

Supplementary Materials: Full-Length Transcriptome Survey and Expression Analysis of *Cassia obtusifolia* to Discover Putative Genes Related to Aurantio-Obtusin Biosynthesis, Seed Formation and Development, and Stress Response

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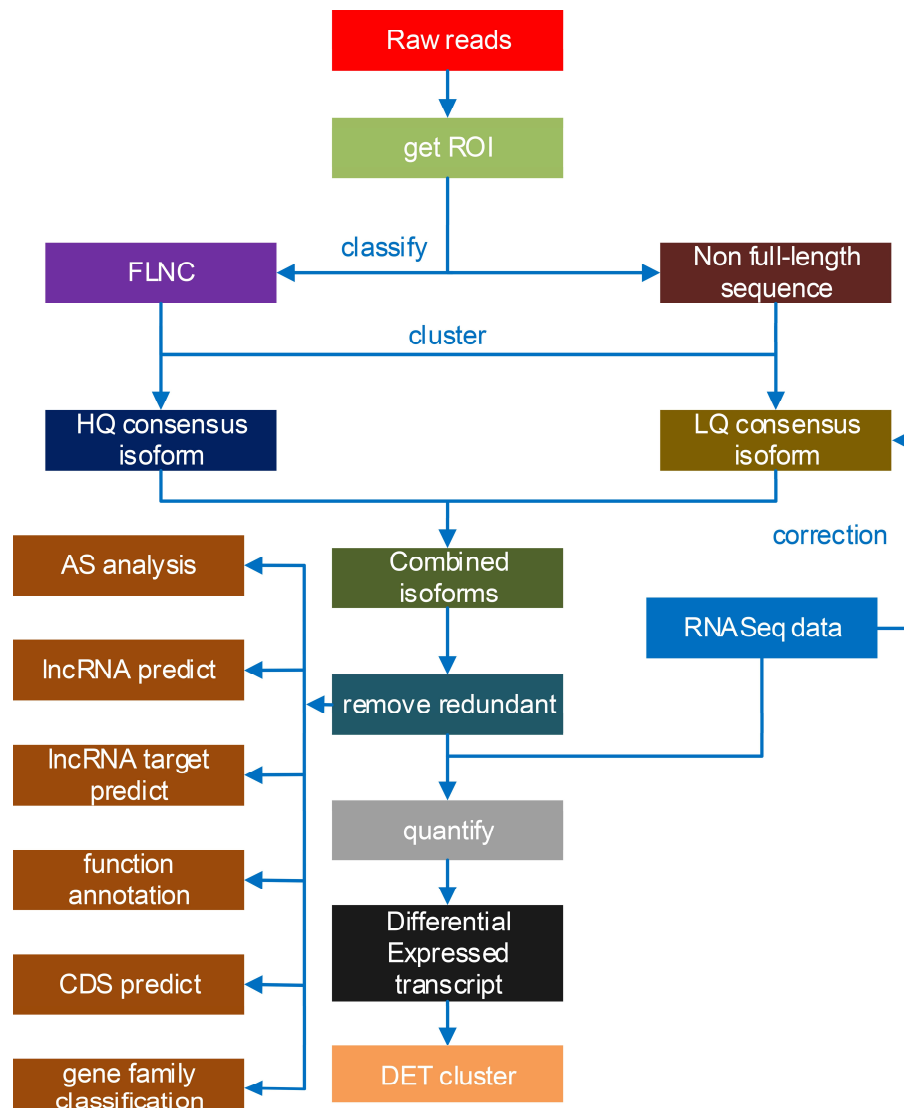


Figure S1. Transcriptome analysis pipeline and strategy used for the hybrid transcriptome assembly and characterization.

