

RS1949 - AutoMap (HG38)

RS1949 HomRegions.tsv

#Chr	Begin	End	Size(Mb)	Nb_variants		Percentage_homozygosity
chr1	13475969		16576166	3.10	140	93.57
chr1	16948577		21424649	4.48	219	99.09
chr1	21426289		37540758	16.11	509	96.46
chr1	111285127		120449120	9.16	220	95.00
chr1	148952762		157519726	8.57	477	95.81
chr2	41404	3388304	3.35 62	95.16		
chr2	15308187		31234951	15.93	380	98.95
chr2	105854871		107826872	1.97	36	88.89
chr2	151617472		152625318	1.01	29	89.66
chr2	181494865		183130387	1.64	34	88.24
chr3	157569553		158732176	1.16	32	96.87
chr4	337904	5525281	5.19 215	98.60		
chr4	8606907	9887445	1.28 48	95.83		
chr4	107645048		108743664	1.10	30	90.00
chr4	125476166		128848913	3.37	29	89.66
chr5	3600022	7690641	4.09 43	100.00		
chr5	7757602	69914070	62.16	745	97.32	
chr5	136429105		138782249	2.35	65	92.31
chr5	154786453		159084571	4.30	58	94.83
chr8	60584391		73071753	12.49	153	95.42
chr8	106770107		116771736	10.00	46	91.30
chr8	124010745		144994708	20.98	577	99.13
chr9	109532879		133205684	23.67	796	97.74
chr9	133208307		135521527	2.31	117	96.58
chr9	135521625		138177023	2.66	290	97.24
chr11	49124286		55554735	6.43	81	96.30
chr11	124158584		134318957	10.16	290	95.86
chr12	4604869	9294381	4.69 311	96.46		
chr12	9294836	11030977	1.74	170	97.06	
chr12	11049290		17360265	6.31	143	97.20
chr12	26695730		27958386	1.26	44	88.64
chr14	81108661		87992936	6.88	42	97.62
chr14	91215544		105624321	14.41	536	98.32
chr15	42142056		43186313	1.04	54	88.89
chr15	68711532		71243119	2.53	50	90.00
chr16	7665019	8779636	1.11 47	91.49		
chr16	11927475		14769992	2.84	36	91.67
chr16	15016220		16362784	1.35	54	96.30
chr16	16398523		23424963	7.03	161	94.41
chr16	25257233		27778579	2.52	26	92.31
chr17	57110293		60008999	2.90	71	94.37
chr17	60009142		74252176	14.24	334	97.31
chr18	75286931		80169229	4.88	69	100.00
chr19	6744892	8889393	2.14 241	95.85		
chr19	8899175	14396290	5.50	332	96.69	
chr19	14396533		15458567	1.06	89	97.75
chr19	22464577		24162481	1.70	31	93.55
chr20	1313429	2558741	1.25 58	94.83		

INFO: 326.4 Mb are in Homozygous Regions (autosomal chromosomes)

AutoMap v1.0 used for analysis

Variant filtering parameters used: DP=8, percaltlow=.25, percalthigh=.75, binomial=.000001, maxgap=10

Other parameters used: window=7, windowthres=5, minsize=1, minvar=25, minperc=88, chrX=No, extend=1

RS1949 - Homozygosity Mapper

score	chr	from (bp)	to (bp)	from SNP	to SNP	build 37	
<i>broad - use this when you expect some genetic heterogeneity</i>							
80	1	15638530	16057052	n/a	n/a	region	genotypes
80	1	17616259	19325637	n/a	n/a	region	genotypes
80	1	23755796	28490843	n/a	n/a	region	genotypes
80	1	155732233	157515771	n/a	n/a	region	genotypes
80	2	15536579	26440319	n/a	n/a	region	genotypes
80	2	28922797	31234951	n/a	n/a	region	genotypes
80	4	1807383	5525281	n/a	n/a	region	genotypes
80	5	7757602	21481665	n/a	n/a	region	genotypes
80	5	37239580	41805423	n/a	n/a	region	genotypes
80	5	51384403	56959540	n/a	n/a	region	genotypes
80	6	32052936	32522036	n/a	n/a	region	genotypes
80	6	32589829	32745710	n/a	n/a	region	genotypes
80	8	133039974	145003654	n/a	n/a	region	genotypes
80	9	114324974	122093180	n/a	n/a	region	genotypes
80	9	131264726	132271888	n/a	n/a	region	genotypes
80	9	133228422	134850172	n/a	n/a	region	genotypes
80	9	135521625	137102909	n/a	n/a	region	genotypes
80	11	125582325	134184820	n/a	n/a	region	genotypes
80	12	4685324	6960259	n/a	n/a	region	genotypes
80	12	9312232	10882381	n/a	n/a	region	genotypes
80	12	12094987	18081163	n/a	n/a	region	genotypes
80	14	95126822	99707755	n/a	n/a	region	genotypes
80	14	100568319	103726947	n/a	n/a	region	genotypes
80	14	103726948	105624321	n/a	n/a	region	genotypes
80	17	68045755	73206638	n/a	n/a	region	genotypes
80	19	7116987	8125795	n/a	n/a	region	genotypes
80	19	8902324	9471416	n/a	n/a	region	genotypes
80	20	62286449	62671912	n/a	n/a	region	genotypes
79	5	34880645	36629427	n/a	n/a	region	genotypes
78	1	154273150	155237903	n/a	n/a	region	genotypes
76	1	113898903	117153461	n/a	n/a	region	genotypes
76	8	67258329	73030477	n/a	n/a	region	genotypes
76	9	129120427	129914769	n/a	n/a	region	genotypes
75	17	60924518	63601186	n/a	n/a	region	genotypes
74	11	49124286	55367959	n/a	n/a	region	genotypes
72	19	14765889	15227726	n/a	n/a	region	genotypes
70	12	7199209	8175287	n/a	n/a	region	genotypes
70	19	10140401	11147080	n/a	n/a	region	genotypes
68	1	19325638	20776009	n/a	n/a	region	genotypes
68	9	127695053	128153052	n/a	n/a	region	genotypes
67	19	13228607	14291566	n/a	n/a	region	genotypes
64	18	76880036	80177972	n/a	n/a	region	genotypes

RS2290 - AutoMap (HG38)

RS2290 HomRegions.tsv

#Chr	Begin	End	Size(Mb)	Nb_variants		Percentage_homozygosity
chr1	55052855		56792812	1.74	32	90.62
chr1	227508301		229654301	2.15	106	93.40
chr3	41249590		42321182	1.07	33	90.91
chr3	46811187		48196481	1.39	67	88.06
chr3	86051159		88317270	2.27	36	100.00
chr3	136930621		138451946	1.52	31	96.77
chr4	2341622	3532402	1.19 76	96.05		
chr4	68496809		69936500	1.44	61	96.72
chr4	86098751		89248967	3.15	86	97.67
chr4	108838313		109851911	1.01	26	92.31
chr4	127710868		130137824	2.43	31	96.77
chr5	10282367		13900236	3.62	50	90.00
chr5	38424906		40949895	2.52	30	90.00
chr5	88197940		126550379	38.35	330	96.97
chr5	129679759		132257680	2.58	27	88.89
chr6	1611782	5972556	4.36 79	89.87		
chr6	27388868		29396548	2.01	39	94.87
chr6	148648256		150800779	2.15	82	100.00
chr8	41734125		47191163	5.46	30	90.00
chr10	79314368		80570049	1.26	103	90.29
chr10	91248495		93074769	1.83	28	100.00
chr12	78217594		80610465	2.39	50	96.00
chr14	60292649		61529300	1.24	27	88.89
chr14	85529270		88192139	2.66	29	93.10
chr15	69023863		70832754	1.81	41	90.24
chr15	85267450		86295233	1.03	45	91.11
chr16	7607430	8735858	1.13 39	92.31		
chr16	47084125		50301239	3.22	33	90.91
chr18	7042495	8705681	1.66 27	88.89		

INFO: 98.64 Mb are in Homozygous Regions (autosomal chromosomes)

AutoMap v1.0 used for analysis

Variant filtering parameters used: DP=8, percaltlow=.25, percalthigh=.75, binomial=.000001, maxgap=10

Other parameters used: window=7, windowthres=5, minsize=1, minvar=25, minperc=88, chrX=No, extend=1

