Dataset EV1

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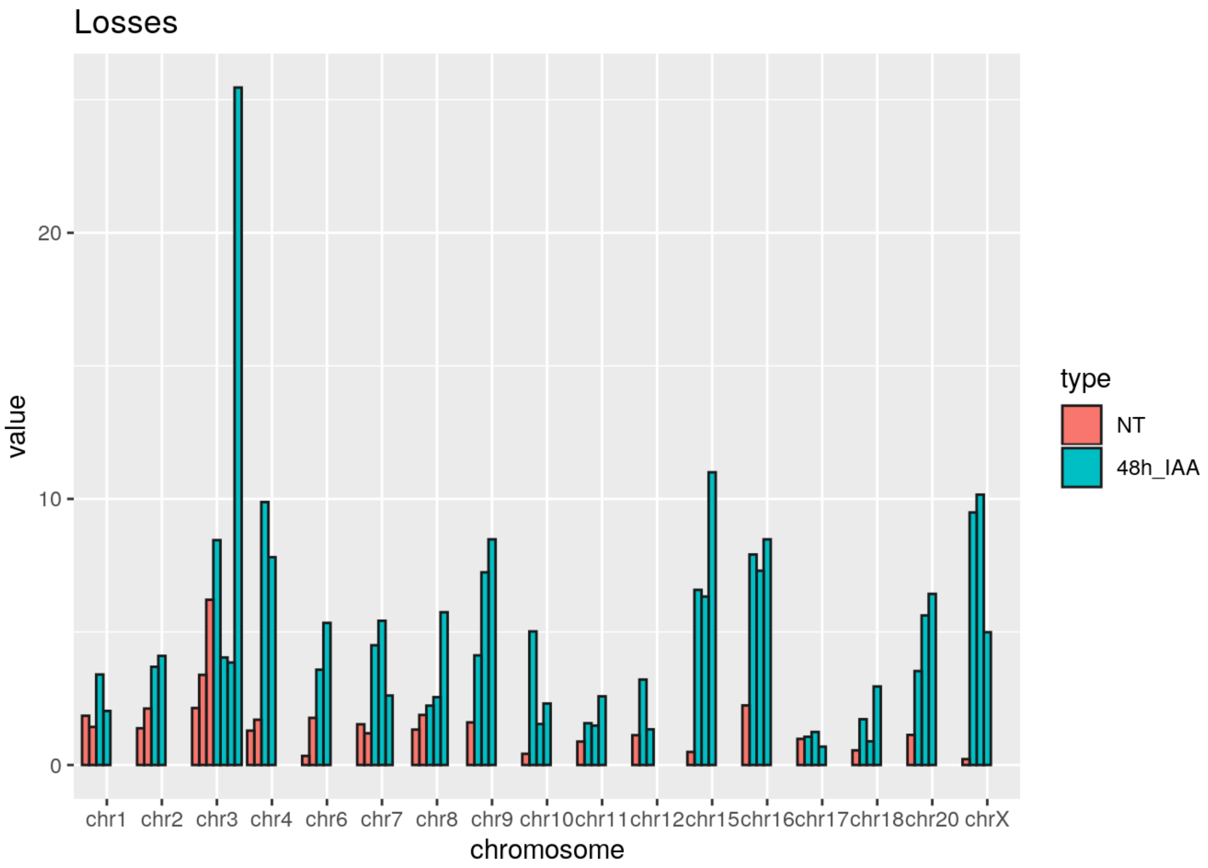
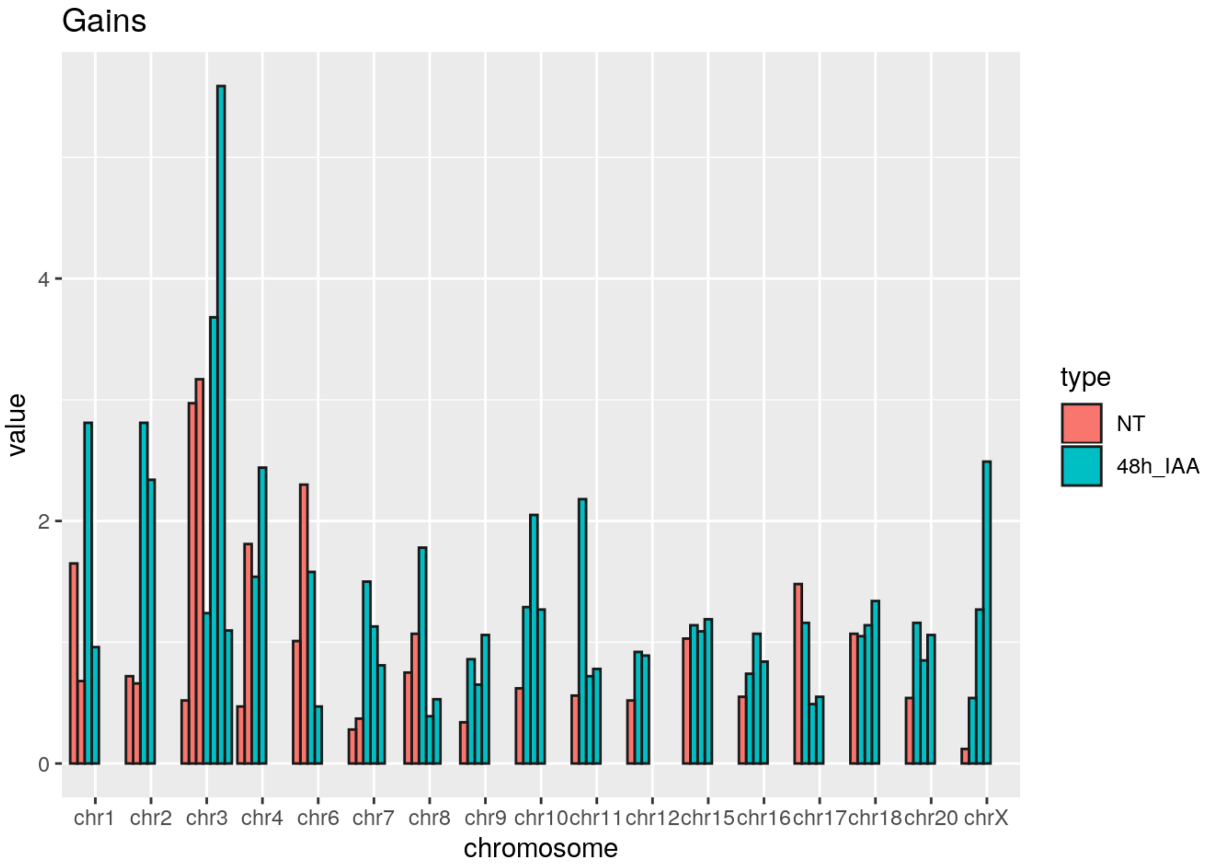
1 Image stream

1.1 Analysis of NT and 48h_IAA data





1.1.1 Model

A generalized linear model is fitted between gains or losses fractions according to chromosomes and type (control or 48h_IAA) with a binomial family.

1.1.2 Results

1.1.2.1 Losses

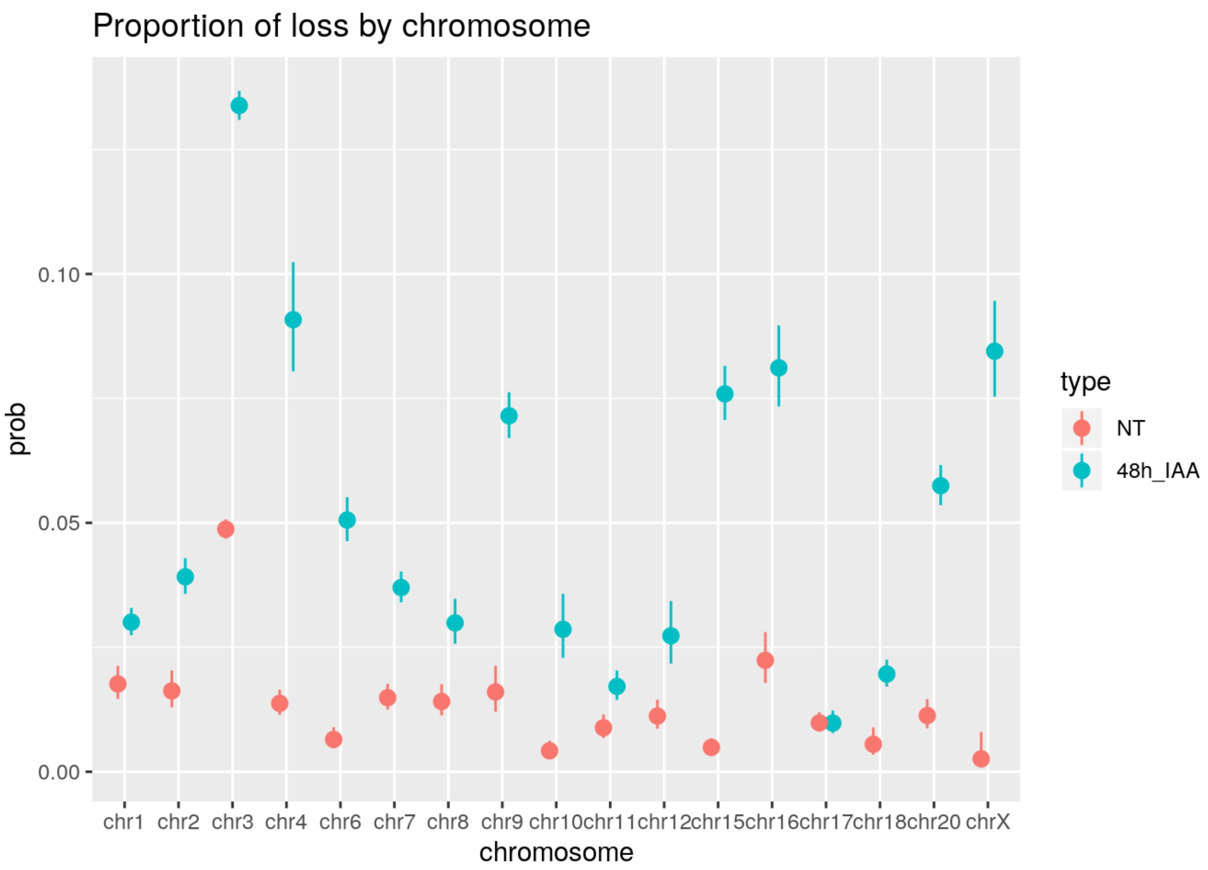
1.1.2.1.1 Estimated proportions for each chromosome

The following table gives the estimated probability for each chromosome with standard error and confidence interval at 95%.

type	chromosome	prob	SE	lower	upper
NT	chr1	0.0176471	0.0016830	0.0146340	0.0212671
48h_IAA	chr1	0.0300561	0.0013954	0.0274385	0.0329150
NT	chr2	0.0162423	0.0018727	0.0129519	0.0203514
48h_IAA	chr2	0.0391582	0.0018278	0.0357289	0.0429021
NT	chr3	0.0487218	0.0009937	0.0468107	0.0507067
48h_IAA	chr3	0.1338195	0.0014837	0.1309381	0.1367544
NT	chr4	0.0137383	0.0012778	0.0114463	0.0164815
48h_IAA	chr4	0.0908059	0.0055890	0.0804301	0.1023712

type	chromosome	prob	SE	lower	upper
NT	chr6	0.0065004	0.0010652	0.0047133	0.0089589
48h_IAA	chr6	0.0505636	0.0022488	0.0463335	0.0551575
NT	chr7	0.0148785	0.0013053	0.0125255	0.0176657
48h_IAA	chr7	0.0369906	0.0015753	0.0340240	0.0402051
NT	chr8	0.0141151	0.0015869	0.0113200	0.0175881
48h_IAA	chr8	0.0299076	0.0022932	0.0257258	0.0347448
NT	chr9	0.0160355	0.0023202	0.0120687	0.0212780
48h_IAA	chr9	0.0715056	0.0023468	0.0670403	0.0762440
NT	chr10	0.0042151	0.0008412	0.0028498	0.0062306
48h_IAA	chr10	0.0286260	0.0032578	0.0228872	0.0357510
NT	chr11	0.0088394	0.0011976	0.0067761	0.0115238
48h_IAA	chr11	0.0171429	0.0014964	0.0144437	0.0203360
NT	chr12	0.0111883	0.0014609	0.0086591	0.0144454
48h_IAA	chr12	0.0273141	0.0031747	0.0217349	0.0342753
NT	chr15	0.0048988	0.0007927	0.0035665	0.0067253
48h_IAA	chr15	0.0759076	0.0027779	0.0706391	0.0815346
NT	chr16	0.0223858	0.0025906	0.0178332	0.0280673
48h_IAA	chr16	0.0811373	0.0041514	0.0733638	0.0896548
NT	chr17	0.0098201	0.0009723	0.0080865	0.0119210
48h_IAA	chr17	0.0097842	0.0011395	0.0077855	0.0122897
NT	chr18	0.0055285	0.0013371	0.0034395	0.0088748
48h_IAA	chr18	0.0196290	0.0013743	0.0171090	0.0225117
NT	chr20	0.0112950	0.0014747	0.0087418	0.0145830
48h_IAA	chr20	0.0574596	0.0020562	0.0535597	0.0616250
NT	chrX	0.0025907	0.0014938	0.0008358	0.0080007
48h_IAA	chrX	0.0844763	0.0049100	0.0753371	0.0946107

Code



1.1.2.1.2 Anova

Anova table on losses model:

Code

term	df	Deviance	Resid..Df	Resid..Dev	p.value
NULL	NA	NA	71	17022.384	NA
chromosome	16	6842.5377	55	10179.847	0
type	1	4064.7422	54	6115.104	0
chromosome:type	16	447.5957	38	5667.509	0

Code

1.1.2.1.3 Comparison of NT and 48h_IAA

Comparison of missegregation rate for each chromosome between NT and 48h_IAA

Code

Code

chr	statistic	p.value	adj_p.value
chr1	25.3700738	0.0000005	0.0000005
chr2	50.7200755	0.0000000	0.0000000
chr3	1955.0787664	0.0000000	0.0000000

chr	statistic	p.value	adj_p.value
chr4	287.9379229	0.0000000	0.0000000
chr6	149.5442011	0.0000000	0.0000000
chr7	88.1363066	0.0000000	0.0000000
chr8	30.5592437	0.0000000	0.0000000
chr9	105.4441833	0.0000000	0.0000000
chr10	69.8637595	0.0000000	0.0000000
chr11	16.9335017	0.0000387	0.0000411
chr12	26.0518815	0.0000003	0.0000004
chr15	282.7812942	0.0000000	0.0000000
chr16	106.4507300	0.0000000	0.0000000
chr17	0.0005745	0.9808776	0.9808776
chr18	25.5551708	0.0000004	0.0000005
chr20	148.5217297	0.0000000	0.0000000
chrX	37.6858090	0.0000000	0.0000000

1.1.2.2 Gains

1.1.2.2.1 Estimated proportions for each chromosome

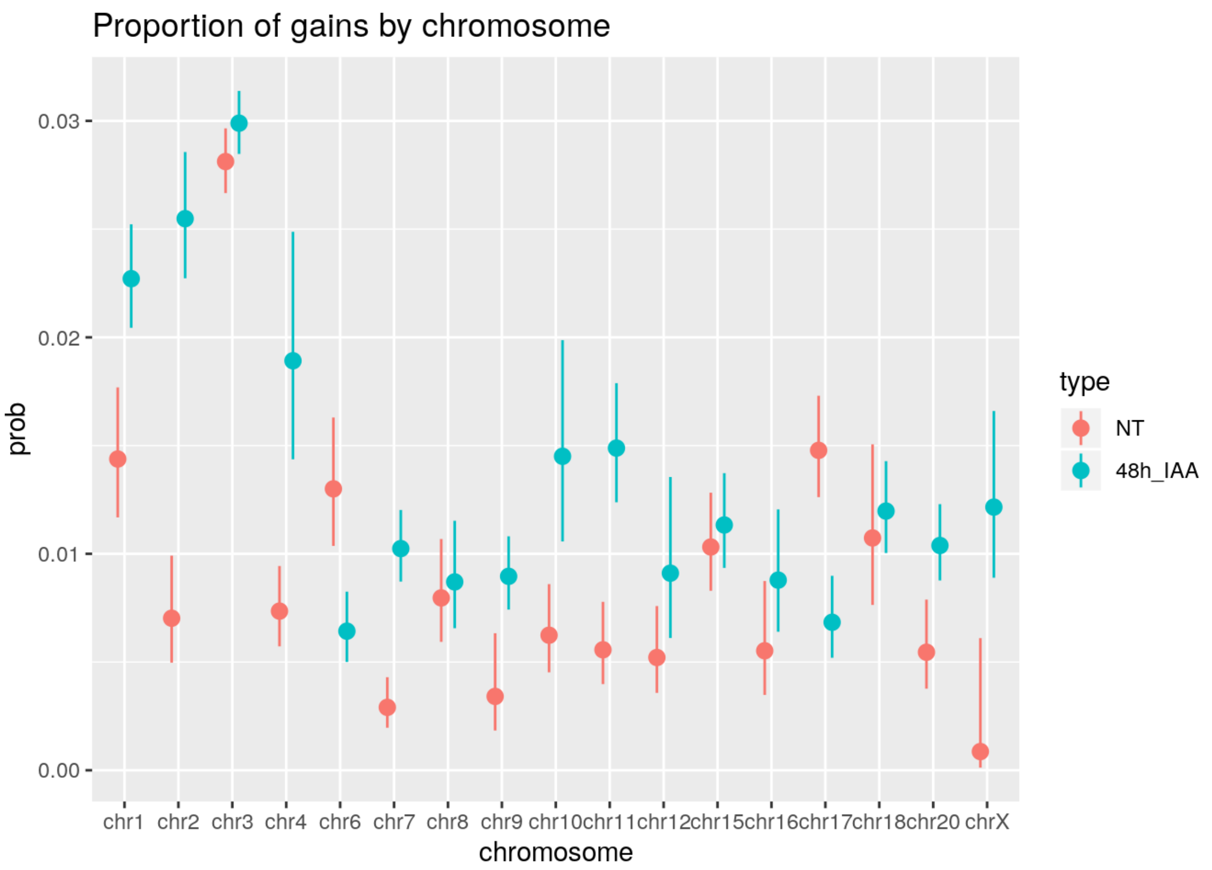
The following table gives the estimated probability for each chromosome with standard error and confidence interval at 95%.

