

Ordering markers using R/qtl and MDSmap+MAPpoly packages

FIT 678 – Genetic Data Analysis for Plant Breeding

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April 19/20, 2022

- Linkage map construction
 - Load data and estimate pairwise recombination fractions
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 - Multidimensional Scale (MDS) by MDSMap + MAPpoly

Linkage map construction

Load data and estimate pairwise recombination fractions

To start with the analysis, we load the data (here, we are using the recombinant inbred line population Z025) using the function `read.cross()`, and estimate the pairwise recombination fractions (and their respective LOD scores) using the function `est.rf()`:

```
library(qtl)
maize <- read.cross(format="csv", file="population_Z025.csv", genotypes=c("0", "1", "2"), cross
  sstype = "riself")
```

```
## --Read the following data:
## 188 individuals
## 1106 markers
## 35 phenotypes
```

```
## Warning in convert2riself(cross): Omitting 14087 genotypes with code==2.
```

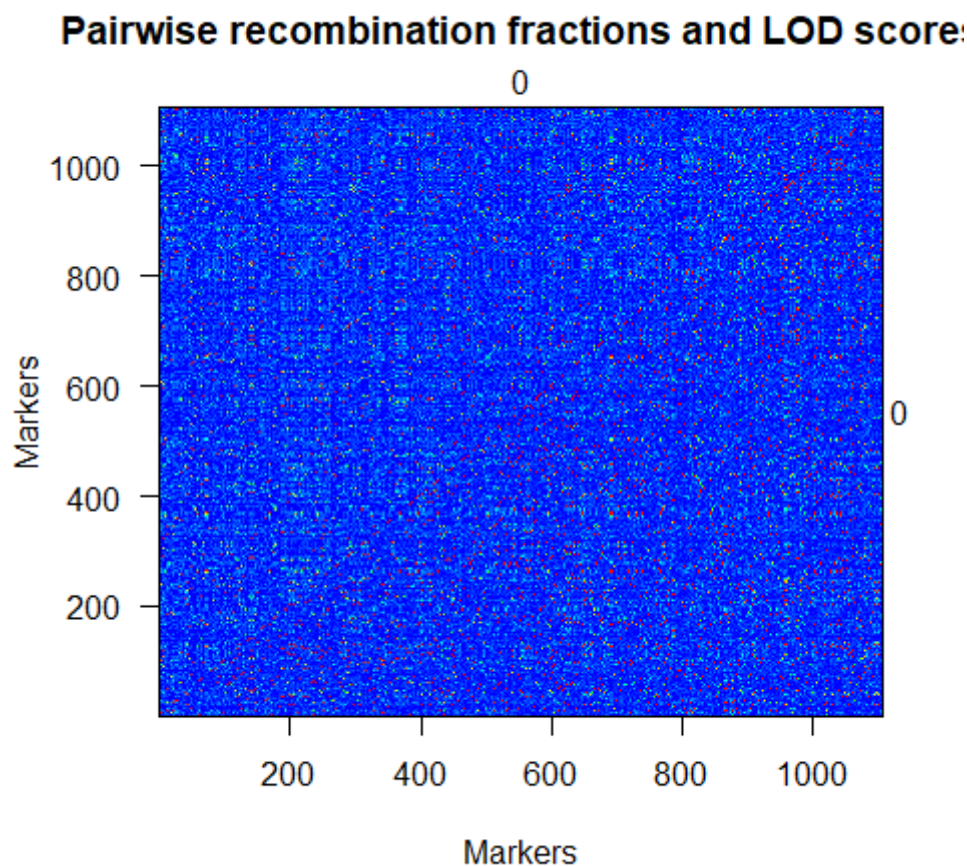
```
## Warning in summary.cross(cross): Some chromosomes > 1000 cM in length; there may be a problem with the genetic map.
## (Perhaps it is in basepairs?)
```

```
## --Cross type: riself
```

Note that there are some warnings regarding:

1: The exclusion of remaining heterozygotes in a RIL population (code==2 is the same as genotype=1); 2: The fact that the map is not estimated yet, so `qt1` package interprets each marker 10 cM apart (which is clearly wrong and we'll fix it).

```
maize <- est.rf(cross = maize)
plotRF(maize, col.scheme = "redblue")
```



From the `plotRF()` function, we notice that 1106 markers have not been assigned to linkage groups yet. In practice, it is recommended to check marker missing data and segregation distortion before grouping, but we will skip it for the sake of time here.

Marker grouping

Once we have the pairwise recombination fraction estimates, we can try to see which markers are in the same linkage group. In order to do so, we need to provide the maximum recombination fraction (`max.rf` argument) and minimum LOD score (`min.lod` argument). These values are provided to the function `formLinkageGroups()` and they are used to see whether two markers are linked or not while avoiding false positives. We will show where these values come from, but you can use them directly in your analysis.

For `max.rf`, we can use something around 0.38, which is the value maximum recombination fraction of 0.50 when converted via Kosambi map function:

$$m_{ij} = \frac{1}{4} \log \left(\frac{1 + 2r_{ij}}{1 - 2r_{ij}} \right)$$

A recombination fraction as big as 0.50 means that two markers are independently segregating (i.e. these two markers are not linked). See below:

```
max.rf <- 0.38
kosambi <- function(r) (1/4)*log((1+(2*r))/(1-(2*r)))
kosambi(r = max.rf)
```

```
## [1] 0.4981075
```

For `min.lod`, we can run Bonferroni correction on the number of tests that we have to perform in order to evaluate marker linkage. The number of tests is the number of marker pairs that we have in our data. As a first guess, we have:

```
(M <- totmar(maize)) # number of markers
```

```
## [1] 1106
```

```
(num.pair <- choose(M, 2)) # number of marker pairs
```

```
## [1] 611065
```

```
(min.lrt <- qchisq(1-(0.05/num.pair), 1)) # min LRT to consider two markers linked
```

```
## [1] 28.7624
```

```
(min.lod <- 0.2172 * min.lrt) # conversion of LRT to LOD
```

```
## [1] 6.247193
```

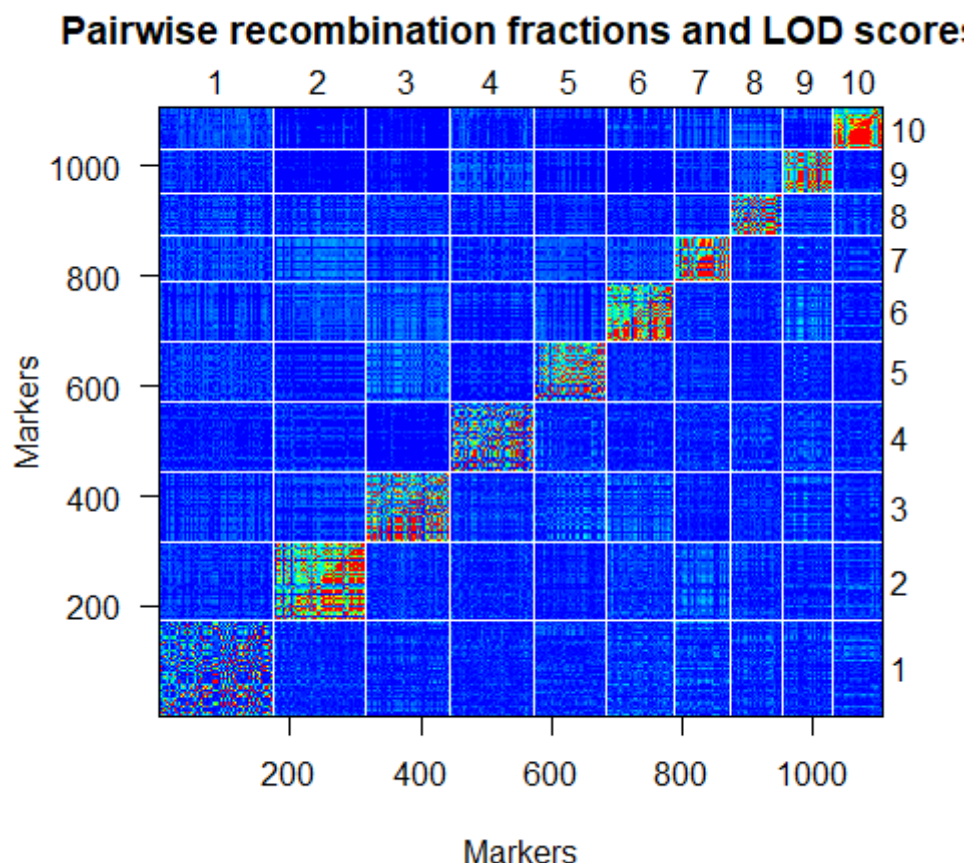
Now, it is time to see how many linkage groups we have. First, we run the function `formLinkageGroups()` with `reorgMarkers = FALSE` just to see how the markers get distributed along the formed linkage groups:

```
lg <- formLinkageGroups(maize, max.rf=max.rf, min.lod=min.lod, reorgMarkers=FALSE)
table(lg[,2])
```

```
##
##  1  2  3  4  5  6  7  8  9 10
## 175 139 130 127 111 106 85 78 78 77
```

We note that there are 10 linkage groups (as expected for maize). Now, we can use `reorgMarkers = TRUE` and update our cross object named `maize` with each marker numbered according to the linkage group it belongs:

```
maize <- formLinkageGroups(maize, max.rf=0.38, min.lod=6.25, reorgMarkers=TRUE)
plotRF(maize, col.scheme = "redblue")
```



The heatmap shows grouped but not yet ordered markers within each linkage group.

Marker ordering

We are going to show two ways of ordering markers. The first way uses the `orderMarkers()` function by R/qtl and usually needs some manual curation. The second way uses the MDS algorithm and it is faster and usually more accurate. You can choose which method you want to use and skip to its specific section, meaning that you do *not* need to run both ways.

Using `orderMarkers` function by R/qtl

R/qtl has a function that runs the Branch-and-Bound algorithm as an possible solution for the Traveling Salesman Problem (TSP) that ordering markers is. It usually provides a good solution. The problem is that Branch-and-Bound is very sensitive to the marker choice that is made to start the algorithm. Therefore, we run it at least a couple of times such that some effect of the first choices can be evaluated.

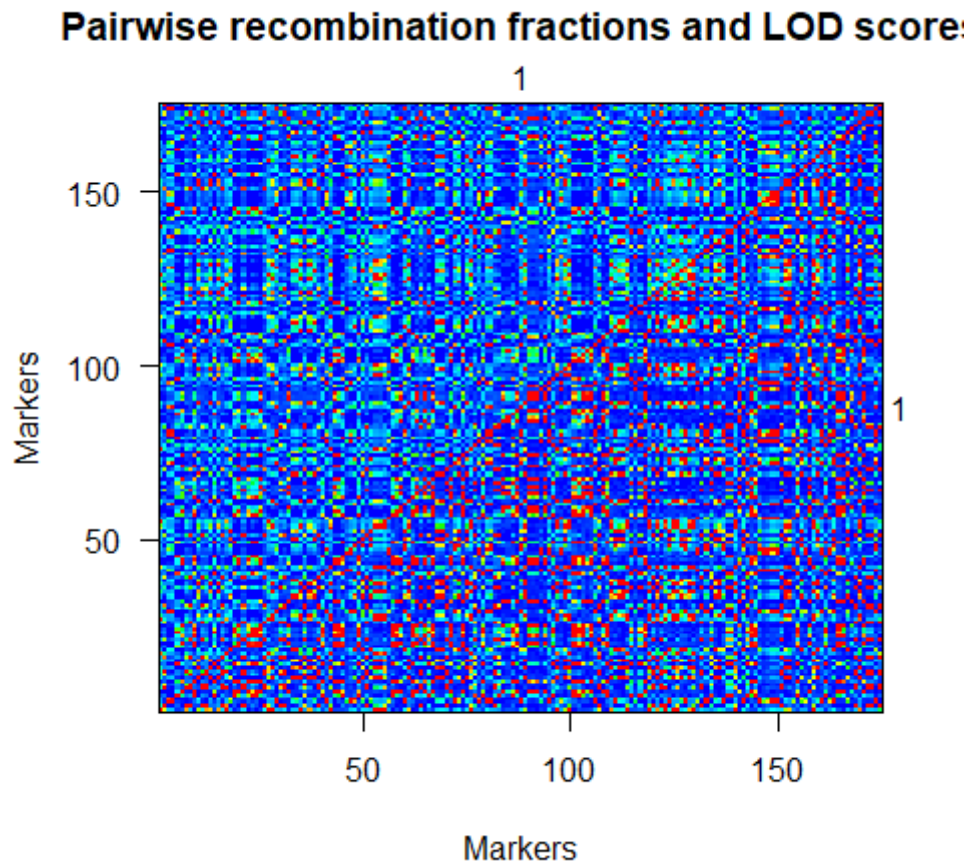
We save the `maize` object under two new object called `maize.bb1` and `maize.bb2`, so we can update the with the results of two runs of the Branch-and-Bound algorithm. In addition, we initialize two objects that will store the log-likelihood of the ordering for each linkage group from both runs:

```
maize.bb1 <- maize
maize.bb2 <- maize
loglik.bb1 <- loglik.bb2 <- c()
```

Linkage group 1

The object `c` stores the number of the chromosome under evaluation.

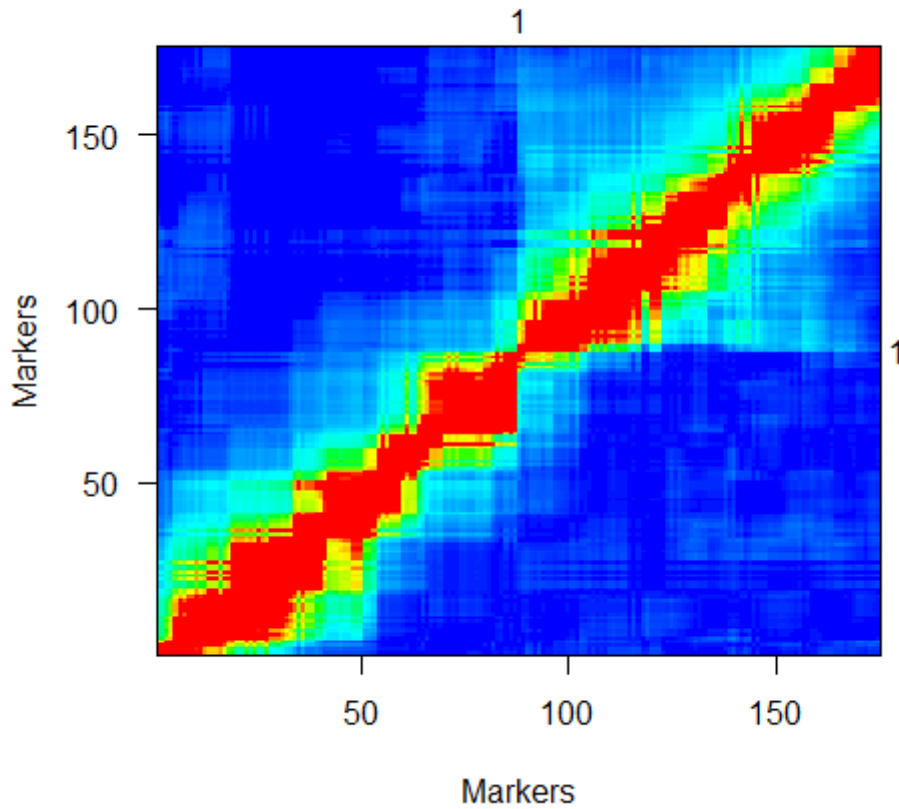
```
c <- 1  
plotRF(maize, chr=c, col.scheme = "redblue")
```



The argument `chr` let us take a closer look into the heatmap of a specific chromosome, whose markers are clearly not ordered.

```
maize.bb1 <- orderMarkers(cross = maize.bb1, chr=c, use.ripple = FALSE, map.function="kosambi")  
plotRF(maize.bb1, chr = c, col.scheme = "redblue")
```

Pairwise recombination fractions and LOD score



```
pull.map(maize.bb1, chr = c)
```

##	PZA01271.1	PZA03613.1	PZA02129.1	PZA02032.1	PHM2244.142
##	0.0000000	0.3003935	3.0214490	5.9395732	11.7259792
##	PHM6238.36	PZA02372.1	PZA00175.2	PZA00181.2	PZA00447.8
##	13.5614240	14.2353070	16.5727377	16.5727427	16.5727477
##	PZA00528.1	PZA02284.1	PZA00106.10	PZA03521.1	PZA00566.5
##	16.5727527	18.5147648	18.5147698	18.5147748	18.5147798
##	PZA00731.7	PZA00887.1	PZA03551.1	csu1171.2	PZB00718.5
##	18.5147848	21.4861669	23.8088191	29.4406497	29.4406547
##	PZA01030.1	PZA02094.9	PZA02393.2	PZA01652.1	PZA00425.11
##	29.4406597	29.4406647	29.4406697	29.4406747	29.4406797
##	PZB00648.5	PZA01497.1	PZA02487.1	PHM3226.15	PHM13619.5
##	29.4406847	29.4406897	31.2848349	31.2848399	31.2848449
##	PHM4531.46	PZB01957.1	PZB02058.1	PZA01348.1	PZA02686.1
##	31.5996172	32.5504777	34.0902393	34.0902443	42.1767749
##	PZA02490.1	PZA01455.1	PZB01662.1	PZA02271.1	PZA02195.1
##	42.1767799	42.1767849	42.1767899	43.2865643	43.6968614
##	PZA00240.6	PZB00872.3	umc13.1	PZA03183.5	PZA00081.18
##	45.9236034	49.9326577	49.9326627	49.9326677	50.2154093
##	PZA03742.1	PZA03243.2	PHM3726.129	PZA00962.1	PZA02376.1
##	50.7844642	50.7844692	50.7844742	50.7844792	50.7844842
##	PHM4913.18	PZA02292.1	PZA03168.5	PZA02737.1	PZA01315.1
##	54.6611780	54.6617714	56.0443542	61.7326447	62.3697197
##	PZA02550.1	PZA03561.1	PZB01062.3	PZA02114.1	PZA01476.1
##	62.3697247	62.3697297	62.3697347	62.3697397	67.9584488
##	PHM5098.25	PZA03189.4	PZA00294.22	PZA01267.3	PZA00752.1
##	68.2686351	68.2686401	68.2686451	75.0176384	76.9493466
##	PZA01135.1	PZA00944.1.2	PZA03240.1.2	PZA03465.1	csu1138.3.4
##	78.3043647	81.0472221	81.0472271	81.0472321	85.2401505
##	PZA03200.2	PZA02070.1	PZA02577.1	PZA01254.2	PZA00939.1
##	85.2401555	85.2401605	85.2401655	86.0866702	86.0866752
##	PZA02750.3	PZA02763.1	PHM9418.11	PZB01235.4	PZA02135.2
##	86.9319637	86.9319687	87.4925658	87.4925708	92.0255392
##	PZA02741.1	an1.5	PZA02191.1	PZA00455.14.16	PZA00068.1
##	92.0255442	94.7059876	97.2689502	97.2689552	102.1892184
##	PHM1968.22	PZA03531.1	PZA00619.3	PZA02467.10	PZA03074.27
##	102.1892234	102.1892284	115.8025686	117.6182429	122.0991466
##	PZA00131.15	PZA01963.15	PZA01216.1	PZA01019.1	PHM5480.17
##	122.4187485	122.4187535	122.4187585	125.1933498	125.1933548
##	PZA01391.1	PZA03194.1	PZA03193.2	PHM12706.14	PZA02014.3
##	125.1933598	128.8603338	128.8603388	128.8603438	129.1771520
##	PZA03265.3	PZA01039.1	PHM6043.19	PZA03741.1	PHM15871.11
##	129.4910916	129.4910966	134.0458500	134.0458550	137.1377011
##	PZA02823.1	PZA02117.1	PZA00658.21	PHM5484.22	PHM4942.12
##	138.8006193	138.8006243	138.8006293	138.8006343	140.3600235
##	PHM2478.22	PZA02186.1	umc128.2	PZA00664.3	PZA03001.15
##	140.3600285	141.2595228	141.2595278	141.2595328	142.5236382
##	PHM4926.16	PZB01647.1	PZA03404.1	PHM16605.19	PZA00381.4
##	142.5236432	142.5236482	149.6812885	149.6812935	149.6812985
##	PZA03301.2	PZA03064.6	PZA02269.3.4	PHM3034.3	PHM14475.7
##	149.6813035	149.6813085	151.7592601	155.5491121	155.5491171
##	kip1.3	glb1.2	PZA00339.4	PZA01588.1	PZA01921.20.19
##	155.5491221	156.3335554	157.8368865	157.8368915	158.8048195
##	PZA02985.5	PHM5526.25	PZA03457.1	PZB00008.1	PZB00895.1
##	159.8543823	159.8543873	160.1940374	164.4565309	164.4565359
##	PZB00063.1	PZA02278.1	PZA02698.3	PZA02520.1	PZA00030.11

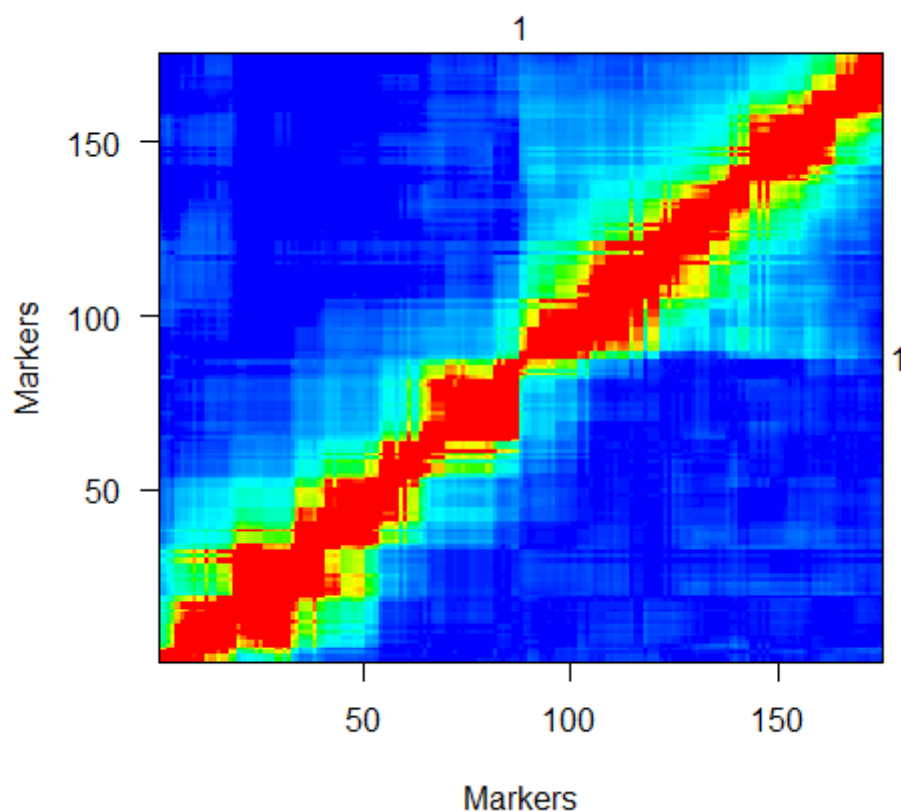
##	164.4565623	165.7603697	169.5840030	174.3181216	174.3181266
##	PZB00114.1	PZA03188.3	PZA02204.1	PZA01978.23	PZA03020.8
##	175.9531456	178.8835165	178.8835215	178.8835265	185.9589731
##	PZA00610.16	PZA00978.1	PZA02957.5	PZA02087.2	PZA01246.1
##	185.9589781	185.9589831	185.9589881	186.6366865	186.6366915
##	PZA00245.20	PHM18705.23	PZB01403.1	PZA03037.2	PZA00894.7
##	187.3142560	187.9785865	187.9785915	190.0428053	190.0428103
##	PZA03305.7.1	PZA02044.1	PZB01227.6	PZA00307.14	PZA00276.18
##	190.6208934	195.4835388	195.4835438	200.3233990	200.3234040
##	PZA00991.2	PZA00235.9	PZA00623.3	PZA02359.10	PZA01238.1.2
##	200.3234090	200.6024741	202.0204076	202.0222843	207.7934729
##	PZA01068.1	PHM9807.9	PZA00343.31	PHM1275.22	PZA00243.25
##	207.7934779	207.7934829	208.4042564	208.4042761	212.2395969
##	PZA00856.2	PZA01239.2	PZA01807.1	PZA00432.4	PHM7616.35
##	212.2396019	212.8504026	214.0573085	214.2008058	214.3473220

```
(loglik.bb1[c] <- attr(maize.bb1$geno[[c]]$map, "loglik"))
```

```
## [1] -2709.611
```

```
maize.bb2 <- orderMarkers(cross = maize.bb2, chr=c, use.ripple = FALSE, map.function="kosambi")
plotRF(maize.bb2, chr = c, col.scheme = "redblue")
```

Pairwise recombination fractions and LOD score



```
pull.map(maize.bb2, chr = c)
```


##	PZA01271.1	PZA03613.1	PZA02129.1	PZA02032.1	PHM2244.142
##	0.0000000	0.3003963	3.0214591	5.9473252	11.7455836
##	PZA02372.1	PHM6238.36	PZA00528.1	PZA00447.8	PZA00181.2
##	13.3027435	14.2749682	15.5633663	15.5633713	15.5633763
##	PZA00175.2	PZA00106.10	PZA02284.1	PZA00731.7	PZA00887.1
##	15.5633813	17.6060553	17.6060603	17.6060653	20.5407327
##	PZA00566.5	PZA03521.1	PZA03551.1	PZA02094.9	PZB01957.1
##	20.5407377	20.5407427	22.7497429	22.7497479	32.4431363
##	PHM4531.46	PZA02487.1	PHM3226.15	PZA00425.11	PHM13619.5
##	33.2645650	33.5436433	33.5436483	34.1048580	34.1048630
##	PZB00718.5	PZB00648.5	PZA02393.2	PZA01652.1	PZA01497.1
##	35.2406095	35.2406145	35.2406195	35.2406245	35.2406295
##	PZA01030.1	csu1171.2	PZB02058.1	PZA01348.1	PZA02686.1
##	35.2406345	35.2406395	40.0222274	40.0222324	47.3682708
##	PZA01455.1	PZB01662.1	PZA02490.1	PZA02271.1	PZA02195.1
##	47.3682758	47.3682808	47.3682858	48.4914939	48.9039010
##	PZA00962.1	PZA02376.1	PZA00240.6	PHM3726.129	PZB00872.3
##	51.1315139	51.1315189	51.1315239	51.1315289	55.1499206
##	PZA03183.5	umc13.1	PZA00081.18	PZA03742.1	PZA03243.2
##	55.1499256	55.1499306	55.4328535	56.0022781	56.0022831
##	PZA02292.1	PHM4913.18	PZA03168.5	PZA02737.1	PZA03561.1
##	59.9100926	59.9100976	61.3027819	67.0386388	67.6796623
##	PZB01062.3	PZA02114.1	PZA02550.1	PZA01476.1	PZA01315.1
##	67.6796673	67.6796723	67.6796773	73.3135709	73.3135759
##	PHM5098.25	PZA00294.22	PZA03189.4	PZA01267.3	PZA00752.1
##	73.6263020	73.6263070	73.6263120	80.4216821	82.3553337
##	PZA01135.1	PZA03240.1.2	PZA00944.1.2	PZA03465.1	PZA02577.1
##	83.6569599	86.1889754	86.1889804	86.1889854	90.8184590
##	PZA02741.1	PZA02135.2	PZA02070.1	PZA03200.2	csu1138.3.4
##	90.8184640	90.8184690	92.2964267	92.2964317	92.2964367
##	PZA00939.1	PZA01254.2	PZA02750.3	PZA02763.1	PZB01235.4
##	93.1497754	93.1497804	94.0013255	94.0013305	94.5661520
##	PHM9418.11	an1.5	PHM1968.22	PZA00455.14.16	PZA02191.1
##	94.5661570	100.9931809	103.5402514	103.5402564	108.4093063
##	PZA03531.1	PZA00068.1	PZA00619.3	PZA02467.10	PZA03074.27
##	108.4093113	108.4093163	121.7656791	123.5820285	128.0629055
##	PZA01216.1	PZA00131.15	PZA01391.1	PHM5480.17	PZA01019.1
##	128.3823339	128.3823389	128.3823439	131.1574920	131.1574970
##	PZA01963.15	PZA03194.1	PHM12706.14	PZA03193.2	PZA02014.3
##	131.1575020	134.8252257	134.8252307	134.8252357	135.1421006
##	PZA01039.1	PHM6043.19	PZA03741.1	PZA03265.3	PHM15871.11
##	135.4556418	140.0119638	140.0119688	140.0119738	143.1037378
##	PZA00658.21	PZA02117.1	PHM5484.22	PHM4942.12	PZA02823.1
##	144.7664515	144.7664565	144.7664615	146.3258113	146.3258163
##	PHM2478.22	umc128.2	PZA02186.1	PZA00664.3	PZA00381.4
##	146.3258213	147.2254544	147.2254594	147.2254644	148.4895661
##	PZB01647.1	PZA03001.15	PHM16605.19	PHM4926.16	PZA03301.2
##	148.4895711	148.4895761	155.6469846	155.6469896	155.6469946
##	PZA03064.6	PZA02269.3.4	PHM3034.3	PZA03404.1	PHM14475.7
##	155.6469996	157.7253188	157.7253238	157.7253288	161.5149359
##	kip1.3	glb1.2	PZA01588.1	PZA00339.4	PZA01921.20.19
##	161.5149409	162.2993774	163.8027157	163.8027207	164.7706501
##	PZA02985.5	PHM5526.25	PZA03457.1	PZB00895.1	PZB00008.1
##	165.8202141	165.8202191	166.1598696	170.4223685	170.4223735
##	PZA02278.1	PZB00063.1	PZA02698.3	PZA02520.1	PZA00030.11

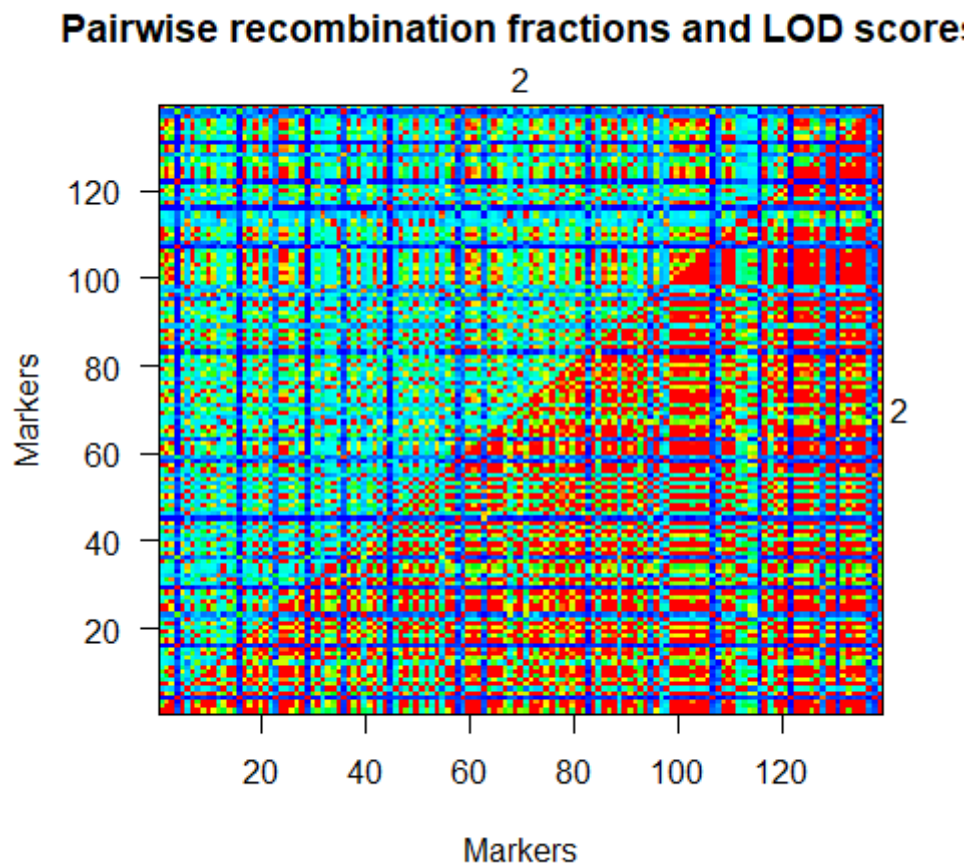
```
## 171.7260717 171.7260767 175.5498409 180.2839768 180.2839818
## PZA01978.23 PZB00114.1 PZA02204.1 PZA00978.1 PZA03020.8
## 181.9192770 181.9192820 184.8490006 191.9250704 191.9250754
## PZA03188.3 PZA02957.5 PZA00610.16 PZA01246.1 PZA02087.2
## 191.9250804 191.9250854 191.9250904 192.6029026 192.9276782
## PZA00245.20 PHM18705.23 PZA03037.2 PZA00894.7 PZB01403.1
## 193.2751390 193.9394333 196.0040747 196.0040797 196.0040847
## PZA03305.7.1 PZB01227.6 PZA02044.1 PZA00276.18 PZA00307.14
## 196.5826410 196.5826460 201.4455279 206.2850389 206.2850439
## PZA00991.2 PZA00235.9 PZA00623.3 PZA02359.10 PZA01238.1.2
## 206.2850489 206.5641139 207.9820349 207.9839232 213.7551142
## PHM9807.9 PZA00343.31 PZA01068.1 PHM1275.22 PZA00243.25
## 213.7551192 213.7551242 213.7551292 214.3659785 218.2012372
## PZA00856.2 PZA01239.2 PZA01807.1 PZA00432.4 PHM7616.35
## 218.2012422 218.8120428 220.0189483 220.1624457 220.3089617
```

```
(loglik.bb2[c] <- attr(maize.bb2$geno[[c]]$map, "loglik"))
```

```
## [1] -2728.051
```

