

Table S1. *MADS-box* gene identified in the hop genome.

Gene ID	Gene name	Contig Location	CDS (bp)	Exon No.	Strand	Protein size (residues)	MW (Da)	pI	Subfamily
g126639.t1	HIMADS01	005050F:261365:267689	648	7	-	215	24191.15	8.66	AGL12
g4287.t1	HIMADS02	000025F:2663950:2669377	747	9	-	248	28673.47	8.96	E(SEP)
000727F.g16.t1	HIMADS03	000727F:300503:306308	732	8	+	243	28010.83	8.78	E(SEP)
000079F.g81.t1	HIMADS04	000079F:2009261:2019723	780	8	+	259	29495.61	7.57	E(SEP)
001022F.g25.t2	HIMADS05	001022F:835353:848110	897	9	-	298	34337.21	7.57	E(SEP)
006765F.g2.t1	HIMADS06	006765F:49016:57362	567	7	+	188	22130.51	9.68	E(SEP)
000139F.g16.t1	HIMADS07	000139F:691180:701232	843	8	-	262	30480.39	8.73	AGL6
000261F.g24.t1	HIMADS08	000261F:1206883:1217085	729	8	+	242	28455.11	8.87	AGL6
000155F.g57.t2	HIMADS09	000155F:1174916:1179017	828	9	-	156	17770.36	9.45	TM8
004947F.g24.t1	HIMADS10	004947F:296392:297739	477	4	+	129	14846.84	9.37	TM8
006412F.g5.t1	HIMADS11	006412F:101506:107824	774	8	+	257	29984.02	8.2	A(AP1-FUL)
005516F.g3.t1	HIMADS12	005516F:100575:106871	771	8	-	256	29778.06	8.97	A(AP1-FUL)
000562F.g29.t1	HIMADS13	000562F:405065:407961	930	7	-	295	33152.62	6.55	B(AP3-PI)
000267F.g44.t1	HIMADS14	000267F:1322662:1327001	1026	11	+	341	38315.62	6.26	MIKC*
000006F.g39.t2	HIMADS15	000006F:1630741:1633244	654	5	+	225	25689.19	7.07	BS(TT16)
008535F.g2.t2	HIMADS16	008535F:35736:40789	628	9	+	208	23976.43	6.55	SVP
003895F.g10.t1	HIMADS17	003895F:119273:124319	588	7	-	195	22415.69	6.86	SVP
004012F.g22.t2	HIMADS18	004012F:362046:365098	519	8	+	152	17407.84	9.3	TM8
002163F.g38.t1	HIMADS19	002163F:484371:488562	765	9	-	254	28867.72	8.23	AGL15
g128133.t1	HIMADS20	005238F:252962:256110	597	8	-	254	28872.72	8.24	AGL15
004180F.g12.t1	HIMADS21	004180F:187393:188704	1140	1	+	379	42912.16	6.83	Beta
000351F.g15.t1	HIMADS22	000351F:597580:601145	1062	13	+	353	40110.17	6.61	MIKC*
000962F.g16.t1	HIMADS23	000962F:609956:612029	603	3	+	200	22140.06	5.75	Alpha
000586F.g19.t1	HIMADS24	000586F:511047:518658	1008	8	+	335	38534.19	8.84	B(AP3-PI)
000238F.g55.t1	HIMADS25	000238F:849739:851157	621	2	+	206	23333.47	6.08	Alpha
001957F.g8.t1	HIMADS26	001957F:323596:325350	1338	2	+	445	48673.45	9.02	Gamma
000887F.g29.t1	HIMADS27	000887F:890609:891924	915	2	+	304	35110.43	5.25	Beta
g39417.t1	HIMADS28	000628F:1010162:1017835	597	7	-	198	22484.65	8.94	AGL6
g90065.t1	HIMADS29	002424F:490038:494465	435	3	-	144	17011.7	9.6	C/D(AG)
g21585.t1	HIMADS30	000253F:1451643:1455810	597	4	-	198	23006.82	9.7	C/D(AG)
g98509.t1	HIMADS31	002879F:359907:364430	531	6	-	176	20176.59	8.77	AGL12
g57516.t1	HIMADS32	001131F:491536:499904	705	6	-	234	26967.13	9.91	C/D(AG)
g120931.t1	HIMADS33	004517F:301077:304561	393	2	+	130	15020.97	10.25	AGL6
g105746.t1	HIMADS34	003321F:169727:172210	630	2	-	209	22689.95	8.91	Alpha
g126627.t1	HIMADS35	005050F:116796:119190	594	1	+	197	21541.38	7.71	Alpha
g145841.t1	HIMADS36	008392F:89967:90690	585	1	-	194	22721.07	8.63	Alpha
g115481.t1	HIMADS37	004059F:231977:232700	585	1	-	194	22663.03	8.84	Alpha
g98489.t1	HIMADS38	002879F:155406:157810	627	1	+	208	22639.82	9.18	Alpha
g70848.t1	HIMADS39	001574F:102007:103540	990	3	-	329	36408.27	9.79	Alpha
g148256.t1	HIMADS40	009280F:58747:62590	867	4	-	288	31504.4	9.49	Alpha
g63684.t1	HIMADS41	001329F:293116:295050	573	2	+	190	20693.75	9.61	Alpha
g116966.t1	HIMADS42	004180F:181006:182210	960	2	+	319	35943.8	8.58	Beta
g115485.t1	HIMADS43	004059F:341647:343290	1297	2	-	431	46701.58	9.36	Alpha
g115484.t1	HIMADS44	004059F::322287:324440	1644	2	-	547	60026.5	9.46	Alpha