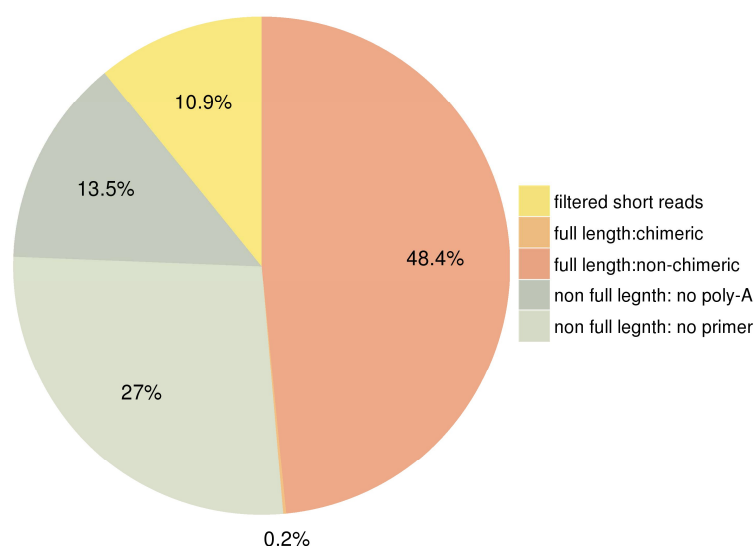


Figure S2. Classification of ROIs.

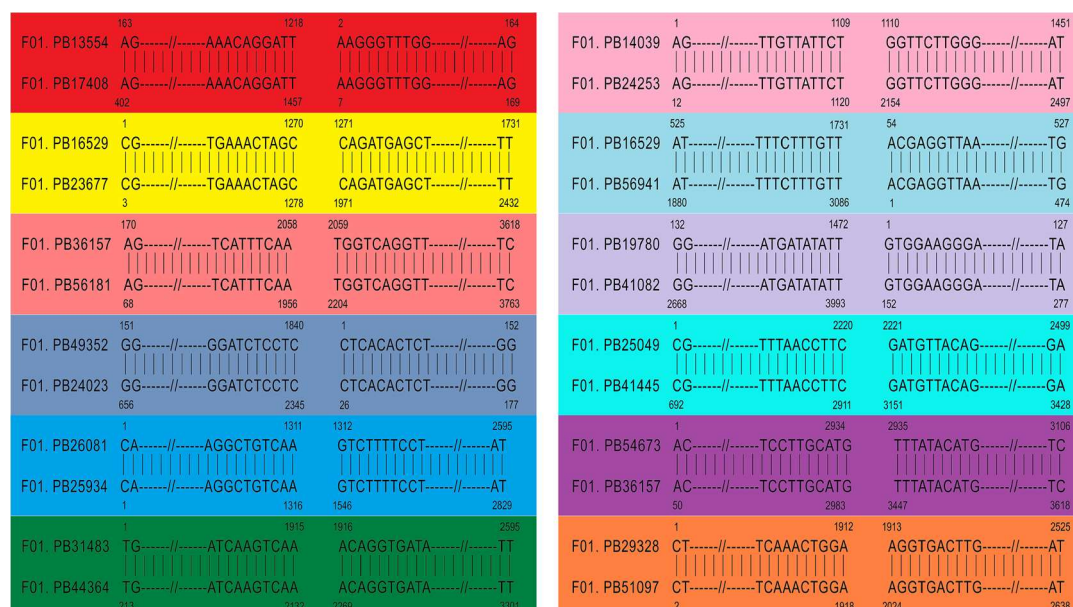


Figure S3. The different alternative splicing isoforms of transcriptional factor genes involved in seed formation and development.

Table S1. Primers used in the study.

Primer	sequence
Oligo(dT)18	GCTGTCAACGATACGCTACGTAACGGCATGACAGTGTTTTTTT
EF1 α 2qFP	TTTTTTTTTTTT TTGAAGAACGGTGATGCAGGTA
EF1 α 2qRP	CACACTCTTGATGACTCCCACA
CoHSP20-1qFP	TTCGACCTTTCTCTCTCGACC
CoHSP20-1qRP	CTCCTCGATCTCCACCTTC
CoHSP20-2qFP	GCTATGCCACAACCAGATGAG
CoHSP20-2qRP	CTGCACTGATGGTGGTGTC
CoHSP20-3qFP	TGCCTTATCGCTTCTACTTCTC
CoHSP20-3qRP	CCTCTAGAGGAAGACGATGATC
CoHSP20-4qFP	CGGTGGTAGAAGGAGCAAC
CoHSP20-4qRP	GGAGCACCTGTTCATCCTC
CoHSP20-5qFP	CAGACAATCCTACACAGTTCCTC
CoHSP20-5qRP	GGTGGAATGGAATCTTGGGC
CoHSP20-6qFP	CCACACACTCTTCTCCTTCTC
CoHSP20-6qRP	CCCAGAGAGATCGCGTGTAG
CoHSP20-7qFP	CTCCGTCAATATCAATGGCTCTC
CoHSP20-7qRP	GAACGCATCTGCCACTGAG
CoHSP20-8qFP	GACTGAGGCAGTGAACCAC
CoHSP20-8qRP	CACGGTCACCTGAATGTCAG
CoUDPG1qFP	CTCTATCTGCTCTGCTCTCCG
CoUDPG1qRP	ACACTTGCTCTGTTCTGAACC
CoUDPG2qFP	GTTCTGAGGACTCAGCGTG
CoUDPG2qRP	AGATCCATCTCGCTCGTCC
CoUDPG3qFP	ACCGTAGCATTCCGTTATTTCTG
CoUDPG3qRP	TGTCGTTCTTCTCCTCGTCG
CoUDPG4qFP	CGCGGAATAGTGTGGAACAG
CoUDPG4qRP	GCTTCAACGACGTCGTCAC
CoUDPG5qFP	CGATCTGCCTTGCTACGTTTAC
CoUDPG5qRP	CCTATGGAGTTGCTTGCTCAC
CoUDPG6qFP	GCGGCTATACAGAACTGCG
CoUDPG6qRP	GCTTCTCCAACCAATCCTTCAC
CoUDPG7qFP	GCTCATGATCTCTTGGATGCC

