Locus 1

Top hit :   position   chr3 : 82'991'172
             alleles (EMMA)   # alleles 1 = 14; # alleles 2 = 8 (do alleles #2 include strain Balb/cJ ?)
             condition / stat control, REMLt
             p-value: **2.593x10⁻⁶**

Locus 2

Significance (based on data with full allele set): INFLATED

Top hit 1 : position   chr3 : 87'719'795 (*Hdgf*)
             alleles (EMMA)   # alleles 1 = 13; # alleles 2 = 7 (-> allele set is incomplete; this is also
                               the case with the imputed CGD1 set of SNPs)
             condition / stat control, REMLt
             p-value: 4.236x10⁻⁶

Top hit 2 : position   chr3 : 87487048 (*Arhgef11*)
             alleles (EMMA)   #alleles 1 =10; # alleles 2 = 10 (-> allele set is incomplete; yet it is
                               complete with the MPD medium size SNP set given below -> it is not
                               clear which alleles are missing in the EMMA III association scan)
             condition / stat control, REMLt
             p-value: 1.031x10⁻⁵

Locus 3

Significance (based on data with full allele set): CORRECT

Top hit 1 : position   chr 4 : 94'807'400 (a single strong hit)
             alleles (EMMA)   # alleles 1 = 17; # alleles 2 = 4
             condition / stat iso1, REMLt
             p-value: **3.351x10⁻⁶**

TOP 100000 regionwide significant SNPs with Isoproterenol_2_PHYSIO_VWI
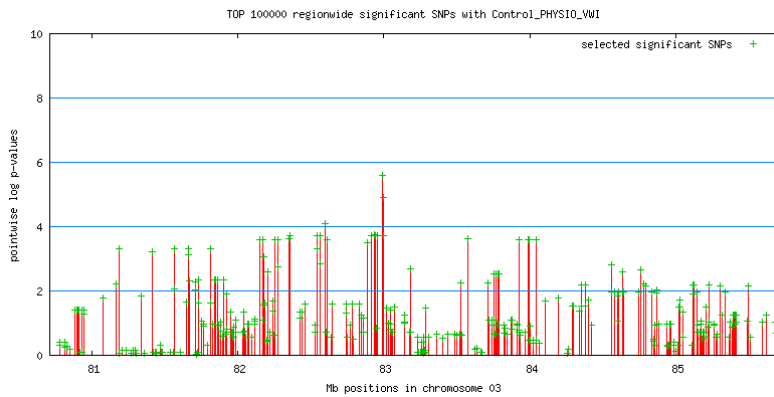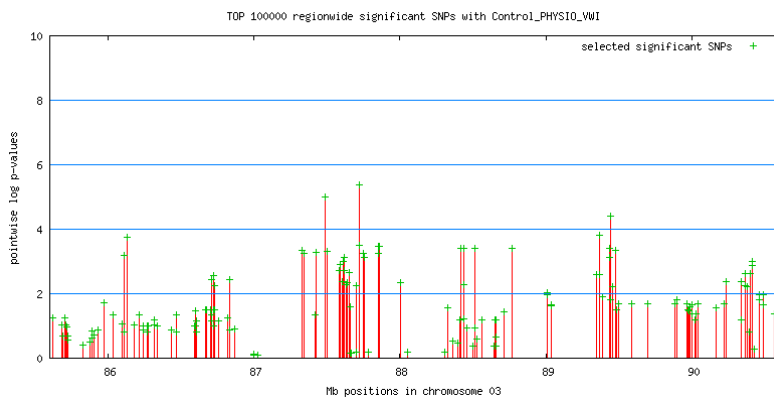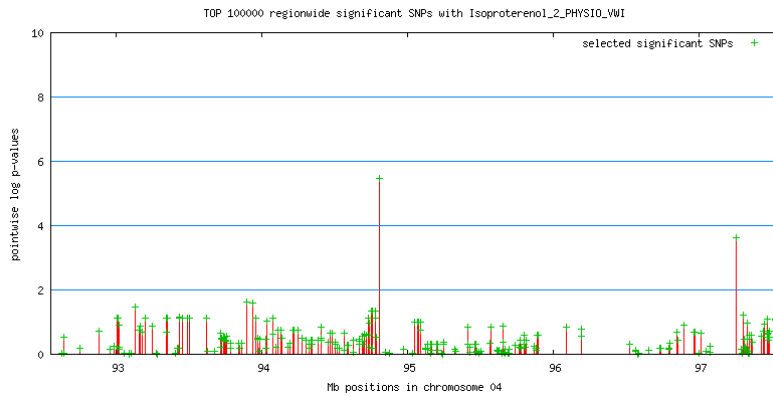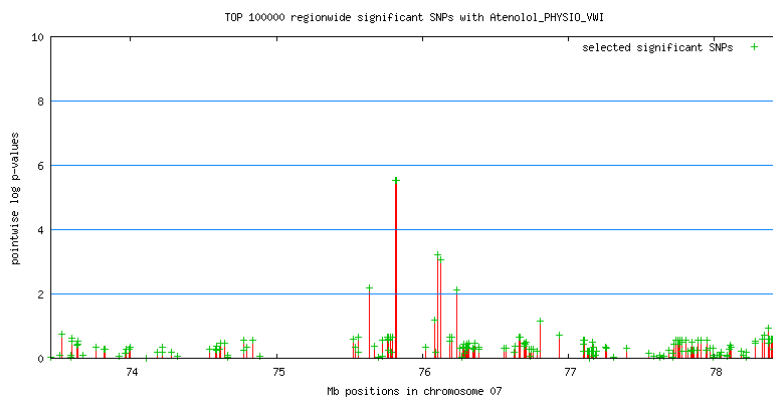
Locus 4

Significance (based on data with full allele set): CORRECT

Top hit 1 : position   chr7 : 75'814'117
             alleles (EMMA)   # alleles 1 = 17; # alleles 2 = 5
             condition / stat atenolol, REMLt
             p-value: **3.038x10^{-6}**

