Table S1. Expression profiles of the tocopherol biosynthesis candidate genes in soybean based on RNAseq data available from RNAsequencing data (http://www.soybase.org/soyseq)

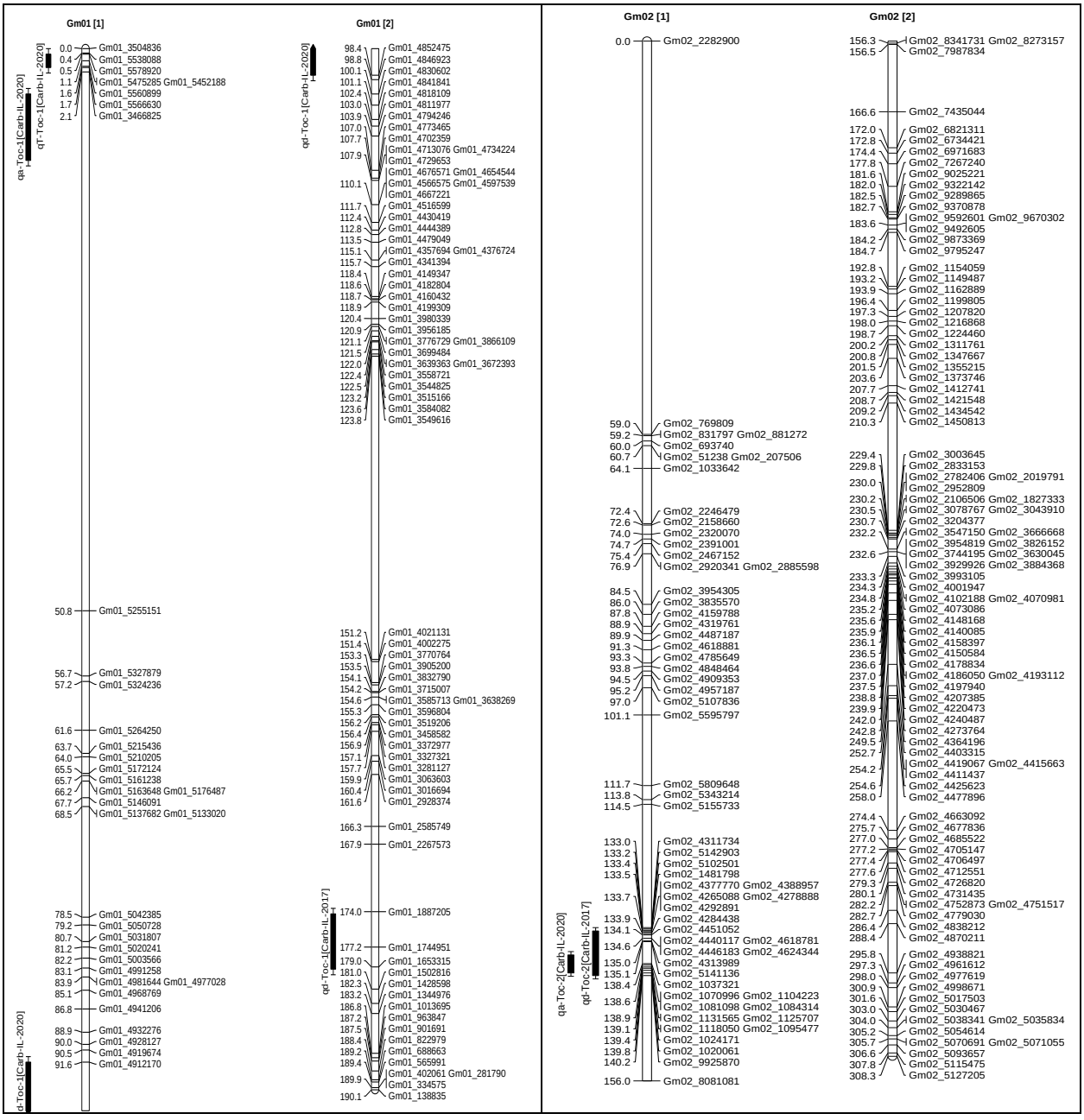
Gene ID	young_leaf	flower	one cm pod	pod shell 10DAF	pod shell 14DAF	seed 10 DAF	seed 14 DAF	seed 21 DAF	seed 25 DAF	seed 28 DAF	seed 35 DAF	seed 42 DAF	root	nodule
Glyma.01G134600	0	31	8	11	4	0	1	0	0	0	0	0	17	8
Glyma.02G002000	372	116	77	101	98	19	24	7	29	22	21	4	1	1
Glyma.02G143700	420	181	249	332	411	86	143	67	112	90	100	69	111	145
Glyma.02G273800	54	67	75	43	31	57	64	39	134	155	369	423	207	176
Glyma.02G284600	2	5	5	1	0	1	4	0	3	2	1	0	1	1
Glyma.03G033100	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Glyma.04G082300	0	34	9	9	5	8	19	3	32	26	60	44	0	0
Glyma.04G082500	47	48	38	46	18	17	25	16	31	46	65	51	8	10
Glyma.05G026200	2036	534	1154	1088	756	158	363	217	743	779	823	556	275	423
