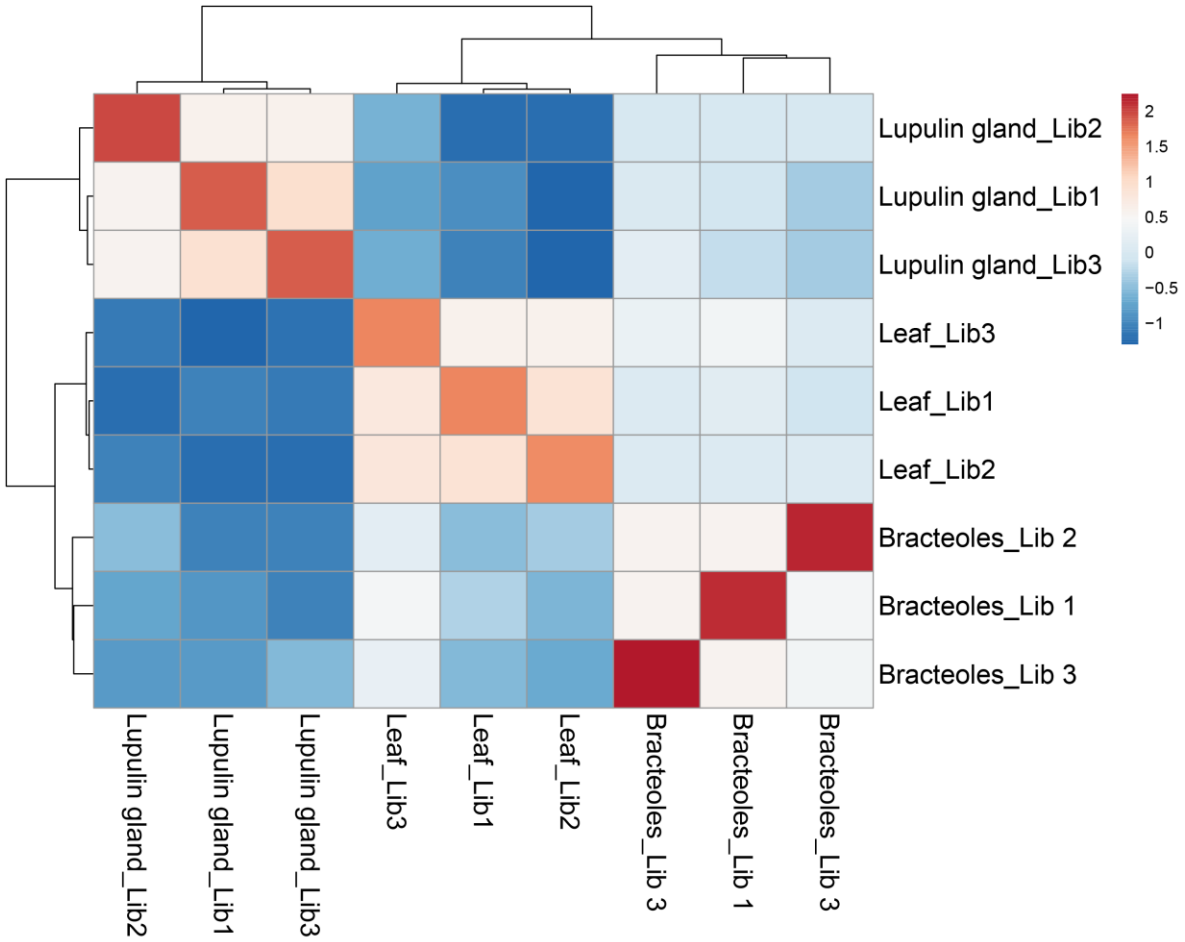


Figure S1: Correlation indices between different samples

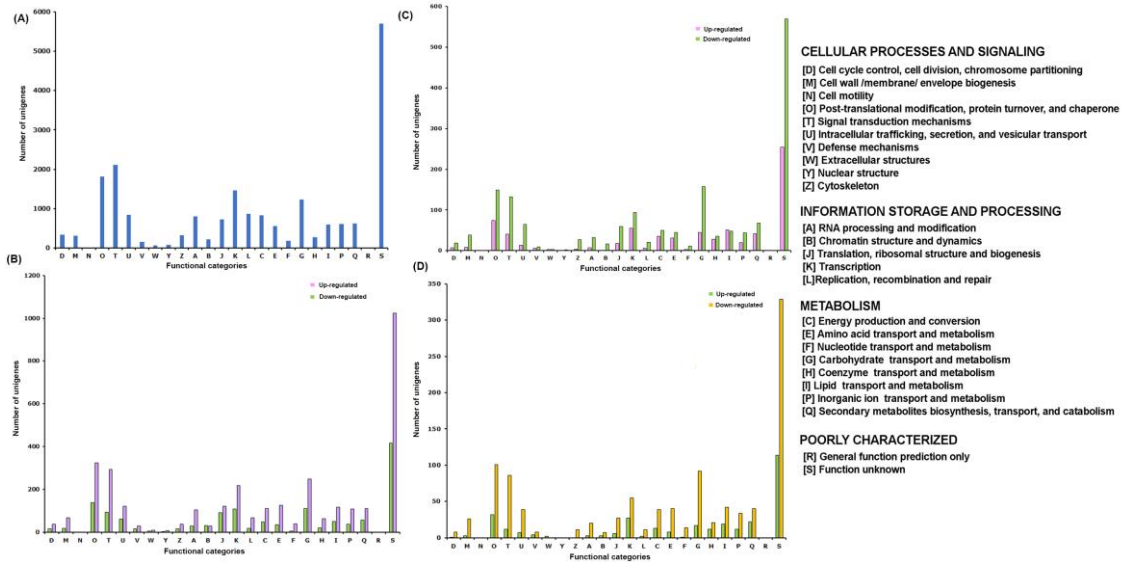


Figure S2. Histogram presentation of clusters of orthologous groups (COGs) classification of unigenes (A) and differentially expressed genes in bract vs leaf (B), lupulin glands vs bract (C) and lupulin glands vs leaf in hop.

