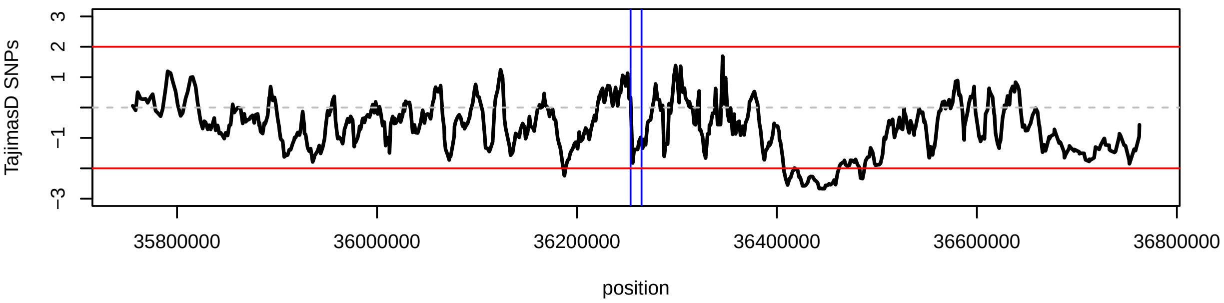

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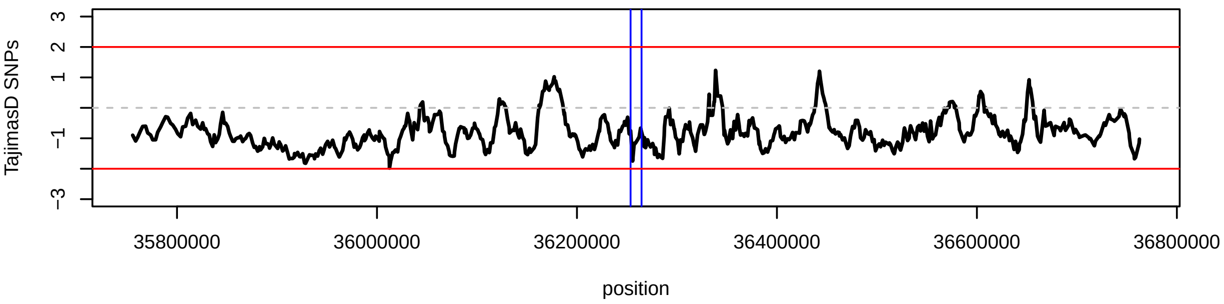

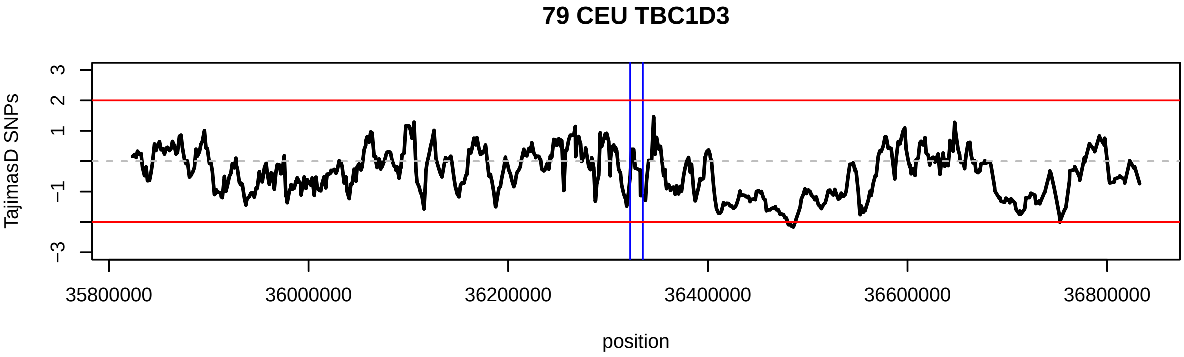
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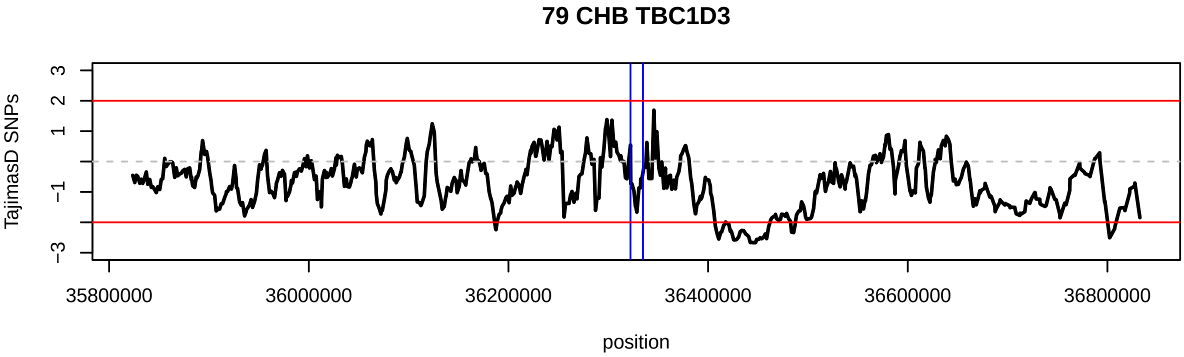
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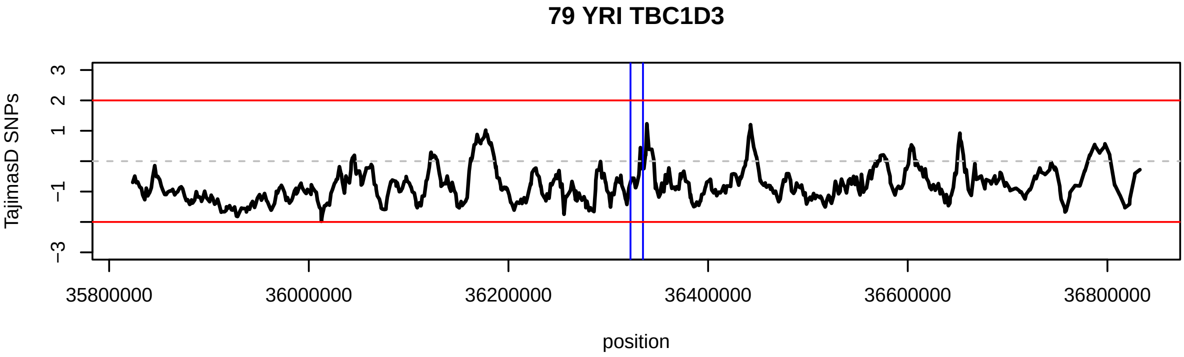
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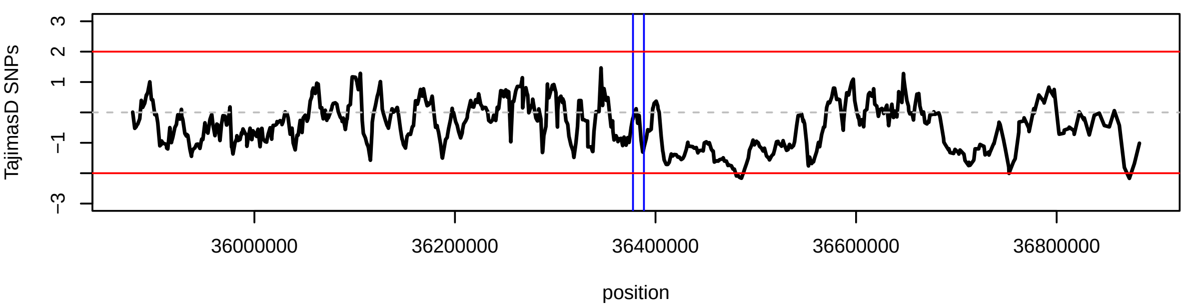
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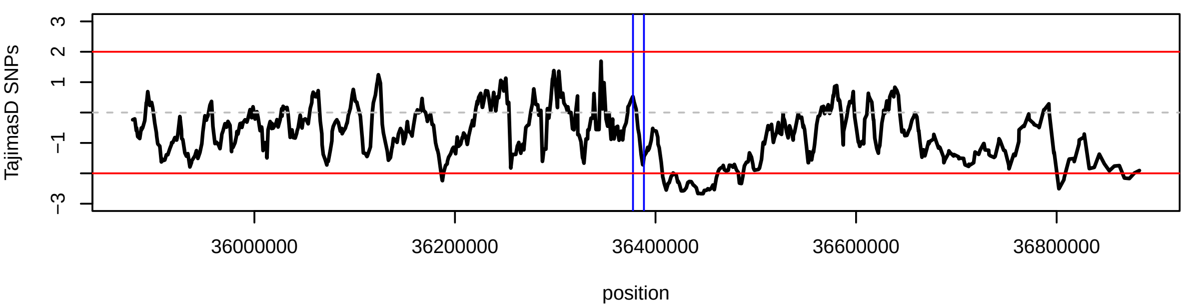
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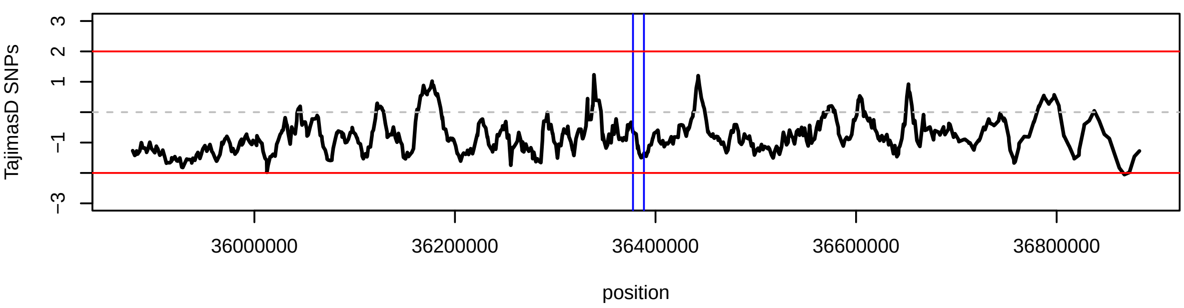
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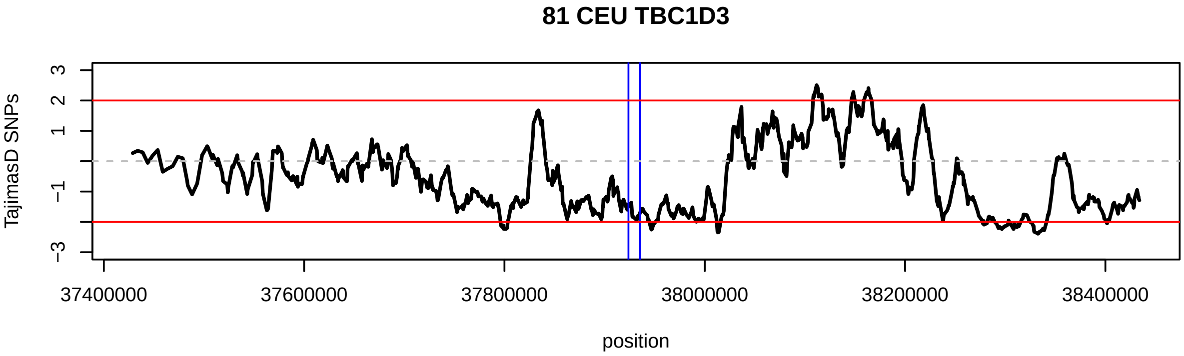

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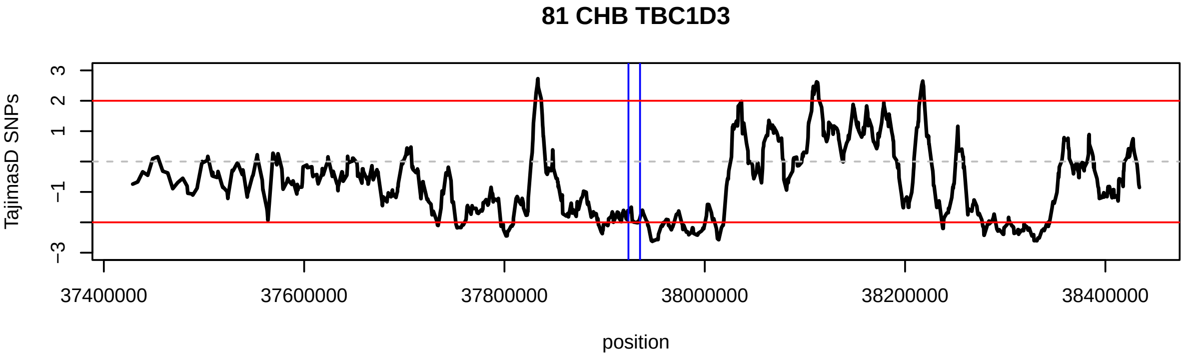

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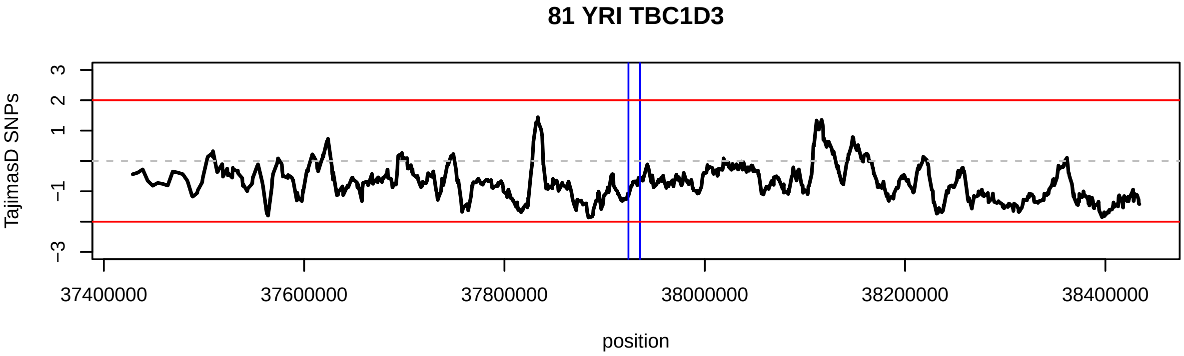

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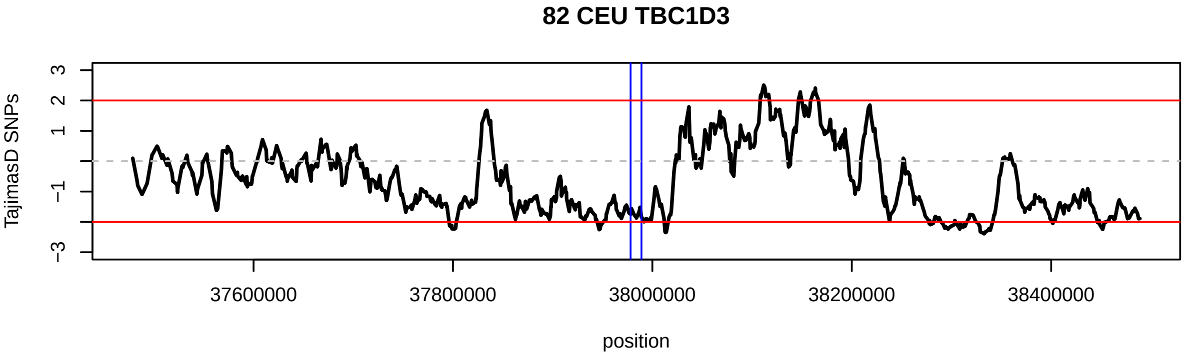
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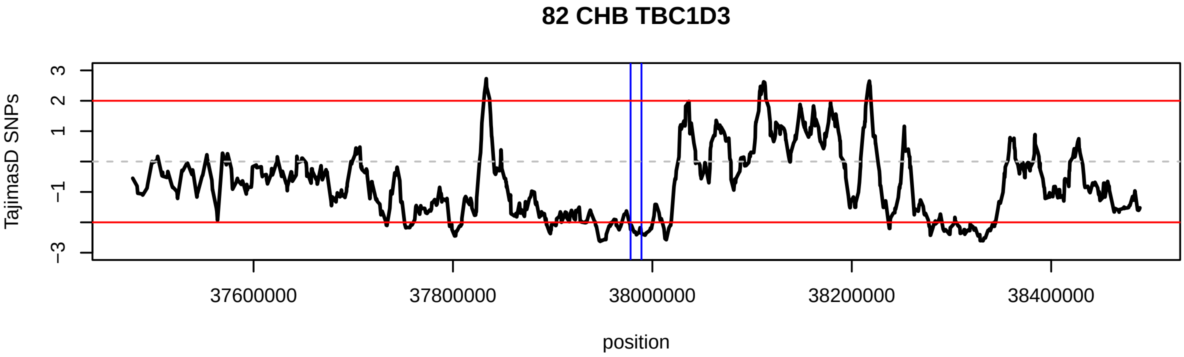
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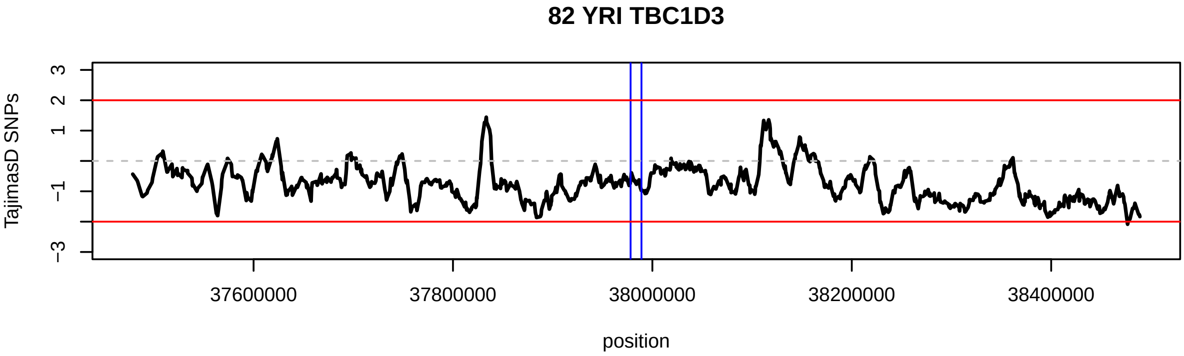
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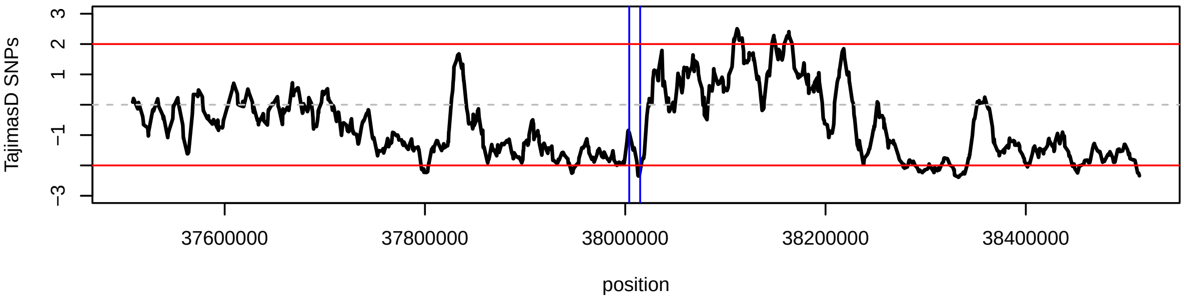

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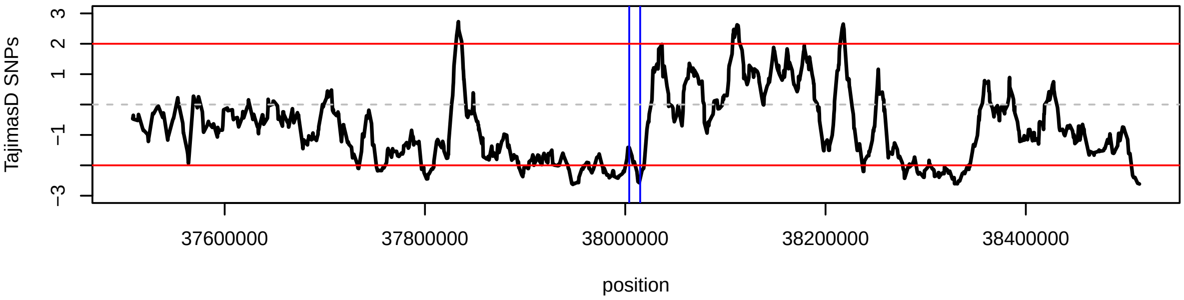

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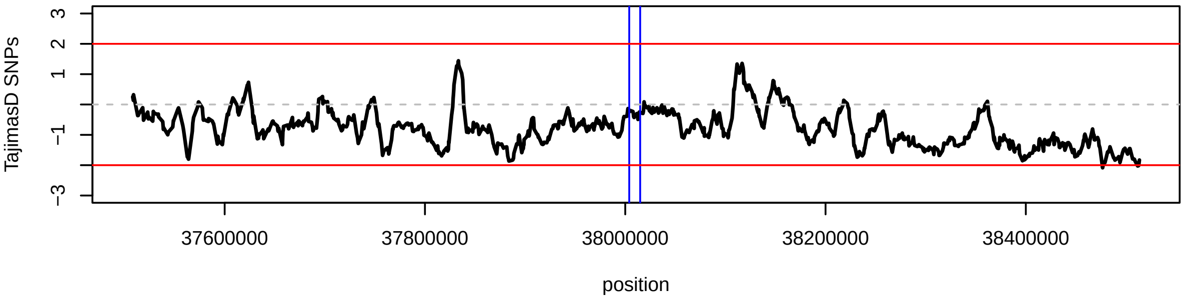

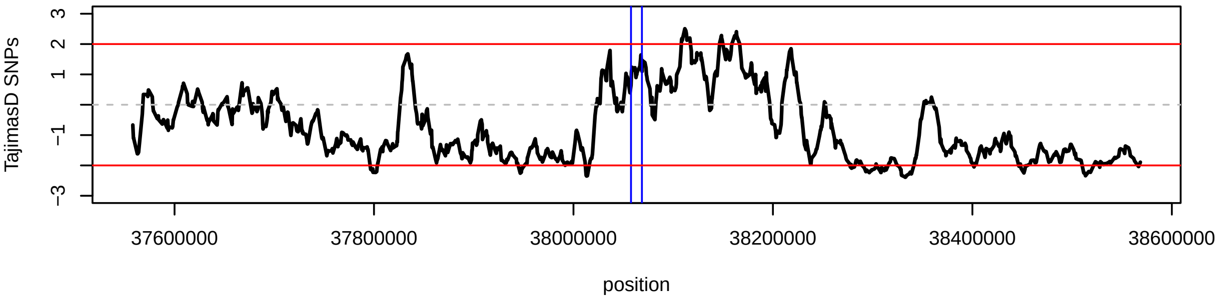

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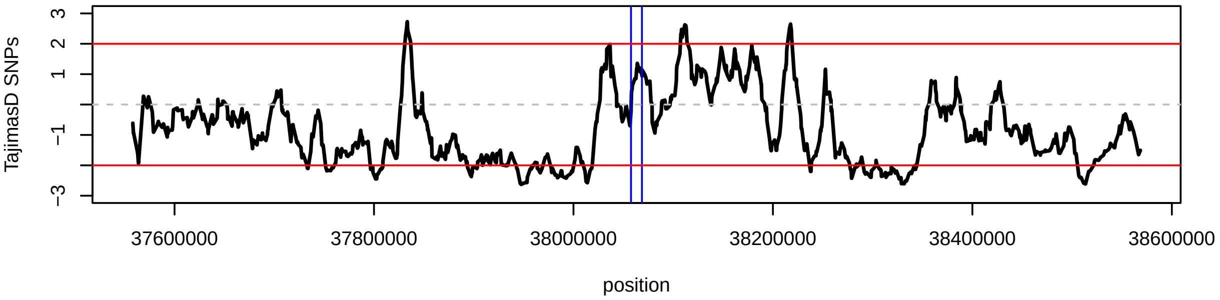

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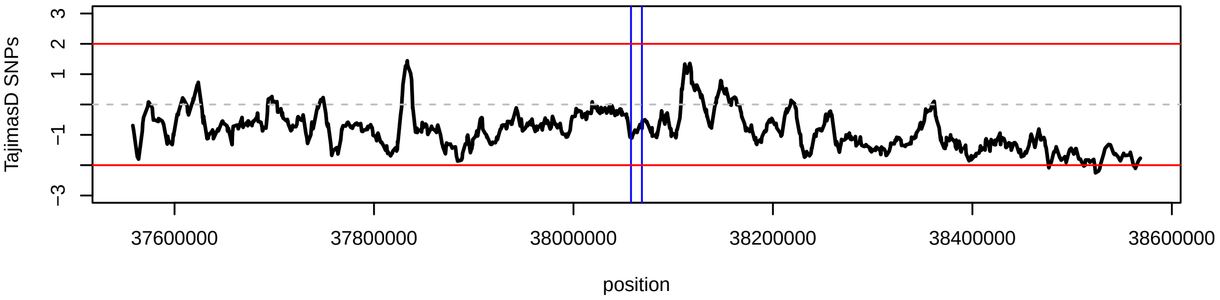

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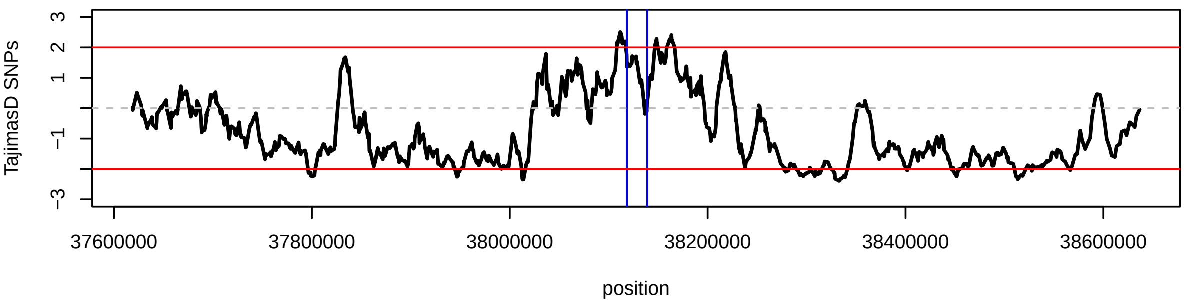

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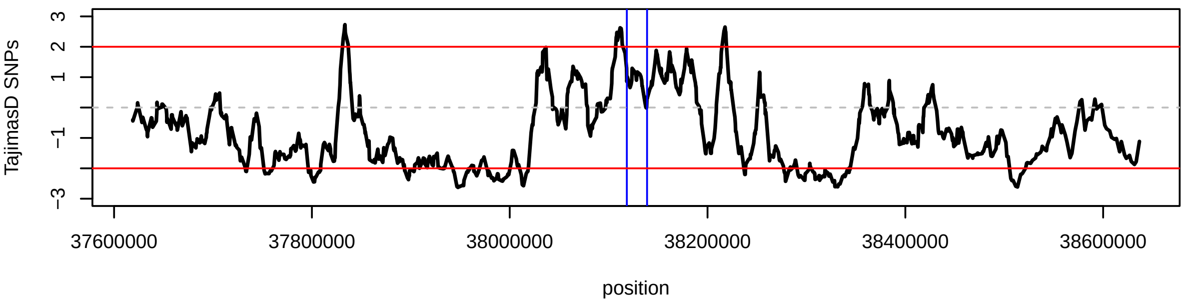

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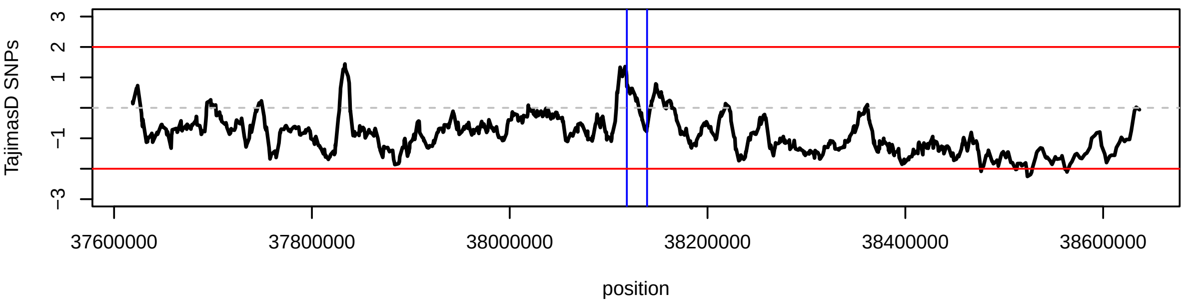

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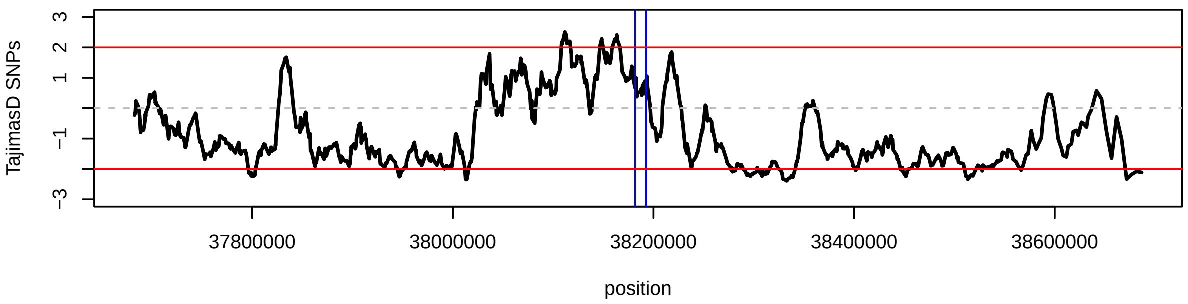

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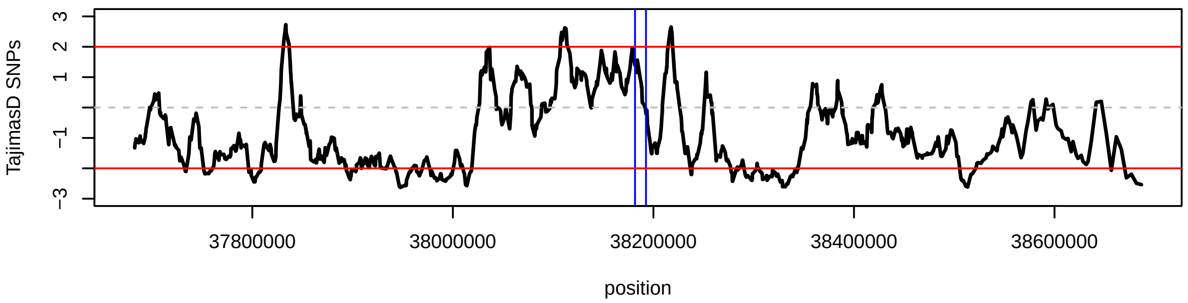