RS2290 - Homozygosity Mapper

score chr from (bp) to (bp) from SNP to SNP build 37

***broad** - use this when you expect some genetic heterogeneity*

80	1	227921436	228458655	n/a	n/a	region	genotypes
80	5	100389728	119196515	n/a	n/a	region	genotypes
80	6	31138400	31464043	n/a	n/a	region	genotypes
80	6	148648256	150800779	n/a	n/a	region	genotypes
80	11	551120	1016640	n/a	n/a	region	genotypes
78	10	133239619	133565402	n/a	n/a	region	genotypes
77	15	89486599	90067575	n/a	n/a	region	genotypes
75	4	86098751	88509857	n/a	n/a	region	genotypes
68	5	95888996	100389594	n/a	n/a	region	genotypes
64	12	52267076	52424720	n/a	n/a	region	genotypes
64	19	15623516	15680322	n/a	n/a	region	genotypes

RS2012 - AutoMap (HG38)

RS2012 HomRegions.tsv

#Chr	Begin	End	Size(Mb)	Nb_variants		Percentage_homozygosity
chr1	24814334		54152762	29.34	853	98.12
chr1	55052643		56726680	1.67	29	89.66
chr1	155047234		156137743	1.09	51	96.08
chr1	209828241		210861363	1.03	27	92.59
chr2	95954090		97142612	1.19	38	97.37
chr2	224499769		227047615	2.55	36	91.67
chr2	232638274		236214741	3.58	97	100.00
chr3	47513652		48567610	1.05	34	94.12
chr3	50187596		51246886	1.06	26	88.46
chr4	1403509	3587776	2.18 165	100.00		
chr4	73151316		74241680	1.09	29	93.10
chr4	74382827		75936011	1.55	46	91.30
chr4	108848743		109944115	1.10	28	89.29
chr5	68296453		69632791	1.34	30	90.00
chr5	76376975		79990745	3.61	94	98.94
chr5	137677661		138782249	1.10	53	94.34
chr7	90167786		92448073	2.28	26	92.31
chr8	20181079		25390071	5.21	185	95.68
chr9	32632292		34088563	1.46	47	91.49
chr9	106722835		109280018	2.56	36	94.44
chr10	6221309	18402089	12.18	283	97.53	
chr10	49178453		52280957	3.10	125	96.80
chr10	101237870		102686071	1.45	54	90.74
chr11	33768722		35176561	1.41	47	89.36
chr11	71527159		73234975	1.71	120	91.67
chr11	104038007		105974196	1.94	27	96.30
chr15	32635758		34527993	1.89	80	98.75
chr15	34556906		66311694	31.75	1004	98.01
chr15	71243119		76259517	5.02	180	91.67
chr15	76261345		82342829	6.08	230	98.70
chr15	82464807		85204210	2.74	110	92.73
chr15	85255622		94855496	9.60	260	98.08
chr16	893361	5239765	4.35 532	98.87		
chr17	5500742	6750049	1.25 37	94.59		
chr17	30556723		31889495	1.33	38	89.47
chr18	43273924		52752316	9.48	157	95.54
chr19	30015399		33800378	3.78	103	96.12
chr22	25851640		29225139	3.37	63	96.83

INFO: 168.47 Mb are in Homozygous Regions (autosomal chromosomes)

AutoMap v1.0 used for analysis

Variant filtering parameters used: DP=8, percaltlow=.25, percalthigh=.75, binomial=.000001, maxgap=10

Other parameters used: window=7, windowthres=5, minsize=1, minvar=25, minperc=88, chrX=No, extend=1

RS2012 - Homozygosity Mapper

broad - use this when you expect some genetic heterogeneity

80	1	176702778	181745330	n/a	n/a	region	genotypes
80	1	183544856	201069559	n/a	n/a	region	genotypes
80	2	68217039	79025836	n/a	n/a	region	genotypes
80	2	113598644	123762966	n/a	n/a	region	genotypes
80	2	207946560	212426475	n/a	n/a	region	genotypes
80	3	187251846	194341097	n/a	n/a	region	genotypes
80	6	21230842	29943445	n/a	n/a	region	genotypes
80	6	29944253	31356374	n/a	n/a	region	genotypes
80	6	31576622	32521801	n/a	n/a	region	genotypes
80	6	32584290	32759159	n/a	n/a	region	genotypes
80	7	29146960	48925545	n/a	n/a	region	genotypes
80	7	146774306	151141913	n/a	n/a	region	genotypes
80	8	213226	4994223	n/a	n/a	region	genotypes
80	9	172167	4793254	n/a	n/a	region	genotypes
80	11	7549609	8776160	n/a	n/a	region	genotypes
80	11	8776162	31102078	n/a	n/a	region	genotypes
80	11	32097119	46382787	n/a	n/a	region	genotypes
80	11	47622725	56375649	n/a	n/a	region	genotypes
80	11	56740404	62616242	n/a	n/a	region	genotypes
80	11	62779019	64315797	n/a	n/a	region	genotypes
80	11	64315859	71527372	n/a	n/a	region	genotypes
80	11	71865771	82732375	n/a	n/a	region	genotypes
80	16	3688960	5097307	n/a	n/a	region	genotypes
80	18	6511760	11610333	n/a	n/a	region	genotypes
80	18	11644684	14183721	n/a	n/a	region	genotypes
80	18	14780065	33683356	n/a	n/a	region	genotypes
80	19	11166556	12432951	n/a	n/a	region	genotypes
80	19	43776828	44473165	n/a	n/a	region	genotypes
80	19	44473230	45609887	n/a	n/a	region	genotypes
80	19	45626960	49044121	n/a	n/a	region	genotypes
80	19	49044189	50260748	n/a	n/a	region	genotypes
80	20	61924300	63276267	n/a	n/a	region	genotypes
78	7	75147946	76440164	n/a	n/a	region	genotypes
77	11	46677944	47622718	n/a	n/a	region	genotypes
75	2	112389661	113577803	n/a	n/a	region	genotypes
75	20	45469923	46055887	n/a	n/a	region	genotypes
73	19	12852443	14381407	n/a	n/a	region	genotypes
70	7	48925712	55497559	n/a	n/a	region	genotypes
69	6	31356433	31572704	n/a	n/a	region	genotypes
68	17	78271698	78502827	n/a	n/a	region	genotypes
66	1	236484250	236731347	n/a	n/a	region	genotypes
65	16	71431703	72054568	n/a	n/a	region	genotypes
64	1	170552235	175014935	n/a	n/a	region	genotypes
64	7	63559111	65091970	n/a	n/a	region	genotypes
64	8	143872650	144040065	n/a	n/a	region	genotypes

RS2210 - AutoMap (HG38)

RS2210.HomRegions.tsv

#Chr	Begin	End	Size(Mb)	Nb_variants		Percentage_homozygosity
chr1	27154266		28200500	1.05	30	93.33
chr1	89289988		91328297	2.04	34	91.18
chr1	91735040		92961312	1.23	32	93.75
chr1	169733446		170947505	1.21	27	88.89
chr2	201636725		203959560	2.32	60	90.00
chr3	46925550		48473670	1.55	63	88.89
chr3	82806586		89413088	6.61	44	88.64
chr4	93207281		96840082	3.63	29	89.66
chr4	119057973		121336795	2.28	48	97.92
chr4	125318831		128946125	3.63	41	92.68
chr6	25689150		29306571	3.62	91	89.01
chr9	131228372		132396600	1.17	73	89.04
chr10	28289366		29421432	1.13	27	92.59
chr10	102066172		103967898	1.90	63	92.06
chr10	116692588		119146428	2.45	31	90.32
chr10	127883985		129766800	1.88	30	96.67
chr11	53635976		56700311	3.06	72	93.06
chr12	49838386		51010684	1.17	64	89.06
chr12	122716390		123841430	1.13	80	96.25
chr16	7653783	8898485	1.24 60	90.00		
chr17	22070615		27560504	5.49	31	90.32
chr18	63497369		66544014	3.05	38	89.47
chr19	23493480		28791121	5.30	34	88.24
chr21	38299554		39528852	1.23	53	92.45
chr21	42434875		43732501	1.30	30	90.00

RS2210 - Homozygosity Mapper

score chr from (bp) to (bp) from SNP to SNP build 37

broad - use this when you expect some genetic heterogeneity

80	12	40237989	40910023	n/a	n/a	region	genotypes
77	16	88699572	88818058	n/a	n/a	region	genotypes
67	12	122716390	123472588	n/a	n/a	region	genotypes

RS2247 - AutoMap (HG38)