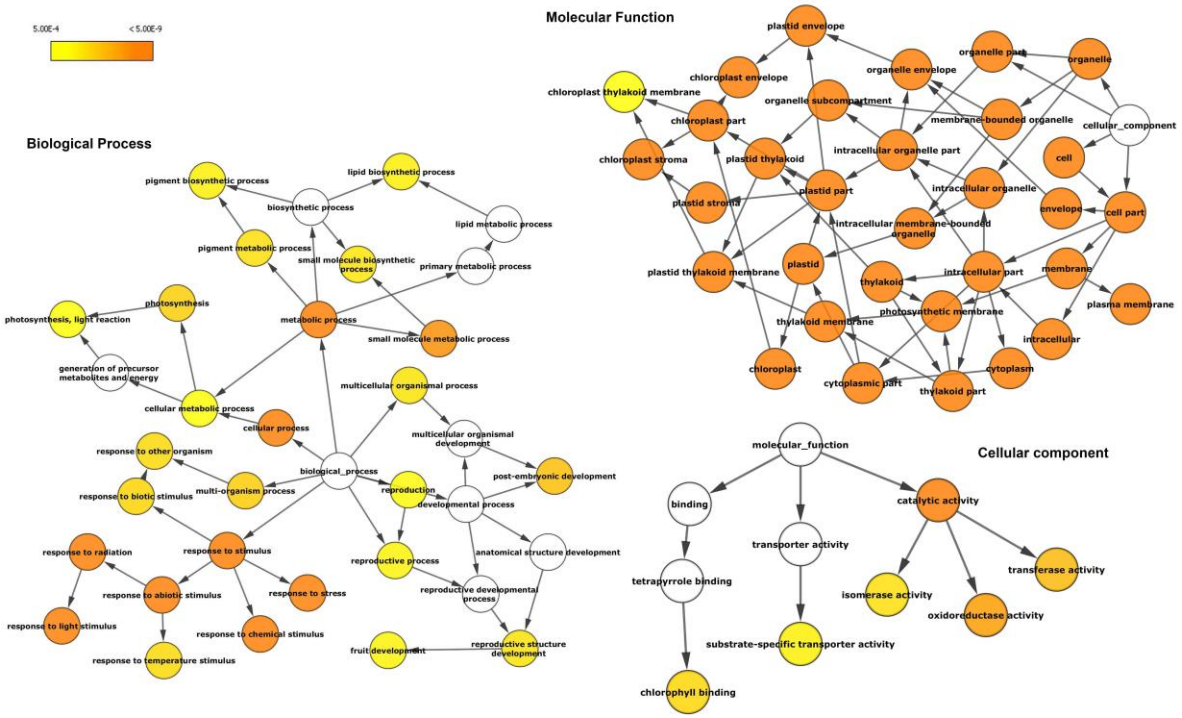


Figure S3. GO enrichment analysis of differentially expressed genes in bract compared to leaf at a significance level p = 0.05, using GO terms from GO Slim. GO term enrichment analysis was carried out by Cytoscape software with a Bingo plug-in. The color of the node represents the (corrected) p-value. White nodes are not significantly over-represented, the other ones are (hypergeometric test, Benjamini & Hochberg False Discovery Rate (FDR) correction), with a color scale ranging from yellow (low) to dark orange (high).