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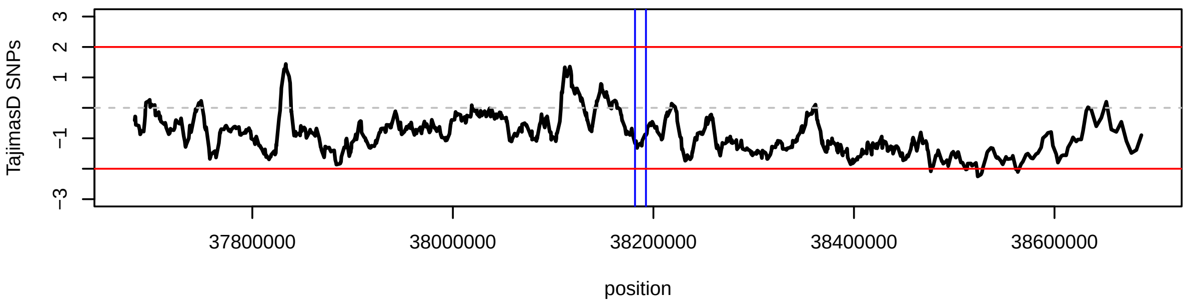

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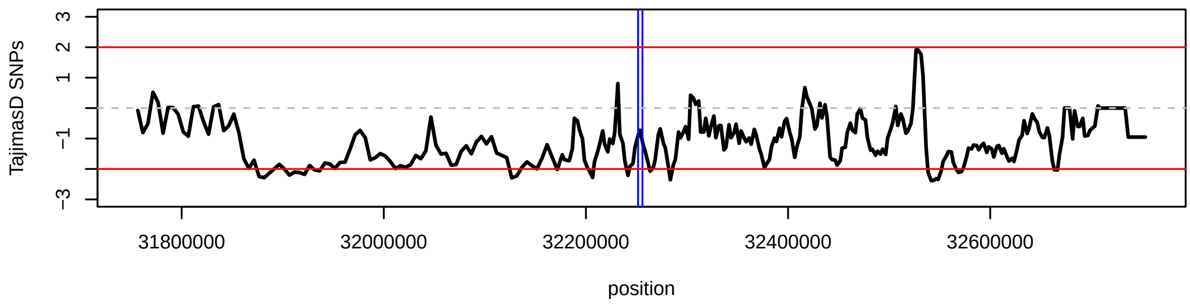

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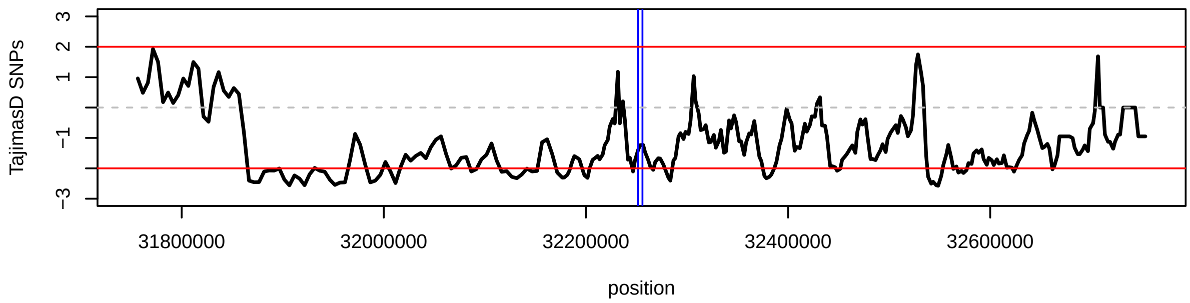

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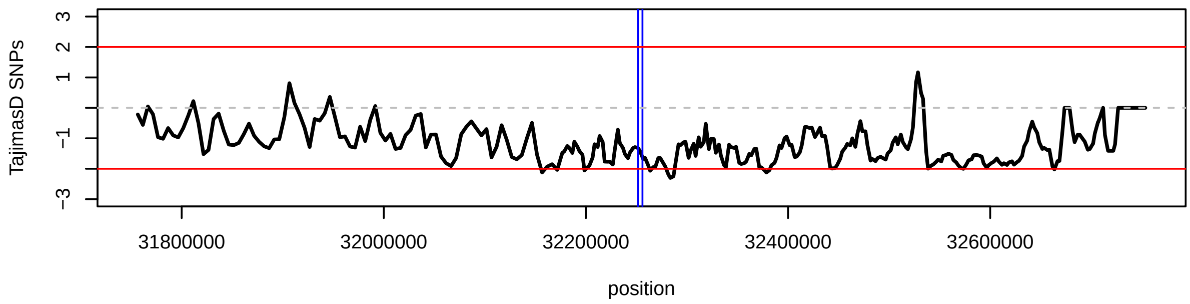

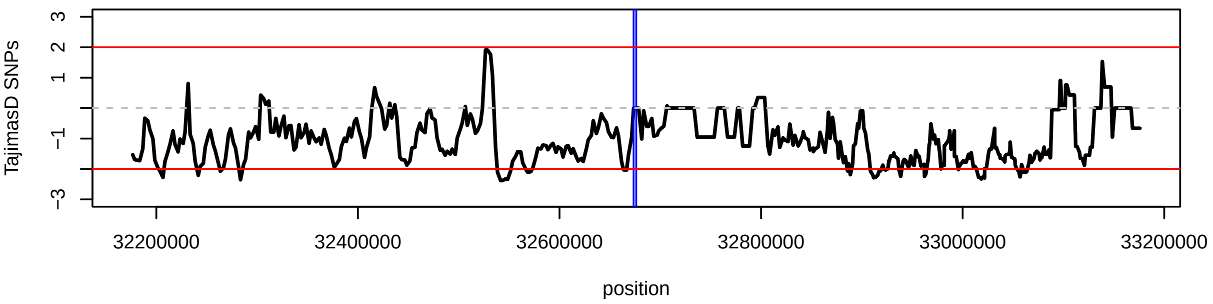

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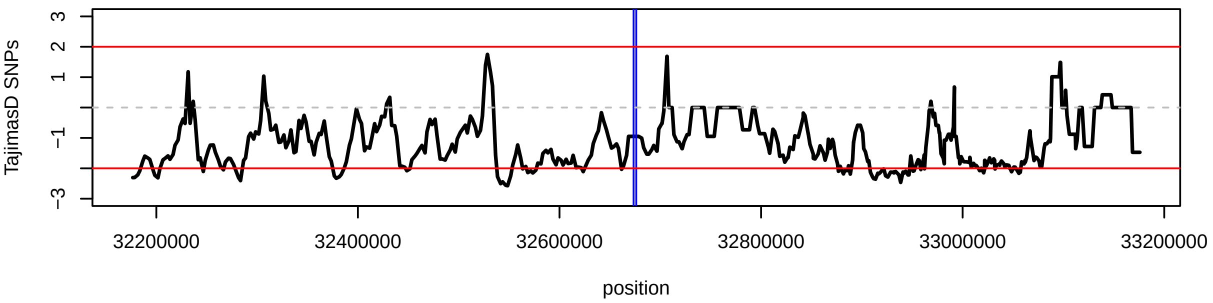

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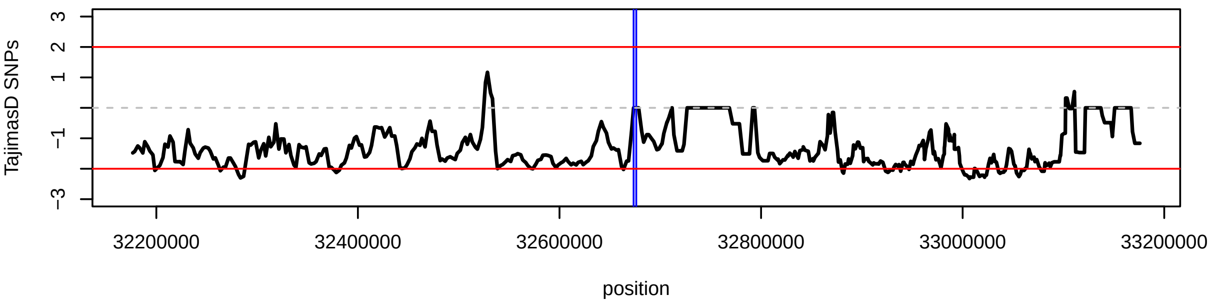

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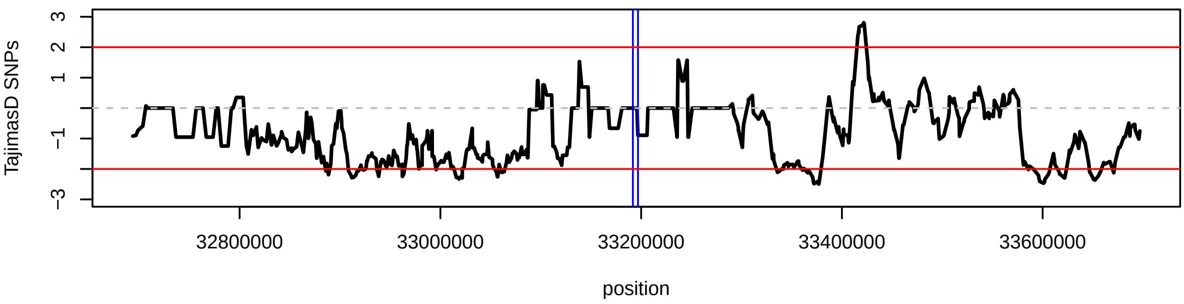
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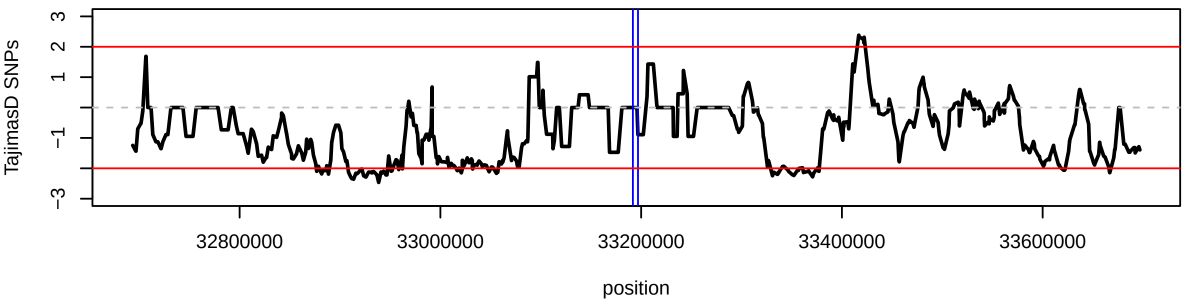
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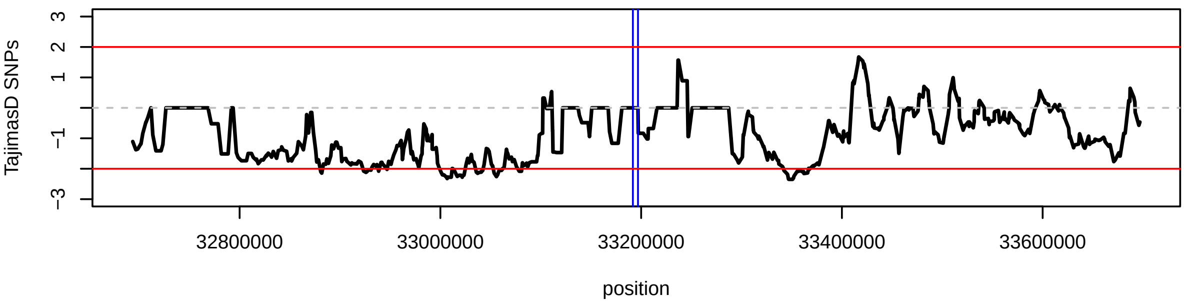
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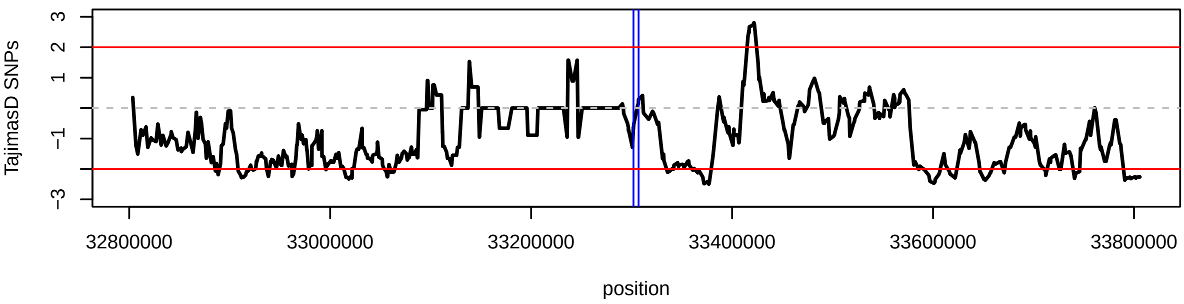

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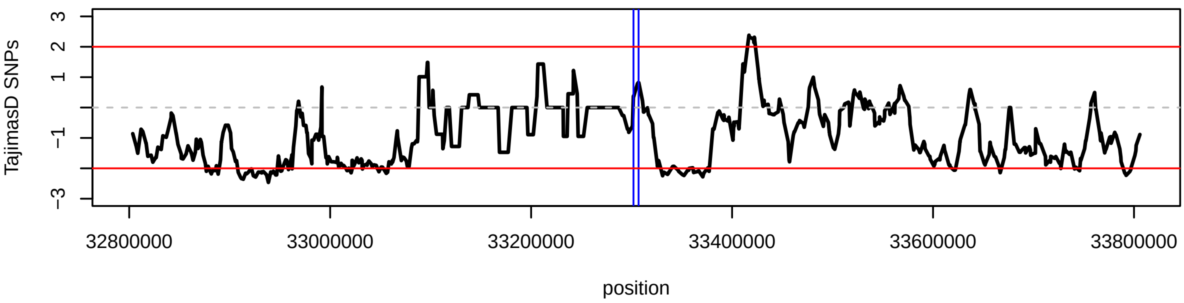

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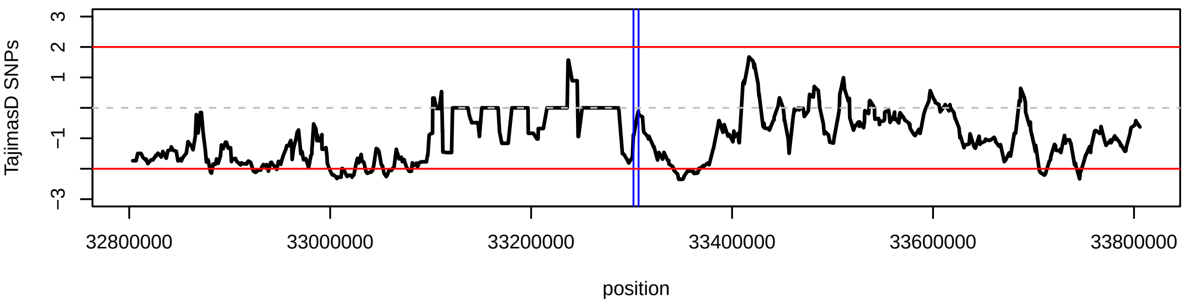

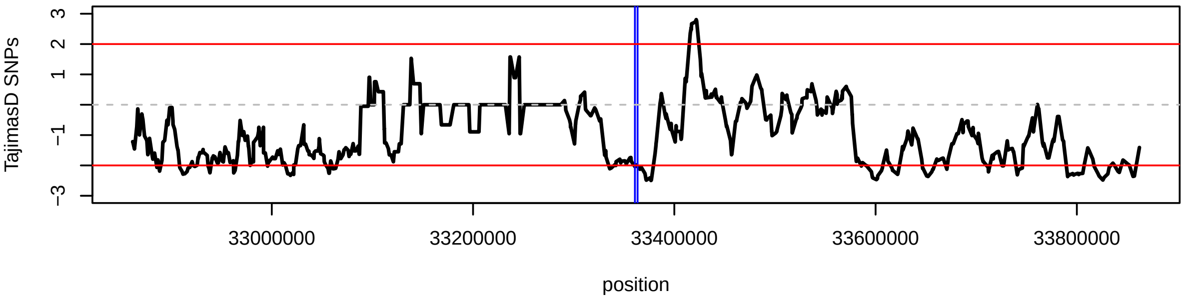

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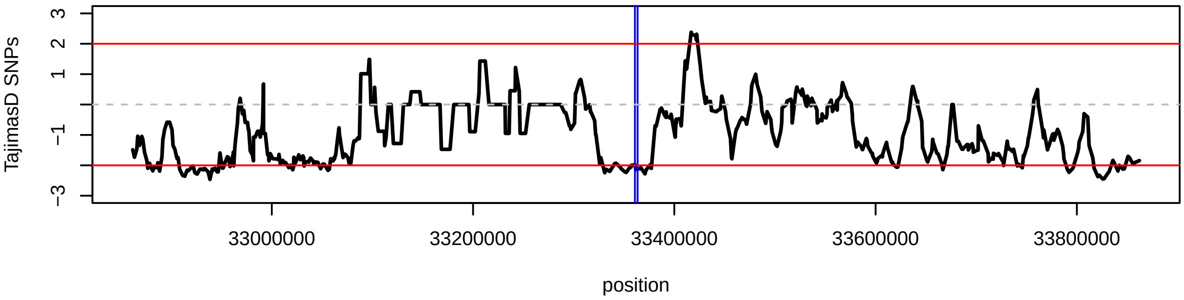

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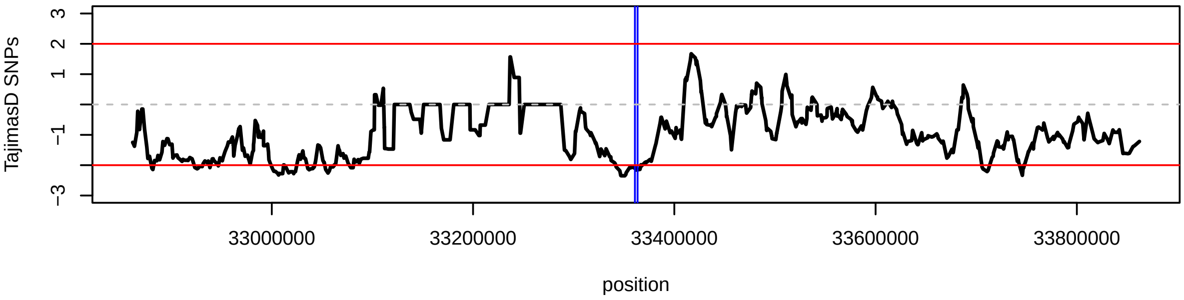

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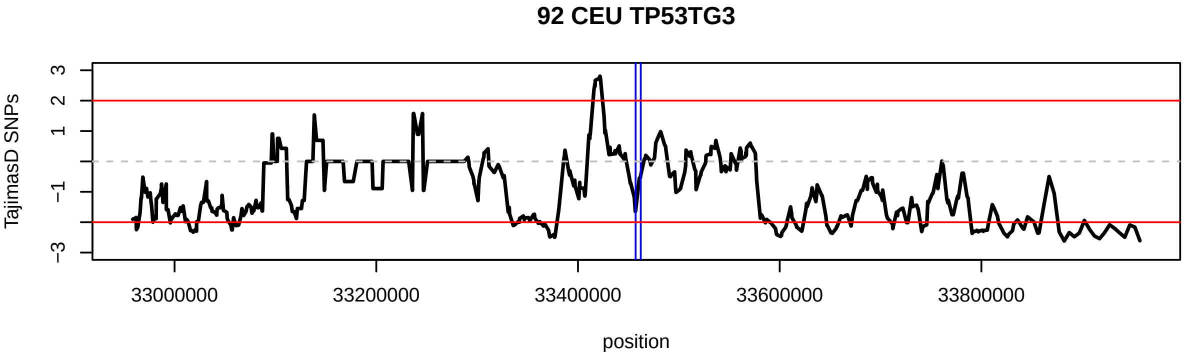
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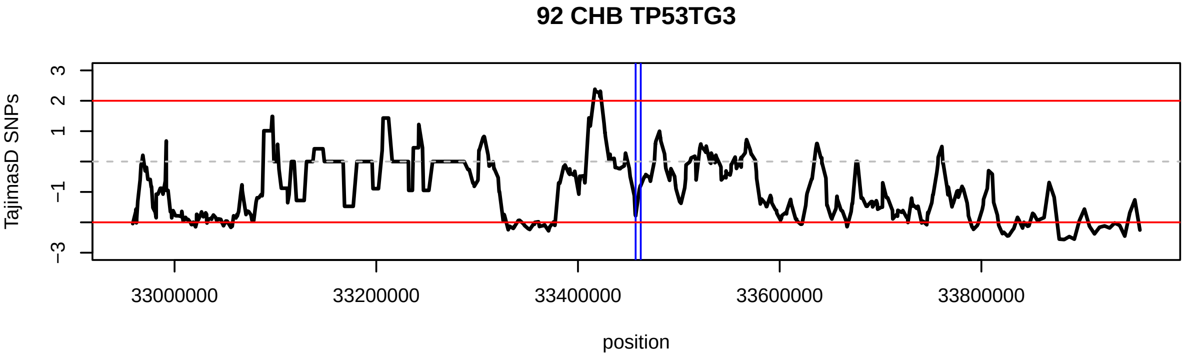
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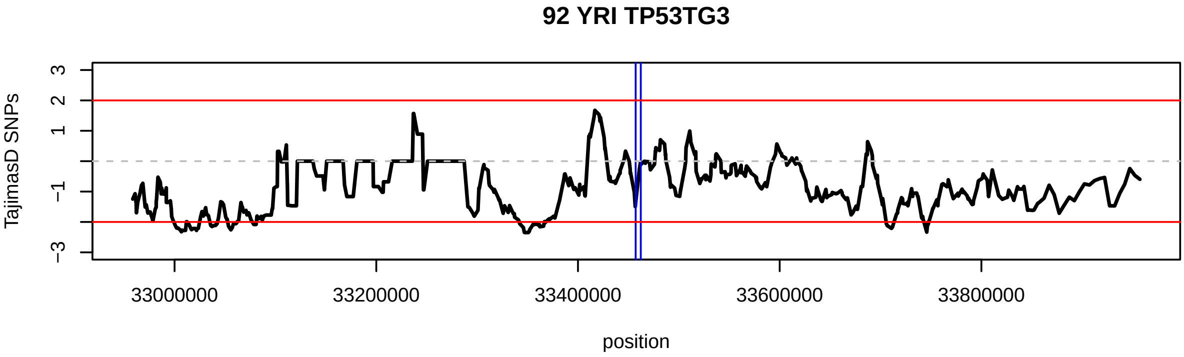
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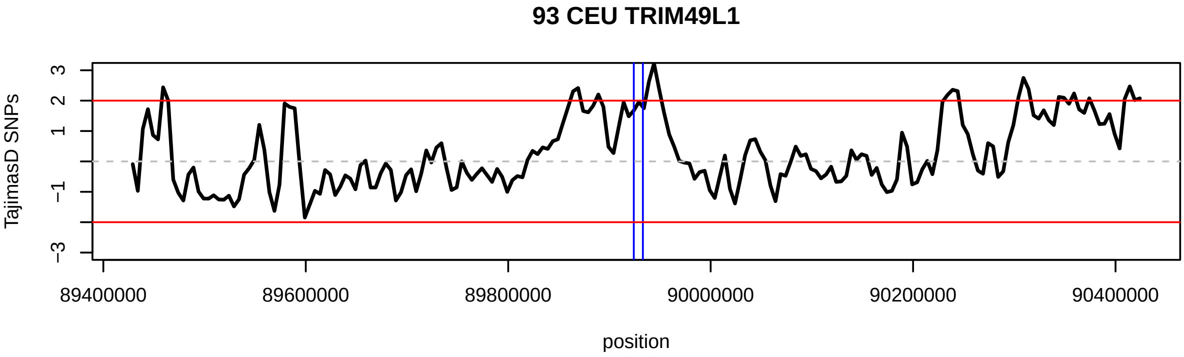
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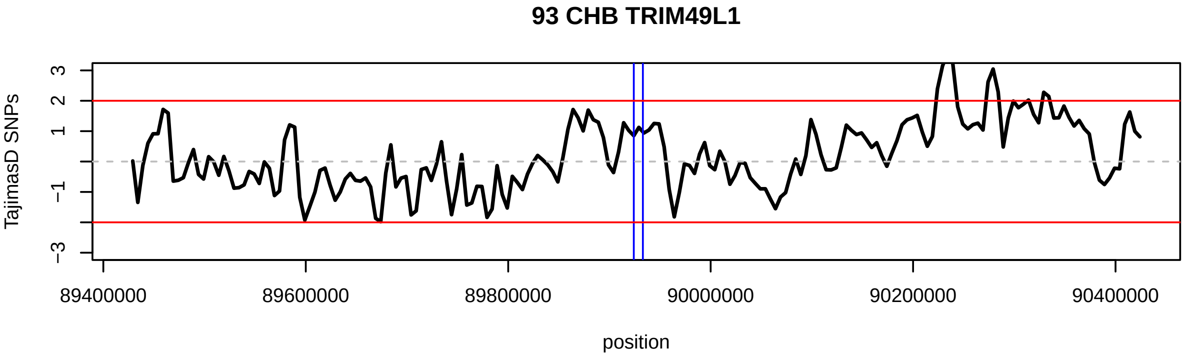
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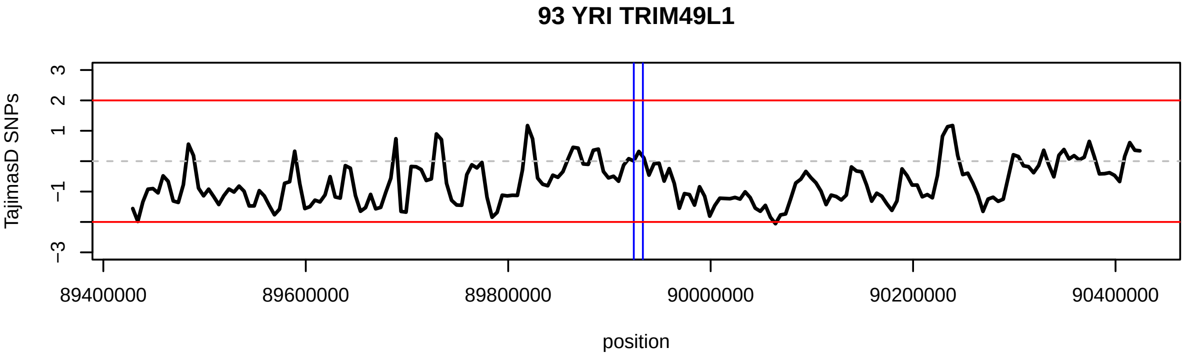
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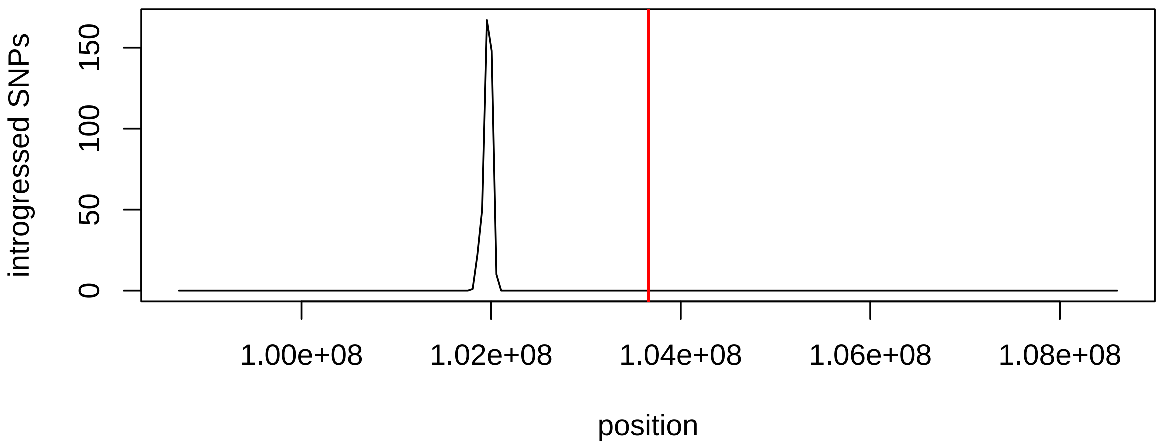

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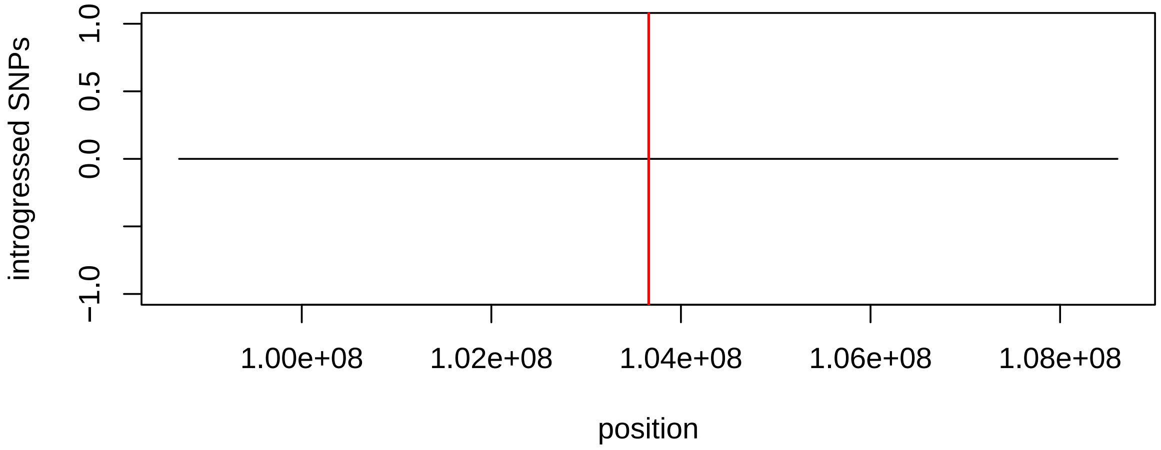

