

Project RIL Population Z015

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Abstract

A molecular linkage map for the maize hybrid of cross between Ye478 and Dan340 was constructed by using 1106 SSR markers. The total map length was 1348.39 cM with an average interval of 10.0 cM. Composite interval mapping was used to identify the plant height (PH) and ear position (EH) QTL at 5 environments based on the phenotypic data of 397 F2:3 families. Then 21 PH and 25 EH relevant QTL were identified. The mean contribution of 12.2% and 14.9% QTL for plant height was identified at the interval of umc2025 - umc1035 on chromosome 1 and umc1822 - bnlg1118 on chromosome 5, respectively. Meanwhile, the mean contribution of 10.2% and 22.8% to ear position were identified at the interval of phi029 - umc1102 on chromosome 3 and phi109188 - bnlg1118 on chromosome 5. The main QTL for PH and EH were both found at the regions of Bin5.05 - 5.07 on chromosome 5. The additive and partial dominant effects were the main genetic basis for plant height and ear position in maize. The effect of population size and environments on QTL mapping were analyzed.

Introduction

you can explain the importance of the crop, the origin of the pop, the meaning of PH for maize and how the different `qtl` mapping approaches might help us to understand the better genetic basis of a trait and guide breeding decisions.

Material and Methods:

Linkage Map

```
library(qtl)
maize <- read.cross(format="csv", file="data/population_Z015.csv", genotypes=c("0", "1", "2"), crosstype=
```

Loading Data

```
## --Read the following data:
##   185 individuals
##   1106 markers
##   33 phenotypes

## Warning in convert2riself(cross): Omitting 13533 genotypes with code==2.

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

## --Cross type: riself
```

```
summary(maize)
```

Data Summary

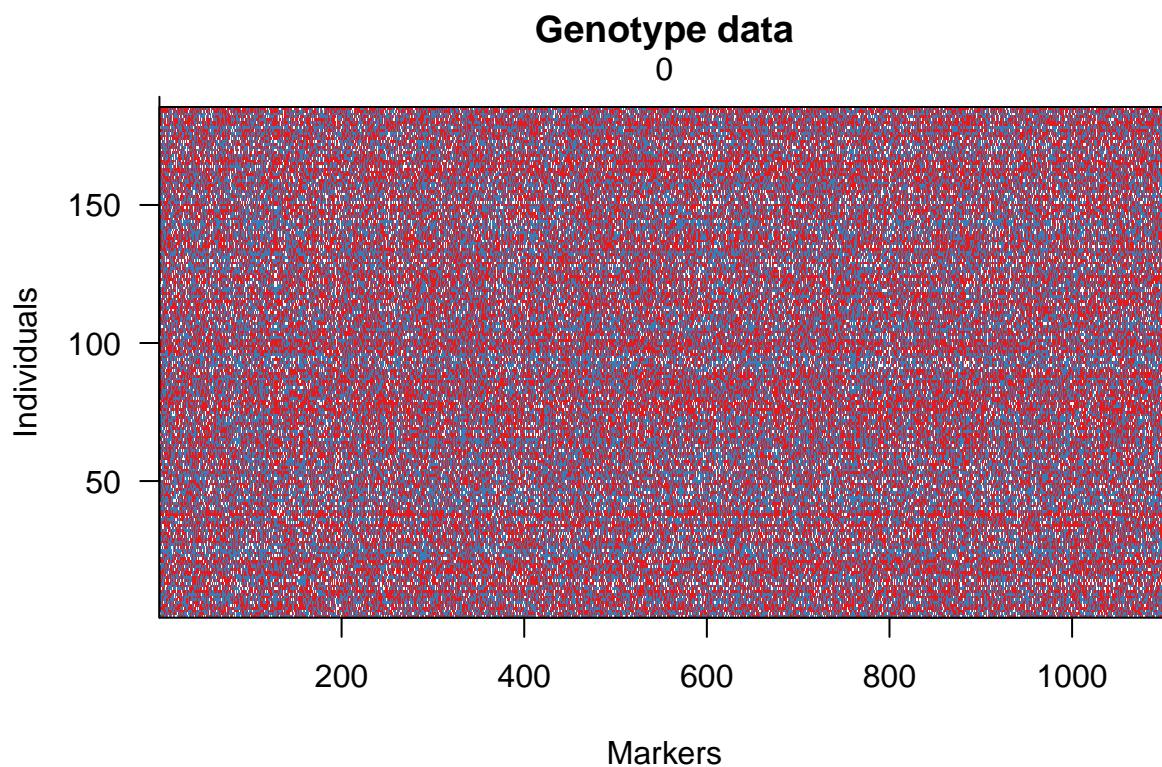
```

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

##      RI strains via selfing
##
##      No. individuals:    185
##
##      No. phenotypes:     33
##      Percent phenotyped: 100
##
##      No. chromosomes:    1
##      Autosomes:          0
##
##      Total markers:      1106
##      No. markers:        1106
##      Percent genotyped: 91.9
##      Genotypes (%):     AA:51.2  BB:48.8

geno.image(maize)

```



```

gt.maize <- geno.table(maize)
gt.maize

```

Chi_squared tests for segregation distortion:

```

##                  chr missing  AA  BB      P.value
## PZB01461.1       0     28  99   58 1.067306e-03

```

## PZA00951.1	0	16	81	88	5.902585e-01
## PHM1870.20	0	17	85	83	8.773706e-01
## PZA03521.1	0	11	89	85	7.617076e-01
## ZHD1.1	0	11	66	108	1.452491e-03
## PZA03488.1	0	4	91	90	9.407483e-01
## PZA02564.2	0	21	73	91	1.598537e-01
## PZA02274.1	0	7	98	80	1.772865e-01
## PHM3668.12	0	16	93	76	1.909777e-01
## PZA03064.6	0	7	82	96	2.940197e-01
## PZA03692.1	0	14	84	87	8.185458e-01
## PZA03191.1.4	0	12	119	54	7.738137e-07
## PHM9695.8	0	8	81	96	2.595442e-01
## PZA03671.1	0	10	60	115	3.215956e-05
## PZB01017.1	0	32	75	78	8.083652e-01
## PZA00912.2	0	11	80	94	2.885367e-01
## PZA03322.5.3	0	27	80	78	8.735811e-01
## PHM4203.11	0	10	88	87	9.397430e-01
## PZA00865.1	0	35	77	73	7.439715e-01
## PZA01447.1	0	15	107	63	7.391071e-04
## PZA02398.2	0	13	93	79	2.857506e-01
## PZA03154.4	0	6	117	62	3.941318e-05
## PZA03265.3	0	22	84	79	6.953315e-01
## PZA01879.1	0	12	80	93	3.229706e-01
## PZA00878.2	0	13	99	73	4.742539e-02
## PZA01238.1.2	0	11	94	80	2.885367e-01
## PZA02427.1	0	32	92	61	1.220361e-02
## PZA01451.1	0	9	82	94	3.657123e-01
## PHM3171.5	0	19	82	84	8.766399e-01
## PHM10321.11	0	24	74	87	3.055786e-01
## PZA01905.12	0	9	91	85	6.510766e-01
## PHM5798.39	0	21	81	83	8.758961e-01
## PZA02490.1	0	8	93	84	4.987350e-01
## PZA02418.2	0	10	90	85	7.054570e-01
## PZA00175.2	0	11	83	91	5.441971e-01
## PZA01946.7	0	12	92	81	4.029780e-01
## PZA01527.1	0	6	89	90	9.404188e-01
## PHM4711.14	0	13	68	104	6.051564e-03
## PZB01647.1	0	11	83	91	5.441971e-01
## PZA02815.25	0	1	79	105	5.527028e-02
## PZA02068.1	0	9	97	79	1.748444e-01
## PZA01993.7	0	13	86	86	1.000000e+00
## PZA00395.2	0	16	94	75	1.438677e-01
## PZA00538.18.15	0	30	101	54	1.599237e-04
## PZA03270.2	0	20	81	84	8.153346e-01
## PZA00181.2	0	11	83	91	5.441971e-01
## PZA00266.7	0	10	79	96	1.987646e-01
## PZA00255.14	0	15	87	83	7.590063e-01
## PZA02033.1	0	10	88	87	9.397430e-01
## PZA02769.1	0	7	88	90	8.808385e-01
## PZA01365.1	0	32	75	78	8.083652e-01
## PHM3637.14	0	10	106	69	5.158958e-03
## PZA00740.3	0	15	91	79	3.573857e-01
## PZA00494.2	0	15	116	54	1.982668e-06
## PZA02329.2	0	25	86	74	3.427817e-01

## PZA00887.1	0	43	71	71	1.000000e+00
## PZA02002.1	0	22	80	83	8.142257e-01
## PHM5480.17	0	15	95	75	1.250469e-01
## PZA02170.1	0	35	57	93	3.288614e-03
## PZA00637.6	0	14	83	88	7.021947e-01
## PZA03452.6	0	10	87	88	9.397430e-01
## PZA01933.3	0	9	93	83	4.509823e-01
## PZB01358.1	0	11	59	115	2.182534e-05
## PZA01028.2	0	9	89	87	8.801685e-01
## PZA02676.2	0	19	82	84	8.766399e-01
## PZA03638.1	0	3	90	92	8.821456e-01
## PHM2478.22	0	8	86	91	7.070485e-01
## PZA00343.31	0	13	91	81	4.457659e-01
## PZA03735.1	0	27	111	47	3.551171e-07
## PZA00440.15.1	0	4	91	90	9.407483e-01
## PZA03602.1	0	11	91	83	5.441971e-01
## PHM6043.19	0	11	88	86	8.794870e-01
## PZA01509.1	0	7	89	89	1.000000e+00
## PHM3078.12	0	23	81	81	1.000000e+00
## PZA01875.1	0	1	79	105	5.527028e-02
## PZA00355.2	0	13	84	88	7.603683e-01
## PZA00261.6	0	17	82	86	7.576207e-01
## PZA02373.1	0	38	69	78	4.579011e-01
## PZB00114.1	0	16	84	85	9.386847e-01
## PZA02018.1	0	9	91	85	6.510766e-01
## PZA02750.3	0	12	92	81	4.029780e-01
## kip1.3	0	20	74	91	1.856864e-01
## PZA02168.1	0	19	82	84	8.766399e-01
## PZA01951.1	0	21	73	91	1.598537e-01
## PZA03577.1	0	6	70	109	3.556921e-03
## PZA02457.1	0	22	80	83	8.142257e-01
## PZA02549.3	0	16	78	91	3.173105e-01
## PZA00213.19	0	12	61	112	1.055535e-04
## PZA00726.8.10	0	17	81	87	6.434288e-01
## PHM3726.129	0	18	90	77	3.144299e-01
## PZA00985.1	0	12	94	79	2.541077e-01
## PZA02751.1	0	13	99	73	4.742539e-02
## PZA03568.1	0	12	84	89	7.038393e-01
## PZA01642.1	0	13	82	90	5.418656e-01
## PZA01804.1	0	10	86	89	8.205958e-01
## PZA02262.3	0	35	80	70	4.142162e-01
## PZA00541.1	0	12	81	92	4.029780e-01
## PZA00060.2	0	13	61	111	1.375881e-04
## PZA01714.1	0	13	90	82	5.418656e-01
## PZA02049.1	0	16	80	89	4.887441e-01
## PHM6238.36	0	11	83	91	5.441971e-01
## PZA00225.8	0	8	57	120	2.186559e-06
## PZA00675.1	0	11	87	87	1.000000e+00
## PZA01799.1.2	0	35	75	75	1.000000e+00
## PZA00030.11	0	10	88	87	9.397430e-01
## PZA02356.7	0	11	92	82	4.483923e-01
## PHM11985.27	0	27	74	84	4.262894e-01
## PZA00528.1	0	11	83	91	5.441971e-01
## PZB00869.4	0	10	91	84	5.967012e-01

## PZA02252.2	0	9	69	107	4.178558e-03
## PHM4586.12	0	11	85	89	7.617076e-01
## PZA02174.2	0	2	72	111	3.939538e-03
## PZA00368.1	0	2	72	111	3.939538e-03
## PZA03054.5	0	14	107	64	1.007972e-03
## PZA03275.4.1	0	34	94	57	2.603740e-03
## PZA00693.3	0	12	58	115	1.466708e-05
## PHM12990.15	0	14	88	83	7.021947e-01
## PZB01957.1	0	10	89	86	8.205958e-01
## PZA00731.7	0	20	82	83	9.379475e-01
## PHM2350.17	0	16	72	97	5.447039e-02
## PZA02015.11	0	29	85	71	2.623317e-01
## PZA02554.1	0	6	88	91	8.225779e-01
## PZA03152.3	0	15	95	75	1.250469e-01
## PZA01589.2	0	17	88	80	5.370940e-01
## PZA02680.1	0	10	94	81	3.257514e-01
## PZA00840.1	0	22	56	107	6.479583e-05
## PZB01115.3	0	19	82	84	8.766399e-01
## PZA00522.12.7	0	17	86	82	7.576207e-01
## PZA00805.1	0	18	85	82	8.164239e-01
## PZA03320.6	0	13	99	73	4.742539e-02
## PZA00473.5	0	28	83	74	4.725858e-01
## PZA01265.1	0	12	99	74	5.733938e-02
## PHM13619.5	0	18	80	87	5.880415e-01
## PZA01552.1	0	28	83	74	4.725858e-01
## PZA03527.1	0	12	99	74	5.733938e-02
## PHM9374.5	0	26	73	86	3.025563e-01
## PZB01457.1	0	12	102	71	1.842889e-02
## PZA03063.21	0	9	89	87	8.801685e-01
## PZB01103.2	0	12	94	79	2.541077e-01
## PZA03634.1	0	21	76	88	3.487367e-01
## PZA02337.4	0	10	77	98	1.124106e-01
## PZA02663.1	0	8	91	86	7.070485e-01
## PHM4503.25	0	14	76	95	1.462331e-01
## PHM1745.16	0	13	114	58	1.955081e-05
## PZA00400.3	0	14	93	78	2.513491e-01
## PZA01209.1	0	2	81	102	1.205750e-01
## PZA00307.14	0	34	72	79	5.689138e-01
## PZA00707.9	0	23	103	59	5.462928e-04
## PZD00015.5	0	15	111	59	6.657149e-05
## PHM4468.13	0	1	79	105	5.527028e-02
## PZA02151.3	0	11	96	78	1.723862e-01
## PZA01690.7	0	12	92	81	4.029780e-01
## PZA02320.1	0	35	80	70	4.142162e-01
## PHM4531.46	0	25	80	80	1.000000e+00
## PZA02271.1	0	10	92	83	4.962917e-01
## PZA02292.1	0	12	92	81	4.029780e-01
## PZA03240.1.2	0	9	88	88	1.000000e+00
## PHM3922.32	0	13	84	88	7.603683e-01
## PZA01195.3	0	8	88	89	9.400837e-01
## PZA00925.2	0	13	55	117	2.273507e-06
## PZA00163.4	0	9	81	95	2.912928e-01
## PZA03578.1	0	14	94	77	1.935933e-01
## PHM3055.9	0	11	95	79	2.251463e-01

## PHM4165.14	0	27	78	80	8.735811e-01
## PHM9914.11	0	25	106	54	3.940158e-05
## PZA02678.1	0	14	100	71	2.657629e-02
## PZA01468.1	0	9	80	96	2.278000e-01
## PZB00054.3	0	10	93	82	4.056789e-01
## PZA03254.1	0	22	80	83	8.142257e-01
## PZA03573.1	0	4	101	80	1.185432e-01
## PZA00521.3	0	11	99	75	6.884504e-02
## PZA02372.1	0	18	78	89	3.946552e-01
## PZA02673.1	0	21	79	85	6.394119e-01
## PZA00243.25	0	13	86	86	1.000000e+00
## PZA03305.7.1	0	9	88	88	1.000000e+00
## PZA02094.9	0	43	71	71	1.000000e+00
## PZB00718.5	0	9	86	90	7.630246e-01
## PZA02456.1	0	26	84	75	4.753840e-01
## PZA02203.1	0	2	81	102	1.205750e-01
## PZA03551.1	0	43	71	71	1.000000e+00
## PZA02011.1	0	10	89	86	8.205958e-01
## PHM15871.11	0	10	89	86	8.205958e-01
## PHM4942.12	0	8	86	91	7.070485e-01
## PZA03116.1	0	37	92	56	3.084571e-03
## PZA02616.1	0	21	98	66	1.246216e-02
## PZA03120.1	0	6	89	90	9.404188e-01
## PZA00466.1	0	8	87	90	8.215951e-01
## PHM4926.16	0	17	79	89	4.404007e-01
## PZA01289.1	0	15	103	67	5.761163e-03
## PZA03529.1	0	12	96	77	1.485862e-01
## PZA00749.1	0	13	99	73	4.742539e-02
## PHM9241.13	0	4	89	92	8.235447e-01
## PHM4080.15	0	43	71	71	1.000000e+00
## PHM2438.28	0	43	76	66	4.013675e-01
## PZA01228.2	0	15	119	51	1.834587e-07
## PHM13673.53	0	16	117	52	5.733031e-07
## PZA00210.1.9	0	32	92	61	1.220361e-02
## PZA03391.1	0	14	88	83	7.021947e-01
## PZB00008.1	0	28	75	82	5.763932e-01
## PZA00838.2	0	25	77	83	6.352563e-01
## PZA01883.2	0	8	83	94	4.083444e-01
## PZA00497.4	0	13	81	91	4.457659e-01
## PZA01575.1	0	11	91	83	5.441971e-01
## PZA02746.2	0	12	87	86	9.393964e-01
## PZD00055.1	0	9	75	101	5.001640e-02
## PZA01001.2	0	10	85	90	7.054570e-01
## PZA00904.1	0	10	89	86	8.205958e-01
## PZA01030.1	0	9	85	91	6.510766e-01
## PZA03135.1	0	5	89	91	8.814975e-01
## PZA02388.1	0	2	72	111	3.939538e-03
## PZA02081.1	0	21	75	89	2.742988e-01
## PHM4913.18	0	21	89	75	2.742988e-01
## PZA02359.10	0	22	85	78	5.834981e-01
## PHM4647.8	0	10	91	84	5.967012e-01
## PZA01122.1	0	6	88	91	8.225779e-01
## PZA02423.1	0	7	94	84	4.535368e-01
## PZA03226.3	0	15	92	78	2.829343e-01

