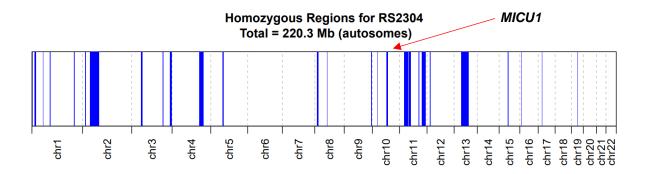
RS2304 (HG38) AutoMap



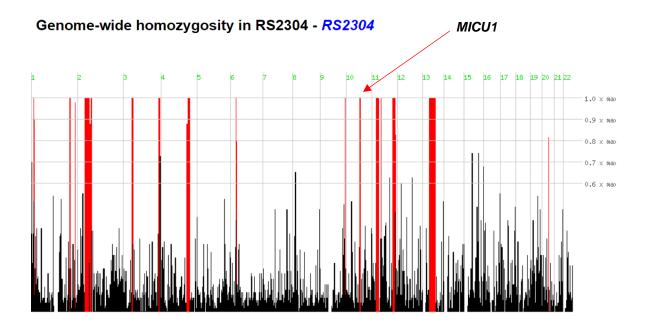
RS2304.HomRegions.tsv

#Chr	Begin	End	Size(Mb))	Nb_variants		Percentage_homozygosity			
chr1	3690968	4774360	1.08	55	98.18					
chr1	13779899	9	1653563	7	2.76	171	98.83			
chr1	16759217	7	18839749	9	2.08	67	98.51			
chr1	55008803	3	56737199	9	1.73	38	94.74			
chr1	89381885		91515092		2.13	38	92.11			
chr1	20593311	L4	2094306	51	3.50	88	100.00			
chr2	11804620	9	1559529	5	3.79	33	93.94			
chr2	37032497	7	8119623	2	44.16	590	96.95			
chr3	45984767	7	4968847	7	3.70	156	98.72			
chr3	49688637	7	5189683	4	2.21	81	100.00			
chr3	15138826	94	15430090	91	2.91	29	93.10			
chr3	18860967	73	19568574	45	7.08	164	96.34			
chr3	19599686	53	19762330	91	1.63	58	100.00			
chr4	13420044	16	1438803	69	9.68	73	94.52			
chr4	14388057	76	15460483	18	10.72	138	97.83			
chr5	58460109	9	6330197	2	4.84	36	91.67			
chr8	10612307	7	1180254	2	1.19	59	91.53			
chr8	12659852	2	17197739	9	4.54	58	96.55			
chr8	60838301	L	6224905	3	1.41	34	91.18			
chr9	13173757	78	1330618	51	1.32	58	96.55			
chr9	13320580	99	13534418	85	2.14	123	99.19			
chr10	26176863	3	27288639	9	1.11	36	97.22			
chr10	69407363	3	7701897	5	7.61	263	98.10			
chr11	22377284	1	42238183	1	19.86	210	98.10			
chr11	45927656	9	5526579	7	9.34	219	95.43			
chr11	93415257	7	9577587	3	2.36	55	100.00			
chr11	11015290	93	12438320	94	14.23	419	99.05			
chr11	12438327	74	1289692	51	4.59	125	97.60			
chr12	13002409	5	14688192	2	1.69	27	88.89			
chr12	18424803	3	1951460	2	1.09	29	89.66			
chr13	34044854	1	7092420	5	36.88	335	100.00			
chr15	41989592	2	4471091	5	2.72	93	88.17			
chr16	7709134	8746097	1.04	31	96.77					
chr17	19041994	1	20503843	1	1.46	58	91.38			
chr19	31279103	3	3299591	5	1.72	38	94.74			
## TNFO	. 220 2 1				: (m-1	sh nama sama s			

^{##} INFO: 220.3 Mb are in Homozygous Regions (autosomal chromosomes)