Glyma.06G084100	165	74	85	99	51	32	36	19	36	35	52	21	45	49
Glyma.06G235500	18	717	19	23	9	8	6	4	19	14	52	41	2	13
Glyma.06G235900	20	644	398	457	187	5	5	3	24	20	24	10	5	57
Glyma.09G222800	32	93	60	76	261	18	25	9	35	21	28	10	212	47
Glyma.10G030600	280	107	160	167	267	42	80	43	87	57	82	27	134	158
Glyma.10G070100	1	3	2	0	0	0	0	0	0	0	0	0	2	0
Glyma.10G070300	0	0	0	0	0	3	2	0	1	0	1	0	3	0
Glyma.10G295300	0	0	0	0	1	2	0	0	0	0	0	0	67	19
Glyma.12G014200	5	125	52	25	41	35	45	25	17	10	7	1	27	0
Glyma.12G014300	152	99	63	61	44	9	18	16	26	22	44	25	9	90
Glyma.12G161500	22	12	111	166	164	66	101	47	180	194	275	103	0	403
Glyma.12G205900	62	103	164	98	55	50	73	50	16	2	7	1	72	12
Glyma.12G233800	91	44	69	73	59	27	49	25	71	34	44	26	88	50
Glyma.13G097800	29	568	21	15	6	60	27	16	15	14	18	6	21	34
Glyma.13G152746	1	0	0	0	0	0	0	0	0	0	0	0	1	1
Glyma.13G152780	16	13	2	1	1	0	0	0	1	0	0	0	0	4
Glyma.13G152814	0	0	0	0	0	0	0	0	0	0	0	0	4	0