Code

type	chromosome	prob	SE	lower	upper
NT	chr1	0.0143791	0.0015218	0.0116821	0.0176876
48h_IAA	chr1	0.0227091	0.0012175	0.0204413	0.0252219
NT	chr2	0.0070237	0.0012373	0.0049712	0.0099152
48h_IAA	chr2	0.0254839	0.0014850	0.0227297	0.0285621
NT	chr3	0.0281210	0.0007630	0.0266635	0.0296558
48h_IAA	chr3	0.0298938	0.0007421	0.0284731	0.0313832
NT	chr4	0.0073512	0.0009378	0.0057237	0.0094369
48h_IAA	chr4	0.0189179	0.0026500	0.0143665	0.0248749

type	chromosome	prob	SE	lower	upper
NT	chr6	0.0130007	0.0015014	0.0103640	0.0162972
48h_IAA	chr6	0.0064258	0.0008201	0.0050028	0.0082502
NT	chr7	0.0029060	0.0005803	0.0019643	0.0042971
48h_IAA	chr7	0.0102403	0.0008403	0.0087179	0.0120254
NT	chr8	0.0079624	0.0011956	0.0059305	0.0106828
48h_IAA	chr8	0.0087004	0.0012503	0.0065626	0.0115265
NT	chr9	0.0034118	0.0010771	0.0018367	0.0063291
48h_IAA	chr9	0.0089589	0.0008582	0.0074242	0.0108074
NT	chr10	0.0062384	0.0010224	0.0045232	0.0085984
48h_IAA	chr10	0.0145038	0.0023357	0.0105710	0.0198704
NT	chr11	0.0055656	0.0009518	0.0039794	0.0077791
48h_IAA	chr11	0.0148837	0.0013959	0.0123816	0.0178823
NT	chr12	0.0052083	0.0009997	0.0035741	0.0075841
48h_IAA	chr12	0.0091047	0.0018500	0.0061098	0.0135476
NT	chr15	0.0103133	0.0011471	0.0082913	0.0128220
48h_IAA	chr15	0.0113311	0.0011101	0.0093496	0.0137268
NT	chr16	0.0055198	0.0012974	0.0034804	0.0087437
48h_IAA	chr16	0.0087841	0.0014187	0.0063981	0.0120492
NT	chr17	0.0147788	0.0011898	0.0126192	0.0173015
48h_IAA	chr17	0.0068355	0.0009539	0.0051986	0.0089833
NT	chr18	0.0107317	0.0018581	0.0076392	0.0150571
48h_IAA	chr18	0.0119737	0.0010775	0.0100357	0.0142805
NT	chr20	0.0054528	0.0010277	0.0037675	0.0078860
48h_IAA	chr20	0.0103833	0.0008957	0.0087670	0.0122940
NT	chrX	0.0008636	0.0008632	0.0001216	0.0061035
48h_IAA	chrX	0.0121571	0.0019348	0.0088946	0.0165963

Code



1.1.2.2.2 Anova

Anova table on gains model:

Code

term	df	Deviance	Resid..Df	Resid..Dev	p.value
NULL	NA	NA	71	3014.620	NA
chromosome	16	1563.33542	55	1451.284	0
type	1	53.44579	54	1397.839	0
chromosome:type	16	233.98125	38	1163.857	0

Code

1.1.2.2.3 Comparison of NT and 48h_IAA

Comparison of missegregation rate for each chromosome between NT and 48h_IAA

Code

chr	statistic	p.value	adj_p.value
chr1	14.9026279	0.0001132	0.0002749
chr2	48.7813944	0.0000000	0.0000000
chr3	2.7636062	0.0964306	0.1252321
chr4	24.8178556	0.0000006	0.0000027

chr	statistic	p.value	adj_p.value
chr6	16.7593565	0.0000424	0.0001202
chr7	34.1600165	0.0000000	0.0000000
chr8	0.1818924	0.6697519	0.6697519
chr9	8.5957306	0.0033695	0.0057282
chr10	13.4688902	0.0002426	0.0005154
chr11	25.5233451	0.0000004	0.0000025
chr12	3.9903461	0.0457617	0.0648290
chr15	0.4032880	0.5253961	0.5954489
chr16	2.6564245	0.1031323	0.1252321
chr17	22.9738102	0.0000016	0.0000056
chr18	0.3151754	0.5745216	0.6104292
chr20	9.6824319	0.0018604	0.0035141
chrX	6.8699504	0.0087657	0.0135470

1.2 Analysis of 48h_IAA data only

1.2.1 Model

A generalized linear model is fitted between gains or losses fractions and chromosomes with a quasibinomial family and weights of observation equal to number of cells.

Code

1.2.2 Results

1.2.2.1 Losses

1.2.2.1.1 Estimated proportions for each chromosome

The following table gives the estimated probability for each chromosome with standard error and confidence interval at 95%.

Code

Code

chromosome	prob	SE	lower	upper
chr1	0.0300561	0.0013954	0.0274385	0.0329150
chr2	0.0391582	0.0018278	0.0357289	0.0429021

chromosome	prob	SE	lower	upper
chr3	0.1338195	0.0014837	0.1309381	0.1367544
chr4	0.0908059	0.0055890	0.0804301	0.1023712
chr6	0.0505636	0.0022488	0.0463335	0.0551575
chr7	0.0369906	0.0015753	0.0340240	0.0402051
chr8	0.0299076	0.0022932	0.0257258	0.0347448
chr9	0.0715056	0.0023468	0.0670403	0.0762440
chr10	0.0286260	0.0032578	0.0228872	0.0357510
chr11	0.0171429	0.0014964	0.0144437	0.0203360
chr12	0.0273141	0.0031747	0.0217349	0.0342753
chr15	0.0759076	0.0027779	0.0706391	0.0815346
chr16	0.0811373	0.0041514	0.0733638	0.0896548
chr17	0.0097842	0.0011395	0.0077855	0.0122897
chr18	0.0196290	0.0013743	0.0171090	0.0225117
chr20	0.0574596	0.0020562	0.0535597	0.0616250
chrX	0.0844763	0.0049100	0.0753371	0.0946107

Code

1.2.2.1.2 Anova

Anova table on losses model:

Code

term	df	Deviance	Resid..Df	Resid..Dev	p.value
NULL	NA	NA	47	171687.515	NA
chromosome	17	166332.2	30	5355.295	0

Code

Wih a p-value of 0.00e+00, we conclude that there is an effect of the chromosomes on the the percentage of losses (i.e. at least one chromosome has a percentage different from the others).

1.2.2.1.3 Test against mean value

Each estimated coefficients is tested against the mean value (0.0520167).

Code

chr	statistic	p.value	adj_p.value
chr1	142.5083941	0.0000000	0.0000000
chr2	37.4845126	0.0000000	0.0000000
chr3	6539.9589926	0.0000000	0.0000000
chr4	78.2764208	0.0000000	0.0000000
chr6	0.4064809	0.5237611	0.5237611

chr	statistic	p.value	adj_p.value
chr7	65.0361652	0.0000000	0.0000000
chr8	53.1995691	0.0000000	0.0000000
chr9	91.9693535	0.0000000	0.0000000
chr10	28.1517897	0.0000001	0.0000001
chr11	166.5455164	0.0000000	0.0000000
chr12	31.4272716	0.0000000	0.0000000
chr15	103.8008640	0.0000000	0.0000000
chr16	73.0073504	0.0000000	0.0000000
chr17	212.4552203	0.0000000	0.0000000
chr18	199.2834362	0.0000000	0.0000000
chr20	7.6882883	0.0055580	0.0059054
chrX	67.0227859	0.0000000	0.0000000

1.2.2.2 Gains

1.2.2.2.1 Estimated proportions for each chromosome

The following table gives the estimated probability for each chromosome with standard error and confidence interval at 95%.

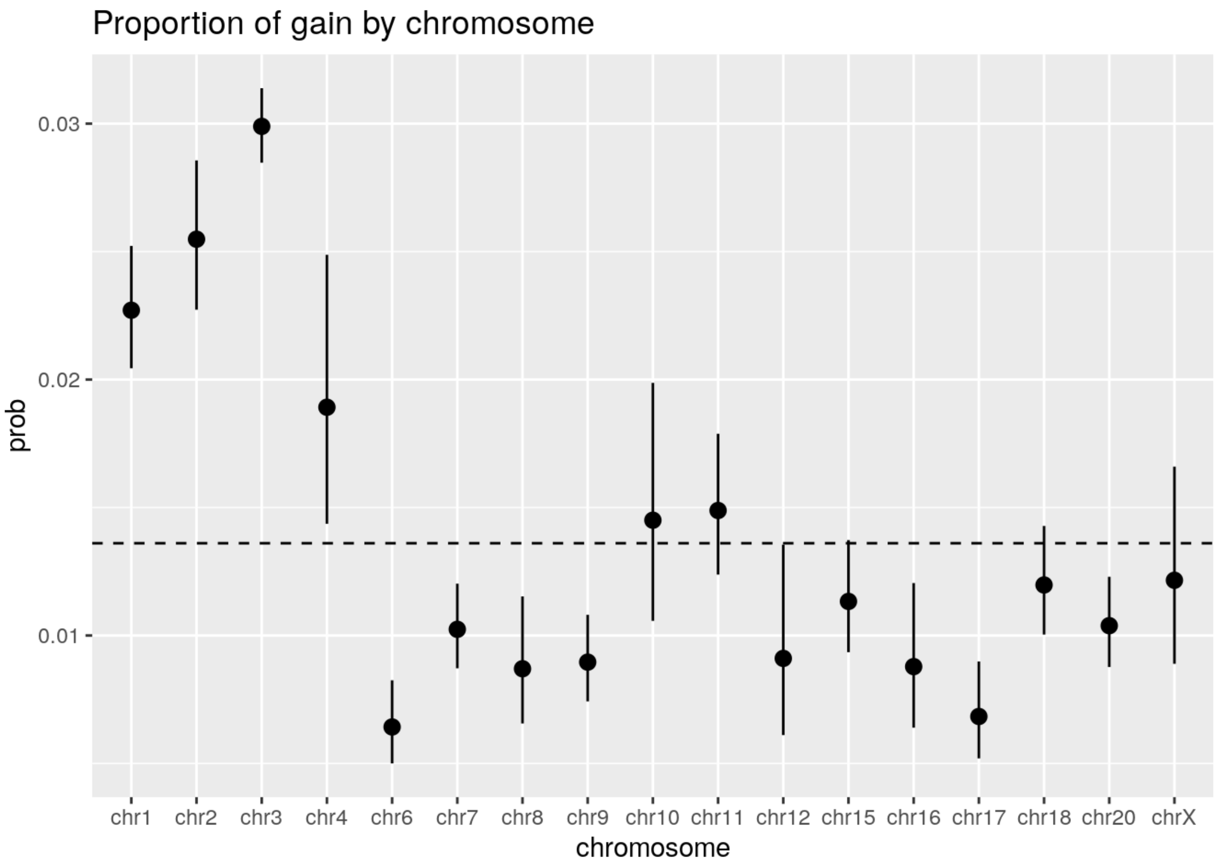
Code

Code

chromosome	prob	SE	lower	upper
chr1	0.0227091	0.0012175	0.0204413	0.0252219
chr2	0.0254839	0.0014850	0.0227297	0.0285621
chr3	0.0298938	0.0007421	0.0284731	0.0313832
chr4	0.0189179	0.0026500	0.0143665	0.0248749
chr6	0.0064258	0.0008201	0.0050028	0.0082502
chr7	0.0102403	0.0008403	0.0087179	0.0120254
chr8	0.0087004	0.0012503	0.0065626	0.0115265
chr9	0.0089589	0.0008582	0.0074242	0.0108074
chr10	0.0145038	0.0023357	0.0105710	0.0198704

chromosome	prob	SE	lower	upper
chr11	0.0148837	0.0013959	0.0123816	0.0178823
chr12	0.0091047	0.0018500	0.0061098	0.0135476
chr15	0.0113311	0.0011101	0.0093496	0.0137268
chr16	0.0087841	0.0014187	0.0063981	0.0120492
chr17	0.0068355	0.0009539	0.0051986	0.0089833
chr18	0.0119737	0.0010775	0.0100357	0.0142805
chr20	0.0103833	0.0008957	0.0087670	0.0122940
chrX	0.0121571	0.0019348	0.0088946	0.0165963

Code



1.2.2.2.2 Anova

Anova table on gains model:

Code

term	df	Deviance	Resid..Df	Resid..Dev	p.value
NULL	NA	NA	47	222427.3404	NA
chromosome	17	221475.4	30	951.8935	0

Code

Wih a p-value of 0.00e+00, we conclude that there is an effect of the chromosomes on the the percentage of losses (i.e. at least one chromosome has a percentage different from the others).

1.2.2.2.3 Test against mean value

Each estimated coefficients is tested against the mean value (0.0136051).

Code

chr	statistic	p.value	adj_p.value
chr1	90.3981205	0.0000000	0.0000000
chr2	114.4579286	0.0000000	0.0000000
chr3	986.6898524	0.0000000	0.0000000
chr4	5.5071233	0.0189392	0.0292696
chr6	34.7662607	0.0000000	0.0000000
chr7	12.0275873	0.0005242	0.0012730
chr8	9.7230188	0.0018197	0.0034373
chr9	19.1054903	0.0000124	0.0000350
chr10	0.1576184	0.6913587	0.6913587
chr11	0.9160349	0.3385182	0.3836540
chr12	3.9240673	0.0475996	0.0674327
chr15	3.4926177	0.0616430	0.0806101
chr16	7.3712824	0.0066274	0.0112665
chr17	24.4764944	0.0000008	0.0000026
chr18	2.0179636	0.1554475	0.1887577
chr20	9.8459144	0.0017021	0.0034373
chrX	0.5006847	0.4791994	0.5091494

1.3 Analysis of NT data only

1.3.1 Model

A generalized linear model is fitted between gains or losses fractions and chromosomes with a quasibinomial family and weights of observation equal to number of cells.

Code

1.3.2 Results

1.3.2.1 Losses

1.3.2.1.1 Estimated proportions for each chromosome

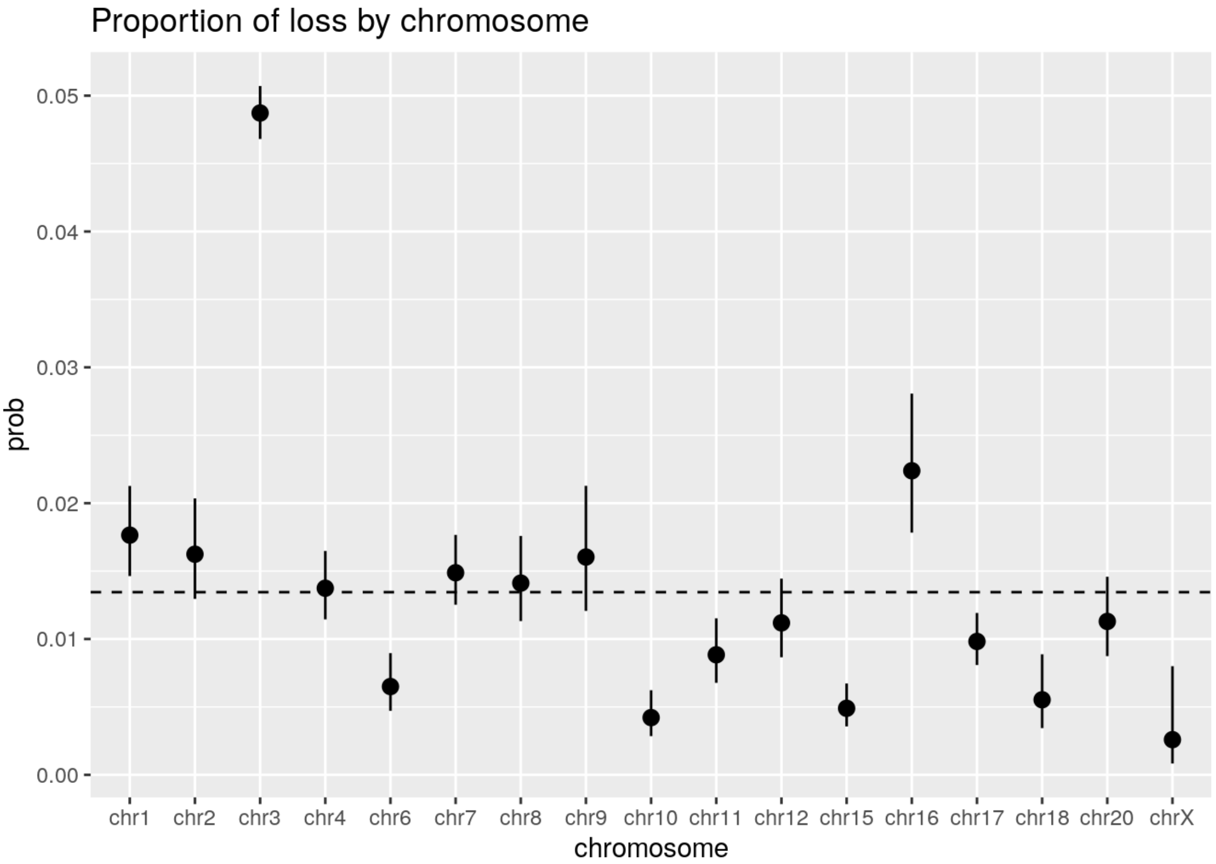
The following table gives the estimated probability for each chromosome with standard error and confidence interval at 95%.

Code

Code

chromosome	prob	SE	lower	upper
chr1	0.0176471	0.0016830	0.0146340	0.0212671
chr2	0.0162423	0.0018727	0.0129519	0.0203514
chr3	0.0487218	0.0009937	0.0468107	0.0507067
chr4	0.0137383	0.0012778	0.0114463	0.0164815
chr6	0.0065004	0.0010652	0.0047133	0.0089589
chr7	0.0148785	0.0013053	0.0125255	0.0176657
chr8	0.0141151	0.0015869	0.0113200	0.0175881
chr9	0.0160355	0.0023202	0.0120687	0.0212780
chr10	0.0042151	0.0008412	0.0028498	0.0062306
chr11	0.0088394	0.0011976	0.0067761	0.0115238
chr12	0.0111883	0.0014609	0.0086591	0.0144454
chr15	0.0048988	0.0007927	0.0035665	0.0067253
chr16	0.0223858	0.0025906	0.0178332	0.0280673
chr17	0.0098201	0.0009723	0.0080865	0.0119210
chr18	0.0055285	0.0013371	0.0034395	0.0088748
chr20	0.0112950	0.0014747	0.0087418	0.0145830
chrX	0.0025907	0.0014938	0.0008358	0.0080007

Code



1.3.2.1.2 Anova

Anova table on losses model:

Code

term	df	Deviance	Resid..Df	Resid..Dev	p.value
NULL	NA	NA	25	160438.7860	NA
chromosome	17	160126.6	8	312.2142	0

Code

Wih a p-value of 0.00e+00, we conclude that there is an effect of the chromosomes on the the percentage of losses (i.e. at least one chromosome has a percentage different from the others).

1.3.2.1.3 Test against mean value

Each estimated coefficients is tested against the mean value (0.0134494).

