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Supporting Online Material for

The Genetic Architecture of Maize Flowering Time

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S1. Materials and Methods:

Germplasm: The germplasm selection process and the design of the population are elaborated in (S*1*). B73 was chosen as the reference line because it is an important founder line of the US maize crop, and it is currently being sequenced. We crossed 25 other lines that maximized world-wide diversity of maize on the basis of prior SSR marker surveys (S*2*). B73 was used as the maternal plant, and F1s were self-fertilized for 5 generations without intentional selection to make the lines. Each line descends from a unique F2 generation plant and also a single F5 generation plant, which was self-fertilized one generation and then sib-mated for one to three generations to create sufficient seed supplies to phenotype in replicated experiments.

Genotyping: The details of the genotyping can be found in (S*3*). Briefly, 7000 lines were scored for 1200 SNP markers. The markers were chosen to maximize information relative to B73. While this resulted in a segregating marker every 1.3cM on average within each family, there were substantial deviations in coverage between families and recombination was quite different between families (S*3*). This mosaic of genotyping results in limitations on the resolution of some of the QTL positions at this time. Each family is represented by 200 lines in the NAM panel, resulting in a final set of 5,000 mapping lines in total.

Genotyping was conducted to score polymorphisms at *Vgt1*and *ZmRap2.7* across the founder lines and lines with recombination events between *Vgt1* and *Vgt2*. Regions surrounding *Vgt1*, where *(S4)* detected SNPs in a set of 95 inbred lines, as well as the entire *ZmRap2.7* gene were PCR amplified and Sanger sequenced in the founders. In addition, a diverse association mapping panel of 282 lines (S5) was scored for variation at *Vgt1* and *ZmRap2.7* with sequencing and indel markers on an agarose gel. The associated marker data are presented in Table S5.

Primers:
Vgt1: GTACCAGCTCCCTCTGCTC; TGGAATGGATGTGAAGTGAG
Best *Rap2.7* Association Primers for sequencing: CCTAGGTGAGCAAGAGCAGA; CTCTGCCATTGCATTTGAT
Rap2.7 Insertion for Gel Scoring: CTAAAGGTCCTTGGAACAGACAGG; GAACTGAAGAAAACCAAGGCAAG

Phenotyping: The 5000 NAM lines were evaluated phenotypically in eight summer environments: Aurora, NY; Clayton, NC; Columbia, MO; and Urbana, IL across two years. Each experiment also included 200 randomly chosen intermated B73 x Mo17 (IBM) RILs plus an association mapping panel of 281 diverse inbred lines representing the global diversity of public maize lines (S*5*). Within each environment, one replicate of each of these 5481 unique lines was grown, but B73 and one other parental founder line were included in each sub-block of 22 plots to permit estimation of within-environment block effects and error variances. Experimental units consisted of plots of 12-25 plants each (depending on the environment), and randomized designs were used. DA and DS were measured as the number of days from planting to the initiation of pollen shed or silk emergence for half the plants within a plot ASI was computed as the difference between DS and DA.

Statistical Analyses:

Field Spatial Correction: Within each environment, mixed linear models were fit including family and line within family genotypic effects; effects of blocks, rows, and columns of the field designs; and spatially correlated residuals (S*6*). Likelihood ratio tests were used to determine which factors explained significant amounts of variation and were to be retained in the model. A combined mixed model across environments was then fitted, using the components of each individual environment model, adding family- and genotype-by-environment interaction terms and permitting heterogeneous spatially correlated error variance structures across environments. In addition, unique genetic variance components were fit for each of the 25 NAM cross families, the IBM, and the association panel. Best linear unbiased predictors (BLUPs) for each line were predicted from the combined analysis model with ASREML version 2.0 software (S*7*),

QTL Mapping approaches: Two approaches, composite interval mapping (CIM) and stepwise regression (SR) (*S8*), were used for QTL mapping. In SR, markers are added sequentially to the model, but can then be dropped if they no longer improve the fit of the model. CIM, using the markers from SR as cofactors to control for background genetic variance, uses maximum likelihood to test putative QTL and estimate their effects at regular intervals along the genome rather than testing only at marker positions. Inclusive CIM (ICIM; *S9*) is a variant of CIM.

In addition, we either mapped QTL on one population at a time or all the populations together. Mapping using all populations at once is referred to as joint mapping. In single population mapping, information on position of QTL is not shared between populations, while joint mapping uses QTL signal across all populations to identify QTL and position the QTL. Single population QTL mapping will not position QTL inaccurately, but it has far less power and precision then joint mapping. Joint mapping is most powerful when QTL are shared between populations.

Marker imputation: Since stepwise regression cannot use individuals with missing marker data, the first step in the analysis was to impute missing data. Since the genetic map is reasonably dense, the probability of double recombinants between any pair of adjacent markers is low. As a result, any interval flanked by markers originating from the same parent is assumed to have originated from that parent. To build the data set, markers within any interval whose nearest known flanking markers were both from B73 were assigned a value of 0. If the flanking markers both came from the non-B73 parent, markers in the intervals were assigned a value of 2. Markers in intervals flanked by a different parent on either side, i.e. recombinant intervals, were assigned a value of 1. Markers in intervals flanked by heterozygotes were assigned a value of 1. Markers in intervals flanked by a heterozygote and a homozygote were assigned a value of 0.5 or 1.5, depending on whether the homozygote carried B73 or non-B73 alleles.

Single Family Step-wise regression: SR was performed on an individual family by fitting markers as covariates rather than as classification variables. The analysis was performed using SAS GLMSELECT or as part of the ICIM software. Markers were allowed to enter the model until the next marker added had a p-value greater than .001, at which point the analysis ended. At each step, markers were allowed to stay in the model as long as their marginal p-values were still less than .001. The significance level of .001 was chosen based on permutation analysis (S*10*).

Joint Stepwise regression: QTL were mapped in combined analysis of all 25 NAM families by joint stepwise regression of flowering time trait BLUPs on markers. In the joint stepwise regression, a family main effect was fit first, and then marker effects nested within families were selected to enter or leave the model based on the p-value calculated for the marginal F-test of that term. An appropriate p-value cutoff was determined to be 0.0001 from permutation tests (S*10*). After the model was fit with stepwise regression, each marker was dropped from the model one at a time and a single best marker was refit. This step checks the fit of each marker using the remaining QTL as background and improves the overall fit of the model to the data.

Inclusive composite interval mapping: QTL were mapped in individual NAM families using inclusive composite interval mapping (ICIM, *S9*), a modification of composite interval mapping (CIM). The method first determined a set of cofactors using stepwise regression to fit individual markers. It then scanned the entire genome at 0.1 cM intervals using maximum likelihood to test putative QTL at each point.

Joint inclusive composite interval mapping: We extended inclusive composite interval mapping (ICIM) to multiple population analysis and proposed a new statistical method. Two steps are included. In the first step, population and population by marker interactions were treated as fixed effects. Each marker has 26 levels (B73 and the other 25) in the consensus map. These parameters were included in a multiple regression model, that is,

$$\mathbf{Y} = b_0 + \boldsymbol{\alpha}\mathbf{u} + \mathbf{X}\boldsymbol{\beta} + \boldsymbol{\varepsilon} \qquad (1)$$

where $\boldsymbol{Y}$ is the vector of phenotypic values, b_0 is the intercept, $\mathbf{u}^T=(u_1, u_2, \ldots, u_{25})$ is the effect vector indicating the cross effect of each founder with the common parent B73; $\boldsymbol{\alpha}$ is the $n \times 25$ incidence matrix relating each family mean u_f (f=1, 2, …, 26) to $\boldsymbol{Y}$; $\boldsymbol{\beta}$ is the $26m \times 1$ effect vector of the $n \times 26m$ incidence matrix $\boldsymbol{X}$; m is the number of markers; n is the total number of families; and ε is the vector of residual variance. To avoid over-fitting the model, we used stepwise regression to estimate the parameters in model (1). If the regression variable was not selected in the model, the corresponding coefficient was set to 0. On the basis of the coefficient estimation, one dimensional scanning was conducted in the second step. In total, the whole genome with the LOD threshold was set to 12.26 to guard against more than 2 false positive linkage results, i.e., genome-wise error rate GWER(2)=12.26 (S*11*).

Significant allele effects: Once significant loci were identified in the joint analysis, significant alleles were determined with a t-test comparison of their parental means versus the B73 allele. We used α=0.05, which from an evaluation of the *P*-value distributions for all alleles at all loci is approximately an 8% FDR. We observed an elevated frequency of alleles with *P*-values between 0.05 and 0.125, so this is likely still undercalling the total number of lines with significant effects. The $\alpha=0.05$ threshold was then used to determine the proportion of families with shared QTL, the number of significant QTL per family, and the significant alleles to predict the parental phenotypes.

QTL×Environment Interactions: QTL-by-environment (QxE) interactions were investigated by fitting the final QTL model based on the line BLUPs computed across all eight environments to a data set containing the BLUPs for each line from each environment analyzed separately. This model was augmented by the inclusion of environment, population-by-environment, and QTL by- environment effects for each QTL. Each QxE interaction was tested based on this general linear model. Any QxE interactions were then included in a similar mixed model that treated both QTL and QxE effects as random. Variance components for each QTL main effect and QxE interaction were estimated from the mixed model in ASREML version 2.0.

Epistasis: Epistasis was tested in two ways: within families separately and in a joint analysis combined across families. To test for epistatic interaction within individual families, we first selected an additive model by stepwise regression within each family separately (using $P < 0.001$ as a significance threshold). Then, we tested all possible pairwise marker interactions to identify the epistatic interaction with smallest p-value when combined with the selected additive model. Finally, permutation tests were used to test the null hypothesis of no epistasis for each family. Permuted data sets were formed by permuting residuals from the main effects only model and adding them back to the predicted values. If the minimum p-value from the original data was smaller than the fifth percentile of minimum p-values from 100 permutation analyses, we declared the presence of at least one significant epistatic interaction within that family.

To test for epistatic interactions across the entire NAM panel, we tested every possible marker pair for interactions (two main effects and one interaction nested within family) in a combined analysis across families and potentially significant interactions were identified as those exceeding the 5% false-discovery rate threshold estimated with the Benjamini-Hochberg procedure (S*12*). Selected marker pairs were then combined with the model developed from the NAM joint linkage additive QTL analysis. The epistatic interaction was deemed significant across families if $P < 0.0001$ in the combined model.

Pleiotropy: A central issue in evaluating pleiotropy in linkage populations is determining whether correlated effects are the product of linked loci or the same gene. So rather than focusing just on the co-localization of the QTL, we used correlations of effects estimates at each locus to evidence that the same QTL were responsible. With 25 families, we could correlate the effects at each locus for each trait against one another. Those with significantly correlated effects are likely to have the same genes and allele series that are producing the correlation. To remove the issues involved with fitting the QTL positions and estimating effects simultaneously, we produced effects estimates for all three traits (DS, DA, ASI) with the loci determined for each trait ($3\times3=9$ sets of estimates total). Then for each locus and each trait comparison, we calculated Pearson correlation between the effect estimates. Counts of significant correlation were determined with $P=0.05$, however, the significant loci were frequently much more significant. From this method, for every pair of traits there are two sets of estimates of proportion of shared pleiotropic loci. For the DS-DA and DS-ASI the two proportions were virtually identical, for DA-ASI there is a slight spread from 14% versus 21%.

Population Structure: For each locus we correlated the effect estimates with *Q* matrix results from the program STRUCTURE, as reported (S*5*). These estimates reflect the relationships between tropical and temperate non-stiff stalks well, but they do a poor job in recognizing the Northern Flint-derived materials that are a small but important proportion of our germplasm. For these correlations, we used a modified Q vector representing tropicalness, so that the Northern lines (Il14H, P39, and Ms71) were set to values of -1; i.e., tropical lines had values near 1; mixed origin lines between 0 and 1, temperate lines had values near 0, and Northern lines were -1. Then for each trait and locus, a Pearson correlation between this population structure vector and the effect estimates for each QTL was calculated.

Table S1. Heritabilities for flowering Traits

Table S2. Summary Joint Linkage Stepwise Model and GxE ASREML Analysis for Days to Anthesis

Table S3. Summary Joint Linkage Stepwise Model and GxE ASREML Analysis for Days to Anthesis

Table S4. Summary Joint Linkage Stepwise Model and GxE ASREML Analysis for Days to Anthesis

Table S5. Associating polymorphisms at Vgt1 and Rap2.7 for the maize 282 association panel.

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Supporting Table 1. Heritabilities for flowering Traits

	ASI	**Days to Anthesis**	**Days to Silk**
Heritability of line BLUPs across all crosses (excluding association panel):			
Heritability of line BLUPs	0.78	0.94	0.94
Heritability of line BLUPs within each cross:			
B73×B97	0.64	0.77	0.77
B73×CML103	0.61	0.78	0.73
B73×CML228	0.68	0.90	0.89
B73×CML247	0.75	0.90	0.89
B73×CML277	0.71	0.92	0.91
B73×CML322	0.72	0.84	0.83
B73×CML333	0.61	0.84	0.82
B73×CML52	0.68	0.88	0.89
B73×CML69	0.67	0.82	0.80
B73×Hp301	0.67	0.83	0.85
B73×Il14H	0.61	0.84	0.86
B73×Ki11	0.69	0.90	0.91
B73×Ki3	0.67	0.84	0.85
B73×Ky21	0.66	0.75	0.81
B73×M162W	0.69	0.82	0.83
B73×M37W	0.65	0.83	0.83
B73×Mo17 (IBM)	0.67	0.84	0.84
B73×Mo18W	0.81	0.88	0.90
B73×MS71	0.63	0.70	0.76
B73×NC350	0.71	0.83	0.84
B73×NC358	0.58	0.75	0.79
B73×Oh43	0.71	0.71	0.81
B73×Oh7B	0.71	0.81	0.80
B73×P39	0.62	0.87	0.86
B73×Tx303	0.80	0.85	0.88
B73×Tzi8	0.81	0.87	0.89
Association Panel	0.79	0.99	0.99
Average within-cross heritability (excluding association panel)	0.68	0.83	0.84
Cross Means (averaged across RILs within a cross)			
B73×B97	1.82	74.06	75.91
B73×CML103	0.26	78.13	78.39
B73×CML228	1.52	79.92	81.88
B73×CML247	1.73	80.58	82.27
B73×CML277	1.46	80.40	81.92
B73×CML322	1.25	77.78	79.16

B73×CML333	2.19	78.20	80.40
B73×CML52	1.53	82.79	84.52
B73×CML69	1.91	79.26	81.18
B73×Hp301	1.68	74.53	76.11
B73×Il14H	1.66	71.81	73.22
B73×Ki11	2.22	79.47	82.12
B73×Ki3	1.81	77.09	79.47
B73×Ky21	1.92	76.28	78.29
B73×M162W	1.28	78.75	80.27
B73×M37W	1.65	77.54	79.20
B73×Mo17 (IBM)	2.09	72.12	74.29
B73×Mo18W	2.70	80.03	82.77
B73×MS71	1.06	71.78	72.36
B73×NC350	1.52	77.76	79.61
B73×NC358	1.53	75.57	77.01
B73×Oh43	1.77	73.79	75.00
B73×Oh7B	2.05	76.30	78.76
B73×P39	1.75	70.20	71.67
B73×Tx303	2.60	78.11	80.77
B73×Tzi8	2.61	78.47	81.39
Association Panel	1.88	78.41	80.06

Minimum and maximum RIL BLUPs across all crosses and association panel:

All Geno Max	6.65	91.20	94.57
All Geno Min	-1.53	66.05	66.83
All Geno Range	8.19	25.15	27.73

Minimum and maximum RIL BLUPs for each cross

B73×B97	(0.1, 3.9)	(70.7, 79.3)	(71.9, 81.2)
B73×CML103	(-1.5, 2)	(74.5, 83.5)	(75.1, 82.6)
B73×CML228	(-0.2, 3.9)	(74.1, 89.2)	(74.5, 91.2)
B73×CML247	(-1.0, 4.9)	(73.1, 89.4)	(75.6, 90.8)
B73×CML277	(-1.0, 4.1)	(75.0, 88.9)	(76.5, 90.2)
B73×CML322	(-1.1, 4.4)	(73.5, 84.1)	(74.3, 86.1)
B73×CML333	(0.6, 4)	(73.6, 84.2)	(76.4, 85.7)
B73×CML52	(-0.2, 3.7)	(78.3, 91.2)	(78.9, 94.6)
B73×CML69	(0.2, 4.3)	(75.2, 86.1)	(76.2, 85.4)
B73×Hp301	(-0.3, 3.5)	(70.5, 80.0)	(71.3, 81.2)
B73×Il14H	(0.1, 3.4)	(67.4, 78.9)	(68.0, 80.1)
B73×Ki11	(0.3, 5.2)	(74.3, 87.6)	(75.8, 92.5)
B73×Ki3	(0.1, 4.2)	(73.0, 82.2)	(74.9, 85.7)
B73×Ky21	(-0.1, 3.7)	(72.5, 79.7)	(73.3, 83.0)
B73×M162W	(-0.5, 4.3)	(74.7, 85.6)	(75.4, 86.8)
B73×M37W	(-0.5, 4.4)	(73.2, 84.0)	(74.8, 85.1)
B73×Mo17 (IBM)	(0.6, 4.7)	(68.0, 78.3)	(68.7, 80.0)
B73×Mo18W	(0.3, 6.7)	(71.9, 86.0)	(73.0, 90.5)
B73×MS71	(-0.2, 3)	(69.2, 75.1)	(68.2, 76.8)
B73×NC350	(-1.0, 3.5)	(71.2, 82.6)	(72.1, 85.3)
B73×NC358	(0.2, 3.3)	(72.5, 80.6)	(72.9, 84.1)

B73×Oh43	(-0.3, 4.3)	(70.9, 77.8)	(70.9, 80.8)
B73×Oh7B	(0.1, 4.5)	(71.9, 80.6)	(73.6, 84.4)
B73×P39	(-0.7, 3.5)	(66.1, 78.5)	(66.8, 80.3)
B73×Tx303	(0.1, 5.5)	(73.8, 85.6)	(75.7, 89.3)
B73×Tzi8	(0.1, 5.8)	(72.6, 86.8)	(73.4, 91.1)
Association Panel	(-0.8, 7.0)	(58.4, 121.2)	(58.7, 125.8)
Founder line BLUPs			
B73	1.05	73.96	75.01
B97	2.62	74.51	77.08
CML103	-0.76	82.64	81.87
CML228	2.10	92.48	94.08
CML247	1.48	93.46	95.00
CML277	2.42	91.10	93.29
CML322	1.81	82.97	85.01
CML333	2.29	84.70	86.96
CML52	1.99	93.87	98.70
CML69	1.31	88.29	89.34
Hp301	1.65	74.93	76.48
Il14H	1.65	69.57	70.89
Ki11	2.71	88.38	91.04
Ki3	1.64	85.20	86.92
Ky21	2.88	80.92	83.87
M162W	-0.59	85.56	85.18
M37W	2.46	79.51	82.32
Mo18W	3.95	86.96	90.49
MS71	0.94	71.63	72.18
NC350	0.40	82.09	82.35
NC358	0.70	77.58	78.10
Oh43	1.24	70.73	71.47
Oh7B	1.90	83.02	85.15
P39	2.03	65.15	66.82
Tx303	2.86	82.64	85.68
Tzi8	2.78	88.72	91.85
Mo17	3.00	72.76	75.49
Founders' Max	3.95	93.87	98.70
Founders' Min	-0.76	65.15	66.82
Founders' Range	4.71	28.72	31.87
Founders' Var	1.14	61.53	68.76

Supporting Table 2. Summary Joint Linkage Stepwise Model and GxE ASREML Analysis for Days to Anthesis

	GLM								Map					ASREML						
Trait	Term	SS	df	MS	F	p	Rsq		marker_numb	marker	chr	pos		G_Gamma	G_Compo	G_Comp/S	GxE_Gamm	GxE_Comp	GxE_Comp	G/GxE
days2anthesis	7	140.6474	25	5.625894	3.131303	2.59E-07	0.002211		m8	PZA00181.	1	15.6		0.00826	0.024218	3.04	0.000566	0.00166	0.71	14.58755
days2anthesis	26	141.4598	25	5.658394	3.149392	2.21E-07	0.002223		m27	PZA00425.	1	37.8		0.010351	0.030352	3.02	0.001085	0.00318	1.14	9.543509
days2anthesis	44	166.3049	25	6.652196	3.70253	1.49E-09	0.002614		m45	PZA03742.	1	60.8		0.012619	0.037	3.09	0.002394	0.007019	2.21	5.271496
days2anthesis	67	392.8678	25	15.71471	8.746615	8.60E-32	0.006175		m68	PZA03465.	1	84.9		0.030789	0.090277	3.3	0.00587	0.017213	4.22	5.244779
days2anthesis	87	171.3702	25	6.854809	3.815302	5.24E-10	0.002694		m88	PZA00619.	1	108.4		0.010405	0.030509	3.1				
days2anthesis	115	170.1478	25	6.805912	3.788087	6.75E-10	0.002674		m116	PZB01647.	1	137.6		0.009315	0.027313	3.14				
days2anthesis	154	199.1385	25	7.965541	4.433522	1.46E-12	0.00313		m155	PZA03037.	1	181.3		0.010192	0.029883	3.2				
days2anthesis	198	174.8552	25	6.994206	3.892889	2.54E-10	0.002748		m199	zfl2.9	2	36.2		0.008476	0.024853	3.15				
days2anthesis	231	386.1484	25	15.44593	8.597017	4.19E-31	0.006069		m232	PHM3457.	2	74.8		0.023611	0.06923	3.31	0.002965	0.008693	2.78	7.963906
days2anthesis	269	136.1405	25	5.445621	3.030965	6.21E-07	0.00214		m270	PZA02731.	2	107.1		0.00859	0.025186	3.02				
days2anthesis	284	382.5854	25	15.30342	8.517692	9.68E-31	0.006013		m285	PZA02471.	2	127.3		0.028091	0.082367	3.35	0.001987	0.005827	2.17	14.13633
days2anthesis	317	159.1752	25	6.367006	3.543797	6.43E-09	0.002502		m318	PZA02427.	3	52.1		0.019152	0.056156	3.11	0.001502	0.004403	1.3	12.75515
days2anthesis	347	175.722	25	7.028878	3.912187	2.12E-10	0.002762		m348	PZA03198.	3	60.5		0.017808	0.052215	3.07	0.000315	0.000923	0.29	56.56485
days2anthesis	367	238.5403	25	9.541612	5.310744	2.56E-16	0.003749		m368	PHM9914.	3	72.9		0.025984	0.07619	3.25	0.002316	0.00679	2.07	11.22009
days2anthesis	401	204.8726	25	8.194903	4.561182	4.23E-13	0.00322		m402	PZA02122.	3	105		0.015425	0.045227	3.12	0.003717	0.010897	3.05	4.150267
days2anthesis	409	226.4805	25	9.059219	5.042249	3.72E-15	0.00356		m410	PZB01457.	3	123.9		0.025285	0.074139	3.24	0.002519	0.007385	2.14	10.03911
days2anthesis	423	133.8097	25	5.352389	2.979074	9.72E-07	0.002103		m424	PZA00402.	3	140.7		0.010286	0.030159	3.06	0.000941	0.00276	1.04	10.92879
days2anthesis	461	265.1611	25	10.60644	5.903416	6.40E-19	0.004168		m462	PZA01759.	4	55.4		0.01411	0.041372	3.25	0.001221	0.003579	1.46	11.56006
days2anthesis	528	168.7738	25	6.75095	3.757495	8.97E-10	0.002653		m529	PZA00694.	4	116.1		0.009641	0.02827	3.19				
days2anthesis	548	207.758	25	8.310319	4.625421	2.26E-13	0.003265		m549	PZA01438.	5	7.2		0.009319	0.027325	3.18				
days2anthesis	618	301.7016	25	12.06806	6.716935	1.50E-22	0.004742		m619	PZA02164.	5	70		0.01631	0.047822	3.32				
days2anthesis	673	158.2692	25	6.330769	3.523628	7.73E-09	0.002488		m674	PZA03167.	5	125.2		0.008298	0.02433	3.11				
days2anthesis	693	128.6262	25	5.145049	2.863671	2.60E-06	0.002022		m694	PZA00355.	6	11.1		0.005876	0.01723	3.03				
days2anthesis	741	141.6067	25	5.664269	3.152662	2.15E-07	0.002226		m742	PZA01462.	6	72.3		0.009201	0.026978	3.13				
days2anthesis	753	183.8458	25	7.353832	4.093052	3.83E-11	0.00289		m754	PZA02688.	6	96.4		0.009697	0.028434	3.08	0.001669	0.004895	1.89	5.808783
days2anthesis	768	174.1109	25	6.964434	3.876318	2.96E-10	0.002737		m769	PZA03624.	7	44.7		0.009529	0.027939	3.09	0.001495	0.004384	1.69	6.372571
days2anthesis	809	172.517	25	6.900681	3.840834	4.13E-10	0.002712		m810	PZA03728.	7	75.3		0.008536	0.025029	3.12				
days2anthesis	834	207.7651	25	8.310605	4.62558	2.26E-13	0.003266		m835	PZA01744.	7	134		0.011317	0.033183	3.23				
days2anthesis	878	142.7292	25	5.709166	3.177651	1.72E-07	0.002243		m879	PZA00908.	8	57.5		0.015947	0.04676	3.1				
days2anthesis	894	512.6517	25	20.50607	11.41342	3.96E-44	0.008058		m895	PZB02155.	8	66.9		0.058075	0.170284	3.33	0.009619	0.028204	5.42	6.037648
days2anthesis	925	196.658	25	7.866321	4.378297	2.49E-12	0.003091		m926	PZA00675.	8	91.3		0.01104	0.032371	3.19				
days2anthesis	972	202.8362	25	8.11345	4.515846	6.58E-13	0.003188		m973	PZA02878.	9	45.2		0.016946	0.049688	2.96	0.013087	0.038374	5.79	1.294834
days2anthesis	996	438.6563	25	17.54625	9.766027	1.71E-36	0.006895		m997	PZA00840.	9	62		0.036182	0.106091	3.33	0.003774	0.011065	2.74	9.588153
days2anthesis	1016	178.3879	25	7.135518	3.971541	1.21E-10	0.002804		m1017	PZA00323.	9	88.5		0.008567	0.025118	3.12				
days2anthesis	1062	678.9068	25	27.15627	15.11485	2.56E-61	0.010671		m1063	PZA00048.	10	42.9		0.042154	0.1236	3.37	0.007347	0.021543	4.77	5.737362
days2anthesis	1097	210.7758	25	8.431034	4.692609	1.17E-13	0.003313		m1098	PZA02049.	10	81.6		0.010824	0.031739	3.18	0.001065	0.003123	1.28	10.16198
days2anthesis	Populatior	221.0124	24	9.208848	5.125531	5.46E-15	0.003474					Pop		0.440099	1.29043	3.13				
days2anthesis	Model	56841.56	924	61.51684	34.23952	0	0.893424					Env		27.495	80.6192	1.87				
days2anthesis	Error	6780.603	3774	1.796662								PopxEnv		0.177555	0.520617	7.29				
												Variance		1	2.93214	120.71				
Building Proc	Stepwise																			
Factors	Markers																			
P	e-4																			

Supporting Table 3. Summary Joint Linkage Stepwise Model and GxE ASREML Analysis for Days to Anthesis

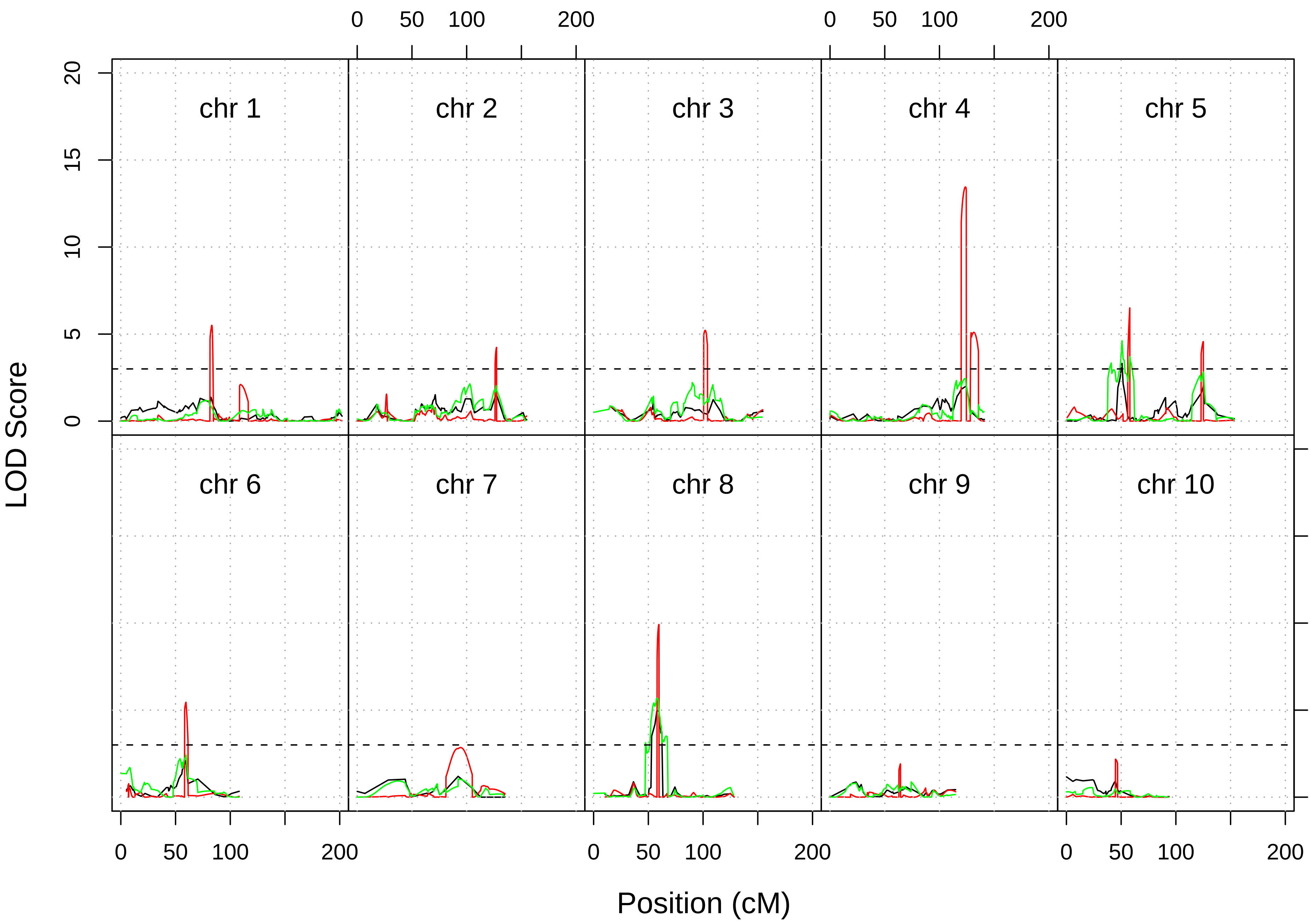
	GLM								Map					ASREML						
Trait	Term	SS	df	MS	F	p	Rsq		marker_nu	marker	chr	pos		G_Gamma	G_Compo	G_Comp/S	GxE_Gamr	GxE_Comp	GxE_Comp	G/GxE
days2silk	26	200.2655	25	8.01062	3.635436	2.79E-09	0.002608		m27	PZA00425.11	1	37.8		0.011609	0.039391	3.08	0.002263	0.007678	2.14	5.130505
days2silk	44	218.0035	25	8.72014	3.957436	1.39E-10	0.002838		m45	PZA03742.1	1	60.8		0.013959	0.047366	3.12	0.002204	0.00748	2.04	6.332265
days2silk	66	612.3494	25	24.49398	11.11603	1.03E-42	0.007973		m67	PZA03240.1/2	1	84.6		0.038225	0.129709	3.35	0.005623	0.01908	4.09	6.798344
days2silk	89	184.3906	25	7.375626	3.347259	3.83E-08	0.002401		m90	PZA03074.27	1	115		0.008923	0.030278	3.06				
days2silk	115	266.5314	25	10.66126	4.838367	2.83E-14	0.00347		m116	PZB01647.1	1	137.6		0.014422	0.048938	3.24				
days2silk	149	283.4126	25	11.3365	5.144813	1.36E-15	0.00369		m150	PZA02087.2	1	178.5		0.011619	0.039426	3.24				
days2silk	200	283.965	25	11.3586	5.154842	1.23E-15	0.003697		m201	PZA01753.1	2	40.6		0.015489	0.052558	3.25	0.001004	0.003407	1.16	15.42762
days2silk	218	158.1345	25	6.325379	2.870629	2.46E-06	0.002059		m219	PZA02058.1	2	63		0.012254	0.04158	3	0.001411	0.004789	1.35	8.683333
days2silk	231	208.2322	25	8.329288	3.780057	7.32E-10	0.002711		m232	PHM3457.6	2	74.8		0.018132	0.061528	3.14	0.001963	0.00666	1.73	9.238325
days2silk	264	196.739	25	7.86956	3.57142	5.02E-09	0.002562		m265	PZA00824.2	2	105.3		0.011434	0.0388	3.1	0.000893	0.003031	0.99	12.80003
days2silk	284	604.3485	25	24.17394	10.97079	4.85E-42	0.007869		m285	PZA02471.5	2	127.3		0.032136	0.109047	3.37	0.001915	0.006497	2.02	16.78493
days2silk	313	177.6782	25	7.107129	3.225408	1.13E-07	0.002313		m314	PZA01765.1	3	33.7		0.008633	0.029293	3.05				
days2silk	324	382.7768	25	15.31107	6.948579	1.40E-23	0.004984		m325	zb21.1	3	55.5		0.026769	0.090835	3.31	0.001073	0.00364	1.22	24.95704
days2silk	367	272.1149	25	10.8846	4.939725	1.04E-14	0.003543		m368	PHM9914.11	3	72.9		0.020883	0.070861	3.26	0.000512	0.001736	0.57	40.81755
days2silk	399	378.8903	25	15.15561	6.878027	2.91E-23	0.004933		m400	PZA00308.24	3	103.7		0.022395	0.075994	3.24	0.004601	0.015613	3.66	4.867536
days2silk	410	440.167	25	17.60668	7.990389	2.62E-28	0.005731		m411	PZA03146.4	3	127.7		0.022917	0.077765	3.33	0.000761	0.002584	0.88	30.0973
days2silk	444	251.9927	25	10.07971	4.574445	3.76E-13	0.003281		m445	PHM8527.2	4	40.4		0.01307	0.044349	3.22				
days2silk	488	199.4802	25	7.979208	3.621181	3.18E-09	0.002597		m489	PZA03116.1	4	75.3		0.010071	0.034174	3.11				
days2silk	509	163.957	25	6.558281	2.976326	9.99E-07	0.002135		m510	PHM4348.16	4	105		0.007277	0.024692	2.96	0.001605	0.005447	1.8	4.533257
days2silk	548	211.1291	25	8.445163	3.832644	4.49E-10	0.002749		m549	PZA01438.1	5	7.2		0.008455	0.02869	3.14				
days2silk	595	157.7863	25	6.311452	2.864308	2.60E-06	0.002054		m596	PHM1870.20	5	63		0.009272	0.031464	3.01				
days2silk	624	144.9732	25	5.798928	2.631711	1.80E-05	0.001888		m625	PZA00148.3	5	76.9		0.008556	0.029034	2.93				
days2silk	658	151.2733	25	6.050931	2.746077	7.02E-06	0.00197		m659	PZA03024.16	5	106.4		0.008742	0.029665	3.05				
days2silk	675	159.5111	25	6.380446	2.895619	1.99E-06	0.002077		m676	PZA01680.3	5	127.2		0.009376	0.031814	3.07				
days2silk	684	174.6462	25	6.985849	3.170368	1.84E-07	0.002274		m685	PZA03047.12	6	6.9		0.009062	0.03075	3.1				
days2silk	705	220.2189	25	8.808755	3.997652	9.53E-11	0.002867		m706	PZA00942.2	6	27.8		0.010209	0.034643	3.11				
days2silk	745	289.5132	25	11.58053	5.255558	4.51E-16	0.00377		m746	PHM4748.16	6	78.6		0.01828	0.062029	3.23	0.002386	0.008096	2.24	7.661929
days2silk	757	143.8952	25	5.75581	2.612143	2.11E-05	0.001874		m758	PZA01875.1	6	108.2		0.007348	0.024935	3.04				
days2silk	770	226.558	25	9.062322	4.112727	3.20E-11	0.00295		m771	PHM15501.9	7	47.8		0.012945	0.043925	3.18				
days2silk	797	162.3146	25	6.492586	2.946512	1.29E-06	0.002113		m798	PZA00986.1	7	63.7		0.008589	0.029145	2.94				
days2silk	815	319.8382	25	12.79353	5.80605	1.76E-18	0.004164		m816	PZA02722.1	7	81.2		0.020507	0.069587	3.28				
days2silk	836	191.9481	25	7.677925	3.484451	1.11E-08	0.002499		m837	PZA01044.1	7	134.4		0.006703	0.022744	3.07				
days2silk	844	176.4452	25	7.057807	3.203024	1.38E-07	0.002297		m845	PHM4711.14	8	18.3		0.006894	0.023393	3.06				
days2silk	894	578.7712	25	23.15085	10.50648	6.86E-40	0.007536		m895	PZB02155.1	8	66.9		0.033961	0.115238	3.34	0.005513	0.018706	4.08	6.16045
days2silk	926	253.4916	25	10.13967	4.601655	2.88E-13	0.003301		m927	PHM1834.47	8	92.1		0.012041	0.040858	3.19	0.000132	0.000448	0.16	91.1195
days2silk	969	272.9778	25	10.91911	4.95539	8.93E-15	0.003554		m970	PZB00959.1	9	44.5		0.015703	0.053285	2.89	0.015209	0.051609	6.2	1.032485
days2silk	997	800.871	25	32.03484	14.53828	1.38E-58	0.010428		m998	PZA00060.2	9	62.2		0.047566	0.161406	3.42	0.001371	0.004653	1.32	34.68956
days2silk	1062	1016.622	25	40.66489	18.45483	1.20E-76	0.013237		m1063	PZA00048.1	10	42.9		0.052015	0.176504	3.43	0.004242	0.014394	3.52	12.26267
days2silk	1102	289.8325	25	11.5933	5.261354	4.25E-16	0.003774		m1103	PZA01001.2	10	91		0.013197	0.04478	3.27				
days2silk	Population	318.5851	24	13.27438	6.024274	8.99E-19	0.004148						PopxEnv	0.325331	1.10395	8.04				
days2silk	Model	68652.59	999	68.72131	31.1876	0	0.893876						Env	26.0004	88.2273	1.87				
days2silk	Error	8150.681	3699	2.203482									Pop	0.549025	1.86301	3.08				
Building Pr	Stepwise																			
Factors	Markers																			
P	e-4																			

Supporting Table 4. Summary Joint Linkage Stepwise Model and GxE ASREML Analysis for Days to Anthesis

	GLM								Map					ASREML						
Trait	Term	SS	df	MS	F	p	Rsq		marker_nu	marker	chr	pos		G_Gamma	G_Compoi	G_Comp/S	GxE_Gamr	GxE_Comp	GxE_Comp	G/GxE
asi	22	35.63	25	1.4252	3.377	2.9E-08	0.007798		m23	PZA02393	1	33.1		0.004682	0.002518	2.77	0.002014	0.001083	2.14	2.325041
asi	71	51.97	25	2.0788	4.925	1.16E-14	0.011375		m72	PZA02763	1	87.9		0.009572	0.005147	2.98	0.003482	0.001872	2.8	2.749129
asi	87	46.17	25	1.8468	4.375	2.51E-12	0.010105		m88	PZA00619	1	108.4		0.007906	0.004251	2.82	0.005246	0.002821	3.71	1.507172
asi	135	87.17	25	3.4868	8.262	1.32E-29	0.019079		m136	PZB00063	1	162.2		0.011424	0.006143	3.19	0.00162	0.000871	1.81	7.0508
asi	200	34.95	25	1.398	3.313	5.1E-08	0.007649		m201	PZA01753	2	40.6		0.005109	0.002747	2.76	0.002962	0.001593	2.84	1.724855
asi	247	58.16	25	2.3264	5.512	3.24E-17	0.012729		m248	PZA01321	2	82.8		0.009812	0.005276	3.06	0.00326	0.001753	2.98	3.010006
asi	282	35.42	25	1.4168	3.357	3.4E-08	0.007752		m283	PZA00804	2	123.9		0.006286	0.00338	2.86	0.002091	0.001125	2.21	3.005967
asi	297	40.36	25	1.6144	3.825	4.7E-10	0.008834		m298	PZA02170	2	151.6		0.008098	0.004354	3.05				
asi	311	74.71	25	2.9884	7.081	3.22E-24	0.016352		m312	PZB01944	3	28.9		0.013435	0.007224	3.1	0.005065	0.002724	3.85	2.652413
asi	324	44.25	25	1.77	4.193	1.45E-11	0.009685		m325	zb21.1	3	55.5		0.007303	0.003927	3	0.000948	0.00051	1.11	7.701247
asi	391	31.6	25	1.264	2.994	8.45E-07	0.006916		m392	PZA01228	3	100.1		0.005174	0.002782	2.96				
asi	461	42.82	25	1.7128	4.058	5.23E-11	0.009372		m462	PZA01759	4	55.4		0.008683	0.004669	3.13				
asi	496	34.63	25	1.3852	3.282	6.8E-08	0.007579		m497	PZA03275	4	85.2		0.005658	0.003042	2.86	0.001624	0.000873	1.83	3.484136
asi	613	48.22	25	1.9288	4.57	3.81E-13	0.010554		m614	PZA00273	5	68.7		0.006685	0.003595	2.87	0.003031	0.00163	2.86	2.205202
asi	648	43.12	25	1.7248	4.087	4E-11	0.009438		m649	PZA03172	5	98.2		0.007586	0.004079	3.04				
asi	672	35.01	25	1.4004	3.318	4.9E-08	0.007663		m673	PZA02015	5	124.9		0.005606	0.003015	2.88				
asi	683	30.79	25	1.2316	2.918	1.63E-06	0.006739		m684	PZA00158	6	5.1		0.005565	0.002993	2.91	0.001082	0.000582	1.31	5.143088
asi	744	41.47	25	1.6588	3.93	1.75E-10	0.009076		m745	PZA00223	6	75.8		0.01105	0.005942	3.03	0.001417	0.000762	1.36	7.800165
asi	751	31.26	25	1.2504	2.963	1.11E-06	0.006842		m752	PZA00889	6	94.1		0.006216	0.003343	2.77	0.001301	0.000699	1.36	4.77886
asi	787	37.9	25	1.516	3.592	4E-09	0.008295		m788	PZA02291	7	49.5		0.006237	0.003354	2.93	0.001193	0.000641	1.37	5.228876
asi	809	32.65	25	1.306	3.094	3.55E-07	0.007146		m810	PZA03728	7	75.3		0.006287	0.003381	2.77	0.001889	0.001016	1.85	3.328431
asi	818	35.57	25	1.4228	3.371	3E-08	0.007785		m819	PHM112.8	7	92.2		0.009467	0.005091	2.95	0.002937	0.001579	2.51	3.223118
asi	842	30.6	25	1.224	2.9	1.89E-06	0.006697		m843	PZA00368	8	17.1		0.005179	0.002785	2.93				
asi	892	55.72	25	2.2288	5.281	3.34E-16	0.012195		m893	PZA03637	8	64.1		0.010488	0.00564	3.06	0.003511	0.001888	3.14	2.987367
asi	924	27.5	25	1.1	2.606	2.2E-05	0.006019		m925	PZB00811	8	89.5		0.003843	0.002066	2.58	0.000462	0.000249	0.56	8.309895
asi	935	30.51	25	1.2204	2.892	2.04E-06	0.006678		m936	PHM14046	8	117.5		0.004777	0.002569	2.87				
asi	969	47.97	25	1.9188	4.546	4.77E-13	0.010499		m970	PZB00959	9	44.5		0.009939	0.005344	2.99	0.004136	0.002224	3.39	2.402681
asi	1002	44.4	25	1.776	4.208	1.26E-11	0.009718		m1003	PZA02397	9	64.5		0.008714	0.004686	3.02	0.001547	0.000832	1.58	5.632369
asi	1070	45.46	25	1.8184	4.308	4.79E-12	0.00995		m1071	PZA01919	10	44.7		0.007376	0.003966	3.01	0.002165	0.001164	2.28	3.406576
asi	Population	28.86	24	1.2025	2.849	4.41E-06	0.006317						Env	0.615168	0.330801	1.85				
asi	Model	2902.24	749	3.87482	9.18	0	0.635209						PopxEnv	0.162253	0.08725	7.12				
asi	ERROR	1666.71	3949	0.422059	.	.							Pop	0.178146	0.095797	2.83				
Building Pr	Stepwise																			
Factors	Markers																			
P	e-4																			

Supporting Table 5. Associating polymorphisms at Vgt1 and Rap2.7 for the maize 282 association panel.