g143617.t1	HIMADS45	007779F:47307:48170	459	2	-	152	17620.07	9.69	Alpha
g93707.t1	HIMADS46	002616F:159796:160380	546	1	+	181	20710.51	9.26	Alpha
g80284.t1	HIMADS47	001966F:73257:73870	501	1	-	166	18423.71	5.68	Alpha
g76680.t1	HIMADS48	001803F:4107:5760	1266	3	-	421	45520.49	9.34	Alpha
g149874.t1	HIMADS49	010116F:52407:53990	597	2	-	198	22248.4	8.78	Alpha
g93699.t1	HIMADS50	002616F:17167:18630	672	1	-	223	25007.1	5.87	Alpha
g149872.t1	HIMADS51	010116F:46656:47370	498	2	+	165	18540.17	5.11	Alpha
g17586.t1	HIMADS52	000193F:209997:216980	474	2	-	157	18031.71	6.52	Alpha
g140155.t1	HIMADS53	007017F:101746:102480	546	1	+	181	20852.1	6.32	Alpha
g69465.t1	HIMADS54	001521F:226037:229000	555	2	-	184	20509.14	5.82	Alpha
g132514.t1	HIMADS55	005766F:205237:206360	723	2	-	240	27195.68	8.72	Beta
g123814.t1	HIMADS56	004793F:82436:83690	987	2	+	328	36872.64	8.84	Beta
g37290.t1	HIMADS57	000578F:1005602:1008466	1256	2	+	395	44459.12	9.34	Beta
g93696.t1	HIMADS58	002616F:866:4050	708	3	+	235	26027.62	9.24	Alpha
g20630.t1	HIMADS59	000238F:870733:872867	759	2	+	252	28642.71	5.71	Alpha
g71695.t1	HIMADS60	001607F:395446:397250	591	2	+	196	22028.87	5.2	Alpha
g34447.t1	HIMADS61	000516F:40106:55690	1148	5	+	359	40443.46	8.84	Alpha
g15081.t1	HIMADS62	000156F:497105:498528	1100	3	-	343	39980.1	4.56	Beta
g110780.t1	HIMADS63	003683F:338687:340750	664	1	-	220	25301.54	4.76	Beta
g32470.t1	HIMADS64	000472F:1676:3320	1247	2	+	392	45421.25	4.55	Beta
000453F.g47.t2	HIMADS65	000453F:1097840:1106375	408	2	-	135	15911.6	9.69	SOC

Table S2. RNA-seq libraries used to hints AUGUSTUS

RNA-seq library	Tissues
SRR10589377	Leaf, bract and lupulin glands
SRR10549511	Leaf, bract and lupulin glands
SRR10541757	Leaf, bract and lupulin glands
SRR10320795	Non-floral Cascade RNA-seq (stem)
SRR10320793	Meristem-Cascade
SRR10320791	Leaf-Cascade
SRR4242068	Roots, sprouts, leaves, stems, flowers, cones
ERR2040411	Young leaves

Table S3. Gene Ontology terms of hop MADS-box genes

Genes	GO terms
HIMADS02	GO:0000977 GO:0000981 GO:0005634 GO:0008134 GO:0045944 GO:0046983
HIMADS03	GO:0000977 GO:0000981 GO:0005634 GO:0008134 GO:0045944 GO:0046983
HIMADS04	GO:0000977 GO:0003700 GO:0005634 GO:0045944 GO:0046983
HIMADS05	GO:0000977 GO:0003700 GO:0005634 GO:0045944 GO:0046983
HIMADS06	GO:0000977 GO:0000981 GO:0005634 GO:0008134 GO:0045944 GO:0046983
HIMADS07	GO:0000977 GO:0000981 GO:0005634 GO:0008134 GO:0045944 GO:0046983
HIMADS08	GO:0000977 GO:0000981 GO:0005634 GO:0008134 GO:0045944 GO:0046983
HIMADS28	GO:0000977 GO:0045944 GO:0046983
HIMADS33	GO:0000977 GO:0000981 GO:0005634 GO:0008134 GO:0010582 GO:0045944 GO:0046983
HIMADS01	GO:0000977 GO:0000981 GO:0005634 GO:0008134 GO:0010228 GO:0045944 GO:0046983 GO:0048364
HIMADS31	GO:0000977 GO:0000981 GO:0005634 GO:0008134 GO:0010228 GO:0045944 GO:0046983 GO:0048364
HIMADS11	GO:0000977 GO:0000981 GO:0005634 GO:0008134 GO:0010582 GO:0045944 GO:0046983
HIMADS12	GO:0000977 GO:0000981 GO:0005634 GO:0008134 GO:0010582 GO:0045944 GO:0046983
HIMADS13	GO:0000977 GO:0003700 GO:0005634 GO:0045944 GO:0046983
HIMADS24	GO:0000977 GO:0003700 GO:0005634 GO:0045944 GO:0046983
HIMADS29	GO:0000977 GO:0000981 GO:0005634 GO:0008134 GO:0016020 GO:0045944 GO:0046983 GO:0048481 GO:0090376
HIMADS30	GO:0000977 GO:0003700 GO:0005634 GO:0045944 GO:0046983 GO:0090376