CoUDPG7qRP	GGTTGGTTATCCAACCACGAC
CoCYP450-1qFP	GACACCACATCCACACTGC
CoCYP450-1qRP	TCACTATCACATGTGTTCTGC
CoCYP450-2qFP	ACGAGAATCCATGCAAGACATC
CoCYP450-2qRP	TCAAAGTAGTGCACAAGGTTGG
CoCYP450-3qFP	CTTGCAAGTGAATCTGAGTGAGG
CoCYP450-3qRP	GATCCAACCTCTTGAGCTACTCTG
CoCYP450-4qFP	TGTGTCAAGATGTGTGCTTGG
CoCYP450-4qRP	TCACATCATCAAAGACAGCATCC
CoCYP450-5qFP	GGTTCTGAGGCTAAGACCATG
CoCYP450-5qRP	GCAGCTCTCATTGCACAATG
CoDXSqFP	CATGTAGTTGCTGTTATTGGCG
CoDXSqRP	CCACTGATCATACCACGAGC
CoIPPSqFP	TTCAGCAACGATCTGCAACG
CoIPPSqRP	GCGAACATTAACATCCCGGAC
CoMDTqFP	CCTTACATGCTCATGATCTCTCG
CoMDTqRP	TTGTGATAGTGTTCCACCGC
CoICSqFP	ATTGCAAGTCGCTTGGAGC
CoICSqRP	ATTGTGTTGATCATTGCCTCGG
CoARFqFP	GTACAGCCAGATGCTATGTGG
CoARFqRP	CCAGATTCTGGTGATTATGCGC
CoLEA1qFP	CGCATTATAACCGAAGCAGTCG
CoLEA1qRP	TGTTATCACATTGCTTCCCGTC
CoLEA2qFP	GAGAATACTGCCGCAGCTAATG
CoLEA2qRP	TCCTCGTCTTCATCATGCTGG
CoLEA3qFP	GTGATGCAATCTGCAGCGTC
CoLEA3qRP	GCTTCTCCTATGGTTATGGCATC
CoNFqFP	GCATCATGCTAGAATGCCATTG
CoNFqRP	TTCAGAGGTAAGCAGGCTGC
CoHBPqFP	GCTCATCGACAAGATGATGTCAC
CoHBPqRP	GATTCAGTGTAGACGAGGTGG
CoMADS1qFP	CGTGGAAGAATGCACAATGAG
CoMADS1qRP	GATATTCAGCCTCACACAGCG
CoMADS2qFP	CAGTCGTGGTCGTCTCTATGAG
CoMADS2qRP	AGTGAGTGTGCTCAAGGCATC