Code

chr	statistic	p.value	adj_p.value
chr1	8.0756940	0.0044863	0.0076267
chr2	2.6701498	0.1022464	0.1580172
chr3	3811.4020426	0.0000000	0.0000000
chr4	0.0521610	0.8193447	0.8193447
chr6	19.8098380	0.0000086	0.0000364

chr	statistic	p.value	adj_p.value
chr7	1.3230119	0.2500522	0.2833925
chr8	0.1844973	0.6675365	0.7092575
chr9	1.4733621	0.2248160	0.2729908
chr10	34.0532863	0.0000000	0.0000000
chr11	9.6392923	0.0019046	0.0040472
chr12	1.9918292	0.1581498	0.2240455
chr15	39.2318413	0.0000000	0.0000000
chr16	19.1926071	0.0000118	0.0000402
chr17	10.1244119	0.0014632	0.0035534
chr18	13.6035286	0.0002258	0.0006397
chr20	1.7916082	0.1807303	0.2363397
chrX	8.2251949	0.0041313	0.0076267

1.3.2.2 Gains

1.3.2.2.1 Estimated proportions for each chromosome

The following table gives the estimated probability for each chromosome with standard error and confidence interval at 95%.

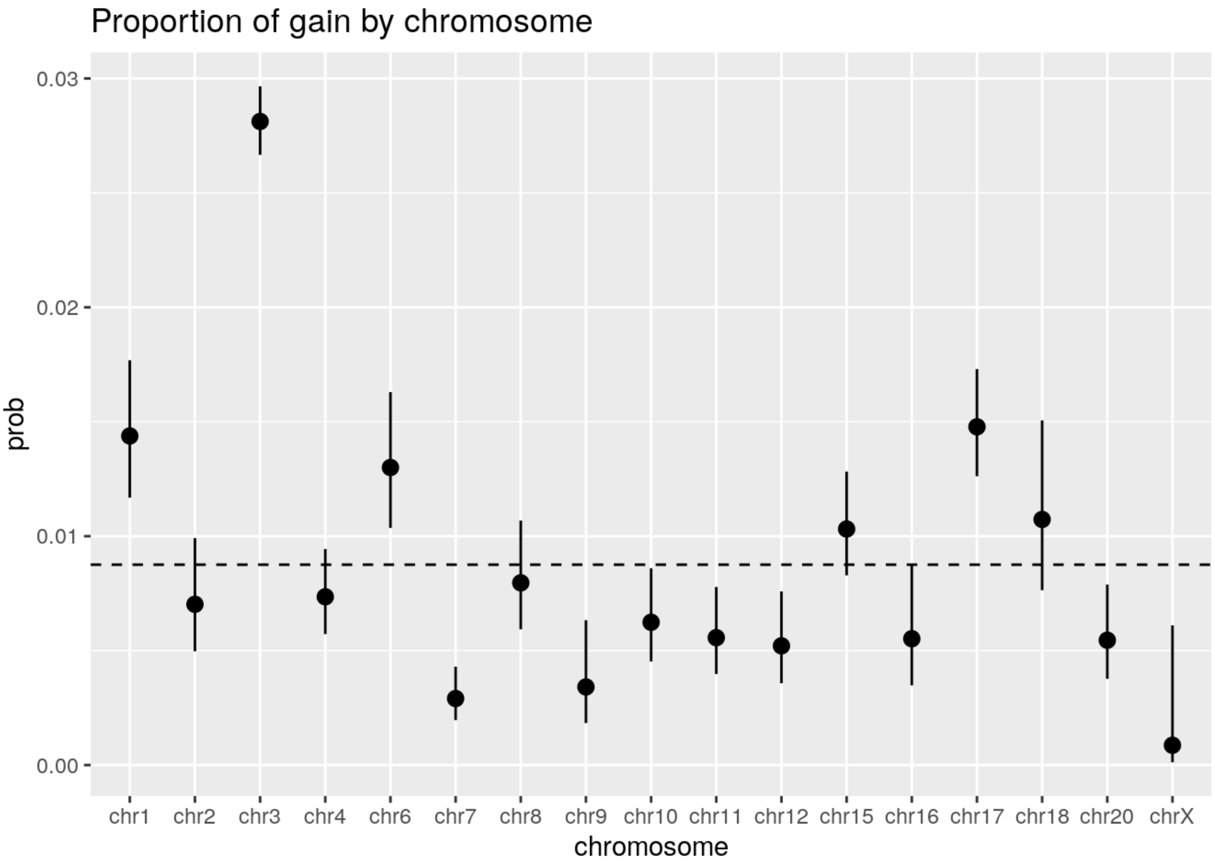
Code

Code

chromosome	prob	SE	lower	upper
chr1	0.0143791	0.0015218	0.0116821	0.0176876
chr2	0.0070237	0.0012373	0.0049712	0.0099152
chr3	0.0281210	0.0007630	0.0266635	0.0296558
chr4	0.0073512	0.0009378	0.0057237	0.0094369
chr6	0.0130007	0.0015014	0.0103640	0.0162972
chr7	0.0029060	0.0005803	0.0019643	0.0042971
chr8	0.0079624	0.0011956	0.0059305	0.0106828
chr9	0.0034118	0.0010771	0.0018367	0.0063291
chr10	0.0062384	0.0010224	0.0045232	0.0085984

chromosome	prob	SE	lower	upper
chr11	0.0055656	0.0009518	0.0039794	0.0077791
chr12	0.0052083	0.0009997	0.0035741	0.0075841
chr15	0.0103133	0.0011471	0.0082913	0.0128220
chr16	0.0055198	0.0012974	0.0034804	0.0087437
chr17	0.0147788	0.0011898	0.0126192	0.0173015
chr18	0.0107317	0.0018581	0.0076392	0.0150571
chr20	0.0054528	0.0010277	0.0037675	0.0078860
chrX	0.0008636	0.0008632	0.0001216	0.0061035

Code



1.3.2.2.2 Anova

Anova table on gains model:

Code

term	df	Deviance	Resid..Df	Resid..Dev	p.value
NULL	NA	NA	25	169059.599	NA
chromosome	17	168847.6	8	211.964	0

Code

Wih a p-value of 0.00e+00, we conclude that there is an effect of the chromosomes on the the percentage of losses (i.e. at least one chromosome has a percentage different from the others).

1.3.2.2.3 Test against mean value

Each estimated coefficients is tested against the mean value (0.0087546).

Code

chr	statistic	p.value	adj_p.value
chr1	21.8476565	0.0000030	0.0000125
chr2	1.5664571	0.2107223	0.2388186
chr3	1806.5331416	0.0000000	0.0000000
chr4	1.8784880	0.1705061	0.2070431
chr6	11.6696236	0.0006353	0.0021600
chr7	30.6408656	0.0000000	0.0000002
chr8	0.3993584	0.5274208	0.5274208
chr9	8.9509349	0.0027733	0.0078576
chr10	4.2852905	0.0384435	0.0594127
chr11	7.0364113	0.0079869	0.0169721
chr12	7.3437029	0.0067298	0.0163438
chr15	2.1667041	0.1410282	0.1844215
chr16	3.8622147	0.0493851	0.0699622
chr17	42.0201092	0.0000000	0.0000000
chr18	1.3802720	0.2400548	0.2550582
chr20	6.3301930	0.0118699	0.0224210
chrX	5.3972473	0.0201685	0.0342865

1.4 Gains and losses pooled

In this part gains and losses are pooled.

Code

Code

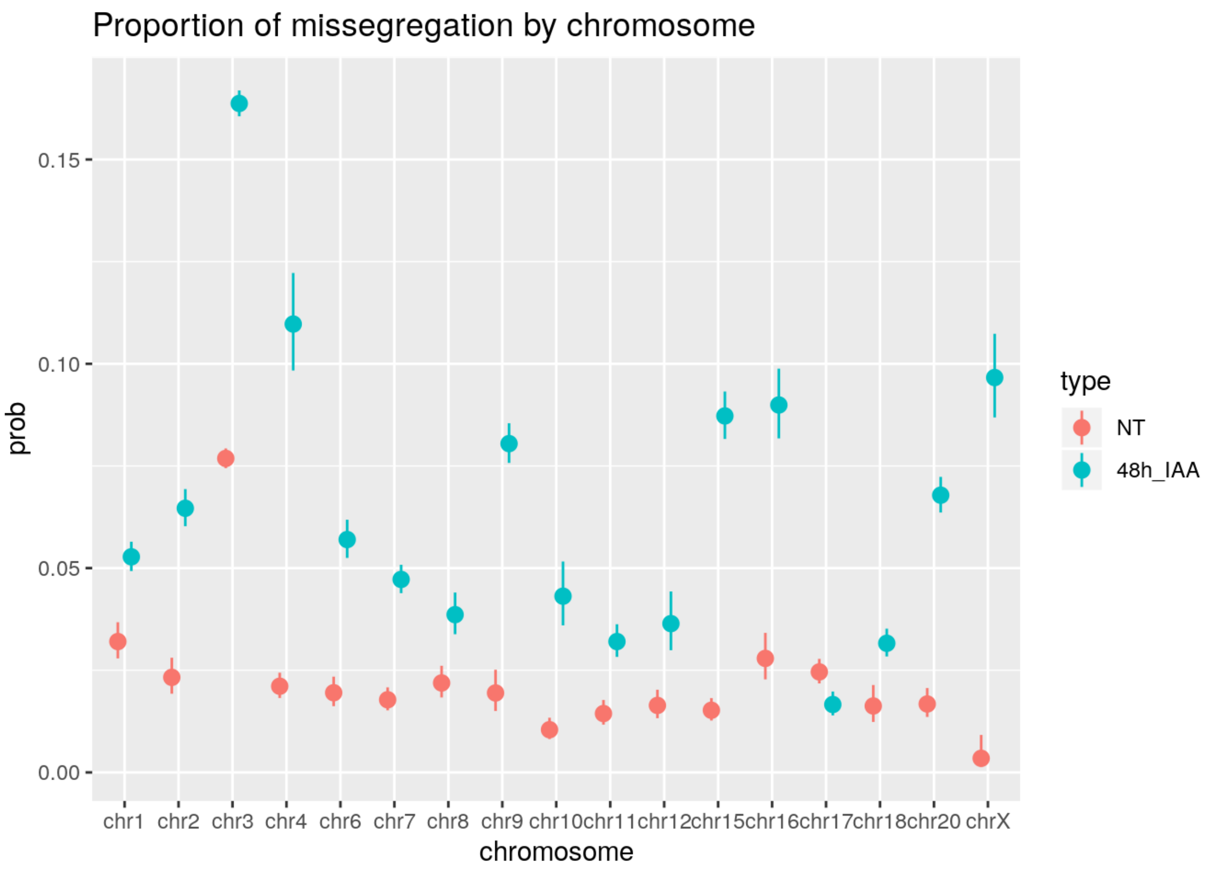
The following table gives the estimated probability for each chromosome with standard error and confidence interval at 95%.

Code

type	chromosome	prob	SE	lower	upper
NT	chr1	0.0320261	0.0022507	0.0278969	0.0367435
48h_IAA	chr1	0.0527652	0.0018271	0.0492967	0.0564631
NT	chr2	0.0232660	0.0022334	0.0192682	0.0280696
48h_IAA	chr2	0.0646422	0.0023171	0.0602466	0.0693348
NT	chr3	0.0768428	0.0012293	0.0744677	0.0792871
48h_IAA	chr3	0.1637134	0.0016125	0.1605774	0.1668984
NT	chr4	0.0210894	0.0015773	0.0182098	0.0244130
48h_IAA	chr4	0.1097238	0.0060794	0.0983632	0.1222186
NT	chr6	0.0195011	0.0018328	0.0162151	0.0234370
48h_IAA	chr6	0.0569894	0.0023793	0.0525013	0.0618360
NT	chr7	0.0177845	0.0014249	0.0151967	0.0208037
48h_IAA	chr7	0.0472309	0.0017705	0.0438794	0.0508248
NT	chr8	0.0218965	0.0019687	0.0183528	0.0261063
48h_IAA	chr8	0.0386079	0.0025938	0.0338334	0.0440256
NT	chr9	0.0194473	0.0025507	0.0150298	0.0251300
48h_IAA	chr9	0.0804645	0.0024774	0.0757406	0.0854559
NT	chr10	0.0104535	0.0013206	0.0081583	0.0133859
48h_IAA	chr10	0.0431298	0.0039688	0.0359872	0.0516141
NT	chr11	0.0144050	0.0015245	0.0117031	0.0177194
48h_IAA	chr11	0.0320266	0.0020297	0.0282786	0.0362527
NT	chr12	0.0163966	0.0017638	0.0132751	0.0202370
48h_IAA	chr12	0.0364188	0.0036487	0.0299054	0.0442861
NT	chr15	0.0152121	0.0013897	0.0127153	0.0181901
48h_IAA	chr15	0.0872387	0.0029597	0.0816095	0.0932168
NT	chr16	0.0279056	0.0028842	0.0227758	0.0341502
48h_IAA	chr16	0.0899214	0.0043494	0.0817531	0.0988180
NT	chr17	0.0245989	0.0015274	0.0217764	0.0277769

type	chromosome	prob	SE	lower	upper
48h_IAA	chr17	0.0166198	0.0014800	0.0139546	0.0197837
NT	chr18	0.0162602	0.0022808	0.0123447	0.0213906
48h_IAA	chr18	0.0316027	0.0017331	0.0283769	0.0351819
NT	chr20	0.0167478	0.0017908	0.0135766	0.0206443
48h_IAA	chr20	0.0678429	0.0022220	0.0636154	0.0723297
NT	chrX	0.0034542	0.0017241	0.0012970	0.0091663
48h_IAA	chrX	0.0966334	0.0052165	0.0868812	0.1073517

Code



Comparison between NT and 48h_IAA

Code

chr	statistic	p.value	adj_p.value
chr1	41.07589	0.0000000	0.0000000
chr2	101.96253	0.0000000	0.0000000
chr3	1665.79160	0.0000000	0.0000000
chr4	313.25350	0.0000000	0.0000000

chr	statistic	p.value	adj_p.value
chr6	110.79740	0.0000000	0.0000000
chr7	123.66870	0.0000000	0.0000000
chr8	25.61210	0.0000004	0.0000005
chr9	115.88498	0.0000000	0.0000000
chr10	82.39314	0.0000000	0.0000000
chr11	42.20581	0.0000000	0.0000000
chr12	29.42617	0.0000001	0.0000001
chr15	332.58568	0.0000000	0.0000000
chr16	108.12927	0.0000000	0.0000000
chr17	13.07481	0.0002993	0.0002993
chr18	19.65932	0.0000093	0.0000098
chr20	161.49131	0.0000000	0.0000000
chrX	46.22516	0.0000000	0.0000000

1.4.1 Pooled data 48h_IAA

Code

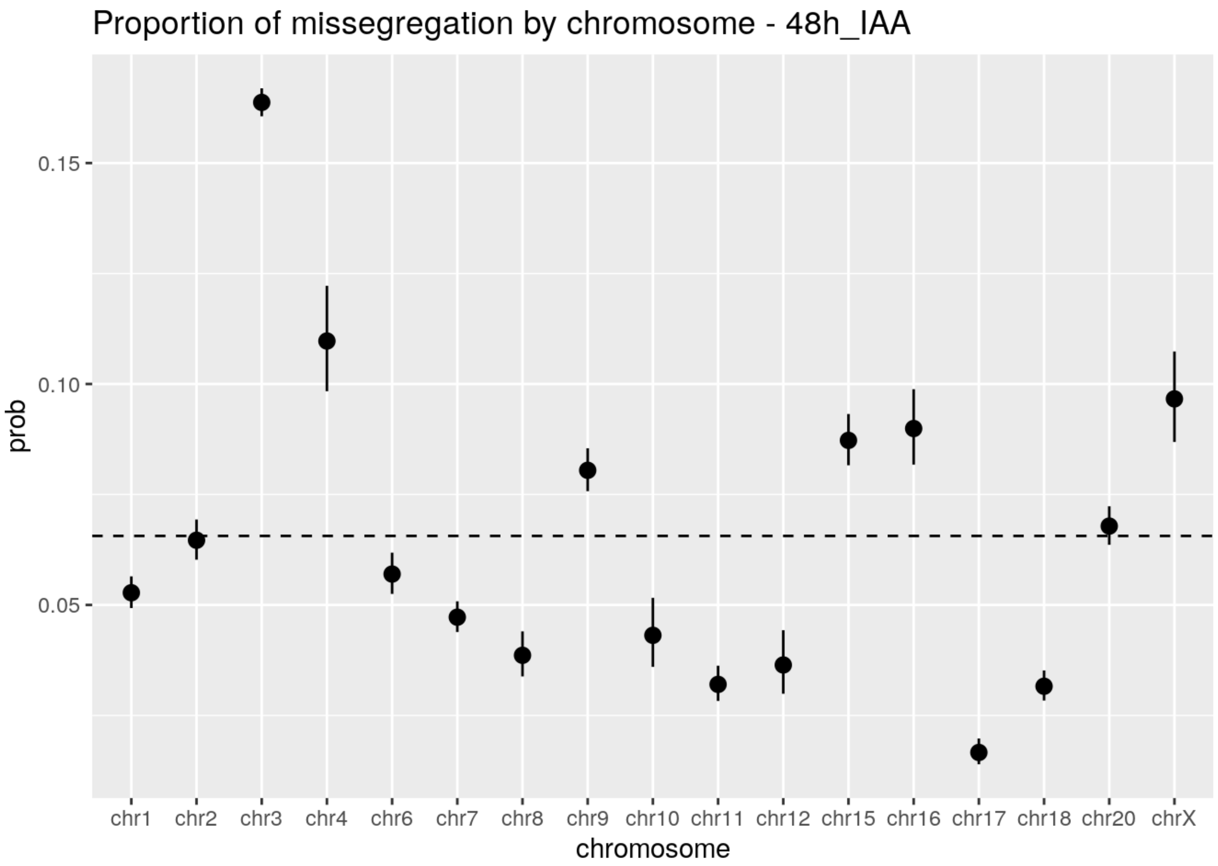
Code

Code

chromosome	prob	SE	lower	upper
chr1	0.0527652	0.0018271	0.0492967	0.0564631
chr2	0.0646422	0.0023171	0.0602466	0.0693348
chr3	0.1637134	0.0016125	0.1605774	0.1668984
chr4	0.1097238	0.0060794	0.0983632	0.1222186
chr6	0.0569894	0.0023793	0.0525013	0.0618360
chr7	0.0472309	0.0017705	0.0438794	0.0508248
chr8	0.0386079	0.0025938	0.0338334	0.0440256
chr9	0.0804645	0.0024774	0.0757406	0.0854559
chr10	0.0431298	0.0039688	0.0359872	0.0516141

chromosome	prob	SE	lower	upper
chr11	0.0320266	0.0020297	0.0282786	0.0362527
chr12	0.0364188	0.0036487	0.0299054	0.0442861
chr15	0.0872387	0.0029597	0.0816095	0.0932168
chr16	0.0899214	0.0043494	0.0817531	0.0988180
chr17	0.0166198	0.0014800	0.0139546	0.0197837
chr18	0.0316027	0.0017331	0.0283769	0.0351819
chr20	0.0678429	0.0022220	0.0636154	0.0723297
chrX	0.0966334	0.0052165	0.0868812	0.1073517

Code


Proportion of missegregation by chromosome - 48h_IAA

Each estimated coefficients is tested against the mean value (0.0656218).

