

## Malaria Genetics & Genomics: Segregation Data

The *Plasmodium falciparum* HB3 X Dd2 cross segregation data table is available below. Microsatellite markers and DNA primer sequences can be retrieved from the [STS database](#) or from the Segregation Table hyperlinks.  
 Last updated: Jan 7, 2000.

Chr	Sequencing Center	Last Update
1	Sanger Centre	99-Sep 22
2	TIGR/NMRC	99-Sep 22
3	Sanger Centre	99-Sep 22
4	Sanger Centre	99-Sep 22
5	Sanger Centre	99-Sep 22
6	Sanger Centre	99-Sep 22
7	Sanger Centre	00-Jan 07
8	Sanger Centre	99-Sep 22
9	Sanger Centre	99-Sep 30
10	TIGR	99-Sep 22
11	TIGR	99-Sep 22
12	Stanford University	99-Sep 30
13	Sanger Centre	99-Nov 26
14	TIGR	99-Sep 22

### Chromosome 1 inheritance in *P. falciparum* HB3xDd2 cross

[Top](#)

Marker	Synonym	Legend for Tables				Next	Parent	Progeny																																					
		STS	GenBank	position	framework			chromosome	DD2	HB3	B1SD	QC13	QC01	B4R3	SC05	TC08	GC03	3BA6	1B55	3BD5	SC01	QC34	QC23	TC05	GC06	D43	C188	C408	116	61	7C3	7C7	7C12	7C16	7C20	7C46	C101	7C111	7C126	7C140	7C159	7C170	7C183	7C421	7C424
C1M38	.	G38005	.	0	2	1	D	H	H	D	D	H	H	D	D	H	D	D	H	D	H	H	D	D	H	H	D	D	D	D	H	D	H	H	D	D	H	H	H	H	H	D	D	H	
C1M17	.	G38006	.	0	2	1	D	H	H	D	D	H	H	D	D	H	D	D	H	D	H	H	D	D	H	H	D	D	D	D	H	D	H	H	D	D	H	H	H	H	H	D	D	H	
RESA	.	.	.	0	2	1	D	H	H	D	D	H	H	D	D	H	D	D	H	D	H	H	D	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
C1M18	.	G38007	.	0	2	1	D	H	H	D	D	H	H	D	D	H	D	D	H	D	H	H	D	D	H	H	D	D	D	D	H	D	H	H	D	D	H	H	H	H	H	D	D	H	
C1M19	.	G38008	.	0	2	1	D	H	H	D	D	H	H	D	D	H	D	D	H	D	H	H	D	D	H	H	D	D	D	D	H	D	H	H	D	D	H	H	H	H	H	D	D	H	
C1M43	.	G42709	.	0	2	1	D	H	H	D	D	H	H	D	D	H	D	D	H	D	H	H	D	D	H	H	D	D	D	D	H	D	H	H	D	D	H	H	H	H	H	D	D	H	
C1M25	.	G37999	.	8.6	2	1	D	H	D	D	D	H	H	D	H	H	D	D	H	D	H	H	D	H	H	H	D	D	D	D	H	D	H	H	D	D	H	H	H	H	H	D	D	H	
C1M24	.	G38004	.	8.6	2	1	D	H	D	D	D	H	H	D	H	H	D	D	H	D	H	H	D	H	H	H	D	D	D	D	H	D	H	H	D	D	H	H	H	H	H	D	D	H	
C1M41	.	G42710	.	11.5	2	1	D	H	D	D	D	H	H	D	H	H	D	D	H	D	H	H	D	D	H	H	D	D	D	D	H	D	H	H	D	D	H	H	H	H	H	D	D	H	
C1M16	.	G38000	.	11.5	2	1	D	H	D	D	D	H	H	D	H	H	D	D	H	D	H	H	D	D	H	H	D	D	D	D	H	D	H	H	D	D	H	H	H	H	H	D	D	H	
C1M39	.	G38001	.	11.5	2	1	D	H	D	D	D	H	H	D	H	H	D	D	H	D	H	H	D	D	H	H	D	D	D	D	H	D	H	H	D	D	H	H	H	H	H	D	D	H	
C1M20	.	G38002	.	11.5	2	1	D	H	D	D	D	H	H	D	H	H	D	D	H	D	H	H	D	D	H	H	D	D	D	D	H	D	H	H	D	D	H	H	H	H	H	D	D	H	
C1M11	.	G38003	.	14.4	3	1	D	H	D	D	D	H	H	D	H	H	D	D	H	D	H	H	D	D	H	H	D	D	D	D	H	D	H	H	D	D	H	H	H	H	H	D	D	H	
B7M97	.	G42711	.	17.3	3	1	D	H	D	D	D	H	H	D	H	H	D	D	H	D	H	H	D	D	H	H	D	D	D	D	H	D	H	H	D	D	H	H	D	H	D	D	H		
CAATP caapt		G37797 X71765		17.3	3	1	D	H	D	D	D	H	H	D	H	H	D	D	H	D	H	H	D	D	H	H	D	D	D	D	H	D	H	H	D	D	H	H	D	H	D	D	H		
C1M10	.	G38009	.	25.9	3	1	D	H	D	D	D	H	H	H	D	H	D	D	H	D	H	H	D	D	H	H	D	D	D	D	H	D	H	H	D	D	H	H	D	H	D	D	H		
C1M32	.	G38010	.	25.9	3	1	D	H	D	D	D	H	H	H	D	H	D	D	H	D	H	H	D	D	H	H	D	D	D	D	H	D	H	H	D	D	H	H	D	H	D	D	H		
C1M29	.	G38011	.	25.9	3	1	D	H	D	D	D	H	H	H	D	H	D	D	H	D	H	H	D	D	H	H	D	D	D	D	H	D	H	H	D	D	H	H	D	H	D	D	H		
C1M27	.	G38012	.	28.8	3	1	D	H	D	D	D	H	H	H	D	H	D	D	H	D	H	H	D	D	H	H	D	D	D	D	H	D	H	H	D	D	H	H	D	H	D	D	H		
C1M8	.	G38013	.	31.7	3	1	D	H	D	D	D	H	H	H	D	H	D	D	H	D	H	H	D	D	H	H	D	D	D	D	H	D	H	H	D	D	H	H	D	H	D	D	H		
C1M4	.	G38014	.	34.6	3	1	D	H	D	D	D	H	H	H	D	H	D	D	H	D	D	H	D	D	H	H	D	D	D	D	H	D	H	H	D	D	H	H	D	H	D	D	H		
C1M31	.	G38015	.	34.6	2	1	D	H	D	D	D	H	H	H	D	H	D	D	H	D	D	H	D	D	H	H	D	D	D	D	H	D	H	H	D	D	H	H	D	H	D	D	H		
C1M30	.	G38016	.	34.6	2	1	D	H	D	D	D	H	H	H	D	H	D	D	H	D	D	H	D	D	H	H	D	D	D	D	H	D	H	H	D	D	H	H	D	H	D	D	H		
C1M12	.	G38017	.	34.6	2	1	D	H	D	D	D	H	H	H	D	H	D	D	H	D	D	H	D	D	H	H	D	D	D	D	H	D	H	H	D	D	H	H	D	H	D	D	H		
GARP	.	G37798 J03998		34.6	2	1	D	H	D	D	D	H	H	H	D	H	D	D	H	D	D	H	D	D	H	H	D	D	D	D	H	D	H	H	D	D	H	H	D	H	D	D	H		
B7M88	.	G42712	.	34.6	2	1	D	H	D	D	D	H	H	H	D	H	D	D	H	D	D	H	D	D	H	H	D	D	D	D	H	D	H	H	D	D	H	H	D	H	D	D	H		
C1M13	.	G38018	.	37.5	3	1	D	H	D	D	D	H	H	H	D	H	D	D	D	D	D	H	D	D	H	H	D	D	D	D	H	D	H	H	D	D	H	H	D	D	H	D	D	H	





C3M47	G37931	60.4	3	3	D	H	D	H	D	D	H	H	D	H	D	H	H	H	D	D	D	H	D	D	H	D	D	H	D	H	H	H	H	H	H	H	H	H	H	H	H	H	D	H	H		
C3M54	G37932	69.0	1	3	D	H	D	H	D	D	H	H	D	H	D	H	H	H	H	H	D	H	D	D	H	D	D	H	D	D	H	H	H	H	H	H	H	H	H	H	H	H	D	H	D	H	H
C3M43	G37988	71.9	3	3	D	H	D	H	D	D	H	H	D	H	D	D	H	H	H	H	D	H	D	D	H	D	D	H	D	D	H	H	H	H	H	H	H	H	H	H	H	D	H	D	H	H	
C3M45	G37933	74.8	1	3	D	H	D	H	D	D	H	H	D	H	D	D	H	H	H	H	D	H	D	D	H	D	D	H	D	D	H	H	H	H	H	H	H	H	H	H	H	D	H	H	H	H	
C3M38	G37987	74.8	1	3	D	H	D	H	D	D	H	H	D	H	D	D	H	H	H	H	D	H	D	D	H	D	D	H	D	D	H	H	H	H	H	H	H	H	H	H	H	D	H	H	H	H	
C3M14	G37911	74.8	1	3	D	H	D	H	D	D	H	H	D	H	D	D	H	H	H	H	D	H	D	D	H	D	D	H	D	D	H	H	H	H	H	H	H	H	H	H	H	D	H	H	H	H	

