

§S6. Assembly and Genetic Map Integration

§S6.1. Chromosome Size Estimates and Comparison to Assembly

Chromosome	Estimated Size [†]	Assembly Size	Estimated Coverage
I	3.8	3.67	96.6%
II	4.2	3.94	93.8%
III	3.5	3.39	96.9%
IV	2.9	2.81	96.9%
V	3.8	2.22	58.4%
VI	3.5	3.34	95.4%
VII	4.5	4.41	98.0%
VIII	5	4.85	97.0%
Unlinked		1.43	
Total	31.2	30.06	96.3%

[†]Chromosome estimated sizes taken from Brody, H., J. Griffith, et al. (1991). "Chromosome-specific recombinant DNA libraries from the fungus *Aspergillus nidulans*." *Nucleic Acids Res* 19(11): 3105-9.

§S6.2. Genetic Map Description and Integration

Around 260 known genetic markers, which have associated sequences, exist for *Aspergillus nidulans*^{4,5}. These 260 genetic markers were filtered to a set of 196 unambiguous sequences with accessions in GenBank. Of these 196 markers, 103 are ordered on the linkage group map whereas the remaining 93 are unordered. The file of genetic markers is available for download at http://www.broad.mit.edu/cgi-bin/annotation/aspergillus/download_license.cgi.

These markers were compared to the current assembly using BLASTN. Where these matches were unique, were of high quality, and contained most or all the gene, we assigned a marker position in one of our contigs. A total of 187 markers were placed uniquely within the assembly and only 14 of the markers showed discrepancies (see below). We used the 187 unique marker alignments to correlate contigs with linkage groups, creating the correlated genetic maps displayed here.

- 28.5 Mb (18 supercontigs) of the 30 Mb assembly or 95% of the assembly, are anchored to the genetic map.
- 26.8 Mb (12 supercontigs) or 89% of the assembly are ordered and oriented.
- 1.7 Mb can only be placed on a linkage group without specifying order or orientation

More detail is available at <http://www.broad.mit.edu/annotation/fungi/aspergillus/markers.html>.

§S6.3. Discrepancies between Assembly and Genetic Map

There are a few cases where marker order on the linkage group map conflicts with the locations of markers in supercontigs. The discrepancies may be due to:

1. Errors in assembly of sequence into contigs or supercontigs

2. Errors in order of markers on the linkage group map
3. Correct but incomplete assembly data: for example, one supercontig may lie within a gap between contigs in another supercontig

The following discrepancies were noted and corrected when related to an error in assembly (see also (<http://www.gla.ac.uk/Acad/IBLS/molgen/aspergillus/>)). *All discrepancies that could be associated with errors in the assembly were corrected prior to analysis.* The order and orientation of contigs within supercontigs in this corrected assembly used for analysis is provided below.

1. **Re-orient Supercontig 9, on LG IV:** *uvrH* and *bimD* map distally while *uvrB* is centromere-proximal
2. **Supercontig 15 should be on LG VI not LG IV:** Supercontig 15 is shown as relating to linkage group IV on the basis of the *pacA* marker. However the clone labelled "*pacA*" has been found to encode a suppressor of *pacA*, and has been renamed "*SuApacA*". *SuApacA* maps on VI, as does *cnxG*, located in contig 169. Telomeric repeats located at the end of contig 170 determine that supercontig 15 is the short left arm of linkage group VI, with contig 170 distal to contig 169.
3. **Supercontig 14 should be on LG VII:** The *alcA* gene is genetically mapped to the short left arm of linkage group VII, and therefore locating supercontig 14 to that position (orientation unknown).
4. **Supercontig 16 should be on LG VIII:** supercontig 16 probably relates to the right arm of linkage group VIII, on the basis of a tentative identification of AN9403.1 as "*pdhA*" (encoding a pyruvate dehydrogenase subunit).
5. **Telomeric simple repeats** are found at:
 - the start of contig 1.134: LG II left end.
 - as stated in item 2, 1.170 (supercontig 15) is clearly the LEFT arm of VI because *cnxG* (meiotically at the left end of VI) locates to 1.169.
 - the start of contig 1.1: right end of LG VIII.
 - on unattached contigs 1.200 and 1.216