Linkage group 2

```
c <- 2
plotRF(maize, chr=c, col.scheme = "redblue")
```



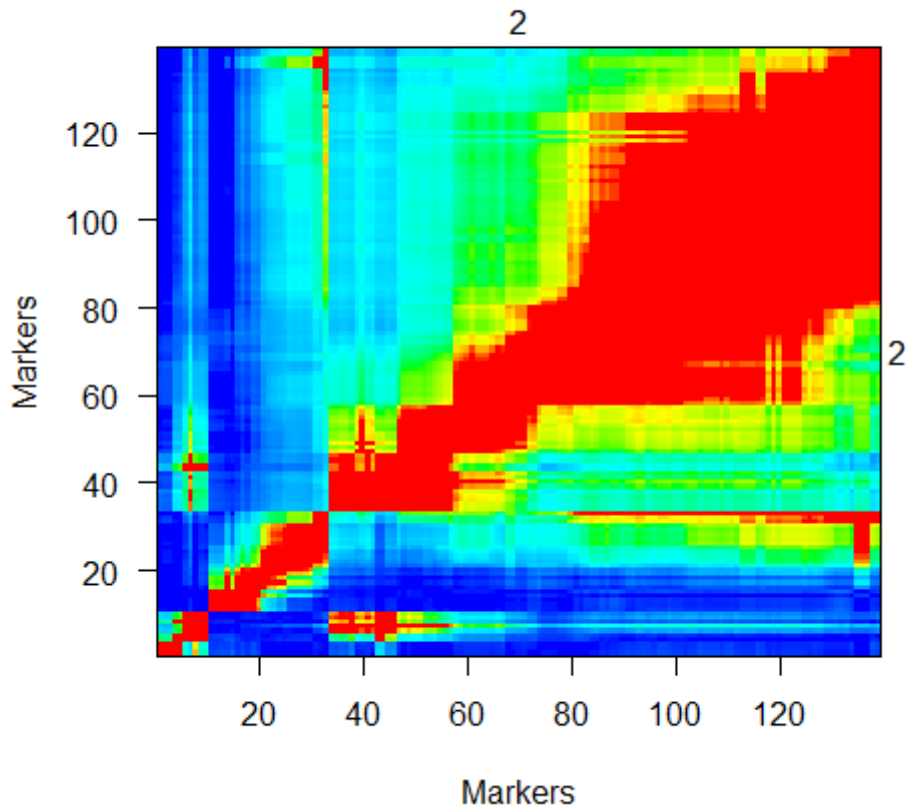
```
maize.bb1 <- orderMarkers(cross = maize.bb1, chr=c, use.ripple = FALSE, map.function="kosambi")  
pull.map(maize.bb1, chr = c)
```

##	PZA02480.1	PZA02769.1	PZA01060.1	PZA02390.1	PZA01140.1
##	0.0000000	0.2727783	0.2727833	14.3955360	15.6728763
##	PZA03167.5	PZA02068.1	PZA00836.1	PZA01259.1	PZA01680.3
##	27.6603670	27.6603720	27.9477903	27.9477953	28.2288527
##	PZA01983.1	PZA01887.1	PZA02367.1	PZA00191.5	PZA00818.1
##	119.4548372	119.7305810	119.7305860	120.9385282	120.9385332
##	PZA01438.1	PHM5359.10	PZA02316.22	PZA01570.1	PHM13122.43
##	129.4840116	131.0113440	131.0113490	133.9256126	134.7265330
##	PZA02653.12	PZA02462.1	PZB00054.3	PZA02753.1	PHM3137.17
##	142.4312825	145.0394640	145.5951338	146.1505969	147.3029967
##	PZB00094.1	PZA02029.21	PZA01371.1	PZA01925.1	PZA00865.1
##	151.0550008	151.0550058	151.1987447	151.3427510	151.6510213
##	PZA01284.6	PZB00079.4	PZA00985.1	PZA02513.1	PZA02060.1
##	160.7150077	161.0066919	161.0066969	189.8678081	189.8678131
##	PZA00395.2	PZA02667.1	PHM3512.186	PZA01265.1	PZA01142.4
##	190.1428641	190.1428691	190.5979380	193.1693084	193.1693134
##	PZB00765.1	PZA02820.17	PZA00545.26	PZA02015.11	PZA00963.3
##	193.1693184	193.3974132	197.9886238	197.9886288	197.9886338
##	PZA00980.1	PZA03024.16	PZA02426.1	PZA00652.17	PZA02411.3
##	197.9886388	206.0454340	208.7046562	208.7046778	208.7046995
##	PHM532.23	PZA00352.23	PZA03320.6	PZA02751.1	PZA03317.1
##	208.7047197	209.2013660	209.9995745	210.4023679	211.2200311
##	PZA02383.1	PZA03172.3	PZA03452.6	PZA01575.1	PZA02356.7
##	211.8288438	212.7375082	218.9950671	219.5543129	220.0838879
##	PZA02408.2	PZA02209.2	PZA03324.1	PHM5296.6	PZA02633.4
##	220.0838929	220.0838979	220.0839029	220.0839079	220.9198150
##	PHM1899.157	PZA01304.1	PZA03714.1	PZA03717.1	PZA01410.1
##	222.6745373	222.6745423	225.3319269	225.3319319	226.7701039
##	PZA00987.1	PZA00300.14	PZA02040.2	PZA00255.14	PZA02641.2
##	226.7701089	228.3813142	228.3813192	230.3882785	232.0206804
##	PZA01294.2.1	PZA03536.1	PZA01763.2	ae1.8.7	PZA02981.2
##	232.0206854	232.0206904	232.7969593	232.7969643	234.2596336
##	PZA00148.3	PZA01796.1	PZA01608.1	PZB01017.1	PZA00067.10
##	235.7255474	237.0856800	238.1015775	239.2147897	240.3280007
##	PZA02164.16	PZA01365.1	PZA00643.13	PZA00881.1	PZA03049.24
##	240.6414858	240.6414908	240.9570248	240.9570298	241.2725614
##	PZA00273.5	PZA01693.1	PZA02818.6	PZA01779.1	PZA01349.2
##	241.9289995	241.9290045	242.2633579	242.2633629	243.2814193
##	PHM5798.39	PZA02862.3	PZA00261.6	PZA01303.1	PZA03677.1
##	243.2814243	243.9123941	243.9123991	244.2257287	244.5390733
##	PZA02525.1	PZB01112.1	PZA01050.1	PHM3171.5	PZA00522.12.7
##	244.5390783	245.1708666	245.4474267	245.7234895	246.0026765
##	PZA03451.5	PHM1870.20	PZA02676.2	PZB00232.2	PZB01115.3
##	246.0026815	246.0026865	246.0026915	246.0026965	246.0027015
##	PZA00222.7	PHM4165.14	PZA00499.3	PHM3691.18	PZA00981.3
##	246.0027065	246.0027115	246.4467331	246.4467381	246.4467431
##	PZA01804.1	PZA00805.1	PZA01563.1	PZA02207.1	PHM4647.8
##	246.4467481	246.4467531	250.5061772	250.5061822	250.5061872
##	PHM12992.5	PZA00996.1	PHM16854.3	PZA01530.1	PZB00869.4
##	250.5061922	250.5061972	250.5062022	250.5062072	250.8420128
##	PZA00934.2	PZA02113.1	PZA00801.1	PHM565.31	PZA01427.1
##	251.1778218	251.1778268	251.1778318	252.8882731	253.6721993
##	PZA03274.4	PZA03226.3	PZA02792.26.25	PZA00517.7	PZA03092.7
##	254.4599692	254.4599742	254.4599792	256.1726454	258.3849165

##	PZA00112.5	PZA01327.1	PZA03578.1	PZA01523.1
##	258.3849215	258.3849265	258.3849315	258.3849365

```
plotRF(maize.bb1, chr = c, col.scheme = "redblue")
```

Pairwise recombination fractions and LOD score



```
(loglik.bb1[c] <- attr(maize.bb1$geno[[c]]$map, "loglik"))
```

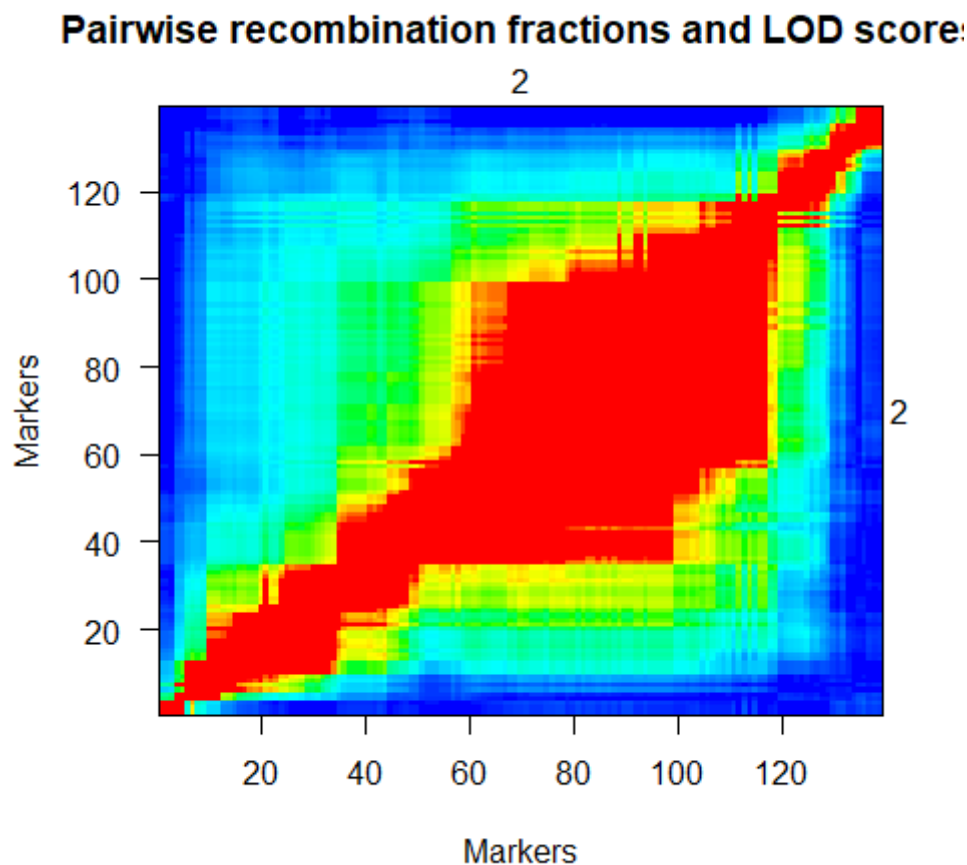
```
## [1] -2002.2
```

```
maize.bb2 <- orderMarkers(cross = maize.bb2, chr=c, use.ripple = FALSE, map.function="kosambi")
pull.map(maize.bb2, chr = c)
```

##	PZA02769.1	PZA01060.1	PZA02480.1	PZA02390.1
##	0.000000000000	0.000005000001	0.281420088296	14.124243479023
##	PZA01140.1	PZA01680.3	PZA00836.1	PZA01259.1
##	15.415287320879	27.385181239327	27.385186239328	27.685025125371
##	PZA03167.5	PZA02015.11	PZA00545.26	PZA02068.1
##	28.008956913837	39.888219888602	39.888224888602	39.888229888603
##	PZA00980.1	PZA00963.3	PHM3512.186	PZA00395.2
##	39.888234888603	39.888239888604	42.509920718287	43.219574479310
##	PZA02667.1	PZA02060.1	PZA02513.1	PZB00765.1
##	43.219579479310	43.530733006844	43.530738006845	43.530743006845
##	PZA01142.4	PZA01265.1	PZA02820.17	PZA03024.16
##	45.560287513125	45.560292513125	45.878515002006	49.262551835388
##	PZA00652.17	PHM532.23	PZA02411.3	PZA02426.1
##	52.158758936675	52.158763936676	52.170824340030	52.418098582361
##	PZA00352.23	PZA03320.6	PZA02751.1	PZA03317.1
##	52.899729032730	53.696723643515	54.100101147187	54.918984536527
##	PZA02383.1	PZA03172.3	PZA03452.6	PZA01575.1
##	55.528994810207	56.439549335998	62.713529088483	63.271349207444
##	PZA03324.1	PZA02356.7	PHM5296.6	PZA02209.2
##	63.801455175479	63.801460175480	63.801465175480	63.801470175481
##	PZA02408.2	PZA02633.4	PZA01304.1	PHM1899.157
##	63.801475175481	64.637735663076	66.393008060711	66.393013060711
##	PZA03714.1	PZA03717.1	PZA01410.1	PZA00987.1
##	69.051293395117	69.051298395118	70.489805746384	70.489810746385
##	PZA00300.14	PZA02040.2	PZA00255.14	PZA03536.1
##	72.102896028693	72.102901028693	74.111607231142	75.741466987173
##	PZA02641.2	PZA01294.2.1	PZA01763.2	ae1.8.7
##	75.741471987174	75.741476987174	76.512243832995	76.512248832996
##	PZA00148.3	PZA02981.2	PZA01796.1	PZA01608.1
##	79.541407451512	79.541412451513	80.901546209174	81.917474541254
##	PZB01017.1	PZA00067.10	PZA01365.1	PZA02164.16
##	81.917479541255	84.206674804562	84.520404081112	84.835416376507
##	PZA00881.1	PZA00643.13	PZA03049.24	PZA01693.1
##	84.835675322736	84.835680322737	85.150920676364	85.806664773048
##	PZA00273.5	PZA02818.6	PZA01779.1	PZA02525.1
##	85.806669773048	86.140643833985	86.140648833985	87.157532740635
##	PHM5798.39	PZA03677.1	PZA01349.2	PZA01303.1
##	87.157537740636	87.157542740636	87.157547740637	87.470772022089
##	PZA00261.6	PZA02862.3	PZB01112.1	PZB00232.2
##	87.784027267862	87.784032267863	89.064975722405	89.908255129439
##	PZA00222.7	PHM3171.5	PZB01115.3	PHM1870.20
##	89.908260129439	89.908265129440	89.908270129440	89.908275129441
##	PZA01050.1	PZA03451.5	PHM4165.14	PZA02676.2
##	89.908280129441	89.908285129442	89.908290129442	89.908295129443
##	PHM3691.18	PZA00522.12.7	PZA01804.1	PZA00996.1
##	90.351164062435	90.351169062436	90.351174062436	90.351179062437
##	PZA00981.3	PZA00805.1	PZA02207.1	PZA00499.3
##	90.351184062437	90.351189062438	90.351194062438	90.351199062439
##	PHM12992.5	PHM16854.3	PZA01530.1	PHM4647.8
##	90.351204062439	94.403374364253	94.403379364254	94.403384364254
##	PZA01563.1	PZB00869.4	PZA00801.1	PZA02113.1
##	94.403389364255	94.738955879174	95.074525838692	95.074530838693
##	PZA01427.1	PZA00934.2	PHM565.31	PZA03274.4
##	96.767984264577	96.767989264578	96.767994264578	98.358546531083
##	PZA03226.3	PZA02792.26.25	PZA00517.7	PZA01327.1

```
## 98.358551531084 98.358556531084 100.051336076647 102.278720570384
## PZA03578.1 PZA00985.1 PZA01523.1 PZA00112.5
## 102.278725570384 102.278730570385 102.278735570385 102.278740570386
## PZA03092.7 PZB00079.4 PZA01284.6 PZA00865.1
## 102.278745570386 113.879253776348 114.184520232048 123.796811346511
## PZA01925.1 PZA01371.1 PZB00094.1 PZA02029.21
## 124.115142004016 124.410125390707 124.410435159070 124.410440159071
## PHM3137.17 PZB00054.3 PZA02753.1 PZA02462.1
## 128.218625397452 129.373729324333 129.373734324333 130.493141624346
## PZA02653.12 PHM13122.43 PHM5359.10 PZA01570.1
## 133.099774224402 140.803643815494 141.604788976714 141.604793976715
## PZA02316.22 PZA01438.1 PZA00191.5 PZA00818.1
## 144.519278418165 146.047391841384 146.047396841384 154.619721269103
## PZA01983.1 PZA02367.1 PZA01887.1
## 155.521000377122 155.808642897715 155.808647897715
```

```
plotRF(maize.bb2, chr = c, col.scheme = "redblue")
```

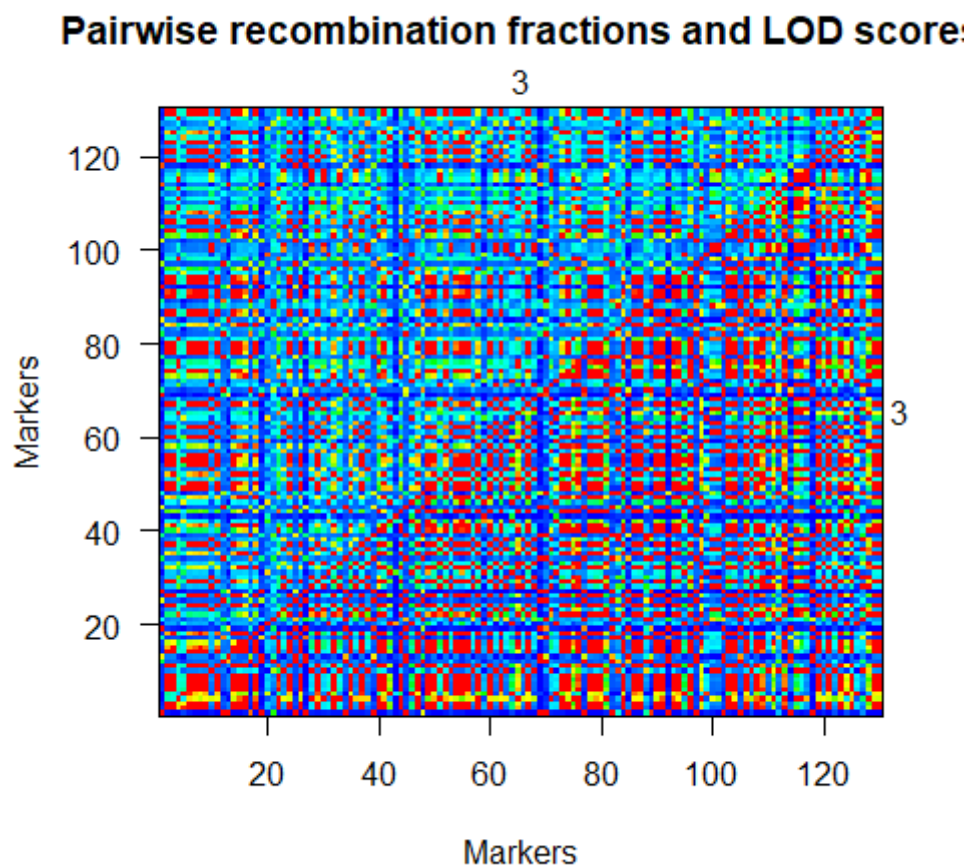


```
(loglik.bb2[c] <- attr(maize.bb2$geno[[c]]$map, "loglik"))
```

```
## [1] -1872.99
```

Linkage group 3

```
c <- 3
plotRF(maize, chr=c, col.scheme = "redblue")
```



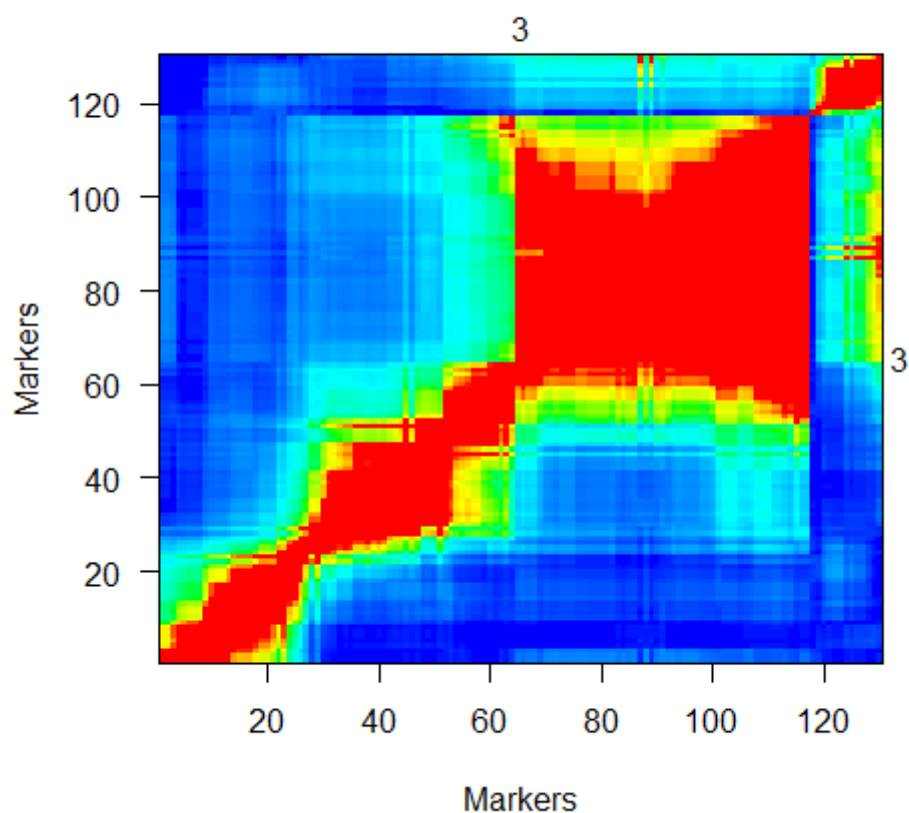
```
maize.bb1 <- orderMarkers(cross = maize.bb1, chr=c, use.ripple = FALSE, map.function="kosambi")
pull.map(maize.bb1, chr = c)
```


##	PZA02423.1	PZA00088.3	PHM2423.33	PZA02182.1
##	0.000000000000	0.000005000001	2.123048532545	6.214762483613
##	PZA01360.3	PHM3852.23	PZA01688.3	PZA00316.10
##	6.844851469440	7.177699698145	7.177704698145	7.177709698146
##	PZA00402.1	PZA03391.1	PHM2672.19	PZA00219.7
##	12.132623760988	15.177545761957	15.177550761957	15.177555761958
##	PZA02668.2	PZA02824.4	PZA02514.1	PZA01233.1
##	16.628123544858	18.754367821563	19.067757128000	19.067762128000
##	PZA02665.2	PHM3342.31	PZA00750.1	PZA01154.1
##	19.067767128001	21.162042631168	23.774199325104	23.774204325105
##	sh2.21	PZB01457.1	PZA03146.4	PZA02616.1
##	23.774209325105	29.439192059250	29.439197059251	32.312115723187
##	PZA02516.1	PZA00538.18.15	PZA02733.1	PZA00892.5
##	34.009655929953	36.191498597082	39.395815354260	44.011715417740
##	PZA03154.4	PZA01501.1	PZA02122.9	PZA01457.1
##	44.011720417740	46.555411510345	48.159036169257	48.534012110587
##	PZA00308.24	PZB01109.1	PZA01035.1	PHM13673.53
##	49.872412716988	50.425861522454	50.425866522455	51.786203462219
##	PZA03744.1	PZA03255.1	PHM824.17	PZA03743.1
##	51.786208462220	51.786213462220	52.410283877194	52.410288877194
##	PZA01228.2	PZA00494.2	PZA03647.1	PZA03191.1.4
##	52.410293877195	54.588336388850	55.234614655734	55.907841880483
##	PZA03735.1	zb27.1	PHM1675.29	PZA01962.12
##	55.907846880484	55.907851880484	55.907856880485	63.538526355918
##	PHM17210.5	PZA02654.3	PZA03733.1	PZA02212.1
##	63.538531355919	63.841234914759	63.841239914759	71.251906442496
##	PZA01726.1	PZA00783.1	PZA03032.19	PZA02402.1
##	71.251911442497	73.211569578044	73.507027054081	73.812864547035
##	PHM1959.26	PZD00027.2	PZA03073.28.26	PHM2885.31
##	75.539900038003	75.539974532495	75.541535424744	77.397501819547
##	PZA00186.4	PZA01396.1	PHM4621.57	PZA00667.2
##	77.754651043897	79.728859427322	79.728864427323	80.973915308239
##	PZA03198.3	PZA02299.16	PHM15449.10	PZA00413.20.18
##	91.835618630567	91.835623630568	91.835628630568	91.835633630569
##	PZA02619.1	PZA00509.1	PHM15474.5	PZA00581.3
##	92.652828023333	93.772571819292	93.772576819292	93.772581819293
##	PZA02296.1	PZA02699.1	PZA02134.3	PHM15899.9
##	93.772586819293	93.772591819294	93.772596819294	94.331602322586
##	PZA03070.9	zb21.1	PZA00380.10	PHM13823.7
##	94.331607322586	94.331612322587	94.331617322587	94.331622322588
##	PZA01114.2	PZA00279.2	PZA00348.11	PZA02255.2
##	94.331627322588	94.331632322589	94.890891750090	94.890896750090
##	PZA01473.1	PZA00210.1.9	PHM4145.18	PZA02427.1
##	94.890901750091	94.890906750091	96.514176649121	96.514181649122
##	PHM4204.69	PZA03054.5	PHM2343.25	PZA00297.2
##	96.514186649122	97.821728491633	97.821733491634	98.371067033599
##	PZA01447.1	PHM5502.31	PZA00265.6	PZA03119.1
##	98.920017599422	99.192872057876	99.192877057876	99.192882057877
##	PZA02589.1	PZA02645.2	PZA02742.1	PZA00707.9
##	99.192887057877	99.465824006015	99.465829006015	99.465834006016
##	PZA00363.7	PZB02002.1	PZD00016.4	PZD00015.5
##	101.268089121740	102.324848966926	102.324853966927	102.324858966927
##	PHM1745.16	PZA02474.1	PZA00920.1	PHM890.20
##	102.948241389670	103.125153082138	103.294040377682	104.356743654137
##	PZB02044.1	PZB02122.1	PHM4955.12	PZA01934.6

```
## 104.356748654137 104.356753654138 105.904327325004 105.904332325005
##      PZA00948.1      PZA00827.1      PHM9914.11      PZB02179.1
## 106.332546519971 106.332551519971 109.001994212273 109.532056033025
##      PZA00828.2      PZA00309.1      PZA02090.1      PZD00038.2
## 109.532061033026 178.324782993852 193.906872277134 198.053392513747
##      PZA02678.1      PZA00100.10      PHM12859.7      PZA00749.1
## 201.911445348668 202.813002412585 202.813007412585 204.113472492974
##      PZA03527.1      PZB01944.1      PZA03212.3      PZA02098.2
## 204.113477492975 204.113482492975 204.113487492976 209.726368765099
##      PZA01765.1      PZA00508.2
## 210.989492427485 215.440577991768
```

```
plotRF(maize.bb1, chr = c, col.scheme = "redblue")
```

Pairwise recombination fractions and LOD score



```
(loglik.bb1[c] <- attr(maize.bb1$geno[[c]]$map, "loglik"))
```

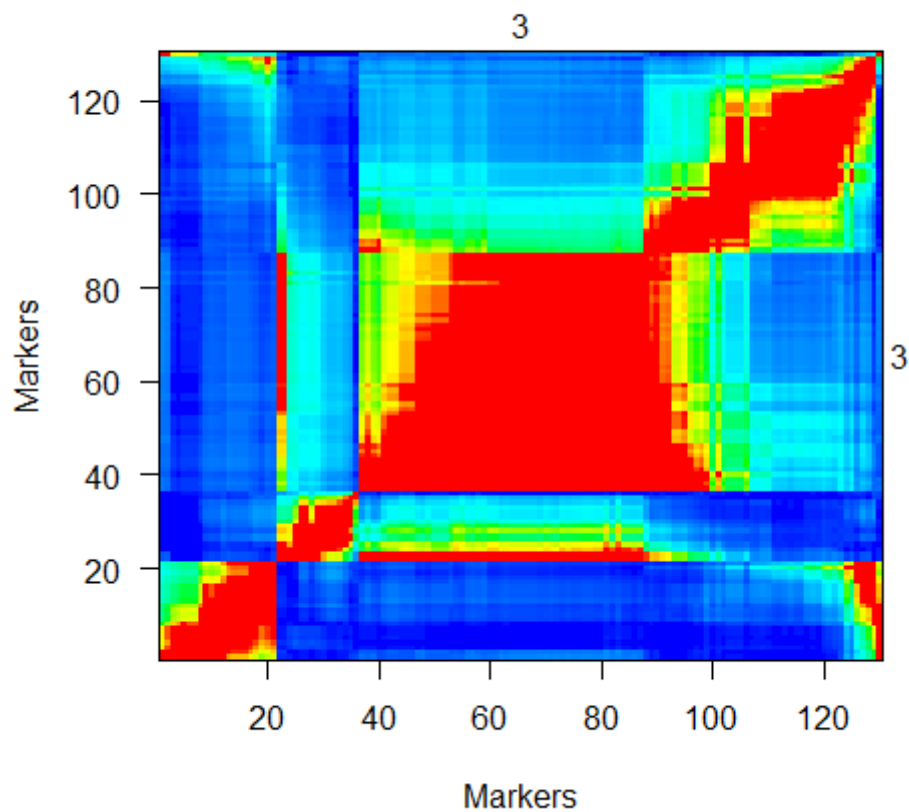
```
## [1] -2026.878
```

```
maize.bb2 <- orderMarkers(cross = maize.bb2, chr=c, use.ripple = FALSE, map.function="kosambi")
pull.map(maize.bb2, chr = c)
```

##	PZA02423.1	PHM2423.33	PZA02182.1	PZA01360.3	PZA00316.10
##	0.000000	2.118121	6.214054	6.844922	7.178349
##	PHM3852.23	PZA01688.3	PZA00402.1	PHM2672.19	PZA03391.1
##	7.178354	7.178359	12.095934	15.124012	15.124017
##	PZA00219.7	PZA02668.2	PZA02824.4	PZA01233.1	PZA02665.2
##	15.124022	16.550093	18.559466	18.858209	18.858214
##	PZA02514.1	PHM3342.31	PZA00750.1	sh2.21	PZA03146.4
##	18.858219	20.747005	21.777864	22.807053	22.807058
##	PZA01154.1	PHM4204.69	PHM4145.18	PZA00508.2	PZA01765.1
##	22.807063	123.084323	123.084328	123.084333	127.540256
##	PZA03212.3	PZA00749.1	PZA02098.2	PZB01944.1	PZA03527.1
##	128.809587	128.809592	128.809597	131.447365	134.089659
##	PHM12859.7	PZA00100.10	PZA02678.1	PZD00038.2	PZA02090.1
##	135.395238	135.395243	136.298140	140.162763	144.313052
##	PZA00309.1	PZA00828.2	PZA00948.1	PZB02179.1	PHM9914.11
##	159.893467	228.701158	228.701163	228.701168	229.231062
##	PZA00827.1	PZA01934.6	PHM4955.12	PZB02122.1	PHM890.20
##	231.889921	232.316439	232.316444	233.857864	233.857890
##	PZB02044.1	PZA02474.1	PZA00920.1	PHM1745.16	PZB02002.1
##	233.857895	234.920386	234.920391	235.267413	235.890685
##	PZD00016.4	PZD00015.5	PZA00363.7	PZA00707.9	PZA02619.1
##	235.890690	235.890695	236.959453	238.513525	238.513530
##	PHM15449.10	PZA00413.20.18	PZA03198.3	PZA02299.16	PZA02742.1
##	239.390036	239.390041	239.390046	239.390051	240.336754
##	PZA02645.2	PZA02296.1	PHM5502.31	PZA03119.1	PZA02589.1
##	240.336759	240.614388	240.614393	240.660449	240.706505
##	PZA02134.3	PZA00265.6	PZA02699.1	PZA01447.1	PZA00279.2
##	240.752561	240.798617	240.844674	240.890730	240.890735
##	PZA00509.1	PHM15474.5	PZA00380.10	PZA00581.3	PZA00297.2
##	240.890740	240.890745	241.448956	241.448961	241.448966
##	PHM13823.7	PZA03070.9	PHM15899.9	zb21.1	PZA01114.2
##	241.448971	241.448976	241.448981	241.448986	241.448991
##	PZA02427.1	PZA00210.1.9	PHM2343.25	PZA03054.5	PZA01473.1
##	243.356756	245.006391	245.006396	245.006401	245.006406
##	PZA02255.2	PZA00348.11	PZA00667.2	PHM4621.57	PZA01396.1
##	245.006411	245.006416	257.633820	258.826482	258.826487
##	PZA00186.4	PHM2885.31	PZD00027.2	PHM1959.26	PZA03073.28.26
##	260.720019	261.073390	262.903055	262.903060	262.903065
##	PZA02402.1	PZA03032.19	PZA00783.1	PZA01726.1	PZA01962.12
##	264.606354	264.907950	265.204099	267.174251	274.193373
##	PZA02212.1	PHM17210.5	PHM1675.29	PZA03733.1	PZA03735.1
##	274.193378	274.193383	274.509591	274.509596	274.509601
##	PZA02654.3	PZA03191.1.4	zb27.1	PZA03647.1	PZA00494.2
##	274.509606	281.714472	281.714477	282.392584	283.041987
##	PHM824.17	PZA01228.2	PZA03744.1	PZA03255.1	PHM13673.53
##	285.223250	285.223255	285.533448	285.842022	285.842027
##	PZA03743.1	PZA00308.24	PZB01109.1	PZA01035.1	PZA01457.1
##	285.842032	287.727977	288.218052	288.218057	289.621237
##	PZA02122.9	PZA01501.1	PZA00892.5	PZA02733.1	PZA03154.4
##	289.994753	291.592027	294.130553	298.682542	298.682547
##	PZA00538.18.15	PZA02516.1	PZA02616.1	PZB01457.1	PZA00088.3
##	301.847632	303.969432	305.592858	308.174366	332.840345

```
plotRF(maize.bb2, chr = c, col.scheme = "redblue")
```

Pairwise recombination fractions and LOD score

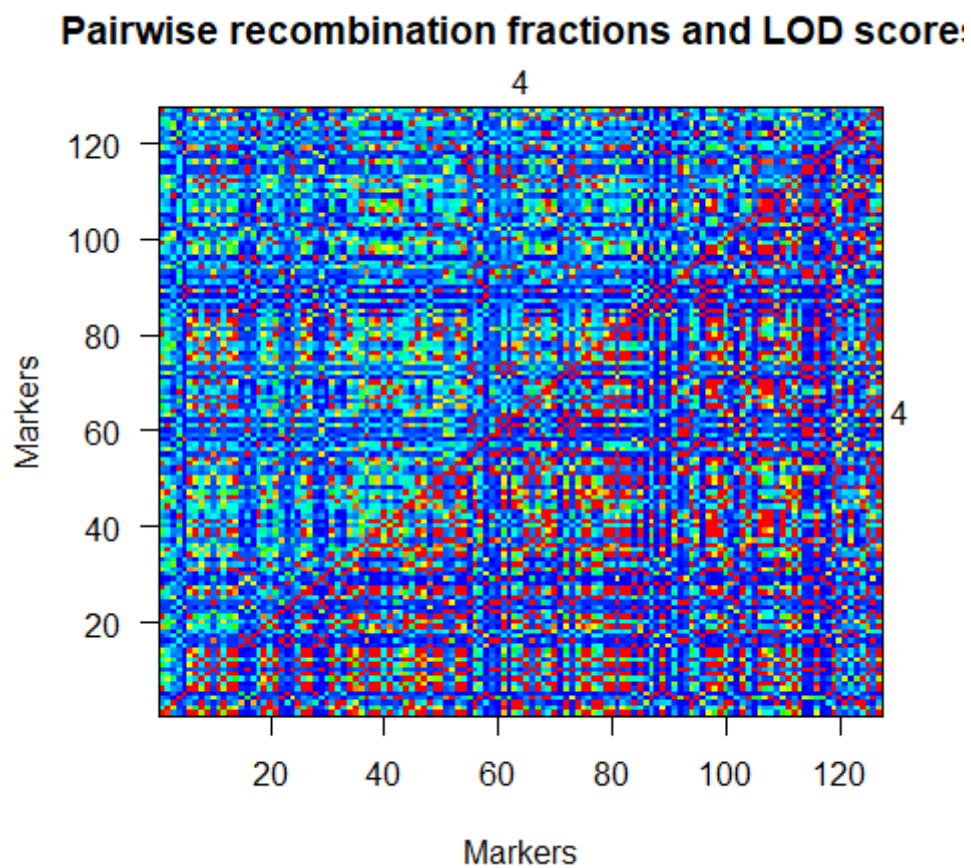


```
(loglik.bb2[c] <- attr(maize.bb2$geno[[c]]$map, "loglik"))
```

```
## [1] -2180.483
```