Chromosome 4 inheritance in *P. falciparum* HB3xDd2 cross

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Previous		Legend for Tables				Next		Parent		Progeny																																											
Marker	Synonym	STS	GenBank	position	framework	chromosome	DD2	HB3	B1SD	QC13	QC01	B4R3	SC05	TC08	GC03	3BA6	1BB5	3BD5	SC01	QC34	QC23	TC05	GC06	D43	C188	C408	116	61	7C3	7C7	7C12	7C16	7C20	7C46	C101	7C111	7C126	7C140	7C159	7C170	7C183	7C421	7C424										
C4M62		G37934		0	3	4	D	H	D	D	H	H	H	H	D	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D				
C4M11		G37935		2.9	2	4	D	H	D	D	H	H	H	H	D	H	D	D	D	D	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D			
C4M82		G37998		2.9	2	4	D	H	D	D	H	H	H	H	D	H	D	D	D	D	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D		
B9M21		G42728		5.8	3	4	D	H	D	D	H	H	H	H	D	D	H	D	D	D	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D		
C4M8		G37937		5.8	3	4	D	H	D	D	H	H	H	H	D	D	H	D	D	D	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D		
XB8M31		G42729		5.8	3	4	D	H	D	D	H	H	H	H	D	D	H	D	D	D	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D		
C4M32		G37936		5.8	3	4	D	H	D	D	H	H	H	H	D	D	H	D	D	D	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D		
C4M35		G37939		8.7	3	4	D	H	D	D	H	H	H	H	D	D	H	D	D	D	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D		
TA79		G38824	AF010567	8.7	3	4	D	H	D	D	H	H	H	H	D	D	H	D	D	D	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D		
PI9605	9605	G37808	T09605	11.6	3	4	D	H	D	D	H	H	H	H	D	D	H	D	D	D	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D		
C4M47		G37940		17.3	3	4	D	H	D	D	H	H	H	H	D	D	D	D	D	D	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D		
C4M31		G37941		20.2	3	4	D	H	D	D	H	H	H	H	D	D	D	D	D	D	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D		
SSP		G37773	M64107	20.2	3	4	D	H	D	D	H	H	H	H	D	D	D	D	D	D	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D		
C4M64		G44695		20.2	3	4	D	H	D	D	H	H	H	H	D	D	D	D	D	D	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D		
C4M50		G37989		20.2	3	4	D	H	D	D	H	H	H	H	D	D	D	D	D	D	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	
C4M49		G37942		20.2	3	4	D	H	D	D	H	H	H	H	D	D	D	D	D	D	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	
pSL10						4	D	H	H	D	H	H	H	H	D	D	H	D	D	D	H	H	D	H																													
pC4.D21						4	D	H	H	D	H	H	H	H	D	D	H	D	D	D	H	H	D	H																													
POLYA		G37809	L18785	25.9	3	4	D	H	H	D	H	H	H	H	D	D	H	D	D	D	H	H	D	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D		
C4M29		G37943		25.9	3	4	D	H	H	D	H	H	H	H	D	D	H	D	D	D	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	
C4M67		G37944		25.9	3	4	D	H	H	D	H	H	H	H	D	D	H	D	D	D	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D
C4M48		G37945		25.9	3	4	D	H	H	D	H	H	H	H	D	D	H	D	D	D	H	H	D	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D
C4M17		G37946		25.9	3	4	D	H	H	D	H	H	H	H	D	D	H	D	D	D	H	H	D	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D
C4M36		G37947		25.9	3	4	D	H	H	D	H	H	H	H	D	D	H	D	D	D	H	H	D	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D
C4M78		G37948		25.9	3	4	D	H	H	D	H	H	H	H	D	D	H	D	D	D	H	H	D	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D
C4M39		G37990		31.6	3	4	D	H	H	D	H	H	H	H	D	D	H	D	D	D	H	H	D	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D
C4M51		G37949		37.3	3	4	D	H	H	D	H	H	H	H	D	D	H	D	D	D	H	H	D	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	
C4M40		G37991		37.3	3	4	D	H	H	D	H	H	H	H	D	D	H	D	D	D	H	H	D	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D
C4M41		G37950		37.3	3	4	D	H	H	D	H	H	H*	H*	D	D	H*	D	D	D	H*	H	D	H*	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	
C4M19		G37954		40.2	3	4	D	H	H	D	H	H	H	H	D	D	H	D	H	D	H	H	D	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	
C4M69		G37956		43.1	3	4	D	H	H	D	H	H	H	H	D	D	H	D	H	D	H	H	D	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D
pSc11.34						4	D	H	H	D	H	H	H	H	D	D	H	D	D	D	H	H	D	H																													
pC4.H31						4	D	H	H	D	H	H	H	H	D	D	H	D	D	D	H	H	D	H																													
DHFR		G37810	M22159	43.1	3	4	D	H	H	D	H	H	H	H	D	D	H	D	H	D	H	H	D	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D		
C4M71		G37952		46.0	3	4	D	H	H	D	H	H	H	H	D	D	H	D	H	D	H	H	D	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	
C3M35		G37953		46																																																	





PF12	G37822	M28889	51.7	3	6	D	H	D	D	H	D	H	H	D	D	D	H	D	D	D	H	H	D	H	H	D	D	D	D	H	H	D	H	H	D	H	H	D
C6/9M17	G42803		54.6	2	6	D	H	D	D	H	D	H	H	D	D	D	H	D	D	D	H	H	D	H	H	D	D	D	D	H	H	D	H	H	D	H	H	D
C6/9M8	G42804		54.6	2	6	D	H	D	D	H	D	H	H	D	D	D	H	D	D	D	H	H	D	H	H	D	D	D	D	H	H	D	H	H	D	H	H	D
C13M48	G42805		54.6	2	6	D	H	D	D	H	D	H	H	D	D	D	H	D	D	D	H	H	D	H	H	D	D	D	D	H	H	D	H	H	D	H	H	D
B5M88	G42806		66.0	3	6	D	H	D	D	H	D	H	H	D	D	D	H	D	D	D	H	H	D	H	H	D	D	D	H	D	H	D	H	D	D	D	D	D
TA87	G38838	AF010571	71.1	3	6	D	H	H	D	H	D	H	H	D	D	D	H	D	D	D	H	H	D	H	H	D	D	D	H	D	H	D	H	D	H	D	H	D
C6/9M12	G42807		71.1	3	6	D	H	H	D	H	D	H	H	D	D	D	H	D	D	D	H	H	D	H	H	D	D	D	H	D	H	D	H	D	H	D	H	D
B5M122	G42808		71.1	3	6	D	H	H	D	H	D	H	H	D	D	D	H	D	D	D	H	H	D	H	H	D	D	D	H	D	H	D	H	D	H	D	H	D
B5M13	G42809		74.6	3	6	D	H	H	D	H	D	H	H	D	D	D	H	D	D	D	H	H	D	H	H	D	D	D	H	D	D	D	H	D	H	D	H	D
B5M1	G42810		80.3	3	6	D	H	H	D	H	D	H	H	D	D	D	H	D	D	D	H	H	D	H	H	D	D	D	H	D	D	D	H	D	H	D	H	D
BM6	G42811		80.3	3	6	D	H	H	D	H	D	H	H	D	D	D	H	D	D	D	H	H	D	H	H	D	D	D	H	D	D	D	H	D	H	D	H	D
B5M30	G42812		80.3	3	6	D	H	H	D	H	D	H	H	D	D	D	H	D	D	D	H	H	D	H	H	D	D	D	H	D	D	D	H	D	H	D	H	D
B5M142	G42813		83.2	3	6	D	H	H	D	H	D	H	H	D	D	D	H	D	D	D	H	H	D	H	H	D	D	D	H	D	D	D	H	D	H	D	H	D
TA67	G38892	AF010560	83.2	3	6	D	H	H	D	H	D	H	H	D	D	D	H	D	D	D	H	H	D	H	H	D	D	D	H	D	H	D	H	D	H	D	H	D
BM70	G42814		86.1	3	6	D	H	H	D	H	D	D	H	D	D	D	H	D	D	D	H	H	D	H	H	D	D	D	H	D	D	D	H	D	H	D	H	D
BM55	G42815		86.1	3	6	D	H	H	D	H	D	D	H	D	D	D	H	D	D	D	H	H	D	H	H	D	D	D	H	D	D	D	H	D	H	D	H	D
BM38	G42816		91.8	3	6	D	H	H	D	H	D	D	H	D	D	D	H	D	D	D	H	H	D	H	H	D	D	D	H	D	D	D	H	D	H	D	H	D
ARA	G37821	X17483	91.8	3	6	D	H	H	D	H	D	D	H	D	D	D	H	D	D	D	H	H	D	H	H	D	D	D	H	D	D	D	H	D	H	D	H	D
ARA4	G37820	X17487	94.7	3	6	D	H	H	D	H	D	D	H	D	D	D	H	D	D	D	H	H	D	H	H	D	D	D	H	D	D	D	H	D	H	H	H	D
B5M8	G42817		97.6	3	6	D	H	H	H	H	D	D	D	D	D	H	D	D	D	D	H	H	D	H	H	D	D	D	H	D	D	D	H	D	H	H	H	D
BM103	G42818		100.5	3	6	D	H	H	H	D	D	D	H	D	D	D	H	D	D	D	H	H	D	H	H	D	D	D	H	D	D	D	H	D	H	H	H	D
B5M110	G42819		103.4	2	6	D	H	H	H	D	D	D	H	D	D	D	H	D	D	D	H	H	D	H	H	D	D	D	H	D	D	D	H	D	H	H	H	D
B5M26	G42820		106.3	3	6	D	H	H	H	D	D	D	H	D	D	D	H	D	D	D	H	H	D	H	H	D	D	D	H	D	D	D	H	D	H	H	H	D