Glyma.13G265200	126	75	84	93	88	32	51	28	83	50	62	33	119	55
Glyma.13G295000	2	17	21	12	8	8	4	1	0	0	0	0	27	1491
Glyma.14G030400	97	706	96	122	39	77	81	38	209	130	111	48	53	55
Glyma.17G061900	21	39	29	26	18	9	6	16	24	16	32	15	10	2
Glyma.17G100700	1567	322	568	556	391	33	83	87	320	240	313	183	44	59
Glyma.20G190100	37	32	15	7	14	14	16	7	20	18	28	8	13	22
Glyma.20G211500	3	2	0	0	0	5	0	0	0	0	3	0	6	2
Glyma.20G245100	0	14	1	1	0	0	1	0	0	0	0	0	21	6

Table S2. QTLs identified in previous studies on Chr. 6.

QTL	Start (cM)	End (cM)	QTL Start	QTL End	Parents	Number loci tested	Lod score	Interval length	Reference
Seed tocopherol, alpha 1-2	96.83	98.83	16106296	16256544	OAC Bayfield X Hefeng 25	107	ND	ND	[35]
Seed tocopherol, alpha 2-2	97.83	107.58	15524734	17218677	Hefeng 25 X OAC Bayfield	606	ND	9.75	[34]
Seed tocopherol, gamma 1-3	100.75	102.75	16029425	16133204	OAC Bayfield X Hefeng 25	107	ND	ND	[35]