Code

chr	statistic	p.value	adj_p.value
chr1	40.181324	0.0000000	0.0000000
chr2	0.176282	0.6745881	0.6745881
chr3	7575.543793	0.0000000	0.0000000

chr	statistic	p.value	adj_p.value
chr4	81.662826	0.0000000	0.0000000
chr6	11.515615	0.0006901	0.0007822
chr7	78.388363	0.0000000	0.0000000
chr8	63.977745	0.0000000	0.0000000
chr9	43.139177	0.0000000	0.0000000
chr10	21.265858	0.0000040	0.0000049
chr11	132.155420	0.0000000	0.0000000
chr12	35.512429	0.0000000	0.0000000
chr15	68.729786	0.0000000	0.0000000
chr16	41.257098	0.0000000	0.0000000
chr17	247.415050	0.0000000	0.0000000
chr18	183.168690	0.0000000	0.0000000
chr20	1.030448	0.3100536	0.3294319
chrX	49.580708	0.0000000	0.0000000

1.4.2 Pooled data NT

Code

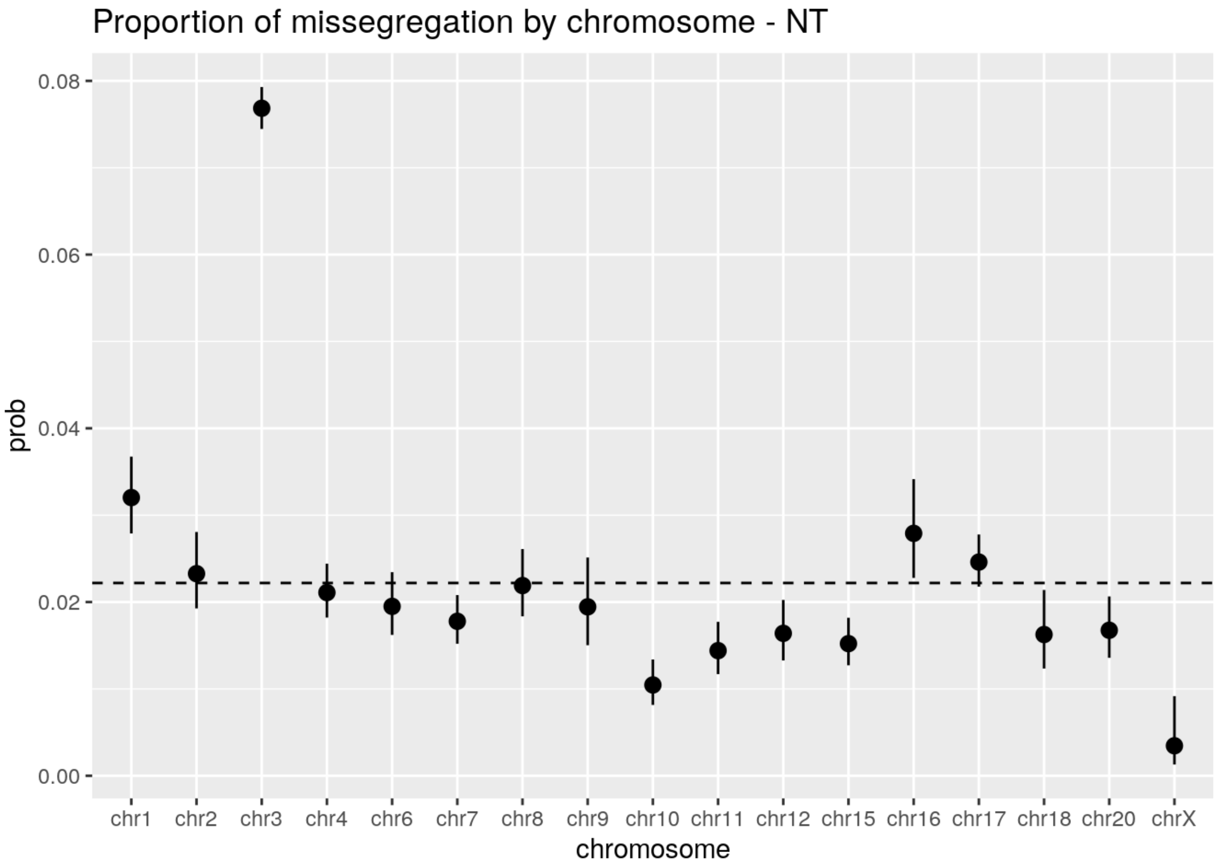
Code

Code

chromosome	prob	SE	lower	upper
chr1	0.0320261	0.0022507	0.0278969	0.0367435
chr2	0.0232660	0.0022334	0.0192682	0.0280696
chr3	0.0768428	0.0012293	0.0744677	0.0792871
chr4	0.0210894	0.0015773	0.0182098	0.0244130
chr6	0.0195011	0.0018328	0.0162151	0.0234370
chr7	0.0177845	0.0014249	0.0151967	0.0208037
chr8	0.0218965	0.0019687	0.0183528	0.0261063
chr9	0.0194473	0.0025507	0.0150298	0.0251300

chromosome	prob	SE	lower	upper
chr10	0.0104535	0.0013206	0.0081583	0.0133859
chr11	0.0144050	0.0015245	0.0117031	0.0177194
chr12	0.0163966	0.0017638	0.0132751	0.0202370
chr15	0.0152121	0.0013897	0.0127153	0.0181901
chr16	0.0279056	0.0028842	0.0227758	0.0341502
chr17	0.0245989	0.0015274	0.0217764	0.0277769
chr18	0.0162602	0.0022808	0.0123447	0.0213906
chr20	0.0167478	0.0017908	0.0135766	0.0206443
chrX	0.0034542	0.0017241	0.0012970	0.0091663

Code


Proportion of missegregation by chromosome - NT

Each estimated coefficients is tested against the mean value (0.0221934).

Code

chr	statistic	p.value	adj_p.value
chr1	26.9458231	0.0000002	0.0000012
chr2	0.2415059	0.6231206	0.6620656

chr	statistic	p.value	adj_p.value
chr3	5622.9066511	0.0000000	0.0000000
chr4	0.4659198	0.4948703	0.5608530
chr6	1.8985907	0.1682362	0.2200011
chr7	7.6733545	0.0056042	0.0119090
chr8	0.0224460	0.8809066	0.8809066
chr9	1.0169818	0.3132360	0.3803580
chr10	35.8847170	0.0000000	0.0000000
chr11	16.8031601	0.0000415	0.0001410
chr12	7.9637519	0.0047723	0.0115900
chr15	17.2083608	0.0000335	0.0001410
chr16	4.8806730	0.0271590	0.0419730
chr17	2.7400127	0.0978640	0.1386407
chr18	4.9466750	0.0261409	0.0419730
chr20	6.9690101	0.0082933	0.0156652
chrX	14.0764406	0.0001755	0.0004973

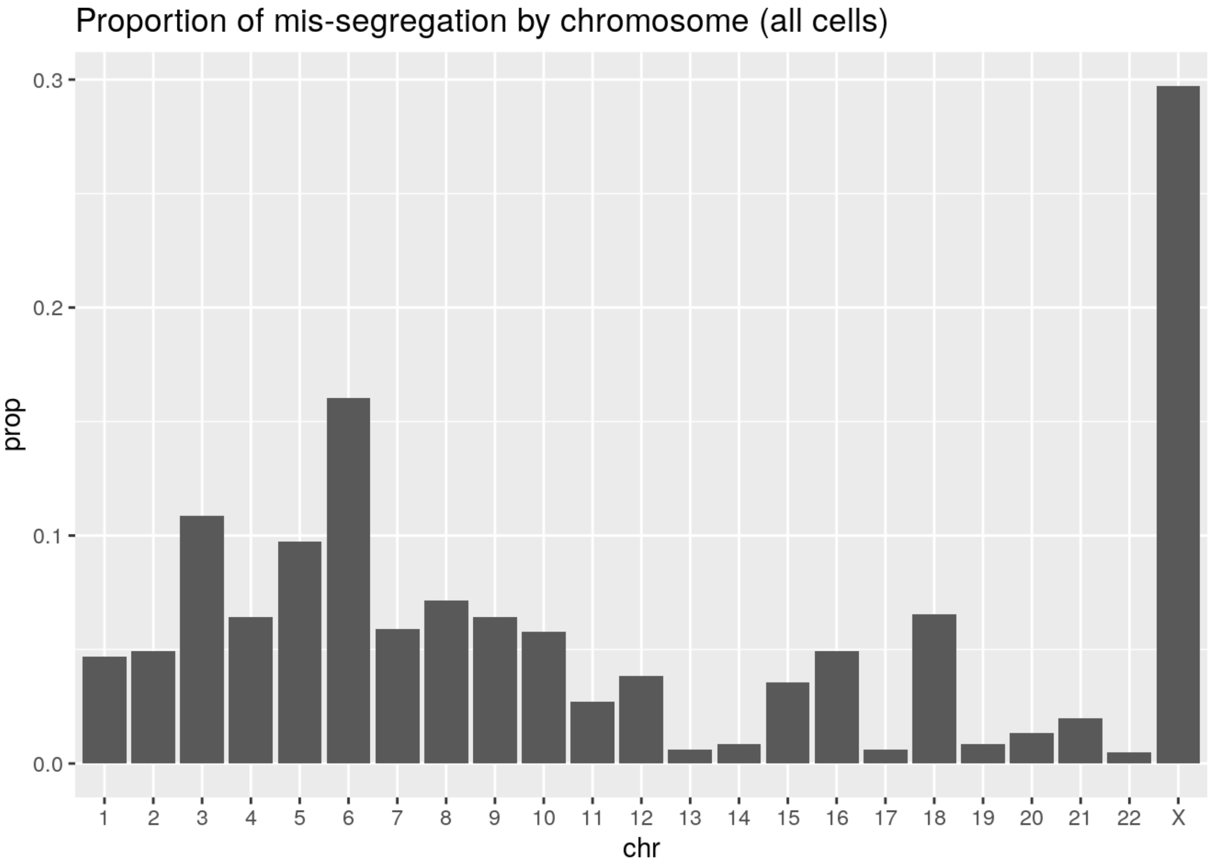
2 Single cell sequencing

2.1 48h_IAA

Data from single cell sequencing are transformed such that mis-segregation is defined as a number of chromosome different from 2 (partial events 1.5 and 2.5 are considered as normal).

Code

Code



2.1.1 Model on missegregated chromosomes only

Code

In this part we only consider chromosomes showing missegrations (1103 events).

A chi-square test allows to see if the probability is the same for each chromosome. With a pvalue of 2.271322910^{-249}, we conclude that the probability proportion of each chromosomes amongst all missegregated chromosome is not the same.

Next a multinomial model is fitted on chromosomes that show missegregation. This model allow to estimate the proportion of each chromosome. For each chromosome, the proportion, its standard error and a confidence interval at 95% is estimated.

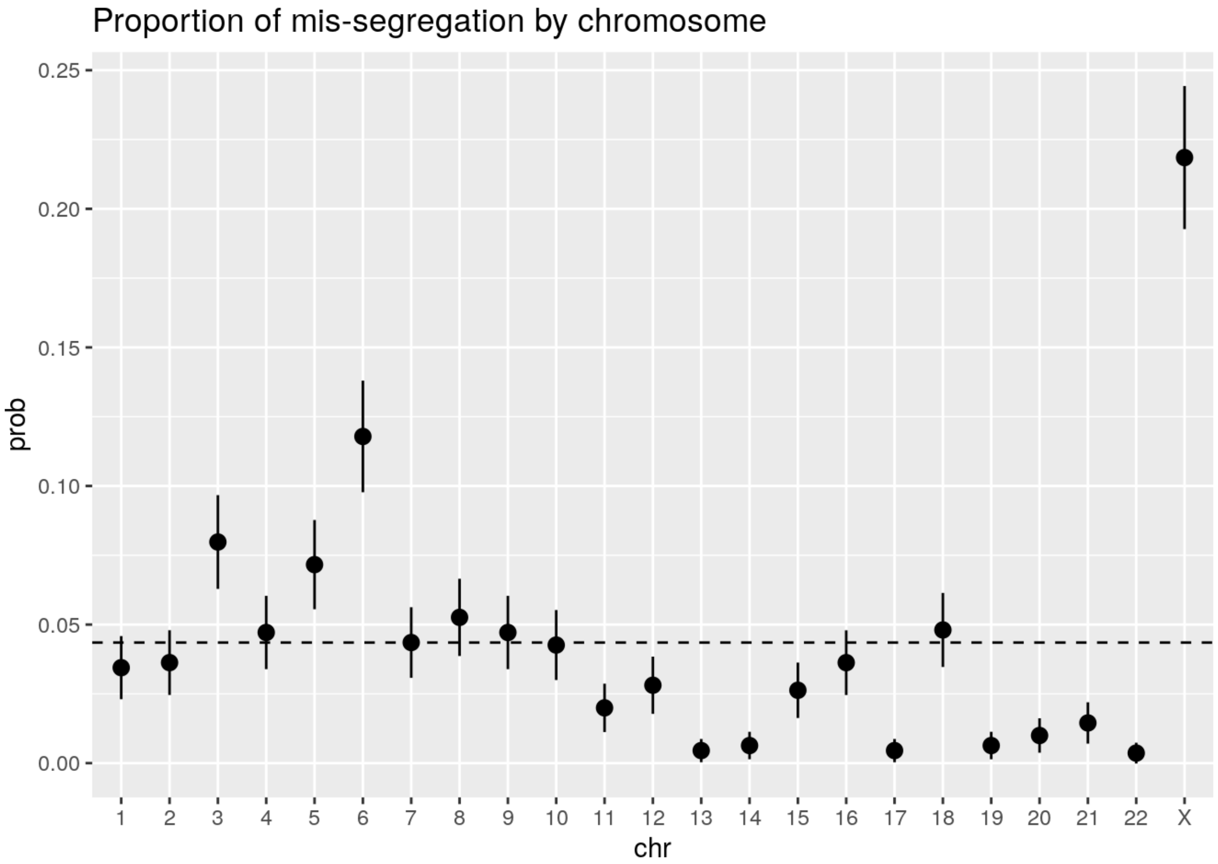
Code

Code

chr	prob	SE	lower	upper
1	0.0344484	0.0054914	0.0230599	0.0458369
2	0.0362694	0.0056294	0.0245948	0.0479440
3	0.0797820	0.0081585	0.0628623	0.0967016
4	0.0471448	0.0063818	0.0339097	0.0603798
5	0.0716217	0.0077642	0.0555197	0.0877236
6	0.1178665	0.0097090	0.0977313	0.1380017
7	0.0435179	0.0061431	0.0307780	0.0562578

chr	prob	SE	lower	upper
8	0.0525858	0.0067207	0.0386479	0.0665237
9	0.0471425	0.0063816	0.0339077	0.0603772
10	0.0426114	0.0060816	0.0299989	0.0552239
11	0.0199468	0.0042099	0.0112160	0.0286776
12	0.0281045	0.0049763	0.0177842	0.0384248
13	0.0045336	0.0020228	0.0003386	0.0087285
14	0.0063474	0.0023913	0.0013882	0.0113065
15	0.0262921	0.0048177	0.0163008	0.0362834
16	0.0362581	0.0056285	0.0245852	0.0479310
17	0.0045336	0.0020228	0.0003386	0.0087285
18	0.0480511	0.0064398	0.0346959	0.0614064
19	0.0063474	0.0023913	0.0013882	0.0113065
20	0.0099739	0.0029920	0.0037688	0.0161790
21	0.0145065	0.0036002	0.0070403	0.0219728
22	0.0036267	0.0018100	-0.0001270	0.0073805
X	0.2184882	0.0124421	0.1926848	0.2442915

Code



Test against value of 4.35% (1/23). The proportion for each chromosome is compared to 1/23 wtih a unilateral binomial test (we test if the proportion is over 1/23).

Code

chr	n	prop	pval
1	38	0.0344515	0.9222989
2	40	0.0362647	0.8658330
3	88	0.0797824	0.0000000
4	52	0.0471442	0.2472229
5	79	0.0716228	0.0000089
6	130	0.1178604	0.0000000
7	48	0.0435177	0.4591489
8	58	0.0525839	0.0631980
9	52	0.0471442	0.2472229
10	47	0.0426111	0.5179231
11	22	0.0199456	0.9999837
12	31	0.0281052	0.9947977
13	5	0.0045331	1.0000000

chr	n	prop	pval
14	7	0.0063463	1.0000000
15	29	0.0262919	0.9981474
16	40	0.0362647	0.8658330
17	5	0.0045331	1.0000000
18	53	0.0480508	0.2043485
19	7	0.0063463	1.0000000
20	11	0.0099728	1.0000000
21	16	0.0145059	0.9999999
22	4	0.0036265	1.0000000
X	241	0.2184950	0.0000000

2.1.2 Model on all chromosomes

In this part we use all the chromosomes, including those from normal cells. We fit a logistic model to assess the probability to be missegregated by chromosome.