Chromosome 7 inheritance in *P. falciparum* HB3xDd2 cross

Top

Previous		Legend for Tables					Next		Parent		Progeny																																					
Marker	Synonym	STS	GenBank	position	framework	chromosome	DD2	HB3	B1SD	QC13	QC01	B4R3	SC05	TC08	GC03	3BA6	1BB5	3BD5	SC01	QC34	QC23	TC05	GC06	D43	C188	C408	116	61	7C3	7C7	7C12	7C16	7C20	7C46	C101	7C111	7C126	7C140	7C159	7C170	7C183	7C421	7C424					
Pr2579	p2579	G37787	T02579	0	2	7	D	H	H	H	D	H	H	H	H	D	D	D	D	D	D	H	D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
C6/9M14		G44701		0	3	7	D	H	H	H	D	H	H	H	H	D	D	D	D	D	D	H	D	H	D	H	D	H	H	H	D	H	H	D	D	H	H	H	H	H	H	H	H	D	D	D	D	
pB300.13				0	3	7	D	H	H	H	D	H	H	H	H	D	D	D	D	D	D	H	D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
pS590.20				0	3	7	D	H	H	H	D	H	H	H	H	D	D	D	D	D	D	H	D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
B5M100	G44400			0	3	7	D	H	H	H	D	H	H	H	H	D	D	D	D	D	D	H	D	H	D	H	D	H	H	H	D	H	H	D	D	H	H	H	H	H	H	H	D	D	D	D		
B5M141	G44401			2.9	2	7	D	H	H	H	H	H	H	H	H	D	D	D	D	D	D	H	D	H	D	H	D	H	H	H	D	H	H	D	D	H	H	H	H	H	H	H	D	D	D	D		
pS590.17						7	D	H	H	H	H	H	H	H	H	D	D	D	D	D	D	H	D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
BM25	G44402			5.8	3	7	D	H	H	H	H	H	H	H	H	D	D	D	D	D	D	H	D	H	D	D	D	H	H	H	D	H	H	D	D	H	H	H	H	H	H	H	D	D	D	D		
B5M2	G44403			5.8	3	7	D	H	H	H	H	H	H	H	H	D	D	D	D	D	D	H	D	H	D	D	D	H	H	H	D	H	H	D	D	H	H	H	H	H	H	H	D	D	D	D		
B5M12	G44404			5.8	3	7	D	H	H	H	H	H	H	H	H	D	D	D	D	D	D	H	D	D	D	D	D	H	H	H	D	H	H	D	D	H	H	H	H	H	H	H	D	D	D	D		
LT103	G38852	AF015468		5.8	3	7	D	H	H	H	H	H	H	H	H	D	D	D	D	D	D	H	D	H	D	D	D	H	H	H	D	H	H	D	D	H	H	H	H	H	H	H	D	D	D	D		
BM2	G44405			5.8	3	7	D	H	H	H	H	H	H	H	H	D	D	D	D	D	D	H	D	H	D	D	D	H	H	H	D	H	H	D	D	H	H	H	H	H	H	D	D	D	D			
PE14D	G38851	AF015462		11.5	3	7	D	H	H	H	H	H	H	H	H	D	D	D	D	D	D	H	D	D	D	D	D	H	H	H	D	H	H	D	D	H	H	H	H	H	H	D	D	D	D			
PE87	G38850	AF015471		14.4	3	7	D	H	H	H	H	H	H	H	H	D	D	D	D	D	D	H	D	D	D	D	D	H	H	H	D	H	H	D	D	H	H	H	H	H	D	D	D	D				
B5M129	G44407			17.3	3	7	D	H	H	H	H	H	H	H	H	D	D	D	D	D	D	H	D	D	D	D	D	H	H	H	D	H	H	D	D	H	H	H	H	H	H	D	D	D	D			
HSP86	G37828	L34027		17.3	3	7	D	H	H	H	H	H	H	H	H	D	D	D	D	D	D	H	D	D	D	D	D	H	H	H	D	H	H	D	D	H	H	H	H	H	H	D	D	D	D			
B5M77	G44408			17.3	3	7	D	H	H	H	H	H	H	H	H	D	D	D	D	D	D	H	D	D	D	D	D	H	H	H	D	H	H	D	D	H	H	H	H	H	D	D	D	D				
B5M97	G44406			17.3	3	7	D	H	H	H	H	H	H	H	H	D	D	D	D	D	D	H	D	D	D	D	D	H	H	H	D	H	H	D	D	H	H	H	H	H	D	D	D	D				
P4	G38833	AF030694		17.3	3	7	D	H	H	H	H	H	H	H	H	D	D	D	D	D	D	H	D	D	D	D	D	H	H	H	D	H	H	D	D	H	H	H	H	H	D	D	D	D				
1H6	p1h6	G37786	AF030694	17.3	3	7	D	H																																								





GP195	G37788	X02919	17.4	3	9	D	H	D	H	H	D	H	H	H	D	D	H	D	H	H	H	D	D	D	D	H	D	D	H	H	H	H	D	H	H	H	H	H	D	D	D			
MMSA	G37834	M19143	17.4	3	9	D	H	D	H	H	D	H	H	H	D	D	H	D	H	H	H	D	D	D	D	H	D	D	H	H	H	H	D	H	H	H	H	H	D	D	D			
BM44	G44483		20.3	3	9	D	H	D	H	H	D	H	H	H	D	D	H	D	H	H	H	D	D	H	D	H	D	D	H	H	H	H	D	H	H	H	H	H	D	D	D			
BM27	G44484		26.0	3	9	D	H	D	H	H	D	H	H	D	D	D	H	D	H	H	H	D	D	D	H	D	H	D	D	H	H	H	H	D	D	H	H	H	H	D	D	D		
C9M108	G44485		34.6	3	9	D	H	D	H	H	D	H	H	D	D	D	H	D	H	H	D	D	D	H	D	H	D	D	D	H	H	H	D	H	H	H	H	H	D	D	D			
C6/9M22	G44486		40.3	3	9	D	H	D	H	H	D	H	H	D	D	D	H	D	H	H	D	D	D	H	D	H	D	D	D	H	H	H	D	D	H	H	H	H	D	H	D			
B7M98	G44487		40.3	3	9	D	H	D	H	H	D	H	H	D	D	D	H	D	H	H	D	D	D	H	D	H	D	D	D	H	H	H	D	D	H	H	H	H	D	H	D			
C6/9M27	G44488		43.2	3	9	D	H	D	H	H	D	H	H	D	D	D	H	D	H	H	D	D	D	H	D	H	D	D	D	H	H	H	D	D	H	H	D	H	D	H	D			
C9M48	G44489		48.9	2	9	D	H	D	H	H	D	H	H	D	H	D	H	D	H	H	D	D	D	H	H	D	D	D	D	H	H	D	D	D	H	H	D	H	D	H	D			
C6/9M46	G44490		48.9	2	9	D	H	D	H	H	D	H	H	D	H	D	H	D	H	H	D	D	D	H	D	H	D	D	D	H	H	D	D	D	H	H	D	H	D	H	D			
BM67	G44491		48.9	3	9	D	H	D	H	H	D	H	H	D	H	D	H	D	H	H	D	D	D	H	D	H	D	D	D	H	H	D	D	D	H	H	D	H	D	H	D			
C9M46	G44492		54.6	3	9	D	H	D	H	H	D	H	H	D	H	D	H	D	H	H	D	H	D	D	H	D	H	D	D	H	H	D	D	H	H	H	D	H	D	H	D			
C9M49	G44493		54.6	3	9	D	H	D	H	H	D	H	H	D	H	D	H	D	H	H	D	H	D	D	H	D	H	D	D	H	H	D	D	H	H	H	D	H	D	H	D			
