

GENETICS

Supporting Information

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Identification of Selection Signatures in Cattle Breeds Selected for Dairy Production

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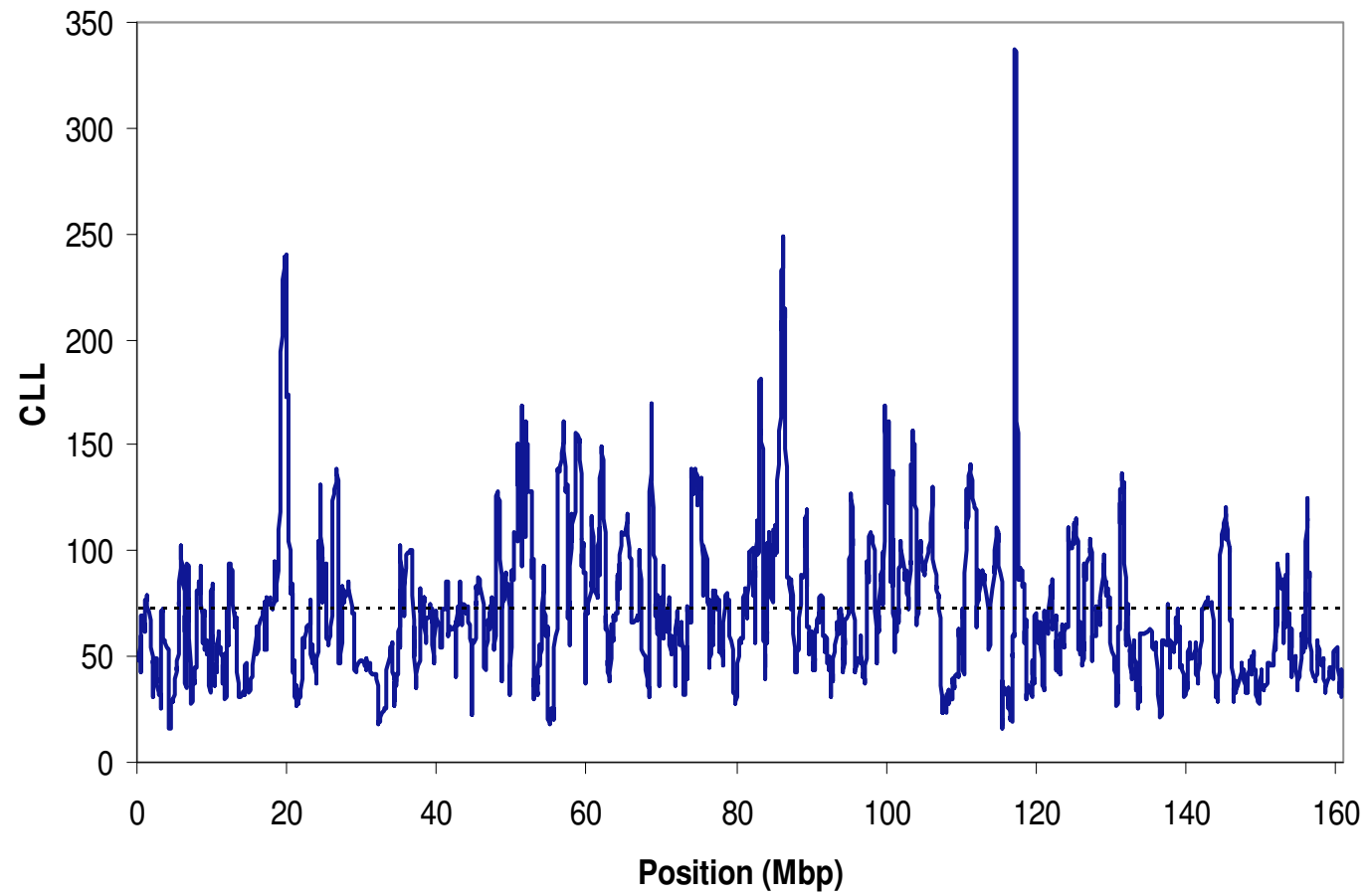


FIGURE S1.—Composite log-likelihood (CLL) for dairy breeds on BTA1. (----- < 0.01 threshold)

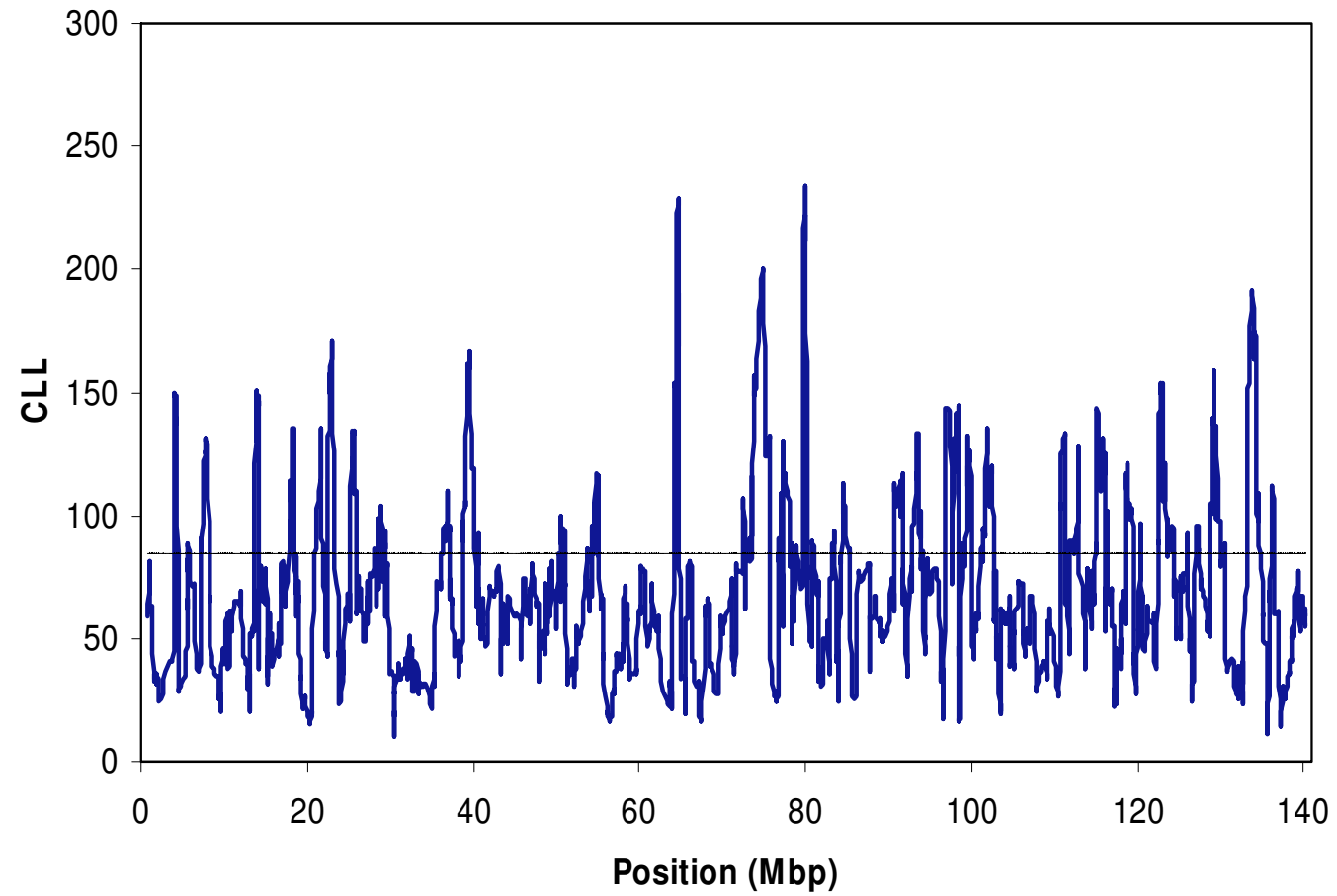


FIGURE S2.—Composite log-likelihood (CLL) for dairy breeds on BTA2. (----- $P < 0.01$ threshold)

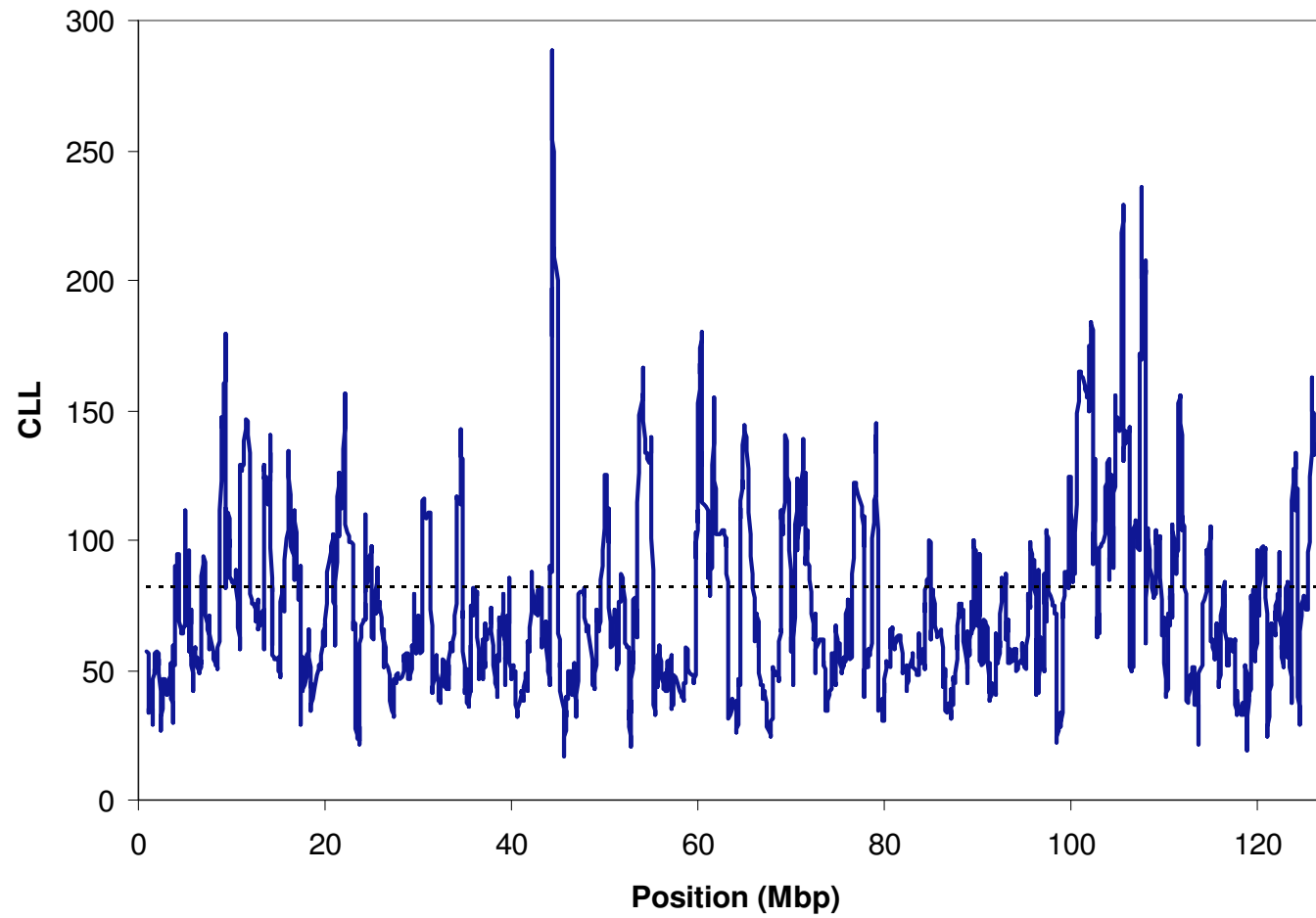


FIGURE S3.—Composite log-likelihood (CLL) for dairy breeds on BTA3. (----- $P < 0.01$ threshold)

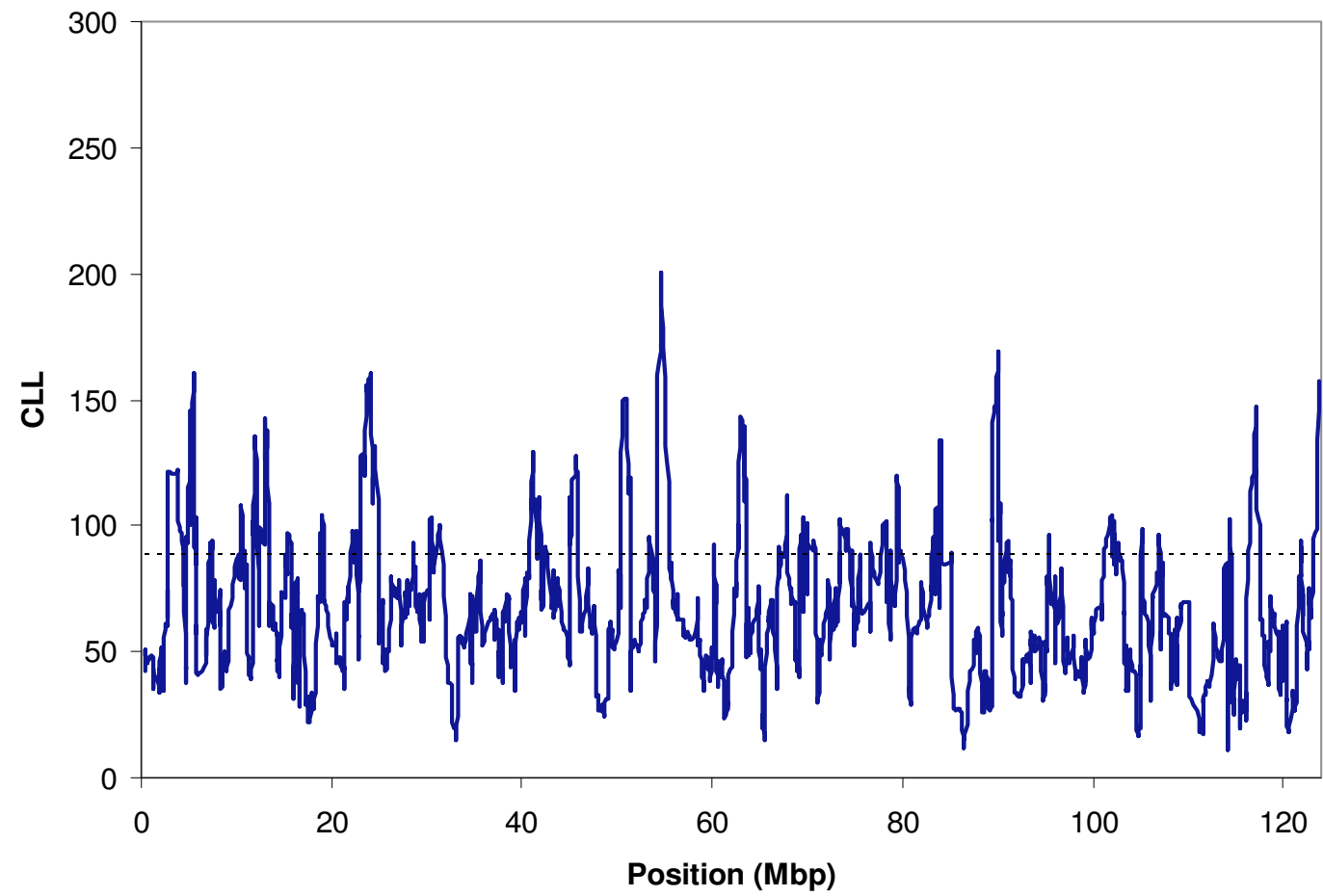


FIGURE S4.—Composite log-likelihood (CLL) for dairy breeds on BTA4. (----- $P < 0.01$ threshold)

