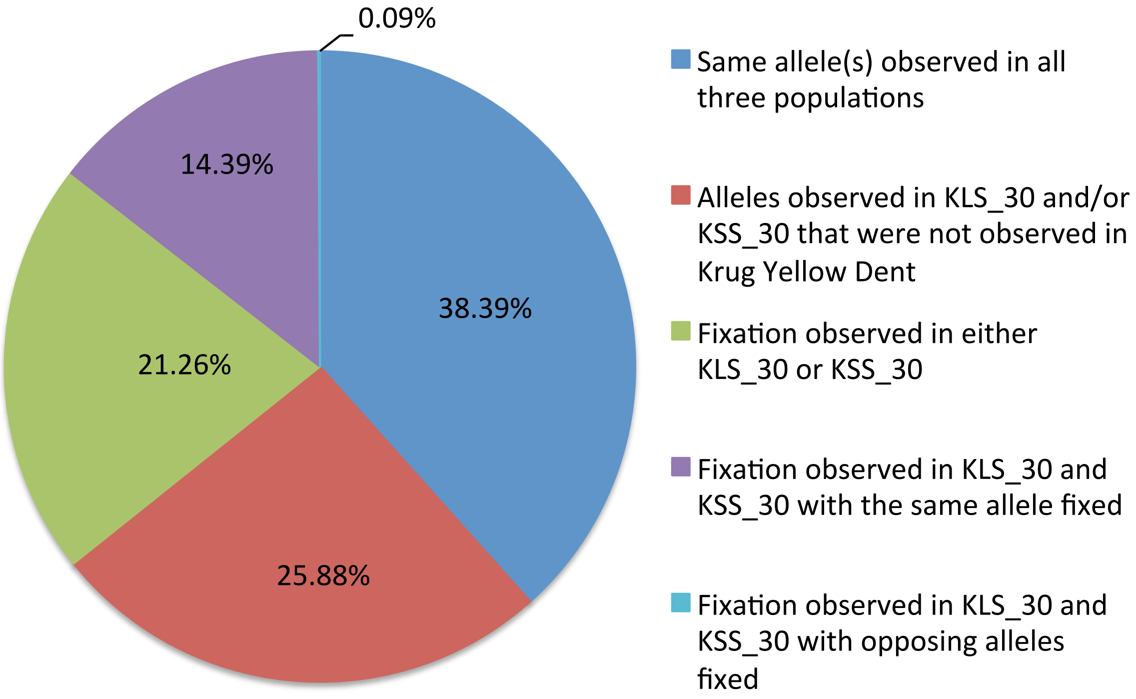
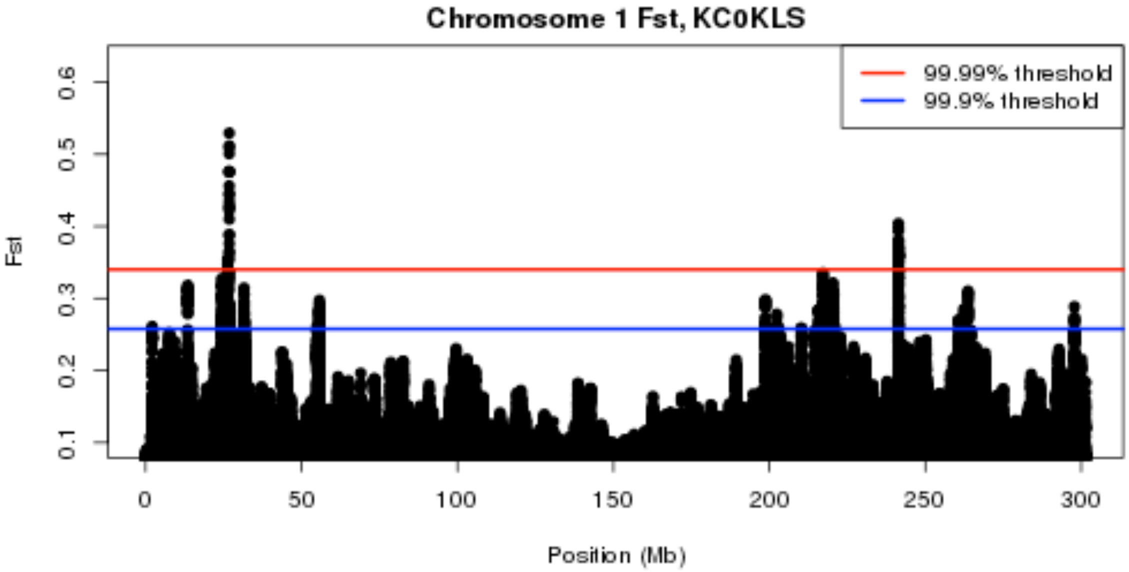
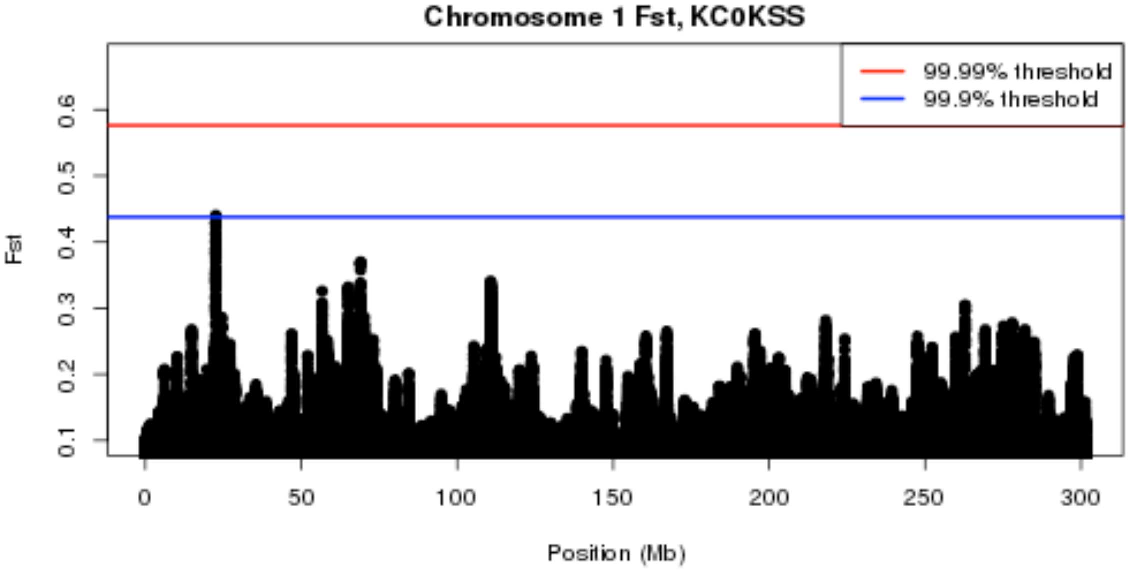
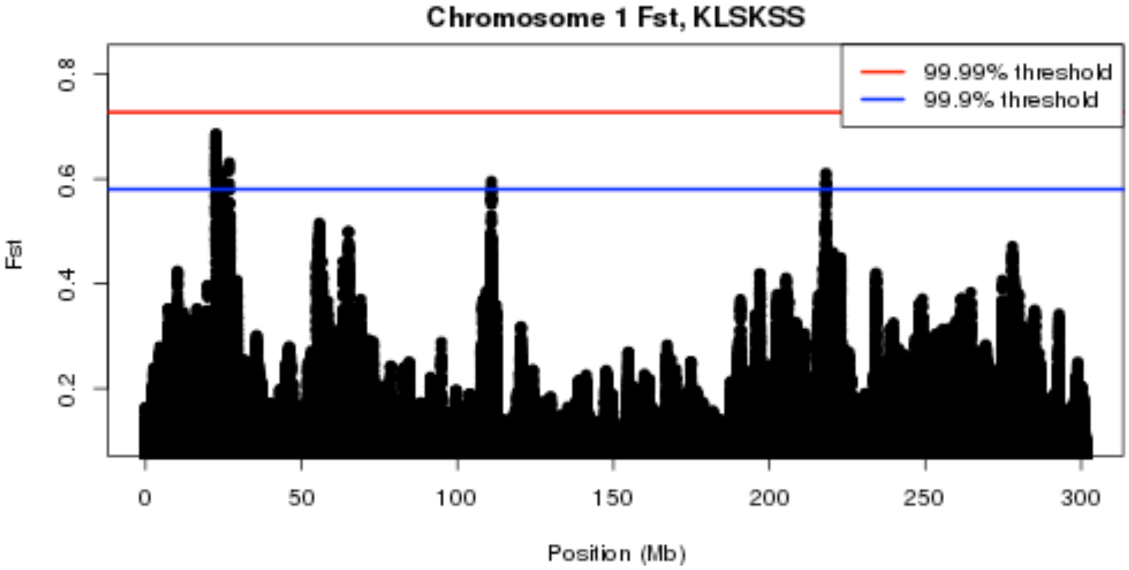
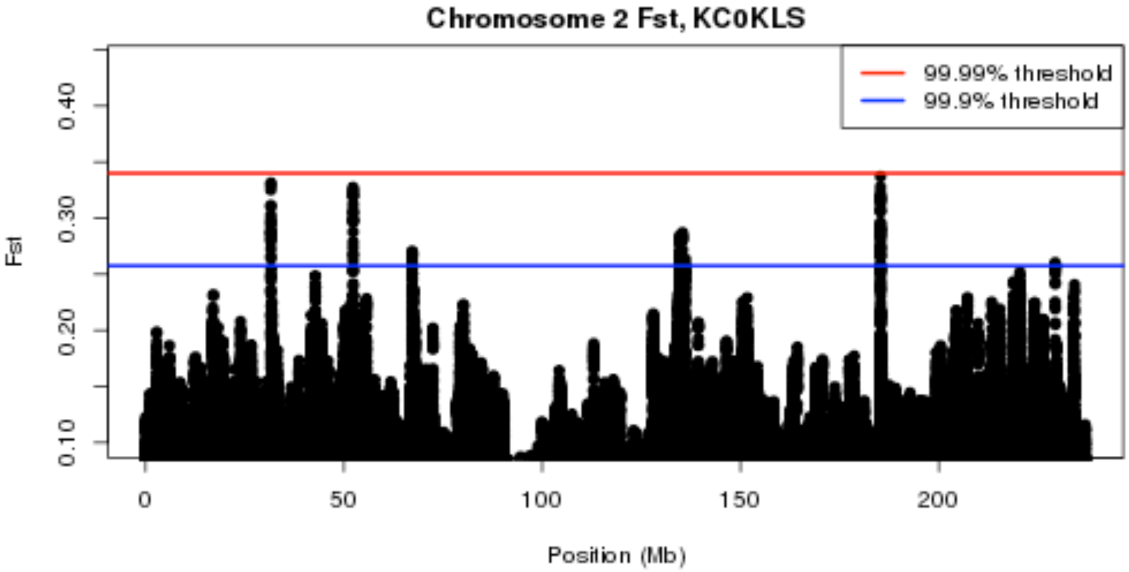


Figure S1 Categorization of single nucleotide polymorphism (SNP) variants within the populations Krug Yellow Dent, KLS_30, and KSS_30.

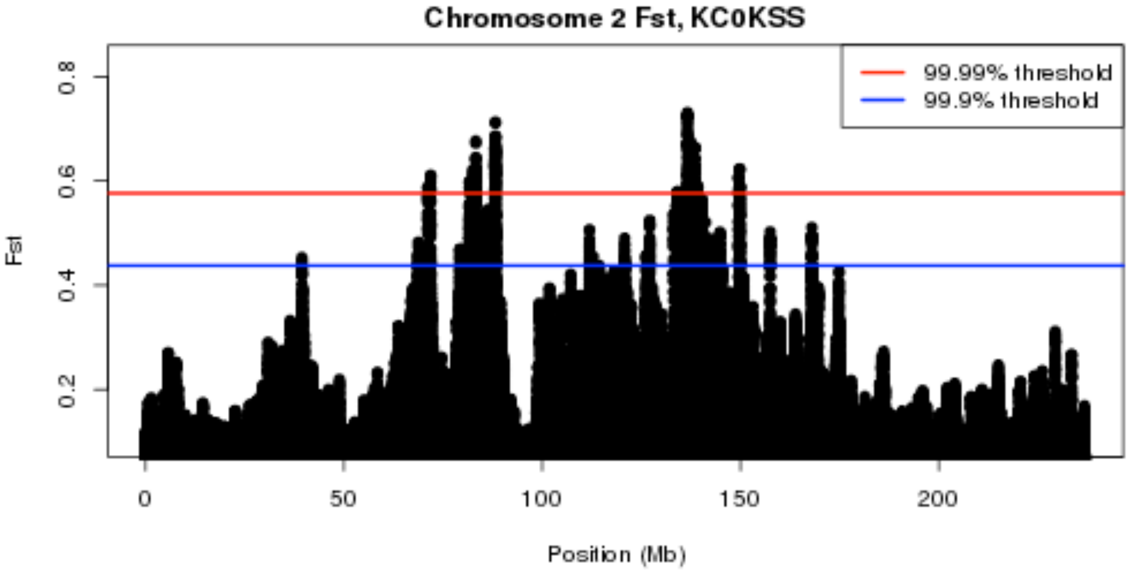

Chromosome 1 Fst, KC0KLS
99.99% threshold
99.9% threshold
Fst
0.1
0.2
0.3
0.4
0.5
0.6
0
50
100
150
200
250
300
Position (Mb)


Chromosome 1 Fst, KC0KSS
99.99% threshold
99.9% threshold
Fst
0.1
0.2
0.3
0.4
0.5
0.6
0
50
100
150
200
250
300
Position (Mb)

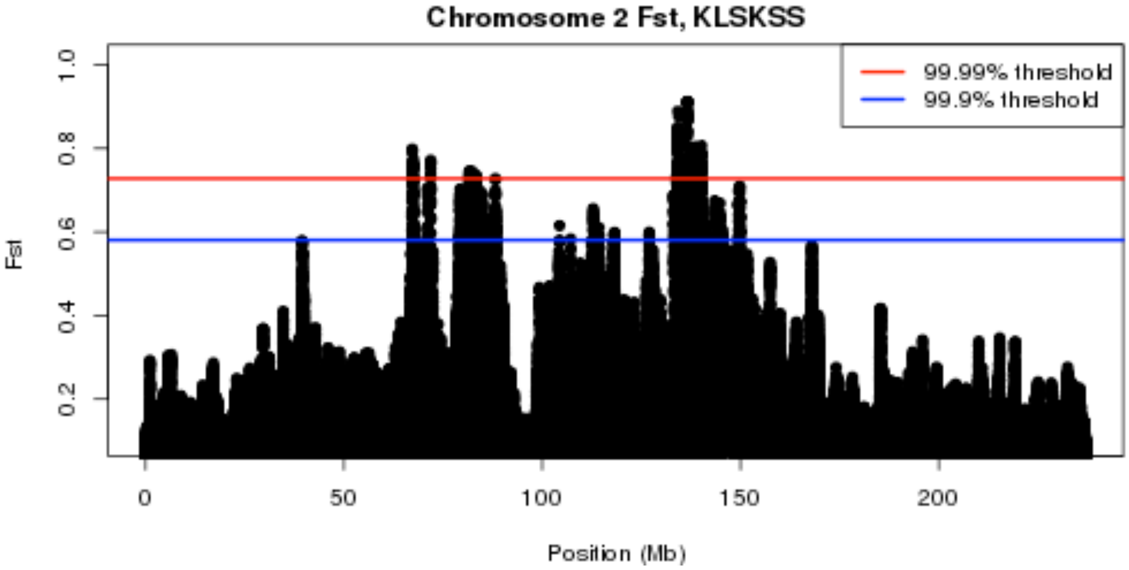

Chromosome 1 Fst, KLSKSS
99.99% threshold
99.9% threshold
Fst
0.2
0.4
0.6
0.8
0
50
100
150
200
250
300
Position (Mb)