§S6.4. *A. nidulans* Assembly Contig Order and Orientation

The following provides the order and orientation of contigs within supercontigs in the corrected *A. nidulans* assembly used for analysis. Supercontigs are ordered from the end of one arm of each chromosome to the end of the other arm although the selection of which arm to start from was arbitrary for each chromosome.

Supercontig	Contig	Contig Length	Contig Orientation	Linkage Group
7	108	352786	-1	1
7	107	444822	-1	1
7	106	67855	-1	1
7	105	277183	-1	1
7	104	297769	-1	1
7	103	69272	-1	1
7	102	132643	-1	1
7	101	209568	-1	1
7	100	337251	-1	1

7	99	2005	-1	1
8	109	233950	1	1
8	110	298245	1	1
8	111	62418	1	1
8	112	353724	1	1
8	113	316066	1	1
8	114	25936	1	1
8	115	127320	1	1
8	116	56802	1	1
36	194	8226	1	1
11	134	78670	1	2
11	135	301041	1	2
11	136	31127	1	2
11	137	32282	1	2
11	138	39791	1	2
11	139	347029	1	2
11	140	26834	1	2
11	141	203328	1	2
11	142	43730	1	2
11	143	30509	1	2
11	144	72448	1	2
11	145	176570	1	2
4	71	8494	-1	2
4	70	41226	-1	2
4	69	80995	-1	2
4	68	250663	-1	2
4	67	254221	-1	2
4	66	88283	-1	2
4	65	278071	-1	2
4	64	203363	-1	2
4	63	41959	-1	2
4	62	201480	-1	2
4	61	865047	-1	2
4	60	68571	-1	2
4	59	177453	-1	2
5	86	112247	-1	3
5	85	34531	-1	3
5	84	621812	-1	3
5	83	55015	-1	3
5	82	44985	-1	3
5	81	156263	-1	3
5	80	335440	-1	3
5	79	209053	-1	3
5	78	353456	-1	3
5	77	132523	-1	3
5	76	153210	-1	3
5	75	213493	-1	3
5	74	12387	-1	3
5	73	3923	-1	3
5	72	17816	-1	3

13	163	91924	-1	3
13	162	65002	-1	3
13	161	266267	-1	3
13	160	146980	-1	3
13	159	58286	-1	3
13	158	283337	-1	3
26	183	10603	1	3
56	214	6579	1	3
9	128	280307	-1	4
9	127	138927	-1	4
9	126	40772	-1	4
9	125	32723	-1	4
9	124	55685	-1	4
9	123	128436	-1	4
9	122	214949	-1	4
9	121	13722	-1	4
9	120	3924	-1	4
9	119	137987	-1	4
9	118	105880	-1	4
9	117	274575	-1	4
10	129	627835	1	4
10	130	308583	1	4
10	131	116788	1	4
10	132	254738	1	4
10	133	81213	1	4
58	216	6436	1	5
6	87	12990	1	5
6	88	183820	1	5
6	89	282268	1	5
6	90	3363	1	5
6	91	6778	1	5
6	92	62660	1	5
6	93	340023	1	5
6	94	523724	1	5
6	95	103820	1	5
6	96	98894	1	5
6	97	24746	1	5
6	98	565485	1	5
15	170	216503	-1	6
15	169	351151	-1	6
3	58	83422	-1	6
3	57	28094	-1	6
3	56	45063	-1	6
3	55	492661	-1	6
3	54	183474	-1	6
3	53	51172	-1	6
3	52	82934	-1	6
3	51	1114266	-1	6
3	50	47652	-1	6
3	49	206454	-1	6