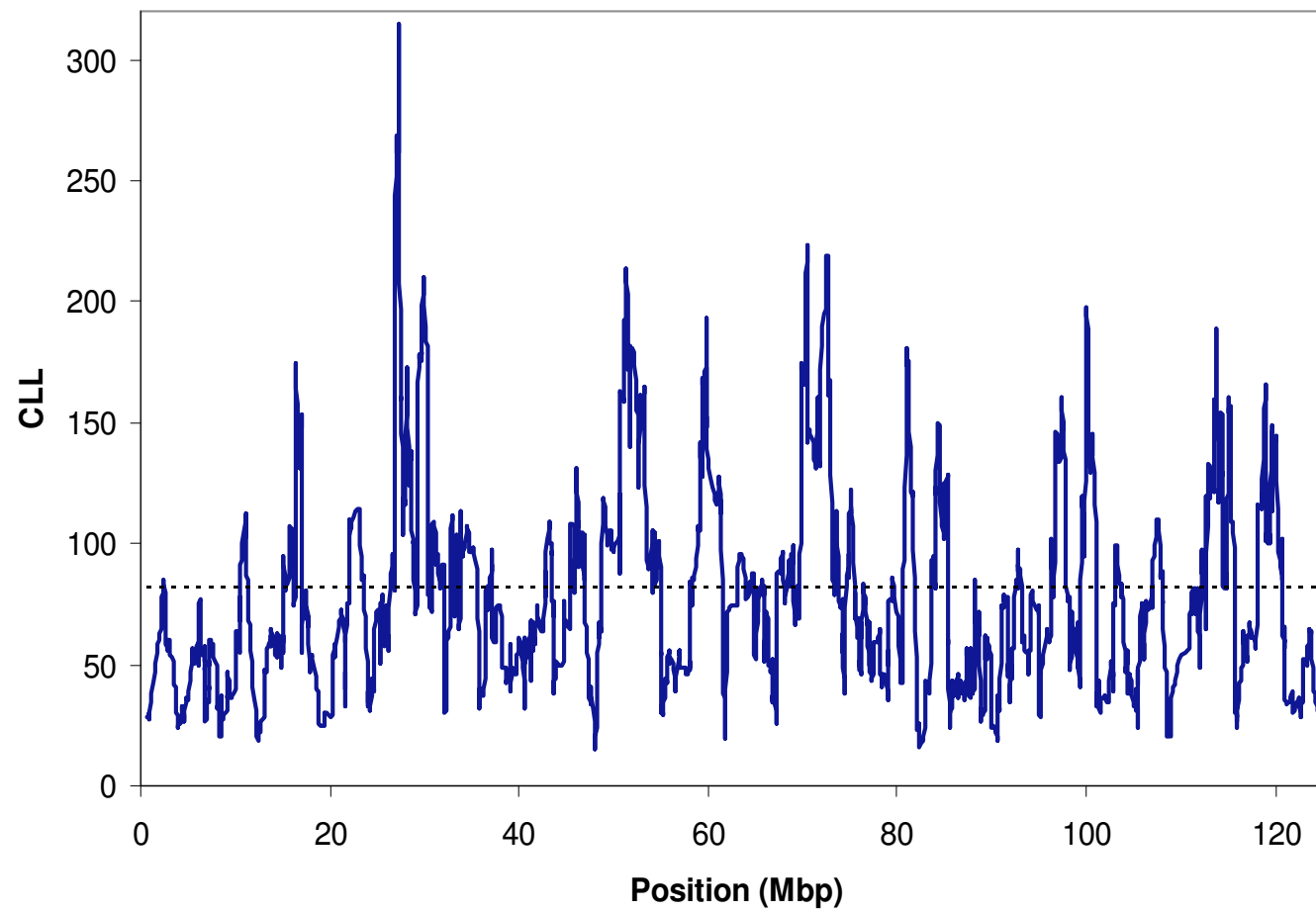


FIGURE S5.—Composite log-likelihood (CLL) for dairy breeds on BTA5. (----- $P < 0.01$ threshold)

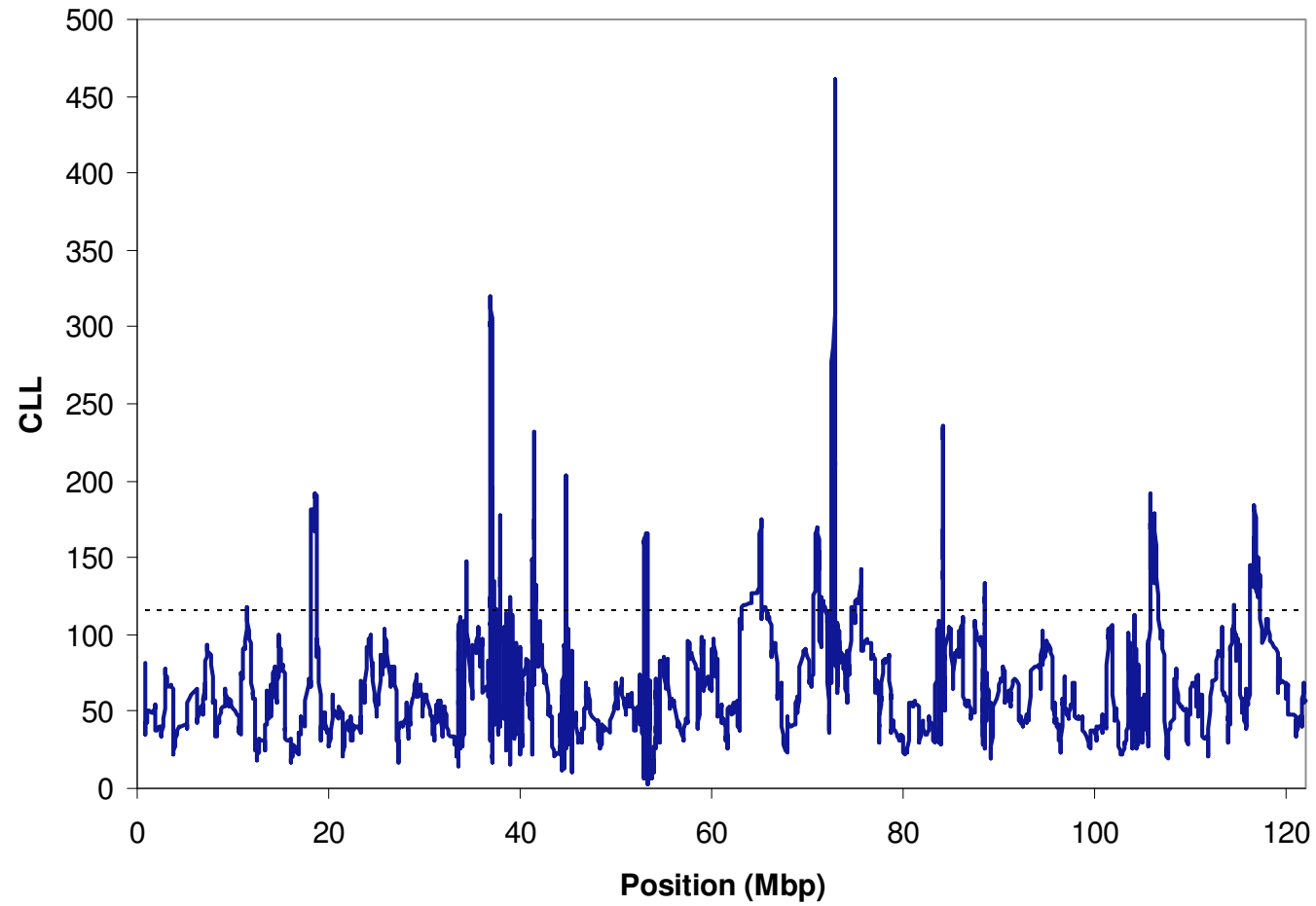


FIGURE S6.—Composite log-likelihood (CLL) for dairy breeds on BTA6. (----- $P < 0.01$ threshold)

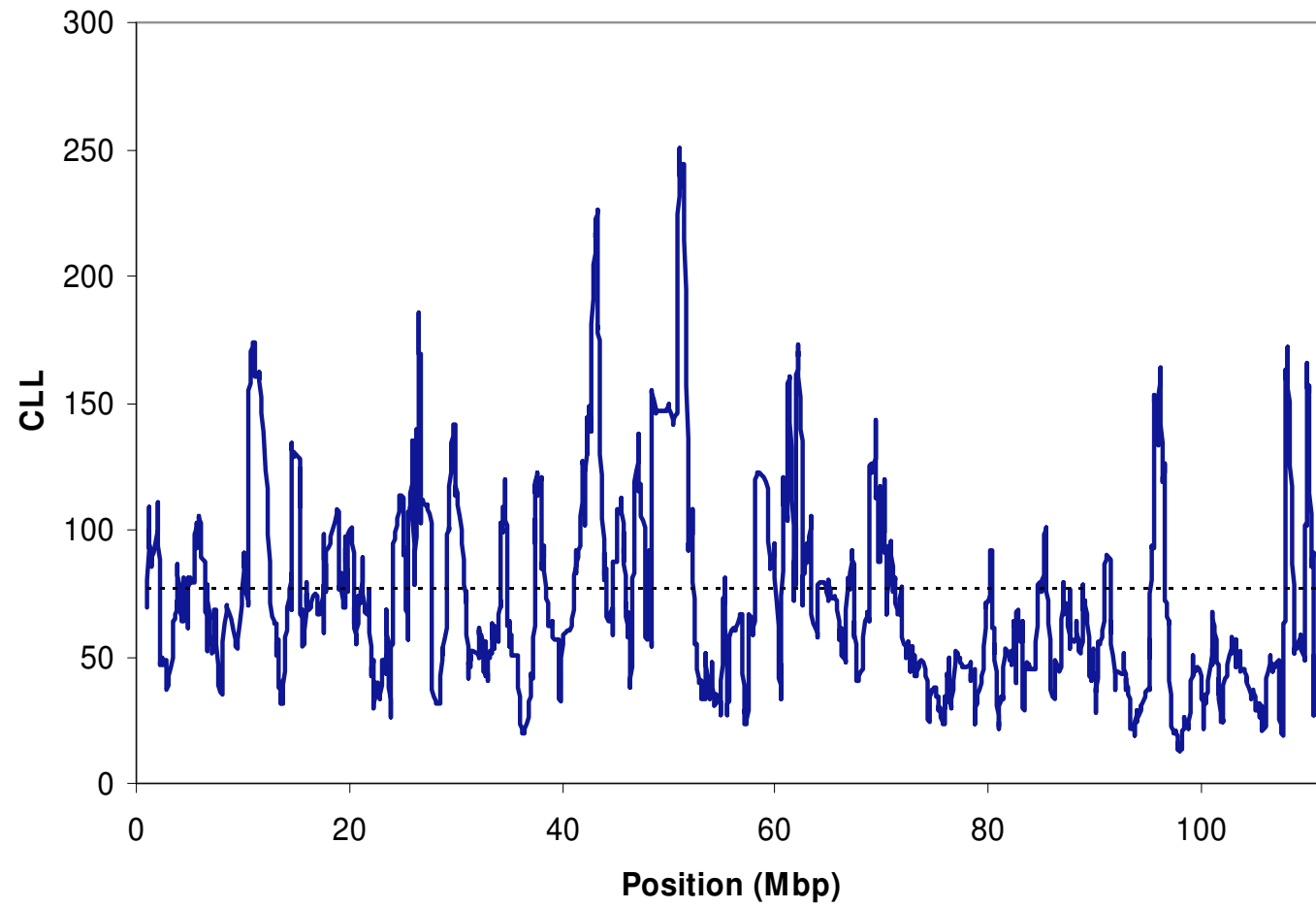


FIGURE S7.—Composite log-likelihood (CLL) for dairy breeds on BTA7. (----- $P < 0.01$ threshold)

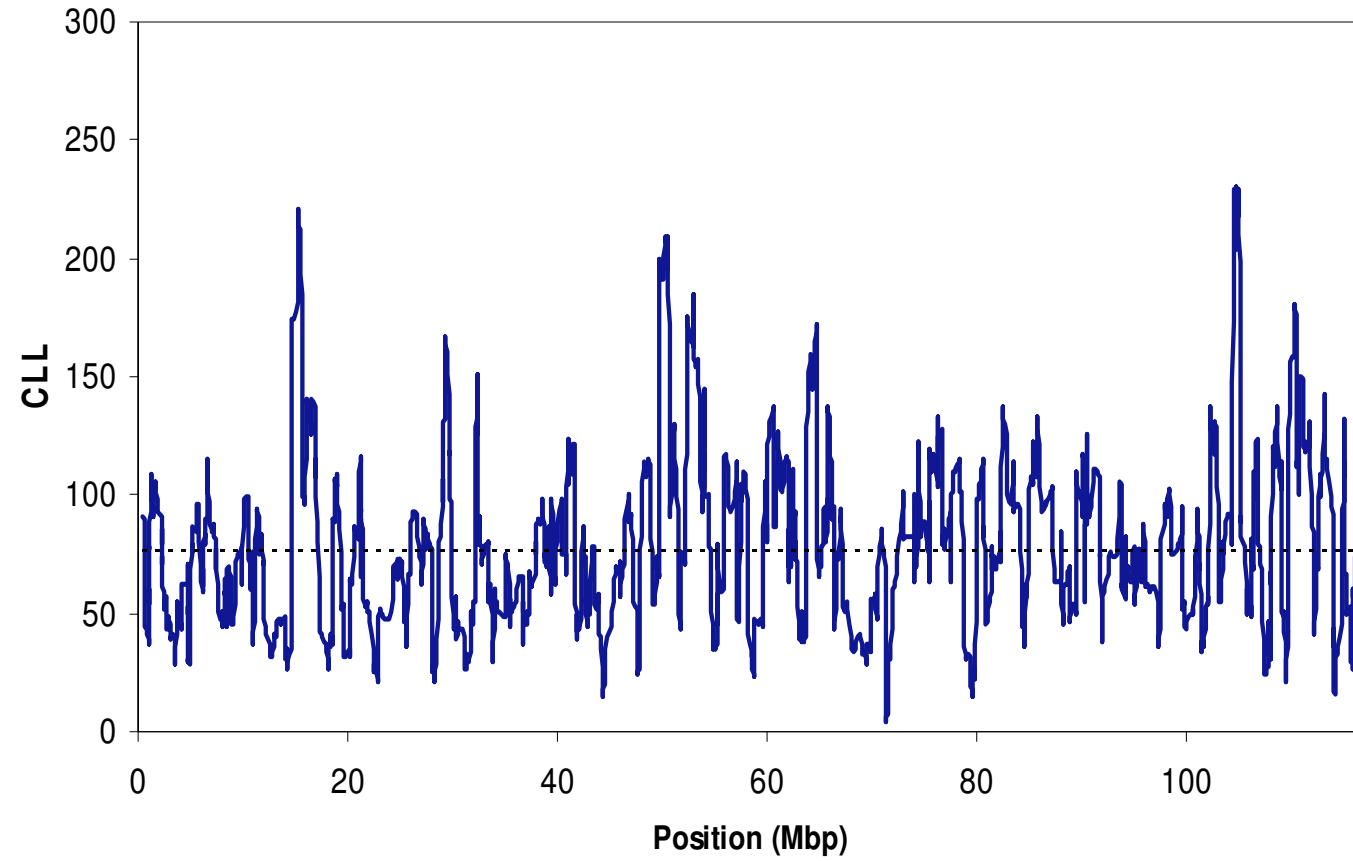


FIGURE S8.—Composite log-likelihood (CLL) for dairy breeds on BTA8. (----- $P < 0.01$ threshold)