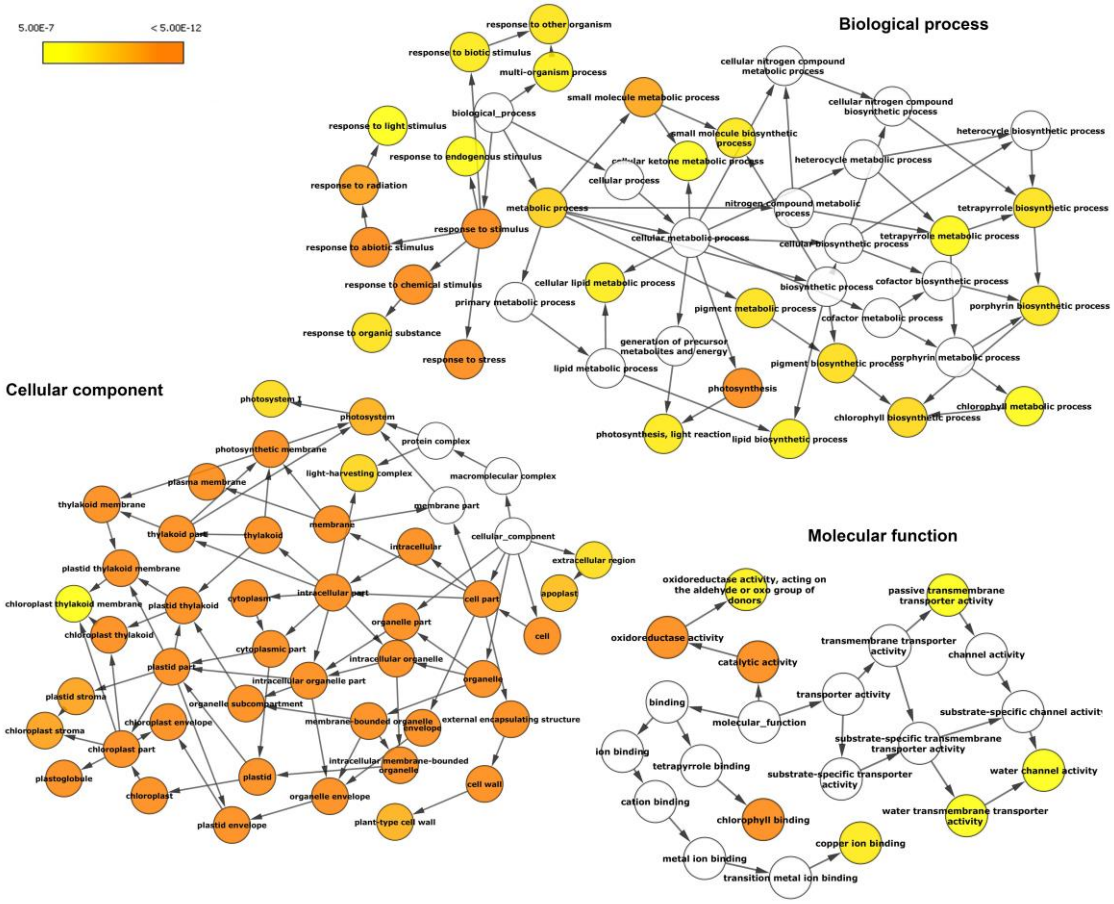


Figure S4. GO enrichment analysis of differentially expressed genes in lupulin glands compared to bract at a significance level p = 0.05, using GO terms from GO Slim. GO term enrichment analysis was carried out by Cytoscape software with a Bingo plug-in. The color of the node represents the (corrected) p-value. White nodes are not significantly over-represented, the other ones are (hypergeometric test, Benjamini & Hochberg False Discovery Rate (FDR) correction), with a color scale ranging from yellow (low) to dark orange (high).