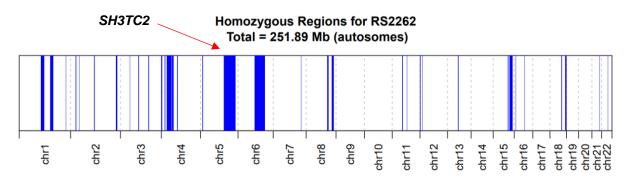
^{##} AutoMap v1.0 used for analysis

RS2304 Homozygosity Mapper



score	chr	from (bp)	to (bp)	from SNP	to SNP	build 37	
broa	ad - l	use this wher	n you expect	some gene	etic heter	ogeneity	
80	1	13782913	16035421	n/a	n/a	region	<u>genotypes</u>
80	1	205933114	209430651	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	2	38300255	47660952	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	2	48461119	61877525	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	2	70297445	74422789	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	3	45984767	49686351	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	3	49691651	51896834	n/a	n/a	region	<u>genotypes</u>
80	3	188874208	195619082	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	4	143880576	154549686	n/a	n/a	region	<u>genotypes</u>
80	6	29588087	29942825	n/a	n/a	region	<u>genotypes</u>
80	9	133208307	134850071	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	10	70529214	75400084	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	11	22859456	33058205	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	11	33286391	40115993	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	11	47734000	49186715	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	11	110164576	117136597	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	11	117136620	124224922	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	13	33835466	39724485	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	13	39724486	70924206	n/a	n/a	<u>region</u>	<u>genotypes</u>
78	1	236484250	236735742	n/a	n/a	region	<u>genotypes</u>
72	1	16948842	18736149	n/a	n/a	<u>region</u>	<u>genotypes</u>
70	2	64104681	69399210	n/a	n/a	<u>region</u>	<u>genotypes</u>
70	4	136355734	143880350	n/a	n/a	region	<u>genotypes</u>
66	11	125620870	126473292	n/a	n/a	<u>region</u>	<u>genotypes</u>
65	20	35466317	35869591	n/a	n/a	<u>region</u>	<u>genotypes</u>
64	6	33009538	33211912	n/a	n/a	region	<u>genotypes</u>

RS2262 (HG38) AutoMap



RS2262.HomRegions.tsv

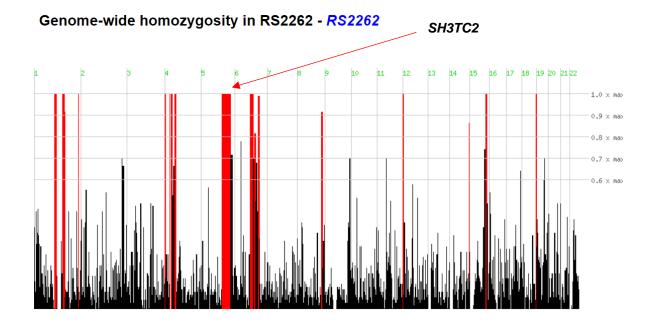
#Chr	Begin End		Size(Mb)		Nb_varia	ants	Percentage_homozygosity	
chr1	104891386	6	12044938			309	97.09	
chr1	149929093		15189508	34	1.97	120	99.17	
	153816674		16520613		11.39		98.03	
	226301129		22749319				94.74	
chr2	23639016		24729843	3	1.09	32	96.87	
chr2	27377372		28618566	5	1.24	48	93.75	
chr2	42055492		43397939	9	1.34	26	96.15	
chr2	113641568	8	11684239	51	3.20	26	88.46	
chr2	219641928	8	22565171	13	6.01	58	96.55	
chr3	45225829		46532766	5	1.31	56	96.43	
	86051159		88950800				96.87	
chr3	135249598	8	13812417		2.87	37	97.30	
chr4	60442	3768062	3.71	214	96.73			
chr4	16512125		18817262			40	90.00	
chr4	25914204		49242839	9	23.33	231	96.54	
chr4	51029884		59117979	9	8.09	100	100.00	
chr4	77075642		79408189	9	2.33	53	92.45	
	9190486							
	112420412					931	98.71	
	80203029		11085876		30.66	279	99.28	
chr6	110858798	8	13082759	97	19.97	222	99.10	
chr7	134579534		13568182		1.10		97.83	
chr8	103372760				5.92	28	100.00	
chr8	125357656	6	13447576	54	9.12	87	97.70	
chr11	49124286		51422246	5	2.30	58	89.66	
chr11	70433660		71538486	5	1.10	46	89.13	
	14838			120	100.00			
chr12	11049329		12717761		1.67		89.86	
chr13	11049329 51029632		52712888	3	1.68	54	88.89	
	71112406		73253373		2.14	43	90.70	
chr15	80597358		82343159	5		37	97.30	
chr15	82463033		92992967			293		
chr16	7607430 8	8735858	1.13	39	94.87			
chr16	49280926		50301239	9	1.02	30	93.33	
chr18	55588156		58019029	5			91.84	
chr18	74156381		90160220				100.00	
chr21	37008356		38575773	3			89.58	
chr22	30664042		31703618	3	1.04	46	97.83	
							chromosomes)	