## PZB02044.1	0	13	114	58	1.955081e-05
## PZA01241.2	0	35	80	70	4.142162e-01
## PZA02878.13	0	13	56	116	4.763176e-06
## PZA02698.3	0	11	85	89	7.617076e-01
## PZA00511.3	0	8	75	102	4.241306e-02
## PHM3512.186	0	8	97	80	2.013206e-01
## PZA01936.4	0	9	92	84	5.464936e-01
## PZA01691.1	0	6	79	100	1.165050e-01
## PZA03659.1	0	13	88	84	7.603683e-01
## PZA02219.2	0	15	95	75	1.250469e-01
## PZA02114.1	0	10	96	79	1.987646e-01
## PHM7616.35	0	8	94	83	4.083444e-01
## PZA00827.1	0	19	108	58	1.041337e-04
## PZA02792.26.25	0	29	83	73	4.233396e-01
## PZB01111.8	0	10	90	85	7.054570e-01
## PZA00706.16	0	11	84	90	6.492108e-01
## PZA03605.1	0	7	91	87	7.643200e-01
## PHM1899.157	0	13	91	81	4.457659e-01
## PZA01089.1	0	15	94	76	1.674214e-01
## PZA01537.2	0	17	82	86	7.576207e-01
## PZA02194.1	0	9	106	70	6.655605e-03
## PZA02397.1	0	12	60	113	5.589196e-05
## PHM15868.56	0	10	90	85	7.054570e-01
## PZA00755.2	0	32	83	70	2.932642e-01
## PZA00828.2	0	15	110	60	1.256538e-04
## PZA03048.18	0	8	86	91	7.070485e-01
## PZA01751.2	0	13	83	89	6.473148e-01
## PHM15961.13	0	2	93	90	8.244958e-01
## PZA00424.1	0	9	97	79	1.748444e-01
## PZA00273.5	0	21	80	84	7.547764e-01
## PZA01791.2	0	11	55	119	1.223290e-06
## PZA02212.1	0	38	102	45	2.585347e-06
## PZA02665.2	0	19	93	73	1.205902e-01
## PHM1511.14	0	37	75	73	8.694171e-01
## PZA00057.2	0	35	89	61	2.224312e-02
## PZA02474.1	0	13	114	58	1.955081e-05
## PZA01457.1	0	14	116	55	3.089375e-06
## PZA02255.2	0	13	107	65	1.362545e-03
## csu1138.3.4	0	9	93	83	4.509823e-01
## PZA02299.16	0	19	108	58	1.041337e-04
## PZA02204.1	0	27	82	76	6.331240e-01
## PZA02376.1	0	16	97	72	5.447039e-02
## PZB00761.1	0	11	55	119	1.223290e-06
## PZA00525.17	0	37	75	73	8.694171e-01
## PZB00183.4	0	26	77	82	6.917172e-01
## PZA02367.1	0	11	103	71	1.526990e-02
## PHM5019.59	0	3	101	81	1.382077e-01
## an1.5	0	11	92	82	4.483923e-01
## PHM3034.3	0	20	74	91	1.856864e-01
## PHM13360.13	0	17	78	90	3.545395e-01
## PZA01410.1	0	23	84	78	6.373519e-01
## PHM3137.17	0	20	88	77	3.918049e-01
## PZA02260.2	0	9	96	80	2.278000e-01
## PZA01796.1	0	17	81	87	6.434288e-01

## PZA02421.1	0	16	101	68	1.113410e-02
## PZA00332.5	0	28	99	58	1.067306e-03
## PZA01445.1	0	9	92	84	5.464936e-01
## PHM565.31	0	12	93	80	3.229706e-01
## PZA01050.1	0	21	82	82	1.000000e+00
## PZA00795.1	0	10	82	93	4.056789e-01
## PZA02296.1	0	16	108	61	2.999020e-04
## PZA01239.2	0	22	84	79	6.953315e-01
## PZB01662.1	0	12	90	83	5.945874e-01
## PHM3155.14	0	28	97	60	3.147820e-03
## PZA02128.3	0	12	92	81	4.029780e-01
## PHM3342.31	0	16	94	75	1.438677e-01
## PZA02527.2	0	9	84	92	5.464936e-01
## PHM3631.47	0	10	85	90	7.054570e-01
## PZA01357.2	0	8	73	104	1.980072e-02
## PHM3993.28	0	7	85	93	5.487559e-01
## PZA03165.1	0	8	95	82	3.284999e-01
## PZA01570.1	0	10	103	72	1.910992e-02
## PHM4786.9	0	11	89	85	7.617076e-01
## PHM16605.19	0	9	81	95	2.912928e-01
## PZA00658.21	0	8	88	89	9.400837e-01
## PZA03698.1	0	11	85	89	7.617076e-01
## PHM2885.31	0	23	106	56	8.552320e-05
## PZA01954.1	0	10	111	64	3.810585e-04
## PZB00547.3	0	7	68	110	1.643731e-03
## PZA02197.1	0	9	75	101	5.001640e-02
## PZA03146.4	0	12	96	77	1.485862e-01
## PZA00941.2	0	12	109	64	6.232560e-04
## PZA03637.1	0	4	89	92	8.235447e-01
## PZA02516.1	0	8	107	70	5.417666e-03
## PZA00118.1.5	0	6	88	91	8.225779e-01
## PZA01044.1	0	9	98	78	1.316680e-01
## PZB00752.1	0	17	88	80	5.370940e-01
## PZA01895.1	0	9	73	103	2.373852e-02
## PZA00944.1.2	0	11	86	88	8.794870e-01
## PHM15899.9	0	25	102	58	5.042182e-04
## PZA01976.9	0	10	106	69	5.158958e-03
## PHM4134.8	0	25	78	82	7.518296e-01
## PHM2749.10	0	2	100	83	2.088709e-01
## PZA02408.2	0	12	91	82	4.938127e-01
## PZB01403.1	0	17	85	83	8.773706e-01
## PHM15331.16	0	32	71	82	3.738433e-01
## PZA00545.26	0	15	95	75	1.250469e-01
## PZA02378.7	0	12	87	86	9.393964e-01
## PZA01371.1	0	11	93	81	3.629714e-01
## PHM4341.42	0	15	94	76	1.674214e-01
## PZA03274.4	0	16	91	78	3.173105e-01
## PHM1766.1	0	8	69	108	3.374168e-03
## PHM9418.11	0	22	85	78	5.834981e-01
## PZA02645.2	0	13	108	64	7.937401e-04
## PZA02683.1	0	1	85	99	3.020282e-01
## PZA02522.1	0	1	84	100	2.381849e-01
## PZB00093.7	0	17	87	81	6.434288e-01
## PZA01315.1	0	9	97	79	1.748444e-01

## PZA02957.5	0	16	89	80	4.887441e-01
## PHM14046.9	0	8	93	84	4.987350e-01
## PZA00517.7	0	16	93	76	1.909777e-01
## PHM3226.15	0	10	86	89	8.205958e-01
## PZA02264.5	0	24	79	82	8.130966e-01
## PZB01227.6	0	8	81	96	2.595442e-01
## PZA01999.3	0	10	65	110	6.697294e-04
## PZA00758.1	0	4	76	105	3.111858e-02
## PHM7922.8	0	5	78	102	7.363827e-02
## PZA00821.1	0	6	76	103	4.358348e-02
## PZA00365.2	0	7	90	88	8.808385e-01
## PZA00444.1	0	16	91	78	3.173105e-01
## PZA00186.4	0	16	109	60	1.637514e-04
## PZA03604.1	0	9	89	87	8.801685e-01
## PZA00235.9	0	13	90	82	5.418656e-01
## PHM1834.47	0	11	88	86	8.794870e-01
## PHM4604.18	0	9	75	101	5.001640e-02
## PZA01909.1.2	0	5	91	89	8.814975e-01
## PZA01186.1	0	16	70	99	2.569642e-02
## PZA01736.1	0	15	90	80	4.431023e-01
## PZA02578.1	0	10	84	91	5.967012e-01
## PZB00895.1	0	14	82	89	5.924401e-01
## PHM15427.11	0	22	80	83	8.142257e-01
## PZA00453.2	0	16	105	64	1.611340e-03
## PZA00610.16	0	15	89	81	5.394982e-01
## PZA00323.3	0	9	75	101	5.001640e-02
## PZA02872.1	0	7	87	91	7.643200e-01
## PZA00866.2	0	16	92	77	2.485632e-01
## PZA01049.1	0	7	87	91	7.643200e-01
## PZA03612.2.1	0	6	87	92	7.086145e-01
## PZA01877.2	0	17	87	81	6.434288e-01
## PZA01281.2	0	10	58	117	8.196700e-06
## PZA00963.3	0	10	96	79	1.987646e-01
## PZA00112.5	0	11	93	81	3.629714e-01
## PZA01414.1	0	8	89	88	9.400837e-01
## PZA00357.19	0	35	80	70	4.142162e-01
## PHM9807.9	0	15	90	80	4.431023e-01
## PZA02566.1	0	5	88	92	7.655945e-01
## PZA02985.5	0	28	75	82	5.763932e-01
## PZA01672.1	0	13	69	103	9.528791e-03
## PZB01009.2.1	0	7	89	89	1.000000e+00
## PZA02095.10	0	8	85	92	5.987824e-01
## PZA00108.4	0	23	70	92	8.390162e-02
## PHM13681.12	0	30	82	73	4.697429e-01
## PZA00981.3	0	32	78	75	8.083652e-01
## PZA03092.7	0	13	88	84	7.603683e-01
## PHM532.23	0	16	95	74	1.062274e-01
## PZA00006.17	0	5	90	90	1.000000e+00
## csu1171.2	0	43	71	71	1.000000e+00
## PZA02643.1	0	12	89	84	7.038393e-01
## PZA03677.1	0	19	83	83	1.000000e+00
## PZA00382.17	0	15	92	78	2.829343e-01
## PZA01060.1	0	7	88	90	8.808385e-01
## PHM15278.6	0	8	86	91	7.070485e-01

## PHM5098.25	0	26	87	72	2.342125e-01
## PZA03624.1	0	43	71	71	1.000000e+00
## PHM5435.25	0	11	83	91	5.441971e-01
## PHM16125.47	0	10	96	79	1.987646e-01
## PZA01039.1	0	8	92	85	5.987824e-01
## PZA02167.2	0	8	86	91	7.070485e-01
## PZB01013.1	0	8	76	101	6.022878e-02
## PZA02613.1	0	11	62	112	1.503503e-04
## PZA03074.27	0	9	99	77	9.725443e-02
## PZA02365.7	0	36	79	70	4.609346e-01
## PZA00509.1	0	15	108	62	4.186506e-04
## PZA02272.3	0	8	76	101	6.022878e-02
## PZA03196.1	0	17	92	76	2.170439e-01
## PZA00219.7	0	18	87	80	5.880415e-01
## PZA00804.1	0	26	84	75	4.753840e-01
## PHM13440.13	0	37	75	73	8.694171e-01
## PZA02964.7	0	10	93	82	4.056789e-01
## PZA01396.1	0	18	108	59	1.495992e-04
## sh2.21	0	14	94	77	1.935933e-01
## PHM12830.14	0	10	90	85	7.054570e-01
## PZA03176.4	0	11	94	80	2.885367e-01
## PZA00613.22	0	46	63	76	2.701811e-01
## PZA02612.1	0	9	92	84	5.464936e-01
## PZA01820.1	0	19	80	86	6.414372e-01
## PZA02087.2	0	16	87	82	7.005224e-01
## PZA03255.1	0	15	116	54	1.982668e-06
## PHM18195.6	0	14	91	80	4.002409e-01
## PZA03639.1	0	4	89	92	8.235447e-01
## PZA01935.10	0	19	76	90	2.772089e-01
## PZA01301.1	0	6	81	98	2.038569e-01
## PZA00130.9	0	10	84	91	5.967012e-01
## PZB01233.1	0	24	79	82	8.130966e-01
## PHM14412.4	0	9	96	80	2.278000e-01
## PZA03651.1	0	34	75	76	9.351407e-01
## PZA02014.3	0	8	93	84	4.987350e-01
## PZB02155.1	0	7	88	90	8.808385e-01
## PZA03531.1	0	10	89	86	8.205958e-01
## PHM13020.10	0	28	83	74	4.725858e-01
## PHM10225.15	0	11	87	87	1.000000e+00
## PZA03081.1	0	27	95	63	1.090328e-02
## PZA02585.2	0	15	92	78	2.829343e-01
## PHM4621.57	0	18	108	59	1.495992e-04
## PZA01271.1	0	6	83	96	3.312169e-01
## PZA01079.1	0	9	77	99	9.725443e-02
## PZA01623.3	0	2	72	111	3.939538e-03
## PZA01715.1.2	0	8	75	102	4.241306e-02
## PZA01062.1	0	14	55	116	3.089375e-06
## PZA00894.7	0	17	85	83	8.773706e-01
## PZA01680.3	0	13	88	84	7.603683e-01
## PZA02269.3.4	0	10	79	96	1.987646e-01
## PZA00793.2	0	4	80	101	1.185432e-01
## PZA03198.3	0	17	107	61	3.867308e-04
## PZA00425.11	0	12	80	93	3.229706e-01
## PZA00860.1	0	26	73	86	3.025563e-01

## PZA00590.1	0	12	80	93	3.229706e-01
## PZA01294.2.1	0	24	82	79	8.130966e-01
## PZA03457.1	0	28	75	82	5.763932e-01
## PZA00652.17	0	12	95	78	1.961889e-01
## PZA03200.2	0	24	85	76	4.781387e-01
## PZB00414.2	0	35	80	70	4.142162e-01
## PZB00221.3	0	9	75	101	5.001640e-02
## PZA02070.1	0	10	92	83	4.962917e-01
## PZA00636.7	0	16	98	71	3.780866e-02
## PZA00513.1	0	14	94	77	1.935933e-01
## PZA01140.1	0	18	86	81	6.988216e-01
## PZA00139.4	0	9	85	91	6.510766e-01
## PZB01109.1	0	20	114	51	9.364494e-07
## PZA03583.1	0	17	88	80	5.370940e-01
## PZA00581.3	0	25	102	58	5.042182e-04
## PZA03606.1	0	9	89	87	8.801685e-01
## PZA02187.1.2	0	15	90	80	4.431023e-01
## PZA00818.1	0	12	100	73	4.009470e-02
## PZA02820.17	0	12	99	74	5.733938e-02
## PZA01677.1	0	13	85	87	8.787937e-01
## PZA00427.3	0	6	87	92	7.086145e-01
## PZA02223.2	0	16	84	85	9.386847e-01
## PZB01899.1	0	18	53	114	2.354719e-06
## PZA02080.1	0	10	81	94	3.257514e-01
## PZA01887.1	0	11	102	72	2.294831e-02
## PZA02090.1	0	12	98	75	8.035022e-02
## PZA01332.2	0	27	95	63	1.090328e-02
## PZA00942.2	0	9	92	84	5.464936e-01
## PHM1307.11	0	18	81	86	6.988216e-01
## PHM2100.21	0	11	84	90	6.492108e-01
## PZA01807.1	0	9	93	83	4.509823e-01
## PZA00240.6	0	18	90	77	3.144299e-01
## PZA02141.1	0	4	75	106	2.121075e-02
## PZA01501.1	0	11	120	54	5.631413e-07
## PZA01257.1	0	4	80	101	1.185432e-01
## PZA01470.1	0	2	83	100	2.088709e-01
## PZA01232.1	0	14	84	87	8.185458e-01
## PZA02133.10	0	37	75	73	8.694171e-01
## PZA02737.1	0	9	97	79	1.748444e-01
## PZA03037.2	0	17	85	83	8.773706e-01
## PZB00772.7	0	10	93	82	4.056789e-01
## PZA00680.3	0	12	86	87	9.393964e-01
## PZA01327.1	0	13	93	79	2.857506e-01
## PHM4303.16	0	18	74	93	1.414902e-01
## PZA00495.5	0	13	83	89	6.473148e-01
## PHM4125.11	0	12	90	83	5.945874e-01
## PZA03385.1	0	12	83	90	5.945874e-01
## PHM5572.19	0	12	81	92	4.029780e-01
## PZA03184.2	0	16	92	77	2.485632e-01
## PZA02060.1	0	11	97	77	1.294698e-01
## PZA01963.15	0	15	95	75	1.250469e-01
## PZA00498.5	0	2	81	102	1.205750e-01
## PZA02426.1	0	14	96	75	1.082937e-01
## PHM15445.25	0	14	83	88	7.021947e-01