RS2247.HomRegions.tsv

#Chr	Begin	End	Size(Mb)	Nb_variants	Percentage_homozygosity
chr1	10658674		11671870	1.01 38	92.11
chr1	36860122		37958181	1.10 28	92.86
chr1	44897320		46203604	1.31 56	92.86
chr1	91735040		94005598	2.27 75	92.00
chr1	204619973		214483121	9.86 271	99.26
chr1	214483419		241857502	27.37 665	98.35
chr2	11133281		33840249	22.71 427	98.83
chr2	34471546		42288248	7.82 65	98.46
chr2	42443887		43720805	1.28 35	97.14
chr2	108660783		110201348	1.54 26	88.46
chr2	119478756		120986649	1.51 40	95.00
chr2	149575863		152144845	2.57 72	90.28
chr2	214108287		215388316	1.28 50	96.00
chr3	52154292		53178367	1.02 136	94.12
chr3	81761365		89107976	7.35 38	92.11
chr4	42455528		45994779	3.54 29	93.10
chr4	143997559		145542814	1.55 29	89.66
chr4	153720337		155214524	1.49 34	94.12
chr5	15936901		20304845	4.37 30	93.33
chr5	111071426		112418840	1.35 31	96.77
chr6	26103770		31356259	5.25 387	97.42
chr6	32589669		93410474	60.82 1370	98.69
chr6	105376288		107070192	1.69 26	88.46
chr7	144401899		152229936	7.83 198	98.48
chr7	152273771		156725313	4.45 55	100.00
chr8	80993298		85643747	4.65 35	100.00
chr8	85644048		97277758	11.63 123	98.37
chr8	141518801		145003393	3.48 299	100.00
chr10	3825121	5277232	1.45 56	91.07	
chr10	72063199		74082394	2.02 35	88.57
chr11	1099002	2159830	1.06 172	98.26	
chr12	663507	1795925	1.13 30	90.00	
chr12	21934004		27958386	6.02 96	93.75
chr12	118082435		121444569	3.36 126	100.00
chr13	18222650		21261333	3.04 191	97.38
chr13	21261421		24587300	3.33 104	95.19
chr13	25097182		40749261	15.65 256	98.83
chr13	102861594		114244779	11.38 223	96.41
chr14	58304914		60159193	1.85 54	88.89
chr14	61019720		62950567	1.93 26	88.46
chr14	96442688		105622067	9.18 366	98.63
chr15	23181632		28174420	4.99 94	92.55
chr15	28547897		30135868	1.59 37	89.19
chr15	30606779		32101283	1.49 53	96.23
chr15	32491556		34386606	1.90 75	97.33
chr15	34556906		43632151	9.08 305	98.36
chr15	43632499		45068982	1.44 30	93.33
chr15	45073611		48247390	3.17 63	96.83
chr15	93073878		101755457	8.68 145	100.00
chr16	17135	1227548	1.21 182	99.45	
chr16	1256972	4360866	3.10 354	97.46	
chr16	7709204	8746097	1.04 34	94.12	
chr16	8848000	10430799	1.58 30	90.00	
chr17	10547499		11629518	1.08 49	93.88
chr17	48189487		49222427	1.03 43	88.37
chr18	77993588		80169229	2.18 32	100.00
chr19	22471624		24162481	1.69 51	88.24
chr20	33791457		35511334	1.72 66	89.39
chr20	49254660		56386407	7.13 84	96.43
chr20	62967547		64328010	1.36 136	97.79
## INFO: 318.96 Mb are in Homozygous Regions (autosomal chromosomes)					
## AutoMap v1.0 used for analysis					
## Variant filtering parameters used: DP=8, percallow=.25, percalhigh=.75, binomial=.000001, maxgap=10					
## Other parameters used: window=7, windowthres=5, minsize=1, minvar=25, minperc=88, chrX=No, extend=1					

RS2247- Homozygosity Mapper

score	chr	from (bp)	to (bp)	from SNP	to SNP	build 37	
<i>broad - use this when you expect some genetic heterogeneity</i>							
80	1	205771298	212068372	n/a	n/a	region	genotypes
80	1	219609937	227493082	n/a	n/a	region	genotypes
80	1	227493774	241711939	n/a	n/a	region	genotypes
80	2	11214485	27243390	n/a	n/a	region	genotypes
80	2	27369223	33840048	n/a	n/a	region	genotypes
80	6	26108147	31029812	n/a	n/a	region	genotypes
80	6	31029892	31354026	n/a	n/a	region	genotypes
80	6	31356458	31711840	n/a	n/a	region	genotypes
80	6	32040674	32521811	n/a	n/a	region	genotypes
80	6	32584463	32745710	n/a	n/a	region	genotypes
80	6	32857218	35787881	n/a	n/a	region	genotypes
80	6	35977442	43071200	n/a	n/a	region	genotypes
80	6	43226535	75085406	n/a	n/a	region	genotypes
80	6	80007993	93410474	n/a	n/a	region	genotypes
80	7	144548450	149892407	n/a	n/a	region	genotypes
80	8	143376704	144398167	n/a	n/a	region	genotypes
80	11	551126	1016609	n/a	n/a	region	genotypes
80	11	1249152	2135306	n/a	n/a	region	genotypes
80	12	23543182	28183780	n/a	n/a	region	genotypes
80	12	118082435	121444569	n/a	n/a	region	genotypes
80	13	18222629	19387711	n/a	n/a	region	genotypes
80	13	25324953	40560901	n/a	n/a	region	genotypes
80	13	105467097	110938373	n/a	n/a	region	genotypes
80	13	110938386	114244779	n/a	n/a	region	genotypes
80	14	97751535	105621899	n/a	n/a	region	genotypes
80	15	34556906	40289927	n/a	n/a	region	genotypes
80	15	40289962	41058568	n/a	n/a	region	genotypes
80	15	41478943	43492237	n/a	n/a	region	genotypes
80	16	17780	1227548	n/a	n/a	region	genotypes
80	16	1257059	2319484	n/a	n/a	region	genotypes
80	16	3069383	4343195	n/a	n/a	region	genotypes
80	20	49481865	54224204	n/a	n/a	region	genotypes
80	20	63009582	64327831	n/a	n/a	region	genotypes
78	15	23687320	28174380	n/a	n/a	region	genotypes
77	15	89486642	90067285	n/a	n/a	region	genotypes
74	8	93700647	96385878	n/a	n/a	region	genotypes
74	14	105741506	105986650	n/a	n/a	region	genotypes
72	7	150293244	151187179	n/a	n/a	region	genotypes
71	8	144400134	145003393	n/a	n/a	region	genotypes
70	1	204619973	205584218	n/a	n/a	region	genotypes
68	11	1099604	1247407	n/a	n/a	region	genotypes
68	15	32528679	34362138	n/a	n/a	region	genotypes
67	1	91735077	93876910	n/a	n/a	region	genotypes
67	1	214483419	218405384	n/a	n/a	region	genotypes
65	2	33840456	42264811	n/a	n/a	region	genotypes
65	15	97969858	100553866	n/a	n/a	region	genotypes

RM4426 - AutoMap (HG38)

RM4426.HomRegions.tsv

#Chr	Begin	End	Size(Mb)	Nb_variants	Percentage_homozygosity
chr1	37794831		39000954	1.21 34	100.00
chr1	60406869		91315856	30.91 445	97.98
chr1	98893205		100484404	1.59 33	93.94
chr1	193141833		197428956	4.29 32	90.62
chr2	38315431		39716915	1.40 41	90.24
chr2	42798067		43828307	1.03 29	89.66
chr2	59682898		85542588	25.86 338	96.15
chr2	106941514		108352488	1.41 26	92.31
chr2	115162299		118942520	3.78 28	92.86
chr2	119685867		121247020	1.56 35	91.43
chr2	152616978		154854845	2.24 26	92.31
chr3	32885908		36169851	3.28 45	95.56
chr3	126551892		127604987	1.05 27	88.89
chr3	131986008		133617116	1.63 37	97.30
chr3	149487795		150762270	1.27 26	88.46
chr5	129397155		132469724	3.07 43	88.37
chr6	134007054		167373063	33.37 549	99.27
chr7	22493833		24285051	1.79 42	90.48
chr7	55492514		56806062	1.31 59	91.53
chr7	82826579		83961536	1.13 27	96.30
chr8	24293915		25316979	1.02 28	89.29
chr9	741041 13110845		12.37	116 93.97	
chr9	98541897		101368187	2.83 48	97.92
chr9	120409378		122144444	1.74 63	98.41
chr11	49146864		51422246	2.28 63	88.89
chr13	75760973		94758491	19.00 80	96.25
chr14	103710853		105625520	1.91 235	93.62
chr15	34752856		45073526	10.32 319	98.75
chr15	45073707		47766017	2.69 46	100.00
chr15	63983446		65384279	1.40 68	88.24
chr16	7595711 8898485	1.30 52		88.46	
chr16	24891113		27429962	2.54 34	88.24
chr16	85112371		90175209	5.06 375	99.47
chr17	41755723		42834437	1.08 68	89.71
chr17	62289439		63509188	1.22 41	90.24
chr18	8343532 11610219	3.27		96 100.00	
chr18	11610625		15004192	3.39 150	95.33
chr18	48948427		50040286	1.09 30	90.00
chr18	59035713		79461207	20.43 212	99.06
chr19	23146138		29526852	6.38 50	92.00
chr20	96321 7778468	7.68 329		99.09	
chr22	25877926		50782271	24.90 913	98.90