^{##} INFO: 251.89 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

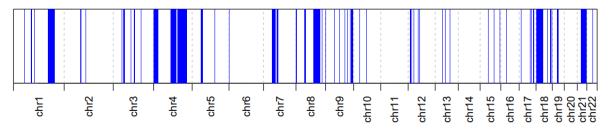
RS2262 Homozygosity Mapper



score	chr	from (bp)	to (bp)	from SNP	to SNP	build 37	
broa	ad - เ	use this whe	n you expect	some gene	etic heter	ogeneity	
80	1	105893150	111697416	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	1	111762784	120157112	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	1	149929093	151895084	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	1	155754524	161548369	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	1	236427359	236795232	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	4	60442	3768062	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	4	25914204	39214773	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	4	52085047	61732971	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	5	112420412	134319338	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	5	134608353	140648036	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	5	141655225	150061432	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	5	150117548	157667763	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	6	80203029	96799933	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	12	552292	3278531	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	15	84186916	90282036	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	18	74147887	80177972	n/a	n/a	<u>region</u>	<u>genotypes</u>
79	6	121654311	129157766	n/a	n/a	<u>region</u>	<u>genotypes</u>
75	1	153995011	155731264	n/a	n/a	<u>region</u>	<u>genotypes</u>
73	1	161548828	164357216	n/a	n/a	<u>region</u>	<u>genotypes</u>
73	8	125436603	132972576	n/a	n/a	<u>region</u>	<u>genotypes</u>
69	14	104889903	104950904	n/a	n/a	<u>region</u>	<u>genotypes</u>
65	6	104852228	109448097	n/a	n/a	<u>region</u>	<u>genotypes</u>

RS2297 (HG38) AutoMap

Homozygous Regions for RS2297 Total = 352.54 Mb (autosomes)

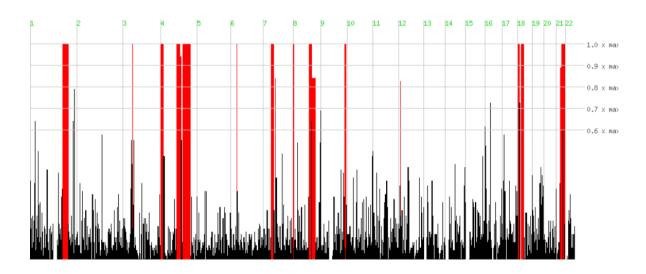


RS2297	Hom Regions.tsv				
#Chr	Begin End	Size(Mb)	Nb_vari	ants	Percentage_homozygosity
chr1	52688244	53793207	1.10	27	88.89
chr1	8663 5966	88983595	2.35	14	92.86
		91328534	2.13	40	92.50
chr1	101996890	104073253	2.08	15	100.00
chr1	171016428	202733925	31.72		99.17
		84688599	5.00		89.66
			1.51		95.45
		45146179	2.39		90.77
		53064759	2.71 1.35	172	94.77
					93.18
				24	
	100898785		4.65		91.43
	136982453 60478 8981454		1.32	21	92.59
	8981834 2241457			97 12	
					96.69
chr4	83462582 102911530	112356901	9.45	124	97.58
				390	
			9.75		92.11
			1.42		100.00
	1515139 2890049		100.00		
	41025253			301	99.34
chr7	63580858	71300517	7.72	113	94.69
chr8	63580858 213226 3128982	2.92 94	100.00		
chr8	41728059	47673299	5.95	27	88.89
chr8	85644048	117171312	31.53	205	99.02
chr8		130116875	1.37	11	90.91
chr9	52625 2028942	1.98 57	100.00		
	41964752		1.15		92.31
		70625419	1.11	24	95.83
					89.47
	107170286			39	
		122120195	1.40		90.70 90.24
		133208251	4.21	277	98.56
	1332 28570			87	
					97.56
		64826405	1.50 2.01	13	92.31
chr12	9997058 1102168				
chr12	13675725	14771094	1.10	18	88.89
chr12	1869 3759	19942516	1.25	13	100.00
chr12	28259462	29516529	1.26	26	92.31
chr12	4989 6945	50930274	1.03	52	90.38
chr12	57108399	59719948	2.61	84	90.48
chr13	36433370	37564593	1.13	11	90.91
chr13	49534116	50823304	1.29	19	94.74
chr13	73062667	75286865	2.22		93.75
	37966571	39741945	1.78	21	95.24
		70051219	1.03		94.74
		99105607	2.14		89.47
		27257702		22	90.91
		11747740	1.20	54	90.74 92.31
		54949462			
		61480239 73285213	1.42 3.76		91.67 89.19
	2729179 3742572		89.74	-	05.15
	5133200 34744976			97 47	
			1.64		88.24
		72543546	2.67	27	92.59
		79461207	2.21		92.31
		28791558	5.43		89.47
		44935616	26.80		98.59
chr22	28030140	29094509	1.06		91.67
## INFO	: 352.54 Mb are :	in Homozygous Re	gions (a	utosomal	chromosomes)
*** 0					