CoMADS3qFP	CCTAAGACATGTGCAGCTGC
CoMADS3qRP	CACTACTGCCATCGTCTCTG
CoMYP1qFP	GAATCTCAGCCTCTCCACTGG
CoMYP1qRP	ATGGCACATCTCTCTTCTCATC
CoMYP2qFP	CTGATATGCTGGCTTGCTTCTC
CoMYP2qRP	GGTTGGCAGAATAGAATGGAGC
CoMYP3qFP	CTCAGATTGCAGCTCAGTTACC
CoMYP3qRP	GGAGAAGCAAGCCAGCATATC
CoNACqFP	CTCGTGATGCACTATCTCTGC
CoNACqRP	GCTTATCTGCACCAGTTGCC
CobHLHqFP	GCAGCCAGACGAAGAACAAC
CobHLHqRP	GATCTGAGAACTCCGAGGTGG
CoWRKYqFP	TGAGGACATCTGCATCTGACG
CoWRKYqRP	CTACAGTAGGTTTCATTGGATGGC
CoYABBY1qFP	TGATACTGTCCTCGCTGTAAGC
CoYABBY1qRP	GGCAGTCCTAGATGGCATAACG
CoYABBY2qFP	CATCATCCTCATCAACTACTGCC
CoYABBY2qRP	CATCGCACAGTCACTGTCTTG
CoZF1qFP	GTCATGACTGGACGGACTGC
CoZF1qRP	GAGGAGTGTGAGCGAAGAAGC
CoZF2qFP	GTCGTCTAGTGCGTTGATGAGC
CoZF2qRP	GCTGCTGCTGATGATGATGATC

Table S2. The putative genes (all with FPKM>10 in seed) related to anthraquinone biosynthesis, seed formation and development, and stress response.

gene ID	Expression in root	Expressio n in stem	Expression in leaf	Expression in flower	Expression in seed	Annotation
F01.PB10020	34.28	21.85	8.31	49.55	285.93	Udp-Glycosyltransferase 91A1
F01.PB10650	22.50	35.32	37.33	11.48	14.38	1-Deoxy-D-Xylulose-5-Ph osphate Synthase
F01.PB10833	0.00	0.31	0.00	2.20	59.35	Udp-Glycosyltransferase 91A1
F01.PB10944	22.93	6.72	0.37	92.22	110.58	Udp-Glycosyltransferase
F01.PB11031	17.92	15.02	4.77	24.54	10.20	Isopentenyl-diphosphate Delta-isomerase II
F01.PB11223	19.52	16.62	9.75	7.62	10.13	Shikimate Kinase
F01.PB11533	30.65	29.44	0.01	46.00	14.55	Cytochrome P450 71A1
F01.PB11581	3.37	1.70	36.68	27.68	34.27	Cytochrome P450 85A
F01.PB11939	7.86	5.22	11.67	2.37	10.95	Udp-Glucuronosyl/Udp-Gl ucosyl Transferase Family Protein
F01.PB12489	32.67	103.54	248.65	118.43	35.50	4-Hydroxy-3-Methylbut-2 -Enyl Diphosphate Reductase

F01.PB1265	30.66	51.48	32.88	12.84	10.50	Chorismate Synthase 1
F01.PB13542	19.44	3.64	3.37	48.45	16.24	Cytochrome P450 734A1
F01.PB13551	15.24	20.43	31.09	34.09	37.09	3-Dehydroquininate Synthase
F01.PB14067	12.09	13.99	8.41	16.74	14.78	Diphosphomevalonate Decarboxylase
F01.PB14731	68.56	29.34	46.03	19.58	17.25	Acyl-Activating Enzyme 5
F01.PB14944	37.50	24.56	12.94	13.22	14.30	3-Phosphoshikimate 1-Carboxyvinyltransferase
F01.PB15276	0.11	1.27	0.11	0.26	21.68	Cytochrome P450 Family 71 Protein
F01.PB15287	3.61	10.32	0.17	2.75	70.82	Cytochrome P450 716B2
F01.PB15419	8.82	6.12	0.00	1.92	19.83	Cytochrome P450 Family 71 Protein
F01.PB15474	10.34	15.82	14.17	89.86	10.49	Cytochrome P450 86B1
F01.PB16224	66.69	42.64	79.16	91.69	31.93	Cytochrome P450 71A24
F01.PB16738	10.35	6.18	0.16	2.80	18.65	Acetyl-Coenzyme A Carboxylase Subunit Alpha
F01.PB16761	9.26	11.91	14.08	15.15	14.59	1-Deoxy-D-Xylulose-5-Phosphate Synthase
F01.PB17172	7.93	0.02	0.06	0.20	18.55	1-Deoxy-D-Xylulose-5-Phosphate Synthase 2