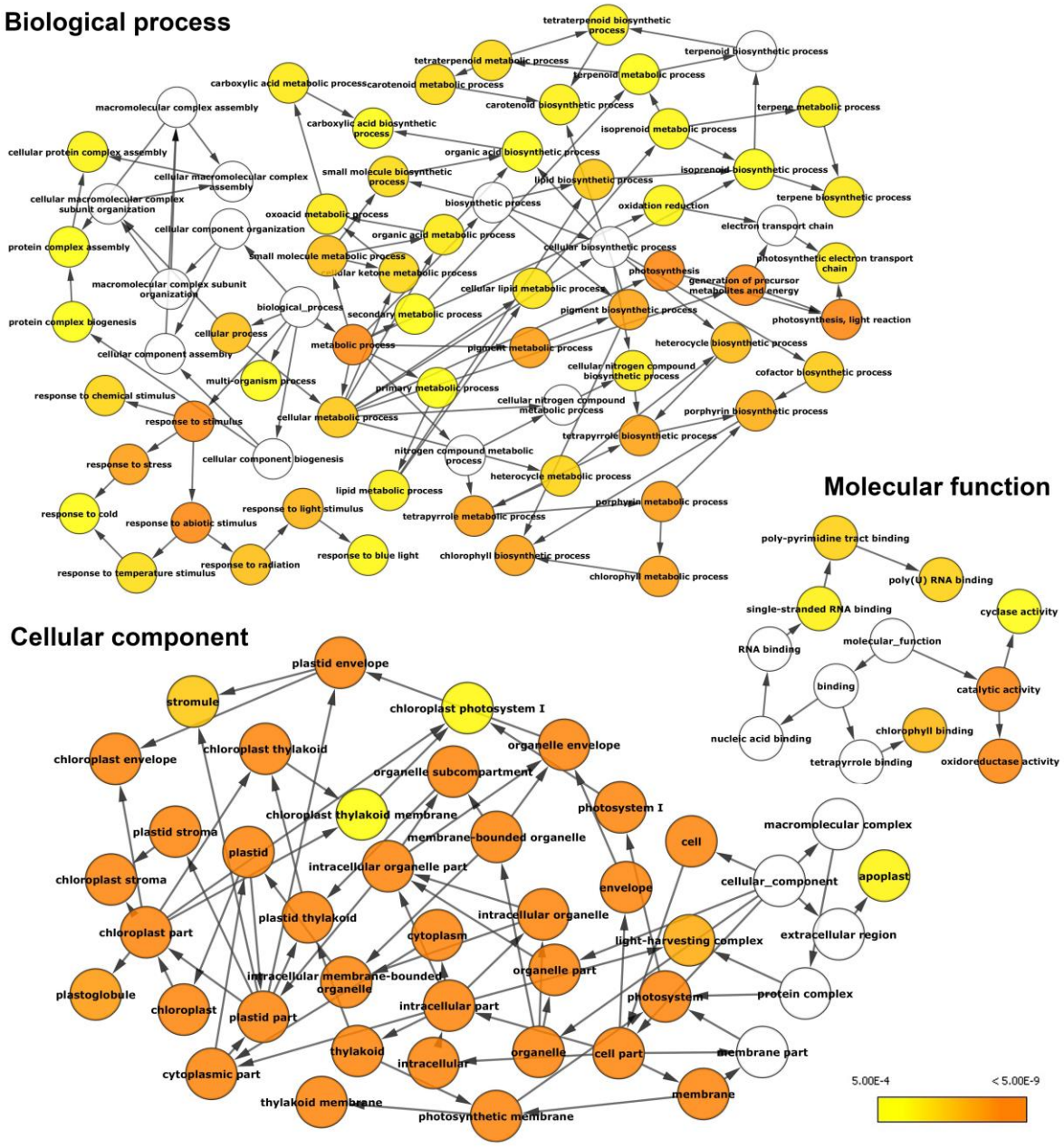


Figure S5. GO enrichment analysis of differentially expressed genes in lupulin glands compared to leaf at a significance level p = 0.05, using GO terms from GO Slim. GO term enrichment analysis was carried out by Cytoscape software with a Bingo plug-in. The color of the node represents the (corrected) p-value. White nodes are not significantly over-represented, the other ones are (hypergeometric test, Benjamini & Hochberg False Discovery Rate (FDR) correction), with a color scale ranging from yellow (low) to dark orange (high).

Table S4. Gene ontology (GO) functional enrichment analysis of differentially expressed genes in pairwise comparison of bracteoles vs leaf in hop.

GO ID	Ontology	Category	Number	Number of	FDR	p-value

			of DEGs	Unigenes in subgroup		
GO:0008152	metabolic process	P	510	8180	1.23E-14	6.23E-18
GO:0044238	primary metabolic process	P	1276	6595	4.80E-22	8.11E-25
GO:0005975	carbohydrate metabolic process	P	168	808	2.12E-03	5.10E-05
GO:0019538	protein metabolic process	P	606	3183	9.83E-08	8.80E-10
GO:0006631	fatty acid metabolic process	P	22	211	2.49E-02	4.71E-04
GO:0006629	lipid metabolic process	P	62	829	1.12E-02	1.86E-04
GO:0090304	nucleic acid metabolic process	P	43	1666	8.01E-03	1.21E-04
GO:0009698	phenylpropanoid metabolic process	P	20	141	1.75E-03	1.81E-05
GO:0019748	secondary metabolic process	P	32	371	3.38E-02	7.15E-04
GO:0009987	cellular process	P	590	10275	3.18E-11	4.30E-14
GO:0006464	protein modification process	P	349	1942	1.09E-02	3.49E-04
GO:0009058	biosynthetic process	P	212	2782	5.03E-11	7.65E-14
GO:0044550	secondary metabolite biosynthetic process	P	21	180	9.40E-03	1.46E-04