Code

The anova table shows a strong effect of the chromosome

Code

term	df	Deviance	Resid..Df	Resid..Dev	p.value
NULL	NA	NA	18653	25858.549	NA
chr	23	18510.74	18630	7347.808	0

Probability of mis-segregation by chromosome with 95% confidence interval:

Code

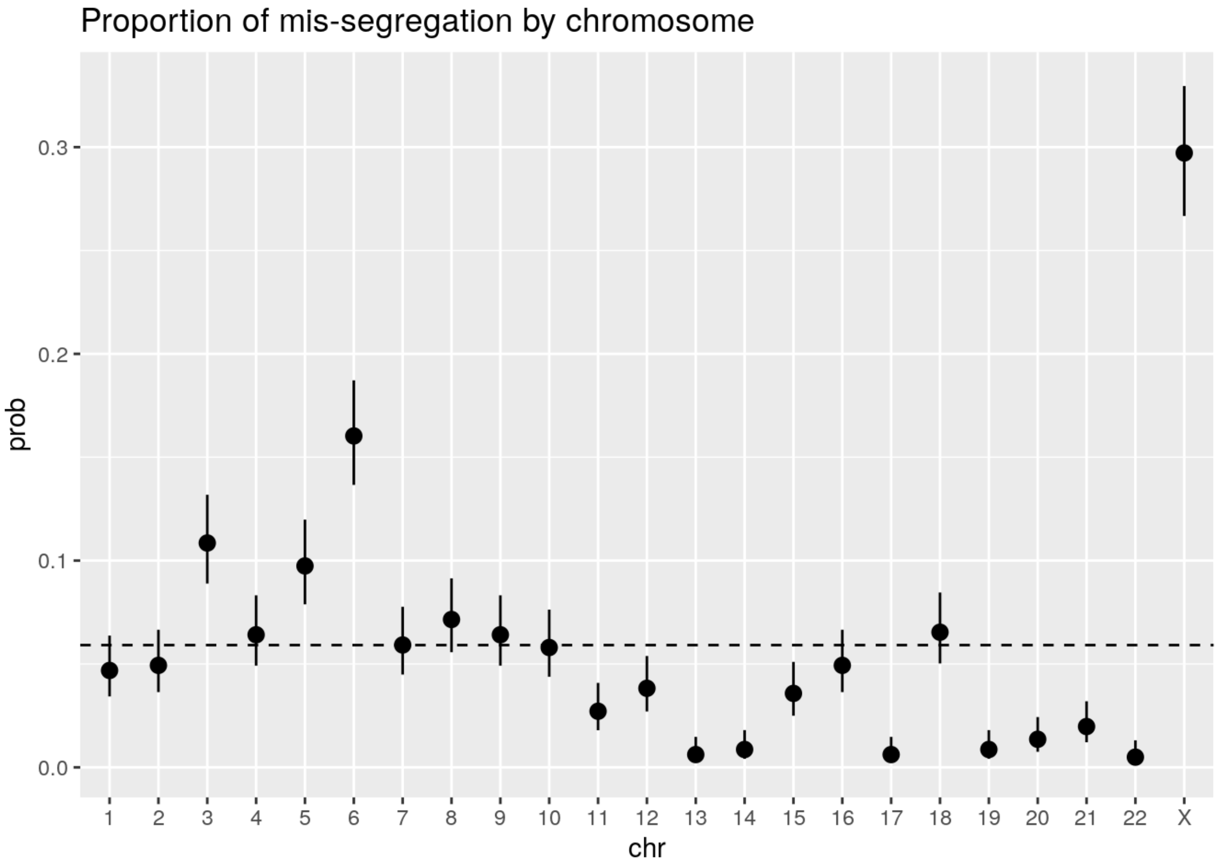
chr	prob	SE	lower	upper
1	0.0468557	0.0074208	0.0342783	0.0637434
2	0.0493218	0.0076037	0.0363812	0.0665475
3	0.1085080	0.0109214	0.0888826	0.1318397
4	0.0641184	0.0086018	0.0491859	0.0831877
5	0.0974106	0.0104121	0.0788235	0.1198106
6	0.1602959	0.0128829	0.1366238	0.1871804

chr	prob	SE	lower	upper
7	0.0591862	0.0082861	0.0448855	0.0776726
8	0.0715166	0.0090486	0.0556873	0.0914100
9	0.0641184	0.0086018	0.0491859	0.0831877
10	0.0579531	0.0082047	0.0438151	0.0762892
11	0.0271270	0.0057045	0.0179267	0.0408527
12	0.0382244	0.0067328	0.0270077	0.0538418
13	0.0061652	0.0027480	0.0025690	0.0147214
14	0.0086313	0.0032481	0.0041204	0.0179916
15	0.0357583	0.0065204	0.0249600	0.0509839
16	0.0493218	0.0076037	0.0363812	0.0665475
17	0.0061652	0.0027480	0.0025690	0.0147214
18	0.0653514	0.0086784	0.0502654	0.0845621
19	0.0086313	0.0032481	0.0041204	0.0179916
20	0.0135635	0.0040617	0.0075269	0.0243228
21	0.0197287	0.0048833	0.0121206	0.0319579
22	0.0049322	0.0024580	0.0018539	0.0130551
X	0.2971640	0.0160478	0.2666991	0.3295450

The plot below shows the proportion of mi-segregration by chromosome with a 95% confidence interval (dotted line at mean value).

Code

Code



2.1.3 Test against mean value.

The coefficients are tested against the mean value of 5.91

Code

chr	statistic	p.value	adj_p.value
1	2.1860293	0.1392679	0.2001976
2	1.3987485	0.2369332	0.3027480
3	34.2716041	0.0000000	0.0000000
4	0.3621302	0.5473255	0.5994518
5	20.8453909	0.0000050	0.0000115
6	134.7385114	0.0000000	0.0000000
7	0.0000419	0.9948356	0.9948356
8	2.2278986	0.1355381	0.2001976
9	0.3621302	0.5473255	0.5994518
10	0.0202767	0.8867670	0.9270746
11	14.1365445	0.0001700	0.0003259
12	6.2619500	0.0123358	0.0202660

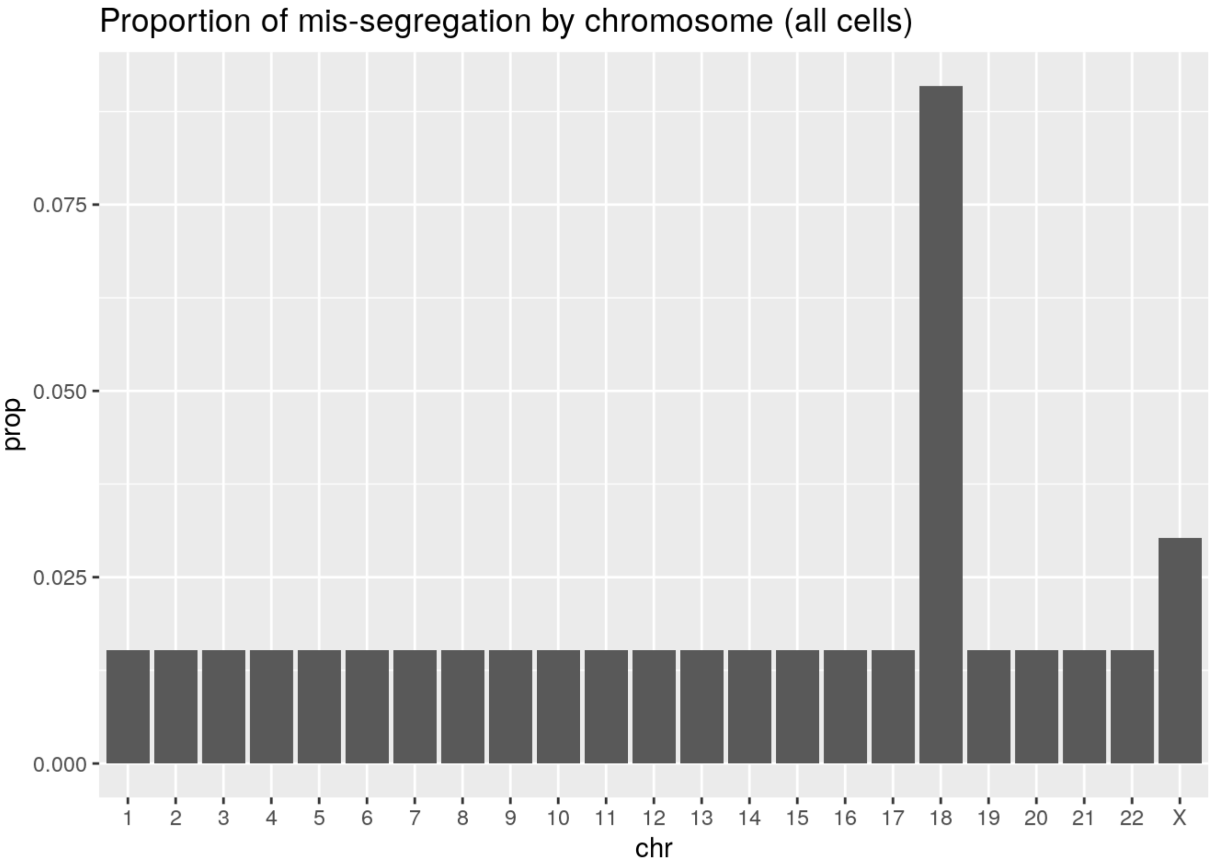
chr	statistic	p.value	adj_p.value
13	26.6584328	0.0000002	0.0000008
14	27.1158843	0.0000002	0.0000008
15	7.7820239	0.0052769	0.0093360
16	1.3987485	0.2369332	0.3027480
17	26.6584328	0.0000002	0.0000008
18	0.5632130	0.4529685	0.5483303
19	27.1158843	0.0000002	0.0000008
20	25.0596959	0.0000006	0.0000014
21	20.3380925	0.0000065	0.0000136
22	25.7217714	0.0000004	0.0000011
X	615.4591244	0.0000000	0.0000000

2.2 NT

Data from single cell sequencing are transformed such that mis-segregation is defined as a number of chromosome different from 2 (partial events 1.5 and 2.5 are considered as normal).

Code

Code



2.2.1 Model on missegregated chromosomes only

Code

In this part we only consider chromosomes showing missegrations (29 events).

A chi-square test allows to see if the probability is the same for each chromosome. With a pvalue of 0.6218038, we conclude that the probability proportion of each chromosomes amongst all missegregated chromosome is not the same.

Next a multinomial model is fitted on chromosomes that show missegregation. This model allow to estimate the proportion of each chromosome. For each chromosome, the proportion, its standard error and a confidence interval at 95% is estimated.

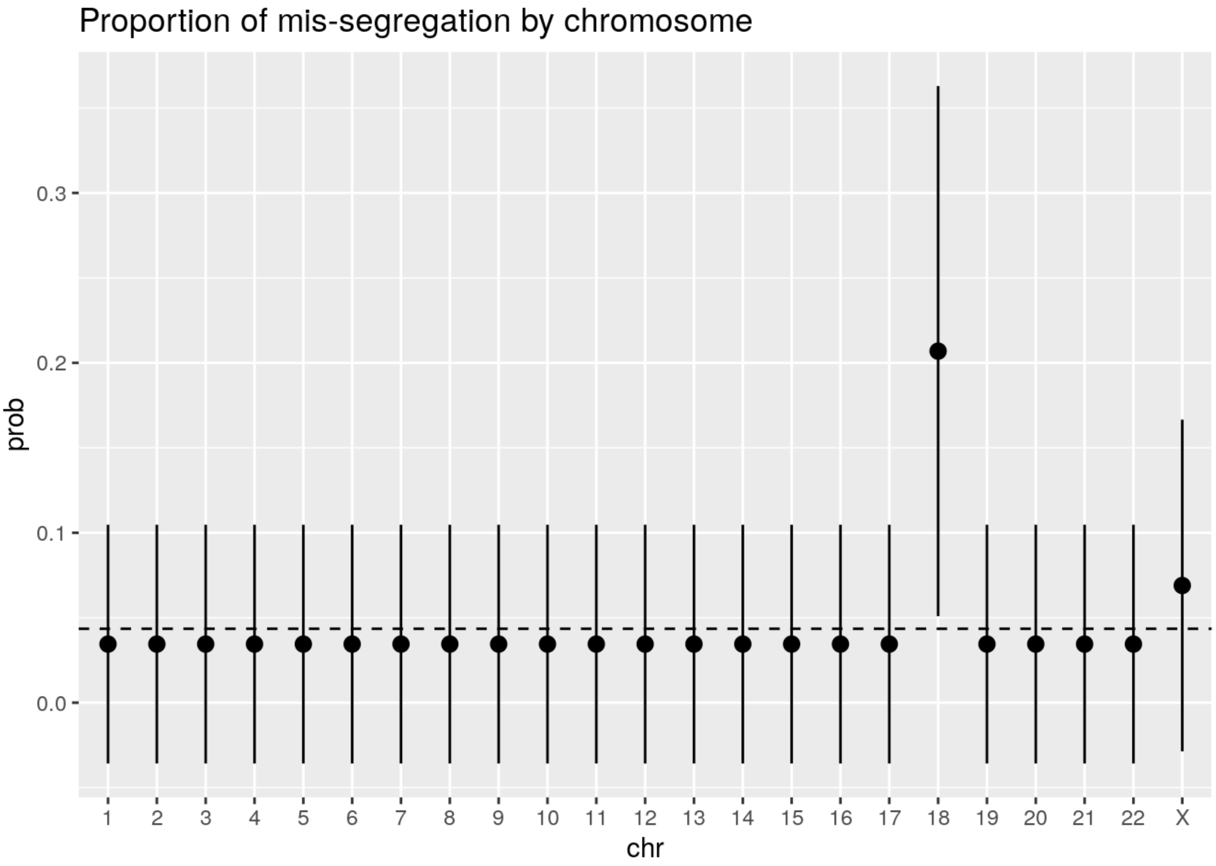
Code

Code

chr	prob	SE	lower	upper
1	0.0344807	0.0338820	-0.0357863	0.1047477
2	0.0344829	0.0338831	-0.0357863	0.1047520
3	0.0344829	0.0338831	-0.0357863	0.1047520
4	0.0344829	0.0338831	-0.0357863	0.1047520
5	0.0344829	0.0338831	-0.0357863	0.1047520
6	0.0344829	0.0338831	-0.0357863	0.1047520
7	0.0344829	0.0338831	-0.0357863	0.1047520

chr	prob	SE	lower	upper
8	0.0344829	0.0338831	-0.0357863	0.1047520
9	0.0344829	0.0338831	-0.0357863	0.1047520
10	0.0344829	0.0338831	-0.0357863	0.1047520
11	0.0344829	0.0338831	-0.0357863	0.1047520
12	0.0344829	0.0338831	-0.0357863	0.1047520
13	0.0344829	0.0338831	-0.0357863	0.1047520
14	0.0344829	0.0338831	-0.0357863	0.1047520
15	0.0344829	0.0338831	-0.0357863	0.1047520
16	0.0344829	0.0338831	-0.0357863	0.1047520
17	0.0344829	0.0338831	-0.0357863	0.1047520
18	0.2068966	0.0752216	0.0508965	0.3628967
19	0.0344829	0.0338831	-0.0357863	0.1047520
20	0.0344829	0.0338831	-0.0357863	0.1047520
21	0.0344829	0.0338831	-0.0357863	0.1047520
22	0.0344829	0.0338831	-0.0357863	0.1047520
X	0.0689656	0.0470544	-0.0286192	0.1665504

Code



Test against value of 4.35% (1/23). The proportion for each chromosome is compared to 1/23 with a unilateral binomial test (we test if the proportion is over 1/23).

Code

chr	n	prop	pval
1	1	0.0344828	0.3612984
2	1	0.0344828	0.3612984
3	1	0.0344828	0.3612984
4	1	0.0344828	0.3612984
5	1	0.0344828	0.3612984
6	1	0.0344828	0.3612984
7	1	0.0344828	0.3612984
8	1	0.0344828	0.3612984
9	1	0.0344828	0.3612984
10	1	0.0344828	0.3612984
11	1	0.0344828	0.3612984
12	1	0.0344828	0.3612984
13	1	0.0344828	0.3612984

chr	n	prop	pval
14	1	0.0344828	0.3612984
15	1	0.0344828	0.3612984
16	1	0.0344828	0.3612984
17	1	0.0344828	0.3612984
18	6	0.2068966	0.0001965
19	1	0.0344828	0.3612984
20	1	0.0344828	0.3612984
21	1	0.0344828	0.3612984
22	1	0.0344828	0.3612984
X	2	0.0689655	0.1301818

2.2.2 Model on all chromosomes

In this part we use all the chromosomes, including those from normal cells. We fit a logistic model to assess the probability to be missegregated by chromosome.

Code

The anova table shows a strong effect of the chromosome

Code

term	df	Deviance	Resid..Df	Resid..Dev	p.value
NULL	NA	NA	1518	2104.3948	NA
chr	23	1828.612	1495	275.7825	0

Probability of mis-segregation by chromosome with 95% confidence interval:

Code

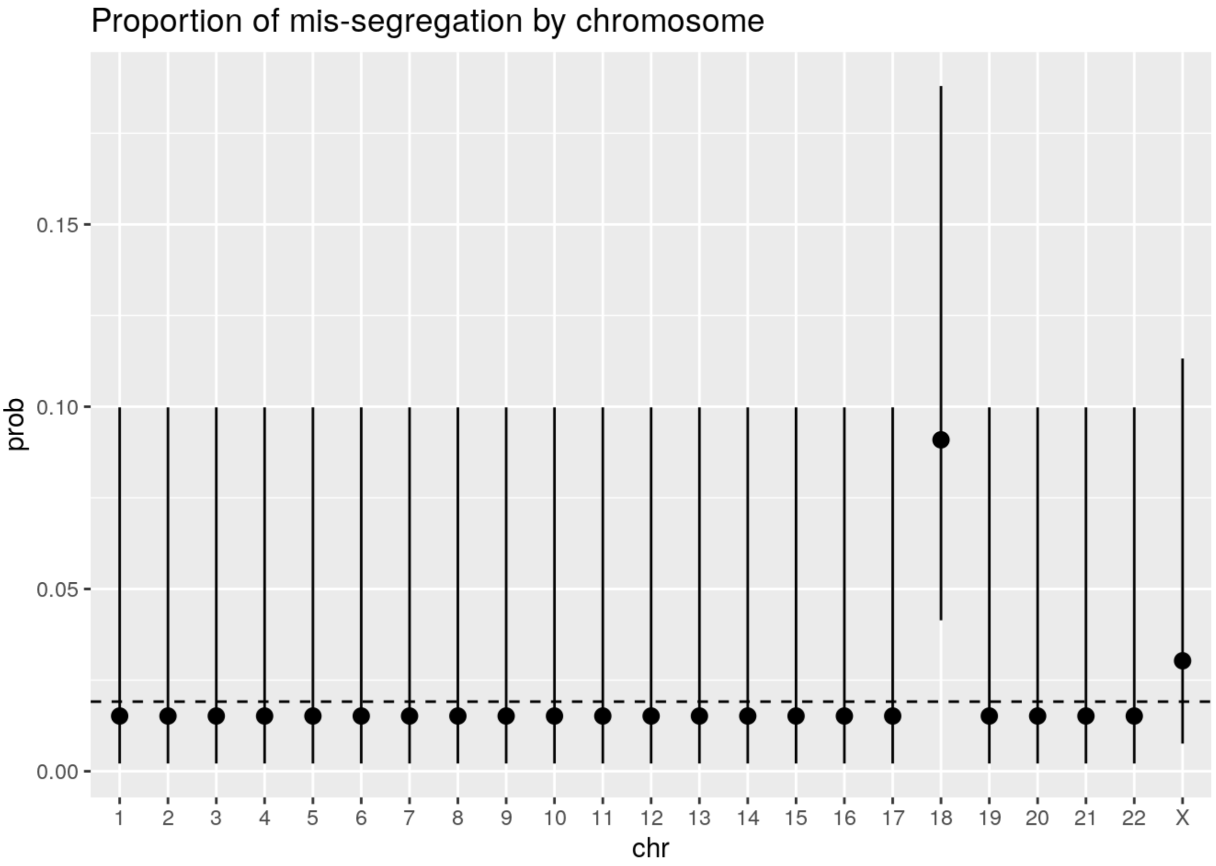
chr	prob	SE	lower	upper
1	0.0151515	0.0150363	0.0021303	0.0998040
2	0.0151515	0.0150363	0.0021303	0.0998040
3	0.0151515	0.0150363	0.0021303	0.0998040
4	0.0151515	0.0150363	0.0021303	0.0998040
5	0.0151515	0.0150363	0.0021303	0.0998040
6	0.0151515	0.0150363	0.0021303	0.0998040

chr	prob	SE	lower	upper
7	0.0151515	0.0150363	0.0021303	0.0998040
8	0.0151515	0.0150363	0.0021303	0.0998040
9	0.0151515	0.0150363	0.0021303	0.0998040
10	0.0151515	0.0150363	0.0021303	0.0998040
11	0.0151515	0.0150363	0.0021303	0.0998040
12	0.0151515	0.0150363	0.0021303	0.0998040
13	0.0151515	0.0150363	0.0021303	0.0998040
14	0.0151515	0.0150363	0.0021303	0.0998040
15	0.0151515	0.0150363	0.0021303	0.0998040
16	0.0151515	0.0150363	0.0021303	0.0998040
17	0.0151515	0.0150363	0.0021303	0.0998040
18	0.0909091	0.0353863	0.0414159	0.1879511
19	0.0151515	0.0150363	0.0021303	0.0998040
20	0.0151515	0.0150363	0.0021303	0.0998040
21	0.0151515	0.0150363	0.0021303	0.0998040
22	0.0151515	0.0150363	0.0021303	0.0998040
X	0.0303030	0.0211003	0.0075913	0.1132120

The plot below shows the proportion of mi-segregration by chromosome with a 95% confidence interval (dotted line at mean value).

