

A

Position	Parent Genotypes			Offspring Genotypes					
	FOGM	F1Mo	F1Fa	1	2	3	4	5	6
79	0/1	1/1	0/0	0/0	0/0	0/1	0/0	0/0	0/0
236	0/0	0/1	0/1	0/1	0/1	1/1	0/1	0/0	0/1
274	0/1	0/0	0/1	0/0	0/0	0/1	0/0	0/0	0/0
409	0/1	0/0	0/1	0/0	0/0	0/1	0/0	0/0	0/0
456	0/0	0/1	0/1	0/1	./.	1/1	0/1	0/0	0/0
540	0/0	0/1	0/1	0/1	0/1	1/1	0/0	0/0	0/1
572	0/1	0/1	0/0	0/1	0/1	0/1	0/1	0/0	0/0
626	0/1	0/0	0/1	./.	0/0	0/1	0/0	0/0	0/0
631	0/1	0/0	0/1	0/0	0/0	0/1	0/0	0/0	0/0
656	1/2	0/2	0/1	0/0	0/1	1/2	0/2	0/1	0/1
660	0/1	0/0	0/1	0/0	0/0	0/1	0/0	0/0	0/1
662	0/1	0/0	0/1	0/0	0/0	0/1	0/0	0/0	0/1
669	0/0	0/1	0/1	0/1	0/1	1/1	0/1	0/0	0/1
674	0/0	0/1	0/1	0/1	0/1	1/1	0/1	0/0	0/1
705	0/1	0/1	0/0	0/1	0/1	0/1	0/1	0/0	0/0
798	0/1	0/1	0/0	0/1	0/1	1/1	0/1	0/0	0/0
819	0/0	0/1	0/1	0/1	0/1	1/1	0/1	0/0	0/1
821	0/1	0/0	0/1	0/0	0/0	0/0	0/0	0/0	0/1
840	0/1	0/0	0/1	0/0	0/0	0/0	0/0	0/0	0/1
842	0/1	0/1	0/0	0/1	0/1	0/1	./.	0/0	0/0
855	0/0	0/1	0/1	0/1	0/1	1/1	0/1	0/0	0/1
937	0/1	0/0	0/1	0/0	0/0	./.	0/0	0/0	0/0
938	0/0	0/1	0/1	0/0	0/1	0/0	0/1	1/1	0/1
986	0/1	0/0	0/1	0/0	0/0	0/1	0/0	0/0	0/1
987	0/1	0/0	0/1	0/0	0/0	0/1	0/0	./.	0/1
1029	0/1	0/0	0/1	0/0	0/0	0/1	0/0	0/0	0/1
1059	0/0	0/1	0/1	0/1	0/1	./.	0/1	0/0	0/0
1121	0/1	0/0	0/1	./.	0/0	0/2	./.	0/0	0/1
1246	0/0	0/1	0/1	0/1	0/1	1/1	0/1	0/0	0/1
1248	0/1	0/1	0/0	0/1	0/1	0/1	0/1	0/0	0/0

B

Parents	Offspring	Type	Reason for rejection
GMF	123456		
HAB	AABAAA	Reject	Invalid parent call
AHH	HHBHAH	Intercross	
HAH	AAHAAA	Reject	Fails MQ threshold
HAH	AAHAAA	Paternal	
AHH	H.BHAA	Intercross	
AHH	HHBAAH	Intercross	
HHA	HHHHAA	Maternal	
HAH	.AHAAA	Paternal	
HAH	AAHAAA	Paternal	
---	-----	Reject	Invalid parent call
HAH	AAHAAH	Paternal	
HAH	AAHAAH	Paternal	
AHH	HHBHAH	Intercross	
AHH	HHBHAH	Intercross	
HHA	HHHHAA	Maternal	
HHA	HHBHAA	Maternal	
AHH	HHBHAH	Intercross	
HAH	AAAAAH	Paternal	
HAH	AAAAAH	Paternal	
HHA	HHH.AA	Maternal	
AHH	HHBHAH	Intercross	
HAH	AA.AAA	Reject	Fails segregation test
AHH	AHBHAH	Intercross	
HAH	AAHAAH	Paternal	
HAH	AAHA.H	Paternal	
HAH	AAHAAH	Paternal	
AHH	HH.HAA	Intercross	
HAH	.AX.AH	Reject	Invalid offspring call 0/2
AHH	HHBHAH	Intercross	
HHA	HHHHAA	Maternal	