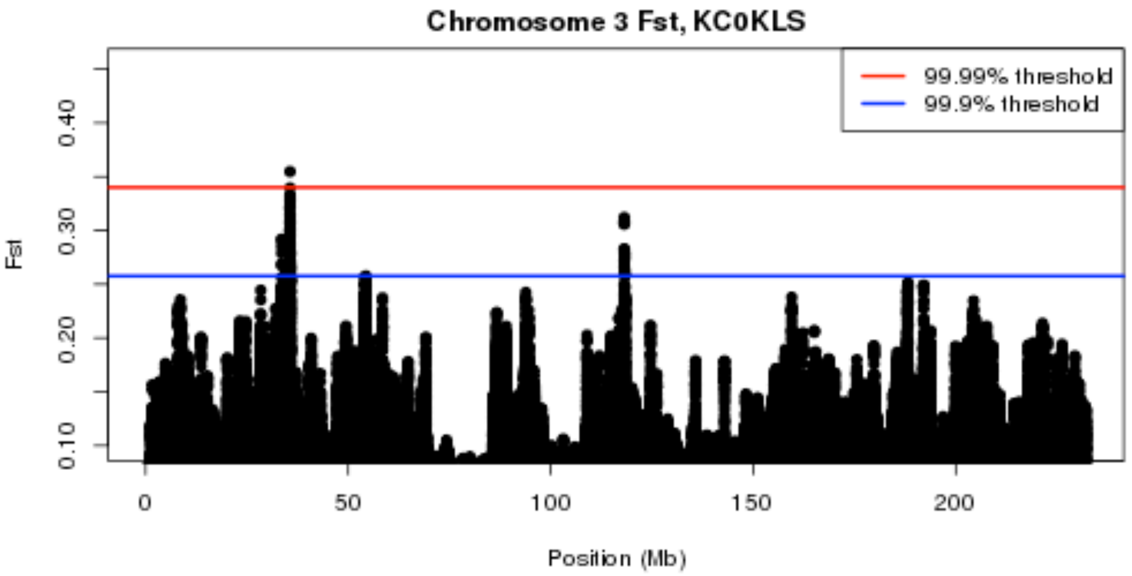
Chromosome 2 Fst, KC0KLS

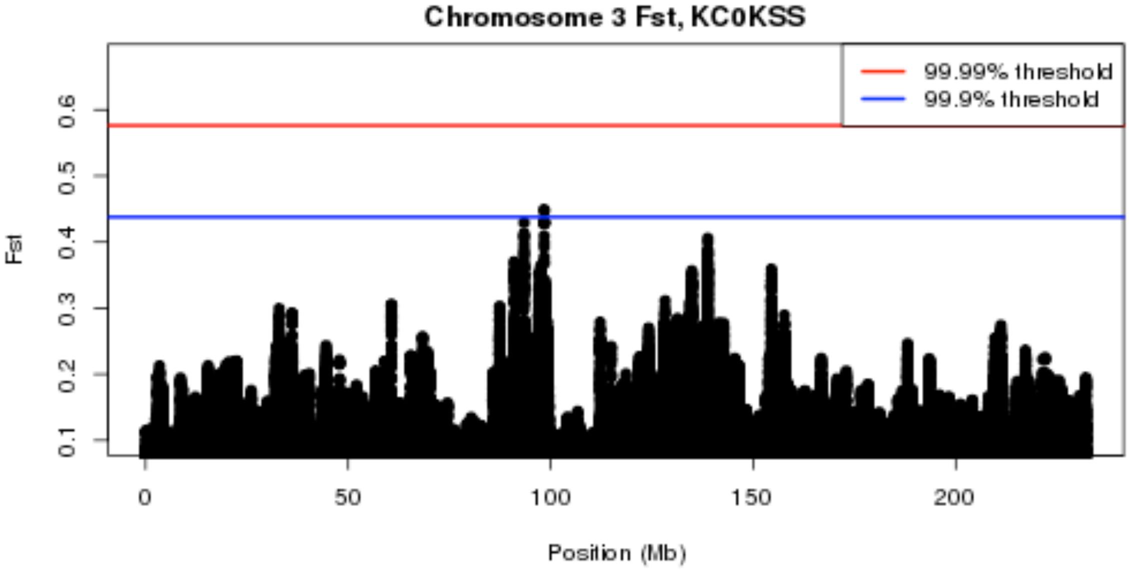


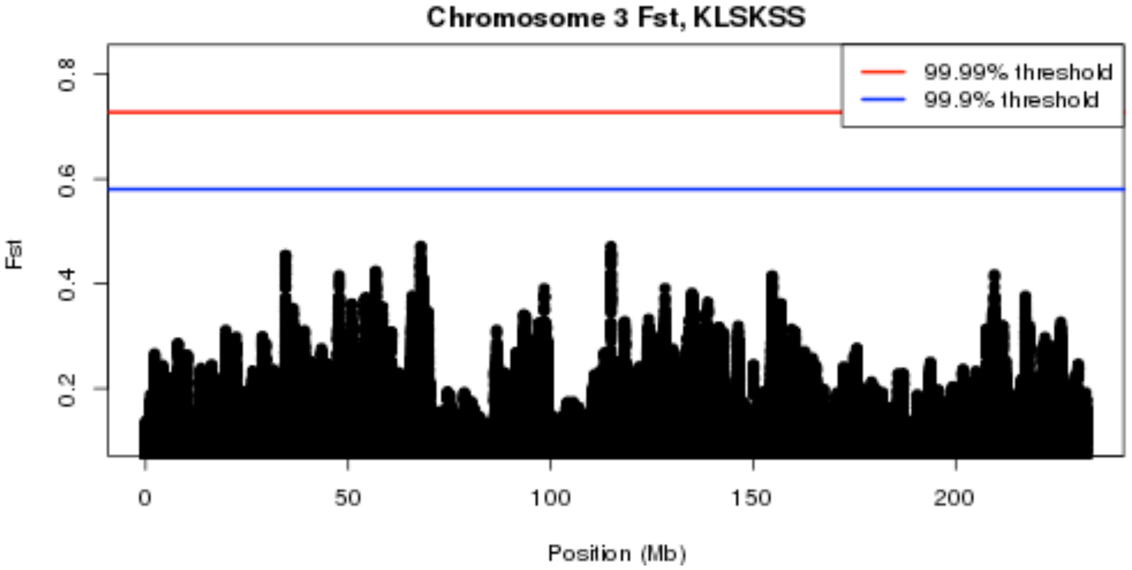
Chromosome 2 Fst, KC0KSS

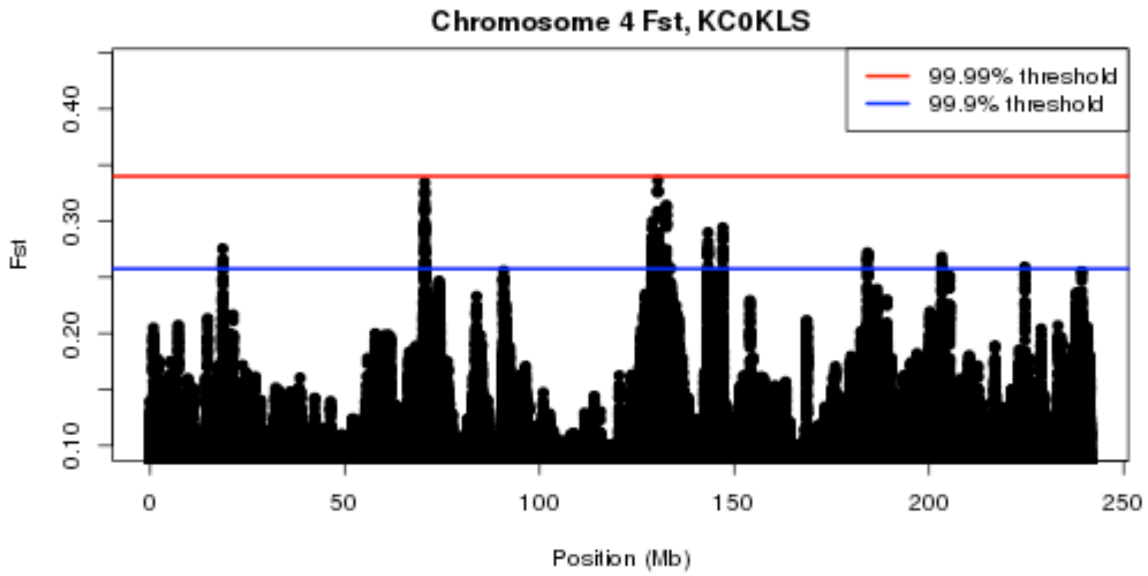


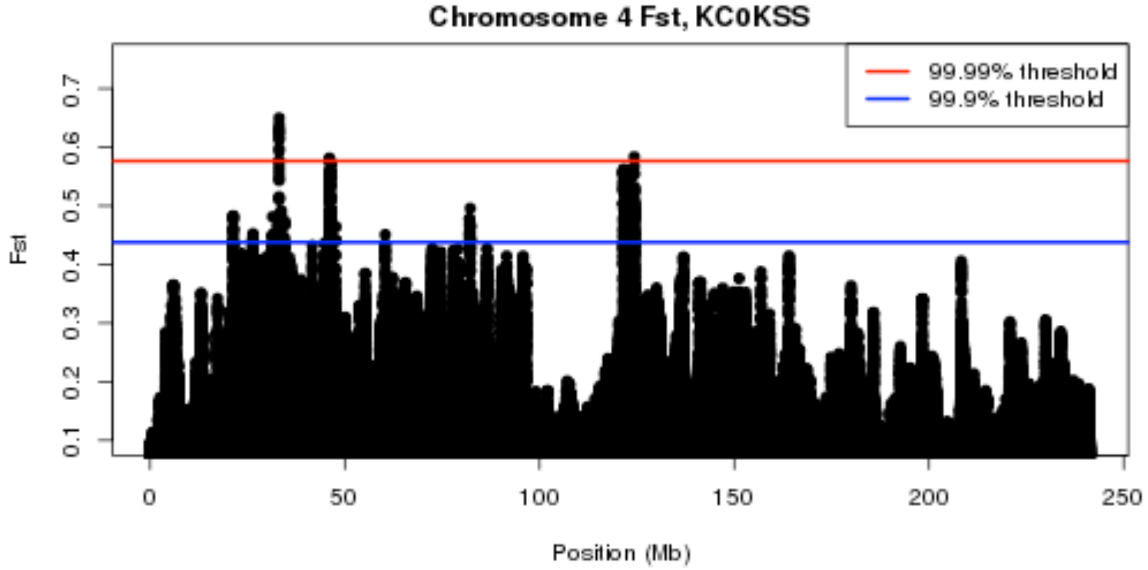
Chromosome 2 Fst, KLSKSS

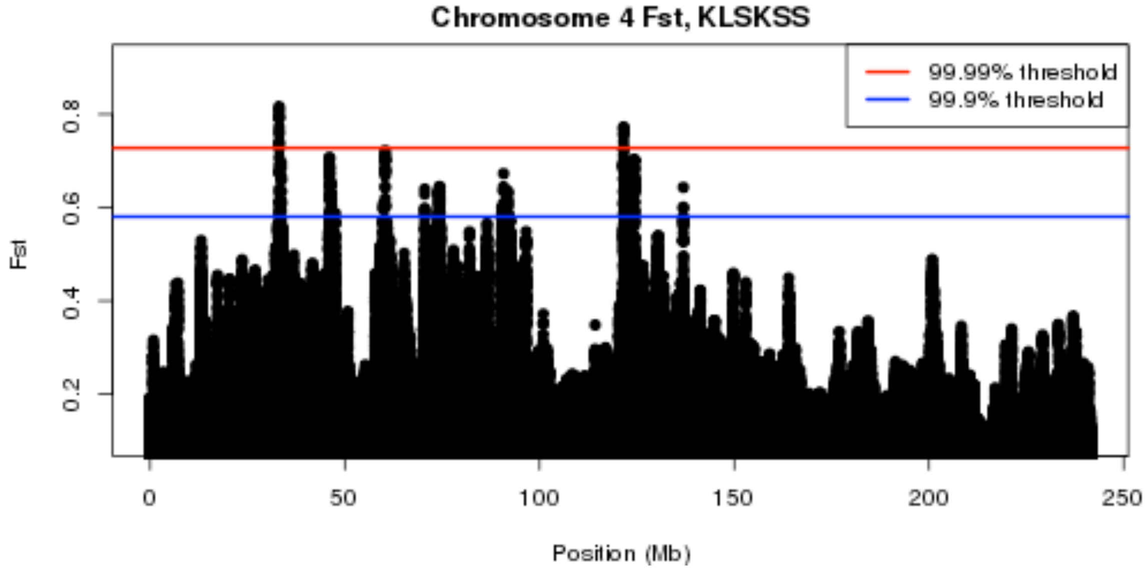

Chromosome 3 Fst, KC0KLS
99.99% threshold
99.9% threshold
Fst
0.10
0.20
0.30
0.40
0
50
100
150
200
Position (Mb)