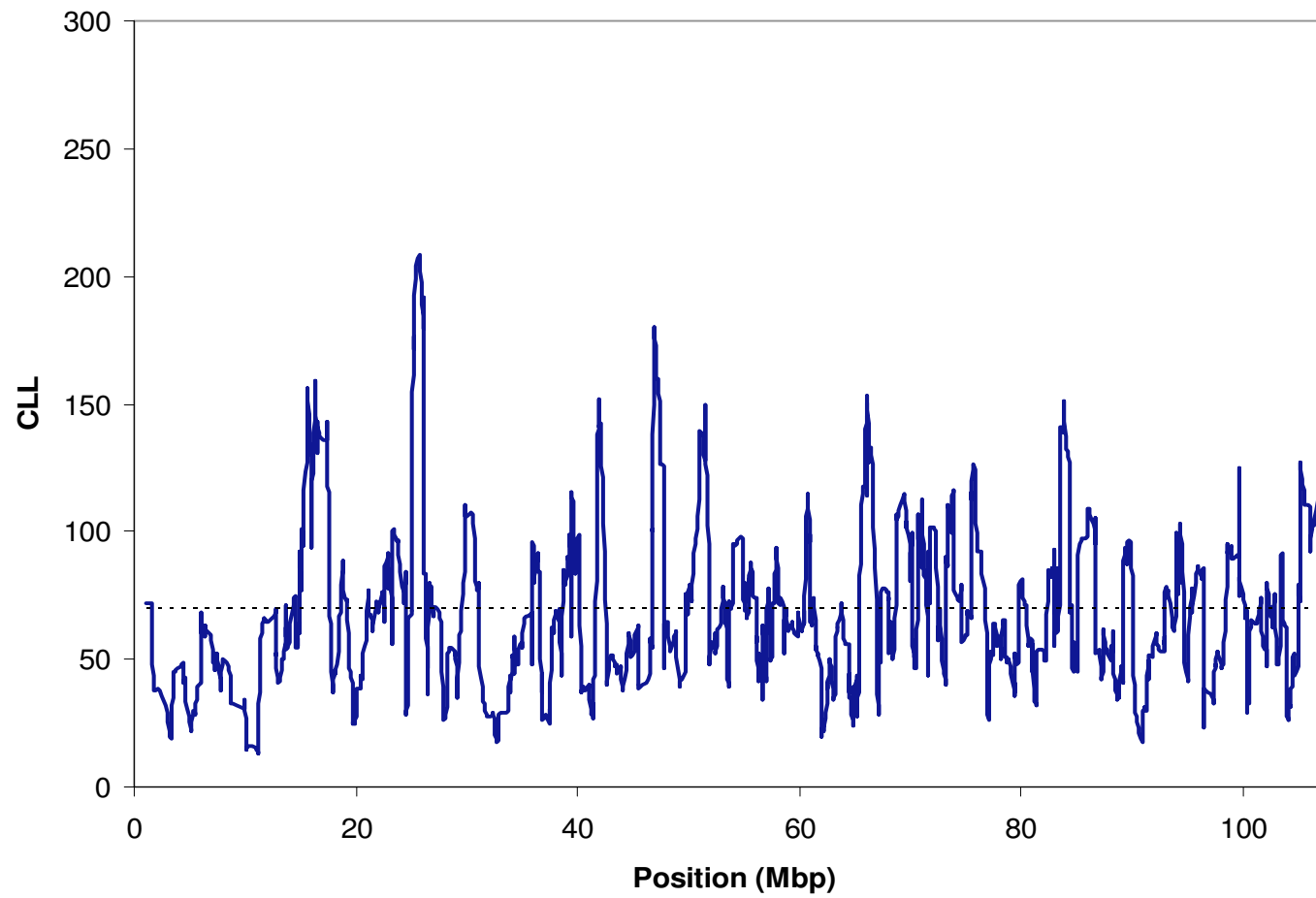


FIGURE S9.—Composite log-likelihood (CLL) for dairy breeds on BTA9. (----- $P < 0.01$ threshold)

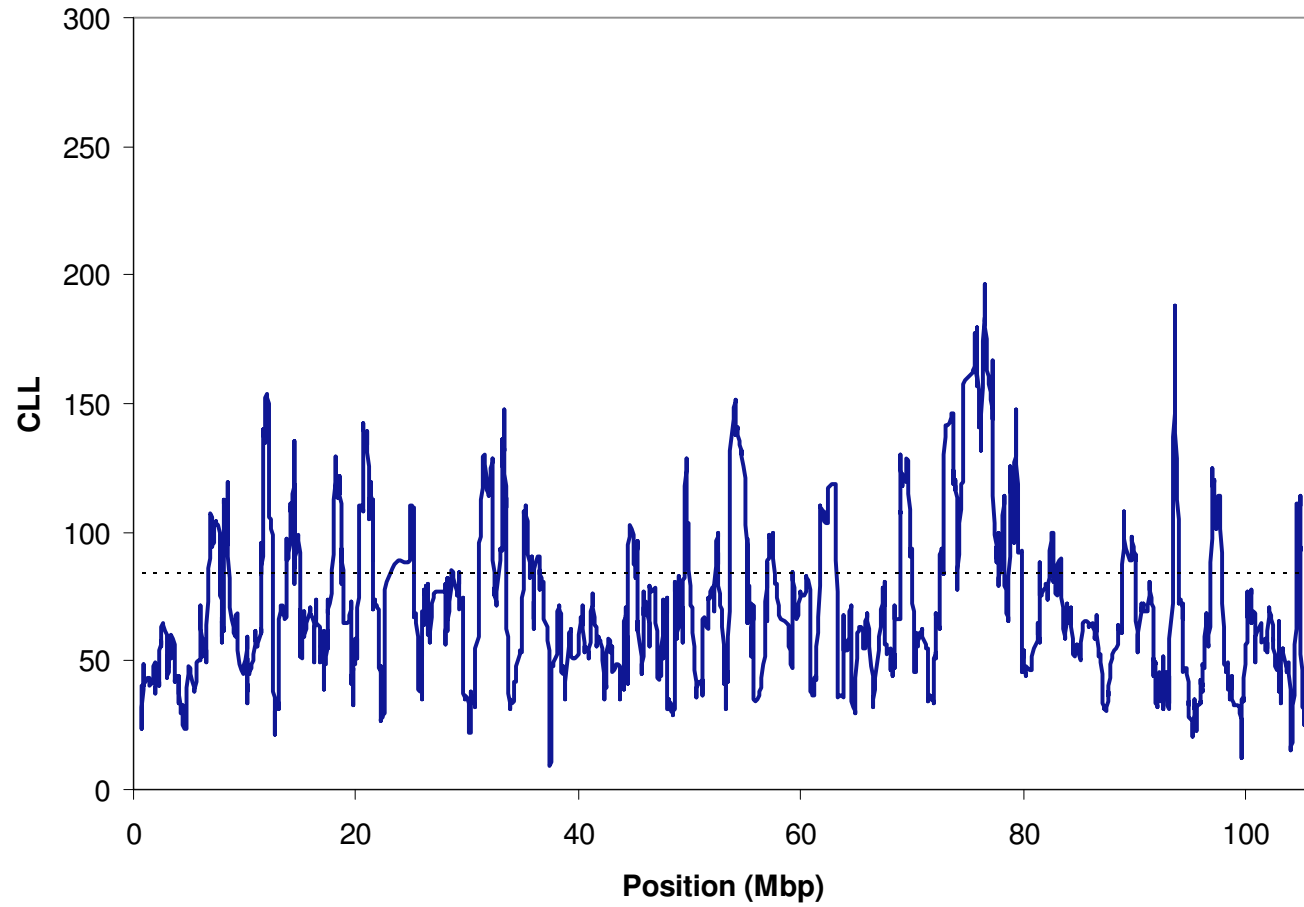


FIGURE S10.—Composite log-likelihood (CLL) for dairy breeds on BTA10. (----- $P < 0.01$ threshold)

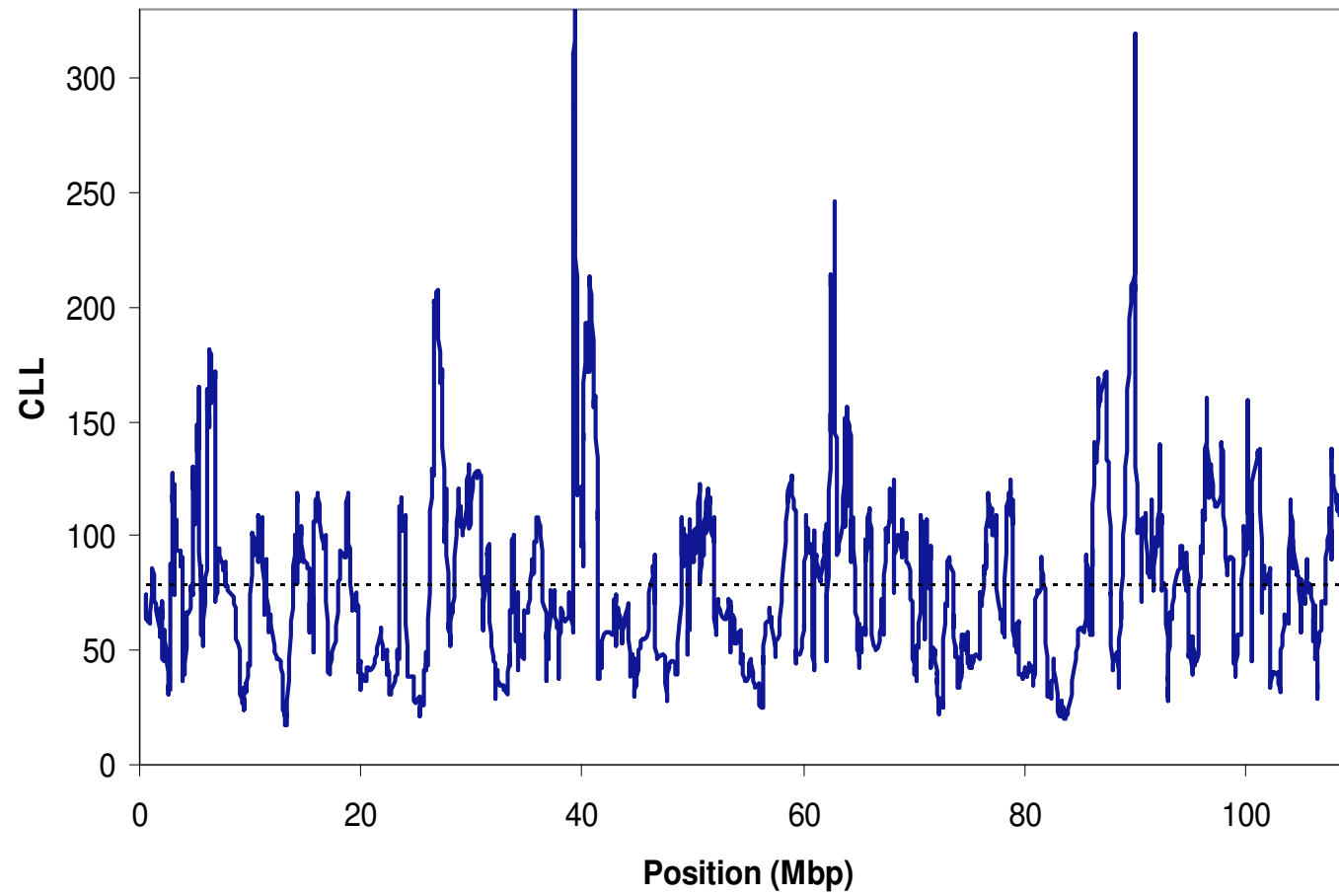


FIGURE S11.—Composite log-likelihood (CLL) for dairy breeds on BTA11. (----- $P < 0.01$ threshold)

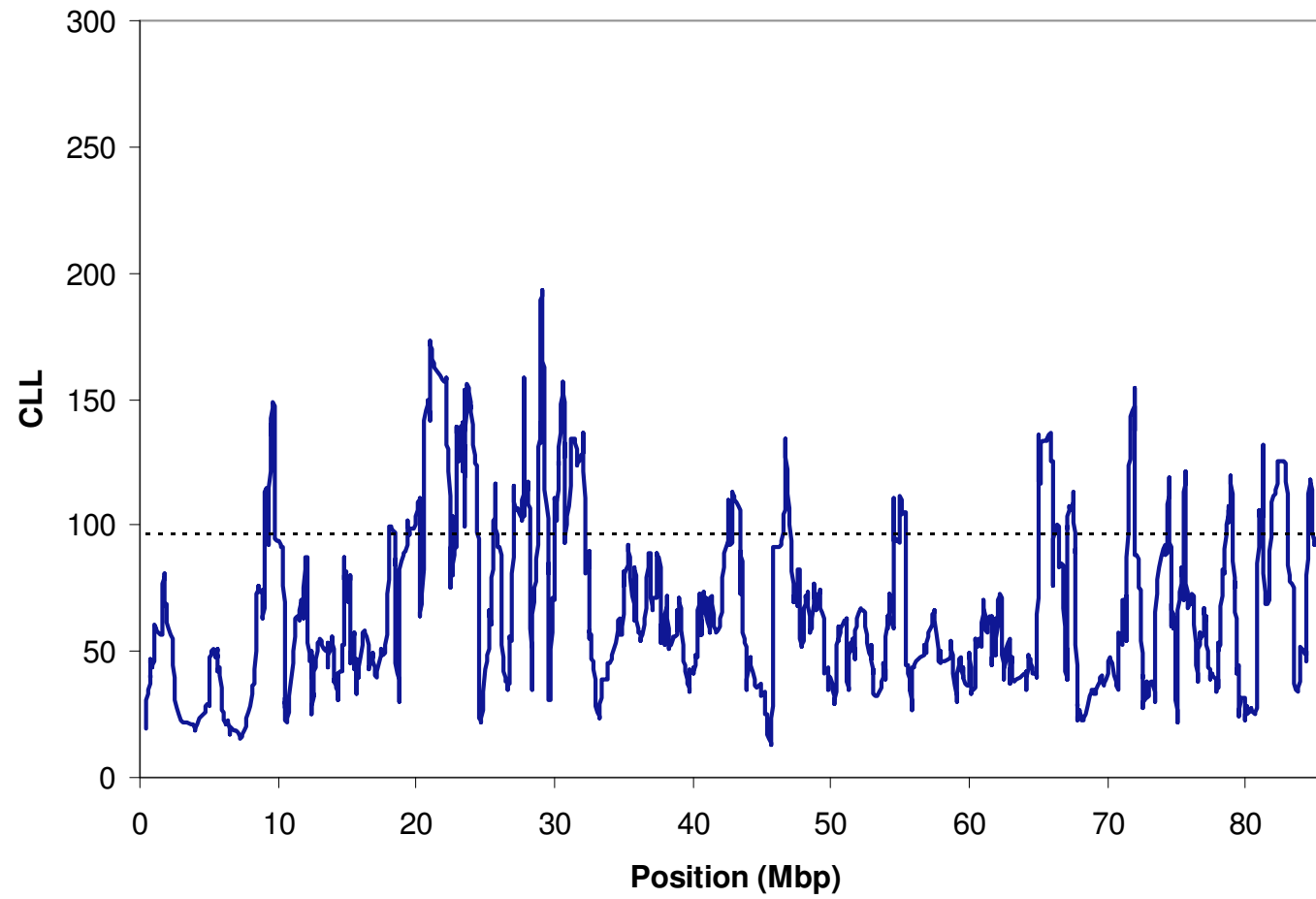


FIGURE S12.—Composite log-likelihood (CLL) for dairy breeds on BTA12. (----- $P < 0.01$ threshold)