GO:0009699	phenylpropanoid biosynthetic process	P	20	116	1.61E-04	1.33E-06
GO:0009056	catabolic process	P	279	1485	4.80E-03	1.33E-04
GO:0015979	photosynthesis	P	51	189	5.97E-18	1.01E-21
GO:0019725	cellular homeostasis	P	59	303	4.56E-01	4.77E-02
GO:0009605	response to external stimulus	P	111	1387	2.44E-06	1.20E-08
GO:0009725	response to hormone	P	119	1599	2.89E-05	1.85E-07
GO:0006952	defense response	P	77	1145	3.15E-02	6.34E-04
GO:0051704	multi-organism process	P	103	1482	2.08E-03	2.18E-05
GO:0055114	oxidation-reduction process	P	99	942	5.14E-11	8.69E-14
GO:0003824	catalytic activity	F	557	8868	1.43E-17	4.63E-21
GO:0016740	transferase activity	F	656	3725	6.95E-04	4.51E-06
GO:0016836	hydrolyase activity	F	15	82	5.05E-03	1.48E-05
GO:0005488	binding	F	539	10024	7.32E-05	9.51E-08
GO:0016301	kinase activity	F	247	1390	2.79E-01	4.88E-03
GO:0016772	transferase activity	F	656	3725	6.95E-04	4.51E-06
GO:0005215	transporter activity	F	259	1418	8.64E-02	1.07E-03
GO:0008135	translation factor activity	F	32	142	7.56E-01	3.04E-02
GO:0005198	structural molecule activity	F	124	502	1.33E-04	6.04E-07
GO:0016853	isomerase activity	F	28	256	1.12E-02	4.01E-05
GO:0016491	oxidoreductase activity	F	63	353	1.00E00	1.60E-01
GO:0016020	membrane	C	471	7769	2.36E-12	5.44E-14
GO:0005737	cytoplasm	C	818	14521	1.25E-20	2.19E-22
GO:0005623	cell	C	1087	22697	1.06E-07	2.83E-09
GO:0043226	organelle	C	935	19561	1.29E-03	5.59E-05
GO:0009536	plastid	C	450	5292	1.08E-41	4.97E-44
GO:0005618	cell wall	C	54	756	2.53E-02	1.38E-03
GO:0005829	cytosol	C	140	2290	4.91E-03	2.31E-04
GO:0005886	plasma membrane	C	38	262	8.59E-08	2.22E-09