Top hit 2 : position   chr7 : 75'824'602
             alleles (EMMA)   # alleles 1 = 17; # alleles 2 = 5
             condition / stat atenolol, REMLt
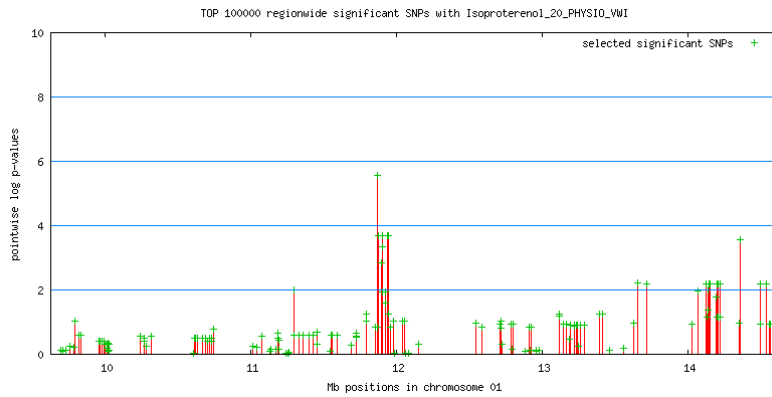   p-value: **3.038x10^{-6}**

TOP 100000 regionwide significant SNPs with Atenolol_PHYSIO_VWI

Locus 5

Significance (based on data with full allele set): INFLATED

Top hit 1 : position   chr 1:11'871'998
             alleles (EMMA)   # alleles 1 = 13; # alleles 2 = 7 (-> allele set is not complete)
             condition / stat iso10, REMLt
             p-value: 2.680x10^{-6}
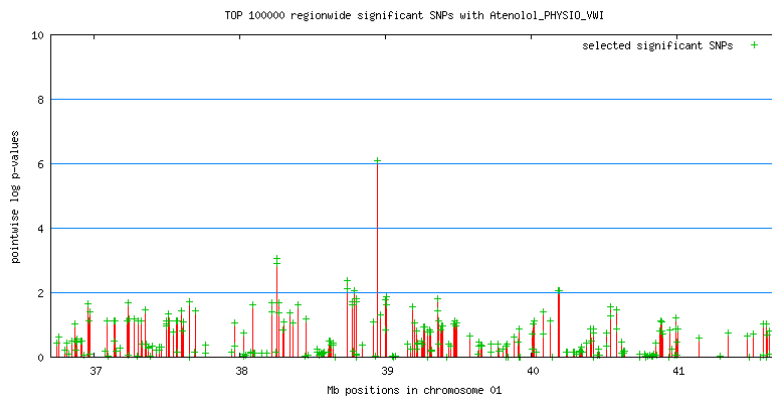
Top hit 2 : position   chr 1:11'899'477
             alleles (EMMA)   #alleles 1 =14; # alleles 2 = 7 (1 missing allele; see matching SNP
             above)
             condition / stat atenolol, LRT
             p-value: 1.351x10^{-6}

Locus 6

Significance (based on data with full allele set): INFLATED ?

Top hit 1 : position: chr 1:38'947'935
             alleles (EMMA):   # alleles 1 = 14; # alleles 2 = 5 (-> allele set is not complete)
             condition / stat: atenolol, LRT
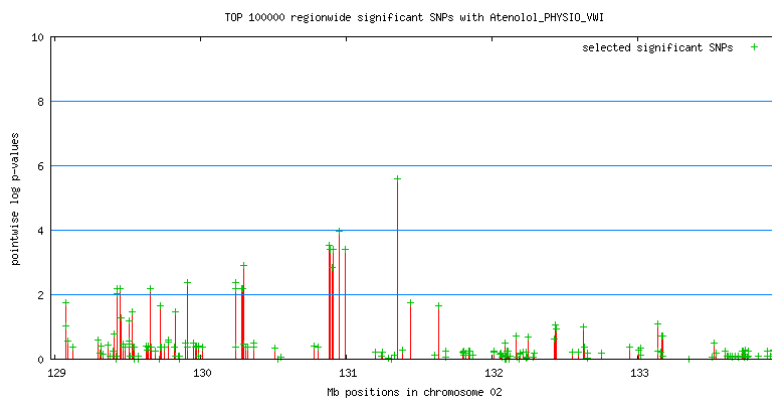   p-value: 8.232×10^{-7}

Locus 7

Significance (based on data with full allele set): CORRECT

Top hit 1 : position   chr 2:131'352'413
             alleles (EMMA) # alleles 1 = 16; # alleles 2 = 6
             condition / stat atenolol, LRT
             p-value: **2.584×10^{-6}**
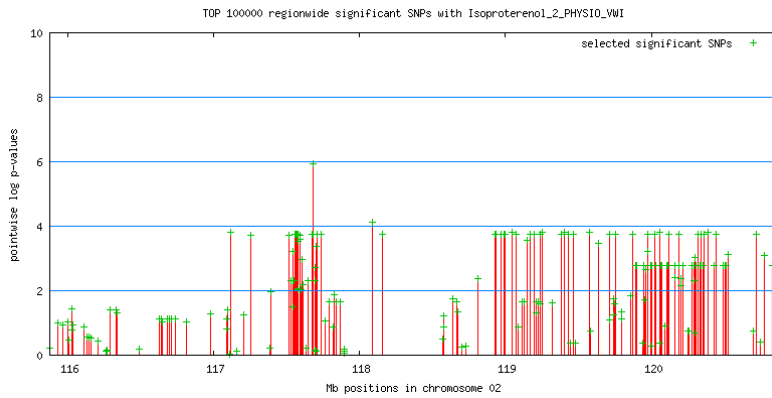
Top hit 2 : position   chr2:130'952'456
             alleles (EMMA) # alleles 1 = 17; # alleles 2 = 4 (incomplete allele set)
             condition / stat atenolol, REMLt
             p-value: 1.439×10^{-5}