LINE	Vgt1 MITE	Rap2.7 GEL	Rap2.7 Seq 568-575	LINE	Vgt1 MITE	Rap2.7 GEL	Rap2.7 Seq 568-575	LINE	Vgt1 MITE	Rap2.7 GEL	Rap2.7 Seq 568-575	LINE	Vgt1 MITE	Rap2.7 GEL	Rap2.7 Seq 568-575	LINE	Vgt1 MITE	Rap2.7 GEL	Rap2.7 Seq 568-575
4226	0	2	NS	**CI3A**	0	2	NS	**E2558W**	0	0	NS	**Mp339**	0	0	NS	**Oh603**	0	0	NS
4722	2	0	NS	**CI64**	0	0	NS	**EP1**	2	2	NS	**MS1334**	2	0	NS	**OH7B**	0	0	0
33-16	0	2	NS	**CI66**	0	2	NS	**F2834T**	0	2	NS	**MS153**	0	0	NS	**Os420**	0	0	NS
38-11	2	0	NS	**CI90C**	0	0	NS	**F44**	0	2	NS	**MS71**	2	0	0	**P39**	2	0	0
A188	2	0	NS	**CI91B**	0	2	NS	**F6**	0	0	NS	**Mt42**	0	0	NS	**Pa762**	2	0	NS
A214N	0	0	NS	**CM105**	2	0	NS	**F7**	2	2	NS	**N192**	0	0	NS	**Pa875**	0	0	NS
A239	0	0	NS	**CM174**	2	0	NS	**GA209**	0	2	NS	**N28Ht**	0	0	NS	**Pa880**	0	0	NS
A272	2	2	NS	**CM37**	2	0	NS	**GT112**	0	2	NS	**N6**	2	2	NS	**Pa91**	2	0	NS
A441-5	0	0	NS	**CM7**	2	0	NS	**H105W**	2	0	NS	**N7A**	0	0	NS	**R109B**	2	0	NS
A554	0	0	NS	**CML10**	0	2	NS	**H49**	0	0	NS	**NC222**	0	0	NS	**R168**	2	0	NS
A556	2	0	NS	**CML103**	0	0	0	**H84**	0	2	NS	**NC230**	0	2	NS	**R177**	2	0	NS
A6	0	2	NS	**CML108**	2	2	NS	**H91**	0	0	NS	**NC232**	0	0	NS	**R229**	0	0	NS
A619	2	0	NS	**CML11**	0	2	NS	**H95**	0	0	NS	**NC236**	0	2	NS	**R4**	0	0	NS
A632	2	0	NS	**CML14**	2	2	NS	**H99**	2	0	NS	**NC238**	0	NS	NS	**SA24**	2	0	NS
A634	0	0	NS	**CML154Q**	0	0	NS	**Hi27**	0	2	NS	**NC250**	0	0	NS	**SC213R**	0	2	NS
A635	0	0	NS	**CML157Q**	2	2	NS	**HP301**	0	2	0	**NC258**	0	2	NS	**SC357**	0	2	NS
A641	2	0	NS	**CML158Q**	0	2	NS	**Hy**	0	0	NS	**NC260**	0	0	NS	**SC55**	0	0	NS
A654	2	0	NS	**CML218**	0	2	NS	**I137TN**	0	0	NS	**NC262**	2	2	NS	**SD40**	0	NS	NS
A659	0	0	NS	**CML220**	0	0	NS	**I205**	0	0	NS	**NC264**	2	0	NS	**SD44**	0	0	NS
A661	0	0	NS	**CML228**	0	2	0	**I29**	2	2	NS	**NC290A**	2	2	NS	**Sg1533**	2	0	NS
A679	2	0	NS	**CML238**	0	0	NS	**IA2132**	2	NS	NS	**NC294**	0	0	NS	**Sg18**	0	2	NS
A680	0	0	NS	**CML247**	0	0	0	**Ia5125**	2	0	NS	**NC296**	0	0	NS	**T232**	0	0	NS
A682	2	0	NS	**CML254**	0	0	NS	**IDS28**	2	0	NS	**NC296A**	0	0	NS	**T234**	0	0	NS
Ab28A	2	0	NS	**CML258**	0	0	NS	**IDS69**	0	2	NS	**NC298**	0	0	NS	**T8**	0	2	NS
B10	0	0	NS	**CML261**	0	0	NS	**IDS91**	0	2	NS	**NC300**	0	0	NS	**Tx303**	0	0	0
B103	0	0	NS	**CML264**	0	2	NS	**Il101**	2	0	NS	**NC302**	0	0	NS	**Tx601**	0	2	NS
B104	0	0	NS	**CML277**	0	0	0	**Il14H**	2	0	0	**NC304**	0	2	NS	**Tzi10**	0	NS	NS
B105	0	0	NS	**CML281**	2	0	NS	**Il677a**	2	0	NS	**NC306**	0	0	NS	**Tzi11**	0	0	NS
B109	0	0	NS	**CML287**	0	0	NS	**K148**	2	2	NS	**NC310**	0	0	NS	**Tzi16**	0	2	NS
B115	0	2	NS	**CML311**	2	2	NS	**K4**	0	0	NS	**NC314**	0	0	NS	**Tzi18**	0	0	NS
B14A	0	0	NS	**CML314**	0	0	NS	**K55**	0	2	NS	**NC318**	0	0	NS	**Tzi25**	0	2	NS
B164	2	0	NS	**CML321**	0	0	NS	**K64**	0	0	NS	**NC320**	0	2	NS	**Tzi8**	0	2	0
B2-good	0	0	NS	**CML322**	0	2	2	**Ki11**	0	0	0	**NC324**	0	0	NS	**Tzi9**	0	2	NS
B37	0	2	NS	**CML323**	0	2	NS	**Ki14**	0	0	NS	**NC326**	0	0	NS	**U267Y**	0	0	NS
B46	0	0	NS	**CML328**	0	2	NS	**Ki2021**	0	0	NS	**NC328**	0	0	NS	**VA102**	2	0	NS
B52	0	2	NS	**CML331**	0	2	NS	**Ki21**	2	2	NS	**NC33**	0	2	NS	**Va14**	0	0	NS
B57	0	2	NS	**CML332**	0	2	NS	**Ki3**	0	0	2	**NC336**	0	0	NS	**Va17**	0	0	NS
B64	0	0	NS	**CML333**	0	2	2	**Ki43**	0	0	NS	**NC338**	0	2	NS	**Va22**	0	0	NS
B68	0	0	NS	**CML341**	0	0	NS	**Ki44**	0	2	NS	**NC340**	0	0	NS	**Va26**	0	0	NS
B73	0	0	0	**CML38**	0	0	NS	**Ky21**	0	0	0	**NC342**	0	2	NS	**Va35**	2	0	NS
B73Htrhm	0	0	NS	**CML45**	0	2	NS	**KY226**	0	0	NS	**NC344**	0	2	NS	**Va59**	2	0	NS
B75	0	0	NS	**CML5**	0	0	NS	**KY228**	0	0	NS	**NC346**	0	0	NS	**Va85**	0	2	NS
B76	0	2	NS	**CML52**	0	2	2	**L317**	2	0	NS	**NC348**	0	0	NS	**Va99**	2	0	NS
B77	0	2	NS	**CML61**	0	2	NS	**L578**	0	2	NS	**NC350**	0	0	0	**VaW6**	0	2	NS
B79	0	0	NS	**CML69**	0	2	2	**M14**	0	0	NS	**NC352**	0	0	NS	**W117Ht**	2	0	NS
B84	0	0	NS	**CML77**	2	2	NS	**M162W**	0	0	0	**NC354**	0	0	NS	**W153R**	0	0	NS
B97	0	0	2	**CML91**	0	2	NS	**M37W**	0	0	0	**NC356**	0	0	NS	**W182B**	0	0	NS
C103	2	0	NS	**CML92**	0	0	NS	**MEF156-55-2**	2	0	NS	**NC358**	0	2	0	**W22**	0	0	NS
C123	2	0	NS	**CMV3**	2	0	NS	**Mo17**	2	2	0	**NC360**	2	2	NS	**W22R-r**	0	0	NS
C49A	0	0	NS	**CO106**	2	0	NS	**Mo18W**	0	2	2	**NC362**	2	2	NS	**W64A**	0	2	NS
CH701-30	0	0	NS	**CO125**	2	0	NS	**MO1W**	0	0	NS	**NC364**	2	2	NS	**WD**	0	0	NS
CH9	0	0	NS	**CO255**	2	0	NS	**Mo24W**	0	2	NS	**NC366**	0	2	NS	**Wf9**	0	0	NS
CI.7	0	2	NS	**D940Y**	0	0	NS	**Mo44**	0	0	NS	**NC368**	0	0	NS	**Yu796_NS**	0	0	NS
CI187-2	2	0	NS	**DE_2**	0	0	NS	**Mo45**	0	2	NS	**ND246**	2	2	NS				
CI21E	0	2	NS	**DE_3**	0	0	NS	**Mo46**	0	0	NS	**Oh40B**	2	0	NS				
CI28A	0	0	NS	**DE1**	0	0	NS	**Mo47**	0	0	NS	**Oh43**	0	0	0				
CI31A	0	2	NS	**DE811**	0	0	NS	**MoG**	0	2	NS	**Oh43E**	2	0	NS				

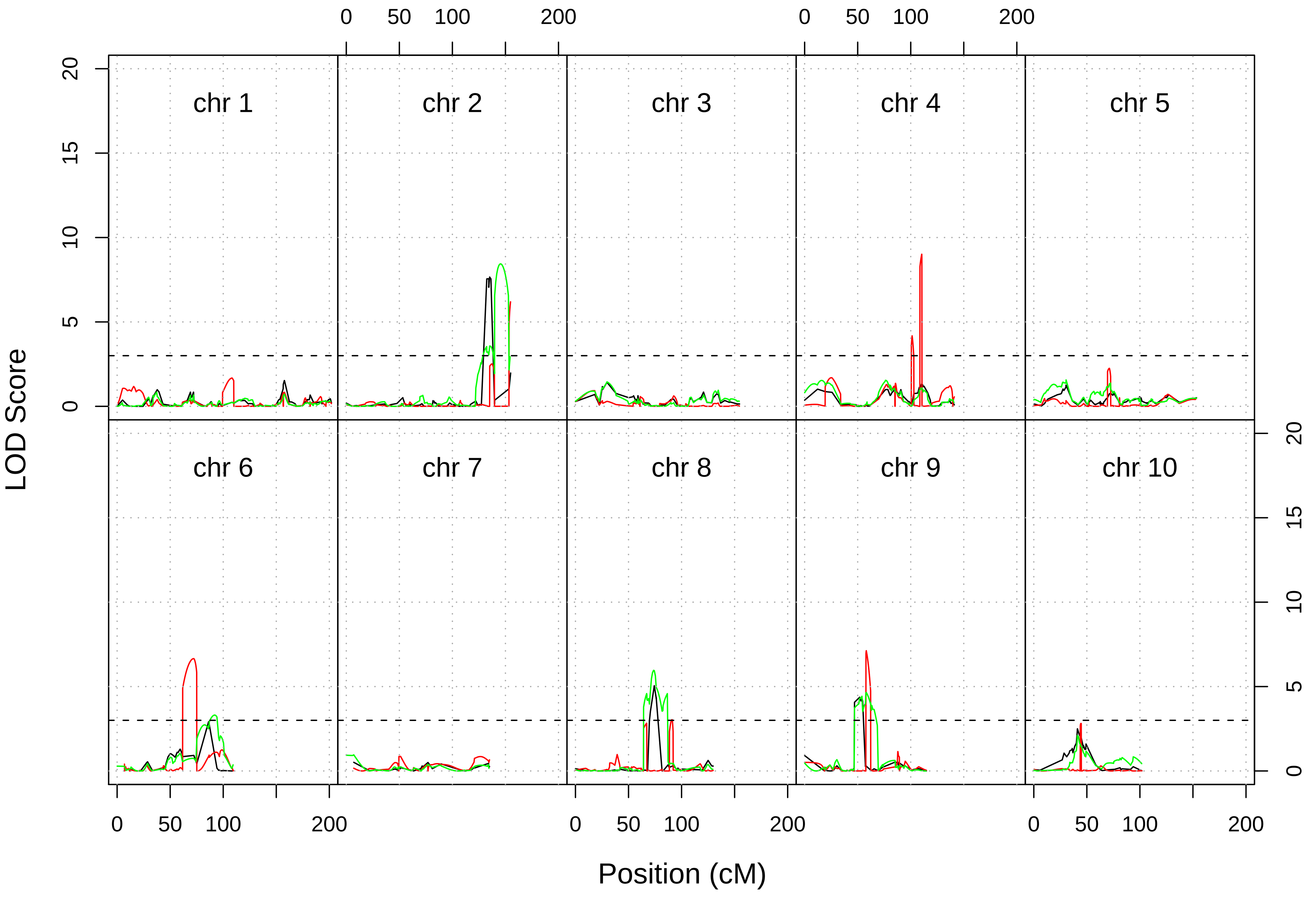


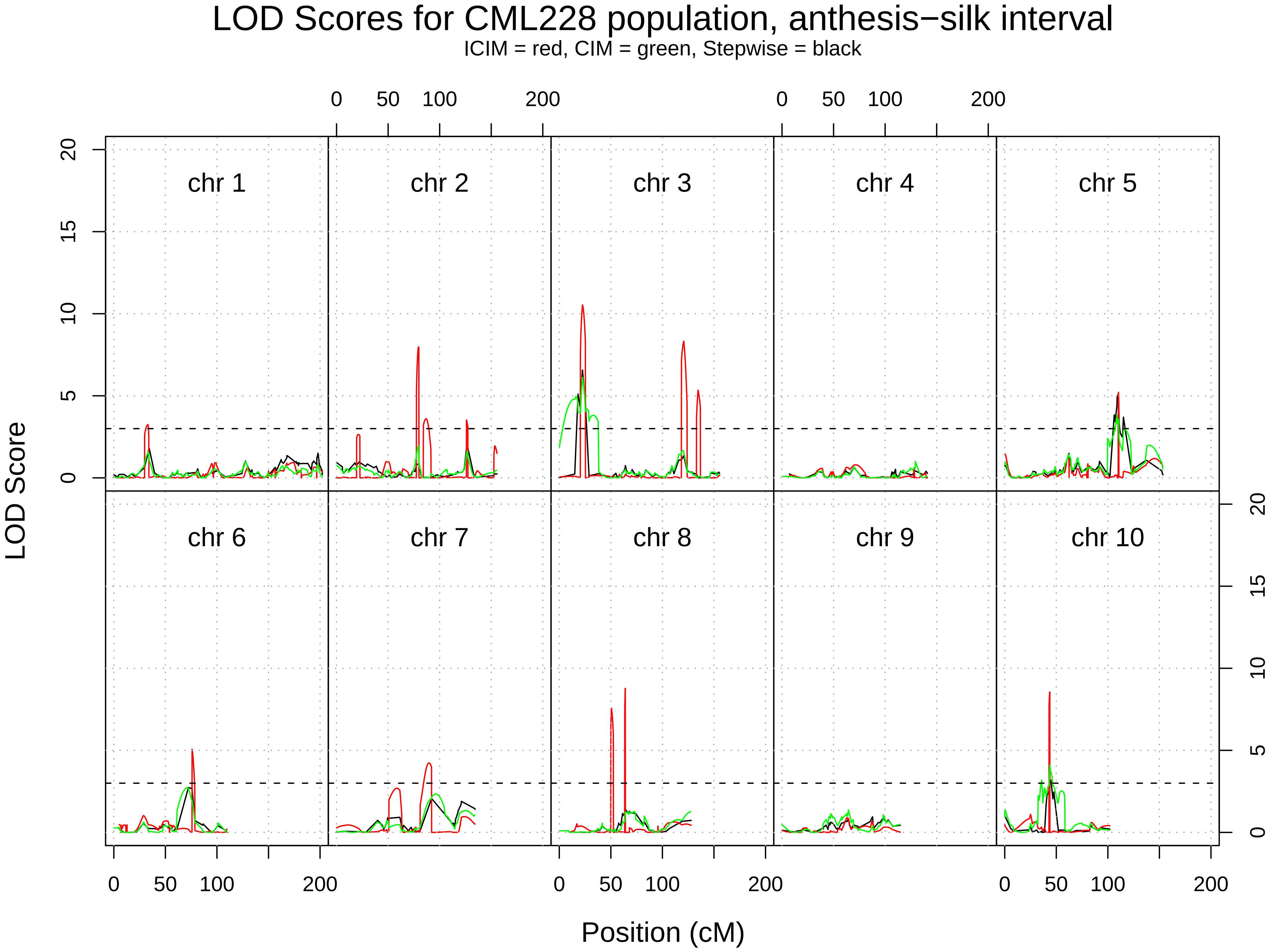
LOD Scores for B97 population, anthesis−silk interval

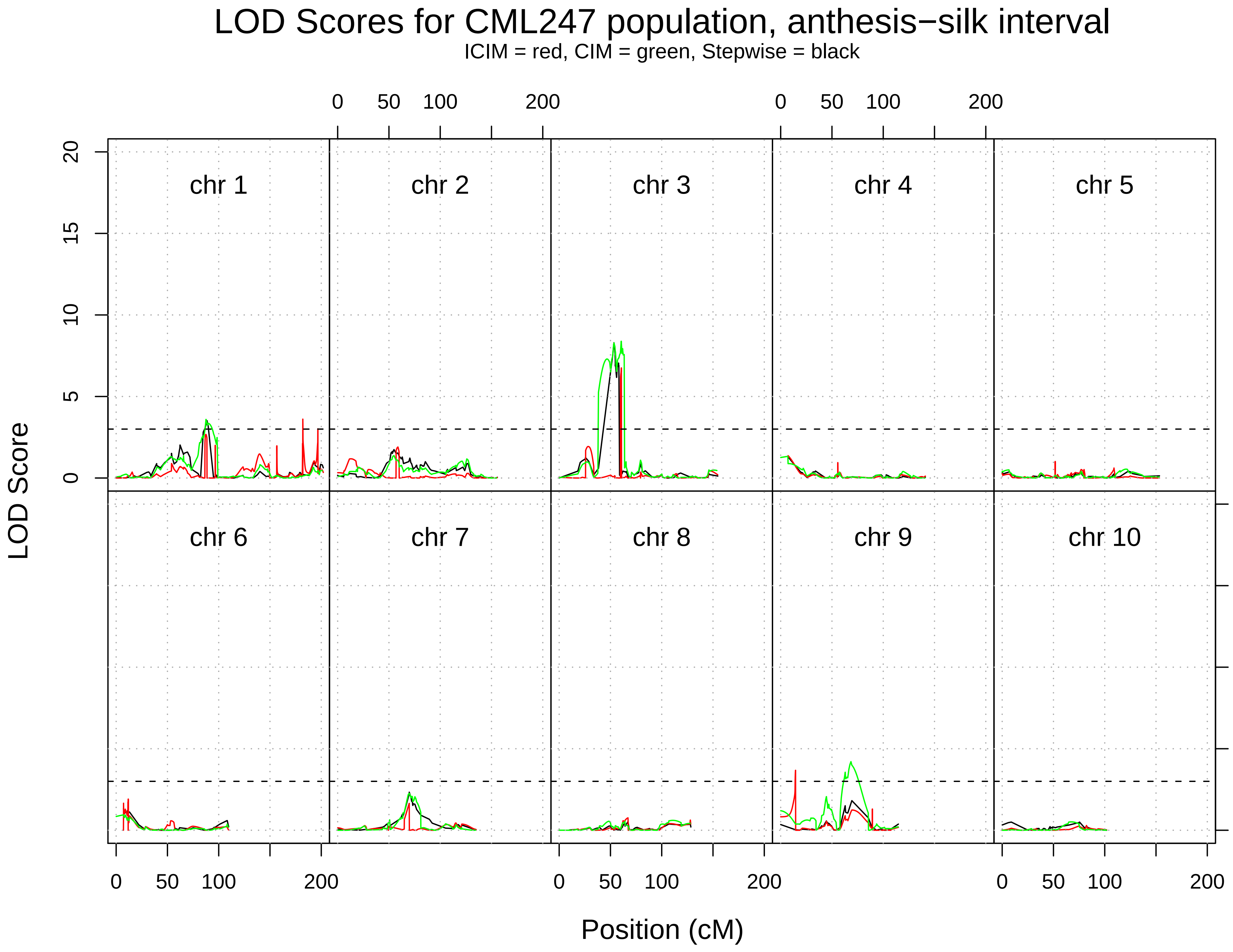
ICIM = red, CIM = green, Stepwise = black

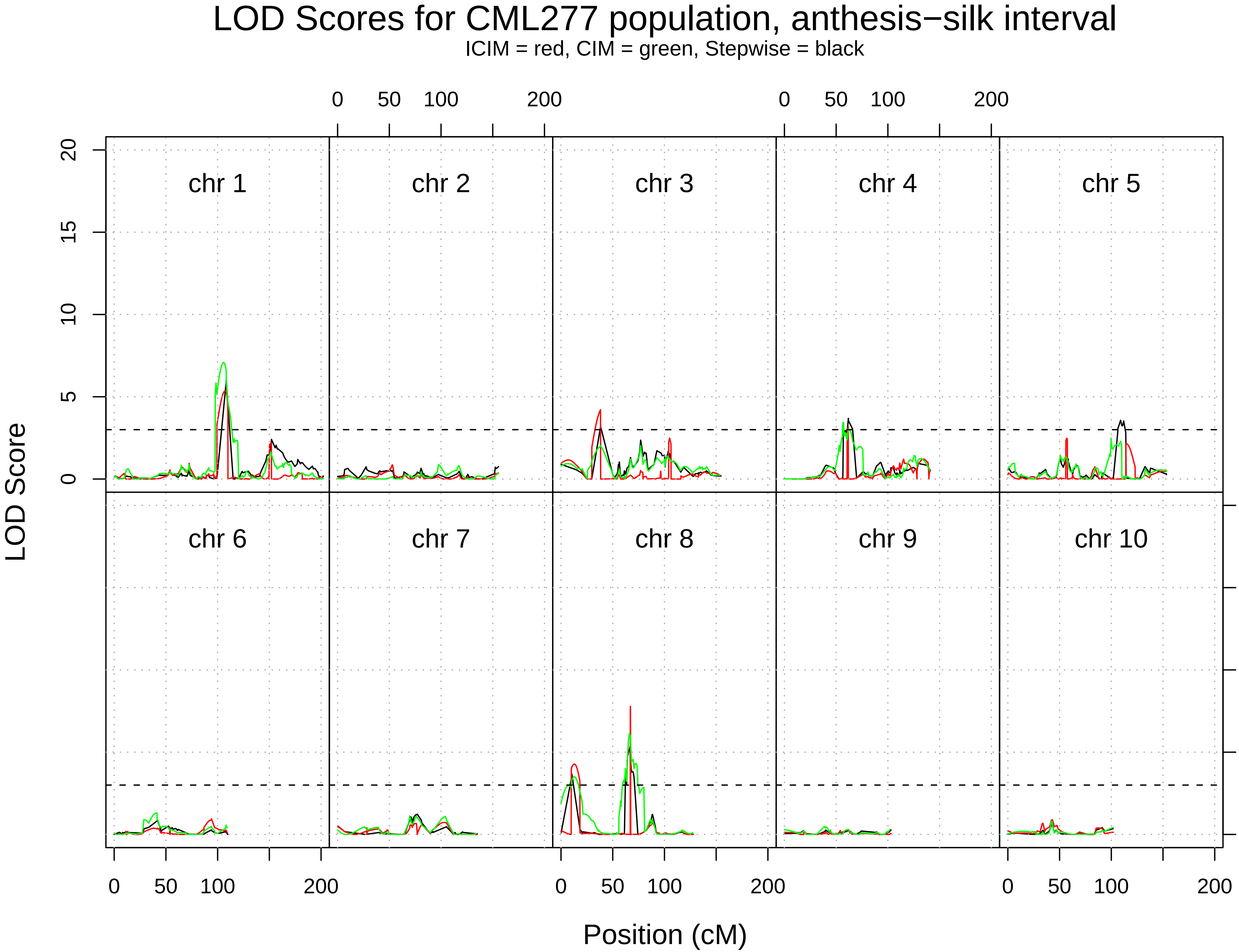
LOD Scores for CML103 population, anthesis−silk interval

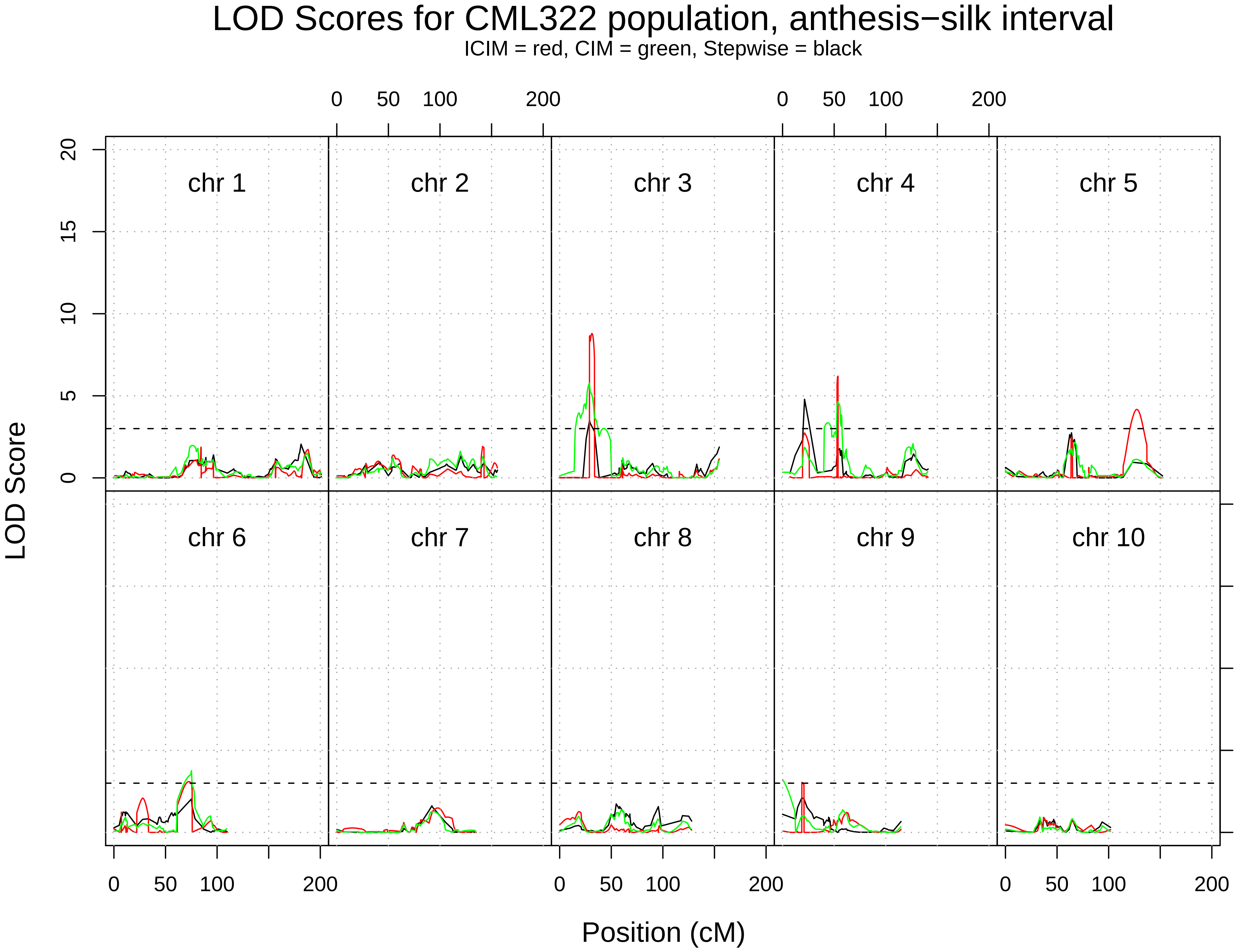
ICIM = red, CIM = green, Stepwise = black




LOD Scores for CML228 population, anthesis−silk interval
ICIM = red, CIM = green, Stepwise = black
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
LOD Score
Position (cM)
0
5
10
15
20
0
50
100
200

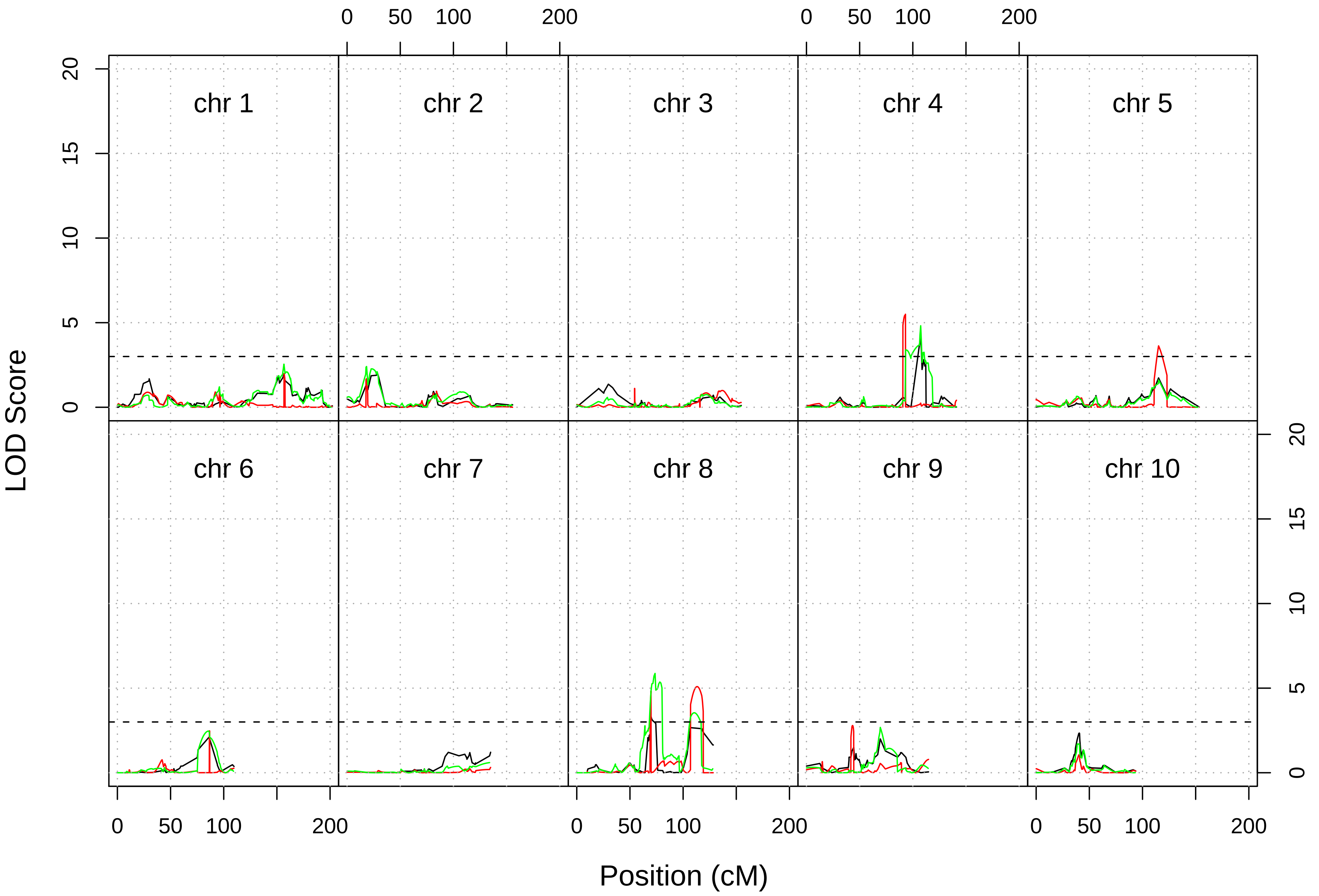

LOD Scores for CML247 population, anthesis−silk interval
ICIM = red, CIM = green, Stepwise = black
LOD Score
Position (cM)
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
0
5
10
15
20
0
50
100
200

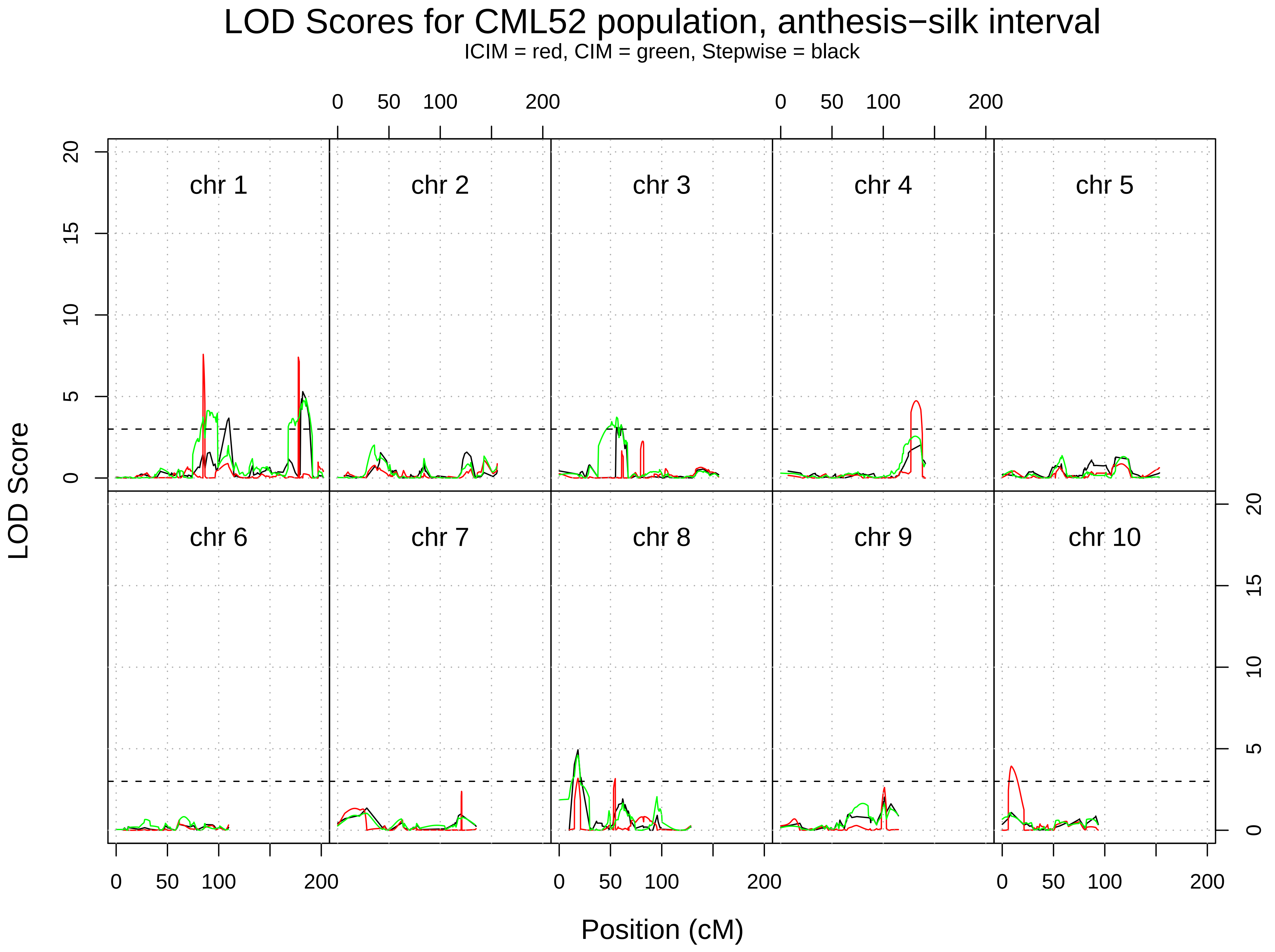

LOD Scores for CML277 population, anthesis−silk interval
ICIM = red, CIM = green, Stepwise = black
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
LOD Score
Position (cM)
0
5
10
15
20
0
50
100
200


LOD Scores for CML322 population, anthesis−silk interval
ICIM = red, CIM = green, Stepwise = black
LOD Score
Position (cM)
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
0
5
10
15
20
0
50
100
200

LOD Scores for CML333 population, anthesis−silk interval

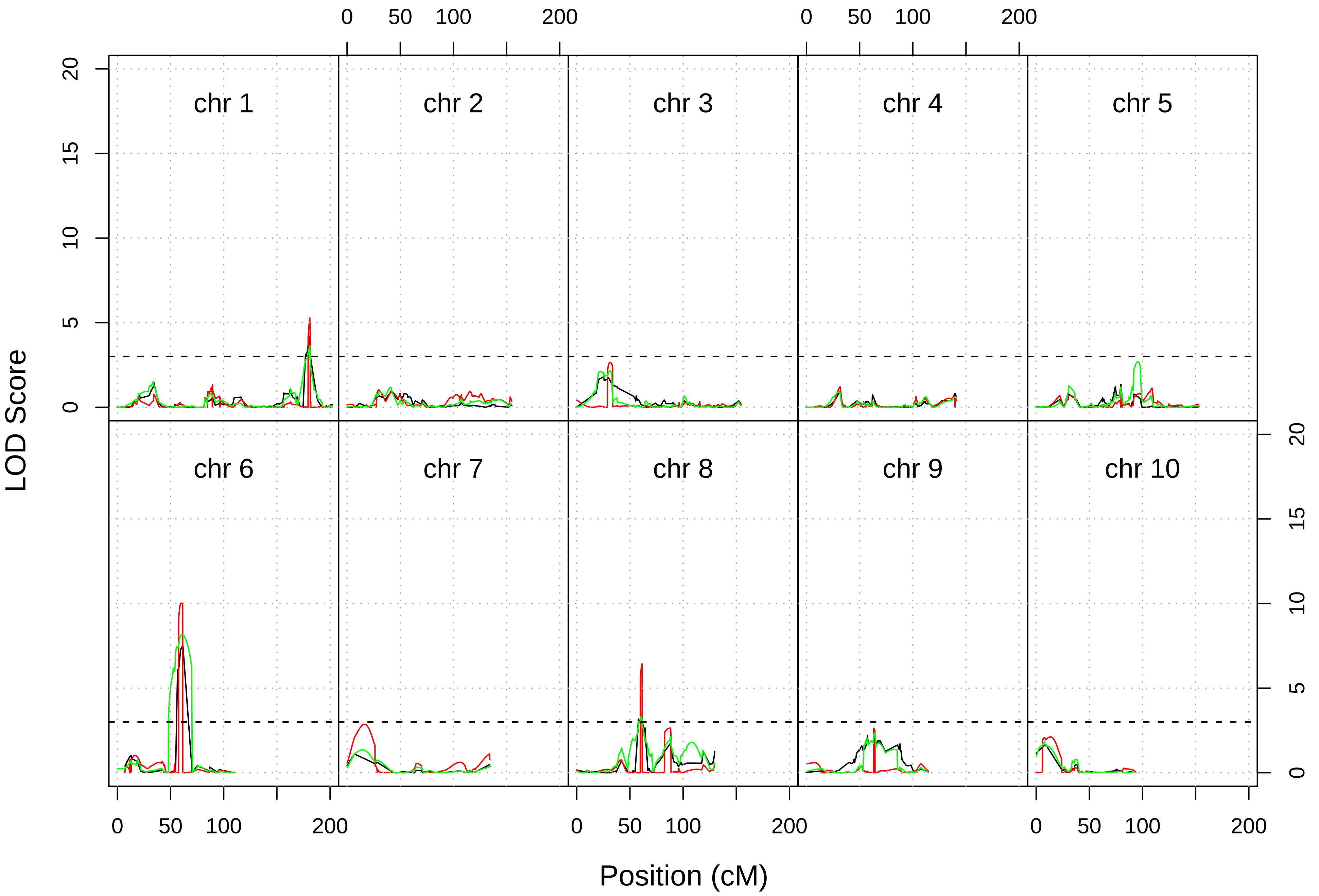
ICIM = red, CIM = green, Stepwise = black