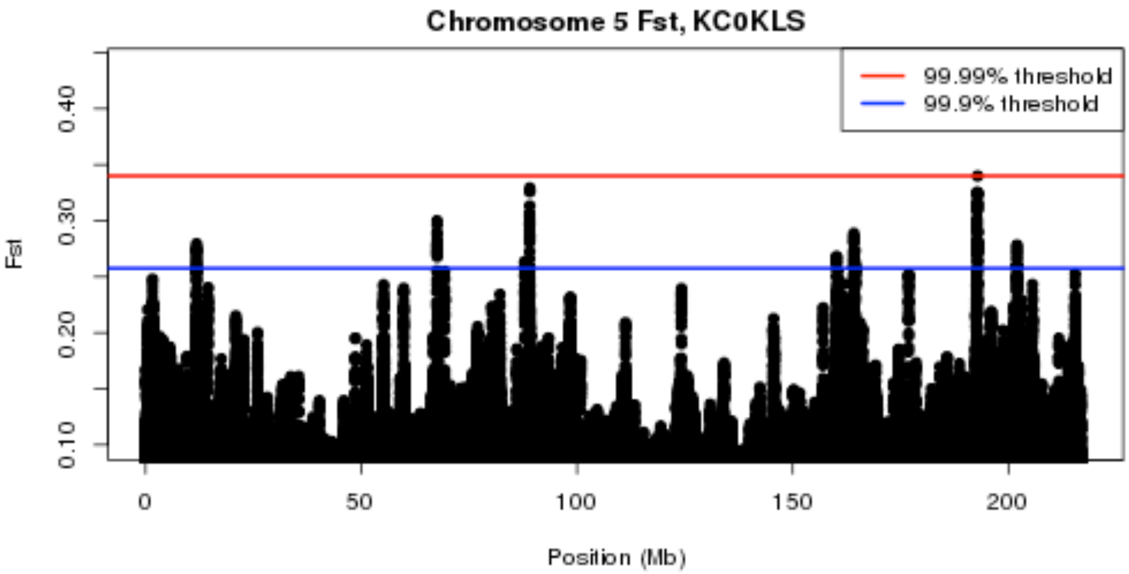

Chromosome 3 Fst, KC0KSS
99.99% threshold
99.9% threshold
Fst
0.1
0.2
0.3
0.4
0.5
0.6
0
50
100
150
200
Position (Mb)

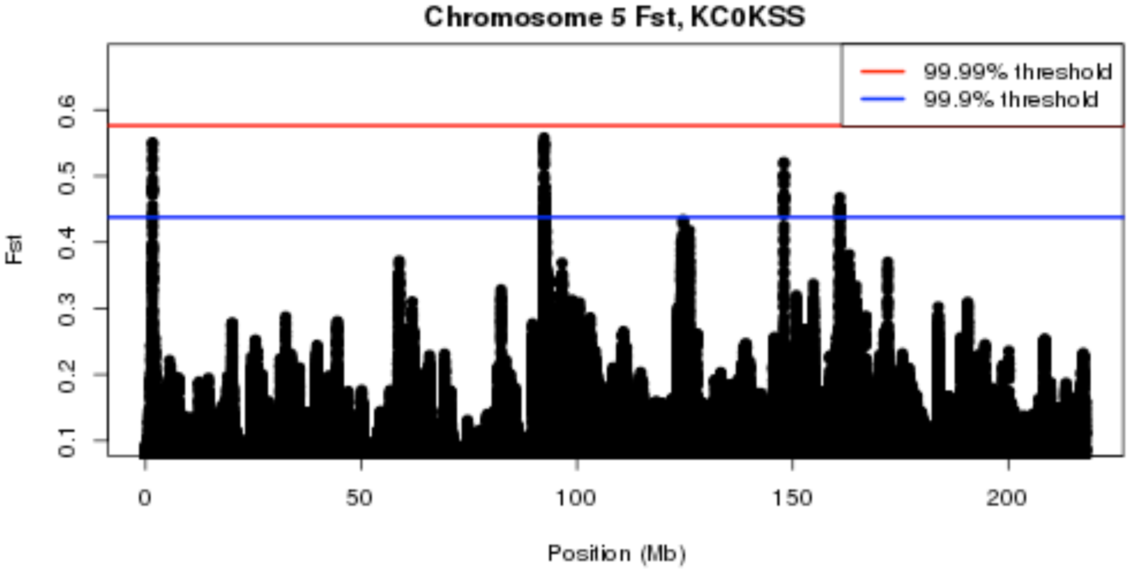

Chromosome 3 Fst, KLSKSS
99.99% threshold
99.9% threshold
Fst
0.2
0.4
0.6
0.8
0
50
100
150
200
Position (Mb)

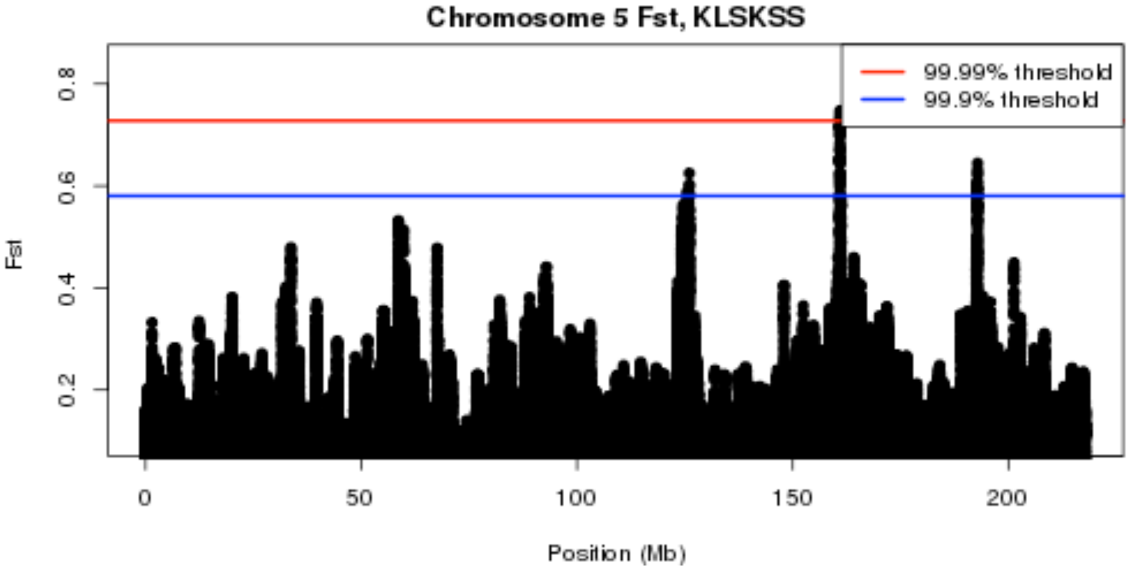

Chromosome 4 Fst, KC0KLS
99.99% threshold
99.9% threshold
Fst
0.10
0.20
0.30
0.40
0
50
100
150
200
250
Position (Mb)

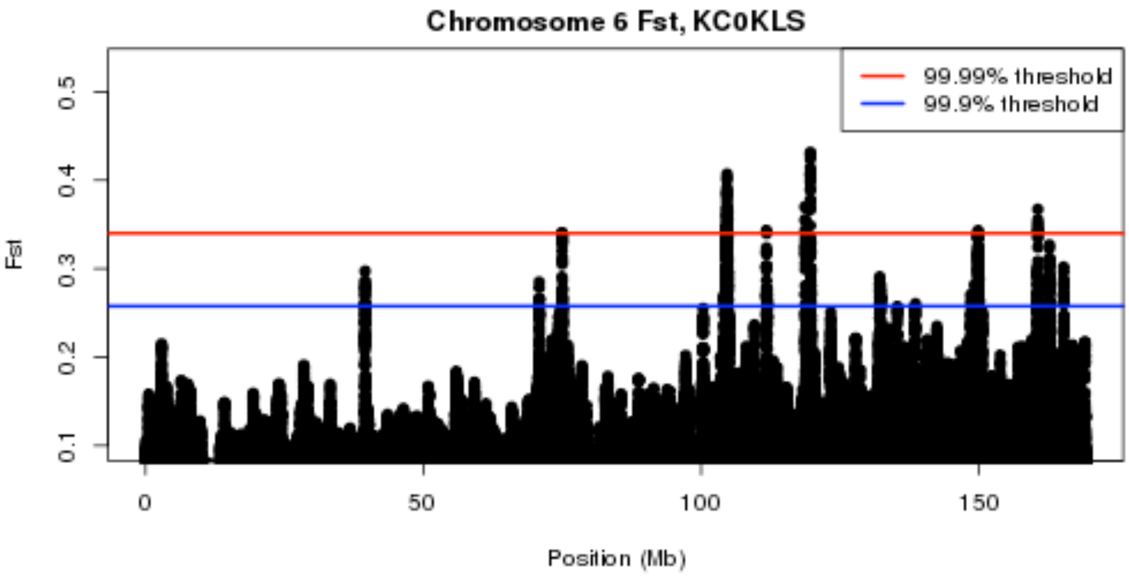

Chromosome 4 Fst, KC0KSS
99.99% threshold
99.9% threshold
Fst
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0
50
100
150
200
250
Position (Mb)

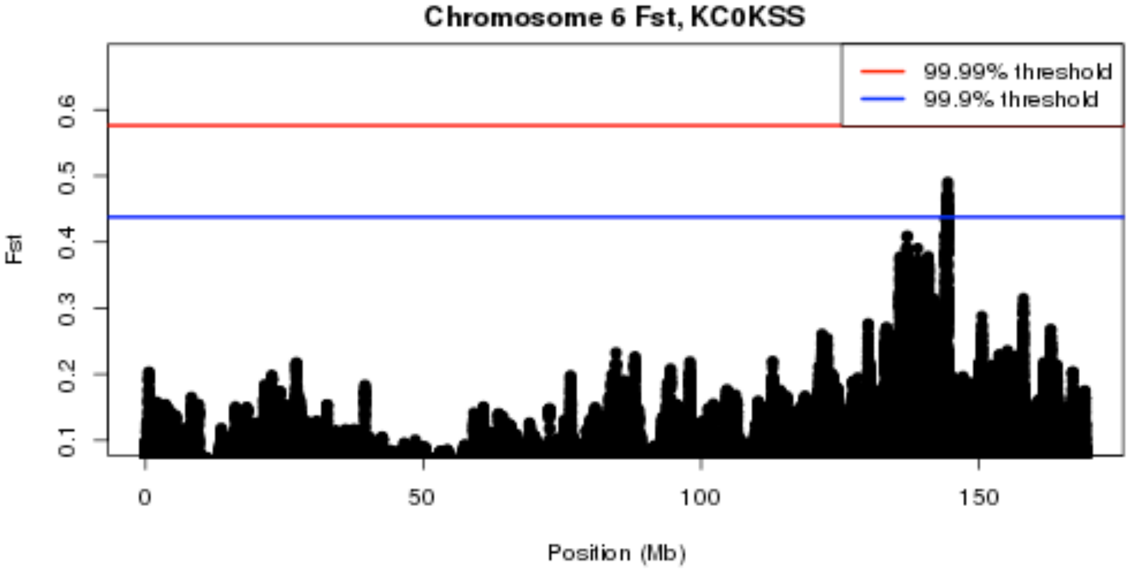

Chromosome 4 Fst, KLSKSS
99.99% threshold
99.9% threshold
Fst
0.2
0.4
0.6
0.8
0
50
100
150
200
250
Position (Mb)