Locus 8

Top hit 1 : position   chr 2:117'682'002
             alleles (EMMA)   # alleles 1 = 15; # alleles 2 = 4 (-> allele set is not complete)
             condition / stat iso 1, REMLt
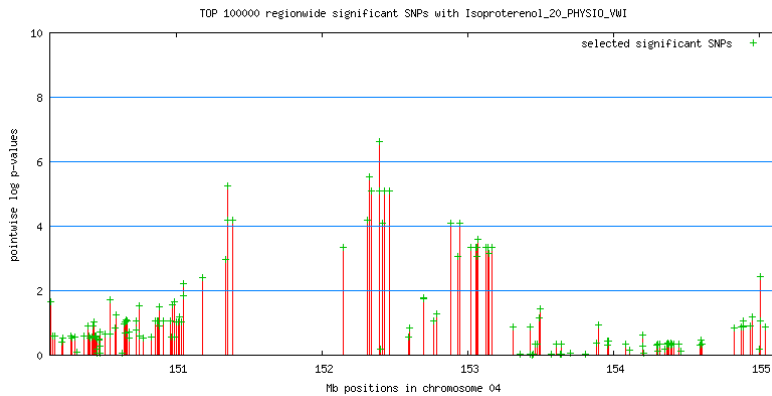   p-value: 1.174×10^{-6}

Locus 9

Top hit 1 : position   chr 4:151'355'820
             alleles (EMMA)   # alleles 1 = 16; # alleles 2 = 5 (allele set is incomplete)
             condition / stat iso 1, REMLt
             p-value: 3.346×10^{-7}
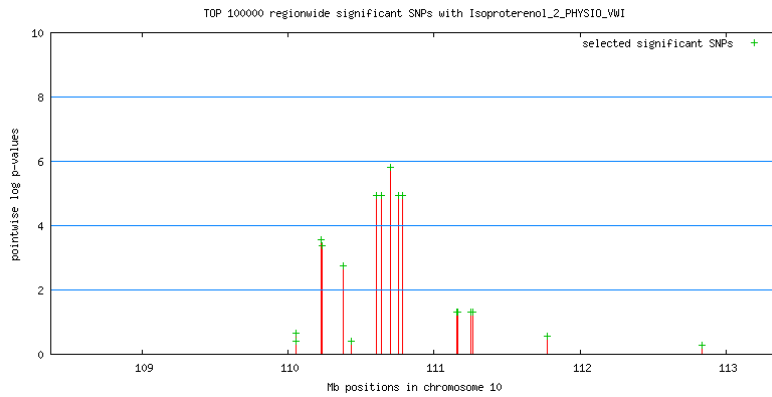
Top hit 2 : position   chr 4:152'394'133
             alleles (EMMA)   # alleles 1 = 17; # alleles 2 = 4 (incomplete allele set)
             condition / stat iso 10, REMLt
p-value: 2.307×10^{-7}

Locus 10
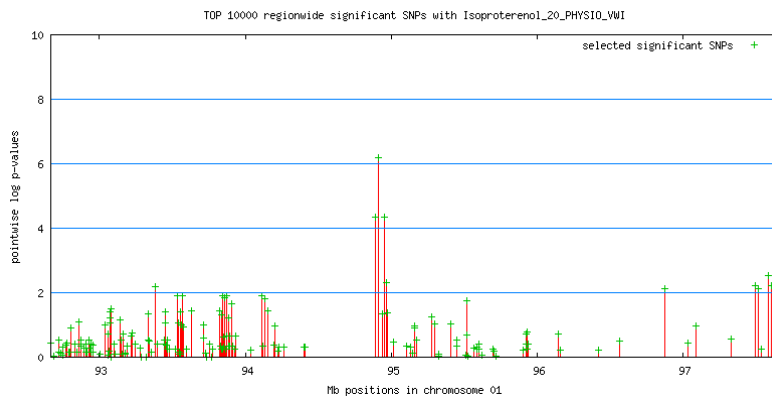
Top hit 1 : position   chr 10:110'702'509
             alleles (EMMA)   # alleles 1 = 16; # alleles 2 = 4 (-> allele set is incomplete)
             condition / stat iso 1, REMLt
             p-value: 1.588×10^{-6}

TOP 100000 regionwide significant SNPs with Isoproterenol_2_PHYSIO_VWI

Locus 11

Significance (based on data with full allele set): INFLATED

Top hit 1 : position   chr 1:94'914'398
            alleles (EMMA)   # alleles 1 = 10; # alleles 2 = 5 (-> allele set is incomplete)
            condition / stat   iso 10, REMLt
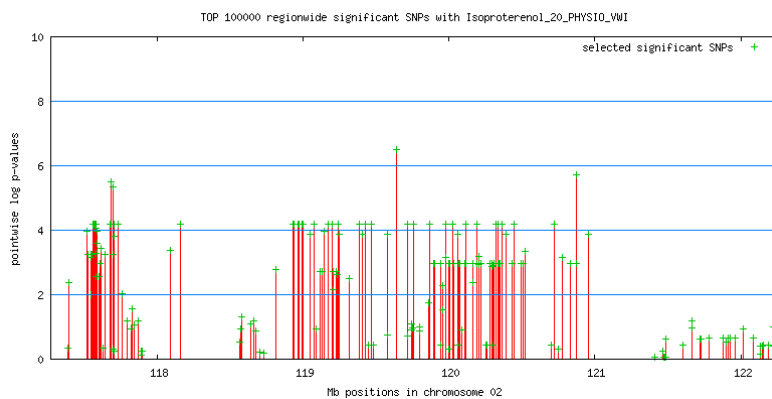   p-value: 6.643×10^{-7}

TOP 10000 regionwide significant SNPs with Isoproterenol_20_PHYSIO_VWI

Locus 12

Significance (based on data with full allele set): INFLATED ?