AutoMap v1.0 used for analysis

RS2297 Homozygosity Mapper

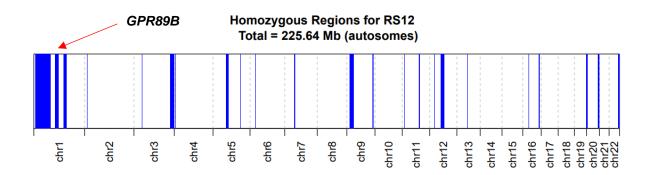
Genome-wide homozygosity in RS2297 - RS2297



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

bro	ad -	use this whe	en you expec	t some gene	etic hetero	ngeneity	
80	1	175330342	186388391	n/a	n/a	region	g <u>enotypes</u>
80	1	186399206	201209630	n/a	n/a	<u>region</u>	g <u>enotypes</u>
80	1	201209954	202733925	n/a	n/a	region	g <u>enotypes</u>
80	3	50351176	52834652	n/a	n/a	region	g <u>enotypes</u>
80	4	59576	1804285	n/a	n/a	region	g <u>enotypes</u>
80	4	1807400	3445057	n/a	n/a	region	g <u>enotypes</u>
80	4	3445065	8981422	n/a	n/a	region	g <u>enotypes</u>
80	4	9248704	15987567	n/a	n/a	region	g <u>enotypes</u>
80	4	86103075	102901141	n/a	n/a	region	<u>genotypes</u>
80	4	119410031	143880509	n/a	n/a	region	g <u>enotypes</u>
80	4	143880576	161385908	n/a	n/a	region	<u>genotypes</u>
80	6	31029892	31377994	n/a	n/a	region	<u>genotypes</u>
80	6	32584435	32741569	n/a	n/a	region	g <u>enotypes</u>
80	7	40860576	44800398	n/a	n/a	region	g <u>enotypes</u>
80	7	44801186	48925545	n/a	n/a	region	g <u>enotypes</u>
80	7	48925839	56813468	n/a	n/a	region	<u>genotypes</u>
80	8	213226	3128982	n/a	n/a	region	g <u>enotypes</u>
80	8	85655705	96784886	n/a	n/a	region	g <u>enotypes</u>
80	9	127824409	128716597	n/a	n/a	<u>region</u>	g <u>enotypes</u>
80	9	129049809	133205798	n/a	n/a	region	g <u>enotypes</u>
80	9	133228570	134727349	n/a	n/a	region	g <u>enotypes</u>
80	18	5133200	11610333	n/a	n/a	region	g <u>enotypes</u>
80	18	20954741	34828936	n/a	n/a	region	g <u>enotypes</u>
80	21	29553539	36387820	n/a	n/a	region	g <u>enotypes</u>
80	21	39127824	44573942	n/a	n/a	region	g <u>enotypes</u>
75	4	102911530	109347459	n/a	n/a	<u>region</u>	g <u>enotypes</u>
71	21	21418616	29321645	n/a	n/a	region	g <u>enotypes</u>
70	21	44573974	44934070	n/a	n/a	region	g <u>enotypes</u>
67	7	63635854	65200707	n/a	n/a	<u>region</u>	g <u>enotypes</u>
67	8	100709671	117171312	n/a	n/a	region	g <u>enotypes</u>
66	12	10218164	11021614	n/a	n/a	<u>region</u>	<u>genotypes</u>