C6/9M19	G44494		54.6	3	9	D	H	D	H	H	D	H	H	D	H	D	H	D	H	H	D	H	D	D	H	D	H	D	D	D	H	H	D	D	H	H	H	D	H	D	H	D		
C9M17	G44495		54.6	3	9	D	H	D	H	H	D	H	H	D	H	D	H	D	H	H	D	H	D	D	H	D	H	D	D	D	H	H	D	D	H	H	H	D	H	D	H	D		
BM54	G44496		54.6	3	9	D	H	D	H	H	D	H	H	D	H	D	H	D	H	H	D	H	D	D	H	D	H	D	D	D	H	H	D	D	H	H	H	D	H	D	H	D		
C9M50	G44497		54.6	3	9	D	H	D	H	H	D	H	H	D	H	D	H	D	H	H	D	H	D	D	H	D	H	D	D	D	H	H	D	D	H	H	H	D	H	D	H	D		
C9M18	G44498		54.6	3	9	D	H	D	H	H	D	H	H	D	H	D	H	D	H	H	D	H	D	D	H	D	H	D	D	D	H	H	D	D	H	H	H	D	H	D	H	D		
C9M15	G44499		54.6	3	9	D	H	D	H	H	D	H	H	D	H	D	H	D	H	H	D	H	D	D	H	D	H	D	D	D	H	H	D	D	H	H	H	D	H	D	H	D		
wh_hrp1			57.5	3	9	D	H	D	H	H	D	D	H	D	H	D	H	D	H	H	D	H	D	D	H	D	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D			
wh_hsp1	G37836	X69121	57.5	3	9	D	H	D	H	H	D	D	H	D	H	D	H	D	H	H	D	H	D	D	D	H	D	D	D	D	H	H	D	D	H	H	H	D	H	D	H	D		
C9M103	G44500		57.5	3	9	D	H	D	H	H	D	D	H	D	H	D	H	D	H	H	D	H	D	D	H	D	H	D	D	D	H	H	D	D	H	H	H	D	H	D	H	D		
C9M106	G44501		57.5	3	9	D	H	D	H	H	D	D	H	D	H	D	H	D	H	H	D	H	D	D	H	D	H	D	D	D	H	H	D	D	H	H	H	D	H	D	H	D		
B5M68	G44502		57.5	3	9	D	H	D	H	H	D	D	H	D	H	D	H	D	H	H	D	H	D	D	H	D	H	D	D	D	H	H	D	D	H	H	H	D	H	D	H	D		
TA61	G38855	AF010557	57.5	3	9	D	H	D	H	H	D	D	H	D	H	D	H	D	H	H	D	H	D	D	H	D	H	D	D	D	H	H	D	D	H	H	H	D	H	D	H	D		
C4M42	G37971		57.5	3	9	D	H	D	H	H	D	D	H	D	H	D	H	D	H	H	D	H	D	D	H	D	H	D	D	D	H	H	D	D	H	H	H	D	H	D	H	D		
C9M20	G44503		60.4	3	9	D	H	D	H	D	D	D	H	D	H	D	H	D	H	H	D	H	D	D	D	H	D	D	D	D	H	H	D	D	H	H	H	D	H	D	H	D		
TA53	G38856	AF010552	60.4	3	9	D	H	D	H	D	D	D	H	D	H	D	H	D	H	H	D	H	D	D	D	H	D	H	D	D	D	H	H	D	D	H	H	H	D	H	D	H	D	
C6/9M20	G44504		66.1	2	9	D	H	D	H	D	D	D	H	D	H	D	H	H	D	H	D	H	D	D	H	D	H	D	D	D	H	H	D	D	H	H	H	D	H	D	H	D		
B7M102	G44505		69.0	3	9	D	H	D	H	D	D	D	H	D	H	D	H	D	H	H	D	H	D	D	D	H	D	D	D	D	H	H	D	D	H	H	H	D	H	D	H	D		
B7M30	G44506		91.9	2	9	D	H	D	H	D	D	D	H	D	D	D	H	D	D	H	H	D	D	D	D	D	D	D	D	D	H	D	D	D	H	D	D	D	D	D	H	D		
C6/9M55	G44507		91.9	2	9	D	H	D	H	D	D	D	H	D	D	D	H	D	D	H	H	D	D	D	D	D	D	D	D	D	H	D	D	D	H	D	D	D	D	D	H	D		
C9M100	G44508		94.8	3	9	D	H	D	H	D	D	D	H	D	D	D	H	D	D	H	H	D	D	D	D	D	D	D	D	D	H	D	D	D	H	D	D	D	D	D	D	D	D	
C9M99	G44509		94.8	3	9	D	H	D	H	D	D	D	H	D	D	D	H	D	D	H	H	D	D	D	D	D	D	D	D	D	D	H	D	D	D	H	D	H	D	D	D	D	D	
C14M117	G44510		94.8	3	9	D	H	D	H	D	D	D	H	D	D	D	H	D	D	H	H	D	D	D	D	D	D	D	D	D	H	D	D	D	H	D	H	D	D	D	D	D	D	
C9M97	G44511		94.8	3	9	D	H	D	H	D	D	D	H	D	D	D	H	D	D	H	H	D	D	D	D	D	D	D	D	D	H	D	D	D	H	D	H	D	D	D	D	D	D	
C9M94	G44512		94.8	3	9	D	H	D	H	D	D	D	H	D	D	D	H	D	D	H	H	D	D	D	D	D	D	D	D	D	H	D	D	D	H	D	H	D	D	D	D	D	D	
C6/9M41-1	G44513		94.8	3	9	D	H	D	H	D	D	D	H	D	D	D	H	D	D	H	H	D	D	D	D	D	D	D	D	D	H	D	D	D	H	D	H	D	D	D	D	D		
C6/9M18	G44514		94.8	3	9	D	H	D	H	D	D	D	H	D	D	D	H	D	D	H	H	D	D	D	D	D	D	D	D	D	H	D	D	D	H	D	H	D	D	D	D	D	D	
C6/9M23	G44515		94.8	3	9	D	H	D	H	D	D	D	H	D	D	D	H	D	D	H	H	D	D	D	D	D	D	D	D	D	D	H	D	D	D	H	D	H	D	D	D	D	D	
BM98	G44516		97.7	3	9	D	H	D	H	D	D	D	H	D	D	D	H	D	D	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	H	D	H	D	D	D	D	D		
C9M98	G44517		100.6	3	9	D	H	D	H	D	D	D	H	D	D	D	H	D	D	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	H	D	D	D	D	D	D	D	D	
C9M110	G44518		103.5	2	9	D	H	D	H	D	D	D	H	D	D	D	H	D	D	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	
RHO3	G37835	M65059	103.5	2	9	D	H	D	H	D	D	D	H	D	D	D	H	D	D	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	
B7M27	G44519		103.5	2	9	D	H	D	H	D	D	D	H	D	D	D	H	D	D	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	
C9M109	G44520		103.5	2	9	D	H	D	H	D	D	D	H	D	D	D	H	D	D	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D
C9M105	G44521		103.5	2	9	D	H	D	H	D	D	D	H	D	D	D	H	D	D	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D
ATGF1	G37837	X15979	103.5	2	9	D	H	D	H	D	D	D	H	D	D	D	H	D	D	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D
B7M57	G44522		106.4	3	9	D	H	D	H	D	D	D	H	D	D	D	H	D	D	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D