Top hit 1 : position   chr 2:119'637'990
            alleles (EMMA)   # alleles 1 = 12; # alleles 2 = 8 (incomplete allele set)
            condition / stat   iso 10, REMLt
            p-value: 3.255×10^{-7}

Top hit 2 : position   chr 2:120'869'441
            alleles (EMMA)   #alleles 1 = 13; # alleles 2 = 7 (incomplete allele set)
            condition / stat   iso 10, REMLt
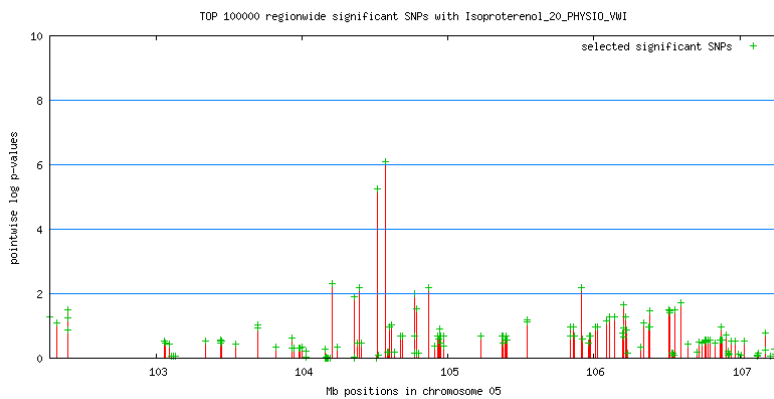   p-value: 1.921×10^{-6}

TOP 100000 regionwide significant SNPs with Isoproterenol_20_PHYSIO_VWI

Locus 13

Top hit 1 : position   chr 5:104'572'764
             alleles (EMMA)   # alleles 1 = 15; # alleles 2 = 5 (-> allele set is not complete)
             condition / stat   iso 10, REMLt
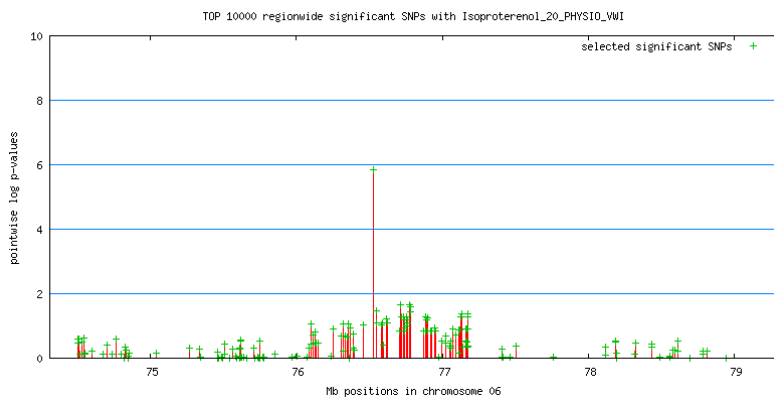   p-value: 8.03×10^{-7}

Top hit 2 : position   chr 5:104'515'280
             alleles (EMMA)   #alleles 1 = 17; # alleles 2 = 4
             condition / stat   iso 10, REMLt
             p-value: 5.597×10^{-6}

TOP 100000 regionwide significant SNPs with Isoproterenol_20_PHYSIO_VWI

Locus 14

Significance (based on data with full allele set): CORRECT

Top hit 1 : position   chr 6:76'524'788
             alleles (EMMA)   # alleles 1 = 12; # alleles 2 = 10
             condition / stat   iso 10, LRT
             p-value: **1.463×10^{-6}**

TOP 10000 regionwide significant SNPs with Isoproterenol_20_PHYSIO_VWI
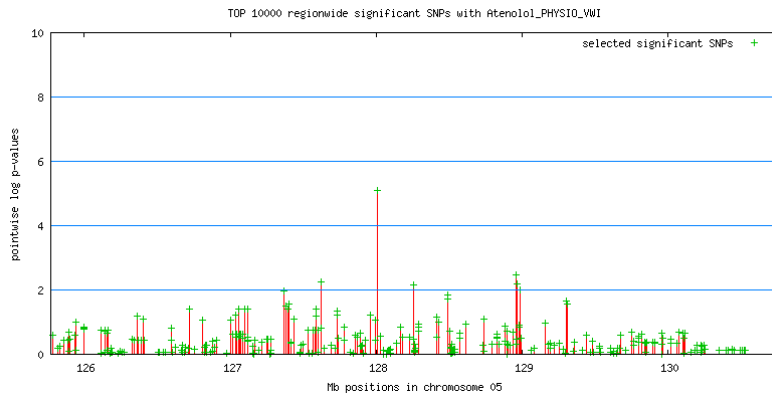
Locus 15

Significance (based on data with full allele set): CORRECT

Top hit 1 : position   chr 5:128'006'028
             alleles (EMMA)   # alleles 1 = 18; # alleles 2 = 4
             condition / stat   atenolol, REMLt
             p-value: **8.338×10^{-6}**

Top hit 2 : position   chr 5:128'006'079
             alleles (EMMA)   #alleles 1 = 18; # alleles 2 = 4
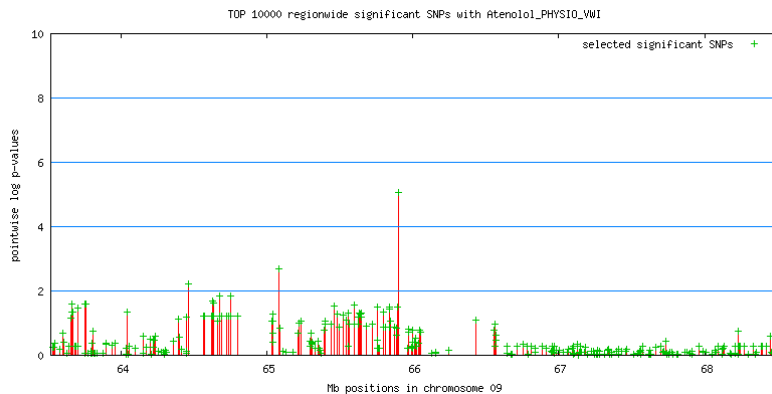   condition / stat   atenolol, REMLt
             p-value: **8.338×10^{-6}**