HIMADS32	GO:0000977 GO:0000981 GO:0005634 GO:0008134 GO:0045944 GO:0046983 GO:0090376
HIMADS19	GO:0000977 GO:0003700 GO:0005634 GO:0045944 GO:0046983
HIMADS20	GO:0000977 GO:0003700 GO:0005634 GO:0045944 GO:0046983
HIMADS09	GO:0000977 GO:0003700 GO:0005634 GO:0045944 GO:0046983
HIMADS10	GO:0000977 GO:0003700 GO:0005634 GO:0045944 GO:0046983
HIMADS18	GO:0000977 GO:0003700 GO:0005634 GO:0045944 GO:0046983
HIMADS15	GO:0000977 GO:0003700 GO:0005634 GO:0008360 GO:0045595 GO:0045944 GO:0046983 GO:0048316 GO:0051302 GO:0080060 GO:0080155 GO:2000029
HIMADS16	GO:0000977 GO:0003700 GO:0005634 GO:0045944 GO:0046983
HIMADS17	GO:0000977 GO:0003700 GO:0005634 GO:0045944 GO:0046983
HIMADS65	GO:0000977 GO:0000981 GO:0005634 GO:0008134 GO:0010048 GO:0032501 GO:0045944 GO:0046983 GO:0048510
HIMADS14	GO:0003677 GO:0046983
HIMADS22	GO:0000981 GO:0000987 GO:0045944 GO:0046983
HIMADS23	GO:0000977 GO:0000981 GO:0005634 GO:0008134 GO:0045944 GO:0046983 GO:0048481
HIMADS25	GO:0000977 GO:0000981 GO:0005634 GO:0006357 GO:0008134 GO:0046983
HIMADS34	GO:0000977 GO:0000981 GO:0005634 GO:0008134 GO:0045944 GO:0046983
HIMADS35	GO:0000977 GO:0000981 GO:0005634 GO:0008134 GO:0045944 GO:0046983
HIMADS36	GO:0000977 GO:0045944 GO:0046983
HIMADS37	GO:0000977 GO:0045944 GO:0046983
HIMADS38	GO:0000977 GO:0000981 GO:0005634 GO:0008134 GO:0046983
HIMADS39	GO:0000977 GO:0000981 GO:0005634 GO:0008134 GO:0045944 GO:0046983
HIMADS40	GO:0000977 GO:0000981 GO:0005634 GO:0008134 GO:0045944 GO:0046983
HIMADS41	GO:0000977 GO:0000981 GO:0005634 GO:0008134 GO:0045944 GO:0046983
HIMADS43	GO:0000977 GO:0000981 GO:0005634 GO:0006357 GO:0008134 GO:0046983
HIMADS44	GO:0000977 GO:0000981 GO:0005634 GO:0008134 GO:0045944 GO:0046983
HIMADS45	GO:0000977 GO:0000981 GO:0005634 GO:0008134 GO:0045944 GO:0046983
HIMADS46	GO:0000977 GO:0000981 GO:0005634 GO:0008134 GO:0045944 GO:0046983
HIMADS47	GO:0000977 GO:0000981 GO:0005634 GO:0008134 GO:0045944 GO:0046983
HIMADS48	GO:0000977 GO:0000981 GO:0005634 GO:0006357 GO:0008134 GO:0046983
HIMADS49	GO:0000977 GO:0000981 GO:0005634 GO:0008134 GO:0045944 GO:0046983
HIMADS50	GO:0000976 GO:0046983
HIMADS51	GO:0000976 GO:0046983
HIMADS52	GO:0000976 GO:0046983
HIMADS53	GO:0000977 GO:0000981 GO:0005634 GO:0006357 GO:0008134 GO:0046983
HIMADS54	GO:0000977 GO:0000981 GO:0005634 GO:0006357 GO:0008134 GO:0046983
HIMADS58	GO:0000977 GO:0005634 GO:0045944 GO:0046983
HIMADS59	GO:0000976 GO:0046983
HIMADS60	GO:0000977 GO:0000981 GO:0005634 GO:0008134 GO:0046983
HIMADS61	GO:0000977 GO:0000981 GO:0005634 GO:0006357 GO:0008134 GO:0046983
HIMADS26	GO:0000977 GO:0000981 GO:0000987 GO:0005634 GO:0008134 GO:0045944 GO:0046983
HIMADS21	GO:0000981 GO:0000987 GO:0045944 GO:0046983
HIMADS27	GO:0003677 GO:0046983
HIMADS42	GO:0000977 GO:0000981 GO:0000987 GO:0005634 GO:0008134 GO:0008360 GO:0045595 GO:0045944 GO:0046983 GO:0048316 GO:0051302 GO:0080060 GO:0080155 GO:2000029
HIMADS55	GO:0003677 GO:0046983
HIMADS56	GO:0003677 GO:0046983
HIMADS57	GO:0003677 GO:0046983
HIMADS62	GO:0003677 GO:0046983
HIMADS63	GO:0003677 GO:0046983
HIMADS64	GO:0003677 GO:0046983