F01.PB17233	33.97	43.65	26.52	64.85	72.33	Isopentenyl-Diphosphate Delta-IsomeraseII
F01.PB1750	8.15	21.20	0.29	3.28	17.99	1-Deoxy-D-Xylulose 5-Phosphate Synthase
F01.PB17587	22.42	31.21	45.16	25.01	11.34	1-Deoxy-D-Xylulose 5-Phosphate Reductoisomerase
F01.PB17961	15.06	13.94	36.50	17.10	11.04	Type III Polyketide Synthase
F01.PB18404	67.74	75.63	41.94	61.54	59.36	Peroxisomal Enoyl-CoA Hydratase/Isomerase Family Protein
F01.PB18582	4.01	73.43	68.29	12.26	43.29	Limonoid Udp-Glucosyltransferase
F01.PB1877	1.90	14.40	0.03	12.02	193.49	Hypothetical Protein Prupe_Ppa010752Mg
F01.PB19520	97.37	22.59	83.83	16.56	27.10	Cytochrome P450 Family 709 Protein
F01.PB19914	7.83	9.93	9.12	13.30	13.90	Mevalonate Diphosphate Decarboxylase
F01.PB20158	4.32	27.18	86.47	8.95	15.78	Cytochrome P450 98A2
F01.PB2045	40.45	20.16	6.01	18.17	18.17	Isopentenyl Diphosphate Isomerase
F01.PB20786	1.65	17.90	66.99	52.29	25.41	Cytochrome P450 Family

					71 Protein	
					4-Diphosphocytidyl-2-C-	
F01.PB21451	10.33	13.63	21.75	21.47	10.20	Methyl-D-Erythritol
						Kinase
F01.PB22057	1.65	1.22	0.00	66.91	173.63	Udp-Glucosyltransferase
						Family Protein
F01.PB22220	1.13	3.07	6.90	9.90	12.90	3-Dehydroquinate
						Synthase
F01.PB22595	5.34	5.45	5.79	14.48	10.82	Cytochrome P450
						Monooxygenase Cyp51G1
F01.PB22877	1.39	0.80	0.05	129.09	536.97	Udp-Glucosyltransferase
						Family Protein
						Polyketide
F01.PB23040	14.74	39.73	145.53	52.37	32.94	Cyclase/Dehydrase And
						Lipid Transport
						Superfamily Protein
F01.PB23612	12.28	44.69	18.59	135.98	41.53	3-Hydroxy-3-Methylglutar
						yl-Coenzyme A Reductase
F01.PB24506	9.52	15.41	20.96	12.72	13.82	Nadph--Cytochrome P450
						Reductase
F01.PB24938	36.15	31.92	43.68	35.56	53.32	3-Phosphoshikimate
						1-Carboxyvinyltransferase
F01.PB25321	3.65	6.54	24.06	16.34	20.70	Phospho-2-Dehydro-3-De
						oxyheptonate Aldolase 2

F01.PB25462	1.66	4.07	8.44	5.63	12.39	Cytochrome P450 97B2
F01.PB2613	0.46	13.12	93.96	18.50	20.22	Cytochrome P450 89A2
F01.PB28214	6.42	3.49	8.34	6.95	14.74	Acyl-Activating Enzyme 16
F01.PB29801	3.81	30.73	1.89	17.50	36.56	1-Deoxy-D-Xylulose 5-Phosphate Synthase
F01.PB30289	3.81	20.48	0.38	94.05	20.48	3-Hydroxy-3-Methylglutar yl-Coenzyme A Reductase 3
F01.PB30570	65.21	35.09	51.61	23.55	19.36	Acyl-Activating Enzyme 5
F01.PB33429	21.55	14.18	2.69	4.60	10.45	Udp-Glycosyltransferase 87A1
F01.PB33635	5.85	18.84	28.70	12.15	12.21	Acyl-Activating Enzyme 1
F01.PB34557	0.08	0.52	0.00	13.43	34.53	Udp-Glucosyltransferase Family Protein
F01.PB3544	4.30	4.07	0.80	19.44	40.65	Cytochrome P450 71A1
F01.PB35649	1.79	7.21	20.64	16.28	20.17	Acetyl-Coenzyme A Carboxylase Carboxyl Transferase Subunit Alpha
F01.PB3977	46.53	28.49	4.19	0.21	10.64	Udp-Glycosyltransferase Acetyl-Coenzyme A
F01.PB40488	5.50	6.18	3.77	7.33	14.63	Carboxylase Carboxyl Transferase Subunit Alpha