RS12 (HG19) AutoMap



RS12 HomRegions.tsv

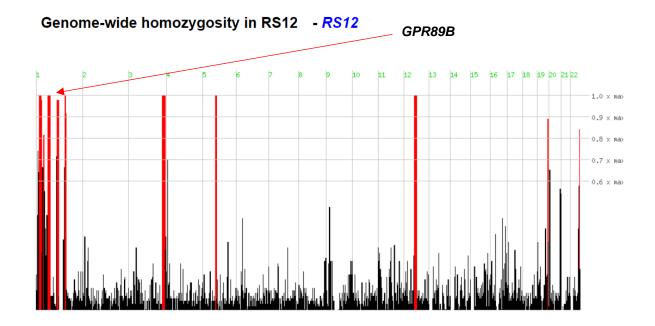
#Chr	Begin End	Size(Mb)	Nb_vari	ants	Percentage_homozygosity
chr1	6418882 1290728	2 6.49	105	95.24	
chr1	13696047	16385131	2.69	88	100.00
chr1	17273493	82432184	65.16	766	98.69
chr1	104068860	120539331	16.47	169	98.22
chr1	145456732	152277210	6.82	119	93.28
chr1	152749045	159802627	7.05	217	100.00
chr2	10566804	12864766	2.30	40	100.00
chr3	38524742	40351484	1.83	30	90.00
chr3	179143941	197765432	18.62	229	93.89
chr4	6374468 8608634	2.23 63	96.83		
chr5	65108215	77425099	12.32	107	91.59
chr5	135287029	137781016	2.49	29	93.10
chr6	26638503	28542424	1.90	26	92.31
chr7	47342857	52153027	4.81	70	94.29
chr9	12708958	33344058	20.64	98	91.84
chr9	127982775	131689361	3.71	94	88.30
chr11	10647702	11944265	1.30	26	88.46
chr11	82996986	86175193	3.18	27	96.30
chr12	21689882	22778701	1.09	29	89.66
chr12	54974803	56079084	1.10	28	89.29
chr12	56348028	71898358	15.55	166	96.39
chr13	51603768	53421432	1.82	31	90.32
chr16	29376400	30510571	1.13	29	93.10
chr16	77910418	81241100	3.33	51	88.24
chr19	56549532	59074653	2.53	128	99.22
chr20	428767 5169877	4.74 99	97.98		
chr20	56190634	62903550	6.71	181	98.34
chr22	43555194	51183255	7.63	186	98.92
UU TNEO	. 225 64 Mb		_: / _		-1

^{##} INFO: 225.64 Mb are in Homozygous Regions (autosomal chromosomes)

^{##} AutoMap v1.0 used for analysis

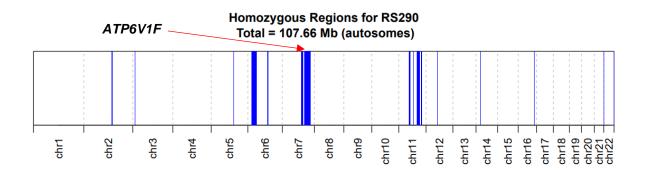
^{##} Variant filtering parameters used: DP=8, percaltlow=.25, percalthigh=.75, binomial=.000001, maxgap=10
Other parameters used: window=7, windowthres=5, minsize=1, minvar=25, minperc=88, chrX=No, extend=1

RS12 Homozygosity Mapper



score	chr	from (bp)	to (bp)	from SNP	to SNP	build 37				
bro	oad -	use this whe	n you expect	you expect some genetic heterogeneity						
80	1	17320118	21896887	n/a	n/a	<u>region</u>	<u>genotypes</u>			
80	1	22329063	26608865	n/a	n/a	<u>region</u>	<u>genotypes</u>			
80	1	63269580	78024345	n/a	n/a	region	<u>genotypes</u>			
80	1	154207635	156785762	n/a	n/a	<u>region</u>	<u>genotypes</u>			
80	3	179143941	195346352	n/a	n/a	<u>region</u>	<u>genotypes</u>			
80	5	70357186	76506914	n/a	n/a	<u>region</u>	<u>genotypes</u>			
80	12	58177379	71158404	n/a	n/a	<u>region</u>	<u>genotypes</u>			
78	1	26646730	32127911	n/a	n/a	<u>region</u>	<u>genotypes</u>			
78	1	111784962	120295872	n/a	n/a	<u>region</u>	<u>genotypes</u>			
73	1	156845492	159802627	n/a	n/a	<u>region</u>	<u>genotypes</u>			
71	19	56572832	58151286	n/a	n/a	<u>region</u>	<u>genotypes</u>			
67	22	47857576	50751529	n/a	n/a	<u>region</u>	<u>genotypes</u>			
65	1	40235489	43779724	n/a	n/a	<u>region</u>	<u>genotypes</u>			