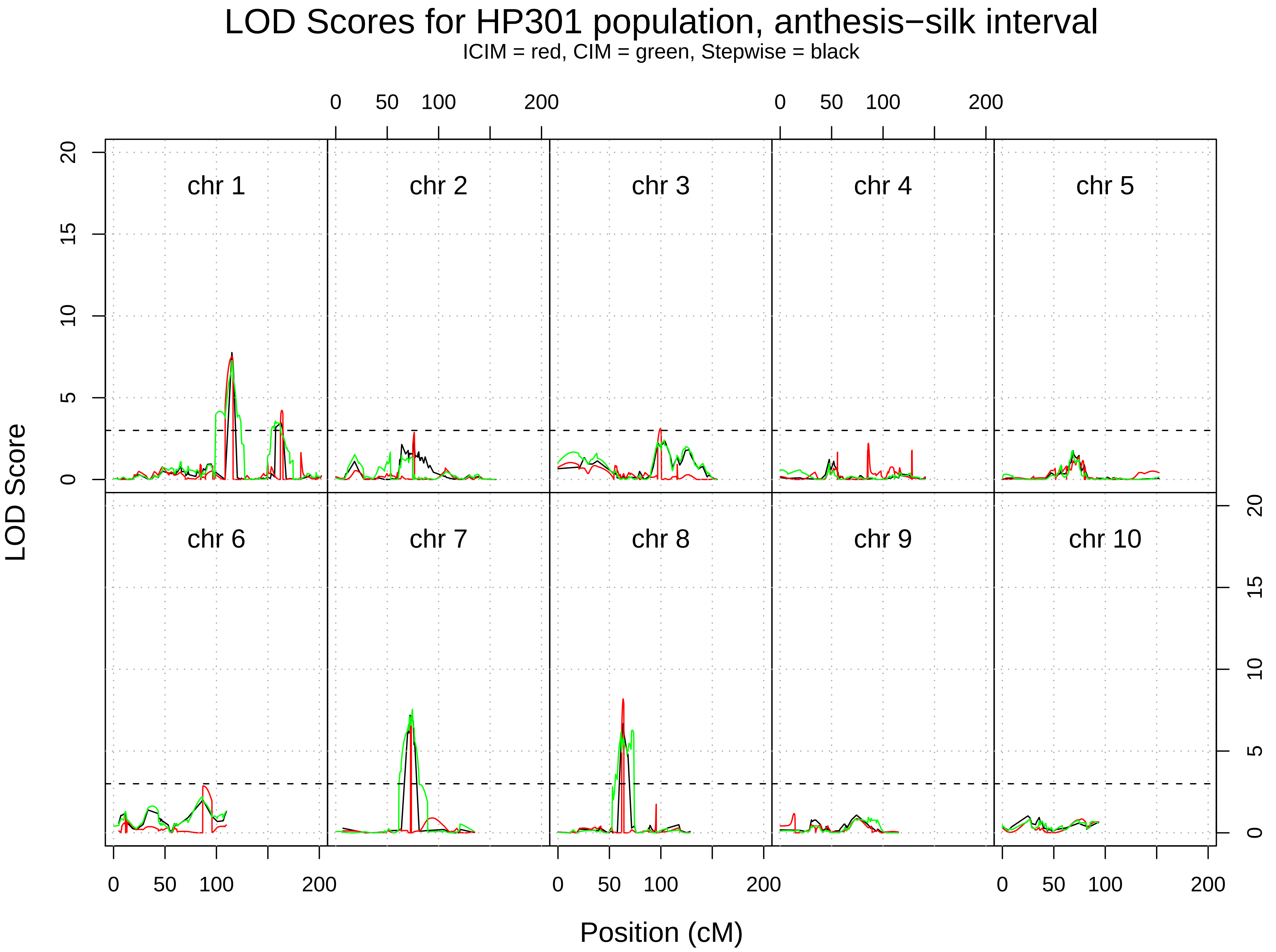


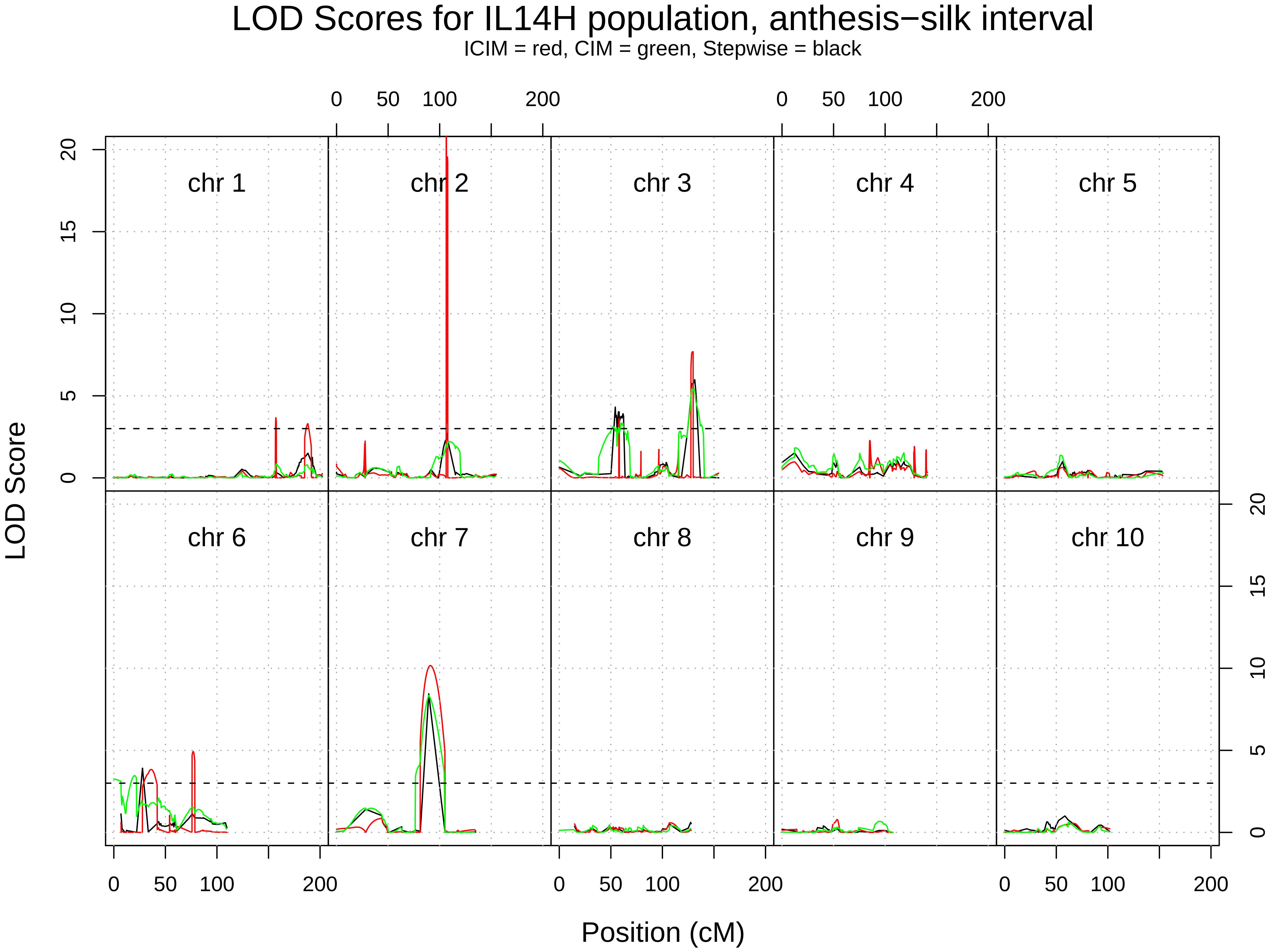

LOD Scores for CML52 population, anthesis−silk interval
ICIM = red, CIM = green, Stepwise = black
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
LOD Score
0
5
10
15
20
Position (cM)
0
50
100
200

LOD Scores for CML69 population, anthesis−silk interval

ICIM = red, CIM = green, Stepwise = black

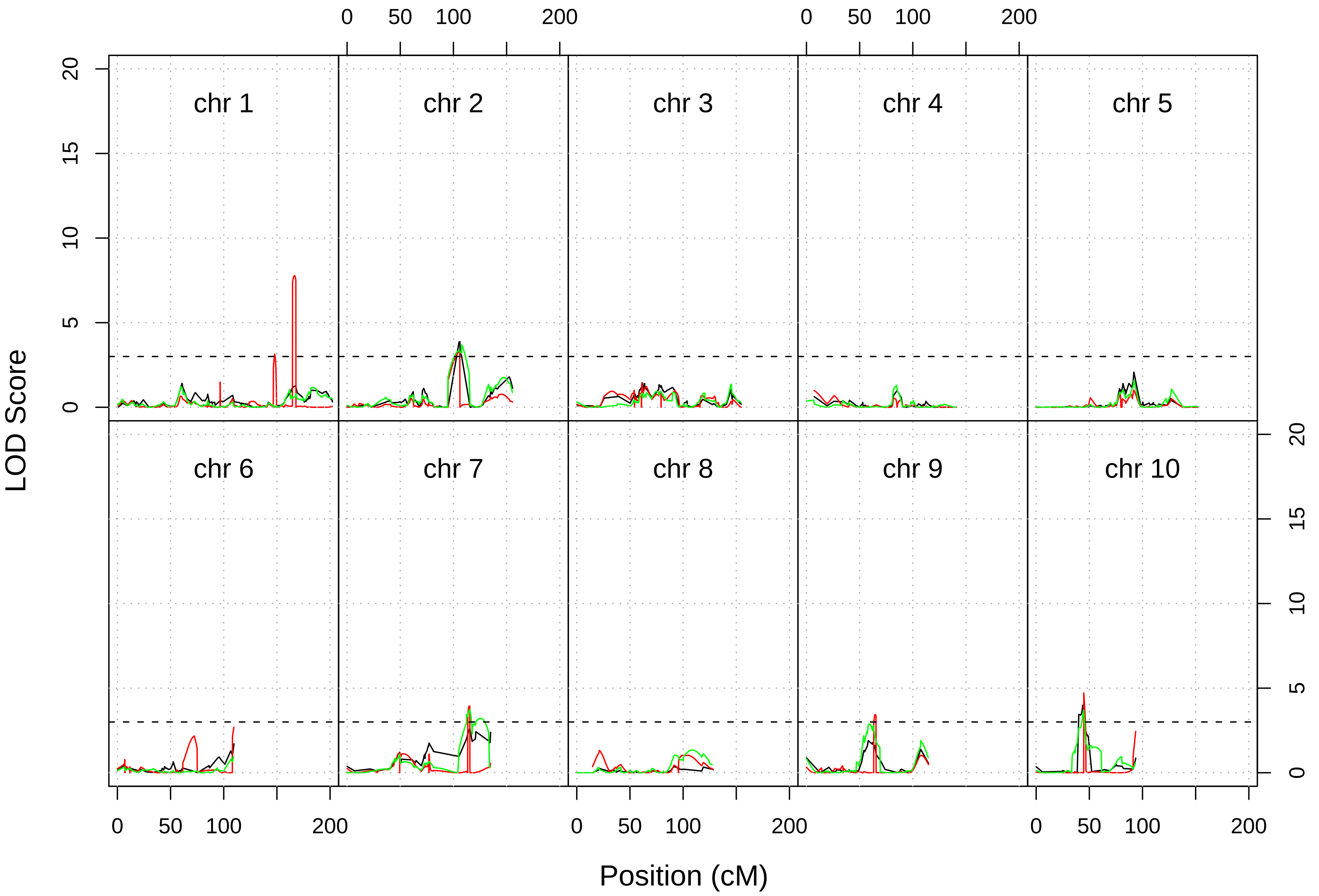


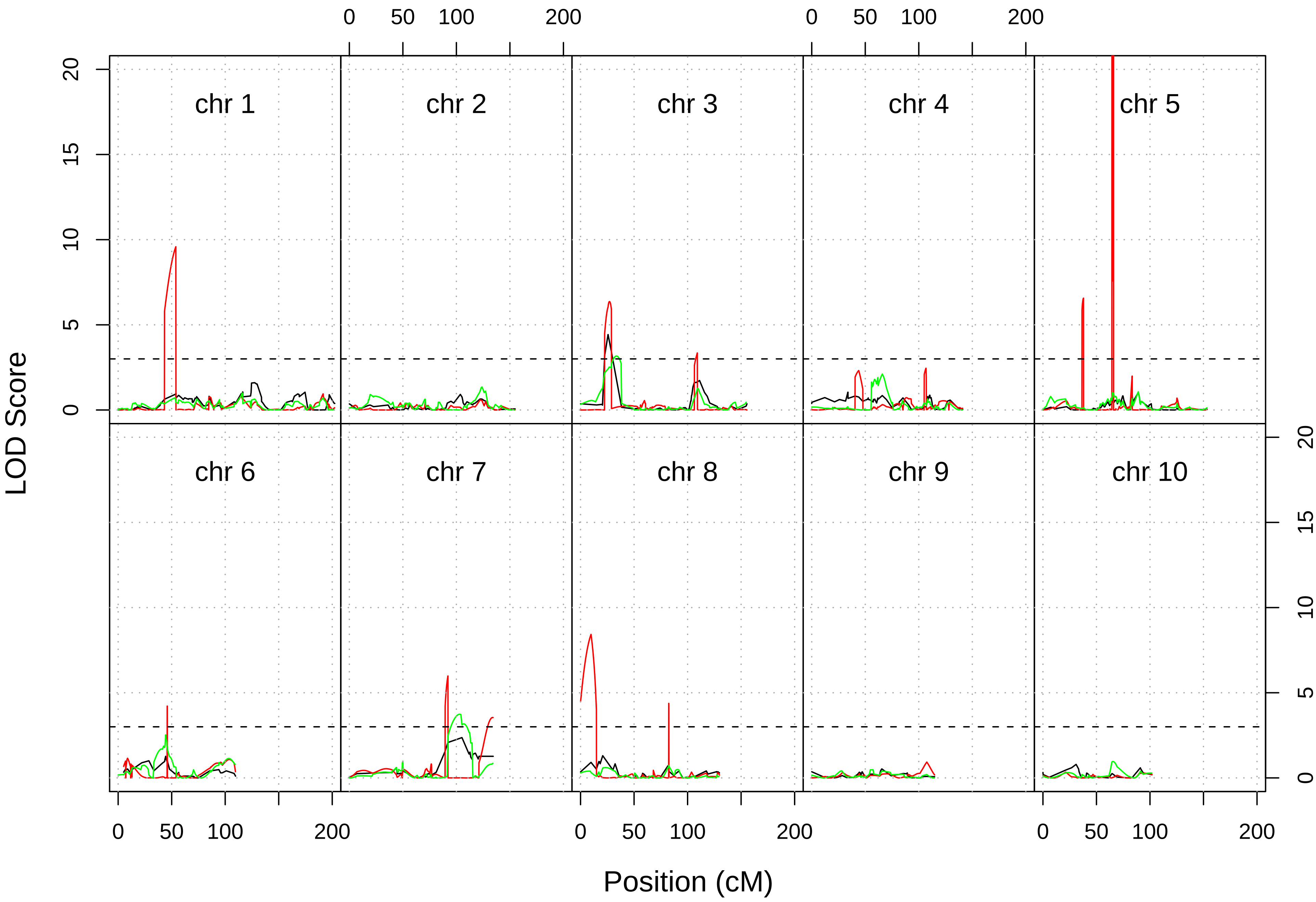

LOD Scores for HP301 population, anthesis−silk interval
ICIM = red, CIM = green, Stepwise = black
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
LOD Score
Position (cM)
0
5
10
15
20
0
50
100
200


LOD Scores for IL14H population, anthesis−silk interval
ICIM = red, CIM = green, Stepwise = black
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
LOD Score
0
5
10
15
20
Position (cM)
0
50
100
200

LOD Scores for KI11 population, anthesis−silk interval

ICIM = red, CIM = green, Stepwise = black



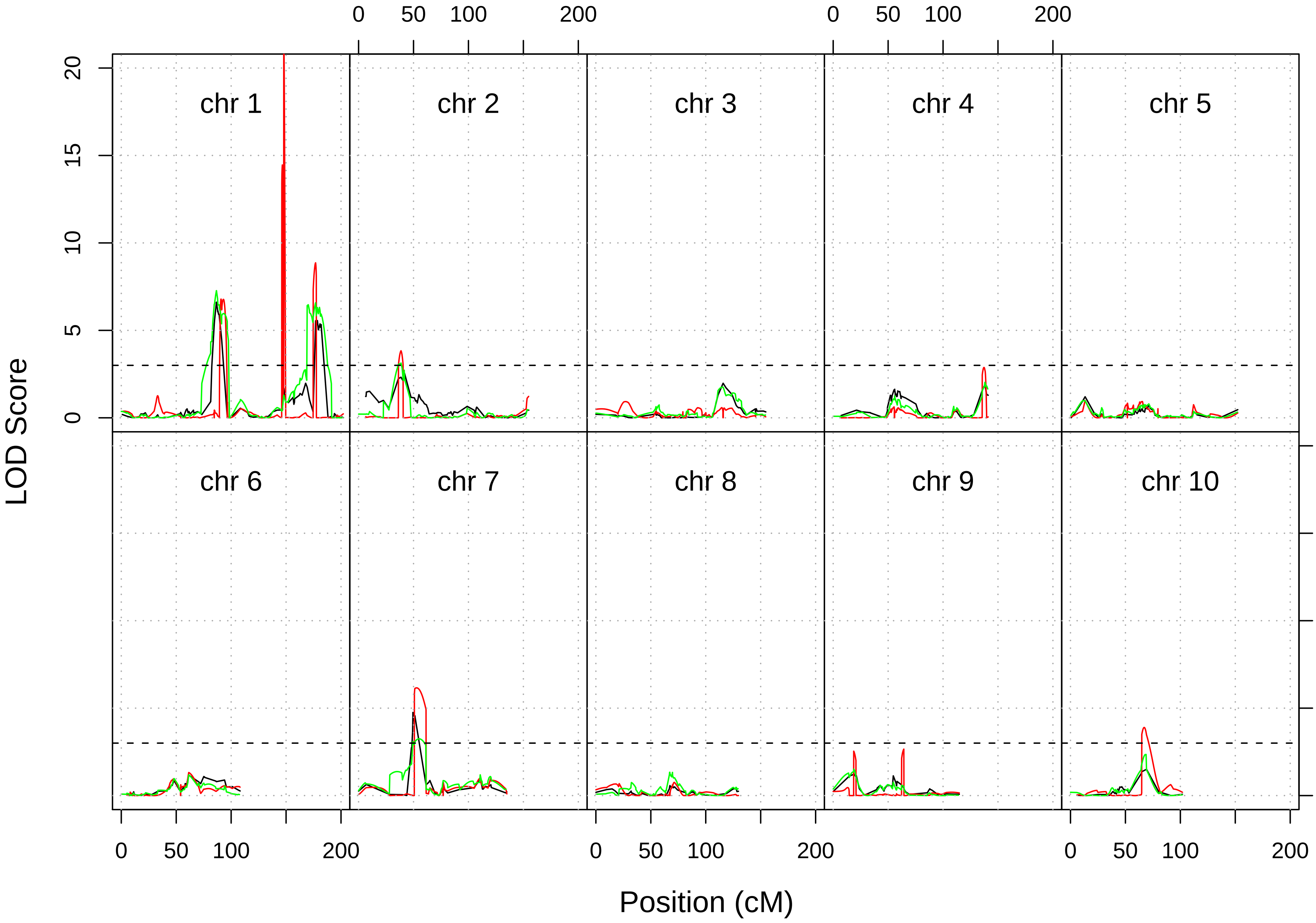


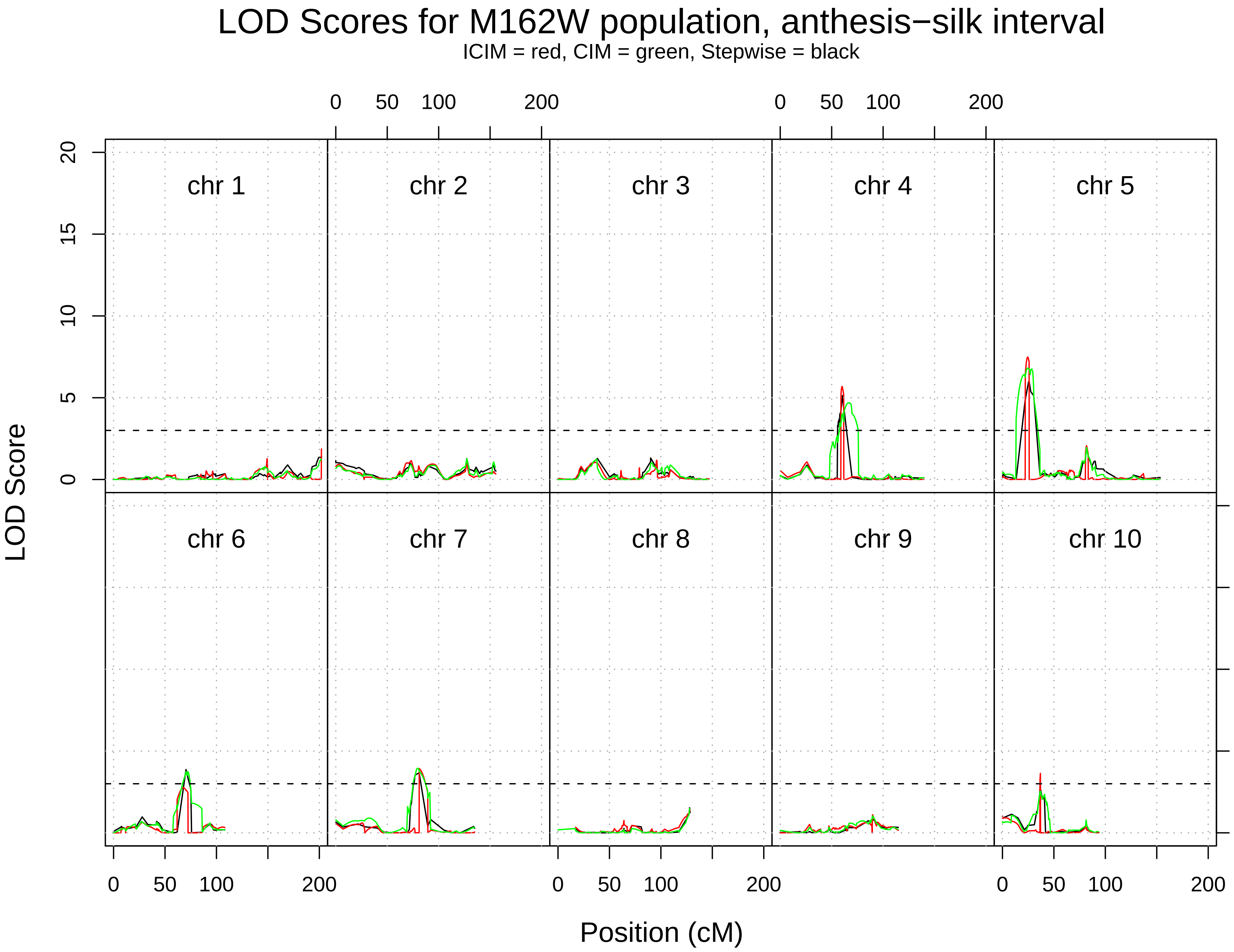
LOD Scores for KI3 population, anthesis−silk interval

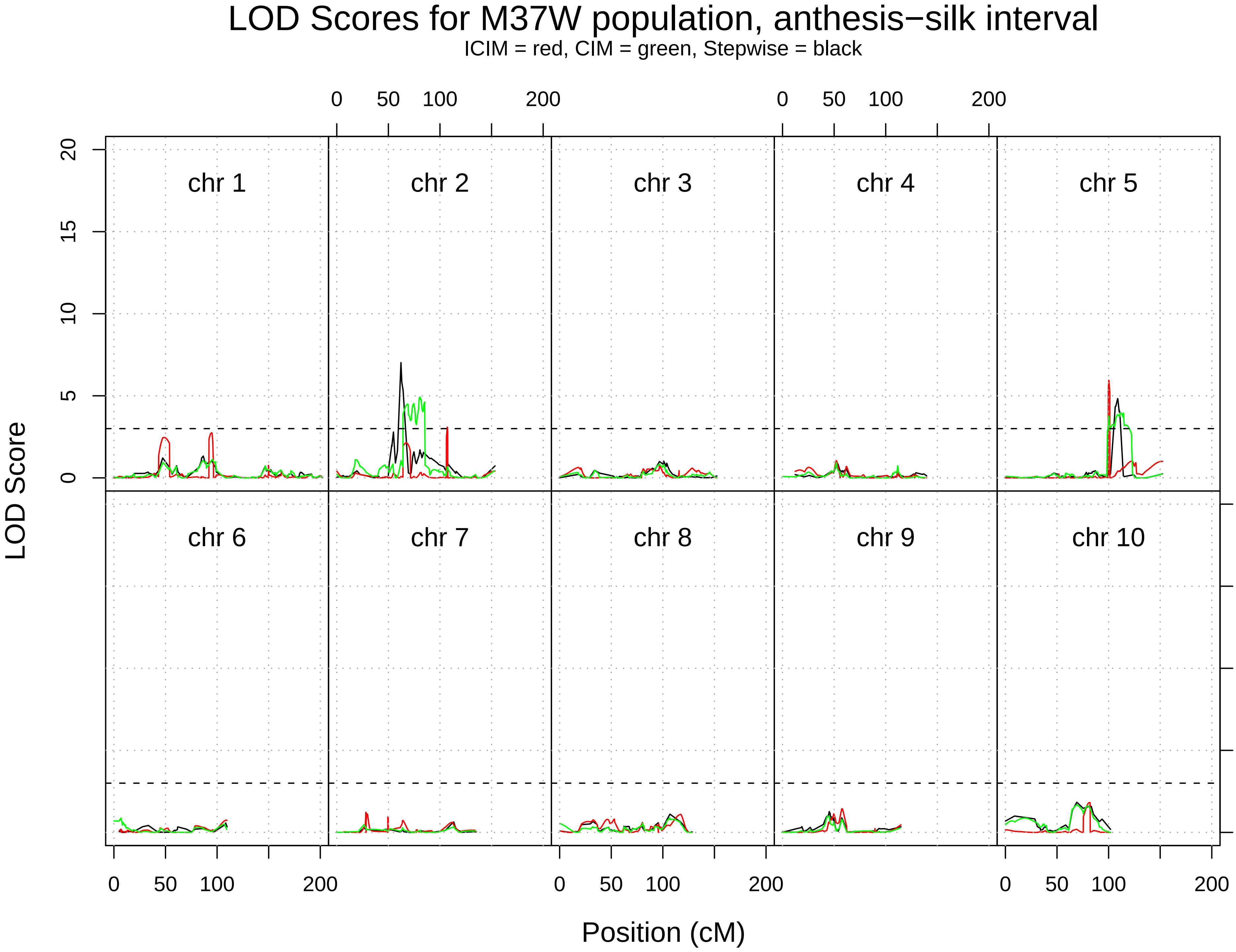
ICIM = red, CIM = green, Stepwise = black

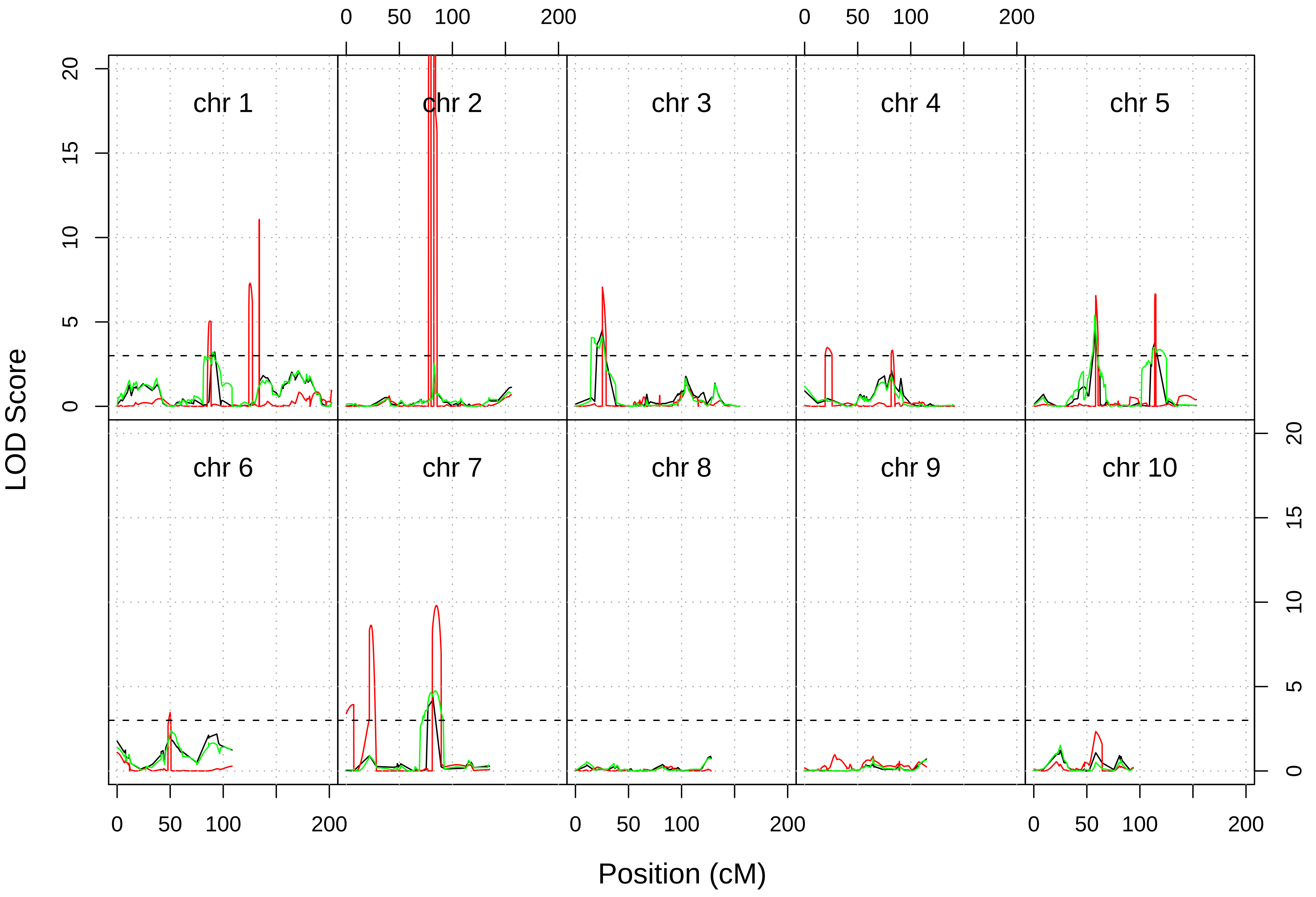
LOD Scores for KY21 population, anthesis−silk interval

ICIM = red, CIM = green, Stepwise = black



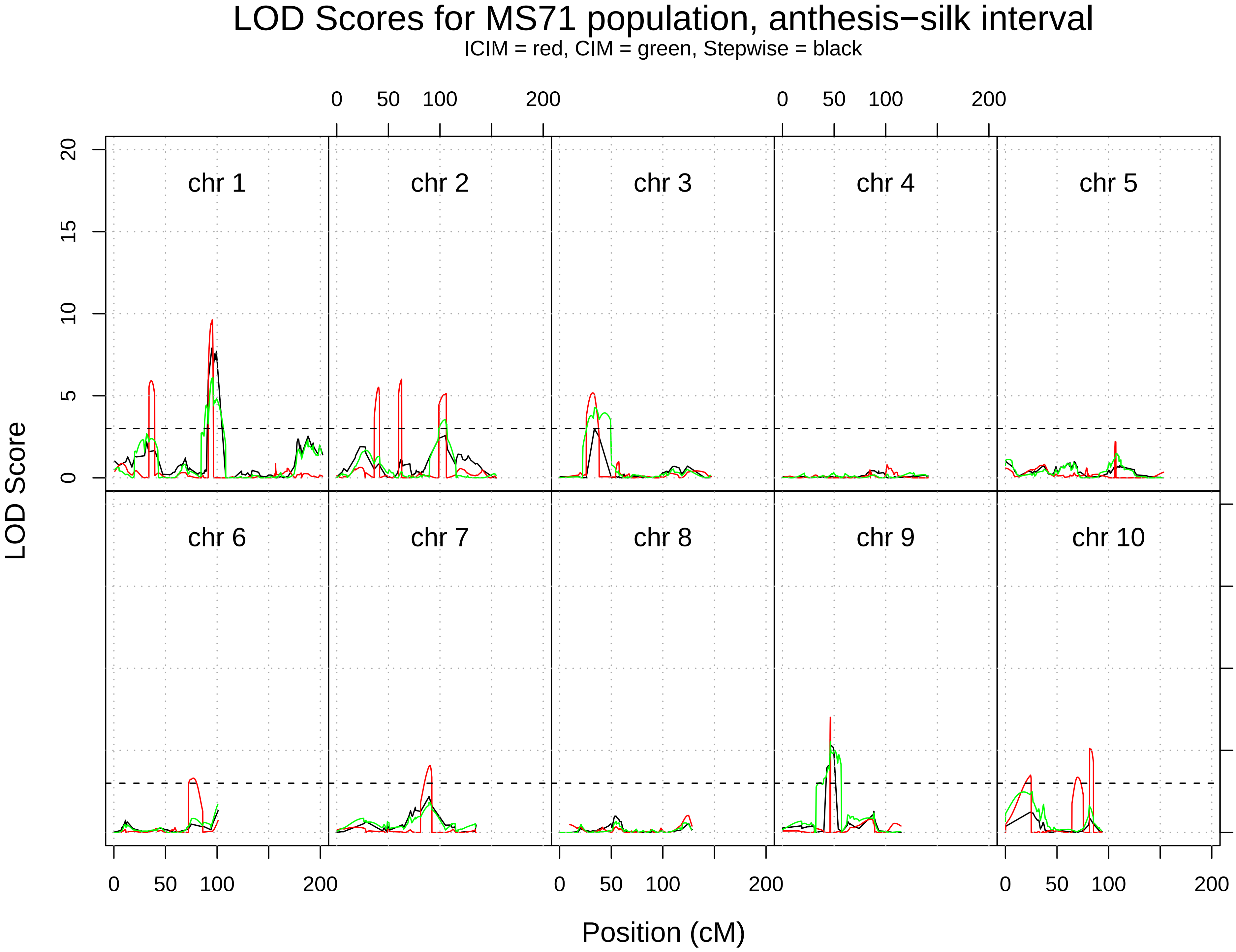

LOD Scores for M162W population, anthesis−silk interval
ICIM = red, CIM = green, Stepwise = black
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
LOD Score
Position (cM)
0
5
10
15
20
0
50
100
200


LOD Scores for M37W population, anthesis−silk interval
ICIM = red, CIM = green, Stepwise = black
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
LOD Score
Position (cM)
0
5
10
15
20
0
50
100
200



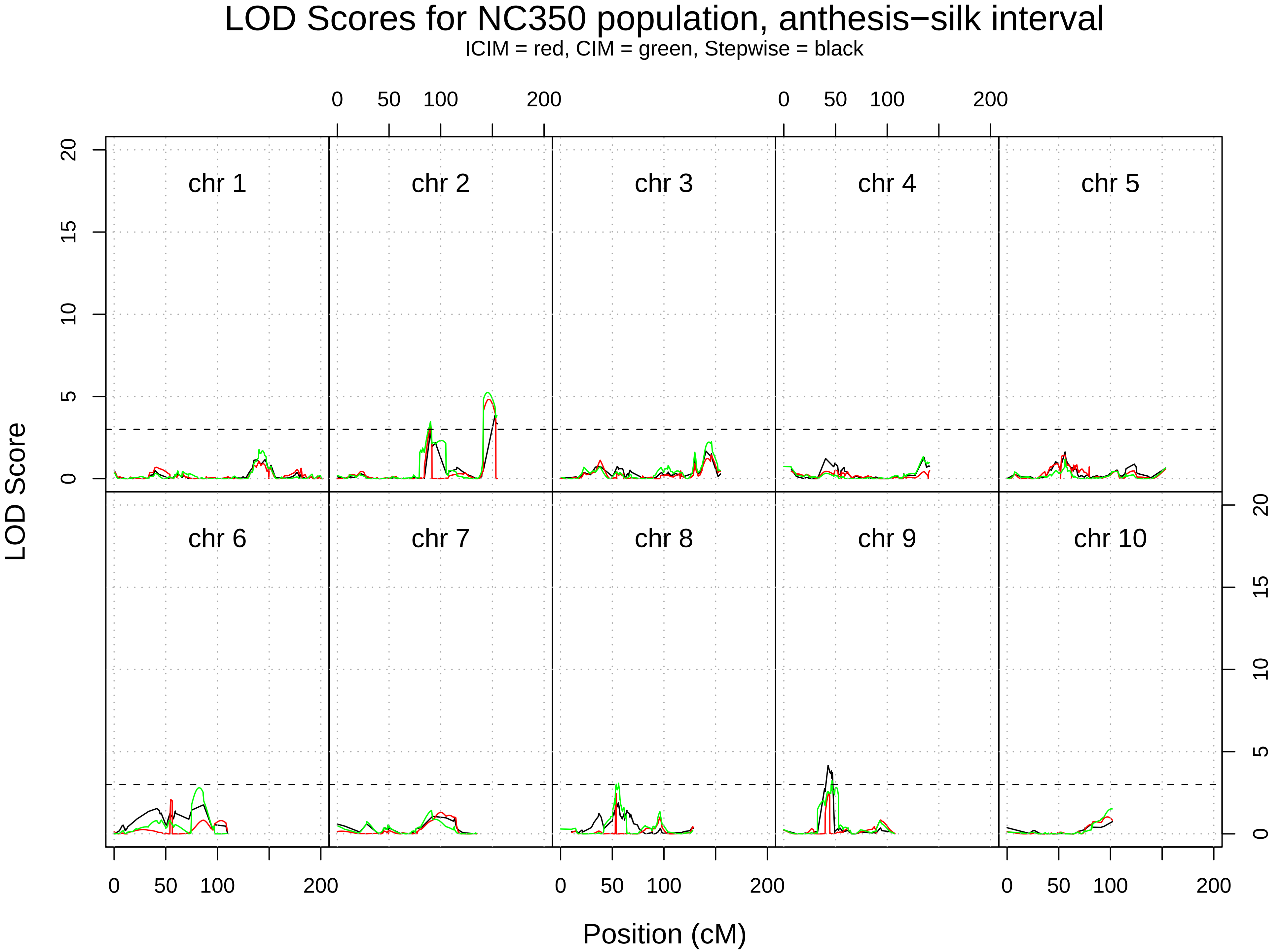
LOD Scores for MO18W population, anthesis−silk interval

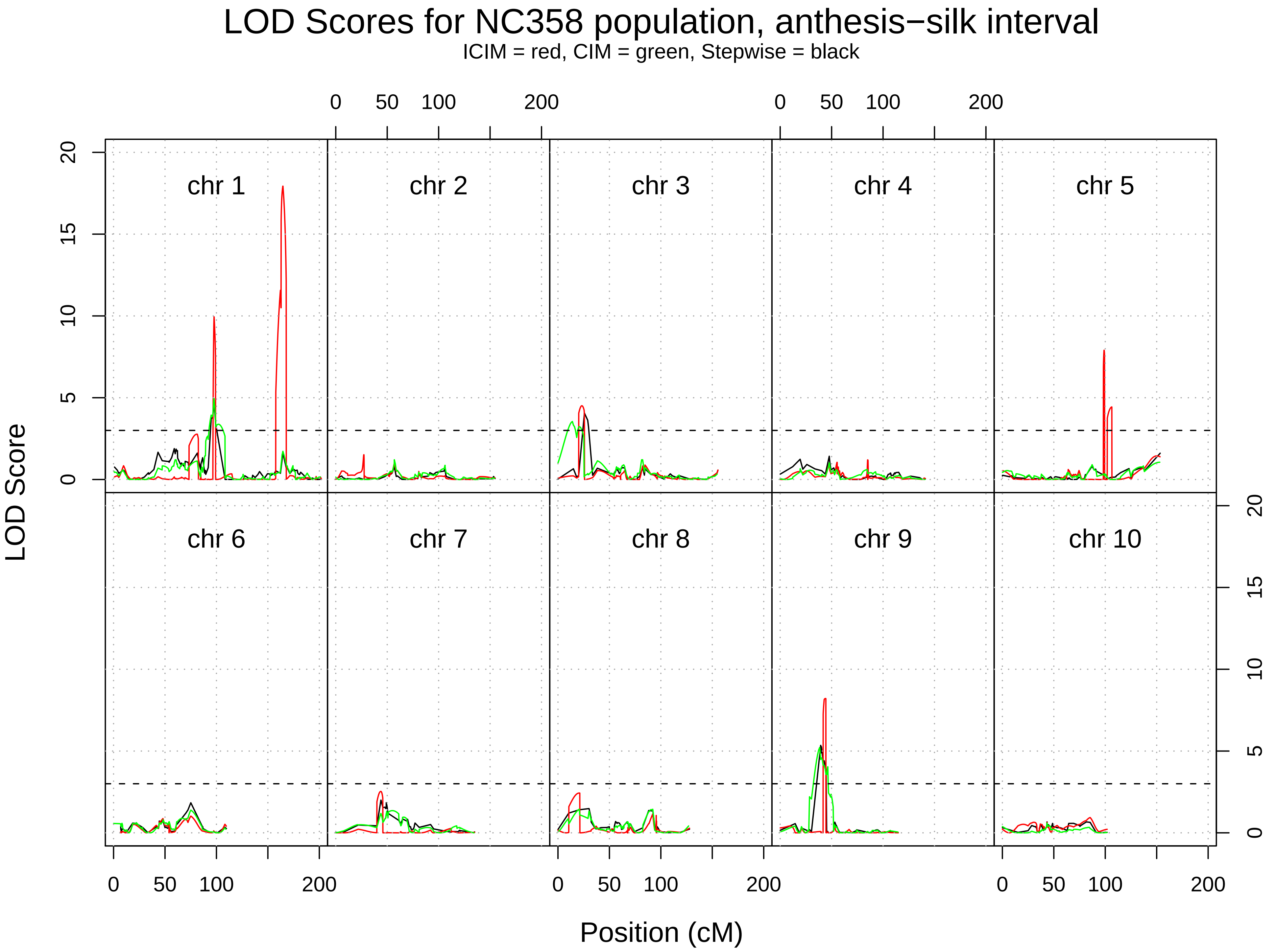
ICIM = red, CIM = green, Stepwise = black