INFO: 257.08 Mb are in Homozygous Regions (autosomal chromosomes)

AutoMap v1.0 used for analysis

Variant filtering parameters used: DP=8, percalflow=.25, percalthigh=.75, binomial=.000001, maxgap=10

Other parameters used: window=7, windowthres=5, minsize=1, minvar=25, minperc=88, chrX=No, extend=1

RM4426 - Homozygosity Mapper

score	chr	from (bp)	to (bp)	from SNP	to SNP	build 37
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<i>broad - use this when you expect some genetic heterogeneity</i>						
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80	1	61455513	74236266	n/a	n/a	region genotypes
80	1	74250831	88983595	n/a	n/a	region genotypes
80	2	70297444	74422789	n/a	n/a	region genotypes
80	6	138499156	155004963	n/a	n/a	region genotypes
80	6	155004966	167196367	n/a	n/a	region genotypes
80	9	842230	11011829	n/a	n/a	region genotypes
80	11	64220727	64927713	n/a	n/a	region genotypes
80	14	20781965	21570431	n/a	n/a	region genotypes
80	14	104018309	105450460	n/a	n/a	region genotypes
80	15	35093137	41852779	n/a	n/a	region genotypes
80	15	41852780	42733012	n/a	n/a	region genotypes
80	16	85112371	88731933	n/a	n/a	region genotypes
80	16	88734600	90093830	n/a	n/a	region genotypes
80	18	8343532	11610163	n/a	n/a	region genotypes
80	18	11644680	14183721	n/a	n/a	region genotypes
80	18	62358225	76880036	n/a	n/a	region genotypes
80	20	478765	3316890	n/a	n/a	region genotypes
80	20	3330791	7914122	n/a	n/a	region genotypes
80	22	30385785	38991280	n/a	n/a	region genotypes
80	22	38991650	42150743	n/a	n/a	region genotypes
80	22	42576927	50782271	n/a	n/a	region genotypes
69	8	143868745	143992685	n/a	n/a	region genotypes
67	2	59022821	63968863	n/a	n/a	region genotypes
66	9	120525129	122144444	n/a	n/a	region genotypes
65	16	1698852	2020163	n/a	n/a	region genotypes
64	13	75760973	94286531	n/a	n/a	region genotypes

RS2021 - AutoMap (HG38)

RS2021 HomRegions.tsv

#Chr	Begin	End	Size(Mb)	Mb_variants	Percentage_homozygosity
chr1	55052855		56737199	1.68 26	92.31
chr1	75541547		77293893	1.75 28	89.29
chr1	96813248		107481214	10.67 65	92.31
chr1	170552235		201077983	30.53 433	98.38
chr2	5496292	9843557	4.35 65	92.31	
chr2	15330878		16553016	1.22 28	100.00
chr2	64592000		79025836	14.43 234	99.57
chr2	111321323		113563173	2.24 107	97.20
chr2	113595774		126899088	13.30 132	96.21
chr2	169198745		170217377	1.02 46	89.13
chr2	196156648		199458729	3.30 57	89.47
chr2	207946560		213297049	5.35 106	100.00
chr3	4362403	9348628	4.99 62	93.55	
chr3	69057154		71754023	2.70 26	88.46
chr3	87052727		89107976	2.06 33	93.94
chr3	186790133		194341178	7.55 126	96.03
chr5	9201861	10377948	1.18	26 100.00	
chr5	25190425		31508826	6.32 27	88.89
chr6	12293904		13584351	1.29 28	92.86
chr6	21230842		29943483	8.71 486	99.38
chr6	29943590		33006774	3.06 671	99.40
chr7	29146960		56019681	26.87 561	99.64
chr7	56944283		65773710	8.83 93	92.47
chr7	65802075		76440164	10.64 174	97.13
chr7	76497524		81950516	5.45 95	90.53
chr7	146774306		152229936	5.46 226	100.00
chr7	152273771		156633598	4.36 50	98.00
chr8	213226	4994223	4.78 116	100.00	
chr9	52705	4834299	4.78 90	97.78	
chr9	19576951		21695461	2.12 26	92.31
chr9	100578593		104764338	4.19 40	90.00
chr9	105619894		110137919	4.52 45	95.56
chr9	117008201		120909242	3.90 43	88.37
chr10	30689359		32188645	1.50 32	100.00
chr10	72102274		73912117	1.81 27	88.89
chr10	96230827		97445929	1.22 39	92.31
chr11	7089012	56375722	49.29	963 99.27	
chr11	56701359		71795884	15.09 874	99.54
chr11	71796215		80989102	9.19 225	98.67
chr11	104873460		105974196	1.10 26	96.15
chr12	14511661		16272409	1.76 47	93.62
chr12	72022455		77025561	5.00 36	88.89
chr12	96223526		98531872	2.31 26	92.31
chr12	113078119		114385382	1.31 30	93.33
chr13	48086244		49725512	1.64 53	96.23
chr16	3674464	5097307	1.42 103	96.12	
chr16	28600799		30555920	1.95 122	90.98
chr16	49638609		52143416	2.50 42	95.24
chr16	71285636		72798719	1.51 96	93.75
chr18	5956503	33683356	27.73	411 96.59	
chr18	75202325		79069525	3.87 36	88.89
chr19	11131368		14467542	3.34 192	95.31
chr19	43747318		50625404	6.88 609	98.69
chr20	13009396		17615510	4.61 47	91.49
chr20	23084705		25215780	2.13 64	96.87
chr20	60570616		63276267	2.71 159	99.37

INFO: 363.47 Mb are in Homozygous Regions (autosomal chromosomes)

AutoMap v1.0 used for analysis

Variant filtering parameters used: DP=8, percalflow=.25, percalhigh=.75, binomial=.000001, maxgap=10

Other parameters used: window=7, windowthres=5, minsize=1, minvar=25, minperc=88, chrX=No, extend=1