Linkage group 4

```
c <- 4
plotRF(maize, chr=c, col.scheme = "redblue")
```



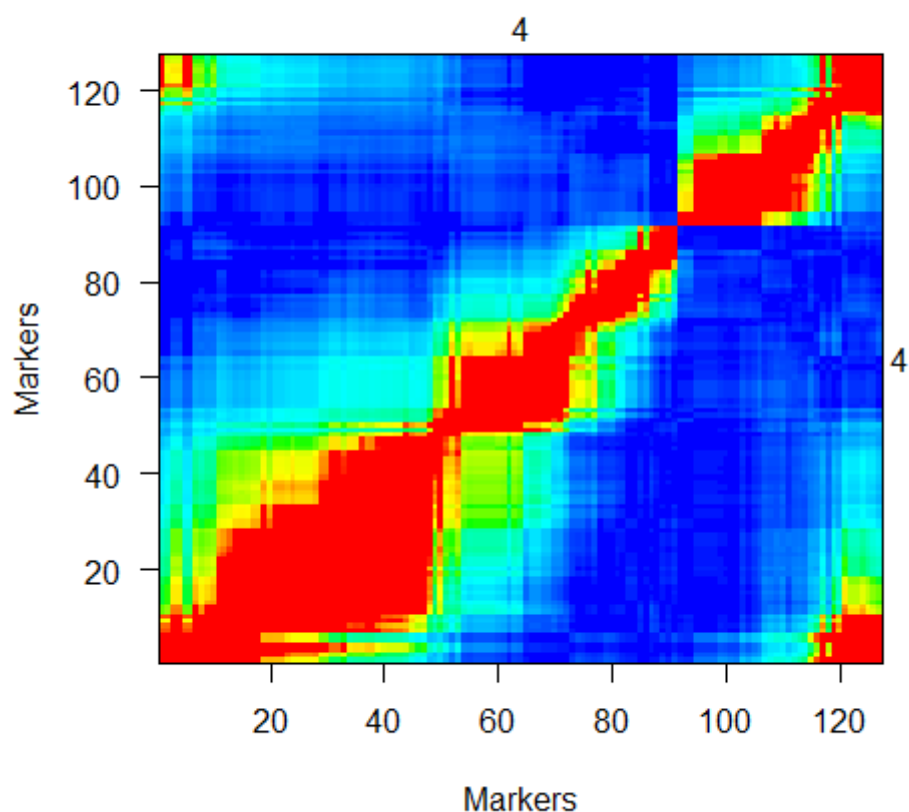
```
maize.bb1 <- orderMarkers(cross = maize.bb1, chr=c, use.ripple = FALSE, map.function="kosambi")
pull.map(maize.bb1, chr = c)
```

##	PZA02080.1	PZA03568.1	PHM4586.12	PZA01374.1
##	0.000000000000	0.000005000001	0.000010000001	0.000015000002
##	PHM1962.33	PZA01755.1	PZA02378.7	PZA01336.1
##	0.000020000002	0.000025000003	4.658940546286	4.658945546287
##	PZA01993.7	PZA02058.1	PZA02496.1	PHM10404.8
##	6.390121571156	6.390126571157	10.154316514124	10.154321514125
##	PZB00183.4	PZA02450.1	PZA02774.1	PZA01820.1
##	10.843629313893	11.416436309736	11.416441309736	11.416446309737
##	PZA02168.1	PZA03629.1	PHM3457.6	PZA00635.7
##	11.760475031346	11.760480031346	13.149935656475	13.149940656475
##	PZA02279.1	PHM10321.11	PZA01902.1	PZA00485.2
##	13.149946008176	13.149951425231	14.537791838719	14.883789643432
##	PZA02549.3	PHM13360.13	PHM4880.179	PHM3626.3
##	15.229478663862	15.229483663863	15.229488663863	15.593659152669
##	PZA02626.1	PZA00029.17	PZA01537.2	PZA01280.2
##	17.563530886168	17.563535886169	18.200613503094	18.200618503094
##	PZA03211.6	PZA01232.1	PZA02939.10	PZA02371.6
##	18.200623503095	20.512983246061	20.512988246061	21.536418394722
##	PZA02465.1	PZA01321.1	PZA03692.1	PZA01638.1
##	21.536423394723	21.536428394723	22.186469106883	22.494592762202
##	PZA00515.10	PZA00637.6	PZA00495.5	PZA03644.1
##	22.494597762203	22.494602762203	22.494607762204	22.494612762204
##	PZA00224.4	PZA03659.1	vdac1a.1	PZA03184.2
##	25.924116418355	26.218868481241	26.218873481242	30.890873797398
##	PZA00755.2	PZA01735.1	PZA03529.1	PHM3055.9
##	38.718067493667	38.718072493667	41.190535798297	42.976041337672
##	PZA02890.4	PZA00824.2	PZA02731.1	PHM3668.12
##	42.976046337673	47.867054385634	48.181921064609	48.181926064610
##	PZA02017.1	PHM7953.11	PZA00803.3	PZA03165.1
##	48.181931064610	48.181936064611	48.181941064611	49.370462952888
##	PHM14412.4	PZA02329.2	PZB01103.2	PHM16125.47
##	49.370467952889	49.370472952889	49.872677468140	49.878271224555
##	PZA02077.1	PZA00390.7	PZA01885.2	PZA02964.7
##	55.445282099561	56.451017781472	56.451022781472	57.536479742335
##	PZB00772.7	PZA03602.1	PZA02456.1	PZA00804.1
##	57.536484742335	60.931474132643	63.617086049217	67.711487051790
##	PZA02680.1	PZA02418.2	PZA02471.5	PZA02012.7
##	70.739298326919	73.923143162193	73.923148162194	75.855690553266
##	PZA00527.10	PZA02453.1	PZA01991.3	PZA00163.4
##	75.855695553266	80.075653915240	81.753770220545	81.753775220546
##	PZA02564.2	PZB01013.1	PZA02266.3	PZA01895.1
##	83.085995115312	83.401994768639	86.737095594105	86.737100594105
##	PZA02727.1	PZA01352.5	PZA02170.1	PHM3094.23
##	89.095501838182	89.095506838183	97.093652405101	97.687733205344
##	PZA03577.1	PZA03321.4	PZD00022.5	PHM5817.15
##	98.530323181975	98.530328181976	101.141258961526	178.136769197281
##	PZA00365.2	PZA00680.3	PZA02133.10	PHM13440.13
##	178.136774197281	178.136779197282	184.449490929485	184.449495929486
##	PHM1511.14	PZA00525.17	PZA02681.8	PZA02175.1
##	184.449500929486	184.449505929487	185.141572693314	186.274840371858
##	PZA00902.1	PZA02264.5	PZA01211.1	PZB01233.1
##	186.274845427180	186.274850427181	189.897579427158	189.897584427159
##	PZA00172.12	PZA00613.22	PZA02208.1	PZA02081.1
##	189.897589427159	189.897594427160	196.923796136883	197.207903596935
##	PZA03747.1	PZA01935.10	PZA03699.1	PZB00901.3.4

```
## 197.481905144933 197.481910144933 200.614797086363 204.719181580191
##      PZA02272.3      PHM5822.15      zfl2.9      PZA00108.4
## 205.016449233908 205.951066201638 211.096231866962 213.706711486920
##      PZA02337.4      PZA01753.1      PZA02417.2      PZA03559.1
## 214.620512898606 214.620517898606 224.375052137356 224.375057137357
##      PZA03142.5      PZA00590.1      PHM6111.5      PZA01879.1
## 229.581733470643 231.365637649365 231.365642649366 231.365647649366
##      PZA03634.1      PZA03228.4      PZA00497.4
## 231.968493294242 231.968498294243 232.826496135996
```

```
plotRF(maize.bb1, chr = c, col.scheme = "redblue")
```

Pairwise recombination fractions and LOD score:



```
(loglik.bb1[c] <- attr(maize.bb1$geno[[c]]$map, "loglik"))
```

```
## [1] -2164.73
```

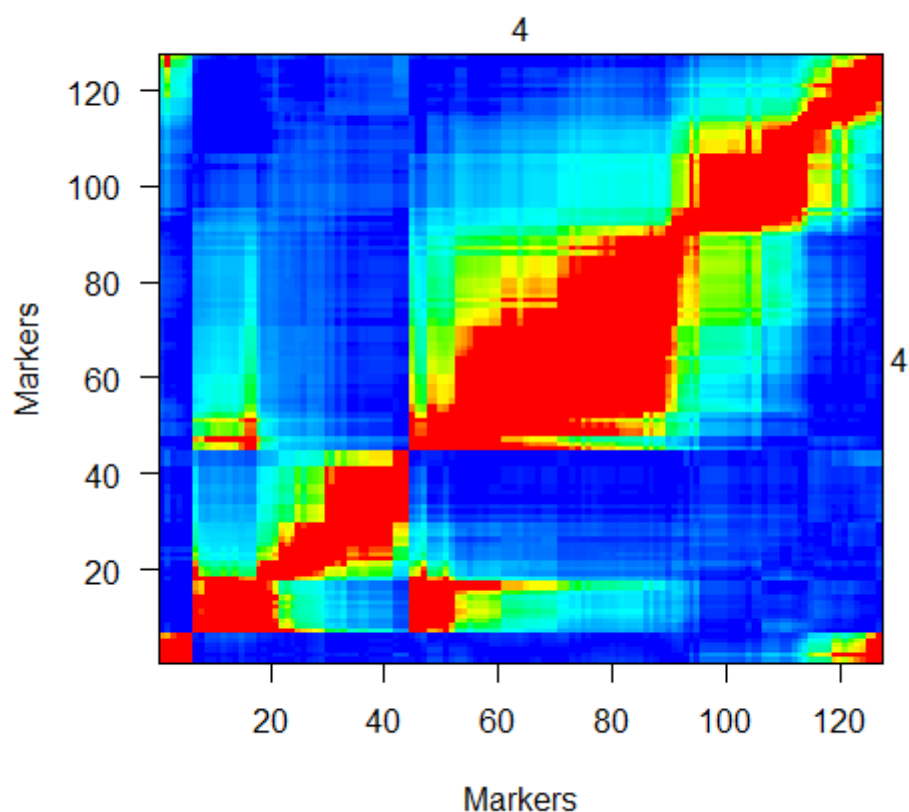
```
maize.bb2 <- orderMarkers(cross = maize.bb2, chr=c, use.ripple = FALSE, map.function="kosambi")
pull.map(maize.bb2, chr = c)
```

##	PZA02170.1	PZA02727.1	PHM3094.23	PZA03321.4
##	0.000000000000	0.000005000001	0.558667529411	1.396724302625
##	PZA03577.1	PZD00022.5	PZA03559.1	PZA02417.2
##	2.652886612909	3.913319564267	389.537031319512	389.537036319512
##	PZA00497.4	PZA00590.1	PZA01879.1	PZA03634.1
##	391.130650999850	392.698624959420	392.698629959420	392.698634959421
##	PHM6111.5	PZA03228.4	PZA03142.5	PZA02080.1
##	392.698639959421	393.262721836198	395.474756973152	395.474761973153
##	PZA01755.1	PZA02337.4	PZA01753.1	PZA00108.4
##	395.474766973153	408.301623299044	408.301628299044	409.196654957529
##	zfl2.9	PZA02272.3	PHM5822.15	PZB00901.3.4
##	411.735457652020	417.974665315076	418.556579719230	419.482413361289
##	PZA03747.1	PZA03699.1	PZA01935.10	PZA02081.1
##	423.589469813843	423.589474813843	426.741646933520	427.016726316963
##	PZA02208.1	PZA01211.1	PZA00613.22	PZB01233.1
##	427.302252672157	434.380720239335	434.380725239336	434.380730239336
##	PZA00172.12	PZA02264.5	PZA00902.1	PZA02681.8
##	434.380735239337	438.005351512867	438.005356512868	439.139186032624
##	PZA02175.1	PZA02133.10	PHM13440.13	PZA00525.17
##	439.139191032624	439.831769339392	439.831774339392	439.831779339393
##	PHM1511.14	PHM5817.15	PZA00365.2	PZA00680.3
##	439.831784339393	446.137223658385	446.137228658385	446.137233658386
##	PZA01374.1	PZA03568.1	PHM1962.33	PZA02378.7
##	535.880516370088	535.880521370088	535.880526370089	540.547008472128
##	PZA02058.1	PZA01336.1	PHM4586.12	PZA01993.7
##	540.547013472128	540.547018472129	540.547023472129	542.279494397271
##	PZA02496.1	PHM10404.8	PZB00183.4	PZA01820.1
##	546.045499137495	546.045504137496	546.734981226977	547.307951002796
##	PZA02774.1	PZA02450.1	PZA02168.1	PZA03629.1
##	547.307956002797	547.307961002797	547.650892814544	547.650897814544
##	PHM10321.11	PHM3457.6	PZA02279.1	PZA00635.7
##	549.073455870844	549.073460870845	549.073465870845	549.073470870846
##	PZA01902.1	PZA00485.2	PHM3626.3	PHM13360.13
##	550.570601824159	550.941202425371	550.941207425371	551.250105202048
##	PZA02549.3	PHM4880.179	PZA02626.1	PZA00029.17
##	551.250110202049	551.250115202049	553.616426344350	553.616431344351
##	PZA01537.2	PZA03211.6	PZA01232.1	PZA01280.2
##	554.266446308277	554.266451308278	556.629574486224	556.629579486224
##	PZA02939.10	PZA02465.1	PZA02371.6	PZA01321.1
##	556.629584486225	557.141966457730	557.661156397550	557.661161397550
##	PZA03692.1	PZA01638.1	PZA00495.5	PZA00637.6
##	558.324379848101	558.638628804954	558.638633804955	558.638638804955
##	PZA00515.10	vdac1a.1	PZA03644.1	PZA03659.1
##	558.638643804956	562.155394687795	562.155399687796	562.155404687796
##	PZA00224.4	PZA03184.2	PZA01735.1	PZA00755.2
##	562.452717849017	566.776136925715	570.376360133628	573.976910463815
##	PZA03529.1	PHM3055.9	PZA02890.4	PZA00824.2
##	576.454975364510	578.244190358090	578.244195358090	583.149044174362
##	PHM7953.11	PHM3668.12	PZA02017.1	PZA00803.3
##	583.463925578828	583.463930578828	583.463935578829	583.463940578829
##	PHM14412.4	PZB01103.2	PHM16125.47	PZA02329.2
##	584.494482648217	584.494487648217	584.494492648218	584.564969478211
##	PZA02731.1	PZA03165.1	PZA02077.1	PZA01885.2
##	584.564974478212	584.852164749990	590.406947586215	591.417503729459
##	PZA00390.7	PZA02964.7	PZB00772.7	PZA03602.1


```
## 591.417508729459 592.507041839335 592.507046839336 595.905108955216
##      PZA02456.1      PZA00804.1      PZA02680.1      PZA02418.2
## 598.591208962648 602.686742573098 605.715424571031 608.899801097811
##      PZA02471.5      PZA00527.10      PZA00163.4      PZA02453.1
## 608.899806097812 610.831913767224 615.051341446535 615.051346446536
##      PZA02012.7      PZA01991.3      PZA02564.2      PZB01013.1
## 615.051351446536 616.737191950087 618.074944739460 618.392077104204
##      PZA02266.3      PZA01895.1      PZA01352.5
## 621.759764719261 621.759769719261 624.092108943737
```

```
plotRF(maize.bb2, chr = c, col.scheme = "redblue")
```

Pairwise recombination fractions and LOD score:

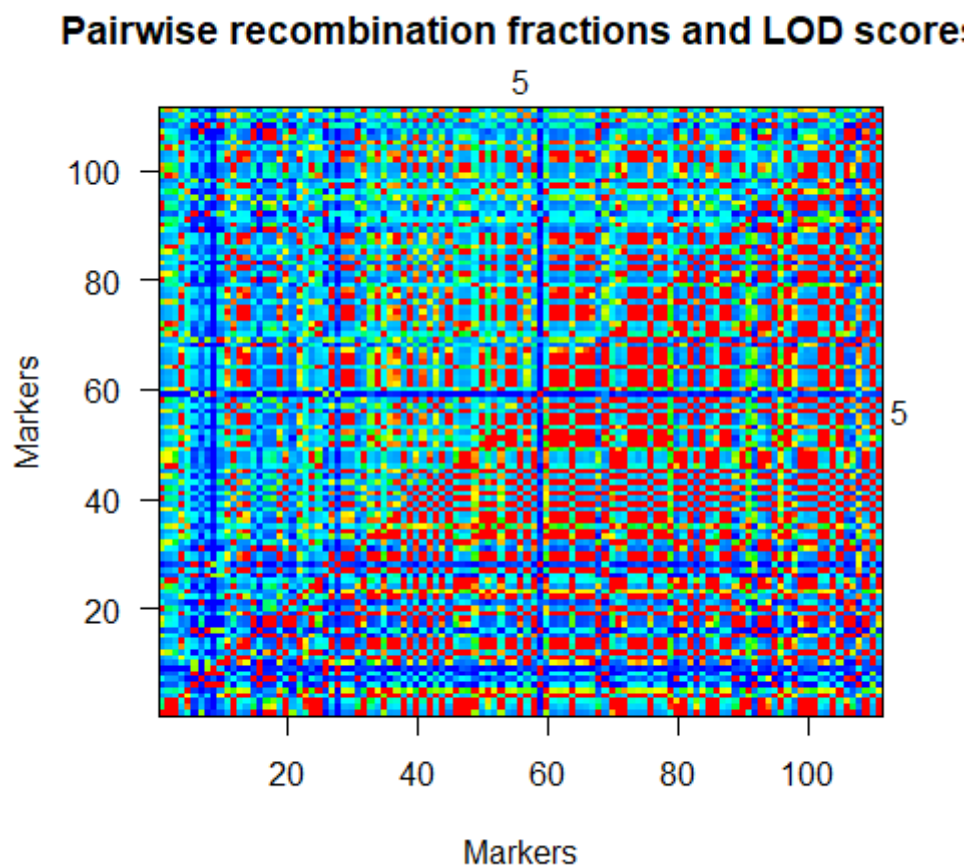


```
(loglik.bb2[c] <- attr(maize.bb2$geno[[c]]$map, "loglik"))
```

```
## [1] -2230.584
```

Linkage group 5

```
c <- 5
plotRF(maize, chr=c, col.scheme = "redblue")
```



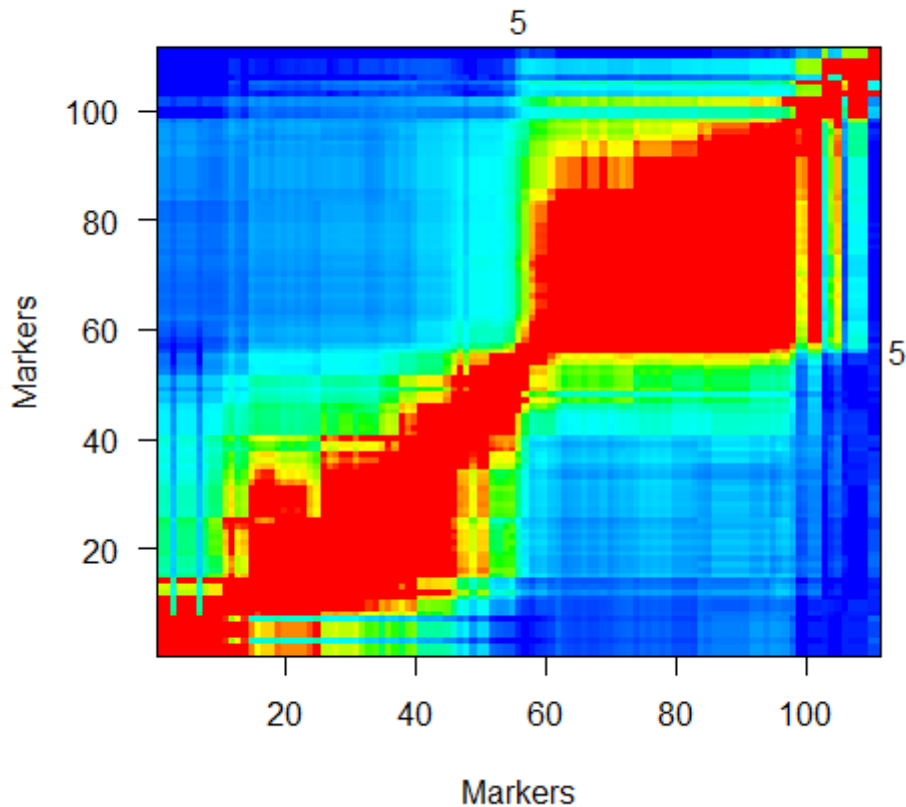
```
maize.bb1 <- orderMarkers(cross = maize.bb1, chr=c, use.ripple = FALSE, map.function="kosambi")
pull.map(maize.bb1, chr = c)
```

##	PZA03322.5.3	PZA03598.1	PZA00682.17.2	PHM4125.11
##	0.000000000000	0.00005000001	0.000010000001	0.000015000002
##	PZA01905.12	PZA02239.12	PZA00282.19	PHM2100.21
##	0.000020000002	0.000025000003	0.000030000003	12.889691249649
##	PZA00529.4	PHM5665.26	PHM5599.20	PZA02151.3
##	14.463596761067	14.463601761067	14.463606984092	20.678133267604
##	PZA00513.1	PZA02585.2	PZA00155.1	PZB01021.1
##	20.678138267604	20.678143267605	27.036873209663	28.314670947869
##	PZA01332.2	PZA03081.1	PZA02479.1	PZA01367.2
##	28.619884622625	28.619889622625	29.867669136583	30.482880068923
##	PZA03155.3	PZA00878.2	PZA00636.7	PZA00521.3
##	30.482885068924	30.482890068924	30.482895068925	32.234308821045
##	PZA00694.6	PZA01810.2	PZA02779.1	PZA02421.1
##	32.825767749117	39.790332448111	39.790337448111	39.790342448112
##	PZA03205.1	PZA01566.1	PZA02614.2	PZA01790.1
##	39.790347448112	39.790352448113	39.790357448113	41.556390279604
##	PHM4348.16	PZA00193.2	PZA00332.5	PZA00344.10
##	42.240785080514	42.240790080515	45.094929824705	46.755406552645
##	PZB01461.1	PZA01766.1	PZA01954.1	PZA00941.2
##	47.176836385714	51.613651774852	52.200129175045	52.200134175046
##	PHM3637.14	PZA02289.2	PZA02194.1	PZA01976.9
##	56.501495507907	56.501500507908	56.501505507908	56.501510507909
##	PZD00030.2	PZA01187.1	PZA01658.1	PZA03275.4.1
##	58.868040969960	58.868604619460	63.566430229147	63.566435229147
##	PZA00271.1	PZA01681.1	PZA01477.3	PHM3155.14
##	68.141829051363	68.141834051364	68.141839051364	70.475602510298
##	PZA01289.1	PZA00453.2	PZA03116.1	PZA01926.1
##	70.779157866043	72.382656859053	73.296769570857	78.575071181326
##	PZA00057.2	PZA02992.15	PZA02982.7	PZA03152.3
##	81.872227229776	86.273207220894	87.326395635362	87.326400635363
##	PZA02147.1	fea2.3	PZB00093.7	PZA03564.1
##	88.520614707405	90.075035488822	90.680040744474	90.980606624158
##	PZA00104.1	PZA02767.1	PZA03203.2	PZA03231.1
##	90.980611624158	90.980616624159	90.980621624159	90.980626624160
##	PZA00218.1	PZA03409.1	PZA00704.1	PZA03459.1
##	90.980631624160	91.281227877791	91.584677015435	91.882346757145
##	PZA02027.1	PHM1307.11	PZA03254.1	PZA03597.1
##	91.882351757145	93.257902387936	93.257907387937	93.257912387937
##	bt2.7.4	PZA03270.2	PZA03587.1	PZA01759.1
##	93.257917387938	93.257922387938	93.257927387939	93.632220638676
##	PHM14055.6	PZA00726.8.10	PZA00445.22	PZA03385.1
##	93.632225638676	93.632230638677	93.920152085604	95.975790960609
##	PZA01751.2	PZA00541.1	PHM13623.14	PZA03247.1
##	96.202764623995	97.875958747526	97.875963747527	97.875968747527
##	PZA01106.3	PZA01713.4	PHM5572.19	PHM15427.11
##	97.875973747528	97.875978747528	97.875983747529	98.679047872688
##	PZA02457.1	PZA02705.1	PZA02002.1	PZA03048.18
##	98.679052872688	98.679057872689	100.581131148824	101.569088508795
##	PZA01422.3	PZA00139.4	PZA01122.1	PZA02138.1
##	102.873382116398	106.030690067252	115.981983824448	116.234564014016
##	PZA02385.6	PHM8527.2	PZA00436.7	PZA00975.1
##	116.234569014016	116.234574014017	125.412644395640	125.412649395641
##	PZA02358.1	PHM1184.26	PZA00683.4	PHM3301.28
##	125.412654395641	144.521939184191	144.521944184192	144.521949184192

```
##          PHM2438.28      PZA02509.15      PZA03227.1
## 144.521954184193 152.989813729025 152.989818729025
```

```
plotRF(maize.bb1, chr = c, col.scheme = "redblue")
```

Pairwise recombination fractions and LOD score



```
(loglik.bb1[c] <- attr(maize.bb1$geno[[c]]$map, "loglik"))
```

```
## [1] -1786.557
```

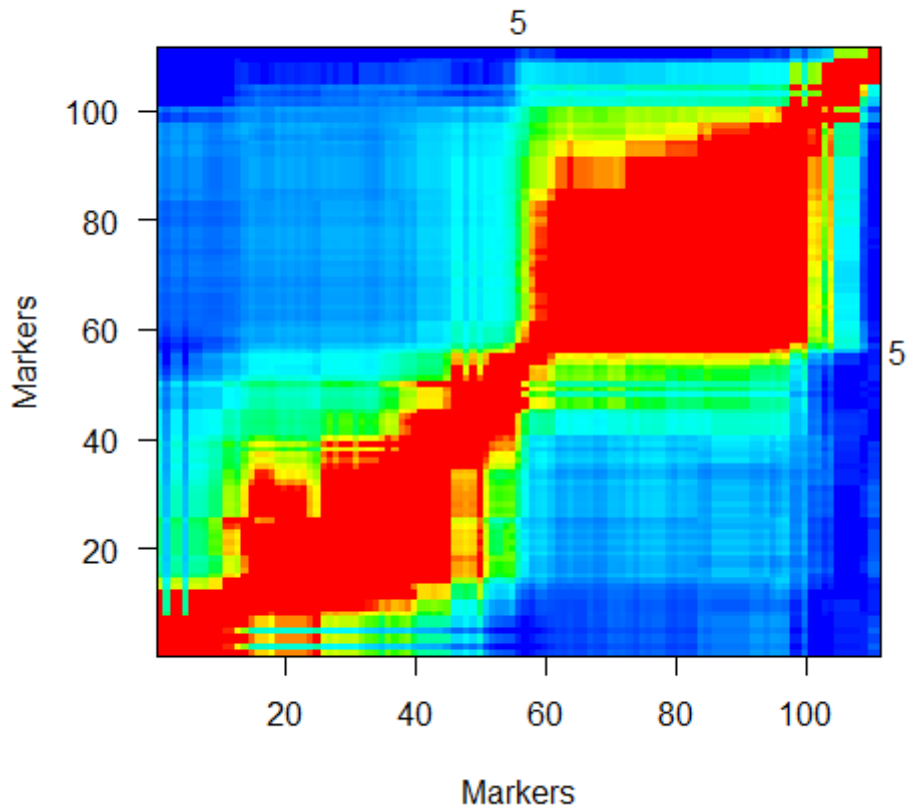
```
maize.bb2 <- orderMarkers(cross = maize.bb2, chr=c, use.ripple = FALSE, map.function="kosambi")
pull.map(maize.bb2, chr = c)
```

##	PZA03598.1	PZA00682.17.2	PZA01905.12	PHM4125.11
##	0.000000000000	0.000005000001	0.000010000001	0.000015000002
##	PZA00282.19	PZA03322.5.3	PZA02239.12	PHM2100.21
##	0.000020000002	0.000025000003	0.000030000003	12.889426946495
##	PHM5665.26	PZA00529.4	PHM5599.20	PZA02585.2
##	14.463138561477	14.463143561478	14.463516812057	14.463920415590
##	PZA00513.1	PZA02151.3	PZA02479.1	PZA01332.2
##	20.674274225615	20.674279225616	27.053730107305	28.508487868624
##	PZA03081.1	PZB01021.1	PZA00155.1	PZA01367.2
##	29.021934268148	29.314190258592	30.578754273474	30.887768007637
##	PZA00636.7	PZA00878.2	PZA03155.3	PZA00521.3
##	30.887773007637	30.887778007638	30.887783007638	32.664015660050
##	PZA00694.6	PZA02614.2	PZA01810.2	PZA02421.1
##	33.254533820728	40.219868975905	40.219873975905	40.219878975906
##	PZA01566.1	PZA03205.1	PZA02779.1	PZA01790.1
##	40.219883975906	40.219888975907	40.219893975907	41.980815820749
##	PZA00193.2	PHM4348.16	PZA00332.5	PZA00344.10
##	42.663462436933	42.663467436934	45.509756755050	47.164562104188
##	PZB01461.1	PZA01954.1	PZA00941.2	PZA01766.1
##	47.561499401122	52.651675957658	52.651680957658	53.351021006292
##	PZA01976.9	PZA02194.1	PZA02289.2	PHM3637.14
##	56.903665253273	56.903670253273	56.903675253274	56.903680253274
##	PZD00030.2	PZA01681.1	PZA01658.1	PZA03275.4.1
##	59.269481052495	63.965529778855	63.965534778855	63.965539778856
##	PZA01477.3	PZA01187.1	PZA00271.1	PHM3155.14
##	63.965544778856	63.965549778857	68.540091264129	70.872669314786
##	PZA01289.1	PZA00453.2	PZA03116.1	PZA01926.1
##	71.176163427970	72.779312825923	73.693223123830	78.971887186102
##	PZA00057.2	PZA02992.15	PZA02982.7	PZA03152.3
##	82.269668261209	86.673334176892	87.706339854312	87.706344854312
##	PZA02147.1	PZA03564.1	PZA03203.2	PZA00218.1
##	88.828862722434	91.463410306764	91.463415306765	91.463420306765
##	PZA03231.1	PZA00104.1	PZA00704.1	PZB00093.7
##	91.463425306766	91.463430306766	91.763784517016	91.763789517017
##	PZA03409.1	fea2.3	PZA03459.1	PZA02027.1
##	91.763794517017	92.368197468069	92.368202468070	92.368207468070
##	PZA03597.1	PZA02767.1	PZA03587.1	PZA03270.2
##	93.767366700758	93.767371700758	93.767376700759	93.767381700759
##	bt2.7.4	PZA03254.1	PZA01759.1	PZA00445.22
##	93.767386700760	93.767391700760	94.151864433636	94.151869433637
##	PHM1307.11	PHM14055.6	PZA00726.8.10	PZA03385.1
##	94.151874433637	94.151879433638	94.151884433638	95.965951571946
##	PZA01751.2	PZA00541.1	PZA01713.4	PZA01106.3
##	96.207534079935	97.938353359499	97.938358359499	97.938363359500
##	PHM13623.14	PZA03247.1	PHM5572.19	PHM15427.11
##	97.938368359500	97.938373359501	97.938378359501	98.750034173511
##	PZA02457.1	PZA02705.1	PZA02002.1	PZA03048.18
##	98.750039173512	98.750044173512	100.658887141617	101.650359629948
##	PZA01422.3	PZA02385.6	PHM8527.2	PZA00139.4
##	102.956385679811	106.119449281787	106.119454281787	106.119459281788
##	PZA01122.1	PZA02138.1	PZA00975.1	PZA02358.1
##	116.076642024995	116.329270782115	125.506351465682	125.506356465683
##	PZA00436.7	PZA00683.4	PHM2438.28	PHM3301.28
##	144.617083137895	144.617088137895	144.617093137896	144.617098137896

```
##          PHM1184.26          PZA03227.1          PZA02509.15
## 144.617103137897 153.084928705567 153.084933705567
```

```
plotRF(maize.bb2, chr = c, col.scheme = "redblue")
```

Pairwise recombination fractions and LOD score!