## PZA00750.1	0	15	93	77	2.197685e-01
## PHM3094.23	0	8	67	110	1.228935e-03
## PZA00271.1	0	14	106	65	1.716501e-03
## PZA01304.1	0	13	91	81	4.457659e-01
## PZA03167.5	0	29	85	71	2.623317e-01
## PZA02753.1	0	11	91	83	5.441971e-01
## PZA03491.1	0	14	87	84	8.185458e-01
## PZA02017.1	0	9	97	79	1.748444e-01
## PZA01925.1	0	11	92	82	4.483923e-01
## PZA03231.1	0	18	86	81	6.988216e-01
## PZA00445.22	0	17	82	86	7.576207e-01
## PZD00022.5	0	6	72	107	8.896061e-03
## PZA00337.4	0	14	88	83	7.021947e-01
## PZA03211.6	0	12	84	89	7.038393e-01
## PHM2343.25	0	32	92	61	1.220361e-02
## PZA02774.1	0	15	80	90	4.431023e-01
## PZA02731.1	0	9	97	79	1.748444e-01
## PZA00619.3	0	8	102	75	4.241306e-02
## PHM5181.10	0	9	84	92	5.464936e-01
## PZA00832.1	0	12	83	90	5.945874e-01
## PZA02487.1	0	10	86	89	8.205958e-01
## PZA01921.20.19	0	28	75	82	5.763932e-01
## PZB00765.1	0	18	94	73	1.041564e-01
## PZA02236.1	0	9	93	83	4.509823e-01
## ae1.8.7	0	17	88	80	5.370940e-01
## PHM18705.23	0	11	90	84	6.492108e-01
## PZB01112.1	0	20	80	85	6.970916e-01
## PHM448.23	0	16	85	84	9.386847e-01
## PZA00948.1	0	11	111	63	2.738363e-04
## PZD00027.2	0	13	112	60	7.340739e-05
## PZA01713.4	0	10	82	93	4.056789e-01
## PHM3978.104	0	5	88	92	7.655945e-01
## PZA03409.1	0	17	87	81	6.434288e-01
## PZA00068.1	0	12	88	85	8.195796e-01
## PHM904.21	0	10	90	85	7.054570e-01
## PZA00571.1	0	28	83	74	4.725858e-01
## PZA02195.1	0	10	93	82	4.056789e-01
## PHM11226.13	0	25	68	92	5.777957e-02
## PZA01233.1	0	15	96	74	9.154127e-02
## PZA00405.7.6	0	12	91	82	4.938127e-01
## PZA01766.1	0	10	111	64	3.810585e-04
## PZA01035.1	0	15	117	53	9.174011e-07
## PHM4353.31	0	13	89	83	6.473148e-01
## PZA02436.1	0	11	85	89	7.617076e-01
## umc128.2	0	10	87	88	9.397430e-01
## PZA01055.1	0	18	89	78	3.946552e-01
## PZA02606.1	0	7	89	89	1.000000e+00
## PZA00766.1	0	16	85	84	9.386847e-01
## PZA03743.1	0	16	118	51	2.551973e-07
## PZA00429.1	0	34	75	76	9.351407e-01
## PZA01688.3	0	11	93	81	3.629714e-01
## PHM1911.173	0	8	87	90	8.215951e-01
## PZA01588.1	0	13	76	96	1.272627e-01
## zb27.1	0	11	120	54	5.631413e-07

## PZA01901.1	0	5	91	89	8.814975e-01
## PZB01042.2	0	14	65	106	1.716501e-03
## PZA01926.1	0	9	105	71	1.038180e-02
## PZB00232.2	0	21	82	82	1.000000e+00
## PZA00020.5	0	13	88	84	7.603683e-01
## PZA01765.1	0	13	92	80	3.601961e-01
## PZA03728.1	0	12	91	82	4.938127e-01
## PZA01246.1	0	12	89	84	7.038393e-01
## PHM13687.14	0	16	94	75	1.438677e-01
## PZA01313.2	0	35	73	77	7.439715e-01
## PHM3925.79	0	2	91	92	9.410723e-01
## PZA00402.1	0	14	88	83	7.021947e-01
## PHM13623.14	0	10	82	93	4.056789e-01
## PZA01005.1	0	16	91	78	3.173105e-01
## PZA02992.15	0	15	96	74	9.154127e-02
## PZA00300.14	0	11	90	84	6.492108e-01
## PZA00987.1	0	23	84	78	6.373519e-01
## PZA02393.2	0	11	87	87	1.000000e+00
## PZA01360.3	0	13	92	80	3.601961e-01
## PZA02454.2	0	8	73	104	1.980072e-02
## PZA02316.22	0	13	102	70	1.468819e-02
## PZA01363.2	0	2	84	99	2.675027e-01
## PZA00111.10	0	15	91	79	3.573857e-01
## PZB00872.3	0	13	95	77	1.699118e-01
## PZA00664.3	0	11	86	88	8.794870e-01
## PHM1675.29	0	16	116	53	1.258779e-06
## PZA01303.1	0	21	81	83	8.758961e-01
## PZA01144.1	0	27	74	84	4.262894e-01
## PZA00589.10	0	12	57	116	7.267939e-06
## PZA00770.1	0	10	88	87	9.397430e-01
## PZA03469.1	0	12	57	116	7.267939e-06
## PZA01618.2	0	13	90	82	5.418656e-01
## PZA00910.1	0	25	65	95	1.770607e-02
## PZA03733.1	0	27	111	47	3.551171e-07
## PZA01349.2	0	21	80	84	7.547764e-01
## PZA01477.3	0	11	107	67	2.426238e-03
## PZA00529.4	0	15	85	85	1.000000e+00
## PHM17210.5	0	17	116	52	7.904640e-07
## PHM12992.5	0	32	78	75	8.083652e-01
## PZA00344.10	0	13	107	65	1.362545e-03
## PZA01106.3	0	10	82	93	4.056789e-01
## PHM4955.12	0	12	111	62	1.950050e-04
## PZA03212.3	0	13	99	73	4.742539e-02
## PZA02514.1	0	15	96	74	9.154127e-02
## PZA01473.1	0	13	107	65	1.362545e-03
## PZA01367.2	0	12	100	73	4.009470e-02
## PZA02702.1	0	11	82	92	4.483923e-01
## PZA03607.1	0	22	81	82	9.375687e-01
## PZA02450.1	0	19	80	86	6.414372e-01
## PZA03451.5	0	17	85	83	8.773706e-01
## PZA01530.1	0	32	78	75	8.083652e-01
## PHM5665.26	0	15	85	85	1.000000e+00
## PZA01073.1	0	19	80	86	6.414372e-01
## PZA01374.1	0	21	80	84	7.547764e-01

## PZA00683.4	0	32	76	77	9.355651e-01
## PZA00739.1	0	25	78	82	7.518296e-01
## PZA02035.5	0	2	89	94	7.116726e-01
## PHM6111.5	0	21	76	88	3.487367e-01
## PZA03227.1	0	8	90	87	8.215951e-01
## PZA02479.1	0	12	99	74	5.733938e-02
## PZA03714.1	0	14	88	83	7.021947e-01
## PHM4905.6	0	16	58	111	4.563558e-05
## PZA00193.2	0	16	104	65	2.699796e-03
## PZA02626.1	0	12	86	87	9.393964e-01
## PZA00067.10	0	32	75	78	8.083652e-01
## PZA01019.1	0	12	93	80	3.229706e-01
## PZA03645.1	0	11	89	85	7.617076e-01
## PZA02550.1	0	10	95	80	2.568393e-01
## PZA00418.2	0	10	90	85	7.054570e-01
## PZA02208.1	0	46	63	76	2.701811e-01
## glb1.2	0	22	73	90	1.830105e-01
## PZA01861.1	0	11	56	118	2.598968e-06
## PHM816.29	0	25	68	92	5.777957e-02
## PZA03363.1	0	9	92	84	5.464936e-01
## PZA02358.1	0	28	76	81	6.898612e-01
## PHM2244.142	0	6	83	96	3.312169e-01
## PZA01819.1	0	12	60	113	5.589196e-05
## PZA03001.15	0	11	83	91	5.441971e-01
## PZA00413.20.18	0	13	109	63	4.523943e-04
## PHM10404.8	0	16	84	85	9.386847e-01
## PZA00158.2	0	26	80	79	9.367899e-01
## PZA02525.1	0	20	81	84	8.153346e-01
## PHM3465.6	0	11	82	92	4.483923e-01
## fea2.3	0	18	88	79	4.861528e-01
## PZA01658.1	0	11	107	67	2.426238e-03
## PHM12625.18	0	14	91	80	4.002409e-01
## PZA00379.2	0	4	80	101	1.185432e-01
## PZA03603.1	0	9	89	87	8.801685e-01
## PZA02164.16	0	32	75	78	8.083652e-01
## PZA01391.1	0	12	97	76	1.103548e-01
## zb21.1	0	25	102	58	5.042182e-04
## PZB00063.1	0	12	84	89	7.038393e-01
## PZA00499.3	0	11	90	84	6.492108e-01
## PZA00978.1	0	12	89	84	7.038393e-01
## PHM10525.9.11	0	6	88	91	8.225779e-01
## PZA00189.23	0	9	91	85	6.510766e-01
## PZA02853.11	0	13	87	85	8.787937e-01
## zf12.9	0	11	77	97	1.294698e-01
## PZA01342.2	0	13	84	88	7.603683e-01
## PZA01278.2	0	5	95	85	4.560565e-01
## PZA03324.1	0	11	92	82	4.483923e-01
## PZA02767.1	0	23	79	83	7.533162e-01
## PZA02722.1	0	16	90	79	3.974669e-01
## PZA01113.1	0	10	92	83	4.962917e-01
## PZA00975.1	0	8	85	92	5.987824e-01
## PZB00409.6	0	13	88	84	7.603683e-01
## PZA00947.1	0	15	57	113	1.746902e-05
## PZA02247.1	0	13	80	92	3.601961e-01

## PZA02981.2	0	16	88	81	5.902585e-01
## PZA00155.1	0	11	99	75	6.884504e-02
## wx1.1	0	10	65	110	6.697294e-04
## PZB00811.1	0	27	78	80	8.735811e-01
## PZA01972.14	0	5	88	92	7.655945e-01
## PZA02381.1	0	9	80	96	2.278000e-01
## PZA03613.1	0	6	83	96	3.312169e-01
## PZA02467.10	0	9	102	74	3.480848e-02
## PZA03470.1	0	11	59	115	2.182534e-05
## PZA02890.4	0	28	88	69	1.294271e-01
## PZA03073.28.26	0	15	112	58	3.448750e-05
## PZA01638.1	0	14	83	88	7.021947e-01
## PZA01523.1	0	15	94	76	1.674214e-01
## PZA00986.1	0	8	96	81	2.595442e-01
## PZA02823.1	0	13	85	87	8.787937e-01
## PHM12706.14	0	8	94	83	4.083444e-01
## PZB01110.6	0	19	58	108	1.041337e-04
## PZA01741.1	0	9	86	90	7.630246e-01
## PHM4757.14	0	34	75	76	9.351407e-01
## PZA00939.1	0	12	90	83	5.945874e-01
## PHM934.19	0	2	93	90	8.244958e-01
## PZA02266.3	0	18	70	97	3.667868e-02
## PZA02328.5	0	35	80	70	4.142162e-01
## PZA03713.1	0	24	89	72	1.803144e-01
## PZA00191.5	0	9	101	75	5.001640e-02
## PZA01810.2	0	16	102	67	7.095945e-03
## PZA03205.1	0	20	100	65	6.435091e-03
## PZA02040.2	0	12	90	83	5.945874e-01
## PZA00962.1	0	9	97	79	1.748444e-01
## PZA03687.1	0	11	91	83	5.441971e-01
## PHM3691.18	0	32	78	75	8.083652e-01
## PZA01919.2	0	12	92	81	4.029780e-01
## PZA03047.12	0	26	80	79	9.367899e-01
## PZA02209.2	0	12	91	82	4.938127e-01
## PHM15474.5	0	15	107	63	7.391071e-04
## PZA01983.1	0	14	100	71	2.657629e-02
## PZA03742.1	0	10	103	72	1.910992e-02
## PZA00029.17	0	12	86	87	9.393964e-01
## PZA00508.2	0	30	85	70	2.282693e-01
## sh1.12.11	0	8	88	89	9.400837e-01
## PZA02182.1	0	7	94	84	4.535368e-01
## PZA00824.2	0	12	94	79	2.541077e-01
## PZA00062.4	0	9	84	92	5.464936e-01
## PZA02984.10	0	13	93	79	2.857506e-01
## PZA00836.1	0	46	73	66	5.526912e-01
## PZA02383.1	0	21	92	72	1.183498e-01
## PZB00901.3.4	0	10	74	101	4.125002e-02
## PZA01141.1	0	16	94	75	1.438677e-01
## PZA02668.2	0	15	90	80	4.431023e-01
## PHM3852.23	0	11	93	81	3.629714e-01
## PZA02344.1	0	8	88	89	9.400837e-01
## PHM3626.3	0	17	80	88	5.370940e-01
## PHM12749.13	0	16	81	88	5.902585e-01
## PZA02688.2	0	7	74	104	2.453827e-02

## PZA01607.1	0	9	91	85	6.510766e-01
## PZA01427.1	0	13	90	82	5.418656e-01
## PZA00276.18	0	11	90	84	6.492108e-01
## PZA01978.23	0	11	86	88	8.794870e-01
## PZA03243.2	0	10	103	72	1.910992e-02
## PZA03235.1	0	17	58	110	6.023531e-05
## PHM4880.179	0	17	78	90	3.545395e-01
## PZA01210.1.2	0	11	90	84	6.492108e-01
## PHM14475.7	0	10	78	97	1.509270e-01
## PHM3896.9	0	13	82	90	5.418656e-01
## PZA02742.1	0	12	108	65	1.078408e-03
## PHM18513.156	0	9	92	84	5.464936e-01
## PZA00282.19	0	9	91	85	6.510766e-01
## PZA03032.19	0	15	112	58	3.448750e-05
## PZA03203.2	0	20	79	86	5.857884e-01
## PZA00708.3	0	12	84	89	7.038393e-01
## PZA01735.1	0	32	83	70	2.932642e-01
## PZA00084.2	0	10	92	83	4.962917e-01
## PHM2551.31	0	7	89	89	1.000000e+00
## PHM5817.15	0	7	90	88	8.808385e-01
## PZA02138.1	0	28	76	81	6.898612e-01
## PZA00285.3	0	35	75	75	1.000000e+00
## PZA01280.2	0	17	82	86	7.576207e-01
## PZA00667.2	0	18	110	57	4.109010e-05
## PZA00090.1	0	9	88	88	1.000000e+00
## PHM2423.33	0	7	94	84	4.535368e-01
## PHM5468.25	0	7	87	91	7.643200e-01
## PZA00566.5	0	20	82	83	9.379475e-01
## PZA02648.2	0	10	59	116	1.641464e-05
## PZA03723.1	0	9	92	84	5.464936e-01
## PHM824.17	0	15	118	52	4.149487e-07
## PZA02207.1	0	32	78	75	8.083652e-01
## PHM13823.7	0	25	102	58	5.042182e-04
## PHM5599.20	0	22	90	73	1.830105e-01
## PZA01284.6	0	13	88	84	7.603683e-01
## PZA01964.29	0	9	91	85	6.510766e-01
## PZB01222.1	0	3	75	107	1.769220e-02
## PZA02289.2	0	9	106	70	6.655605e-03
## PZA01787.1	0	7	87	91	7.643200e-01
## PZA00635.7	0	20	77	88	3.918049e-01
## PZA01029.1	0	17	89	79	4.404007e-01
## PZA01866.1	0	16	58	111	4.563558e-05
## PHM4818.15	0	9	91	85	6.510766e-01
## PZA02763.1	0	13	91	81	4.457659e-01
## PZA01426.1	0	2	89	94	7.116726e-01
## PZA03189.4	0	9	94	82	3.657123e-01
## PZA01154.1	0	20	91	74	1.856864e-01
## PZA02284.1	0	20	82	83	9.379475e-01
## PZB01658.1	0	31	83	71	3.335503e-01
## PZA01462.1	0	16	68	101	1.113410e-02
## PZA02741.1	0	24	85	76	4.781387e-01
## PZB01235.4	0	22	85	78	5.834981e-01
## PZA02699.1	0	15	108	62	4.186506e-04
## PZA02417.2	0	14	78	93	2.513491e-01