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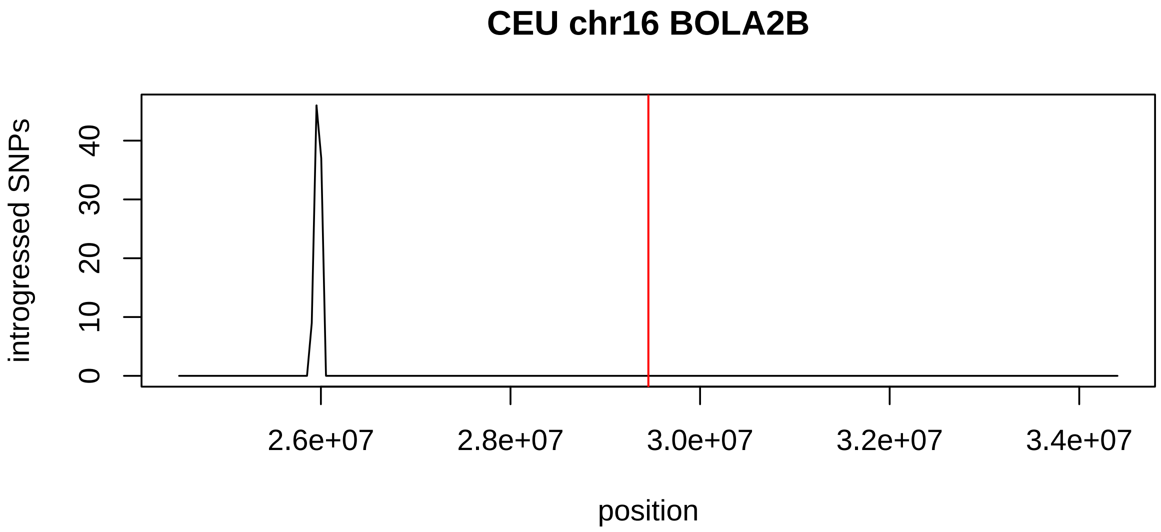
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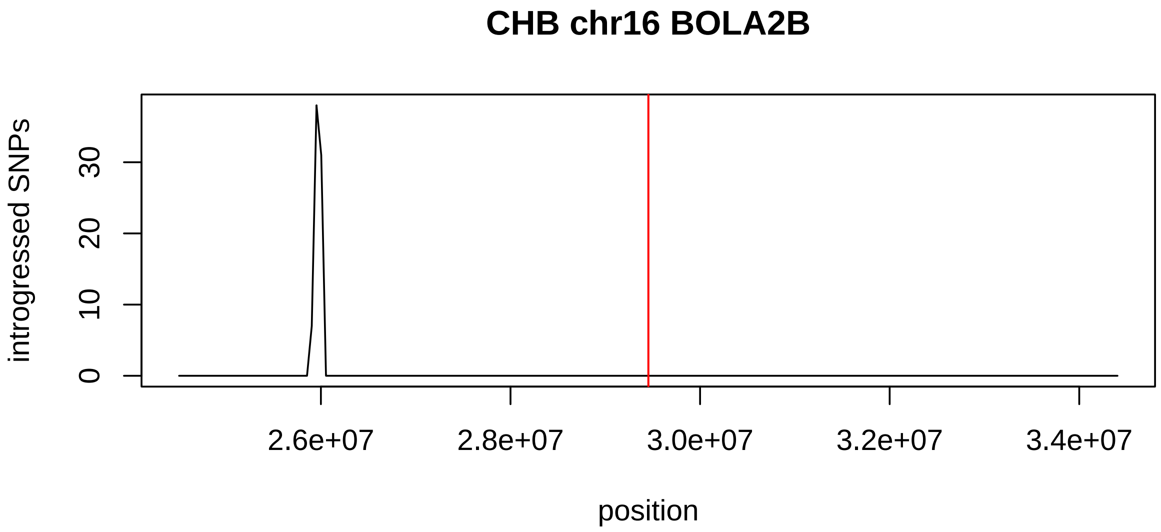
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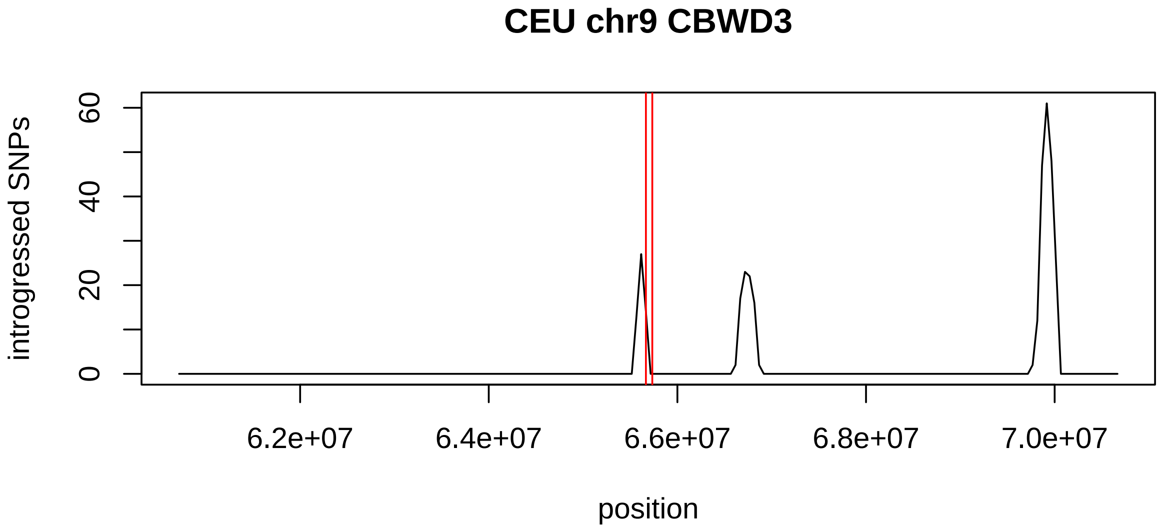
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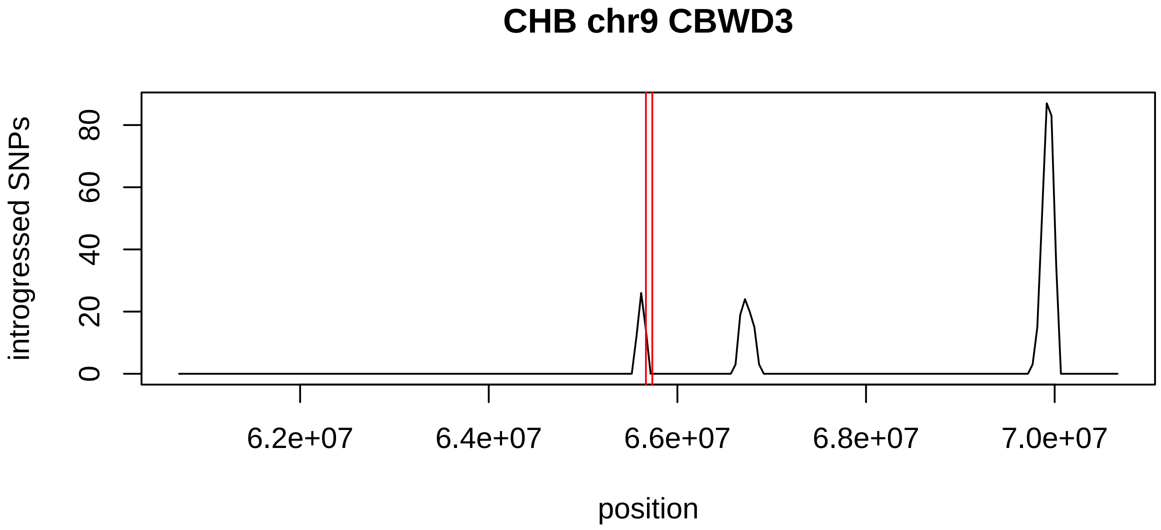
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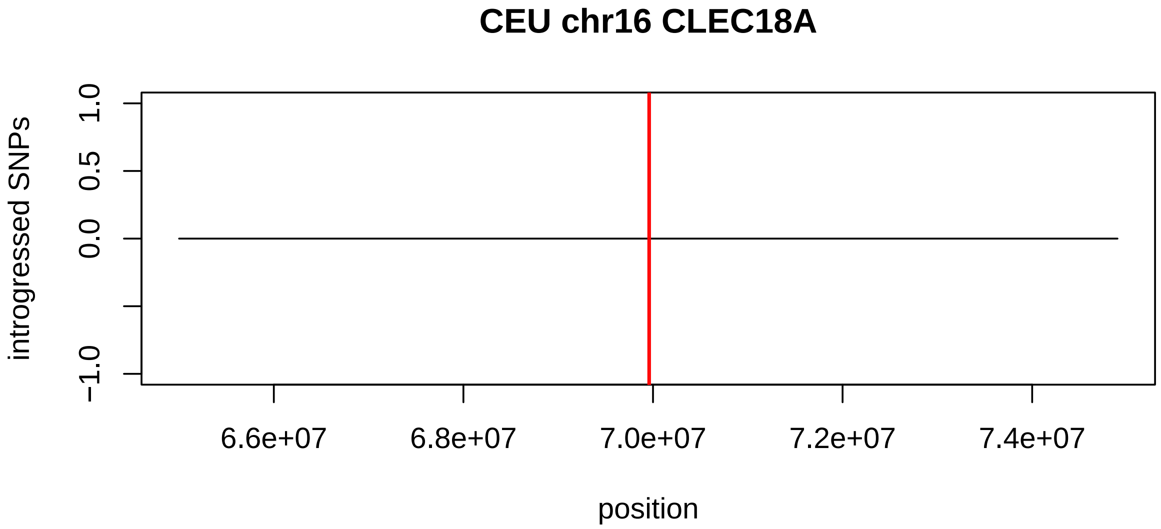
position



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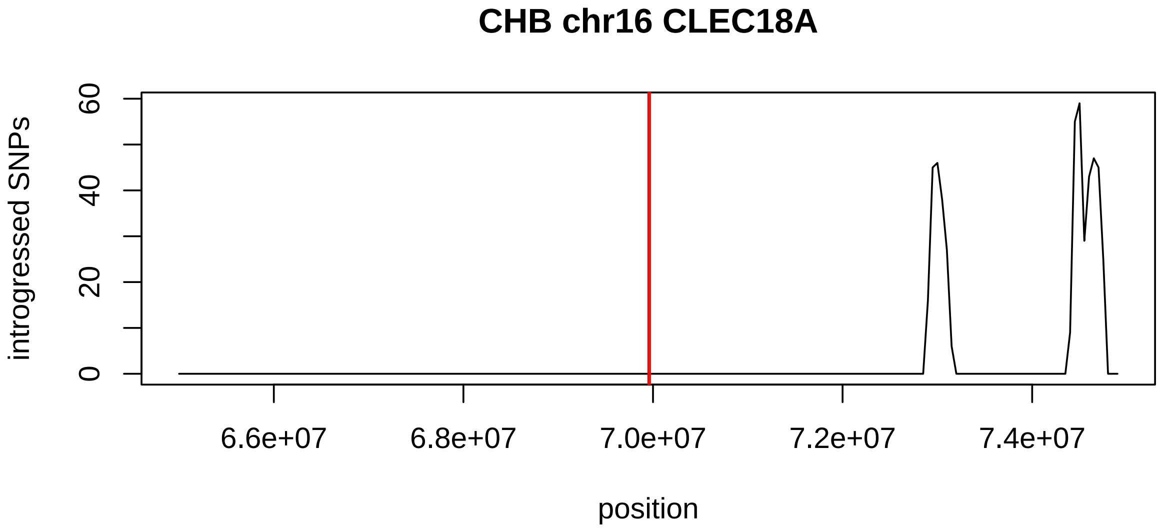

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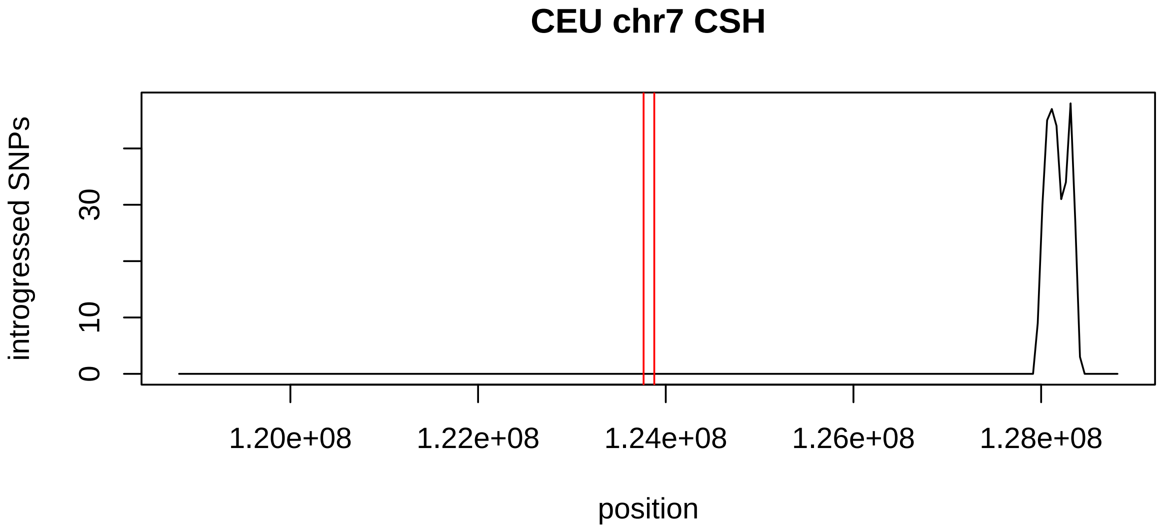

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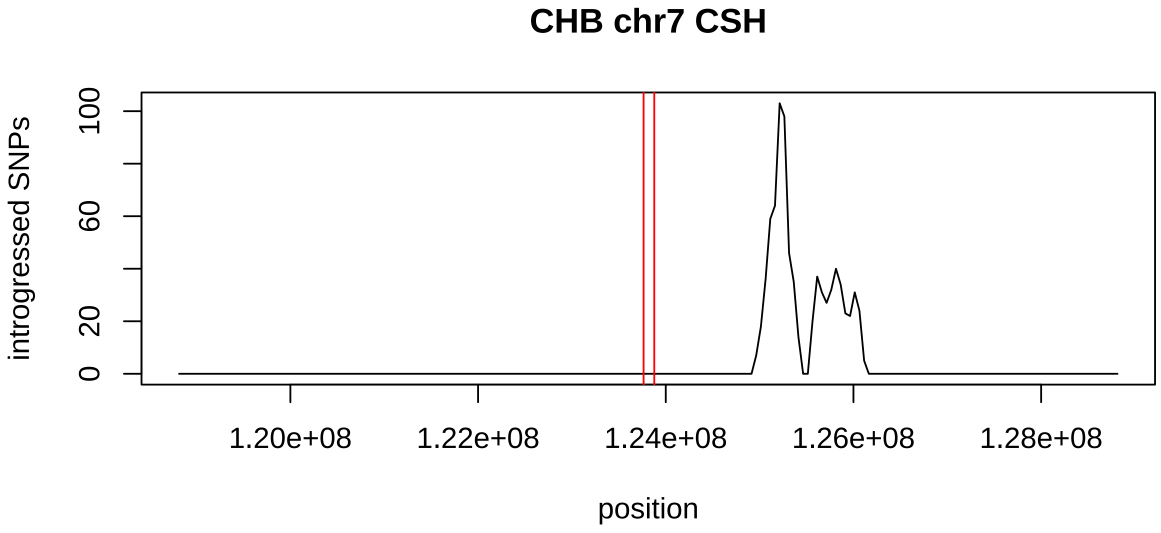

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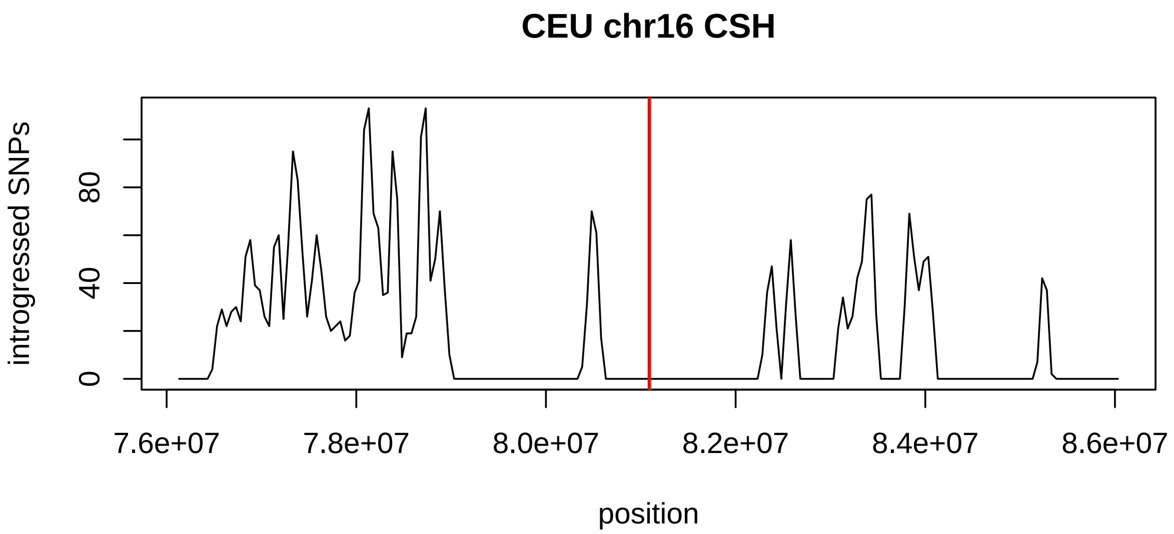

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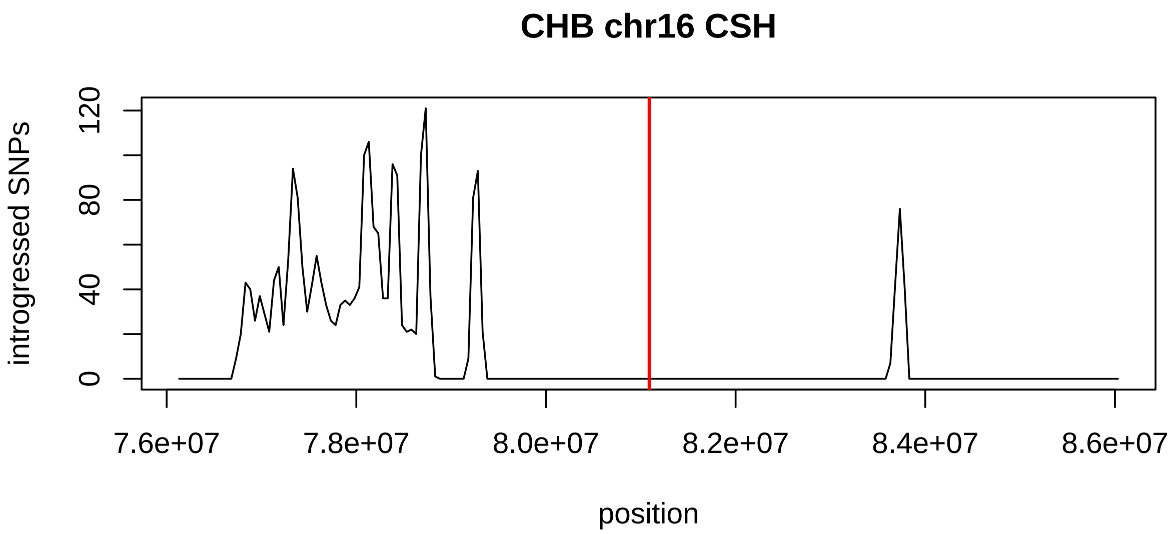

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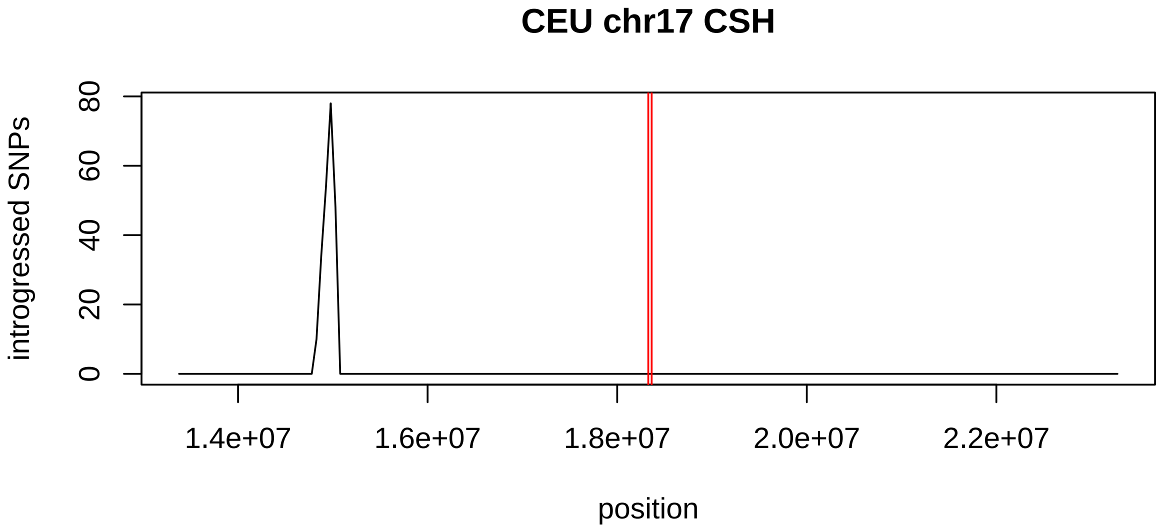
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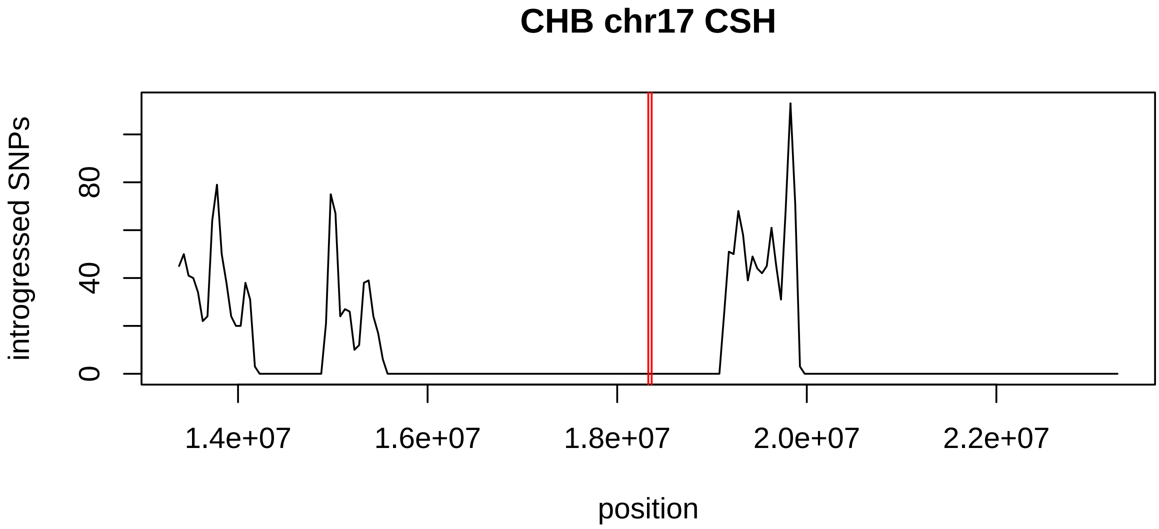
2.2e+07
position


CHB chr17 CSH
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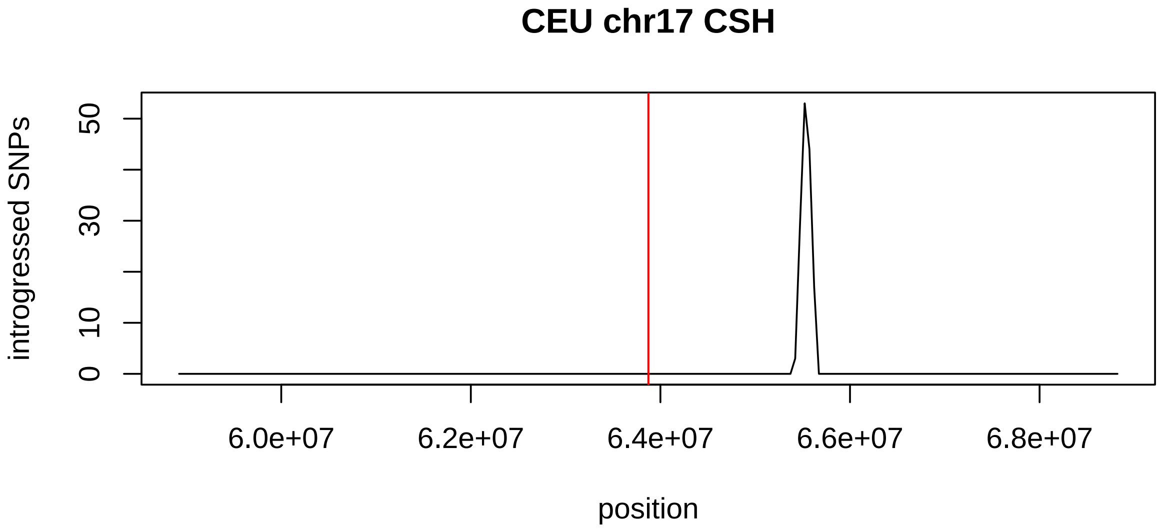
position



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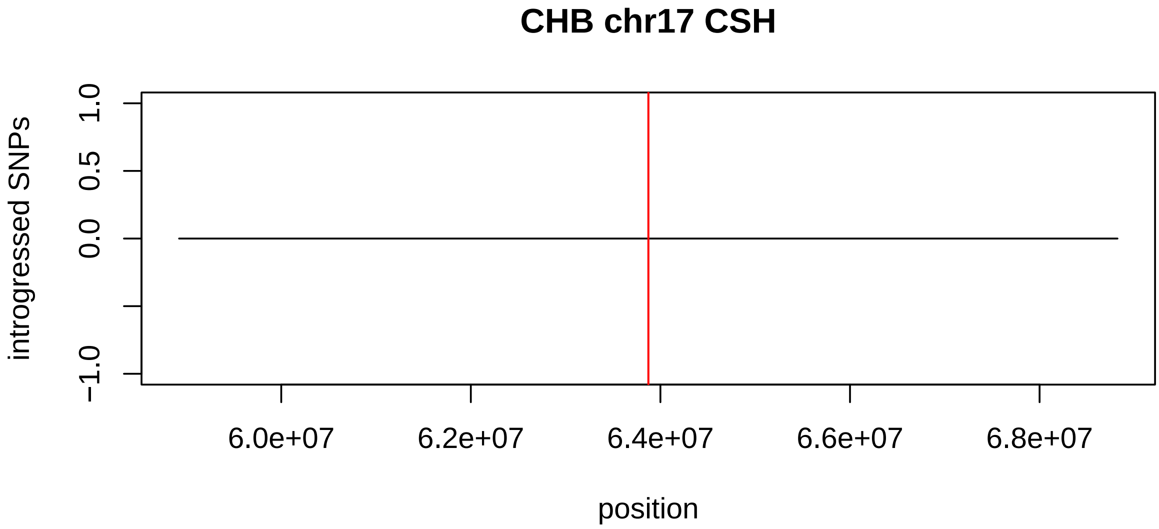

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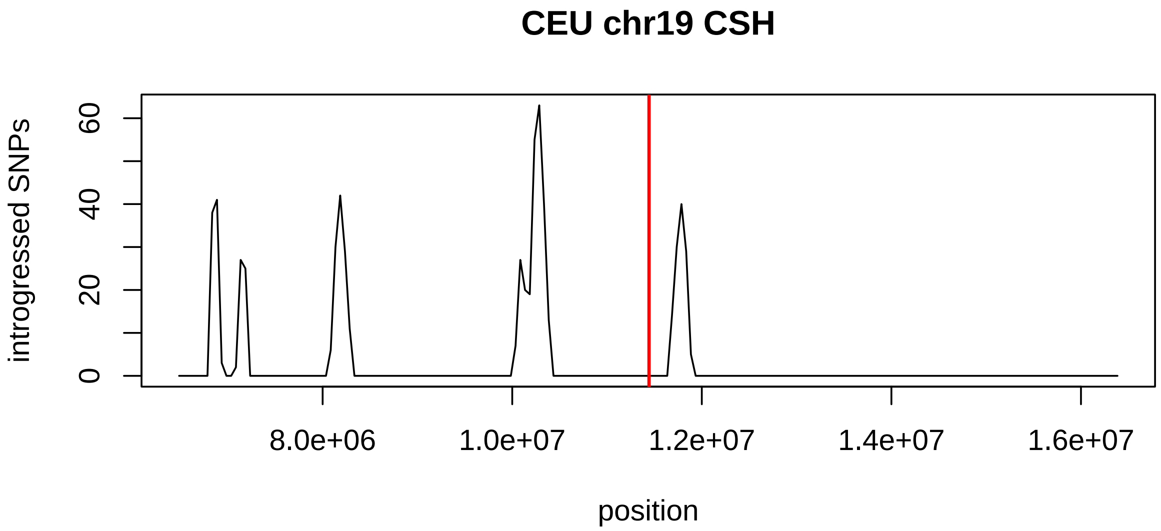
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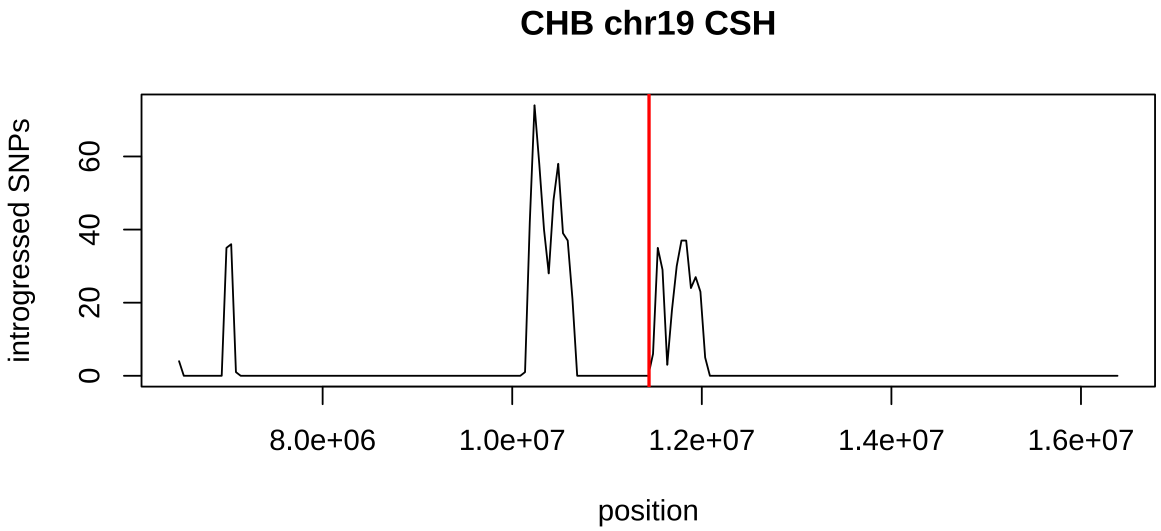
1.4e+07
1.6e+07
position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introgressed SNPs
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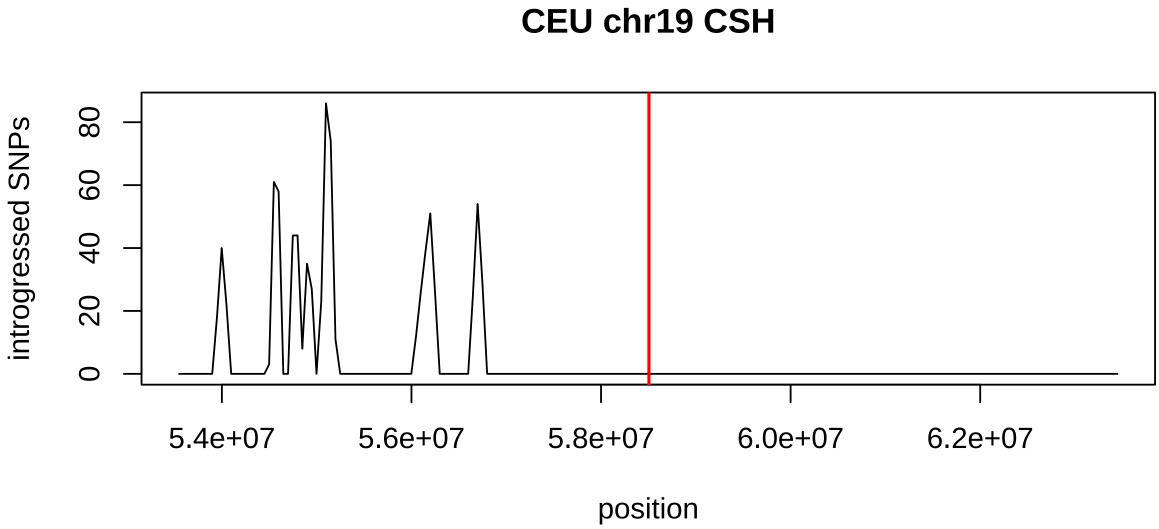
1.6e+07
position