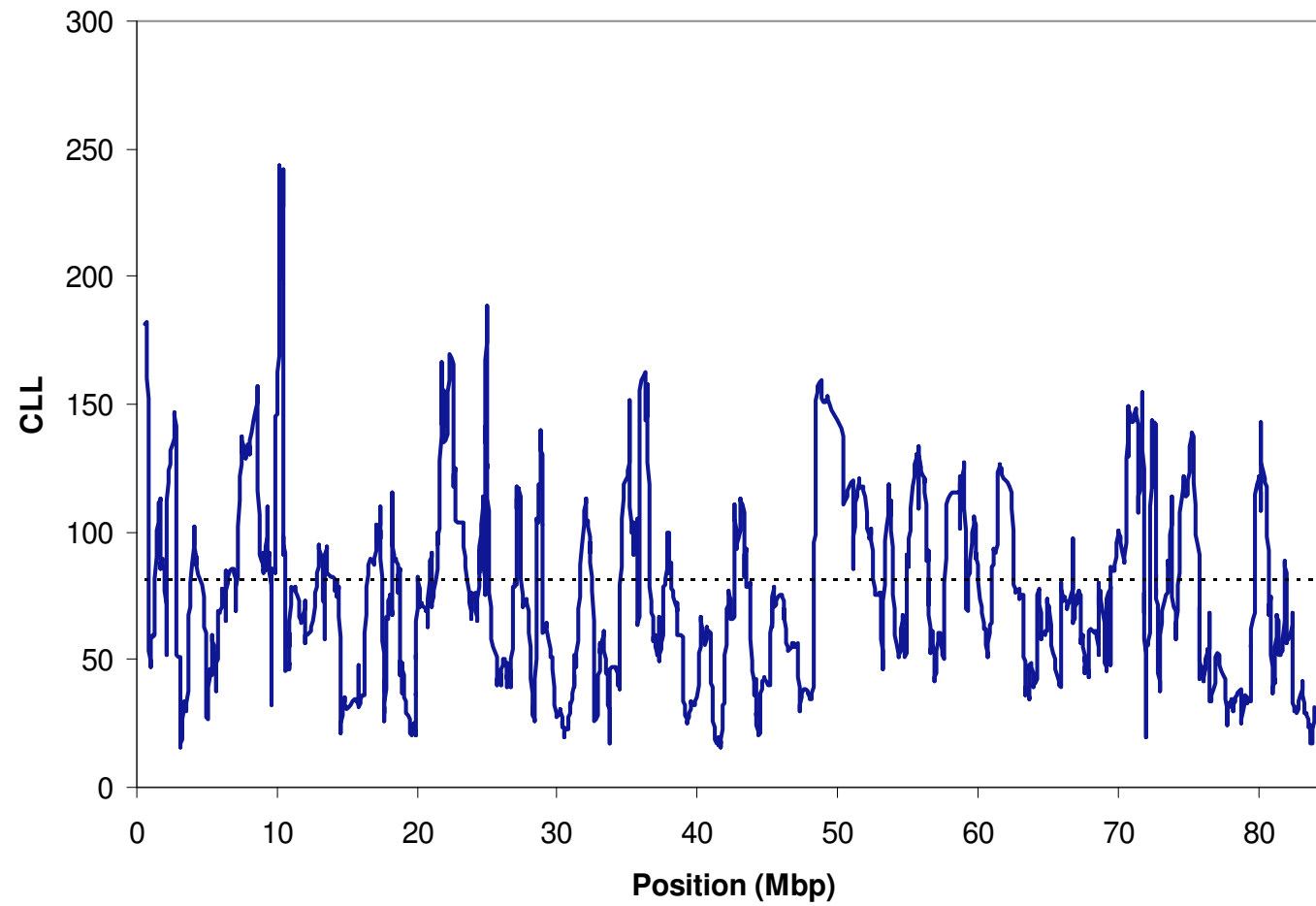


FIGURE S13.—Composite log-likelihood (CLL) for dairy breeds on BTA13. (----- $P < 0.01$ threshold)

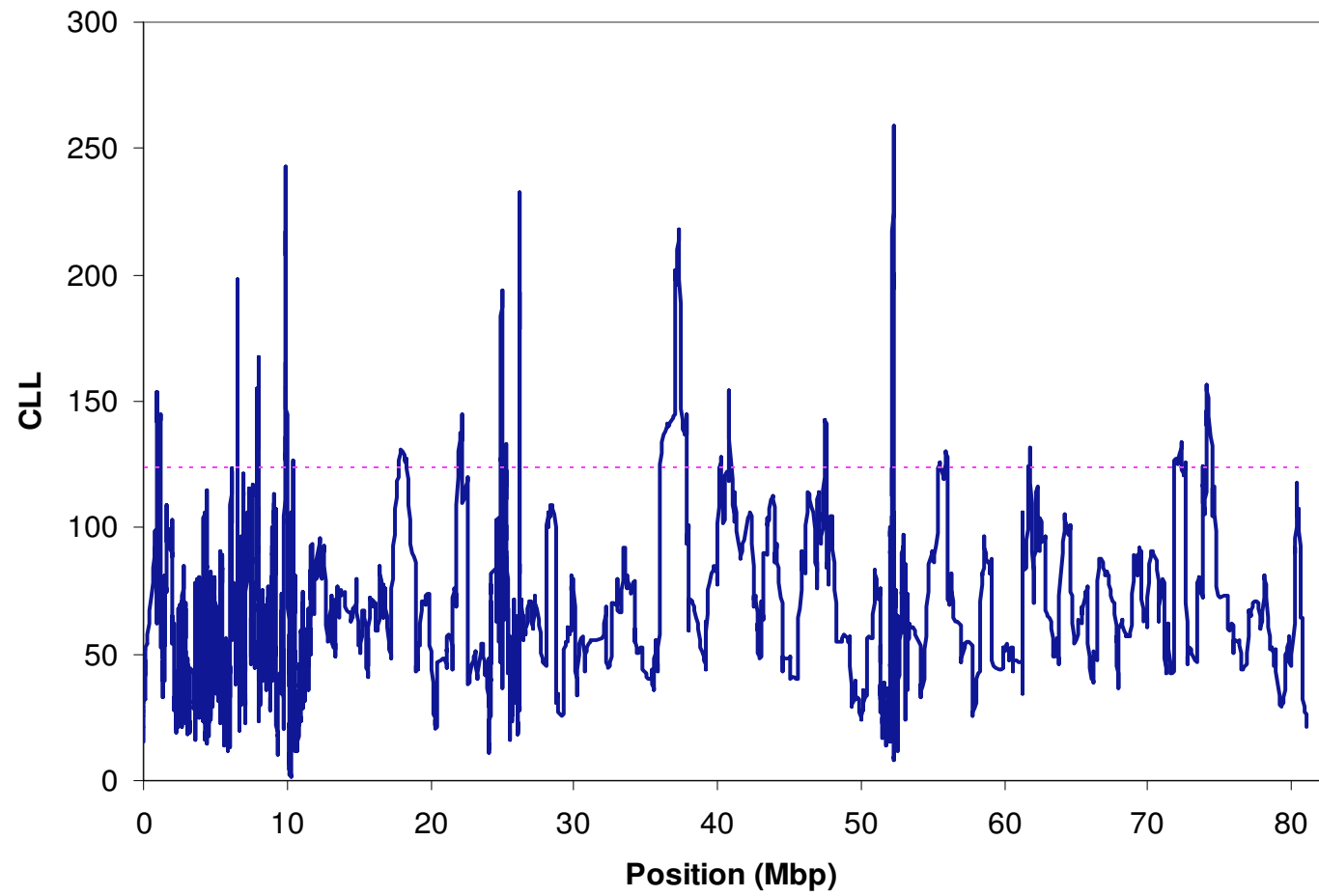


FIGURE S14.—Composite log-likelihood (CLL) for dairy breeds on BTA14. (----- P < 0.01 threshold)

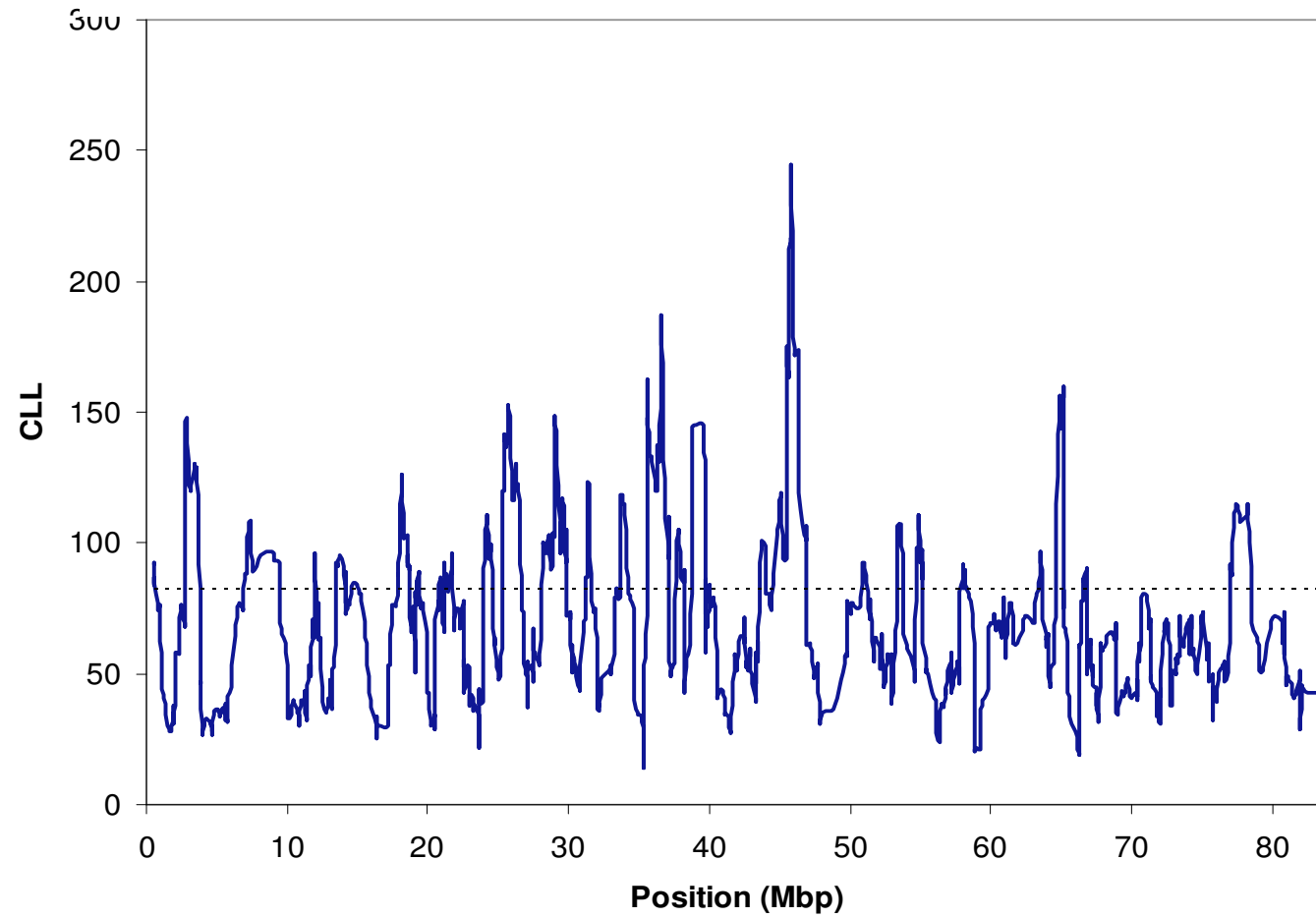


FIGURE S15.—Composite log-likelihood (CLL) for dairy breeds on BTA15. (----- $P < 0.01$ threshold)

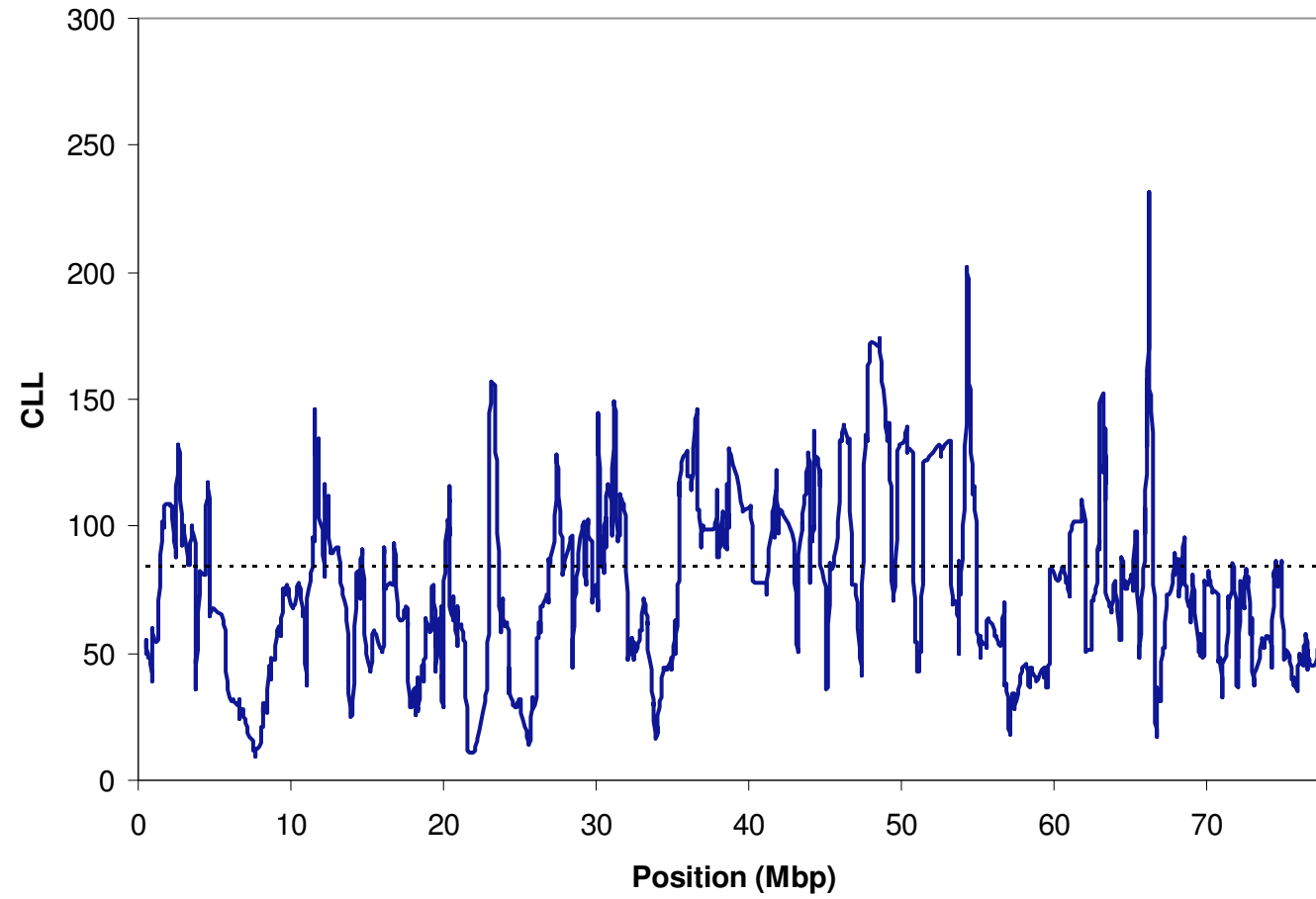


FIGURE S16.—Composite log-likelihood (CLL) for dairy breeds on BTA16. (----- $P < 0.01$ threshold)