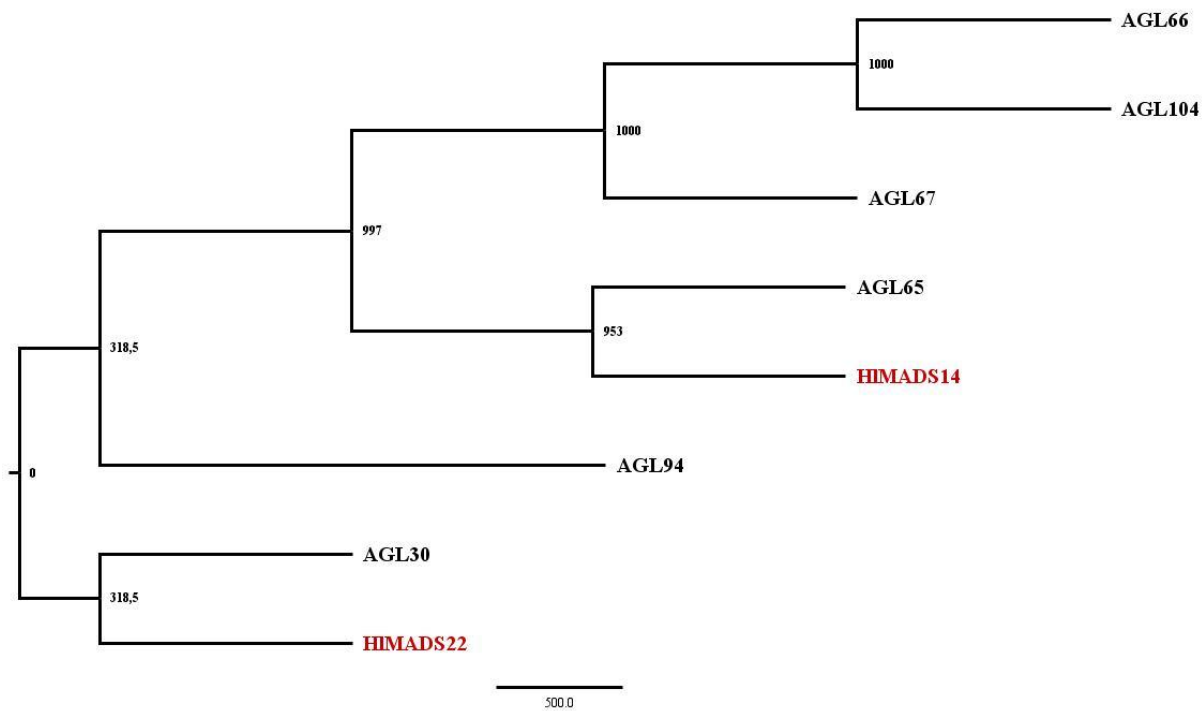


Figure S1. Phylogenetic tree of MIKC*-type MADS-box proteins of *H. lupulus* (2, red), *Arabidopsis* (6).