TOP 10000 regionwide significant SNPs with Atenolol_PHYSIO_VWI

Locus 16

Significance (based on data with full allele set): CORRECT

Top hit 1 : position   chr 9:65'899'904
            alleles (EMMA)   # alleles 1 = 18; # alleles 2 = 4
            condition / stat   atenolol, REMLt
            p-value: **8.396x10^{-6}**

Top hit 2 : position   chr 9:64'463'047
            alleles (EMMA)   #alleles 1 = 13; # alleles 2 = 7
            condition / stat   iso 10, REMLt
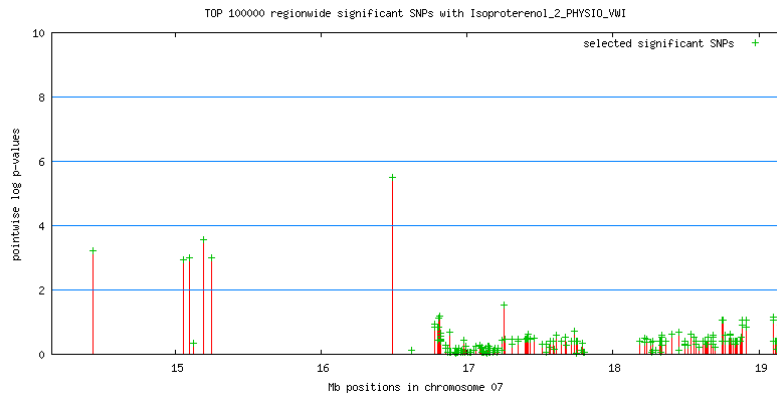   p-value: 1.743x10^{-5}

TOP 10000 regionwide significant SNPs with Atenolol_PHYSIO_VWI

Locus 17

Significance (based on data with full allele set): INFLATED ?

Top hit 1 : position   chr 7:16'488'107
            alleles (EMMA)   # alleles 1 = 14; # alleles 2 = 5 (-> allele set is not complete)
            condition / stat   iso 1, REMLt
            p-value: 3.162x10^{-6}
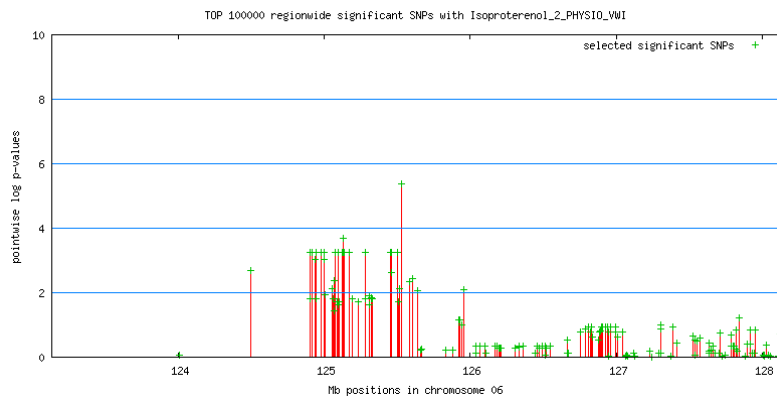
Top hit 2 : position   chr 7:15'194'001
            alleles (EMMA)   #alleles 1 = 13; # alleles 2 = 5
            condition / stat   iso 10, REMLt
            p-value: 6.614x10^{-6}

Locus 18

Significance (based on data with full allele set): CORRECT

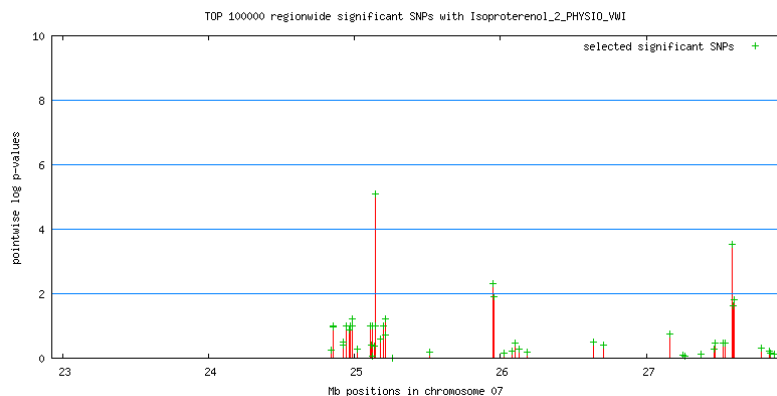Top hit 1 : position   chr 6:125'528'422
            alleles (EMMA)   # alleles 1 = 17; # alleles 2 = 5
            condition / stat   iso 1, REMLT
            p-value: **4.072x10^{-6}**

Locus 19

Significance (based on data with full allele set): CORRECT

Top hit 1 : position   chr 7:25'140'278
            alleles (EMMA)   # alleles 1 = 18; # alleles 2 = 4
            condition / stat   iso 1, REMLt
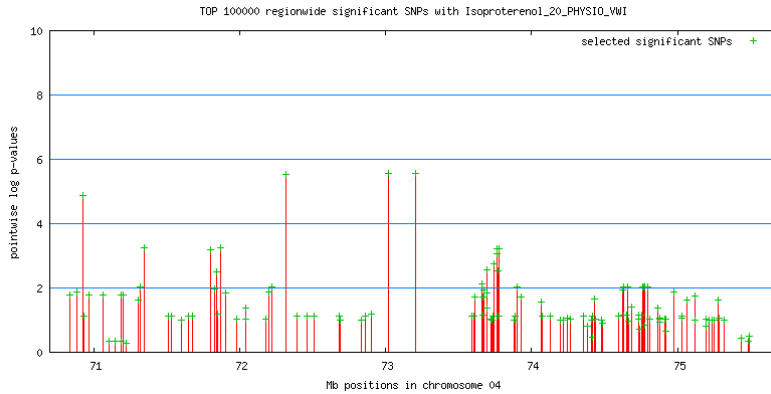   p-value: **8.226x10^{-6}**