CEU chr19 CSH
introgressed SNPs
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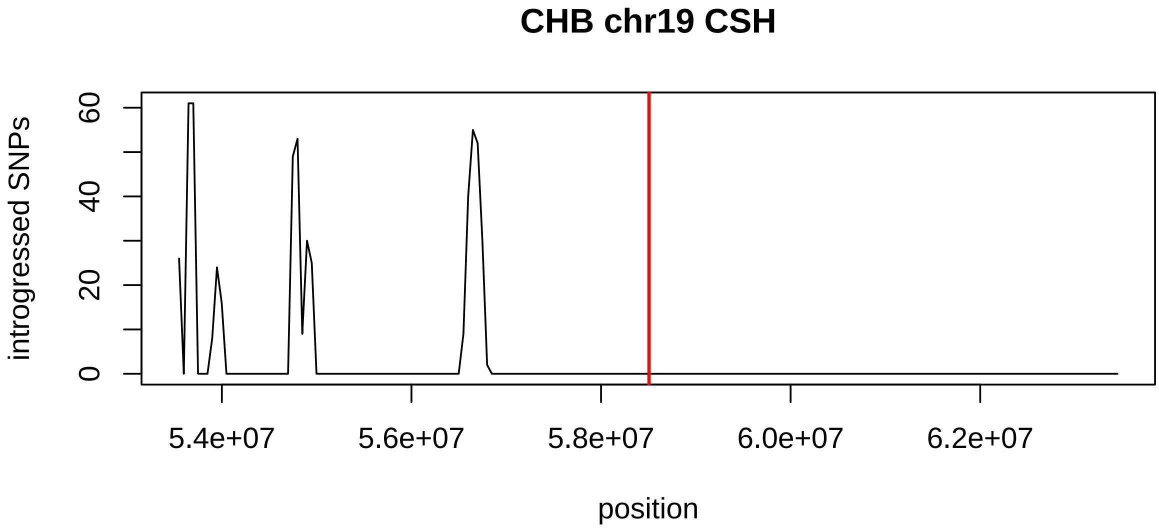
6.2e+07
position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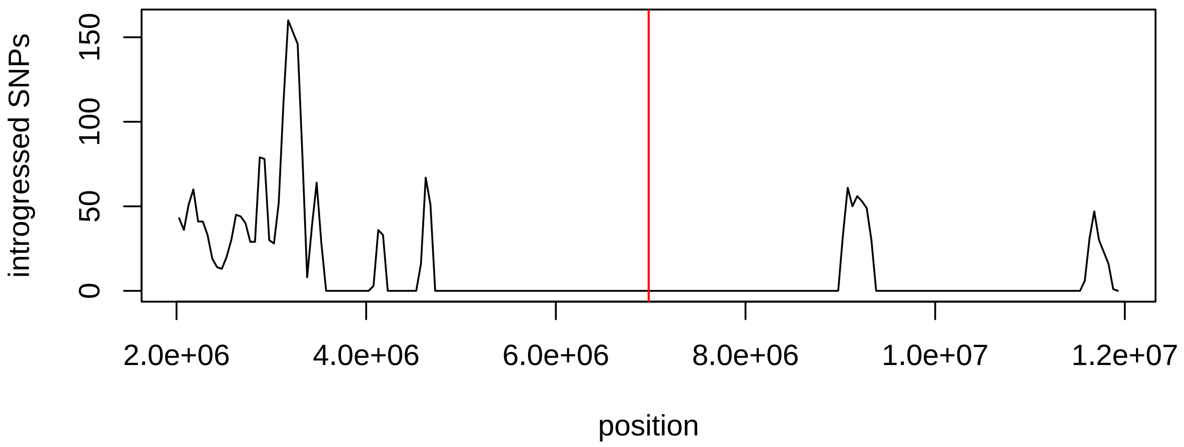
6.2e+07
position

CEU chr8 DEFA1



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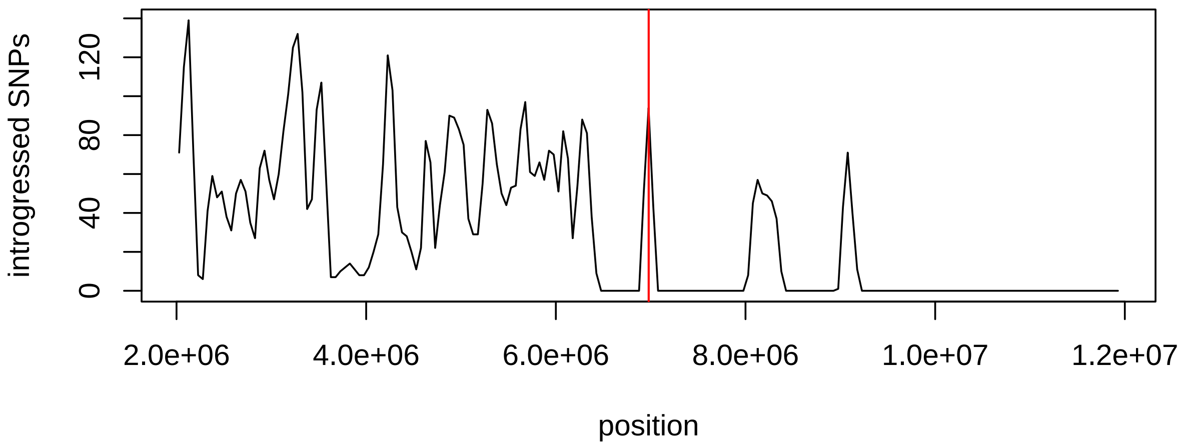

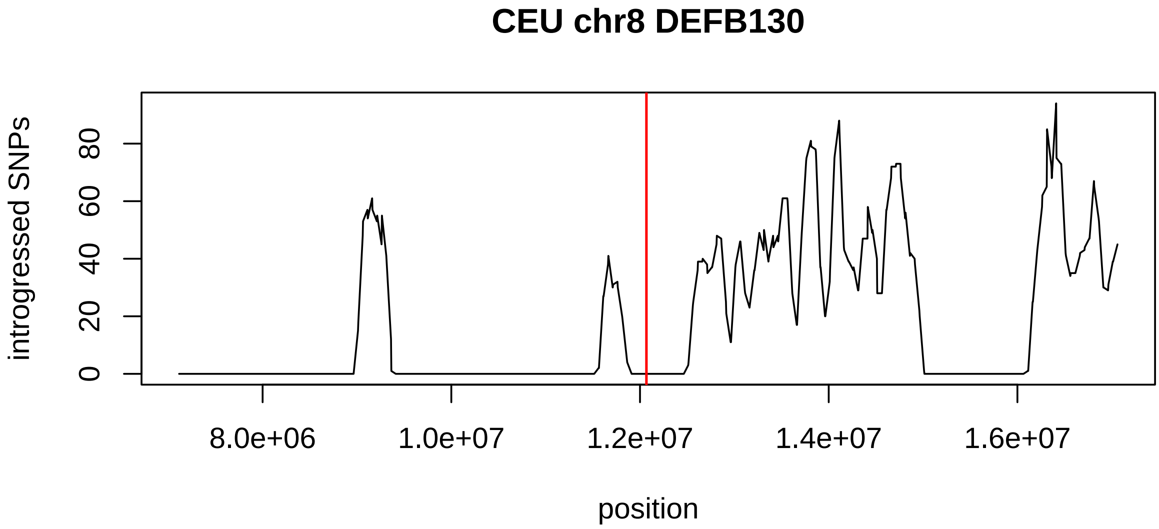
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introgressed SNPs
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80
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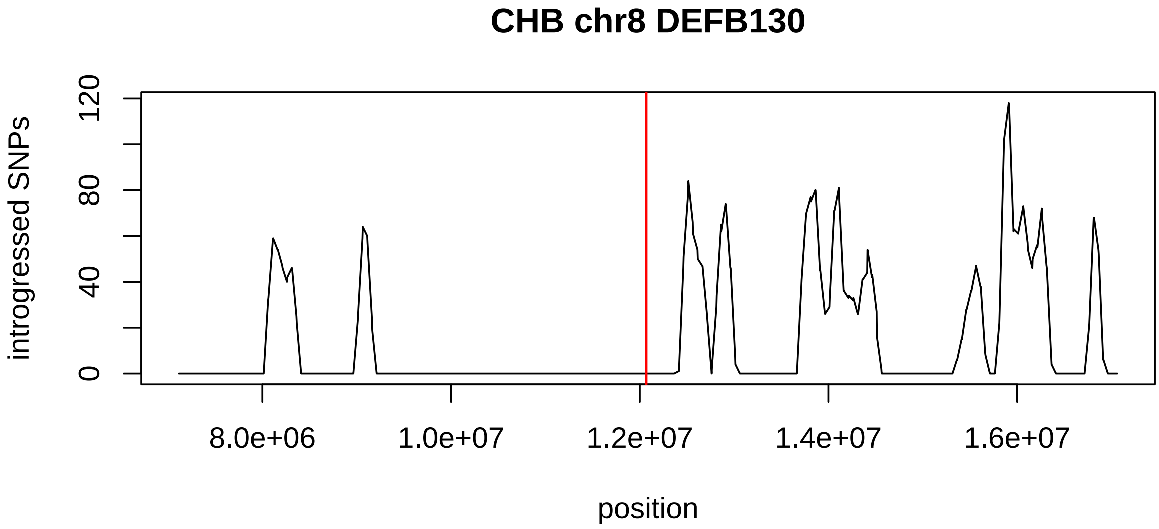
1.6e+07
position


CHB chr8 DEFB130
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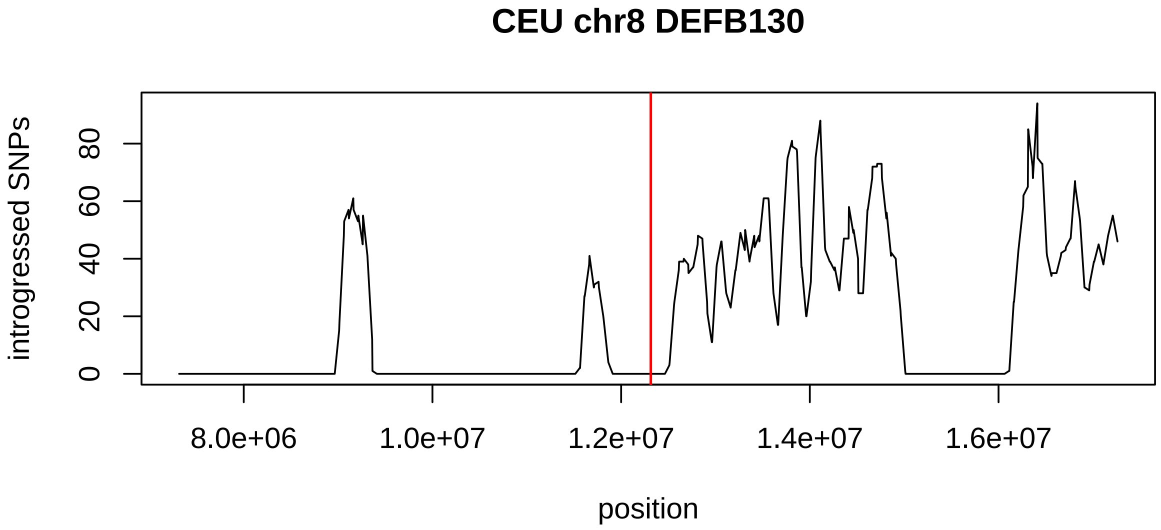
1.6e+07
position



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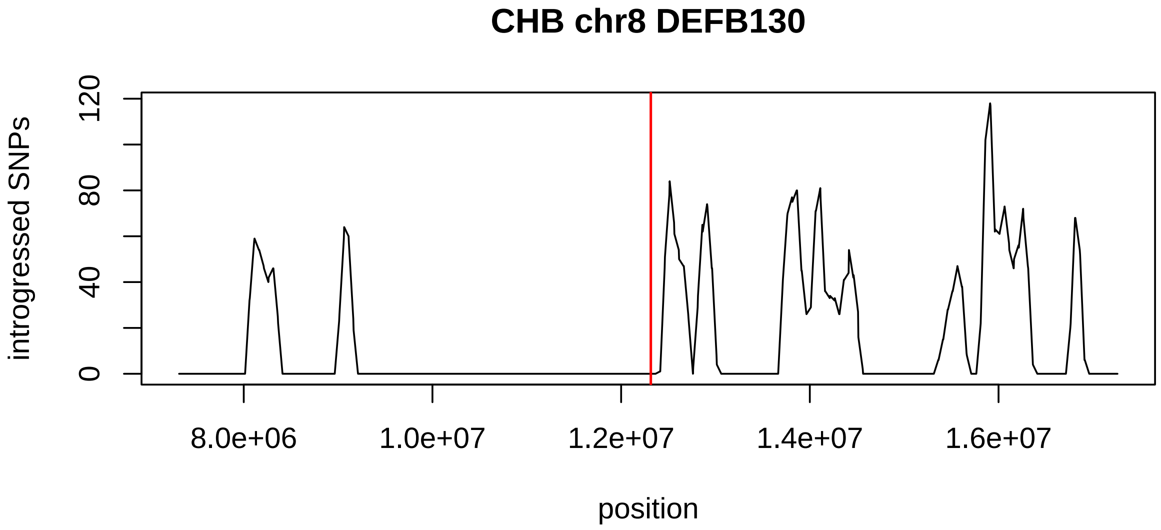

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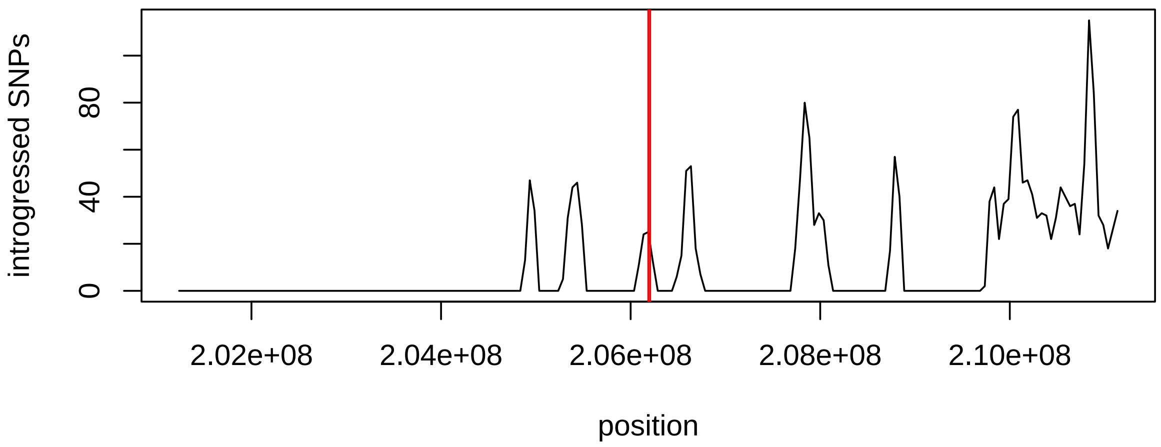
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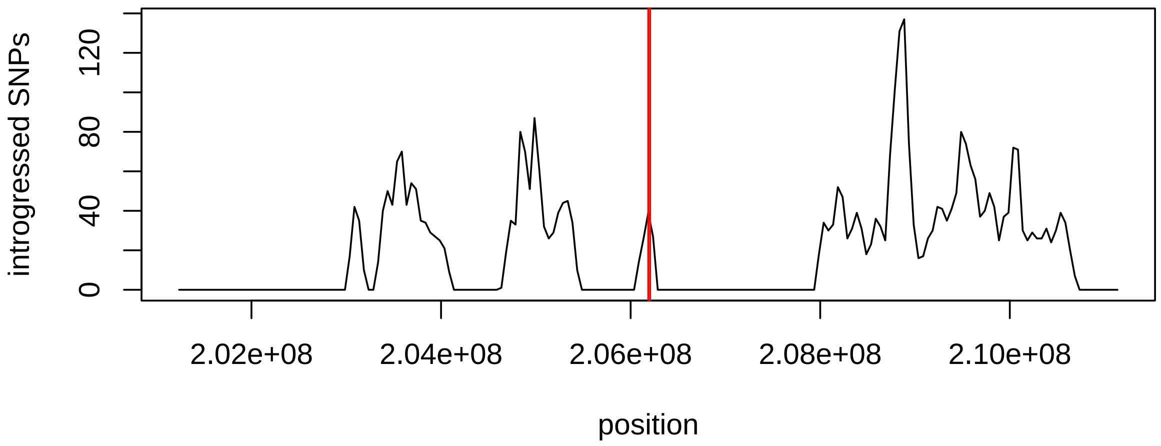
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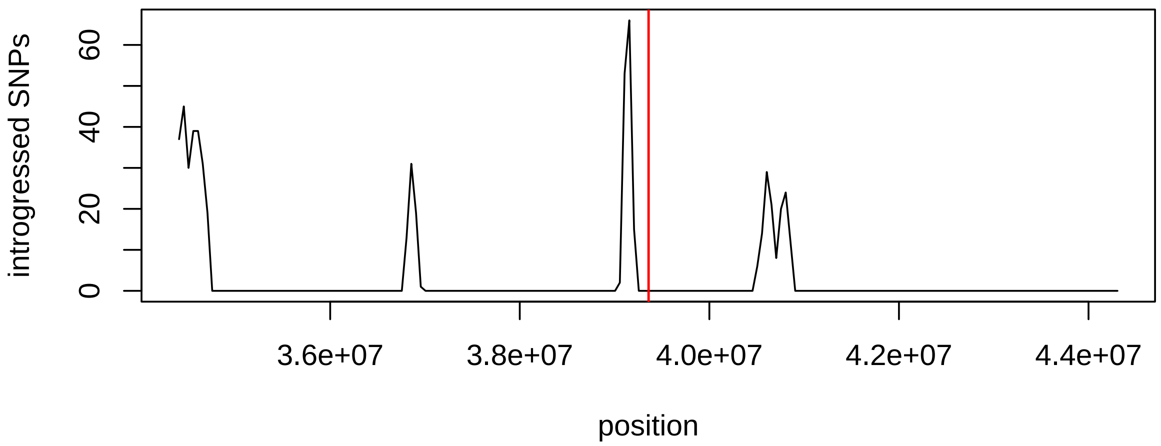
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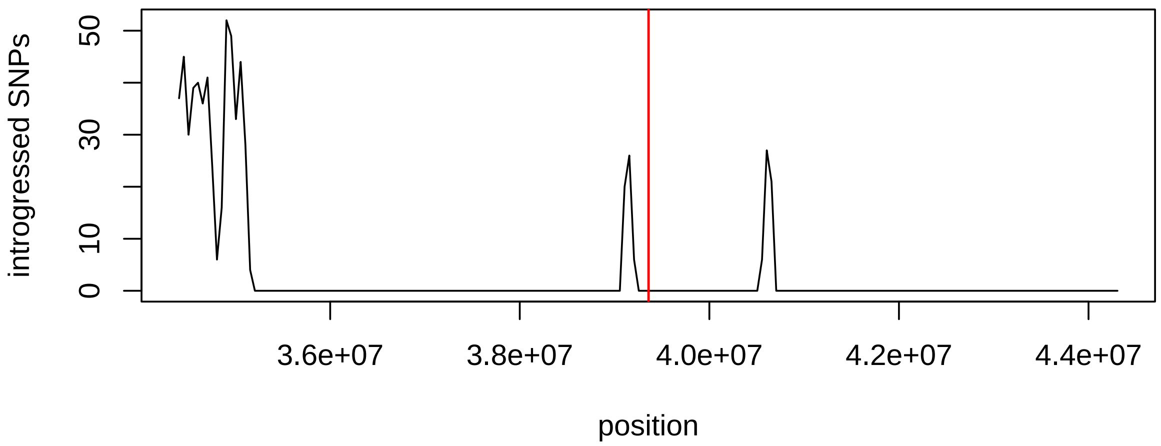
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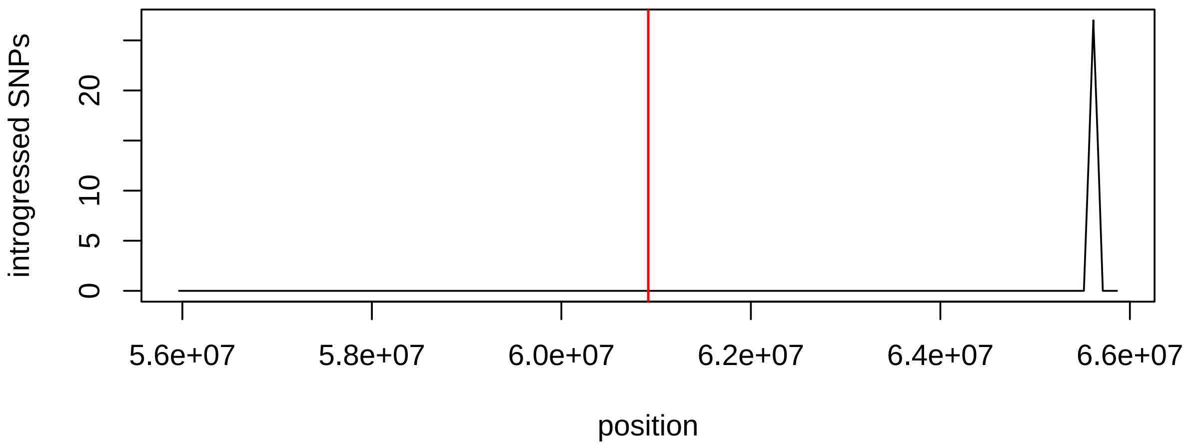

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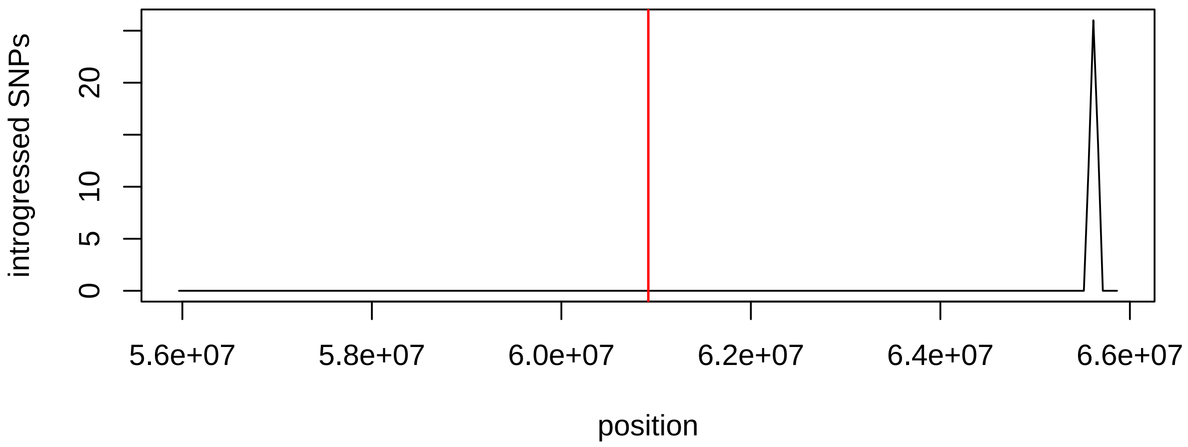

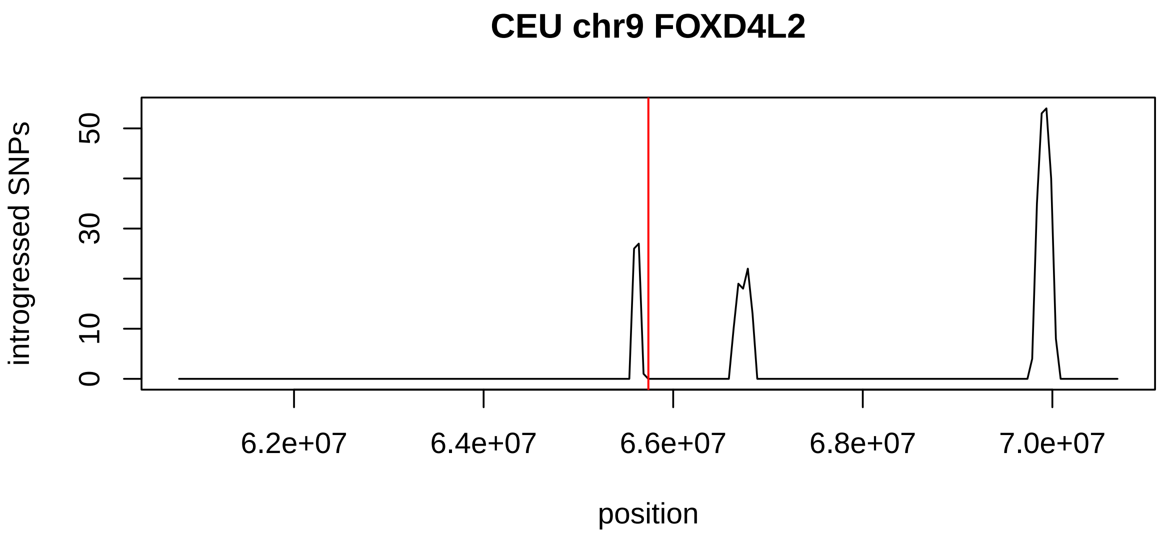
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30
50
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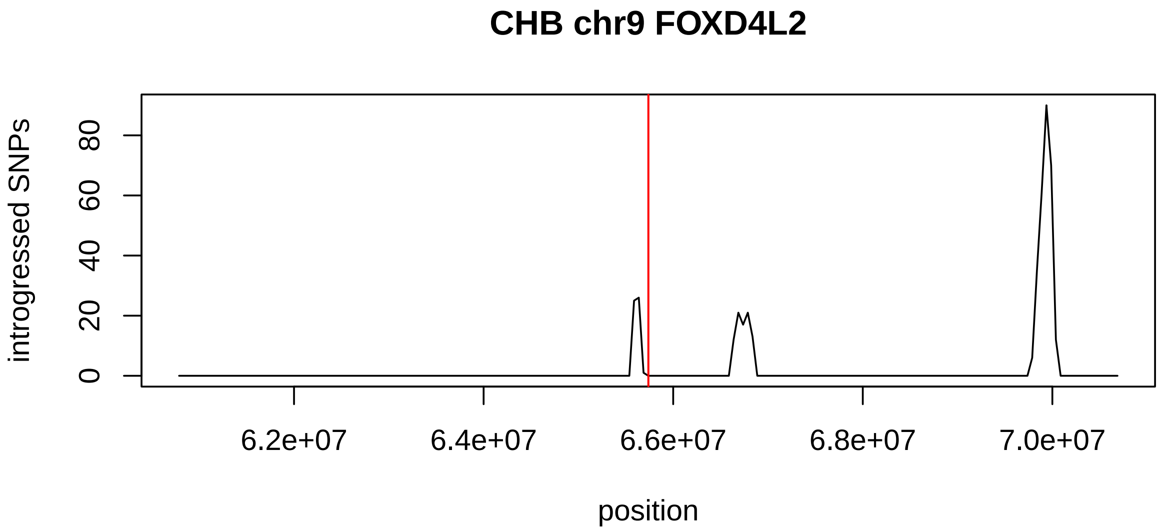
6.6e+07
6.8e+07
7.0e+07
position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introgressed SNPs
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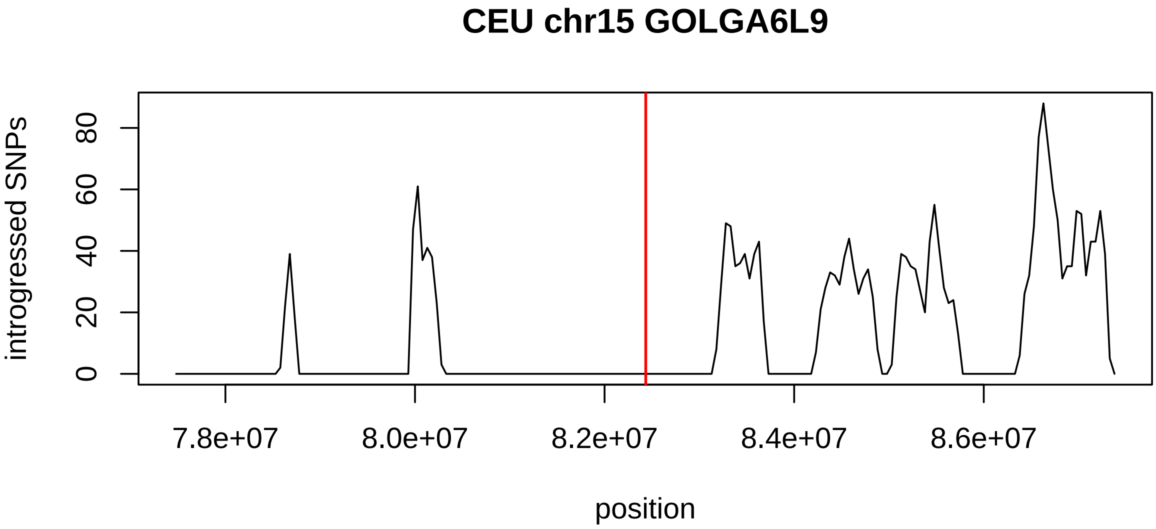
position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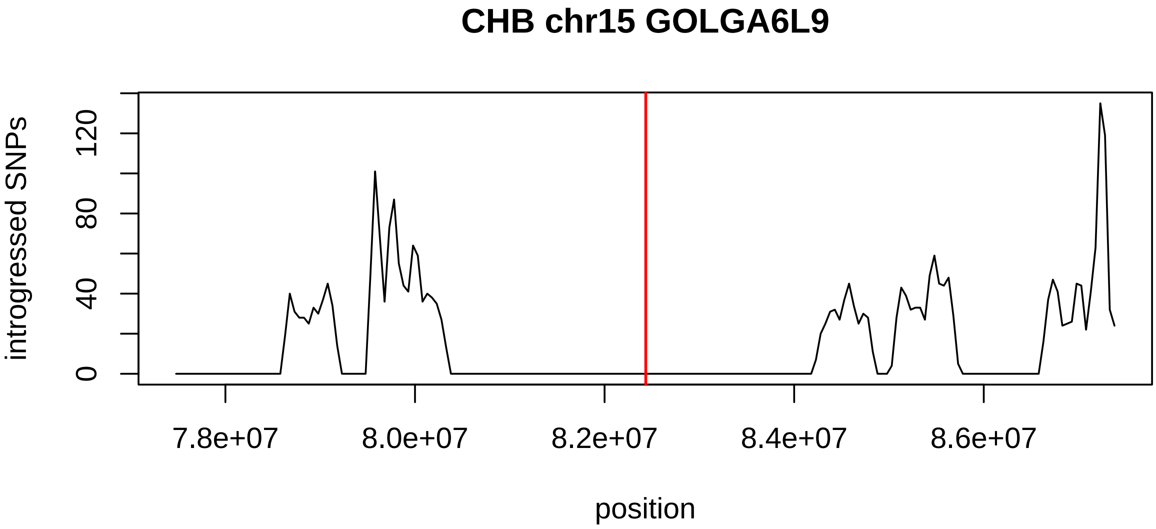
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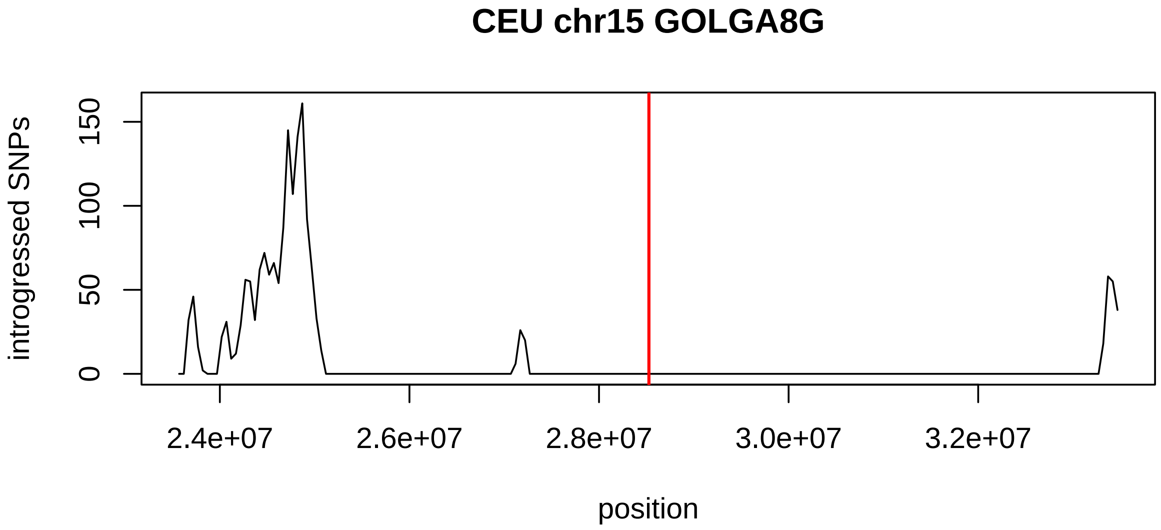
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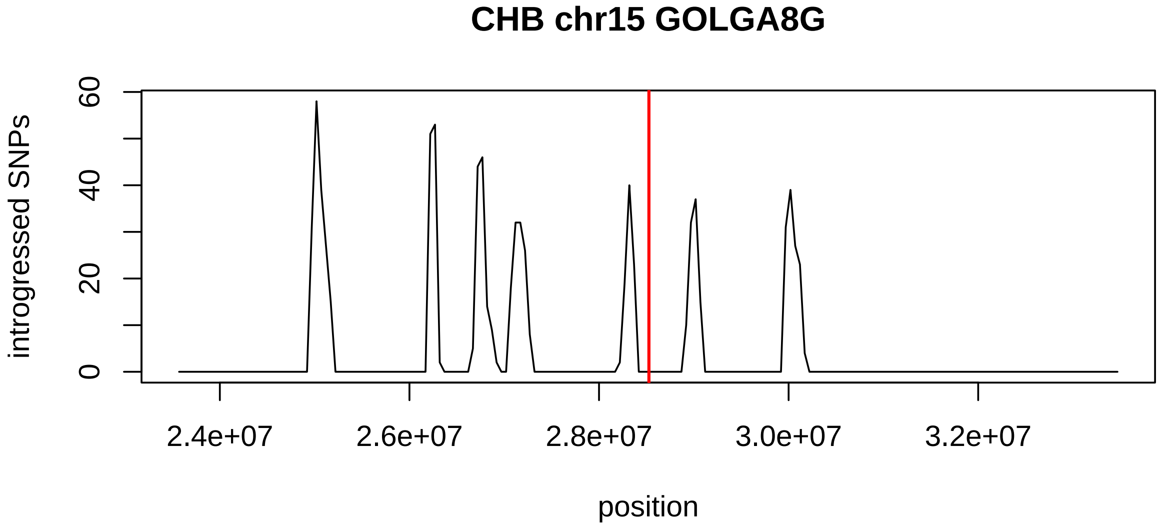
position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40
60
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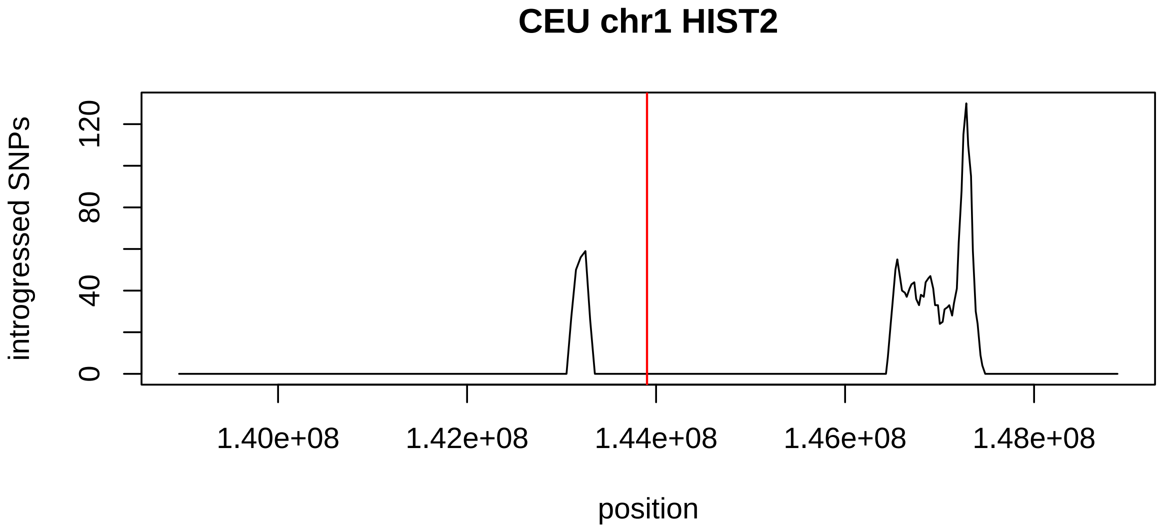
position