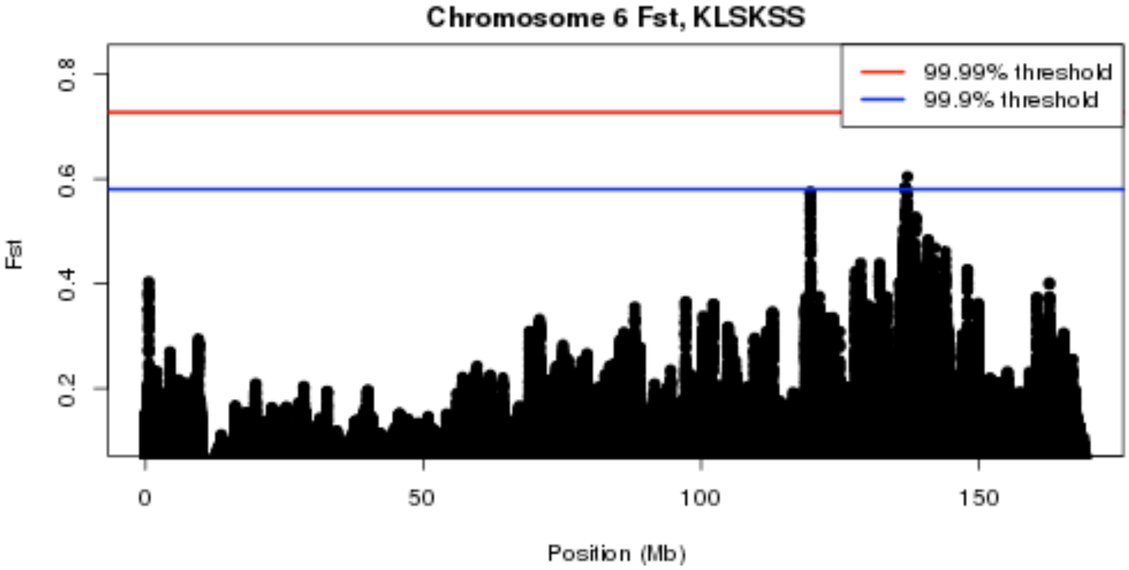

Chromosome 5 Fst, KC0KLS

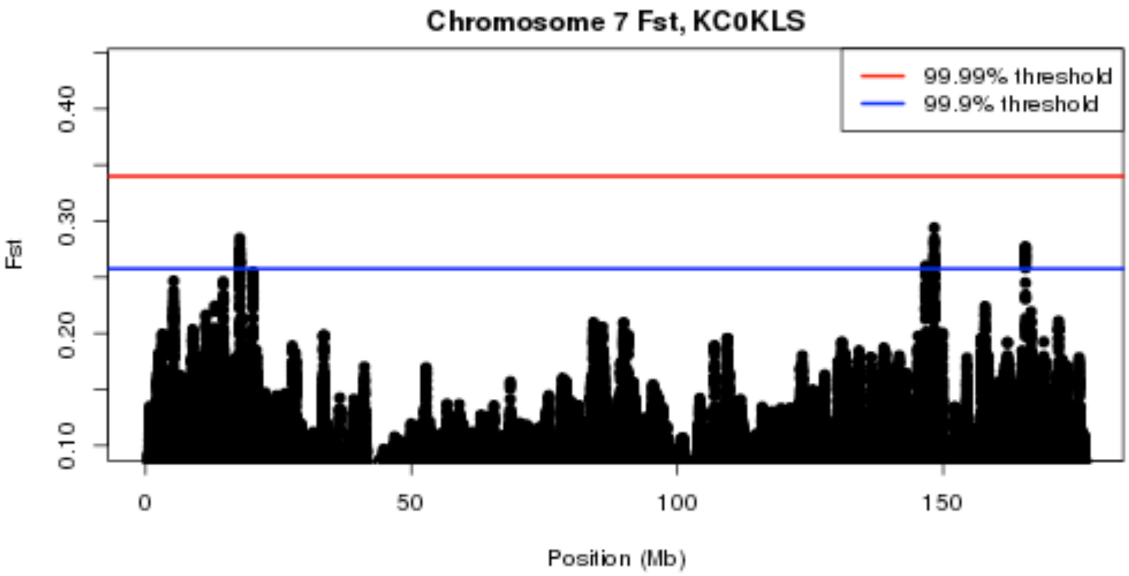

Chromosome 5 Fst, KC0KSS

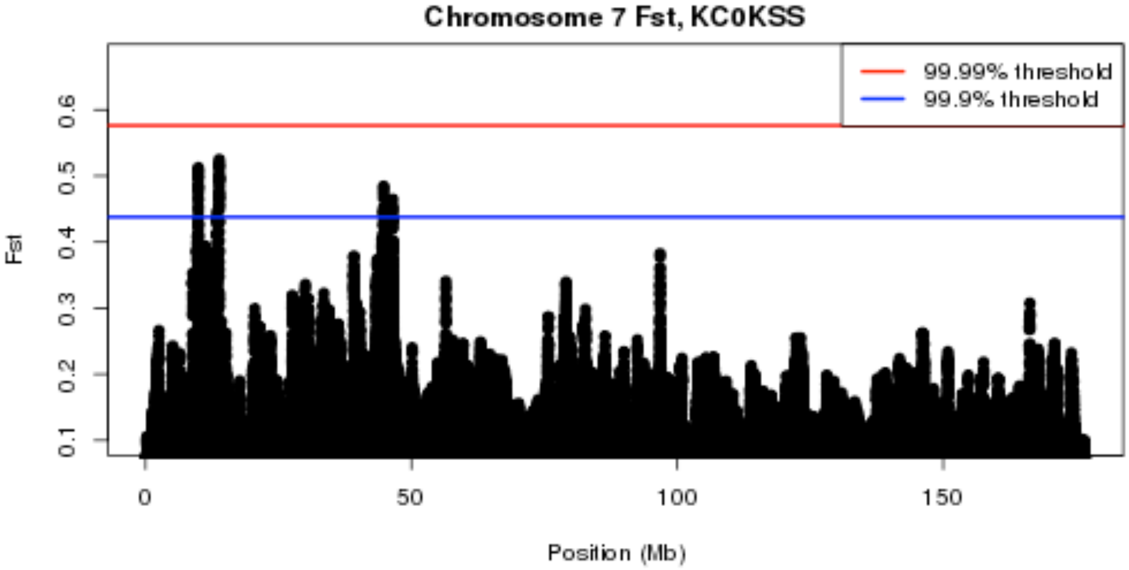

Chromosome 5 Fst, KLSKSS

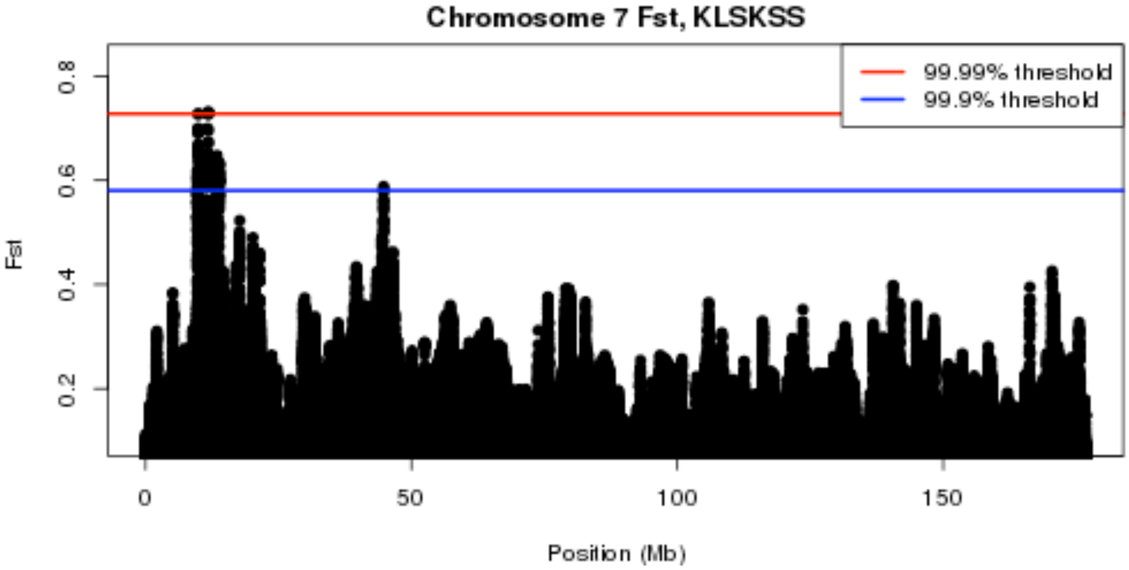

Chromosome 6 Fst, KC0KLS
99.99% threshold
99.9% threshold
Fst
0.1
0.2
0.3
0.4
0.5
0
50
100
150
Position (Mb)

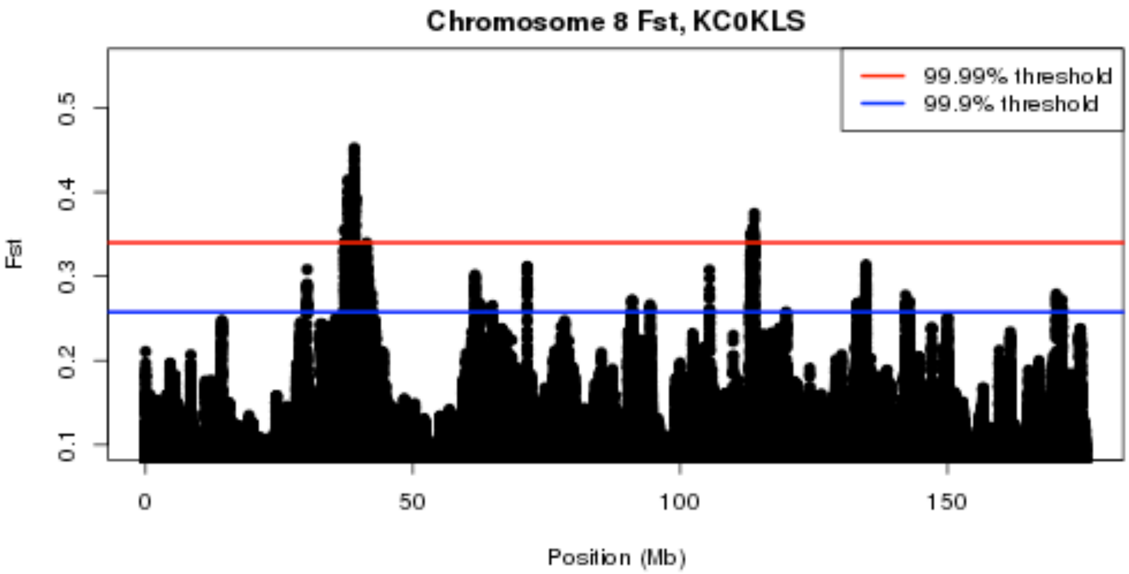

Chromosome 6 Fst, KC0KSS
99.99% threshold
99.9% threshold
Fst
0.1
0.2
0.3
0.4
0.5
0.6
0
50
100
150
Position (Mb)

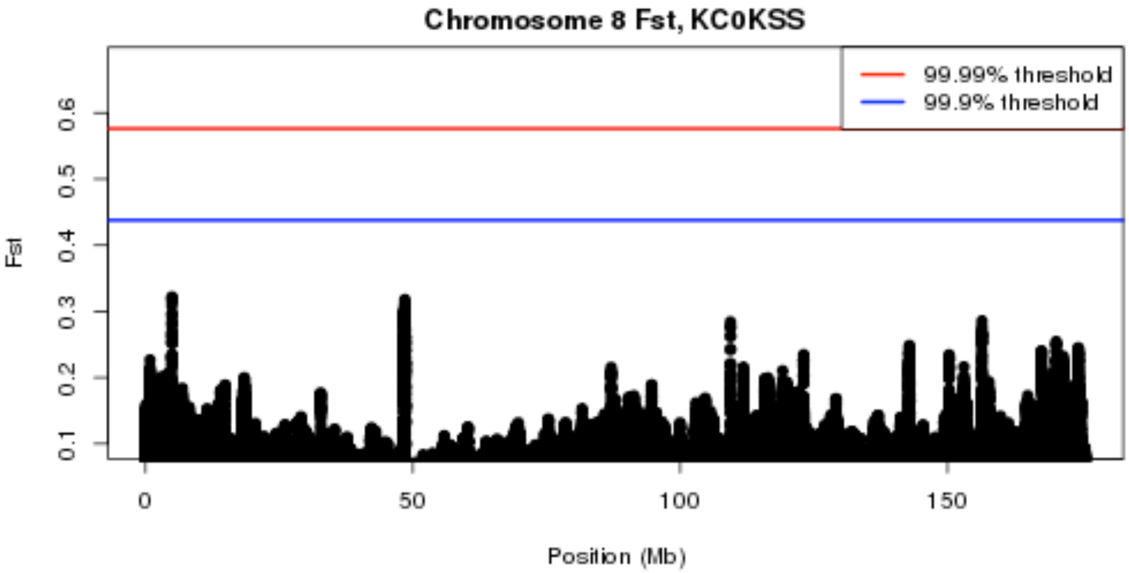

Chromosome 6 Fst, KLSKSS
99.99% threshold
99.9% threshold
Fst
0.2
0.4
0.6
0.8
0
50
100
150
Position (Mb)