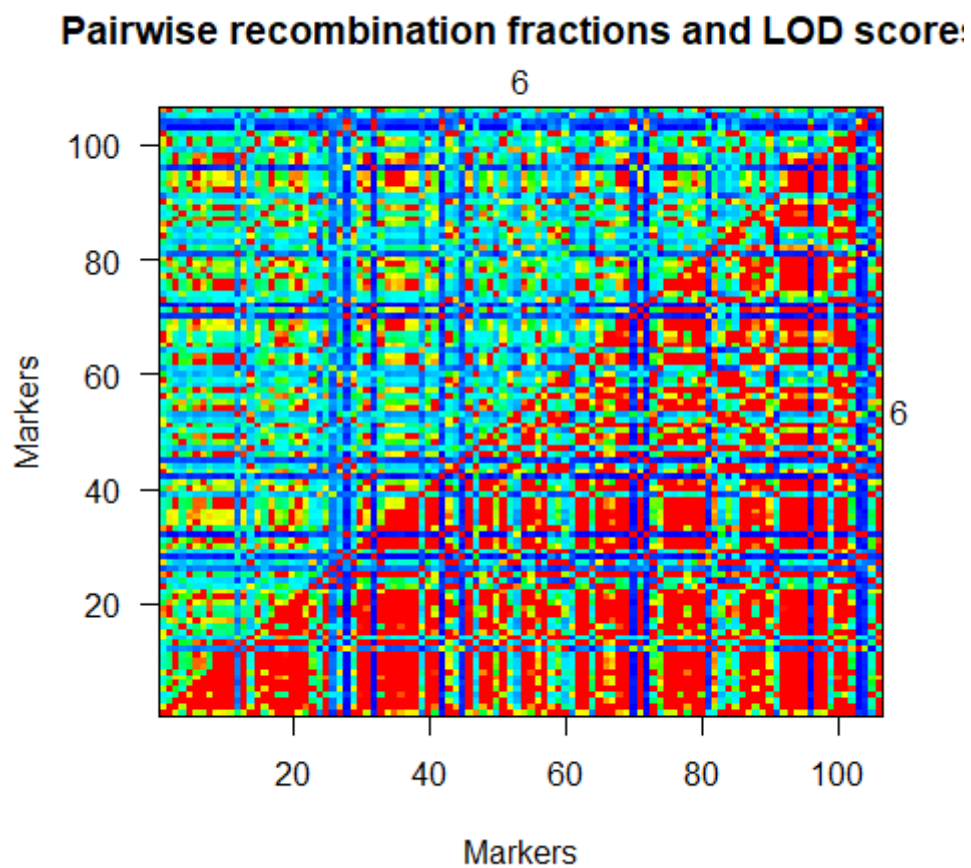


```
(loglik.bb2[c] <- attr(maize.bb2$geno[[c]]$map, "loglik"))
```

```
## [1] -1770.147
```

Linkage group 6

```
c <- 6
plotRF(maize, chr=c, col.scheme = "redblue")
```

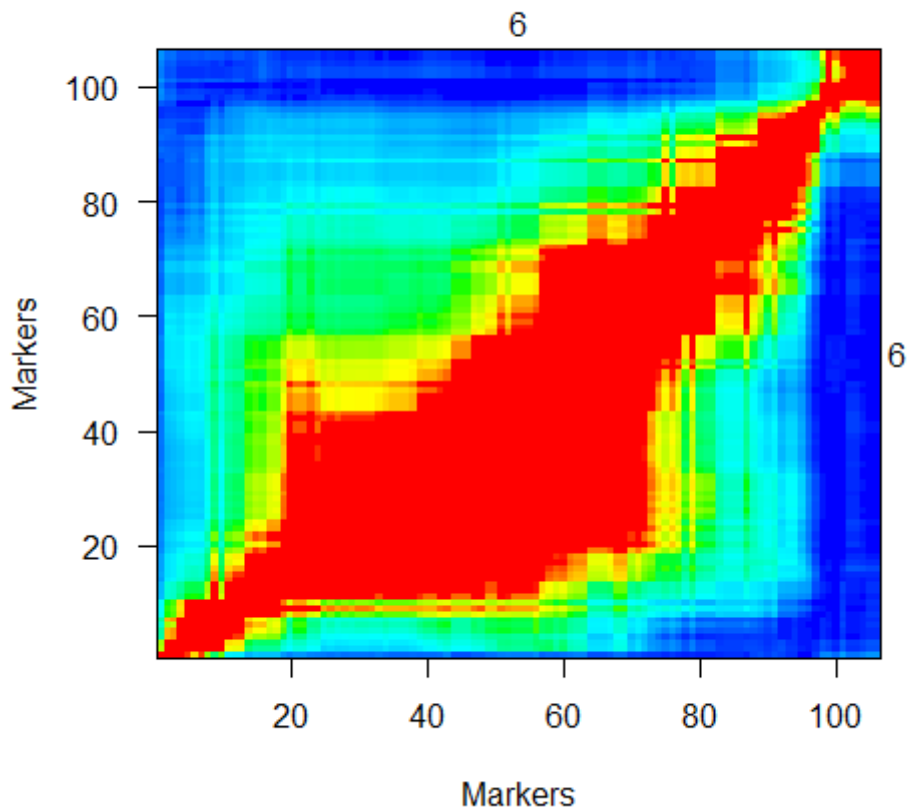


```
maize.bb1 <- orderMarkers(cross = maize.bb1, chr=c, use.ripple = FALSE, map.function="kosambi")  
pull.map(maize.bb1, chr = c)
```

##	PZA02388.1	PZA02174.2	PZA01600.2	PZA01623.3	PZA00058.1
##	0.000000	8.201328	8.201333	13.307052	14.841360
##	PHM4711.14	PZA00368.1	PZA00416.7	PZA03178.1	PZA01601.1
##	16.373005	16.373010	19.013646	19.345439	19.345444
##	PZA01691.1	PZA01951.1	PHM9695.8	PZA01079.1	PZA02955.3
##	27.985631	28.987027	28.987032	32.516981	33.138486
##	PZA01357.2	PZA02454.2	PZA02528.1	PHM1978.111	PHM2350.17
##	34.179988	35.689129	35.689134	38.191134	40.313685
##	PZA01186.1	PHM6428.11	PZA01196.2	PZA00758.1	PZA00717.15
##	40.313690	40.313695	40.313700	40.313705	42.743824
##	PZA02203.1	PZA01257.1	PZA00793.2	PZA01960.1	PZA00498.5
##	42.743829	42.743834	42.743839	42.743844	42.743849
##	PZA01209.1	PZA00379.2	PHM11114.7	PZA01470.1	PZA01297.1
##	42.743854	42.743859	43.383214	43.700504	44.666519
##	PZA01363.2	PZA02522.1	PZA01301.1	PZA02683.1	PHM3978.104
##	44.666524	44.666529	44.666534	45.473846	46.273071
##	PZA00908.2	PZA03135.1	PZA02019.1	PZA00739.1	PZA03579.1
##	46.273076	46.590959	46.908734	49.740386	49.740391
##	PHM4134.8	PZA02566.1	PZA01972.14	PZA03012.7	PZA01072.1
##	49.740396	51.600088	51.600093	52.273078	52.273083
##	PZA02748.3	PHM934.19	PZA03637.1	PZA03639.1	PZA03638.1
##	52.933759	52.933764	54.274832	54.274837	54.274842
##	PHM3993.28	PZB02155.1	PZA01038.1	PZA00118.1.5	PHM10525.9.11
##	54.612207	57.442558	57.765046	58.057540	58.057545
##	PZA03612.2.1	PHM5468.25	PZA01049.1	PHM448.23	PZA00770.1
##	58.638955	58.639010	58.639015	60.119836	60.119841
##	PZA00766.1	PZA02033.1	PZA01787.1	PHM14152.18	PZA00090.1
##	60.119846	60.119851	60.119856	60.119861	61.374822
##	PHM4203.11	PZA02011.1	PZA00429.1	PZA03651.1	PZA03182.5
##	61.374827	61.687630	64.032705	65.576279	65.576284
##	PZA03650.1	PHM4757.14	PHM12749.13	PZA00951.1	PZA01741.1
##	65.576289	68.126117	70.675945	70.675950	71.266724
##	PHM15278.6	PZA03698.1	PZB00811.1	PZA00706.16	PHM3465.6
##	71.266729	71.266734	76.660341	76.660346	76.660351
##	PHM15623.10	PZA00838.2	PZA00675.1	PHM1834.47	PZA00460.3.8
##	76.660356	76.660361	77.642638	80.298692	82.950283
##	PZA02746.2	PZA00362.1	PZA00020.5	PZA01316.1	PHM4786.9
##	82.950288	84.392199	85.756188	87.099288	88.532691
##	PZA00904.1	PZA01964.29	PHM14046.9	PHM14104.23	PZA00189.23
##	92.600422	95.659851	103.968454	106.268611	106.268616
##	PZA00760.1	PZA02281.3	PZA00071.2	PHM5019.59	PZA01290.1
##	111.611612	116.405924	116.405929	116.995530	116.995535
##	PHM2749.10				
##	116.995540				

```
plotRF(maize.bb1, chr = c, col.scheme = "redblue")
```


Pairwise recombination fractions and LOD score



```
(loglik.bb1[c] <- attr(maize.bb1$geno[[c]]$map, "loglik"))
```

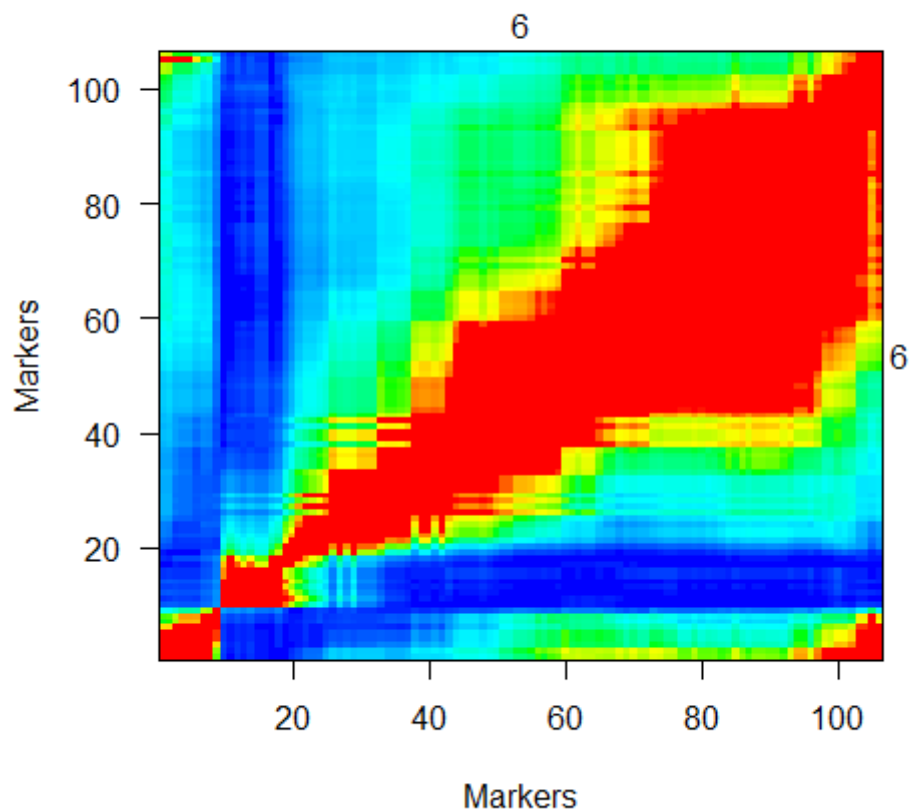
```
## [1] -1555.402
```

```
maize.bb2 <- orderMarkers(cross = maize.bb2, chr=c, use.ripple = FALSE, map.function="kosambi")
pull.map(maize.bb2, chr = c)
```

##	PZA01601.1	PZA00416.7	PHM4711.14	PZA00058.1	PZA00368.1
##	0.0000000	0.2889094	2.6907090	2.6907140	2.6907190
##	PZA01623.3	PZA02174.2	PZA01600.2	PZA02388.1	PZA00760.1
##	5.8289056	10.8711861	10.8711911	19.0347648	61.6169722
##	PHM14104.23	PHM2749.10	PHM5019.59	PZA01290.1	PZA00071.2
##	61.6169772	65.2700832	65.2700882	65.2700932	65.9058132
##	PZA02281.3	PZA00189.23	PHM14046.9	PZA01964.29	PZA00904.1
##	65.9058182	73.4812523	75.7937709	83.9672861	87.0328536
##	PHM4786.9	PZA01316.1	PZA00020.5	PZA00362.1	PZA00460.3.8
##	91.1001700	92.5330174	93.8756168	95.2363805	96.6701044
##	PZB00811.1	PHM1834.47	PZA00675.1	PZA02746.2	PZA00706.16
##	102.3376236	102.3376286	102.3376336	102.3376386	103.3138247
##	PHM15623.10	PHM3465.6	PZA00838.2	PHM15278.6	PZA03698.1
##	103.3138297	103.3138347	103.3138397	108.6918530	108.6918580
##	PZA01741.1	PHM12749.13	PZA03651.1	PZA03182.5	PZA00951.1
##	108.6918630	109.2809701	114.6797621	114.6797671	114.6797721
##	PZA03650.1	PHM4757.14	PZA00429.1	PZA02011.1	PHM4203.11
##	114.6797771	114.6797821	116.2206800	118.5626615	118.8752133
##	PZA00770.1	PHM448.23	PZA00090.1	PZA00766.1	PZA02033.1
##	118.8752183	118.8752233	118.8752283	118.8756604	120.1303600
##	PZA01787.1	PHM14152.18	PZA01049.1	PHM5468.25	PZA03612.2.1
##	121.6075846	121.6093392	121.6110750	121.6110800	121.6110850
##	PHM10525.9.11	PZA00118.1.5	PZA01038.1	PZB02155.1	PHM3993.28
##	122.1925814	122.1925864	122.4851459	122.8077041	125.6387710
##	PZA03638.1	PZA02748.3	PZA03637.1	PZA03639.1	PHM934.19
##	125.9761764	125.9761814	125.9761864	125.9761914	127.3175460
##	PZA03012.7	PZA01072.1	PZA02566.1	PZA03579.1	PZA01972.14
##	127.9781569	127.9781619	128.6511323	130.5112963	130.5113013
##	PZA00739.1	PHM4134.8	PZA02019.1	PZA03135.1	PHM3978.104
##	130.5113063	130.5113113	133.3433847	133.6612000	133.9791153
##	PZA00908.2	PZA01297.1	PZA02522.1	PZA02683.1	PZA01363.2
##	133.9791203	135.6156038	135.6156088	135.6156138	135.6156188
##	PZA01470.1	PZA01301.1	PHM11114.7	PZA01960.1	PZA01196.2
##	136.5816301	136.5816351	136.8990528	137.5384708	137.5384758
##	PZA00498.5	PZA00717.15	PZA01209.1	PZA02203.1	PZA00379.2
##	137.5384808	137.5384858	137.5384908	137.5384958	137.5385008
##	PZA00793.2	PZA01257.1	PHM2350.17	PHM6428.11	PZA01186.1
##	137.5385058	137.5385108	137.5385158	139.9376983	139.9377033
##	PZA00758.1	PHM1978.111	PZA02528.1	PZA02454.2	PZA01357.2
##	139.9377083	142.0353673	144.4823695	144.4823745	145.9440190
##	PZA02955.3	PZA01079.1	PHM9695.8	PZA01951.1	PZA03178.1
##	146.9482271	147.5198035	150.7463555	150.7463605	151.6718695
##	PZA01691.1				
##	151.6718745				

```
plotRF(maize.bb2, chr = c, col.scheme = "redblue")
```

Pairwise recombination fractions and LOD score

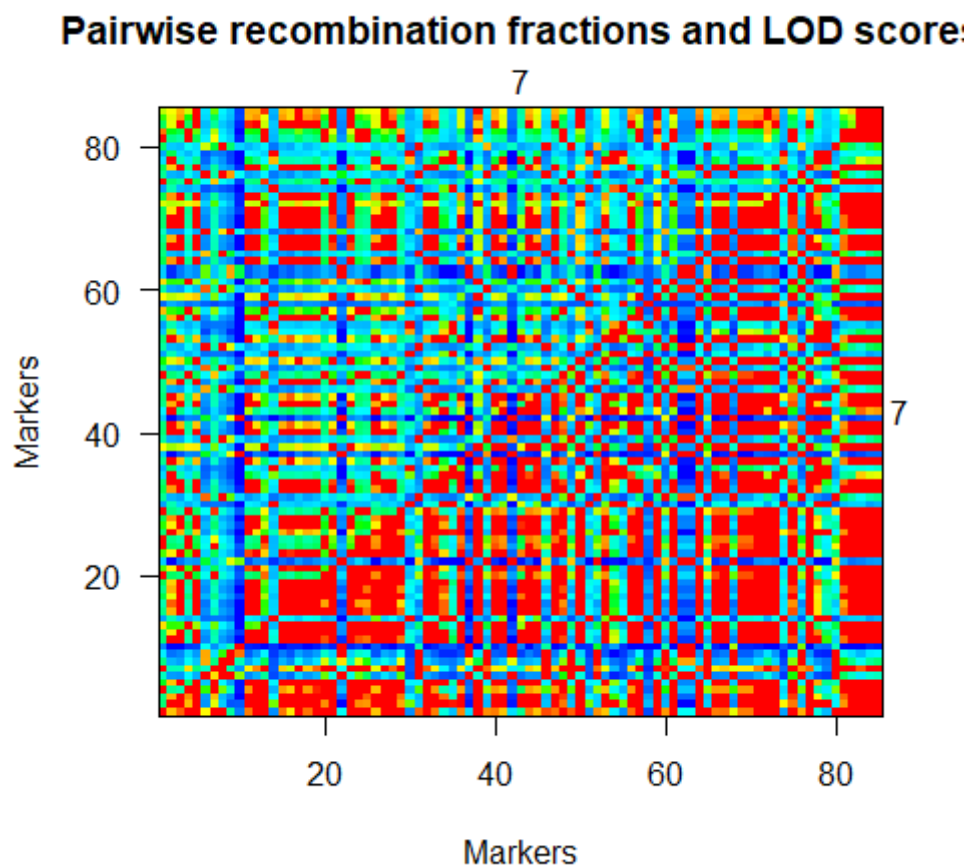


```
(loglik.bb2[c] <- attr(maize.bb2$geno[[c]]$map, "loglik"))
```

```
## [1] -1603.393
```

Linkage group 7

```
c <- 7
plotRF(maize, chr=c, col.scheme = "redblue")
```



```
maize.bb1 <- orderMarkers(cross = maize.bb1, chr=c, use.ripple = FALSE, map.function="kosambi")  
pull.map(maize.bb1, chr = c)
```

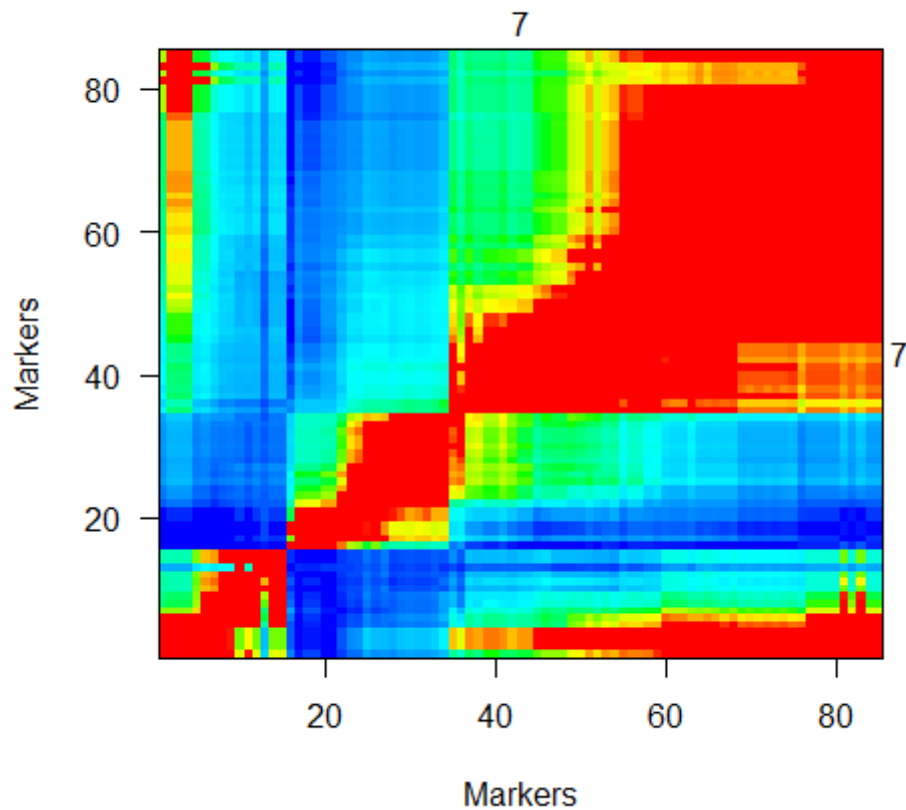
```

##      PZA03416.7      PZB01042.2      PZA00860.1      zb7.2
## 0.0000000000000 0.000005000001 0.000010000001 0.000015000002
##      PZA02702.1      PHM5181.10      PZA02344.1      PZA01386.3
## 2.829472827479 8.393155044571 8.393160044572 10.996621483656
##      PZA00466.1      PHM1218.6      PZA01195.3      PZA01799.1.2
## 11.299093061106 13.490229156490 13.490234156490 13.490239156491
##      PHM3925.79      sh1.12.11      PZA00285.3      PZA03573.1
## 32.564883227559 32.564888227560 32.564893227560 139.446199863081
##      PZA00708.3      PHM1911.173      PHM13681.12      PZA00832.1
## 149.619607252534 149.619612252534 149.619617252535 151.273792148576
##      PHM15445.25      PHM4303.16      PZA00912.2      PZA02381.1
## 151.273797148577 156.303576633678 160.233145703649 161.360059151566
##      PZA01715.1.2      PZA00511.3      PHM4604.18      PZA00323.3
## 163.426279766438 163.426284766438 164.026359224766 165.550353281318
##      PZA02197.1      PHM11226.13      PZB00221.3      PZD00055.1
## 165.735852802653 165.912321124493 165.912326124493 165.912331124494
##      PHM816.29      PZA01369.1      PHM1766.1      PZA02252.2
## 166.221633654423 168.684335695118 182.032543693435 182.032548693436
##      PZA02235.14      PZA01096.1      PZA03670.1      PZA02111.1
## 186.095550479267 186.095555479268 188.134118425280 188.134123425281
##      PZA03671.1      PZA02397.1      PHM4905.6      PZA01866.1
## 188.134128425281 188.425001429015 189.001332660854 189.001337660854
##      PHM3330.25      PZA00213.19      PZA00060.2      PZA00840.1
## 190.599567182330 191.225014352032 191.585537020559 191.585542020560
##      PZA01819.1      PZA02325.4      PZA03235.1      PZA02613.1
## 194.080387852140 194.082406417098 195.431327080372 195.431332080373
##      PZA03470.1      PZA00015.5      PZA00225.8      PZA00152.1
## 199.200235836794 199.590696343295 202.438454704801 202.438459704802
##      PZB01358.1      PZA01281.2      PZB01899.1      PZA03596.1
## 202.438464704802 203.259012138160 203.259017138161 204.594049912303
##      PZA01062.1      PZA02545.1      PZA00947.1      PZA01791.2
## 204.594054912304 204.594059912304 204.594064912305 204.901829939930
##      PZA01861.1      PZB00761.1      PZA03057.3      PZA00925.2
## 204.901834939930 205.201916883883 205.501998818769 205.502003818769
##      PZA03469.1      PZA02878.13      PZA00589.10      PZA00693.3
## 206.106111220853 206.106116220854 206.106121220854 206.106126220855
##      PZB00014.1      PZA03036.6      PZB00959.1      PZA02648.2
## 206.106131220856 206.106136220856 206.106141220857 207.185871874911
##      wx1.1      PZA01999.3      PZB00540.3      PZB01110.6
## 207.185876874911 207.185881874912 207.185886874912 207.185891874913
##      PZA03058.22.21      ZHD1.1      PHM9374.5      PZB00544.2
## 211.067077945713 211.067082945713 211.067087945714 211.067092945714
##      PZB00547.3
## 211.067097945715

```

```
plotRF(maize.bb1, chr = c, col.scheme = "redblue")
```

Pairwise recombination fractions and LOD score



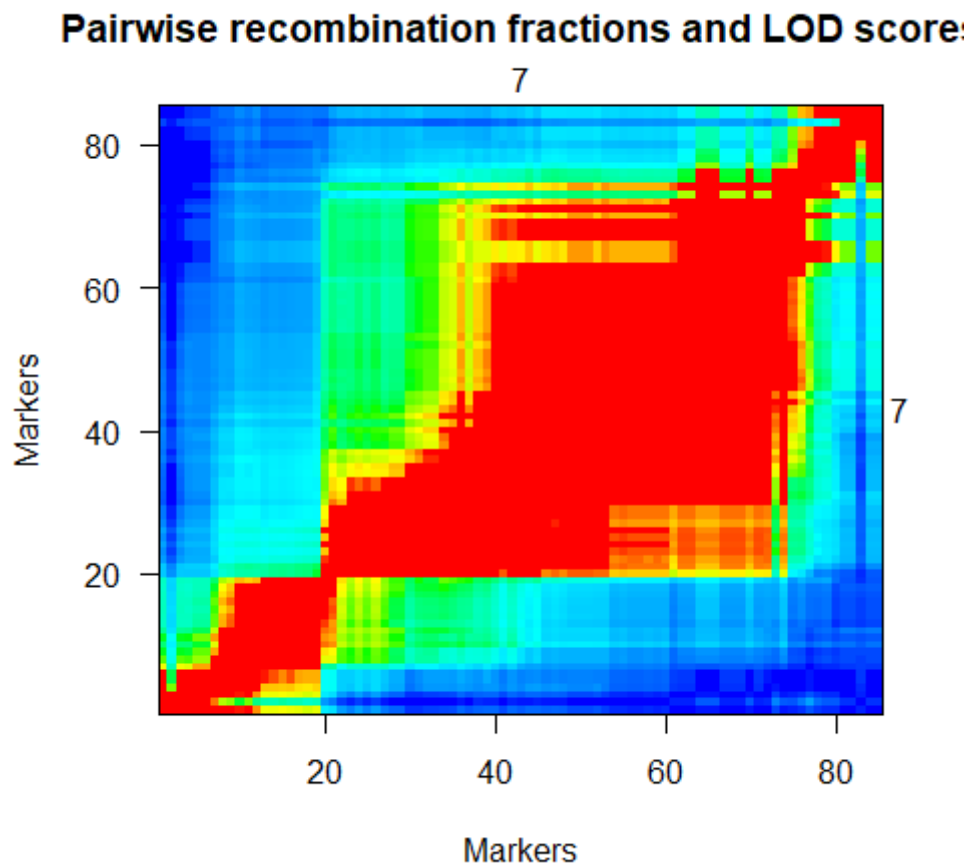
```
(loglik.bb1[c] <- attr(maize.bb1$geno[[c]]$map, "loglik"))
```

```
## [1] -1351.731
```

```
maize.bb2 <- orderMarkers(cross = maize.bb2, chr=c, use.ripple = FALSE, map.function="kosambi")
pull.map(maize.bb2, chr = c)
```

##	PHM1911.173	PZA03573.1	PHM13681.12	PZA00708.3
##	0.000000000000	0.000005000001	0.000010000001	10.173948654865
##	PHM15445.25	PZA00832.1	PHM4303.16	PZA00912.2
##	11.827154831133	11.827159831134	16.857074500055	20.786747541014
##	PZA02381.1	PZA01715.1.2	PZA00511.3	PHM4604.18
##	21.913671064139	23.979910782033	23.979915782034	24.579995681500
##	PZA00323.3	PZD00055.1	PZB00221.3	PZA02197.1
##	26.103744330165	26.467087054022	26.467347313829	26.467352313829
##	PHM11226.13	PHM816.29	PZA01369.1	PZA02252.2
##	26.766958428724	26.776528408729	29.239302562420	42.587513020857
##	PHM1766.1	PZA01096.1	PZA02111.1	PZA02235.14
##	46.650560481879	46.650565481879	48.689628065023	48.689633065024
##	PZA03670.1	PZA03671.1	PZA02397.1	PHM4905.6
##	48.689638065024	48.689643065025	48.980521924627	49.556864940226
##	PZA01866.1	PHM3330.25	PZA00213.19	PZA00840.1
##	49.556869940226	51.155442921115	51.781020853652	52.141770569531
##	PZA00060.2	PZA01819.1	PZA02325.4	PZA03235.1
##	52.141775569531	54.627471598104	54.627476598104	55.974097307693
##	PZA02613.1	PZA03470.1	PZA00015.5	PZB01358.1
##	55.974102307694	59.721684759643	60.109750728359	62.997344823117
##	PZA00225.8	PZA00152.1	PZB01899.1	PZA00947.1
##	62.997349823118	62.997354823118	63.828069645931	63.828074645932
##	PZA01281.2	PZA02545.1	PZA03596.1	PZA01062.1
##	63.828079645932	65.179385947838	65.179390947838	65.179395947839
##	PZA00925.2	PZA01791.2	PZB00761.1	PZA01861.1
##	65.491453700669	65.491458700669	65.491463700670	65.491468700670
##	PZA03057.3	PZA03036.6	PZB00959.1	PZA00589.10
##	66.103835918622	66.716234757208	66.716239757208	66.716244757209
##	PZB00014.1	PZA02878.13	PZA03469.1	PZA00693.3
##	66.716249757209	66.716254757210	66.716259757210	66.716264757211
##	PZA02648.2	PZB00540.3	PZB00547.3	zb7.2
##	67.823077270398	67.823082270399	67.823087270399	71.920272138127
##	PZB01042.2	PZA00860.1	PZB00544.2	wx1.1
##	71.920277138128	71.920282138128	71.920287138129	71.920292138129
##	PZA01999.3	PZA03058.22.21	PZB01110.6	ZHD1.1
##	71.920297138130	71.920302138130	71.920307138131	71.920312138131
##	PZA03416.7	PHM9374.5	PZA02702.1	PHM5181.10
##	81.406076449378	81.406081449379	84.493952806905	90.289228570786
##	PZA02344.1	PZA01386.3	PZA00466.1	PZA01195.3
##	90.289233570786	92.923941692972	93.226554499978	95.419550769431
##	sh1.12.11	PHM1218.6	PHM3925.79	PZA00285.3
##	114.573468180497	114.573473180497	114.573478180498	114.573483180498
##	PZA01799.1.2			
##	114.573488180499			

```
plotRF(maize.bb2, chr = c, col.scheme = "redblue")
```



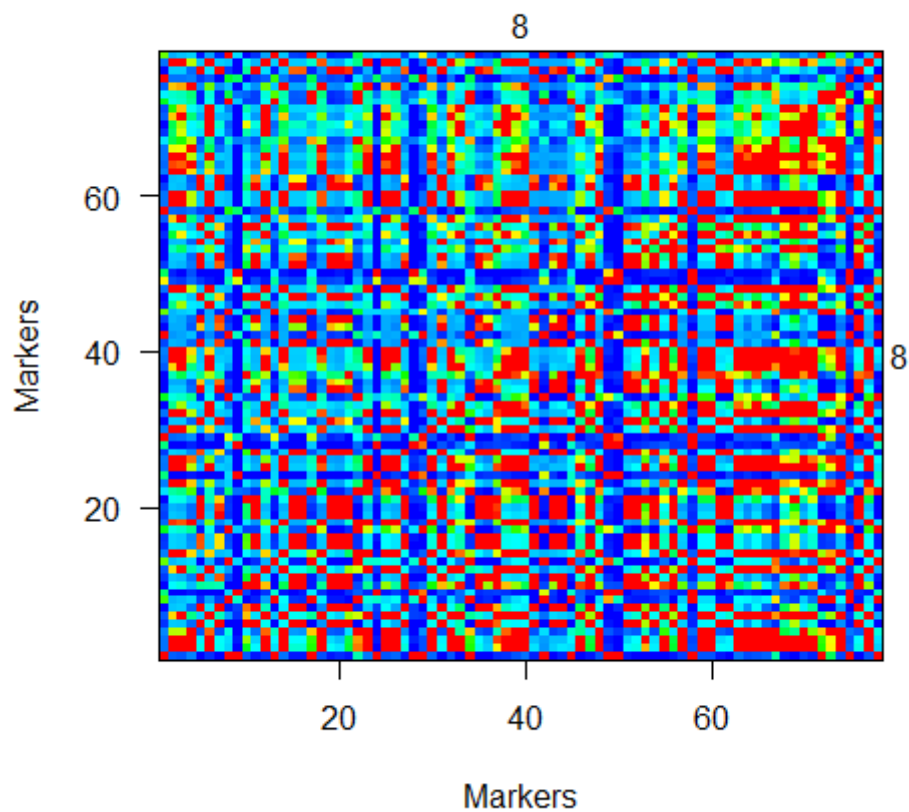
```
(loglik.bb2[c] <- attr(maize.bb2$geno[[c]]$map, "loglik"))
```

```
## [1] -1308.089
```

Linkage group 8

```
c <- 8
plotRF(maize, chr=c, col.scheme = "redblue")
```


Pairwise recombination fractions and LOD score

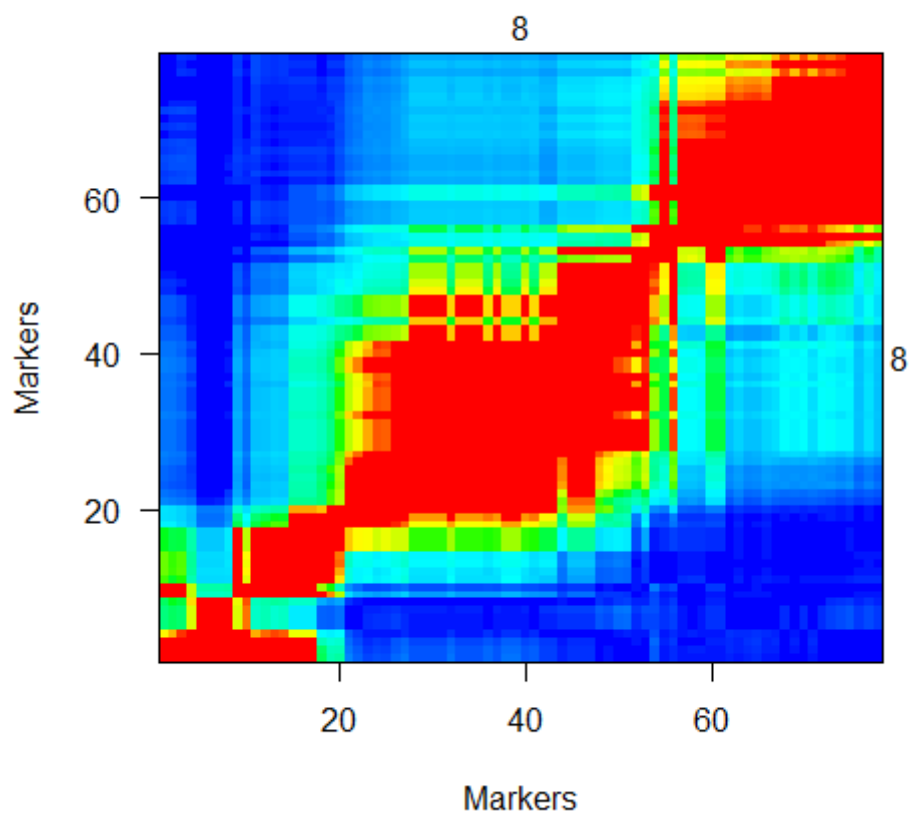


```
maize.bb1 <- orderMarkers(cross = maize.bb1, chr=c, use.ripple = FALSE, map.function="kosambi")
pull.map(maize.bb1, chr = c)
```