RS2021 - Homozygosity Mapper

score chr from (bp) to (bp) from SNP to SNP build 37

broad - use this when you expect some genetic heterogeneity

80	1	176702778	181745330	n/a	n/a	region	genotypes
80	1	183544856	201089559	n/a	n/a	region	genotypes
80	2	68217039	79025836	n/a	n/a	region	genotypes
80	2	113588844	123762966	n/a	n/a	region	genotypes
80	2	207948580	212428475	n/a	n/a	region	genotypes
80	3	187251848	194341097	n/a	n/a	region	genotypes
80	6	21230842	29943445	n/a	n/a	region	genotypes
80	6	29944253	31358374	n/a	n/a	region	genotypes
80	6	31576622	32521801	n/a	n/a	region	genotypes
80	6	32584290	32759159	n/a	n/a	region	genotypes
80	7	29148960	48925545	n/a	n/a	region	genotypes
80	7	148774306	151141913	n/a	n/a	region	genotypes
80	8	213226	4994223	n/a	n/a	region	genotypes
80	9	172167	4793254	n/a	n/a	region	genotypes
80	11	7549609	8776160	n/a	n/a	region	genotypes
80	11	8776162	31102078	n/a	n/a	region	genotypes
80	11	32097119	46382787	n/a	n/a	region	genotypes
80	11	47622725	56375649	n/a	n/a	region	genotypes
80	11	56740404	62616242	n/a	n/a	region	genotypes
80	11	62779019	64315797	n/a	n/a	region	genotypes
80	11	64315859	71527372	n/a	n/a	region	genotypes
80	11	71865771	82732375	n/a	n/a	region	genotypes
80	16	3688960	5097307	n/a	n/a	region	genotypes
80	18	6511760	11610333	n/a	n/a	region	genotypes
80	18	11644684	14183721	n/a	n/a	region	genotypes
80	18	14780065	33683356	n/a	n/a	region	genotypes
80	19	11166556	12432951	n/a	n/a	region	genotypes
80	19	43776828	44473165	n/a	n/a	region	genotypes
80	19	44473230	45608887	n/a	n/a	region	genotypes
80	19	45626960	49044121	n/a	n/a	region	genotypes
80	19	49044189	50260748	n/a	n/a	region	genotypes
80	20	61924300	63276267	n/a	n/a	region	genotypes
78	7	75147946	76440164	n/a	n/a	region	genotypes
77	11	46677944	47622718	n/a	n/a	region	genotypes
75	2	112388661	113577803	n/a	n/a	region	genotypes
75	20	45469923	46055887	n/a	n/a	region	genotypes
73	19	12852443	14381407	n/a	n/a	region	genotypes
70	7	48925712	55497559	n/a	n/a	region	genotypes
69	6	31356433	31572704	n/a	n/a	region	genotypes
68	17	78271698	78502827	n/a	n/a	region	genotypes
66	1	236484250	236731347	n/a	n/a	region	genotypes
65	16	71431703	72054568	n/a	n/a	region	genotypes
64	1	170552235	175014935	n/a	n/a	region	genotypes
64	7	63559111	65091970	n/a	n/a	region	genotypes
64	8	143872650	144040065	n/a	n/a	region	genotypes

RS1901- AutoMap (HG38)

RS1901 HomRegions.tsv

#Chr	Begin	End	Size(Mb)	Nb_variants	Percentage_homozygosity
chr1	3869625	7749668	3.88 98	96.94	
chr1	31756312		34218862	2.46 49	97.96
chr1	55008803		56692378	1.68 32	90.62
chr1	58631181		67660413	9.03 146	100.00
chr1	149934520		151532302	1.60 92	91.30
chr1	159535507		165563768	6.03 221	99.10
chr1	200174314		201211017	1.04 45	100.00
chr1	201211044		203496264	2.29 147	100.00
chr1	235809567		243050459	7.24 144	100.00
chr2	8683033	9846033	1.16 48	89.58	
chr2	16553027		31388163	14.84 397	98.74
chr3	197630	6956457	6.76 79	96.20	
chr3	46925550		48580541	1.65 65	95.38
chr3	83692473		88095920	4.40 29	93.10
chr4	138562023		148435364	9.87 127	92.13
chr5	43245820		44305207	1.06 26	88.46
chr5	122440606		124708735	2.27 35	91.43
chr6	28579175		29670657	1.09 51	92.16
chr6	46746861		52516387	5.77 111	97.30
chr6	99383666		116453096	17.07 204	97.06
chr6	116453332		127416743	10.96 122	98.36
chr7	2795235	5919633	3.12 103	96.12	
chr7	28410346		35634260	7.22 143	100.00
chr7	105981066		128254297	22.27 192	98.44
chr8	23574801		25886741	2.31 55	90.91
chr9	5467955	8338847	2.87 53	92.45	
chr9	87004875		90216772	3.13 58	96.55
chr9	93335634		94587384	1.25 36	91.67
chr10	120905455		122242024	1.34 26	88.46
chr11	8230374	13388824	5.16	165 97.58	
chr11	20606933		36081678	15.47 228	97.81
chr11	74697339		95175494	20.48 324	98.15
chr11	101997684		105753169	3.76 120	95.83
chr11	107962122		110093461	2.13 29	89.66
chr11	118902729		120115459	1.21 69	95.65
chr11	130672987		131911740	1.24 31	100.00
chr12	46207273		47791384	1.58 36	94.44
chr13	48317700		51020605	2.70 58	94.83
chr13	76957226		80336657	3.38 28	89.29
chr14	67729919		68869865	1.14 37	91.89
chr15	23440775		26937210	3.50 45	97.78
chr15	63626108		64675455	1.05 40	95.00
chr16	11730	1383765	1.37 229	99.13	
chr16	50100097		55823423	5.72 117	94.87
chr16	55828971		57916153	2.09 150	99.33
chr16	68909389		69976613	1.07 35	91.43
chr17	55561443		57597062	2.04 34	94.12
chr18	11644846		31318238	19.67 188	97.87
chr20	35271872		36632483	1.36 41	95.12

INFO: 251.78 Mb are in Homozygous Regions (autosomal chromosomes)

AutoMap v1.0 used for analysis

Variant filtering parameters used: DP=8, percalflow=.25, percalhigh=.75, binomial=.000001, maxgap=10

Other parameters used: window=7, windowthres=5, minsize=1, minvar=25, minperc=88, chrX-No, extend=1

RS1901 - Homozygosity Mapper

score chr from (bp) to (bp) from SNP to SNP build 37

broad - use this when you expect some genetic heterogeneity

80	1	4712657	7467936	n/a	n/a	region	genotypes
80	1	58631181	65364614	n/a	n/a	region	genotypes
80	1	159598582	161548369	n/a	n/a	region	genotypes
80	1	161548828	165563768	n/a	n/a	region	genotypes
80	1	201211072	203496264	n/a	n/a	region	genotypes
80	1	235809567	243050459	n/a	n/a	region	genotypes
80	2	17284808	24821047	n/a	n/a	region	genotypes
80	2	25938357	28550170	n/a	n/a	region	genotypes
80	2	240140467	241071915	n/a	n/a	region	genotypes
80	6	32584454	32741569	n/a	n/a	region	genotypes
80	6	99613748	110858764	n/a	n/a	region	genotypes
80	6	116453340	127342558	n/a	n/a	region	genotypes
80	7	3140916	5847457	n/a	n/a	region	genotypes
80	7	30626980	35634260	n/a	n/a	region	genotypes
80	7	105981066	123129324	n/a	n/a	region	genotypes
80	11	8776160	10773884	n/a	n/a	region	genotypes
80	11	20783789	31681741	n/a	n/a	region	genotypes
80	11	32097119	36081678	n/a	n/a	region	genotypes
80	11	74697695	89753194	n/a	n/a	region	genotypes
80	16	17593	1357791	n/a	n/a	region	genotypes
80	16	50633388	55820284	n/a	n/a	region	genotypes
80	16	55829106	57915320	n/a	n/a	region	genotypes
80	18	20954987	31318238	n/a	n/a	region	genotypes
80	19	15548002	15878920	n/a	n/a	region	genotypes
79	6	32116560	32371571	n/a	n/a	region	genotypes
78	11	102452429	104037228	n/a	n/a	region	genotypes
77	2	28593947	31388163	n/a	n/a	region	genotypes
76	4	138562023	143880509	n/a	n/a	region	genotypes
76	6	110858798	116453096	n/a	n/a	region	genotypes
73	1	873967	1091327	n/a	n/a	region	genotypes

T3-ST-12 - AutoMap (HG38)