Table S5. Gene ontology (GO) functional enrichment analysis of differentially expressed genes in pairwise comparison lupulin glands vs bracteoles in hop.

GO ID	Ontology	Category	Number of DEGs	Number of Unigenes in subgroup	FDR	p-value
GO:0008152	metabolic process	P	848	8180	4.12E-20	2.09E-23
GO:0044238	primary metabolic process	P	196	2714	1.00E+00	4.47E-01
GO:0005975	carbohydrate metabolic process	P	98	808	1.82E-03	3.14E-05
GO:0019538	protein metabolic process	P	273	3183	5.40E-01	5.24E-02
GO:0006631	fatty acid metabolic process	P	37	211	1.12E-03	1.65E-05
GO:0006629	lipid metabolic process	P	110	829	2.66E-05	1.94E-07
GO:0090304	nucleic acid metabolic process	P	91	1666	2.82E-02	9.33E-04
GO:0009698	phenylpropanoid metabolic process	P	30	141	3.08E-04	3.59E-06
GO:0019748	secondary metabolic process	P	53	371	2.75E-03	5.48E-05
GO:0009987	cellular process	P	1003	10275	1.07E-17	9.02E-21
GO:0006464	protein modification process	P	154	1942	1.00E+00	6.27E-01

GO:0009058	biosynthetic process	P	357	2782	2.75E-17	2.79E-20
GO:0044550	secondary metabolite biosynthetic process	P	32	180	3.21E-03	6.56E-05
GO:0009699	phenylpropanoid biosynthetic process	P	28	116	1.07E-04	9.22E-07
GO:0009056	catabolic process	P	162	1485	1.28E-03	2.04E-05
GO:0015979	photosynthesis	P	61	189	4.28E-15	7.23E-18
GO:0019725	cellular homeostasis	P	24	303	1.00E+00	8.28E-01
GO:0009605	response to external stimulus	P	185	1387	1.78E-09	6.34E-12
GO:0009725	response to hormone	P	226	1599	2.72E-14	5.99E-17
GO:0006952	defense response	P	139	1145	6.27E-05	5.09E-07
GO:0051704	multi-organism process	P	172	1482	4.30E-05	3.42E-07
GO:0055114	oxidation-reduction process	P	144	942	7.69E-11	2.47E-13
GO:0003824	catalytic activity	F	920	8868	5.38E-23	1.75E-26
GO:0016740	transferase activity	F	330	3725	3.27E-01	6.25E-03
GO:0016836	hydrolyase activity	F	19	82	1.36E-02	7.94E-05
GO:0005488	binding	F	926	10024	4.49E-09	4.38E-12
GO:0016301	kinase activity	F	111	1390	1.00E+00	6.42E-01
GO:0005215	transporter activity	F	139	1418	2.91E-01	5.20E-03
GO:0008135	translation factor activity	F	9	142	1.00E+00	7.50E-01
GO:0005198	structural molecule activity	F	63	502	4.33E-02	3.51E-04
GO:0016853	isomerase activity	F	33	256	3.46E-01	7.53E-03