Seed tocopherol, gamma 2-3	94.65	101.75	16106296	16221044	Hefeng 25 X OAC Bayfield	606	ND	7.5	[34]
Seed tocopherol, total 1-1	96.83	98.83	16106296	16256544	OAC Bayfield X Hefeng 25	107	ND	ND	[35]
Seed tocopherol, total 1-2	100.75	102.75	16133204	16029425	OAC Bayfield X Hefeng 25	107	ND	ND	[35]
Seed tocopherol, total 2-1	96.83	98.83	16106296	16256544	Hefeng 25 X OAC Bayfield	606	ND	ND	[34]
Seed tocopherol, total 2-2	94.65	101.75	16106296	16221044	Hefeng 25 X OAC Bayfield	606	ND	7.1	[34]
qδTC-6	116.9	118	42091687	43647797	TK780 X B04009	ND	4.7	ND	[7]
qγTC-6	74.5	76.5	14027025	14268479	TK780 X B04009	ND	5.6	ND	[7]

Table S3. Positions of SNPs between Forrest and Williams 82 cultivars in the promoter of the tocopherol cyclase candidate gene (GmTC06, Glyma.06G084100).

Region	Position	Williams 82	Forrest
5'UTR	6464552	G	A
	6465186	G	A
	6465268	C	T
	6465403	A	G
	6465466	C	T
	6465531	G	T
	6465536	G	A
	6465698	T	C
	6465744	G	C