3	48	95913	-1	6
3	47	137873	-1	6
3	46	103482	-1	6
3	45	83158	-1	6
3	44	17771	-1	6
14	168	229305	-1	7
14	167	41972	-1	7
14	166	41526	-1	7
14	165	114598	-1	7
14	164	150254	-1	7
2	22	276296	1	7
2	23	67024	1	7
2	24	43525	1	7
2	25	229102	1	7
2	26	389371	1	7
2	27	113764	1	7
2	28	98898	1	7
2	29	525887	1	7
2	30	89802	1	7
2	31	2490	1	7
2	32	435990	1	7
2	33	2149	1	7
2	34	177275	1	7
2	35	84073	1	7
2	36	96901	1	7
2	37	75346	1	7
2	38	233386	1	7
2	39	240080	1	7
2	40	150763	1	7
2	41	64302	1	7
2	42	99573	1	7
2	43	338545	1	7
16	171	24092	1	8
16	172	523550	1	8
16	173	11633	1	8
1	21	2196	-1	8
1	20	21570	-1	8
1	19	71437	-1	8
1	18	175793	-1	8
1	17	347844	-1	8
1	16	451587	-1	8
1	15	178329	-1	8
1	14	364334	-1	8
1	13	249512	-1	8
1	12	174100	-1	8
1	11	61200	-1	8
1	10	175166	-1	8
1	9	14258	-1	8
1	8	49390	-1	8
1	7	773302	-1	8

1	6	266891	-1	8
1	5	450355	-1	8
1	4	155056	-1	8
1	3	127977	-1	8
1	2	168814	-1	8
1	1	10851	-1	8
12	146	11447	1	0
12	147	5126	1	0
12	148	4102	1	0
12	149	38673	1	0
12	150	109819	1	0
12	151	72894	1	0
12	152	53749	1	0
12	153	403022	1	0
12	154	34335	1	0
12	155	40523	1	0
12	156	11675	1	0
12	157	136262	1	0
17	174	26679	1	0
18	175	19880	1	0
19	176	15731	1	0
20	177	14522	1	0
21	178	12319	1	0
22	179	11756	1	0
23	180	11235	1	0
24	181	10660	1	0
25	182	10620	1	0
27	184	2754	1	0
27	185	7835	1	0
28	186	10198	1	0
29	187	10087	1	0
30	188	10072	1	0
31	189	10019	1	0
32	190	9210	1	0
33	191	9200	1	0
34	192	9030	1	0
35	193	8744	1	0
37	195	8077	1	0
38	196	8076	1	0
39	197	7797	1	0
40	198	7688	1	0
41	199	7686	1	0
42	200	7501	1	0
43	201	7389	1	0
44	202	7303	1	0
45	203	7055	1	0
46	204	6994	1	0
47	205	6930	1	0
48	206	6924	1	0
49	207	6880	1	0

50	208	6838	1	0
51	209	6773	1	0
52	210	6735	1	0
53	211	6721	1	0
54	212	6710	1	0
55	213	6639	1	0
57	215	6468	1	0
59	217	2295	1	0
59	218	4089	1	0
60	219	6367	1	0
61	220	6090	1	0
62	221	5785	1	0
63	222	5781	1	0
64	223	5626	1	0
65	224	5623	1	0
66	225	5462	1	0
67	226	5454	1	0
68	227	5437	1	0
69	228	5427	1	0
70	229	5381	1	0
71	230	5336	1	0
72	231	5185	1	0
73	232	5001	1	0
74	233	4981	1	0
75	234	4876	1	0
76	235	4760	1	0
77	236	4673	1	0
78	237	4650	1	0
79	238	4644	1	0
80	239	4316	1	0
81	240	3963	1	0
82	241	3865	1	0
83	242	3786	1	0
84	243	3623	1	0
85	244	3100	1	0
86	245	3093	1	0
87	246	3023	1	0
88	247	2515	1	0
89	248	2259	1	0