Chromosome 10 inheritance in *P. falciparum* HB3xDd2 cross

Top

Previous		Legend for Tables					Next		Parent		Progeny																																
Marker	Synonym	STS	GenBank	position	framework	chromosome	DD2	HB3	B1SD	QC13	QC01	B4R3	SC05	TC08	GC03	3BA6	1BB5	3BD5	SC01	QC34	QC23	TC05	GC06	D43	C188	C408	116	61	7C3	7C7	7C12	7C16	7C20	7C46	C101	7C111	7C126	7C140	7C159	7C170	7C183	7C421	7C424
pMBP3				0	3	10	D	H	H	D	H	H	D	D	D	D	H</																										

B7M48	G44525		11.5	3	10	D	H	H	D	H	H	D	D	D	D	H	H	H	H	D	D	H	D	D	D	H	H	H	H	H	D	H	H	H	D	D	H	H	D	H	D
B7M115	G44529		17.2	3	10	D	H	H	D	H	H	D	D	H	D	H	D	H	H	D	D	H	D	D	D	H	H	H	H	H	D	H	H	H	D	D	H	H	D	H	D
B7M45	G44526		17.2	3	10	D	H	H	D	H	H	D	D	H	D	H	D	H	H	D	D	H	D	D	D	H	H	H	H	H	D	H	H	H	D	D	H	H	D	H	D
B7M45-2	G44527		17.2	3	10	D	H	H	D	H	H	D	D	H	D	H	D	H	H	D	D	H	D	D	D	H	H	H	H	H	D	H	H	H	D	D	H	H	D	H	D
ARA5	G37811	X17488	17.2	3	10	D	H	H	D	H	H	D	D	H	D	H	D	H	H	D	D	H	D	D	D	H	H	H	H	H	D	H	H	H	D	D	H	H	D	H	D
B7M28	G44531		17.2	3	10	D	H	H	D	H	H	D	D	H	D	H	D	H	H	D	D	H	D	D	D	H	H	H	H	H	D	H	H	H	D	D	H	H	D	H	D
B7M24	G44528		17.2	3	10	D	H	H	D	H	H	D	D	H	D	H	D	H	H	D	D	H	D	D	D	H	H	H	H	H	D	H	H	H	D	D	H	H	D	H	D
B7M79	G44532		20.1	3	10	D	H	H	D	H	H	D	D	H	D	H	D	H	H	D	D	H	D	D	D	H	H	H	H	H	D	H	H	H	D	D	H	D	D	H	D
B7M78	G44533		20.1	3	10	D	H	H	D	H	H	D	D	H	D	H	D	H	H	D	D	H	D	D	D	H	H	H	H	H	D	H	H	H	D	D	H	D	D	H	D
B7M69	G44534		20.1	3	10	D	H	H	D	H	H	D	D	H	D	H	D	H	H	D	D	H	D	D	D	H	H	H	H	H	D	H	H	H	D	D	H	D	D	H	D
C9M35	G44530		23.0	3	10	D	H	H	D	H	H	D	D	H	D	H	D	H	H	D	D	H	D	D	D	H	D	H	H	H	.	.	.	.	.	.	.	.	.	.	.
HPRT	G37814	M88110	31.6	3	10	D	H	H	D	H	H	D	D	H	D	H	D	H	H	D	D	H	D	H	D	H	D	H	H	D	H	H	H	D	D	H	D	D	H	D	
ACT1	G37815	M22719	31.6	3	10	D	H	H	D	H	H	D	D	H	D	H	D	H	H	D	D	H	D	H	D	D	H	H	H	D	H	H	H	D	D	H	D	D	H	D	
LW40	.	.	31.6	3	10	D	H	H	D	H	H	D	D	H	D	H	D	H	H	D	D	H	D	H	D	H	D	H	H	.	.	.	.	.	.	.	.	.	.	.	
QF122	G37813	M18825	31.6	3	10	D	H	H	D	H	H	D	D	H	D	H	D	H	H	D	D	H	D	H	D	D	H	H	H	D	H	H	H	D	D	H	D	D	H	D	
C3M65	G44535		31.6	3	10	D	H	H	D	H	H	D	D	H	D	H	D	H	H	D	D	H	D	H	D	D	H	H	H	D	H	H	H	D	D	H	D	D	H	D	
BM23	G44536		31.6	3	10	D	H	H	D	H	H	D	D	H	D	H	D	H	H	D	D	H	D	H	D	D	H	H	H	D	H	H	H	D	D	H	D	D	H	D	
TA111	G38830	AF010518	31.6	3	10	D	H	H	D	H	H	D	D	H	D	H	D	H	H	D	D	H	D	H	D	D	H	H	H	D	H	H	H	D	D	H	D	D	H	D	
B7M72	G44537		34.5	3	10	D	H	H	D	H	H	D	D	H	D	H	D	H	H	D	D	H	D	H	D	D	H	H	H	D	H	H	H	D	D	H	D	D	H	D	
B7M104	G44538		.	.	10	D	H	H	H	H	D	D	H	D	H	D	H	H	H	D	D	H	D	H	D	D	H	H	H	D	H	H	H	D	D	H	D	D	H	D	
TA77	G38816	AF010565	.	.	10	D	H	H	H	H	D	D	D	H	D	H	D	H	H	D	D	H	D	H	D	D	H	H	H	D	H	H	H	D	D	H	D	D	H	D	
POLYD	G37838	X62423	40.2	3	10	D	H	H	D	H	D	D	D	H	D	H	D	H	D	D	H	D	H	D	D	H	H	H	D	H	H	H	D	D	H	D	D	H	D		
B7M77	G44539		40.2	3	10	D	H	H	D	H	D	D	D	H	D	H	D	H	D	D	H	D	H	D	D	H	H	H	D	H	H	H	D	D	H	D	D	H	D		
B7M6	G44540		45.9	3	10	D	H	H	H	H	D	D	D	H	D	H	D	H	D	D	D	H	D	H	D	D	H	H	H	D	H	H	H	D	D	H	D	D	H	D	
B7M46	G44541		45.9	3	10	D	H	H	H	H	D	D	D	H	D	H	D	H	D	D	D	H	D	H	D	D	H	H	H	D	H	H	H	D	D	H	D	D	H	D	
TA50	G38859	AF010550	45.9	3	10	D	H	H	H	H	D	D	D	H	D	H	D	H	D	D	D	H	D	H	D	D	H	H	H	D	H	H	H	D	D	H	D	D	H	D	
B7M58	G44542		51.6	3	10	D	H	H	H	H	D	D	D	H	D	H	D	H	D	H	H	D	H	D	D	H	H	H	D	H	H	H	D	D	H	D	D	H	D		
B7M23	G44543		51.6	3	10	D	H	H	H	H	D	D	D	H	D	H	D	H	D	H	D	H	D	H	D	D	H	H	H	D	H	H	H	D	H	D	D	H	D		
TA2	G38860	AF010532	51.6	3	10	D	H	H	H	H	D	D	D	H	D	H	D	H	D	H	D	H	D	H	D	D	H	H	H	D	H	H	H	D	D	H	D	D	H	D	
B7M14	G44544		51.6	3	10	D	H	H	H	H	D	D	D	H	D	H	D	H	D	H	D	H	D	H	D	D	H	H	H	D	H	H	H	D	D	H	D	D	H	D	
TA91	G38861	AF010573	51.6	3	10	D	H	H	H	H	D	D	D	H	D	H	D	H	D	H	D	H	D	H	D	D	H	H	H	D	H	H	H	D	D	H	D	D	H	D	
TA126	G38817	AF010525	51.6	3	10	D	H	H	H	H	D	D	D	H	D	H	D	H	D	H	D	H	D	H	D	D	H	H	H	D	H	H	H	D	D	H	D	D	H	D	
B7M100	G44545		51.6	3	10	D	H	H	H	H	D	D	D	H	D	H	D	H	D	H	D	H	D	H	D	D	H	H	H	D	H	H	H	D	D	H	D	D	H	D	
Pfs25	.	.	65.9	3	10	D	H	H	H	H	D	D	D	D	D	D	H	D	H	D	H	-	-	-	-	-	-	-	.	.	.	.	.	.	.	.	.	.	.		
B7M92	G44546		65.9	3	10	D	H	H	H	H	D	D	D	D	D	D	H	D	H	D	H	D	D	H	D	D	H	H	H	D	H	H	H	D	D	H	D	D	D	D	
B7M62	G44547		71.6	3	10	D	H	H	H	H	D	D	D	D	D	D	H	D	H	H	D	D	H	D	D	H	H	H	D	H	H	H	D	D	D	D	D	D	D	D	
pSL4	.	.	71.6	3	10	D	H	H	H	H	D	D	D	D	D	D	H	D	H	H	H	-	-	-	-	-	-	-	.	.	.	.	.	.	.	.	.	.	.		
C4M1	G37972		71.6	3	10	D	H	H	H	H	D	D	D	D	D	D	H	D	H	H	D	D	H	D	D	H	H	H	D	H	H	H	D	D	D	D	D	D	D	D	
B7M42	G44548		71.6	3	10	D	H	H	H	H	D	D	D	D	D	D	H	D	H	H	D	D	H	D	D	D	H	H	H	D	H	H	H	D	D	D	D	D	D	D	
TA40	G38858	AF010542	74.5	3	10	D	H	H	H	H	D	D	D	D	D	D	H	D	H	H	D	D	H	D	D	D	H	H	H	D	H	H	H	D	D	D	D	D	D	D	
B7M19	G44549		80.2	3	10	D	H	H	H	H	D	D	D	D	D	D	H	D	H	H	D	D	H	D	D	H	D	D	H	H	H	D	D	H	H	H	D	D	D	D	D
C4M43	G37973		83.1	3	10	D	H	H	H	H	D	D	D	D	D	D	H	D	H	H	D	D	H	D	D	H	H	H	H	D	D	H	H	H	D	D	D	D	D	D	
B7M113	G44550		83.1	3	10	D	H	H	H	H	D	D	D	D	D	D	H	D	H	H	D	D	H	D	D	H	H	H	H	D	D	H	H	H	D	D	D	D	D	D	
LSA	.	.	.	.	10	D	H	-	H	H	H	D	D	D	D	D	H	H	D	H	H	-	-	-	-	-	-	-	.	.	.	.	.	.	.	.	.	.	.		
SAG	G37789	M10129	.	.	10	D	H	-	H	H	H	D	D	D	D	D	H	H	D	H	H	-	-	-	-	-	-	-	.	.	.	.	.	.	.	.	.	.	.		
B7M18	G44551		83.1	3	10	D	H	H	H	H	D	D	D	D	D	D	H	D	H	H	D	D	H	D	D	H	H	H	H	D	H	H	H	D	D	D	D	D	D		
TA80	G38857	AF010568	86.0	3	10	D	H	H	H	H	D	D	D	D	D	D	H	D	H	H	D	D	H	D	D	H	H	H	H	D	H	H	D	H	D	D	D	D	D	D	
pSL6	.	.	.	.	10	D	H	H	H	H	D	D	D	D	D	D	H	D	H	H	H	-	-	-	-	-	-	-	.	.	.	.	.	.	.	.	.	.	.		
B7M93	G44552		88.9	3	10	D	H	H	H	H	D	D	D	D	D	D	H	D	H	H	D	D	H	D	D	H	H	H	H	D	H	H	D	H	D	D	D	D	D		
p11_1	11-1	G37842	X07453	94.6	3	10	D	H	H	H*	H	H	H*	D	D	D	D	H	H	D	H	H	H	D	D	H	D	D	H	D	H	D	H	D	H	D	D	D	D		