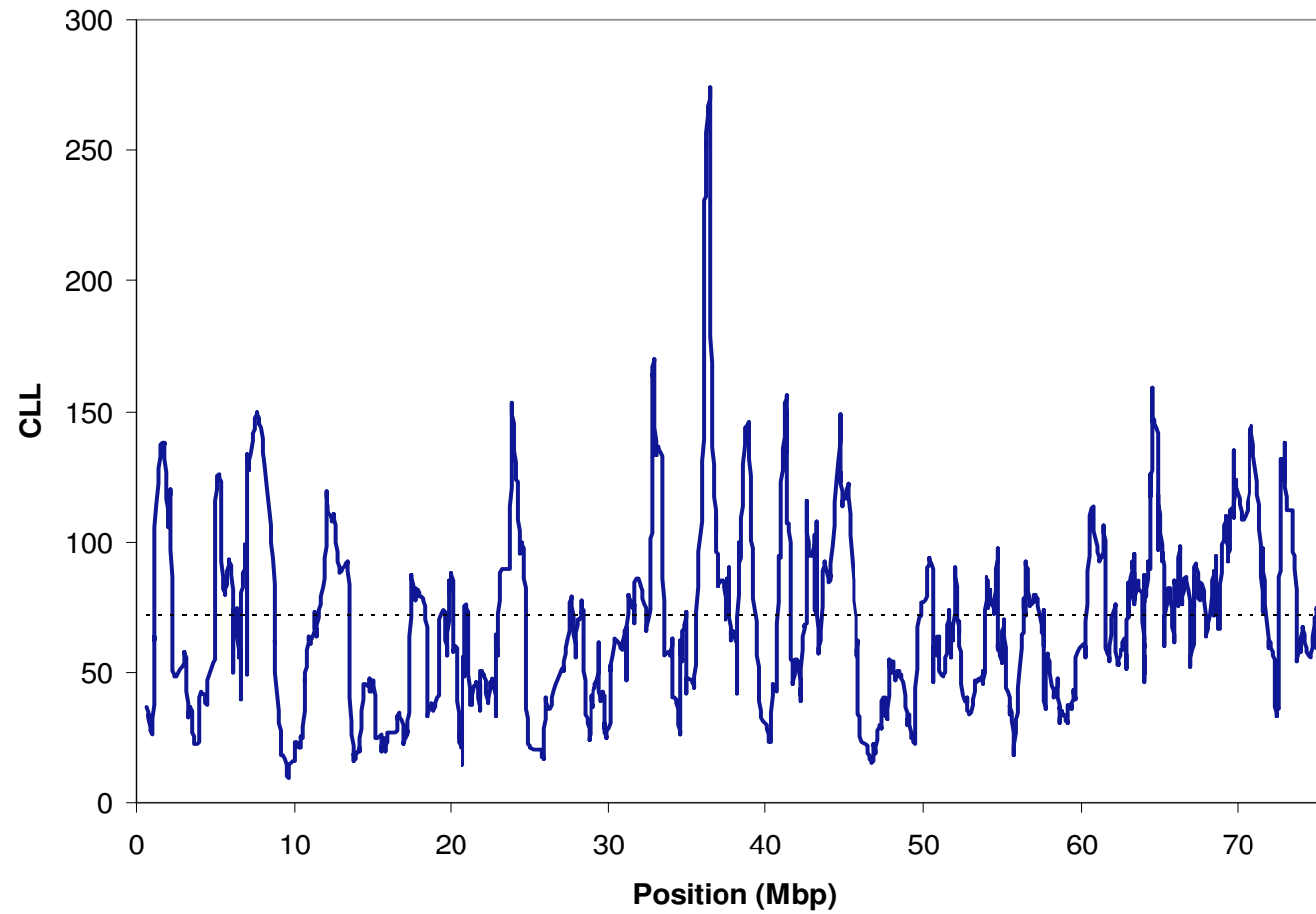


FIGURE S17.—Composite log-likelihood (CLL) for dairy breeds on BTA17. (----- $P < 0.01$ threshold)

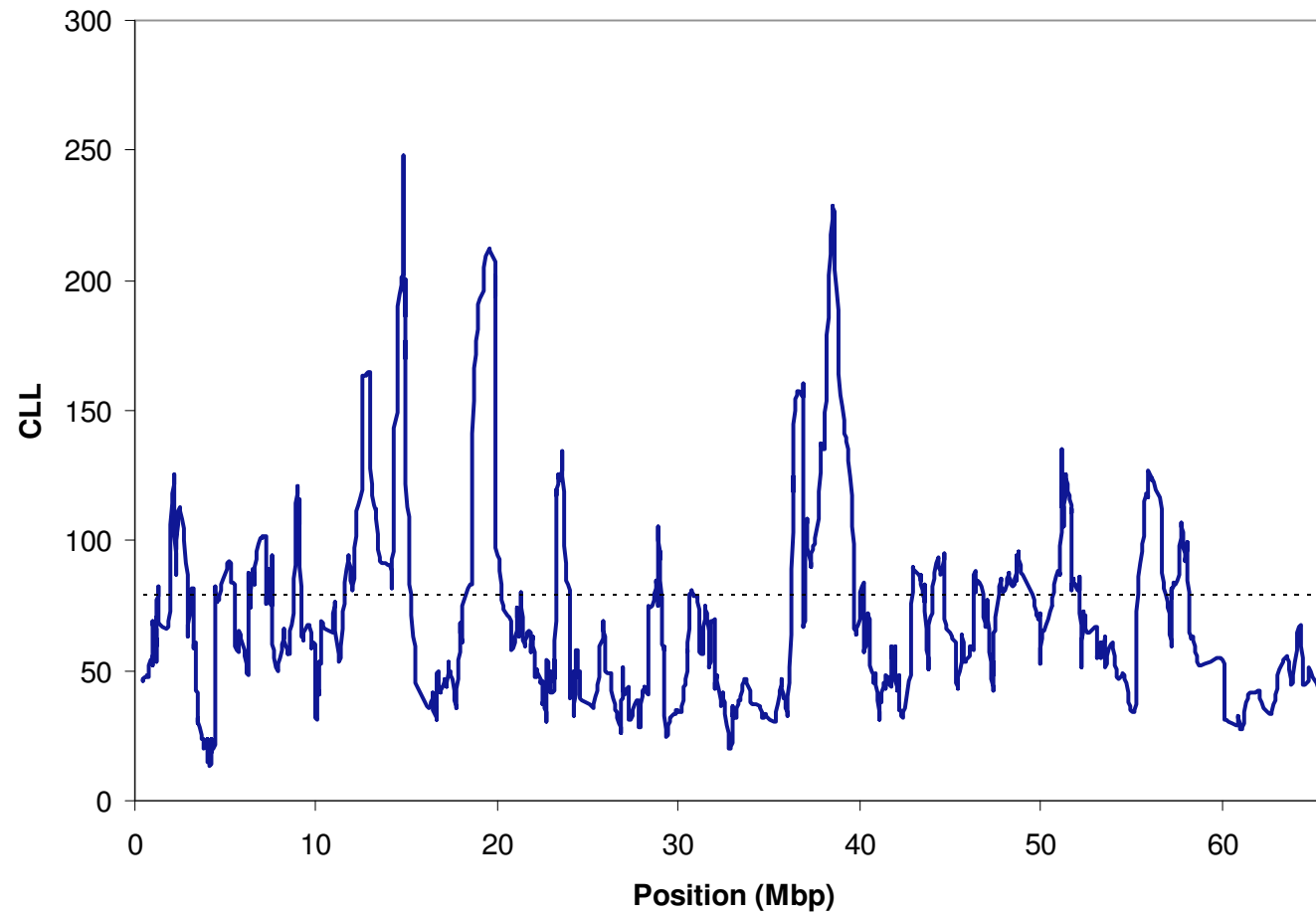


FIGURE S18.—Composite log-likelihood (CLL) for dairy breeds on BTA18. (----- $P < 0.01$ threshold)

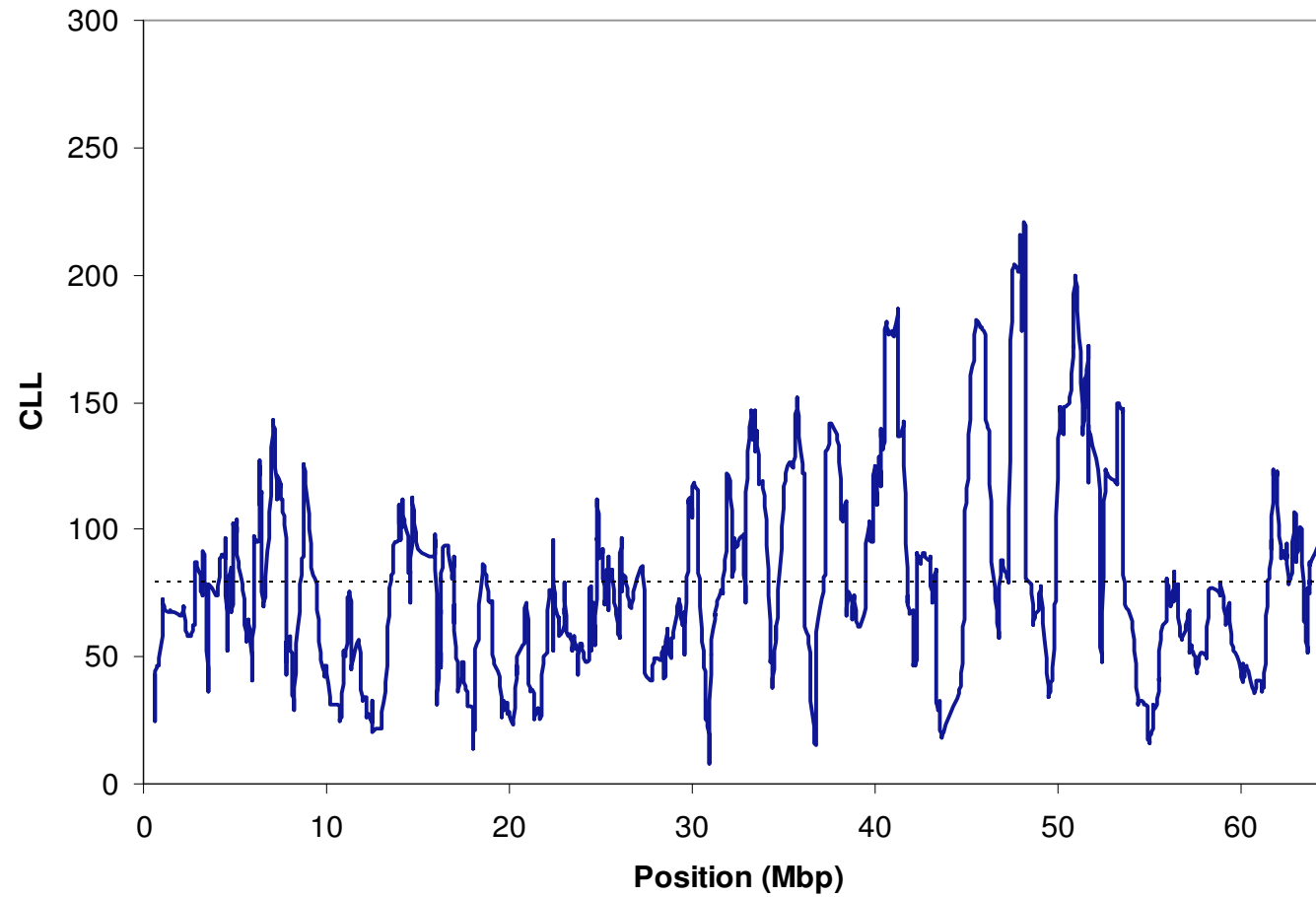


FIGURE S19.—Composite log-likelihood (CLL) for dairy breeds on BTA19. (----- $P < 0.01$ threshold)

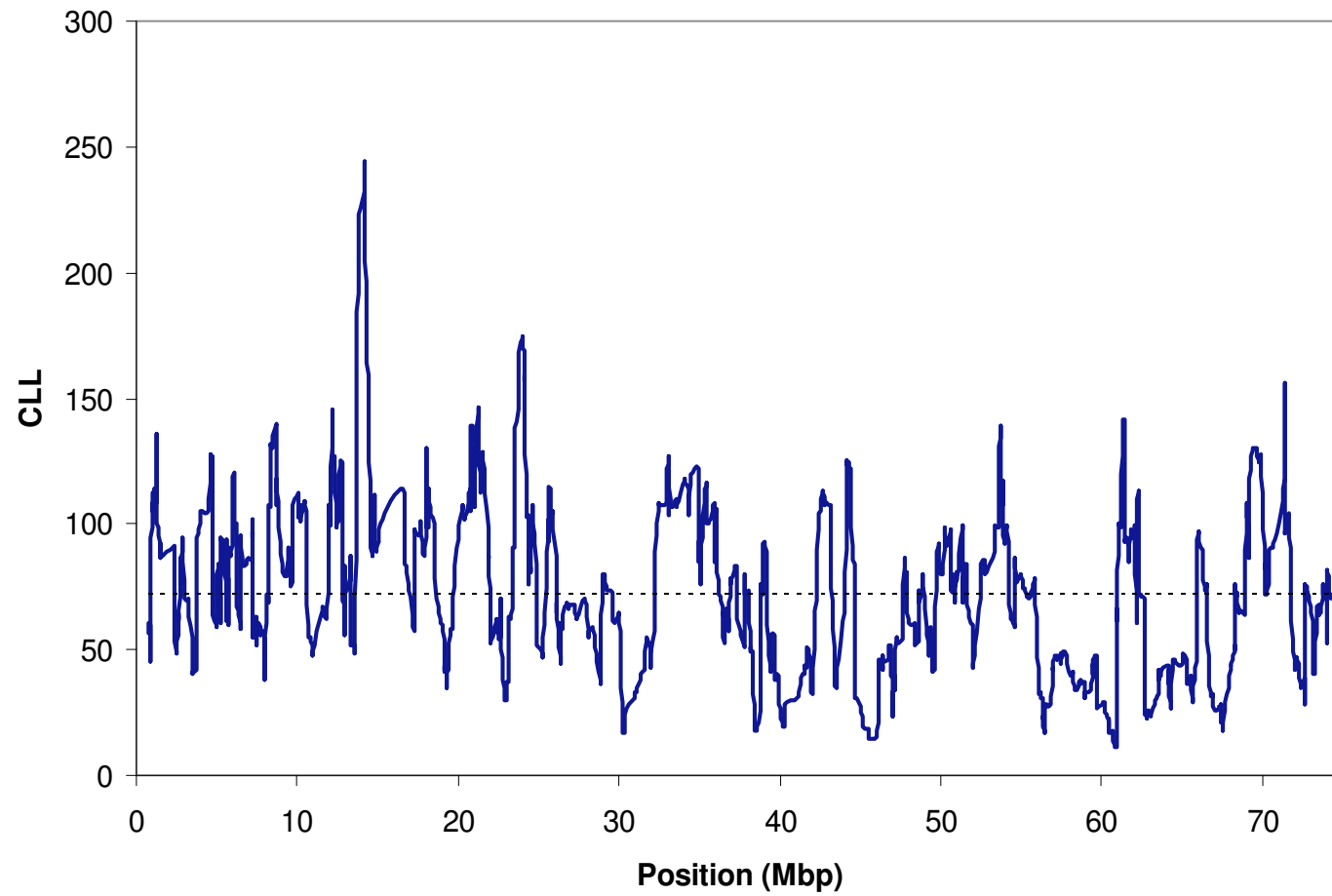


FIGURE S20.—Composite log-likelihood (CLL) for dairy breeds on BTA20. (----- $P < 0.01$ threshold)