## PZA02012.7	0	16	80	89	4.887441e-01
## PZA01597.1	0	14	85	86	9.390437e-01
## PZA01348.1	0	12	90	83	5.945874e-01
## PZA01455.1	0	8	92	85	5.987824e-01
## PZA03670.1	0	10	60	115	3.215956e-05
## PZA01753.1	0	12	75	98	8.035022e-02
## PHM16437.20	0	16	90	79	3.974669e-01
## PZA00455.14.16	0	12	91	82	4.938127e-01
## PZA01216.1	0	15	96	74	9.154127e-02
## PZA03193.2	0	8	94	83	4.083444e-01
## PZA02545.1	0	11	57	117	5.400699e-06
## PHM7953.11	0	11	96	78	1.723862e-01
## PZA03247.1	0	11	82	92	4.483923e-01
## PZB02122.1	0	17	110	58	6.023531e-05
## PZA00980.1	0	7	97	81	2.304305e-01
## PZA01438.1	0	26	94	65	2.145674e-02
## vdac1a.1	0	12	88	85	8.195796e-01
## PZA00803.3	0	10	96	79	1.987646e-01
## PZA01196.2	0	16	72	97	5.447039e-02
## PZA03536.1	0	16	87	82	7.005224e-01
## PZA00316.10	0	11	93	81	3.629714e-01
## PZA03036.6	0	14	56	115	6.426682e-06
## PZA02077.1	0	10	93	82	4.056789e-01
## PZA02396.14	0	18	89	78	3.946552e-01
## PZA00432.4	0	8	94	83	4.083444e-01
## PZA01068.1	0	16	90	79	3.974669e-01
## PZA01763.2	0	18	87	80	5.880415e-01
## PZA03587.1	0	22	80	83	8.142257e-01
## PZA00348.11	0	14	107	64	1.007972e-03
## PZA01422.3	0	29	76	80	7.487740e-01
## PHM5359.10	0	16	100	69	1.709699e-02
## PZA02221.20	0	7	86	92	6.529131e-01
## PZA02134.3	0	15	108	62	4.186506e-04
## PZA03741.1	0	18	85	82	8.164239e-01
## PZA01995.2	0	42	73	70	8.019126e-01
## PZA02235.14	0	13	61	111	1.375881e-04
## PZA02633.4	0	11	91	83	5.441971e-01
## PZA02371.6	0	14	84	87	8.185458e-01
## PZA02465.1	0	14	84	87	8.185458e-01
## PZA02854.13	0	17	90	78	3.545395e-01
## PZA03070.9	0	25	102	58	5.042182e-04
## PZA02528.1	0	8	72	105	1.312233e-02
## PHM112.8	0	40	74	71	8.032552e-01
## PZA00647.9	0	35	80	70	4.142162e-01
## PZA00007.1	0	10	84	91	5.967012e-01
## PZB00942.1	0	11	82	92	4.483923e-01
## PZA01369.1	0	12	75	98	8.035022e-02
## PZA03564.1	0	23	79	83	7.533162e-01
## PZA01726.1	0	16	112	57	2.328935e-05
## PZD00038.2	0	16	100	69	1.709699e-02
## PZA01386.3	0	7	88	90	8.808385e-01
## PZA00881.1	0	22	79	84	6.953315e-01
## PZA03559.1	0	11	77	97	1.294698e-01
## PZA02478.7	0	15	85	85	1.000000e+00

## PZA02779.1	0	17	102	66	5.478553e-03
## PZA00015.5	0	11	60	114	4.244896e-05
## PZA00485.2	0	16	81	88	5.902585e-01
## PZA01254.2	0	11	90	84	6.492108e-01
## PZB00094.1	0	20	88	77	3.918049e-01
## PZA02278.1	0	12	84	89	7.038393e-01
## PZA02948.24	0	7	90	88	8.808385e-01
## PZB00540.3	0	9	66	110	9.111189e-04
## PZB01944.1	0	16	94	75	1.438677e-01
## PHM8909.12	0	29	78	78	1.000000e+00
## PZA03579.1	0	25	78	82	7.518296e-01
## PZA00436.7	0	32	76	77	9.355651e-01
## PZA01114.2	0	25	102	58	5.042182e-04
## PZA00214.1	0	29	78	78	1.000000e+00
## PZA03416.7	0	9	81	95	2.912928e-01
## PHM3765.7	0	8	83	94	4.083444e-01
## PZA02019.1	0	7	88	90	8.808385e-01
## PZA00515.10	0	14	83	88	7.021947e-01
## PZA01292.1	0	13	92	80	3.601961e-01
## PZA02402.1	0	19	109	57	5.437422e-05
## PHM890.20	0	13	114	58	1.955081e-05
## PZA00814.1	0	21	87	77	4.348797e-01
## PZA00132.17	0	13	89	83	6.473148e-01
## PZA03178.1	0	28	64	93	2.064294e-02
## PZA03744.1	0	16	118	51	2.551973e-07
## PHM1978.111	0	8	75	102	4.241306e-02
## PZA02941.7	0	13	86	86	1.000000e+00
## PHM15623.10	0	11	84	90	6.492108e-01
## PHM13122.43	0	15	101	69	1.411639e-02
## PZA02939.10	0	14	84	87	8.185458e-01
## PZA00783.1	0	16	111	58	4.563558e-05
## PZA01267.3	0	6	100	79	1.165050e-01
## PZA00362.1	0	13	88	84	7.603683e-01
## PZA03057.3	0	13	55	117	2.273507e-06
## PHM14104.23	0	26	84	75	4.753840e-01
## PZA02186.1	0	11	86	88	8.794870e-01
## PZA00279.2	0	15	107	63	7.391071e-04
## PZA00902.1	0	14	86	85	9.390437e-01
## PZA02589.1	0	16	107	62	5.370974e-04
## PZA00079.1	0	13	84	88	7.603683e-01
## PZA02029.21	0	11	93	81	3.629714e-01
## PZA00218.1	0	20	81	84	8.153346e-01
## PZA00934.2	0	9	95	81	2.912928e-01
## PZA00717.15	0	4	80	101	1.185432e-01
## PZA03102.9	0	16	79	90	3.974669e-01
## PHM16854.3	0	11	90	84	6.492108e-01
## PHM1968.22	0	12	89	84	7.038393e-01
## PZA02513.1	0	8	100	77	8.384743e-02
## PZD00030.2	0	11	102	72	2.294831e-02
## PZA00363.7	0	19	108	58	1.041337e-04
## PZA01779.1	0	19	81	85	7.562110e-01
## PHM8527.2	0	8	84	93	4.987350e-01
## PZA00463.3	0	11	79	95	2.251463e-01
## PZA01316.1	0	13	85	87	8.787937e-01

## PZA01962.12	0	15	116	54	1.982668e-06
## PZA00416.7	0	13	68	104	6.051564e-03
## PZA02470.2	0	14	84	87	8.185458e-01
## PZA02117.1	0	22	83	80	8.142257e-01
## PZA03461.1	0	12	95	78	1.961889e-01
## PZA01755.1	0	10	81	94	3.257514e-01
## PZA00390.7	0	10	93	82	4.056789e-01
## PZB01308.1	0	13	80	92	3.601961e-01
## PZA01211.1	0	13	82	90	5.418656e-01
## PZA03166.1	0	12	93	80	3.229706e-01
## PZA03012.7	0	2	92	91	9.410723e-01
## PZA01456.2	0	22	85	78	5.834981e-01
## PZA03459.1	0	17	89	79	4.404007e-01
## PZA00104.1	0	18	83	84	9.383194e-01
## PZA00892.5	0	10	117	58	8.196700e-06
## PZA00908.2	0	5	87	93	6.547208e-01
## PHM1184.26	0	6	94	85	5.011435e-01
## PZA02619.1	0	11	110	64	4.880131e-04
## PZA03049.24	0	24	80	81	9.371829e-01
## zb7.2	0	32	63	90	2.904902e-02
## PZA02113.1	0	17	91	77	2.800872e-01
## PZA02818.6	0	20	80	85	6.970916e-01
## PZB02058.1	0	11	88	86	8.794870e-01
## PZA02325.4	0	11	61	113	8.076797e-05
## PZA01542.1	0	18	89	78	3.946552e-01
## PZA00920.1	0	13	114	58	1.955081e-05
## PZA02044.1	0	34	72	79	5.689138e-01
## PZA00222.7	0	17	85	83	8.773706e-01
## PZA00294.22	0	13	94	78	2.224692e-01
## PZA00131.15	0	10	98	77	1.124106e-01
## PZA00106.10	0	11	89	85	7.617076e-01
## PHM5794.13	0	17	75	93	1.649148e-01
## PZA02969.9	0	9	83	93	4.509823e-01
## PZA00695.3	0	4	93	88	7.101556e-01
## PZA01601.1	0	4	73	108	9.280908e-03
## PHM15501.9	0	43	71	71	1.000000e+00
## PZB02179.1	0	15	110	60	1.256538e-04
## PHM4348.16	0	15	105	65	2.155976e-03
## PHM14152.18	0	7	89	89	1.000000e+00
## PZA01608.1	0	16	79	90	3.974669e-01
## PZA00760.1	0	4	97	84	3.339029e-01
## PZA01096.1	0	33	54	98	3.585225e-04
## PZA03155.3	0	13	98	74	6.725250e-02
## PZA03321.4	0	7	70	108	4.396446e-03
## PZA01652.1	0	43	71	71	1.000000e+00
## PHM4748.16	0	33	68	84	1.943659e-01
## PHM3457.6	0	24	74	87	3.055786e-01
## PZA00308.24	0	15	116	54	1.982668e-06
## PZA02614.2	0	20	100	65	6.435091e-03
## PZA02032.1	0	7	85	93	5.487559e-01
## PZA01729.1	0	28	83	74	4.725858e-01
## PZA03629.1	0	20	81	84	8.153346e-01
## PZA01693.1	0	21	80	84	7.547764e-01
## PZB00544.2	0	10	65	110	6.697294e-04

## PZA02129.1	0	6	83	96	3.312169e-01
## PZA01591.1	0	28	83	74	4.725858e-01
## PZA02239.12	0	11	90	84	6.492108e-01
## PZB00605.1	0	4	94	87	6.028504e-01
## PZA02111.1	0	10	59	116	1.641464e-05
## PZA00682.17.2	0	9	91	85	6.510766e-01
## bt2.7.4	0	17	82	86	7.576207e-01
## PZA03183.5	0	13	95	77	1.699118e-01
## PZA00148.3	0	30	78	77	9.359812e-01
## PZA03194.1	0	10	93	82	4.056789e-01
## PHM11114.7	0	2	82	101	1.601639e-01
## PZA01497.1	0	43	71	71	1.000000e+00
## PZA03717.1	0	13	89	83	6.473148e-01
## PZA00996.1	0	32	78	75	8.083652e-01
## PZB00648.5	0	9	86	90	7.630246e-01
## PHM7898.10	0	11	85	89	7.617076e-01
## PZB00014.1	0	12	57	116	7.267939e-06
## PZA02577.1	0	24	85	76	4.781387e-01
## PZA02449.13	0	14	93	78	2.513491e-01
## PZA03650.1	0	34	75	76	9.351407e-01
## PZA02385.6	0	25	77	83	6.352563e-01
## PZA02862.3	0	17	82	86	7.576207e-01
## PZA03301.2	0	9	84	92	5.464936e-01
## PZA03561.1	0	10	96	79	1.987646e-01
## PHM537.22	0	17	90	78	3.545395e-01
## PZA01566.1	0	15	103	67	5.761163e-03
## PZD00033.3	0	15	86	84	8.780884e-01
## lac1.3	0	18	88	79	4.861528e-01
## PZA03027.12	0	17	74	94	1.228226e-01
## PZA03020.8	0	16	89	80	4.887441e-01
## PZA02453.1	0	16	80	89	4.887441e-01
## PZA03069.8.4	0	4	92	89	8.235447e-01
## PZA00856.2	0	13	86	86	1.000000e+00
## PZA00309.1	0	1	101	83	1.845161e-01
## PZA02667.1	0	7	99	79	1.338572e-01
## PZA03168.5	0	12	92	81	4.029780e-01
## PZA01072.1	0	4	90	91	9.407483e-01
## PZA03344.2	0	43	71	71	1.000000e+00
## PZB00959.1	0	10	58	117	8.196700e-06
## PZA02048.2	0	18	89	78	3.946552e-01
## PHM5822.15	0	29	65	91	3.737299e-02
## PZA02480.1	0	7	86	92	6.529131e-01
## PZA02520.1	0	16	84	85	9.386847e-01
## PZA00071.2	0	2	104	79	6.459465e-02
## PZA01991.3	0	9	81	95	2.912928e-01
## PZA00048.1	0	15	93	77	2.197685e-01
## PZA00265.6	0	16	107	62	5.370974e-04
## PZA02955.3	0	14	72	99	3.894746e-02
## PZA01259.1	0	15	89	81	5.394982e-01
## PZA03142.5	0	10	84	91	5.967012e-01
## PZA03228.4	0	13	82	90	5.418656e-01
## PZA00694.6	0	11	98	76	9.535232e-02
## PZA03747.1	0	32	70	83	2.932642e-01
## PZA01960.1	0	4	80	101	1.185432e-01

## PHM5502.31	0	15	106	64	1.276314e-03
## PZA01533.2	0	15	85	85	1.000000e+00
## PZA00058.1	0	13	68	104	6.051564e-03
## PZA02386.2	0	40	74	71	8.032552e-01
## PZA02654.3	0	16	117	52	5.733031e-07
## PZB01062.3	0	9	95	81	2.912928e-01
## PZA00527.10	0	9	86	90	7.630246e-01
## PZA00752.1	0	7	98	80	1.772865e-01
## PZA03598.1	0	9	91	85	6.510766e-01
## PHM5526.25	0	28	75	82	5.763932e-01
## PZA02191.1	0	17	88	80	5.370940e-01
## PZA01230.1	0	9	92	84	5.464936e-01
## PZA02733.1	0	30	101	54	1.599237e-04
## PZD00072.2	0	6	89	90	9.404188e-01
## PZA02705.1	0	11	85	89	7.617076e-01
## PZA01902.1	0	15	80	90	4.431023e-01
## PZA00460.3.8	0	13	88	84	7.603683e-01
## PZA00801.1	0	11	94	80	2.885367e-01
## PZA01681.1	0	34	94	57	2.603740e-03
## PHM14055.6	0	17	81	87	6.434288e-01
## PHM2828.83	0	7	88	90	8.808385e-01
## PZA03596.1	0	10	60	115	3.215956e-05
## PZA02727.1	0	12	69	104	7.790879e-03
## PZA03404.1	0	18	76	91	2.457497e-01
## PHM12859.7	0	15	99	71	3.175334e-02
## PZA02135.2	0	24	85	76	4.781387e-01
## PZB01021.1	0	11	99	75	6.884504e-02
## PZA00152.1	0	14	57	114	1.307185e-05
## PHM4204.69	0	18	93	74	1.414902e-01
## PZA02175.1	0	37	75	73	8.694171e-01
## PZA01187.1	0	9	104	72	1.586133e-02
## PZA03465.1	0	9	88	88	1.000000e+00
## PZA02509.15	0	7	91	87	7.643200e-01
## PZA01038.1	0	7	88	90	8.808385e-01
## PZA02058.1	0	9	88	88	1.000000e+00
## PZD00054.1	0	14	91	80	4.002409e-01
## PZA00933.3	0	13	86	86	1.000000e+00
## PZA00616.13	0	36	79	70	4.609346e-01
## PZA01600.2	0	2	72	111	3.939538e-03
## PHM9162.135	0	17	90	78	3.545395e-01
## PZA00297.2	0	25	102	58	5.042182e-04
## PHM2672.19	0	18	87	80	5.880415e-01
## PZA02281.3	0	2	104	79	6.459465e-02
## PZA02471.5	0	10	90	85	7.054570e-01
## PZA02279.1	0	24	74	87	3.055786e-01
## PZA00505.6	0	10	87	88	9.397430e-01
## PZA00623.3	0	13	90	82	5.418656e-01
## PZA00409.17	0	15	85	85	1.000000e+00
## PZA02098.2	0	16	93	76	1.909777e-01
## PZA03644.1	0	17	83	85	8.773706e-01
## PZA02961.6	0	12	84	89	7.038393e-01
## PHM6428.11	0	16	70	99	2.569642e-02
## PZA01142.4	0	22	92	71	1.000014e-01
## PZA01744.1	0	38	79	68	3.642668e-01