RS290 (HG19) AutoMap



RS290.HomRegions.tsv

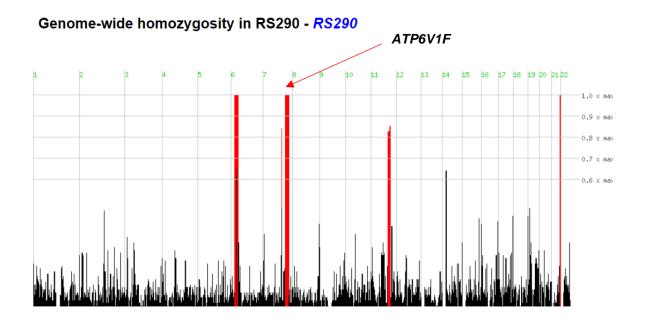
#Chr	Begin	End	Size(Mb)	Nb_vari	ants	Percentage_homozygosity
chr2	1364074	45	141457985	5.05	29	89.66
chr3	1106409	1	12571420	1.51	26	88.46
chr5	1104487	53	112676191	2.23	32	90.62
chr6	1767524	6	29910289	12.24	201	99.50
chr6	2991328	2	41533579	11.62	709	99.86
chr6	4190378	3	42933874	1.03	26	92.31
chr6	9762637	4	102312104	4.69	34	91.18
chr7	9522192	7	100547307	5.33	103	93.20
chr7	1006786	10	102147284	1.47	58	93.10
chr7	1106290	54	140218464	29.59	246	98.37
chr11	4982919	3	56143156	6.31	44	88.64
chr11	7123845	3	72296039	1.06	36	88.89
chr11	8981930	4	104971210	15.15	134	97.01
chr11	1104530	09	113114313	2.66	44	88.64
chr12	5655911	3	57627717	1.07	38	89.47
chr14	2001020	7	21215692	1.21	58	96.55
chr16	7924607	8	81211496	1.97	36	88.89
chr21	4632165	9	47978321	1.66	100	96.00
chr22	4894233	9	50750879	1.81	32	90.62
		4.4				

^{##} INFO: 107.66 Mb are in Homozygous Regions (autosomal chromosomes)

^{##} AutoMap v1.0 used for analysis

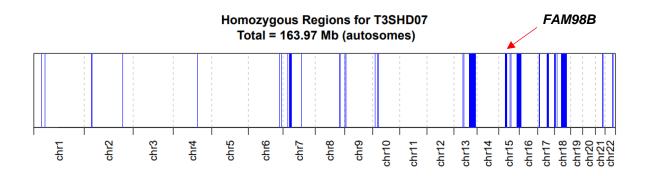
^{##} Variant filtering parameters used: DP=8, percaltlow=.25, percalthigh=.75, binomial=.000001, maxgap=10
Other parameters used: window=7, windowthres=5, minsize=1, minvar=25, minperc=88, chrX=No, extend=1

RS290 Homozygosity Mapper



score	chr	from (bp)	to (bp)	from SNP	to SNP	build 37					
broad - use this when you expect some genetic heterogeneity											
80	6	17675246	29760352	n/a	n/a	<u>region</u>	genotypes				
80	6	30229076	31323048	n/a	n/a	<u>region</u>	genotypes				
80	6	31324210	32008198	n/a	n/a	<u>region</u>	<u>genotypes</u>				
80	6	32552081	38820599	n/a	n/a	<u>region</u>	genotypes				
80	7	120906759	130148869	n/a	n/a	<u>region</u>	genotypes				
80	7	130297119	140055425	n/a	n/a	<u>region</u>	<u>genotypes</u>				
80	21	46602483	47978321	n/a	n/a	<u>region</u>	<u>genotypes</u>				
68	11	99690428	104971210	n/a	n/a	region	genotypes				
67	7	99705771	100547211	n/a	n/a	region	genotypes				
66	11	89819304	99690286	n/a	n/a	region	genotypes				