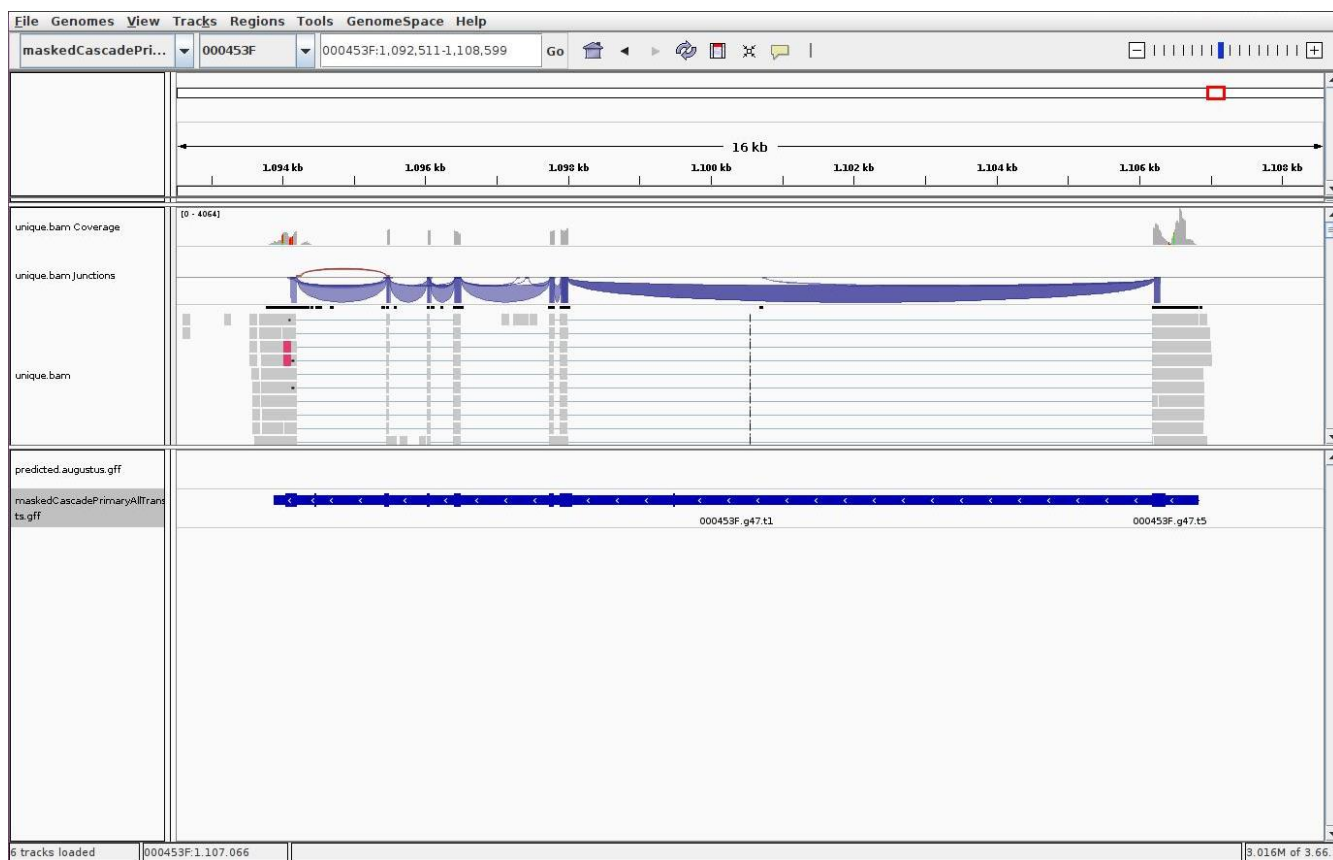


Figure S2. RNAseq reads on the gene 000453F.g47.