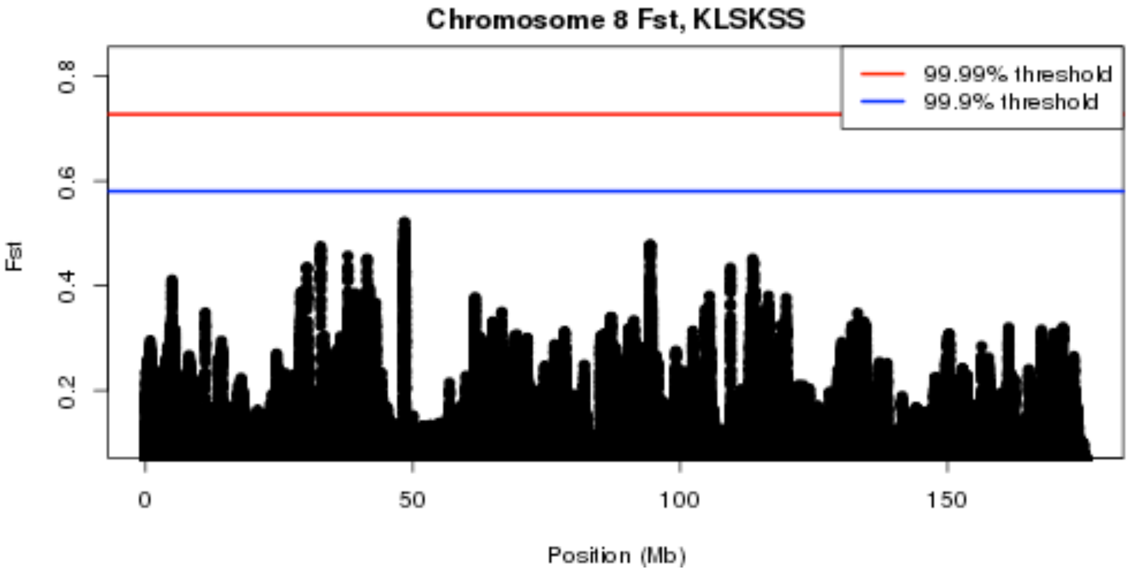

Chromosome 7 Fst, KC0KLS

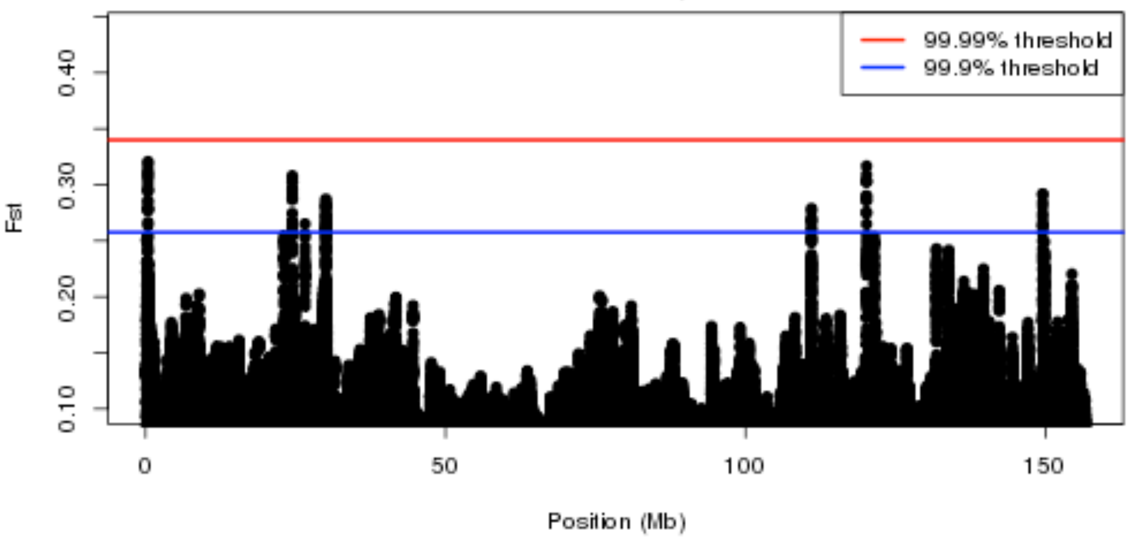

Chromosome 7 Fst, KC0KSS

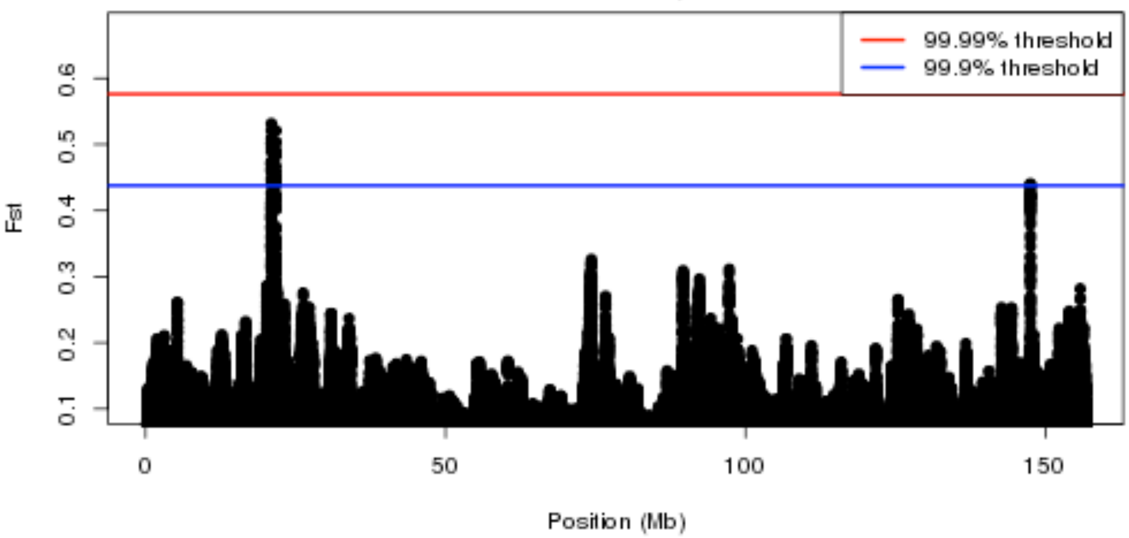

Chromosome 7 Fst, KLSKSS

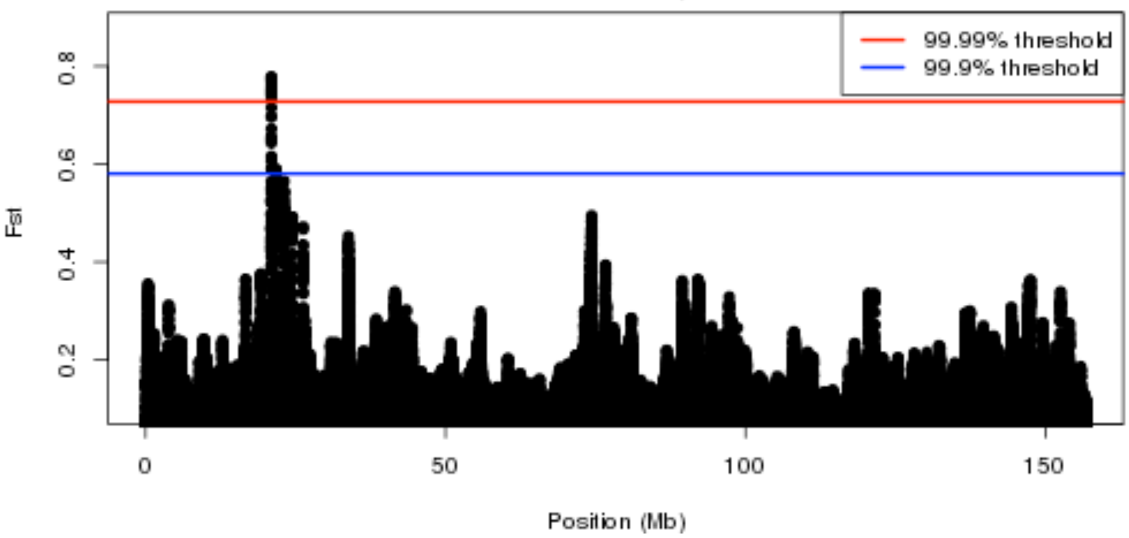

Chromosome 8 Fst, KC0KLS
Fst
0.1
0.2
0.3
0.4
0.5
0
50
100
150
Position (Mb)
99.99% threshold
99.9% threshold

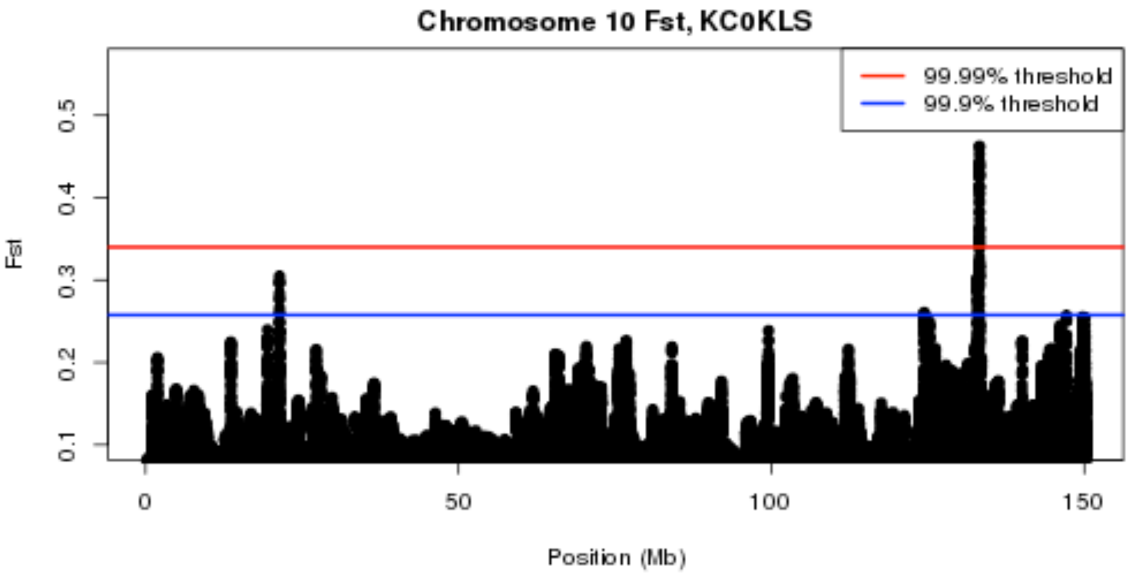

Chromosome 8 Fst, KC0KSS
Fst
0.1
0.2
0.3
0.4
0.5
0.6
0
50
100
150
Position (Mb)
99.99% threshold
99.9% threshold

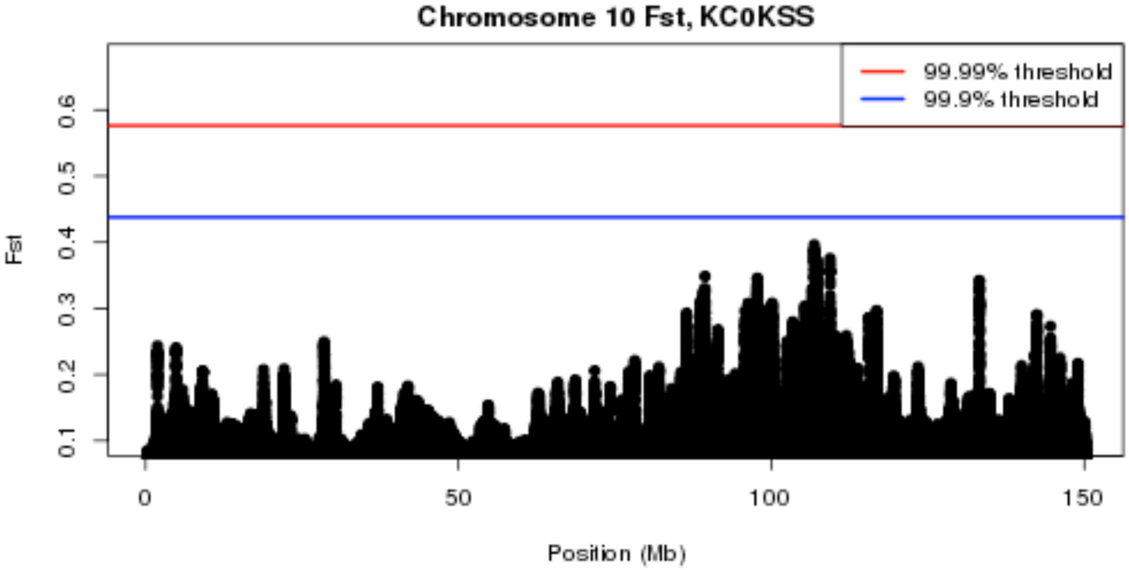

Chromosome 8 Fst, KLSKSS
Fst
0.2
0.4
0.6
0.8
0
50
100
150
Position (Mb)
99.99% threshold
99.9% threshold


Chromosome 9 Fst, KC0KLS


Chromosome 9 Fst, KC0KSS


Chromosome 9 Fst, KLSKSS


Chromosome 10 Fst, KC0KLS
99.99% threshold
99.9% threshold
Fst
0.1
0.2
0.3
0.4
0.5
0
50
100
150
Position (Mb)


Chromosome 10 Fst, KC0KSS
99.99% threshold
99.9% threshold
Fst
0.1
0.2
0.3
0.4
0.5
0.6
0
50
100
150
Position (Mb)

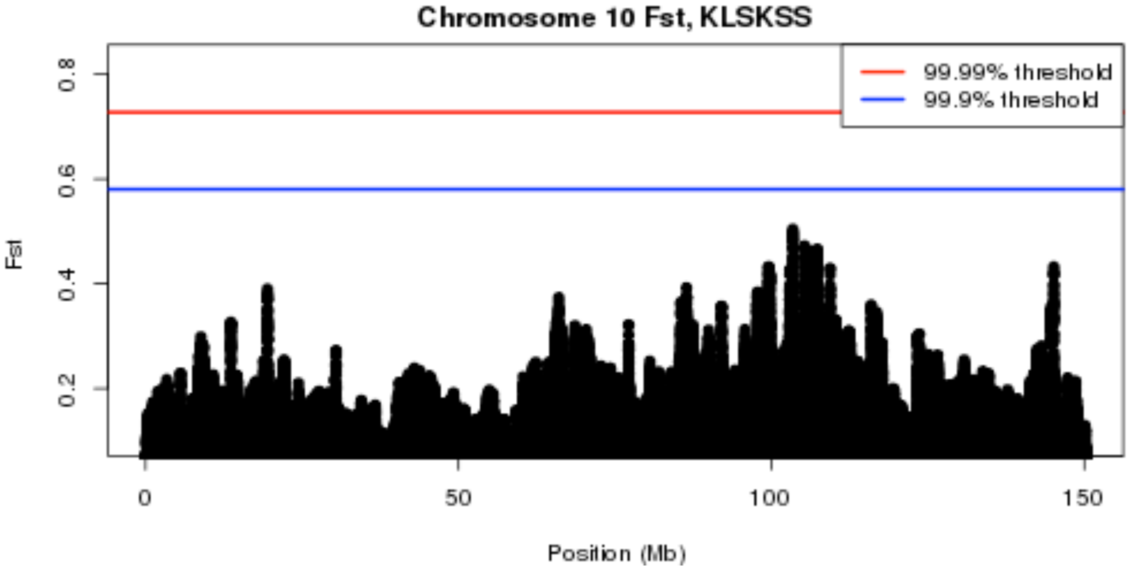

Chromosome 10 Fst, KLSKSS
99.99% threshold
99.9% threshold
Fst
0.2
0.4
0.6
0.8
0
50
100
150
Position (Mb)

Figure S2 F_{ST} values for each of the maize chromosomes. F_{ST} values were calculated using a 25-single nucleotide polymorphism (SNP) sliding window approach. Comparisons were made between Krug Yellow Dent and KLS_30, Krug Yellow Dent and KSS_30, and KLS_30 and KSS_30.

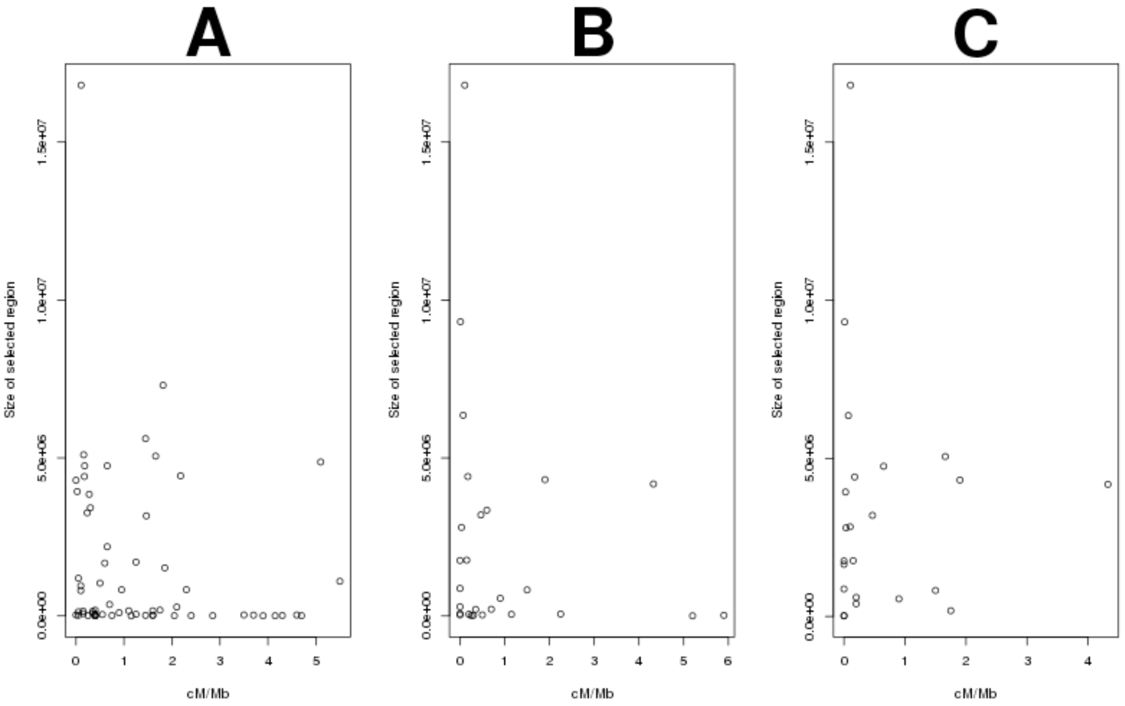


Figure S3 Region size versus relative recombination rate for each region identified as putatively under selection in the Krug long-term selection populations at the 99.9% outlier threshold. A) Regions identified by comparing Krug Yellow Dent to KLS_30, B) Regions identified by comparing Krug Yellow Dent to KSS_30, C) Regions identified by comparing KLS_30 and KSS_30. For all, relative levels of recombination across the genome were approximated based on recombination frequencies in the intermated B73 x Mo17 population. No significant correlations were observed.