	6465768	A	T
	6465948	CATATTCA	-
	6466025	T	C
	6466060	GCACGTGAGGTTTAACAAGTTGATTT	-
	6466090	C	G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Gm01 [2]
Gm02 [1]
Gm02 [2]
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qd-Toc-1[Carb-IL-2020]
qa-Toc-2[Carb-IL-2020]
qd-Toc-2[Carb-IL-2017]
qd-Toc-1[Carb-IL-2017]
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0.5 Gm01_5578920
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1.6 Gm01_5560899
1.7 Gm01_5566630
2.1 Gm01_3466825
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56.7 Gm01_5327879
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63.7 Gm01_5215436
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79.2 Gm01_5050728
80.7 Gm01_5031807
81.2 Gm01_5020241
82.2 Gm01_5003566
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83.9 Gm01_4981644 Gm01_4977028
85.1 Gm01_4968769
86.8 Gm01_4941206
88.9 Gm01_4932276
90.0 Gm01_4928127
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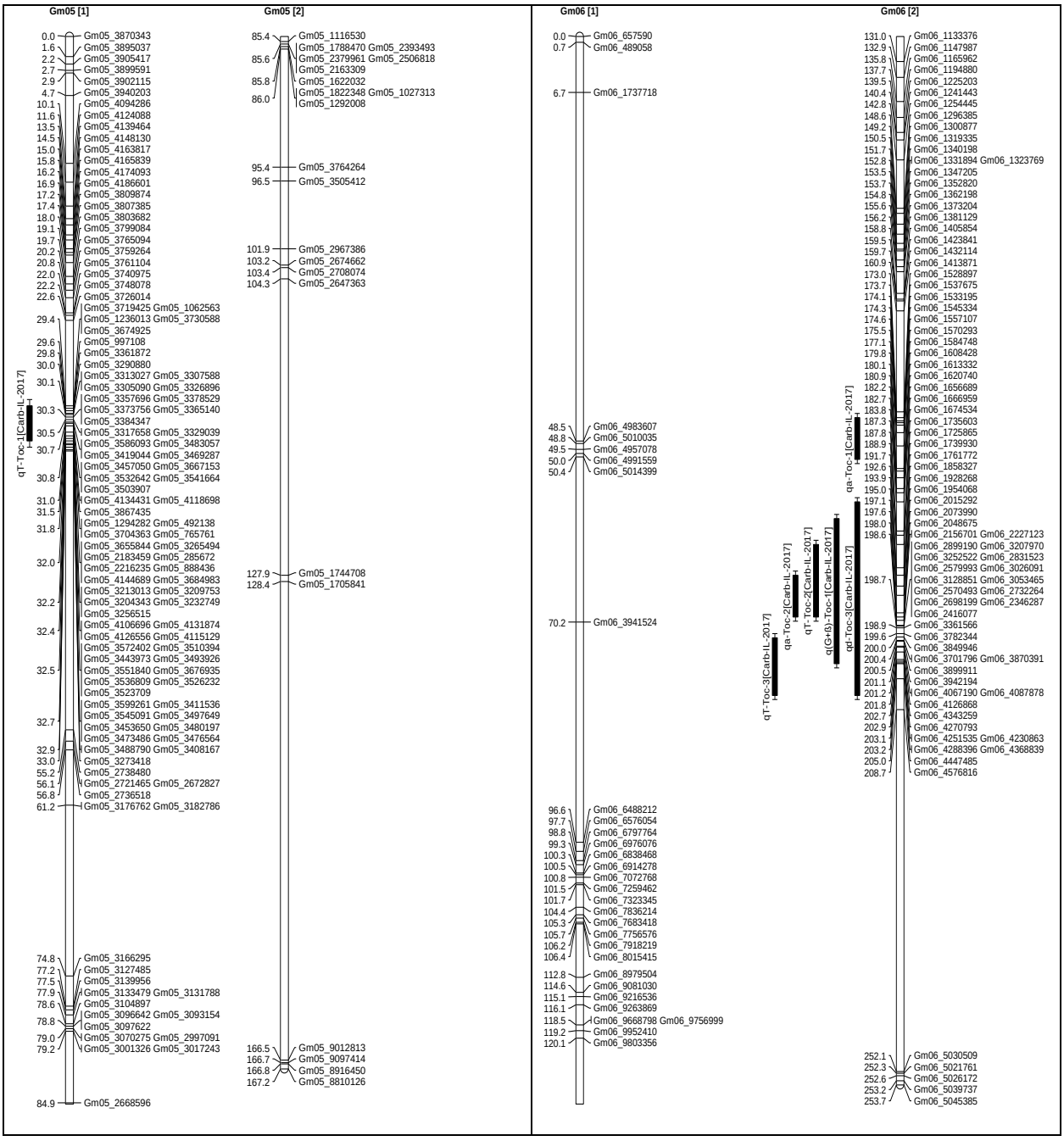
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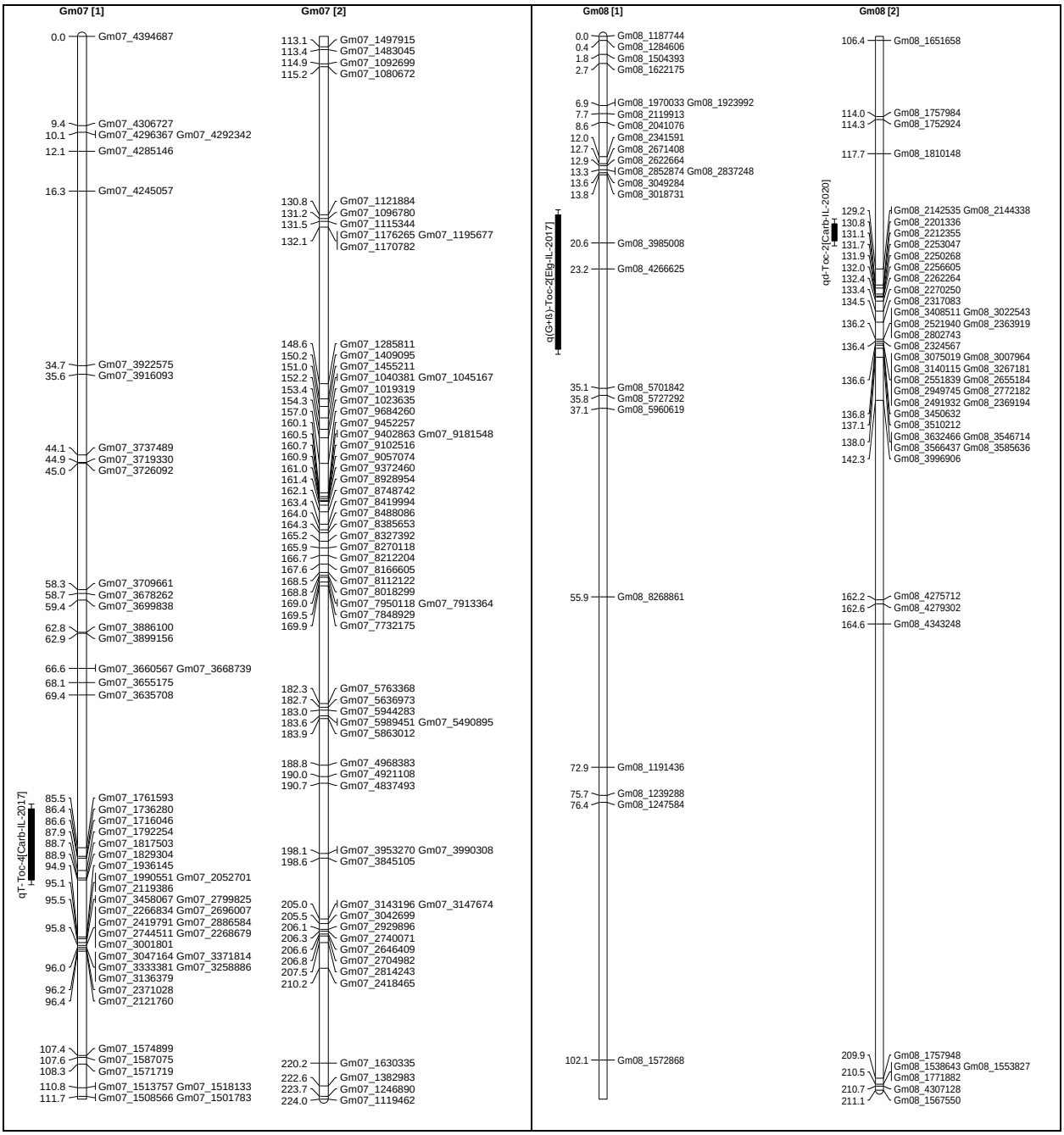
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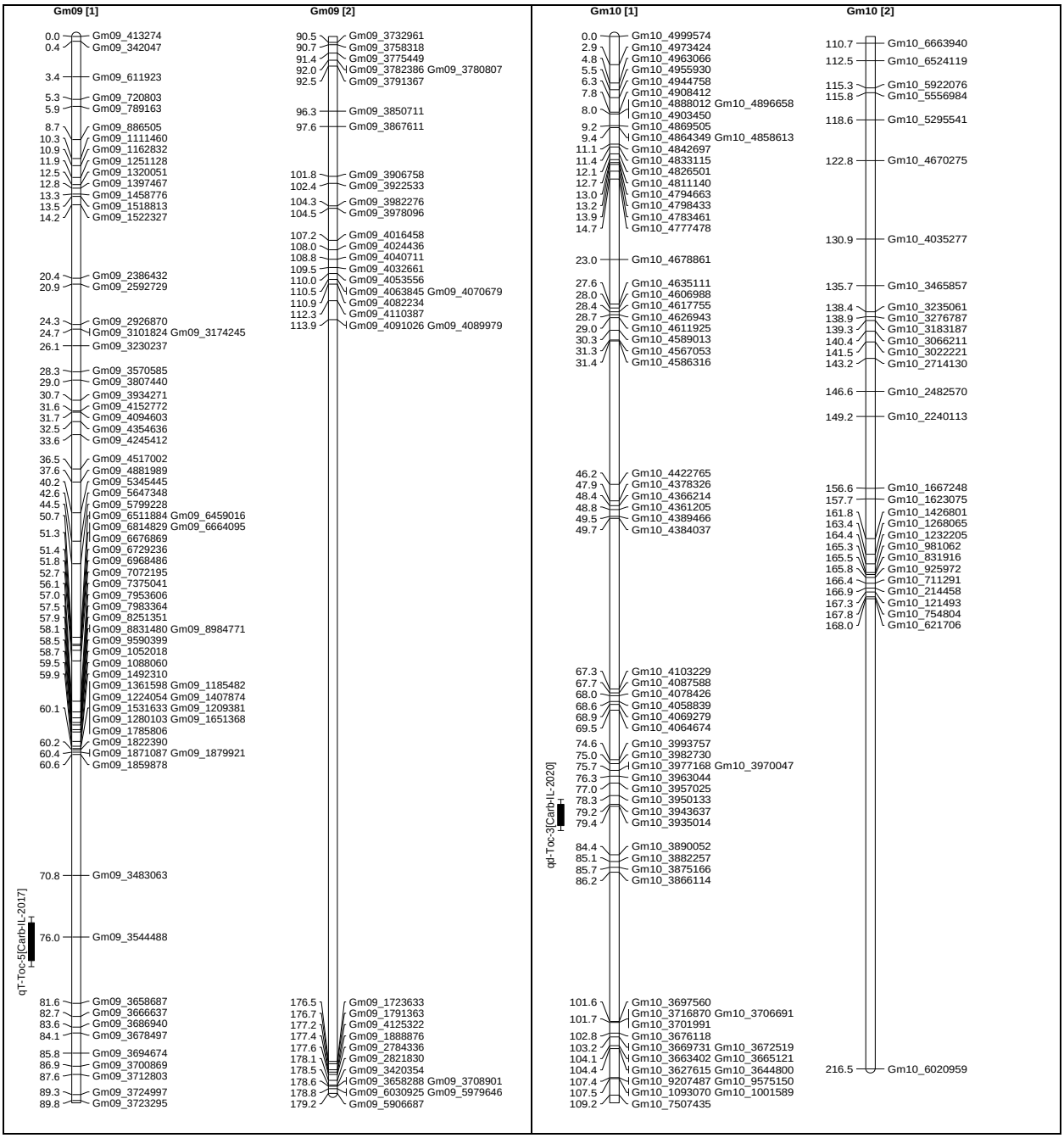
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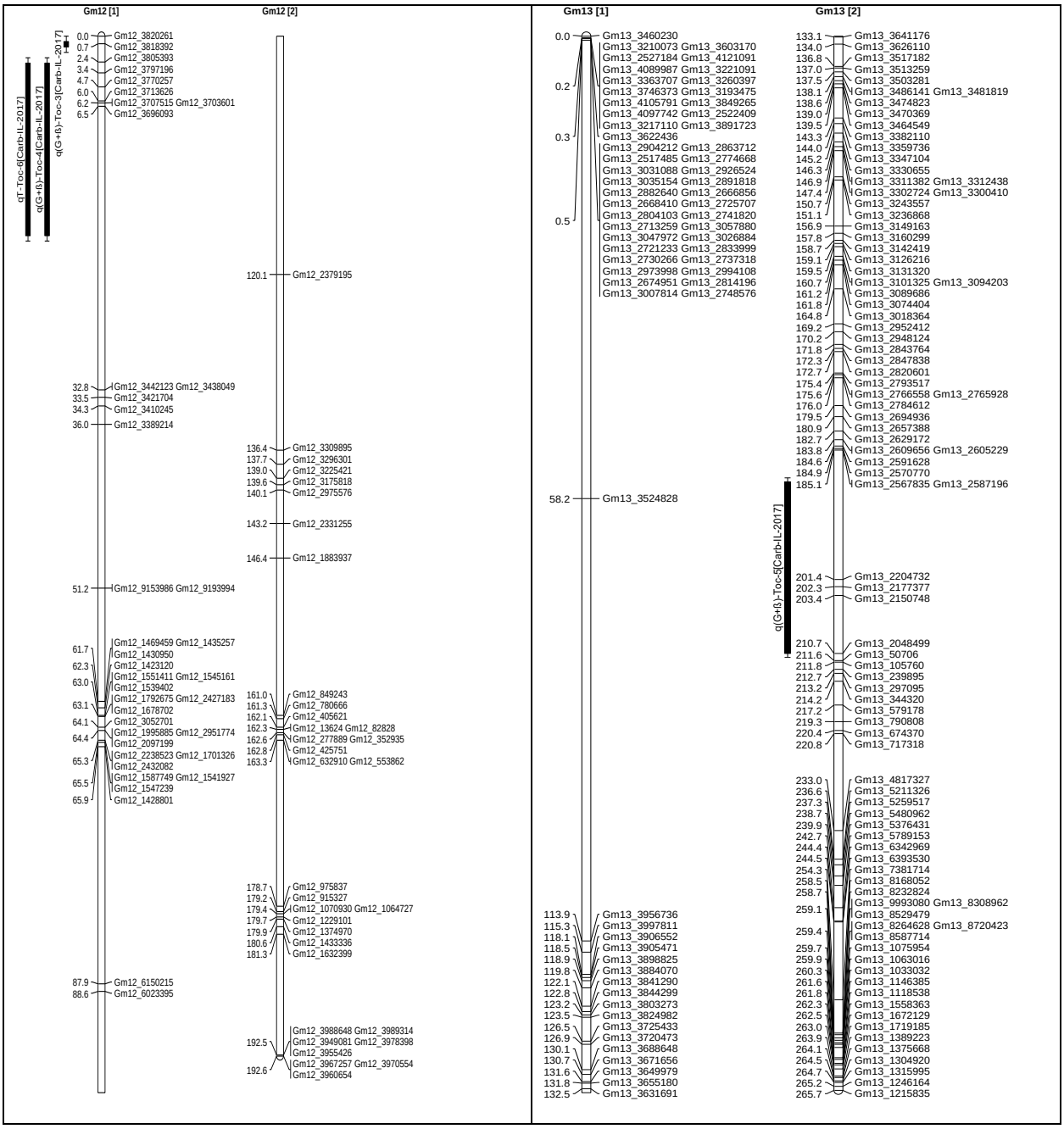
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q(G+f)-Toc-3[Carb-IL-2017]
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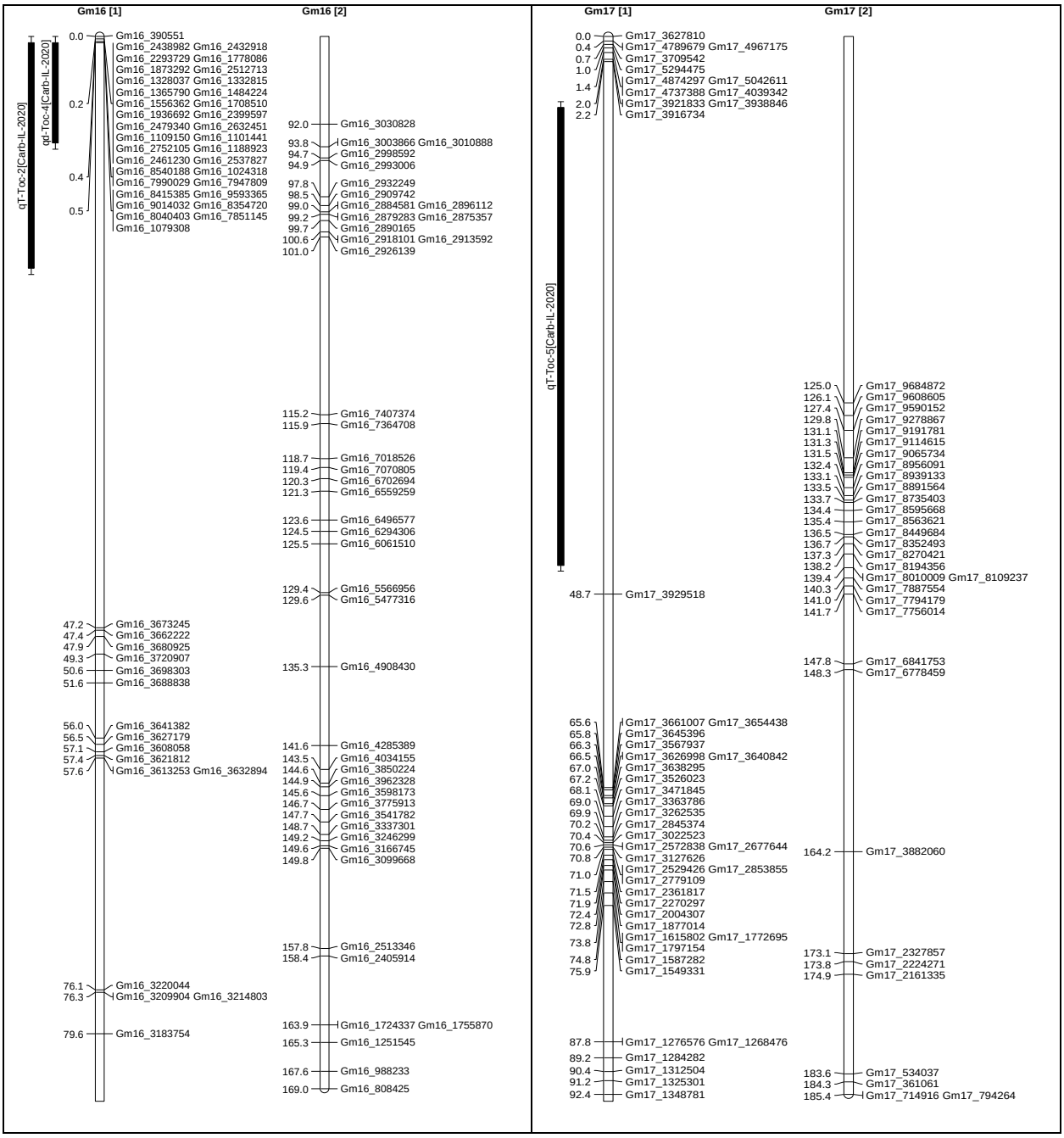
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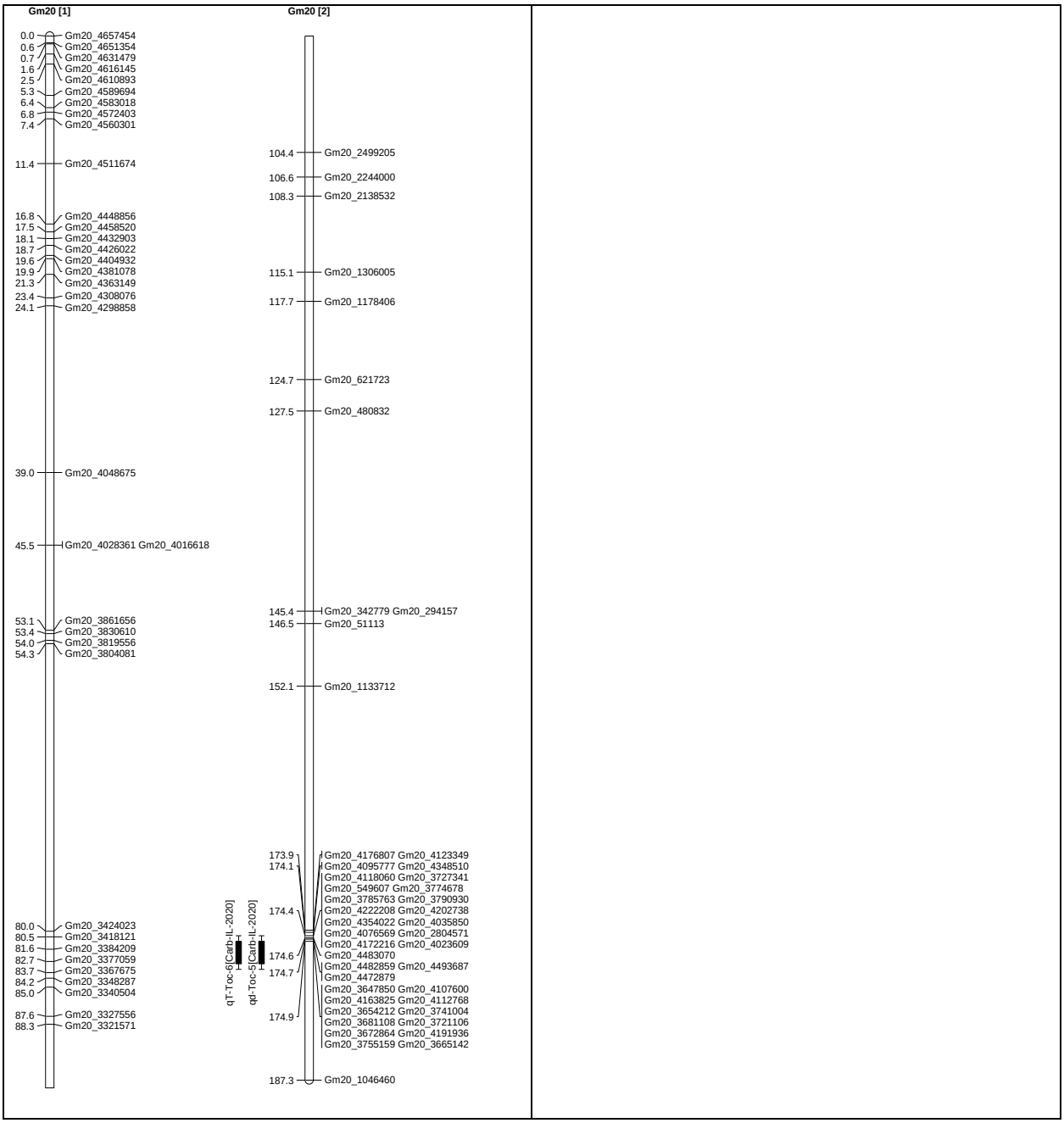
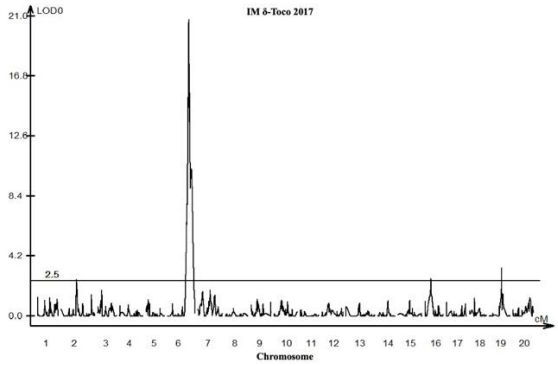


Figure S1. Positions of QTL that control seed α-Tocopherol (α-Toc), δ-Tocopherol (δ-Toc), (γ+β)-Tocopherol ((γ+β)-Toc), and Total-Tocopherols (T-Toc) contents on chromosomes 1, 2, 5, 6, 7, 8, 9, 10, 12, 13, 16, 17, and 20. The QTL