##	PZA00821.1	PZA02688.2	PZB01222.1	PZA02141.1	PZA02815.25
##	0.0000000	0.6101723	1.2582481	6.0147530	14.3563574
##	PHM4468.13	PZA01875.1	PZA00910.1	PHM7922.8	PZA00889.2
##	14.3563624	14.6337946	17.2867227	34.2893077	34.2893127
##	PZA01468.1	PZA00266.7	PZB01569.7	PHM4503.25	PHM5794.13
##	41.5634646	41.8458301	42.1685346	42.1685396	44.6305588
##	PZA00223.4	PHM4748.16	PZA03027.12	PZA01462.1	PZA01672.1
##	47.0859821	49.5414047	51.9986754	54.6438408	57.2384741
##	PZA02436.1	PZA01342.2	PZA01144.1	PZA02247.1	PHM11985.27
##	65.0051118	65.8746116	66.9541304	67.9641768	67.9641818
##	PZA03102.9	PZB01308.1	PZA00473.5	PZA01591.1	PZB00414.2
##	68.7952833	69.8076380	72.2545646	72.2545696	72.2545746
##	PZA01884.1	PZB00942.1	PZA00357.19	PZA01552.1	PZA02328.5
##	72.2545796	72.2545846	72.2545896	72.2545946	72.2545996
##	PZA02478.7	PZA01618.2	PZA02148.1	PZA02673.1	PZA02262.3
##	72.2546046	72.2546096	72.2546146	72.2546196	72.2546246
##	PZA02187.1.2	PZA01729.1	PHM13020.10	PZA00382.17	PZA00571.1
##	72.2546296	78.2522830	78.2522880	84.0703386	84.0703436
##	PZA01055.1	lac1.3	PZA01736.1	PZA01589.2	PZA02396.14
##	84.0703486	84.0703536	84.9734779	85.4187156	86.7449796
##	PZA02048.2	PZA03461.1	PZA01029.1	PZA00942.2	PZA03488.1
##	86.7449846	95.7959722	95.7959835	103.3106302	103.3106352
##	PZB01658.1	PHM2551.31	PZA00006.17	PZB01009.2.1	PZA00214.1
##	103.3106402	114.2844838	114.2844888	114.2844938	114.2844988
##	PHM8909.12	PZA03069.8.4	PZA02606.1	PZA00543.12	PZA00427.3
##	114.2845038	115.7208357	115.7208407	115.7208457	115.7208507
##	PZD00072.2	PZA01425.2	PZA01509.1	PZA01527.1	PZA03120.1
##	115.7208557	116.7100055	117.6901279	117.6901329	117.6901379
##	PZA00355.2	PZA01901.1	PZA03063.21	PZA02948.24	PZA00440.15.1
##	117.6901429	118.3861637	119.0610944	119.3329389	120.1576368
##	PZA00158.2	PZA03047.12	PHM15961.13		
##	122.7182325	122.7182375	122.7182425		

```
plotRF(maize.bb1, chr = c, col.scheme = "redblue")
```

Pairwise recombination fractions and LOD score



```
(loglik.bb1[c] <- attr(maize.bb1$geno[[c]]$map, "loglik"))
```

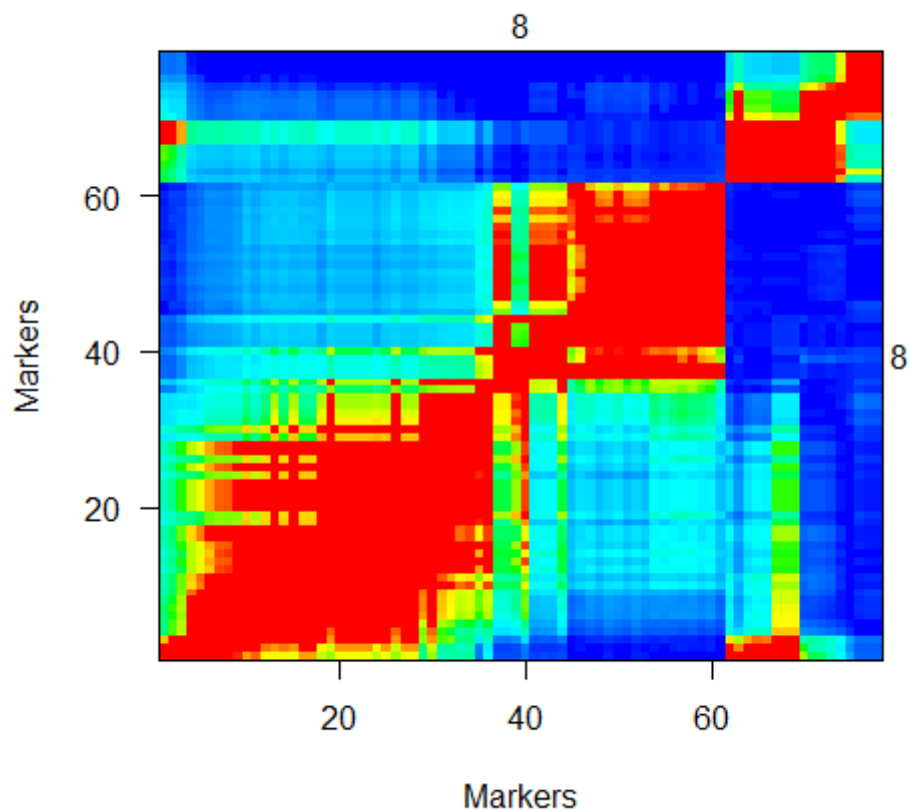
```
## [1] -1343.448
```

```
maize.bb2 <- orderMarkers(cross = maize.bb2, chr=c, use.ripple = FALSE, map.function="kosambi")
pull.map(maize.bb2, chr = c)
```

##	PZA03027.12	PZA01462.1	PZA01672.1	PZA02436.1	PZA01342.2
##	0.000000	2.543026	5.070278	12.750559	13.622749
##	PZA01144.1	PHM11985.27	PZA02247.1	PZA03102.9	PZB00942.1
##	14.707844	15.203951	15.699978	16.529679	17.540978
##	PZB01308.1	PZA02478.7	PZA00357.19	PZA02187.1.2	PZA01552.1
##	17.540983	19.975292	19.975297	19.975302	19.975307
##	PZA02148.1	PZA02673.1	PHM13020.10	lac1.3	PZA00473.5
##	19.975312	19.975317	25.972079	25.972084	25.972089
##	PZA02262.3	PZA01591.1	PZA01884.1	PZA01729.1	PZA02328.5
##	25.972094	25.972099	25.972104	25.972109	25.972114
##	PZA00571.1	PZA01618.2	PZB00414.2	PZA00382.17	PZA01055.1
##	25.972119	25.972124	25.972129	31.788565	31.788570
##	PZA01736.1	PZA01589.2	PZA02048.2	PZA02396.14	PZA03461.1
##	32.691429	33.136531	34.462394	34.462399	43.510072
##	PZA01029.1	PHM8909.12	PZA00214.1	PZA00942.2	PZB01658.1
##	43.510077	51.022729	51.022734	51.022739	51.022744
##	PZB01009.2.1	PHM2551.31	PZA00006.17	PZA03488.1	PZA00158.2
##	61.933202	61.933207	61.933212	61.933217	70.458815
##	PZA03047.12	PZA01425.2	PZA00543.12	PZD00072.2	PZA00355.2
##	70.458830	76.887292	76.887297	76.887302	76.887307
##	PZA03069.8.4	PZA02606.1	PZA00427.3	PZA03120.1	PZA01527.1
##	76.887312	76.887317	76.887322	78.857923	78.857928
##	PZA01509.1	PZA03063.21	PZA01901.1	PZA02948.24	PZA00440.15.1
##	79.543422	80.228916	80.228921	80.500893	81.325779
##	PHM15961.13	PZA01468.1	PHM7922.8	PZA00266.7	PZB01569.7
##	83.882029	152.528457	152.676869	152.824864	153.124714
##	PHM4503.25	PZA00223.4	PHM5794.13	PHM4748.16	PZA00889.2
##	153.124719	153.124724	153.124729	153.124734	160.629230
##	PZA00821.1	PZA02688.2	PZB01222.1	PZA02141.1	PZA00910.1
##	162.754488	163.399408	164.077099	169.363579	176.089613
##	PZA01875.1	PHM4468.13	PZA02815.25		
##	178.738193	179.014200	179.014205		

```
plotRF(maize.bb2, chr = c, col.scheme = "redblue")
```

Pairwise recombination fractions and LOD score



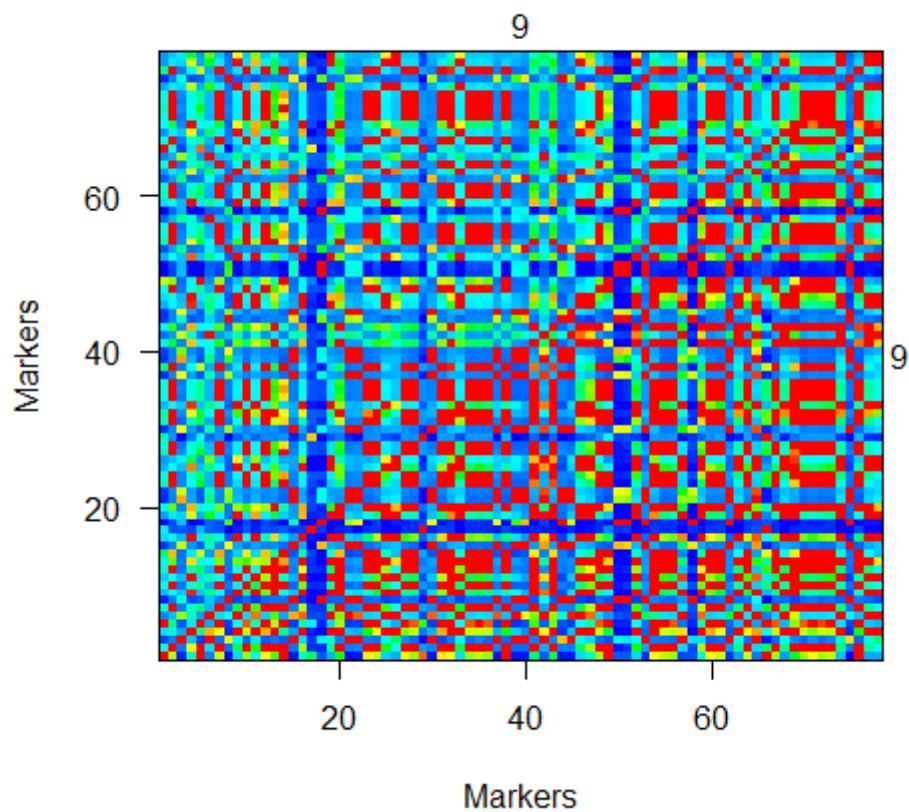
```
(loglik.bb2[c] <- attr(maize.bb2$geno[[c]]$map, "loglik"))
```

```
## [1] -1424.652
```

Linkage group 9

```
c <- 9
plotRF(maize, chr=c, col.scheme = "redblue")
```

Pairwise recombination fractions and LOD score

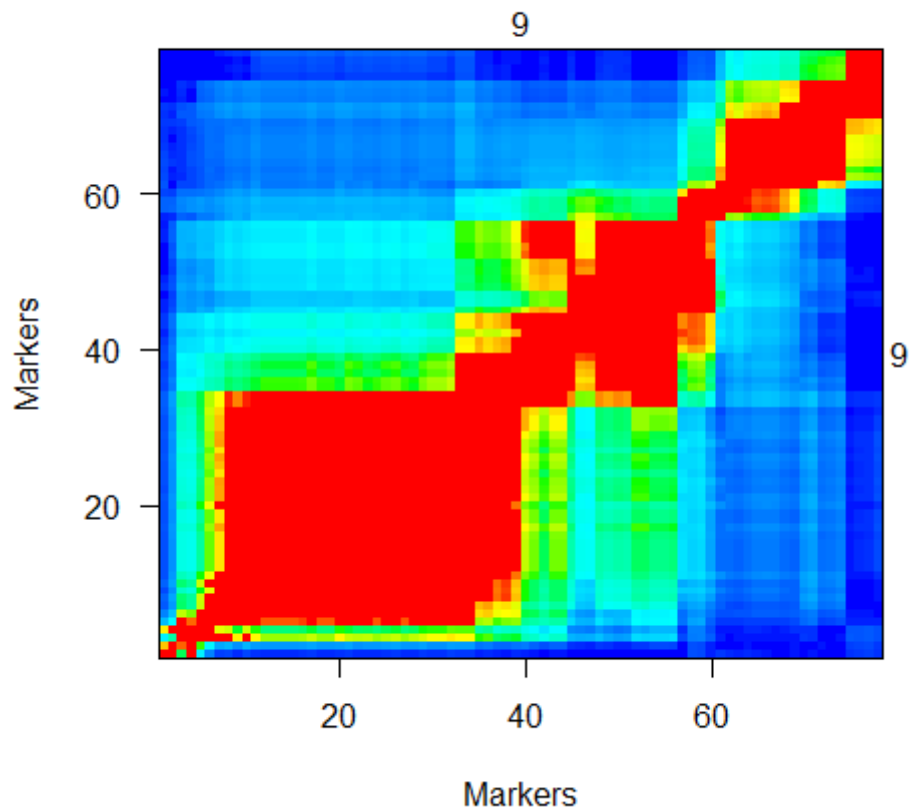


```
maize.bb1 <- orderMarkers(cross = maize.bb1, chr=c, use.ripple = FALSE, map.function="kosambi")
pull.map(maize.bb1, chr = c)
```

##	PZA01426.1	PZA02035.5	PHM3078.12	PHM9241.13	PZA01909.1.2	PZA02872.1
##	0.000000	4.988858	24.362085	24.362090	27.894807	31.518326
##	PZA00256.27	PZA03624.1	PZA03344.2	PHM4080.15	PZA00132.17	PZA01607.1
##	35.340666	38.527281	38.527286	38.527291	38.527296	41.709039
##	PZA03723.1	PZA01230.1	PZA02612.1	PHM12830.14	PZA02291.1	PHM4818.15
##	41.709044	41.709049	41.709054	41.709059	41.709064	41.709069
##	PZA01445.1	PHM15501.9	PHM904.21	PZA00084.2	PHM4353.31	PZA03363.1
##	41.709074	41.709079	41.709084	41.709089	41.709094	41.709099
##	PZA00418.2	PZA03645.1	PZA01936.4	PZA03687.1	PZA01210.1.2	PZA02018.1
##	41.709104	41.709109	41.709114	41.709119	42.150813	42.618204
##	PZA01113.1	PZA01933.3	PZA02236.1	PZA02365.7	PZA01690.7	PZA00616.13
##	42.618209	43.109431	43.109436	43.109441	55.157585	55.157590
##	PZA00986.1	PZA01946.7	PZA02352.1	PZA02643.1	PZB00752.1	PZD00054.1
##	55.809871	55.809876	57.497134	62.807798	64.456174	64.456179
##	PZA03583.1	PZA01714.1	PHM9162.135	PHM16437.20	PZA02722.1	PZA00405.7.6
##	64.456184	64.456189	70.407081	73.459883	73.459888	76.871840
##	PZA02854.13	PZA03728.1	PZA03166.1	PZA02449.13	PZA02984.10	PZA00740.3
##	77.222728	77.543673	77.543678	79.262546	79.262551	79.547295
##	PZA01542.1	PZA00111.10	PZA03176.4	PHM112.8	PZA02260.2	PZA02386.2
##	79.547300	79.547305	93.086877	96.585539	96.585544	98.651684
##	PZA00795.1	PHM7898.10	PZA02373.1	PZA02223.2	PHM10225.15	PZA01533.2
##	107.523944	113.005901	113.005906	113.713652	114.021894	114.026207
##	PZA00505.6	PZA01802.3	PZA01414.1	PZA01028.2	PZA00386.4	PZB00605.1
##	114.642566	114.642571	116.643523	120.252530	120.586424	122.673041
##	PZA01278.2	PZA00695.3	PZA01744.1	PZA00424.1	PZA01044.1	PZA02274.1
##	122.673046	122.965479	133.577531	134.270961	134.270966	134.949937

```
plotRF(maize.bb1, chr = c, col.scheme = "redblue")
```

Pairwise recombination fractions and LOD score



```
(loglik.bb1[c] <- attr(maize.bb1$geno[[c]]$map, "loglik"))
```

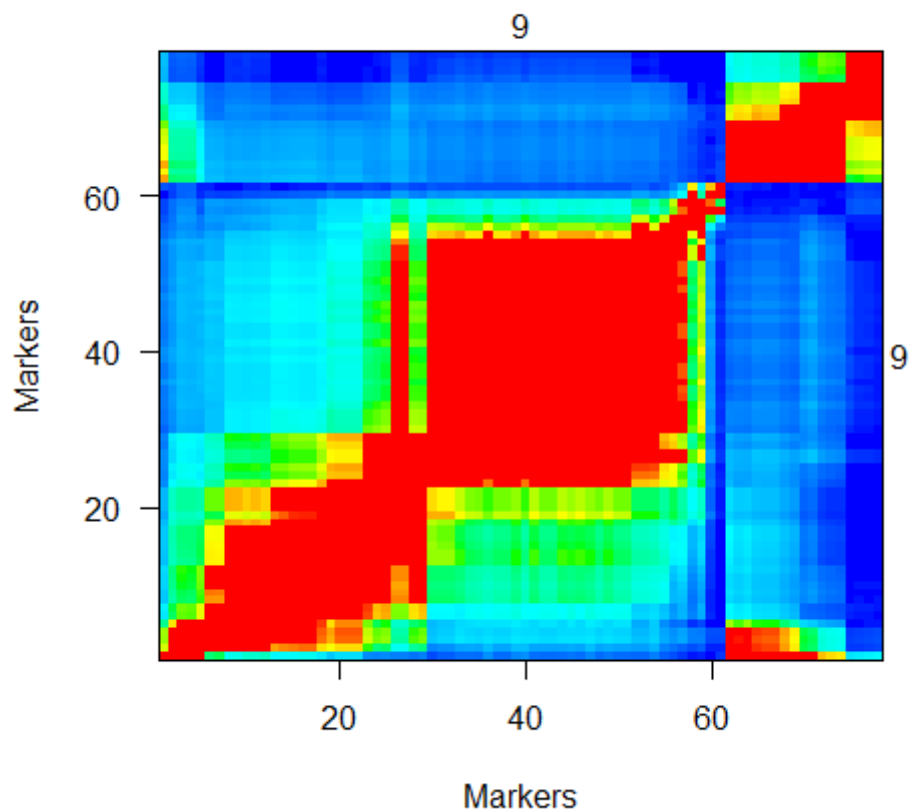
```
## [1] -1451.878
```

```
maize.bb2 <- orderMarkers(cross = maize.bb2, chr=c, use.ripple = FALSE, map.function="kosambi")
pull.map(maize.bb2, chr = c)
```


##	PZA00795.1	PZA02386.2	PZA02260.2	PHM112.8	PZA03176.4	PHM16437.20
##	0.000000	7.767678	9.832863	9.832868	13.516398	20.727169
##	PZA02722.1	PZA03728.1	PZA03166.1	PZA02854.13	PHM9162.135	PZA00405.7.6
##	20.727174	25.047734	25.047739	25.328543	25.434451	25.540383
##	PZA02984.10	PZA02449.13	PZA00111.10	PZA00740.3	PZA01542.1	PZD00054.1
##	28.036230	28.036235	28.203367	28.370499	28.370504	30.927066
##	PZA02643.1	PZB00752.1	PZA03583.1	PZA01714.1	PZA02352.1	PZA00986.1
##	32.695343	32.695348	32.695353	32.695358	38.063896	39.762800
##	PZA01946.7	PZA02236.1	PZA02365.7	PZA00616.13	PZA01690.7	PZA01933.3
##	39.762805	40.415864	40.415869	40.415874	40.415879	52.448312
##	PZA02018.1	PZA01113.1	PZA01210.1.2	PHM12830.14	PZA01445.1	PZA00132.17
##	52.938430	52.938454	53.405898	53.847644	53.847649	53.847654
##	PZA03723.1	PZA01607.1	PHM4353.31	PHM15501.9	PZA03645.1	PZA02612.1
##	53.847659	53.847664	53.847669	53.847674	53.847679	53.847684
##	PZA01936.4	PZA02291.1	PZA00084.2	PHM904.21	PZA03687.1	PZA01230.1
##	53.847689	53.847694	53.847699	53.847704	53.847709	53.847714
##	PZA00418.2	PHM4818.15	PZA03363.1	PZA03624.1	PHM4080.15	PZA03344.2
##	53.847719	53.847724	53.847729	57.030286	57.030291	57.030296
##	PZA00256.27	PZA02872.1	PZA01909.1.2	PHM9241.13	PHM3078.12	PZA02035.5
##	60.217102	64.040065	67.664104	71.197023	71.197028	90.588482
##	PZA01426.1	PZA02373.1	PZA02223.2	PHM7898.10	PZA01533.2	PHM10225.15
##	95.579544	166.453582	167.069036	167.069041	167.371849	167.371854
##	PZA00505.6	PZA01802.3	PZA01414.1	PZA01028.2	PZA00386.4	PZA00695.3
##	167.981314	168.942857	169.904626	173.475739	173.806012	175.451169
##	PZA01278.2	PZB00605.1	PZA02274.1	PZA01044.1	PZA00424.1	PZA01744.1
##	175.779985	175.779990	188.003173	188.667193	189.006449	189.346085

```
plotRF(maize.bb2, chr = c, col.scheme = "redblue")
```

Pairwise recombination fractions and LOD score

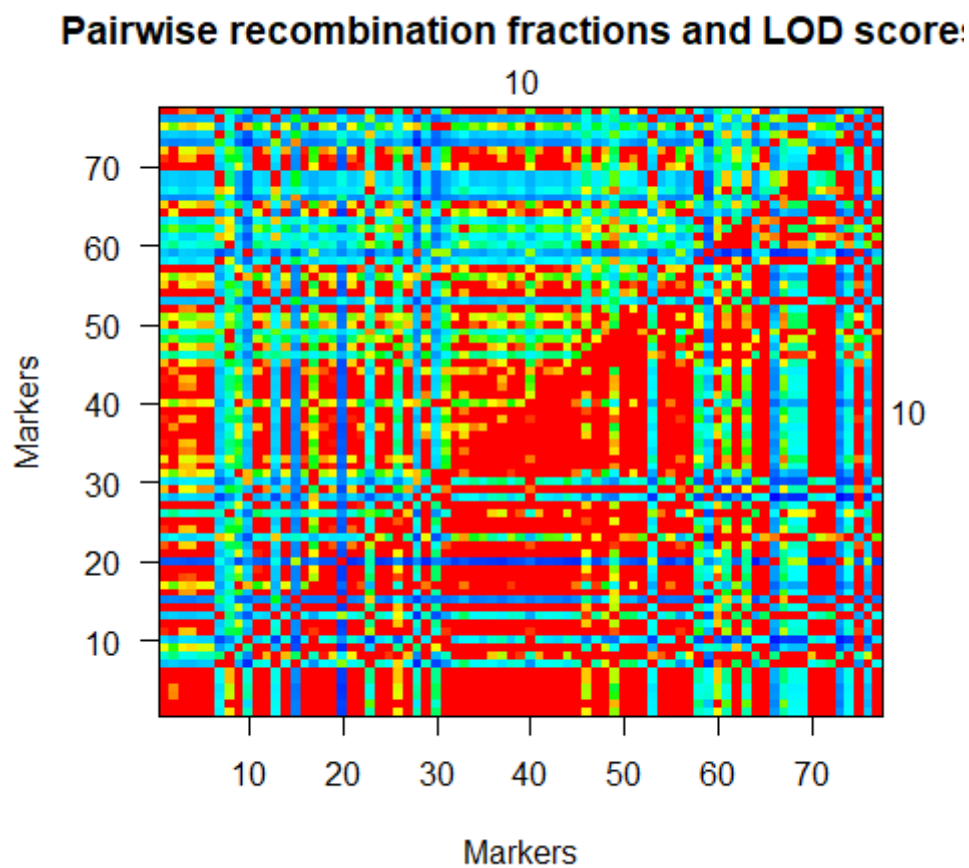


```
(loglik.bb2[c] <- attr(maize.bb2$geno[[c]]$map, "loglik"))
```

```
## [1] -1445.71
```

Linkage group 10

```
c <- 10
plotRF(maize, chr=c, col.scheme = "redblue")
```

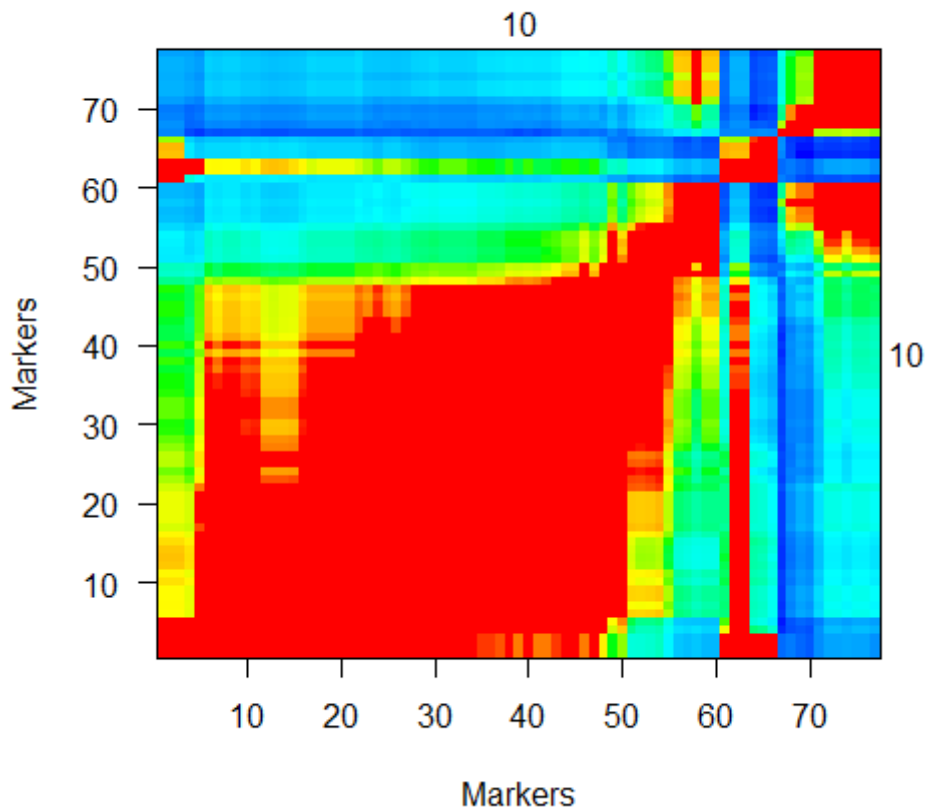


```
maize.bb1 <- orderMarkers(cross = maize.bb1, chr=c, use.ripple = FALSE, map.function="kosambi")  
pull.map(maize.bb1, chr = c)
```

##	PZA02095.10	PHM3765.7	PZA01883.2	PZB01301.5
##	0.000000000000	0.000005000001	0.000010000001	0.000015000002
##	PHM15331.16	PZD00033.3	PZA01597.1	PZA02853.11
##	2.943116687852	5.838494884217	5.838499884217	5.838504884218
##	PZA03491.1	PHM3922.32	PZA00079.1	PHM3896.9
##	5.838509884218	6.420672385991	6.420677385991	7.299088732605
##	PZA00463.3	PZA01642.1	PZA02961.6	PZA02470.2
##	7.299093732606	7.299098732606	7.299103732607	8.500447422408
##	PZA01677.1	PZA00933.3	PHM2770.19	PZA02941.7
##	9.293028029560	9.293033029560	9.293038029561	9.293043029561
##	PZA00409.17	PZA01877.2	PZB00409.6	PZA01619.1
##	9.293048029562	10.091340570513	11.233600434181	11.233605434182
##	PZA00337.4	PHM12990.15	PZA00814.1	PZA02398.2
##	11.233610434182	11.233615434183	11.523305206091	12.633652940762
##	PHM18195.6	PZA00444.1	PZA00048.1	PHM537.22
##	12.633781820236	12.633786820237	12.633791820237	12.633796820238
##	PZA00400.3	PHM12625.18	PZA01919.2	PZA01292.1
##	12.633801820238	12.633806820239	12.800765883658	12.967725894681
##	PZA02128.3	PZA01089.1	PZA02219.2	PHM4341.42
##	13.135047487402	13.716410041220	14.296499246744	14.296504246745
##	PHM13687.14	PZA01141.1	PZA03713.1	PZA01005.1
##	14.296509246745	14.595073877923	15.196134910752	15.832811301963
##	PZA00866.2	PZA00647.9	PZA03196.1	PZA01241.2
##	15.832816301963	15.832821301964	15.832826301964	18.499360824655
##	PZB01111.8	PZA02320.1	PZA01456.2	PHM18513.156
##	21.379097008087	21.379102008087	26.095227298669	27.336124394132
##	PHM15868.56	PZA02663.1	PZA01995.2	PZA03603.1
##	27.801243514861	28.266449623960	30.901674727333	34.936716828639
##	PZA03605.1	PZA03607.1	PZA03604.1	PZA03606.1
##	34.936721828639	34.936726828640	34.936731828640	34.936736828640
##	PHM3631.47	PHM2828.83	PZA01451.1	PZA01313.2
##	84.389916107399	84.389921107399	84.389926107400	89.094616702769
##	PZA02221.20	PZA02554.1	PZA02527.2	PZA00062.4
##	90.821181001387	92.551807550976	135.360602427269	143.244758347951
##	PZA01001.2	PZA02578.1	PZA02167.2	PZA00007.1
##	147.524239119803	147.825209221318	156.466585320467	156.850385202227
##	PZA02969.9	PZA01073.1	PZA02049.1	PHM5435.25
##	156.850390202228	156.850395202228	157.349083966439	157.847786280537
##	PZA00130.9			
##	158.348101709486			

```
plotRF(maize.bb1, chr = c, col.scheme = "redblue")
```

Pairwise recombination fractions and LOD score



```
(loglik.bb1[c] <- attr(maize.bb1$geno[[c]]$map, "loglik"))
```

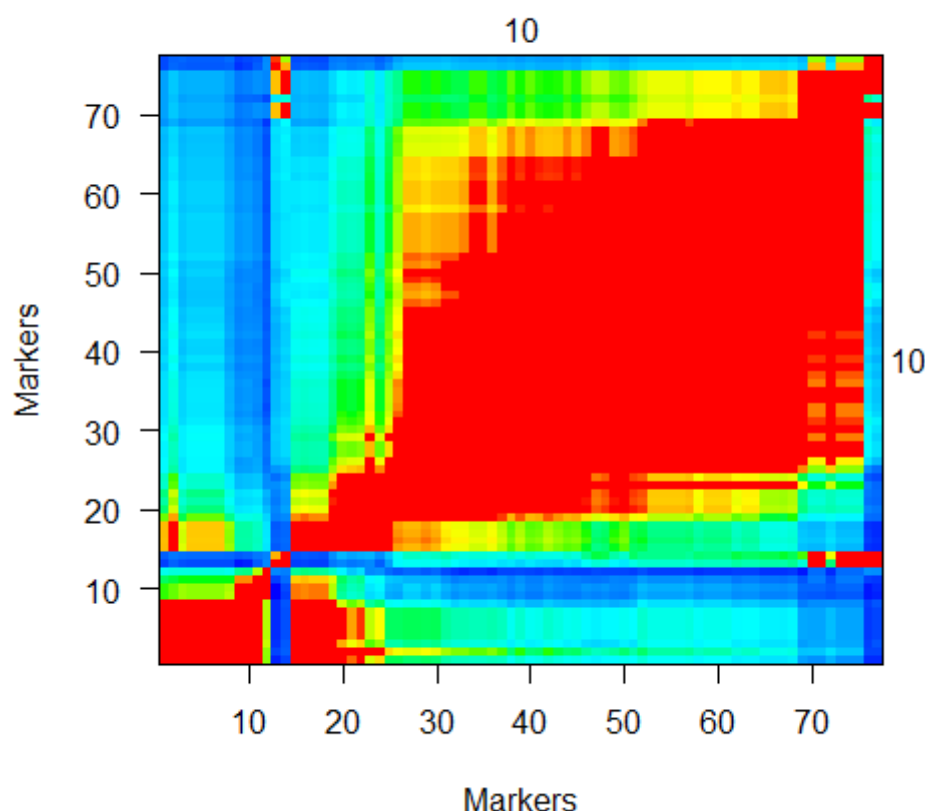
```
## [1] -1226.465
```

```
maize.bb2 <- orderMarkers(cross = maize.bb2, chr=c, use.ripple = FALSE, map.function="kosambi")
pull.map(maize.bb2, chr = c)
```

##	PZA00130.9	PZA03607.1	PZA01073.1	PZA00007.1
##	0.000000000000	0.000005000001	1.536006465536	1.536011465537
##	PZA02969.9	PHM5435.25	PZA02049.1	PZA02167.2
##	1.536016465537	1.536021465538	1.536026465538	1.918538466352
##	PZA02578.1	PZA01001.2	PZA00062.4	PZA02527.2
##	10.560592006181	10.861597103997	15.141731458688	23.056473693650
##	PZA01313.2	PHM3631.47	PZA03604.1	PZA03603.1
##	69.183155836936	73.735970463463	123.995476728935	123.995481728936
##	PZA03605.1	PZA03606.1	PZA01995.2	PZA02663.1
##	123.995486728936	123.995491728937	128.031206385987	130.663657187693
##	PHM18513.156	PHM15868.56	PZB01111.8	PZA01456.2
##	131.602604222142	131.602609222143	132.842597000651	132.842602000652
##	PZA02320.1	PZA01241.2	PZA01005.1	PZA03196.1
##	137.554496772686	140.420883174706	143.071236191521	143.071241191522
##	PZA00647.9	PZA00866.2	PZA03713.1	PZA01141.1
##	143.071246191522	143.071251191523	143.704409056716	144.302173461295
##	PHM13687.14	PZA01089.1	PHM4341.42	PZA02219.2
##	144.599121472981	144.599126472982	144.599131472982	144.599136472983
##	PZA02128.3	PHM537.22	PZA01292.1	PZA02398.2
##	145.752860532405	146.280132702141	146.280137702142	146.280142702142
##	PHM18195.6	PZA01919.2	PZA00444.1	PZA00400.3
##	146.280147702143	146.280152702143	146.280157702144	146.280162702144
##	PHM12625.18	PZA00814.1	PHM12990.15	PZA00337.4
##	146.280167702145	147.425494120742	147.905355574444	147.905360574444
##	PZA01619.1	PZA00048.1	PZB00409.6	PZA01877.2
##	148.688914041644	148.688919041644	149.289110342085	150.443721224444
##	PHM2770.19	PZA02941.7	PZA00409.17	PZA00933.3
##	151.436518101816	151.436523101817	151.436528101817	151.436533101818
##	PZA01677.1	PZA01597.1	PZA03491.1	PZA02853.11
##	151.436538101818	151.918808281904	151.918822763585	151.918837218100
##	PZD00033.3	PHM3922.32	PZA00079.1	PZA02470.2
##	151.918851693757	152.602370607631	152.602375607631	152.602380607632
##	PHM3896.9	PZA01642.1	PZA00463.3	PZA02961.6
##	153.666634179617	153.666639179618	153.666644179618	153.666649179619
##	PHM15331.16	PZA02095.10	PHM3765.7	PZB01301.5
##	156.244976034172	159.216561169757	159.216566169758	159.216571169758
##	PZA01451.1	PZA01883.2	PHM2828.83	PZA02221.20
##	159.216621527138	159.216671885553	159.216722335108	189.217338707812
##	PZA02554.1			
##	189.217343707813			

```
plotRF(maize.bb2, chr = c, col.scheme = "redblue")
```

Pairwise recombination fractions and LOD score



```
(loglik.bb2[c] <- attr(maize.bb1$geno[[c]]$map, "loglik"))
```

```
## [1] -1226.465
```

Manual adjustments from orderMarkers() output

Before any manual adjustments to the marker orderings, we need to check which runs of `orderMarkers()` performed best for each linkage group. In order to do so, we should look at linkage group lengths, maximum space between two consecutive markers (a.k.a. gap) and their log-likelihoods. Higher log-likelihoods indicate better (i.e. more likely) maps.