Locus 20

Significance (based on data with full allele set): INFLATED but p-value still below 10^{-5} (provided that alleles are correct)

Top hits 1/2: position   chr 4:73'016'585 and chr 4:73'202'146
            alleles (EMMA)   # alleles 1 = 13; # alleles 2 = 7 (-> allele set is not complete)

	condition / stat	iso 10, REMLt
	p-value:	2.659×10^{-6}
Top hit 3 :	position	chr 4:72'313'856
	alleles (EMMA)	#alleles 1 = 15; # alleles 2 = 7
	condition / stat	iso 10, REMLt
	p-value:	**2.840×10^{-6}**

TOP 100000 regionwide significant SNPs with Isoproterenol_20_PHYSIO_VWI

Locus 21

Significance (based on data with full allele set): INFLATED ?

Top hit 1 :	position	chr 4:82'834'365
	alleles (EMMA)	# alleles 1 = 9; # alleles 2 = 11 (-> allele set is not complete)
	condition / stat	iso 10, REMLt
	p-value:	3.179×10^{-6}
Top hit 2 :	position	chr 4:83'326'905
	alleles (EMMA)	#alleles 1 = 10; # alleles 2 = 11
	condition / stat	iso 10, REMLt
	p-value:	1.239×10^{-5}

TOP 100000 regionwide significant SNPs with Isoproterenol_20_PHYSIO_VWI

Locus 22

Significance (based on data with full allele set): CORRECT

Top hit 1 :	position	chr 6:145'091'729
	alleles (EMMA)	# alleles 1 = 16; # alleles 2 = 6
	condition / stat	iso 10, REMLt
	p-value:	**4.025×10^{-6}**

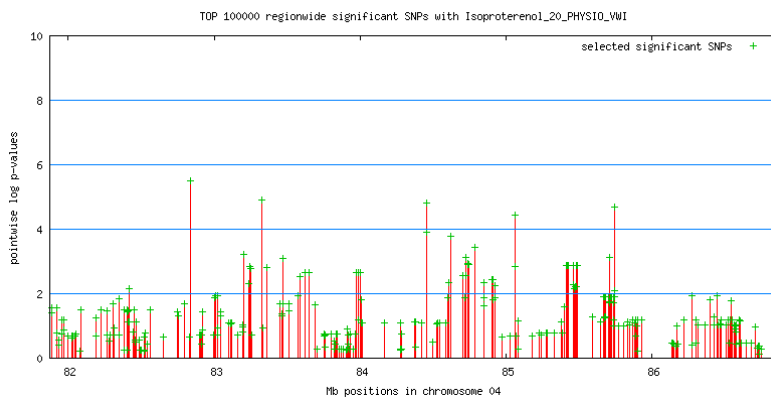**Locus 23**

Significance (based on data with full allele set): INFLATED

Top hit 1 : position   chr 6:5'476'010
alleles (EMMA)   # alleles 1 = 13; # alleles 2 = 5 (-> allele set is not complete)
condition / stat   iso 10, REMLt
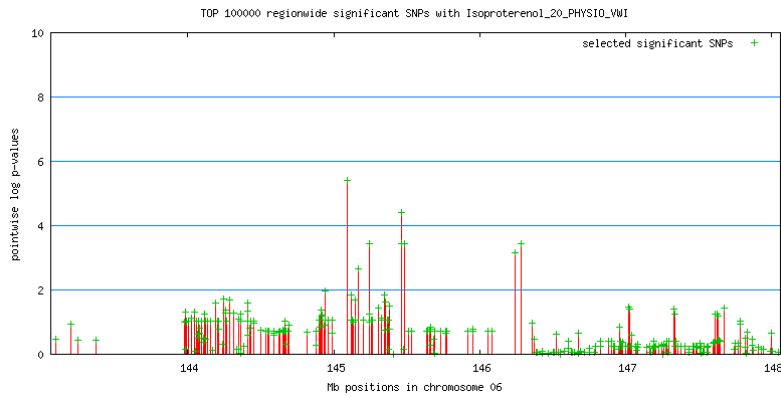p-value: 4.607×10^{-6}

Locus 24

Significance (based on data with full allele set): INFLATED ?

Top hit 1 : position   chr 18:60'889'758
alleles (EMMA)   # alleles 1 = 12; # alleles 2 = 7 (-> the allele set is incomplete)
condition / stat   iso 10, LRT
p-value: 2.488×10^{-6}

Locus 25

Significance (based on data with full allele set): CORRECT (under-estimated ?)

Top hit 1 : position   chr 4:135'298'806
alleles (EMMA)   # alleles 1 = 16; # alleles 2 = 5 (-> allele set is not complete)
condition / stat   control, LRT

