Supplemental Table 3

Correspondences of Cotton Chromosomal Regions with *Arabidopsis* Duplications

Cotton Chr[a]	Length		Length of syntenic regions				% of total syntenic regions associated with indicated number of *Arabidopsis* chromosomes									
			CS2		FISH		CS2	FISH	CS2	FISH	CS2	FISH	CS2	FISH	CS2	FISH
	cM	% genome	cM	%	cM	%	1[b]	1	2	2	3	3	4	4	>5	>5
C01	195.4	8.4	107.4	55.0	54.7	28.0	82.4	84.1	17.6	15.9	0.0	0.0	0.0	0.0	0.0	0.0
C02	176.4	7.6	100.7	57.1	70.5	40.0	60.9	63.8	21.3	32.5	17.9	3.7	0.0	0.0	0.0	0.0
C03	120.7	5.2	90.6	75.1	74.9	62.1	30.4	60.3	39.3	33.9	10.5	5.7	0.0	0.0	19.9	0.0
C04	183.8	7.9	70.3	38.2	39.5	21.5	35.6	88.6	20.9	11.4	31.9	0.0	11.7	0.0	0.0	0.0
C05	191.9	8.3	155.6	81.1	48.6	25.3	52.6	93.6	21.5	6.4	19.7	0.0	0.0	0.0	6.2	0.0
C06	172.6	7.4	84.0	48.7	26.6	15.4	39.4	51.9	53.5	44.7	7.1	3.4	0.0	0.0	0.0	0.0
C07	217.2	9.3	141.2	65.0	90.5	41.7	45.0	66.1	28.8	29.2	19.2	4.8	0.0	0.0	6.9	0.0
C08	159.5	6.9	126.0	79.0	59.3	37.2	65.9	49.2	15.4	41.3	14.1	8.3	3.7	1.2	0.9	0.0
C09	264.6	11.4	173.8	65.7	76.7	29.0	60.8	84.4	27.8	13.2	3.3	1.6	8.1	0.9	0.0	0.0
C10	172.6	7.4	69.7	40.4	54.9	31.8	85.1	83.6	14.9	16.4	0.0	0.0	0.0	0.0	0.0	0.0
C11	170.2	7.3	86.6	50.9	45.1	26.5	65.4	89.6	29.0	8.2	5.7	2.2	0.0	0.0	0.0	0.0
C12	101.7	4.4	49.4	48.6	24.5	24.1	53.8	78.0	31.0	13.5	15.2	8.6	0.0	0.0	0.0	0.0
C13	198.1	8.5	116.8	59.0	46.3	23.4	44.0	77.8	17.9	22.2	19.1	0.0	7.5	0.0	11.5	0.0
Total	2324.7	100.0	1372.1	59.0	712.1	30.6	55.6	73.8	25.5	23.0	12.5	3.0	2.6	0.2	3.8	0.0

[a] Based on the hypothetical ancestral chromosomes: does not correspond to published nomenclature for modern tetraploid chroosomes (Rong et al 2004)

[b] Number of chromosome segments involved in synteny

Supplemental Table 4

Correspondence of *Arabidopsis* α Duplications with Cotton Hypothetical Ancestral Chromosomes