						2-C-Methyl-D-Erythritol
F01.PB43	38.11	110.15	211.74	58.07	28.13	2,4-Cyclodiphosphate Synthase
F01.PB432	63.66	38.25	146.61	20.94	199.77	Udp-Glucosyl Transferase 73B3
F01.PB46801	30.87	57.69	74.98	36.01	21.79	Chorismate Synthase 1
F01.PB46863	16.72	2.92	14.79	17.42	23.21	Udp-Glucosyl Transferase 85A2
F01.PB46950	17.22	14.91	2.92	44.48	145.41	Udp-Glycosyltransferase
F01.PB47063	62.46	23.56	2.41	13.73	12.49	Udp-Glucosyltransferase Family Protein
F01.PB47348	0.02	0.18	3.08	2.69	30.39	Hydroquinone Glucosyltransferase
F01.PB47552	0.02	0.08	0.06	0.13	12.03	Cytochrome P450 71A1
F01.PB47927	1.18	2.06	4.47	7.47	10.47	3-Dehydroquinone Synthase
F01.PB48318	4.00	4.27	6.42	9.42	12.42	Shikimate Dehydrogenase
F01.PB4860	0.49	13.86	94.92	13.44	19.45	Cytochrome P450 Monooxygenase Cyp89A28
F01.PB49420	56.97	42.64	24.42	18.26	22.85	Cyclin-Dependent Kinase
F01.PB49500	2.70	3.97	7.77	2.07	17.73	Protein PHYLLO, chloroplastic
F01.PB49521	12.34	10.73	0.00	34.07	41.40	Udp-Glycosyltransferase

F01.PB49848	5.08	33.61	6.04	11.15	22.08	1-Deoxy-D-Xylulose-5-Phosphate Synthase
F01.PB49988	21.15	18.34	15.06	15.29	15.67	Acyl-Activating Enzyme 17
F01.PB50624	0.06	0.75	0.03	3.80	14.16	3-Phosphoshikimate 1-Carboxyvinyltransferase
F01.PB5440	2.66	1.48	0.28	5.14	19.64	Udp-Glycosyltransferase
F01.PB5577	19.80	30.57	0.06	137.59	57.62	Udp-Glycosyltransferase
F01.PB5630	76.16	27.03	6.79	90.89	13.15	3-Ketoacyl-CoA Synthase 11
F01.PB5637	4.69	1.93	0.62	11.95	157.10	Udp-Glycosyltransferase
F01.PB6061	2.18	3.78	5.16	8.16	11.16	3-Dehydroquinate Synthase
F01.PB7847	36.20	89.05	190.84	353.99	20.71	Udp-Glycosyltransferase
F01.PB797	35.25	68.09	106.10	68.77	12.70	4-Hydroxy-3-Methylbut-2-Enyl Diphosphate Reductase
F01.PB7996	5.83	20.21	0.70	7.35	13.60	1-Deoxyxylulose-5-Phosphate Synthase
F01.PB8269	0.00	0.00	0.00	18.71	120.79	Udp-Glycosyltransferase
F01.PB8827	0.59	3.95	3.05	20.32	298.11	Udp-Glycosyltransferase
F01.PB8896	29.66	41.46	4.14	20.59	17.85	Phospho-2-Dehydro-3-Deoxyheptonate Aldolase 1

F01.PB9034	0.00	0.00	0.00	0.00	23.62	Udp-Glycosyltransferase
F01.PB9323	195.06	65.14	77.29	19.48	54.72	Udp-Glycosyltransferase
F01.PB9394	23.19	12.07	0.84	18.32	13.47	4-Hydroxy-3-Methylbut-2 -Enyl Diphosphate Reductase
F01.PB9468	1.33	14.05	0.07	20.38	320.70	Cytochrome P450 71A26
F01.PB9810	0.17	0.11	2.13	8.10	205.83	Udp-Glycosyltransferase
F01.PB4662	81.60	86.47	81.13	186.78	161.05	Udp-Glycosyltransferase
F01.PB12588	18.64	21.86	17.19	14.18	17.26	Glabra2 Expression Modulator
F01.PB10	217.20	224.88	112.20	234.23	138.96	Late Embryogenesis Abundant Hydroxyproline-Rich Glycoprotein
F01.PB10002	19.20	14.78	9.66	7.16	14.69	Gata Transcription Factor 24
F01.PB10007	40.21	106.06	172.46	86.60	20.43	Myb Transcription Factor Myb118 Isoform X1
F01.PB10028	11.58	10.78	2.54	5.98	14.30	Zinc Finger Ccch Domain-Containing Protein 32-Like Isoform X1
F01.PB10228	43.47	132.59	1.74	44.27	12.48	Auxin-Responsive Protein Iaa27