LOD Scores for MS71 population, anthesis−silk interval

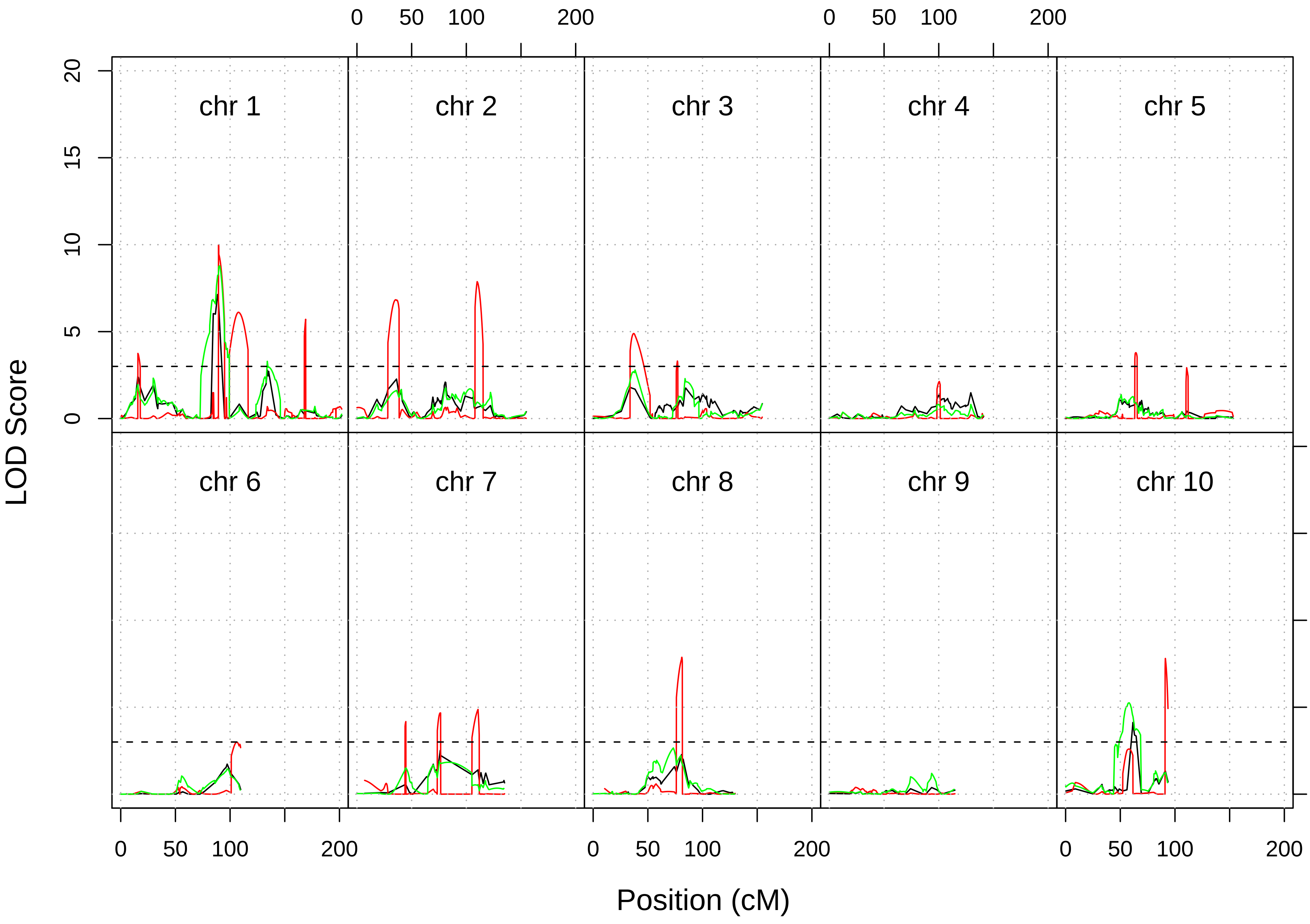
ICIM = red, CIM = green, Stepwise = black


LOD Scores for NC350 population, anthesis−silk interval
ICIM = red, CIM = green, Stepwise = black
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
LOD Score
0
5
10
15
20
0
50
100
200
Position (cM)


LOD Scores for NC358 population, anthesis−silk interval
ICIM = red, CIM = green, Stepwise = black
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
LOD Score
0
5
10
15
20
Position (cM)
0
50
100
200

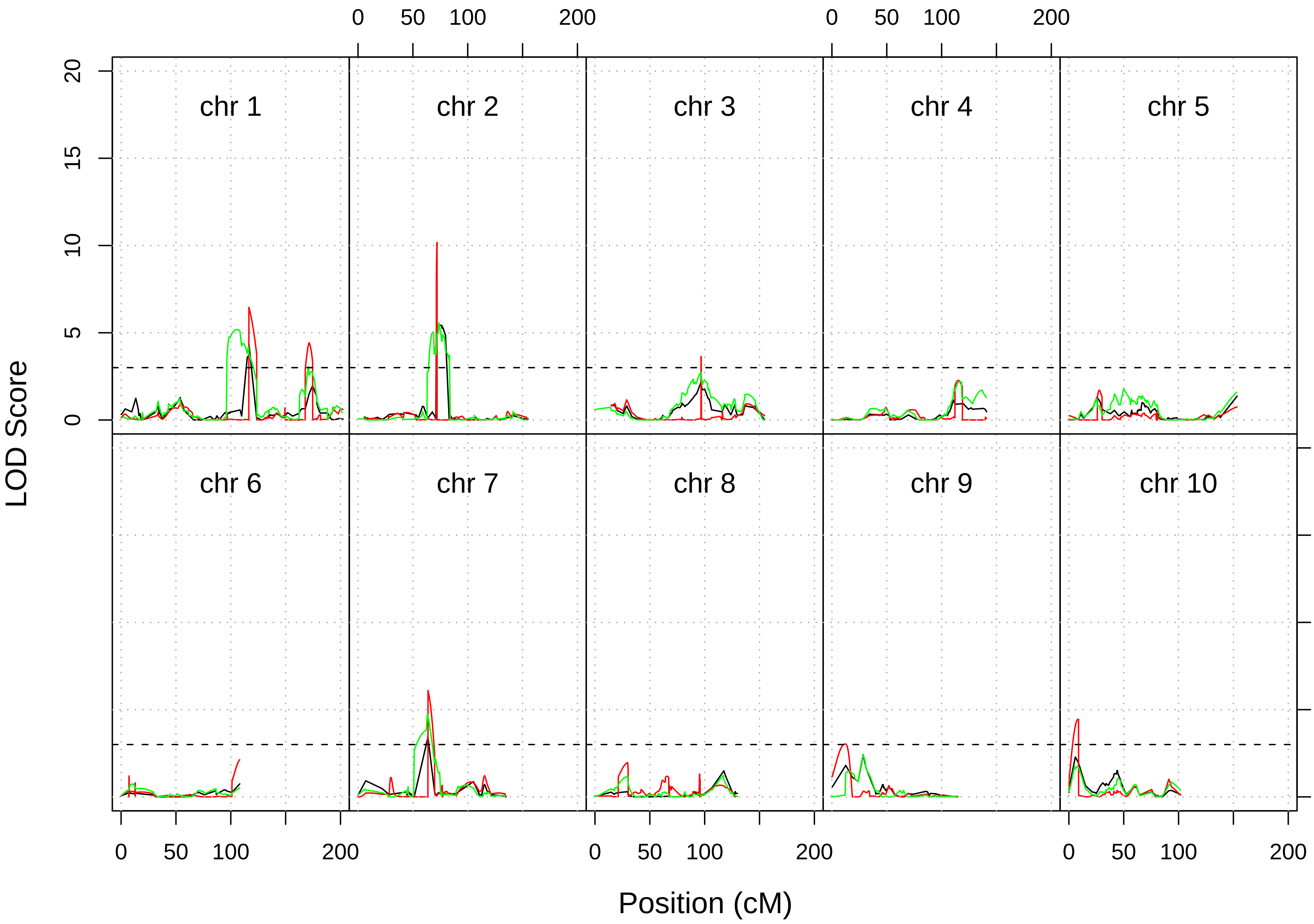
LOD Scores for OH43 population, anthesis−silk interval

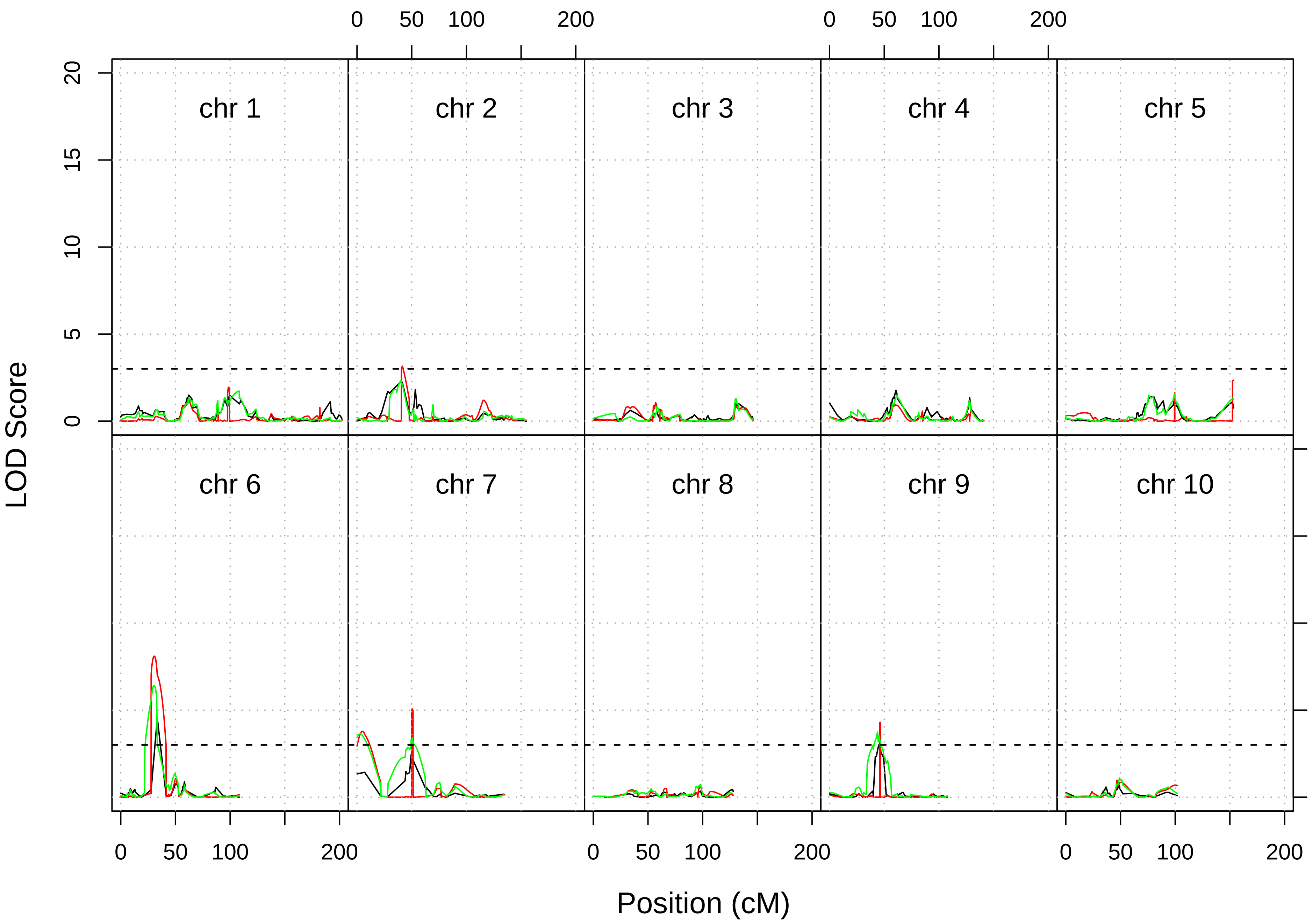
ICIM = red, CIM = green, Stepwise = black



LOD Scores for OH7B population, anthesis−silk interval

ICIM = red, CIM = green, Stepwise = black



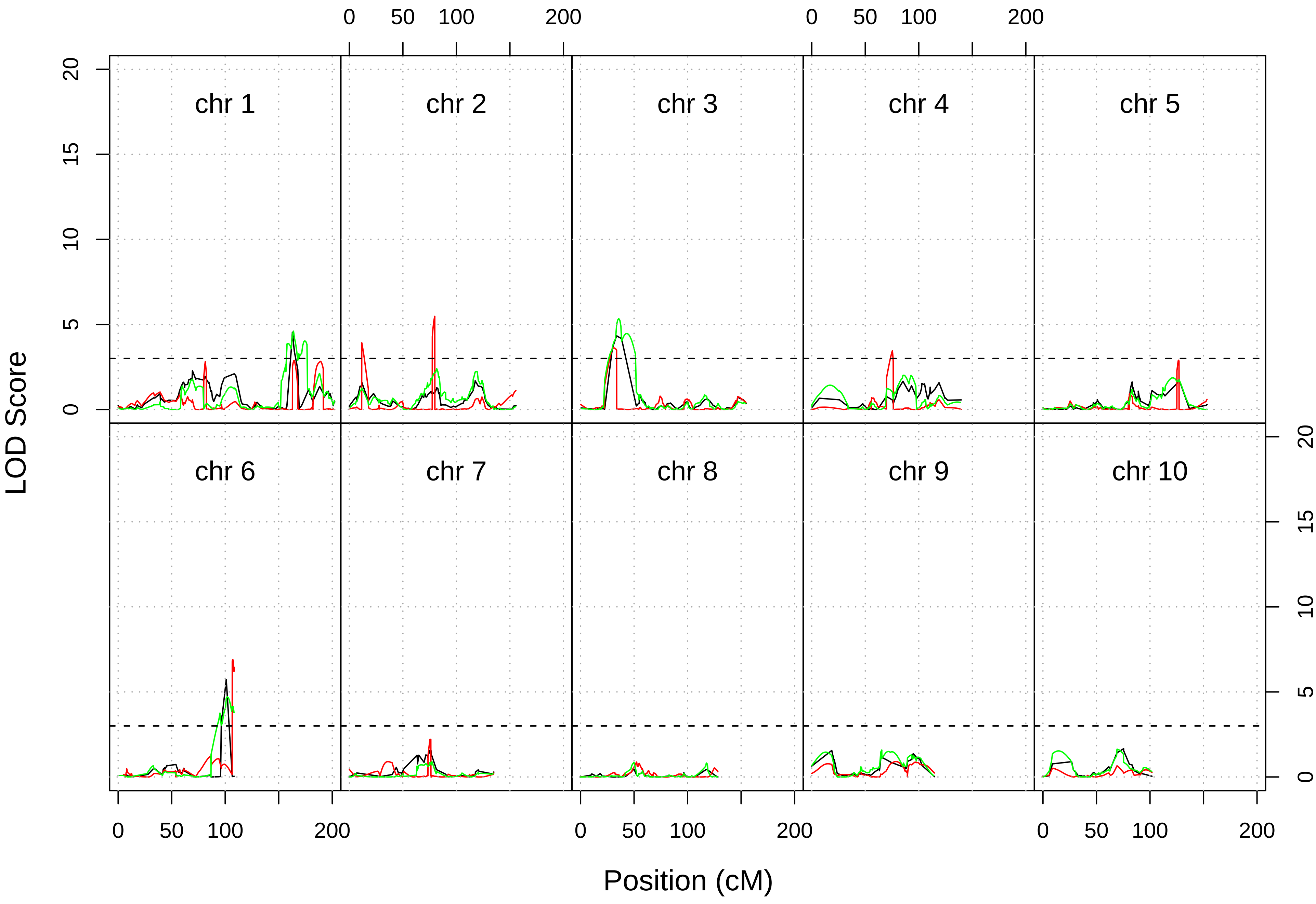


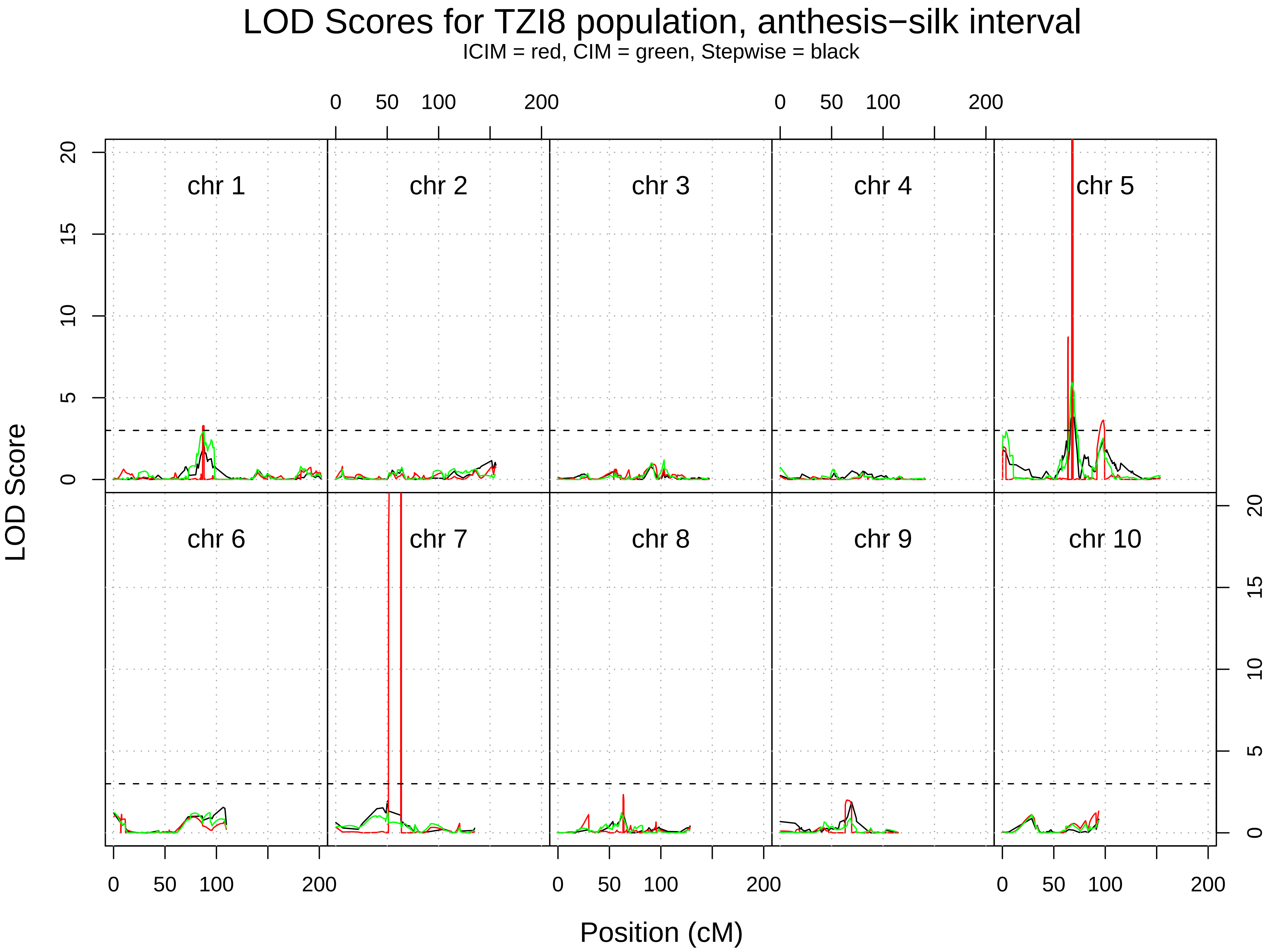
LOD Scores for P39 population, anthesis−silk interval

ICIM = red, CIM = green, Stepwise = black

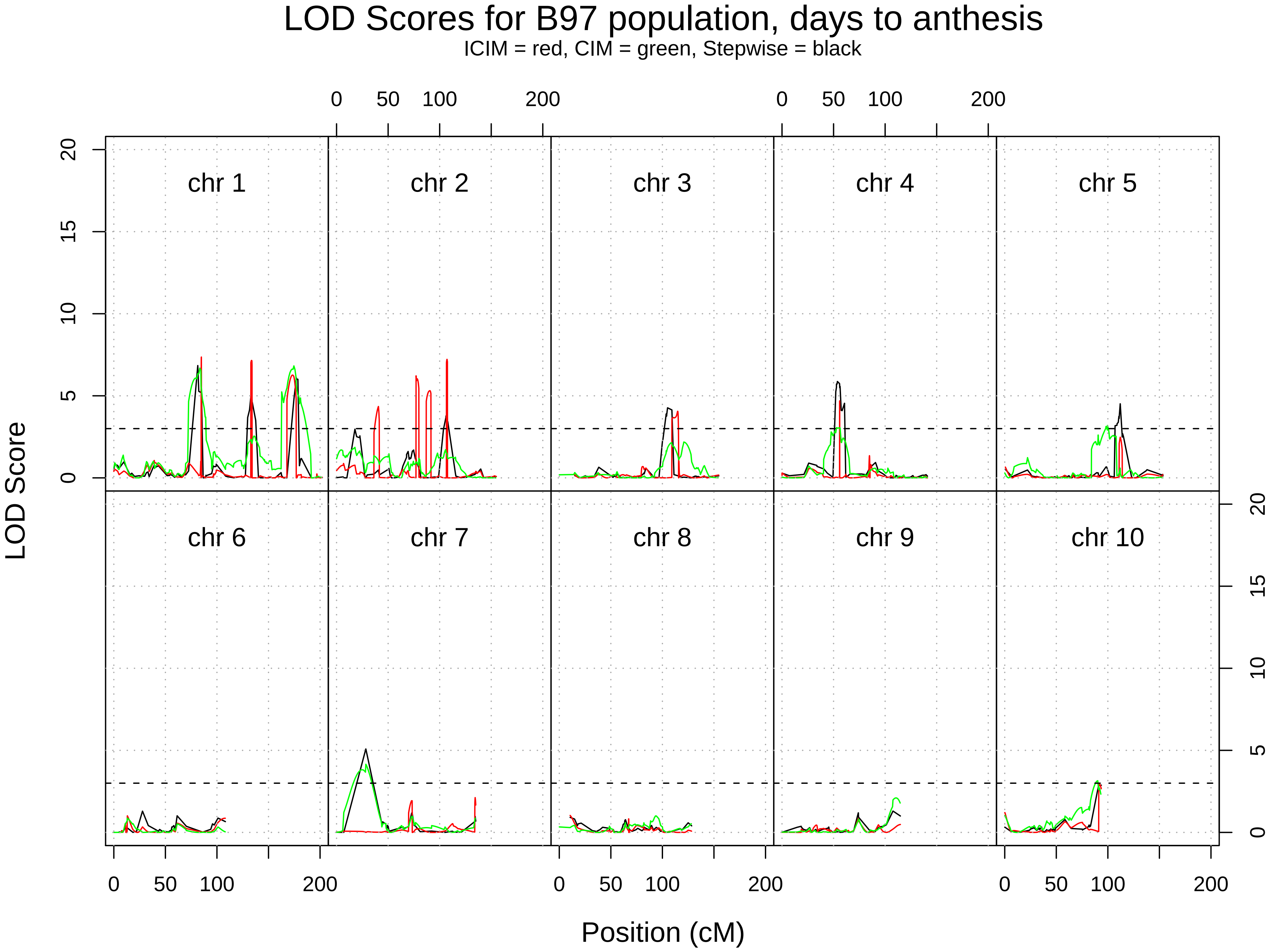
LOD Scores for TX303 population, anthesis−silk interval

ICIM = red, CIM = green, Stepwise = black



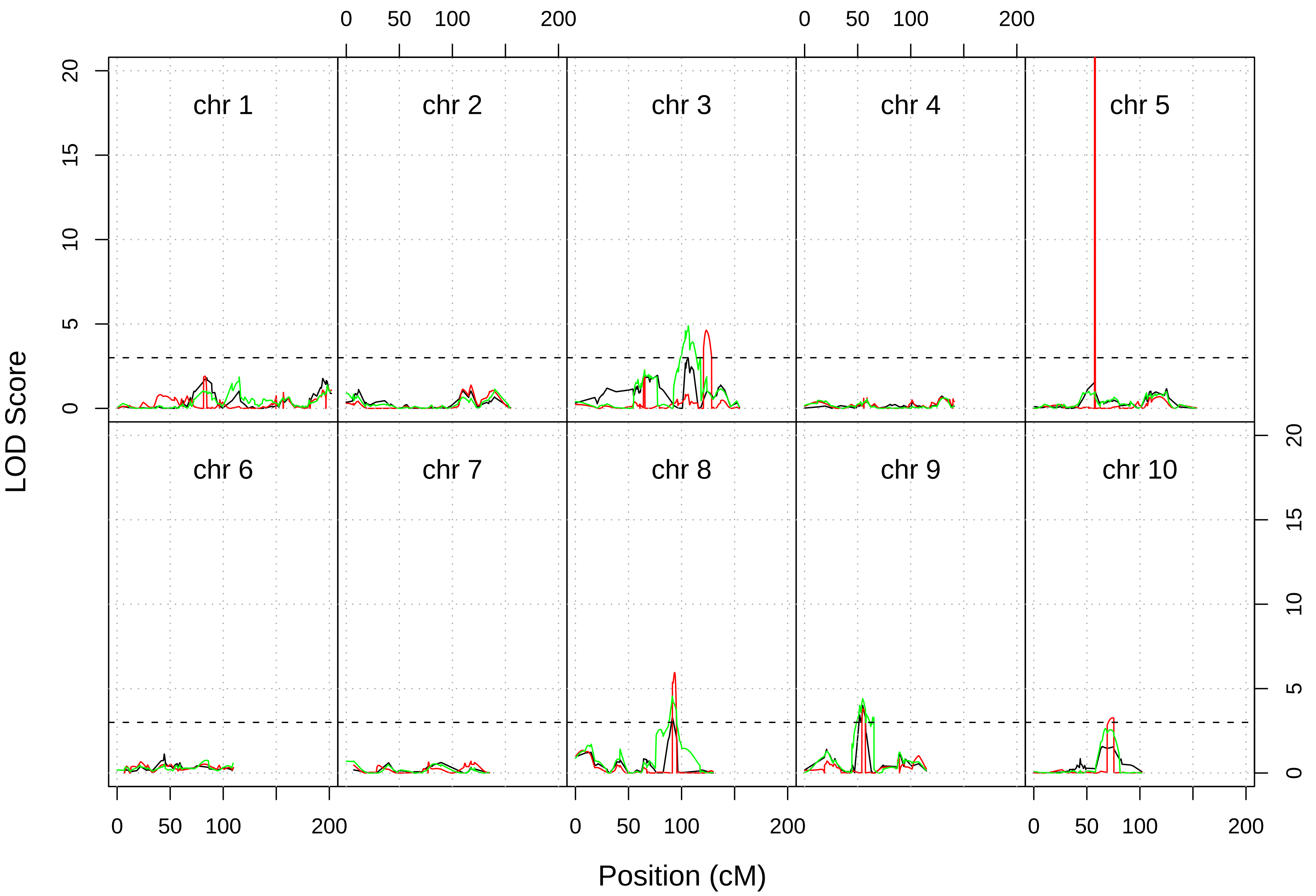

LOD Scores for TZI8 population, anthesis−silk interval

ICIM = red, CIM = green, Stepwise = black



LOD Scores for B97 population, days to anthesis

ICIM = red, CIM = green, Stepwise = black

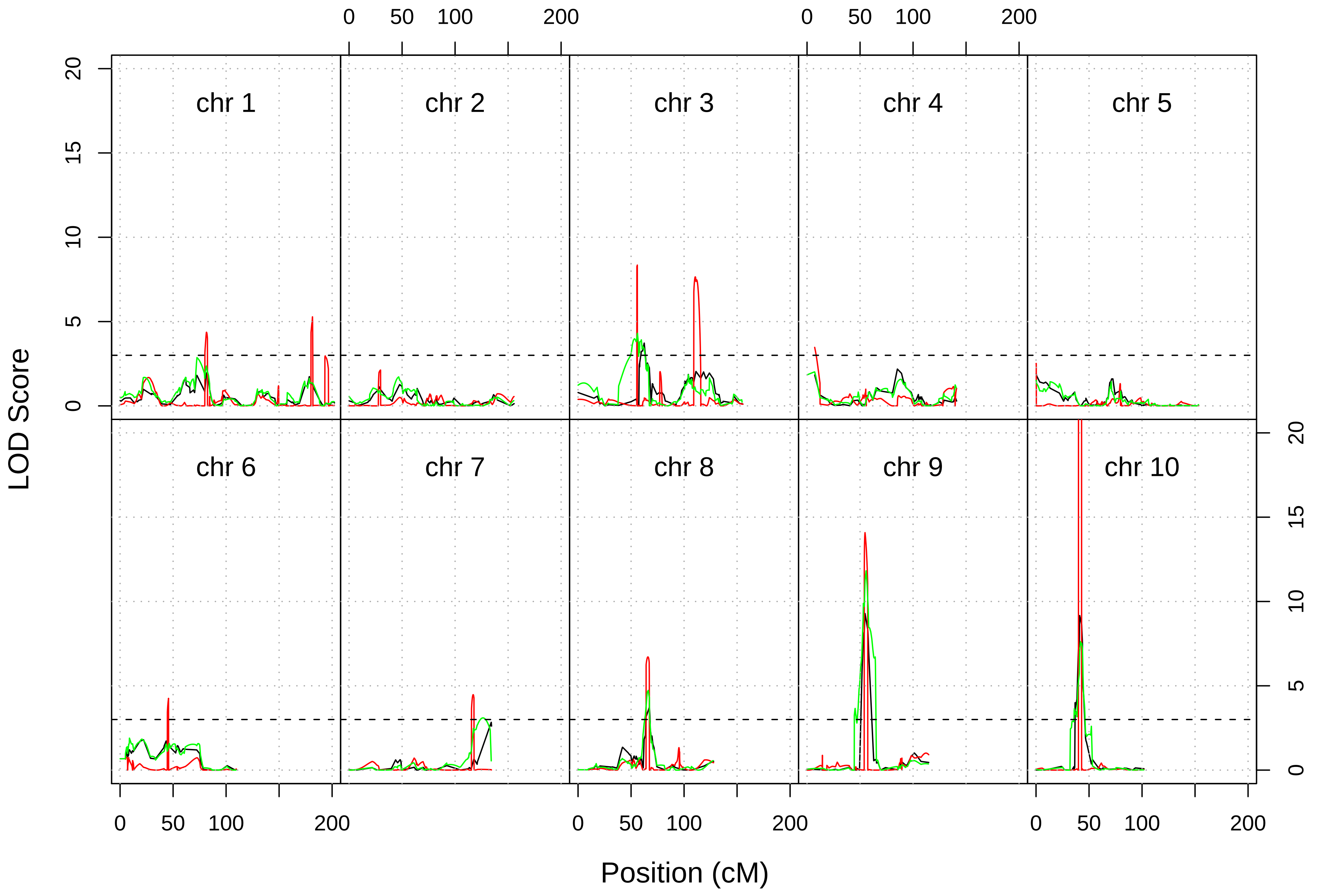


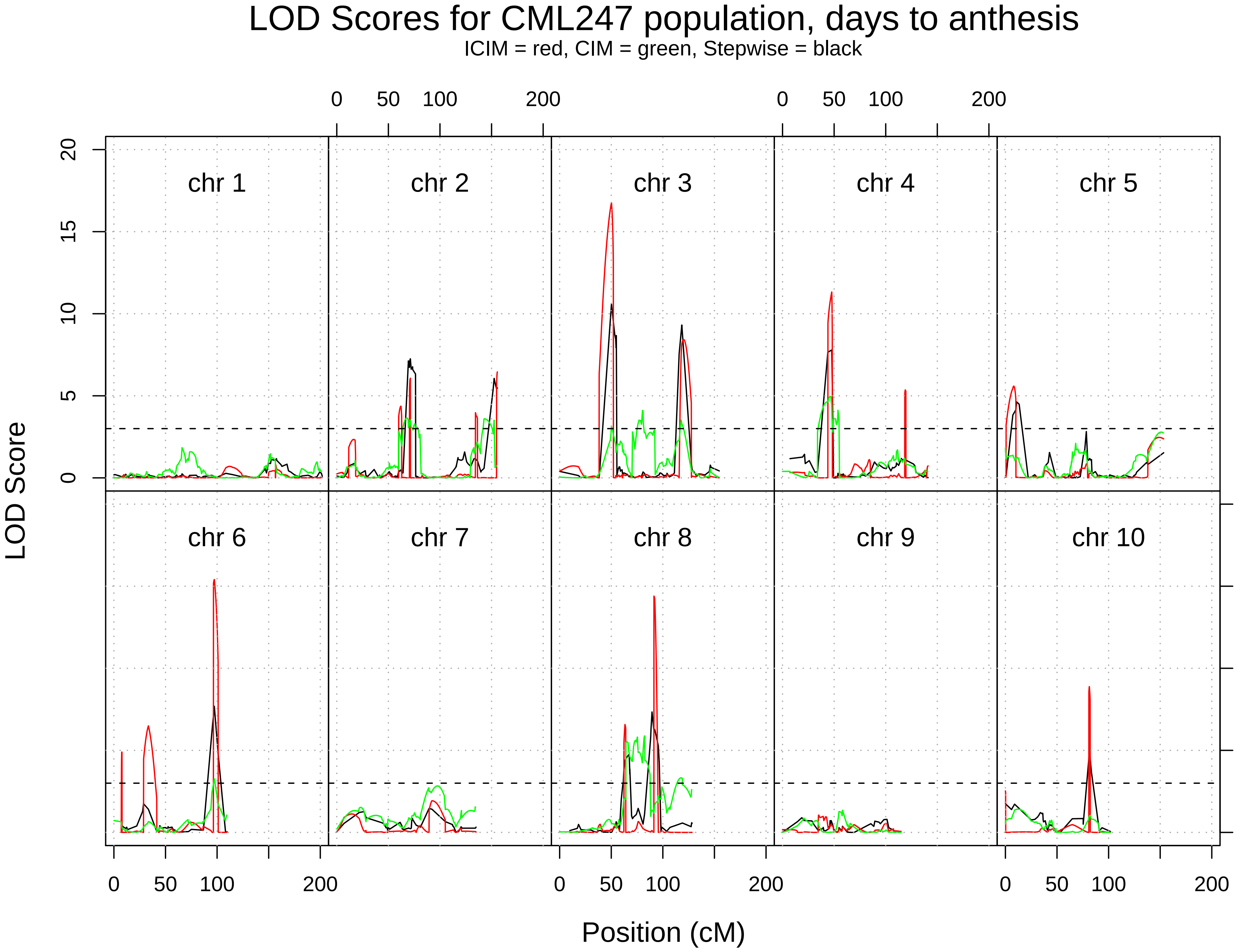
LOD Scores for CML103 population, days to anthesis

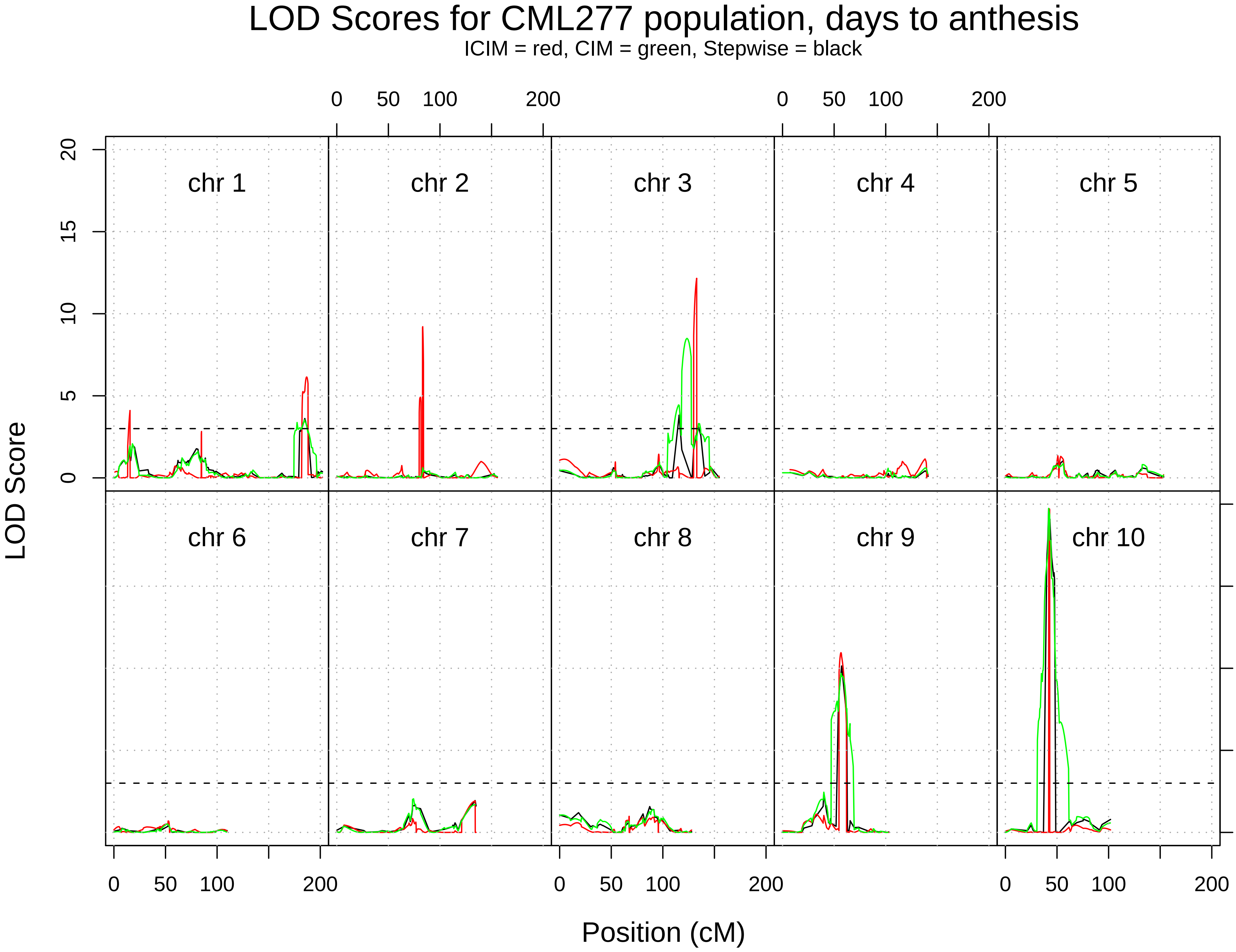
ICIM = red, CIM = green, Stepwise = black

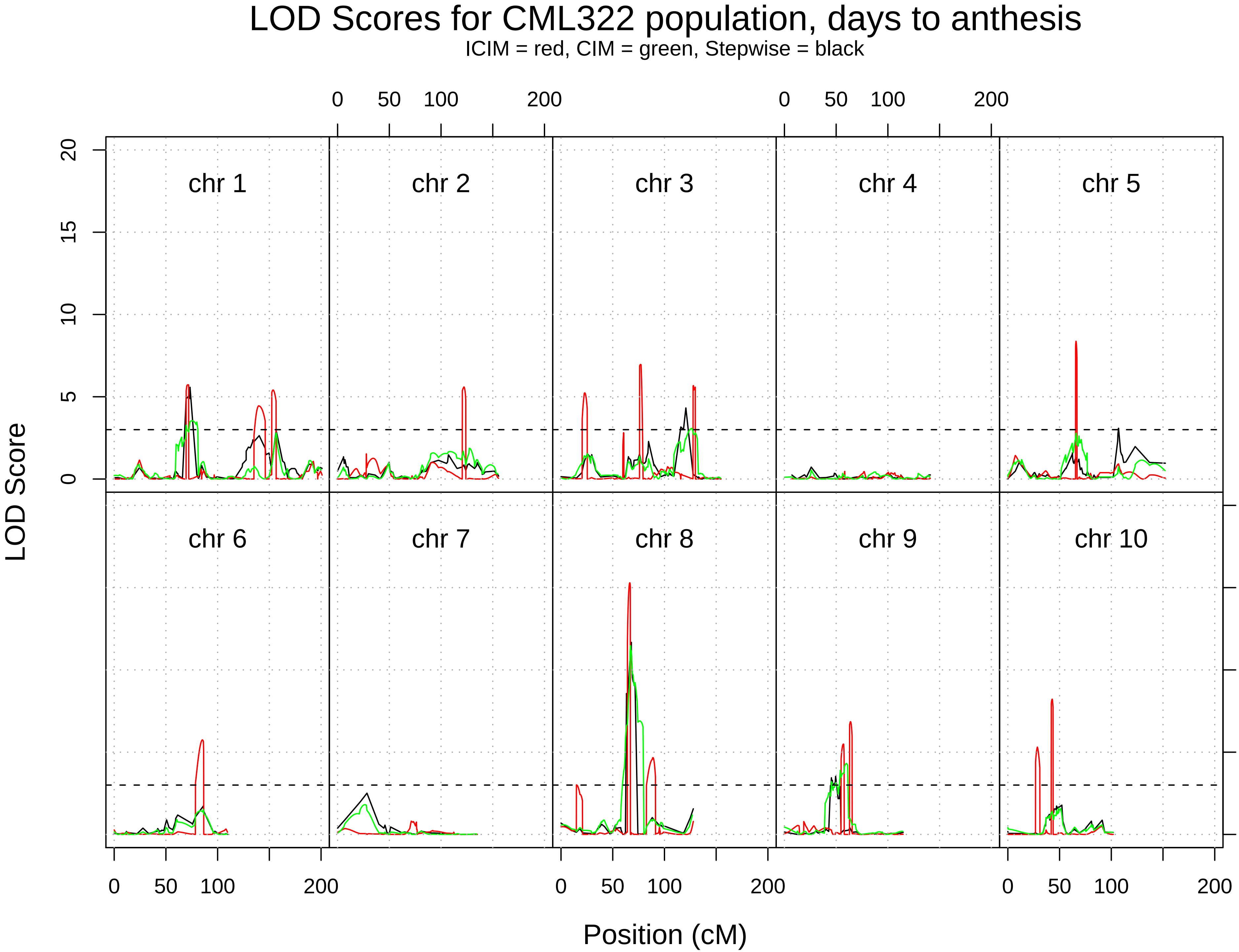
LOD Scores for CML228 population, days to anthesis