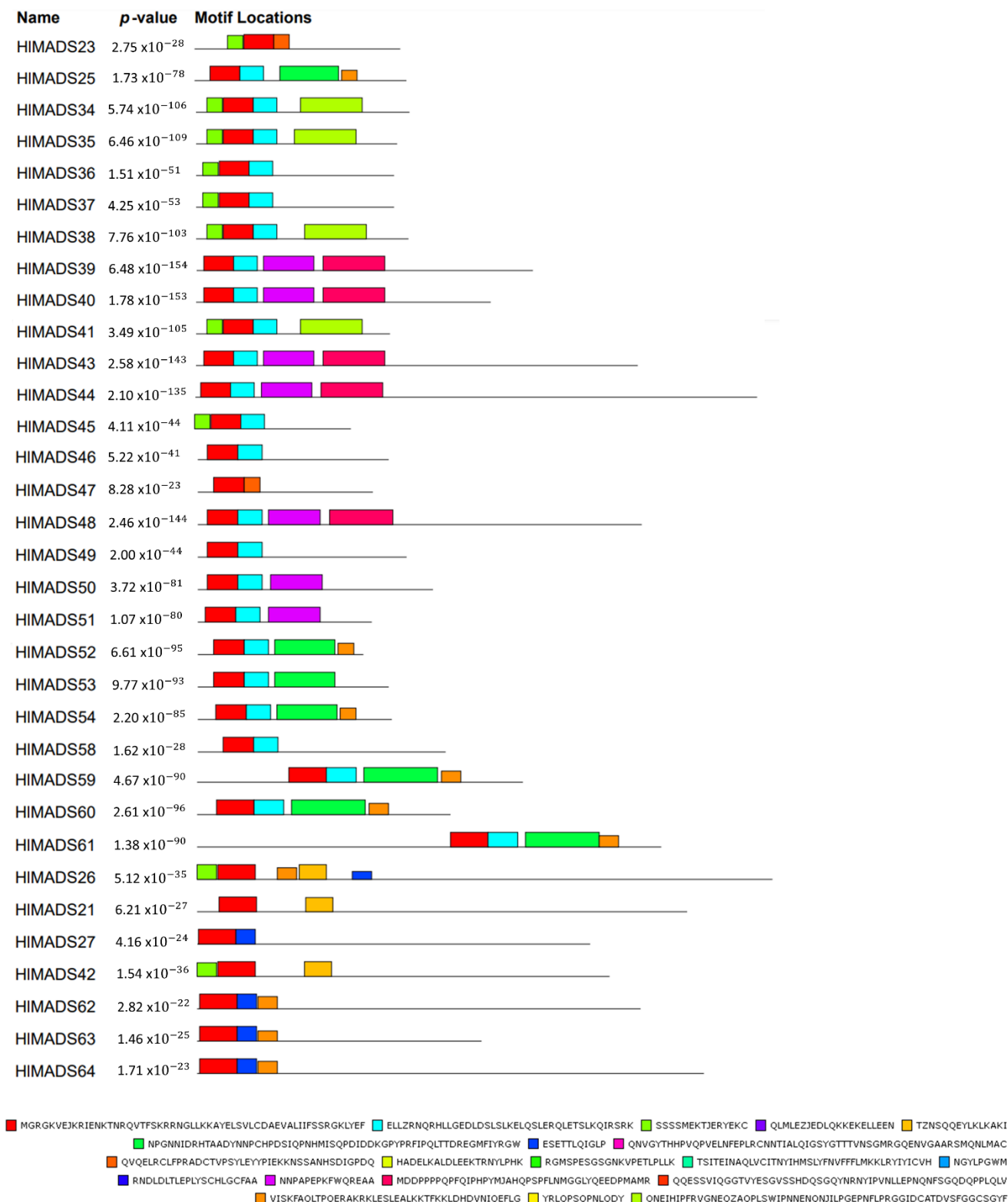


Figure S3. Motifs distribution of the hop MADS-box proteins. Protein sequences are represented by black lines, and the conserved motifs are represented by colored boxes. The motif consensus sequences are shown in the legend.

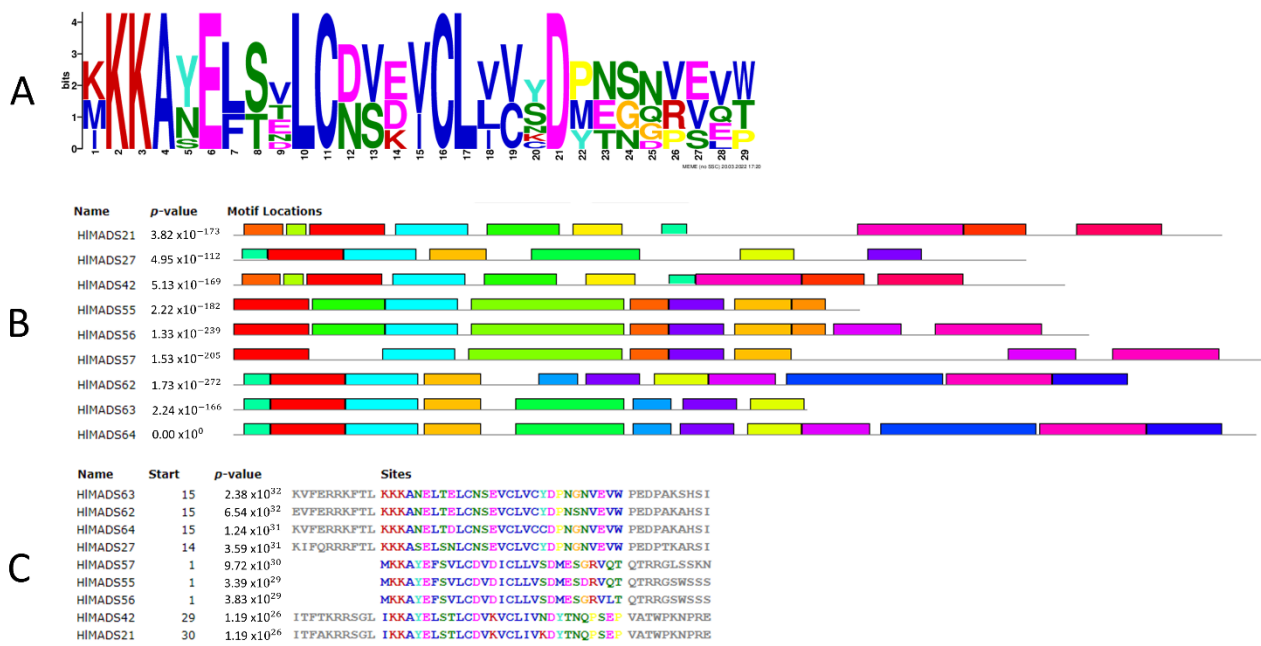


Figure S4. Motifs distribution of the hop MADS-box proteins of β -subfamily members. Protein sequences are represented by black lines, and the conserved motifs are represented by colored boxes. **A:** Logo of MADS-box domain. **B:** Motifs distribution of the hop MADS-box proteins of β -subfamily members. **C:** Amino acid residue sequences of selected MADS-box domains.