p-value: **7.542x10⁻⁶**

TOP 100000 regionwide significant SNPs with Control_PHYSIO_VWI

selected significant SNPs +

Locus 26

Significance (based on data with full allele set): presumably CORRECT / false positive
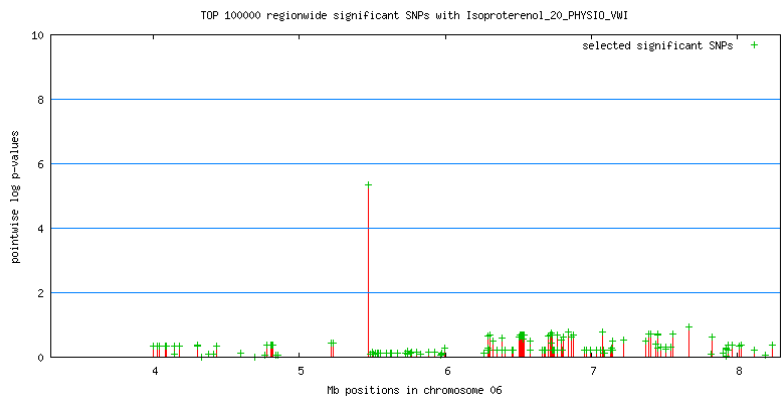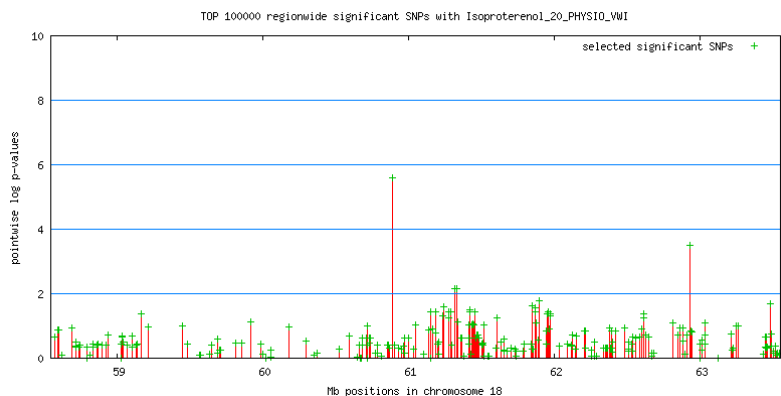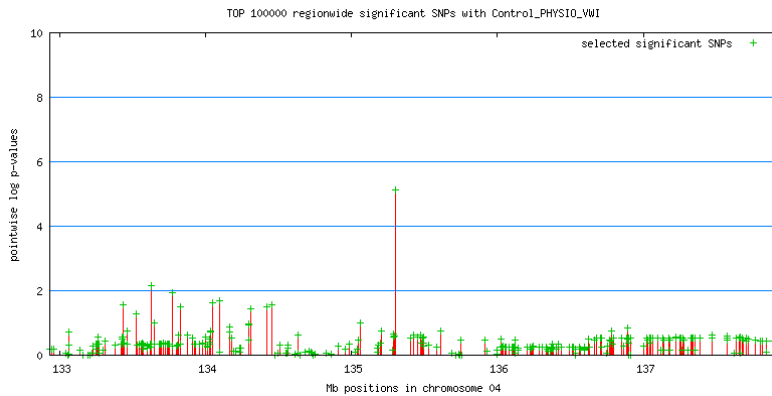
Top hit 1 : position   chr 5:45'736'224
            alleles (EMMA)   # alleles 1 = 10; # alleles 2 = 12
            condition / stat iso 1, LRT
            p-value: **6.138x10⁻⁶**

Top hit 2 : position   chr 5:45'776'195
            alleles (EMMA)   # alleles 1 = 10; # alleles 2 = 12
            condition / stat iso 1, LRT
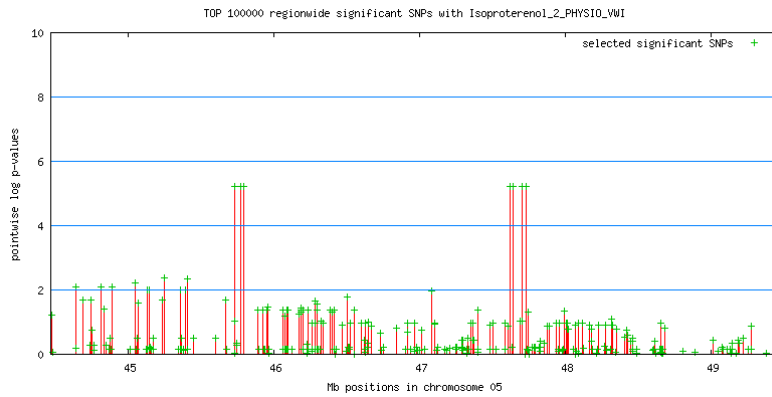   p-value: 6.138x10⁻⁶

and
Locus 27

Significance (based on data with full allele set): presumably CORRECT / false positive

Top hits 1-4: positions   chr   5:47'619'864;   chr5:   47'638'996;   chr5:47'704'974;   and
              chr5:47'729'042
              alleles (EMMA)   # alleles 1 = 10; # alleles 2 = 12
              condition / stat iso 1, REMLt
              p-value: **6.138x10⁻⁶**

Top hit 2 : position   chr5: 47'638'996
            alleles (EMMA)   # alleles 1 = 10; # alleles 2 = 12
            condition / stat iso 1, REMLt
            p-value: 6.138x10⁻⁶

Top hit 3 : position   chr5:47'704'974
            alleles (EMMA)   # alleles 1 = 10; # alleles 2 = 12
            condition / stat iso 1, REMLt
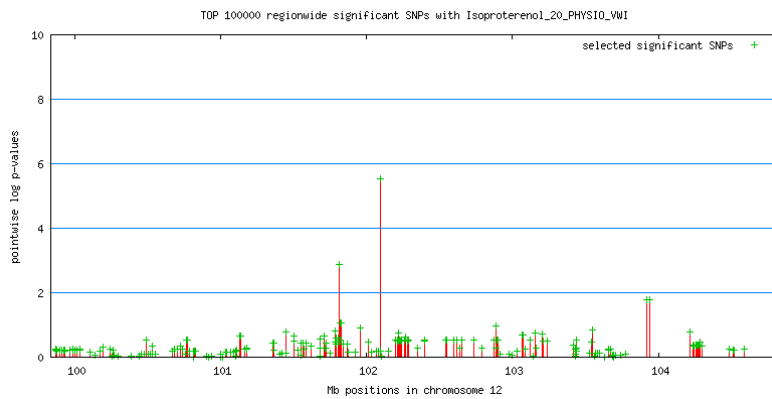   p-value: 6.138x10⁻⁶

