

Additional file 5

T. reesei Rut-C30 reassembly (based on genome sequence from T. reesei QM6a)

65 scaffolds from the JGI reference genome (33.3Mb - 99.5% of the genome) have been reassembled in 7 chromosomes, as follows :

CHR I

	scaffold	start	end	direction	comment
7	full	1	1 429 972	-1	
12	full	1	1 022 062	-1	
43	full	1	74 996	-1	
21	full	1	576 034	-1	
55	full	1	33 670	?	centromere (consistent with QM6a)
4	translocation	1	748 277	1	manual correction according to (Vitikainen et al. 2010)
22	translocation	139 515	541 456	1	

size : 4 287 553 (with 100bp Ns spacers between each scaffold)

CHR II

	scaffold	start	end	direction	comment
31	fragment	1	224 034	-1	split location corrected as in QM6a reassembly
41	full	1	80 626	-1	
25	full	1	439 677	1	
68	full	1	10 734	1	
10	full	1	1 156 739	-1	
66	full	1	11 200	?	centromere (consistent with QM6a)
59	full	1	18 517	?	centromere (consistent with QM6a)
8	full	1	1 408 331	1	
34	full	1	166 473	-1	
26	full	1	433 400	1	
14	full	1	861 070	-1	
23	full	1	512 080	-1	
54	full	1	34 758	1?	
36	full	1	136 855	-1	
27	full	1	433 262	-1	
28	fragment	367 024	407 093	?	split location corrected as in QM6a reassembly
67	full	1	11 021	1?	

size : 5 980 447 (with 100bp Ns spacers between each scaffold)

CHR III

	scaffold	start	end	direction	comment
45	full	1	65 952	-1	
69	full	1	10 696	-1?	
35	full	1	152 537	1	
32	full	1	230 370	-1	
11	full	1	1 155 933	-1	
40	full	1	89 857	1	
					centromere location consistent with QM6a (no scaffold reliably assembled)
2	translocation	546 704	2 007 221	-1	manual correction according to (Vitikainen et al. 2010)
4	translocation	748 278	1 204 862	-1	
4	translocation	1 204 863	1 832 615	1	manual correction according to (Vitikainen et al. 2010)
49		1	46 304	?	
48	translocation	1	1 666	1	
2	translocation	154 748	546 703	-1	manual correction according to (Vitikainen et al. 2010)
2	fragment	1	98 434	-1	split location corrected as in QM6a reassembly
6	full	1	1 455 714	-1	

size : 6 245 475 (with 100bp Ns spacers between each scaffold)

CHR IV

	scaffold	start	end	direction	comment
64	full	1	14 482	1	
19	full	1	663 018	-1	
17	full	1	797 352	1	
56	full	1	32 194	?	centromere (consistent with QM6a)
20	full	1	629 213	-1	
1	fragment	2 981 735	3 756 989	1	split location corrected as in QM6a reassembly
5	fragment	1 584 116	1 729 360	1	split location corrected as in QM6a reassembly
13	full	1	891 309	-1	
2	fragment	99 435	154 747	-1	split location corrected as in QM6a reassembly
38	full	1	125 035	-1	
33	full	1	207 997	-1	

size : 4 337 413 (with 100bp Ns spacers between each scaffold)

CHR V

	scaffold	start	end	direction	comment
46	full	1	62 252	1	telomere repeats
30	full	1	247 268	1	
42	full	1	78 584	1	
53	full	1	36 593	-1?	
18	full	1	685 578	1	
61	full	1	15 406	?	centromere (consistent with QM6a)
60	full	1	15 714	?	centromere (consistent with QM6a)
28	fragment	1	366 023	-1	split location corrected as in QM6a reassembly
1	fragment	1	2 471 118	1	split location corrected as in QM6a reassembly

size : 3 979 336 (with 100bp Ns spacers between each scaffold)

CHR VI

	scaffold	start	end	direction	comment
47	full	1	50 543	-1	
15	deletion	1	1 555	1	manual correction according to (Seidl et al. 2008)
15	deletion	86 603	837 556	1	
44	full	1	66 247	-1?	
62	full	1	15 337	?	
1	fragment	2 471 169	2 980 271	-1	split location corrected as in QM6a reassembly
50	full	1	45 663	-1	
37	full	1	132 540	1	
51	full	1	43 169	-1?	centromere (consistent with QM6a)
39	full	1	105 148	1	
9	full	1	1 219 543	-1	
22	translocation	1	139 476	1	manual correction according to (Vitikainen et al. 2010)
48	translocation	1 667	48 367	1	
5	fragment	1	1 583 115	-1	split location corrected as in QM6a reassembly

size : 4 710 394 (with 100bp Ns spacers between each scaffold)

CHR VII

	scaffold	start	end	direction	comment
29	full	1	382 182	-1	
24	full	1	501 049	-1	
16	full	1	824 923	-1	
52	full	1	41 083	?	centromere (consistent with QM6a)
3	full	1	1 910 749	-1	

size : 3 660 386 (with 100bp Ns spacers between each scaffold)

>scaffold_57

	scaffold	start	end	direction	comment
57	full	1	25 756	1	centromere signature but not reliably assembled

>scaffold_58

	scaffold	start	end	direction	comment
58	full	1	21 040	1	centromere signature but not reliably assembled

>scaffold_63

scaffold	start	end	direction
63 full	1	14 539	1

>scaffold_65

scaffold	start	end	direction
65 full	1	12 580	1

centromere signature but not reliably assembled

>scaffold_70

scaffold	start	end	direction
70 full	1	8 513	1

>scaffold_71

scaffold	start	end	direction
71 full	1	6 846	1

>scaffold_72

scaffold	start	end	direction
72 full	1	6 811	1

>scaffold_73

scaffold	start	end	direction
73 full	1	6 421	1

>scaffold_74

scaffold	start	end	direction
74 full	1	5 890	1

>scaffold_75

scaffold	start	end	direction
75 full	1	5 683	1

>scaffold_76

scaffold	start	end	direction
76 full	1	5 459	1

>scaffold_77

scaffold	start	end	direction
77 full	1	5 371	1

>scaffold_78

scaffold	start	end	direction
78 full	1	5 154	1

>scaffold_79

scaffold	start	end	direction
79 full	1	4 691	1

>scaffold_80

scaffold	start	end	direction
80 full	1	4 619	1

>scaffold_81

scaffold	start	end	direction
81 full	1	4 614	1

>scaffold_82

scaffold	start	end	direction
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82	full	1	4 370	1
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>scaffold_83

scaffold		start	end	direction
83	full	1	3 796	1

>scaffold_84

scaffold		start	end	direction
84	full	1	3 468	1

>scaffold_85

scaffold		start	end	direction
85	full	1	3 089	1

>scaffold_86

scaffold		start	end	direction
86	full	1	3 000	1

>scaffold_87

scaffold		start	end	direction
87	full	1	2 158	1