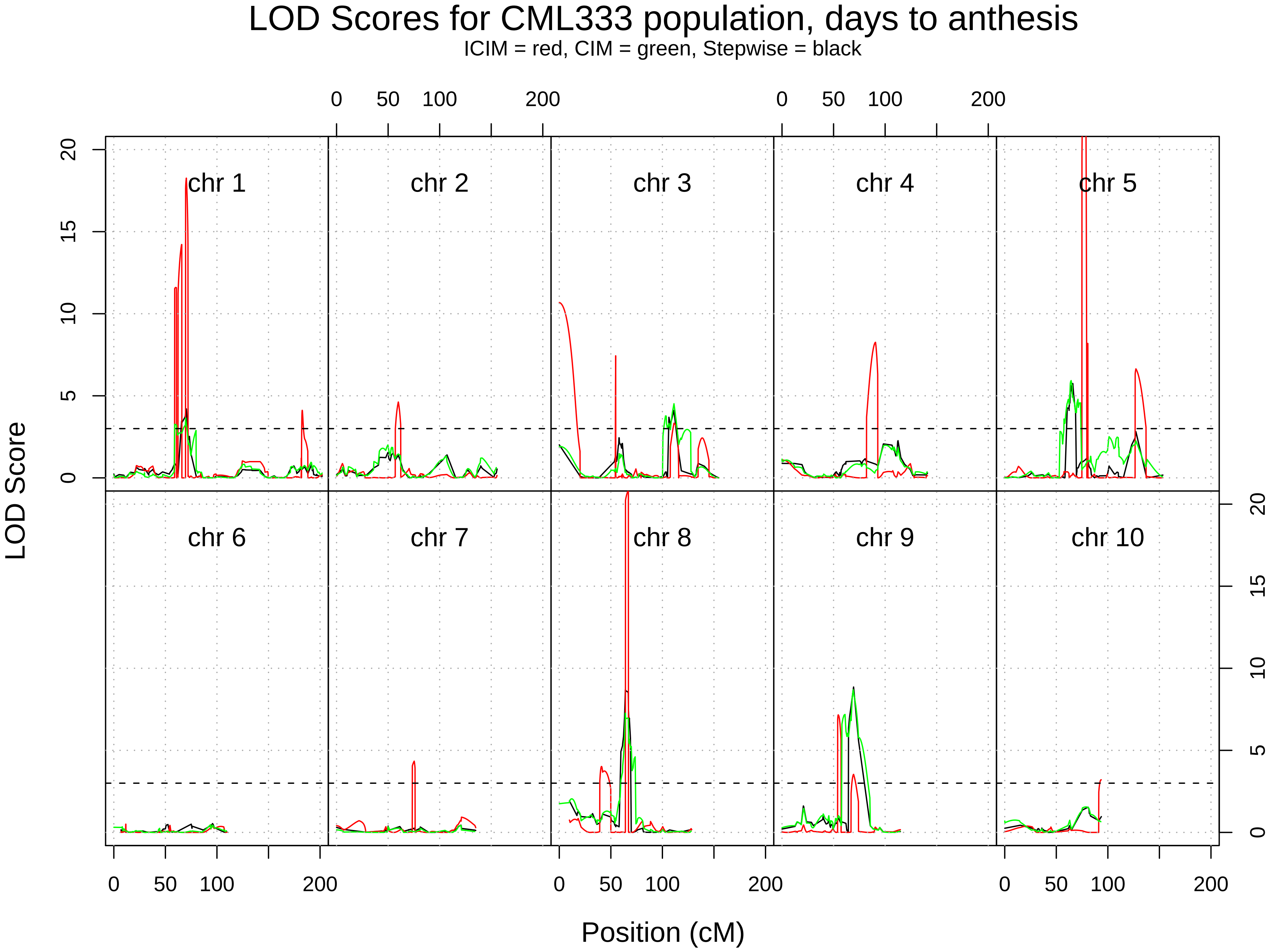
ICIM = red, CIM = green, Stepwise = black




LOD Scores for CML247 population, days to anthesis
ICIM = red, CIM = green, Stepwise = black
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
LOD Score
Position (cM)
0
5
10
15
20
0
50
100
200

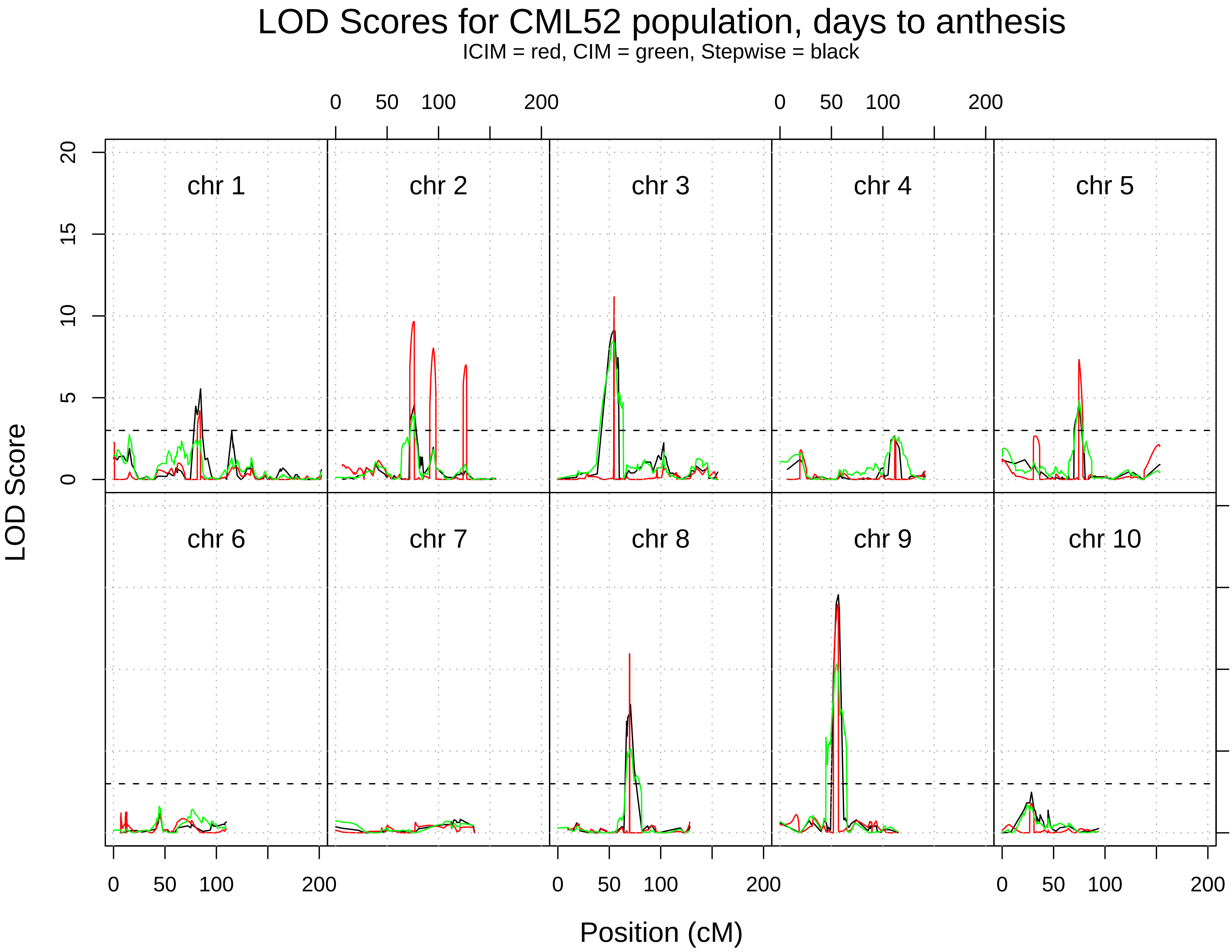

LOD Scores for CML277 population, days to anthesis
ICIM = red, CIM = green, Stepwise = black
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
LOD Score
0
5
10
15
20
Position (cM)
0
50
100
200

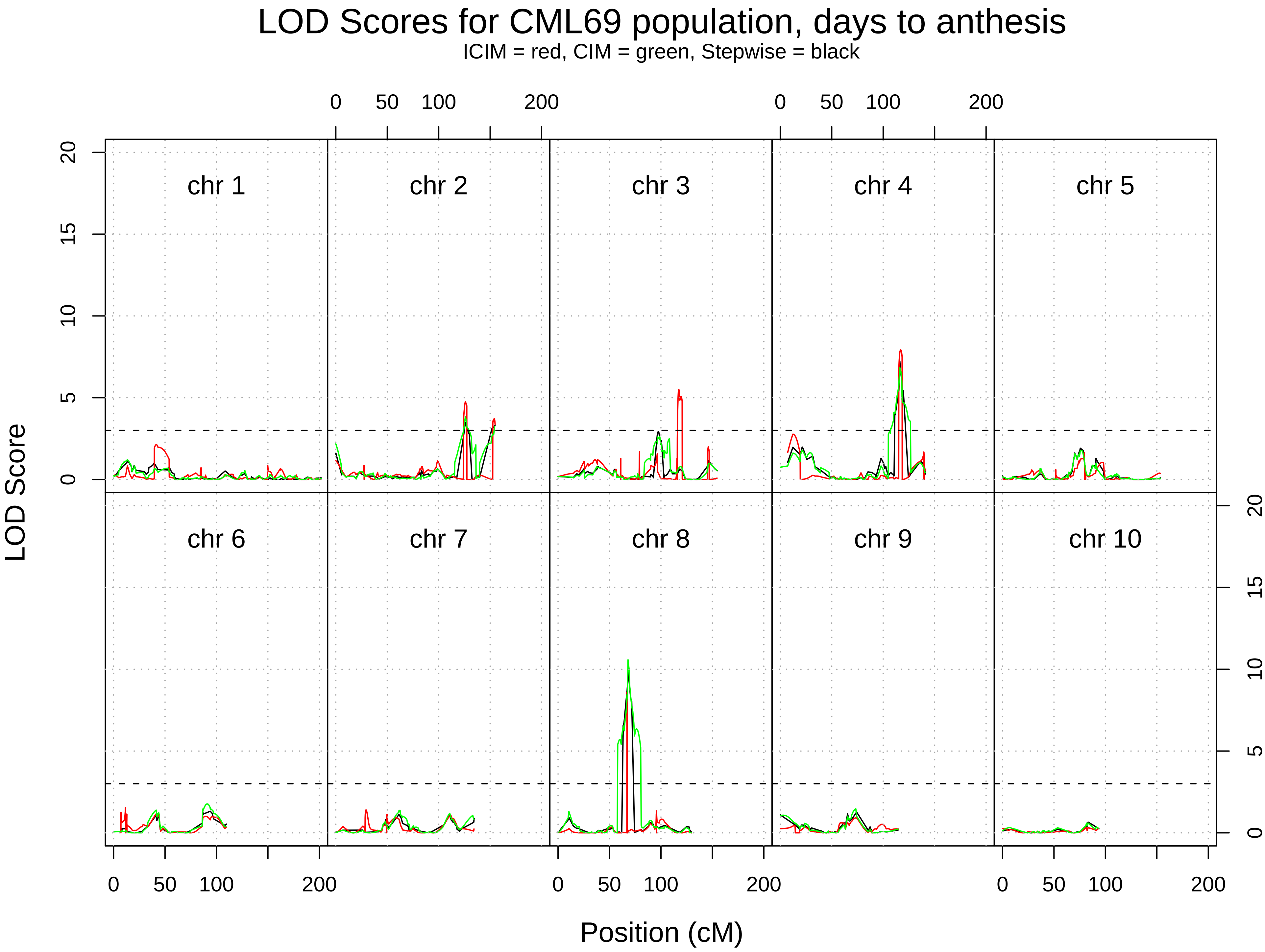

LOD Scores for CML322 population, days to anthesis
ICIM = red, CIM = green, Stepwise = black
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
LOD Score
Position (cM)
0
5
10
15
20
0
50
100
200

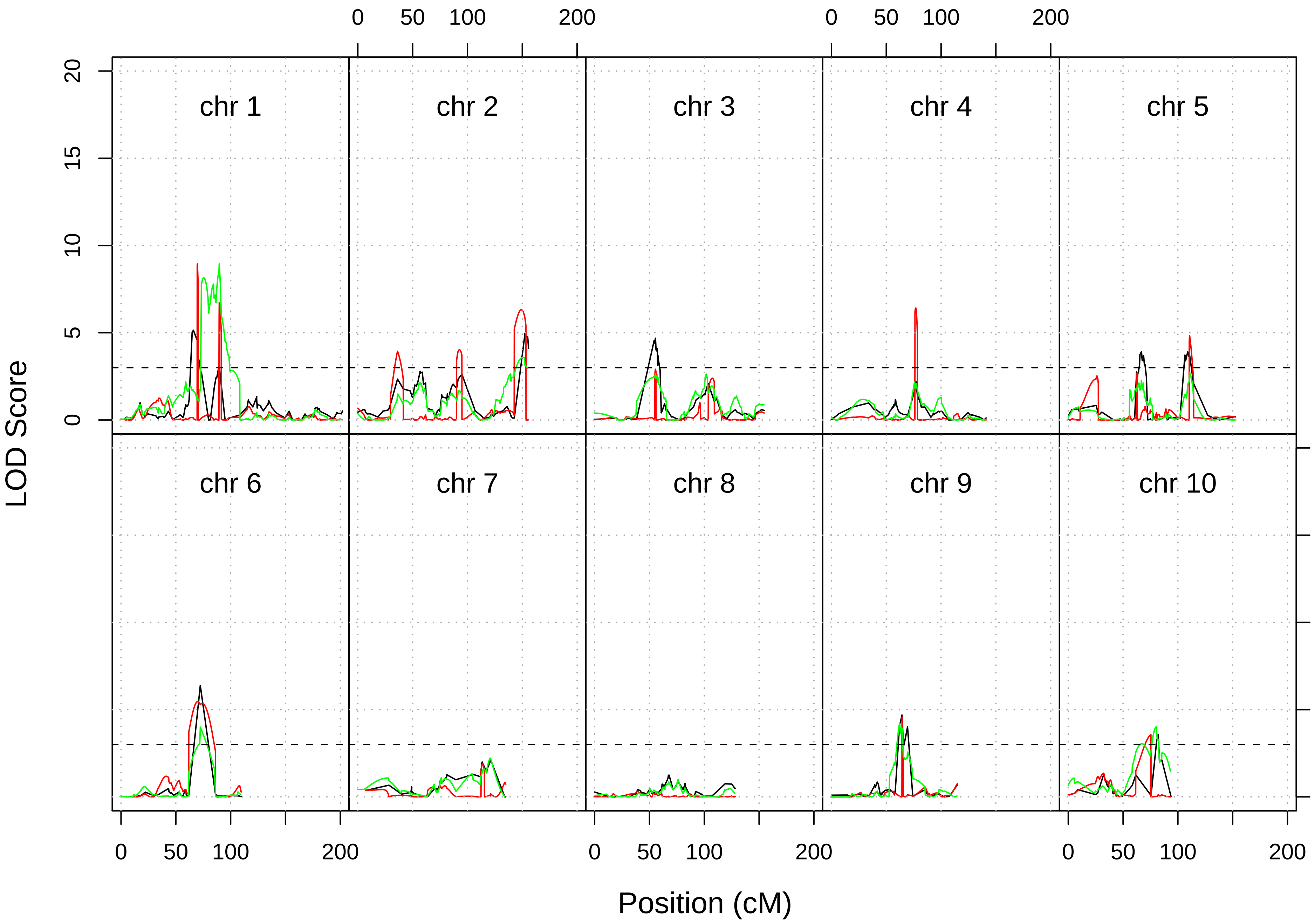


LOD Scores for CML333 population, days to anthesis

ICIM = red, CIM = green, Stepwise = black

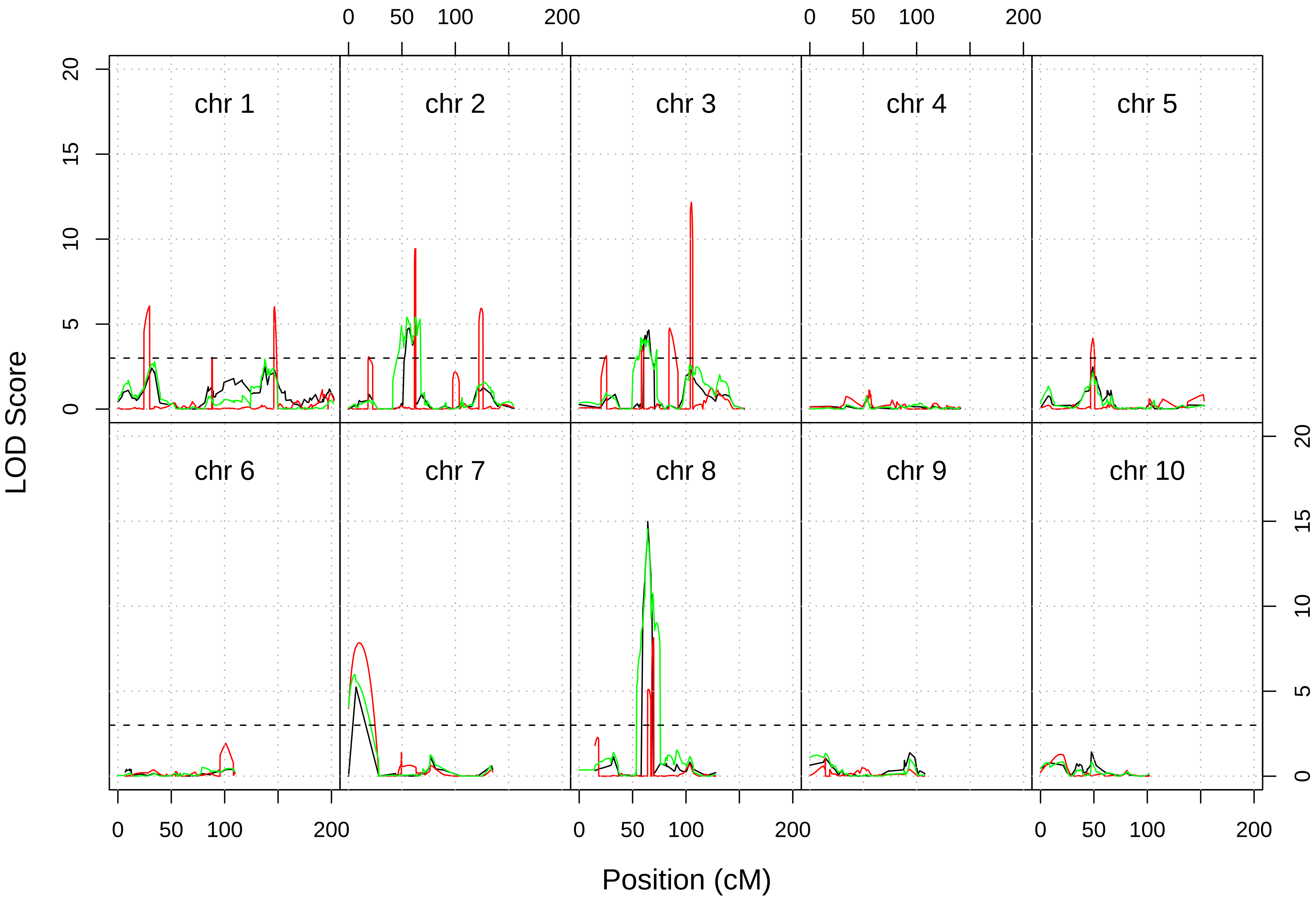
LOD Scores for CML52 population, days to anthesis
ICIM = red, CIM = green, Stepwise = black
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
LOD Score
Position (cM)
0
5
10
15
20
0
50
100
200


LOD Scores for CML69 population, days to anthesis
ICIM = red, CIM = green, Stepwise = black
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
LOD Score
Position (cM)
0
5
10
15
20
0
50
100
200



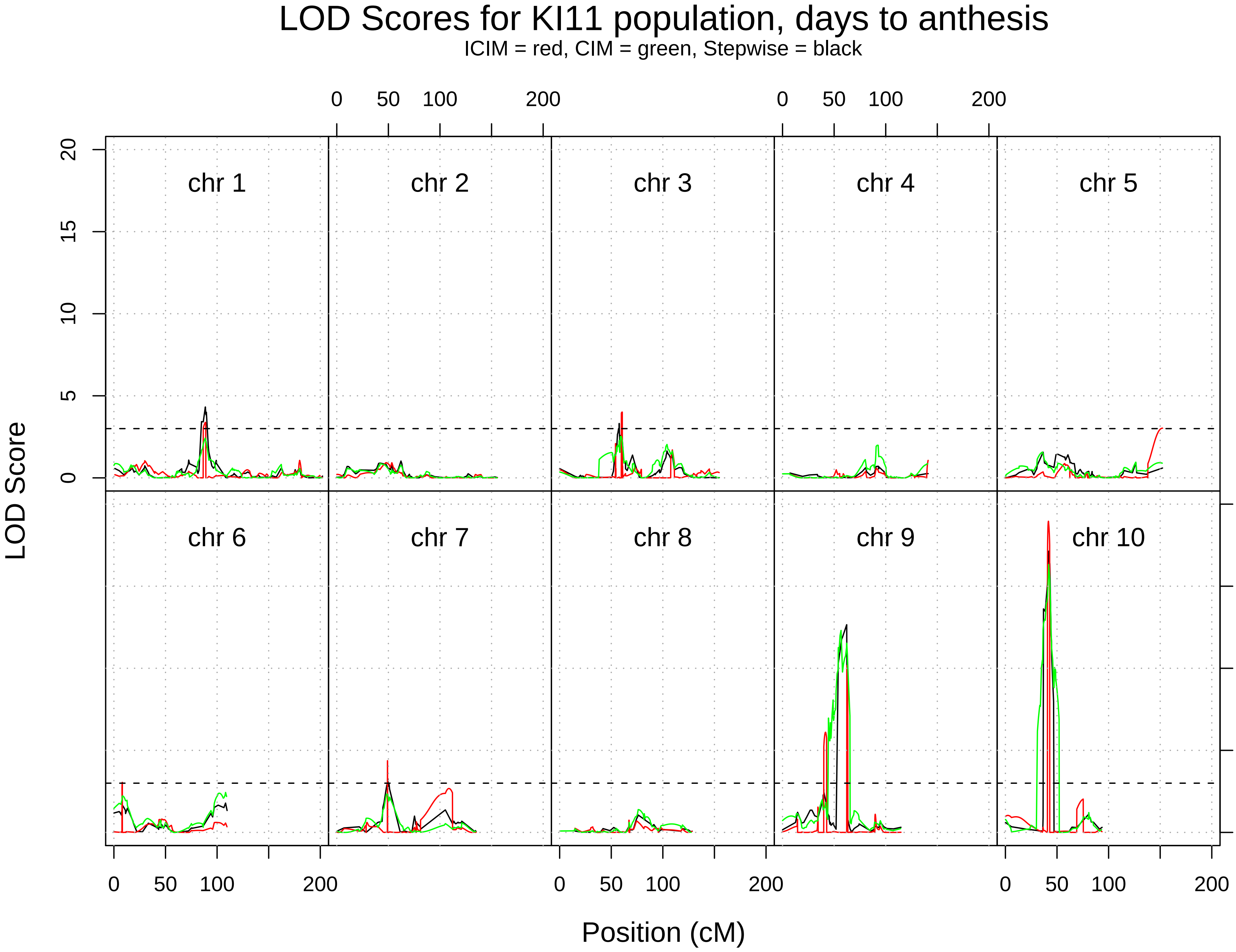
LOD Scores for HP301 population, days to anthesis

ICIM = red, CIM = green, Stepwise = black



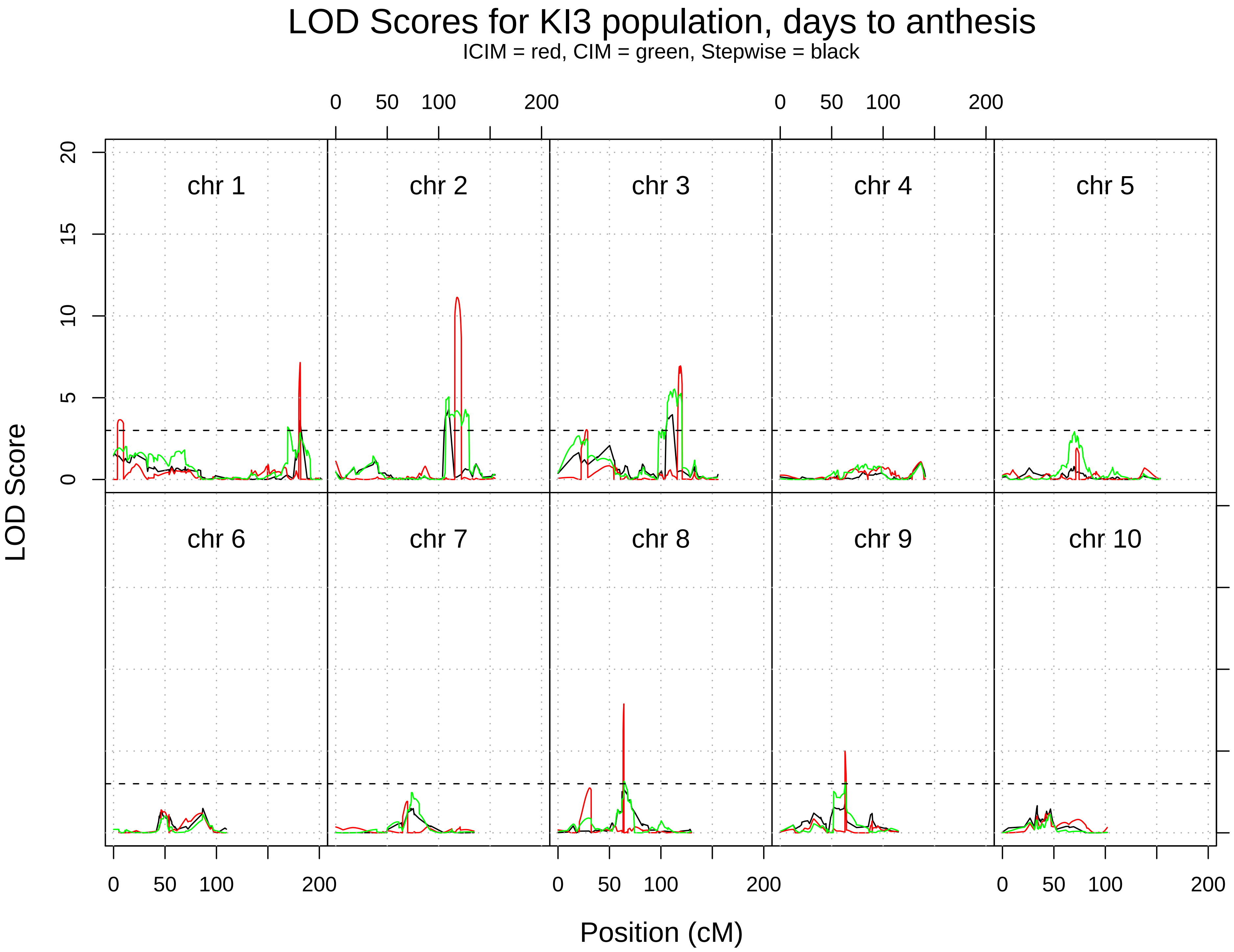
LOD Scores for IL14H population, days to anthesis

ICIM = red, CIM = green, Stepwise = black



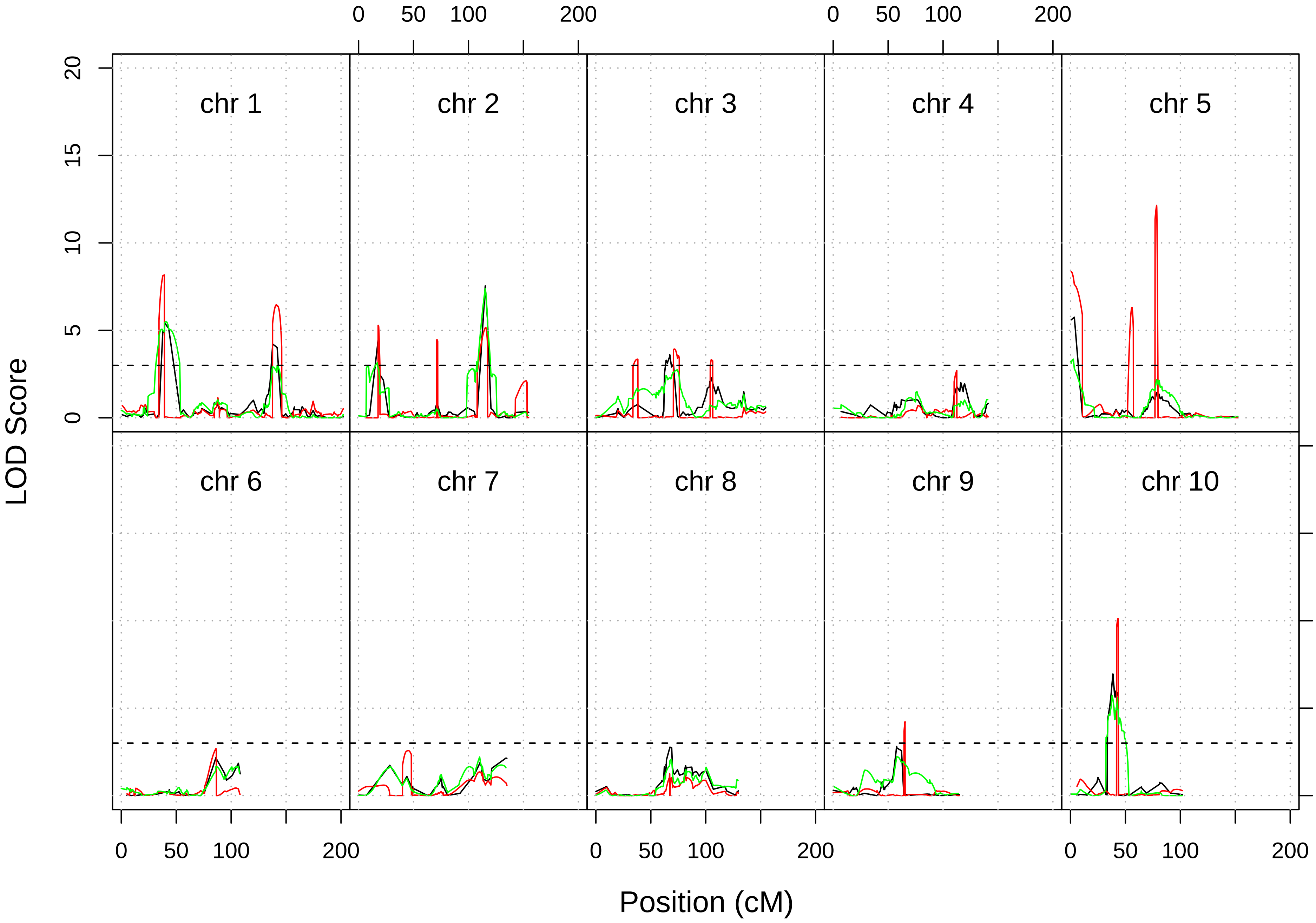
LOD Scores for KI11 population, days to anthesis

ICIM = red, CIM = green, Stepwise = black



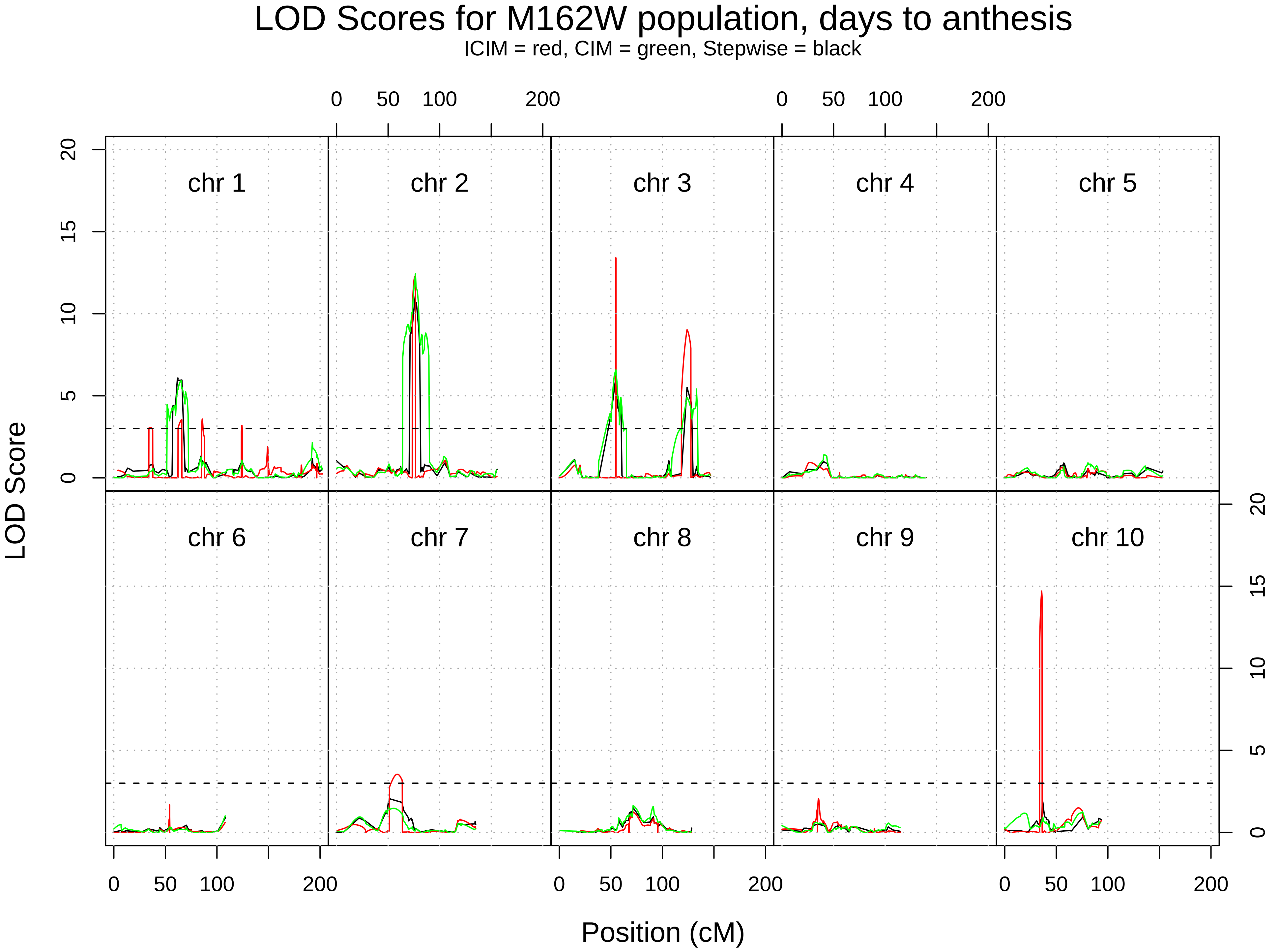
LOD Scores for KI3 population, days to anthesis

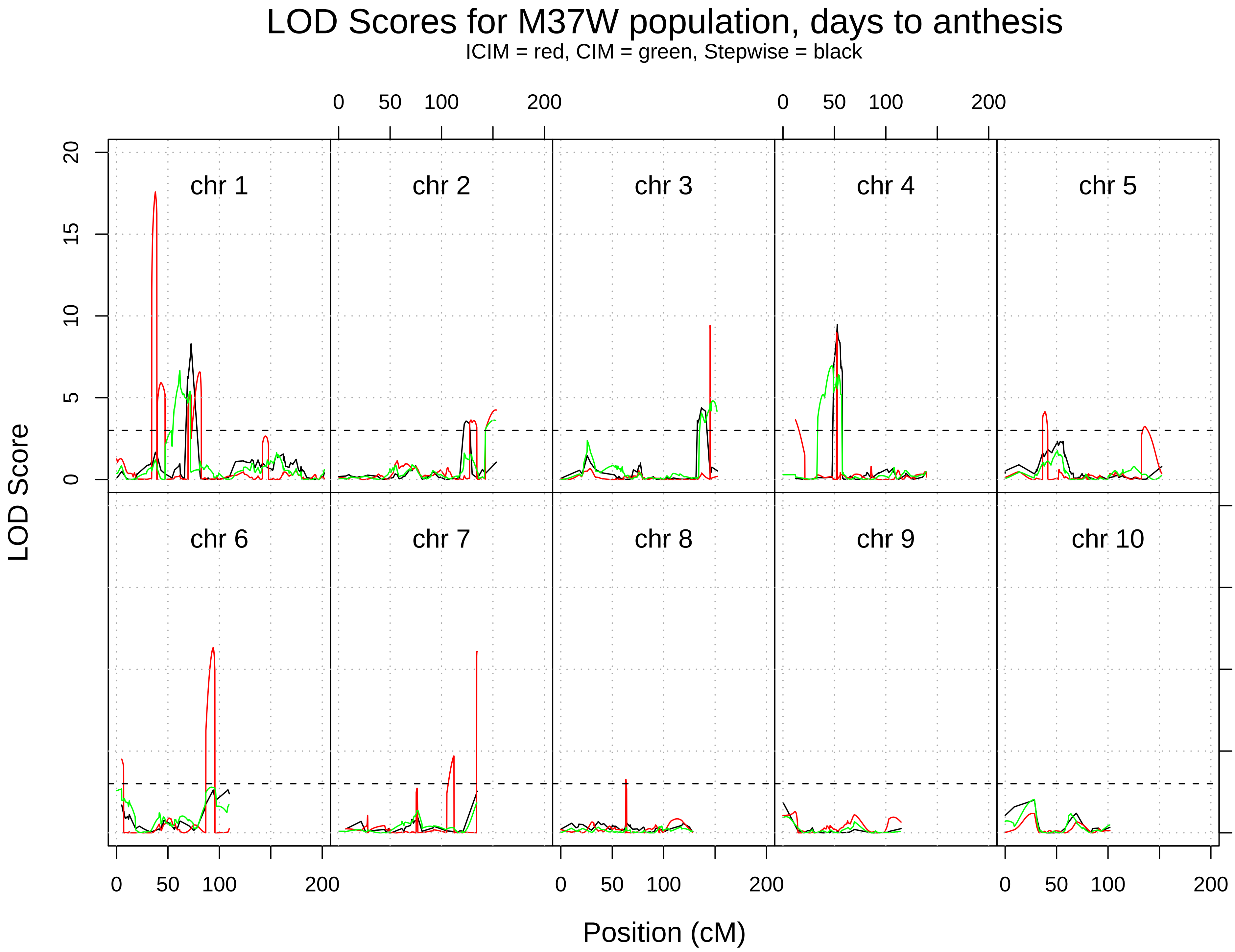
ICIM = red, CIM = green, Stepwise = black

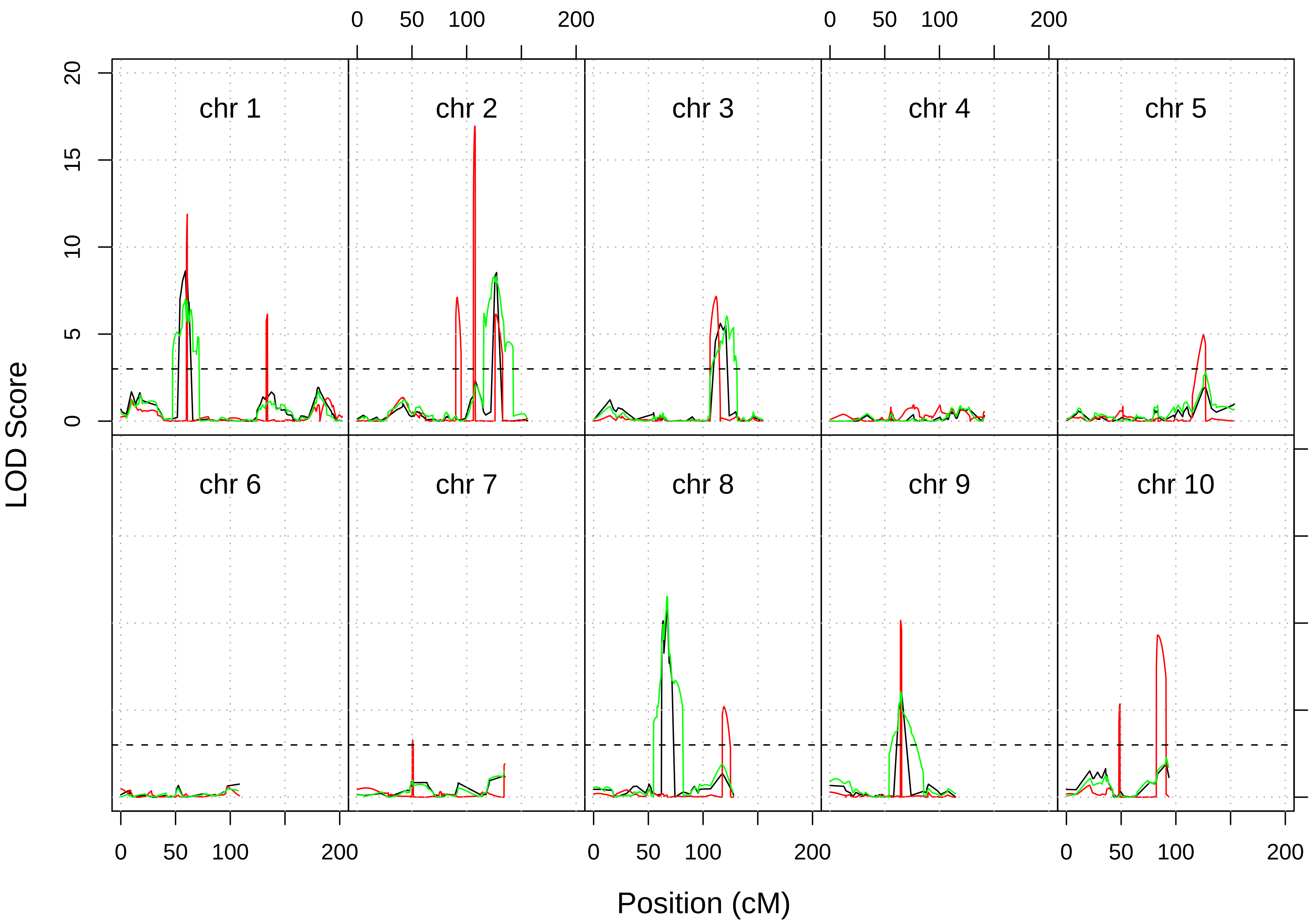


LOD Scores for KY21 population, days to anthesis

ICIM = red, CIM = green, Stepwise = black

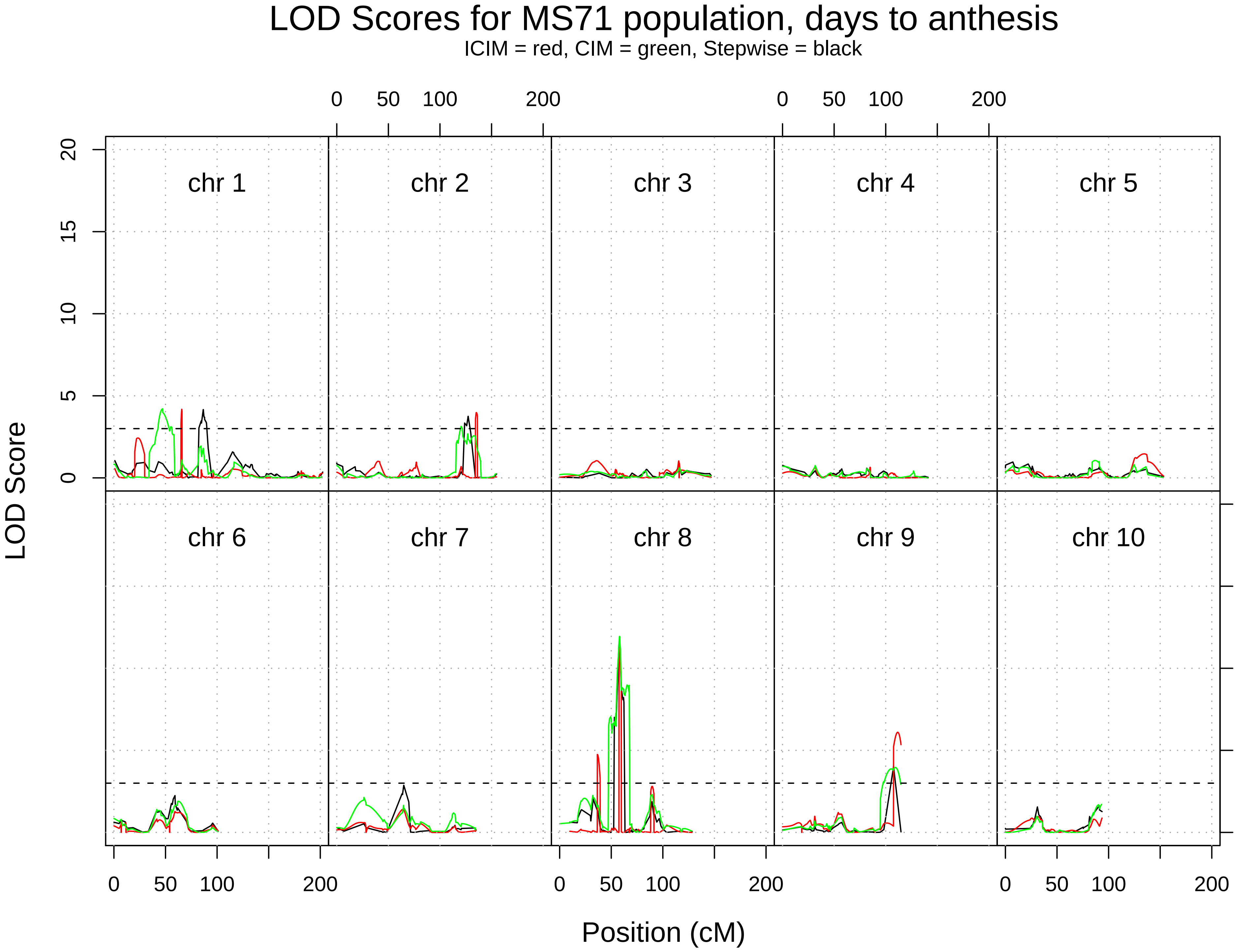

LOD Scores for M162W population, days to anthesis
ICIM = red, CIM = green, Stepwise = black
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
LOD Score
Position (cM)
0
5
10
15
20
0
50
100
200