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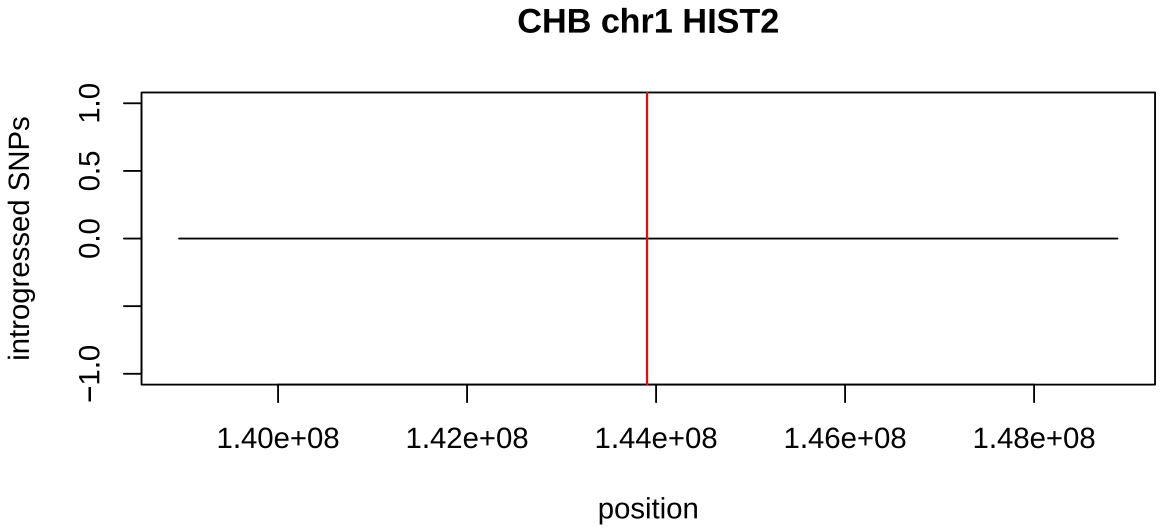

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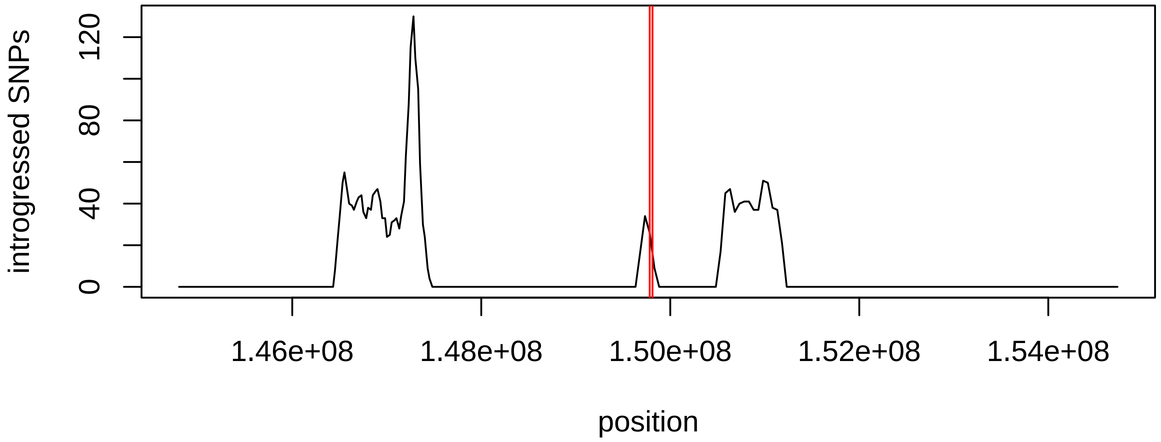

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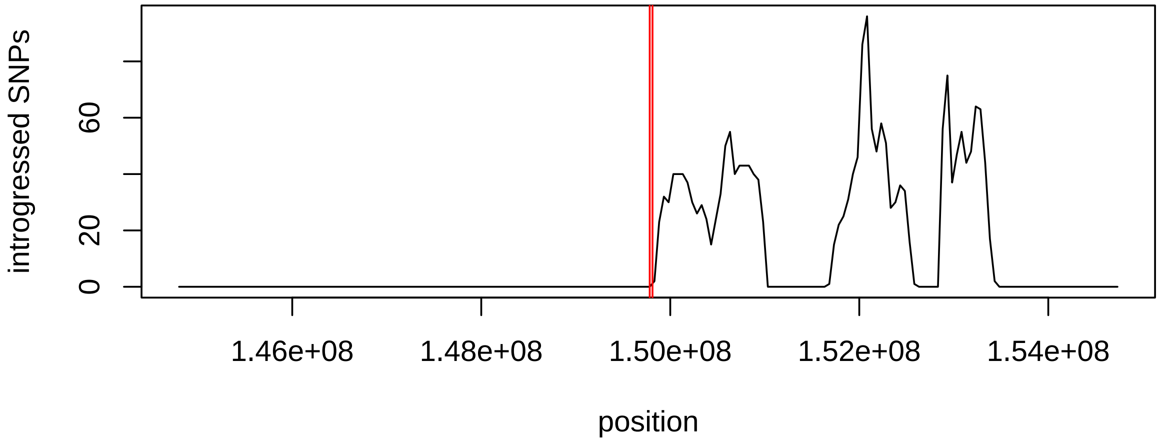

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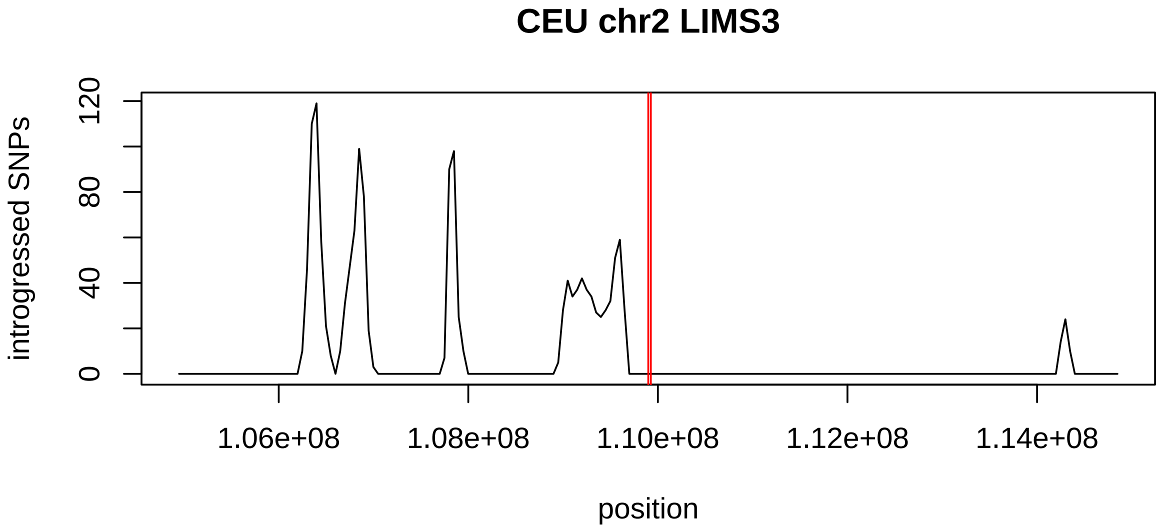
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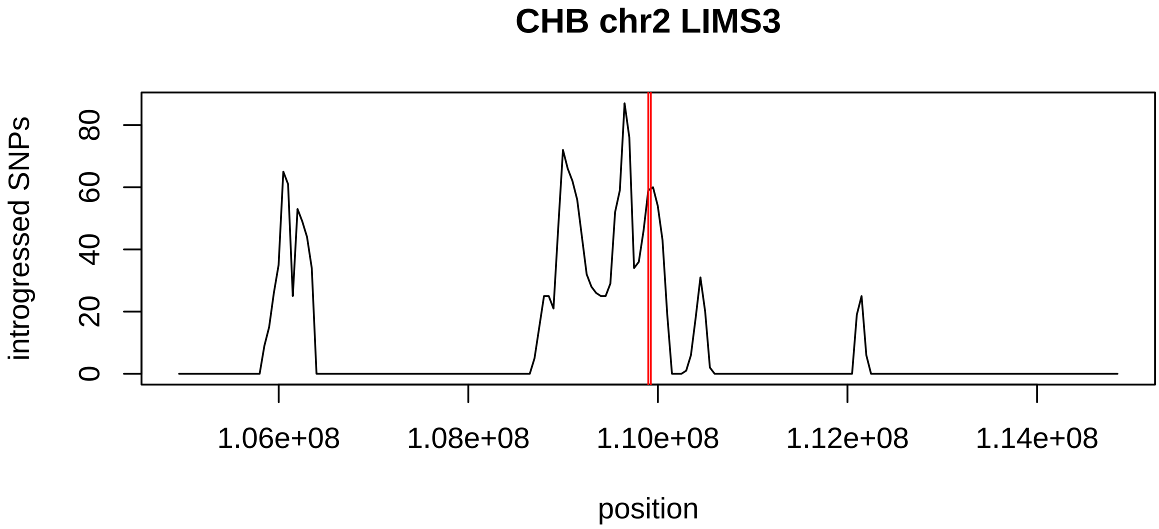
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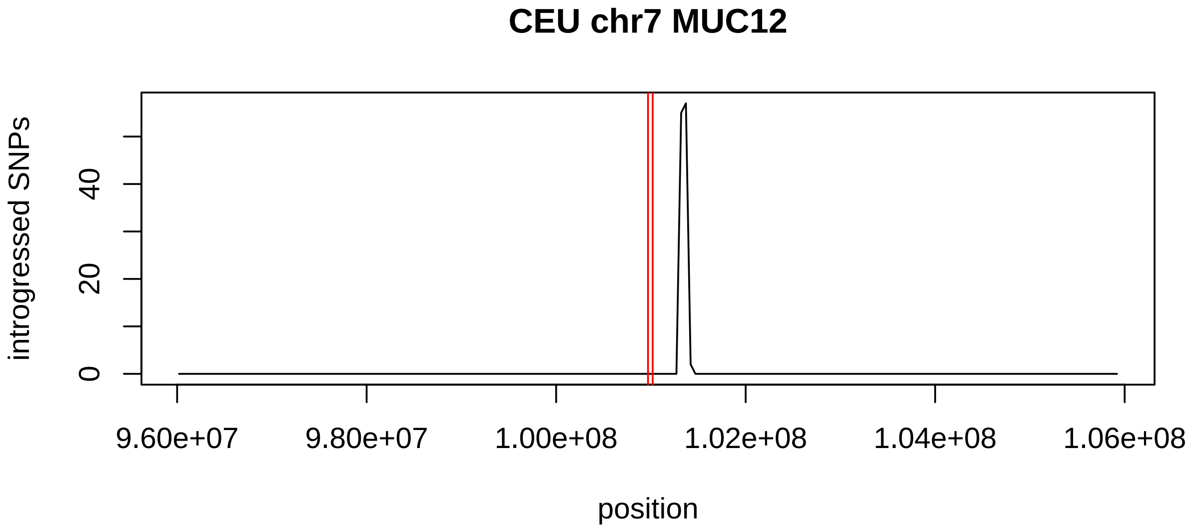
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1.02e+08
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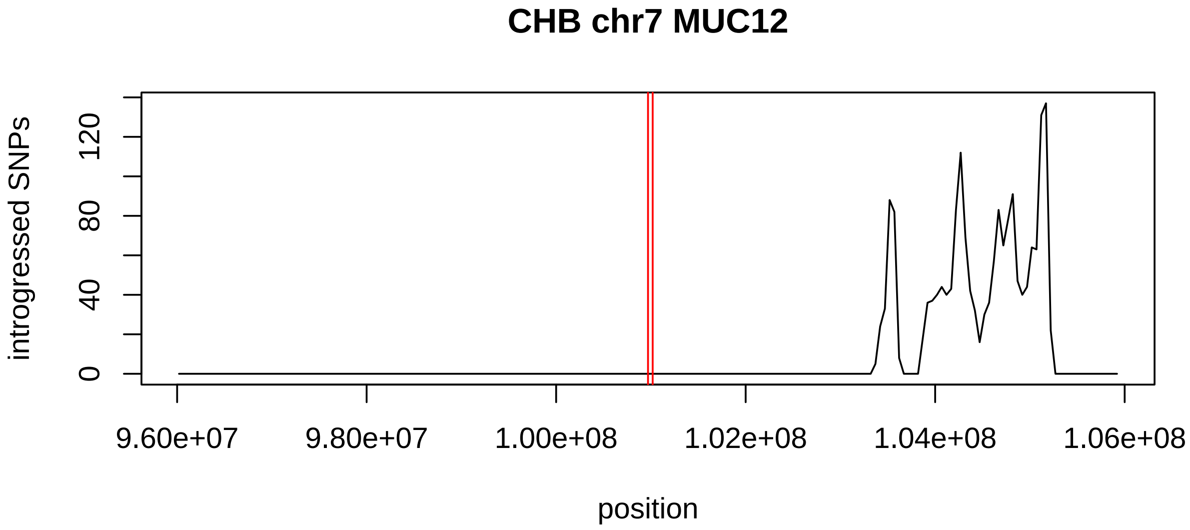
1.06e+08
position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introgressed SNPs
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1.00e+08
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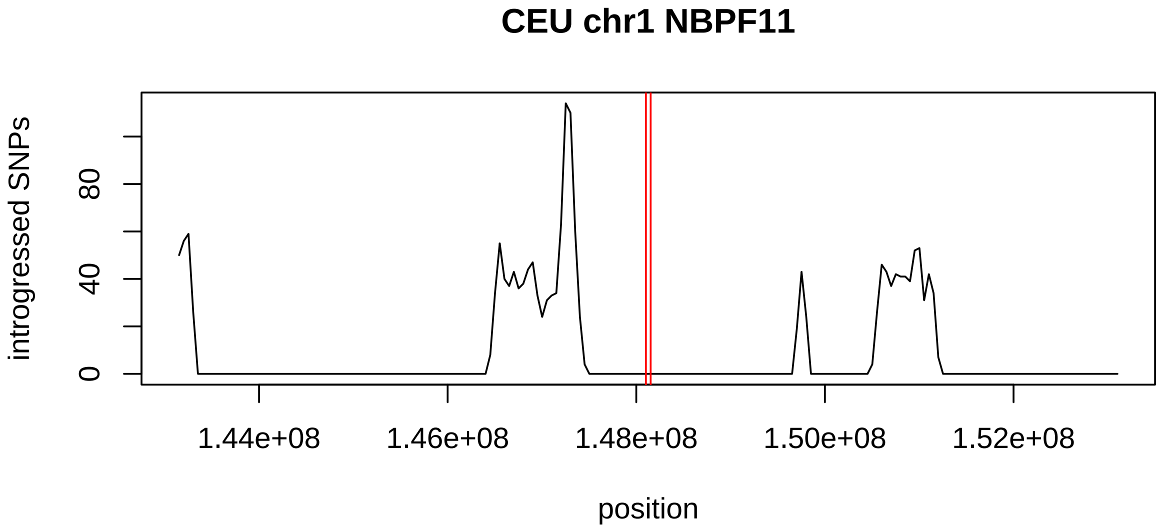
1.06e+08
position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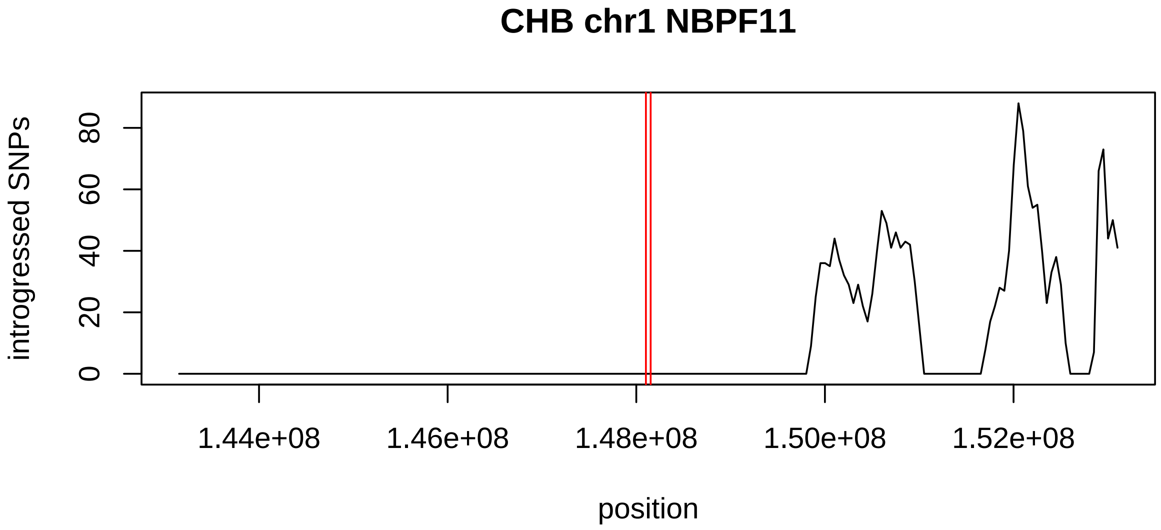
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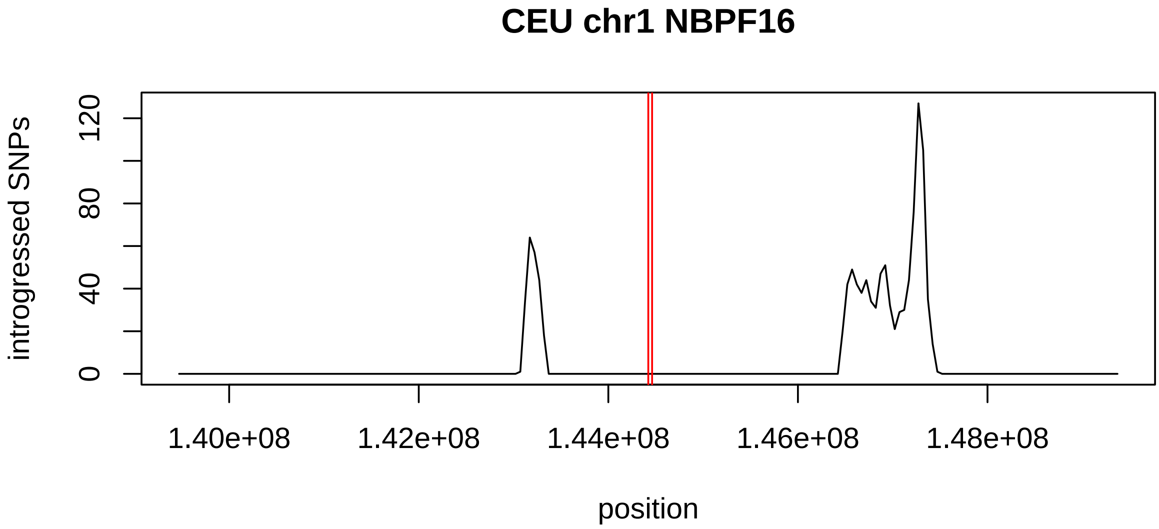
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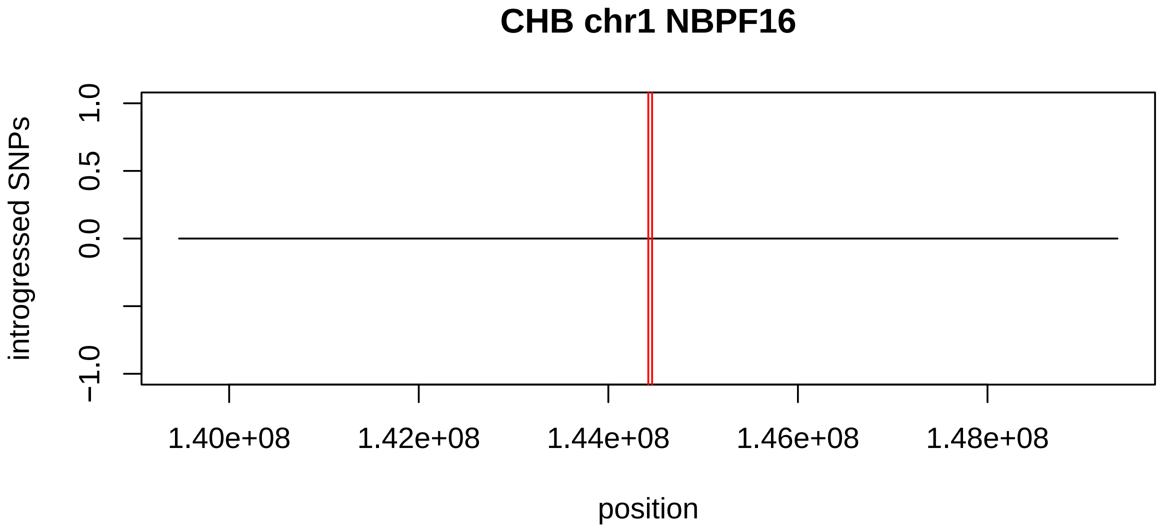
position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introgressed SNPs
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1.0
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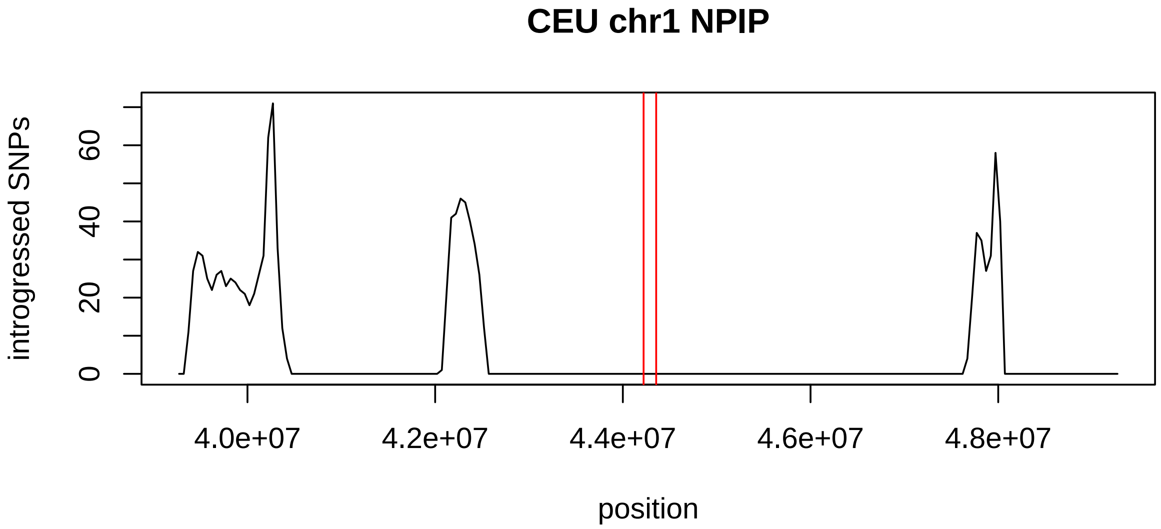
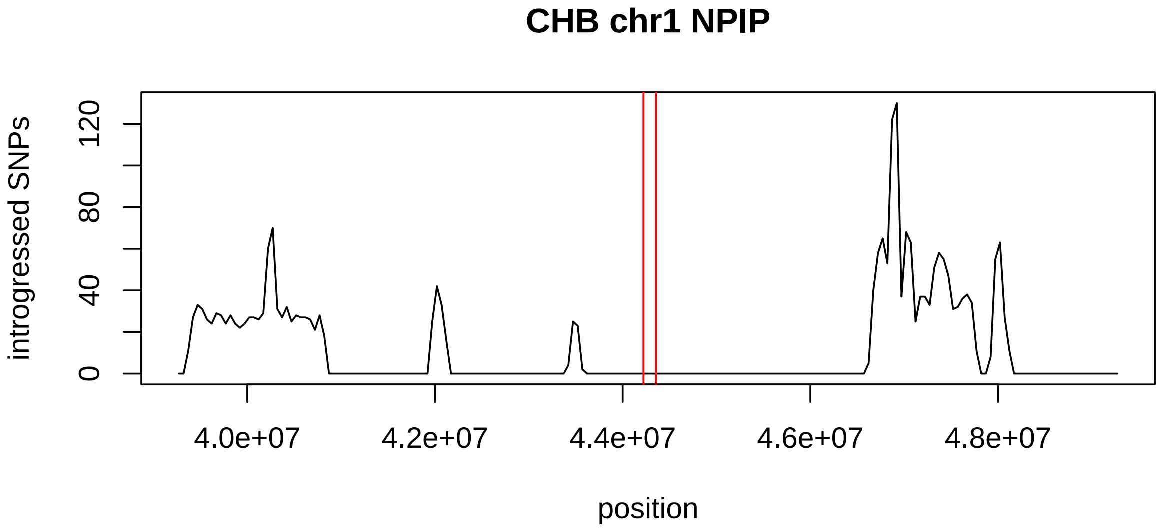
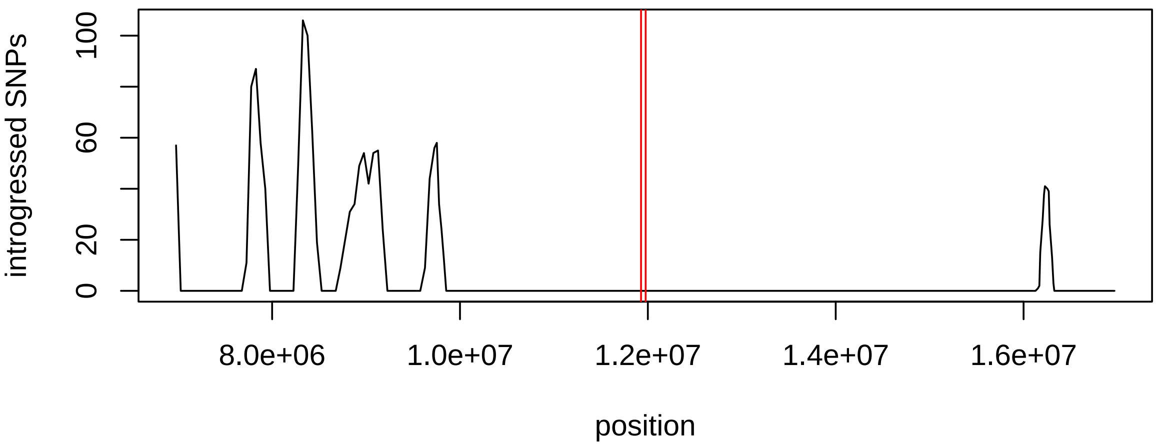
1.48e+08
position