Chromosome 11 inheritance in *P. falciparum* HB3xDd2 cross

Top

Previous		Legend for Tables				Next		Parent		Progeny																																			
Marker	Synonym	STS	GenBank	position	framework	chromosome	DD2	HB3	B1SD	QC13	QC01	B4R3	SC05	TC08	GC03	3BA6	1BB5	3BD5	SC01	QC34	QC23	TC05	GC06	D43	C188	C408	116	61	7C3	7C7	7C12	7C16	7C20	7C46	C101	7C111	7C126	7C140	7C159	7C170	7C183	7C421	7C424		
S11_1f	.	.	.	0	2	11	D	H	-	D	D	H	H	D	.	H	H	H	H	H	D	H	D	-	-	-	-	-	-	-	-	-	.	.	.	.	.	.	.	.	.	.	.	.	.
S370.7_1	.	.	.	.	.	11	D	H	H	D	H	H	D	D	H	H	D	H	H	H	D	H	D	-	-	-	-	-	-	-	-	.	.												







TA47	.	G38819	AF010547	44.1	3	13	D	H	D	D	D	H	H	H	D	H	D	D	D	D	D	D	D	H	D	H	D	D	H	H	D	H	H	H	D	D	D	D	H	H				
C13M43	.	G44623	.	44.1	3	13	D	H	D	D	D	H	H	H	D	H	D	D	D	D	D	D	D	H	D	H	D	D	H	H	D	H	H	H	D	D	D	D	H	H				
C13M97	.	G44624	.	47.0	3	13	D	H	D	D	D	H	H	H	D	H	D	D	D	D	D	D	D	H	D	H	D	D	H	H	H	H	H	H	H	D	D	D	D	H	H			
TA56	.	G38877	AF010554	47.0	3	13	D	H	D	D	D	H	H	H	D	H	D	D	D	D	D	D	D	H	D	H	D	D	H	H	H	H	H	H	H	D	D	D	D	H	H			
C13M87	.	G44625	.	52.7	3	13	D	H	D	D	D	H	H	H	D	H	H	H	D	D	D	D	D	D	H	D	H	D	D	H	H	H	H	H	H	H	H	D	D	D	D	H	H	
C13M95	.	G44626	.	58.4	3	13	D	H	D	D	D	H	H	H	D	H	H	H	D	D	D	D	D	D	H	D	D	D	D	H	H	H	H	H	H	H	H	D	D	D	D	H	H	
TA116	.	G38875	AF010520	58.4	3	13	D	H	D	D	D	H	H	H	D	H	H	H	D	D	D	D	D	D	H	D	D	D	D	H	H	H	H	H	H	H	H	D	D	D	D	H	H	
C14M101	.	G44627	.	58.4	3	13	D	H	D	D	D	H	H	H	D	H	H	H	D	D	D	D	D	D	H	D	D	D	D	H	H	H	H	H	H	H	H	H	D	D	D	D	H	H
C14M84	.	G44628	.	58.4	3	13	D	H	D	D	D	H	H	H	D	H	H	H	D	D	D	D	D	D	H	D	D	D	D	H	H	H	H	H	H	H	H	D	D	D	D	H	H	
p7BP27	.	.	.	.	.	13	D	H	D	D	D	H	H	H	H	-	H	H	H	D	D	D	D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
C13M63	.	G44629	.	64.1	3	13	D	H	D	H	D	H	H	H	D	H	H	H	D	D	D	D	D	D	D	D	D	D	D	H	H	H	H	H	H	H	H	D	D	D	D	H	H	
Pf2488	p2488	G37774	TO2488	64.1	3	13	D	H	D	H	D	H	H	H	D	H	H	H	D	D	D	D	D	D	D	D	D	D	D	H	H	H	H	H	H	H	H	D	D	D	D	H	H	
B7M9	.	G44630	.	64.1	3	13	D	H	D	H	D	H	H	H	D	H	H	H	D	D	D	D	D	D	D	D	D	D	D	D	H	H	H	H	H	H	H	H	D	D	D	D	H	H
C13M86	.	G44631	.	64.1	3	13	D	H	D	H	D	H	H	H	D	H	H	H	D	D	D	D	D	D	D	D	D	D	D	D	H	H	H	H	H	H	H	H	D	D	D	D	H	H
TA49	.	G38874	AF010549	64.1	3	13	D	H	D	H	D	H	H	H	D	H	H	H	D	D	D	D	D	D	D	D	D	D	D	H	H	H	H	H	H	H	H	D	D	D	D	H	H	
C13M17	.	G44632	.	72.7	3	13	D	H	D	H	D	H	D	H	H	D	H	H	H	D	D	D	D	D	D	D	D	D	D	D	H	H	H	H	H	H	H	D	D	D	D	H	H	
C13M18	.	G44633	.	72.7	3	13	D	H	D	H	D	H	D	H	H	D	H	H	H	D	D	D	D	D	D	D	D	D	D	D	H	H	H	H	H	H	H	D	D	D	D	H	H	
C14M12	.	G41090	.	72.7	3	13	D	H	D	H	D	H	D	H	H	D	H	H	H	D	D	D	D	D	D	D	D	D	D	D	H	H	H	H	H	H	H	D	D	D	D	H	H	
C1M53	.	G44634	.	72.7	3	13	D	H	D	H	D	H	D	H	H	D	H	H	H	D	D	D	D	D	D	D	D	D	D	D	H	H	H	H	H	H	H	D	D	D	D	H	H	
C13M10	.	G44635	.	72.7	3	13	D	H	D	H	D	H	D	H	H	D	H	H	H	D	D	D	D	D	D	D	D	D	D	D	D	H	H	H	H	H	H	D	D	D	D	H	H	
C13M13	.	G44636	.	72.7	3	13	D	H	D	H	D	H	D	H	H	D	H	H	H	D	D	D	D	D	D	D	D	D	D	D	D	H	H	H	H	H	H	D	D	D	D	H	H	
TRAP	.	G37858	X13022	75.6	3	13	D	H	D	H	D	H	D	D	H	D	H	H	H	D	D	D	D	D	D	D	D	D	D	D	H	H	H	H	H	H	H	D	D	D	D	H	H	
C13M36	.	G44637	.	75.6	3	13	D	H	D	H	D	H	D	D	H	D	H	H	H	D	D	D	D	D	D	D	D	D	D	D	H	H	H	H	H	H	H	D	D	D	D	H	H	
C1M70	.	G44638	.	78.5	3	13	D	H	D	H	D	H	D	D	H	D	H	H	H	D	D	D	D	D	D	D	D	D	D	D	H	H	H	H	H	H	H	D	D	D	D	H	H	
C13M27	.	G44639	.	81.4	3	13	D	H	D	H	D	H	D	D	H	D	H	H	H	D	D	D	D	D	D	D	D	D	D	D	H	H	H	H	H	H	H	D	D	D	D	H	H	
C13M45	.	G44640	.	81.4	3	13	D	H	D	H	D	H	D	D	H	D	H	H	H	D	D	D	D	D	D	D	D	D	D	D	H	H	H	H	H	H	H	D	D	D	D	H	H	
C13M46	.	G44641	.	81.4	3	13	D	H	D	H	D	H	D	D	H	D	H	H	H	D	D	D	D	D	D	D	D	D	D	D	D	H	H	H	H	H	H	D	D	D	D	H	H	
C14M74	.	G44642	.	84.3	3	13	D	H	D	H	D	H	D	D	H	D	H	H	H	D	D	D	D	D	D	D	D	D	D	D	D	H	H	H	H	H	H	H	D	D	D	D	H	H
C14M83	.	G44643	.	87.2	3	13	D	H	D	H	D	H	D	D	H	D	H	H	H	D	D	D	D	D	D	D	D	D	D	D	H	H	H	H	H	H	H	D	D	D	D	H	H	
C14M94	.	G44644	.	92.9	3	13	D	H	D	H	D	H	D	D	H	D	H	H	H	D	D	H	D	D	H	D	D	D	D	D	H	H	H	H	H	H	H	D	D	D	D	D	H	
C13M75	.	G44645	.	92.9	3	13	D	H	D	H	D	H	D	D	H	D	H	H	H	D	D	H	D	D	H	D	D	D	D	D	H	H	H	H	H	H	H	D	D	D	D	D	H	
C1M61	.	G44651	.	95.8	3	13	D	H	D	H	D	H	D	D	H	D	H	H	H	D	D	H	D	H	H	D	D	D	D	H	H	H	H	H	H	H	D	D	D	D	D	H		
C13M40	.	G44649	.	95.8	3	13	D	H	D	H	D	H	D	D	H	D	H	H	H	D	D	H	D	H	H	D	D	D	D	D	H	H	H	H	H	H	D	D	D	D	D	H		
C13M84	.	G44650	.	95.8	3	13	D	H	D	H	D	H	D	D	H	D	H	H	H	D	D	H	D	H	H	D	D	D	D	D	D	H	H	H	H	H	H	D	D	D	D	D	H	
C1M60	.	G44646	.	95.8	3	13	D	H	D	H	D	H	D	D	H	D	H	H	H	D	D	H	D	H	H	D	D	D	D	D	H	H	H	H	H	H	H	D	D	D	D	D	H	
C13M33	.	G44647	.	95.8	3	13	D	H	D	H	D	H	D	D	H	D	H	H	H	D	D	H	D	H	H	D	D	D	D	D	H	H	H	H	H	H	H	D	D	D	D	D	H	
C13M59	.	G44648	.	95.8	3	13	D	H	D	H	D	H	D	D	H	D	H	H	H	D	D	H	D	H	H	D	D	D	D	D	H	H	H	H	H	H	H	D	D	D	D	D	H	
C13M96	.	G44652	.	98.7	3	13	D	H	D	H	D	H	D	D	H	D	H	H	H	D	D	H	D	H	D	H	D	D	D	D	H	H	H	H	H	H	D	D	D	D	D	H		
C13M28	.	G44653	.	98.7	3	13	D	H	D	H	D	H	D	D	H	D	H	H	H	D	D	H	D	H	D	H	D	D	D	D	H	H	H	H	H	H	D	D	D	D	D	H		
C14M81	.	G44654	.	98.7	3	13	D	H	D	H	D	H	D	D	H	D	H	H	H	D	D	H	D	H	H	D	D	D	D	D	D	H	H	H	H	H	D	D	D	D	D	H		
C1M69	.	G44655	.	101.6	3	13	D	H	D	H	D	H	D	D	H	D	H	H	H	D	D	H	D	H	H	D	D	D	D	D	H	H	H	H	H	H	D	D	D	D	D	H		
C13M15	.	G44656	.	107.3	3	13	D	H	H	H	D	H	D	D	H	D	H	H	H	D	D	H	D	H	H	D	D	D	D	D	H	H	H	D	H	H	H	D	D	D	D	D	H	
C12M49	.	G38798	.	107.3	3	13	D	H	H	H	D	H	D	D	H	D	H	H	H	D	D	H	D	H	H	D	D	D	D	D	H	H	H	D	H	H	H	D	D	D	D	D	H	
C14M66	.	G44657	.	107.3	3	13	D	H	H	H	D	H	D	D	H	D	H	H	H	D	D	H	D	H	H	D	D	D	D	D	H	H	H	D	H	H	H	D	D	D	D	D	H	
POLY3	.	G37859	M73770	107.3	3	13	D	H	H	H	D	H	D	D	H	D	H	H	H	D	D	H	D	H	H	D	D	D	D	D	H	H	H	D	H	H	H	D	D	D	D	D	H	
C13M2	.	G44658	.	107.3	3	13	D	H	H	H	D	H	D	D	H	D	H	H	H	D	D	H	D	H	H	D	D	D	D	D	D	H	H	H	D	H	H	H	D	D	D	D	D	H
C13M90	.	G44659	.	107.3	3	13	D	H	H	H	D	H	D	D	H	D	H	H	H	D	D	H	D	H	H	D	D	D	D	D	D	H	H	H	D	H	H	H	D	D	D	D	D	H
C14M106	.	G44660	.	107.3	3	13	D	H	H	H	D	H	D	D	H	D	H	H	H	D	D	H	D	H	H	D	D	D	D	D	D	H	H	H	D	H	H	H	D	D	D	D	D	H
pE3	.	.	.	113.0	3	13	D	H	-	H	D	H	D	D	H	D	H	H	H	D	D	H	H	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
pC13.E14	.	.	.	113.0	3	13	D	H	-	H	D	H	D	D	H	D	H	H	H	D	D	H	H	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	
TA133	.	G38879	AF010528	113.0	3	13	D	H	H	H	D	H	D	D	H	D	H	H	H	D	D	H	H	H	D	D	D	D	D	H	D	H	H	H	H	H	H	D	D	D	D	D	H	
C14M73	.	G44661	.	127.3	3	13	D	H	D	H	D	H	D	D	D	D	H																											