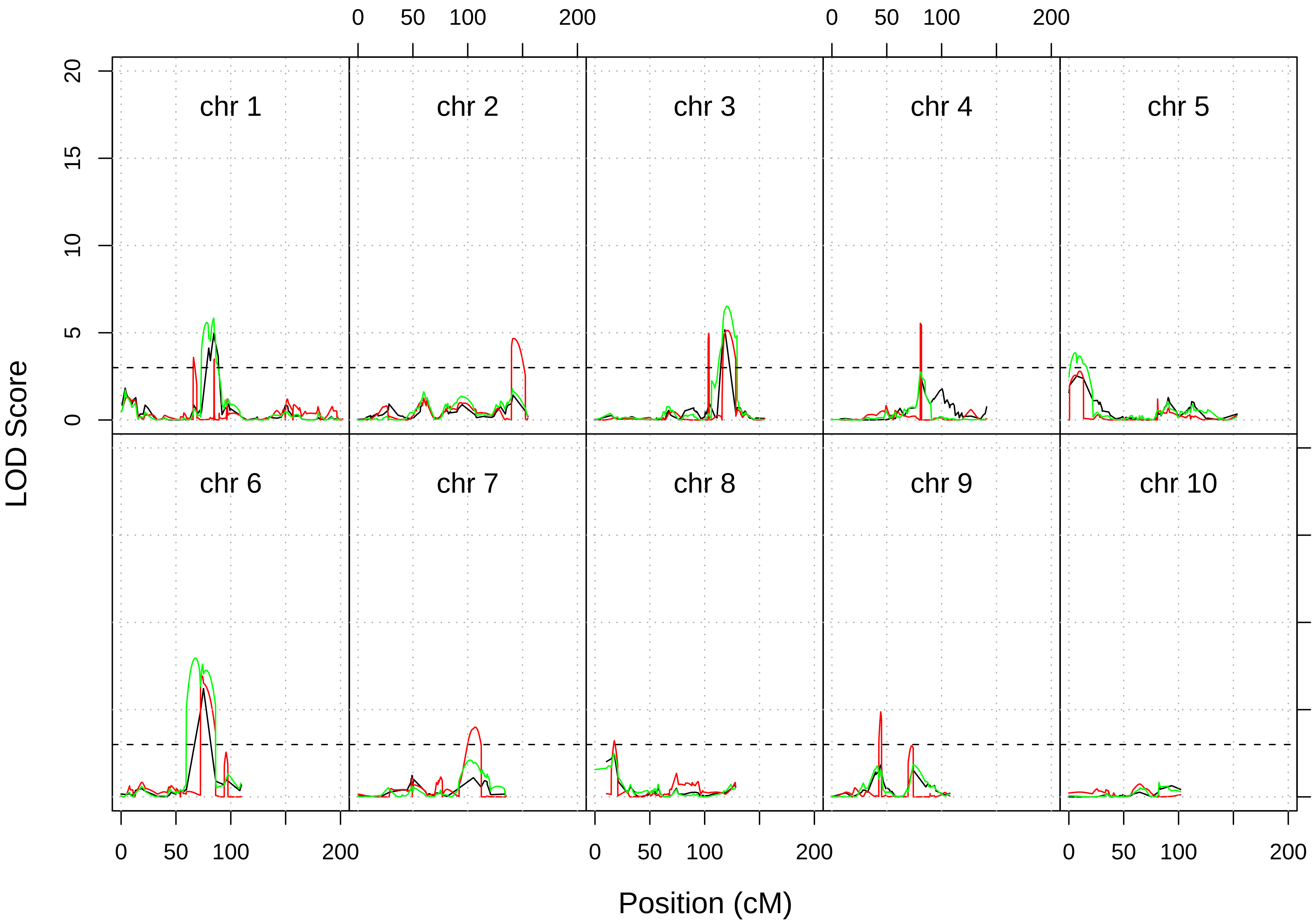

LOD Scores for M37W population, days to anthesis
ICIM = red, CIM = green, Stepwise = black
LOD Score
Position (cM)
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
0
5
10
15
20
0
50
100
200



LOD Scores for MO18W population, days to anthesis

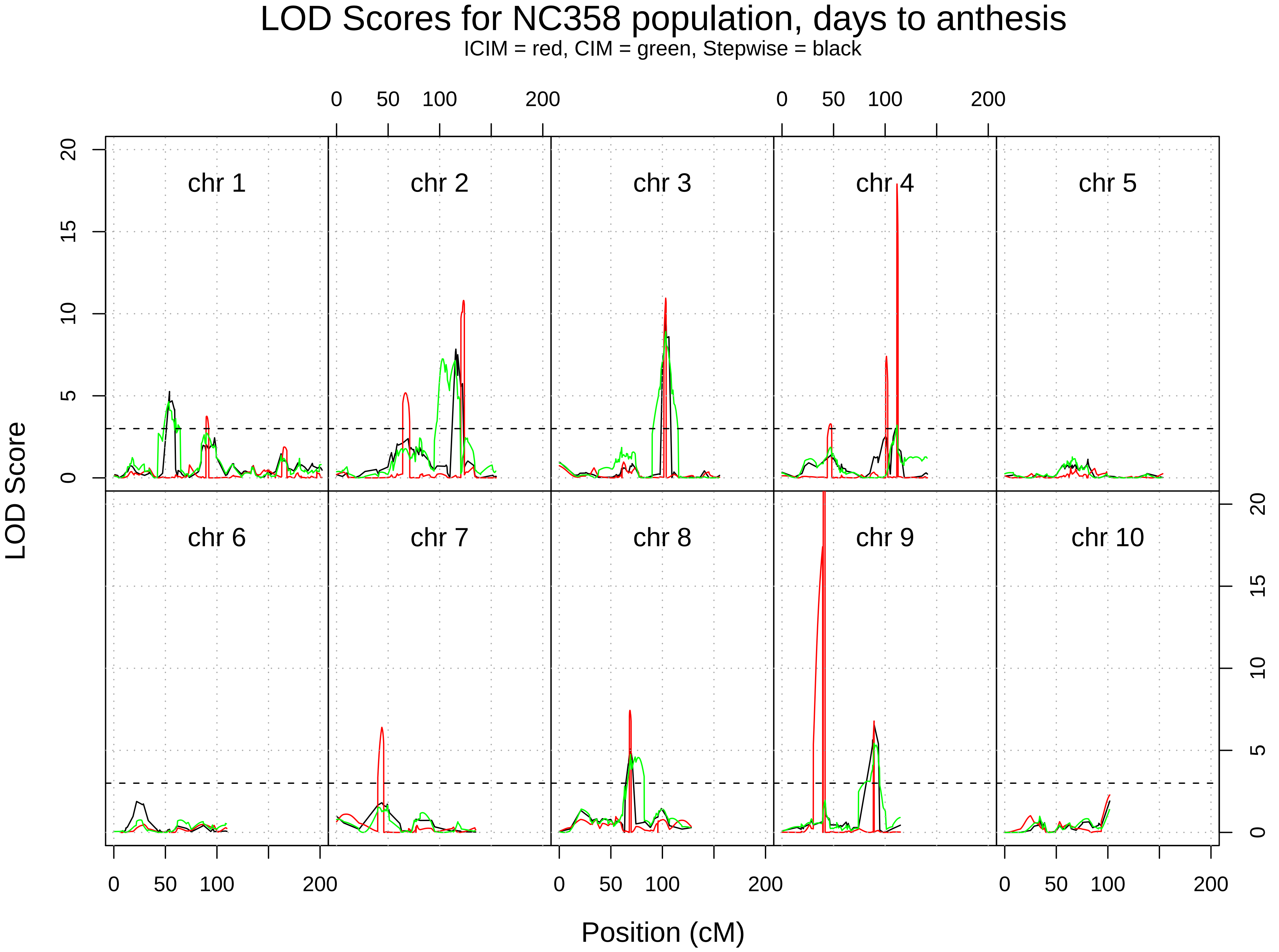
ICIM = red, CIM = green, Stepwise = black

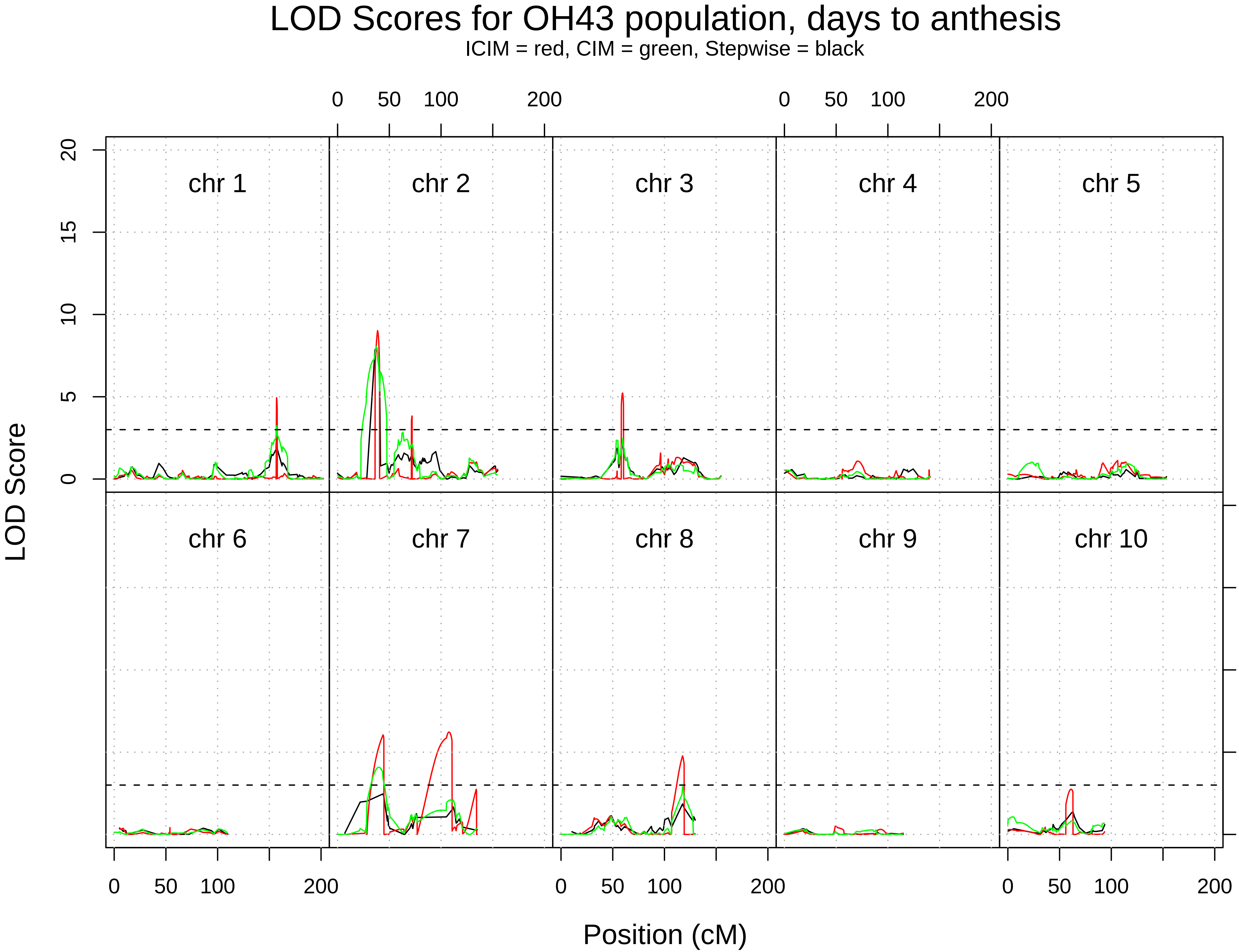

LOD Scores for MS71 population, days to anthesis
ICIM = red, CIM = green, Stepwise = black
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
LOD Score
0
5
10
15
20
Position (cM)
0
50
100
200

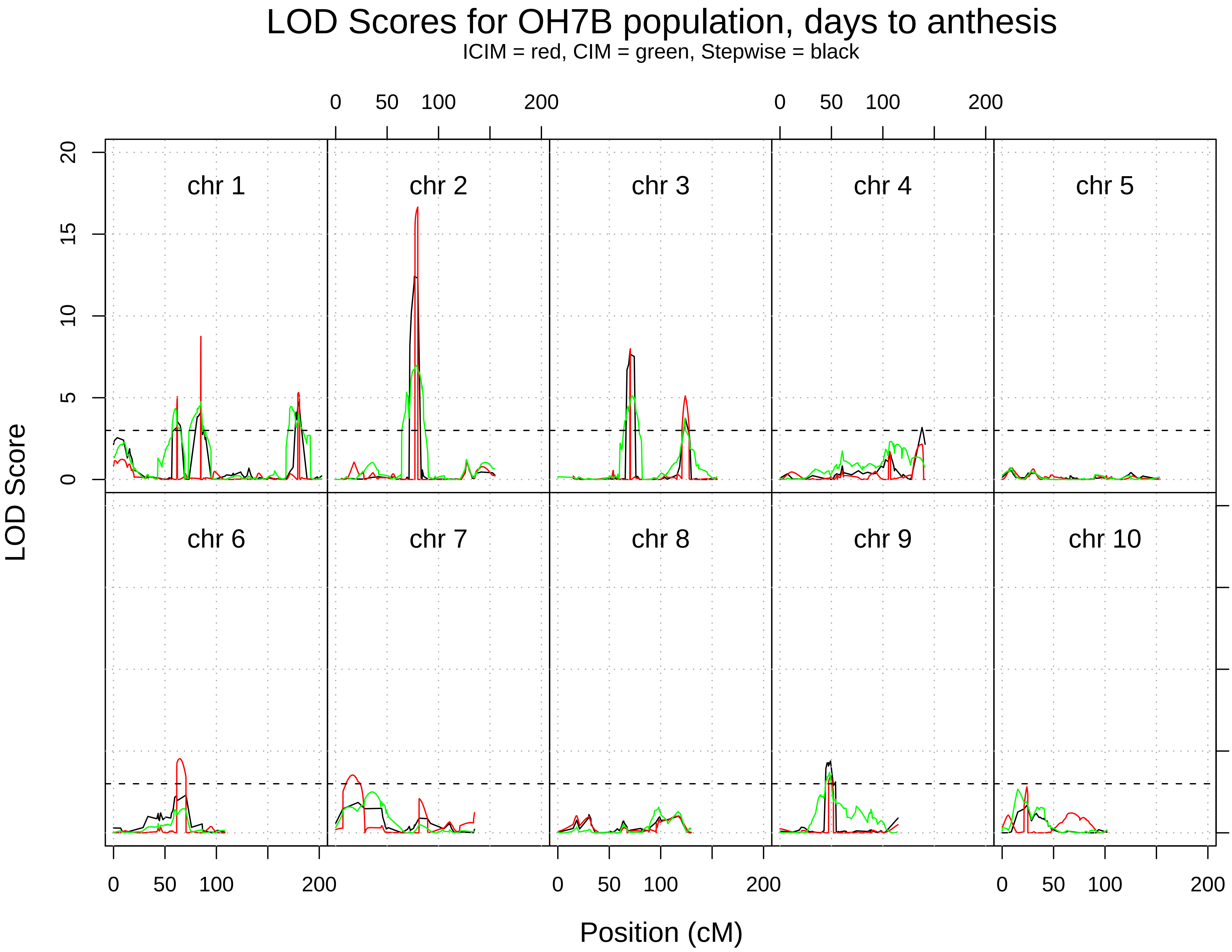


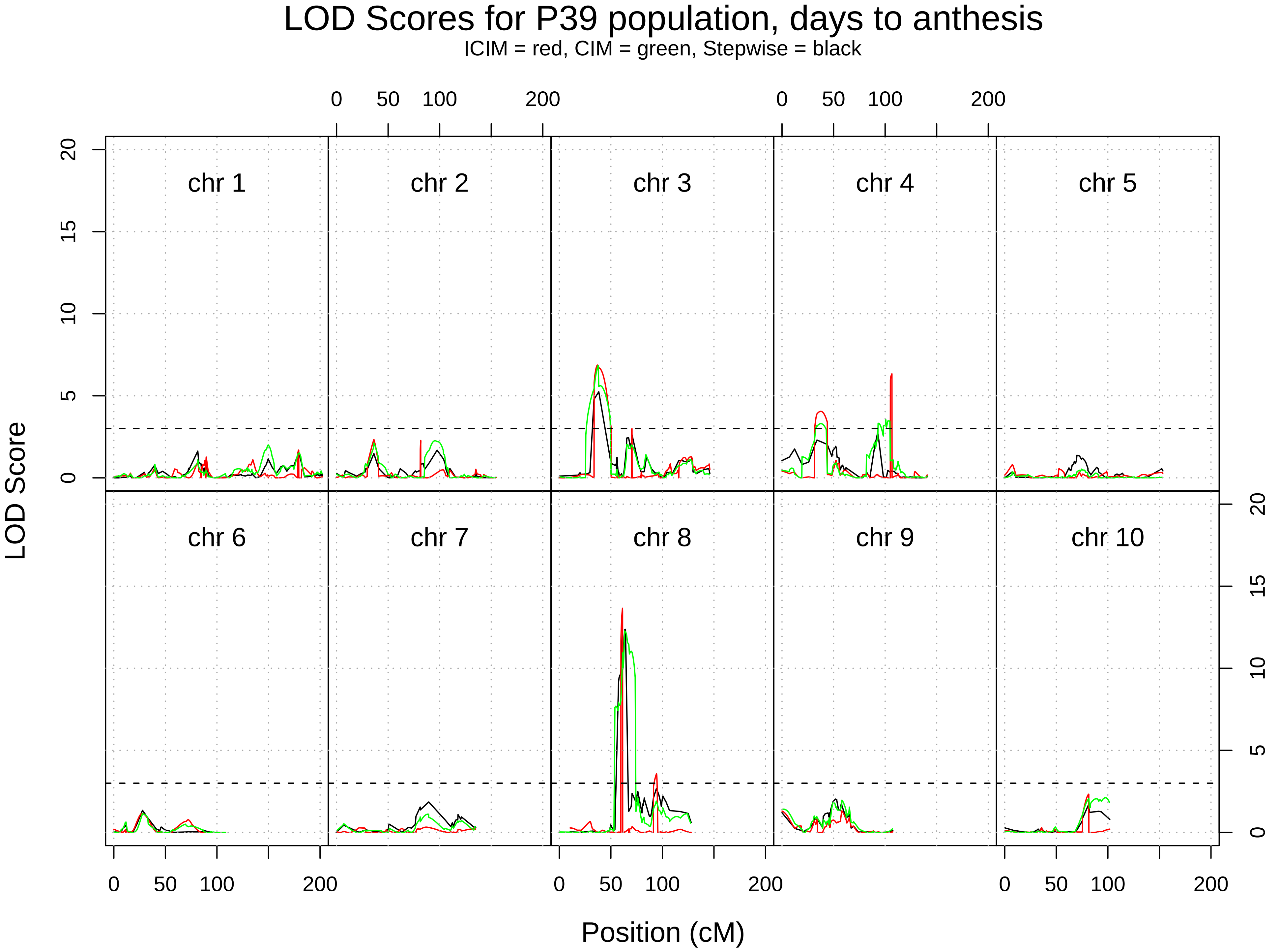
LOD Scores for NC350 population, days to anthesis

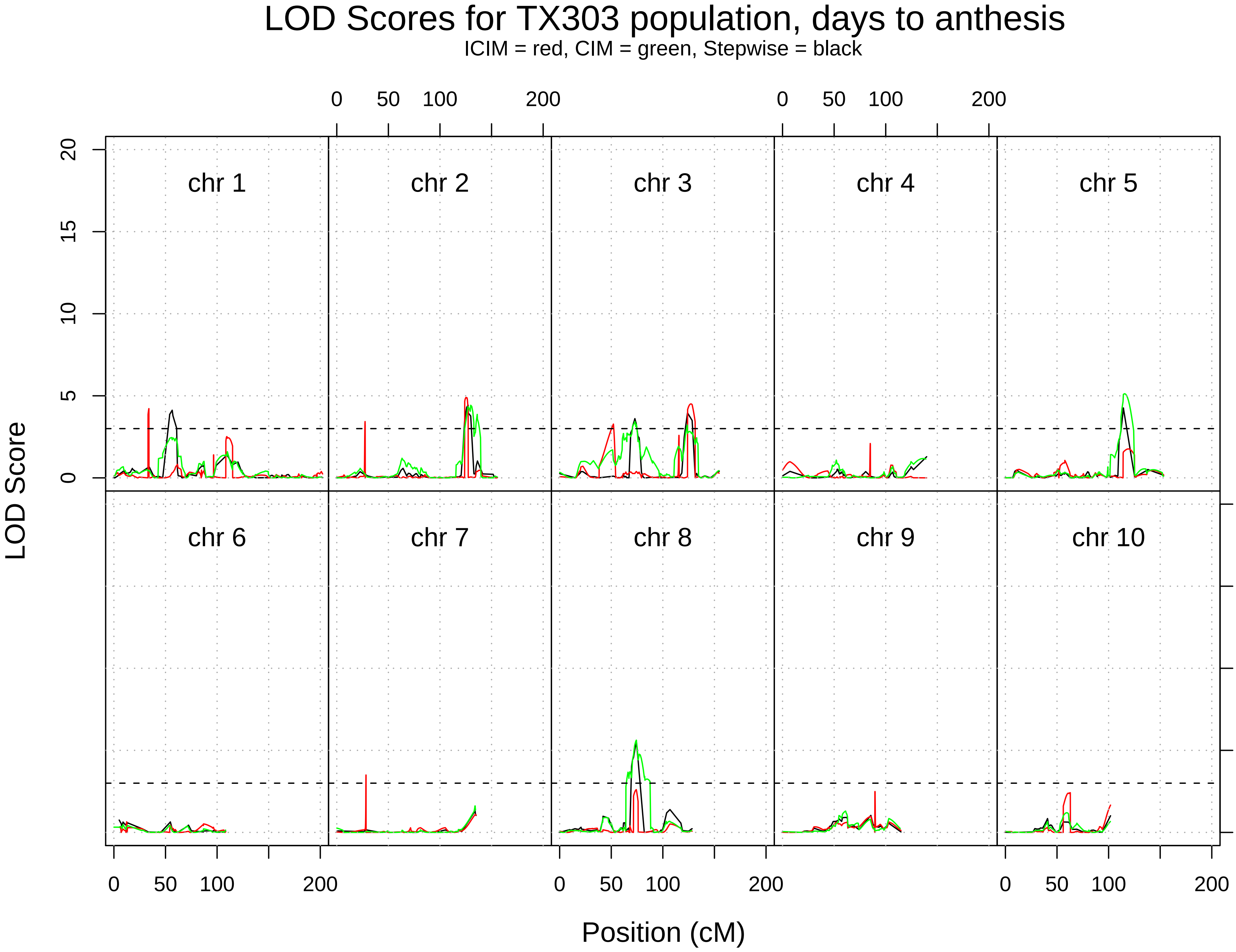
ICIM = red, CIM = green, Stepwise = black


LOD Scores for NC358 population, days to anthesis
ICIM = red, CIM = green, Stepwise = black
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
LOD Score
0
5
10
15
20
Position (cM)
0
50
100
200


LOD Scores for OH43 population, days to anthesis
ICIM = red, CIM = green, Stepwise = black
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
LOD Score
Position (cM)
0
5
10
15
20
0
50
100
200

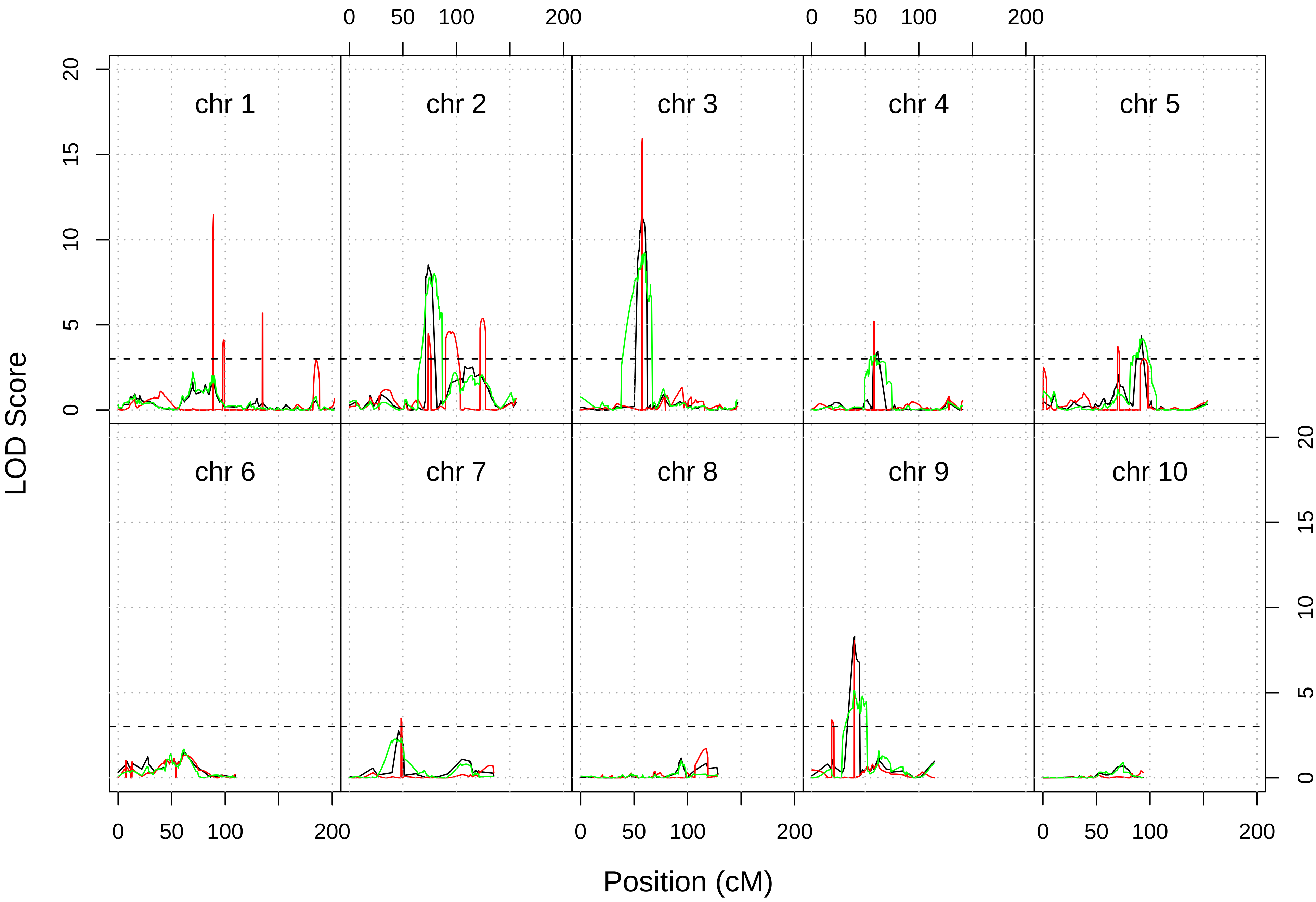

LOD Scores for OH7B population, days to anthesis
ICIM = red, CIM = green, Stepwise = black
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
LOD Score
Position (cM)
0
5
10
15
20
0
50
100
200


LOD Scores for P39 population, days to anthesis
ICIM = red, CIM = green, Stepwise = black
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
LOD Score
Position (cM)
0
50
100
200
0
5
10
15
20


LOD Scores for TX303 population, days to anthesis
ICIM = red, CIM = green, Stepwise = black
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
LOD Score
0
5
10
15
20
Position (cM)
0
50
100
200

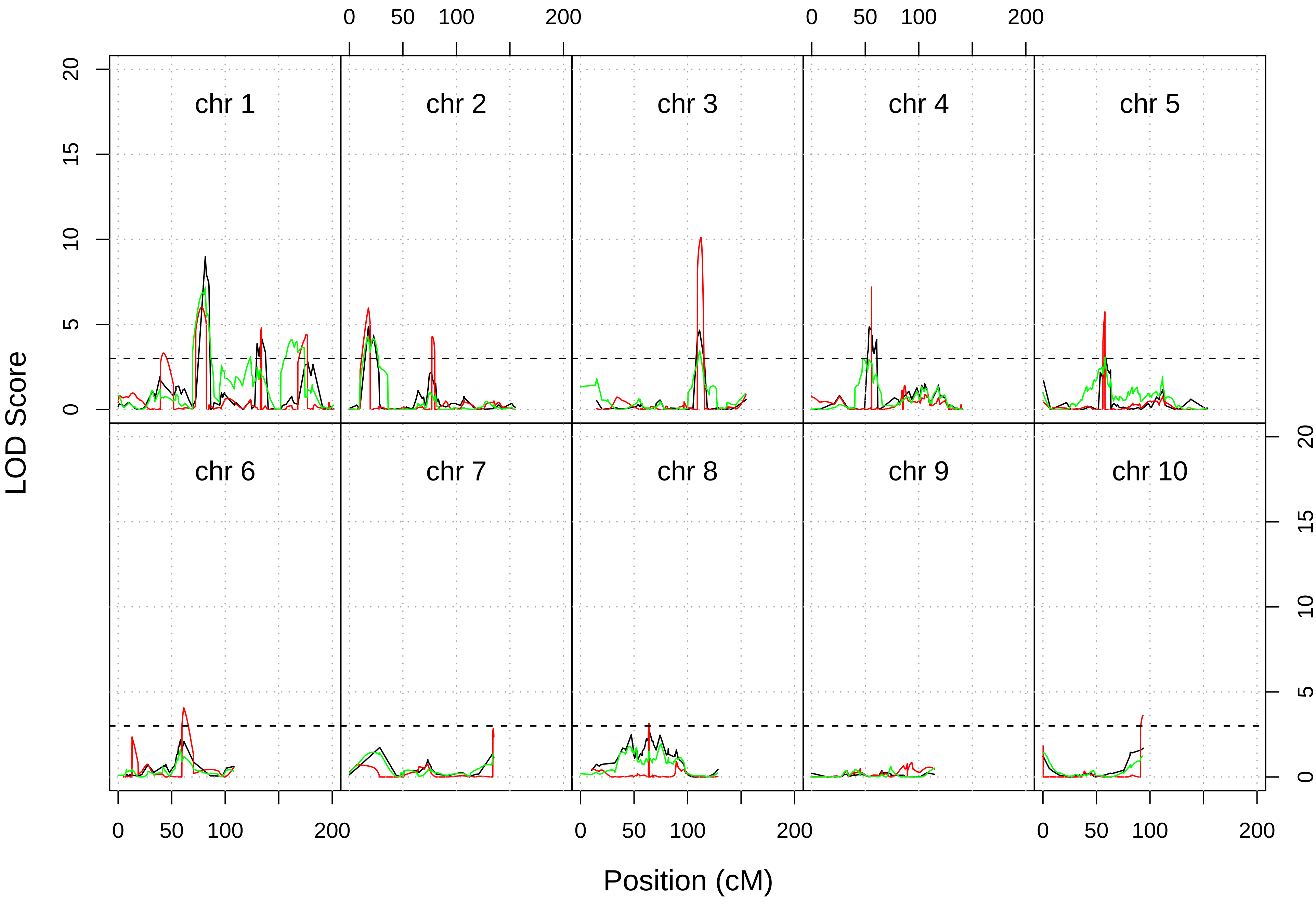
LOD Scores for TZI8 population, days to anthesis

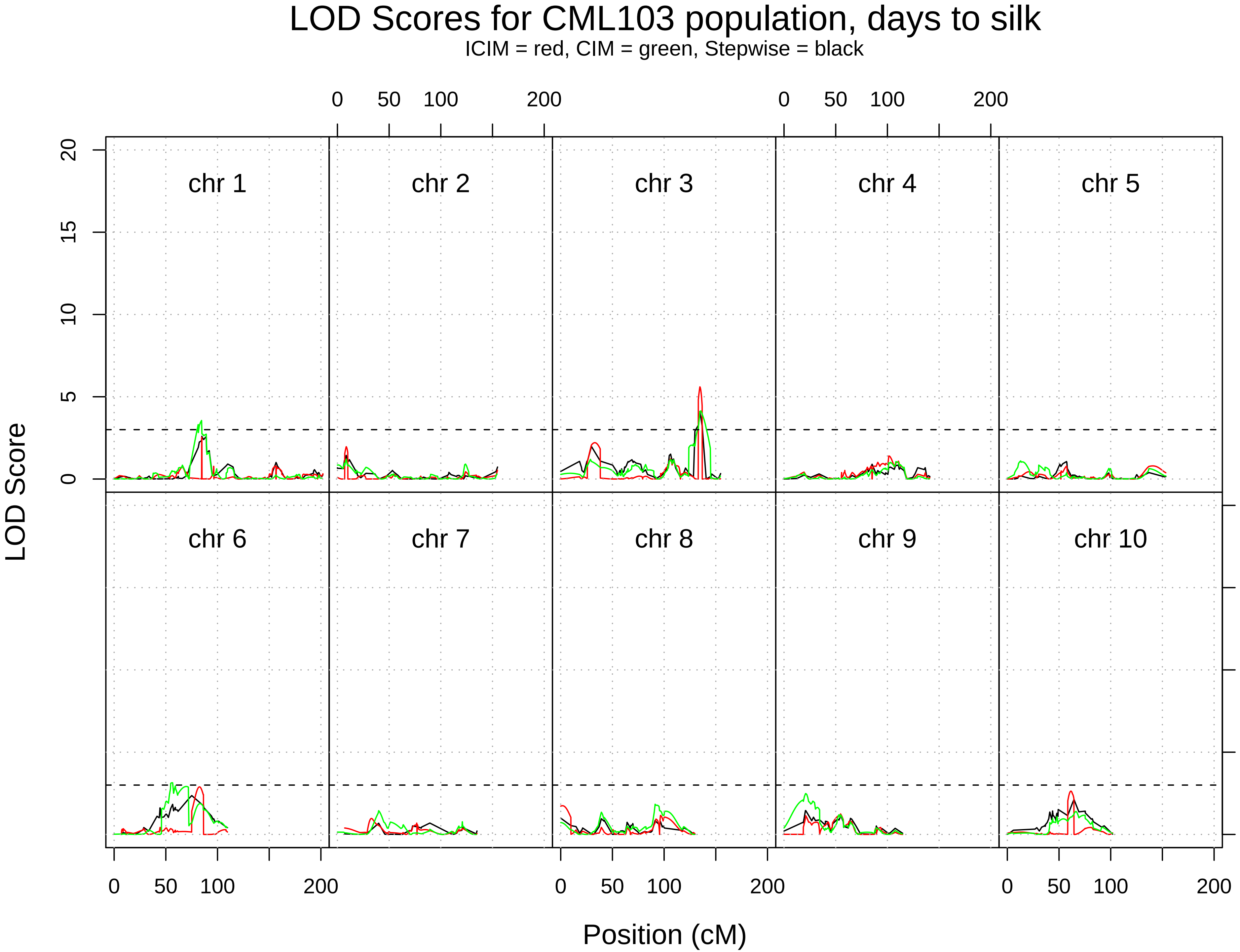
ICIM = red, CIM = green, Stepwise = black

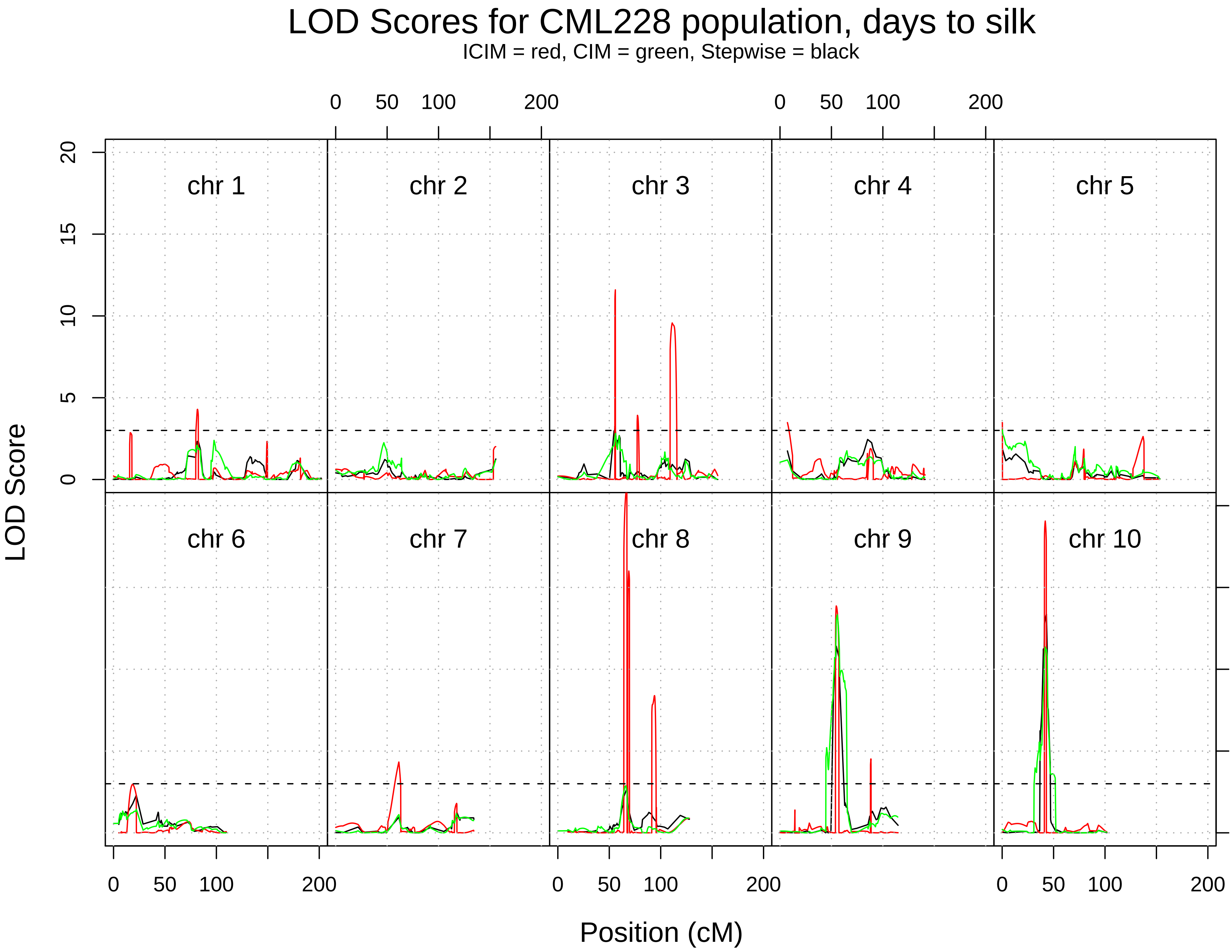


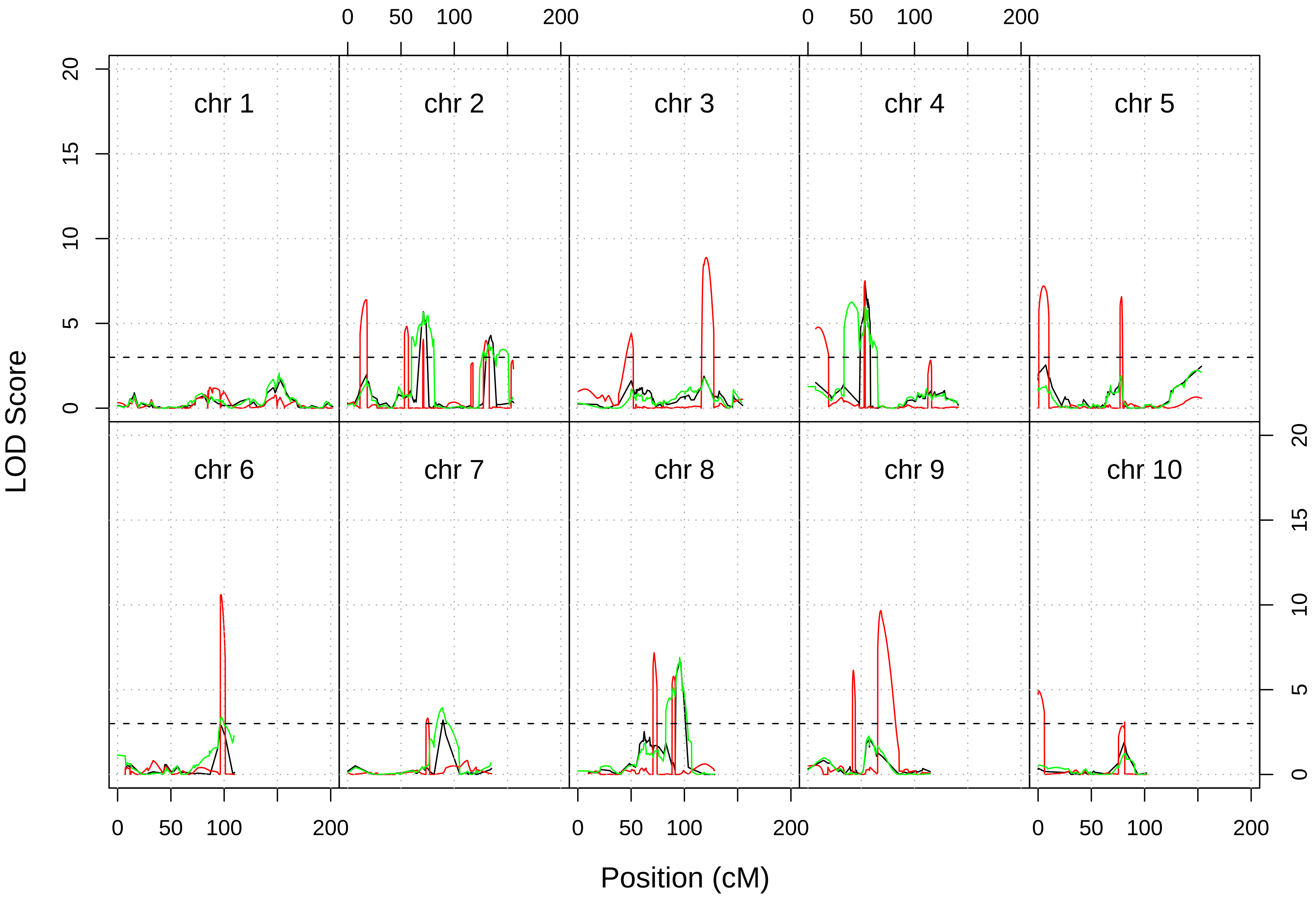
LOD Scores for B97 population, days to silk