## PZA02462.1	0	10	93	82	4.056789e-01
## PZA01336.1	0	10	85	90	7.054570e-01
## PZA03699.1	0	17	79	89	4.404007e-01
## PZA01934.6	0	12	111	62	1.950050e-04
## PHM4145.18	0	16	95	74	1.062274e-01
## PZA01476.1	0	9	98	78	1.316680e-01
## PZA03119.1	0	14	107	64	1.007972e-03
## PZA00543.12	0	11	86	88	8.794870e-01
## PZA03317.1	0	13	99	73	4.742539e-02
## PZA00224.4	0	26	85	74	3.830138e-01
## PZA00100.10	0	14	99	72	3.894746e-02
## PZA01135.1	0	8	94	83	4.083444e-01
## PZA01290.1	0	2	101	82	1.601639e-01
## PZA00256.27	0	43	71	71	1.000000e+00
## PHM2770.19	0	14	85	86	9.390437e-01
## PZB01569.7	0	11	76	98	9.535232e-02
## PZD00016.4	0	15	111	59	6.657149e-05
## PZA03597.1	0	22	80	83	8.142257e-01
## PZA02982.7	0	15	95	75	1.250469e-01
## PZA01790.1	0	16	102	67	7.095945e-03
## PHM1218.6	0	8	88	89	9.400837e-01
## PZA02148.1	0	21	79	85	6.394119e-01
## PZA01885.2	0	10	93	82	4.056789e-01
## PZA02824.4	0	13	97	75	9.344782e-02
## PZA01321.1	0	13	84	88	7.603683e-01
## PZA00088.3	0	7	94	84	4.535368e-01
## PZA02411.3	0	15	95	75	1.250469e-01
## PZA01563.1	0	10	91	84	5.967012e-01
## PHM3301.28	0	8	92	85	5.987824e-01
## PZA00991.2	0	13	90	82	5.418656e-01
## PHM15449.10	0	17	107	61	3.867308e-04
## PZA02496.1	0	16	84	85	9.386847e-01
## PZA03647.1	0	18	115	52	1.087609e-06
## PZA02686.1	0	8	92	85	5.987824e-01
## PZA00352.23	0	20	94	71	7.336593e-02
## PZA02681.8	0	37	75	73	8.694171e-01
## PZA02122.9	0	20	113	52	2.045831e-06
## PZA02653.12	0	9	96	80	2.278000e-01
## PZA03172.3	0	15	93	77	2.197685e-01
## PZA03024.16	0	22	92	71	1.000014e-01
## PZA02291.1	0	10	90	85	7.054570e-01
## PZA00223.4	0	16	75	94	1.438677e-01
## PZA01352.5	0	9	71	105	1.038180e-02
## PZA01297.1	0	1	84	100	2.381849e-01
## PZA02027.1	0	18	88	79	4.861528e-01
## PZA01425.2	0	13	84	88	7.603683e-01
## PZA02748.3	0	5	90	90	1.000000e+00
## PZA02641.2	0	16	88	81	5.902585e-01
## PZA01884.1	0	35	80	70	4.142162e-01
## PZA03188.3	0	13	91	81	4.457659e-01
## PZA00704.1	0	17	87	81	6.434288e-01
## PZA00381.4	0	9	84	92	5.464936e-01
## PZB01301.5	0	32	71	82	3.738433e-01
## PZA01759.1	0	17	81	87	6.434288e-01

```

## PZA02352.1      0      11  92  82 4.483923e-01
## PHM5296.6      0      11  92  82 4.483923e-01
## umc13.1        0      13  95  77 1.699118e-01
## PZA00172.12    0      46  63  76 2.701811e-01
## PZA00081.18    0      10 100  75 5.878172e-02
## PHM1959.26     0      17 110  58 6.023531e-05
## PZA03182.5     0      8   85  92 5.987824e-01
## PZA00386.4     0      9   88  88 1.000000e+00
## PHM3330.25     0      11  60 114 4.244896e-05
## PZA02147.1     0      16  93  76 1.909777e-01
## PHM1962.33     0      10  81  94 3.257514e-01
## PZA01619.1     0      12  92  81 4.029780e-01
## PZA02390.1     0      13  92  80 3.601961e-01
## PZA01802.3     0      20  82  83 9.379475e-01
## PZB00079.4     0      13  88  84 7.603683e-01
## PZA00245.20    0      12  88  85 8.195796e-01
## PHM5484.22     0      9   90  86 7.630246e-01
## PZA00643.13    0      24  79  82 8.130966e-01
## PHM1275.22     0      19  85  81 7.562110e-01
## PZA00380.10    0      25 102  58 5.042182e-04
## PZA03058.22.21 0      11  80  94 2.885367e-01
## PZB02002.1     0      15 111  59 6.657149e-05
## PZA00339.4     0      10  79  96 1.987646e-01
## PZA00447.8     0      9   85  91 6.510766e-01
## PZA00889.2     0      5   78 102 7.363827e-02

```

```
head(gt.maize)
```

```

##          chr missing AA  BB      P.value
## PZB01461.1  0      28 99  58 0.001067306
## PZA00951.1  0      16 81  88 0.590258451
## PHM1870.20  0      17 85  83 0.877370556
## PZA03521.1  0      11 89  85 0.761707564
## ZHD1.1       0      11 66 108 0.001452491
## PZA03488.1  0      4  91  90 0.940748272

```

```
table(gt.maize$P.value <0.05)
```

```

##
## FALSE  TRUE
## 865    241
table(gt.maize$P.value <0.05/totmar(maize))

```

```

##
## FALSE  TRUE
## 1043    63

```

```

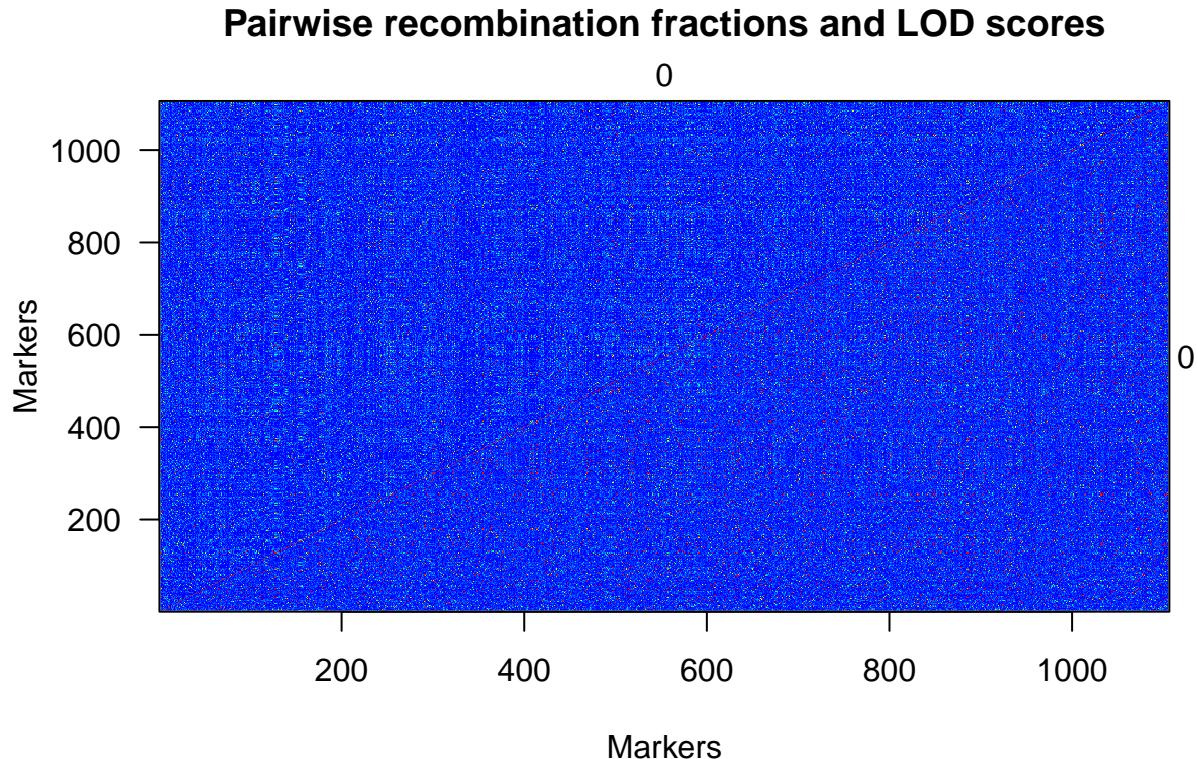
maize <- est.rf(cross = maize)
dim(maize$rf)

```

Estimation of the pairwise or two-point recombination fractions:

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

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



Again, this `heatmap` presents both the estimates (above diagonal) and LOD scores (below diagonal). The `heatmap` shows more blue, colder colors for non-linked markers (i.e. $r \approx 0.5$ and low LOD), and more red, warmer colors for the linked markers (i.e. $r < 0.35$ and high LOD). It can now see how many groups are formed by these markers:

```
maize <- formLinkageGroups(maize, max.rf=0.38, min.lod=6.25, reorgMarkers=TRUE)
summary(maize)
```

Marker grouping:

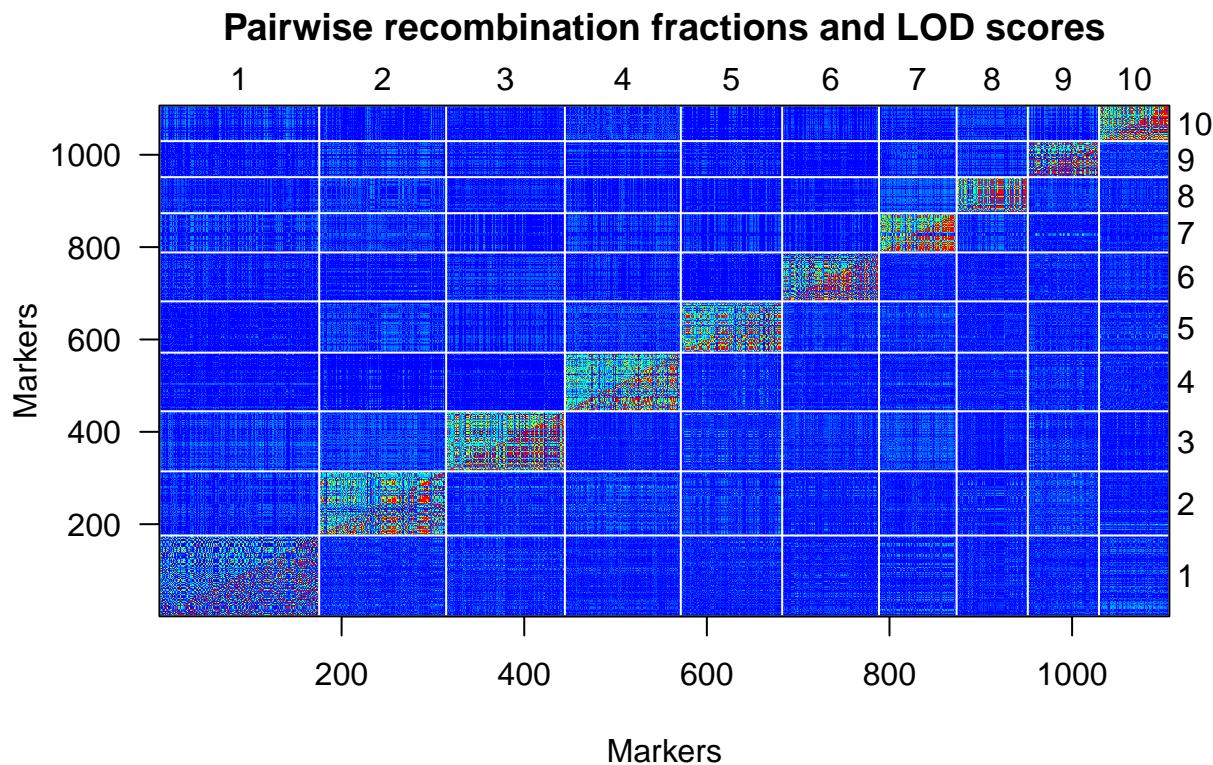
```
## Warning in summary.cross(maize): Some chromosomes > 1000 cM in length; there may be a problem with the
##   (Perhaps it is in basepairs?)

##   RI strains via selfing
##
##   No. individuals:    185
##
##   No. phenotypes:     33
##   Percent phenotyped: 100
##
##   No. chromosomes:    10
##   Autosomes:          1 2 3 4 5 6 7 8 9 10
##
##   Total markers:      1106
```

```

##      No. markers:      175 139 130 127 111 106 85 78 78 77
##      Percent genotyped: 91.9
##      Genotypes (%):    AA:51.2  BB:48.8
plotRF(maize, col.scheme = "redblue")

```



Marker Ordering: is done by using Multidimensional Scale (MDS) from `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/qt1, and it returns a new order that can be used by `switch.order()` R/qt1 function to yield a newly ordered linkage group.

First, `MAPpoly` package was installed and MDS algorithm used to build a chosen linkage group.

```
#library(mappoly)
```

```

#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)]
#  rec.mat[lower.tri(rec.mat)] <- mat[lower.tri(mat)]
#  rec.mat[upper.tri(rec.mat)] <- t(rec.mat)[upper.tri(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()
```

```
#for(c in 1:10) {
# mds.ord <- getMDSorder(cross = maize.mds, chr = c)
# maize.mds <- switch.order(cross = maize.mds, chr=c, order=mds.ord)
# plotRF(maize.mds, chr=c, col.scheme = "redblue")
# print(pull.map(maize.mds, chr = c))
# print(loglik.mds[c] <- attr(maize.mds$geno[[c]]$map, "loglik"))
#}
```

Reordering markers into each of the 10 linkage groups:

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

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

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

```
#save.image("maize_mds.Rdata")
```

```
load("maize_mds.RData")
```

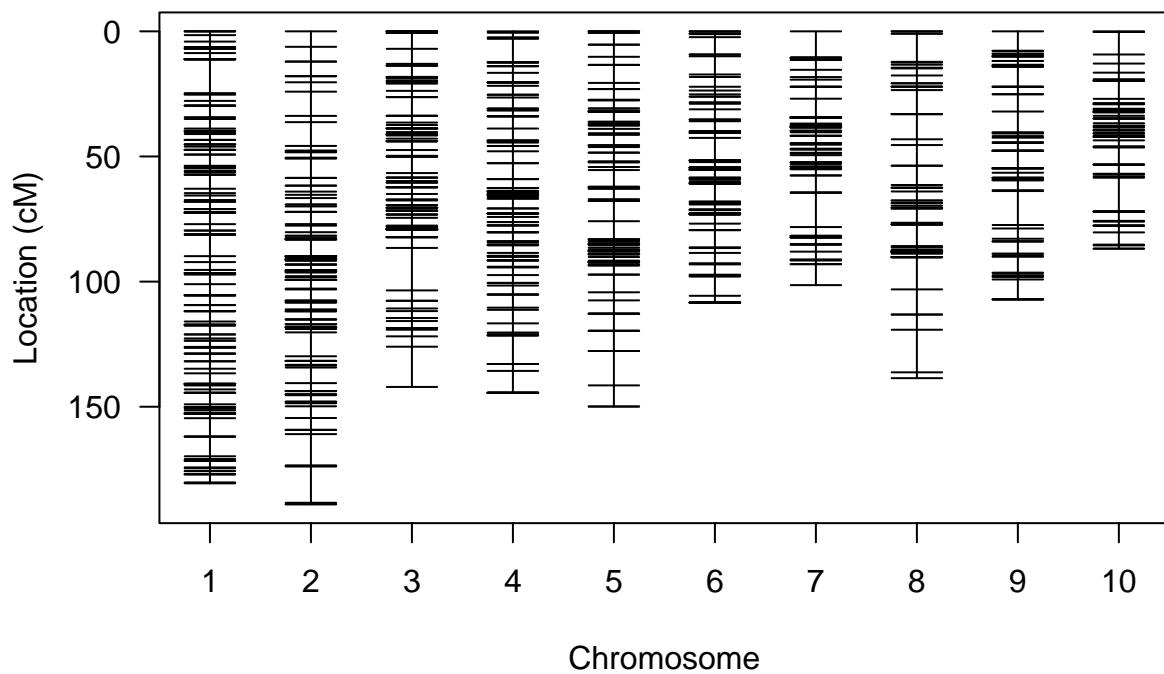
```
summaryMap(maize.mds)
```

Final map:

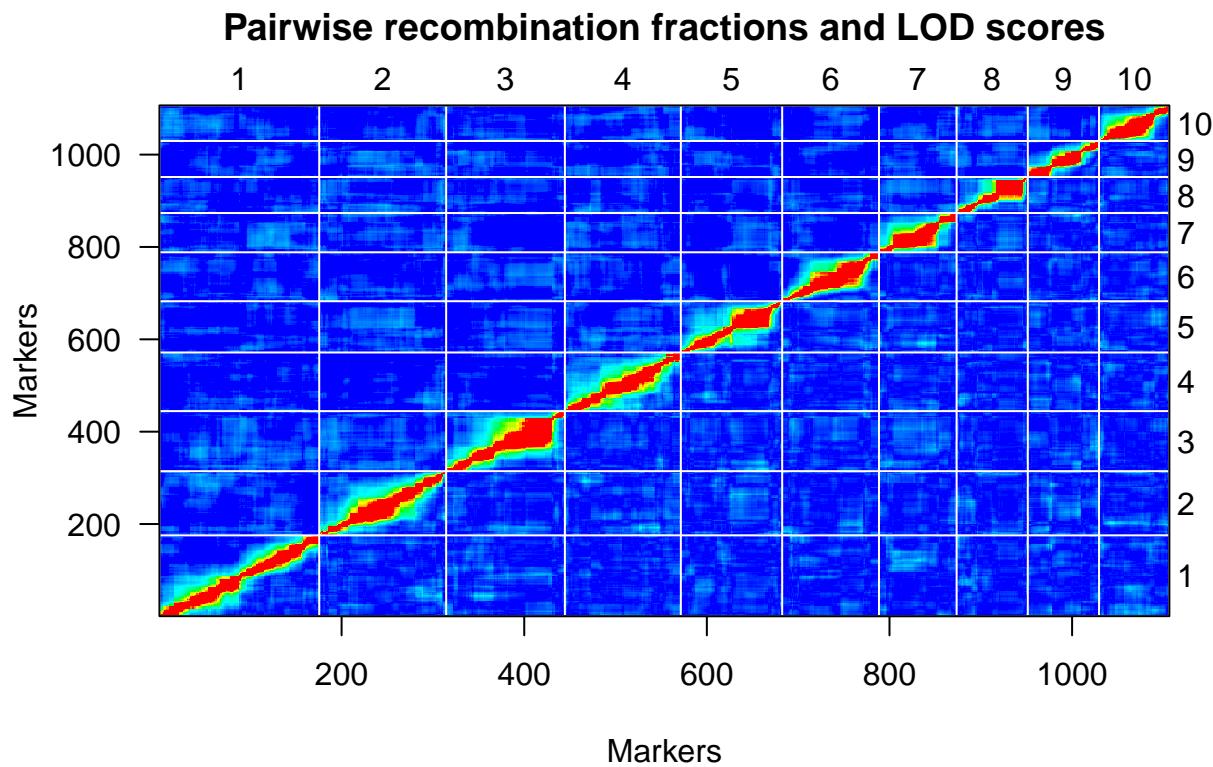
```
##      n.mar length ave.spacing max.spacing
## 1        175   180.6       1.0      13.6
## 2        139   189.0       1.4      14.5
## 3        130   142.1       1.1      17.0
## 4        127   144.5       1.1      11.5
## 5        111   149.9       1.4      13.8
## 6        106   108.4       1.0       9.0
## 7         85   101.4       1.2      13.6
## 8         78   138.6       1.8      17.0
## 9         78   107.1       1.4      13.6
## 10        77    86.8       1.1      13.5
## overall   1106  1348.4       1.2      17.0
```

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

Genetic map



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



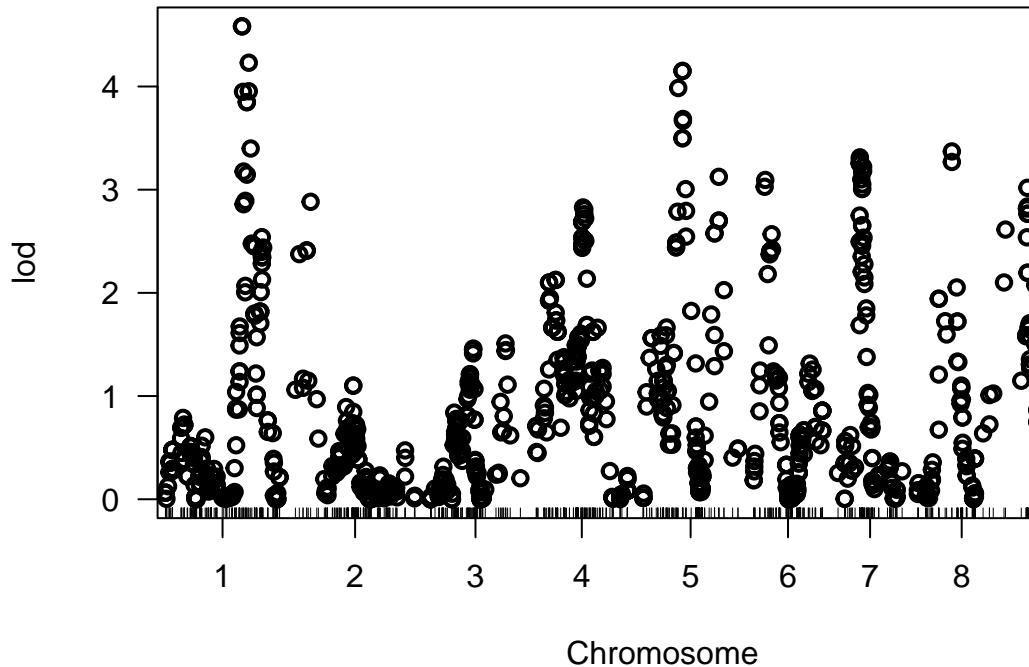
QTL Mapping

Used the linkage map to perform interval mapping (IM) for the trait "PlantHeight". Do not forget to run permutation tests to identify the LOD threshold to declare QTL at an alpha level of 0.05. Results for the QTL peak within each QTL region should be presented as a table showing QTL chromosome and location of its peak, their effects, associated LOD scores, and R-squared.

Approximate critical values previously obtained from permutation tests (ideally, should be run separately for each population):

```
maize.mr <- scanone(maize.mds, pheno.col = "PlantHeight", method = "mr")
plot(maize.mr, type = "p", main = "Single marker analysis (SMA)")
```

Single marker analysis (SMA)



```
Single marker analysis (SMA)
```

```
summary(maize.mr)
```

```
##          chr      pos    lod
## PZB01647.1      1 121.11 4.58
## PZA01887.1      2  24.10 2.88
## PHM12859.7      3 118.57 1.51
## PZA00635.7      4   74.17 2.83
## PZA03275.4.1    5   62.15 4.15
## PZA00904.1      6   18.24 3.09
## PZB00547.3      7   34.57 3.31
## PZA02722.1      8   53.70 3.37
## PZA01901.1      9    9.69 3.02
## PZA02095.10     10  12.87 4.14
```

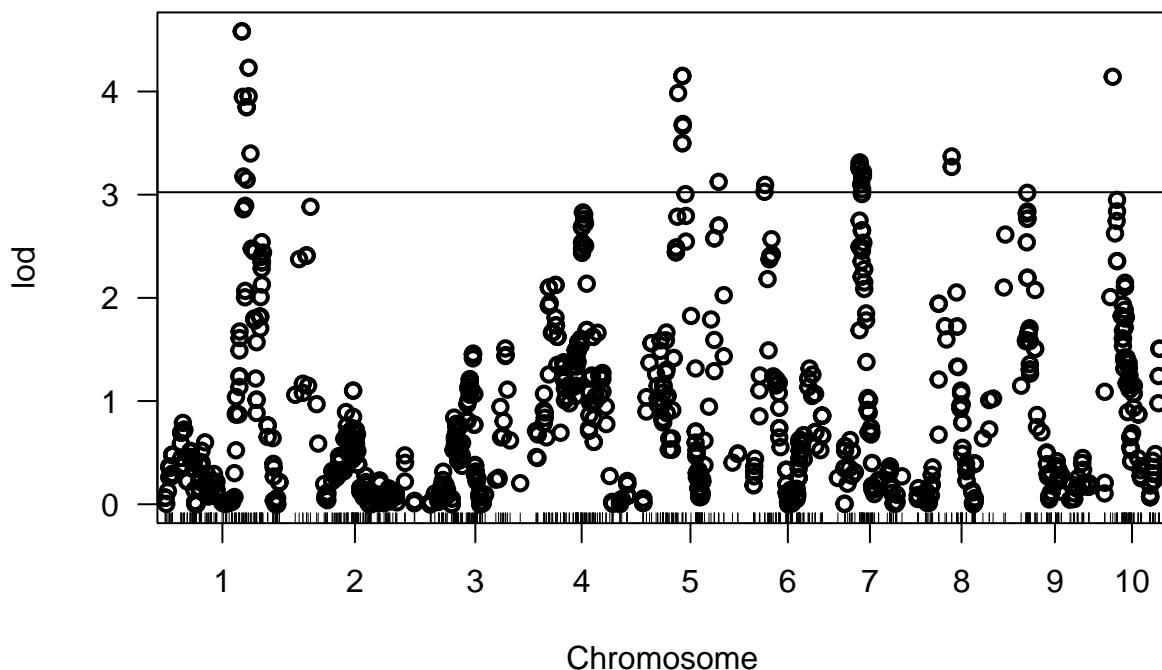
```
maize.perm.mr <- scanone(cross = maize.mds, pheno.col = "PlantHeight", method = "mr",
                           n.perm = 1000, verbose = FALSE, n.cluster = 2)
```

```
## -Running permutations via a cluster of 2 nodes.
```

```
lod.sma <- summary(maize.perm.mr, alpha = 0.05)
```

```
plot(maize.mr, type = "p", main = "Single marker analysis (SMA)") +abline(h = lod.sma)
```

Single marker analysis (SMA)



```
## integer(0)
maize.mr.sig <- summary(maize.mr, perms = maize.perm.mr, alpha = 0.05)
maize.mr.sig
```

```
##           chr   pos   lod
## PZA03001.15    1 121.1 4.58
## PZA01681.1     5  62.2 4.15
## PZA00904.1     6 18.2 3.09
## PZB00547.3     7 34.6 3.31
## PZA02722.1     8 53.7 3.37
## PZA02095.10    10 12.9 4.14
```

```
maize.mds <- calc.genoprob(cross = maize.mds, step = 1)
maize.im <- scanone(cross = maize.mds, pheno.col = "PlantHeight", method = "hk")
summary(maize.im)
```

Interval mapping (IM)

```
##           chr   pos   lod
## PZB01647.1     1 121.11 4.14
## PZA01887.1     2  24.10 2.81
## PZA00948.1     3  67.58 1.60
## c4.loc77        4  77.00 3.06
## c5.loc58        5  58.00 4.44
## c6.loc18        6  18.00 3.23
## c7.loc39        7  39.00 3.30
```

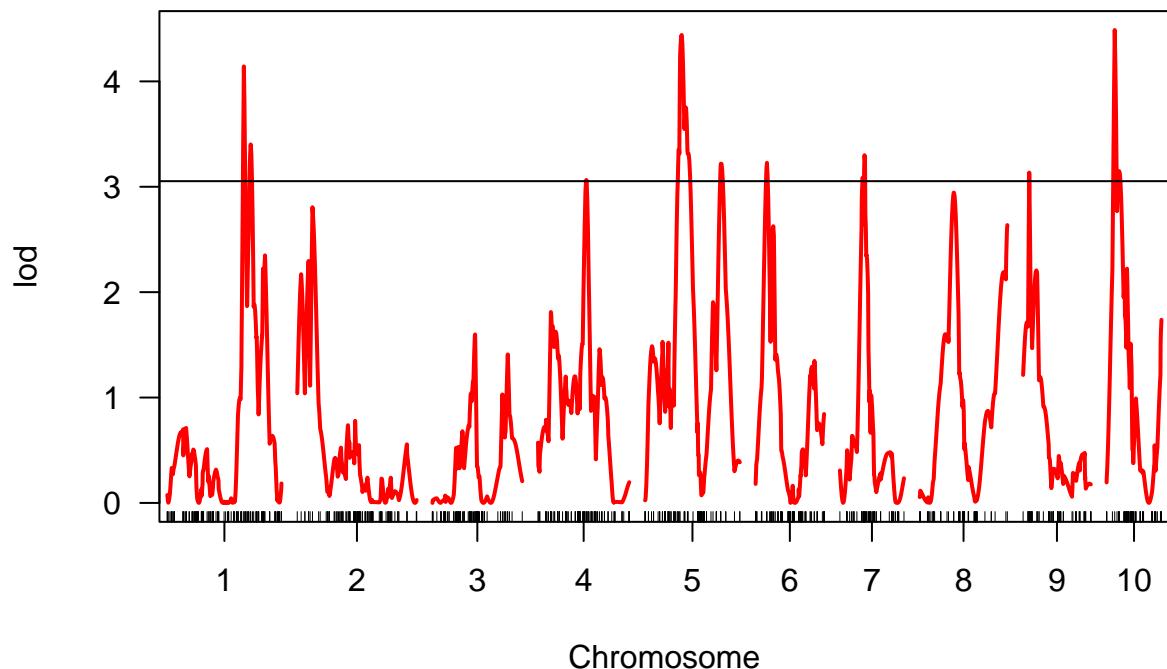
```

## c8.loc54      8  54.00 2.94
## PZA01901.1   9   9.69 3.13
## PZA02095.10 10  12.87 4.49

#perm.im <- scanone(cross = maize.mds, pheno.col = "PlantHeight", method = "hk", n.perm = 1000, n.clust
#save(perm.im, file = "perm.im.RData")
load("perm.im.RData")
lod.im <- summary(perm.im, alpha = 0.05)
plot(maize.im, col = "red", main = "Interval mapping (IM)")+abline(h= lod.im)

```

Interval mapping (IM)



```
## integer(0)
```

Notice we can use `maize.im.sig` to extract the chromosomes (`chr`) and positions (`pos`) of our significant QTL:

Finally, the `makeqtl()` and `fitqtl()` are used to show the QTL effect estimates for an RIL population based on an object derived from the function `sim.gen()` :

We can also build a multiple QTL model, including all three QTL:

```
maize.im.sig <- summary(maize.im, perms = perm.im, alpha = 0.05)
maize.im.sig
```

	chr	pos	lod
## PZB01647.1	1	121.11	4.14
## c4.loc77	4	77.00	3.06
## c5.loc58	5	58.00	4.44
## c6.loc18	6	18.00	3.23
## c7.loc39	7	39.00	3.30

```

## PZA01901.1      9   9.69 3.13
## PZA02095.10    10  12.87 4.49
chr <- maize.im.sig$chr
chr

## [1] 1 4 5 6 7 9 10
## Levels: 1 2 3 4 5 6 7 8 9 10
pos <- maize.im.sig$pos
pos

## [1] 121.112323 77.000000 58.000000 18.000000 39.000000 9.688036 12.869866
maize.mds <- sim.gen( cross = maize.mds, step = 1)
maize.im.qtl <- makeqtl(cross = maize.mds, chr = chr, pos = pos)
maize.im.qtl

## QTL object containing imputed genotypes, with 16 imputations.
##
##          name chr      pos n.gen
## Q1  10121.1    1 121.112      2
## Q2  4077.0     4 77.000      2
## Q3  5058.0     5 58.000      2
## Q4  6018.0     6 18.000      2
## Q5  7039.0     7 39.000      2
## Q6  909.7      9 9.688      2
## Q7  10012.9    10 12.870      2

formula.im <- as.formula(paste("y", paste0("Q", c(1:length(maize.im.sig$pos))),
                                collapse = "+"), sep = " ~ "))
maize.im.fit <- fitqtl(cross = maize.mds, pheno.col = "PlantHeight",
                        qtl = maize.im.qtl, formula = formula.im, get.est = TRUE)
summary(maize.im.fit)

##
## fitqtl summary
##
## Method: multiple imputation
## Model: normal phenotype
## Number of observations : 185
##
## Full model result
## -----
## Model formula: y ~ Q1 + Q2 + Q3 + Q4 + Q5 + Q6 + Q7
##
##          df      SS      MS      LOD      %var Pvalue(Chi2) Pvalue(F)
## Model    7 16837.14 2405.3059 23.13593 43.78117          0          0
## Error 177 21620.36 122.1489
## Total 184 38457.50
##
##
## Drop one QTL at a time ANOVA table:
## -----
##          df Type III SS      LOD      %var F value Pvalue(Chi2) Pvalue(F)
## 10121.1  1      3431.2 5.917 8.922 28.091      0.000 3.41e-07 ***
## 4077.0   1      986.7 1.793 2.566 8.077      0.004 0.005009 **

```

```

## 5058.0   1    1712.1 3.062 4.452 14.017      0.000 0.000245 ***
## 6018.0   1     570.6 1.047 1.484  4.672      0.028 0.032008 *
## 7039.0   1    2531.8 4.449 6.583 20.727      0.000 9.82e-06 ***
## 909.7    1    1357.1 2.446 3.529 11.110      0.001 0.001045 **
## 10012.9   1    1722.1 3.079 4.478 14.098      0.000 0.000235 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##
## Estimated effects:
## -----
##          est       SE      t
## Intercept 156.5637  0.8884 176.231
## 10121.1    -4.5121  0.8667 -5.206
## 4077.0     2.3726  0.8563  2.771
## 5058.0     3.1564  0.8950  3.527
## 6018.0     -1.8499  0.8664 -2.135
## 7039.0     4.0699  0.9131  4.457
## 909.7      2.8030  0.8505  3.296
## 10012.9    3.0967  0.8437  3.670