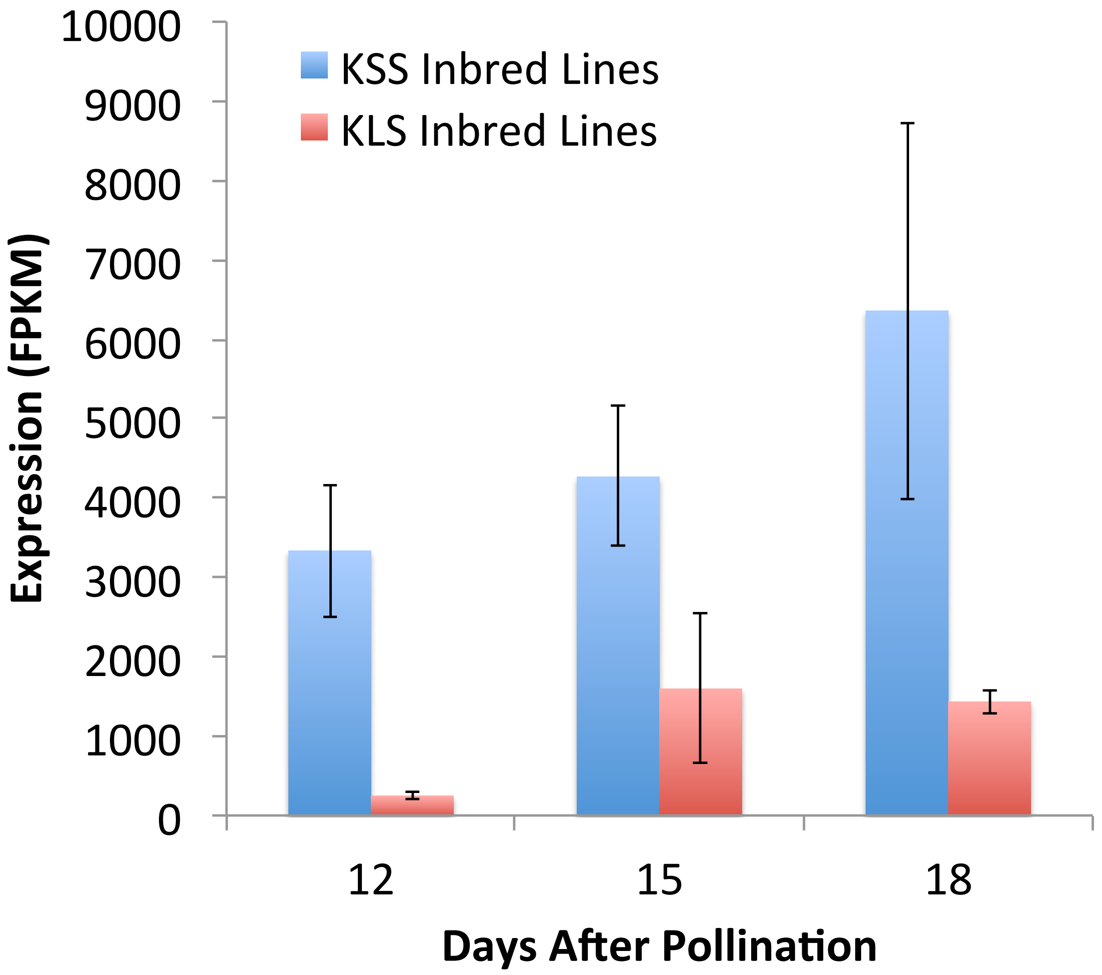


Figure S4 Average endosperm transcript abundance estimates for inbred lines derived from the KSS_30 and KLS_30 populations for the *Opaque2* gene. Error bars show standard deviations calculated from three biological replicates. Data for this figure was obtained from (SEKHON *et al.* 2014).

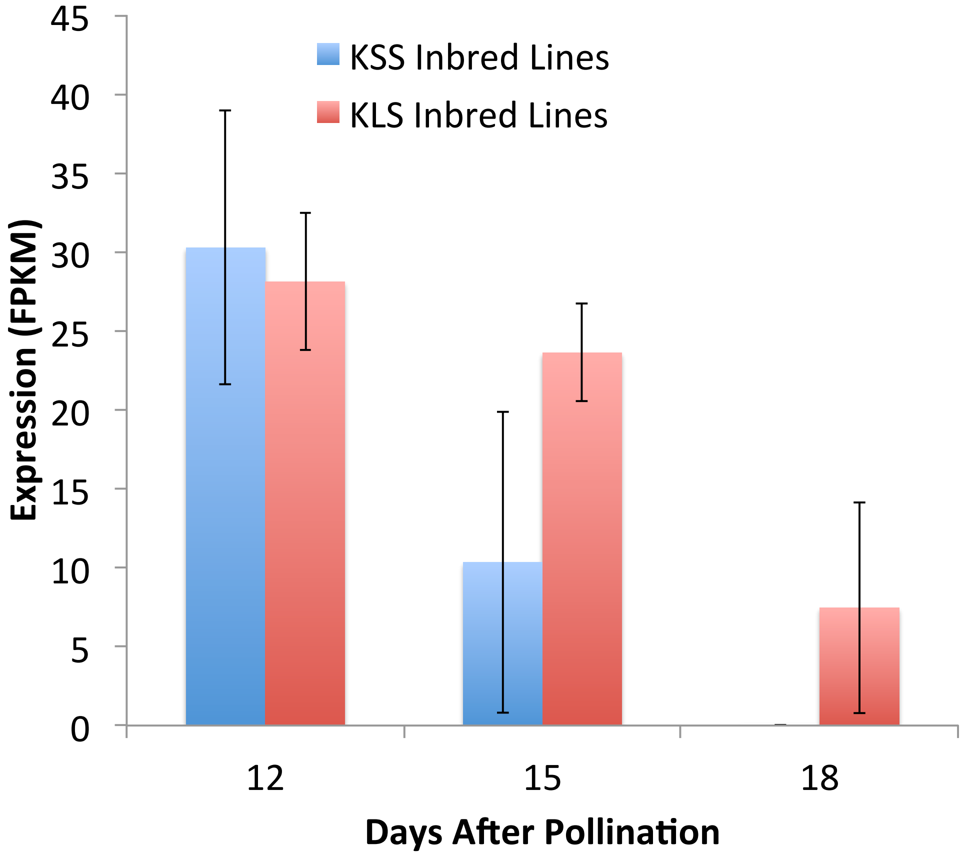


Figure S5 Average endosperm transcript abundance estimates for inbred lines derived from the KSS_30 and KLS_30 populations for the gene GRMZM2G069078. Error bars show standard deviations calculated from three biological replicates. Data for this figure was obtained from (SEKHON *et al.* 2014)

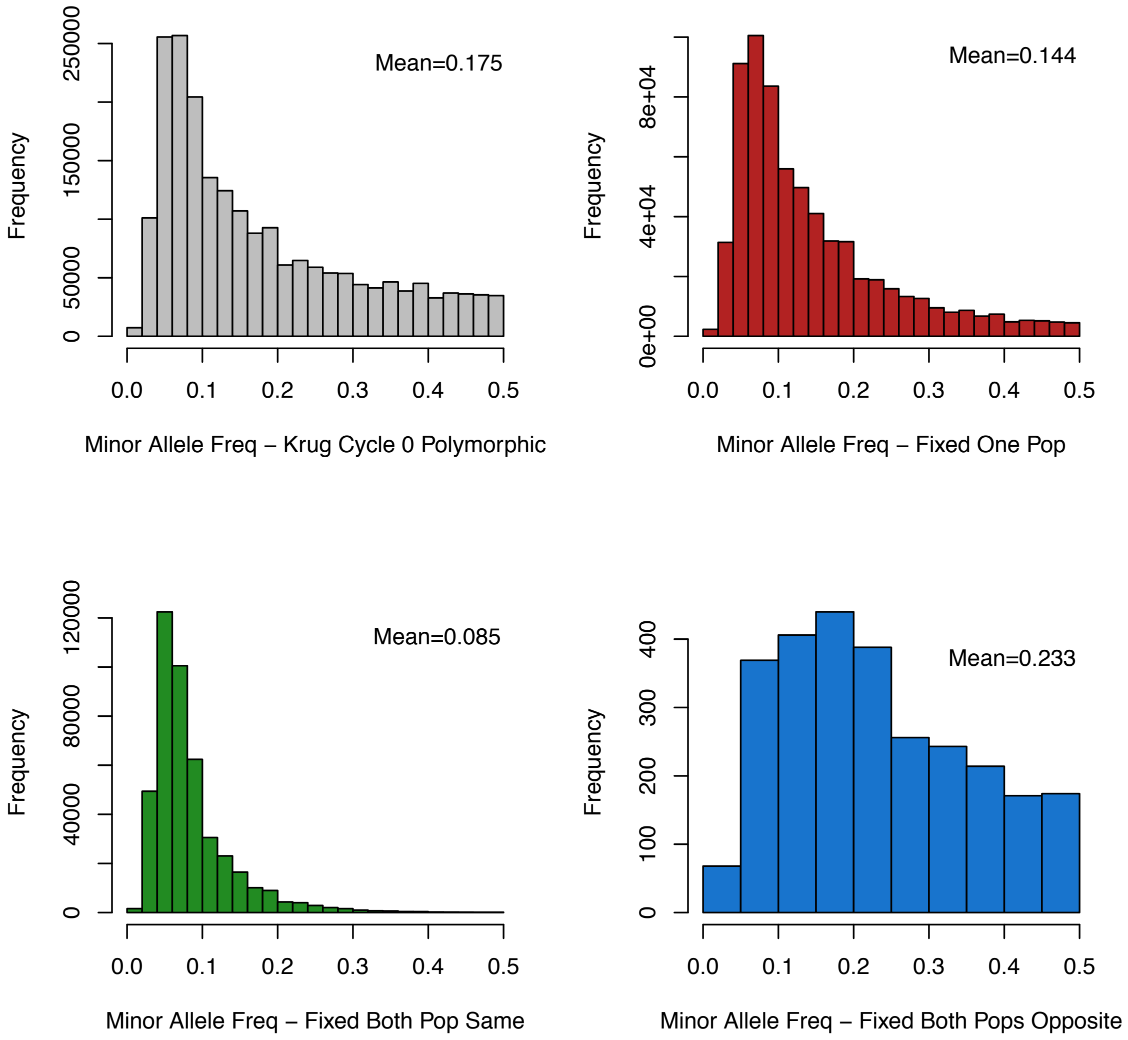
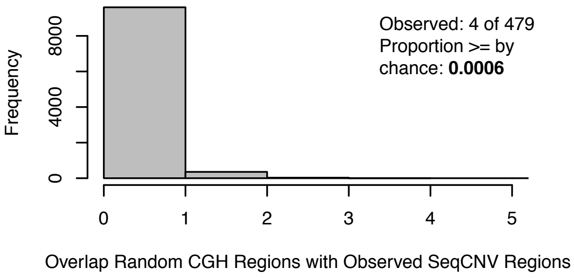
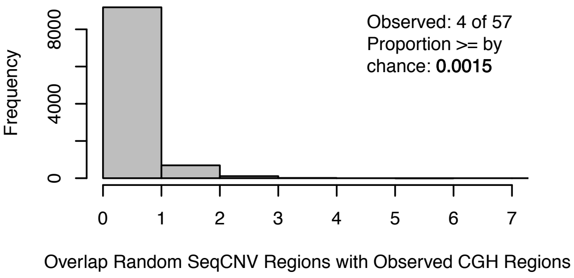
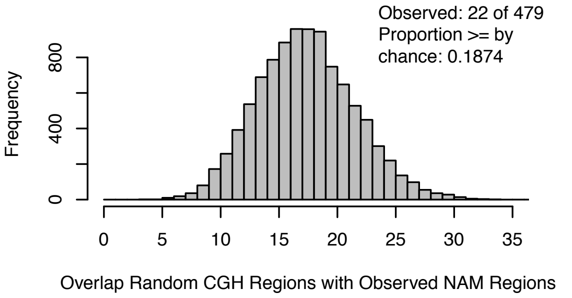
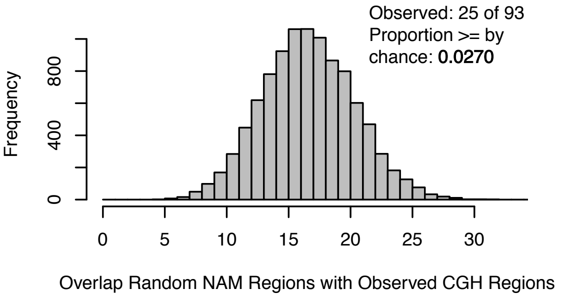


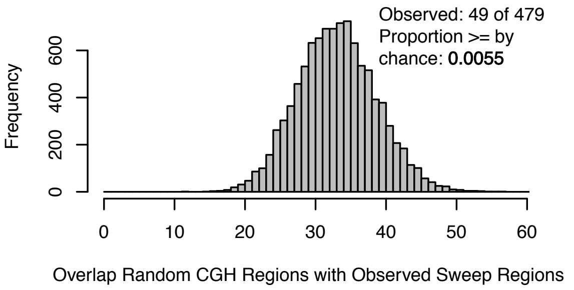
Figure S6 Empirical minor allele frequency for 2,056,663 SNPs that were polymorphic in the Krug Yellow Dent population and subsets of these SNPs that were fixed in one or both of the selected populations. 664,056 SNPs reached fixation in only one population (red), 444,599 SNPs reached fixation in both populations with the same fixed allele (green), and 2,729 SNPs reads in both populations reached fixation in both populations with oppositely fixed SNPs (blue).