ICIM = red, CIM = green, Stepwise = black



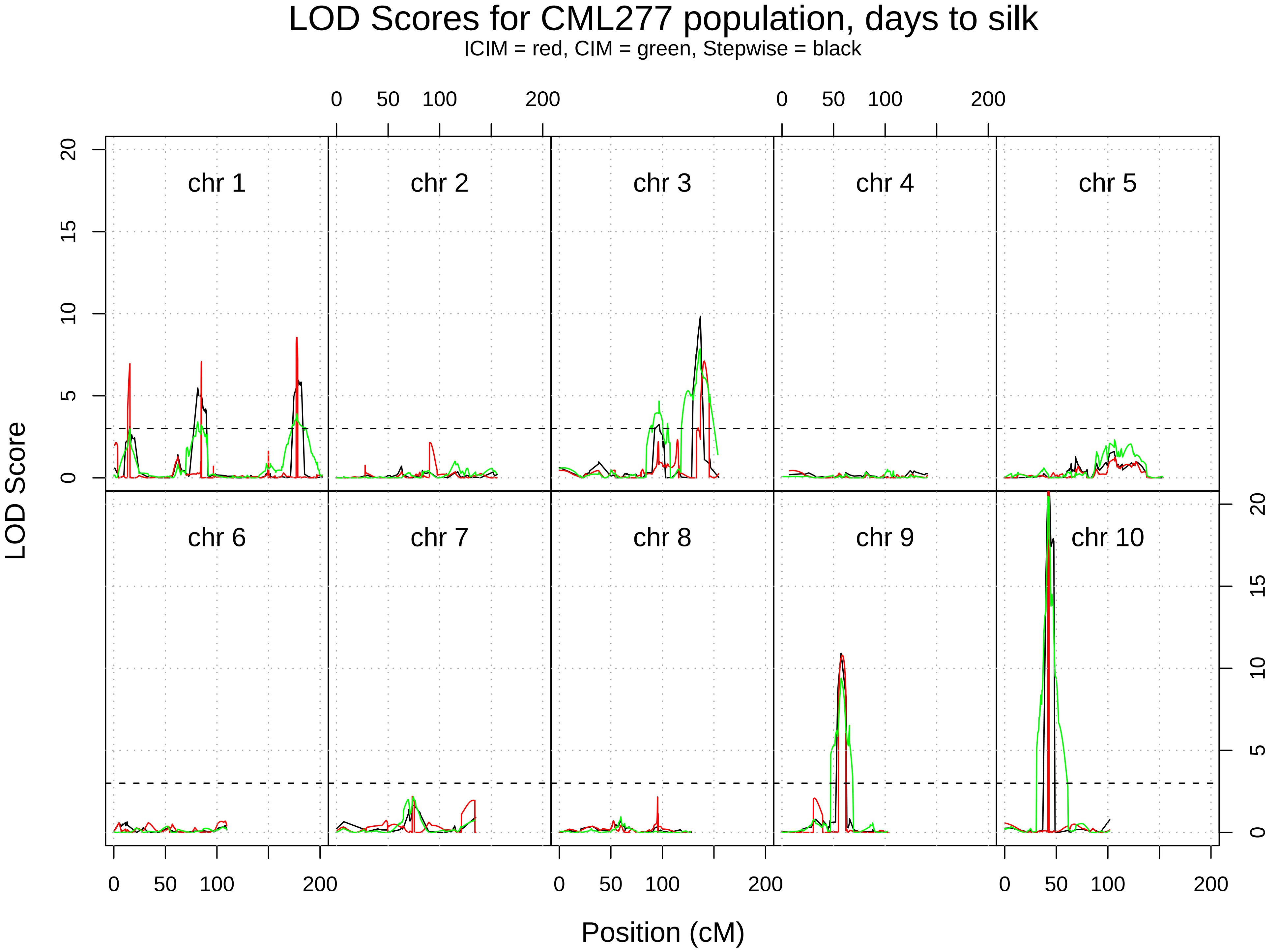

LOD Scores for CML103 population, days to silk
ICIM = red, CIM = green, Stepwise = black
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
LOD Score
Position (cM)
0
5
10
15
20
0
50
100
200

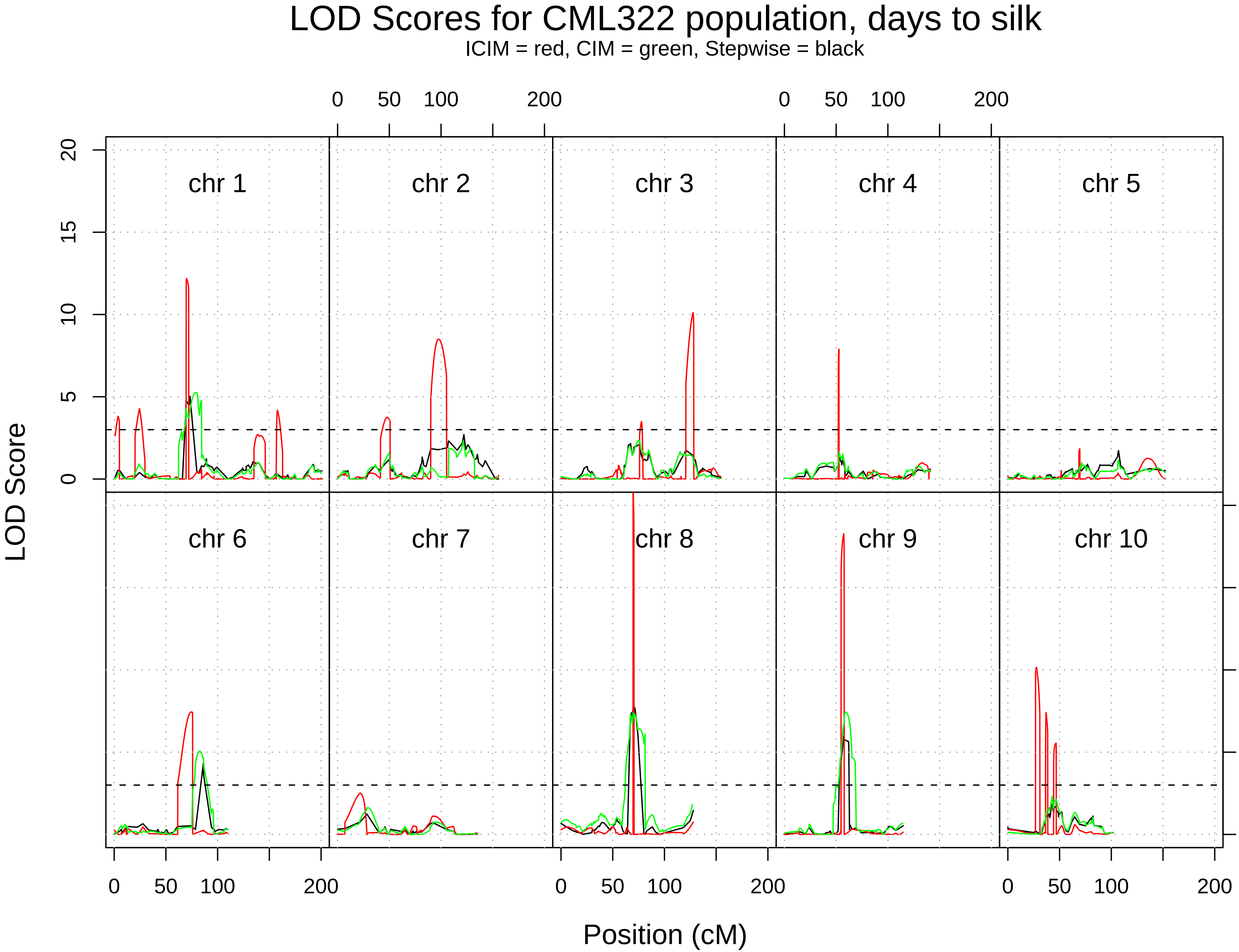

LOD Scores for CML228 population, days to silk
ICIM = red, CIM = green, Stepwise = black
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
LOD Score
Position (cM)
0
50
100
200
0
5
10
15
20

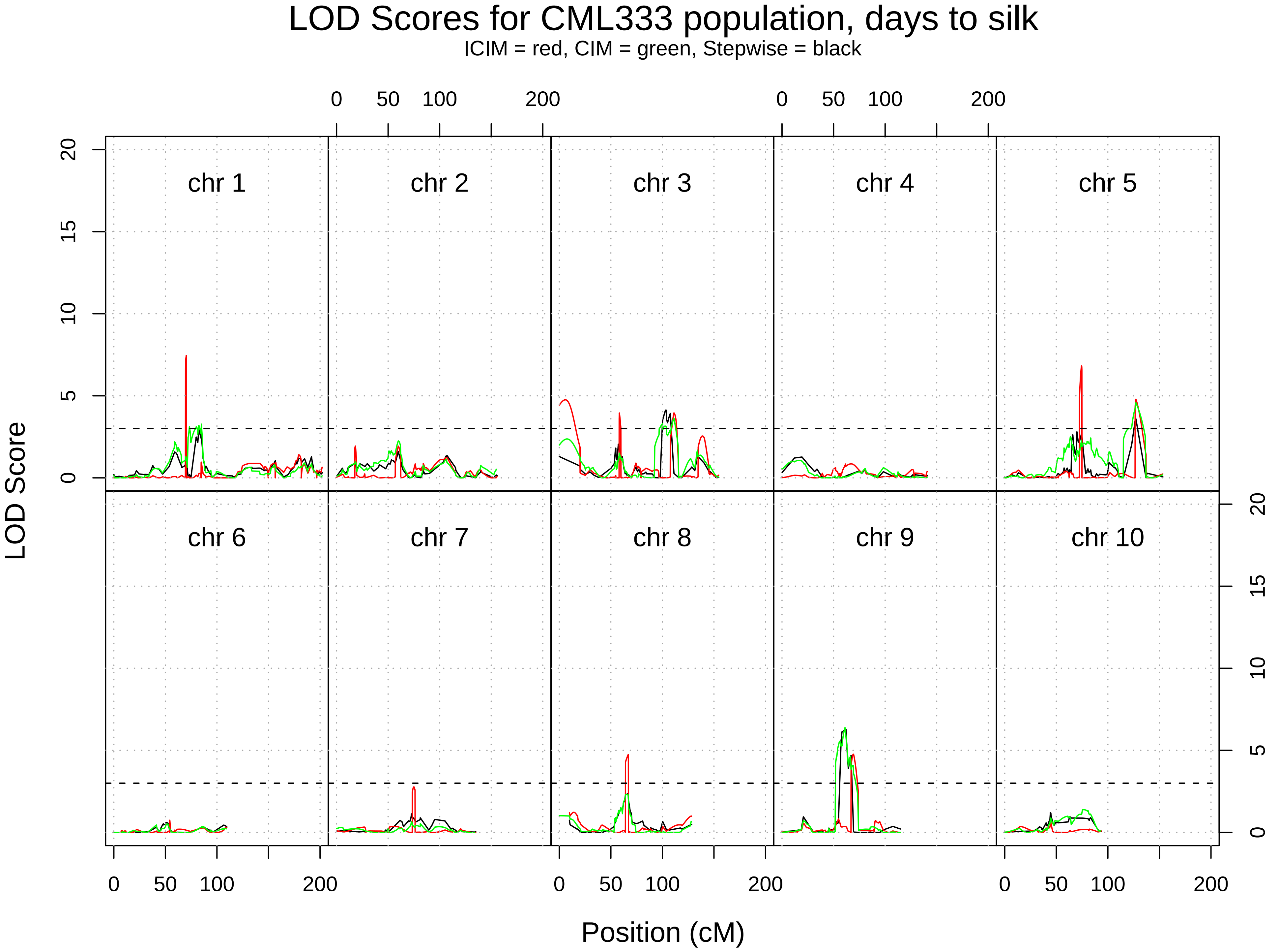


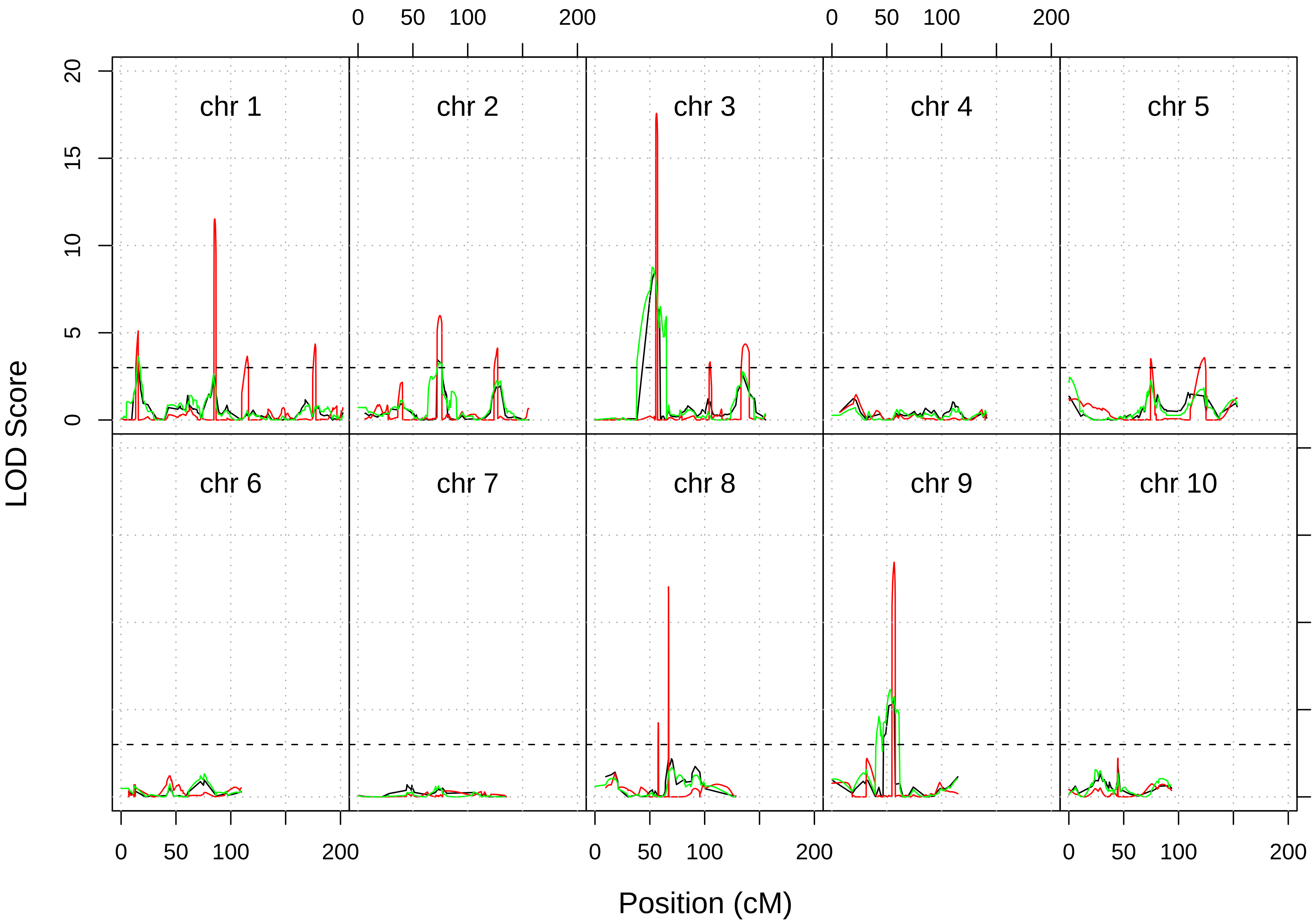
LOD Scores for CML247 population, days to silk

ICIM = red, CIM = green, Stepwise = black


LOD Scores for CML277 population, days to silk
ICIM = red, CIM = green, Stepwise = black
LOD Score
Position (cM)
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
0
5
10
15
20
0
50
100
200

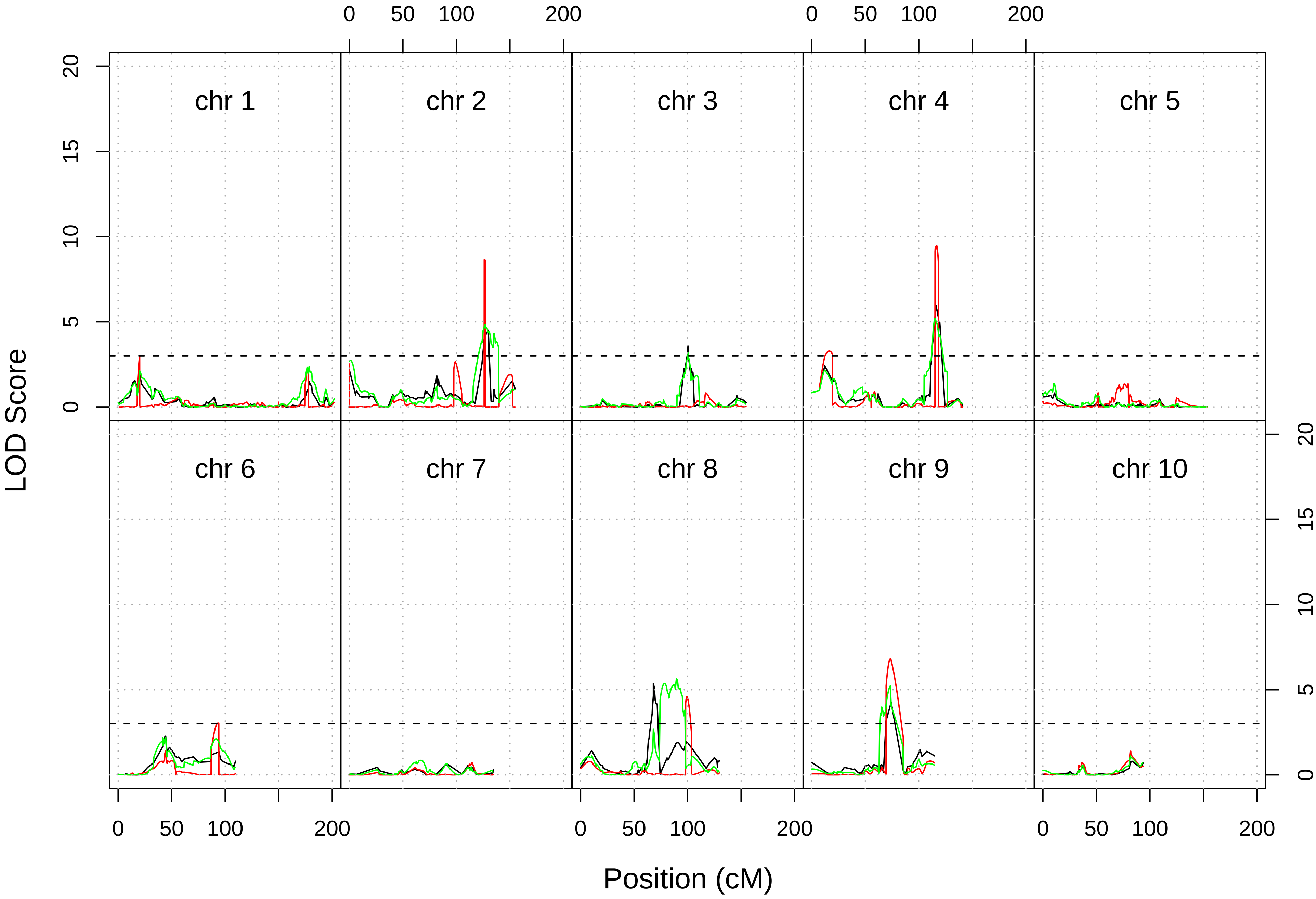

LOD Scores for CML322 population, days to silk
ICIM = red, CIM = green, Stepwise = black
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
LOD Score
0
5
10
15
20
Position (cM)
0
50
100
200


LOD Scores for CML333 population, days to silk
ICIM = red, CIM = green, Stepwise = black
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
LOD Score
Position (cM)
0
5
10
15
20
0
50
100
200



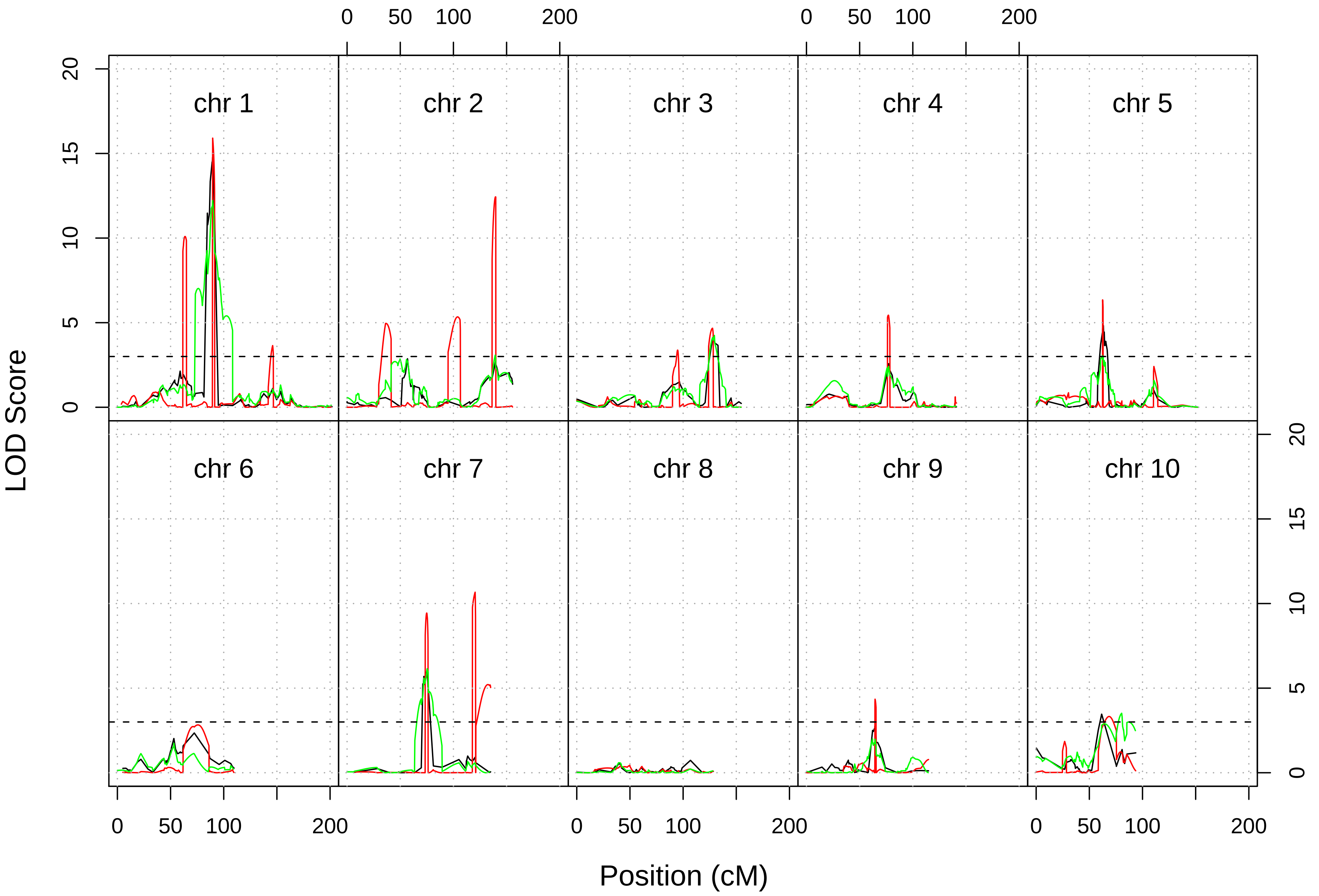
LOD Scores for CML52 population, days to silk

ICIM = red, CIM = green, Stepwise = black



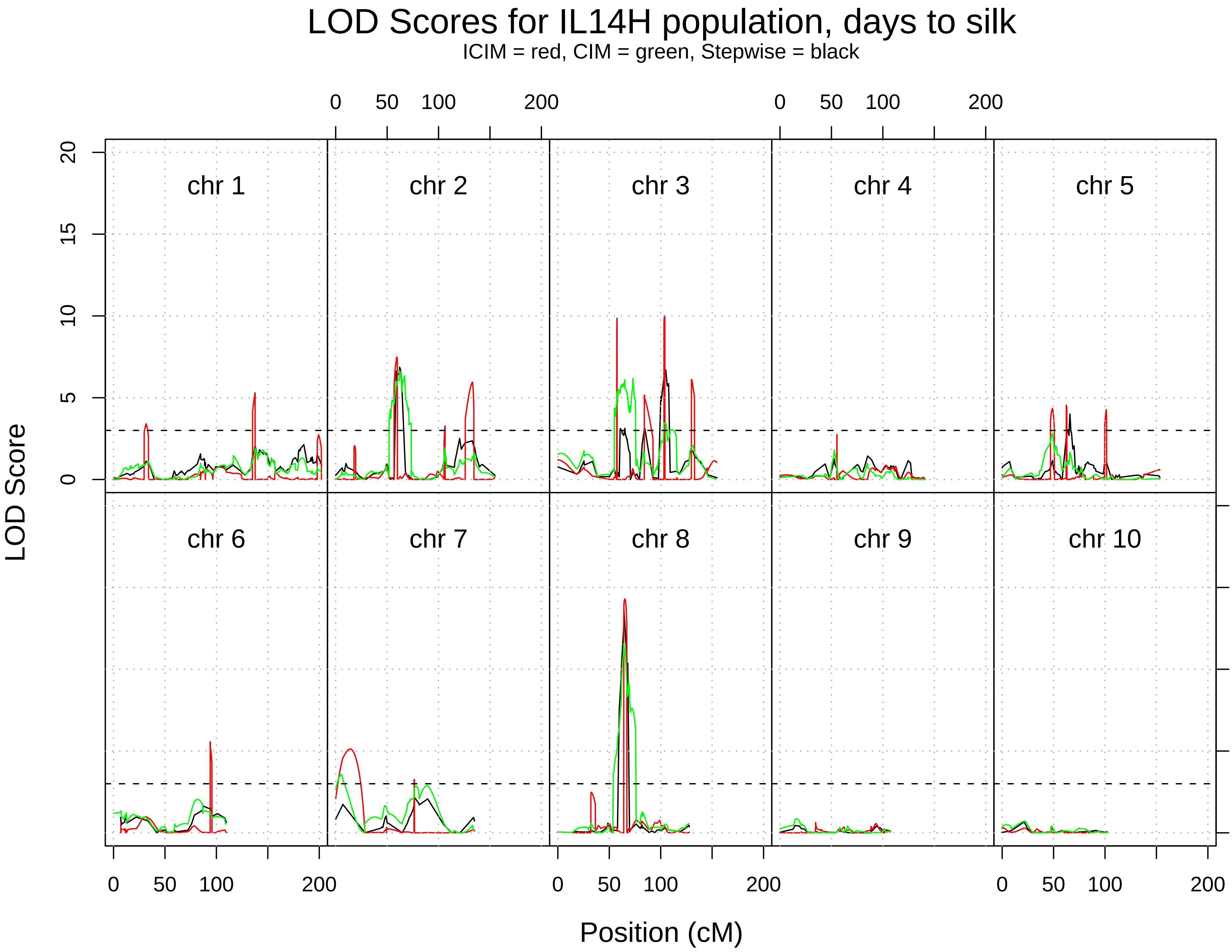
LOD Scores for CML69 population, days to silk

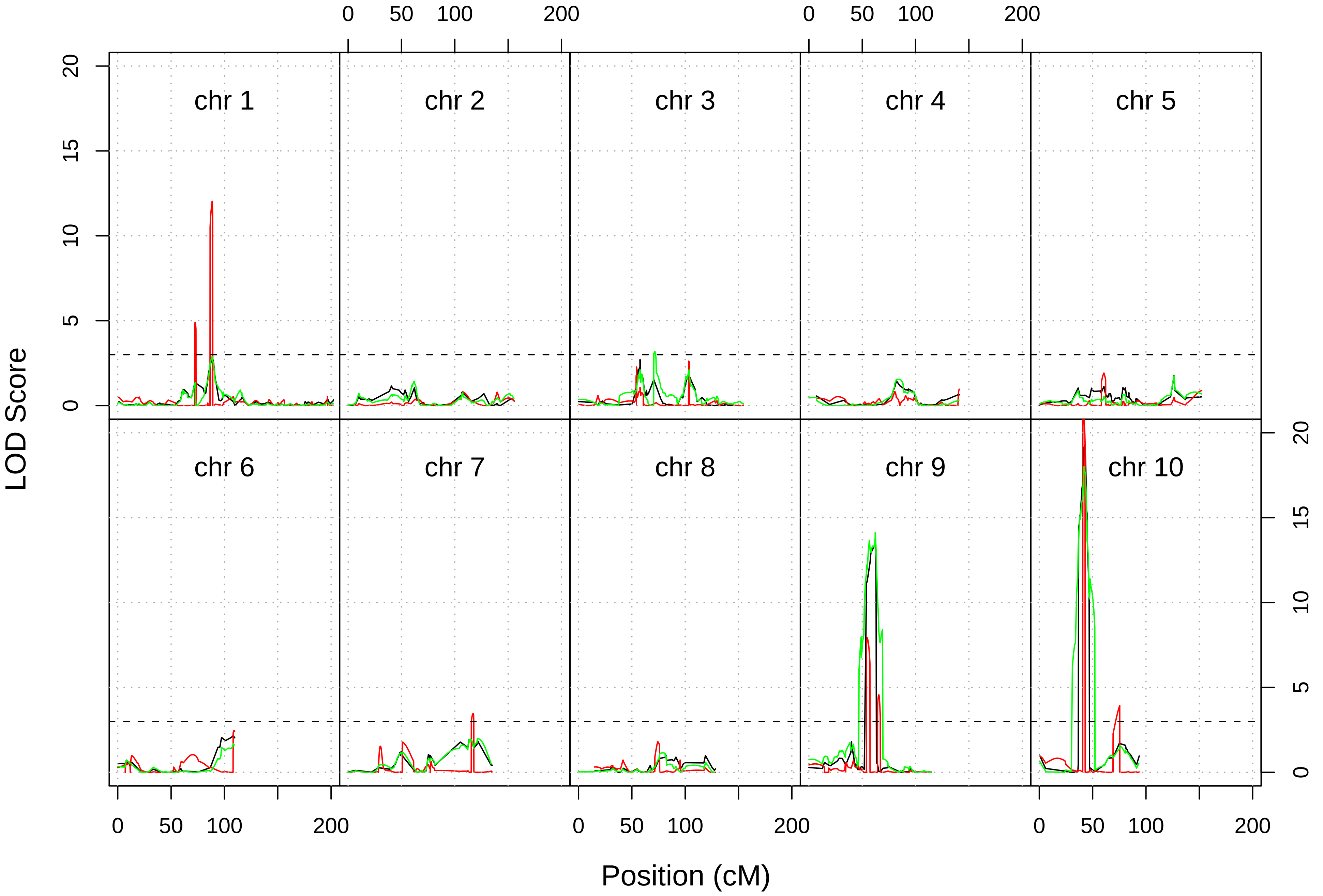
ICIM = red, CIM = green, Stepwise = black



LOD Scores for HP301 population, days to silk

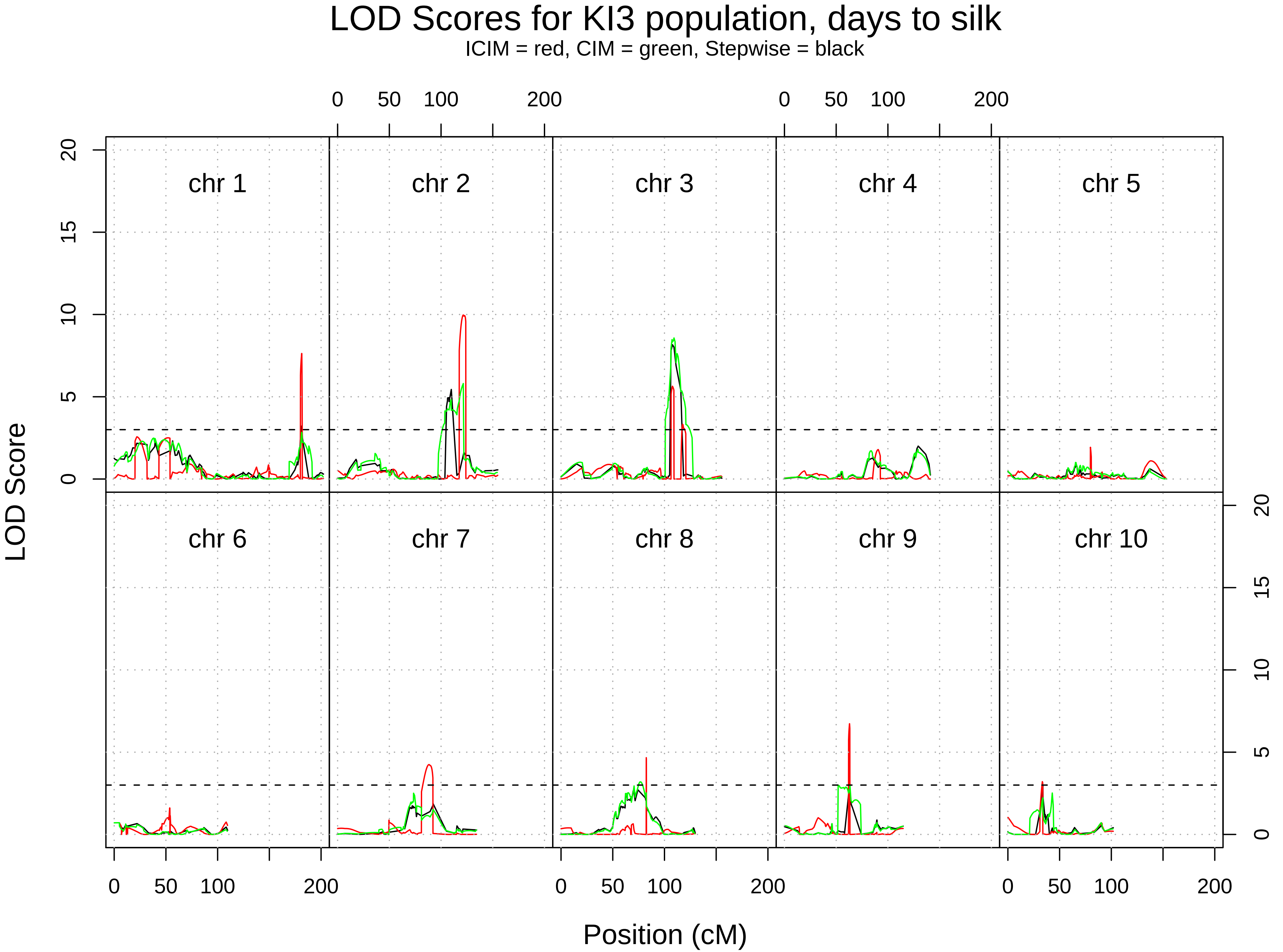
ICIM = red, CIM = green, Stepwise = black


LOD Scores for IL14H population, days to silk
ICIM = red, CIM = green, Stepwise = black
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
LOD Score
Position (cM)
0
5
10
15
20
0
50
100
200



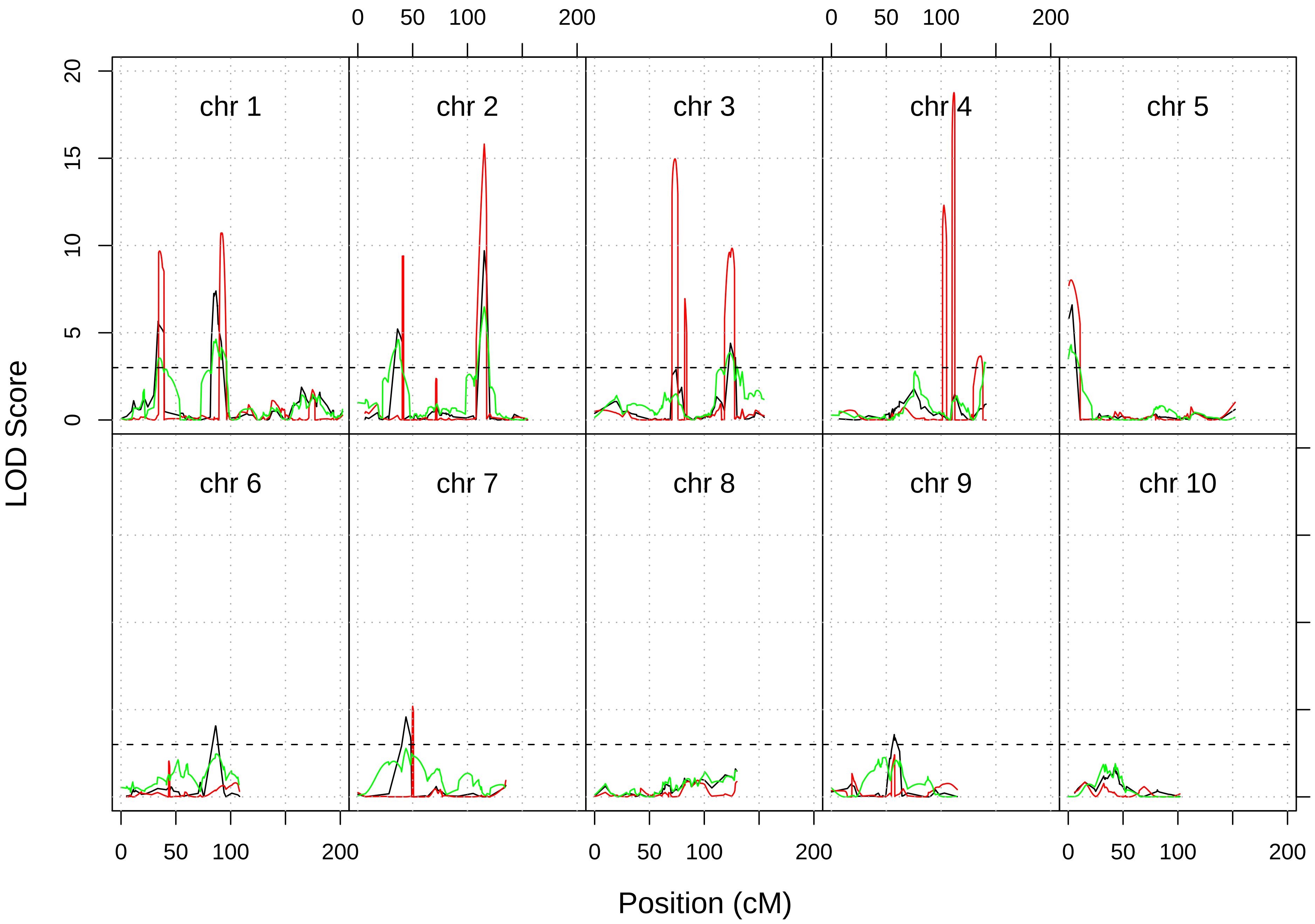
LOD Scores for KI11 population, days to silk