T3-SHD-07 (HG38) AutoMap



T3SHD07. Hom Regions. tsv

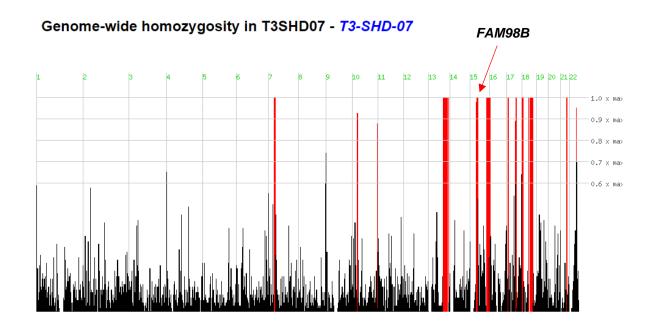
		,					
#Chr	Begin End		Size(Mb))	Nb_varia	ants	Percentage_homozygosity
	36180210						
chr1	55040188		56579217		1.54	29	93.10
chr2	37028663	3	39768768		2.74	50	94.00
chr2	18901014	17	19020002	27	1.19	36	88.89
chr4	11902689				1.60		97.67
chr6	15104186	96	15209896	50	1.06	32	93.75
chr6	16066423		16316623				88.89
chr7	22856612	2	24285140	9	1.43	42	100.00
chr7	30976403	3	38245048	3	7.27	136	98.53
chr7	38245375	5	41689849	5	3.44	43	95.35
chr7	90268389	9	92397873	3	2.13	39	89.74
					2.74	26	96.15
		2123639			98.31		
chr9	4850436	6554589	1.70		92.59		
chr10	12026543		14530645		2.50	70	91.43
chr10	24433017	7	28873235		4.44		97.40
chr13	43214022	2	45596474		2.38	45	93.33
chr13	49377057	7	50823304		1.45	36	91.67
chr13	75817336	5	108820538		33.00	232	95.26
chr15	30516504	1	32158503	3	1.64	61	90.16
					9.32		97.98
chr15	55498183	3	56631597	7	1.13	27	96.30
chr15	60385961	L	62254261	L	1.87	26	92.31
chr15	88032954	1	99974289	9	11.94	250	98.80
chr16	1465414	7676755	6.21	378	97.62		
chr16	7693416	8779636	1.09	38	92.11		
chr17	7342187	11632786)	4.29	248	98.79	
chr17	46694746	9	54930294	1	8.24	250	97.20
chr18	348265	6947144	6.60	87	96.55		
chr18	12718648	3	14132403	3	1.41	27	88.89
chr18	32677037	7	59469637	7	26.79	330	98.18
chr21	32584269	9	36487362	2	3.90	98	96.94
chr22	36239710	9	39233324	1	2.99	119	95.80
## INFO:	163.97	Mb are i	in Homozy	gous Reg	gions (au	utosomal	chromosomes)

^{##} INFO: 163.97 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-SHD-07 Homozygosity Mapper



score	chr	from (bp)	to (bp)	from SNP	to SNP	build 37	
broad - use this when you expect some genetic heterogeneity							
80	7	31092621	36686871	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	13	79371937	108659427	n/a	n/a	region	<u>genotypes</u>
80	15	34893611	40166370	n/a	n/a	region	<u>genotypes</u>
80	15	88184105	99792594	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	16	1474084	3069019	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	16	3069383	4987497	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	17	7347840	11629398	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	17	50143520	53953552	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	18	346821	6942296	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	18	34864078	59469637	n/a	n/a	<u>region</u>	<u>genotypes</u>
80	21	32584269	36391463	n/a	n/a	<u>region</u>	<u>genotypes</u>
78	15	32776687	34893609	n/a	n/a	<u>region</u>	<u>genotypes</u>
76	22	36261743	37724034	n/a	n/a	<u>region</u>	<u>genotypes</u>
74	10	24433017	28437096	n/a	n/a	region	<u>genotypes</u>
71	17	46710944	48113563	n/a	n/a	region	<u>genotypes</u>
70	10	133240280	133532307	n/a	n/a	<u>region</u>	<u>genotypes</u>