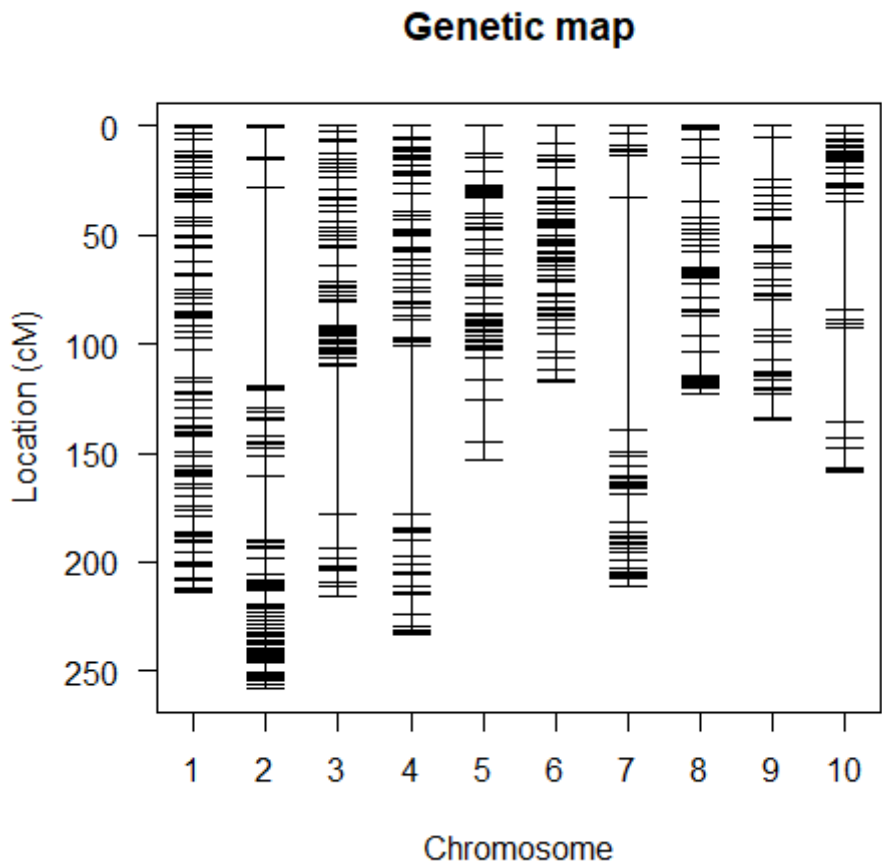
We combine the information from the function `summaryMap()` with the one gathered in the objects `loglik.bb1` and `loglik.bb1` from each respective run:

```
knitr::kable(cbind(summaryMap(maize.bb1), log.likelihood=c(loglik.bb1, sum(loglik.bb1))))
```

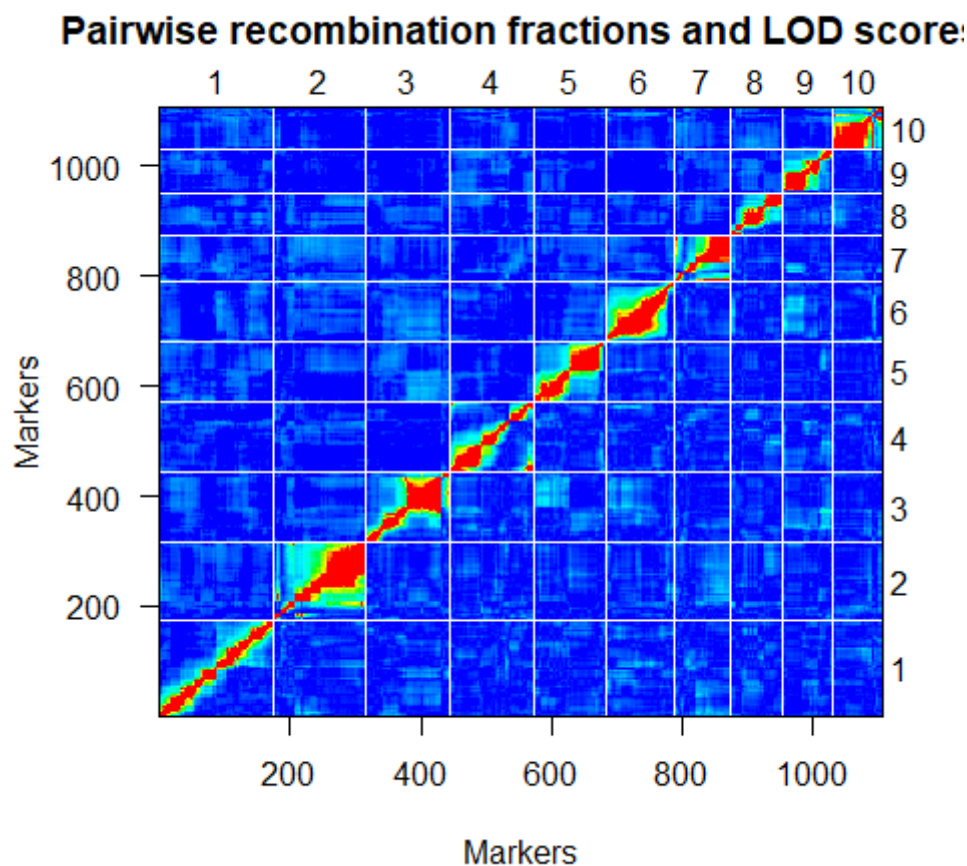
	n.mar	length	ave.spacing	max.spacing	log.likelihood
1	175	214.3473	1.231881	13.613340	-2709.611
2	139	258.3849	1.872355	91.225984	-2002.200
3	130	215.4406	1.670082	68.792722	-2026.878
4	127	232.8265	1.847829	76.995510	-2164.730
5	111	152.9898	1.390816	19.109285	-1786.557

	n.mar	length	ave.spacing	max.spacing	log.likelihood
6	106	116.9955	1.114243	8.640187	-1555.402
7	85	211.0671	2.512704	106.881307	-1351.731
8	78	122.7182	1.593743	17.002585	-1343.448
9	78	134.9499	1.752597	19.373227	-1451.878
10	77	158.3481	2.083528	49.453179	-1226.465
overall	1106	1818.0681	1.658821	106.881307	-17618.901

```
plotMap(maize.bb1)
```



```
plotRF(maize.bb1, col.scheme = "redblue")
```

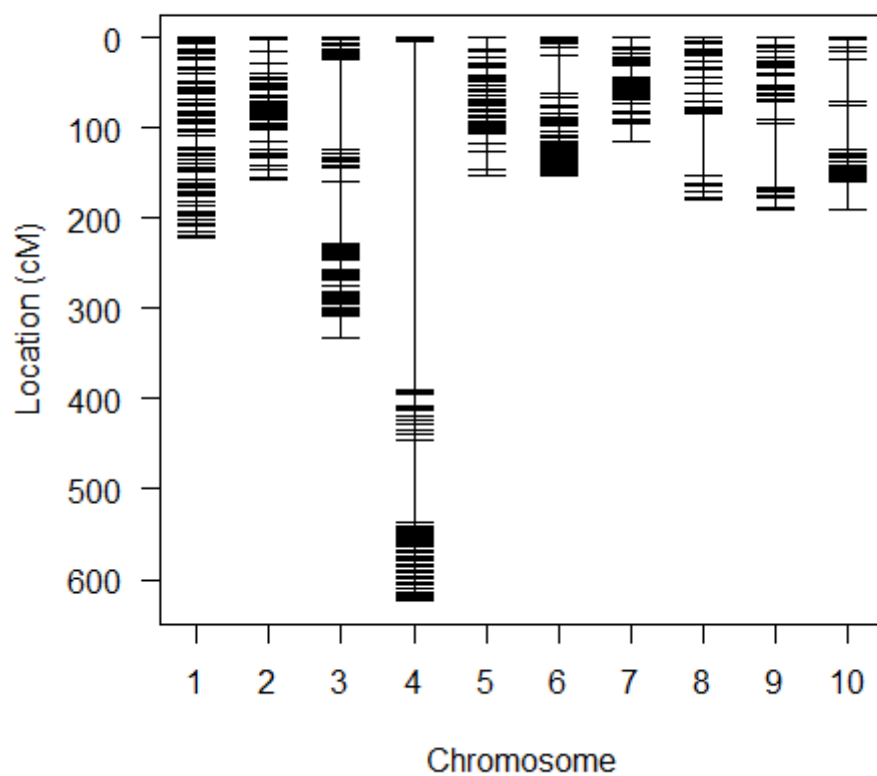



```
knitr::kable(cbind(summaryMap(maize.bb2), log.likelihood=c(loglik.bb2, sum(loglik.bb2))))
```

	n.mar	length	ave.spacing	max.spacing	log.likelihood
1	175	220.3090	1.266144	13.35636	-2728.051
2	139	155.8086	1.129048	13.84282	-1872.990
3	130	332.8403	2.580158	100.27726	-2180.483
4	127	624.0921	4.953112	385.62371	-2230.584
5	111	153.0849	1.391681	19.11073	-1770.147
6	106	151.6719	1.444494	42.58221	-1603.393
7	85	114.5735	1.363970	19.15392	-1308.089
8	78	179.0142	2.324860	68.64643	-1424.652
9	78	189.3461	2.459040	70.87404	-1445.710
10	77	189.2173	2.489702	50.25951	-1226.465
overall	1106	2309.9580	2.107626	385.62371	-17790.563

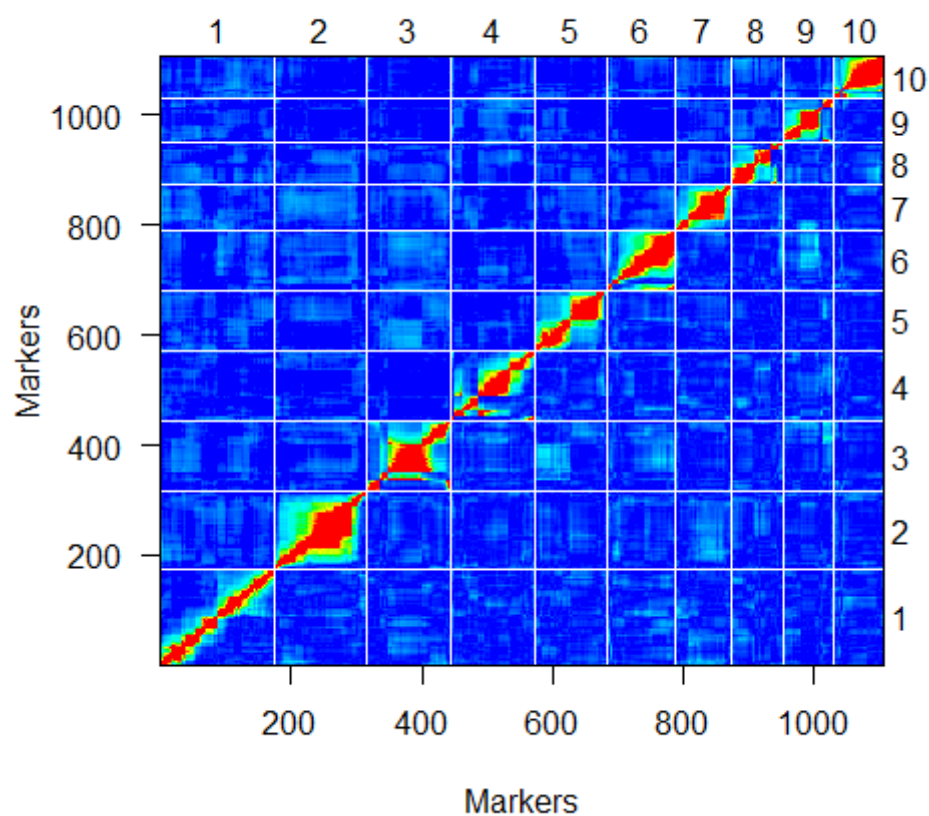
```
plotMap(maize.bb2 )
```

Genetic map



```
plotRF(maize.bb2, col.scheme = "redblue")
```

Pairwise recombination fractions and LOD score



```
save.image("maize_bb.RData")
```

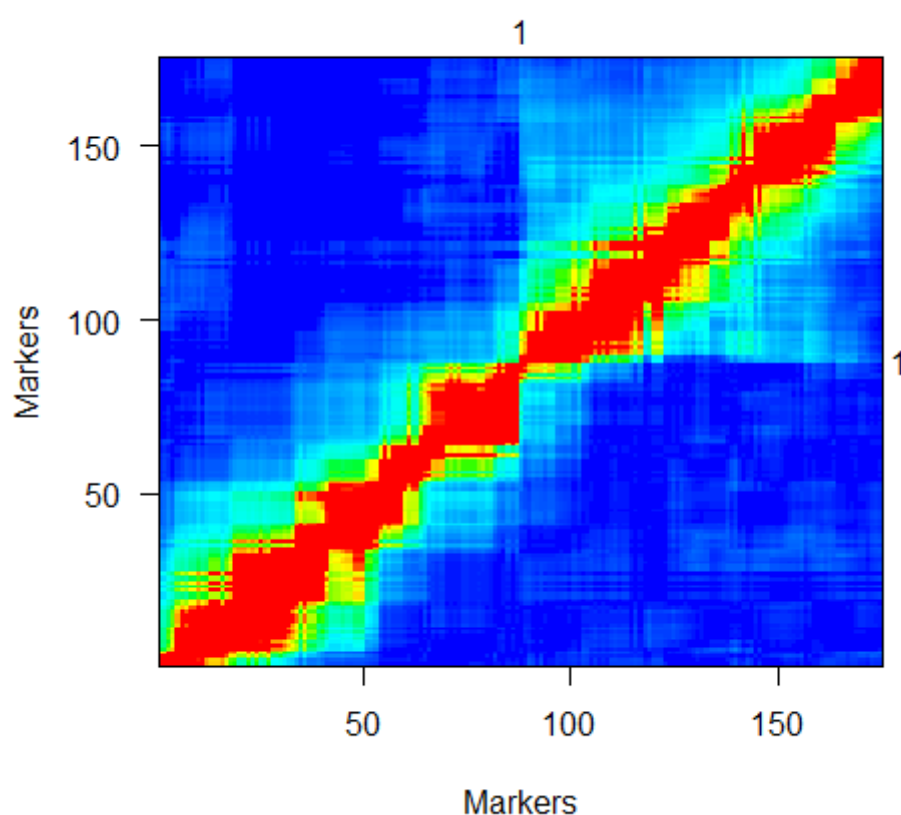
Now, we can select the best order so far, that we can still try to improve by making manual adjustments for each linkage group. As an strategy to improve marker ordering, we will find where the major gaps are, and fix it by moving the block of markers to its most likely position when looking at the heatmap.

Linkage group 1

From the map summary tables, we notice that from the first run of Branch-and-Bound (`maize.bb1`) provided a better map than the second run ($-2697 > -2711$) even though its length was slightly greater ($215 > 214$).

```
plotRF(maize.bb1, chr = 1, col.scheme = "redblue")
```

Pairwise recombination fractions and LOD score:



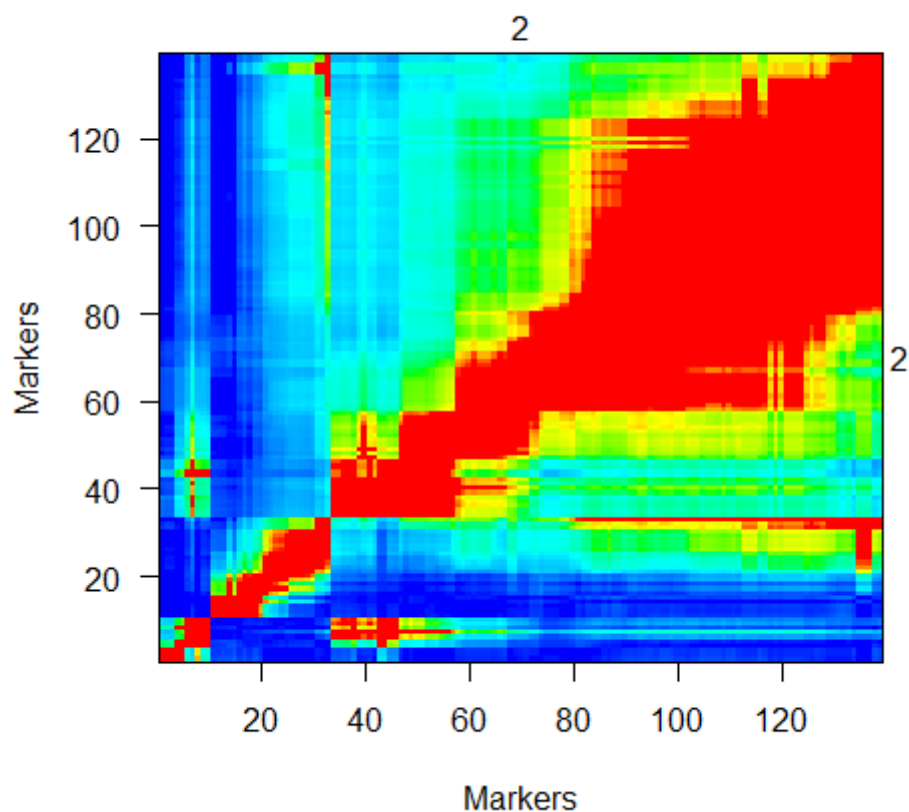
By looking at its heatmap, there seems to be small inversions, but no bigger inversions that can be easily corrected manually, so we keep it as is. Small inversions can be fixed by the function `ripple()`. However, this function is not well optimized in R/qtl for many markers, so we can avoid it at this point.

Linkage group 2

For linkage group 2, the first run also provided greater log-likelihood ($-2006 > -2016$), with a length of 259 cM and a gap as big as 91 cM, so we need to fix it. From the heatmap, we notice that there are three subgroups of markers, where the one in the middle seems misplaced. We locate the markers on each side by looking at the major gaps.

```
plotRF(maize.bb1, chr = 2, col.scheme = "redblue")
```

Pairwise recombination fractions and LOD score



```
(gaps <- tail(sort(diff(maize.bb1$geno[[2]]$map)), 2))
```

```
## PZA02513.1 PZA01983.1
## 28.86111 91.22598
```

```
match(names(gaps), names(maize.bb1$geno[[2]]$map))
```

```
## [1] 34 11
```

```
maize.bb1 <- switch.order(maize.bb1, chr = 2, order = c(1:10,35:139,34:11), error.prob = 0)
```

```
## Warning in est.map(cross, chr = chr, error.prob = error.prob, map.function =
## map.function, : Didn't converge!
```

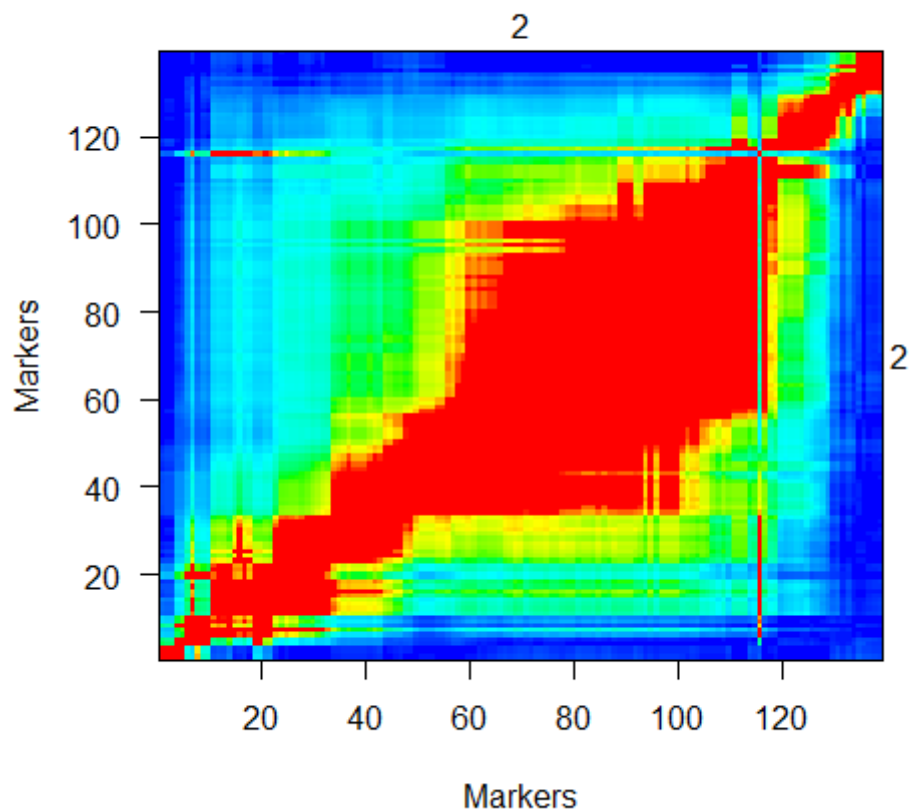
```
pull.map(maize.bb1, chr = 2)
```

##	PZA02480.1	PZA02769.1	PZA01060.1	PZA02390.1	PZA01140.1
##	0.0000000	0.2785523	0.2785523	16.3842941	17.6901802
##	PZA03167.5	PZA02068.1	PZA00836.1	PZA01259.1	PZA01680.3
##	31.3930827	31.3930828	31.6821116	31.6821116	31.9695403
##	PZA02060.1	PZA00395.2	PZA02667.1	PHM3512.186	PZA01265.1
##	50.4333489	50.7096405	50.7096406	51.2671779	54.0454575
##	PZA01142.4	PZB00765.1	PZA02820.17	PZA00545.26	PZA02015.11
##	54.0454576	54.0454576	54.3279875	59.1745817	59.1745817
##	PZA00963.3	PZA00980.1	PZA03024.16	PZA02426.1	PZA00652.17
##	59.1745818	59.1745818	67.9057171	70.6472722	70.7925674
##	PZA02411.3	PHM532.23	PZA00352.23	PZA03320.6	PZA02751.1
##	70.9378626	70.9379072	71.8759079	72.8020835	73.2062170
##	PZA03317.1	PZA02383.1	PZA03172.3	PZA03452.6	PZA01575.1
##	74.0297379	74.6416892	75.5714895	82.2269330	82.7898496
##	PZA02356.7	PZA02408.2	PZA02209.2	PZA03324.1	PHM5296.6
##	83.3239477	83.3239477	83.3239478	83.3239478	83.3239479
##	PZA02633.4	PHM1899.157	PZA01304.1	PZA03714.1	PZA03717.1
##	84.1692137	85.9594625	85.9594625	88.7041038	88.7041038
##	PZA01410.1	PZA00987.1	PZA00300.14	PZA02040.2	PZA00255.14
##	90.1701592	90.1701593	91.8083475	91.8083476	93.8562725
##	PZA02641.2	PZA01294.2.1	PZA03536.1	PZA01763.2	ae1.8.7
##	95.5126403	95.5126404	95.5126404	96.2892762	96.2892763
##	PZA02981.2	PZA00148.3	PZA01796.1	PZA01608.1	PZB01017.1
##	99.4110173	99.4110174	100.7842337	101.8065881	101.8065882
##	PZA00067.10	PZA02164.16	PZA01365.1	PZA00643.13	PZA00881.1
##	104.1380844	104.4518458	104.4518459	104.7675258	104.7675259
##	PZA03049.24	PZA00273.5	PZA01693.1	PZA02818.6	PZA01779.1
##	105.0832058	105.7418933	105.7418934	106.0762654	106.0762654
##	PZA01349.2	PHM5798.39	PZA02862.3	PZA00261.6	PZA01303.1
##	107.1012085	107.1012085	107.7345629	107.7345630	108.0481049
##	PZA03677.1	PZA02525.1	PZB01112.1	PZA01050.1	PHM3171.5
##	108.3616220	108.3616221	108.9957045	108.9957045	108.9957046
##	PZA00522.12.7	PZA03451.5	PHM1870.20	PZA02676.2	PZB00232.2
##	109.8538445	109.8538446	109.8538446	109.8538447	109.8538447
##	PZB01115.3	PZA00222.7	PHM4165.14	PZA00499.3	PHM3691.18
##	109.8538448	109.8538448	109.8538449	110.3026143	110.3026144
##	PZA00981.3	PZA01804.1	PZA00805.1	PZA01563.1	PZA02207.1
##	110.3026144	110.3026145	110.3026145	114.5470519	114.5470520
##	PHM4647.8	PHM12992.5	PZA00996.1	PHM16854.3	PZA01530.1
##	114.5470520	114.5470521	114.5470521	114.5470522	114.5470522
##	PZB00869.4	PZA00934.2	PZA02113.1	PZA00801.1	PHM565.31
##	114.8840728	115.2210934	115.2210934	115.2210935	116.9717417
##	PZA01427.1	PZA03274.4	PZA03226.3	PZA02792.26.25	PZA00517.7
##	116.9717418	118.6133867	118.6133868	118.6133868	120.3643121
##	PZA03092.7	PZA00112.5	PZA01327.1	PZA03578.1	PZA01523.1
##	122.6326074	122.6326075	122.6326075	122.6326076	122.6326076
##	PZA02513.1	PZA00985.1	PZB00079.4	PZA01284.6	PZA00865.1
##	165.0344229	200.7879093	200.7879093	201.0844667	210.9098221
##	PZA01925.1	PZA01371.1	PZA02029.21	PZB00094.1	PHM3137.17
##	211.2199414	211.3640117	211.5080820	211.5080821	215.4106281
##	PZA02753.1	PZB00054.3	PZA02462.1	PZA02653.12	PHM13122.43
##	216.5804004	216.5804005	217.7238342	220.4018743	228.7105578
##	PZA01570.1	PZA02316.22	PHM5359.10	PZA01438.1	PZA00818.1
##	229.5335731	232.5494069	232.5494070	234.1296962	243.4336433

##	PZA00191.5	PZA02367.1	PZA01887.1	PZA01983.1
##	243.4336433	244.6573964	244.6573964	244.9390873

```
plotRF(maize.bb1, chr = 2, col.scheme = "redblue")
```

Pairwise recombination fractions and LOD score



```
(loglik.bb1[2] <- attr(maize.bb1$geno[[2]]$map, "loglik"))
```

```
## [1] -2096.184
```

And we can keep doing this for every linkage group. However, another alternative delivers better ordering in general much more efficiently.

Multidimensional Scale (MDS) by MDSMap + MAPpoly

MDSMap implements the MDS algorithm, and MAPpoly has a nice wrapper function called `mds_mappoly`. This function only needs the recombination fraction matrix estimated by R/ql, and it returns a new order that can be used by `switch.order()` R/ql function to yield a newly ordered linkage group.

First, we need to install MAPpoly package and use the function below to get the order given by the MDS algorithm for a chosen linkage group. You need to run it first so it becomes available into R before you actually use it:

```
## # install.packages("mappoly") # you just need to run this one time
getMDSorder <- function(cross, chr){
  markers <- match(names(cross$geno[[chr]]$map), colnames(cross$rf))
  mat <- cross$rf[markers,markers]
  rec.mat <- lod.mat <- matrix(rep(NA, length(markers)^2), nrow = length(markers))
  colnames(rec.mat) <- colnames(lod.mat) <- rownames(rec.mat) <- rownames(lod.mat) <- colnames(mat)
  lod.mat[upper.tri(lod.mat)] <- mat[upper.tri(mat)]
  lod.mat[lower.tri(lod.mat)] <- t(lod.mat)[lower.tri(lod.mat)]; image(lod.mat)
  rec.mat[lower.tri(rec.mat)] <- mat[lower.tri(mat)]
  rec.mat[upper.tri(rec.mat)] <- t(rec.mat)[upper.tri(rec.mat)]; image(rec.mat)
  input.mat <- NULL
  input.mat$rec.mat <- rec.mat
  input.mat$lod.mat <- lod.mat
  mds.map <- mappoly::mds_mappoly(input.mat)
  mds.ord <- match(as.character(mds.map$locimap$locus), colnames(mat))
  return(mds.ord)
}
```

We'll create a new object called `maize.mds` which is a copy of our original cross object `maize`, so that we can update the ordering within `maize.mds` only. In addition, we'll create an empty object called `loglik.mds` to store the log-likelihood of the orderings obtained using MDS:

```
maize.mds <- maize
loglik.mds <- c()
```

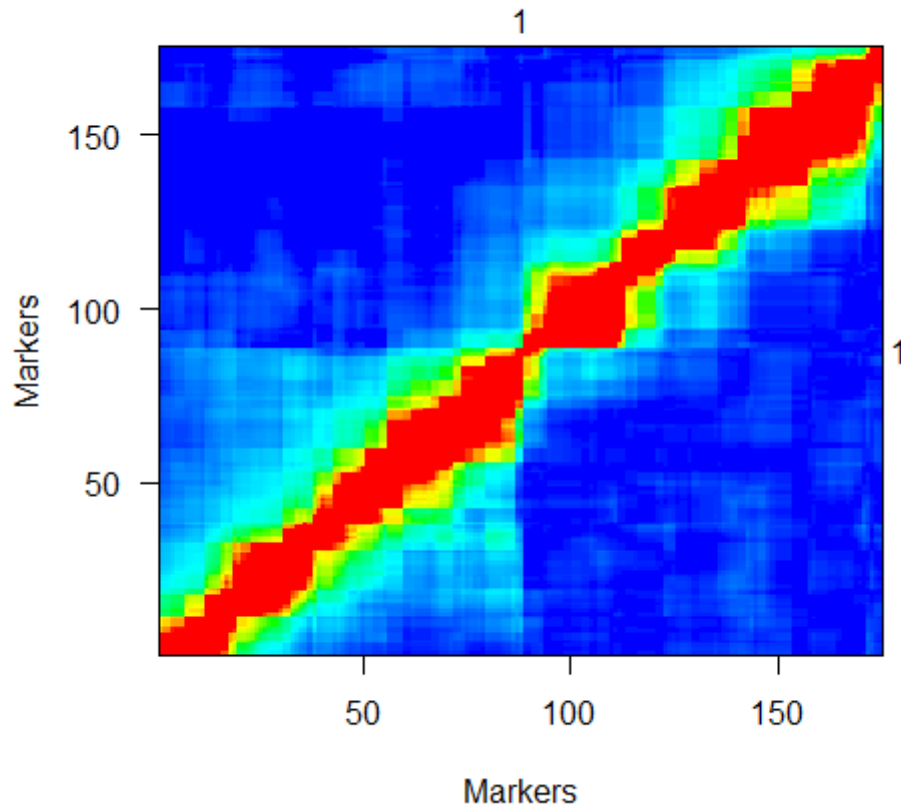
Linkage group 1

```
c <- 1
mds.ord <- getMDSorder(cross = maize.mds, chr = c)
```

```
## Stress: 0.66501
## Mean Nearest Neighbour Fit: 4.68811
```

```
maize.mds <- switch.order(cross = maize.mds, chr=c, order=mds.ord, maxit = 10000, tol=1e-5)
plotRF(maize.mds, chr=c, col.scheme = "redblue")
```

Pairwise recombination fractions and LOD score



```
pull.map(maize.mds, chr = c)
```


##	PHM7616.35	PZA00432.4	PZA01807.1	PZA01239.2	PZA00856.2
##	0.0000000	0.2916593	0.2917507	1.5132131	2.1278390
##	PZA00243.25	PHM1275.22	PZA00343.31	PZA01068.1	PZA01238.1.2
##	2.1278395	6.1107345	6.7254066	6.7254071	6.7254076
##	PHM9807.9	PZA02359.10	PZA00623.3	PZA00235.9	PZA00991.2
##	7.0230911	12.7206442	14.1695009	14.1695014	14.4495582
##	PZA00276.18	PZA00307.14	PZA02044.1	PZB01227.6	PZA03305.7.1
##	14.4495587	14.4495592	19.5245101	24.6254419	24.6254424
##	PZA03037.2	PZA00894.7	PZB01403.1	PHM18705.23	PZA00245.20
##	24.6254429	25.2071098	27.3137543	27.3137548	27.9824936
##	PZA02087.2	PZA01246.1	PZA00978.1	PZA03020.8	PZA02957.5
##	28.6646431	28.6646436	29.3469289	29.3469294	29.3469299
##	PZA03188.3	PZA00610.16	PZA02204.1	PZA01978.23	PZB00114.1
##	29.3469304	29.3469309	36.9218926	39.9373845	39.9373850
##	PZA02520.1	PZA00030.11	PZA02698.3	PZA02278.1	PZB00063.1
##	41.5994106	41.5994111	46.5573092	50.5270023	51.8478351
##	PZB00008.1	PZB00895.1	PZA03457.1	PZA02985.5	PHM5526.25
##	51.8478356	51.8478361	56.2918000	56.6324981	57.6930963
##	PZA01921.20.19	PZA00339.4	PZA01588.1	glb1.2	PHM14475.7
##	57.6930968	58.6704767	58.6704772	60.1964052	60.9869919
##	PHM3034.3	kip1.3	PZA02269.3.4	PZA03404.1	PHM16605.19
##	60.9869924	60.9869929	64.9203411	67.0406781	67.0406786
##	PHM4926.16	PZA03301.2	PZA03064.6	PZA00381.4	PZB01647.1
##	74.7099698	74.7099703	74.7099708	74.7099713	74.7099718
##	PZA03001.15	PZA02186.1	PZA00664.3	umc128.2	PHM4942.12
##	74.7099723	75.9900508	75.9900513	75.9900518	75.9900523
##	PHM2478.22	PZA02823.1	PZA00658.21	PHM5484.22	PZA02117.1
##	76.8978921	76.8978926	78.4813273	80.1717445	80.1717450
##	PHM15871.11	PZA03741.1	PHM6043.19	PZA03265.3	PZA01039.1
##	80.1717455	83.3593080	83.3593085	83.3593090	88.1219414
##	PZA02014.3	PZA03193.2	PHM12706.14	PZA03194.1	PZA01019.1
##	88.4364142	88.7542331	88.7542336	88.7542341	92.5553820
##	PZA01963.15	PHM5480.17	PZA01391.1	PZA00131.15	PZA01216.1
##	95.4073445	95.4073450	95.4073455	95.4073460	95.4073465
##	PZA03074.27	PZA02467.10	PZA00619.3	PZA03531.1	PZA00068.1
##	95.7279740	100.4066846	102.2561149	117.6983959	117.6983964
##	PHM1968.22	PZA02191.1	PZA00455.14.16	an1.5	PZA02135.2
##	117.6983969	117.6983974	122.9049520	125.5903291	128.4589076
##	PZA03200.2	PZA02577.1	PZA02741.1	PZA02070.1	csu1138.3.4
##	130.2088648	130.2088653	130.2088658	130.2088663	130.2088668
##	PZA01254.2	PZA00939.1	PZA02763.1	PZA02750.3	PHM9418.11
##	131.1870647	131.1870652	132.0858283	132.0858288	132.6795868
##	PZB01235.4	PZA00944.1.2	PZA03465.1	PZA03240.1.2	PZA01135.1
##	132.6795873	134.6551423	134.6551428	134.6551433	137.7316509
##	PZA00752.1	PZA01267.3	PHM5098.25	PZA03189.4	PZA00294.22
##	139.1589508	141.1499877	148.3857878	148.3857883	148.3857888
##	PZA01476.1	PZB01062.3	PZA03561.1	PZA01315.1	PZA02114.1
##	148.6969089	154.5935674	154.5935679	154.5935684	154.5935689
##	PZA02550.1	PZA02737.1	PZA03168.5	PZA02292.1	PHM4913.18
##	154.5935694	155.2346010	161.2703277	162.6828562	162.6828567
##	PZB00872.3	PZA03183.5	umc13.1	PZA00081.18	PZA03243.2
##	166.3267172	166.3267177	166.3267182	166.6332092	167.2813455
##	PZA03742.1	PZA02376.1	PHM3726.129	PZA00962.1	PZA00240.6
##	167.2813460	167.2813465	167.2813470	167.2813475	170.2657951
##	PZA02195.1	PZA02271.1	PZA02686.1	PZB01662.1	PZA01455.1