F01.PB107	0.50	0.37	0.24	0.26	488.41	Transcription Factor Hbp-1B(C38)
F01.PB10770	0.42	2.43	32.41	0.43	16.56	Homeobox Protein, Putative
F01.PB10793	285.95	194.53	31.67	25.04	18.74	Homeobox-Leucine Zipper Protein Athb-6-Like Isoform X2
F01.PB11208	41.52	40.88	2.41	11.77	20.36	Bzip Transcription Factor Bzip124
F01.PB11229	62.38	69.00	63.82	40.18	28.95	Zinc Finger, C3Hc4 Type (Ring Finger) Family Protein Isoform 1
F01.PB11410	78.76	59.94	53.43	68.50	26.32	Transcription Factor Bhlh47
F01.PB11550	623.17	450.16	6.49	10.66	74.14	Nac Transcription Factor-Like Protein
F01.PB1180	0.00	0.00	0.00	0.00	11.76	Late Embryogenesis Abundant Protein D-34-Like
F01.PB11820	196.24	51.59	54.45	25.16	29.00	Zinc Finger Ccch Domain-Containing Protein 49
F01.PB11904	12.89	10.87	4.60	16.99	22.73	Protein Auxin Response 4
F01.PB1192	206.45	193.69	27.01	80.31	23.17	Auxin Response Factor 6-Like Isoform X3

F01.PB11937	174.75	246.80	29.77	98.68	53.30	Auxin-Responsive Protein Iaa9
F01.PB1207	44.37	27.70	27.83	26.86	28.06	Transcription Factor Bhlh14
F01.PB12154	0.04	0.64	0.00	15.10	104.94	Zinc Finger Ccch Domain-Containing Protein 2]
F01.PB12157	1.30	54.90	0.64	24.09	26.71	Transcription Factor Bhlh148
F01.PB12201	14.69	17.94	7.67	10.49	10.46	Zinc Finger Protein Magpie
F01.PB123	56.17	73.11	36.52	30.36	18.61	Transcription Factor Bhlh104
F01.PB12333	23.14	36.49	15.25	24.99	16.86	Nuclear Transcription Factor Y Subunit C-9
F01.PB12406	122.37	69.73	24.20	93.59	25.69	Putative Myb-Related Protein 20
F01.PB12499	105.11	104.44	215.65	25.98	21.60	Zinc Finger Protein Constans-Like 5
F01.PB12556	145.28	135.23	85.23	107.14	97.21	Transcription Factor Ilr3-Like Isoform 1
F01.PB12599	2.96	4.92	0.42	53.89	98.20	Zinc Finger Ccch Domain-Containing Protein 2-Like

F01.PB12611	0.08	0.05	1.04	74.22	14.55	K-Box Region And Mads-Box Transcription Factor Family Protein Isoform 1
F01.PB1262	161.32	122.68	23.67	63.60	70.53	Auxin-Responsive Protein Iaa9-Like Isoform X2
F01.PB12679	27.41	28.79	21.24	44.14	12.73	Ring Finger And Chy Zinc Finger Domain-Containing Protein 1-Like Isoform X1
F01.PB12856	96.10	62.76	12.39	28.51	21.43	Putative Wrky Transcription Factor 21
F01.PB13177	5.41	15.16	33.40	53.26	69.92	Zinc-Finger Homeodomain Protein 9
F01.PB13285	14.02	7.39	11.75	8.89	10.04	Transcription Factor Bhlh122-Like Isoform X1
F01.PB13301	0.78	0.59	0.14	8.58	14.52	Zinc Finger Ccch Domain-Containing Protein 2
F01.PB13756	3.03	3.12	2.53	0.00	13.72	Zinc Finger Ccch Domain-Containing Protein 11
F01.PB13831	38.00	52.00	40.70	28.48	49.71	Zinc Finger Ccch Domain-Containing Protein 40