Top hit 4 : position   chr5:47'729'042
            alleles (EMMA)   # alleles 1 = 10; # alleles 2 = 12
            condition / stat iso 1, REMLt
            p-value: 6.138x10⁻⁶

TOP 100000 regionwide significant SNPs with Isoproterenol_2_PHYSIO_VWI

Locus 28

Significance (based on data with full allele set): INFLATED
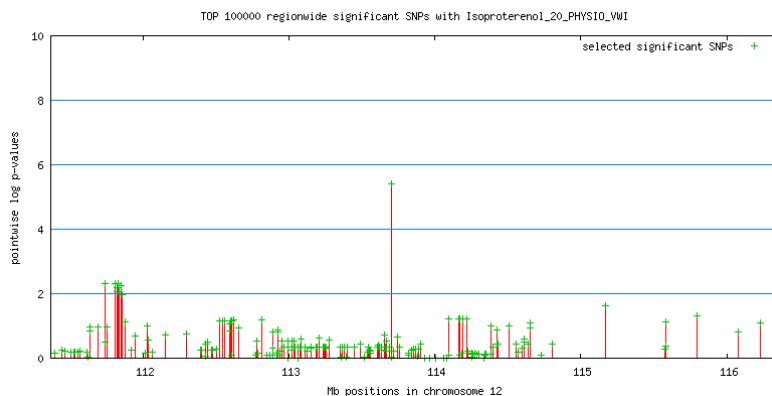
Top hit 1 : position   chr 12:102'095'964
             alleles (EMMA)   # alleles 1 = 12; # alleles 2 = 8 (-> allele set is not complete)
             condition / stat iso 10, LRT
             p-value: 2.973×10^{-6}

TOP 100000 regionwide significant SNPs with Isoproterenol_20_PHYSIO_VWI

Locus 29

Significance (based on data with full allele set): INFLATED

Top hit 1 : position   chr 12:113'701'753 and chr12:113'701'290
             alleles (EMMA)   # alleles 1 = 12; # alleles 2 = 9 (-> allele set is incomplete)
             condition / stat iso 10, LRT
             p-value: 3.884×10^{-6}

TOP 100000 regionwide significant SNPs with Isoproterenol_20_PHYSIO_VWI
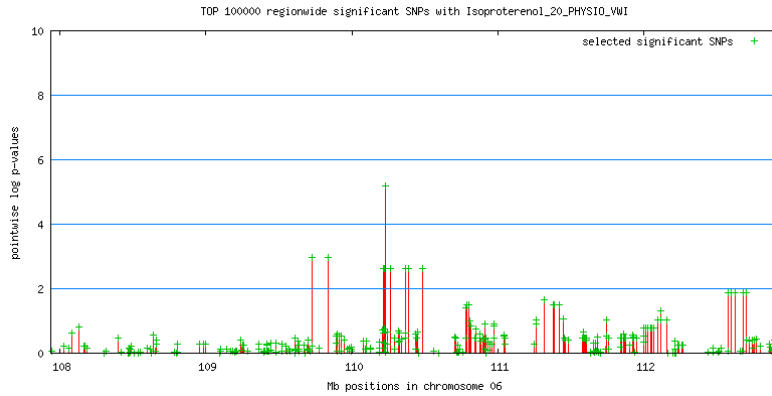
Locus 30

Significance (based on data with full allele set): presumably CORRECT / false positive

Top hit 1 : position   chr 6:110'232'069
             alleles (EMMA)   # alleles 1 = 13; # alleles 2 = 9
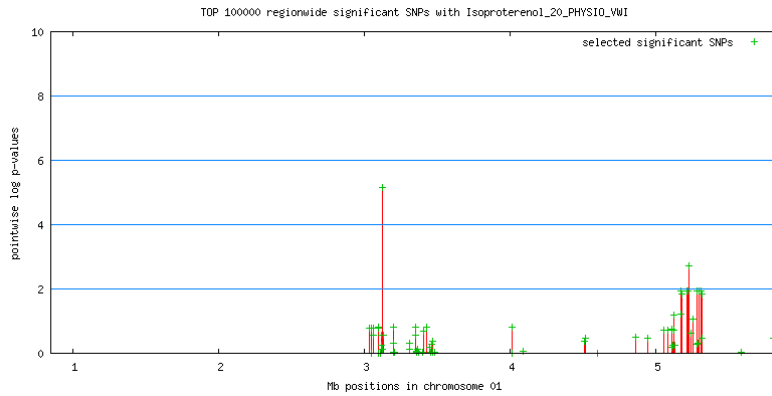   condition / stat iso 10, LRT

p-value: 6.407×10^{-6}

TOP 100000 regionwide significant SNPs with Isoproterenol_20_PHYSIO_VWI

Locus 31

Significance (based on data with full allele set): presumably CORRECT / false positive

Top hit 1 : position   chr 1:3'125'499
            alleles (EMMA)   # alleles 1 = 8; # alleles 2 = 14
            condition / stat   iso 10, LRT
            p-value: 7.007×10^{-6}

TOP 100000 regionwide significant SNPs with Isoproterenol_20_PHYSIO_VWI

Locus 32

Significance (based on data with full allele set): presumably CORRECT / false positive

Top hit 1 : position   chr 17:12'465'938, 12′503′901, and 12′539′636
            alleles (EMMA)   # alleles 1 = 13; # alleles 2 = 9
            condition / stat   iso 10, LRT
            p-value: **8.838×10^{-6}**

Top hit 2 : position   chr 17:12'503'901
            alleles (EMMA)   # alleles 1 = 13; # alleles 2 = 9
            condition / stat   iso 10, LRT
            p-value: 8.838×10^{-6}

Top hit 3 : position   17:12'539'636
            alleles (EMMA)   # alleles 1 = 13; # alleles 2 = 9
            condition / stat   iso 10, LRT
            p-value: 8.838×10^{-6}

TOP 100000 regionwide significant SNPs with Isoproterenol_20_PHYSIO_VWI