Ara Dupli	Length		Length of syntenic regions				% of total syntenic regions associated with indicated number of cotton chromosomes									
			CS2		Fish		CS2	Fish	CS2	Fish	CS2	Fish	CS2	Fish	CS2	Fish
	Gene#	% genome	Gene#	%	Gene#	%	1[a]	1	2	2	3	3	4	4	>5	>5
α01	625	2.7	121	19.3	180	28.8	100.0	77.2	0.0	22.8	0.0	0.0	0.0	0.0	0.0	0.0
α02	1021	4.4	573	56.1	281	27.5	54.5	59.1	33.7	33.8	11.9	7.1	0.0	0.0	0.0	0.0
α03	943	4.1	616	65.3	329	34.9	51.0	50.2	14.6	49.8	19.2	0.0	15.3	0.0	0.0	0.0
α04	422	1.8	188	44.5	142	33.6	86.7	36.6	13.3	63.4	0.0	0.0	0.0	0.0	0.0	0.0
α05	2413	10.4	1225	50.7	694	28.8	52.9	63.7	23.7	35.7	13.1	0.6	10.3	0.0	0.0	0.0
α06	644	2.8	401	62.2	277	43.0	37.4	53.8	47.9	26.0	14.7	20.2	0.0	0.0	0.0	0.0
α07	441	1.9	153	34.7	55	12.5	99.3	100.0	1.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0
α08	1583	6.8	741	46.8	263	16.6	73.4	79.1	26.6	20.9	0.0	0.0	0.0	0.0	0.0	0.0
α09	260	1.1	170	65.4	65	25.0	18.2	100.0	75.9	0.0	5.9	0.0	0.0	0.0	0.0	0.0
α10	2411	10.4	1301	54.0	784	32.5	72.9	71.2	21.6	18.9	5.5	8.3	0.0	1.7	0.0	0.0
α11	2321	10.0	1316	56.7	1031	44.4	40.0	52.0	28.8	44.6	15.4	3.0	5.7	0.4	10.0	0.0
α12	1180	5.1	755	64.0	419	35.5	65.2	87.4	19.7	12.6	6.6	0.0	8.5	0.0	0.0	0.0
α13	289	1.3	270	93.4	99	34.3	63.7	44.4	21.5	55.6	14.8	0.0	0.0	0.0	0.0	0.0
α14	956	4.1	758	79.3	232	24.3	26.6	51.3	25.3	47.0	44.1	1.7	4.0	0.0	0.0	0.0
α15	771	3.3	270	35.0	112	14.5	42.6	48.2	57.4	32.1	0.0	19.6	0.0	0.0	0.0	0.0
α16	419	1.8	187	44.6	29	6.9	34.8	100.0	65.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0
α17	393	1.7	0	0.0	93	23.7	0.0	95.7	0.0	4.3	0.0	0.0	0.0	0.0	0.0	0.0
α18	445	1.9	379	85.2	201	45.2	31.7	49.8	24.5	49.8	26.9	1.0	5.0	0.0	11.9	0.0
α19	413	1.8	98	23.7	46	11.1	100.0	23.9	0.0	76.1	0.0	0.0	0.0	0.0	0.0	0.0
α20	829	3.6	367	44.3	73	8.8	44.4	90.4	39.5	9.6	16.1	0.0	0.0	0.0	0.0	0.0
α21	737	3.2	346	47.0	203	27.5	100.0	91.1	0.0	8.9	0.0	0.0	0.0	0.0	0.0	0.0
α22	1159	5.0	844	72.8	310	26.7	49.8	74.8	32.5	25.2	17.1	0.0	0.7	0.0	0.0	0.0
α23	364	1.6	307	84.3	124	34.1	21.8	90.3	35.2	9.7	42.0	0.0	1.0	0.0	0.0	0.0
α24	267	1.2	126	47.2	18	6.7	100.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
αS01	170	0.7	83	48.8	70	41.2	100.0	0.0	0.0	88.6	0.0	11.4	0.0	0.0	0.0	0.0
αS02	221	1.0	213	96.4	41	18.6	27.7	58.5	72.3	41.5	0.0	0.0	0.0	0.0	0.0	0.0
αS03	125	0.5	78	62.4	0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
αS04	443	1.9	189	42.7	118	26.6	84.7	95.8	15.3	4.2	0.0	0.0	0.0	0.0	0.0	0.0
αS05	191	0.8	135	70.7	43	22.5	100.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
αS06	265	1.1	117	44.2	55	20.8	100.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
αS07	92	0.4	0	0.0	22	23.9	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
αS08	257	1.1	75	29.2	30	11.7	100.0	33.3	0.0	66.7	0.0	0.0	0.0	0.0	0.0	0.0
αS09	58	0.3	0	0.0	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
αS10	44	0.2	0	0.0	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Total	23172	100.0	12402	53.5	6439	27.8	56.5	65.6	26.3	30.8	12.5	3.3	3.4	0.3	1.4	0.0

[a] Number of chromosome segments involved in synteny

Supplemental Table 5

Percentage of Cotton Chromosomal Regions Showing Duplications in Hypothetical Ancestral Cotton Genome

Cotton Chr.[a]	Length		Length of syntenic regions				% of total syntenic regions associated with indicated number of chromosomes									
			CS2		FISH		CS2	FISH	CS2	FISH	CS2	FISH	CS2	FISH	CS2	FISH
	cM	% genome	cM	%	cM	%	1[b]	1	2	2	3	3	4	4	>5	>5
C01	195.4	8.4	62.4	31.9	38.7	19.8	47.4	61.8	39.1	21.4	13.5	12.7	0.0	4.1	0.0	0.0
C02	176.4	7.6	120	68.0	46.0	32.0	58.8	99.1	36.6	0.9	4.7	0.0	0.0	0.0	0.0	0.0
C03	120.7	5.2	46.6	40.8	45.2	39.6	45.3	80.5	47.4	19.5	7.3	0.0	0.0	0.0	0.0	0.0
C04	183.8	7.9	90.4	49.2	27.4	14.9	47.3	32.1	26.1	67.9	13.2	0.0	7.9	0.0	5.5	0.0
C05	191.9	8.3	95.7	49.9	83.8	43.7	46.4	67.7	23.6	23.2	15.8	9.2	7.9	0.0	6.3	0.0
C06	172.6	7.4	110.7	64.1	72.4	41.9	37.8	36.2	35.3	63.8	23.7	0.0	3.3	0.0	0.0	0.0
C07	217.2	9.3	104.1	47.9	34.1	15.7	39.6	100.0	47.3	0.0	13.2	0.0	00.0	0.0	0.0	0.0
C08	159.5	6.9	91.6	57.4	19.3	12.1	61.2	94.3	15.9	5.7	14.5	0.0	8.3	0.0	0.0	0.0
C09	264.6	11.4	127.4	48.1	72.8	27.5	57.7	80.1	21.0	16.1	14.1	3.8	4.8	0.0	2.4	0.0
C10	172.6	7.4	71.4	41.4	12.7	7.4	65.3	100.0	34.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0
C11	170.2	7.3	96.7	56.8	40.8	24.0	49.5	83.1	10.9	16.7	18.6	0.2	14.6	0.0	6.4	0.0
C12	101.7	4.4	66.2	65.1	30.6	30.1	51.4	69.0	11.2	20.6	14.7	10.5	14.5	0.0	8.3	0.0
C13	198.1	8.5	116.9	59.0	40.3	20.3	49.0	100.0	14.1	0.0	9.2	0.0	7.3	0.0	20.4	0.0
Total	2324.7	100.0	1200.1	51.8	564.1	24.3	50.6	73.8	27.1	22.6	12.8	3.3	5.3	0.3	4.1	0.0

[a] Based on hypothetical ancestral chromosomes: does not correspond to published nomenclature for modern tetraploid chromosomes (Rong et al 2004).

[b] Number of chromosome segments involved in synteny: data in columns is percentage of total syntenic regions associated with indicated numbers of chromosomes