have been identified in F×W82 grown in two environments in Carbondale, IL over two years (2017 and 2020). Legend: (γ+β)=(G+β) and (Carb-IL)=Carbondale, IL.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12.6
8.4
4.2
0.0
2.5
cM
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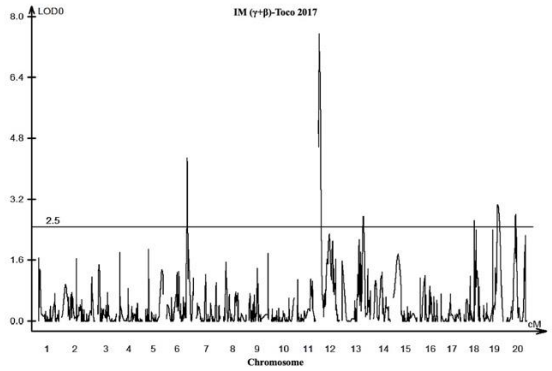
Chromosome


IM (γ+β)-Toco 2017
LOD0
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6.4
4.8
3.2
1.6
0.0
2.5
cM
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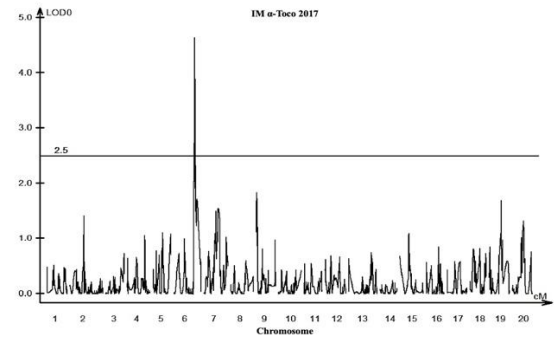
Chromosome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4.0
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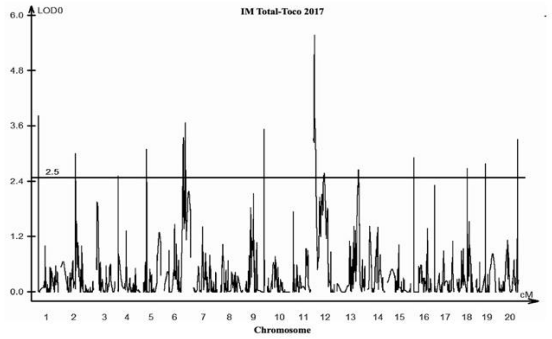
Chromosome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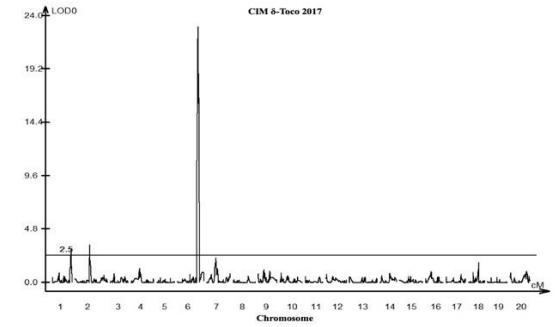
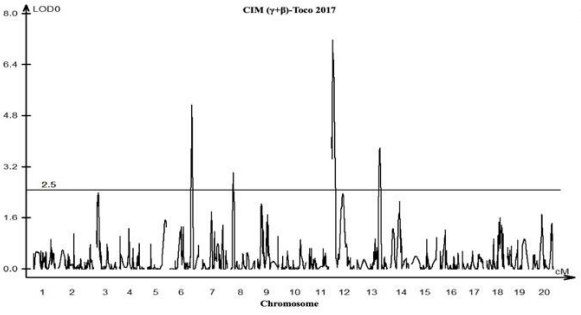
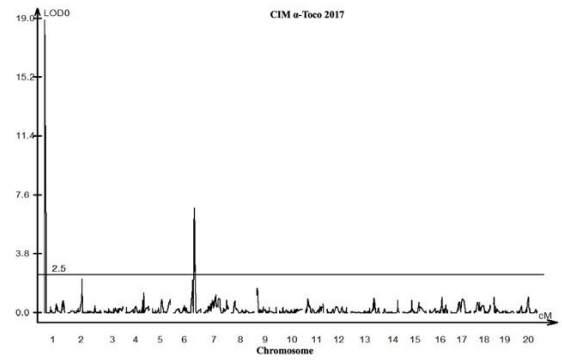
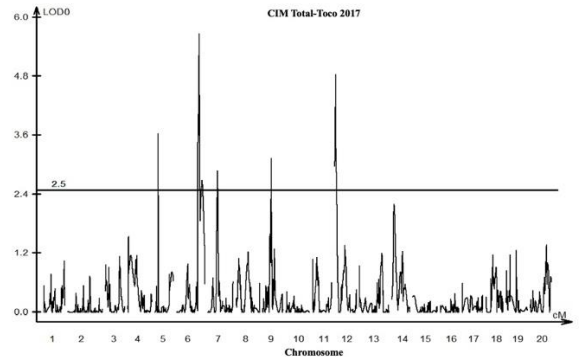