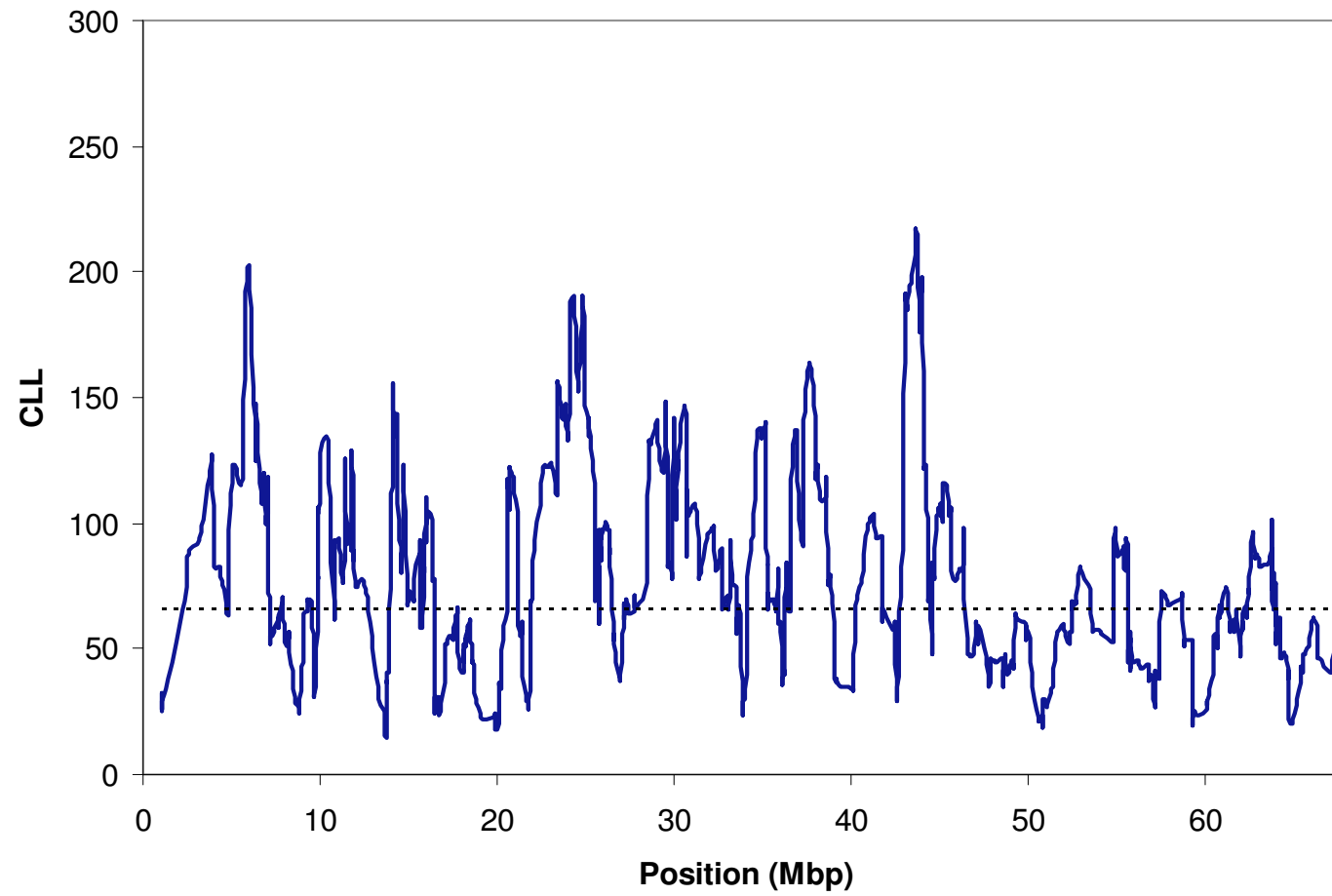


FIGURE S21.—Composite log-likelihood (CLL) for dairy breeds on BTA21. (----- $P < 0.01$ threshold)

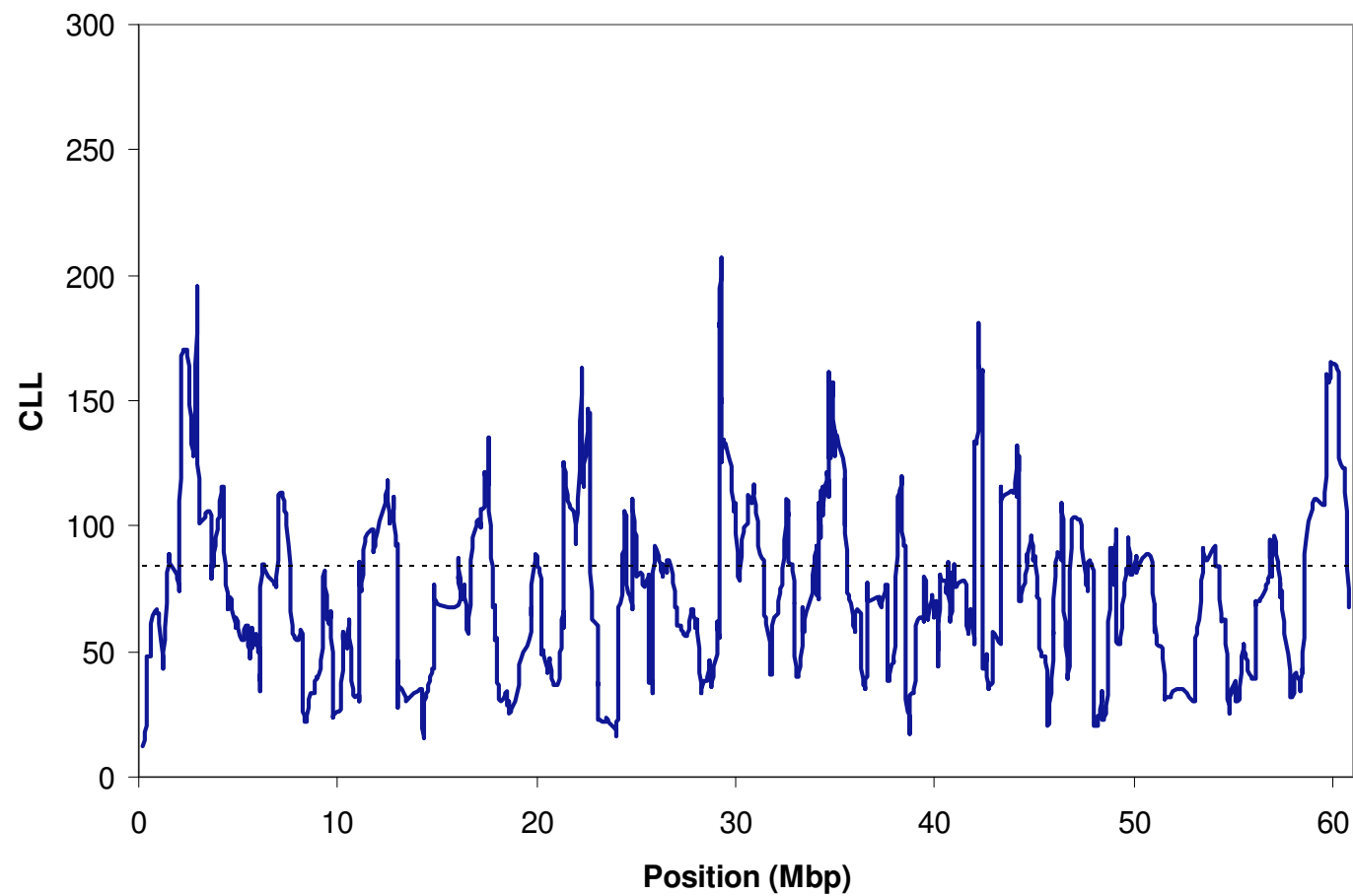


FIGURE S22.—Composite log-likelihood (CLL) for dairy breeds on BTA22. (----- $P < 0.01$ threshold)

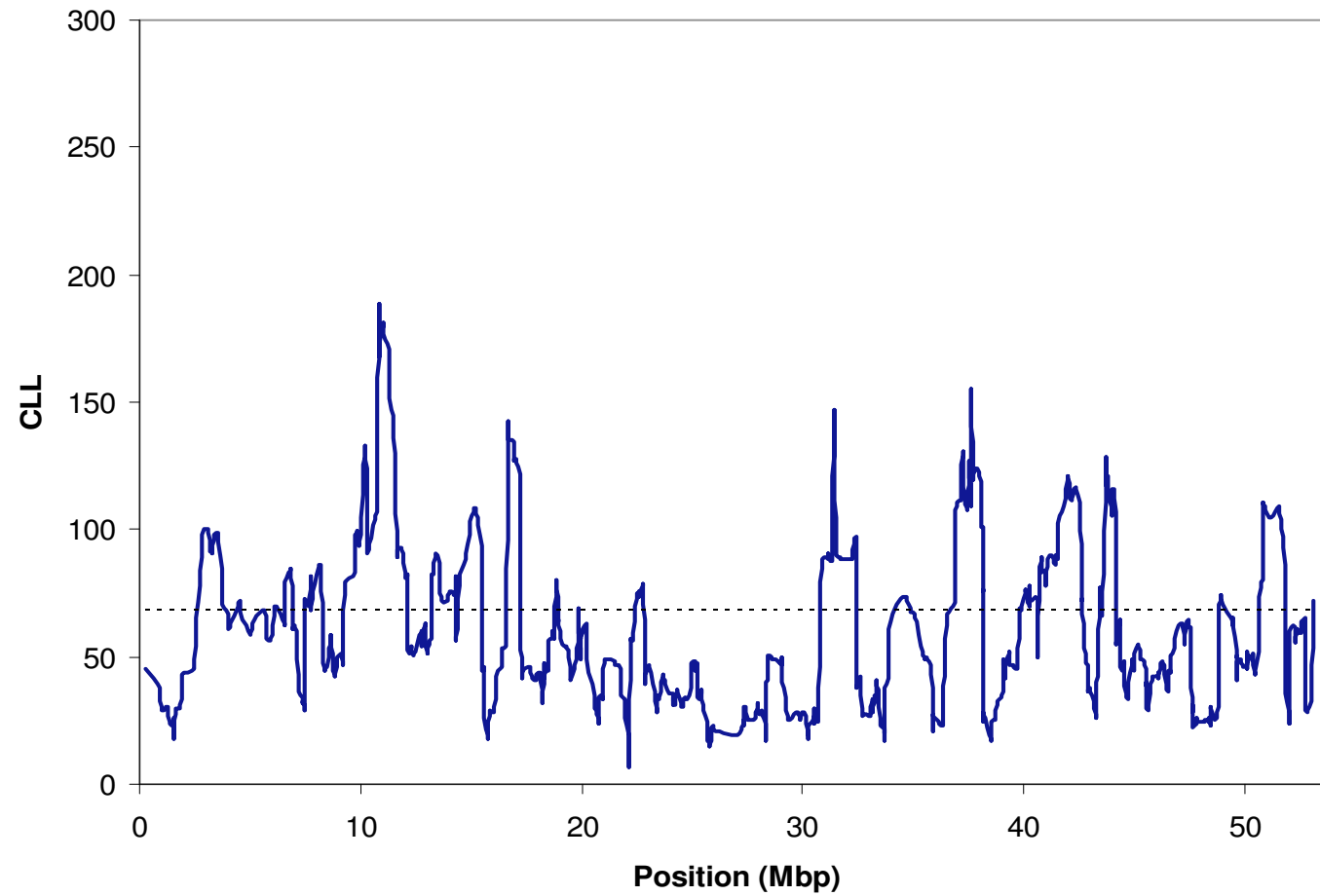


FIGURE S23.—Composite log-likelihood (CLL) for dairy breeds on BTA23. (----- $P < 0.01$ threshold)

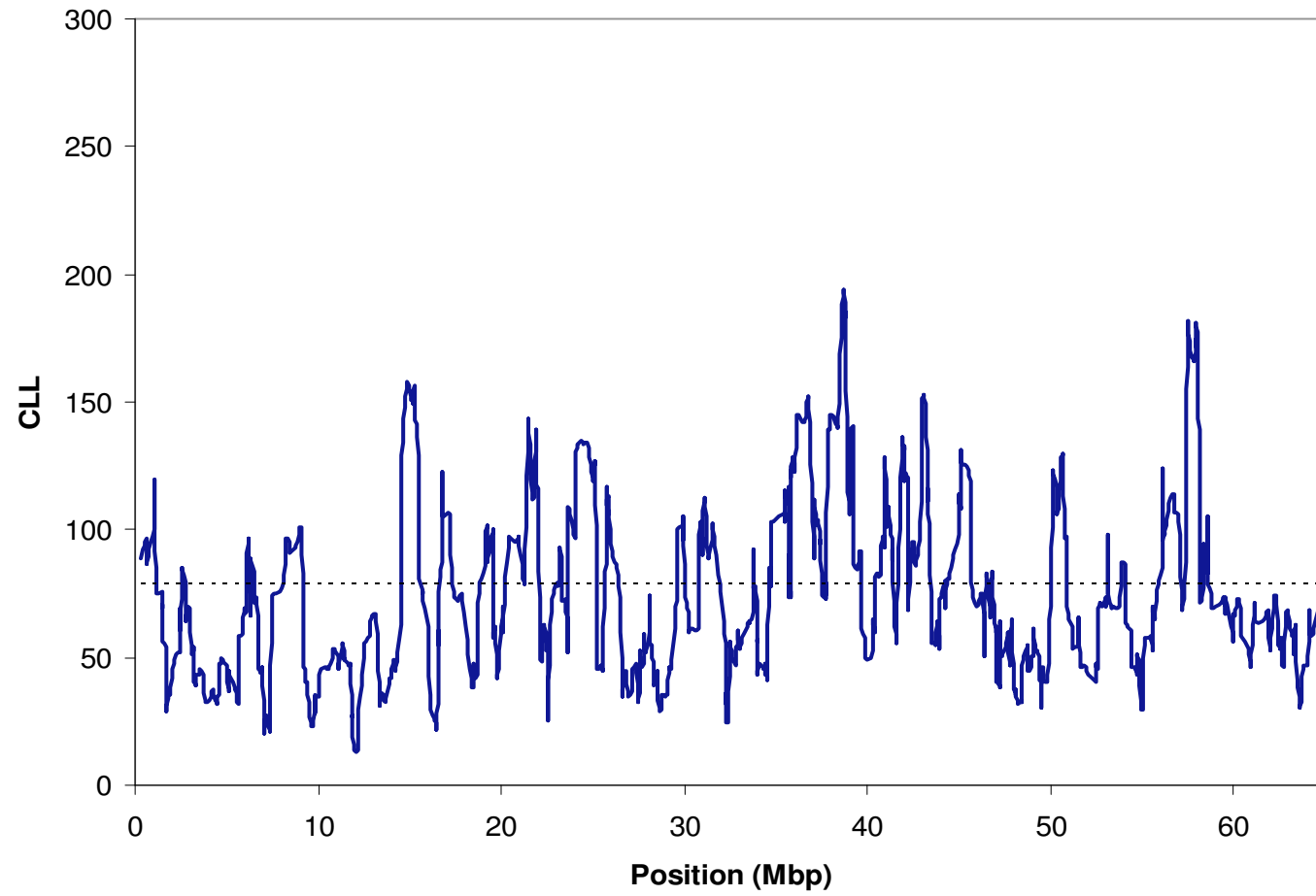


FIGURE S24.—Composite log-likelihood (CLL) for dairy breeds on BTA24. (----- $P < 0.01$ threshold)