CEU chr1 NPIP



CHB chr1 NPIP



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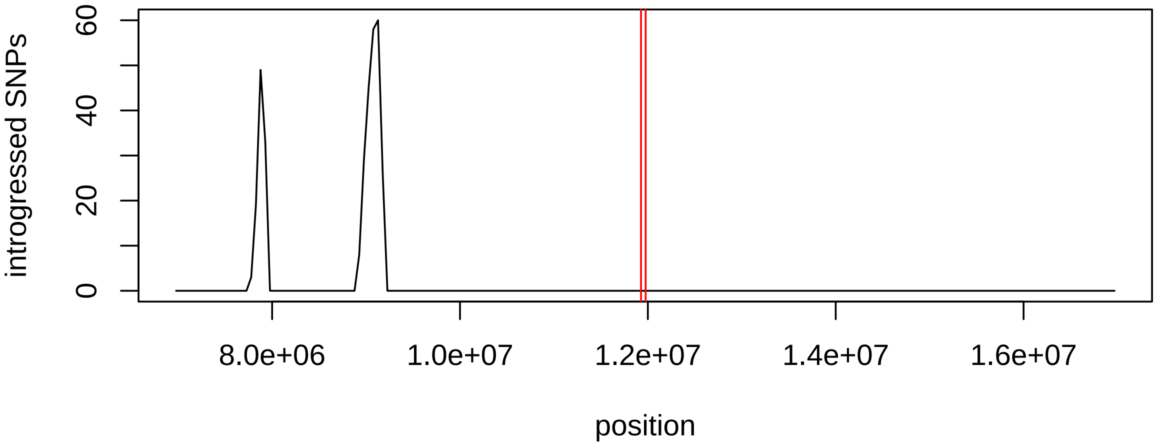

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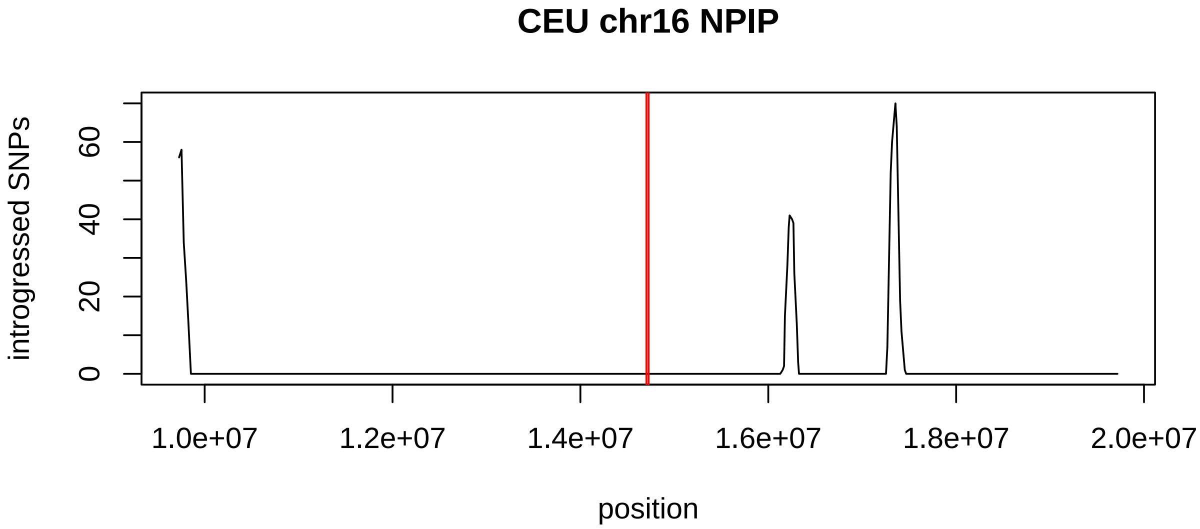

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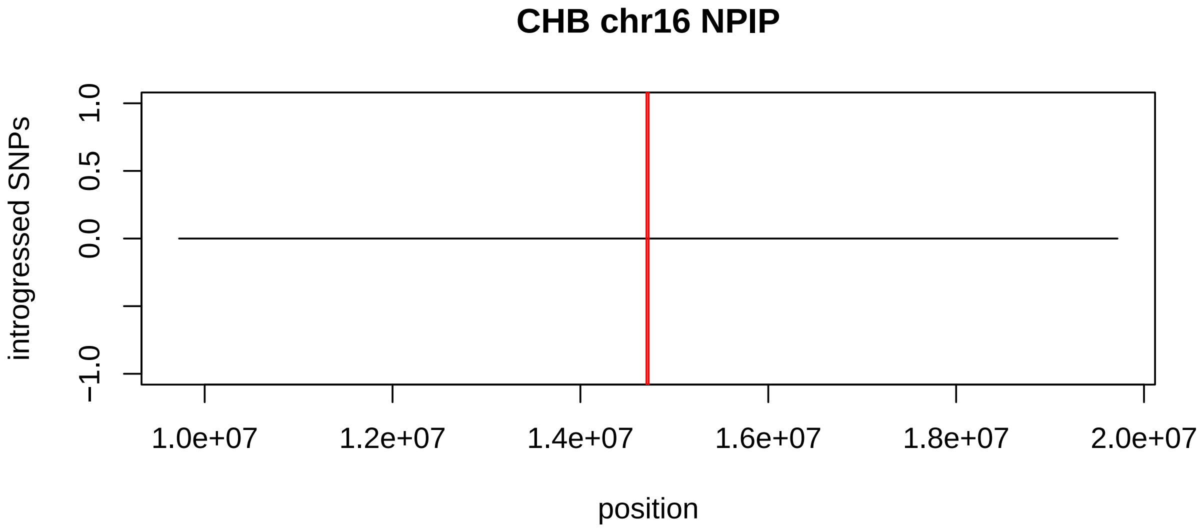
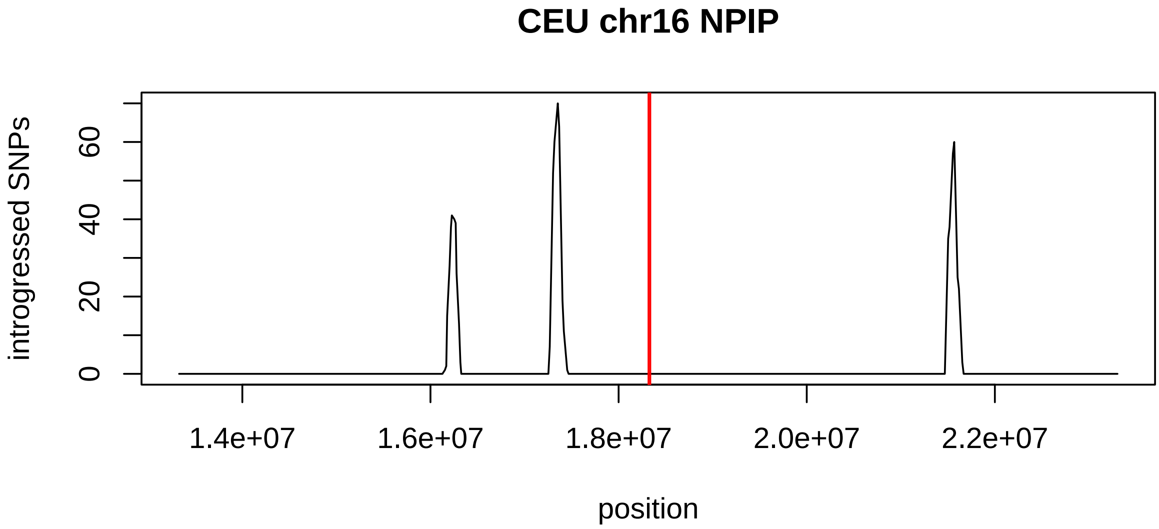


CHB chr16 NPIP



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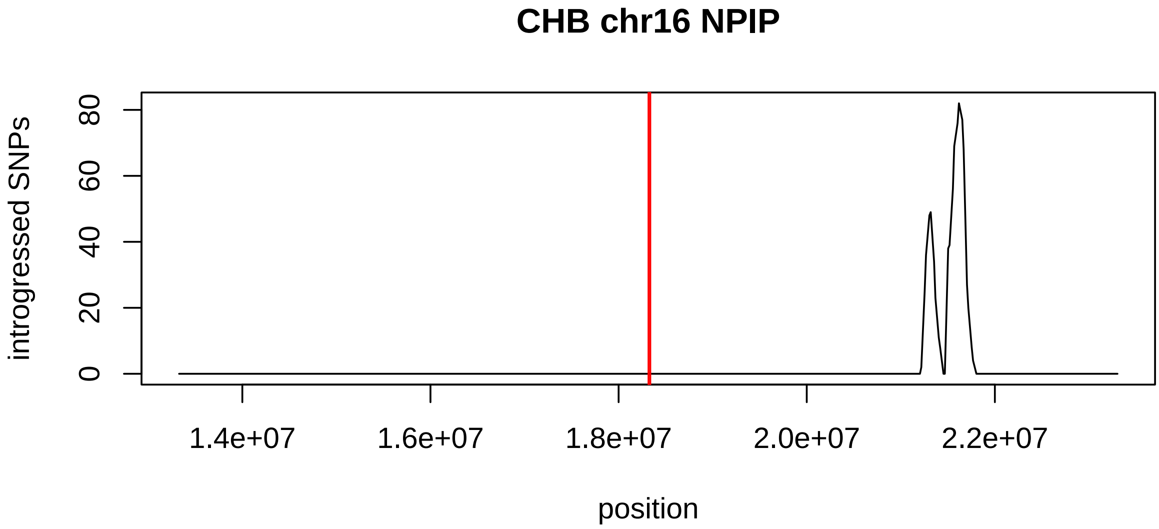
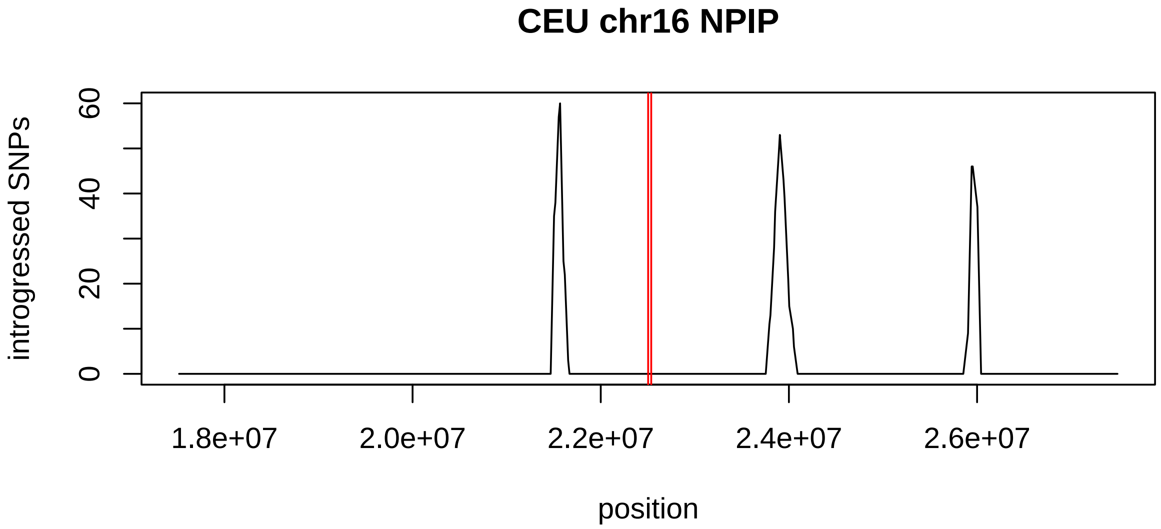


CHB chr16 NPIP


CEU chr16 NPIP
introgressed SNPs
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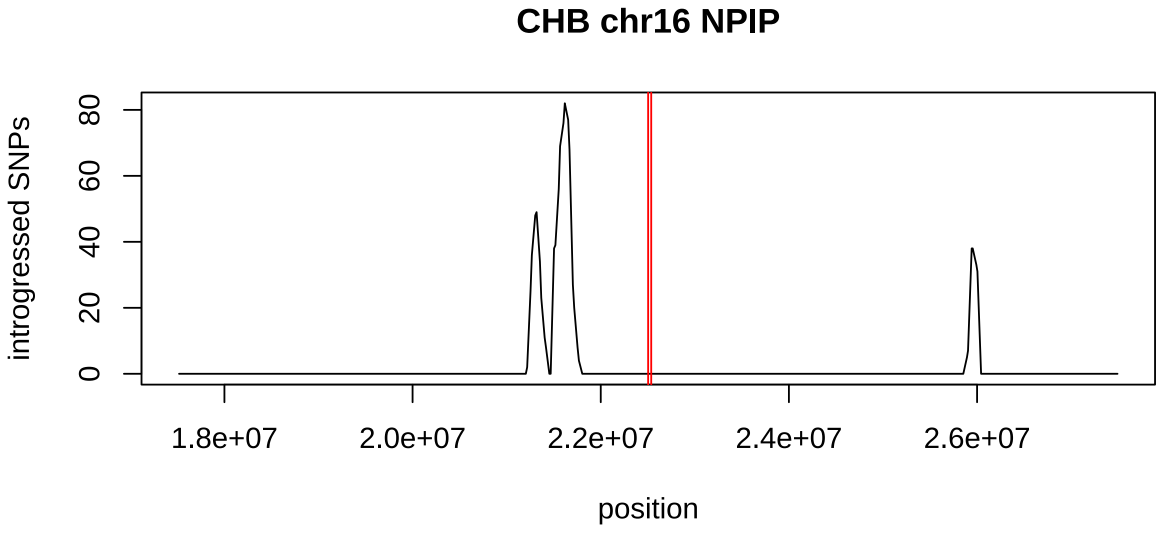
2.6e+07
position


CHB chr16 NPIP
introgressed SNPs
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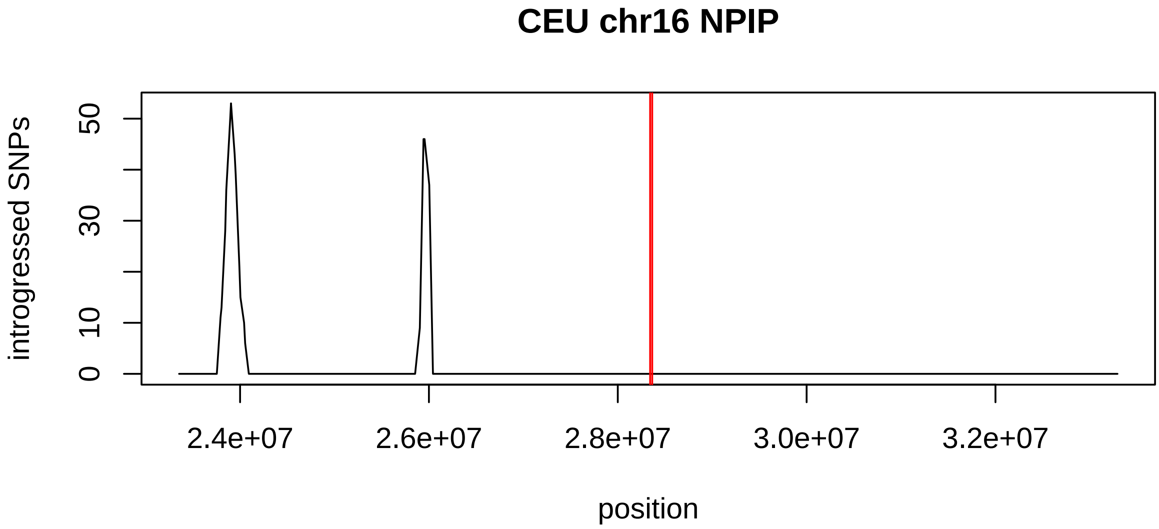
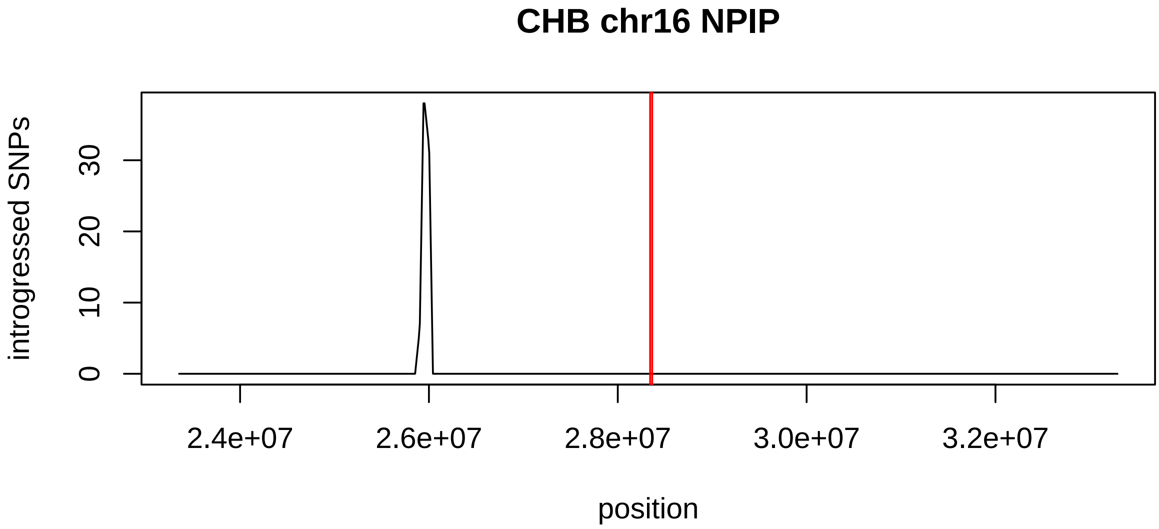
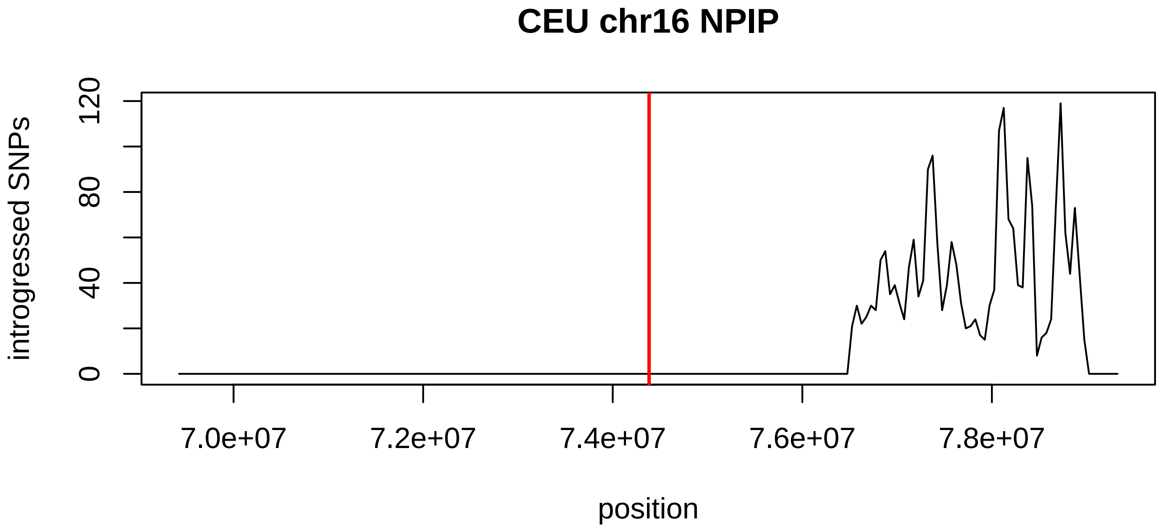
position



CEU chr16 NPIP



CHB chr16 NPIP


CEU chr16 NPIP
introgressed SNPs
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80
120
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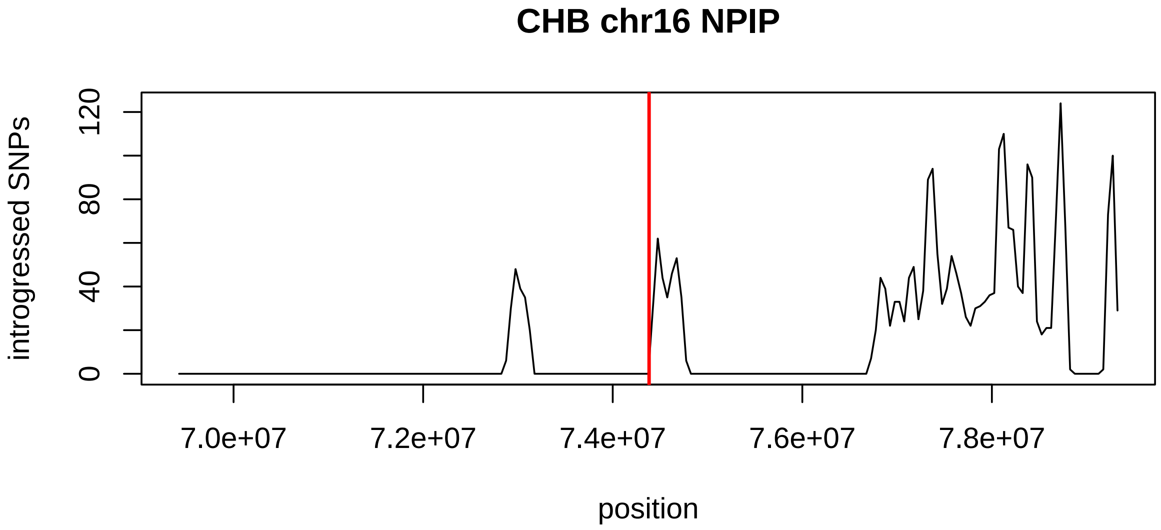
7.2e+07
7.4e+07
7.6e+07
7.8e+07
position


CHB chr16 NPIP
introgressed SNPs
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80
120
7.0e+07
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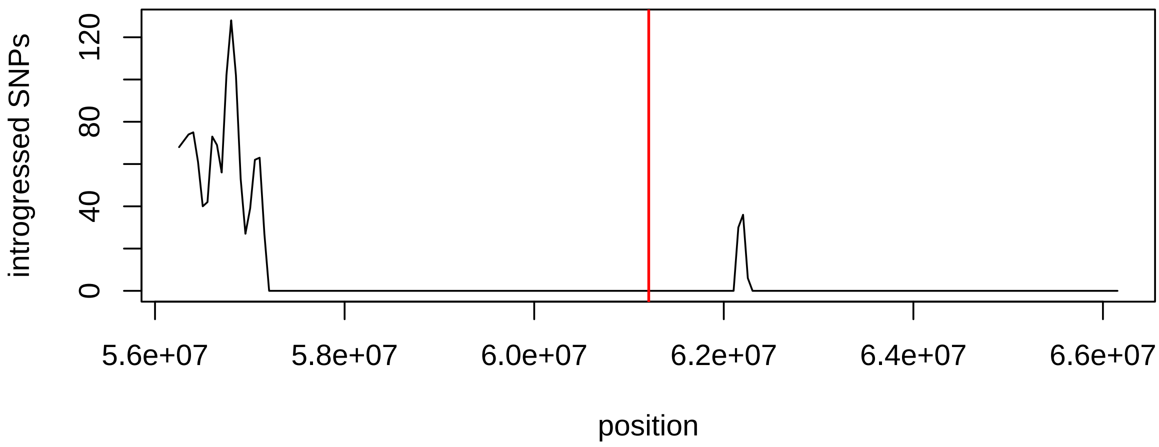
7.8e+07
position



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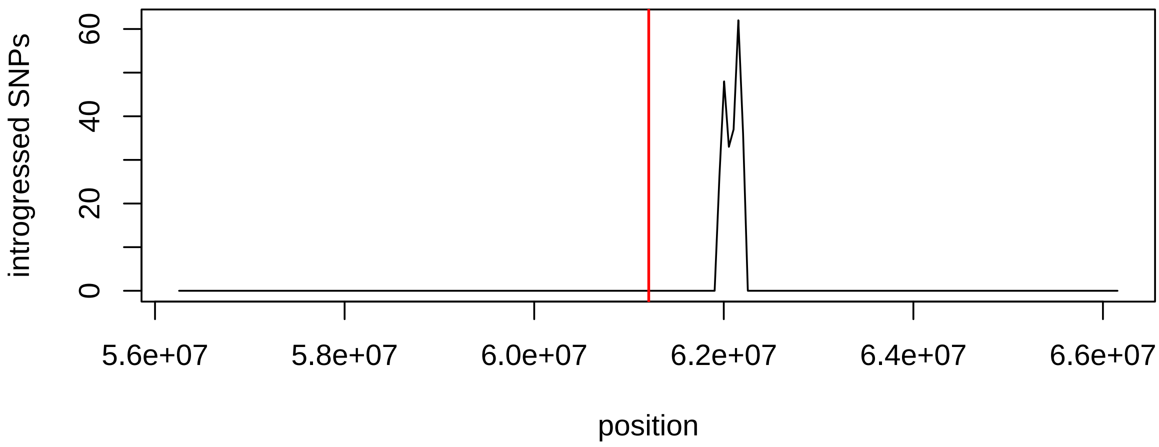
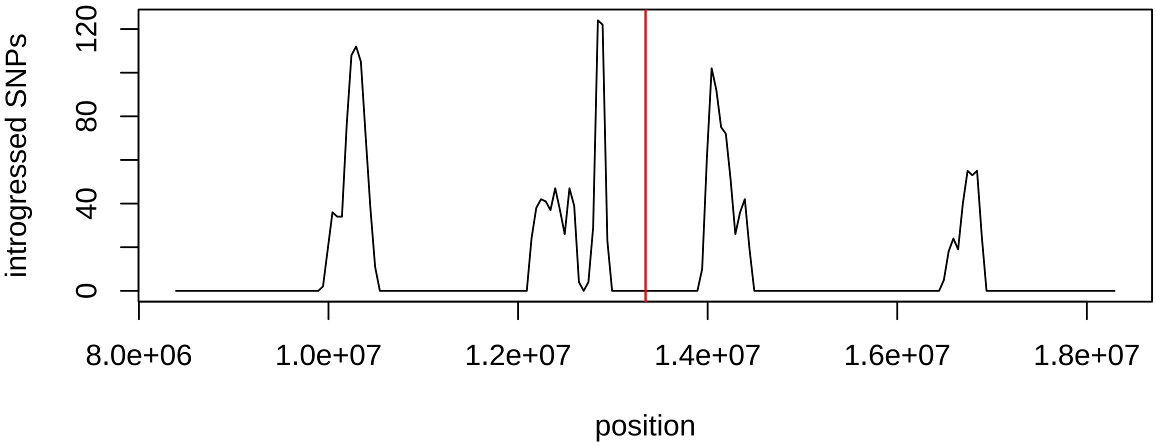
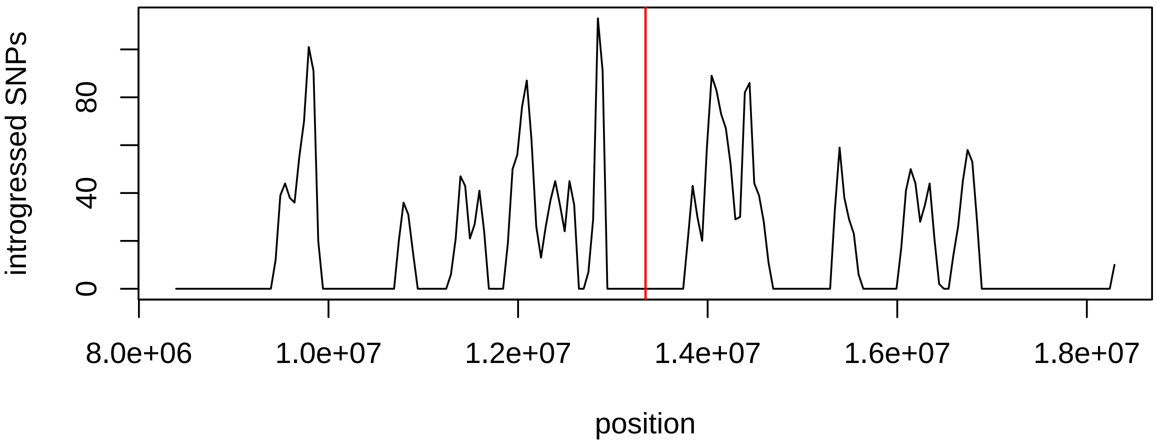


