

Accession	Origin	AIMS Stock #	Library	Read Length	Library insert size/bp ^b			Sequence Produced /Gb ^c			Coverage ^d		de-novo contig size/bp ^e			# denovo contigs	total contig length /Mb	
					25%	median	75%	total	mapped	rmdup	library	total	longest	N50	N90			
Bur-0	Ireland	CS6643	download ^a	35				1.60	1.16	0.80	6.69	27.39	24654	1984	279	260365	111.29	
			bur PhaseII	51	385	406	416	2.97	2.77	2.48	20.69							
Can-0	Canary Isles	CS6660	can Phase I	36	178	188	198	4.67	4.43	3.21	26.86	54.25	22495	1736	266	273359	111.31	
			can PhaseII	51	462	483	499	4.76	4.37	3.28	27.39							
Ct-1	Italy	CS6674	ct Phase I	36	196	206	217	5.18	4.91	3.78	31.60	57.40	21849	1854	268	270434	111.41	
			ct PhaseII	51	407	422	438	4.35	4.07	3.09	25.81							
Edi-0	Scotland	CS6688	edi Phase I	36	160	171	183	4.97	4.44	3.46	28.95	57.92	22926	1906	221	322787	117.04	
			edi PhaseII	51	409	420	429	5.06	4.76	3.47	28.97							
Hi-0	Netherlands	CS6736	hi Amplified	36	358	375	391	1.02	0.94	0.86	7.23	41.29	19083	1441	236	306478	112.09	
			hi Nonamp	36	380	393	406	1.78	1.65	1.48	12.38							
			hi Phase I	36	198	208	218	4.06	3.89	2.60	21.69							
Kn-0	Lithuania	CS6762	kn Phase I	36	209	224	239	4.83	4.05	2.59	21.63	41.35	18886	1524	186	385673	127.67	
			kn PhaseII	51	354	370	385	2.94	2.57	2.36	19.72							
Ler-0	Germany	CS20	ler Phase I	36	213	230	249	5.14	4.31	2.70	22.60	38.85	17955	1372	228	315154	113.15	
			ler PhaseII	51	403	410	417	2.50	2.30	1.95	16.26							
Mt-0	Libya	CS1380	mt Phase I	36	154	181	211	4.12	3.88	3.42	28.54	39.13	7478	646	182	404940	113.46	
			mt PhaseII	51	1394	1504	1613	2.33	1.88	1.27	10.59							
No-0	Germany	CS6805	no Phase I	36	178	187	196	5.20	4.84	2.92	24.43	45.56	20011	1901	253	284666	112.80	
			no PhaseII	51	304	315	327	3.17	2.96	2.53	21.13							
Oy-0	Norway	CS6824	oy Phase I	36	186	194	203	4.94	4.69	3.64	30.41	60.98	28033	1756	266	272178	111.35	
			oy PhaseII	51	420	431	440	5.14	4.83	3.66	30.57							
Po-0	Germany	CS6839	po Phase I	36	164	170	176	3.64	3.06	2.31	19.29	48.38	19320	1258	190	414957	119.92	
			po PhaseII	51	400	413	421	5.08	4.79	3.48	29.09							
Rsch-4	Russia	CS6850	rsch Phase I	36	187	205	225	5.04	4.42	2.62	21.91	50.41	22767	1780	256	281651	112.17	
			rsch PhaseII	51	398	409	418	5.01	4.64	3.41	28.50							
Sf-2	Spain	CS6857	sf Phase I	36	174	179	183	2.95	2.80	1.94	16.25	45.39	22295	1886	266	272602	111.46	
			sf PhaseII	51	375	383	390	5.11	4.78	3.49	29.14							
Tsu-0	Japan	CS6874	tsu Phase I	36	178	189	199	4.91	4.72	3.41	28.50	57.61	20007	1761	263	274548	112.15	
			tsu PhaseII	51	390	416	426	4.97	4.63	3.48	29.11							

Wil-2	Russia	CS6889	wil2 Phase I	36	165	170	174	3.42	3.21	2.21	18.48	46.06	19784	1826	269	273385	111.33
			wil2 PhaseII	51	452	460	467	4.81	4.52	3.30	27.58						
Ws-0	Russia	CS6891	ws Phase I	36	381	406	429	4.66	3.49	1.72	14.39	44.57	28032	1732	231	329115	124.97
			ws_tsl	36	376	403	426	1.60	1.28	0.93	7.78						
			ws PhaseII	51	210	215	220	3.58	3.22	2.68	22.40						
Wu-0	Germany	CS6897	wu Phase I	36	191	204	216	3.14	2.99	2.07	17.27	35.04	23074	1955	273	264048	111.26
			wu PhaseII	51	354	393	410	2.69	2.50	2.13	17.77						
Zu-0	Germany	CS6902	zu Phase I	36	138.5	191	207	3.93	3.41	2.57	21.51	42.08	23671	1807	219	317803	116.42
			zu PhaseII	51	233.5	346	411	3.04	2.87	2.46	20.56						

Supplemental Table Accession_statistics

^a publicly available data downloaded from the Weigel lab. All other data were generated specifically for this project

^b library insert size estimated from alignment of paired-end reads to TAIR10; 25%, 75% are quartiles.

^c total: amount in Gb of sequence generated after standard quality control filtering; mapped: amount mapped to TAIR10; rmdup: amount mapped after removing duplicate reads

^d coverage is the total length of rmdup sequence divided by 0.11966775 Gb (TAIR10 genome length)

^e de-novo contigs were generated by SOAPdenovo. Lengths are for contigs, ignoring scaffolds. Only contigs at least 50bp long included. N50, N90 are threshold lengths such that 50% and 90% of contigs are longer, respectively.