##	172.5910042	173.0026341	174.1255240	174.1255245	174.1255250
##	PZA02490.1	PZA01348.1	PZB02058.1	PZB01957.1	PHM4531.46
##	174.1255255	174.1255260	182.8918986	184.4538549	185.4143233
##	PHM3226.15	PZA02487.1	PHM13619.5	PZA00425.11	PZB00648.5
##	185.7302422	185.7302427	186.3203706	187.5499995	187.5500000
##	PZA02393.2	PZB00718.5	PZA01030.1	csu1171.2	PZA02094.9
##	187.5500005	187.5500010	187.5500015	187.5500020	187.5500025
##	PZA01497.1	PZA01652.1	PZA03551.1	PZA00887.1	PZA03521.1
##	187.5500030	187.5500035	193.5072734	195.8972517	198.9670928
##	PZA00566.5	PZA00106.10	PZA02284.1	PZA00731.7	PZA00447.8
##	198.9670933	198.9670938	198.9670943	198.9670948	198.9670953
##	PZA00175.2	PZA00528.1	PZA00181.2	PHM6238.36	PZA02372.1
##	201.0688409	201.0688414	201.0688419	202.3758041	203.3609214
##	PHM2244.142	PZA02032.1	PZA02129.1	PZA03613.1	PZA01271.1
##	204.9456788	211.0815229	214.0928428	216.8878893	217.1891882

```
(loglik.mds[c] <- attr(maize.mds$geno[[c]]$map, "loglik"))
```

```
## [1] -2625.751
```

Linkage group 2

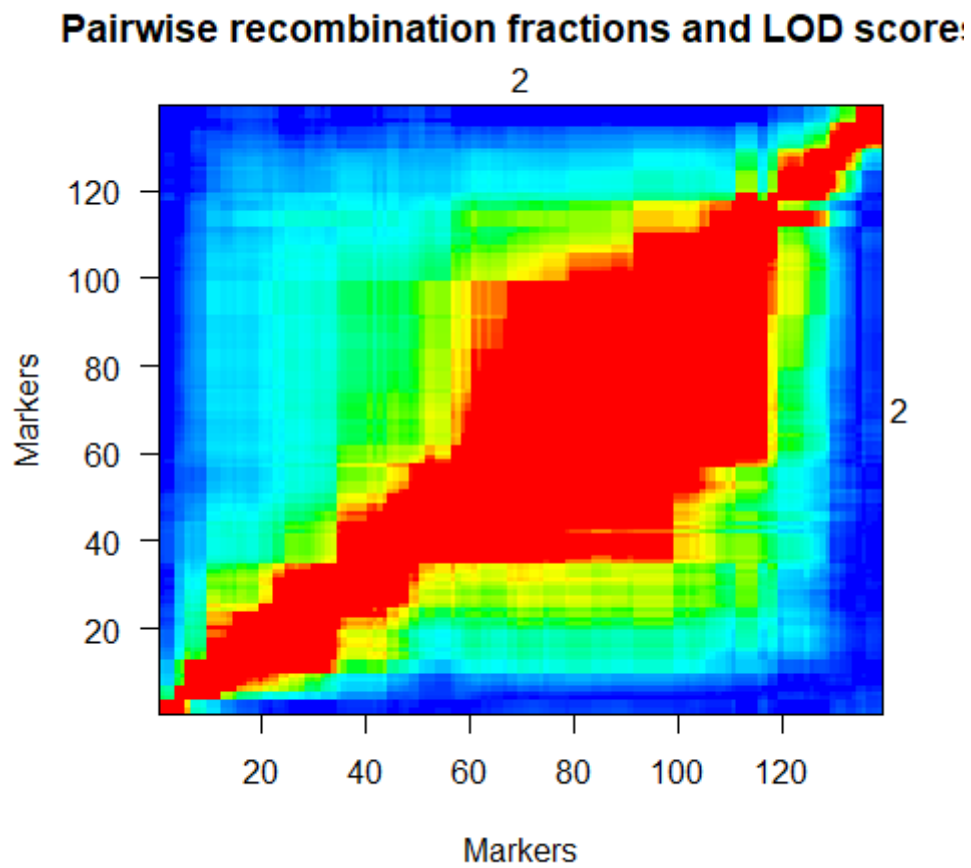
```
c <- 2
mds.ord <- getMDSorder(cross=maize.mds, chr=c)
```

```
## Stress: 0.40791
## Mean Nearest Neighbour Fit: 3.26572
```

```
maize.mds <- switch.order(cross = maize.mds, chr=c, order=mds.ord)
```

```
## Warning in est.map(cross, chr = chr, error.prob = error.prob, map.function =
## map.function, : Didn't converge!
```

```
plotRF(maize.mds, chr=c, col.scheme = "redblue")
```



```
pull.map(maize.mds, chr = c)
```

##	PZA02480.1	PZA01060.1	PZA02769.1	PZA02390.1	PZA01140.1
##	0.0000000	0.2735224	0.2735225	16.6816981	17.9868420
##	PZA00836.1	PZA01680.3	PZA01259.1	PZA03167.5	PZA02068.1
##	31.3430012	31.3430012	31.6438684	31.9688171	45.2468366
##	PZA00545.26	PZA02015.11	PZA00980.1	PZA00963.3	PHM3512.186
##	45.2468367	45.2468367	45.2468368	45.2468368	47.9371677
##	PZA00395.2	PZA02667.1	PZA02060.1	PZA02513.1	PZB00765.1
##	48.6518484	48.6518484	48.9639654	48.9639654	48.9639655
##	PZA01265.1	PZA02820.17	PZA01142.4	PZA03024.16	PZA00652.17
##	51.0352244	51.3545677	51.3545677	54.8510307	57.8301153
##	PZA02411.3	PHM532.23	PZA02426.1	PZA00352.23	PZA03320.6
##	57.8301154	57.8301154	58.0901966	58.5741377	59.3769046
##	PZA02751.1	PZA03317.1	PZA02383.1	PZA03172.3	PZA03452.6
##	59.7816292	60.6069034	61.2203877	62.1389605	68.7288665
##	PZA01575.1	PHM5296.6	PZA02209.2	PZA02356.7	PZA03324.1
##	69.2377613	69.7235204	69.7235205	69.7235205	69.7235206
##	PZA02408.2	PZA01304.1	PZA02633.4	PHM1899.157	PZA03717.1
##	69.7235206	72.4245536	73.7476561	75.1496813	77.6504578
##	PZA03714.1	PZA01410.1	PZA00987.1	PZA00300.14	PZA02040.2
##	77.6504578	79.1185064	79.1185064	80.7639010	80.7639010
##	PZA00255.14	ae1.8.7	PZA01763.2	PZA02641.2	PZA03536.1
##	82.7917561	84.4169358	84.4169358	85.0195697	85.0195697
##	PZA01294.2.1	PZA02981.2	PZA00148.3	PZA01796.1	PZA01608.1
##	85.0195698	89.0780714	89.0780714	90.4516674	91.4741061
##	PZB01017.1	PZA00067.10	PZA02164.16	PZA01365.1	PZA00881.1
##	91.4741062	93.8205515	94.1374918	94.1374918	94.4559249
##	PZA00643.13	PZA03049.24	PZA01693.1	PZA00273.5	PZA02818.6
##	94.4559249	94.7743553	95.4426755	95.4426755	95.7829297
##	PZA01779.1	PZA00261.6	PZA02862.3	PZA01303.1	PZA01349.2
##	95.7829298	96.1228949	96.1228949	96.4628648	96.7806711
##	PHM5798.39	PZA03677.1	PZA02525.1	PZB01112.1	PZA01050.1
##	96.7806711	96.7806712	96.7806712	97.4227221	98.2821076
##	PHM3171.5	PZB00232.2	PHM4165.14	PZA02676.2	PZB01115.3
##	98.2821077	98.2821077	98.2821078	98.2821078	98.2821079
##	PZA03451.5	PHM1870.20	PZA01804.1	PZA00222.7	PZA00522.12.7
##	98.2821079	98.2821080	98.2821080	98.2821081	98.2821081
##	PZA00805.1	PHM12992.5	PZA00499.3	PZA02207.1	PHM16854.3
##	98.7312172	103.0043253	103.0043254	103.0043254	103.0043255
##	PZA00981.3	PZA00996.1	PHM3691.18	PZA01530.1	PZA01563.1
##	103.0043255	103.0043256	103.0043256	103.0043257	103.0043257
##	PHM4647.8	PZB00869.4	PZA00801.1	PZA02113.1	PZA00934.2
##	103.0043258	103.3419859	103.6796495	103.6796496	103.6796496
##	PHM565.31	PZA01427.1	PZA02792.26.25	PZA03274.4	PZA03226.3
##	105.4075554	107.0293548	107.0293549	107.0293549	107.0293550
##	PZA00517.7	PZA00112.5	PZA01327.1	PZA03092.7	PZA00985.1
##	108.7504343	111.0262117	111.0262117	111.0262118	111.0262118
##	PZA01523.1	PZA03578.1	PZA01284.6	PZB00079.4	PZA00865.1
##	111.0262119	111.0262119	124.4653564	124.7511326	135.3360545
##	PZA02029.21	PZB00094.1	PZA01371.1	PZA01925.1	PHM3137.17
##	135.9721772	135.9721772	135.9721783	136.2255724	140.4977344
##	PZA02753.1	PZB00054.3	PZA02462.1	PZA02653.12	PHM13122.43
##	141.6699098	141.6699098	142.8104307	145.5042367	153.8991226
##	PZA01570.1	PHM5359.10	PZA02316.22	PZA01438.1	PZA00191.5
##	154.7036022	157.7023617	157.7023617	159.2539701	159.2539701

```
##      PZA00818.1      PZA01983.1      PZA01887.1      PZA02367.1
##      168.5562764      169.4656849      169.7541558      169.7541558
```

```
(loglik.mds[c] <- attr(maize.mds$geno[[c]]$map, "loglik"))
```

```
## [1] -1910.858
```

Linkage group 3

```
c <- 3
mds.ord <- getMDSorder(cross=maize.mds, chr=c)
```

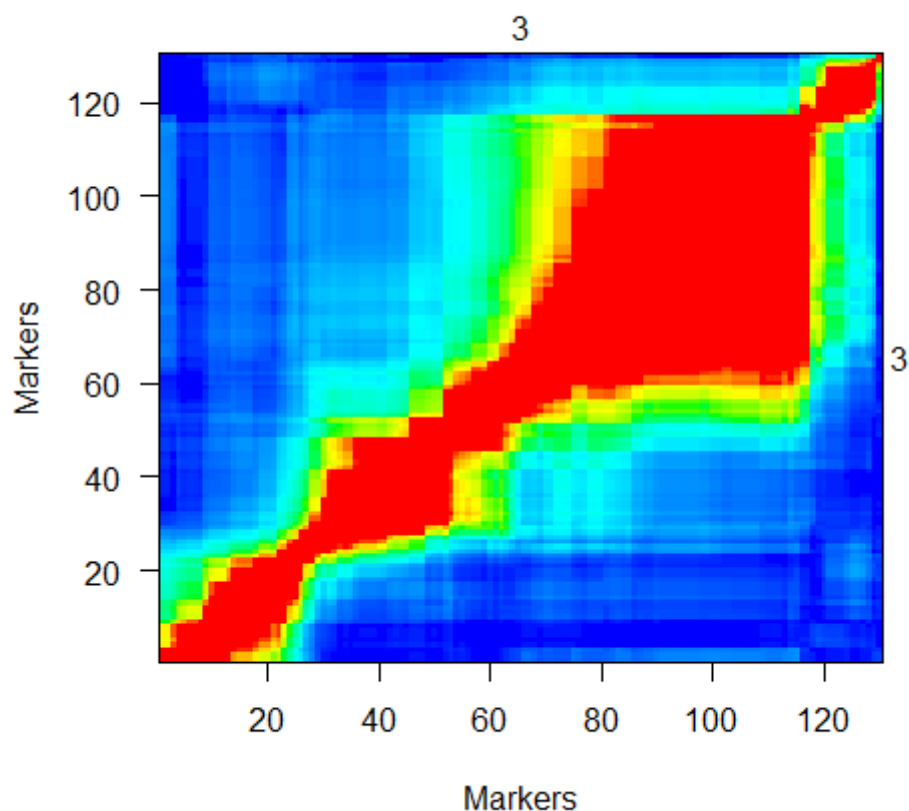
```
## Stress: 0.26315
## Mean Nearest Neighbour Fit: 3.65432
```

```
maize.mds <- switch.order(cross = maize.mds, chr=c, order=mds.ord)
```

```
## Warning in est.map(cross, chr = chr, error.prob = error.prob, map.function =
## map.function, : Didn't converge!
```

```
plotRF(maize.mds, chr=c, col.scheme = "redblue")
```

Pairwise recombination fractions and LOD score



```
pull.map(maize.mds, chr = c)
```

##	PZA00088.3	PZA02423.1	PHM2423.33	PZA02182.1	PZA01360.3
##	0.00000000	0.00000005	2.16810328	6.42705112	7.06111013
##	PHM3852.23	PZA01688.3	PZA00316.10	PZA00402.1	PZA03391.1
##	7.39506630	7.39506635	7.39506640	12.59508260	15.73265889
##	PZA00219.7	PHM2672.19	PZA02668.2	PZA02824.4	PZA02665.2
##	15.73265894	15.73265899	17.20425879	19.37566350	19.69003064
##	PZA01233.1	PZA02514.1	PHM3342.31	PZA01154.1	PZA00750.1
##	19.69003069	19.69003074	21.82807734	24.50969829	24.50969834
##	sh2.21	PZA03146.4	PZB01457.1	PZA02616.1	PZA02516.1
##	24.50969839	24.50969844	30.49704898	33.45265210	35.17943741
##	PZA00538.18.15	PZA02733.1	PZA03154.4	PZA00892.5	PZA01501.1
##	37.40943717	40.71768978	40.71768983	45.54779347	48.15629146
##	PZA02122.9	PZA01457.1	PZA00308.24	PZB01109.1	PZA01035.1
##	49.78655974	50.16313725	51.52018067	52.07702068	52.07702073
##	PZA03255.1	PHM13673.53	PZA03744.1	PZA03743.1	PHM824.17
##	53.45866455	54.08838967	54.08838972	54.08838977	54.08838982
##	PZA01228.2	PZA00494.2	PZA03647.1	zb27.1	PZA03191.1.4
##	54.08838987	56.32174985	56.97658188	57.66054114	57.66054119
##	PHM1675.29	PZA03735.1	PZA03733.1	PZA02654.3	PHM17210.5
##	57.66054124	57.66054129	57.66054134	65.40233271	65.71874848
##	PZA01962.12	PZA02212.1	PZA01726.1	PZA00783.1	PZA03032.19
##	65.71874853	65.71874858	73.21857399	75.22525645	75.52197322
##	PZA02402.1	PZD00027.2	PHM1959.26	PZA03073.28.26	PHM2885.31
##	75.83562133	77.63753797	77.63753802	77.63753807	79.56033954
##	PZA00186.4	PHM4621.57	PZA01396.1	PZA00667.2	PHM9914.11
##	79.91697350	79.91697355	82.32807356	83.83083170	86.23089505
##	PZA00828.2	PZB02179.1	PZA00948.1	PZA00827.1	PZA01934.6
##	86.99509384	86.99509389	86.99509394	89.39699292	89.86364938
##	PHM4955.12	PZB02044.1	PZB02122.1	PHM890.20	PZA00920.1
##	89.86364943	91.51339351	91.51339356	91.51339361	92.62753198
##	PZA02474.1	PHM1745.16	PZD00016.4	PZD00015.5	PZB02002.1
##	92.62753789	92.94624672	93.62992830	93.62992835	93.62992840
##	PZA00363.7	PZA02299.16	PZA00413.20.18	PHM15449.10	PZA03198.3
##	94.93943882	95.47112927	95.47112932	95.47112937	95.47112942
##	PZA02619.1	PZA00707.9	PZA02742.1	PZA02645.2	PHM5502.31
##	96.42429680	97.03625882	97.03625887	97.03625892	97.33243119
##	PZA02699.1	PZA03119.1	PZA02296.1	PZA02134.3	PZA00265.6
##	97.59201858	97.59716040	97.60229900	97.60743760	97.61257620
##	PZA00509.1	PZA02589.1	PHM15474.5	PZA01447.1	PZA00279.2
##	97.61771480	97.62285340	97.62798812	97.62798817	97.62798823
##	PZA00581.3	PHM15899.9	PZA03070.9	PZA00380.10	PZA00297.2
##	98.22574139	98.22574145	98.22574150	98.22574155	98.22574160
##	PHM13823.7	zb21.1	PZA01114.2	PZA00210.1.9	PZA03054.5
##	98.22574165	98.22574170	98.22574175	98.83292173	98.83292178
##	PZA01473.1	PZA00348.11	PZA02255.2	PHM2343.25	PZA02427.1
##	98.83292183	98.83292188	98.83292193	98.83292198	101.12737911
##	PHM4204.69	PHM4145.18	PZA00508.2	PZA01765.1	PZA02098.2
##	101.12737916	101.12737921	121.73129591	126.50890240	127.79091975
##	PZA00749.1	PZB01944.1	PZA03212.3	PZA03527.1	PHM12859.7
##	133.77563328	133.77563333	133.77563338	133.77563343	135.10690613
##	PZA00100.10	PZA02678.1	PZD00038.2	PZA02090.1	PZA00309.1
##	135.10690618	136.02168309	140.05629215	144.40536750	162.49245203

```
loglik.mds[c] <- attr(maize.mds$geno[[c]]$map, "loglik")
```

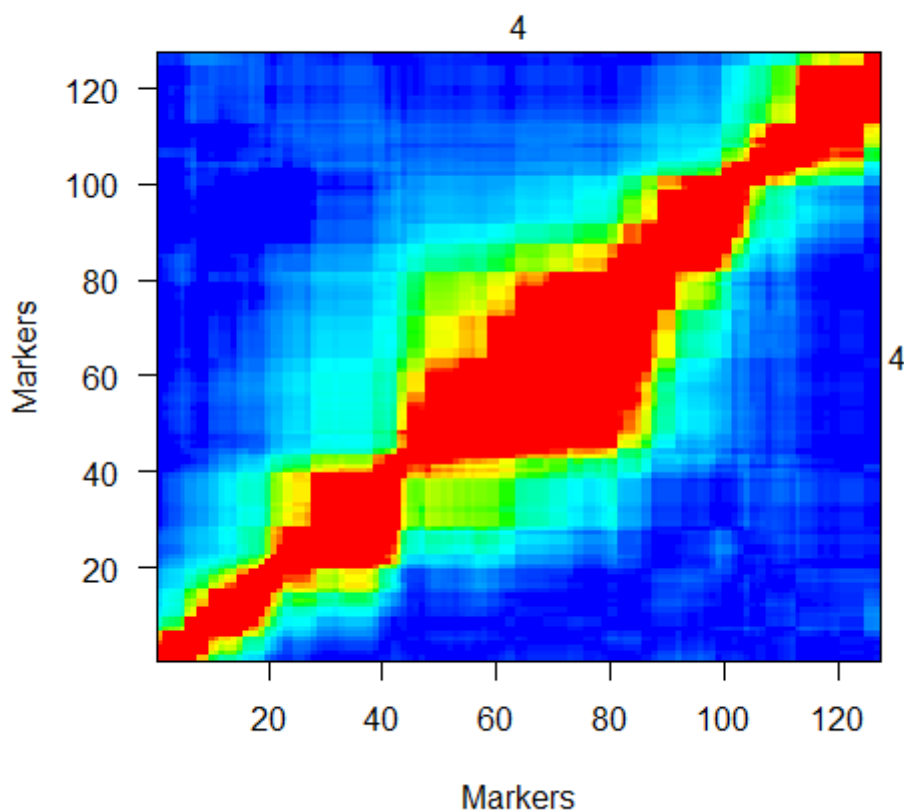
Linkage group 4

```
c <- 4  
mds.ord <- getMDSorder(cross=maize.mds, chr=c)
```

```
## Stress: 0.52258  
## Mean Nearest Neighbour Fit: 3.83517
```

```
maize.mds <- switch.order(cross = maize.mds, chr=c, order=mds.ord)  
plotRF(maize.mds, chr=c, col.scheme = "redblue")
```

Pairwise recombination fractions and LOD score



```
pull.map(maize.mds, chr = c)
```

##	PZD00022.5	PZA03577.1	PZA03321.4	PHM3094.23	PZA02170.1	PZA02727.1
##	0.000000	2.682006	2.682006	3.532523	4.131237	4.131237
##	PZA01352.5	PZA02266.3	PZA01895.1	PZB01013.1	PZA02564.2	PZA01991.3
##	12.772980	15.186685	15.186685	18.633796	18.950862	20.301147
##	PZA00163.4	PZA02453.1	PZA02012.7	PZA00527.10	PZA02418.2	PZA02471.5
##	20.301147	22.007830	26.405621	26.405621	28.375506	28.375507
##	PZA02680.1	PZA00804.1	PZA02456.1	PZA03602.1	PZA02964.7	PZB00772.7
##	31.660662	34.780097	39.042021	41.799708	45.309694	45.309694
##	PZA00390.7	PZA01885.2	PZA02077.1	PZA02329.2	PZA03165.1	PZB01103.2
##	46.410278	46.410278	47.429062	53.286728	53.286728	53.836340
##	PHM14412.4	PHM16125.47	PZA02731.1	PZA00803.3	PZA02017.1	PHM3668.12
##	53.836340	53.836340	55.039279	55.039279	55.039279	55.039280
##	PHM7953.11	PZA00824.2	PHM3055.9	PZA02890.4	PZA03529.1	PZA00755.2
##	55.039280	55.354452	55.354452	60.458250	62.275257	64.808626
##	PZA01735.1	PZA03184.2	vdac1a.1	PZA03659.1	PZA00224.4	PZA03644.1
##	64.808626	73.244181	78.131942	78.131942	78.427456	81.972058
##	PZA00637.6	PZA00495.5	PZA00515.10	PZA01638.1	PZA03692.1	PZA02371.6
##	81.972058	81.972058	81.972058	81.972058	82.280954	82.934705
##	PZA01321.1	PZA02465.1	PZA01232.1	PZA02939.10	PZA01280.2	PZA01537.2
##	82.934705	83.968660	83.968660	83.968660	83.968660	83.968660
##	PZA03211.6	PZA02626.1	PZA00029.17	PHM3626.3	PZA00485.2	PHM13360.13
##	86.334524	86.975373	86.975373	88.983791	88.983791	89.352295
##	PZA02549.3	PHM4880.179	PZA01902.1	PHM10321.11	PHM3457.6	PZA02279.1
##	89.352295	89.352295	89.741265	89.741265	89.741265	89.741265
##	PZA00635.7	PZA03629.1	PZA02168.1	PZA01820.1	PZA02450.1	PZA02774.1
##	91.335092	92.907389	92.907389	93.250001	93.250001	93.250001
##	PZB00183.4	PHM10404.8	PZA02496.1	PZA01993.7	PZA02378.7	PZA02058.1
##	93.836163	94.542921	94.542921	98.724183	100.582551	100.582551
##	PZA01336.1	PHM4586.12	PZA01374.1	PZA03568.1	PHM1962.33	PZA02080.1
##	100.582551	100.582551	100.582551	106.056479	106.056479	106.056479
##	PZA01755.1	PZA03142.5	PZA01879.1	PZA00590.1	PHM6111.5	PZA03634.1
##	106.056480	110.843391	112.869608	113.221711	113.221711	113.221712
##	PZA03228.4	PZA00497.4	PZA02417.2	PZA03559.1	PZA02337.4	PZA01753.1
##	113.873463	114.916511	116.737234	116.737234	116.737234	127.894936
##	PZA00108.4	zfl2.9	PHM5822.15	PZA02272.3	PZB00901.3.4	PZA03699.1
##	128.812230	131.489501	136.899168	137.845622	138.144686	142.433986
##	PZA03747.1	PZA01935.10	PZA02081.1	PZA02208.1	PZA00613.22	PZA01211.1
##	142.433986	145.664765	145.939220	146.224154	153.741844	153.741844
##	PZA00172.12	PZB01233.1	PZA02175.1	PZA02681.8	PZA02264.5	PZA00902.1
##	153.741844	153.741844	157.074642	157.074642	158.089741	158.089741
##	PHM13440.13	PHM1511.14	PZA00525.17	PZA02133.10	PZA00365.2	PZA00680.3
##	159.867562	159.867562	159.867563	159.867563	166.532756	166.532756
##	PHM5817.15					
##	166.532756					

```
loglik.mds[c] <- attr(maize.mds$geno[[c]]$map, "loglik")
```

Linkage group 5

```
c <- 5
mds.ord <- getMDSorder(cross=maize.mds, chr=c)
```



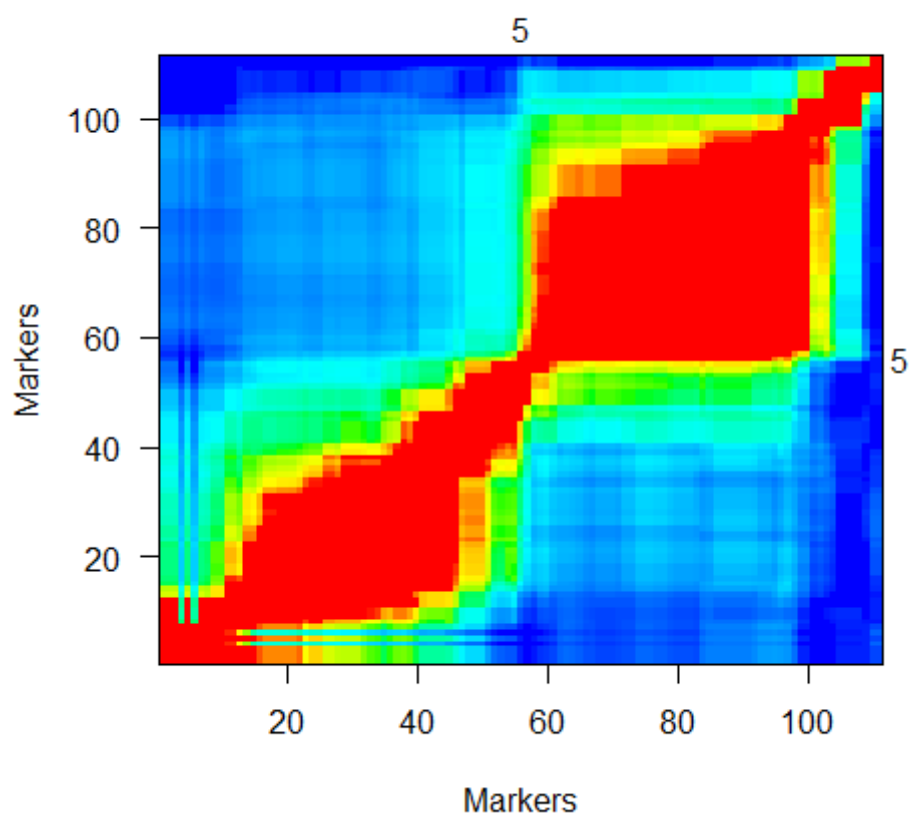
```
## Stress: 0.37657  
## Mean Nearest Neighbour Fit: 3.1279
```

```
maize.mds <- switch.order(cross = maize.mds, chr=c, order=mds.ord)
```

```
## Warning in est.map(cross, chr = chr, error.prob = error.prob, map.function =  
## map.function, : Didn't converge!
```

```
plotRF(maize.mds, chr=c, col.scheme = "redblue")
```

Pairwise recombination fractions and LOD score!



```
pull.map(maize.mds, chr = c)
```

##	PHM4125.11	PZA02239.12	PZA03598.1	PZA00282.19	PZA01905.12
##	0.00000000	0.00000005	0.00000010	0.00000015	0.00000020
##	PZA00682.17.2	PZA03322.5.3	PHM2100.21	PHM5665.26	PZA00529.4
##	0.00000025	0.00000030	14.83528629	16.45814809	16.45814814
##	PHM5599.20	PZA02585.2	PZA00513.1	PZA02151.3	PZA00694.6
##	16.45814819	16.45814824	23.25660985	23.25660990	26.66361991
##	PZA00521.3	PZA00878.2	PZA01367.2	PZA03155.3	PZA00636.7
##	27.34246955	29.26920310	29.26920315	29.26920329	29.26920343
##	PZA00155.1	PZA02479.1	PZB01021.1	PZA03081.1	PZA01332.2
##	29.58861372	29.91822412	30.99034864	31.28837711	31.82391317
##	PZA02614.2	PZA02421.1	PZA02779.1	PZA01810.2	PZA01566.1
##	33.54988818	33.54988823	33.54988828	33.54988833	33.54988838
##	PZA03205.1	PZA01790.1	PZA00193.2	PHM4348.16	PZA00332.5
##	33.54988843	35.41497041	36.13210875	36.13210880	39.10630735
##	PZB01461.1	PZA00344.10	PZA00941.2	PZA01954.1	PZA01766.1
##	40.23402589	41.06877787	45.54652810	45.54652815	46.26109123
##	PZA02289.2	PZA02194.1	PHM3637.14	PZA01976.9	PZD00030.2
##	49.97224294	49.97224299	49.97224304	49.97224309	52.39586156
##	PZA01187.1	PZA03275.4.1	PZA01658.1	PZA01477.3	PZA01681.1
##	52.39586161	57.31708684	57.31708689	57.31708694	57.31708699
##	PZA00271.1	PHM3155.14	PZA01289.1	PZA00453.2	PZA03116.1
##	62.10538711	64.49442056	64.79907079	66.42940167	67.35218529
##	PZA01926.1	PZA00057.2	PZA02992.15	PZA02982.7	PZA03152.3
##	72.91266583	76.31970508	80.91537344	81.97665259	81.97665264
##	PZA02147.1	PZA03459.1	fea2.3	PZA02027.1	PZA00704.1
##	83.24133911	84.89300559	84.89300564	84.89300569	84.89300574
##	PZA03409.1	PZB00093.7	PZA03203.2	PZA03231.1	PZA00104.1
##	85.50090098	85.50090103	85.80608560	85.80608565	85.80608570
##	PZA03564.1	PZA00218.1	PZA02767.1	PZA03254.1	bt2.7.4
##	85.80608575	85.80608580	86.82834397	86.82834402	86.82834407
##	PZA03587.1	PZA03597.1	PZA03270.2	PHM1307.11	PHM14055.6
##	86.82834412	86.82834417	86.82834422	87.00199817	87.19621666
##	PZA00726.8.10	PZA01759.1	PZA00445.22	PZA01751.2	PZA03385.1
##	87.19621671	87.19621676	87.49452650	89.94033352	90.32293616
##	PZA01713.4	PHM5572.19	PHM13623.14	PZA01106.3	PZA03247.1
##	91.65113222	91.65113227	91.65113232	91.65113237	91.65113242
##	PZA00541.1	PZA02705.1	PZA02457.1	PHM15427.11	PZA02002.1
##	91.65113247	92.48352746	92.48352751	92.48352756	94.42360649
##	PZA03048.18	PZA01422.3	PZA00139.4	PZA02385.6	PHM8527.2
##	95.42220615	96.74567590	100.00899749	110.95259474	110.95259479
##	PZA01122.1	PZA02138.1	PZA02358.1	PZA00975.1	PHM2438.28
##	110.95259484	111.20586620	121.22252402	121.22252407	121.22252412
##	PHM3301.28	PZA00436.7	PZA00683.4	PHM1184.26	PZA02509.15
##	121.22252417	121.22252422	121.22252427	143.90383557	153.08362903
##	PZA03227.1				
##	153.08362908				

```
loglik.mds[c] <- attr(maize.mds$geno[[c]]$map, "loglik")
```