ICIM = red, CIM = green, Stepwise = black



LOD Scores for KI3 population, days to silk

ICIM = red, CIM = green, Stepwise = black

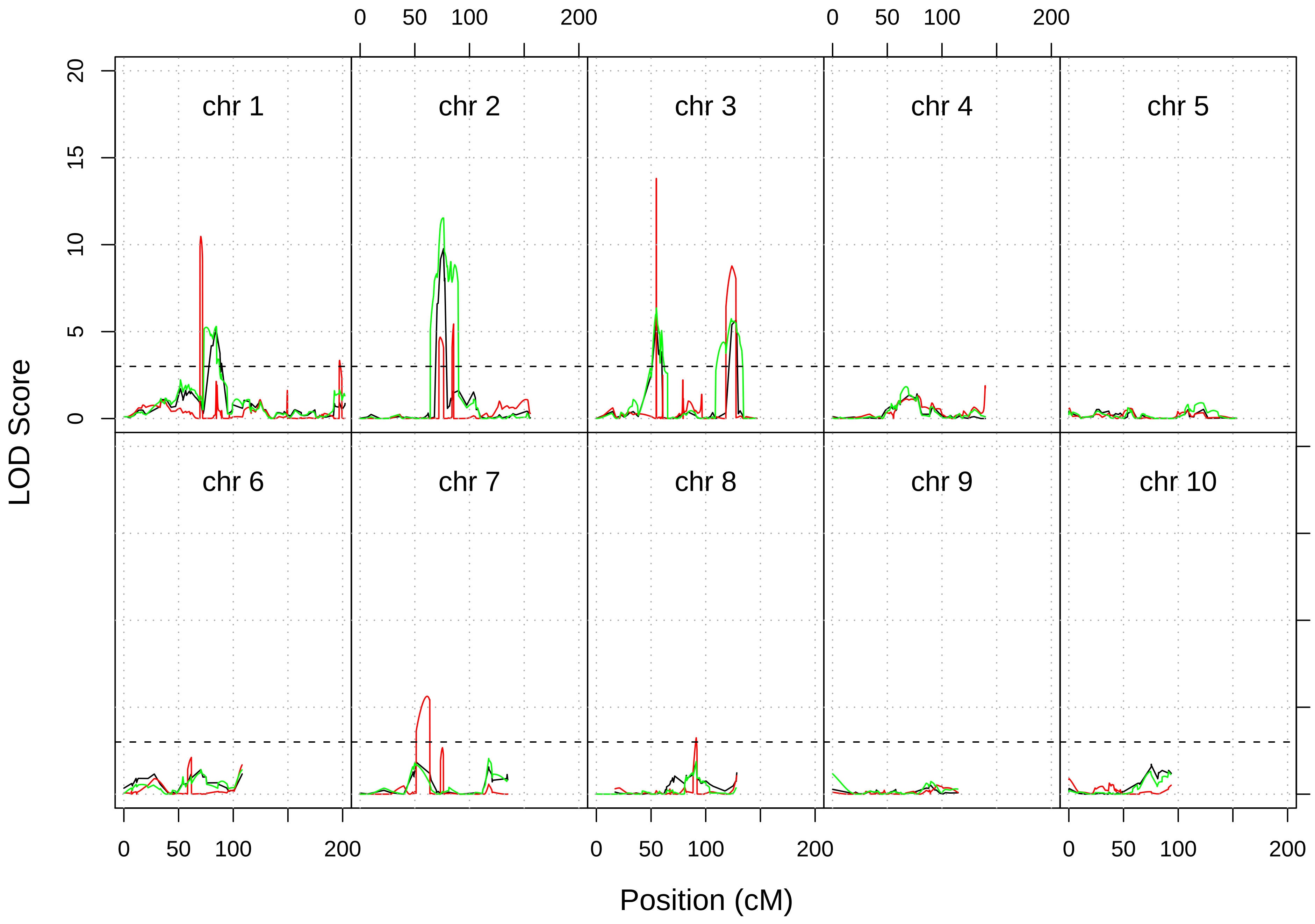


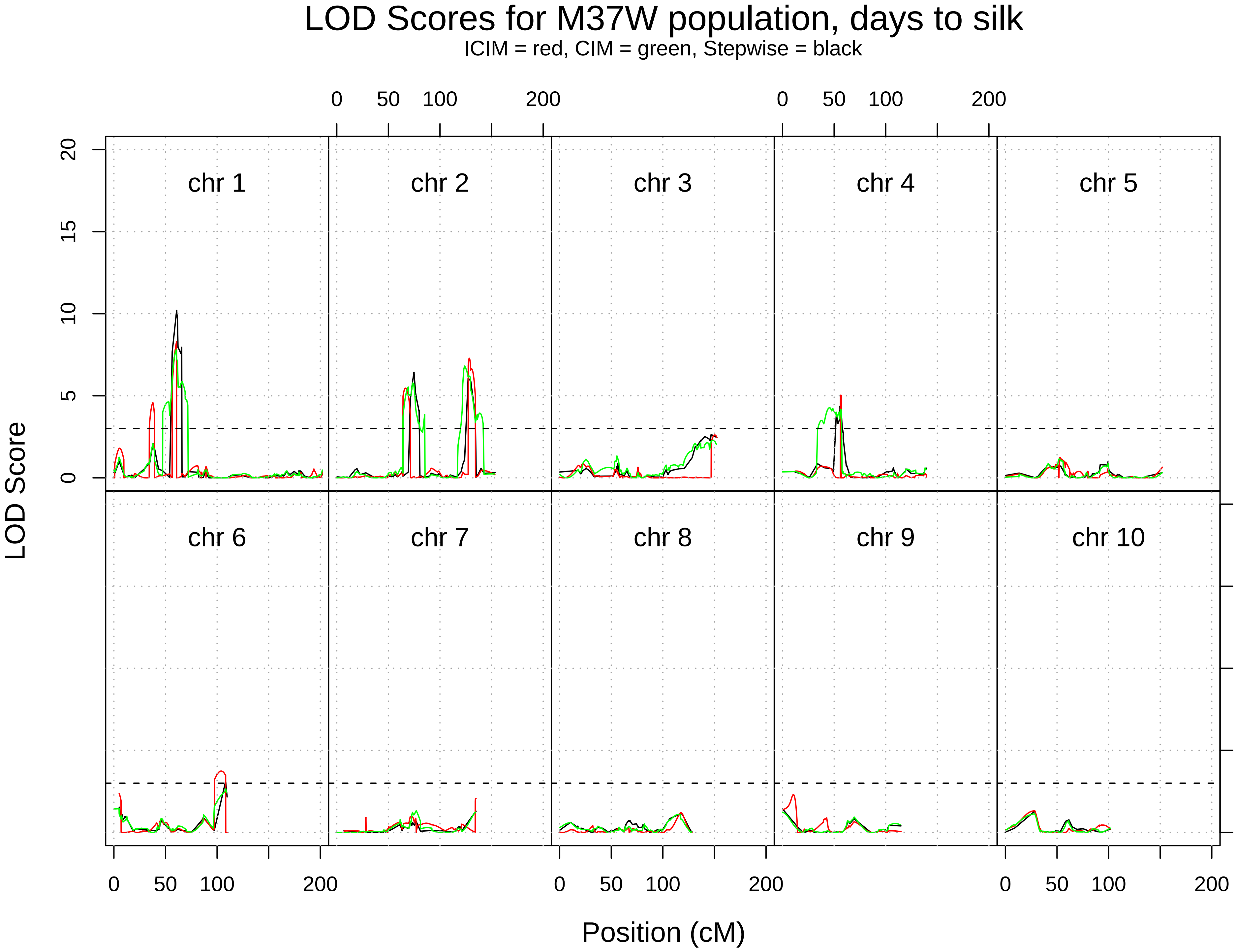
LOD Scores for KY21 population, days to silk

ICIM = red, CIM = green, Stepwise = black

LOD Scores for M162W population, days to silk

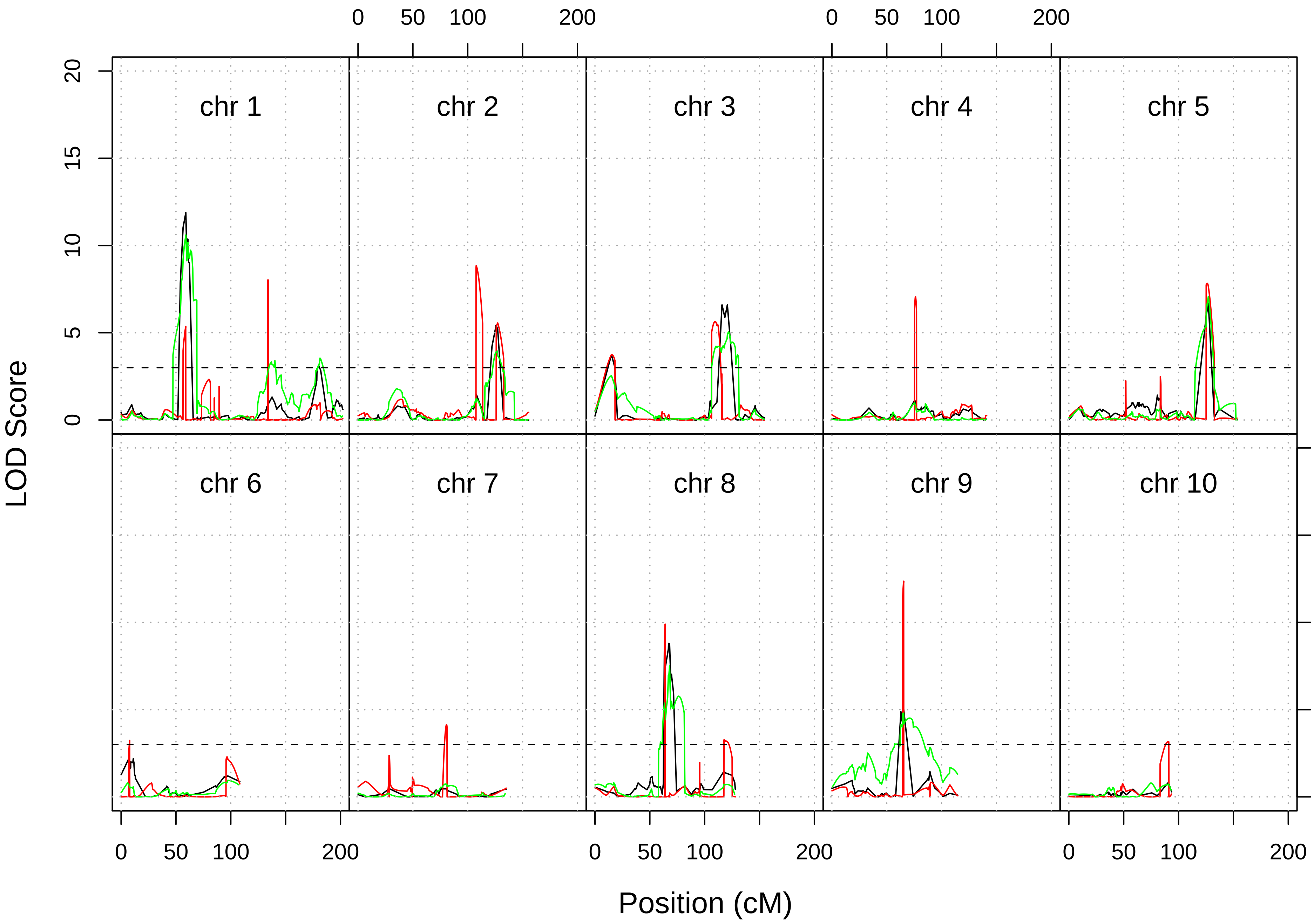
ICIM = red, CIM = green, Stepwise = black





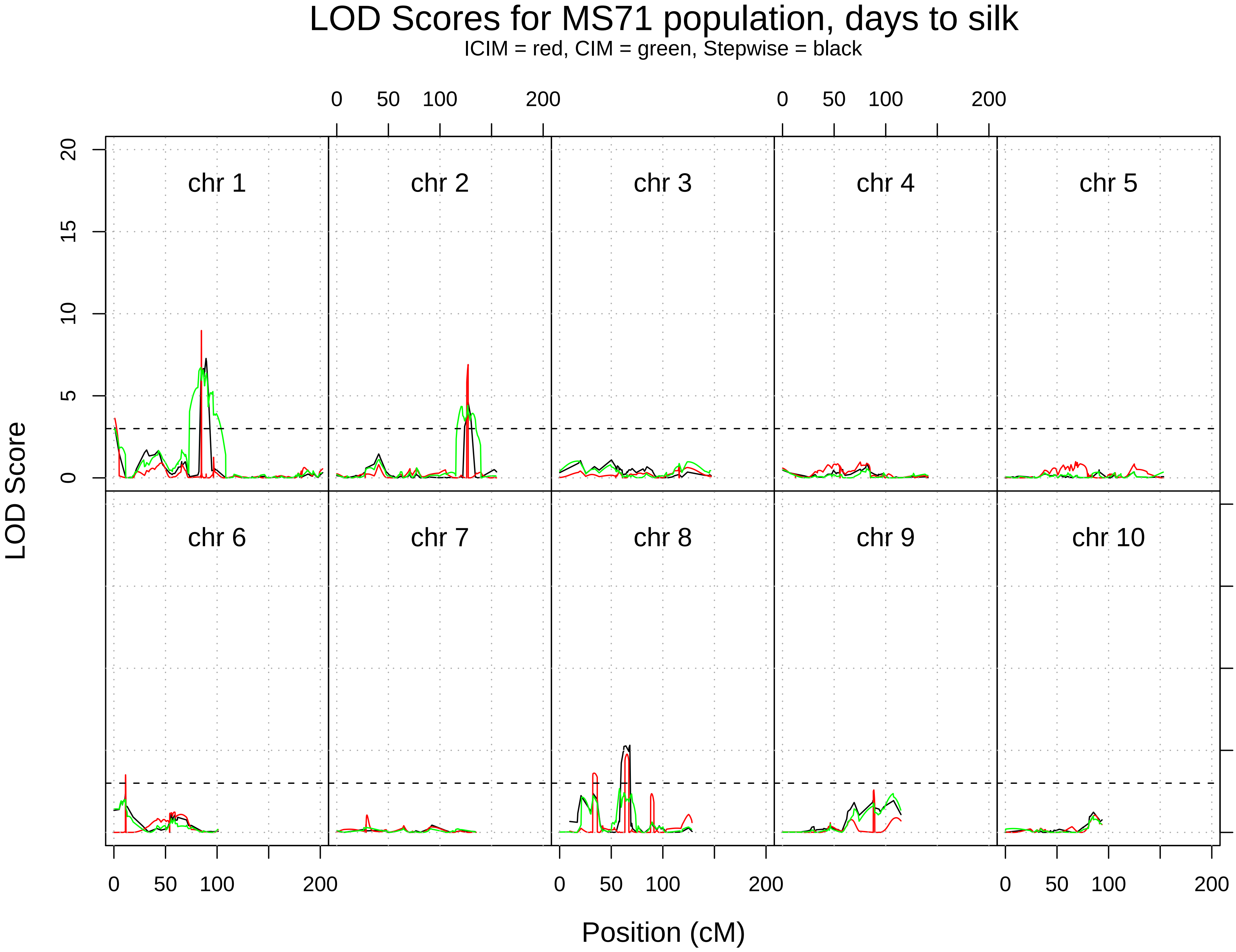
LOD Scores for M37W population, days to silk

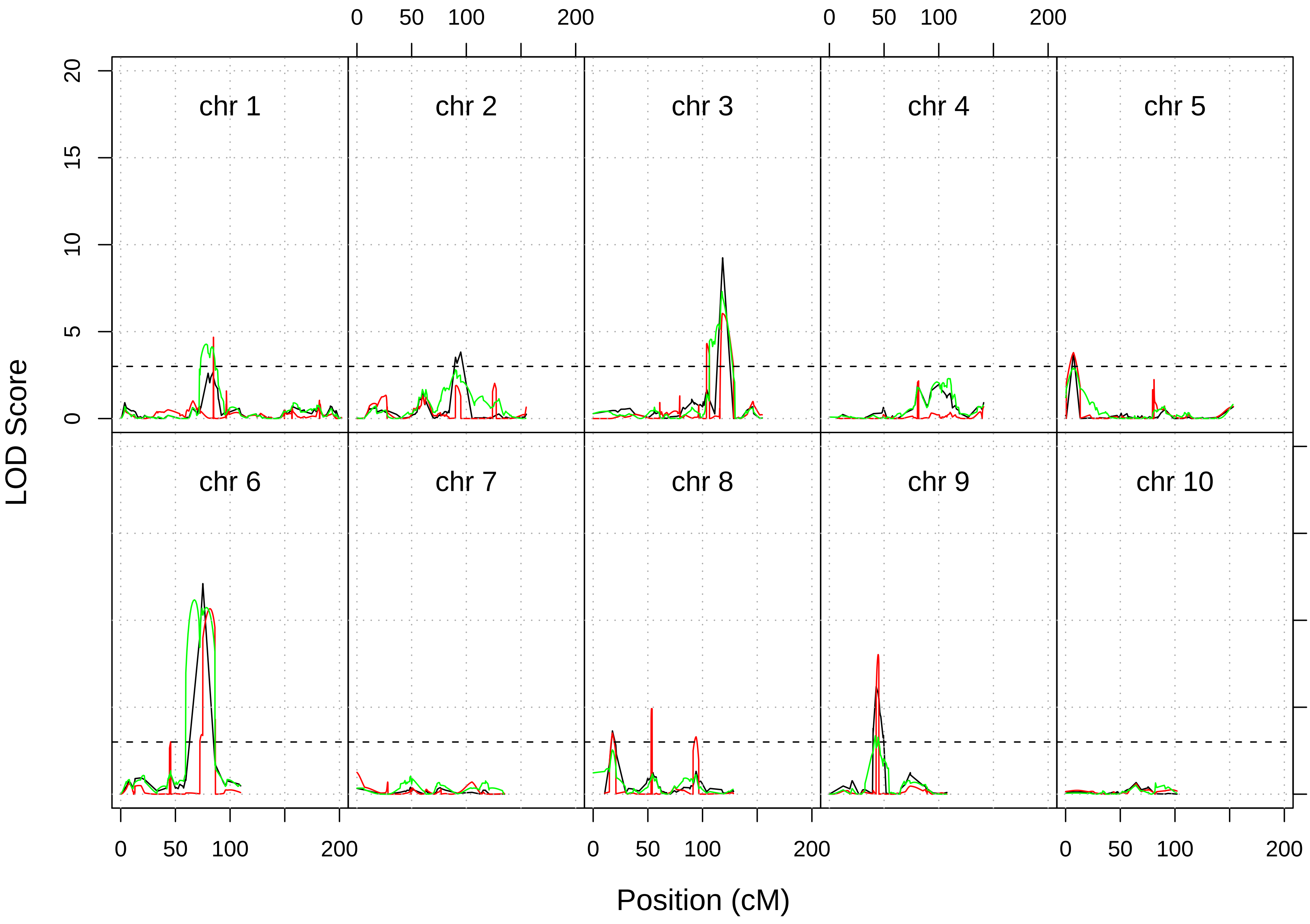
ICIM = red, CIM = green, Stepwise = black



LOD Scores for MO18W population, days to silk

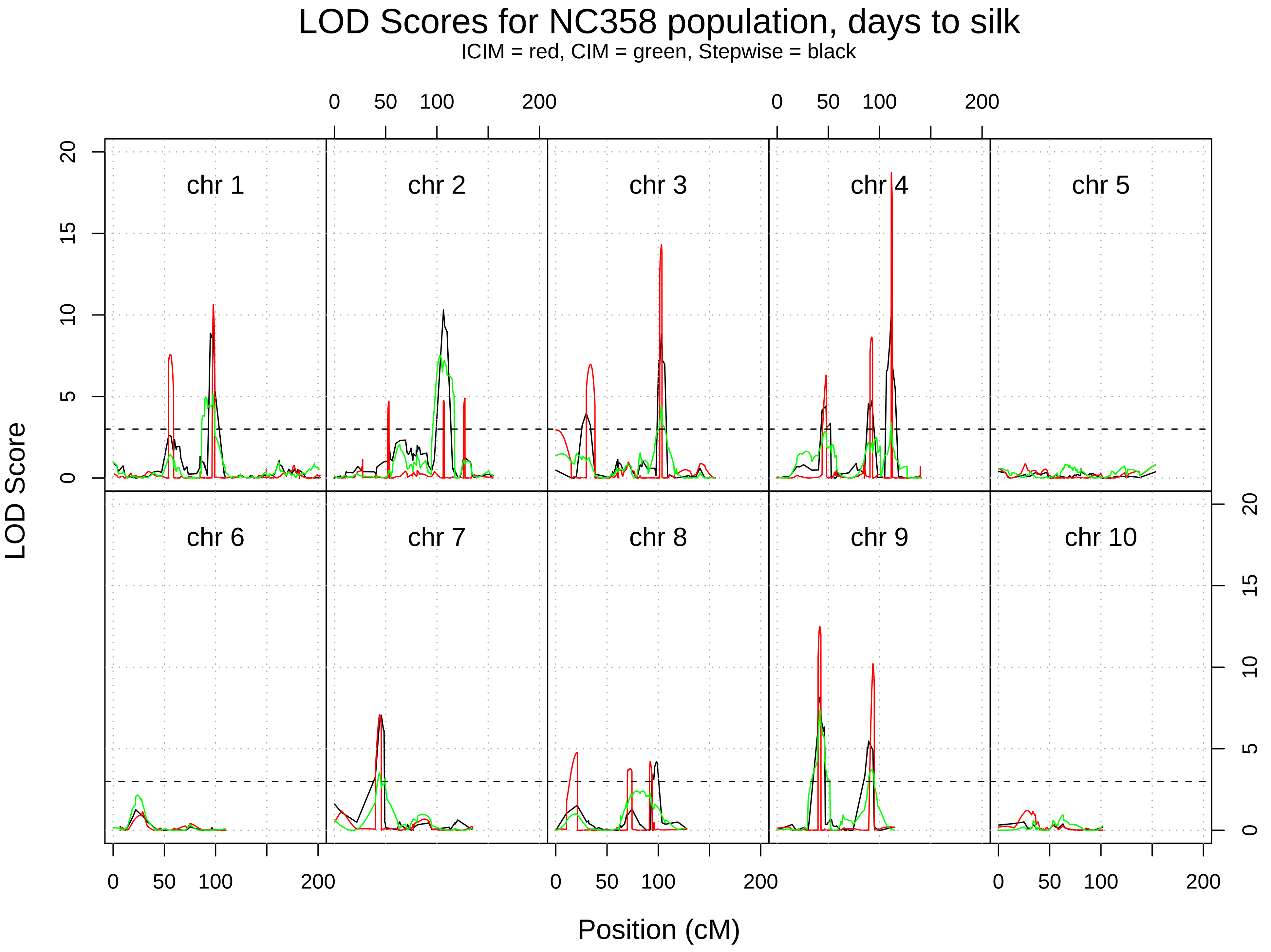
ICIM = red, CIM = green, Stepwise = black


LOD Scores for MS71 population, days to silk
ICIM = red, CIM = green, Stepwise = black
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
LOD Score
Position (cM)
0
5
10
15
20
0
50
100
200



LOD Scores for NC350 population, days to silk

ICIM = red, CIM = green, Stepwise = black

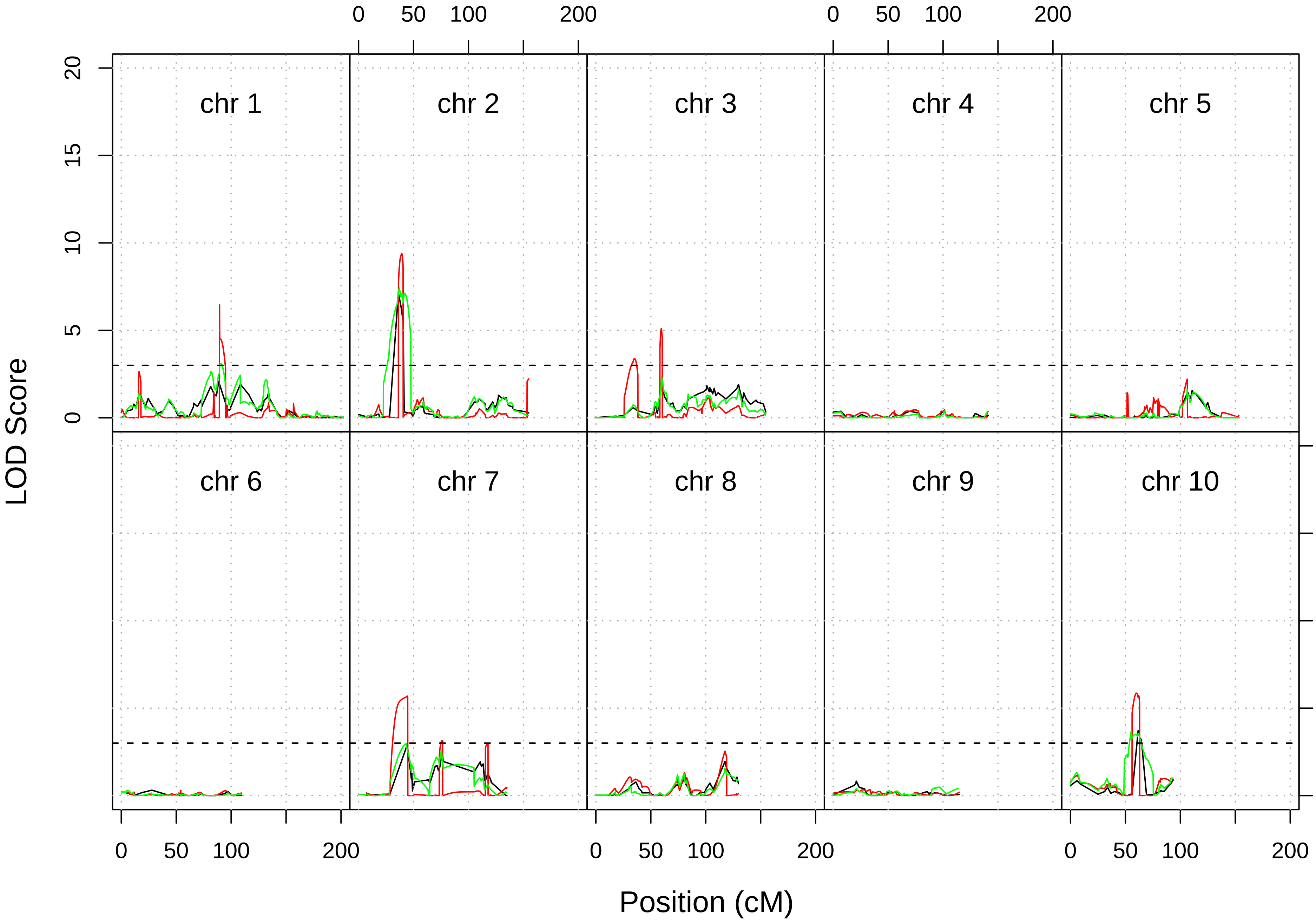


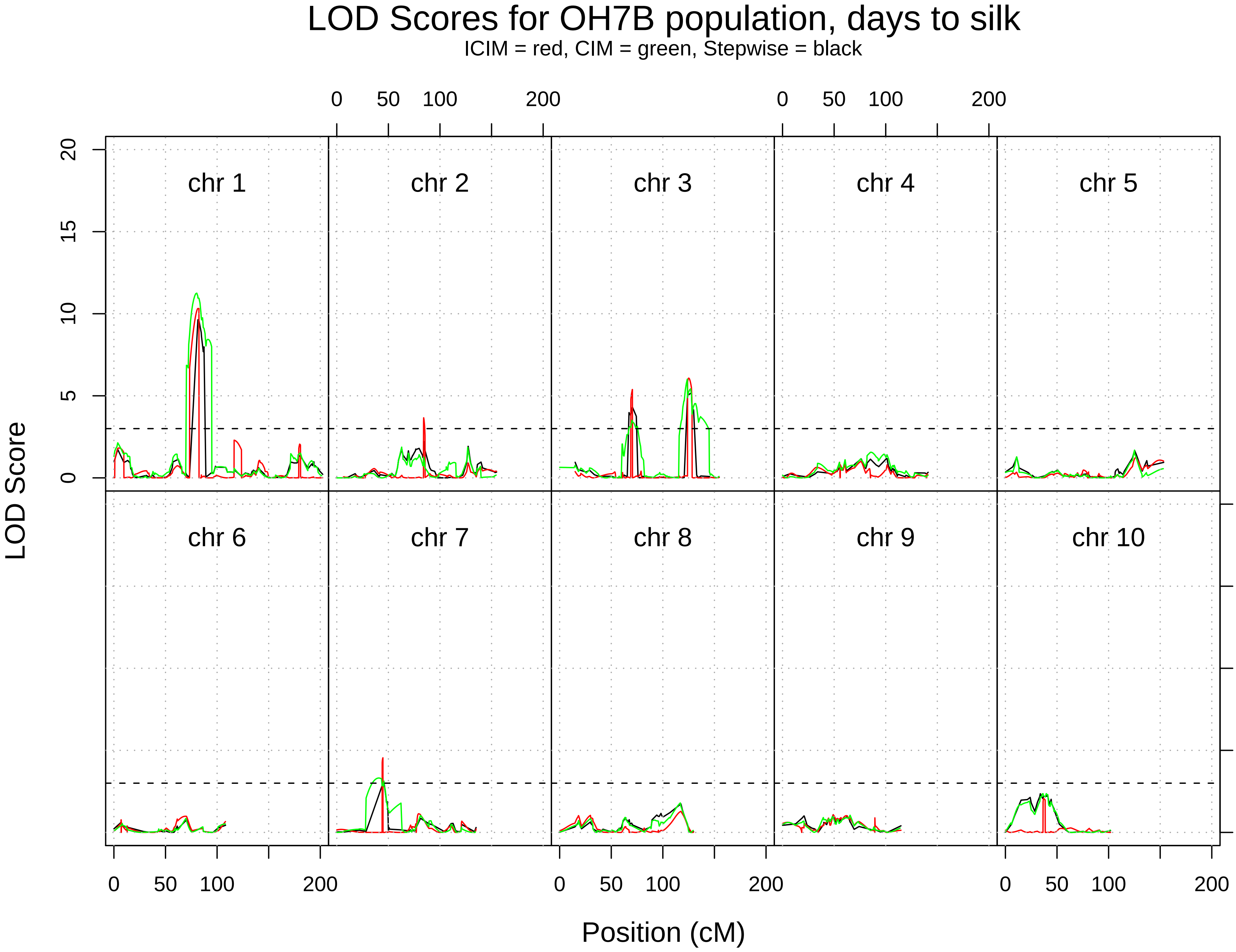
LOD Scores for NC358 population, days to silk

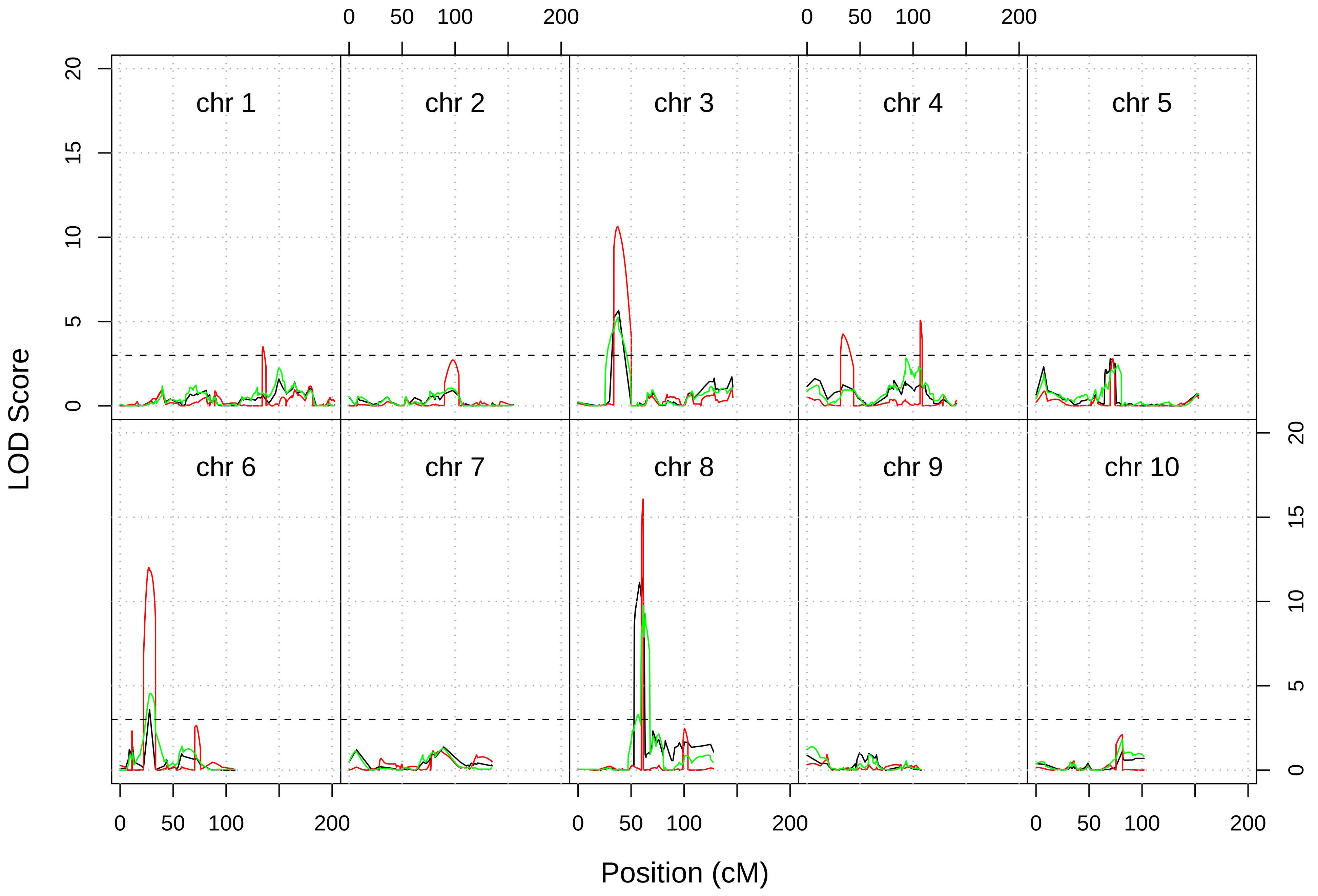
ICIM = red, CIM = green, Stepwise = black

LOD Scores for OH43 population, days to silk

ICIM = red, CIM = green, Stepwise = black

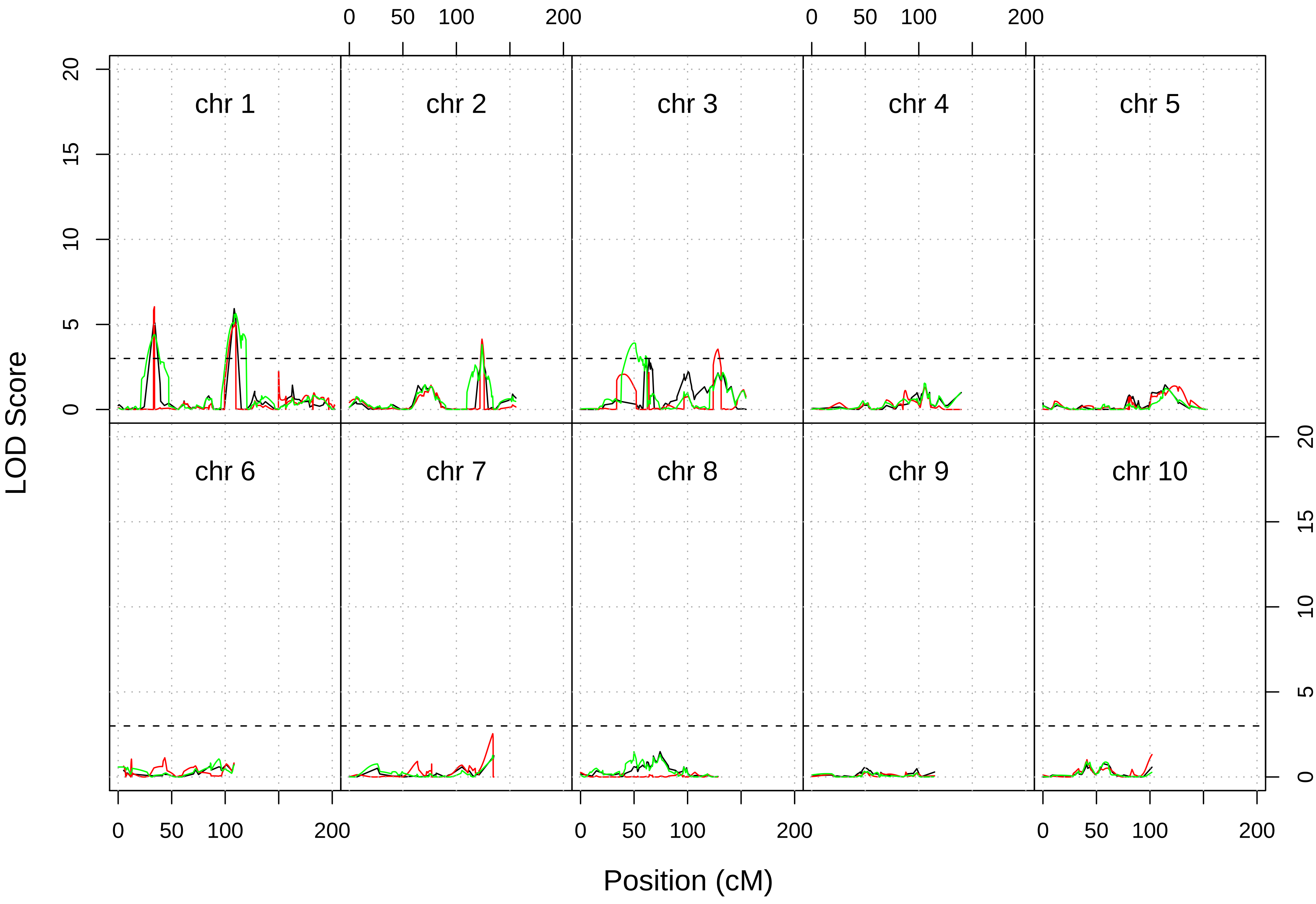



LOD Scores for OH7B population, days to silk
ICIM = red, CIM = green, Stepwise = black
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
LOD Score
0
5
10
15
20
Position (cM)
0
50
100
200



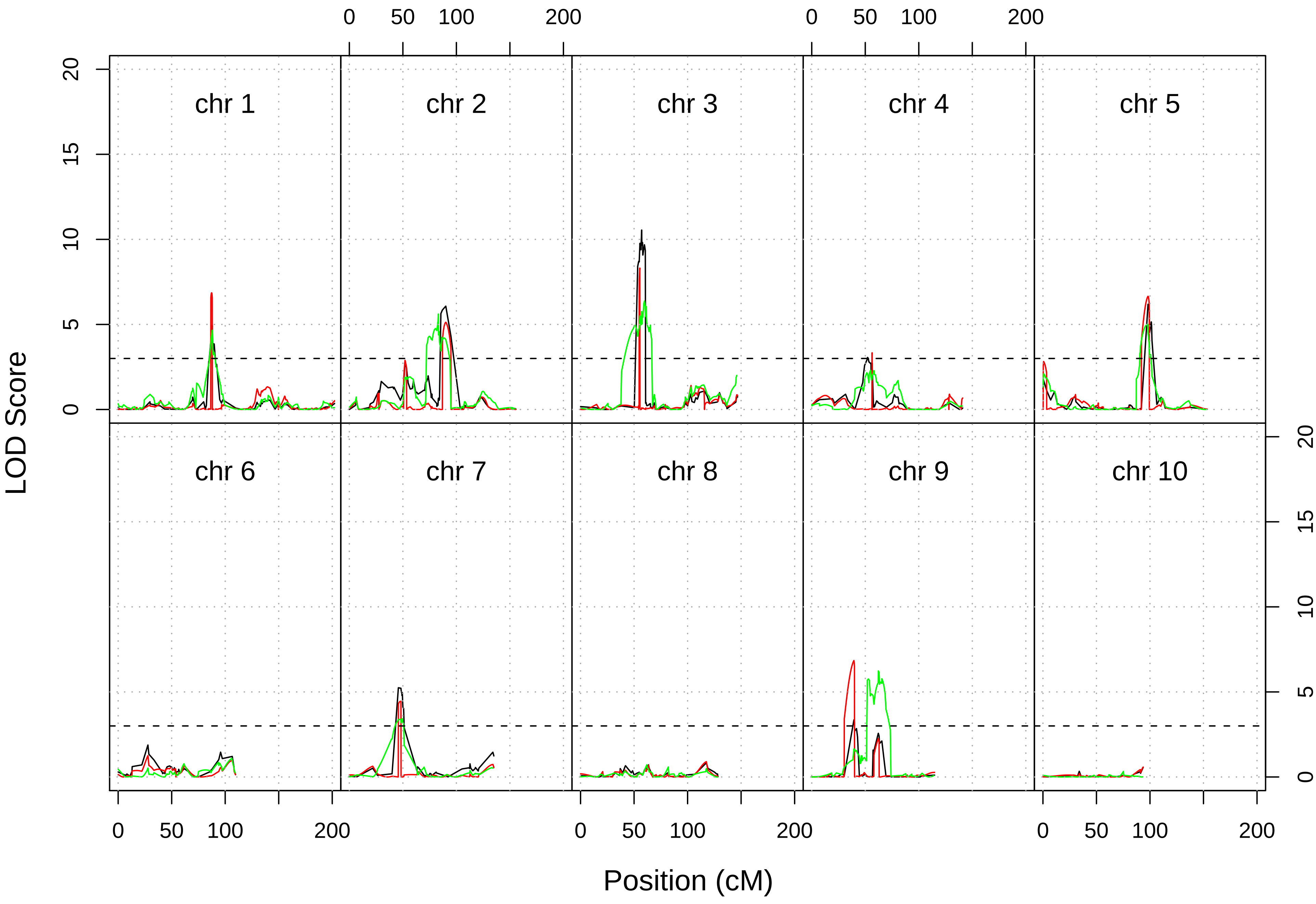
LOD Scores for P39 population, days to silk

ICIM = red, CIM = green, Stepwise = black



LOD Scores for TX303 population, days to silk

ICIM = red, CIM = green, Stepwise = black



LOD Scores for TZI8 population, days to silk

ICIM = red, CIM = green, Stepwise = black