GO:0016491	oxidoreductase activity	F	219	1492	8.40E-15	5.46E-18
GO:0016020	membrane	C	833	7769	2.07E-25	2.86E-27
GO:0005737	cytoplasm	C	1340	14521	5.10E-21	8.94E-23
GO:0005623	cell	C	1865	22697	4.69E-13	1.21E-14
GO:0043226	organelle	C	631	5381	3.69E-26	3.40E-28
GO:0009536	plastid	C	635	5292	2.22E-28	6.15E-31
GO:0005618	cell wall	C	129	756	1.67E-13	4.01E-15
GO:0005829	cytosol	C	245	2290	9.06E-06	4.01E-07
GO:0005886	plasma membrane	C	387	3572	4.13E-10	1.26E-11

Table S6. Gene ontology (GO) functional enrichment analysis of differentially expressed genes in pairwise comparison of lupulin glands vs leaf in hop.

GO ID	Ontology	Category	Number of DEGs	Number of Unigenes in subgroup	FDR	p-value
GO:0008152	metabolic process	P	510	8180	1.23E-14	6.23E-18
GO:0044238	primary metabolic process	P	333	6595	2.49E-01	1.04E-02
GO:0005975	carbohydrate metabolic process	P	55	808	1.13E-01	3.43E-03
GO:0019538	protein metabolic process	P	142	3183	1.00E+00	9.64E-01
GO:0006631	fatty acid metabolic process	P	22	211	2.49E-02	4.71E-04
GO:0006629	lipid metabolic process	P	62	829	1.12E-02	1.86E-04
GO:0090304	nucleic acid metabolic process	P	43	1666	8.01E-03	1.21E-04
GO:0009698	phenylpropanoid metabolic process	P	20	141	1.75E-03	1.81E-05
GO:0019748	secondary metabolic process	P	32	371	3.38E-02	7.15E-04
GO:0009987	cellular process	P	590	10275	3.18E-11	4.30E-14
GO:0006464	protein modification process	P	77	1942	1.00E+00	3.31E-01
GO:0009058	biosynthetic process	P	212	2782	5.03E-11	7.65E-14
GO:0044550	secondary metabolite biosynthetic process	P	21	180	9.40E-03	1.46E-04
GO:0009699	phenylpropanoid biosynthetic process	P	20	116	1.61E-04	1.33E-06
GO:0009056	catabolic process	P	20	182	2.90E-02	5.69E-04
GO:0015979	photosynthesis	P	51	189	5.97E-18	1.01E-21
GO:0019725	cellular homeostasis	P	13	99	4.35E-02	9.71E-04
GO:0009605	response to external stimulus	P	390	5729	4.10E-15	1.39E-18
GO:0009725	response to hormone	P	119	1599	2.89E-05	1.85E-07
GO:0006952	defense response	P	77	1145	3.15E-02	6.34E-04
GO:0051704	multi-organism process	P	103	1482	2.08E-03	2.18E-05
GO:0055114	oxidation-reduction process	P	99	942	5.14E-11	8.69E-14
GO:0003824	catalytic activity	F	557	8868	1.43E-17	4.63E-21
GO:0016740	transferase activity	F	183	3725	1.00E+00	1.60E-01