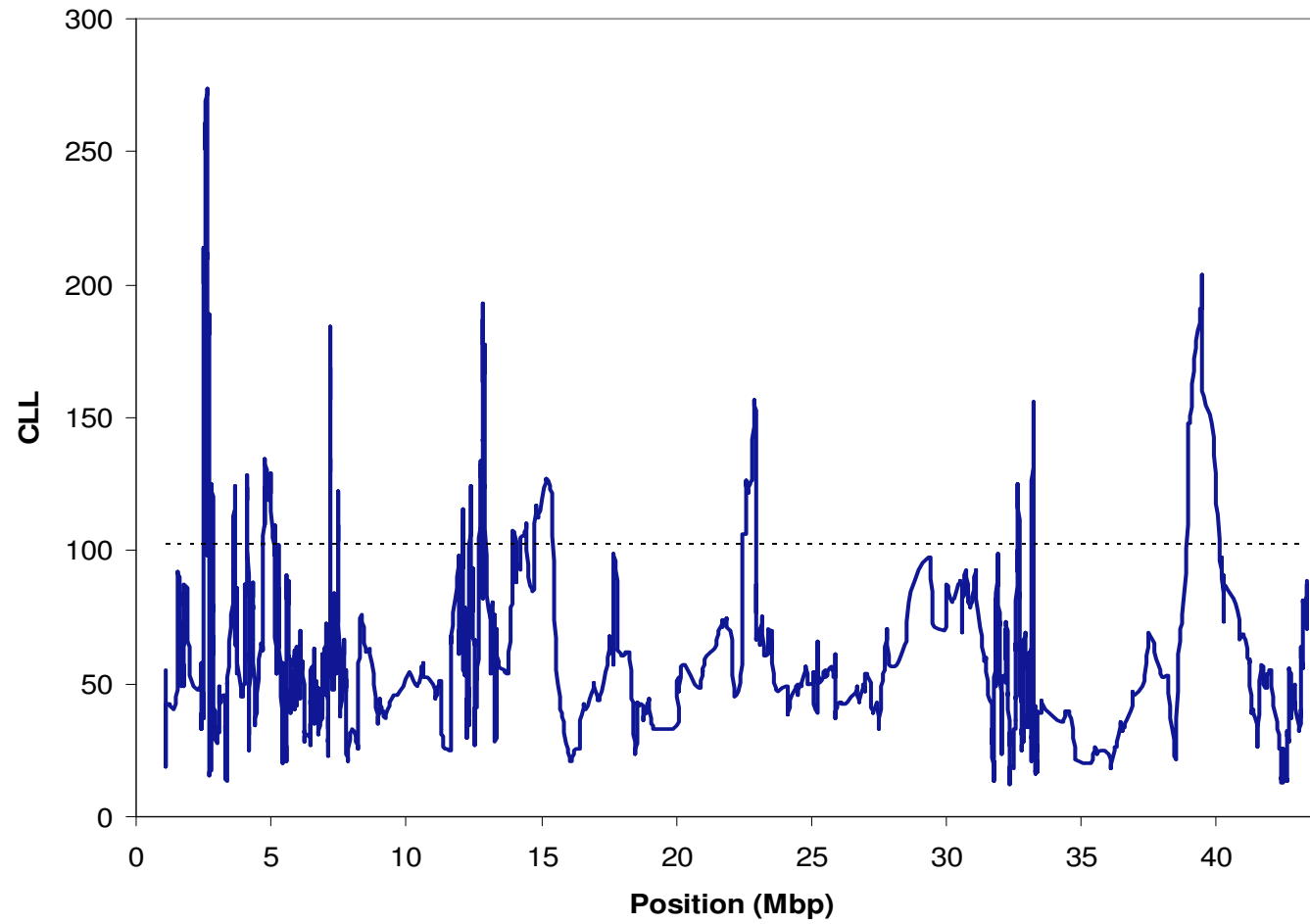


FIGURE S25.—Composite log-likelihood (CLL) for dairy breeds on BTA25. (----- $P < 0.01$ threshold)

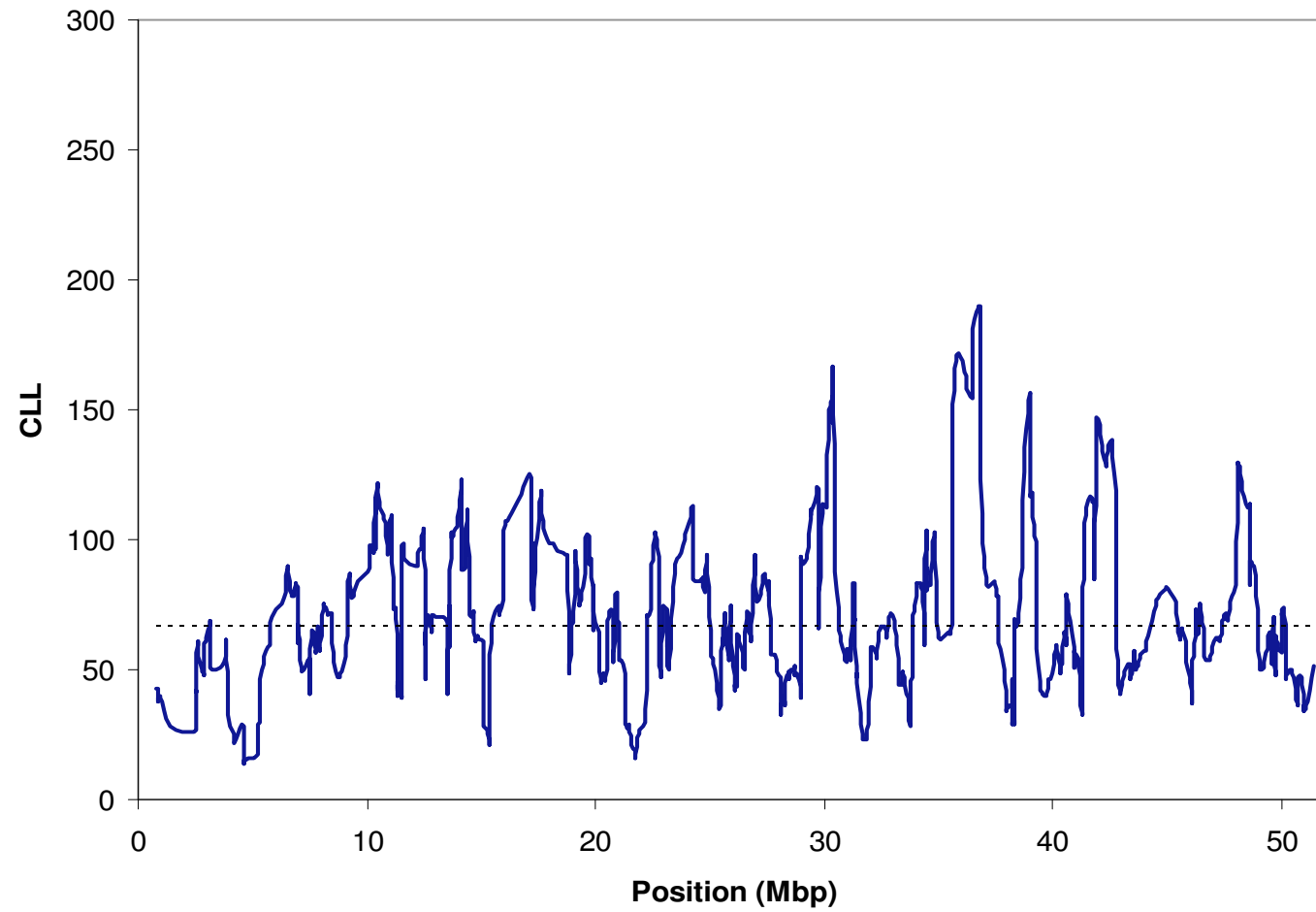


FIGURE S26.—Composite log-likelihood (CLL) for dairy breeds on BTA26. (----- $P < 0.01$ threshold)

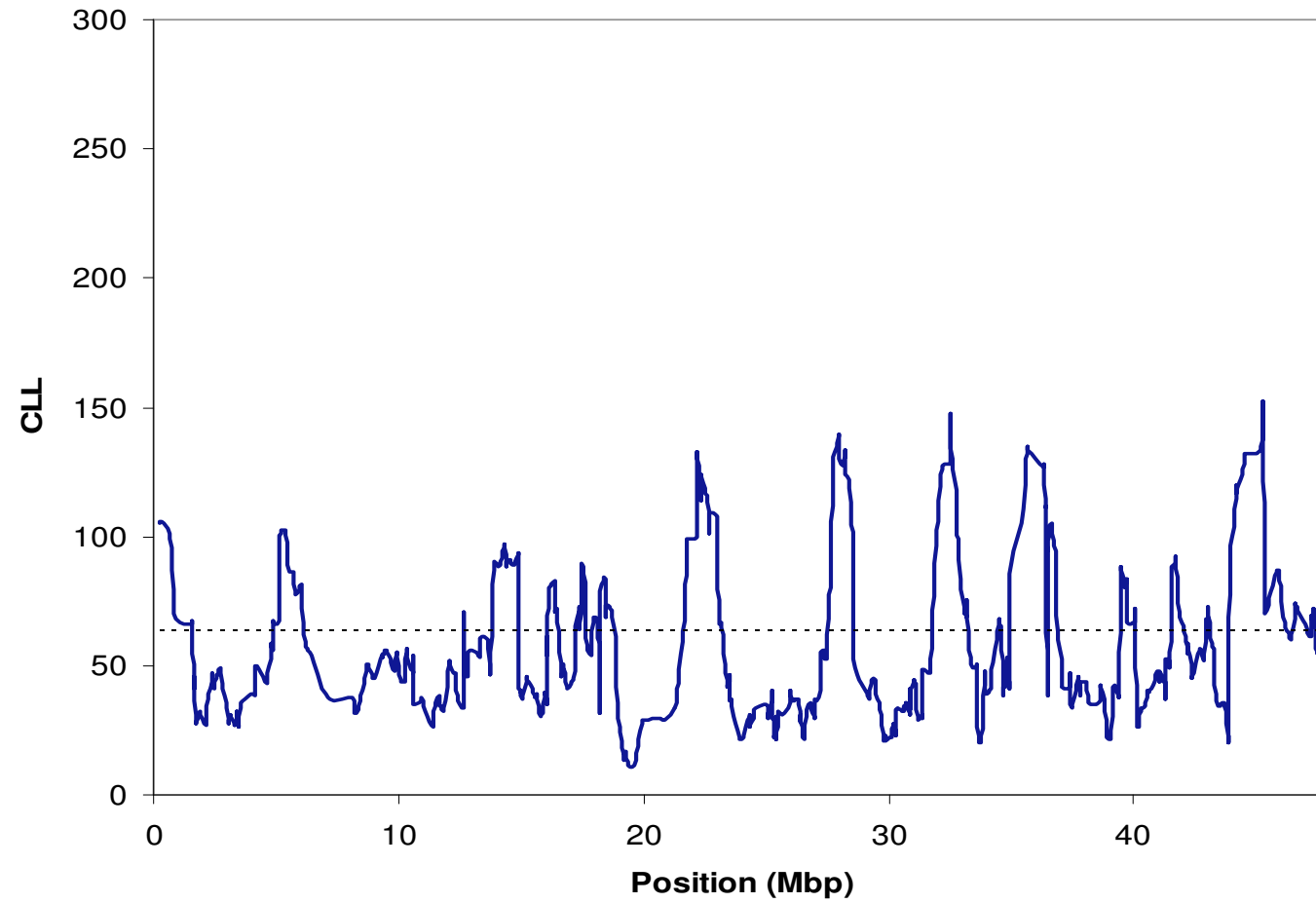


FIGURE S27.—Composite log-likelihood (CLL) for dairy breeds on BTA27. (----- $P < 0.01$ threshold)

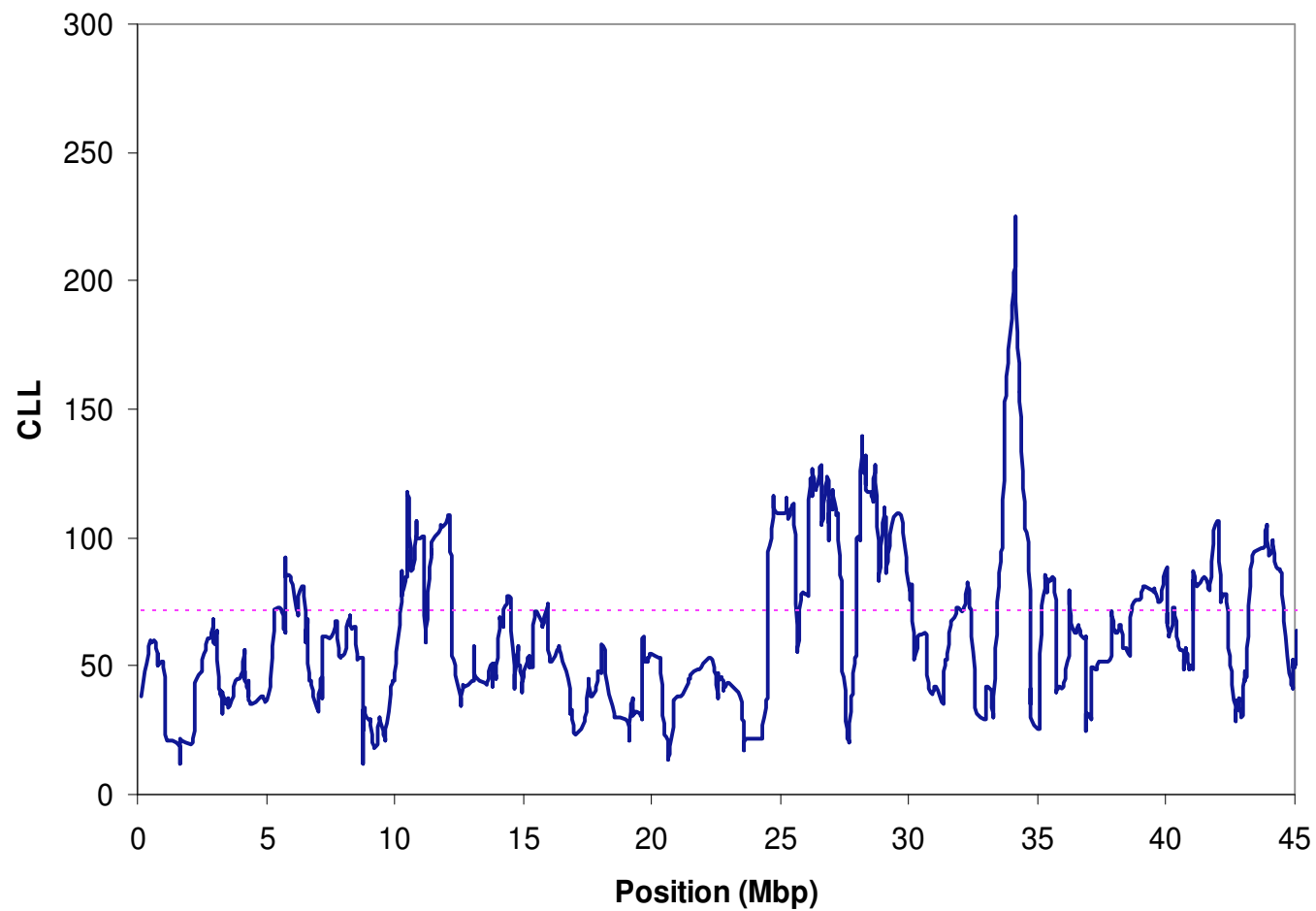


FIGURE S28.—Composite log-likelihood (CLL) for dairy breeds on BTA28. (----- $P < 0.01$ threshold)