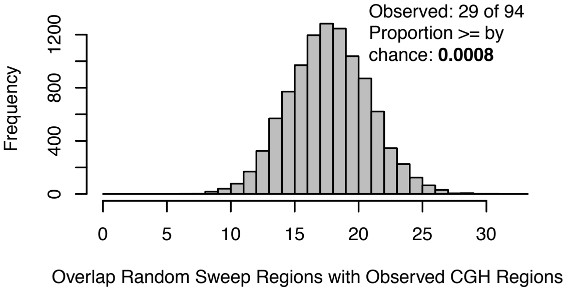

Frequency
0
4000
8000
Observed: 4 of 479
Proportion >= by
chance: **0.0006**
0
1
2
3
4
5
Overlap Random CGH Regions with Observed SeqCNV Regions

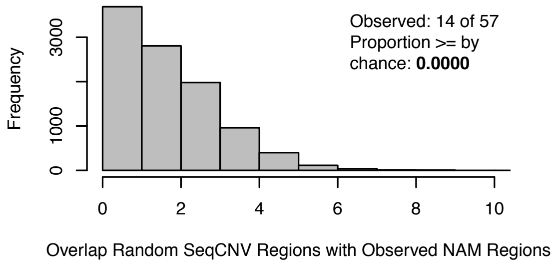

Frequency
0
4000
8000
Observed: 4 of 57
Proportion >= by
chance: **0.0015**
0
1
2
3
4
5
6
7
Overlap Random SeqCNV Regions with Observed CGH Regions

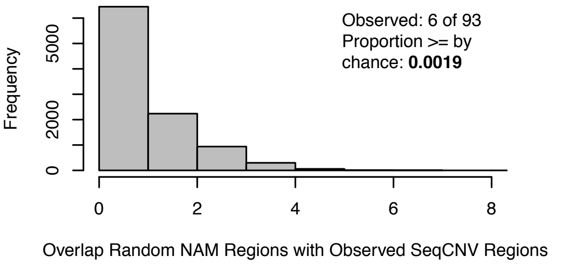

Frequency
0
400
800
Observed: 22 of 479
Proportion >= by
chance: 0.1874
0
5
10
15
20
25
30
35
Overlap Random CGH Regions with Observed NAM Regions

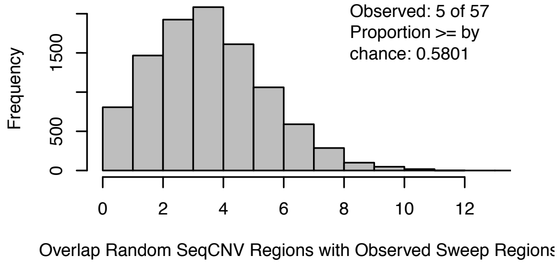

Frequency
0
400
800
Observed: 25 of 93
Proportion >= by
chance: **0.0270**
0
5
10
15
20
25
30
Overlap Random NAM Regions with Observed CGH Regions

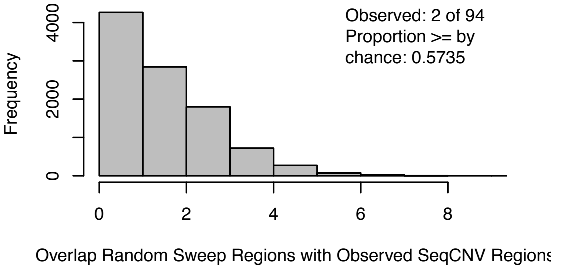

Frequency
0
200
400
600
Observed: 49 of 479
Proportion >= by
chance: **0.0055**
0
10
20
30
40
50
60
Overlap Random CGH Regions with Observed Sweep Regions


Frequency
0
400
800
1200
Observed: 29 of 94
Proportion >= by
chance: **0.0008**
0
5
10
15
20
25
30
Overlap Random Sweep Regions with Observed CGH Regions


Frequency
0
1000
3000
Observed: 14 of 57
Proportion >= by
chance: **0.0000**
0
2
4
6
8
10
Overlap Random SeqCNV Regions with Observed NAM Regions


Frequency
0
2000
5000
Observed: 6 of 93
Proportion >= by
chance: **0.0019**
0
2
4
6
8
Overlap Random NAM Regions with Observed SeqCNV Regions


Frequency
0
500
1500
Observed: 5 of 57
Proportion >= by
chance: 0.5801
0
2
4
6
8
10
12
Overlap Random SeqCNV Regions with Observed Sweep Regions


Frequency
0
2000
4000
Observed: 2 of 94
Proportion >= by
chance: 0.5735
0
2
4
6
8
Overlap Random Sweep Regions with Observed SeqCNV Regions

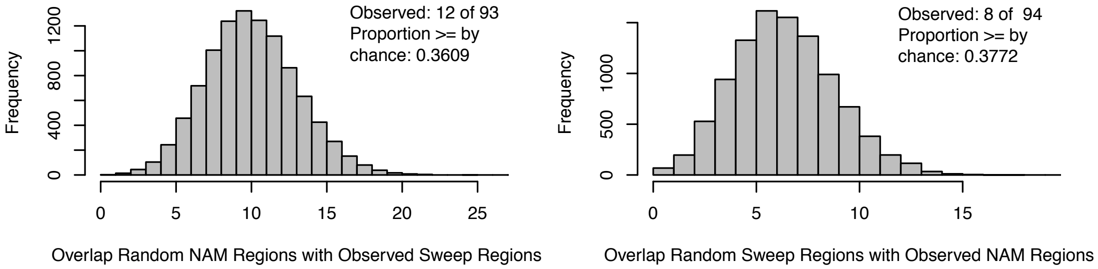


Figure S7 Simulation experiment testing the pair-wise overlap between each source of evidence [comparative genome hybridization (CGH) copy number variation (CNV) regions, sequence depth CNV regions (SeqCNV), regions exceeding the 99.9% outlier threshold (Sweep Regions), and regions identified in the nested association mapping (NAM) population] by chance compared with the empirically observed overlap. Regions with the empirically observed size were randomly placed throughout the genome 10,000 for each source of evidence. Comparisons were then made between the random data and observed data to test the overlap that was observed by chance.

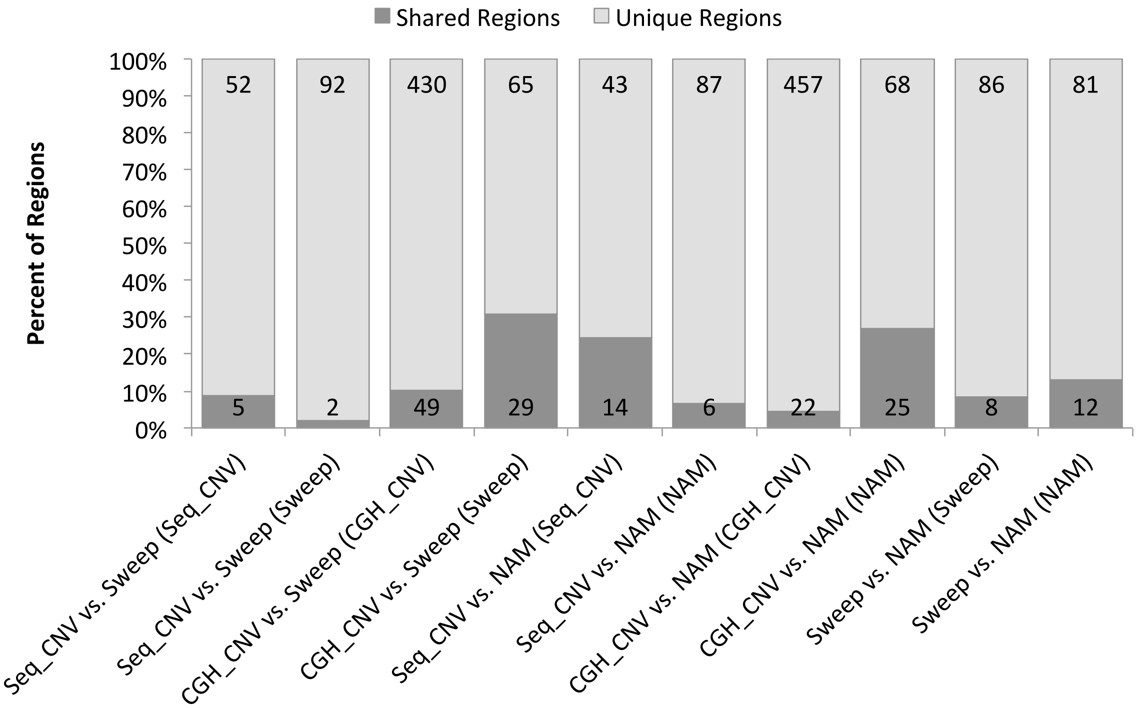


Figure S8 Pair-wise comparisons of overlapping variable regions in the Krug Yellow Dent divergent long-term selection experiment for seed size and quantitative trait loci for seed weight in the maize nested association (NAM) population. Type of variation in parenthesis following the pair-wise comparison description indicates which type of variation the bar pertains to. A comparison with NAM SNPs required regions to be within 500kb to be considered shared regions and for all other comparisons 10kb overlap was required.

Table S1 Candidate regions under selection during 30 generations of selection for seed size, at the 99.9% level. Regions were identified using F_{ST} values and a 25-single nucleotide polymorphism (SNP) sliding window approach. Comparisons were made between Krug Yellow Dent and KLS_30, Krug Yellow Dent and KSS_30, and KLS_30 and KSS_30. One indicates a difference and zero indicates no difference for the region.

Region	Chromosome	Start	End	Krug Yellow Dent vs. KLS_30	Krug Yellow Dent vs. KSS_30	KLS_30 vs. KSS_30	Number of Genes in Region
1	chr1	2088034	2099502	1	0	0	2
2	chr1	13507647	13537594	1	0	0	1
3	chr1	22511847	26826200	0	1	1	103
4	chr1	24438690	31739806	1	0	0	169
5	chr1	54928624	55758694	1	0	0	18
6	chr1	110877561	110898319	0	0	1	0
7	chr1	198652274	203086089	1	0	0	100
8	chr1	210227884	210245719	1	0	0	1
9	chr1	215729004	220787144	1	0	1	92
10	chr1	241280862	241441394	1	0	0	7
11	chr1	260539402	263706680	1	0	0	74
12	chr1	297792787	297796118	1	0	0	1
13	chr10	21394962	21401418	1	0	0	1
14	chr10	124383915	124428189	1	0	0	1
15	chr10	132885971	133247775	1	0	0	9
16	chr2	31592504	31644896	1	0	0	2
17	chr2	39419610	39427387	0	1	0	2
18	chr2	52315602	52324852	1	0	0	1
19	chr2	67149060	71899682	1	0	1	44
20	chr2	68731886	72080518	0	1	0	33
21	chr2	79033475	88346653	0	1	1	79
22	chr2	104374659	107211278	0	0	1	27
23	chr2	111890936	118244338	0	1	1	70
24	chr2	120764979	120833500	0	1	0	1
25	chr2	126240290	127110286	0	1	1	6
26	chr2	133138750	149941557	1	1	1	215
27	chr2	157461751	157483350	0	1	0	1
28	chr2	167971120	168003596	0	1	0	2
29	chr2	185293453	185305296	1	0	0	1
30	chr2	229346615	229355363	1	0	0	1
31	chr3	33560667	35750525	1	0	0	39
32	chr3	54372654	54403213	1	0	0	0
33	chr3	98358330	98391049	0	1	0	0
34	chr3	118149134	118294301	1	0	0	3
35	chr4	18677194	18683044	1	0	0	1
36	chr4	21278849	21337830	0	1	0	2
37	chr4	26373871	26423688	0	1	0	3

38	chr4	31360987	34558254	0	1	1	52
39	chr4	45849344	47615468	0	1	1	12
40	chr4	59868197	60425643	0	1	1	8
41	chr4	70497566	74434332	1	0	1	46
42	chr4	82008572	82215823	0	1	0	6
43	chr4	90311130	91962113	0	0	1	8
44	chr4	121554377	124356978	0	1	1	27
45	chr4	128919570	133670654	1	0	0	48
46	chr4	136905695	136928673	0	0	1	0
47	chr4	143240267	147090538	1	0	0	59
48	chr4	184169869	184450981	1	0	0	7
49	chr4	203316217	203332954	1	0	0	0
50	chr4	224661121	224666412	1	0	0	0
51	chr5	1591098	1611277	0	1	0	3
52	chr5	11820020	11823805	1	0	0	1
53	chr5	67479937	67630316	1	0	0	5
54	chr5	87886831	89078200	1	0	0	18
55	chr5	92352752	92644615	0	1	0	2
56	chr5	125437902	126041703	0	0	1	4
57	chr5	147926211	147981089	0	1	0	1
58	chr5	160128174	164541434	1	1	1	81
59	chr5	192685362	192867950	1	0	1	3
60	chr5	201980075	201986492	1	0	0	1
61	chr6	39475298	39536174	1	0	0	0
62	chr6	70833345	75128389	1	0	0	67
63	chr6	104020474	104846933	1	0	0	14
64	chr6	111743312	111905380	1	0	0	3
65	chr6	118700694	119737122	1	0	0	16
66	chr6	132125931	132306220	1	0	0	7
67	chr6	136744931	137145831	0	0	1	8
68	chr6	138564837	138585701	1	0	0	1
69	chr6	144188428	144399049	0	1	0	2
70	chr6	148547648	150068199	1	0	0	39
71	chr6	160413038	165284918	1	0	0	233
72	chr7	9710307	13889417	0	1	1	87
73	chr7	17688939	17714548	1	0	0	2
74	chr7	44745316	46501661	0	1	1	25
75	chr7	146699976	148403614	1	0	0	48
76	chr7	165464112	165470747	1	0	0	2
77	chr8	30179302	30251700	1	0	0	1
78	chr8	37221664	42322860	1	0	0	57
79	chr8	61632813	64896557	1	0	0	55
80	chr8	71301175	71431155	1	0	0	1

81	chr8	90964543	94385148	1	0	0	51
82	chr8	105466415	105566934	1	0	0	2
83	chr8	113063388	114015951	1	0	0	19
84	chr8	119830324	119832288	1	0	0	1
85	chr8	133152921	134822866	1	0	0	46
86	chr8	142114111	142915956	1	0	0	19
87	chr8	170308877	171403851	1	0	0	49
88	chr9	384383	408227	1	0	0	0
89	chr9	20905213	21728170	0	1	1	14
90	chr9	24459413	30070094	1	0	0	130
91	chr9	110988581	110997371	1	0	0	1
92	chr9	120081323	120160910	1	0	0	2
93	chr9	147488930	147492242	0	1	0	1
94	chr9	149518807	149547799	1	0	0	6

Table S2 Candidate regions under selection during 30 generations of selection for seed size, at the 99.99% level. Regions were identified using F_{ST} values and a 25-single nucleotide polymorphism (SNP) sliding window approach. Comparisons were made between Krug Yellow Dent and KLS_30, Krug Yellow Dent and KSS_30, and KLS_30 and KSS_30. One indicates a difference and zero indicates no difference for the region.

Region	Chromosome	Start	End	Krug Yellow Dent vs. KLS_30	Krug Yellow Dent vs. KSS_30	KLS_30 vs. KSS_30	Number of Genes in Region
1	chr1	26329612	26830886	1	0	0	13
2	chr1	241368710	241403853	1	0	0	3
3	chr10	133216883	133233948	1	0	0	1
4	chr2	67171728	71897890	0	1	1	43
5	chr2	81659356	88321220	0	1	1	57
6	chr2	133888415	140323700	0	1	1	71
7	chr2	149509536	149793812	0	1	0	3
8	chr3	35626227	35655007	1	0	0	0
9	chr4	33053660	33128631	0	1	1	3
10	chr4	46050068	46061870	0	1	0	0
11	chr4	121594579	121609805	0	0	1	1
12	chr4	124305534	124320863	0	1	0	0
13	chr5	160954183	160971691	0	0	1	0
14	chr6	74962790	75080845	1	0	0	2
15	chr6	104456206	104843865	1	0	0	7
16	chr6	111761479	111767828	1	0	0	1
17	chr6	118702716	119665910	1	0	0	15
18	chr6	149827936	149835542	1	0	0	1
19	chr6	160589531	160606591	1	0	0	3
20	chr7	9901060	11800787	0	0	1	38
21	chr8	37229750	39230104	1	0	0	24
22	chr8	113178318	114007931	1	0	0	16
23	chr9	20905875	20973896	0	0	1	3

Table S3 Number of base pairs in the 2.1Gb maize v2 reference assembly with a given coverage range for each of the population pools. M=million.

	Population		
Coverage	Krug Yellow Dent	KLS_30	KSS_30
0	759M	859M	792M
1-5	523M	568M	447M
6-10	219M	225M	183M
11-15	144M	143M	127M
15-20	106M	99M	100M
21-25	81M	68M	82M
26-30	63M	45M	69M
31-40	86M	43M	105M
41-50	47M	12M	70M
>51	37M	4M	89M

Table S4 Genes within candidate regions under selection at the 99.9% level that were in a gene coexpression network module that distinguished KLS_30 and KSS_30 derived inbred lines and was enriched with cell cycle genes.