Code

Code



2.2.3 Test against mean value.

The coefficients are tested against the mean value of 1.91

chr	statistic	p.value	adj_p.value
1	0.0547699	0.8149619	0.8149619
2	0.0547699	0.8149619	0.8149619
3	0.0547699	0.8149619	0.8149619
4	0.0547699	0.8149619	0.8149619
5	0.0547699	0.8149619	0.8149619
6	0.0547699	0.8149619	0.8149619
7	0.0547699	0.8149619	0.8149619
8	0.0547699	0.8149619	0.8149619
9	0.0547699	0.8149619	0.8149619
10	0.0547699	0.8149619	0.8149619
11	0.0547699	0.8149619	0.8149619
12	0.0547699	0.8149619	0.8149619

chr	statistic	p.value	adj_p.value
13	0.0547699	0.8149619	0.8149619
14	0.0547699	0.8149619	0.8149619
15	0.0547699	0.8149619	0.8149619
16	0.0547699	0.8149619	0.8149619
17	0.0547699	0.8149619	0.8149619
18	14.5986963	0.0001330	0.0030592
19	0.0547699	0.8149619	0.8149619
20	0.0547699	0.8149619	0.8149619
21	0.0547699	0.8149619	0.8149619
22	0.0547699	0.8149619	0.8149619
X	0.4335837	0.5102357	0.8149619

---

3 FISH data

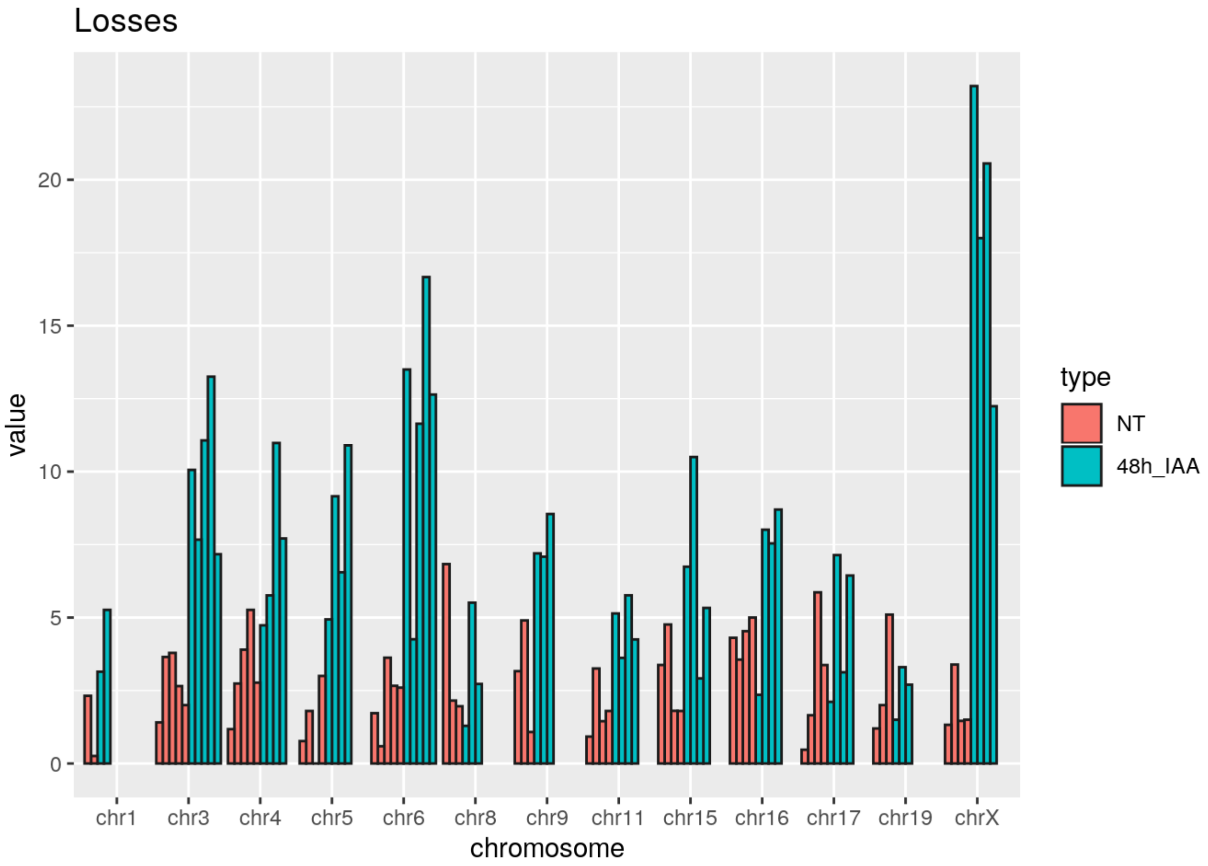
FISH data are analysed in the same way as Image stream.

Code

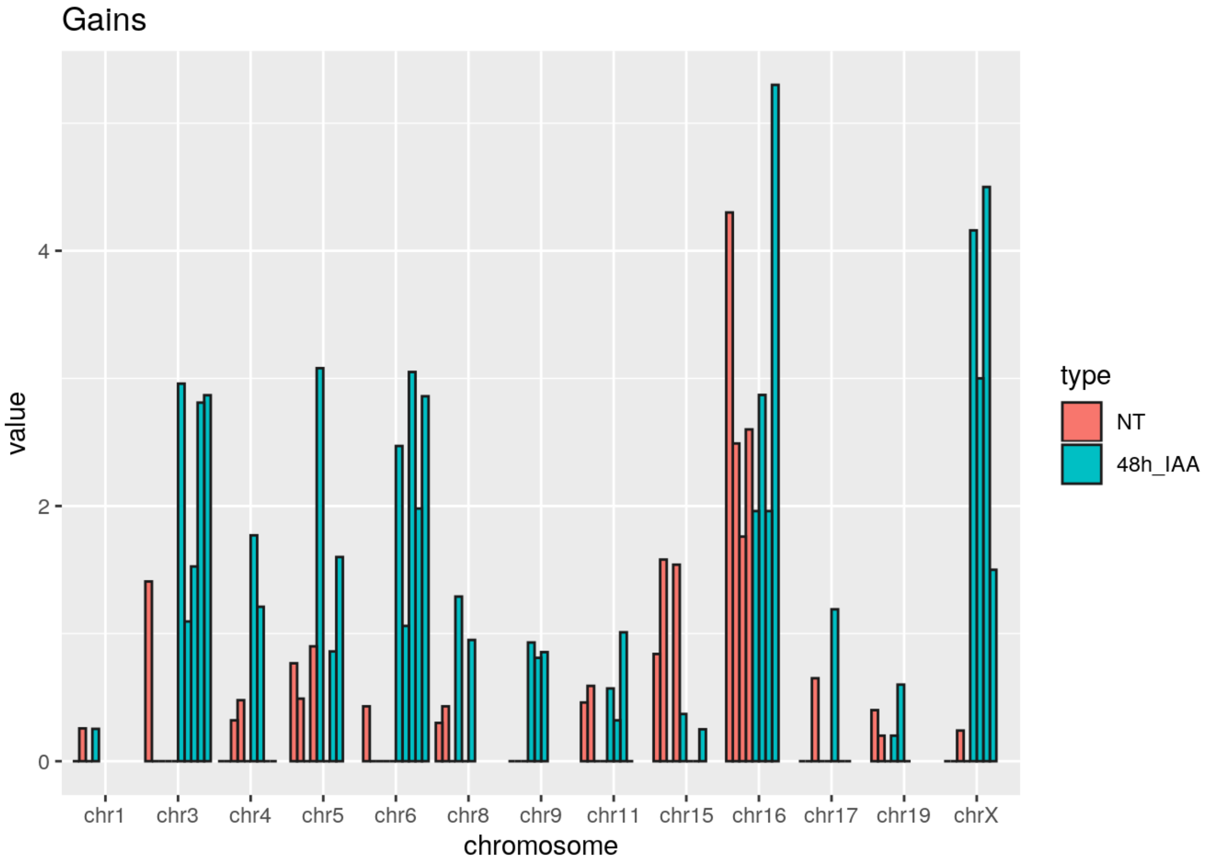
3.1 Analysis of NT and 48h_IAA data

Code

Code



Code



3.1.1 Model

A generalized linear model is fitted between gains or losses fractions according to chromosomes and type (control or 48h_IAA) with a binomial family.

Code

3.1.2 Results

3.1.2.1 Losses

3.1.2.1.1 Estimated proportions for each chromosome

The following table gives the estimated probability for each chromosome with standard error and confidence interval at 95%.

Code

type	chromosome	prob	SE	lower	upper
NT	chr1	0.0160226	0.0038548	0.0099832	0.0256211
48h_IAA	chr1	0.0432900	0.0077307	0.0304300	0.0612415
NT	chr3	0.0279931	0.0034232	0.0220104	0.0355429
48h_IAA	chr3	0.0904075	0.0059080	0.0794766	0.1026741
NT	chr4	0.0349170	0.0043919	0.0272602	0.0446257
48h_IAA	chr4	0.0749814	0.0071758	0.0620738	0.0903146
NT	chr5	0.0124224	0.0025199	0.0083398	0.0184662
48h_IAA	chr5	0.0714286	0.0070993	0.0587048	0.0866562
NT	chr6	0.0257048	0.0032223	0.0200905	0.0328355
48h_IAA	chr6	0.1258081	0.0073952	0.1120139	0.1410311
NT	chr8	0.0382022	0.0064253	0.0274208	0.0529919
48h_IAA	chr8	0.0334661	0.0050768	0.0248241	0.0449780
NT	chr9	0.0365169	0.0049707	0.0279312	0.0476123
48h_IAA	chr9	0.0744804	0.0063087	0.0630209	0.0878282
NT	chr11	0.0187683	0.0032865	0.0133025	0.0264199
48h_IAA	chr11	0.0438175	0.0050148	0.0349754	0.0547682
NT	chr15	0.0252672	0.0048923	0.0172595	0.0368511
48h_IAA	chr15	0.0574810	0.0067673	0.0455675	0.0722734
NT	chr16	0.0444096	0.0047087	0.0360426	0.0546089
48h_IAA	chr16	0.0735450	0.0060042	0.0626095	0.0862148
NT	chr17	0.0316319	0.0046927	0.0236211	0.0422419

type	chromosome	prob	SE	lower	upper
48h_IAA	chr17	0.0497367	0.0052588	0.0403849	0.0611161
NT	chr19	0.0221551	0.0033028	0.0165271	0.0296418
48h_IAA	chr19	0.0257009	0.0034207	0.0197833	0.0333285
NT	chrX	0.0169492	0.0033610	0.0114778	0.0249629
48h_IAA	chrX	0.1641921	0.0109478	0.1438447	0.1867899

3.1.2.1.2 Anova

Anova table on losses model:

Code

term	df	Deviance	Resid..Df	Resid..Dev	p.value
NULL	NA	NA	98	1142.4348	NA
type	1	469.4442	97	672.9906	0
chromosome	12	278.4129	85	394.5777	0
type:chromosome	12	160.5050	73	234.0727	0

Code

3.1.2.1.3 Comparison of NT and 48h_IAA

Comparison of missegregation rate for each chromosome between NT and 48h_IAA

Code

chr	statistic	p.value	adj_p.value
chr1	11.038887	0.0008922	0.0010544
chr3	50.386352	0.0000000	0.0000000
chr4	36.548455	0.0000000	0.0000000
chr5	33.840479	0.0000000	0.0000000
chr6	73.842801	0.0000000	0.0000000
chr8	6.742240	0.0094156	0.0102003
chr9	37.456177	0.0000000	0.0000000
chr11	14.446210	0.0001442	0.0001875
chr15	23.131114	0.0000015	0.0000025

chr	statistic	p.value	adj_p.value
chr16	37.151724	0.0000000	0.0000000
chr17	18.892279	0.0000138	0.0000200
chr19	2.966745	0.0849927	0.0849927
chrX	93.752389	0.0000000	0.0000000

3.1.2.2 Gains

3.1.2.2.1 Estimated proportions for each chromosome

The following table gives the estimated probability for each chromosome with standard error and confidence interval at 95%.

Code

type	chromosome	prob	SE	lower	upper
NT	chr1	0.0009425	0.0009421	0.0001327	0.0066588
48h_IAA	chr1	0.0014430	0.0014420	0.0002032	0.0101688
NT	chr3	0.0012920	0.0007454	0.0004168	0.0039980
48h_IAA	chr3	0.0207980	0.0029401	0.0157532	0.0274133
NT	chr4	0.0022896	0.0011435	0.0008596	0.0060842
48h_IAA	chr4	0.0051967	0.0019591	0.0024794	0.0108596
NT	chr5	0.0046584	0.0015492	0.0024256	0.0089282
48h_IAA	chr5	0.0129179	0.0031128	0.0080452	0.0206803
NT	chr6	0.0008292	0.0005861	0.0002074	0.0033091
48h_IAA	chr6	0.0263550	0.0035721	0.0201889	0.0343385
NT	chr8	0.0033708	0.0019428	0.0010876	0.0103975
48h_IAA	chr8	0.0071713	0.0023819	0.0037354	0.0137240
NT	chr9	0.0000000	0.0000002	0.0000000	1.0000000
48h_IAA	chr9	0.0086605	0.0022264	0.0052277	0.0143152
NT	chr11	0.0017595	0.0010150	0.0005676	0.0054408
48h_IAA	chr11	0.0036014	0.0014676	0.0016189	0.0079926
NT	chr15	0.0097182	0.0030582	0.0052367	0.0179657
48h_IAA	chr15	0.0016906	0.0011944	0.0004229	0.0067336

type	chromosome	prob	SE	lower	upper
NT	chr16	0.0261233	0.0036458	0.0198533	0.0343041
48h_IAA	chr16	0.0317460	0.0040328	0.0247258	0.0406763
NT	chr17	0.0007189	0.0007186	0.0001013	0.0050849
48h_IAA	chr17	0.0011703	0.0008270	0.0002927	0.0046667
NT	chr19	0.0025176	0.0011245	0.0010483	0.0060340
48h_IAA	chr19	0.0028037	0.0011430	0.0012601	0.0062264
NT	chrX	0.0006780	0.0006777	0.0000955	0.0047963
48h_IAA	chrX	0.0279476	0.0048710	0.0198306	0.0392540

3.1.2.2.2 Anova

Anova table on gains model:

Code

term	df	Deviance	Resid..Df	Resid..Dev	p.value
NULL	NA	NA	98	602.6248	NA
type	1	90.40428	97	512.2205	0
chromosome	12	252.42945	85	259.7911	0
type:chromosome	12	105.54838	73	154.2427	0

Code

3.1.2.2.3 Comparison of NT and 48h_IAA

Comparison of missegregation rate for each chromosome between NT and 48h_IAA

Code

chr	statistic	p.value	adj_p.value
chr1	0.0908163	0.7631419	0.8267371
chr3	9.4911115	0.0020647	0.0067103
chr4	2.5593227	0.1096456	0.1781740
chr5	6.5215169	0.0106577	0.0277100
chr6	11.0426055	0.0008904	0.0038585
chr8	3.7232853	0.0536587	0.0996519

chr	statistic	p.value	adj_p.value
chr9	4.6376669	0.0312775	0.0677679
chr11	1.5444238	0.2139605	0.3090541
chr15	0.2279205	0.6330700	0.7481737
chr16	12.3658937	0.0004372	0.0038585
chr17	0.0312679	0.8596441	0.8596441
chr19	1.0209330	0.3122978	0.4059872
chrX	11.3015295	0.0007744	0.0038585

3.2 Analysis of 48h_IAA data only

3.2.1 Model

A generalized linear model is fitted between gains or losses fractions and chromosomes with a quasibinomial family and weights of observation equal to number of cells.

Code

3.2.2 Results

3.2.2.1 Losses

3.2.2.1.1 Estimated proportions for each chromosome

The following table gives the estimated probability for each chromosome with standard error and confidence interval at 95%.