Linkage group 6

```
c <- 6
mds.ord <- getMDSorder(cross=maize.mds, chr=c)
```

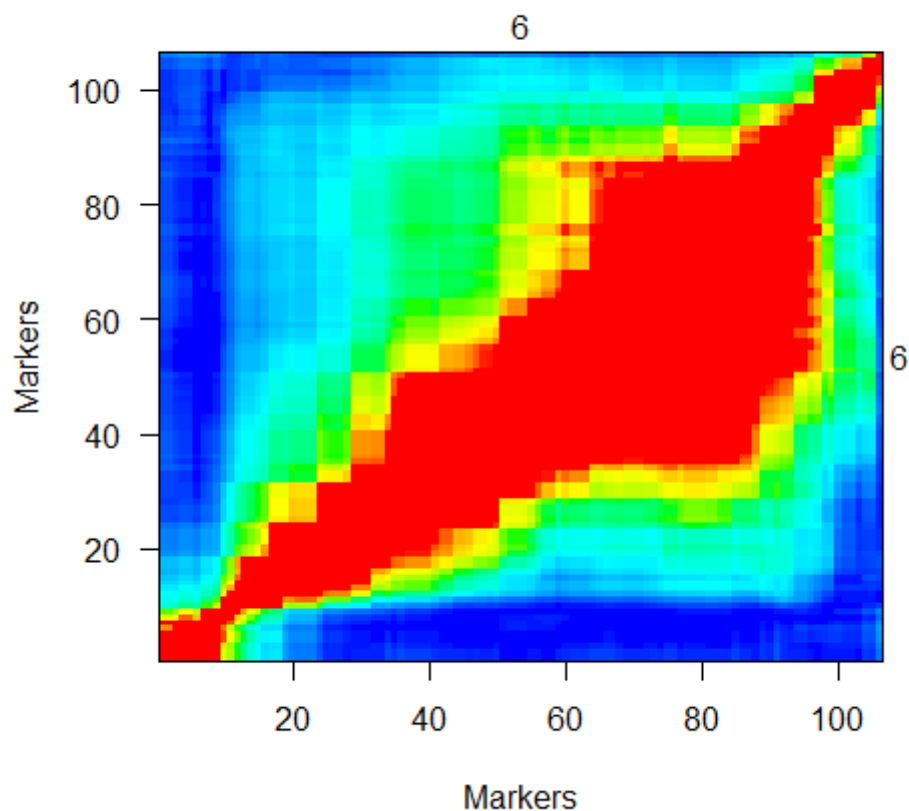
```
## Stress: 0.16427  
## Mean Nearest Neighbour Fit: 3.58911
```

```
maize.mds <- switch.order(cross = maize.mds, chr=c, order=mds.ord)
```

```
## Warning in est.map(cross, chr = chr, error.prob = error.prob, map.function =  
## map.function, : Didn't converge!
```

```
plotRF(maize.mds, chr=c, col.scheme = "redblue")
```

Pairwise recombination fractions and LOD score!



```
pull.map(maize.mds, chr = c)
```

```
## PZA00071.2 PZA02281.3 PHM5019.59 PZA01290.1 PHM2749.10
## 0.00000000 0.00000005 0.63575193 4.79661119 4.79661124
## PZA00760.1 PHM14104.23 PZA00189.23 PHM14046.9 PZA01964.29
## 4.79661129 4.79661134 10.46629996 12.83389299 21.84462564
## PZA00904.1 PHM4786.9 PZA01316.1 PZA00020.5 PZA00362.1
## 24.99699143 29.22125419 30.67291934 32.03190287 33.40942373
## PZA00460.3.8 PHM1834.47 PZA02746.2 PZA00675.1 PZB00811.1
## 34.86242766 34.86242771 34.86242776 40.84165820 41.82654088
## PHM15623.10 PHM3465.6 PZA00706.16 PZA00838.2 PZA01741.1
## 41.82654093 41.82654098 41.82654103 41.82654108 47.49346266
## PZA03698.1 PHM15278.6 PHM12749.13 PZA00951.1 PZA03182.5
## 47.49346271 47.49346276 48.08604264 53.77576972 53.77576977
## PHM4757.14 PZA03650.1 PZA03651.1 PZA00429.1 PZA02011.1
## 53.77576982 53.77576987 53.77576992 55.34042230 57.73723752
## PZA00090.1 PHM448.23 PZA00766.1 PZA00770.1 PHM4203.11
## 58.05076684 58.05076689 58.05076694 58.05076699 58.05076704
## PZA02033.1 PZA01787.1 PHM14152.18 PHM5468.25 PZA01049.1
## 59.32168623 60.82453644 60.82453649 60.82453654 60.82453659
## PZA03612.2.1 PZA00118.1.5 PHM10525.9.11 PZA01038.1 PZB02155.1
## 60.82453664 61.40938151 61.70246184 61.70273851 62.02630762
## PHM3993.28 PZA03639.1 PZA03638.1 PZA03637.1 PZA02748.3
## 64.93688395 65.27535233 65.27535238 65.27535243 65.27535248
## PHM934.19 PZA03012.7 PZA01072.1 PZA02566.1 PZA01972.14
## 66.63438426 67.29921145 67.29921150 67.97644093 69.87021503
## PZA03579.1 PZA00739.1 PHM4134.8 PZA02019.1 PZA03135.1
## 69.87021508 69.87021513 69.87021518 72.78089606 73.09957648
## PZA00908.2 PHM3978.104 PZA02683.1 PZA02522.1 PZA01297.1
## 73.41836692 73.41836697 75.08086703 75.08086708 75.08086713
## PZA01363.2 PZA01301.1 PZA01470.1 PHM11114.7 PHM2350.17
## 75.08086718 75.08086723 76.05588438 76.37407752 77.01730659
## PZA01196.2 PZA01960.1 PZA01209.1 PZA02203.1 PZA00498.5
## 77.01730664 77.01730669 77.01730674 77.01730679 77.01730684
## PZA00793.2 PZA00379.2 PZA01257.1 PZA00717.15 PZA00758.1
## 77.01730689 77.01730694 77.01730699 77.01730704 79.50614143
## PZA01186.1 PHM6428.11 PHM1978.111 PZA02454.2 PZA02528.1
## 81.67334984 81.67334989 81.67334994 84.23811131 84.23811136
## PZA01357.2 PZA02955.3 PZA01079.1 PHM9695.8 PZA01951.1
## 85.76999900 86.82239945 87.44768948 91.10219547 91.10219552
## PZA01691.1 PZA03178.1 PZA01601.1 PZA00416.7 PHM4711.14
## 92.11363700 101.49531838 101.49531843 101.82818413 104.53860963
## PZA00368.1 PZA00058.1 PZA01623.3 PZA01600.2 PZA02174.2
## 104.53860968 104.53860973 107.81072332 113.16989553 113.16989558
## PZA02388.1
## 122.04076928
```

```
loglik.mds[c] <- attr(maize.mds$geno[[c]]$map, "loglik")
```

Linkage group 7

```
c <- 7
mds.ord <- getMDSorder(cross=maize.mds, chr=c)
```

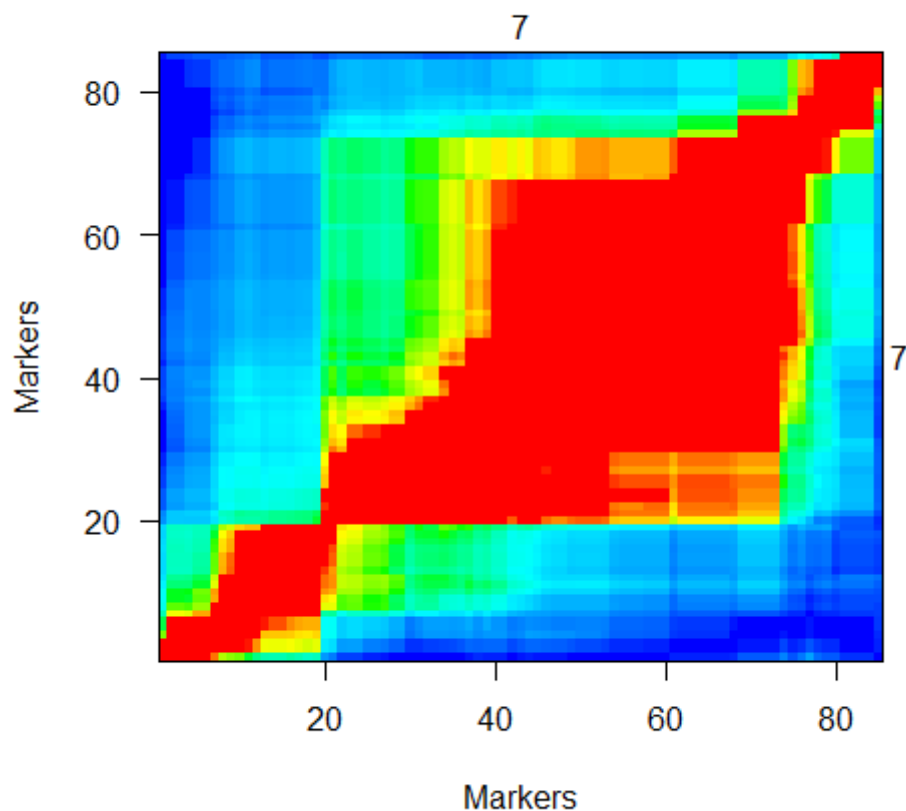
```
## Stress: 0.36936  
## Mean Nearest Neighbour Fit: 3.4612
```

```
maize.mds <- switch.order(cross = maize.mds, chr=c, order=mds.ord)
```

```
## Warning in est.map(cross, chr = chr, error.prob = error.prob, map.function =  
## map.function, : Didn't converge!
```

```
plotRF(maize.mds, chr=c, col.scheme = "redblue")
```

Pairwise recombination fractions and LOD score!



```
pull.map(maize.mds, chr = c)
```

##	PZA03573.1	PHM1911.173	PHM13681.12	PZA00708.3	PHM15445.25
##	0.00000000	0.00000005	0.00000010	11.20197116	12.88250325
##	PZA00832.1	PHM4303.16	PZA00912.2	PZA02381.1	PZA00511.3
##	12.88250330	18.16499362	22.24890550	23.38873060	23.38873065
##	PZA01715.1.2	PHM4604.18	PZA00323.3	PZD00055.1	PZA02197.1
##	25.49768017	26.10115099	27.64814226	27.64814280	27.64814285
##	PZB00221.3	PHM11226.13	PHM816.29	PZA01369.1	PZA02252.2
##	28.01310654	28.01311472	28.32332977	30.84669964	45.95587836
##	PHM1766.1	PZA01096.1	PZA02235.14	PZA03671.1	PZA03670.1
##	50.18383343	50.18383348	52.26446247	52.26446252	52.26446257
##	PZA02111.1	PZA02397.1	PHM4905.6	PZA01866.1	PHM3330.25
##	52.26446262	52.55618761	53.13585231	53.13585236	54.75997903
##	PZA00213.19	PZA00060.2	PZA00840.1	PZA01819.1	PZA02325.4
##	55.38947169	55.75152368	55.75152373	58.29884779	59.66322405
##	PZA02613.1	PZA03235.1	PZA03470.1	PZA00015.5	PZB01358.1
##	59.66322410	63.55130698	63.55130703	63.94124801	66.91219660
##	PZA00152.1	PZA00225.8	PZB01899.1	PZA01281.2	PZA00947.1
##	66.91219665	66.91219670	66.91219675	67.74971749	69.11934161
##	PZA03596.1	PZA02545.1	PZA01062.1	PZA01861.1	PZA01791.2
##	69.11934166	69.11934171	69.11934176	69.43237395	69.43237400
##	PZB00761.1	PZA00925.2	PZA03057.3	PZB00959.1	PZA00693.3
##	69.43237405	69.43237410	70.04849226	70.66464257	70.66464262
##	PZA02878.13	PZA03036.6	PZB00014.1	PZA00589.10	PZA03469.1
##	70.66464267	70.66464272	70.66464277	70.66464282	70.66464287
##	PZA02648.2	PZA01999.3	PZB00540.3	PZB01110.6	wx1.1
##	71.78371316	71.78371321	71.78371326	71.78371331	71.78371336
##	PZB00547.3	PZB00544.2	ZHD1.1	PZA03058.22.21	PHM9374.5
##	71.78371341	71.78371346	76.04812730	86.42927149	86.42927154
##	PZB01042.2	PZA00860.1	zb7.2	PZA03416.7	PZA02702.1
##	86.42927159	86.42927164	86.42927169	86.42927174	89.61240314
##	PHM5181.10	PZA02344.1	PZA01386.3	PZA00466.1	PZA01195.3
##	95.74276209	95.74276214	98.44685177	98.75038035	100.99145355
##	PHM1218.6	sh1.12.11	PZA00285.3	PZA01799.1.2	PHM3925.79
##	123.72775118	123.72775123	123.72775128	123.72775133	123.72775138

```
loglik.mds[c] <- attr(maize.mds$geno[[c]]$map, "loglik")
```

Linkage group 8

```
c <- 8
mds.ord <- getMDSorder(cross=maize.mds, chr=c)
```

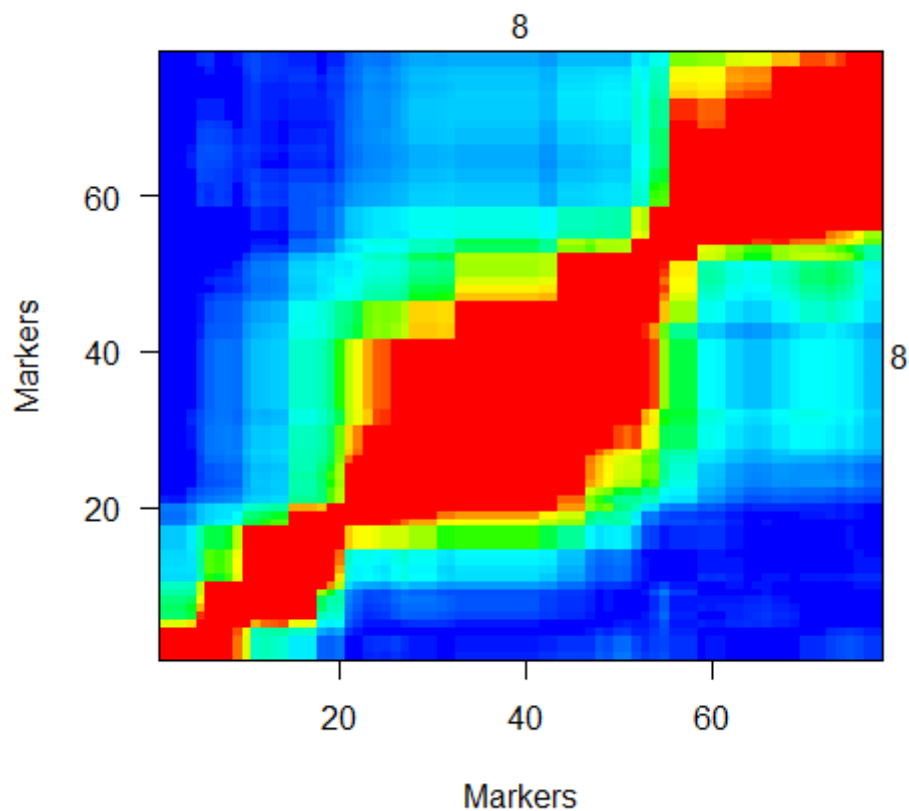
```
## Stress: 0.56341
## Mean Nearest Neighbour Fit: 3.98981
```

```
maize.mds <- switch.order(cross = maize.mds, chr=c, order=mds.ord)
```

```
## Warning in est.map(cross, chr = chr, error.prob = error.prob, map.function =
## map.function, : Didn't converge!
```

```
plotRF(maize.mds, chr=c, col.scheme = "redblue")
```

Pairwise recombination fractions and LOD score



```
pull.map(maize.mds, chr = c)
```

```
## PZA01875.1 PZA02815.25 PHM4468.13 PZA00910.1 PZA02141.1
## 0.0000000 0.2719726 0.2719727 3.3214799 10.4642071
## PZB01222.1 PZA02688.2 PZA00821.1 PZA00889.2 PHM7922.8
## 16.0443384 16.7435413 17.4126199 19.6362149 28.3838017
## PZA01468.1 PZA00266.7 PHM4503.25 PZB01569.7 PHM4748.16
## 28.3838018 28.6658355 28.9859595 28.9861794 42.3346096
## PHM5794.13 PZA00223.4 PZA03027.12 PZA01462.1 PZA01672.1
## 42.3346097 42.3346097 42.3346098 45.0285301 47.6759220
## PZA02436.1 PZA01342.2 PZA01144.1 PHM11985.27 PZA02247.1
## 55.9794179 56.8531555 57.9402256 58.9559002 58.9559002
## PZA03102.9 PZB01308.1 PZA02673.1 PZB00942.1 PZA02148.1
## 59.7901478 60.8125522 63.3182412 63.3182412 63.3182413
## PZA02478.7 PZA02187.1.2 PZA02328.5 PZA01591.1 PZA01884.1
## 63.3182413 63.3182414 69.6752119 69.6752120 69.6752120
## PZA01552.1 PZA01618.2 PZA00473.5 PZB00414.2 PZA02262.3
## 69.6752121 69.6752121 69.6752122 69.6752122 69.6752123
## PZA00357.19 PZA01729.1 PHM13020.10 PZA00571.1 PZA01055.1
## 69.6752123 69.6752124 69.6752124 69.6752125 69.6752125
## lac1.3 PZA00382.17 PZA01736.1 PZA01589.2 PZA02396.14
## 69.6752126 75.8318339 76.7424864 77.1896704 78.5334511
## PZA02048.2 PZA01029.1 PZA03461.1 PZB01658.1 PZA00942.2
## 78.5334511 78.5334512 88.4004717 88.4004717 96.4751727
## PZA03488.1 PZA00214.1 PHM8909.12 PZA00006.17 PHM2551.31
## 108.6423263 108.6423263 108.6423264 108.6423264 108.6423265
## PZB01009.2.1 PZD00072.2 PZA02606.1 PZA03069.8.4 PZA00543.12
## 108.6423265 110.0991242 110.0991242 110.0991243 110.0991243
## PZA00427.3 PZA01425.2 PZA00355.2 PZA01527.1 PZA01509.1
## 110.0991244 110.0991244 110.0991245 112.1495672 113.5589389
## PZA01901.1 PZA03120.1 PZA03063.21 PZA02948.24 PZA00440.15.1
## 113.5589390 113.5589390 113.5589391 113.8315918 114.6630962
## PZA03047.12 PHM15961.13 PZA00158.2
## 117.2892487 117.2892487 117.2892488
```

```
loglik.mds[c] <- attr(maize.mds$geno[[c]]$map, "loglik")
```

Linkage group 9

```
c <- 9
mds.ord <- getMDSorder(cross=maize.mds, chr=c)
```

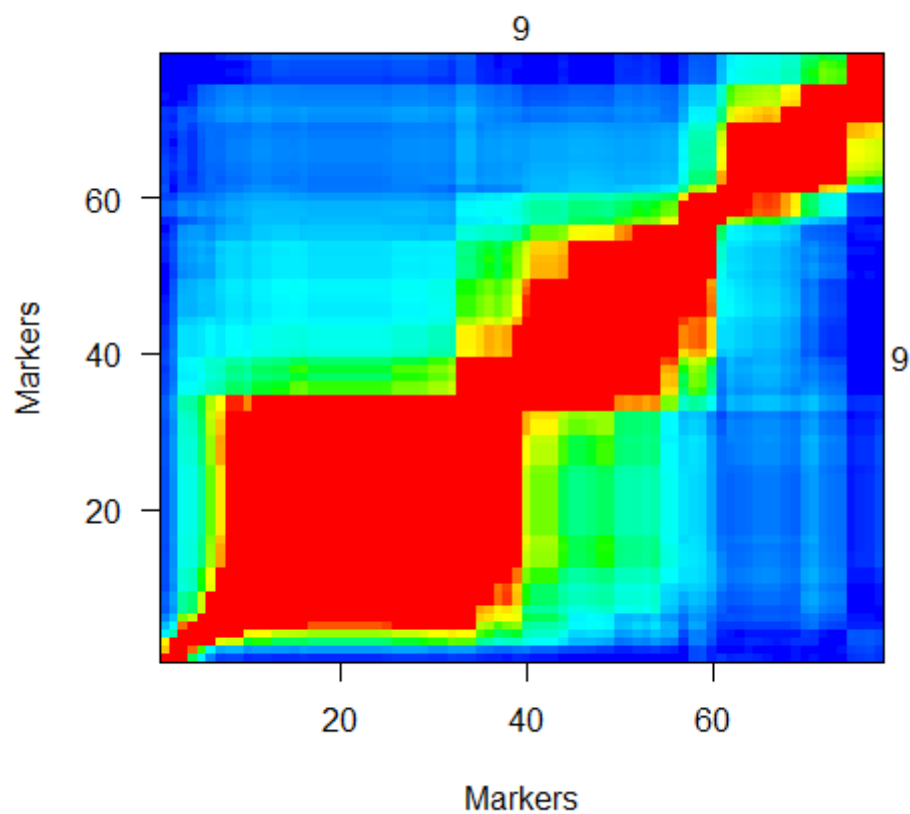
```
## Stress: 0.32333
## Mean Nearest Neighbour Fit: 4.80369
```

```
maize.mds <- switch.order(cross = maize.mds, chr=c, order=mds.ord)
```

```
## Warning in est.map(cross, chr = chr, error.prob = error.prob, map.function =
## map.function, : Didn't converge!
```

```
plotRF(maize.mds, chr=c, col.scheme = "redblue")
```


Pairwise recombination fractions and LOD score



```
pull.map(maize.mds, chr = c)
```

```
## PZA01426.1 PZA02035.5 PHM9241.13 PHM3078.12 PZA01909.1.2 PZA02872.1
## 0.000000 5.237332 28.273487 28.273487 31.930902 35.685660
## PZA00256.27 PHM4080.15 PZA03624.1 PZA03344.2 PHM15501.9 PZA00132.17
## 39.654022 42.941750 42.941751 42.941751 46.224952 46.224952
## PHM4353.31 PZA03687.1 PZA00084.2 PZA00418.2 PZA02612.1 PHM4818.15
## 46.224952 46.224952 46.224952 46.224952 46.224953 46.224953
## PZA03363.1 PZA01230.1 PZA03723.1 PZA01607.1 PZA01445.1 PZA01936.4
## 46.224953 46.224953 46.224953 46.224953 46.224953 46.224953
## PHM12830.14 PZA02291.1 PZA03645.1 PHM904.21 PZA01210.1.2 PZA02018.1
## 46.224953 46.224953 46.224953 46.224953 46.668642 47.138242
## PZA01113.1 PZA01933.3 PZA02236.1 PZA02365.7 PZA00616.13 PZA01690.7
## 47.138242 47.631877 47.631877 47.631877 61.103677 61.759973
## PZA00986.1 PZA01946.7 PZA02352.1 PZA02643.1 PZB00752.1 PZA03583.1
## 61.759973 61.759973 63.487038 69.168495 69.168495 69.168495
## PZA01714.1 PZD00054.1 PZA00740.3 PZA01542.1 PZA00111.10 PZA02449.13
## 69.168495 70.979504 73.617579 73.617579 73.782677 73.954178
## PZA02984.10 PZA03728.1 PZA03166.1 PHM9162.135 PZA02854.13 PZA00405.7.6
## 73.954178 75.949773 75.949774 76.290676 76.290676 76.664296
## PHM16437.20 PZA02722.1 PZA03176.4 PZA02260.2 PHM112.8 PZA02386.2
## 80.307585 80.307585 88.066708 91.881350 91.881350 93.970681
## PZA00795.1 PZA02373.1 PHM7898.10 PZA02223.2 PHM10225.15 PZA01533.2
## 103.636301 109.422057 110.134705 110.134705 110.443952 110.443952
## PZA00505.6 PZA01802.3 PZA01414.1 PZA01028.2 PZA00386.4 PZA00695.3
## 111.068562 111.068563 113.113497 116.897772 117.235984 118.945837
## PZA01278.2 PZB00605.1 PZA01744.1 PZA00424.1 PZA01044.1 PZA02274.1
## 119.279564 119.279564 131.576524 132.274388 132.274388 132.958006
```

```
loglik.mds[c] <- attr(maize.mds$geno[[c]]$map, "loglik")
```

Linkage group 10

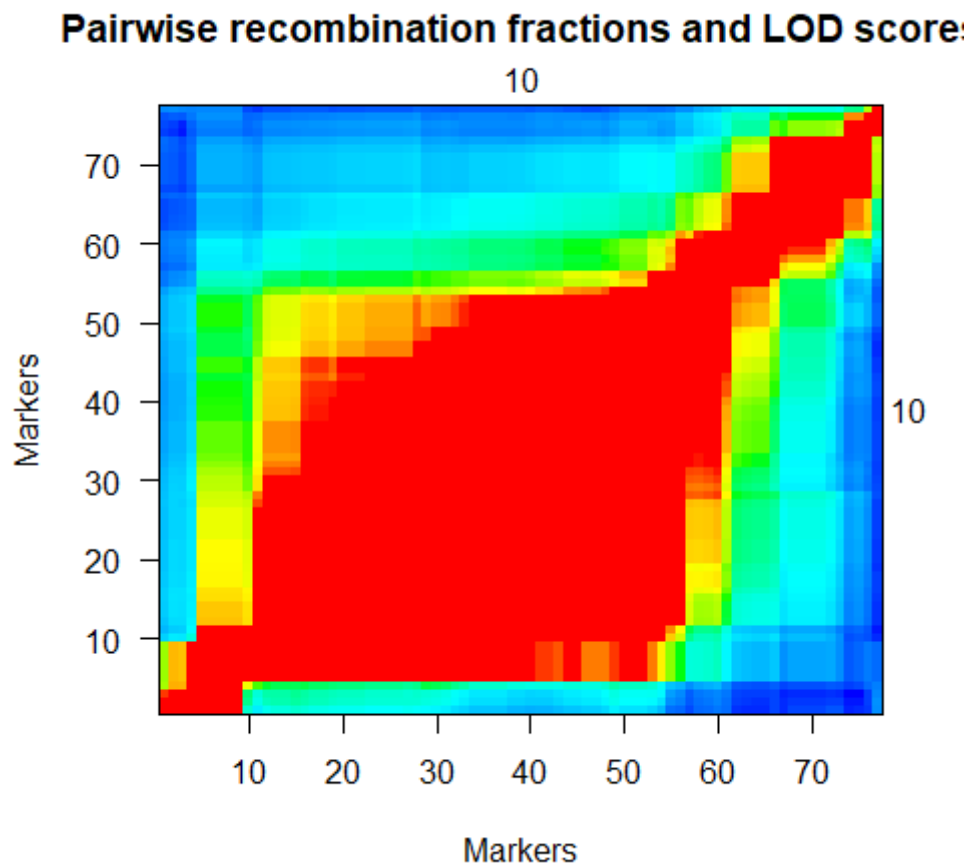
```
c <- 10
mds.ord <- getMDSorder(cross=maize.mds, chr=c)
```

```
## Stress: 0.18846
## Mean Nearest Neighbour Fit: 3.39309
```

```
maize.mds <- switch.order(cross = maize.mds, chr=c, order=mds.ord)
```

```
## Warning in est.map(cross, chr = chr, error.prob = error.prob, map.function =
## map.function, : Didn't converge!
```

```
plotRF(maize.mds, chr=c, col.scheme = "redblue")
```



```
pull.map(maize.mds, chr = c)
```

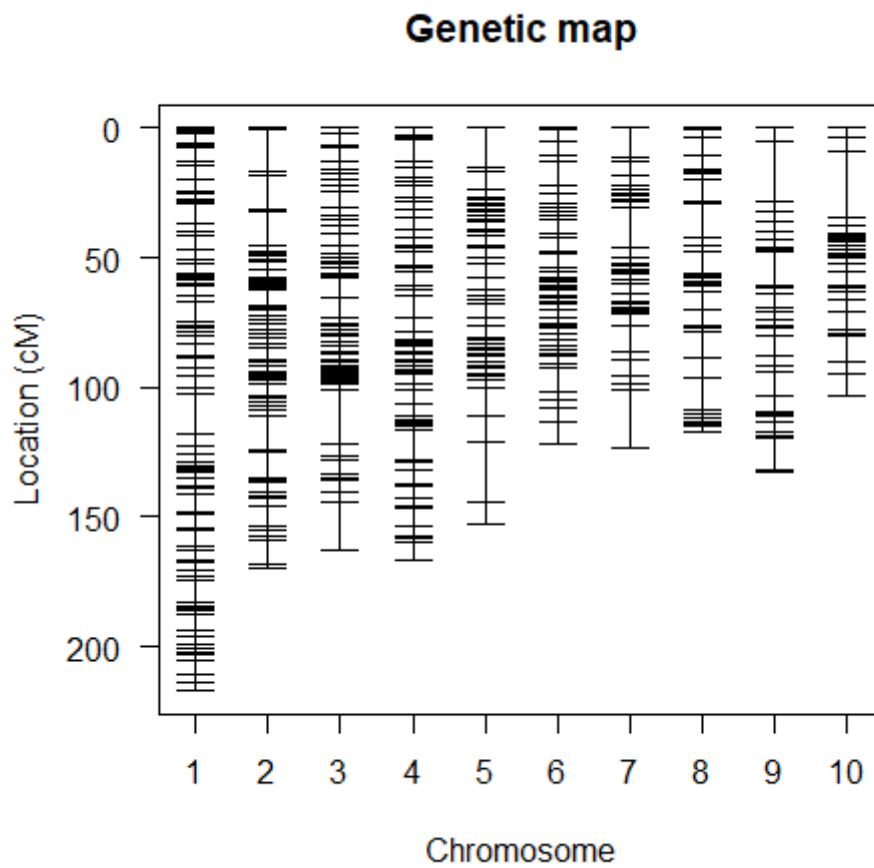
```
## PZA02554.1 PZA02221.20 PZA01313.2 PHM3631.47 PHM3765.7 PHM2828.83
## 0.000000 3.745946 3.745946 8.866913 34.590826 34.590826
## PZA01451.1 PZA02095.10 PZA01883.2 PZB01301.5 PHM15331.16 PZA00463.3
## 34.590826 34.590826 34.590826 34.590826 37.677986 40.321616
## PHM3896.9 PZA01642.1 PZA02961.6 PHM3922.32 PZA00079.1 PZA02470.2
## 40.321616 40.321616 40.321616 41.400724 41.400724 41.400725
## PZA01597.1 PZD00033.3 PZA03491.1 PZA02853.11 PHM2770.19 PZA00933.3
## 42.086091 42.086091 42.086091 42.086091 42.579110 42.579110
## PZA00409.17 PZA02941.7 PZA01677.1 PZA01877.2 PHM12990.15 PZA00337.4
## 42.579110 42.579110 42.579110 43.583900 44.911421 44.954192
## PZB00409.6 PZA00814.1 PZA01619.1 PZA00400.3 PZA02398.2 PZA00048.1
## 45.022458 45.327366 45.632197 46.451001 46.451001 46.451001
## PHM537.22 PHM18195.6 PHM12625.18 PZA00444.1 PZA01292.1 PZA01919.2
## 46.451001 46.451001 46.451001 46.451002 46.451002 46.451002
## PZA02128.3 PZA01089.1 PHM4341.42 PZA02219.2 PHM13687.14 PZA01141.1
## 47.031464 48.199701 48.199701 48.199701 48.199702 48.497762
## PZA03713.1 PZA00866.2 PZA03196.1 PZA01005.1 PZA00647.9 PZA01241.2
## 49.099572 49.741108 49.741108 49.741108 49.741108 52.482640
## PZA02320.1 PZB01111.8 PZA01456.2 PHM18513.156 PHM15868.56 PZA02663.1
## 55.476504 55.476504 60.504161 61.807532 62.805065 62.805065
## PZA01995.2 PZA03603.1 PZA03605.1 PZA03606.1 PZA03604.1 PZA03607.1
## 65.768481 70.576110 70.576110 70.576110 70.576110 70.576110
## PZA00130.9 PZA02969.9 PHM5435.25 PZA00007.1 PZA02049.1 PZA01073.1
## 77.691664 79.671187 79.671187 79.671187 79.671187 79.671187
## PZA02167.2 PZA02578.1 PZA01001.2 PZA00062.4 PZA02527.2
## 80.106755 89.886841 90.190653 94.689032 103.258961
```

```
loglik.mds[c] <- attr(maize.mds$geno[[c]]$map, "loglik")
```

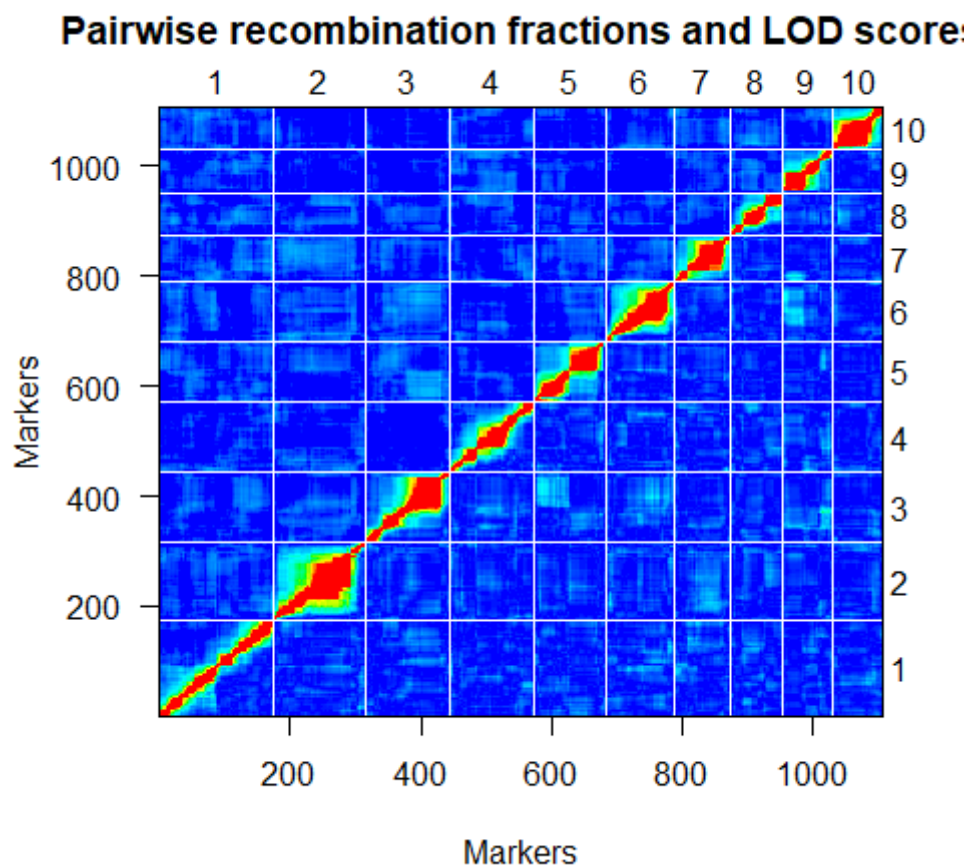
```
knitr::kable(cbind(summaryMap(maize.mds), log.likelihood=c(loglik.mds, sum(loglik.mds))))
```

	n.mar	length	ave.spacing	max.spacing	log.likelihood
1	175	217.1892	1.248214	15.442281	-2625.751
2	139	169.7542	1.230103	16.408176	-1910.858
3	130	162.4925	1.259631	20.603917	-1886.990
4	127	166.5328	1.321689	11.157701	-2072.313
5	111	153.0836	1.391669	22.681311	-1666.601
6	106	122.0408	1.162293	9.381681	-1549.291
7	85	123.7278	1.472949	22.736298	-1308.084
8	78	117.2892	1.523237	13.348430	-1276.050
9	78	132.9580	1.726727	23.036154	-1366.151
10	77	103.2590	1.358670	25.723913	-1124.173
overall	1106	1468.3269	1.339714	25.723913	-16786.261

```
plotMap(maize.mds)
```



```
plotRF(maize.mds, col.scheme = "redblue")
```



```
save.image("maize_mds.RData")
```