T3ST12 HomRegions.tsv

#Chr	Begin	End	Size(Mb)	Nb_variants		Percentage_homozygosity
chr1	44842022		46192656	1.35	54	96.30
chr1	48436880		58630794	10.19	171	97.08
chr1	58631107		66628605	8.00	121	98.35
chr1	75227908		76307755	1.08	26	96.15
chr1	169862852		179035523	9.17	133	96.24
chr1	236394471		241500602	5.11	157	97.45
chr2	14178946		16565629	2.39	40	92.50
chr2	38698468		39716915	1.02	35	94.29
chr2	106844018		108329577	1.49	27	100.00
chr2	196271334		199760858	3.49	40	92.50
chr2	201749909		203956771	2.21	36	91.67
chr2	215336184		219906502	4.57	279	98.57
chr3	56737223		58103867	1.37	40	95.00
chr3	82807041		88317270	5.51	39	92.31
chr3	11750927		126499316	8.95	236	96.61
chr4	3588166	4894170	1.31 34	94.12		
chr5	54857206		55883224	1.03	45	91.11
chr5	70220125		72115891	1.90	26	92.31
chr5	103025380		128278099	25.25	238	98.32
chr5	177440942		178727174	1.29	66	95.45
chr7	1155698	2213351	1.06 60	88.33		
chr7	8157347	15686441	7.53	63	98.41	
chr7	31552877		33019795	1.47	48	91.67
chr7	64679146		66998208	2.32	64	93.75
chr7	140473302		142060167	1.59	37	89.19
chr7	142774389		144259649	1.49	100	99.00
chr7	144372860		152229936	7.86	246	98.37
chr7	152273771		159232490	6.96	112	99.11
chr8	33389167		37829231	4.44	28	89.29
chr8	118952044		130847522	11.90	129	96.90
chr9	7174773	33795705	26.62	267	99.63	
chr9	33798301		39073680	5.28	185	98.38
chr9	119512969		120997808	1.48	32	93.75
chr9	129042506		131588771	2.55	223	95.07
chr10	15132925		27981683	12.85	239	98.33
chr10	37145055		38646304	1.50	46	93.48
chr10	44983986		46234232	1.25	41	90.24
chr10	54527929		59352215	4.82	28	92.86
chr10	78054561		100746346	22.69	496	99.19
chr10	125896805		127008624	1.11	28	92.86
chr11	47815856		55265797	7.45	153	92.81
chr11	62433986		64315797	1.88	124	98.39
chr11	64315859		71802871	7.49	479	99.58
chr11	71802999		73235095	1.43	99	98.99
chr11	127003697		134347569	7.34	106	99.06
chr12	31252236		32305822	1.05	34	88.24
chr12	45992065		49794651	3.80	121	97.52
chr12	113471252		119520263	6.05	70	95.71
chr13	46276492		52820901	6.54	139	97.84
chr13	66228207		84145972	17.92	110	97.27
chr13	91693325		104052694	12.36	213	99.06
chr14	28264641		34486324	6.22	50	98.00
chr15	67832515		70052277	2.22	52	90.38
chr16	88736424		90167912	1.43	176	97.73
chr20	96321	6006566	5.91 248	98.39		
chr21	26954622		29458073	2.50	31	93.55

INFO: 315.04 Mb are in Homozygous Regions (autosomal chromosomes)

AutoMap v1.0 used for analysis

Variant filtering parameters used: DP=8, percaltlow=.25, percalthigh=.75, binomial=.000001, maxgap=10

Other parameters used: window=7, windowthres=5, minsize=1, minvar=25, minperc=88, chrX=No, extend=1

T3-ST-12 - Homozygosity Mapper

score chr from (bp) to (bp) from SNP to SNP build 37

***broad** - use this when you expect some genetic heterogeneity*

80	1	48497626	54614939	n/a	n/a	region	genotypes
80	1	54614956	58630807	n/a	n/a	region	genotypes
80	1	170958432	179035523	n/a	n/a	region	genotypes
80	1	236427516	240811913	n/a	n/a	region	genotypes
80	2	215336184	219906502	n/a	n/a	region	genotypes
80	3	116850137	126106996	n/a	n/a	region	genotypes
80	7	144372860	151187179	n/a	n/a	region	genotypes
80	7	154795797	159232490	n/a	n/a	region	genotypes
80	8	118952044	130800670	n/a	n/a	region	genotypes
80	9	7174773	16418873	n/a	n/a	region	genotypes
80	9	16582892	28149040	n/a	n/a	region	genotypes
80	9	34835276	36141820	n/a	n/a	region	genotypes
80	9	129095910	131475956	n/a	n/a	region	genotypes
80	10	22539904	27331583	n/a	n/a	region	genotypes
80	10	78054561	99660526	n/a	n/a	region	genotypes
80	11	62616244	64315749	n/a	n/a	region	genotypes
80	11	64874301	66554456	n/a	n/a	region	genotypes
80	11	67215719	71527289	n/a	n/a	region	genotypes
80	11	71538486	73235095	n/a	n/a	region	genotypes
80	11	127098582	134985836	n/a	n/a	region	genotypes
80	12	46269120	49067099	n/a	n/a	region	genotypes
80	13	46276492	51908600	n/a	n/a	region	genotypes
80	13	65310849	85794985	n/a	n/a	region	genotypes
80	13	95062895	105467097	n/a	n/a	region	genotypes
80	16	88736424	89546571	n/a	n/a	region	genotypes
80	20	499958	5922871	n/a	n/a	region	genotypes
78	16	89578759	90093906	n/a	n/a	region	genotypes
74	7	142774516	143811094	n/a	n/a	region	genotypes
73	1	58631181	62578974	n/a	n/a	region	genotypes
72	11	49035075	54591643	n/a	n/a	region	genotypes
69	5	113010735	119165286	n/a	n/a	region	genotypes
69	7	8157347	15387331	n/a	n/a	region	genotypes

RS1048 - AutoMap (HG38)

RS1048.HomRegions.tsv

#Chr	Begin	End	Size(Mb)	Nb_variants		Percentage_homozygosity
chr1	109486240		121512104	12.03	123	91.87
chr1	149676574		158054379	8.38	141	95.04
chr2	98709684		128181234	29.47	126	96.03
chr2	137814477		174086285	36.27	140	97.14
chr3	24639973		64138955	39.50	275	97.09
chr3	76607070		106495432	29.89	63	100.00
chr3	126268918		170784256	44.52	166	99.40
chr3	195510732		197765432	2.25	57	89.47
chr4	53428	3590711	3.54	114	99.12	
chr4	3590911	13627943	10.04	88	95.45	
chr4	78987157		97127869	18.14	77	96.10
chr5	5200430	8869235	3.67	29	93.10	
chr5	137754695		140682958	2.93	56	96.43
chr5	156946803		179729625	22.78	127	97.64
chr6	90402482		136582497	46.18	157	96.82
chr6	136599836		166307718	29.71	153	98.69
chr7	12620804		32623477	20.00	99	97.98
chr8	72982161		101608919	28.63	59	98.31
chr11	62766431		64367862	1.60	47	93.62
chr12	50151977		52307145	2.16	27	100.00
chr12	125621419		133795960	8.17	61	95.08
chr13	102366825		110408608	8.04	34	97.06
chr14	61448128		71455425	10.01	77	93.51
chr14	105268228		106471268	1.20	103	89.32
chr15	34678933		63054439	28.38	225	98.22
chr16	64341	8620014	8.56	275	96.73	
chr16	46764482		59713621	12.95	97	97.94
chr16	70680850		74127515	3.45	28	96.43
chr16	85145977		90233804	5.09	126	96.83
chr17	6115	10216442	10.21	236	98.31	
chr19	52130488		59082605	6.95	245	95.92
chr21	34638859		37410477	2.77	28	89.29
chr21	38593609		48063476	9.47	239	97.91
chr22	47068935		51183255	4.11	92	96.74

INFO: 511.05 Mb are in Homozygous Regions (autosomal chromosomes)

AutoMap v1.0 used for analysis

Variant filtering parameters used: DP=8, percaltlow=.25, percalthigh=.75, binomial=.000001, maxgap=10

Other parameters used: window=7, windowthres=5, minsize=1, minvar=25, minperc=88, chrX=No, extend=1

RS1048 - Homozygosity Mapper

score	chr	from (bp)	to (bp)	from SNP	to SNP	build 37	
<i>broad - use this when you expect some genetic heterogeneity</i>							
80	1	112305406	120611496	n/a	n/a	region	genotypes
80	1	153636471	158054379	n/a	n/a	region	genotypes
80	2	158275111	174086285	n/a	n/a	region	genotypes
80	3	44846477	48681765	n/a	n/a	region	genotypes
80	3	50112589	58351660	n/a	n/a	region	genotypes
80	3	126340553	142231062	n/a	n/a	region	genotypes
80	3	142272275	169988364	n/a	n/a	region	genotypes
80	4	4239587	9245679	n/a	n/a	region	genotypes
80	5	175533585	178293256	n/a	n/a	region	genotypes
80	6	90660954	136582417	n/a	n/a	region	genotypes
80	6	136914852	166307718	n/a	n/a	region	genotypes
80	7	14026357	32598138	n/a	n/a	region	genotypes
80	8	72981327	101586133	n/a	n/a	region	genotypes
80	14	64443258	70496919	n/a	n/a	region	genotypes
80	15	35664406	52239617	n/a	n/a	region	genotypes
80	15	52506937	62539781	n/a	n/a	region	genotypes
80	16	436701	1291385	n/a	n/a	region	genotypes
80	16	1291622	2607730	n/a	n/a	region	genotypes
80	16	3119384	5289860	n/a	n/a	region	genotypes
80	16	48234421	59772778	n/a	n/a	region	genotypes
80	16	88593210	90232872	n/a	n/a	region	genotypes
80	17	767330	2965978	n/a	n/a	region	genotypes
80	17	2966525	5036205	n/a	n/a	region	genotypes
80	17	5334804	10206595	n/a	n/a	region	genotypes
80	19	52888074	54006913	n/a	n/a	region	genotypes
80	19	55175073	56274086	n/a	n/a	region	genotypes
80	19	56284587	58385748	n/a	n/a	region	genotypes
80	21	39213020	46012160	n/a	n/a	region	genotypes
80	21	46012240	48063476	n/a	n/a	region	genotypes
80	22	47370343	51183255	n/a	n/a	region	genotypes
76	8	144946818	145245647	n/a	n/a	region	genotypes
75	14	105268228	105416262	n/a	n/a	region	genotypes
74	4	88048318	95508108	n/a	n/a	region	genotypes
72	5	160049355	172385267	n/a	n/a	region	genotypes
67	1	149676574	152186699	n/a	n/a	region	genotypes
67	3	38938299	43607224	n/a	n/a	region	genotypes
66	2	148701099	157425502	n/a	n/a	region	genotypes
65	16	70926445	74425702	n/a	n/a	region	genotypes
64	1	110304092	112240038	n/a	n/a	region	genotypes
64	2	114356066	127816743	n/a	n/a	region	genotypes