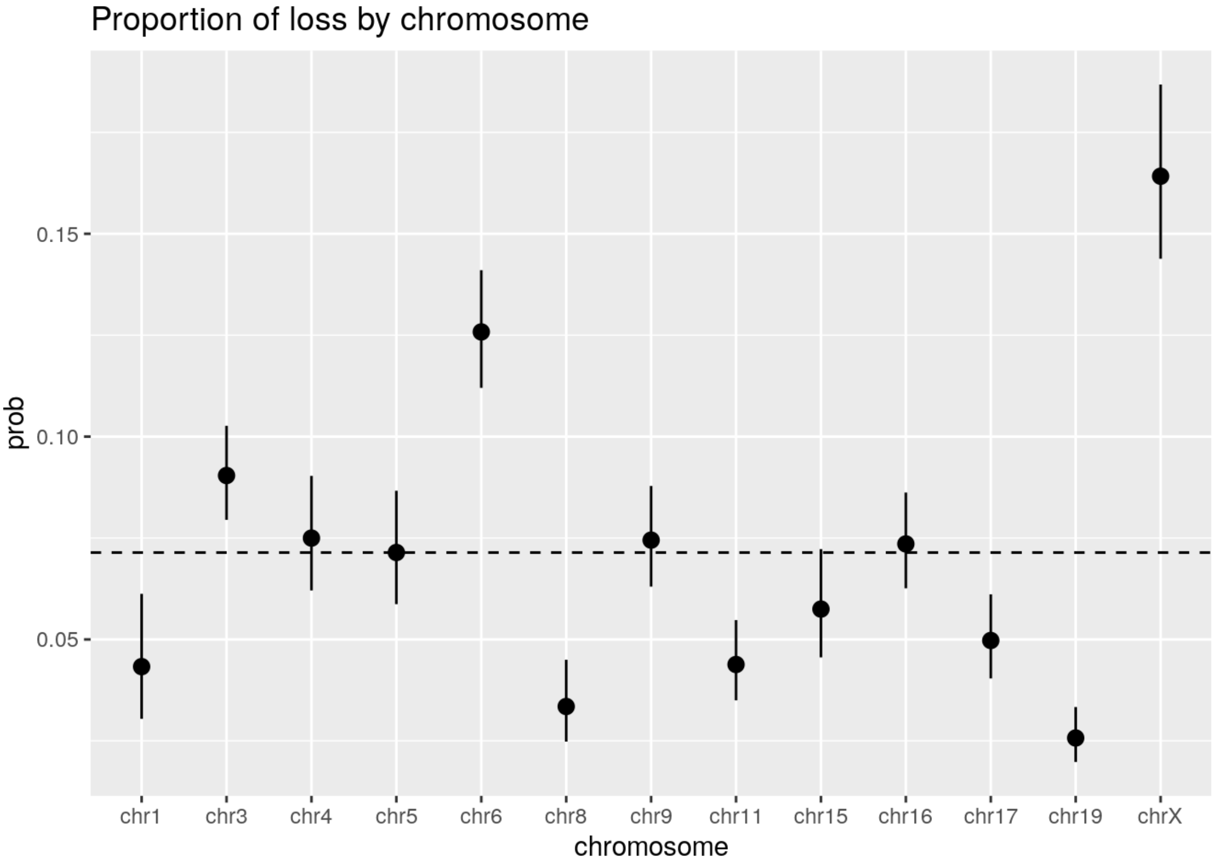
Code

Code

chromosome	prob	SE	lower	upper
chr1	0.0432900	0.0077307	0.0304300	0.0612415
chr3	0.0904075	0.0059080	0.0794766	0.1026741
chr4	0.0749814	0.0071758	0.0620738	0.0903146
chr5	0.0714286	0.0070993	0.0587048	0.0866562
chr6	0.1258081	0.0073952	0.1120139	0.1410311
chr8	0.0334661	0.0050768	0.0248241	0.0449779
chr9	0.0744804	0.0063087	0.0630209	0.0878282
chr11	0.0438175	0.0050148	0.0349754	0.0547682

chromosome	prob	SE	lower	upper
chr15	0.0574810	0.0067673	0.0455675	0.0722734
chr16	0.0735450	0.0060042	0.0626095	0.0862148
chr17	0.0497367	0.0052588	0.0403849	0.0611161
chr19	0.0257009	0.0034207	0.0197833	0.0333285
chrX	0.1641921	0.0109478	0.1438447	0.1867899

Code



3.2.2.1.2 Anova

Anova table on losses model:

Code

term	df	Deviance	Resid..Df	Resid..Dev	p.value
NULL	NA	NA	49	18252.4970	NA
chromosome	13	18137.59	36	114.9054	0

Code

Wih a p-value of 0.00e+00, we conclude that there is an effect of the chromosomes on the the percentage of losses (i.e. at least one chromosome has a percentage different from the others).

3.2.2.1.3 Test against mean value

Each estimated coefficients is tested against the mean value (0.0714104).

Code

chr	statistic	p.value	adj_p.value
chr1	8.0729807	0.0044930	0.0073011
chr3	12.7521078	0.0003556	0.0007705
chr4	0.2589817	0.6108206	0.7325121
chr5	0.0000065	0.9979586	0.9979586
chr6	86.8600057	0.0000000	0.0000000
chr8	25.8481370	0.0000004	0.0000012
chr9	0.2461236	0.6198179	0.7325121
chr11	18.7070789	0.0000152	0.0000396
chr15	3.4460598	0.0634027	0.0915817
chr16	0.1298549	0.7185825	0.7784644
chr17	11.9583960	0.0005440	0.0010103
chr19	61.3474444	0.0000000	0.0000000
chrX	138.2108039	0.0000000	0.0000000

3.2.2.2 Gains

3.2.2.2.1 Estimated proportions for each chromosome

The following table gives the estimated probability for each chromosome with standard error and confidence interval at 95%.

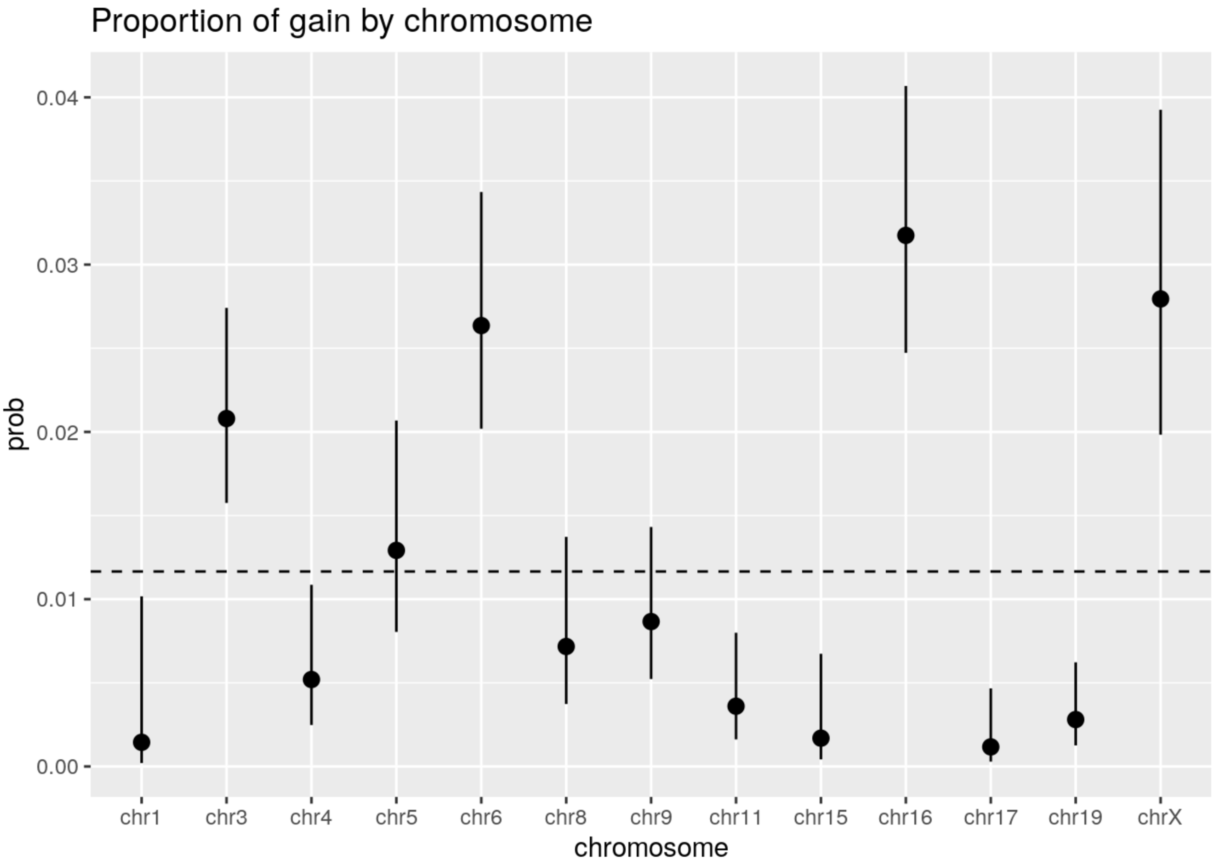
Code

Code

chromosome	prob	SE	lower	upper
chr1	0.0014430	0.0014420	0.0002032	0.0101688
chr3	0.0207980	0.0029401	0.0157532	0.0274133
chr4	0.0051967	0.0019591	0.0024794	0.0108596
chr5	0.0129179	0.0031128	0.0080452	0.0206803
chr6	0.0263550	0.0035721	0.0201889	0.0343385
chr8	0.0071713	0.0023819	0.0037354	0.0137240

chromosome	prob	SE	lower	upper
chr9	0.0086605	0.0022264	0.0052277	0.0143152
chr11	0.0036014	0.0014676	0.0016189	0.0079926
chr15	0.0016906	0.0011944	0.0004229	0.0067336
chr16	0.0317460	0.0040328	0.0247258	0.0406763
chr17	0.0011703	0.0008270	0.0002927	0.0046667
chr19	0.0028037	0.0011430	0.0012601	0.0062264
chrX	0.0279476	0.0048710	0.0198306	0.0392540

Code



3.2.2.2.2 Anova

Anova table on gains model:

Code

term	df	Deviance	Resid..Df	Resid..Dev	p.value
NULL	NA	NA	49	25853.30692	NA
chromosome	13	25763.34	36	89.96192	0

Code

Wih a p-value of 0.00e+00, we conclude that there is an effect of the chromosomes on the the percentage of losses (i.e. at least one chromosome has a percentage different from the others).

3.2.2.2.3 Test against mean value

Each estimated coefficients is tested against the mean value (0.011654).

Code

chr	statistic	p.value	adj_p.value
chr1	4.4002983	0.0359326	0.0467124
chr3	16.6172801	0.0000457	0.0001486
chr4	4.6155734	0.0316829	0.0457642
chr5	0.1823541	0.6693579	0.6693579
chr6	35.6347262	0.0000000	0.0000000
chr8	2.1461663	0.1429264	0.1689130
chr9	1.3374309	0.2474876	0.2681115
chr11	8.3586519	0.0038386	0.0071287
chr15	7.5190272	0.0061051	0.0099207
chr16	60.7573910	0.0000000	0.0000000
chr17	10.6501980	0.0011006	0.0023846
chr19	12.2968850	0.0004537	0.0011797
chrX	24.7110359	0.0000007	0.0000029

3.3 Analysis of NT data only

3.3.1 Model

A generalized linear model is fitted between gains or losses fractions and chromosomes with a quasibinomial family and weights of observation equal to number of cells.

Code

3.3.2 Results

3.3.2.1 Losses

3.3.2.1.1 Estimated proportions for each chromosome

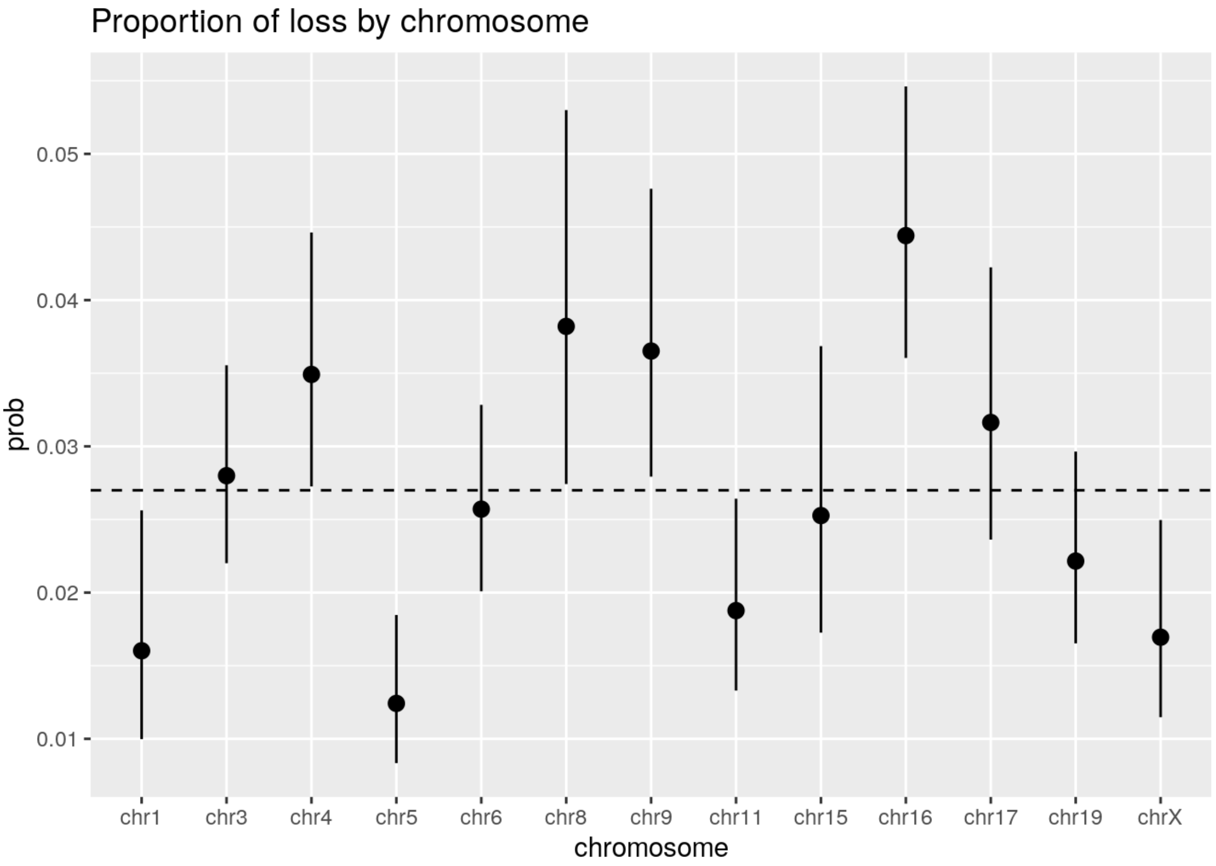
The following table gives the estimated probability for each chromosome with standard error and confidence interval at 95%.

Code

Code

chromosome	prob	SE	lower	upper
chr1	0.0160226	0.0038548	0.0099832	0.0256211
chr3	0.0279931	0.0034232	0.0220104	0.0355429
chr4	0.0349170	0.0043919	0.0272602	0.0446257
chr5	0.0124224	0.0025199	0.0083398	0.0184662
chr6	0.0257048	0.0032223	0.0200905	0.0328355
chr8	0.0382022	0.0064253	0.0274208	0.0529919
chr9	0.0365169	0.0049707	0.0279312	0.0476123
chr11	0.0187683	0.0032865	0.0133025	0.0264199
chr15	0.0252672	0.0048923	0.0172595	0.0368511
chr16	0.0444096	0.0047087	0.0360426	0.0546089
chr17	0.0316319	0.0046927	0.0236211	0.0422419
chr19	0.0221551	0.0033028	0.0165271	0.0296418
chrX	0.0169492	0.0033610	0.0114778	0.0249629

Code


Proportion of loss by chromosome

3.3.2.1.2 Anova

Anova table on losses model:

Code

term	df	Deviance	Resid..Df	Resid..Dev	p.value
NULL	NA	NA	50	24442.2009	NA
chromosome	13	24323.03	37	119.1672	0

Code

Wih a p-value of 0.00e+00, we conclude that there is an effect of the chromosomes on the the percentage of losses (i.e. at least one chromosome has a percentage different from the others).

3.3.2.1.3 Test against mean value

Each estimated coefficients is tested against the mean value (0.0269969).

Code

chr	statistic	p.value	adj_p.value
chr1	4.7510280	0.0292808	0.0677617
chr3	0.0877083	0.7671110	0.7671110
chr4	4.1473602	0.0416995	0.0677617
chr5	14.8333531	0.0001174	0.0007634
chr6	0.1532767	0.6954235	0.7671110
chr8	4.2087671	0.0402156	0.0677617
chr9	4.8733626	0.0272743	0.0677617
chr11	4.3445802	0.0371269	0.0677617
chr15	0.1171550	0.7321408	0.7671110
chr16	21.6090867	0.0000033	0.0000435
chr17	1.1350842	0.2866935	0.3727015
chr19	1.7664049	0.1838276	0.2655288
chrX	5.5632399	0.0183414	0.0677617

3.3.2.2 Gains

3.3.2.2.1 Estimated proportions for each chromosome

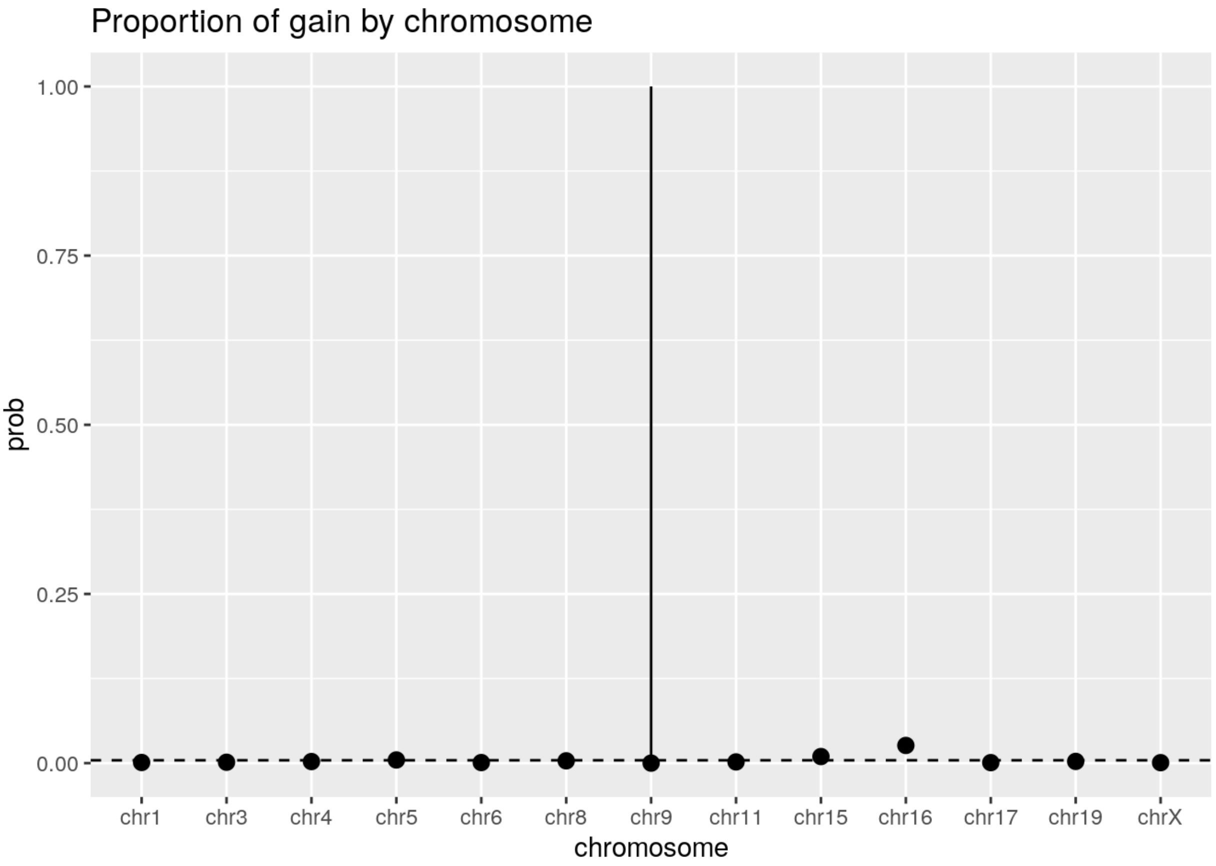
The following table gives the estimated probability for each chromosome with standard error and confidence interval at 95%.