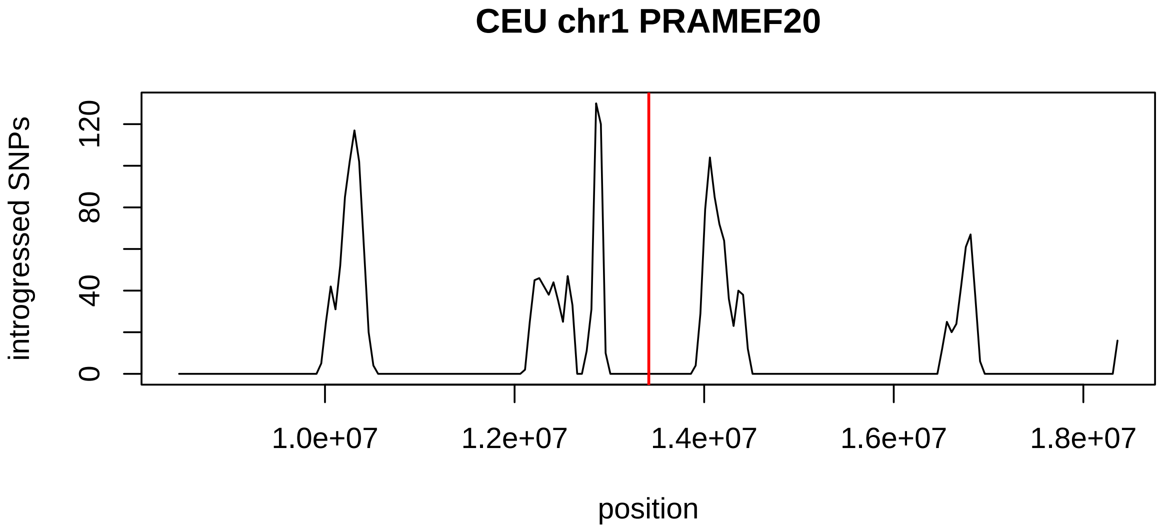
CHB chr11 PGA3

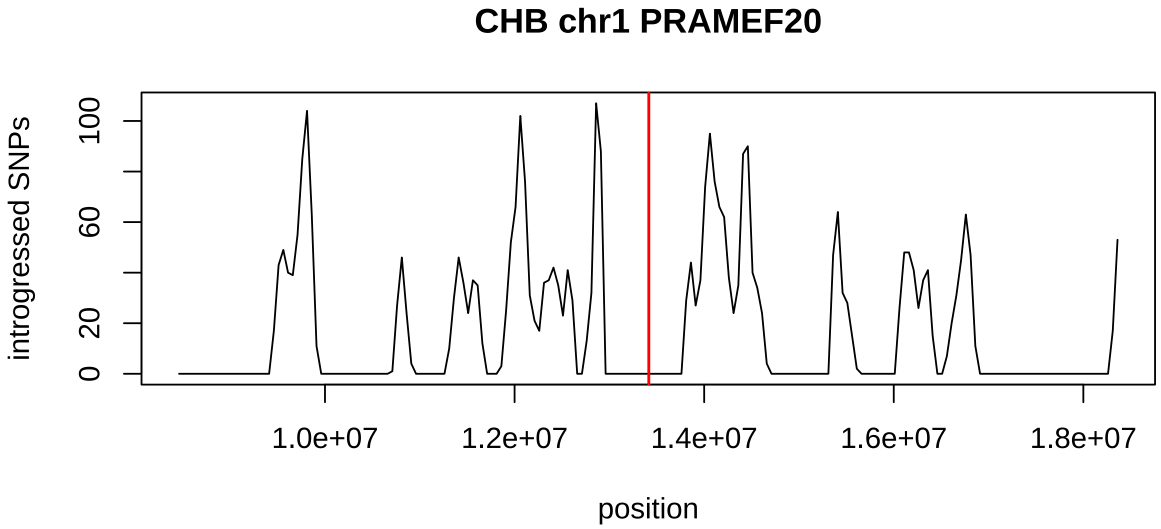


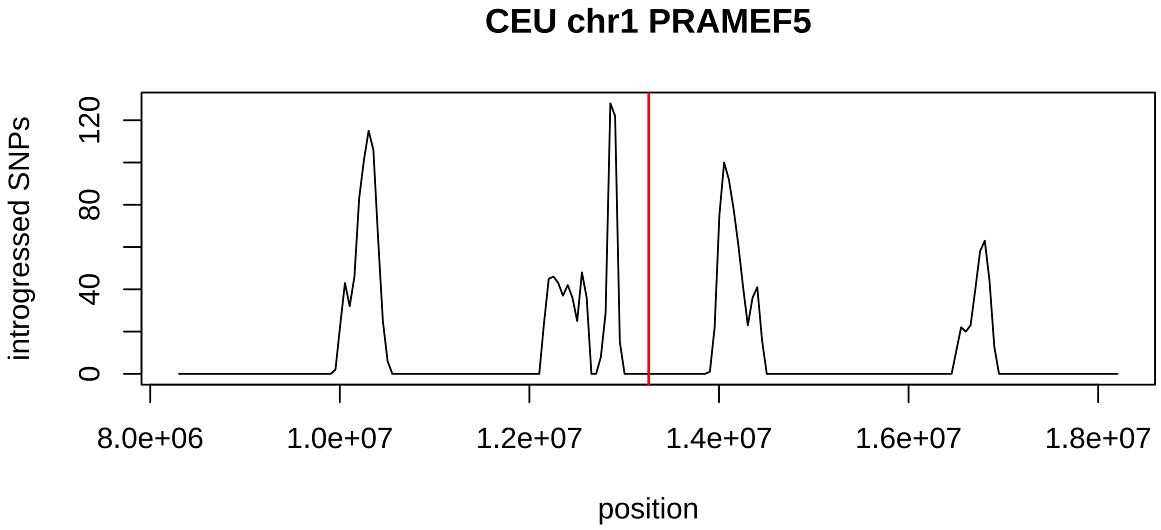
CEU chr1 PRAMEF14



CHB chr1 PRAMEF14


CEU chr1 PRAMEF20
introgressed SNPs
0
40
80
120
1.0e+07
1.2e+07
1.4e+07
1.6e+07
1.8e+07
position


CHB chr1 PRAMEF20
introgressed SNPs
0
20
60
100
1.0e+07
1.2e+07
1.4e+07
1.6e+07
1.8e+07
position



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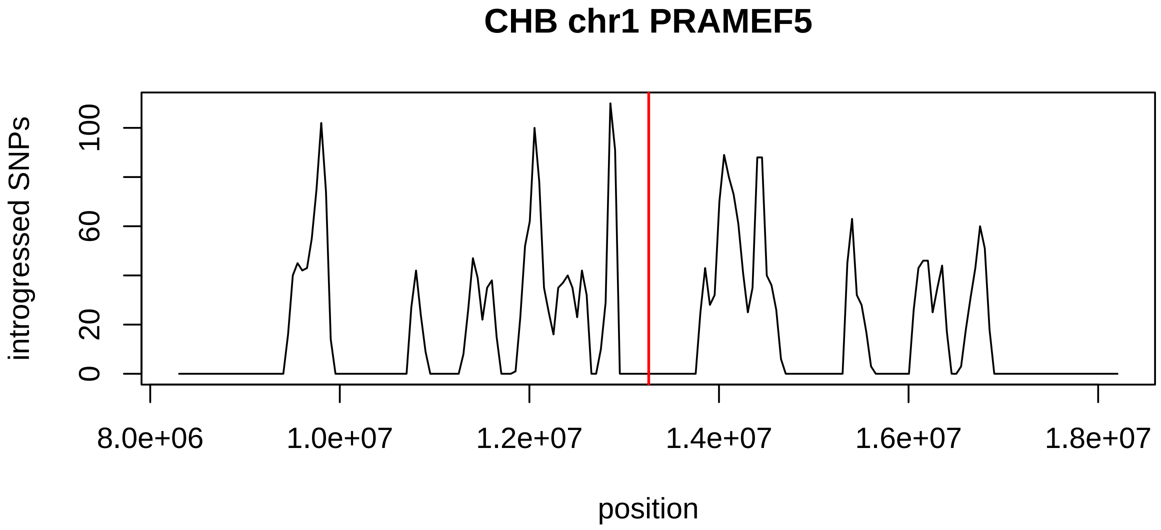

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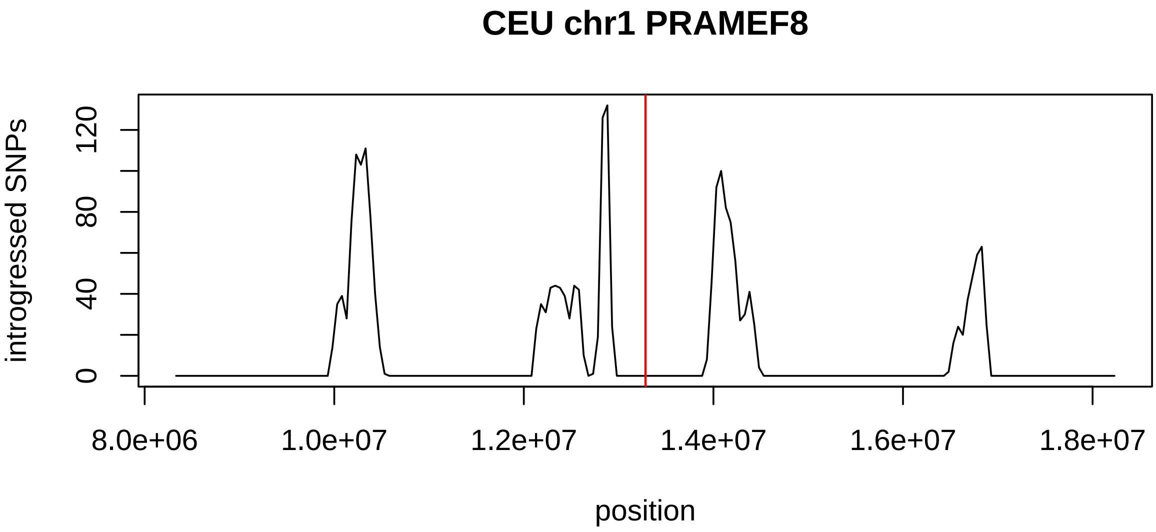
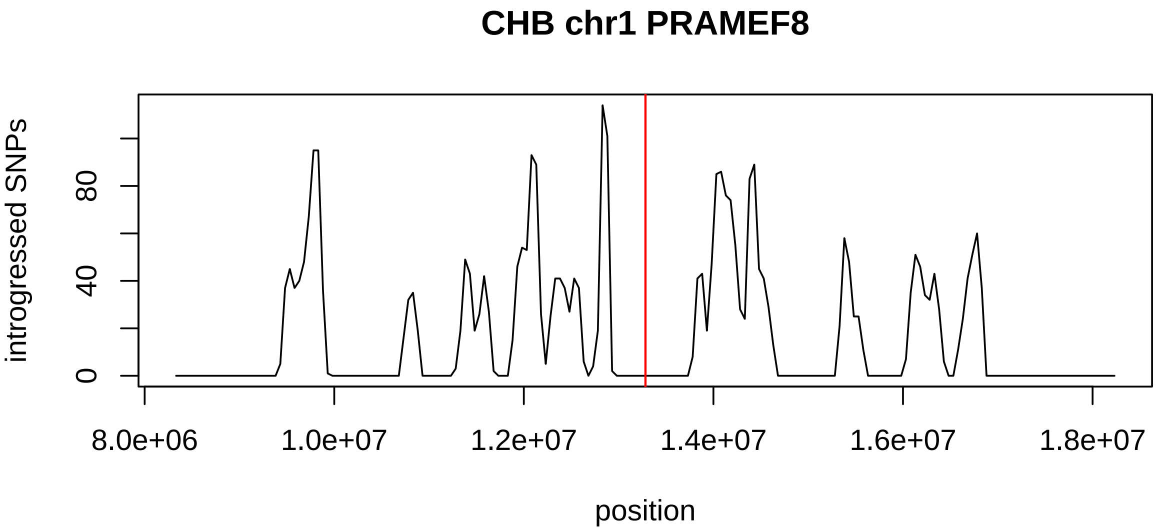
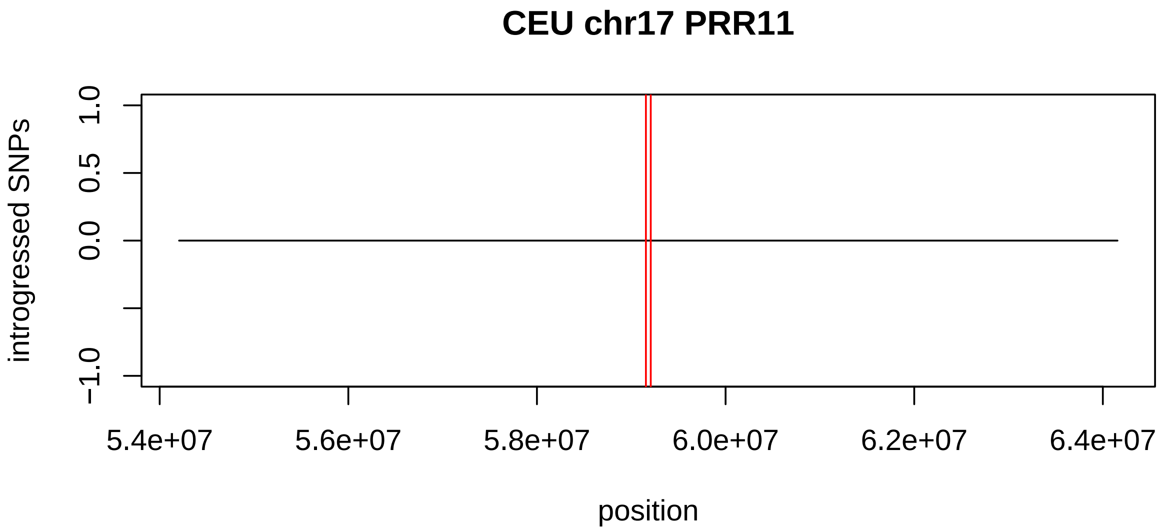

CEU chr1 PRAMEF8


CHB chr1 PRAMEF8


CEU chr17 PRR11
introgressed SNPs
1.0
0.5
0.0
−1.0
5.4e+07
5.6e+07
5.8e+07
6.0e+07
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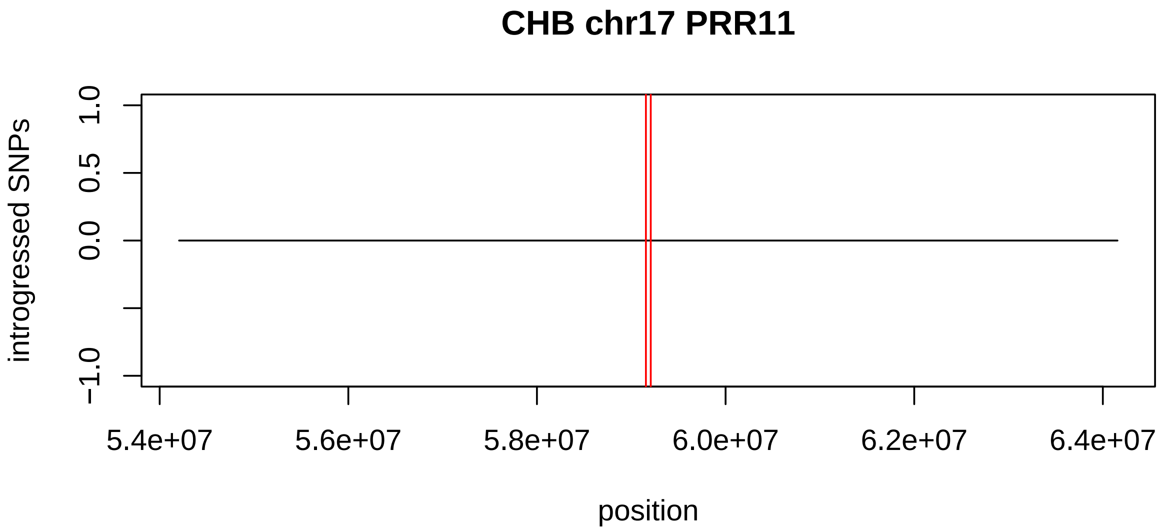
6.4e+07
position


CHB chr17 PRR11
introgressed SNPs
1.0
0.5
0.0
−1.0
5.4e+07
5.6e+07
5.8e+07
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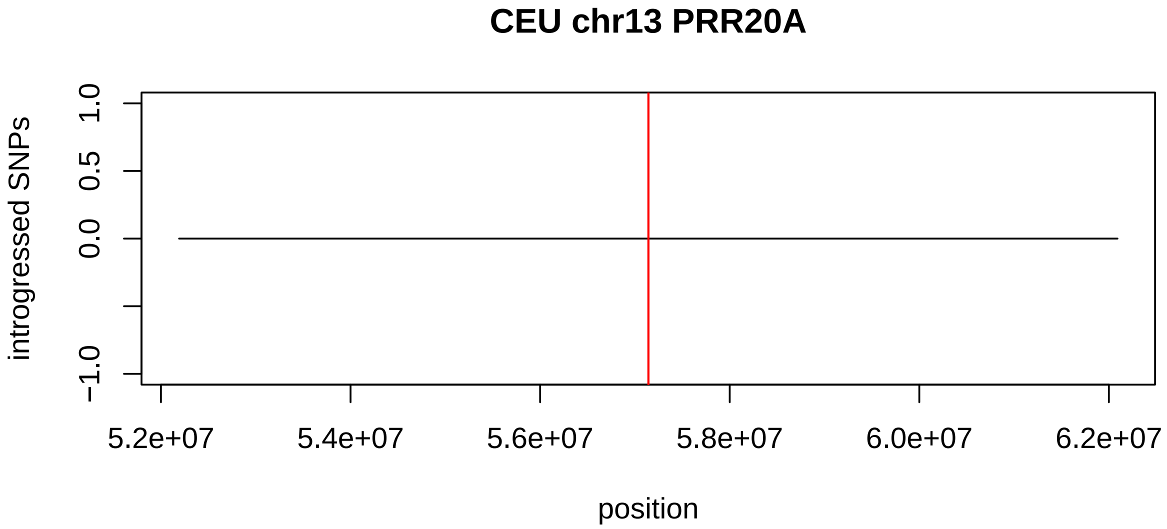
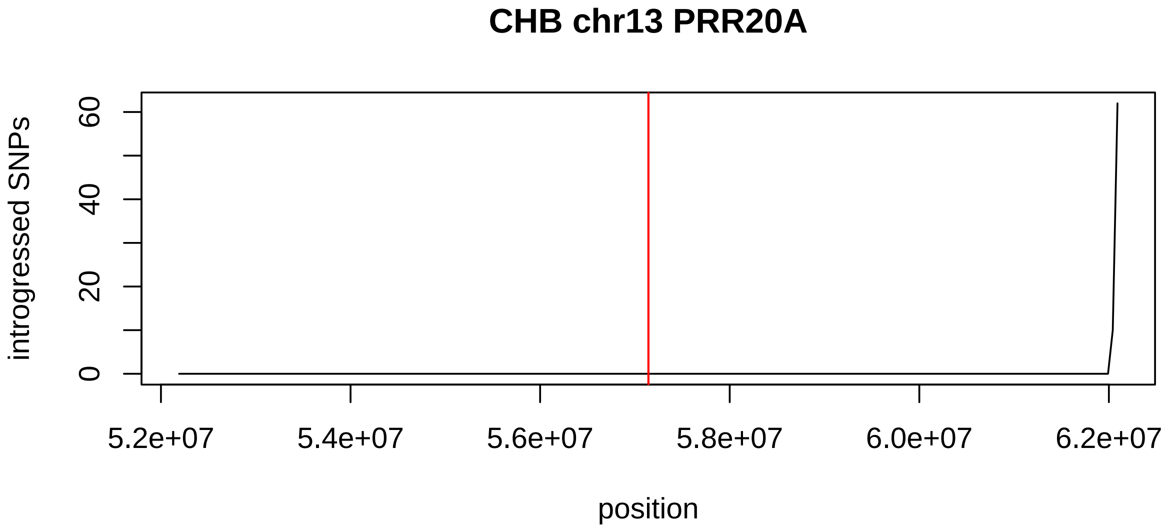
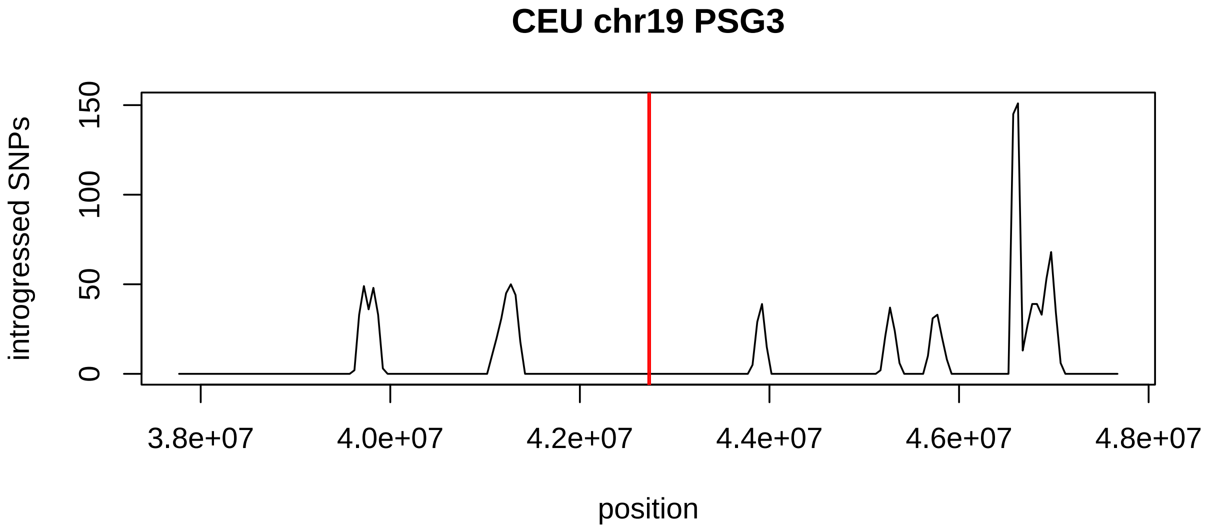
6.2e+07
6.4e+07
position



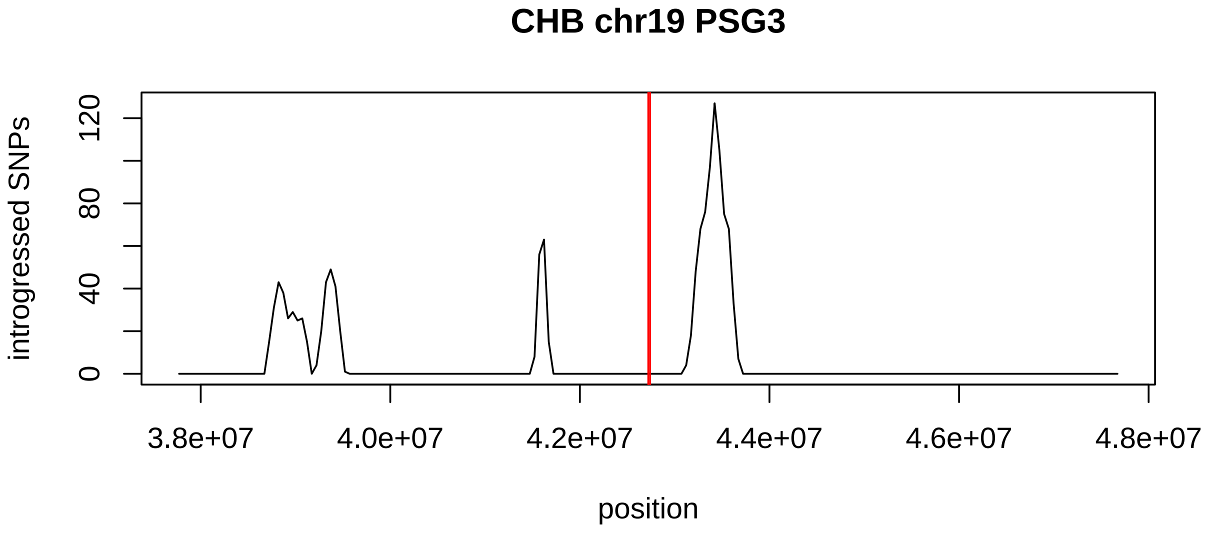
CEU chr13 PRR20A



CHB chr13 PRR20A

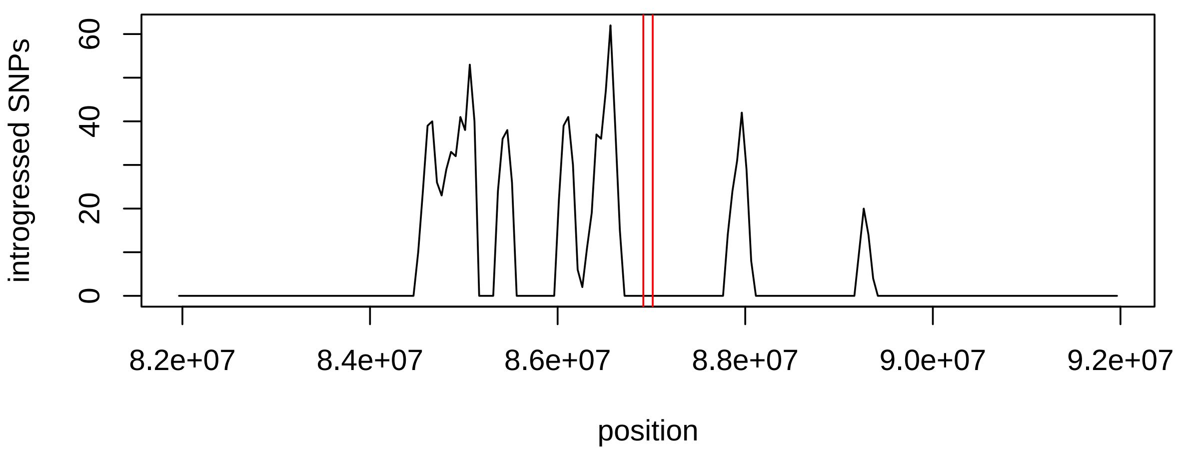


CEU chr19 PSG3

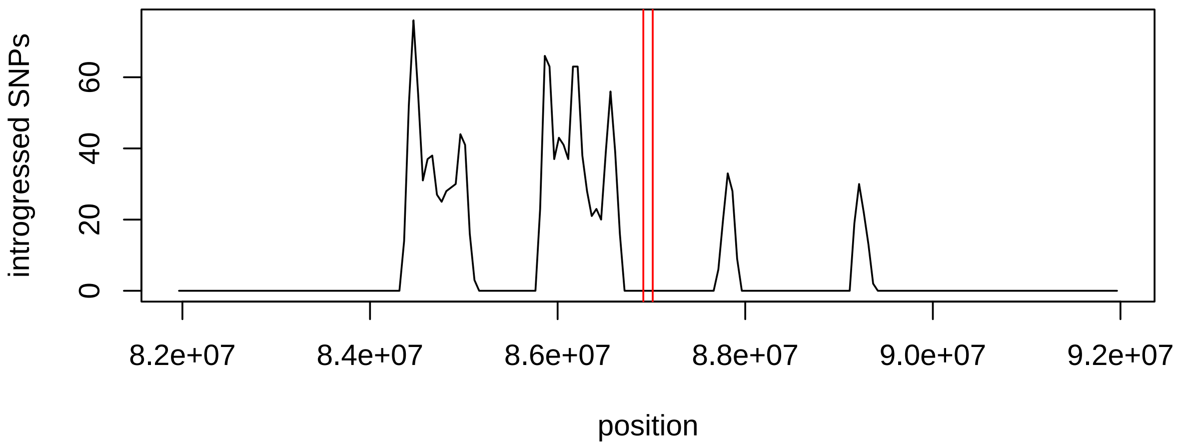


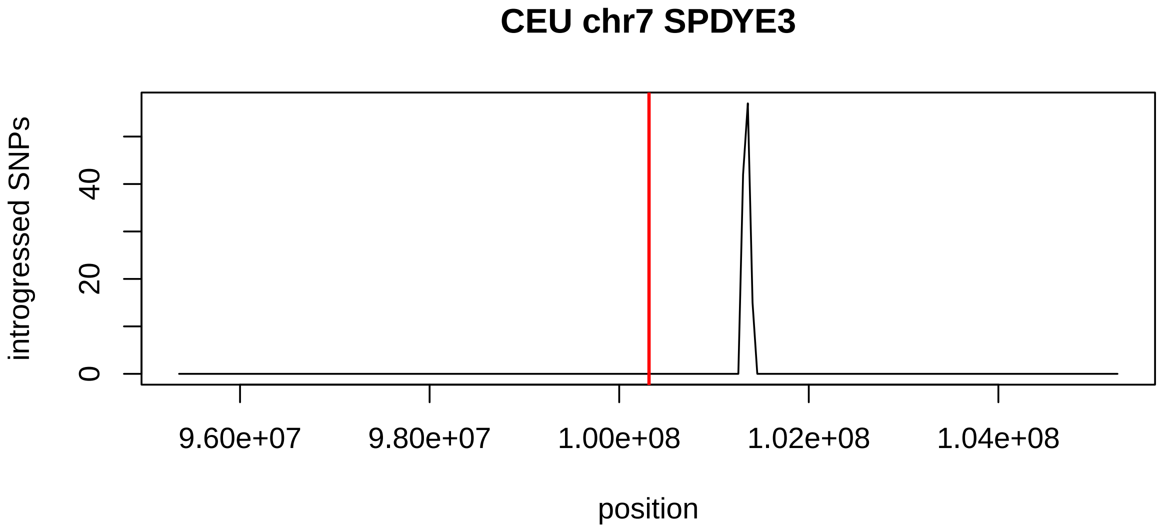
CHB chr19 PSG3

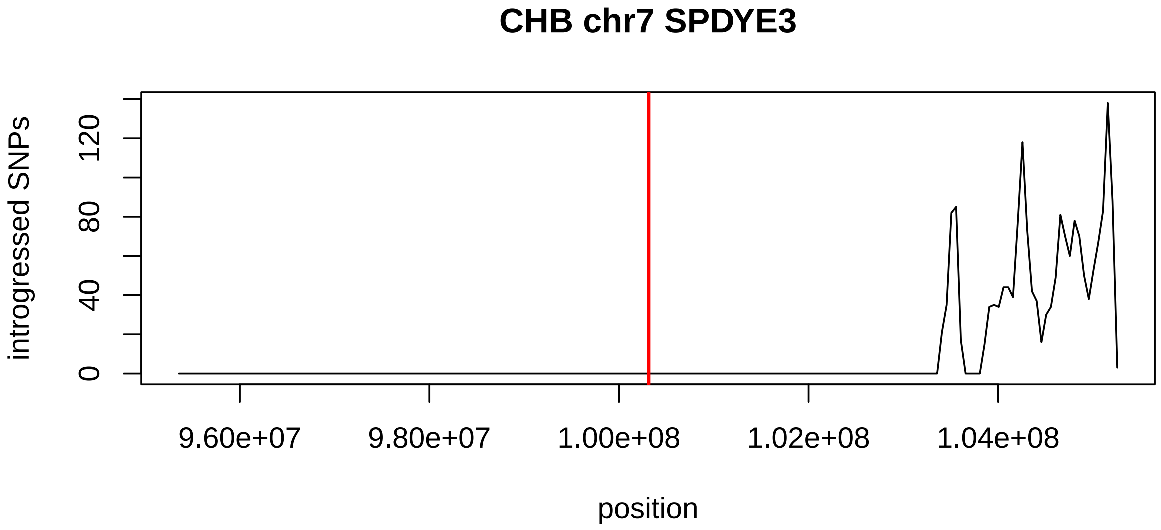
CEU chr2 RGPD1

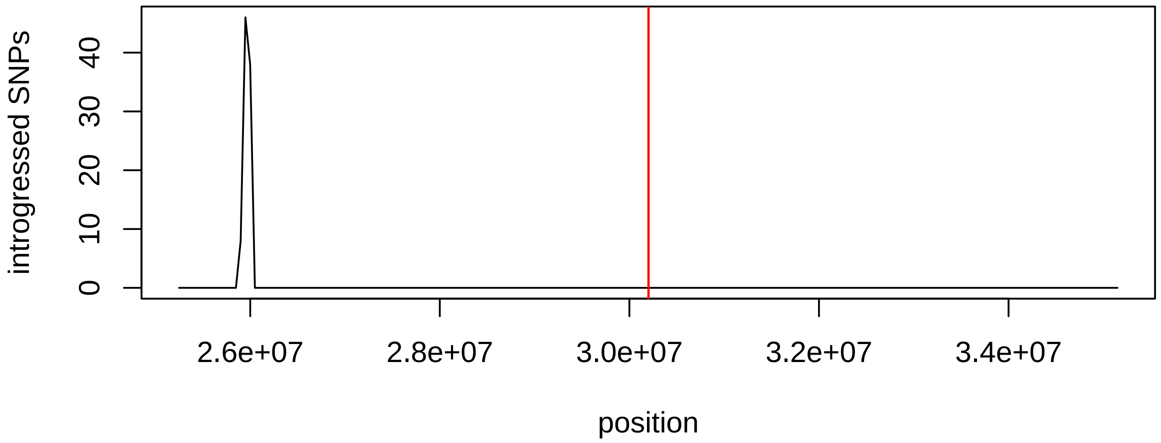


CHB chr2 RGPD1

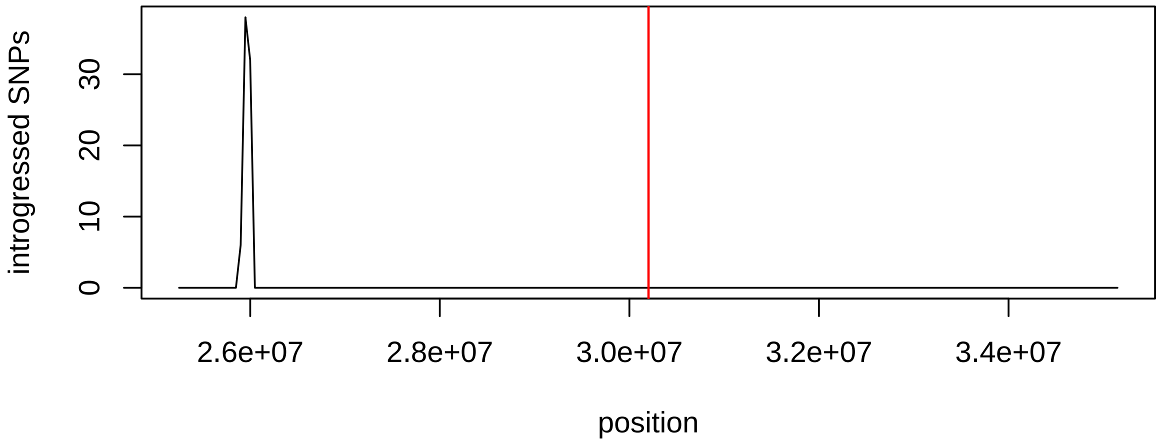



CEU chr7 SPDYE3
introgressed SNPs
0
20
40
9.60e+07
9.80e+07
1.00e+08
1.02e+08
1.04e+08
position