RS2326 - AutoMap (HG38)

RS2326.HomRegions.tsv

#Chr	Begin	End	Size(Mb)	Nb_variants		Percentage_homozygosity
chr1	55009006		56645496	1.64	33	93.94
chr1	91735040		93115467	1.38	31	100.00
chr1	218437320		227493885	9.06	214	94.86
chr1	227506730		239907303	12.40	330	98.48
chr2	45895	2922665	2.88 59	98.31		
chr2	8747296	9955245	1.21 55	89.09		
chr2	130656603		178431939	47.78	627	97.77
chr2	178451163		204959601	26.51	382	99.74
chr3	10146744		19346813	9.20	204	99.02
chr3	30844314		36380572	5.54	70	98.57
chr3	64647828		75630725	10.98	115	97.39
chr3	105541674		128622053	23.08	586	98.98
chr3	138950380		156457320	17.51	191	99.48
chr3	188180166		195781576	7.60	210	95.71
chr3	195783347		198153259	2.37	105	100.00
chr4	125479670		136355088	10.88	49	93.88
chr6	33665750		35455712	1.79	91	93.41
chr7	1093535	3158155	2.06 117	97.44		
chr7	27102038		34658310	7.56	157	94.27
chr7	63580858		65773665	2.19	54	98.15
chr7	65788154		72999753	7.21	66	100.00
chr7	73005557		100949503	27.94	589	97.28
chr7	101034344		102329332	1.29	78	96.15
chr7	102541698		129451774	26.91	321	96.88
chr7	155707522		159232490	3.52	63	98.41
chr8	2076680	3493840	1.42 73	97.26		
chr8	100924055		110645285	9.72	108	99.07
chr8	127416578		132622568	5.21	47	89.36
chr9	117696	2057318	1.94 58	98.28		
chr9	111597344		112817728	1.22	26	88.46
chr9	120394483		122144444	1.75	66	89.39
chr9	129001735		130265876	1.26	94	90.43
chr10	71344147		80233654	8.89	167	92.22
chr10	80235484		101020555	20.79	459	99.78
chr11	20090946		36431956	16.34	224	98.21
chr11	40660010		44903487	4.24	47	100.00
chr11	45953579		47276650	1.32	34	88.24
chr11	48164558		56700220	8.54	185	95.68
chr11	112071532		133656970	21.59	628	98.09
chr12	4596151	5647617	1.05 39	89.74		
chr12	49999589		51191521	1.19	60	88.33
chr14	59315153		63280916	3.97	67	95.52
chr15	36614332		45073526	8.46	388	96.65
chr15	45073594		60382232	15.31	317	99.37
chr15	74451605		75785647	1.33	55	89.09
chr15	88568488		92712089	4.14	180	99.44
chr16	6654748	10538055	3.88	74	90.54	
chr20	96321	3705601	3.61 244	98.77		
chr20	34122904		36187629	2.06	85	88.24
chr20	46128252		53941395	7.81	138	97.10
chr21	14013728		18294209	4.28	29	100.00
chr21	36487368		38392289	1.90	51	90.20
chr22	48780408		50776695	2.00	185	98.92

INFO: 435.71 Mb are in Homozygous Regions (autosomal chromosomes)

AutoMap v1.0 used for analysis

Variant filtering parameters used: DP=8, percaltlow=.25, percalthigh=.75, binomial=.000001, maxgap=10

Other parameters used: window=7, windowthres=5, minsize=1, minvar=25, minperc=88, chrX=No, extend=1

RS2326 - Homozygosity Mapper

score chr from (bp) to (bp) from SNP to SNP build 37

broad - use this when you expect some genetic heterogeneity

80	1	729454	1090292	n/a	n/a	region	genotypes
80	1	220813204	225786845	n/a	n/a	region	genotypes
80	1	235138181	236603878	n/a	n/a	region	genotypes
80	2	157324272	168802693	n/a	n/a	region	genotypes
80	2	168802696	174310876	n/a	n/a	region	genotypes
80	2	178543036	204965268	n/a	n/a	region	genotypes
80	3	11871288	19346813	n/a	n/a	region	genotypes
80	3	105545332	122752560	n/a	n/a	region	genotypes
80	3	122759194	128622053	n/a	n/a	region	genotypes
80	3	138950380	147940254	n/a	n/a	region	genotypes
80	3	147940255	156457320	n/a	n/a	region	genotypes
80	3	189310328	195620029	n/a	n/a	region	genotypes
80	6	32642790	32668172	n/a	n/a	region	genotypes
80	7	1158358	2945727	n/a	n/a	region	genotypes
80	7	29445295	34658370	n/a	n/a	region	genotypes
80	7	83648383	97990216	n/a	n/a	region	genotypes
80	7	98191556	100949503	n/a	n/a	region	genotypes
80	7	107554459	128397151	n/a	n/a	region	genotypes
80	10	80235484	101018011	n/a	n/a	region	genotypes
80	11	20097827	36229496	n/a	n/a	region	genotypes
80	11	48949215	56331267	n/a	n/a	region	genotypes
80	11	112148818	117136597	n/a	n/a	region	genotypes
80	11	117208910	119160518	n/a	n/a	region	genotypes
80	11	119160520	125572592	n/a	n/a	region	genotypes
80	11	125620870	133842215	n/a	n/a	region	genotypes
80	15	41219843	42733278	n/a	n/a	region	genotypes
80	15	45073594	51689396	n/a	n/a	region	genotypes
80	15	51949699	59768792	n/a	n/a	region	genotypes
80	15	88568481	92712089	n/a	n/a	region	genotypes
80	20	96321	3705601	n/a	n/a	region	genotypes
80	20	46128252	53941395	n/a	n/a	region	genotypes
80	22	50208430	50777650	n/a	n/a	region	genotypes
79	7	102678568	107258425	n/a	n/a	region	genotypes
79	15	36950239	40289927	n/a	n/a	region	genotypes
75	8	2085509	3493572	n/a	n/a	region	genotypes
73	2	135345468	143435582	n/a	n/a	region	genotypes
72	8	103918418	109523215	n/a	n/a	region	genotypes
71	7	101037032	102329332	n/a	n/a	region	genotypes
70	1	229302783	231366498	n/a	n/a	region	genotypes
70	2	150471770	156568990	n/a	n/a	region	genotypes
70	3	30844314	36380572	n/a	n/a	region	genotypes
69	7	77055404	83616727	n/a	n/a	region	genotypes
69	10	133239619	133528756	n/a	n/a	region	genotypes
68	6	33685671	35411243	n/a	n/a	region	genotypes
68	22	49265502	50109670	n/a	n/a	region	genotypes
65	10	73674883	79510497	n/a	n/a	region	genotypes
64	3	64686798	69310577	n/a	n/a	region	genotypes

RS2320 - AutoMap (HG38)