C14M27	G44666		130.9	3	13	D	H	D	H	D	H	D	D	D	D	H	H	D	H	D	H	H	H	H	H	H	D	H	D	H	H	H	H	D	H	H	D	H	D	H	H		
C14M126	G44667		135.9	3	13	D	H	D	H	D	H	D	D	D	D	D	H	D	H	H	H	H	H	H	H	D	H	D	D	D	D	H	H	H	H	D	H	H	D	H	D	H	H
TA14	G38885	AFO10530	138.8	3	13	D	H	D	H	D	H	D	D	D	D	D	H	D	H	H	H	H	H	H	D	H	D	D	H	D	H	H	H	D	D	H	H	D	H	D	H	H	
C13M81	G44668		144.5	3	13	D	H	D	H	D	H	D	D	D	D	H	D	H	H	H	H	H	H	H	D	H	D	D	H	D	H	H	H	D	D	H	H	H	H	D	H	H	
C1M59	G44669		144.5	3	13	D	H	D	H	D	H	D	D	D	D	H	D	H	H	H	H	H	H	H	D	H	D	D	H	D	H	H	H	D	D	H	H	H	H	D	H	H	
C13M32	G44670		144.5	3	13	D	H	D	H	D	H	D	D	D	D	H	D	H	H	H	H	H	H	H	D	H	D	D	H	D	H	H	H	D	D	H	H	H	H	D	H	H	
B8M6	G44671		150.2	3	13	D	H	D	H	D	H	D	D	D	D	D	D	H	H	H	H	H	H	H	D	H	D	D	H	D	H	H	H	D	D	H	H	H	H	D	H	H	
B5M146	G44672		150.2	3	13	D	H	D	H	D	H	D	D	D	D	D	H	H	H	H	H	H	H	D	H	D	D	H	D	H	H	H	D	D	H	H	H	H	D	H	H		
C13M67	G44673		155.9	3	13	D	H	H	H	D	H	D	D	D	D	D	H	H	H	H	H	H	H	D	H	D	H	H	H	H	H	D	D	H	H	D	H	H	H	H	H		
C13M12	G44674		158.8	3	13	D	H	H	H	D	H	D	D	D	D	D	H	H	H	D	H	H	D	H	D	H	D	D	H	D	H	H	H	D	D	H	H	D	H	H	H	H	
C1M67	G44675		158.8	3	13	D	H	H	H	D	H	D	D	D	D	D	H	H	H	D	H	H	D	H	D	H	D	D	H	D	H	H	H	D	D	H	H	D	H	H	H	H	
C13M68	G44676		158.8	3	13	D	H	H	H	D	H	D	D	D	D	D	H	H	H	D	H	H	D	H	D	H	D	D	H	D	H	H	H	D	D	H	H	D	H	H	H	H	
C14M107	G44677		158.8	3	13	D	H	H	H	D	H	D	D	D	D	D	H	H	H	D	H	H	D	H	D	H	D	D	H	D	H	H	H	D	D	H	H	D	H	H	H	H	
C13M37	G44678		158.8	3	13	D	H	H	H	D	H	D	D	D	D	D	H	H	H	D	H	H	D	H	D	H	D	D	H	D	H	H	H	D	D	H	H	D	H	H	H	H	
C13M77	G44679		164.5	3	13	D	H	H	H	D	H	D	D	D	D	D	H	H	D	D	H	H	D	H	D	H	D	D	H	D	H	H	H	D	D	H	H	D	H	H	H	H	
C13M6	G44680		164.5	3	13	D	H	H	H	D	H	D	D	D	D	D	H	H	D	D	H	H	D	H	D	H	D	D	H	D	H	H	H	D	D	H	H	D	H	H	H	H	
VAPA	G37860	L08200	164.5	3	13	D	H	H	H	D	H	D	D	D	D	D	H	H	D	D	H	H	D	H	D	H	D	D	H	D	H	H	H	D	D	H	H	D	H	H	H	H	
C13M22	G44681		164.5	3	13	D	H	H	H	D	H	D	D	D	D	D	H	H	D	D	H	H	D	H	D	H	D	D	H	D	H	H	H	D	D	H	H	D	H	H	H	H	
C13M14	G44682		164.5	3	13	D	H	H	H	D	H	D	D	D	D	D	H	H	D	D	H	H	D	H	D	H	D	D	H	D	H	H	H	D	D	H	H	D	H	H	H	H	
C13M79	G44686		170.2	3	13	D	H	H	D	D	H	D	D	D	D	D	H	H	D	D	H	H	D	H	D	H	D	D	H	D	H	H	H	D	D	H	H	D	H	H	H	H	
C1M68	G44687		170.2	3	13	D	H	H	D	D	H	D	D	D	D	D	H	H	D	D	H	H	D	H	D	H	D	D	H	D	H	H	H	D	D	H	H	D	H	H	H	H	
TA107	G38880	AFO10516	170.2	3	13	D	H	H	D	D	H	D	D	D	D	D	H	H	D	D	H	H	D	H	D	H	D	H	D	H	H	H	D	D	H	H	D	H	H	H	H		
PF18153	G37861	T18153	170.2	3	13	D	H	H	D	D	H	D	D	D	D	D	H	H	D	D	H	H	D	H	D	H	D	H	D	H	H	H	D	D	H	H	D	H	H	H	H		
C14M45	G44688		170.2	3	13	D	H	H	D	D	H	D	D	D	D	D	H	H	D	D	H	H	D	H	D	H	D	D	H	D	H	H	H	D	D	H	H	D	H	H	H	H	
C14M43	G44690		170.2	3	13	D	H	H	D	D	H	D	D	D	D	D	H	H	D	D	H	H	D	H	D	H	D	D	H	D	H	H	H	D	D	H	H	D	H	H	H	H	
C13M38	G44689		173.1	3	13	D	H	H	D	D	H	D	D	D	D	D	H	H	D	D	H	H	D	H	D	H	D	D	H	D	H	H	H	D	D	H	H	D	H	H	H	H	
TA46	G38820	AFO10546	173.1	3	13	D	H	H	D	D	H	D	D	D	D	D	H	H	D	D	H	H	D	H	D	H	D	D	H	D	H	H	H	D	D	H	H	D	H	H	H	H	
C13M56	G44685		178.8	3	13	D	H	H	D	D	H	D	D	D	D	D	H	H	D	D	H	H	D	H	D	H	D	D	H	D	H	H	H	D	D	H	H	D	H	H	H	H	
C13M73	G44683		178.8	3	13	D	H	H	D	D	H	D	D	D	D	D	H	H	D	D	H	H	D	H	D	H	D	D	H	D	H	H	H	D	D	H	H	D	H	H	H	H	
C13M51	G44684		178.8	3	13	D	H	H	D	D	H	D	D	D	D	D	H	H	D	D	H	H	D	H	D	H	D	D	H	D	H	H	H	D	D	H	H	D	H	H	H	H	
TA58	G38813	AFO10555	184.5	3	13	D	H	H	D	D	H	D	D	D	D	D	H	H	D	D	H	H	D	H	D	D	H	D	D	H	H	D	H	D	D	D	H	D	H	H	H	H	

Chromosome 14 inheritance in *P. falciparum* HB3xDd2 cross

Top

Previous		Legend for Tables				Parent		Progeny																																									
Marker	Synonym	STS	GenBank	position	framework	chromosome	DD2	HB3	B1SD	QC13	QC01	B4R3	SC05	TC08	GC03	3BA6	1BB5	3BD5	SC01	QC34	QC23	TC05	GC06	D43	C188	C408	116	61	7C3	7C7	7C12	7C16	7C20	7C46	C101	7C111	7C126	7C140	7C159	7C170	7C183	7C421	7C424						
C14M48		G41083		0	3	14	D	H	H	H	D	D	D	D	D	D	H	D	D	H	H	H	H	H	D	D	D	D	D	D	D	D	D	D	D	H	H	D	D	H	D	H	D	H	H	H			
C14M59		G41082		5.7	3	14	D	H	H	H	D	D	D	D	D	D	H	D	D	D	H	H	H	H	H	D	D	D	D	D	D	D	D	D	D	D	H	D	D	D	D	H	D	H	D	H	H		
C14M89		G41085		11.4	3	14	D	H	H	H	D	D	D	D	D	H	H	D	D	H	H	H	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	H	H	D	H	H		
C14M128		G41086		11.4	3	14	D	H	H	H	D	D	D	D	D	H	H	D	D	H	H	H	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	H	H	D	H	H		
C14M111		G41084		14.3	3	14	D	H	H	H	D	D	D	D	D	H	H	D	D	H	H	H	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	H	D	H	H		
C14M100		G41081		14.3	3	14	D	H	H	H	D	D	D	D	D	H	H	D	D	H	H	H	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	H	D	H	H	
C14M118		G41087		17.2	3	14	D	H	H	H	D	D	D	D	D	H	H	D	D	H	H	H	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	H	D	H	H	
C14M52		G44700		25.8	3	14	D	H	H	H	D	D	H	H	H	H	H	D	H	H	H	H	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	H	D	H	H	
C14M79		G42698		25.8	3	14	D	H	H	H	D	D	H	H	H	H	H	D	H	H	H	H	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	H	D	H	H
C14M108		G42699		28.7	3	14	D	H	H	H	D	D	H	H	H	H	D	D	H	H	H	H	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	H	D	H	H	
RHO1		G37777	M32853	28.7	3	14	D	H	H	H	D	D	H	H	H	H	D	D	H	H	H	H	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	H	D	H	H	
C14M6		G42700		28.7	3	14	D	H	H	H	D	D	H	H	H	H	D	D	H	H	H	H	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	H	D	H	H
pSc11.87						14	D	H	H	H	D	D	H	H	H	H	D	D	H	H	H	H	H																										
C14M11		G42701		31.6	3	14	D	H	H	H	D	D	H	H	H	H	D	D	H	H	H	H	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	H	D	D	H	H	
ACT2		G37871	M22718	31.6	3	14	D	H	H	H	D	D	H	H	H	H	D	D	H	H	H	H	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	H	D	H	H	
C14M71		G42702		31.6	3	14	D	H	H	H	D	D	H	H	H	H	D	D	H	H	H	H	H	H	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	H	D	D	H	H	
C13M98		G42703		31.6	3	14	D	H	H	H	D	D	H	H	H	H	D	D	H	H	H	H	H	H	D																								