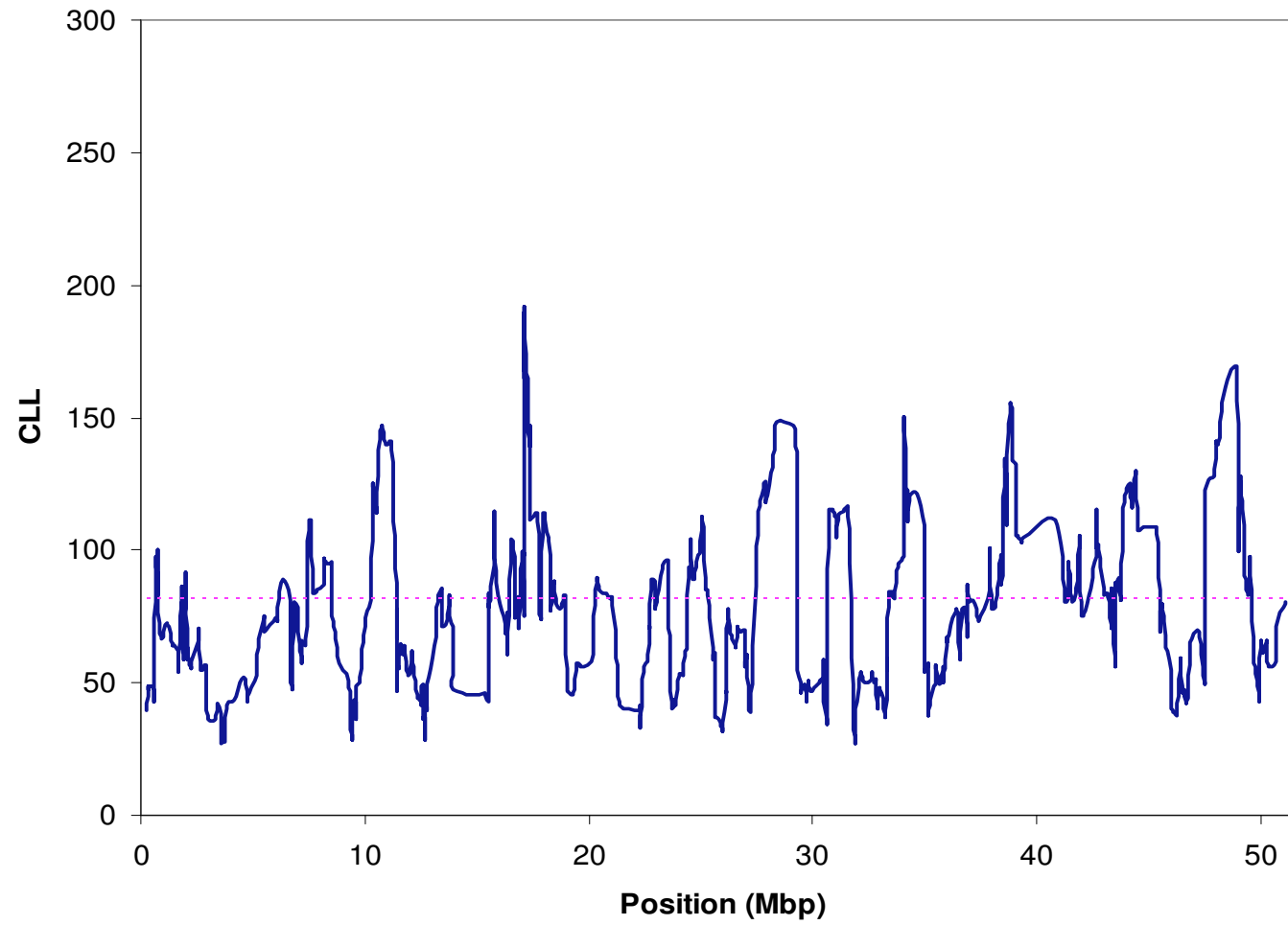


FIGURE S29.—Composite log-likelihood (CLL) for dairy breeds on BTA29. (----- $P < 0.01$ threshold)

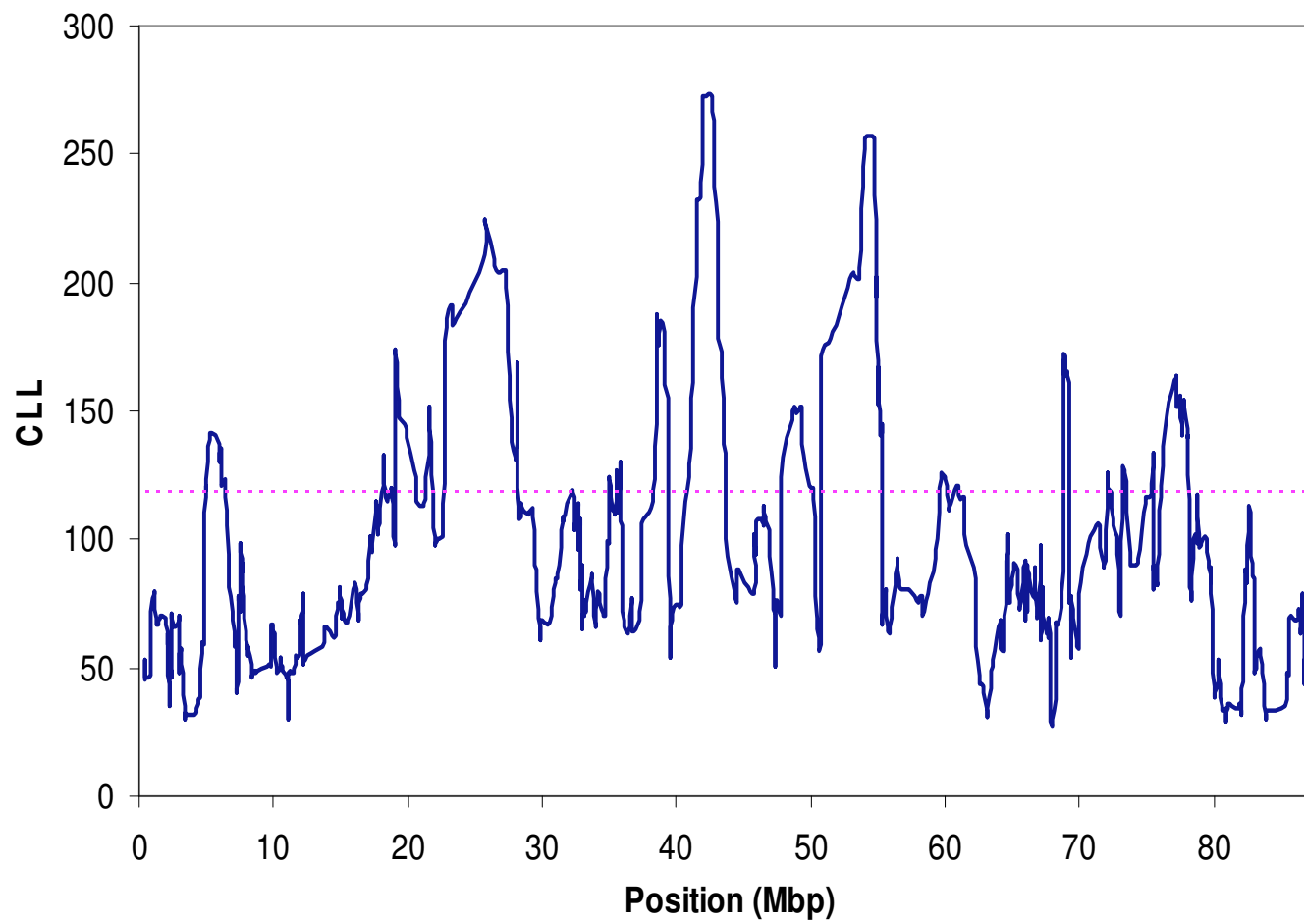


FIGURE S30.—Composite log-likelihood (CLL) for dairy breeds on the X chromosome. (----- $P < 0.01$ threshold)

TABLE S1**A sample of potassium channel related genes, their locations and the significance of CLL in their respective genomic regions**

Gene	Chromosome	Location (Mbp)	P-value ^a
KCNMB2 potassium large conductance calcium-activated channel, subfamily M, beta member 2	1	90497302 to 90533714	<0.01
LOC539609 similar to calcium-activated potassium channel beta 3 subunit	1	90178175 to 90189020	<0.05
KCNJ6 potassium inwardly-rectifying channel, subfamily J, member 6	1	153203304 to 153302300	<0.01
KCTD18 potassium channel tetramerisation domain containing 18	2	93326843 to 93347668	<0.01
LOC528741 similar to Potassium voltage-gated channel subfamily KQT member 4	3	112355459 to 112397271	<0.01
KCTD17 potassium channel tetramerisation domain containing 17	5	81355293 to 81365551	<0.01
KCTD8 potassium channel tetramerisation domain containing 8	6	65617020 to 65880230	<0.01
KCNIP4 Kv channel interacting protein 4	6	41419999 to 41522915	<0.01
KCTD9 potassium channel tetramerisation domain containing 9	8	76553678 to 76634800	<0.01
KCNN2 potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2	10	2774232 to 2941240	<0.01
KCNK10 potassium channel, subfamily K, member 10	10	102914246 to 103002706	N.S.
LOC787307 similar to potassium channel, subfamily K, member 13	10	104750054 to 104868308	<0.01
KCNT1 potassium channel, subfamily T, member 1	11	107250180 to 107296127	<0.01
KCMF1 potassium channel modulatory factor 1	11	51702094 to 51734247	<0.01
KCNRG potassium channel regulator	12	18849412 to 18854893	<0.01
KCTD12 potassium channel tetramerisation domain containing 12	12	52443570 to 52445112	N.S. ^b
KCNV1, potassium channel, subfamily V, member 1	14	52285517 to 52291616	<0.01
KCNK9 potassium channel, subfamily K, member 9	14	2992665 to 2993414	N.S.
KCNC1 potassium voltage-gated channel, Shaw-related subfamily, member 1	15	33443470 to 33478009	<0.01
KCNAB2 potassium voltage-gated channel, shaker-related subfamily, beta member 2	16	44432964 to 44488939	<0.01
KCNK2 potassium channel, subfamily K, member 2	16	66195133 to 66332411	<0.01
KCTD10 potassium channel tetramerisation domain containing 10	17	66989274 to 67018624	<0.01
KCTD15 potassium channel tetramerisation domain containing 15	18	43672614 to 43687280	<0.01
KCNN4 potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4	18	51704024 to 51717711	<0.01
KCNK6 potassium channel, subfamily K, member 6	18	47597197 to 47605452	<0.01

KCTD11 potassium channel tetramerisation domain containing 11	19	27430450 to 27433058	<0.01
KCNMB1 potassium large conductance calcium-activated channel, subfamily M, beta member 1	20	879685 to 892344	<0.01
KCTD6 potassium channel tetramerisation domain containing 6	22	43720967 to 43723995	<0.01
KCTD20 potassium channel tetramerisation domain containing 20	23	10658756 to 10694823	<0.01
KCNK17 potassium channel, subfamily K, member 17	23	13661306 to 13673969	<0.01
KCTD1 potassium channel tetramerisation domain containing 1	24	31526407 to 31532051	<0.01
KCTD1 potassium channel tetramerisation domain containing 1	24	31252383 to 31331532	<0.01
KCTD5 potassium channel tetramerisation domain containing 5	25	2655433 to 2676088	<0.01
KCTD13 potassium channel tetramerisation domain containing 13	25	28157084 to 28170312	<0.05
KCTD7 potassium channel tetramerisation domain containing 7	25	29978110 to 29988583	<0.05
KCNK18 potassium channel, subfamily K, member 18	26	37920930 to 37933177	N.S.
LOC524144 similar to potassium channel, subfamily U, member 1	27	34349739 to 34419158	<0.01
KCNK4 potassium channel, subfamily K, member 4	29	44377105 to 44387219	<0.01
KCTD21 potassium channel tetramerisation domain containing 21	29	18831873 to 18850491	<0.01
KCND1 potassium voltage-gated channel, Shal-related subfamily, member 1	X	55447620 to 55453611	<0.01

^a genome-wide

^b P < 0.01 in the Holstein breed

TABLE S2

Genomic locations (Chromosome, location of first and last SNP in windows and center SNP of window with greatest CLL) of SNP windows with significant CLL ($P < 0.01$, genome-wide) in three dairy breeds.

Chromosome	Start SNP	End SNP	Location of Greatest CLL (bp)
1	73492000	74862396	74635914
2	97907848	98533769	98350061
3	44433212	44983850	44433721
3	94928170	96195939	95699976
3	104551311	105634768	105516858
4	13168178	13607786	13171355
4	116130595	117126810	117074929
5	26855330	27767731	27358666
5	29246452	30554866	29886837
5	72095403	73062135	72588495
6	38223328	38301284	38233961
6	72361646	72806193	72801968
6	73014776	73089763	73081515
7	42147869	43508330	43191723
7	54879866	55554527	55241236
7	87691601	87785340	87784971
8	59915903	60838709	60573312
8	62653224	63495631	62677841
8	103552067	104972023	104695202
8	110698964	111986506	110868569
9	61529984	62077535	62003379
9	93158942	94535491	94365053
11	3081133	3944051	3156303
11	13907535	14359910	14156735
11	27098047	27938345	27363167
11	99936121	100288369	100428971
11	100609317	101622893	101237153
13	17970190	18620789	18253417
13	47952596	49438058	48808020
15	4524164	5511180	5024958
15	20854382	21699914	21252577
16	66176557	66663719	66232833
16	72012474	72290010	72055590
17	7043203	9062498	7692717
17	37646557	38959892	38959892
17	40822701	41375934	41268654
17	74934058	75634272	75040960
18	6650248	7270967	7209080
18	14111894	14857895	14857880

18	36952233	37573693	37107399
19	24714049	25232094	24840946
19	32837903	33567180	33263855
20	1064802	2353627	1226415
20	3544207	4694229	4627110
20	13649048	14814996	14123694
20	23160387	24112262	24019852
20	24359518	24919337	24666139
20	26897274	28458537	27855634
20	33559072	35062871	34953908
20	39393523	39946848	40263756
21	9837926	10619360	10408616
21	11820092	12649861	11820092
21	14151339	14320140	12649861
21	24827201	25180217	24827395
21	36564029	38217250	37659445
21	61343351	61961853	61592669
23	9243597	10694782	10171362
23	14779113	15458536	15148464
23	22317454	22872332	22575044
23	36897757	37801219	37558866
24	21489085	22432882	21489085
24	40765006	41411977	40979414
24	54892828	56094597	56265972
24	57224647	58173539	57520410
24	58206568	59493016	58588510
25	2685017	2745210	2701126
26	9275306	10962162	10441938
26	11500747	12530395	12496998
26	35419392	37460372	36779948
26	43849120	45492807	44975793
27	266427	1676820	266630
27	3954652	4816213	4622510
27	4833631	5535961	5367942
27	12474380	13175592	12637209
27	14415472	15071069	14856065
27	32180919	33185899	32492485
27	46709833	48228143	47366352
29	38611283	38775982	39310845

TABLE S3

Genomic locations (Chromosome, location of first and last SNP in windows and center SNP of window with greatest CLL) of SNP windows with significant CLL ($P < 0.25$, genome wide) in all five dairy breeds

Chromosome	Start SNP	End SNP	Location of Greatest CLL (bp)
1	69915599	70265608	70163287
1	109935324	111953500	111188614
2	64218856	64792978	64640561
4	8879649	10574834	10541198
5	27989563	29195425	28624790
5	33793313	35644135	33834359
5	73062135	74052334	73634208
5	99515505	100475202	99998862
5	105874101	107789222	107583301
6	63097961	65672360	65061093
7	26478900	28581752	26567785
8	102483790	103230023	102680398
8	109596861	110698964	110444685
9	24700523	26153478	26054472
9	60476473	60969754	60819485
9	77364393	78193820	77629138
9	98619640	100150571	99619205
10	105580939	106191883	105996383
11	17998250	19466646	18795224
11	70453484	70881571	70566731
13	61085727	63245599	61619058
15	6488096	9992399	7426452
15	25296841	26542437	25767576
15	35603443	37051045	36632901
15	38723497	39760998	39618626
15	64604389	65208287	65146035
16	22886605	23784394	23133906
18	50146867	51734876	51189694
19	4854373	5614645	5075583
19	46014590	47984865	47897746
20	60977058	62089345	61351502
20	71369712	71530743	71369875
21	33032960	33844730	33251422
21	33852145	35259414	35149769
23	50641847	51839638	51514190
24	16734137	17601902	16734288
24	44978575	45664478	45090507
24	59589744	60914533	60272305
26	3901836	4624902	4494144

27	27597833	28549227	27942513
27	43906621	45458022	45238475
29	7145531	9221822	7628919
29	14798487	15536124	15359492
29	42351793	43111752	42690175