Code

Code

chromosome	prob	SE	lower	upper
chr1	0.0009425	0.0009421	0.0001327	0.0066588
chr3	0.0012920	0.0007454	0.0004168	0.0039980
chr4	0.0022896	0.0011435	0.0008596	0.0060842
chr5	0.0046584	0.0015492	0.0024256	0.0089282
chr6	0.0008292	0.0005861	0.0002074	0.0033091
chr8	0.0033708	0.0019428	0.0010876	0.0103975
chr9	0.0000000	0.0000002	0.0000000	1.0000000
chr11	0.0017595	0.0010150	0.0005676	0.0054408
chr15	0.0097182	0.0030582	0.0052367	0.0179657
chr16	0.0261233	0.0036458	0.0198533	0.0343041
chr17	0.0007189	0.0007186	0.0001013	0.0050849
chr19	0.0025176	0.0011245	0.0010483	0.0060340
chrX	0.0006780	0.0006777	0.0000955	0.0047963

Code



3.3.2.2.2 Anova

Anova table on gains model:

Code

term	df	Deviance	Resid..Df	Resid..Dev	p.value
NULL	NA	NA	50	28547.42270	NA
chromosome	13	28483.14	37	64.28078	0

Code

Wih a p-value of 0.00e+00, we conclude that there is an effect of the chromosomes on the the percentage of losses (i.e. at least one chromosome has a percentage different from the others).

3.3.2.2.3 Test against mean value

Each estimated coefficients is tested against the mean value (0.0042229).

Code

chr	statistic	p.value	adj_p.value
chr1	2.2569648	0.1330145	0.2161486
chr3	4.2234601	0.0398688	0.1295735
chr4	1.5048880	0.2199208	0.3176634
chr5	0.0870525	0.7679583	0.8319548
chr6	5.3174682	0.0211127	0.0914882
chr8	0.1530317	0.6956548	0.8221375
chr9	0.0001485	0.9902760	0.9902760
chr11	2.3083258	0.1286826	0.2161486
chr15	6.9708675	0.0082847	0.0538508
chr16	165.6721921	0.0000000	0.0000000
chr17	3.1450374	0.0761583	0.1650096
chr19	1.3430169	0.2465026	0.3204534
chrX	3.3566557	0.0669339	0.1650096

3.4 Pooled data

Code

3.4.1 Model on all data.

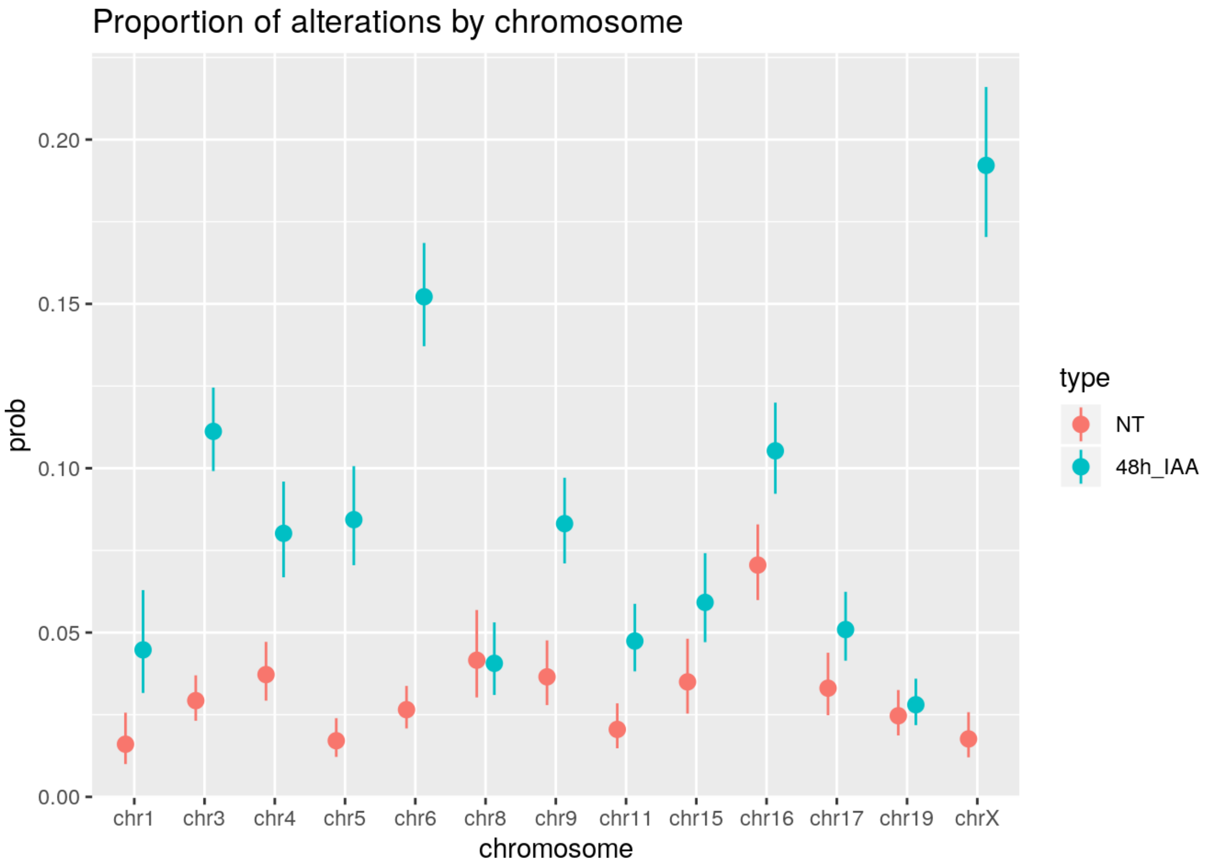
Code

Code

type	chromosome	prob	SE	lower	upper
NT	chr1	0.0160226	0.0038548	0.0099832	0.0256211
48h_IAA	chr1	0.0447330	0.0078525	0.0316319	0.0629079
NT	chr3	0.0292851	0.0034990	0.0231533	0.0369794
48h_IAA	chr3	0.1112054	0.0064770	0.0991303	0.1245481
NT	chr4	0.0372066	0.0045282	0.0292807	0.0471737
48h_IAA	chr4	0.0801782	0.0073994	0.0668213	0.0959304
NT	chr5	0.0170807	0.0029479	0.0121679	0.0239292
48h_IAA	chr5	0.0843465	0.0076607	0.0704947	0.1006255
NT	chr6	0.0265340	0.0032725	0.0208211	0.0337604
48h_IAA	chr6	0.1521631	0.0080095	0.1371201	0.1685341
NT	chr8	0.0415730	0.0066910	0.0302667	0.0568552
48h_IAA	chr8	0.0406375	0.0055736	0.0310149	0.0530819
NT	chr9	0.0365169	0.0049707	0.0279312	0.0476123
48h_IAA	chr9	0.0831409	0.0066341	0.0710288	0.0971025
NT	chr11	0.0205279	0.0034340	0.0147743	0.0284572
48h_IAA	chr11	0.0474190	0.0052070	0.0381957	0.0587334
NT	chr15	0.0349854	0.0057280	0.0253391	0.0481227
48h_IAA	chr15	0.0591716	0.0068599	0.0470732	0.0741375
NT	chr16	0.0705329	0.0058525	0.0598892	0.0829015
48h_IAA	chr16	0.1052910	0.0070600	0.0922341	0.1199520
NT	chr17	0.0330697	0.0047946	0.0248584	0.0438715
48h_IAA	chr17	0.0509070	0.0053171	0.0414395	0.0623967
NT	chr19	0.0246727	0.0034809	0.0186957	0.0324973
48h_IAA	chr19	0.0280374	0.0035685	0.0218293	0.0359462
NT	chrX	0.0176271	0.0034264	0.0120288	0.0257629

type	chromosome	prob	SE	lower	upper
48h_IAA	chrX	0.1921397	0.0116432	0.1703451	0.2159969

Code


Proportion of alterations by chromosome

Comparison of missegregation rate for each chromosome between NT and 48h_IAA

Code

chr	statistic	p.value	adj_p.value
chr1	11.9275060	0.0005531	0.0007989
chr3	104.0642063	0.0000000	0.0000000
chr4	25.4038759	0.0000005	0.0000010
chr5	68.4016976	0.0000000	0.0000000
chr6	178.4491133	0.0000000	0.0000000
chr8	0.0115849	0.9142868	0.9142868
chr9	27.6394293	0.0000001	0.0000004
chr11	17.6256467	0.0000269	0.0000499
chr15	6.9021942	0.0086090	0.0111917
chr16	14.1698347	0.0001670	0.0002714

chr	statistic	p.value	adj_p.value
chr17	5.8537380	0.0155440	0.0183702
chr19	0.4527973	0.5010095	0.5427603
chrX	149.1562400	0.0000000	0.0000000

3.4.2 Pooled 48h_IAA

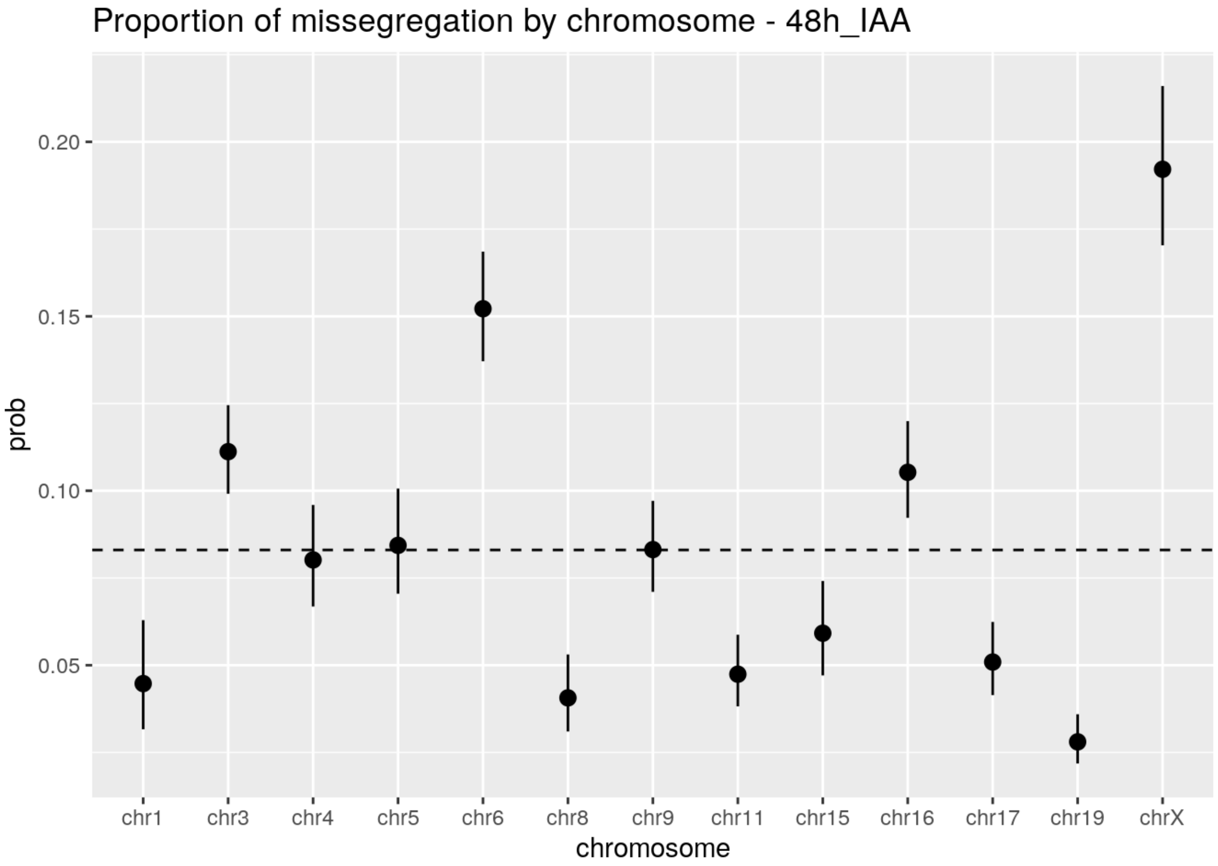
Code

Code

Code

chromosome	prob	SE	lower	upper
chr1	0.0447330	0.0078525	0.0316319	0.0629079
chr3	0.1112054	0.0064770	0.0991303	0.1245481
chr4	0.0801782	0.0073994	0.0668213	0.0959304
chr5	0.0843465	0.0076607	0.0704947	0.1006255
chr6	0.1521631	0.0080095	0.1371201	0.1685341
chr8	0.0406375	0.0055736	0.0310149	0.0530819
chr9	0.0831409	0.0066341	0.0710288	0.0971025
chr11	0.0474190	0.0052070	0.0381957	0.0587334
chr15	0.0591716	0.0068599	0.0470732	0.0741375
chr16	0.1052910	0.0070600	0.0922341	0.1199520
chr17	0.0509070	0.0053171	0.0414395	0.0623967
chr19	0.0280374	0.0035685	0.0218293	0.0359462
chrX	0.1921397	0.0116432	0.1703451	0.2159969

Code



Each estimated coefficients is tested against the mean value (0.0830285).

Code

chr	statistic	p.value	adj_p.value
chr1	12.8755390	0.0003329	0.0005410
chr3	24.3555763	0.0000008	0.0000017
chr4	0.1437194	0.7046111	0.8327222
chr5	0.0300268	0.8624294	0.9342985
chr6	121.4355526	0.0000000	0.0000000
chr8	28.2371914	0.0000001	0.0000003
chr9	0.0002874	0.9864743	0.9864743
chr11	26.9345154	0.0000002	0.0000005
chr15	8.7464091	0.0031021	0.0040328
chr16	12.2332706	0.0004694	0.0006781
chr17	22.6387436	0.0000020	0.0000036
chr19	76.3073634	0.0000000	0.0000000
chrX	165.7552473	0.0000000	0.0000000

3.4.3 Pooled NT

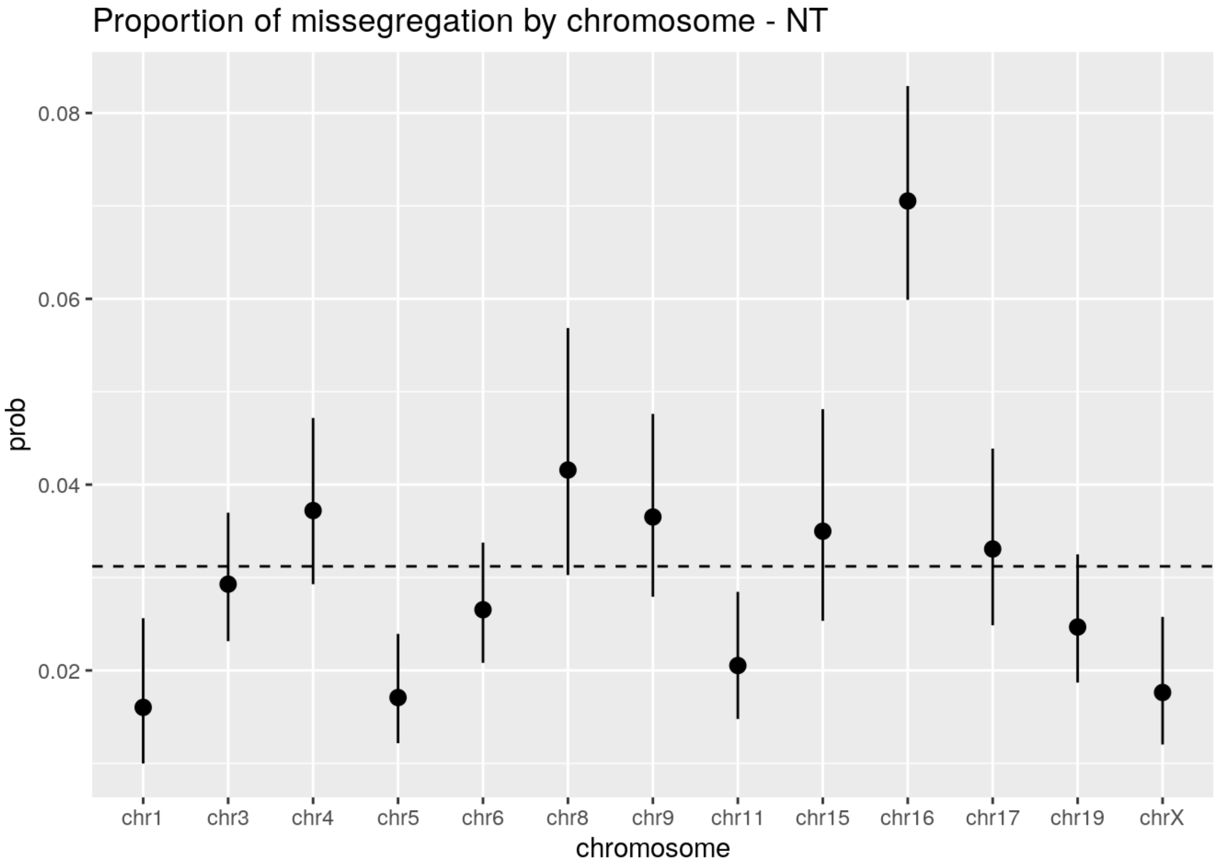
Code

Code

Code

chromosome	prob	SE	lower	upper
chr1	0.0160226	0.0038548	0.0099832	0.0256211
chr3	0.0292851	0.0034990	0.0231533	0.0369794
chr4	0.0372066	0.0045282	0.0292807	0.0471737
chr5	0.0170807	0.0029479	0.0121679	0.0239292
chr6	0.0265340	0.0032725	0.0208211	0.0337604
chr8	0.0415730	0.0066910	0.0302667	0.0568552
chr9	0.0365169	0.0049707	0.0279312	0.0476123
chr11	0.0205279	0.0034340	0.0147743	0.0284572
chr15	0.0349854	0.0057280	0.0253391	0.0481227
chr16	0.0705329	0.0058525	0.0598892	0.0829015
chr17	0.0330697	0.0047946	0.0248584	0.0438715
chr19	0.0246727	0.0034809	0.0186957	0.0324973
chrX	0.0176271	0.0034264	0.0120288	0.0257629

Code



Each estimated coefficients is tested against the mean value (0.0312027).

Code

chr	statistic	p.value	adj_p.value
chr1	7.7815508	0.0052782	0.0171543
chr3	0.2823494	0.5951654	0.6447626
chr4	2.0775126	0.1494836	0.2429108
chr5	12.3491131	0.0004412	0.0028678
chr6	1.7351314	0.1877569	0.2712044
chr8	3.1430240	0.0762523	0.1652133
chr9	1.3273923	0.2492697	0.3240506
chr11	6.3291988	0.0118766	0.0308791
chr15	0.4865182	0.4854846	0.5737545
chr16	92.1614835	0.0000000	0.0000000
chr17	0.1603574	0.6888277	0.6888277
chr19	2.7878278	0.0949829	0.1763968
chrX	8.7404308	0.0031123	0.0134867