GO:0016836	hydrolyase activity	F	15	82	5.05E-03	1.48E-05
GO:0005488	binding	F	539	10024	7.32E-05	9.51E-08
GO:0016301	kinase activity	F	63	1390	1.00E+00	8.42E-01
GO:0016772	transferase activity	F	183	3725	1.00E+00	1.60E-01
GO:0005215	transporter activity	F	62	1418	1.00E+00	9.47E-01
GO:0008135	translation factor activity	F	6	142	1.00E+00	1.00E+00
GO:0005198	structural molecule activity	F	22	502	1.00E+00	1.00E+00
GO:0016853	isomerase activity	F	28	256	1.12E-02	4.01E-05
GO:0016491	oxidoreductase activity	F	143	1492	2.93E-13	1.90E-16
GO:0016020	membrane	C	471	7769	1.36	2.36E-12
GO:0005737	cytoplasm	C	818	14521	1.27	1.25E-20
GO:0005623	cell	C	1087	22697	1.08	1.06E-07
GO:0043226	organelle	C	935	19561	1.07	1.29E-03
GO:0009536	plastid	C	450	5292	1.91	1.08E-41
GO:0005618	cell wall	C	54	756	1.61	2.53E-02
GO:0005829	cytosol	C	140	2290	1.37	4.91E-03
GO:0005886	plasma membrane	C	38	497	1.72	3.85E-02

Table S7 Primers used for qRT-PCR analyses.

S.No	Primer Name	Sequence (5' - 3')
1	PAL-F	CCGAAGTCTTGTCAGCCATT
2	PAL-R	TGGGGTGATGTCCTAAGAGC
3	4CL-F	TCCGATAGCCTTAACGGTTG
4	4CL-R	CCATAGCCCTGTCCAAGTGT
5	C4H-F	CCACTGGAAGAAGCCAGAAG
6	C4H-R	TCTGCACCAAACGTCCAATA
7	CHS_H1-F	TCACCAACAGCGAGCACA
8	CHS_H1-R	GGTGATCTTCGACTTGGGC
9	OMT1-F	TAAAGGAACAGTGGTGGACGTTG
10	OMT1-R	ACCGCATCAGCACTAGGAATTGA
11	PT1-F	ACAACAACAACAACACCTCTAACA
12	PT1-R	CTTGCAGCTGAAAATTGATAAAG
13	VPS-F	ACTCCGATTGGGATTAATGACTG
14	VPS-R	GTACTCGCTCAGCATTTCAC
15	CHS4-F	TCTGGACTAATGCTTCACTTAAT
16	CHS4-R	AATCTCTAATCCCAATTTCCC
17	DFR-F	CGAAGAAGTTGACAGATTTGGG
18	DFR-R	TTGGTTTGATGGGTAAGAGGA
19	CHI_F	CAACTGCCCTCAACTCAA
20	CHI_R	TTTCTTCCTCAAGCCAAC
21	*Hl*bHLH2-F	AGCGGGTTGACTAGTGTG
22	*Hl*bHLH2-R	ACTTGCACCGTTGTCTCTG
23	*Hl*WRKY1-F	AGATTGATCAGAGCTCCGACAGT
24	*Hl*WRKY1-R	CTTCCTCCATCTATAGCCATCATC
25	*Hl*Myb7-F	CCAGCCAGACCAATTGAAGAG
26	*Hl*Myb7-R	CAAGCCCAAGAAATCATAACCA
27	*Hl*Myb8-F	GGATGATCAGCAGAAACGAC
28	*Hl*Myb8-F	CAACACAAAAACGACAACTGG
29	ERT_F	AAGTGGGGGAAATGGGTATC
30	ERT_R	GCAATCTCCGGTGGACTATT
31	SHCT_F	TCGGAAATGTCCTATCCTGTC
32	SHCT_R	CTTTGAACGAAGTGCCTCTACC

33	DRH-F	ATTCCCACTAAGCGTCAAACC
34	DRH-R	ATCTGCTCTAACCTCCTCTGT