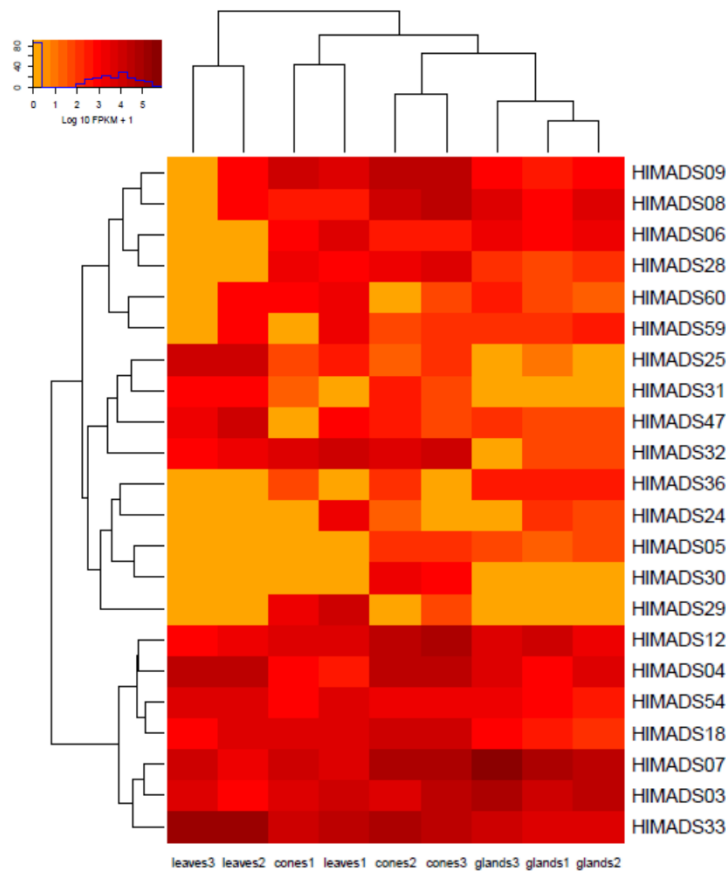


Figure S5. Expression profile of the hop MADS-box genes in three RNAseq libraries from cones, leaves, and glands.