```

```
#save.image("maize_im.RData")
```

```

perm.cim <- 7.4
#maize.cim10 <- cim(cross = maize.mds, pheno.col = "PlantHeight", method = "hk", n.marcovar = 2 * sqrt(n
#save(maize.cim10, file = "maize.cim10.RData")
load("maize.cim10.RData")
summary(maize.cim10)

```

Composite interval mapping (CIM)

```

##          chr  pos  lod
## c1.loc122   1 122.0 24.51
## c2.loc54    2  54.0  5.26
## PZA00892.5  3  36.5  1.65
## c4.loc76    4  76.0  7.76
## c5.loc120   5 120.0  7.62
## PZA01079.1  6  93.1  1.03
## PZA01062.1  7  39.7  7.99
## c8.loc58    8  58.0  3.60
## PZA02478.7  9  56.5  3.66
## PZA02578.1 10  85.5  4.38

```

```
summary(maize.cim10, threshold = perm.cim)
```

```

##          chr  pos  lod
## c1.loc122   1 122.0 24.51
## c4.loc76    4  76.0  7.76
## c5.loc120   5 120.0  7.62
## PZA01062.1  7  39.7  7.99

```

```

#maize.cim15 <- cim(cross = maize.mds, pheno.col = "PlantHeight", method = "hk", n.marcovar = 2 * sqrt(n
#save(maize.cim15, file = "maize.cim15.RData")
load("maize.cim15.RData")
summary(maize.cim15)

```

```

##          chr pos    lod
## c1.loc122     1 122 18.28
## PZA01608.1   2 103  3.34
## c3.loc2       3   2  3.64
## c4.loc74      4  74  6.19
## c5.loc120     5 120  6.57
## c6.loc16      6  16  1.25
## c7.loc38      7  38  8.32
## c8.loc134     8 134  5.93
## c9.loc46      9  46  2.55
## c10.loc86     10 86  4.42
summary(maize.cim15, threshold = perm.cim)

##          chr pos    lod
## c1.loc122     1 122 18.28
## c7.loc38      7  38  8.32

#maize.cim20 <- cim(cross = maize.mds, pheno.col = "PlantHeight", method = "hk", n.marcovar = 2 * sqrt(
#save(maize.cim20, file = "maize.cim20.RData")
load("maize.cim20.RData")
summary(maize.cim20)

##          chr pos    lod
## c1.loc122     1 122.0 16.51
## PZA01887.1   2  24.1  5.37
## PHM1675.29   3  47.4  4.09
## c4.loc74      4  74.0  5.04
## c5.loc120     5 120.0  5.69
## PZA02746.2   6  28.3  1.12
## PZB01110.6   7  34.6  7.14
## c8.loc128     8 128.0  5.84
## PZA02247.1   9  59.5  3.47
## PZA02578.1   10 85.5  4.20
summary(maize.cim20, threshold = perm.cim)

##          chr pos    lod
## c1.loc122     1 122 16.5

#maize.cimInf <- cim(cross = maize.mds, pheno.col = "PlantHeight", method = "hk", n.marcovar = 2 * sqrt(
#save(maize.cimInf, file = "maize.cimInf.RData")
load("maize.cimInf.RData")
summary(maize.cimInf)

##          chr pos    lod
## PZB01647.1   1 121.1 17.056
## c2.loc94      2  94.0  2.871
## c3.loc56      3  56.0  0.545
## c4.loc74      4  74.0  5.681
## c5.loc120     5 120.0 10.392
## PZA02388.1   6 108.4  2.950
## PZA00693.3   7  37.5  7.835
## c8.loc128     8 128.0  4.312
## c9.loc50      9  50.0  4.844
## c10.loc14     10 14.0  7.113

```

```

summary(maize.cimInf, threshold = perm.cim)

##           chr   pos   lod
## PZB01647.1    1 121.1 17.06
## c5.loc120     5 120.0 10.39
## PZA00693.3    7  37.5  7.84

```

The green dots represent the location of markers selected as covariates (cofactors) for the CIM search with window = Inf.

Noticed that the QTL on chromosome 1 and 3 that we had identified using IM is right below the threshold for the CIM analysis - so we called them suggestive QTL here. Depending on the researcher's decision, we could low the threshold a bit to include it as a QTL using CIM, which is probably okay. We'll see, however, a better way to deal with it when running a multiple-QTL model, which is our next topic.

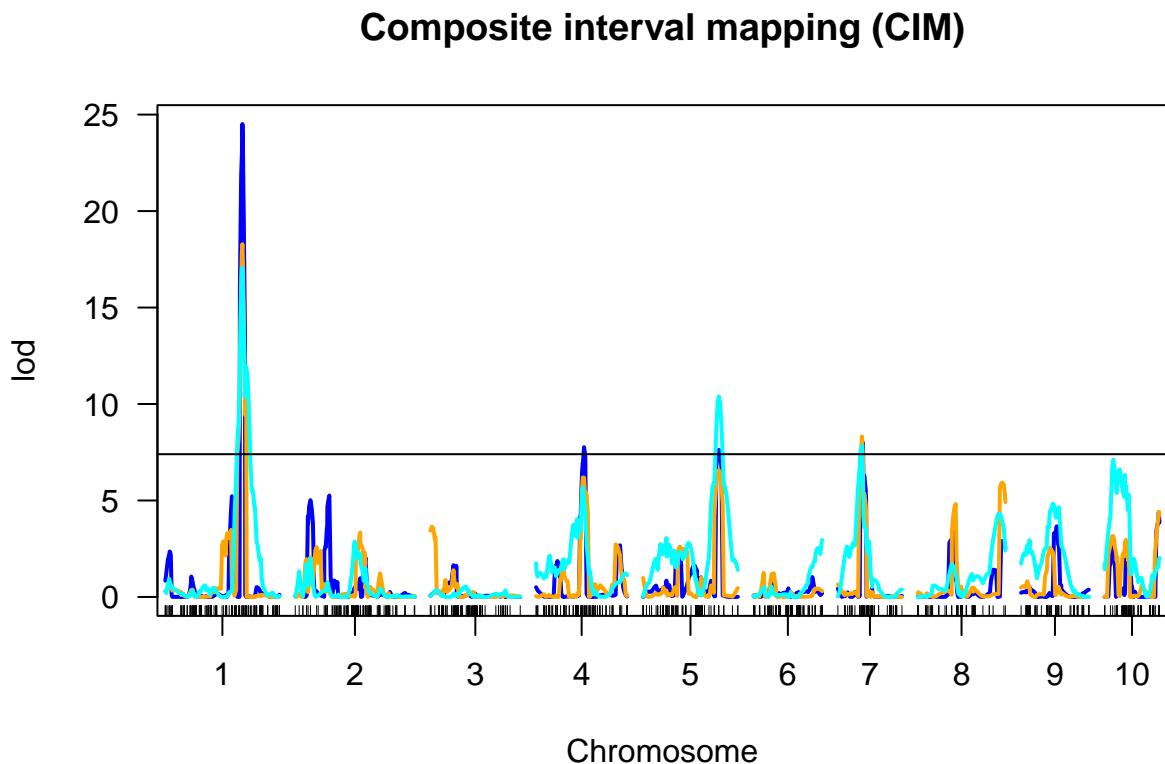
Right now, suppose we want to investigate the QTL estimates under CIM with window = 10 . We just need to store the QTL chromosomes and positions from our selected model (CIM with)

However, we noticed that only one QTL on chromosome 1 is listed (the one with the highest LOD score). We need to find the other one by looking at the positions in that chromosome that have a LOD score greater than our threshold of 7.39:

```

plot(maize.cim10, maize.cim15, maize.cimInf, col = c("blue", "orange", "cyan")), main = "Composite interval mapping (CIM)"

```



```

## integer(0)
maize.cim.sig <- summary(maize.cim10, threshold = perm.cim)
maize.cim.sig

```

```

##           chr   pos   lod

```

```

## c1.loc122      1 122.0 24.51
## c4.loc76       4  76.0  7.76
## c5.loc120      5 120.0  7.62
## PZA01062.1    7  39.7  7.99

peak.markers <- which(maize.cim10$lod[maize.cim10$chr == 1] > 7.4)
maize.cim10$lod[peak.markers]

## [1] 16.10694 21.81860 22.91849 22.91849 24.50957 23.78671 20.87421 20.87421
## [9] 20.18195 13.58196 13.20975

maize.cim10$pos[peak.markers]

## [1] 118.0000 120.0000 121.1123 121.1123 122.0000 122.7166 123.6104 123.6104
## [9] 124.0000 126.0000 126.0952

chr <- c(1, maize.cim.sig$chr)
pos <- c(124, maize.cim.sig$pos)
chr

## [1] 1 1 4 5 7

pos

## [1] 124.00000 122.00000 76.00000 120.00000 39.70343

In order to show the QTL effect estimates for an RIL population, we need to use the function sim.geno(), then makeqtl() and fitqtl():

maize.mds <- sim.geno(maize.mds, step = 1)
maize.cim.qtl <- makeqtl(cross = maize.mds, chr = chr, pos = pos)
maize.cim.qtl

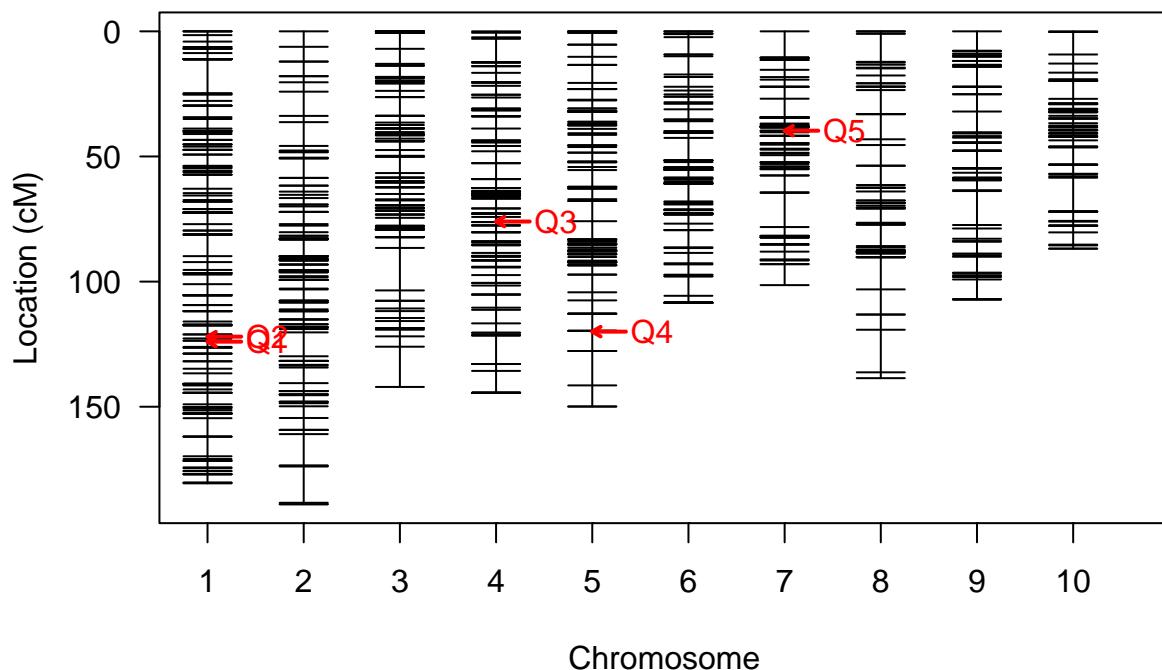
## QTL object containing imputed genotypes, with 16 imputations.

## name chr pos n.gen
## Q1 10124.0 1 124.000 2
## Q2 10122.0 1 122.000 2
## Q3 4076.0 4  76.000 2
## Q4 50120.0 5 120.000 2
## Q5 7039.7 7  39.703 2

plot(maize.cim.qtl)

```

Genetic map



```

formula <- as.formula(paste("y", paste0("Q", c(1:length(maize.cim.sig$pos)),
                                         collapse = "+"), sep = " ~ "))
maize.cim.fit <- fitqtl(cross = maize.mds, pheno.col = "PlantHeight",
                           qtl = maize.cim.qtl, formula = formula, get.est = TRUE)
summary(maize.cim.fit)

##
##      fitqtl summary
##
## Method: multiple imputation
## Model: normal phenotype
## Number of observations : 185
##
## Full model result
## -----
## Model formula: y ~ Q1 + Q2 + Q3 + Q4
##
##          df        SS        MS       LOD      %var Pvalue(Chi2)   Pvalue(F)
## Model     4  9789.352 2447.3381 11.80128 25.45499 4.452028e-11 7.874845e-11
## Error  180 28668.145   159.2675
## Total  184 38457.498
##
##
## Drop one QTL at a time ANOVA table:
## -----
##          df Type III SS       LOD      %var F value Pvalue(Chi2)   Pvalue(F)

```

```

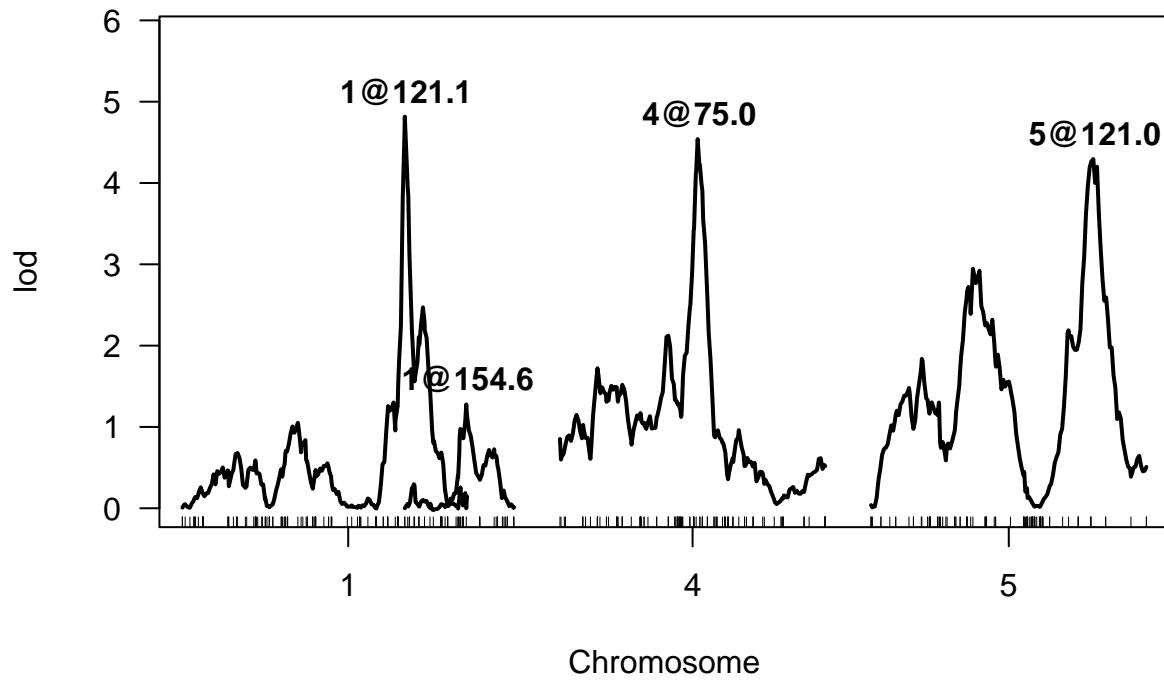
## 10124.0 1      149.3 0.2087 0.3883 0.9377      0.327  0.33418
## 10122.0 1      1177.4 1.6169 3.0615 7.3925      0.006  0.00719 **
## 4076.0   1      3186.6 4.2341 8.2860 20.0077     0.000  1.36e-05 ***
## 50120.0  1      3316.4 4.3975 8.6236 20.8229     0.000  9.30e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##
## Estimated effects:
## -----
##           est        SE        t
## Intercept 157.3957  0.9337 168.575
## 10124.0    2.1817  2.5730  0.848
## 10122.0   -6.6339  2.5469 -2.605
## 4076.0     4.1652  0.9576  4.350
## 50120.0    4.2321  0.9371  4.516

maize.ref <- refineqtl(cross = maize.mds, pheno.col = "PlantHeight", qtl = maize.cim.qtl, formula = fo

## pos: 124 122 76 120
## Iteration 1
##   Q1 pos: 124 -> 154.5864
##   LOD increase:  0.931
##   Q3 pos: 76 -> 75
##   LOD increase:  0.096
##   Q2 pos: 122 -> 121.1123
##   LOD increase:  0.421
##   Q4 pos: 120 -> 121
##   LOD increase:  0.026
## all pos: 124 122 76 120 -> 154.5864 121.1123 75 121
## LOD increase at this iteration:  1.475
## Iteration 2
##   Q4 pos: 121 -> 121
##   LOD increase:  0
##   Q3 pos: 75 -> 75
##   LOD increase:  0
##   Q1 pos: 154.5864 -> 154.5864
##   LOD increase:  0
##   Q2 pos: 121.1123 -> 121.1123
##   LOD increase:  0
## all pos: 154.5864 121.1123 75 121 -> 154.5864 121.1123 75 121
## LOD increase at this iteration:  0
## overall pos: 124 122 76 120 -> 154.5864 121.1123 75 121
## LOD increase overall:  1.475

plotLodProfile(maize.ref)