RS2320.HomRegions.tsv

#Chr	Begin	End	Size(Mb)	Nb_variants		Percentage_homozygosity
chr1	66777341		69839075	3.06	34	88.24
chr1	196673839		197921672	1.25	43	90.70
chr1	223856582		225289844	1.43	32	90.62
chr2	114309408		118942520	4.63	26	92.31
chr2	118994490		120986649	1.99	65	90.77
chr3	87052727		88318756	1.27	27	96.30
chr3	135248526		138103363	2.85	37	94.59
chr4	8871251	9908299	1.04 39	92.31		
chr5	53083447		55276335	2.19	28	89.29
chr5	153494089		156922351	3.43	42	90.48
chr8	23703135		40153911	16.45	294	96.26
chr8	141518320		143043095	1.52	82	100.00
chr9	124804099		126381156	1.58	40	90.00
chr11	47339533		50422253	3.08	154	90.26
chr12	4662516	5920988	1.26 27	88.89		
chr12	11078088		12094660	1.02	32	90.62
chr12	79292133		80460849	1.17	37	91.89
chr12	122792202		123898053	1.11	90	94.44
chr13	21261438		23660230	2.40	29	100.00
chr14	55063402		56491529	1.43	53	98.11
chr15	50309870		51342058	1.03	45	95.56
chr16	7709204	8747977	1.04 36	100.00		
chr20	35126172		36155242	1.03	83	92.77
chr21	44973175		45992837	1.02	34	88.24
chr22	31093589		32254213	1.16	54	94.44

INFO: 59.44 Mb are in Homozygous Regions (autosomal chromosomes)

AutoMap v1.0 used for analysis

Variant filtering parameters used: DP=8, percaltlow=.25, percalthigh=.75, binomial=.000001, maxgap=10

Other parameters used: window=7, windowthres=5, minsize=1, minvar=25, minperc=88, chrX=No, extend=1

RS2320 - Homozygosity Mapper

score chr from (bp) to (bp) from SNP to SNP build 37

broad - use this when you expect some genetic heterogeneity

80	2	131264458	131591936	n/a	n/a	region	genotypes
80	8	25345721	30679706	n/a	n/a	region	genotypes
80	8	141518320	143043095	n/a	n/a	region	genotypes
78	1	236111318	236731347	n/a	n/a	region	genotypes
73	8	38060117	40153911	n/a	n/a	region	genotypes
72	11	47734000	49186715	n/a	n/a	region	genotypes
69	12	122792202	123513500	n/a	n/a	region	genotypes
67	19	15669937	15871728	n/a	n/a	region	genotypes

RS2278 - AutoMap (HG38)

RS2278.HomRegions.tsv

#Chr	Begin	End	Size(Mb)	Nb_variants	Percentage_homozygosity
chr1	32223920		33519370	1.30 49	89.80
chr1	81427173		100390923	18.96 309	96.76
chr1	115058907		117414666	2.36 52	96.15
chr1	229325277		236041790	6.72 92	96.74
chr1	245686793		246842858	1.16 35	91.43
chr2	12724640		15591962	2.87 34	97.06
chr2	25954329		33840249	7.89 258	98.06
chr2	38070996		42053160	3.98 40	97.50
chr2	55027585		57384408	2.36 37	89.19
chr2	151607640		152628171	1.02 26	88.46
chr2	162272314		180987269	18.71 332	98.19
chr3	46925550		48372725	1.45 64	89.06
chr3	56959003		58078847	1.12 36	97.22
chr3	86051159		88317270	2.27 36	97.22
chr3	193668450		195618483	1.95 46	95.65
chr4	48016744		49242842	1.23 40	97.50
chr4	71486879		77773052	6.29 131	93.89
chr4	125318831		129136560	3.82 51	90.20
chr4	139888739		141229706	1.34 30	93.33
chr4	186274219		188092005	1.82 33	90.91
chr5	54857975		55916618	1.06 47	93.62
chr5	75688945		79986721	4.30 99	93.94
chr5	112209973		113294190	1.08 27	96.30
chr6	14117907		18122275	4.00 40	90.00
chr7	84999673		88210213	3.21 47	89.36
chr7	121440998		129212540	7.77 156	95.51
chr8	213226	3107722	2.89 93	96.77	
chr8	60576300		61714951	1.14 38	89.47
chr8	70842805		73292418	2.45 42	95.24
chr10	13201345		18402089	5.20 148	98.65
chr10	26777047		27987344	1.21 55	92.73
chr10	97771814		99387935	1.62 51	98.04
chr10	113141442		118685944	5.54 128	98.44
chr10	118693656		119823044	1.13 44	90.91
chr10	119919501		122143618	2.22 37	89.19
chr10	130283727		133625131	3.34 181	100.00
chr11	104037228		106746764	2.71 28	92.86
chr11	110179777		120229082	10.05 346	99.13
chr11	128485181		133924839	5.44 77	94.81
chr12	9298801	10434322	1.14	174 91.95	
chr12	11092206		19457097	8.36 144	95.83
chr12	77032996		92531139	15.50 110	99.09
chr12	92531288		94140511	1.61 26	92.31
chr13	110242803		112398248	2.16 66	95.45
chr14	50007344		51243825	1.24 68	95.59
chr14	60658222		63949800	3.29 40	95.00
chr15	51377428		54264061	2.89 48	89.58
chr17	9162781	10343766	1.18	52 90.38	
chr17	49217994		50536476	1.32 96	94.79
chr19	610209	2823259	2.21 279	98.21	
chr19	12508116		39879656	27.37 1301	98.46
chr19	39902877		45601994	5.70 383	97.65
chr21	38878842		40062914	1.18 49	93.88
chr21	43029807		46658699	3.63 277	99.28
chr22	40418632		41958385	1.54 43	93.02

INFO: 235.3 Mb are in Homozygous Regions (autosomal chromosomes)

AutoMap v1.0 used for analysis

Variant filtering parameters used: DP=8, percalflow=.25, percalhigh=.75, binomial=.000001, maxgap=10

Other parameters used: window=7, windowthres=5, minsize=1, minvar=25, minperc=88, chrX=No, extend=1

RS2278 - Homozygosity Mapper

score chr from (bp) to (bp) from SNP to SNP build 37

***broad** - use this when you expect some genetic heterogeneity*

80	1	81427173	88983595	n/a	n/a	region	genotypes
80	1	88983716	94903018	n/a	n/a	region	genotypes
80	1	229325277	235138181	n/a	n/a	region	genotypes
80	2	25994812	33839969	n/a	n/a	region	genotypes
80	2	163611850	174399899	n/a	n/a	region	genotypes
80	2	174750180	180987269	n/a	n/a	region	genotypes
80	4	73258354	77160591	n/a	n/a	region	genotypes
80	5	75832405	79876313	n/a	n/a	region	genotypes
80	6	29670697	29852393	n/a	n/a	region	genotypes
80	7	122040729	128857406	n/a	n/a	region	genotypes
80	8	213226	3106481	n/a	n/a	region	genotypes
80	10	113141442	118009040	n/a	n/a	region	genotypes
80	10	132912614	133625131	n/a	n/a	region	genotypes
80	11	112961669	117207770	n/a	n/a	region	genotypes
80	11	117226141	118883762	n/a	n/a	region	genotypes
80	11	118897757	120226789	n/a	n/a	region	genotypes
80	12	12111448	19129736	n/a	n/a	region	genotypes
80	19	1037750	2811790	n/a	n/a	region	genotypes
80	19	14765889	15878886	n/a	n/a	region	genotypes
80	19	15879061	17286672	n/a	n/a	region	genotypes
80	19	17286690	22180994	n/a	n/a	region	genotypes
80	19	22181059	32999523	n/a	n/a	region	genotypes
80	19	32999710	35527505	n/a	n/a	region	genotypes
80	19	38830954	39877634	n/a	n/a	region	genotypes
80	19	39902984	41004197	n/a	n/a	region	genotypes
80	19	41432789	43361347	n/a	n/a	region	genotypes
80	19	43378743	44158121	n/a	n/a	region	genotypes
80	21	44601173	46658699	n/a	n/a	region	genotypes
79	12	9575063	10434322	n/a	n/a	region	genotypes
77	10	16520459	18402089	n/a	n/a	region	genotypes
77	19	36315529	38500798	n/a	n/a	region	genotypes
75	1	227816266	228318960	n/a	n/a	region	genotypes
72	21	43032314	44574233	n/a	n/a	region	genotypes
71	19	44267351	45319426	n/a	n/a	region	genotypes
68	10	13201345	16520445	n/a	n/a	region	genotypes
68	11	128809316	133918974	n/a	n/a	region	genotypes
65	10	130283727	132912579	n/a	n/a	region	genotypes