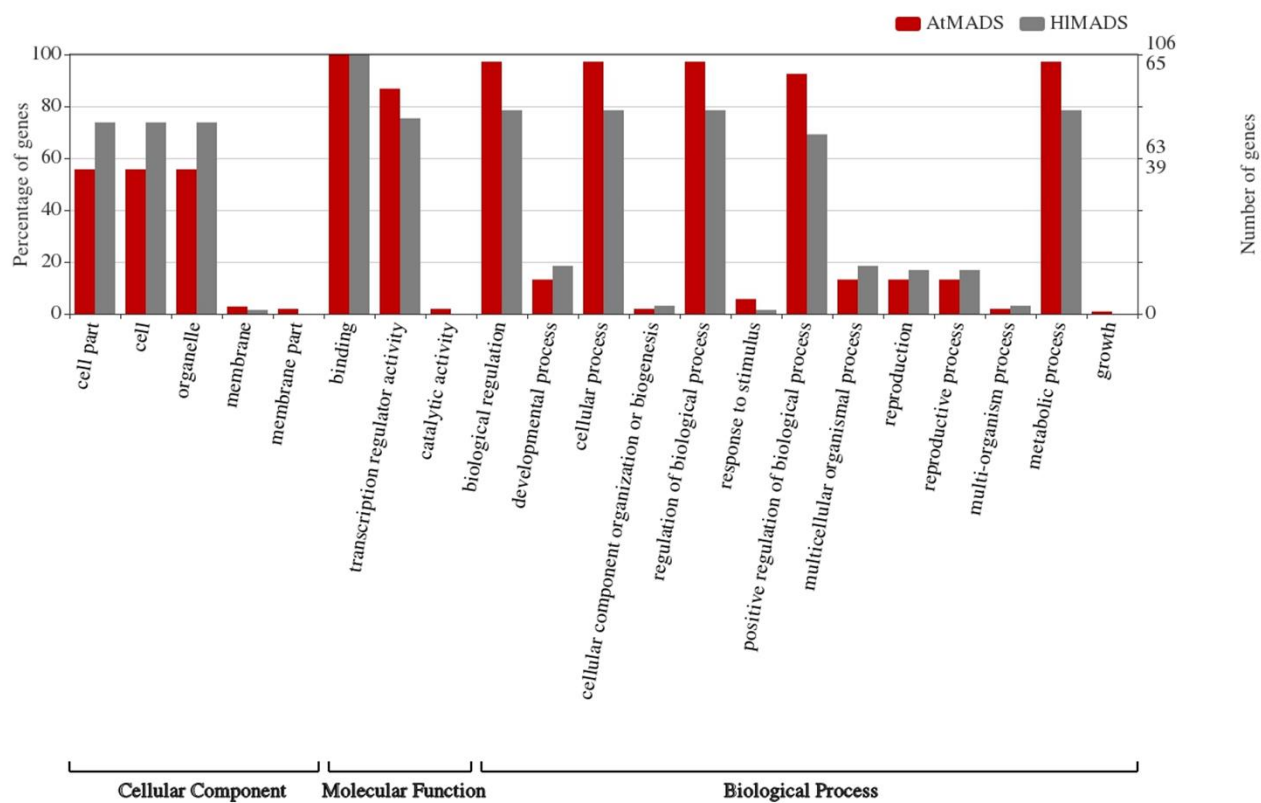


Figure S6. Gene Ontology classification of MADS-box genes in hop and *Arabidopsis*.

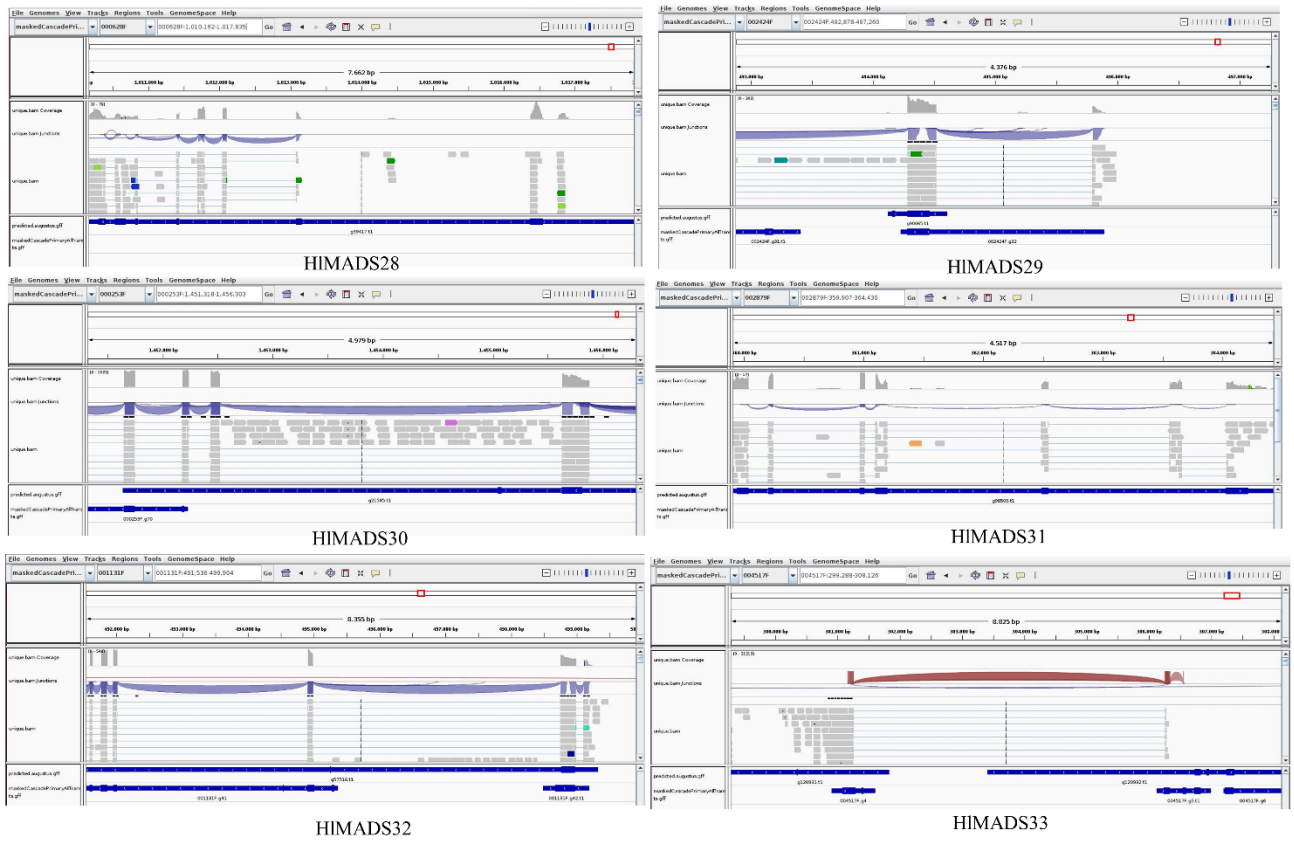


Figure S7. RNAseq reads that are uniquely mapped on 6 novel MADS-box genes (*HIMADS28-33*).