C

Maternal	Paternal	Intercross
123456	123456	123456
		HHBHAH
	AAHAAA	
		H.BHAA
		HHBAAH
HHHHAA		
	.AHAAA	
	AAHAAA	
	AAHAAH	
	AAHAAH	
		HHBHAH
		HHBHAH
HHHHAA		
HHBHAA		
		BHBHAH
	HAAAHA	
	HAAAHA	
HHH.AA		
		BHBHAH
		AHBHAH
	HAHAAH	
	HAHA.H	
	HAHAAH	
		BH.HAA
HHHHAA		BHBHAH

D

Maternal	Paternal	Intercross	Position
123456	123456	123456	
		HHBHAH	79
		HHBHAH	236
			274
	AAHAAA		409
		HHBHAH	456
		HHBHAH	540
HHHHAA			572
	AAHAAA		626
	AAHAAA		631
			656
	AAHAAH		660
	AAHAAH		662
		HHBHAH	669
		HHBHAH	674
HHHHAA			705
HHHHAA			798
		BHBHAH	819
	HAHAAH		821
	HAHAAH		840
HHHHAA			842
		BHBHAH	855
		BHBHAH	937
		BHBHAH	938
	HAHAAH		986
	HAHAAH		987
	HAHAAH		1029
		BHBHAH	1059
		BHBHAH	1121
HHHHAA		BHBHAH	1246
HHHHAA		BHBHAH	1248

E

Start	End	Maternal	Paternal	Intercross
1	235			
236	408			HHBHAH
409	571		AABAAA	HHBHAH
572	631	BBBBAA	AAHAAA	HHBHAH
632	659	BBBBAA		HHBHAH
660	662	BBBBAA	AAHAAH	HHBHAH
663	674	BBBBAA		HHBHAH
675	818	BBBBAA		
819	820	BBBBAA		BHBHAH
821	1029	BBBBAA	BABAAB	BHBHAH
1030	1246	BBBBAA		BHBHAH
1247	1248	BBBBAA		
1249	1789			

F

Start	End	Maternal	Paternal	Intercross
1	235			
236	408	BBBBAA	AABAAB	HHBHAH
409	571	BBBBAA	AABAAB	HHBHAH
572	631	BBBBAA	AABAAB	HHBHAH
632	659	BBBBAA	AABAAB	HHBHAH
660	662	BBBBAA	AABAAB	HHBHAH
663	674	BBBBAA	AABAAB	HHBHAH
675	818	BBBBAA		
819	820	BBBBAA	BABAAB	BHBHAH
821	1029	BBBBAA	BABAAB	BHBHAH
1030	1246	BBBBAA	BABAAB	BHBHAH
1247	1248	BBBBAA		
1249	1789			

G

Start	End	Maternal	Paternal	Intercross	Chromosome	cM
1	235				-	-
236	674	BBBBAA	AABAAB	HHBHAH	18	1.45
675	818	BBBBAA			18	-
819	1246	BBBBAA	BABAAB	BHBHAH	18	2.889
1247	1248	BBBBAA			18	-
1249	1789				-	-

Figure S1

Figure S1 Linkage map construction from raw low coverage genomic SNPs. The figure shows the process of calling markers for one scaffold region from raw SNPs (A) to final chromosome and marker assignment (G). See Supplementary Methods for full discussion. (A) Raw SNPs for 30 positions with GATK VCF calls for parents (F0GM, F0 Grandmother; F1Mo, F1 Mother; F1Fa, F1Father) and offspring (1-6; in the actual study, 69 offspring were present). (B) Assignment of SNPs to marker types. G=F0 Grandmother, M=F1 Mother, F=F1 Father. A=homozygous for allele A, B=homozygous for allele B, H=heterozygous for A and B, '.'=missing, '-'=invalid. (C) Separation of genotypes into marker types and grouping of SNPs into marker sub-regions. Marker sub-regions are bound by horizontal black lines and connected by vertical grey lines. Erroneous genotypes (at this point unknown to the algorithm) in red. (D) Consensus genotypes for all sub-regions. Bold, imputed or corrected genotypes. (E) Collapsed marker regions. Regions with maternal, paternal and intercross markers shown in bold; consistent genotypes in green, inconsistent genotypes in red. (F) Corrected and imputed marker regions. (G) Final collapsed maternal, paternal and intercross marker regions used to build linkage map, with resulting chromosome and cM marker assignments.