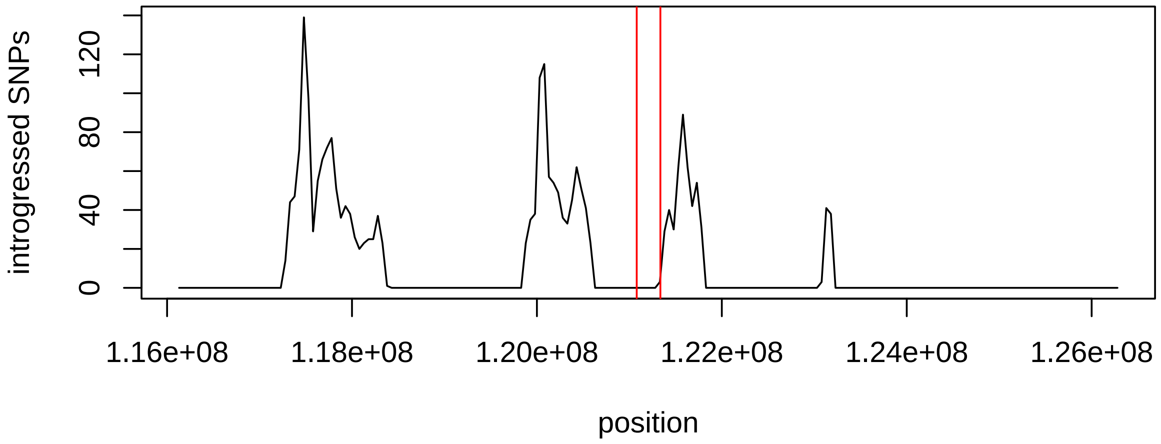

CHB chr7 SPDYE3
introgressed SNPs
0
40
80
120
9.60e+07
9.80e+07
1.00e+08
1.02e+08
1.04e+08
position



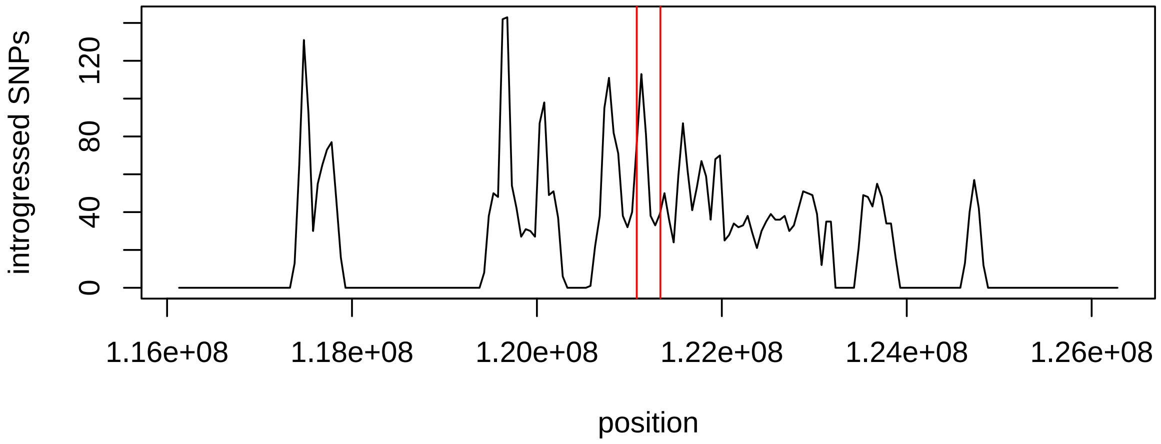
CEU chr16 SULT1A3



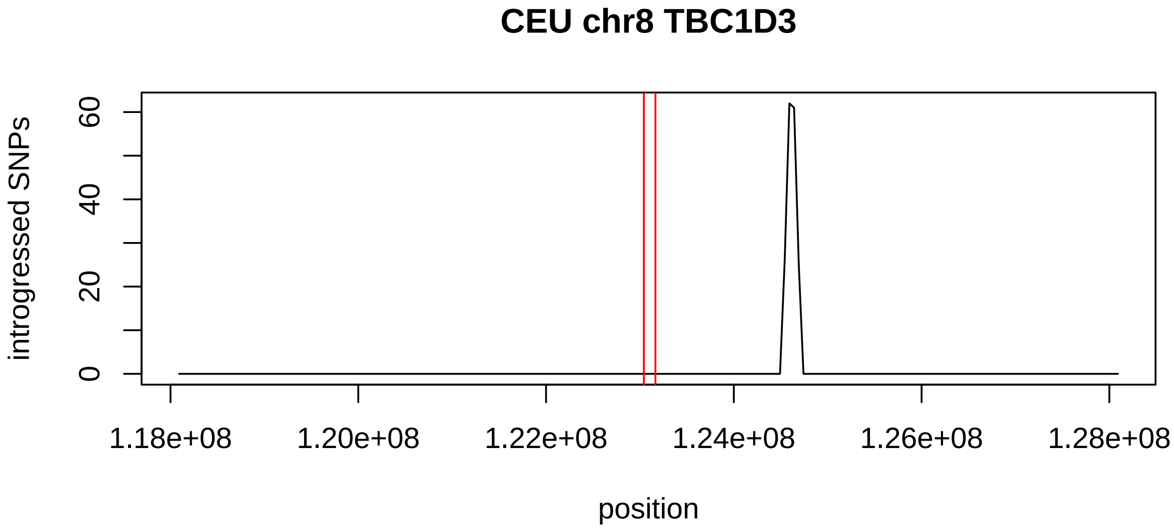
CHB chr16 SULT1A3

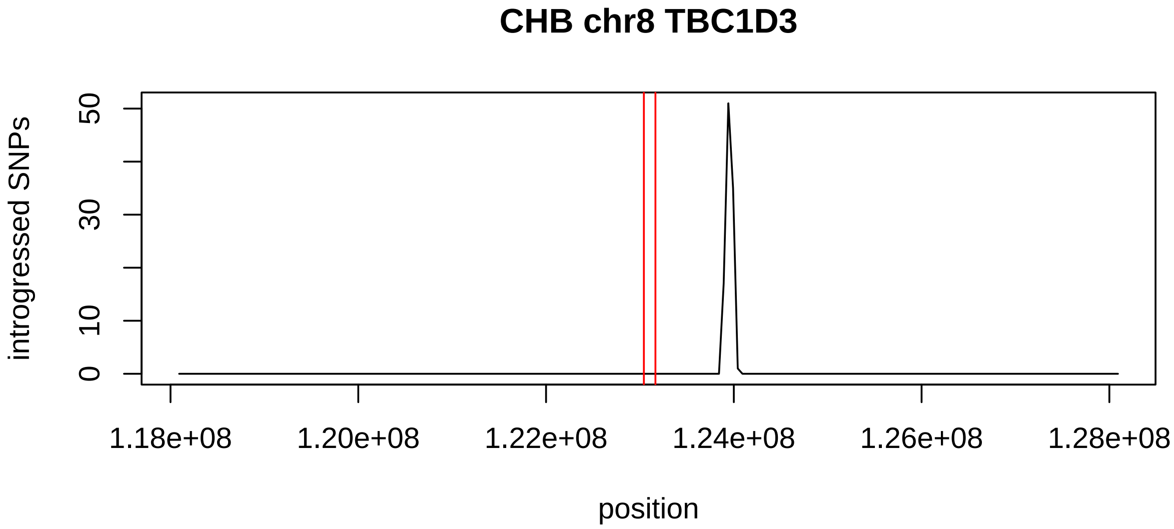


CEU chr6 TBC1D3



CHB chr6 TBC1D3


CEU chr8 TBC1D3
introgressed SNPs
0
20
40
60
1.18e+08
1.20e+08
1.22e+08
1.24e+08
1.26e+08
1.28e+08
position


CHB chr8 TBC1D3
introgressed SNPs
0
10
30
50
1.18e+08
1.20e+08
1.22e+08
1.24e+08
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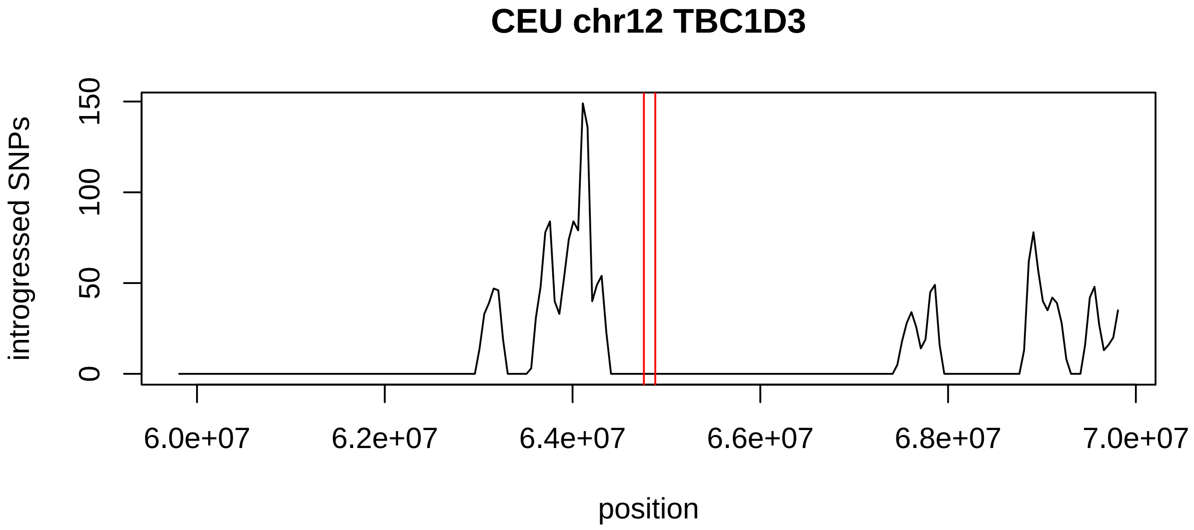
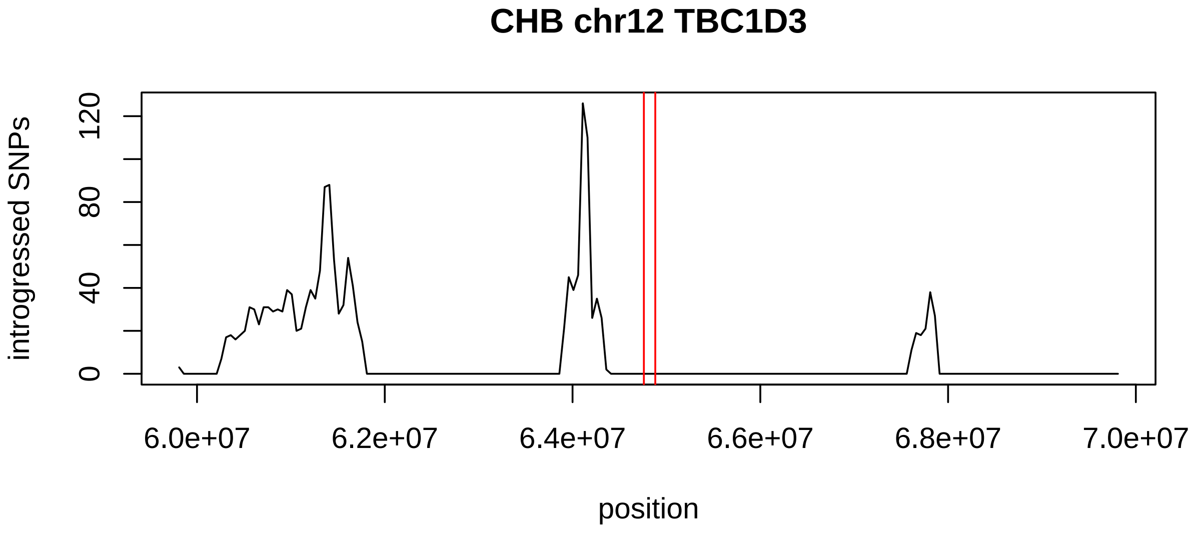
1.28e+08
position

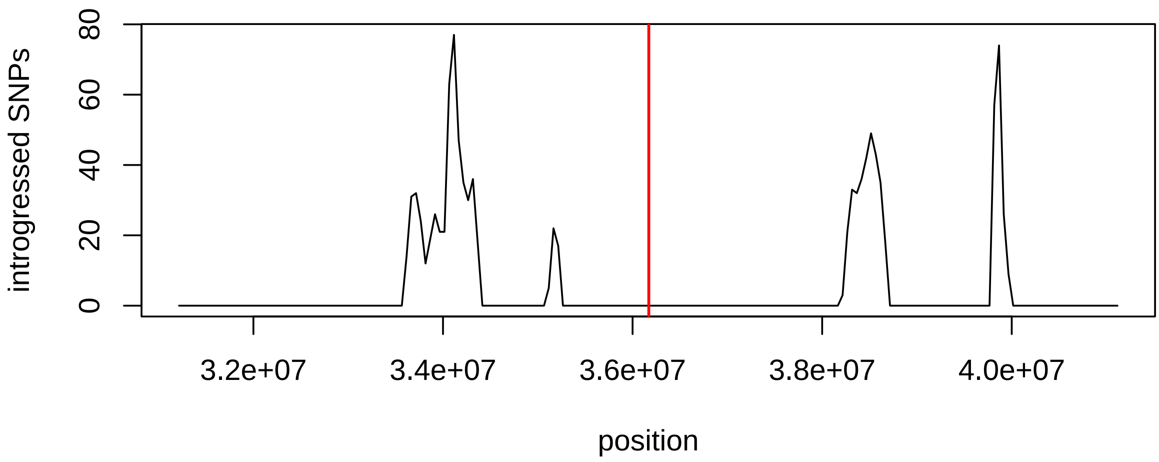


CEU chr12 TBC1D3

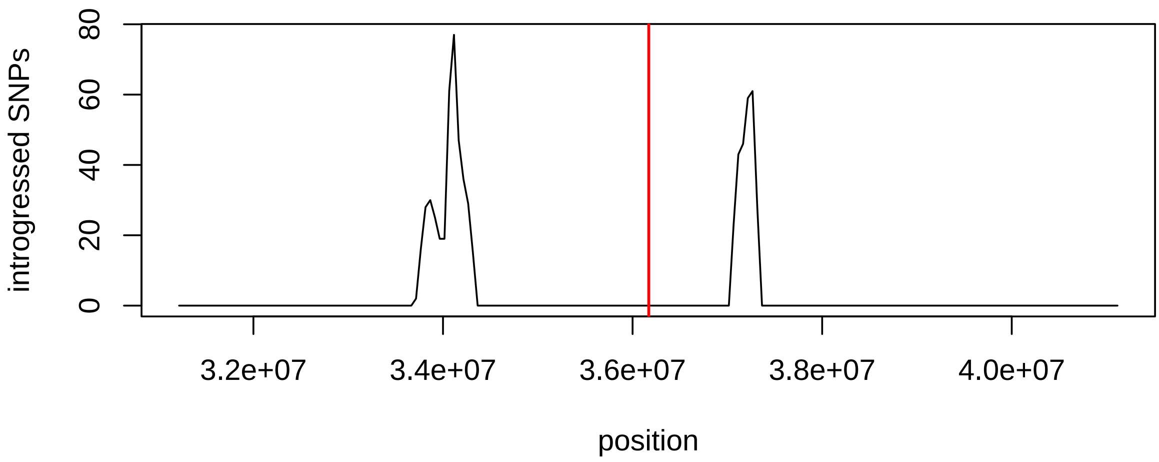


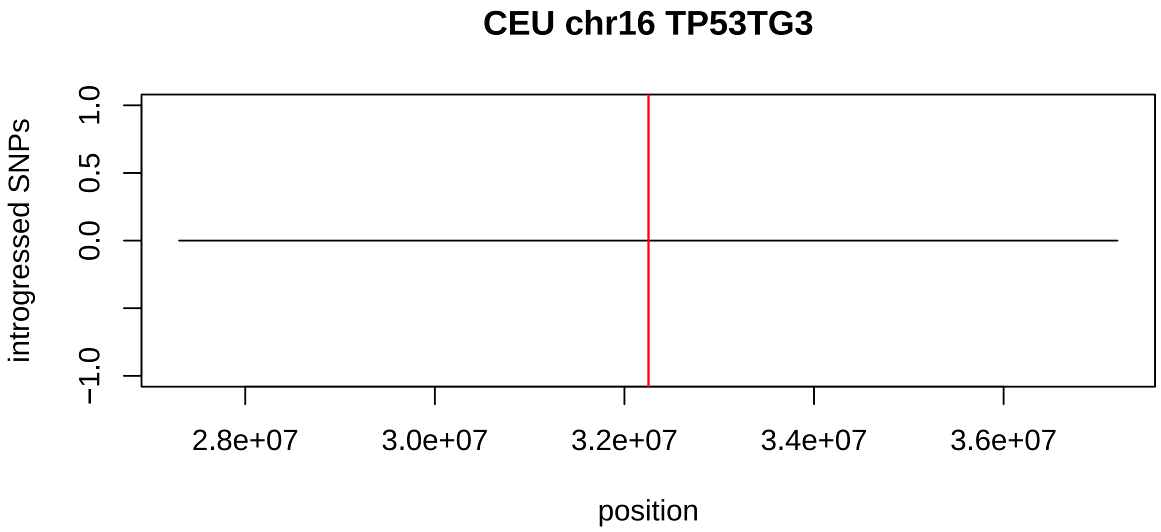
CHB chr12 TBC1D3

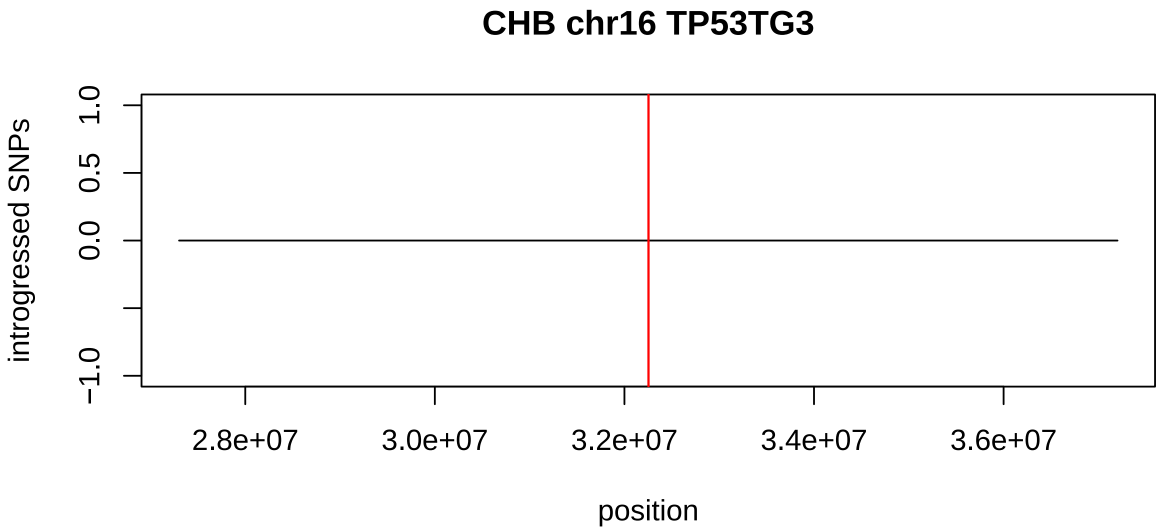
CEU chr17 TBC1D3

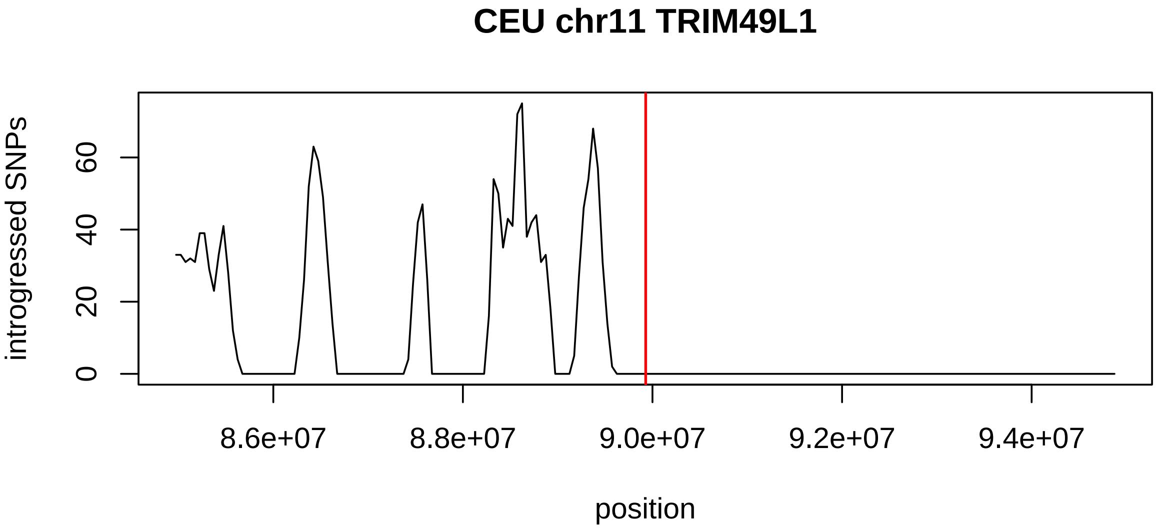


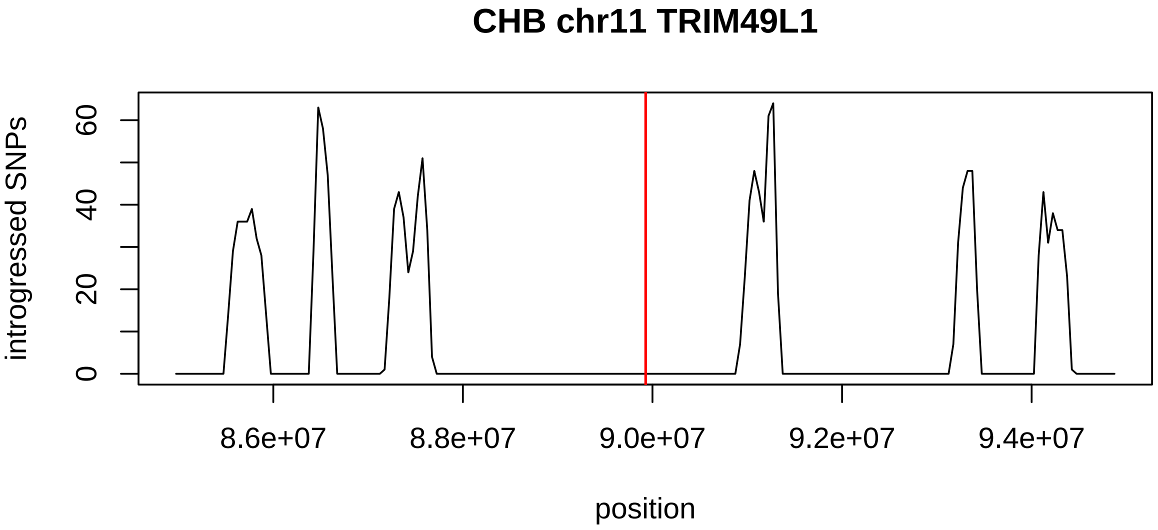
CHB chr17 TBC1D3

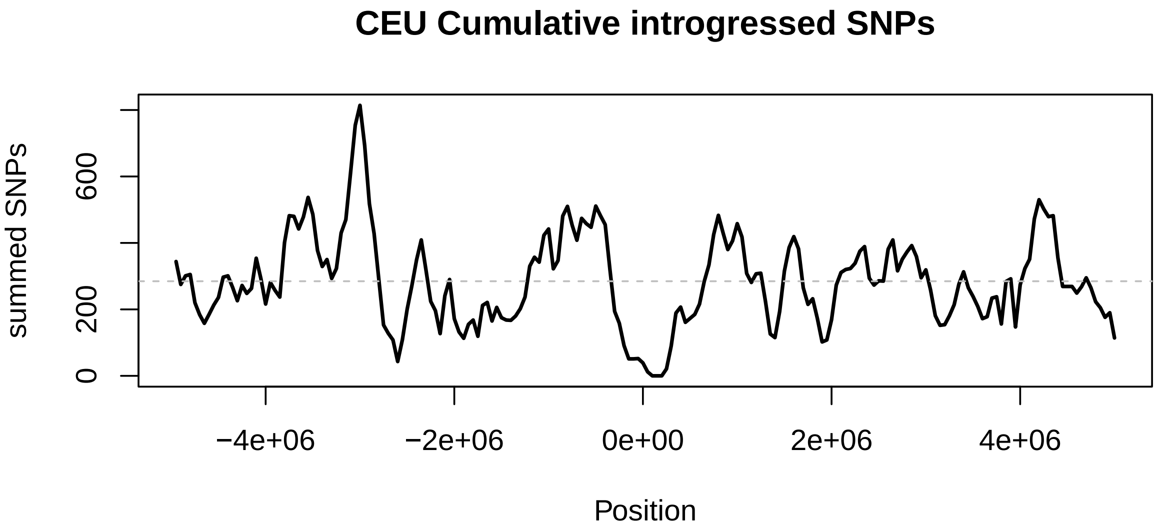


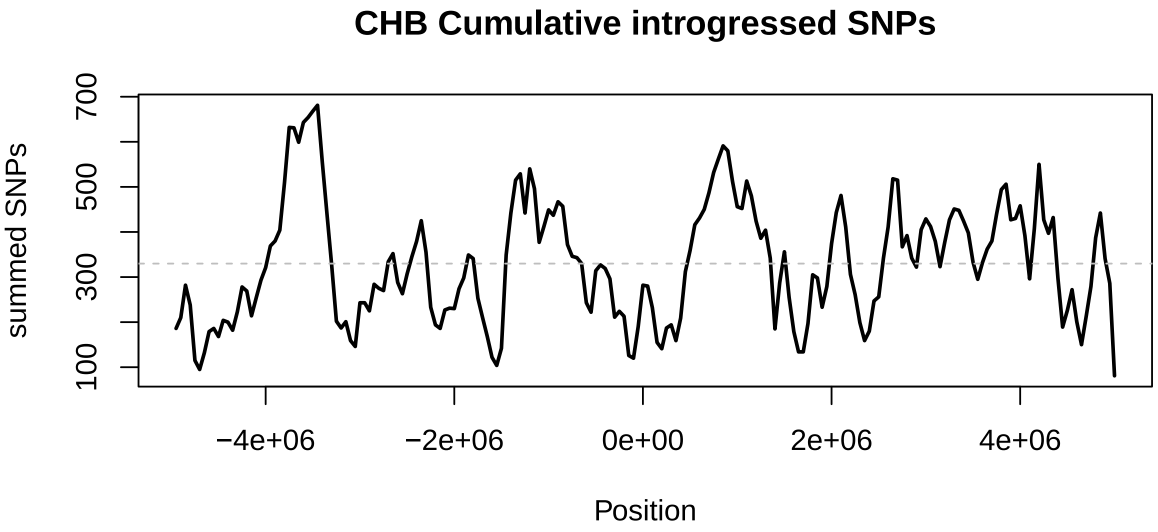

CEU chr16 TP53TG3
introgressed SNPs
−1.0
0.0
0.5
1.0
2.8e+07
3.0e+07
3.2e+07
3.4e+07
3.6e+07
position


CHB chr16 TP53TG3
introgressed SNPs
−1.0
0.0
0.5
1.0
2.8e+07
3.0e+07
3.2e+07
3.4e+07
3.6e+07
position


CEU chr11 TRIM49L1
introgressed SNPs
0
20
40
60
8.6e+07
8.8e+07
9.0e+07
9.2e+07
9.4e+07
position


CHB chr11 TRIM49L1
introgressed SNPs
0
20
40
60
8.6e+07
8.8e+07
9.0e+07
9.2e+07
9.4e+07
position


CEU Cumulative introgressed SNPs


CHB Cumulative introgressed SNPs