2.4
1.2
0.0
2.5
cM
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
Chromosome


CIM δ-Toco 2017
LOD0
24.0
19.2
14.4
9.6
4.8
0.0
2.5
cM
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
Chromosome


CIM (γ+β)-Toco 2017
LOD0
8.0
6.4
4.8
3.2
1.6
0.0
2.5
cM
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
Chromosome


CIM α-Toco 2017
LOD0
19.0
15.2
11.4
7.6
3.8
0.0
2.5
cM
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
Chromosome


CIM Total-Toco 2017
LOD0
6.0
4.8
3.6
2.4
1.2
0.0
2.5
cM
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
Chromosome

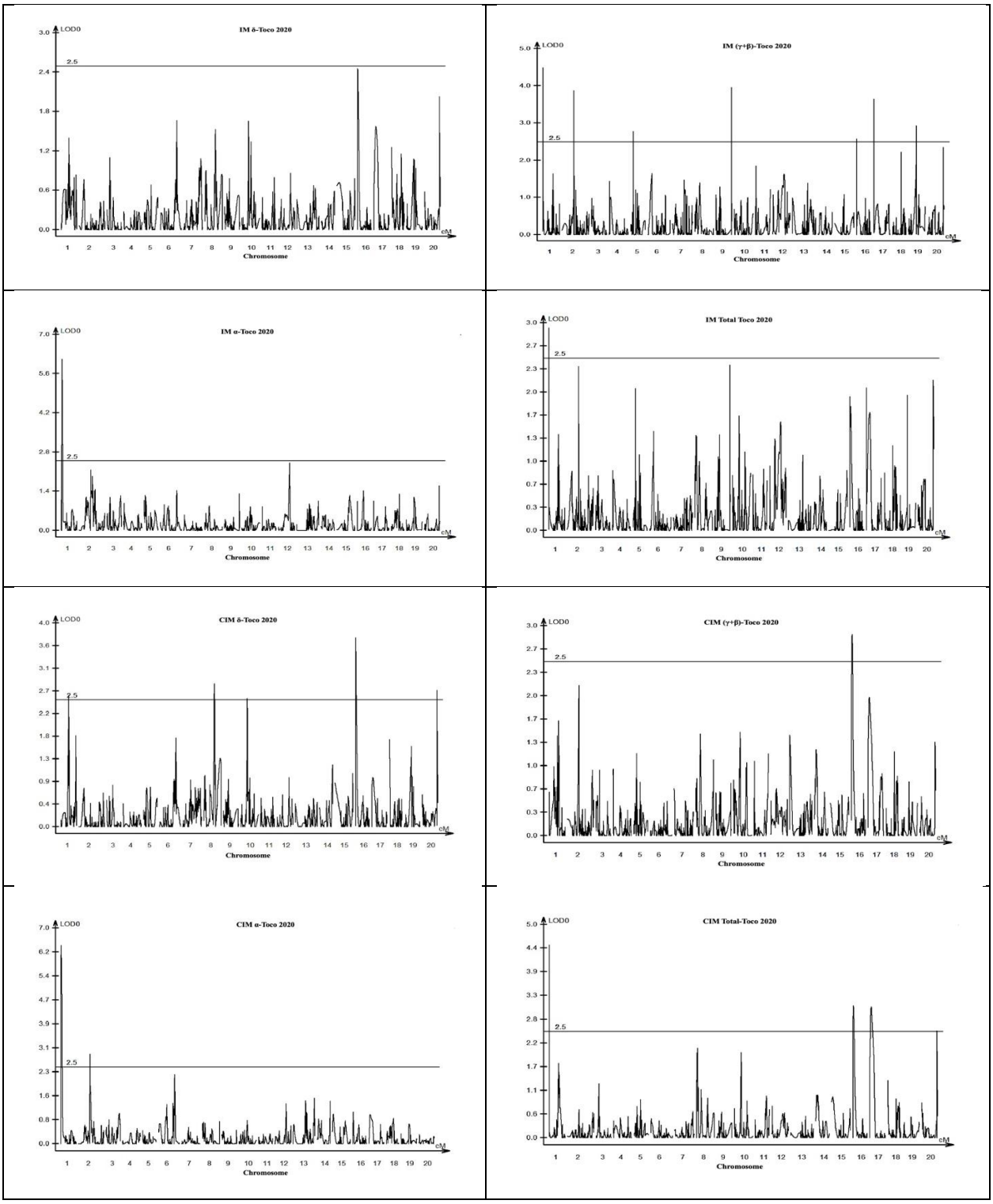


Figure S2. QTL that control seed *α*-Tocopherol (*α*-Toc), *δ*-Tocopherol (*δ*-Toc), (γ+β)-Tocopherol ((γ+β)-Toc), and Total-Tocopherols (T-Toc) contents identified by IM and CIM methods in the F×W82 RIL population grown in two environments in Carbondale, IL over two years (2017 and 2020).