

**Table S3.** Attribution of 21 contigs to the 20 chromosomes described by Ma *et al* (4) using flanking non-*msg* genes.

<b>Non-<i>msg</i> gene no. in assembled subtelomeres (Fig. 3 and S6a)</b>	<b>Function</b>	<b>Contig no.</b>	<b>Fig. no.</b>	<b>Locus Ma et al (4) assembly</b>	<b>Identity to locus Ma et al (4) assembly %</b>	<b>Chromosome no. Ma et al (4) (= supercontig no.)</b>	<b>Size chromosome (bps)</b>	<b>Position non-<i>msg</i> gene</b>
1	hypothetical protein	54	3	T551_01652	99	6	518165	479400-480758
2	hypothetical protein (helicase)	54	3	T551_01651	99	6	518165	476141-478700
3	hypothetical protein	18	3	T551_01851	99	7	454917	427758-428464
4	hypothetical protein	18	3	T551_01852	99	7	454917	429499-430704
5	hypothetical protein	26	3	T551_02779	100	13	364210	13192-15820
6	thiamine pyrophosphokinase	26	3	T551_02780	99	13	364210	15966-16885
7	hypothetical protein	45	3	T551_03102	100	14	360840	326441-327418
8	hypothetical protein	45	3	T551_03101	99	14	360840	322728-325661
9	amidophosphoribosyltransferase	74	3	T551_03398	99	16	301115	283900-285098
10	hypothetical protein	74	3	T551_03399	99	16	301115	285293-285886
11	hypothetical protein	59	3	T551_02607	99	11	401875	393657-394969
12	hypothetical protein	59	3	T551_02608	99	11	401875	395025-395689
13	hypothetical protein	55	3	T551_01666	99	7	454917	22474-26897
14	hypothetical protein	55	3	T551_01667	96	7	454917	20227-21266
15	60S ribosomal protein L28	6	3	T551_03406	100	17	269959	25639-26302
16	potassium/sodium efflux P-type ATPase	6	3	T551_03405	99	17	269959	20501-24017
17	hypothetical protein	98	3	T551_02615	100	12	394971	21306-22104
18	hypothetical protein	98	3	T551_02614	99	12	394971	15560-20701
19	hypothetical protein	24	3	T551_02440	99	11	401875	23902-25162
20	hypothetical protein	24	3	T551_02439	99	11	401875	20725-22665
21	hypothetical protein	84	S7a	T551_03252	100	15	322061	293986-294980
22	hypothetical protein	84	S7a	T551_03253	95	15	322061	295229-297205
23	hypothetical protein	106	S7a	T551_02048	99	8	454558	428498-430616
24	hypothetical protein (cyclin)	106	S7a	T551_02049	99	8	454558	431088-432680
25	hypothetical protein	105	S7a	T551_03662	99	20	72378	38975-41550
26	hypothetical protein	105	S7a	T551_03663	96	20	72378	41885..>44219
2	hypothetical protein	53	S7a	T551_00329	97	2	626993	26418-28129

28	hypothetical protein	53	S7a	T551_00328	99	2	626993	22974-26267
29	hypothetical protein	33	S7a	T551_01433	99	6	518165	20112-22438
30	hypothetical protein	33	S7a	T551_01432	99	6	518165	16995-19594
31	hypothetical protein	149	S7a	T551_01863	99	8	454558	20988-22187
32	mevalonate kinase	149	S7a	T551_01862	100	8	454558	19454-20919
33	hypothetical protein	44	S7a	T551_01188	100	5	557778	15123-16823
34	rRNA adenine N(6)-methyltransferase	44	S7a	T551_01189	100	5	557778	17377-18597
35	hypothetical protein	147	S7a	T551_00608	99	3	621393	6402-7384
36	hypothetical protein	147	S7a	T551_00607	97	3	621393	4794-5465
37	metalloendopeptidase	124	S7a	T551_03640	93	19	73066	58200-62230
38	ferrochelataase	124	S7a	T551_03639	98	19	73066	55462-56880
39	nuclear distribution protein PAC1	88	S7a	T551_02769	100	12	394971	363742-369964
40	hypothetical protein	88	S7a	T551_02770	100	12	394971	370261-371738
41 (flanking UCS;	transketolase	72	S7a	T551_00004	100	1 (carrying UCS)	635195	6182-8357
42 (flanking UCS;	hypothetical protein	72	S7a	T551_00003	100	1 (carrying UCS)	635195	3430-4836