C14M113	G41024	48.8	2	14	D	H	H	H	D	D	H	H	H	H	D	D	H	H	D	H	D	D	D	D	H	H	H	D	D	H	D	D	D	H	H	D	D	H	D	D	H	D	H	H	
C14M105	G41025	48.8	2	14	D	H	H	H	D	D	H	H	H	H	D	D	H	H	D	H	D	D	D	D	H	H	H	D	D	H	D	D	D	H	H	D	D	H	D	D	H	D	H	H	
C14M95	G41026	48.8	2	14	D	H	H	H	D	D	H	H	H	H	D	D	H	H	D	H	D	D	D	D	H	H	H	D	D	H	D	D	D	H	H	D	D	H	D	D	H	D	H	H	
C14M42	G41027	48.8	2	14	D	H	H	H	D	D	H	H	H	H	D	D	H	H	D	H	D	D	D	D	H	H	H	D	D	H	D	D	D	H	H	D	D	H	D	D	H	D	H	H	
C14M91	G41028	48.8	2	14	D	H	H	H	D	D	H	H	H	H	D	D	H	H	D	H	D	D	D	D	H	H	H	D	D	H	D	D	D	H	H	D	D	H	D	D	H	D	H	H	
C14M41	G41029	48.8	2	14	D	H	H	H	D	D	H	H	H	H	D	D	H	H	D	H	D	D	D	D	H	H	H	D	D	H	D	D	D	H	H	D	D	H	D	D	H	D	H	H	
C14M47	G41030	48.8	2	14	D	H	H	H	D	D	H	H	H	H	D	D	H	H	D	H	D	D	D	D	H	H	H	D	D	H	D	D	D	H	H	D	D	H	D	D	H	D	H	H	
C14M68	G41023	51.7	2	14	D	H	D	H	D	D	H	H	H	H	D	D	H	H	D	H	D	D	D	D	H	H	H	D	D	H	D	D	D	H	H	D	D	H	D	D	H	D	H	H	
C14M39	G42706	54.6	2	14	D	H	D	H	D	D	H	H	H	H	D	D	H	H	D	H	D	D	D	D	H	H	D	D	D	H	D	D	D	H	H	D	D	H	D	D	H	D	H	H	
C14M40	G41021	54.6	2	14	D	H	D	H	D	D	H	H	H	H	D	D	H	H	D	H	D	D	D	D	H	H	D	D	D	H	D	D	D	H	H	D	D	H	D	D	H	D	H	H	
C14M4	G41022	54.6	2	14	D	H	D	H	D	D	H	H	H	H	D	D	H	H	D	H	D	D	D	D	H	H	D	D	D	H	D	D	D	H	H	D	D	H	D	D	H	D	H	H	
C14M82	G41032	63.2	3	14	D	H	H	H	D	D	H	H	H	H	D	H	H	H	D	H	D	D	D	D	H	H	D	D	H	H	D	D	D	H	H	D	D	H	D	D	H	D	H	H	
LW74	.	63.2	3	14	D	H	H	H	D	D	H	H	H	H	D	H	H	H	D	H	D	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
C13M54	G42734	63.2	3	14	D	H	H	H	D	D	H	H	H	H	D	H	H	H	D	H	D	D	D	D	H	H	D	D	H	D	D	D	H	H	D	D	H	D	D	H	D	H	H		
C14M58	G41033	63.2	3	14	D	H	H	H	D	D	H	H	H	H	D	H	H	H	D	H	D	D	D	D	H	H	D	D	H	D	D	D	H	H	D	D	H	D	D	H	D	H	H		
C14M129	G41034	77.5	3	14	D	H	H	H	D	D	D	H	D	H	D	H	H	H	D	H	D	H	D	D	H	H	H	D	H	H	D	D	D	D	H	H	D	D	H	D	D	H	D	H	H
TA13	G38887	AF010527	80.4	3	14	D	H	H	H	D	D	D	H	D	H	D	H	D	H	D	H	D	H	D	D	H	H	H	D	H	H	D	D	D	D	H	D	D	H	D	H	H	H		
C14M61	G41038	83.3	3	14	D	H	H	H	D	D	D	H	D	H	D	H	D	H	D	H	D	H	D	H	H	D	H	H	D	H	H	D	D	D	D	H	D	D	H	D	H	H	H		
C14M99	G41039	83.3	3	14	D	H	H	H	D	D	D	H	D	H	D	H	D	H	D	H	D	H	D	H	H	D	H	H	D	H	H	D	D	D	D	H	D	D	H	D	H	H	H		
C14M14	G41040	83.3	3	14	D	H	H	H	D	D	D	H	D	H	D	H	D	H	D	H	D	H	D	H	H	H	D	H	H	D	D	D	D	H	H	D	D	H	D	D	H	D	H	H	
C14M30	G41035	89.0	3	14	D	H	D	H	D	D	D	H	D	H	D	H	D	H	D	H	D	H	D	H	H	D	H	H	H	H	H	D	D	D	D	H	D	D	H	D	D	H	H		
C14M29	G41037	89.0	3	14	D	H	D	H	D	D	D	H	D	H	D	H	D	H	D	H	D	H	D	H	H	D	H	H	H	H	H	D	D	D	D	H	D	D	H	D	D	H	D	H	H
TA22	G38886	AF010534	89.0	3	14	D	H	D	H	D	D	D	H	D	H	D	H	D	H	D	H	D	H	H	D	H	H	H	H	H	D	D	D	D	H	D	D	H	D	H	D	H	H		
CAL	G37870	M99442	94.7	3	14	D	H	D	H	D	D	D	H	D	H	D	H	D	H	D	H	D	H	H	H	H	D	H	H	H	D	D	D	D	H	D	D	H	D	D	H	D	H	H	
GPI	G37867	J05544	106.1	3	14	D	H	H	H	D	D	D	H	D	H	H	H	D	H	D	H	D	H	H	H	H	D	H	H	H	D	D	D	D	H	D	D	D	D	D	D	D	D	H	H
C14M78	G41041	106.1	3	14	D	H	H	H	D	D	D	H	D	H	H	D	H	D	H	D	H	D	H	H	H	H	D	H	H	H	D	D	D	D	H	D	D	D	D	D	D	D	D	H	H
PIPGI	.	106.1	3	14	D	H	H	H	D	D	D	H	D	H	H	D	H	D	H	D	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
M41K2	G37872	114.7	3	14	D	H	H	H	D	D	D	H	D	H	D	H	D	H	D	H	D	H	D	H	H	H	H	D	H	D	H	H	D	D	H	D	H	D	D	D	D	D	H	H	
ATB	atb2	G37796	.	14	D	H	H	H	D	D	D	H	D	H	D	H	D	H	D	H	D	H	D	H	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
RRR1	G37865	L22057	117.6	3	14	D	H	H	H	D	D	D	H	D	H	D	H	D	H	D	H	D	H	D	H	H	H	D	D	H	D	H	H	D	D	H	D	H	D	D	D	D	D	H	H
C14M115	G41042	117.6	3	14	D	H	H	H	D	D	D	H	D	H	D	H	D	H	D	H	D	H	D	H	H	H	D	D	H	D	H	H	D	D	H	D	H	D	D	D	D	D	D	H	H
C14M65	G41036	117.6	3	14	D	H	H	H	D	D	D	H	D	H	D	H	D	H	D	H	D	H	D	H	H	H	D	D	H	D	H	H	D	D	H	D	H	D	D	D	D	D	D	H	H
C14M36	G41043	117.6	3	14	D	H	H	H	D	D	D	H	D	H	D	H	D	H	D	H	D	H	D	H	H	H	D	D	H	D	H	H	D	D	H	D	H	D	D	D	D	D	D	H	H
C14M53	G42707	120.5	3	14	D	H	H	H	D	D	D	H	D	H	D	H	D	H	D	H	D	H	D	H	H	H	D	D	H	D	H	H	D	D	H	D	H	D	D	D	D	D	D	H	H
TA88	G38888	AF010572	120.5	3	14	D	H	H	H	D	D	D*	H	D	H	D	H	D	H	D	H	D	H	D	H	H	H	D	D	H	D	D	H	D	H	D	H	D	D	D	D	D	D	H	H
pSc11.90	.	123.4	3	14	D	H	H	H	D	D	H	H	D	H	D	H	D	H	D	H	D	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
LW54	.	123.4	3	14	D	H	H	H	D	D	H	H	D	H	D	H	D	H	D	H	D	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
LW55	.	123.4	3	14	D	H	H	H	D	D	H	H	D	H	D	H	D	H	D	H	D	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
C14M51	G41044	123.4	3	14	D	H	H	H	D	D	H	H	D	H	D	H	D	H	D	H	D	H	H	H	D	D	H	D	D	H	D	D	H	D	H	D	D	D	D	D	D	D	H	H	
C14M17	G41045	123.4	3	14	D	H	H	H	D	D	H	H	D	H	D	H	D	H	D	H	D	H	D	H	H	H	D	D	H	D	D	H	D	D	H	D	H	D	H	D	D	D	D	H	H
C14M120	G41046	123.4	3	14	D	H	H	H	D	D	H	H	D	H	D	H	D	H	D	H	D	H	D	H	H	H	D	D	H	D	D	H	D	D	H	D	H	D	D	D	D	D	D	H	H
C14M109	G41047	123.4	3	14	D	H	H	H	D	D	H	H	D	H	D	H	D	H	D	H	D	H	D	H	H	H	D	D	H	D	D	H	D	D	H	D	H	D	D	D	D	D	D	H	H
TPI	tpi	G37794	L01655	123.4	3	14	D	H	H	H	D	D	H	H	D	H	D	H	D	H	D	H	D	H	H	H	D	D	H	D	D	H	D	D	H	D	H	D	D	D	D	D	D	H	H
C14M104	G41048	123.4	3	14	D	H	H	H	D	D	H	H	D	H	D	H	D	H	D	H	D	H	D	H	H	H	D	D	H	D	D	H	D	D	H	D	H	D	D	D	D	D	D	H	H
M41KD	G37873	A13477,A00785	123.4	3	14	D	H	H	H	D	D	H	H	D	H	D	H	D	H	D	H	D	H	H	H	D	D	H	D	D	H	D	D	H	D	H	D	D	D	D	D	D	D	H	H
C14M54	G41049	123.4	3	14	D	H	H	H	D	D	H	H	D	H	D	H	D	H	D	H	D	H	D	H	H	H	D	D	H	D	D	H	D	D	H	D	H	D	D	D	D	D	D	H	H
C14M77	G41050	123.4	3	14	D	H	H	H	D	D	H	H	D	H	D	H	D	H	D	H	D	H	D	H	H	H	D	D	H	D	D	H	D	D	H	D	H	D	D	D	D	D	D	H	H
C14M9	G41051	123.4	3	14	D	H	H	H	D	D	H	H	D	H	D	H	D	H	D	H	D	H	D	H	H	H	D	D	H	D	D	H	D	D	H	D	H	D	D	D	D	D	D	H	H
C14M96	G41052	123.4	3	14	D	H	H	H	D	D	H	H	D	H	D	H	D	H	D	H	D	H	D	H	H	H	D	D	H	D	D	H	D	D	H	D	H	D	D	D	D	D	D	H	H
C14M80	G41053	126.3	3	14	D	H	H	D	D	D	H	H	D	H	D	H	D	H	D	H	D	H	D	H	H	H	D	D	H	D	D	H	D	D	H	D	H	D	D	D	D				



D	Dd2 genotype (aqua)	
H*	D*	* for third allele. H* is the third allele from HB3 parent and D* is the third allele from Dd2 parent. Note: * indicate non-canonical alleles from spontaneous microsatellite mutations in the parental populations.
Gene conversion candidate. A gene conversion is a non-reciprocal process of genetic change in which one DNA sequence directs the conversion of a different, usually homologous, DNA partner to its own sequence. In meiotic gene conversion, one allele of a pair is changed to the sequence of its partner. This is a distinct process from reciprocal chromatid exchange.		
Empty allele or no PCR product; Amplified HB3 band is present, but Dd2 band is not present.		

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