```



```
#perm.mim <- scantwo(maize.mds, pheno.col = "PlantHeight", method = "hk", n.perm = 1000, n.cluster = 2)
#save(perm.mim, file = "perm.mim.RData")
load("perm.mim.RData")
threshold.mim <- summary(perm.mim, alpha = 0.05)
threshold.mim
```

Multiple Interval Mapping (MIM)

```
## (1000 permutations)
##   full fv1 int add av1 one
## 5% 6.44 4.78 4.01 5.1 2.93 3.07
penalties <- calc.penalties(perm.mim)
penalties
```

```
##      main     heavy     light
## 3.069812 4.008667 1.705571
```

```
maize.step <- stepwiseqtl(maize.mds, pheno.col = "PlantHeight", max.qtl = 6, method = "hk", penalties =
```

Main effect

```
## -Initial scan
## initial lod: 4.487229
## ** new best ** (pLOD increased by 1.4174)
##   no.qtl = 1   pLOD = 1.417417   formula: y ~ Q1
```

```

## -Step 1
## ---Scanning for additive qtl
##     plod = 3.194404
## ---Scanning for QTL interacting with Q1
##     plod = 1.511306
## ---Refining positions
##     no.qtl = 2   pLOD = 3.194404   formula: y ~ Q1 + Q2
## ** new best ** (pLOD increased by 1.777)
## -Step 2
## ---Scanning for additive qtl
##     plod = 5.525958
## ---Scanning for QTL interacting with Q1
##     plod = 3.822307
## ---Scanning for QTL interacting with Q2
##     plod = 3.874844
## ---Look for additional interactions
##     plod = 1.511306
## ---Refining positions
##     no.qtl = 3   pLOD = 5.525958   formula: y ~ Q1 + Q2 + Q3
## ** new best ** (pLOD increased by 2.3316)
## -Step 3
## ---Scanning for additive qtl
##     plod = 7.063851
## ---Scanning for QTL interacting with Q1
##     plod = 5.644448
## ---Scanning for QTL interacting with Q2
##     plod = 5.411262
## ---Scanning for QTL interacting with Q3
##     plod = 5.421449
## ---Look for additional interactions
##     plod = 3.874844
## ---Refining positions
##     no.qtl = 4   pLOD = 7.063851   formula: y ~ Q1 + Q2 + Q3 + Q4
## ** new best ** (pLOD increased by 1.5379)
## -Step 4
## ---Scanning for additive qtl
##     plod = 7.165081
## ---Scanning for QTL interacting with Q1
##     plod = 6.100364
## ---Scanning for QTL interacting with Q2
##     plod = 5.476568
## ---Scanning for QTL interacting with Q3
##     plod = 5.567667
## ---Scanning for QTL interacting with Q4
##     plod = 6.269987
## ---Look for additional interactions
##     plod = 5.603833
## ---Refining positions
##     Moved a bit
##     no.qtl = 5   pLOD = 7.222111   formula: y ~ Q1 + Q2 + Q3 + Q4 + Q5
## ** new best ** (pLOD increased by 0.1583)
## -Step 5
## ---Scanning for additive qtl
##     plod = 7.717983

```

```

## ---Scanning for QTL interacting with Q1
##     plod = 7.390984
## ---Scanning for QTL interacting with Q2
##     plod = 6.030969
## ---Scanning for QTL interacting with Q3
##     plod = 6.192371
## ---Scanning for QTL interacting with Q4
##     plod = 6.118072
## ---Scanning for QTL interacting with Q5
##     plod = 6.79887
## ---Look for additional interactions
##     plod = 5.845643
## ---Refining positions
## --- Moved a bit
##     no.qtl = 6 pLOD = 7.812867 formula: y ~ Q1 + Q2 + Q3 + Q4 + Q5 + Q6
## ** new best ** (pLOD increased by 0.5908)
## -Starting backward deletion
## ---Dropping Q6
##     no.qtl = 5 pLOD = 6.952984 formula: y ~ Q1 + Q2 + Q3 + Q4 + Q5
## ---Refining positions
## --- Moved a bit
## ---Dropping Q5
##     no.qtl = 4 pLOD = 7.051856 formula: y ~ Q1 + Q2 + Q3 + Q4
## ---Refining positions
## --- Moved a bit
## ---Dropping Q4
##     no.qtl = 3 pLOD = 5.525958 formula: y ~ Q1 + Q2 + Q3
## ---Refining positions
## ---Dropping Q3
##     no.qtl = 2 pLOD = 3.194404 formula: y ~ Q1 + Q2
## ---Refining positions
## ---Dropping Q2
##     no.qtl = 1 pLOD = 1.417417 formula: y ~ Q1
## ---Refining positions
## ---One last pass through refineqtl

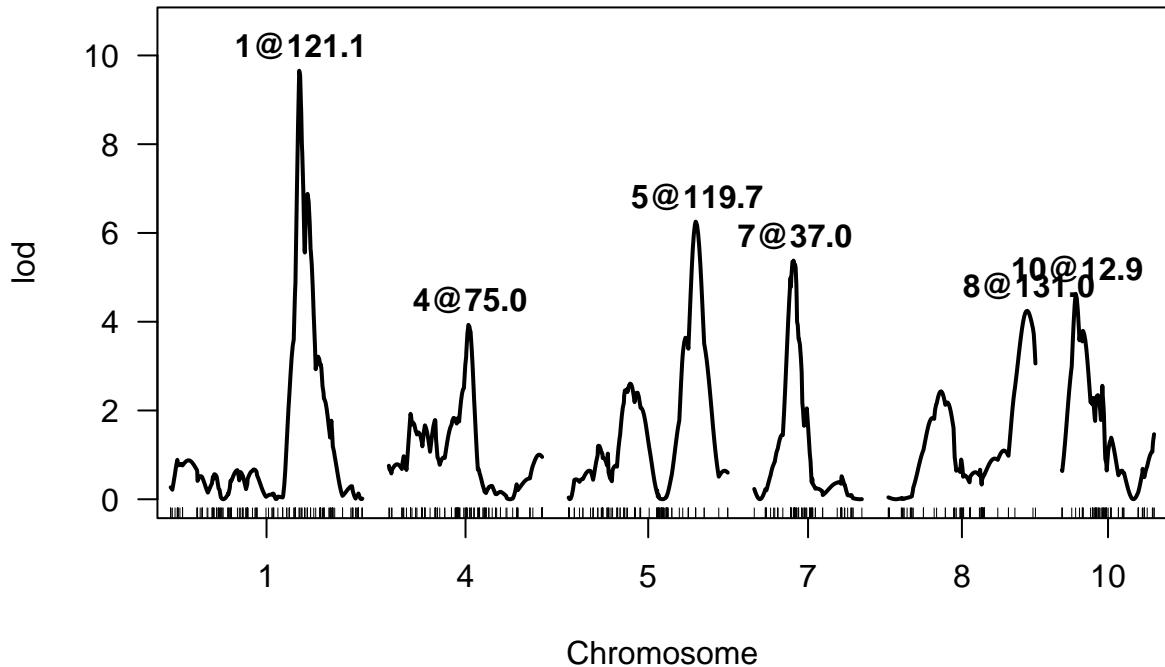
summary(maize.step)

## QTL object containing genotype probabilities.
##
##      name chr    pos n.gen
## Q1 10121.1   1 121.11     2
## Q2 4075.0    4  75.00     2
## Q3 50119.7   5 119.66     2
## Q4 7037.0    7  37.00     2
## Q5 80131.0   8 131.00     2
## Q6 10012.9   10 12.87    2
##
## Formula: y ~ Q1 + Q2 + Q3 + Q4 + Q5 + Q6
##
## pLOD: 7.813

plotLodProfile(maize.step, main ="PlantHeight")

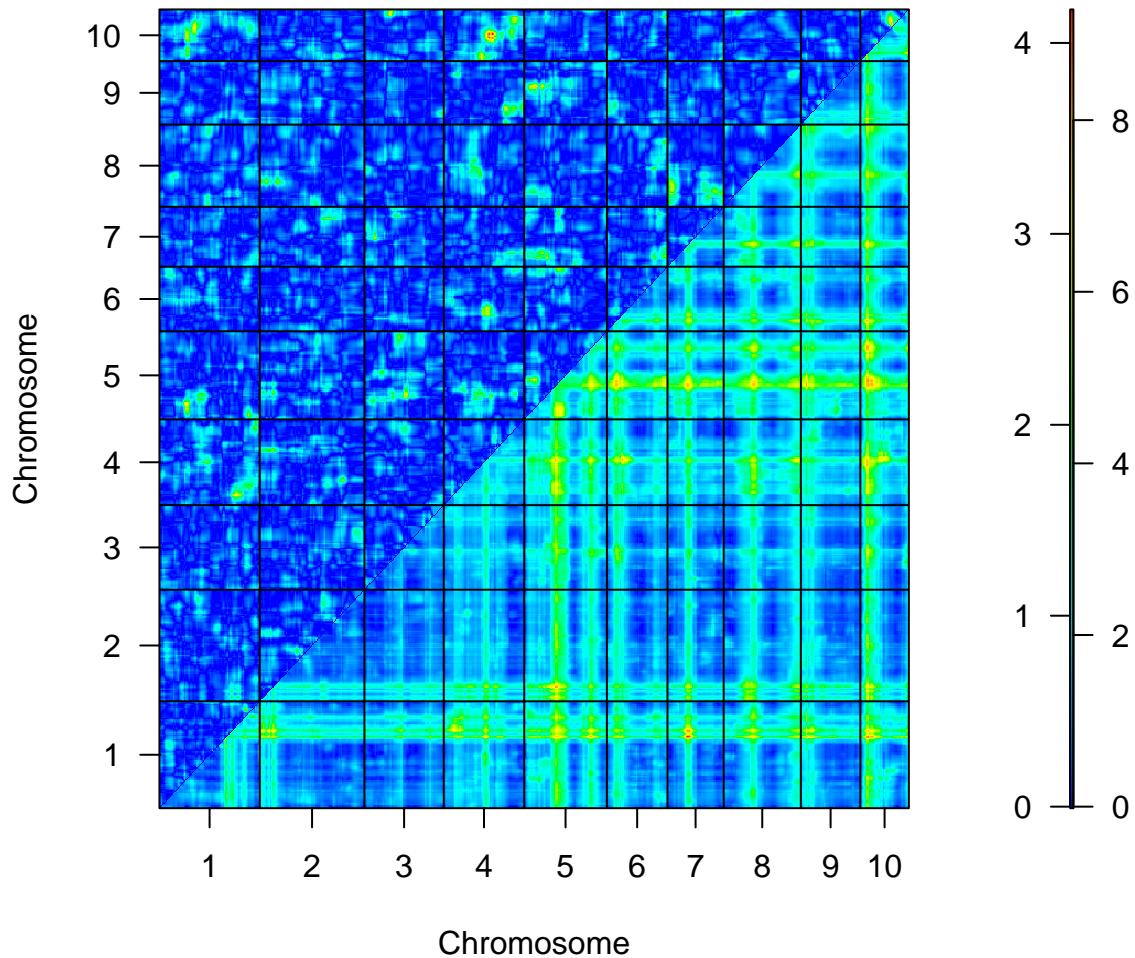
```

PlantHeight



```
#maize.mds <- calc.genoprob(maize.mds, step = 2)
#maize.two <- scantwo(maize.mds, pheno.col = "PlantHeight", method = "hk", n.cluster = 2)
#save(maize.two, file = "maize.two.RData")

load("maize.two.RData")
plot(maize.two, col.scheme = "redblue")
```



```
summary(maize.two)
```

	pos1f	pos2f	lod.full	lod.fv1	lod.int	pos1a	pos2a	lod.add	lod.av1
## c1 :c1	106	122	5.64	1.823	0.03700	106	122	5.60	1.786
## c1 :c2	132	24	7.25	3.428	1.16498	122	24	6.08	2.263
## c1 :c3	122	68	5.49	1.675	0.19302	122	120	5.30	1.482
## c1 :c4	122	76	7.50	3.679	0.00613	122	76	7.49	3.673
## c1 :c5	122	120	7.93	3.488	0.08971	122	120	7.84	3.398
## c1 :c6	122	18	6.45	2.629	0.10913	122	18	6.34	2.520
## c1 :c7	122	36	9.27	5.454	0.08435	122	36	9.19	5.369
## c1 :c8	122	52	7.20	3.384	0.01122	122	52	7.19	3.373
## c1 :c9	122	10	8.11	4.293	0.69859	122	10	7.41	3.595
## c1 :c10	122	14	8.64	4.523	0.03631	122	14	8.60	4.487
## c2 :c2	24	72	3.91	1.137	0.40611	6	24	3.50	0.731
## c2 :c3	24	120	4.16	1.391	0.05765	24	120	4.10	1.334
## c2 :c4	24	76	5.81	2.751	0.32870	24	76	5.48	2.422
## c2 :c5	24	58	8.28	3.841	1.54517	24	56	6.74	2.295

## c2 :c6	24	18	5.21	1.987	0.00739	24	18	5.21	1.980
## c2 :c7	24	36	6.43	3.347	0.31492	24	36	6.12	3.032
## c2 :c8	24	138	6.24	3.294	0.01395	24	138	6.22	3.280
## c2 :c9	18	10	5.78	2.766	0.40586	24	10	5.37	2.360
## c2 :c10	24	14	7.27	3.152	0.29785	24	14	6.97	2.855
## c3 :c3	68	86	3.77	2.335	0.84544	68	86	2.92	1.489
## c3 :c4	68	76	4.46	1.402	0.14866	68	76	4.31	1.253
## c3 :c5	78	58	6.11	1.670	0.44662	68	58	5.66	1.224
## c3 :c6	66	18	5.72	2.490	0.44993	68	18	5.27	2.040
## c3 :c7	56	38	5.36	2.273	0.85768	66	40	4.50	1.415
## c3 :c8	120	54	4.51	1.564	0.04156	120	54	4.47	1.523
## c3 :c9	120	10	4.64	1.626	0.00136	120	10	4.64	1.625
## c3 :c10	68	14	6.93	2.811	0.56843	68	14	6.36	2.243
## c4 :c4	28	76	4.39	1.325	0.41726	28	76	3.97	0.908
## c4 :c5	76	56	7.89	3.452	0.47173	76	58	7.42	2.981
## c4 :c6	76	28	7.88	4.654	2.31260	76	18	5.57	2.342
## c4 :c7	76	38	5.69	2.602	0.03723	76	40	5.65	2.565
## c4 :c8	76	132	6.83	3.764	0.72311	76	138	6.10	3.041
## c4 :c9	76	10	5.56	2.503	0.00361	76	10	5.56	2.500
## c4 :c10	68	12	7.93	3.814	1.44786	76	14	6.48	2.366
## c5 :c5	16	68	7.27	2.835	0.37399	58	122	6.90	2.461
## c5 :c6	64	18	8.07	3.629	0.24778	64	18	7.82	3.381
## c5 :c7	58	36	8.02	3.579	0.03229	58	36	7.99	3.547
## c5 :c8	60	56	7.77	3.331	0.13920	58	54	7.63	3.192
## c5 :c9	58	10	8.22	3.781	0.53252	58	10	7.69	3.248
## c5 :c10	66	14	8.46	4.022	0.24666	66	14	8.22	3.776
## c6 :c6	18	92	5.25	2.028	0.33042	18	88	4.92	1.698
## c6 :c7	18	40	6.30	3.071	0.20512	28	36	6.09	2.866
## c6 :c8	18	138	6.79	3.567	0.73411	18	138	6.06	2.833
## c6 :c9	28	10	6.19	2.962	0.59134	18	10	5.60	2.370
## c6 :c10	18	12	7.73	3.609	0.82172	18	12	6.90	2.787
## c7 :c7	28	36	4.26	1.179	0.11576	0	36	4.15	1.063
## c7 :c8	38	54	6.24	3.156	0.30408	36	138	5.94	2.851
## c7 :c9	36	10	6.19	3.106	0.11261	36	10	6.08	2.993
## c7 :c10	36	12	7.21	3.089	0.00500	36	12	7.20	3.084
## c8 :c8	54	138	6.26	3.321	0.16220	54	138	6.10	3.159
## c8 :c9	138	10	6.00	2.989	0.63096	138	10	5.37	2.358
## c8 :c10	138	14	6.61	2.494	0.14232	138	14	6.47	2.352
## c9 :c9	10	40	3.98	0.963	0.26551	10	94	3.71	0.698
## c9 :c10	10	12	6.98	2.862	0.55067	10	14	6.43	2.312
## c10:c10	14	86	6.87	2.749	0.50126	14	86	6.37	2.248

Discussion

Conclusion

References