

T. reesei QM6a reassembly

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	
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 - direction uncertainty
4	full	1 1 832 615	1	
49	full	1 46 304	-1?	direction uncertainty
48	full	1 48 367	1	
5	fragment	1 1 583 115	-1	split location identified by Ns gap

size : **6 647 935** (with 100bp Ns spacers between each scaffold)

CHR II

scaffold	start	end	direction	
31	fragment	1 224 034	-1	telomere repeats (4 duplications of the telomere sequence have been deleted, 7kb)
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 - direction and order uncertainty
59	full	1 18 517	?	centromere - direction and order uncertainty
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?	direction uncertainty
36	full	1 136 855	-1	
27	full	1 433 262	-1	
28	fragment	367 024 407 093	?	split location identified by Ns gap - direction uncertainty
67	full	1 11 021	1?	direction uncertainty

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

CHR III

scaffold	start	end	direction	
45	full	1 65 952	-1	telomere repeats OK
69	full	1 10 696	?	direction uncertainty
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 position (no centromere scaffold reliable assembled)
2	fragment	154 748 2 007 204	-1	split location uncertainty (154 748 was chosen here after alignment with fragment 1-98434)
2	fragment	1 98 434	-1	split location identified by Ns gap
6	full	1 1 455 714	-1	telomere repeats OK

size : **5 112 650** (with 100bp Ns spacers between each scaffold)

CHR IV

scaffold	start	end	direction	
64	full	1 14 482	1	telomere repeats
19	full	1 663 018	-1	
17	full	1 797 352	1	
56	full	1 32 194	?	centromere - direction uncertainty
20	full	1 629 213	-1	
1	fragment	2 981 735 3 756 989	1	split location identified by Ns gap
5	fragment	1 584 116 1 729 360	1	split location identified by Ns gap
13	full	1 891 309	-1	
2	fragment	99 435 154 747	-1	split location uncertainty (around 152 to 158 kb, 154747 chosen after alignment of the 2 other fragments)
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	
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	-1?	centromere - direction and order uncertainty
60	full	1 15 714	1?	centromere - direction and order uncertainty
28	fragment	1 366 023	-1	split location identified by Ns gap
1	fragment	1 2 471 118	1	telomere repeats - split location identified by Ns gap and presence of telomere repeats

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

CHR VI

scaffold	start	end	direction
47	full	1 50 543	-1?
15	full	1 837 556	1
44	full	1 66 247	-1
62	full	1 15 337	-1?
1	fragment	2 471 169 2 980 271	-1
50	full	1 45 663	-1
37	full	1 132 540	1
51	full	1 43 169	?
39	full	1 105 148	1
9	full	1 1 219 543	-1
22	full	1 541 456	1

remarks

direction uncertainty

direction uncertainty

split location identified by Ns gap and presence of telomere repeats on the other side

size : 3 567 305 (with 100bp Ns spacers between each scaffold)

CHR VII

scaffold	start	end	direction
29	full	1 382 182	-1
24	full	1 501 049	-1
16	full	1 824 923	-1
52	full	1 41 083	?
3	full	1 1 910 749	-1

centromere - direction uncertainty

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

>scaffold_57

scaffold	start	end	direction
57	full	1 25 756	1

centromere signature but not reliably assembled

>scaffold_58

scaffold	start	end	direction
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
82	full	1 4 370	1

>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