Chr	Start	End	99.9% Level Region	Krug Yellow Dent vs. KLS_30	Krug Yellow Dent vs. KSS_30	KLS_30 vs. KSS_30	Gene in Coexpression Module
chr1	198652274	203086089	7	1	0	0	GRMZM2G055968
chr1	260539402	263706680	11	1	0	0	GRMZM2G351304
chr2	79033475	88346653	21	0	1	1	GRMZM2G177596
chr2	104374659	107211278	22	0	0	1	GRMZM2G141814
chr2	133138750	149941557	26	1	1	1	GRMZM2G006765
chr2	133138750	149941557	26	1	1	1	GRMZM2G042897
chr4	70497566	74434332	41	1	0	1	GRMZM2G147756
chr4	128919570	133670654	45	1	0	0	GRMZM2G087323
chr6	118700694	119737122	65	1	0	0	GRMZM2G159953
chr6	160413038	165284918	71	1	0	0	GRMZM2G096389
chr6	160413038	165284918	71	1	0	0	GRMZM2G310758
chr6	160413038	165284918	71	1	0	0	GRMZM5G892879
chr7	9710307	13889417	72	0	1	1	GRMZM2G101036
chr7	9710307	13889417	72	0	1	1	GRMZM2G446921
chr7	146699976	148403614	75	1	0	0	AC196961.2_FG003
chr8	37221664	42322860	78	1	0	0	GRMZM2G120202
chr8	170308877	171403851	87	1	0	0	GRMZM2G069078
chr9	24459413	30070094	90	1	0	0	GRMZM2G050329
chr9	24459413	30070094	90	1	0	0	GRMZM2G136838

Table S5 Regions with copy number variation (CNV) between KLS_30 and KSS_30 based on read depth variation. Average read depth was determined in 5kb windows in both populations. CNV windows were defined as having an absolute value greater than 2 for the number of standard deviations (SD) away from the mean in KLS_30 minus the number of standard deviations away from the mean in KSS_30.

Chr	Region Start	Region Stop	Krug Yellow Dent SD From Mean	KLS_30 SD from Mean	KSS_30 SD From Mean	Absolute Value of KLS_30 SD Minus KSS_30 SD
1	235001	240000	6.20	3.54	5.81	2.27
1	203910001	203915000	32.13	36.10	29.50	6.60
1	234470001	234475000	9.85	6.52	8.83	2.31
1	234500001	234505000	8.74	5.46	8.02	2.56
1	234510001	234515000	10.74	6.57	9.38	2.81
1	234525001	234530000	6.38	3.88	6.34	2.46
1	234545001	234550000	2.00	7.27	0.28	6.99
1	234605001	234610000	19.13	13.87	16.02	2.15
1	234640001	234645000	11.68	6.30	10.07	3.76
1	234645001	234650000	23.55	10.47	20.49	10.02
1	234650001	234655000	4.62	1.99	4.03	2.04
1	234720001	234725000	30.96	17.98	26.04	8.05
1	234725001	234730000	32.95	19.19	27.93	8.74
1	234730001	234735000	26.88	15.52	22.49	6.97
1	234735001	234740000	22.14	13.38	18.65	5.27
2	65000001	65005000	9.96	11.93	9.33	2.60
2	77820001	77825000	9.52	5.09	8.19	3.10
2	77825001	77830000	20.88	9.50	18.85	9.35
2	77865001	77870000	8.97	5.59	7.65	2.06
2	77870001	77875000	24.74	16.35	22.08	5.73
2	77875001	77880000	30.42	18.85	26.10	7.25
2	77880001	77885000	13.41	7.95	11.53	3.57
2	172080001	172085000	31.16	35.19	31.35	3.84
2	172085001	172090000	14.78	9.31	14.01	4.70
2	172110001	172115000	26.79	30.90	25.12	5.78
2	172115001	172120000	53.85	60.10	51.33	8.77
2	174415001	174420000	1.82	5.69	-0.06	5.74
3	74660001	74665000	11.29	4.59	9.86	5.27
3	209600001	209605000	5.97	4.05	6.10	2.05
4	111670001	111675000	2.75	9.63	0.53	9.10
4	172415001	172420000	9.54	6.01	9.02	3.01
5	189240001	189245000	7.91	4.43	6.65	2.22
5	209940001	209945000	23.61	24.51	20.82	3.69
5	209945001	209950000	22.73	24.76	19.44	5.32
5	209960001	209965000	3.94	5.56	-0.32	5.88
5	209990001	209995000	19.42	22.00	18.48	3.52
5	210290001	210295000	4.68	6.30	4.11	2.18

6	20610001	20615000	7.53	6.25	8.27	2.02
6	60760001	60765000	9.35	11.79	8.53	3.26
6	104230001	104235000	17.50	12.94	16.65	3.71
6	160755001	160760000	10.34	7.23	9.34	2.11
6	160765001	160770000	68.65	72.54	63.99	8.55
6	160770001	160775000	33.42	27.46	30.52	3.06
6	160785001	160790000	12.43	5.81	11.82	6.01
7	18050001	18055000	9.32	11.19	8.66	2.53
7	44725001	44730000	25.12	29.51	22.88	6.63
8	80365001	80370000	8.94	5.13	8.89	3.75
8	97340001	97345000	1.68	1.18	3.21	2.03
8	97350001	97355000	2.11	1.61	3.85	2.23
8	146460001	146465000	9.07	10.99	8.45	2.54
9	6950001	6955000	21.67	14.18	17.76	3.58
9	6955001	6960000	17.92	11.16	15.19	4.03
9	57980001	57985000	11.86	5.65	10.62	4.97
9	67980001	67985000	14.12	9.01	12.19	3.18
9	68025001	68030000	19.43	13.21	17.14	3.93
10	34105001	34110000	27.75	13.75	22.70	8.95
10	121000001	121005000	16.96	10.89	15.30	4.41

Tables S6-S7

Available for download as Excel files at http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.114.167155/-/DC1

Table S6 Comparative genome hybridization (CGH) normalized intensities for four inbreds generated from KLS_30 and five inbreds generated from KSS_30.

Table S7 Joint linkage analysis results for 20-kernel seed weight in the maize nested association mapping (NAM) population.

Table S8 Single nucleotide polymorphisms (SNPs) contained in a single forward regression genome wide association analysis (GWAS) model for 20-kernel seed weight in the maize nested association mapping (NAM) population. Effect is relative to B73.

Marker	chr	AGPv2 Position	cM	Effect	P value
PZE0123124739	1	23,099,268	39.91	-0.07	1.11E-16
PZE01201470169	1	201,639,860	115.12	-0.11	1.24E-09
PZE01237261221	1	237,965,327	140.05	-0.11	3.95E-15
PZE0207620470	2	7,663,333	22.98	-0.06	5.77E-17
PZE0219925121	2	20,005,607	50.23	0.15	1.15E-10
PZE0228682197	2	28,761,283	60.29	0.06	2.21E-17
PZE02207653607	2	210,665,344	116.70	0.11	2.08E-09
PZE0305630836	3	5,850,072	21.63	0.09	1.39E-08
PZE03182929802	3	184,677,342	94.84	0.13	1.35E-15
PZE03209569396	3	211,128,687	120.01	-0.16	5.34E-13
PZE04207608568	4	201,957,506	108.82	0.08	2.04E-20
PZE0545748962	5	46,424,011	59.89	-0.11	1.89E-15
PZE05209672404	5	210,474,175	129.99	0.25	1.87E-13
PZE0692901122	6	64,157,406	19.51	0.08	2.05E-09
PZE06159136863	6	159,014,181	80.65	-0.08	1.20E-10
PZE07148539524	7	154,191,204	86.44	0.09	1.15E-08
PZE07156647853	7	162,259,418	99.46	0.06	4.55E-14
PZE08103597003	8	104,822,548	58.93	-0.05	3.20E-13
PZE0961486830	9	NA	45.68	0.19	4.67E-24
PZE09131782056	9	136,179,349	66.59	0.06	2.23E-12
PZE1025657301	10	25,657,714	35.72	-0.09	7.26E-10

Table S9 Resampling model inclusion probability (RMIP) analysis results for 20-kernel seed weight in the maize nested association mapping (NAM) population. Only markers with bootstrap support in five or more subsamples are reported. Effect is relative to B73. The reported *P* values are the lowest significant *P* value that was observed across the 100 subsamples.

Marker	Chr	AGPv2 Position	cM	RMIP	Effect	P value
PZE0122275486	1	22,247,033	39.19	16	-0.12	6.15E-13
PZE0123077638	1	23,067,629	39.87	11	-0.07	8.38E-13
PZE0123124739	1	23,099,268	39.91	16	-0.07	5.61E-12
PZE0123662144	1	23,566,708	40.47	25	-0.07	5.02E-11
PZE0125025863	1	24,931,627	41.89	8	-0.08	6.15E-13
PZE0139180321	1	39,111,110	57.09	5	0.07	1.51E-09
PZE01201470169	1	201,639,860	115.12	9	-0.12	4.18E-09
PZE01233561761	1	234,219,193	138.59	39	-0.14	3.91E-11
PZE01237261221	1	237,965,327	140.05	40	-0.11	6.16E-11
PZE01292560885	1	293,627,855	192.50	12	-0.06	5.79E-10
PZE01292868532	1	293,935,502	193.21	5	-0.05	1.81E-09
PZE0205818953	2	5,817,525	17.74	8	-0.07	3.99E-11
PZE0207620470	2	7,663,333	22.98	48	-0.06	6.57E-11
PZE0207910201	2	7,953,064	23.73	9	-0.07	6.71E-11
PZE0219925121	2	20,005,607	50.23	18	0.16	1.84E-09
PZE0221648470	2	21,726,433	52.73	6	0.09	2.99E-09
PZE0228682191	2	28,761,277	60.29	6	0.07	3.63E-11
PZE0228682197	2	28,761,283	60.29	14	0.07	1.54E-13
PZE0229550868	2	29,117,510	61.21	6	0.06	2.48E-10
PZE0235758316	2	35,272,110	64.57	9	0.08	2.81E-14
PZE0238058171	2	37,572,981	66.09	6	0.07	5.49E-16
PZE0239176813	2	38,696,485	66.82	8	0.10	1.85E-10
PZE0240222660	2	39,757,715	67.51	29	0.11	5.75E-09
PZE0240904916	2	40,439,971	67.94	6	0.08	6.88E-11
PZE02207653607	2	210,665,344	116.70	6	0.13	1.99E-09
PZE0302919491	3	2,957,042	8.69	9	0.06	2.46E-09
PZE0305630836	3	5,850,072	21.63	8	0.10	8.31E-09
PZE03116146291	3	119,926,252	59.37	13	0.10	6.65E-09
PZE03177053561	3	178,806,797	88.27	6	0.15	1.15E-11
PZE03178447133	3	180,203,027	90.04	12	0.11	7.81E-12
PZE03182929802	3	184,677,342	94.84	65	0.13	2.99E-10
PZE03209569396	3	211,128,687	120.01	77	-0.16	1.39E-09
PZE04207608568	4	201,957,506	108.82	48	0.08	5.12E-13
PZE04207758758	4	202,107,696	108.86	23	0.07	3.74E-14
PZE04212652195	4	207,024,058	110.04	5	0.07	1.32E-14
PZE0536484165	5	37,174,222	58.23	14	-0.15	4.28E-12
PZE0545435902	5	46,110,951	59.83	10	-0.15	1.70E-10
PZE0545748962	5	46,424,011	59.89	21	-0.11	6.11E-12

PZE0566973506	5	67,673,484	64.68	6	-0.08	1.42E-11
PZE0567955527	5	68,647,181	64.90	6	-0.13	5.99E-13
PZE0570378999	5	71,092,575	65.73	9	-0.11	6.41E-12
PZE05209219847	5	210,021,618	128.36	9	0.18	8.04E-11
PZE05209416262	5	210,218,033	129.07	8	0.26	5.92E-11
PZE05209450970	5	210,252,741	129.19	5	0.26	1.84E-10
PZE05209890414	5	210,694,868	130.78	14	0.19	1.00E-10
PZE05212784052	5	213,583,963	142.19	20	0.19	8.37E-11
PZE05213906088	5	214,718,607	147.42	11	0.19	5.70E-10
PZE0690543233	6	91,646,020	17.51	7	0.08	4.93E-09
PZE0692901122	6	64,157,406	19.51	12	0.10	5.92E-09
PZE0696785554	6	96,541,043	22.94	6	0.15	1.08E-08
PZE06159136863	6	159,014,181	80.65	19	-0.08	6.37E-09
PZE06163919721	6	163,822,182	95.67	35	-0.09	5.30E-09
PZE07148539524	7	154,191,204	86.44	34	0.10	1.64E-08
PZE07156061393	7	161,697,119	98.24	6	0.09	1.04E-12
PZE07156647853	7	162,259,418	99.46	22	0.08	2.07E-10
PZE07157275574	7	162,985,624	100.76	18	0.09	6.83E-12
PZE07158131612	7	163,824,440	102.53	13	0.08	1.03E-11
PZE07160221189	7	165,945,883	107.21	13	0.06	5.46E-10
PZE07168993370	7	174,761,756	134.00	5	0.20	5.90E-09
PZE0801360932	8	1,375,719	2.97	9	-0.13	1.11E-08
PZE0832831580	8	32,859,653	51.21	5	-0.07	8.73E-12
PZE08103155726	8	104,380,896	58.78	12	-0.06	6.77E-11
PZE08103597003	8	104,822,548	58.93	12	-0.06	5.10E-11
PZE08109869427	8	111,192,862	60.88	9	-0.06	7.05E-12
PZE08112249901	8	113,634,215	61.49	7	-0.06	3.90E-11
PZE08156324673	8	157,638,136	83.03	6	-0.06	6.12E-11
PZE0961486830	9	NA	45.68	56	0.19	1.76E-15
PZE0985093978	9	88,002,312	46.49	5	0.22	9.81E-11
PZE0986885631	9	89,813,289	46.80	19	0.20	2.14E-13
PZE0988184281	9	91,122,357	47.01	6	0.20	3.83E-19
PZE09131781985	9	136,179,278	66.59	9	0.06	2.98E-09
PZE09131782056	9	136,179,349	66.59	9	0.06	3.98E-09
PZE09137421592	9	141,828,934	76.37	5	0.08	9.82E-09
PZE1025657301	10	25,657,714	35.72	25	-0.09	1.44E-08
PZE1030835021	10	30,870,720	36.00	17	-0.09	1.38E-08
PZE1036843968	10	52,676,288	36.08	6	-0.07	1.21E-08