F01.PB13938	89.38	16.88	16.57	23.29	14.09	Lob Domain-Containing Protein 38
F01.PB14074	318.80	237.25	60.93	118.86	19.31	Transcription Factor C2H2
						Late Embryogenesis
F01.PB14103	7.22	14.96	23.96	33.29	11.03	Abundant
						Hydroxyproline-Rich Glycoprotein
F01.PB14123	11.12	7.99	12.04	77.05	13.14	Nac-Like Transcription Factor
F01.PB14289	88.92	172.24	50.50	44.10	16.08	Homeobox Protein, Putative Isoform 1
F01.PB14325	20.78	20.62	25.79	18.08	10.91	Bzip Transcription Factor Bzip56 Precursor
F01.PB14399	18.00	18.92	7.33	41.59	63.63	Myb Family Transcription Factor
F01.PB14532	48.69	53.77	32.41	41.73	41.90	Nuclear Transcription Factor Y Subunit C-9
F01.PB14683	0.95	0.21	0.32	1.15	20.49	Transcription Factor Bhlh67
F01.PB14812	30.94	11.41	4.79	5.97	13.11	Morc Family Cw-Type Zinc Finger Protein 4
F01.PB1490	125.22	72.81	14.98	100.85	17.22	Putative Myb-Related Protein 20
F01.PB15014	144.86	55.78	33.31	55.86	179.77	Nac Domain-Containing

					Protein 100	
					Atp-Dependent Zinc	
F01.PB15050	27.61	26.51	18.78	21.09	12.13	Metalloprotease Ftsh 4, Mitochondrial
						Predicted: Mads-Box
F01.PB15377	0.00	0.06	0.00	0.00	37.11	Transcription Factor 18-Like Isoform X1
						Zinc Finger Ccch
F01.PB1543	33.77	23.37	12.85	12.02	17.01	Domain-Containing Protein 40
						Squamosa
F01.PB15433	16.66	19.14	10.97	8.88	15.52	Promoter-Binding-Like Protein
						Zinc Finger Protein
F01.PB15651	5.30	23.26	12.00	11.25	21.20	Jackdaw
						Auxin-Responsive Protein
F01.PB15751	69.36	91.76	20.49	60.46	81.92	Iaa9-Like Isoform X1
						Gras Family Transcription Factor
F01.PB15956	144.47	70.52	19.86	24.02	24.46	
						Zinc Finger Ccch
F01.PB16052	56.10	23.32	13.77	12.14	26.31	Domain-Containing Protein 25-Like Isoform X1
						Wrky Transcription Factor
F01.PB16108	81.48	43.82	21.92	35.10	12.12	17-Like

F01.PB16131	0.15	0.08	0.08	16.21	108.74	Zinc Finger Family Protein
F01.PB16143	188.81	140.79	101.24	67.45	10.88	Zinc Finger A20 And An1 Domain-Containing Stress-Associated Protein 5
F01.PB16222	13.27	9.45	0.70	65.71	41.05	Ring Finger And Chy Zinc Finger Domain-Containing Protein 1
F01.PB16242	110.42	86.96	29.70	26.28	14.85	Homeobox Protein Knotted-1-Like 7
F01.PB16338	397.62	202.35	29.02	78.44	52.02	Nac Domain Protein
F01.PB16499	43.94	27.57	31.04	16.79	88.73	Nuclear Transcription Factor Y Subunit A-1
F01.PB16529	50.03	33.82	24.47	24.81	24.23	Zinc Finger Protein 207
F01.PB16736	10.07	9.58	9.86	7.46	14.26	C2H2 Type Zf-Met: Zinc-Finger Protein
F01.PB16736	10.07	9.58	9.86	7.46	14.26	C2H2 Type Zf-Met: Zinc-Finger Protein
F01.PB1685	163.23	131.53	12.60	36.10	79.04	Chy And Ctchy And Ring-Type Zinc Finger Proteintruncatula]
F01.PB16852	37.09	21.39	12.62	16.78	10.27	Gamyb-Binding Protein Family Protein

F01.PB16996	0.00	0.07	0.07	4.19	20.82	Protein Yabby 4
F01.PB17056	34.37	38.45	15.80	19.28	21.49	Transcription Factor Bhlh148-Like
F01.PB17111	45.18	55.64	32.02	26.52	11.15	Transcription Factor C2H2
F01.PB17249	32.94	34.25	29.59	17.61	14.21	Zinc Finger Protein
F01.PB17278	42.28	22.80	19.11	7.25	29.21	Nuclear Transcription Factor Y Subunit A-7-Like Isoformx2
F01.PB17297	50.62	36.28	48.02	318.54	47.22	Nac Transcription Factor-Like Protein
F01.PB17408	51.25	31.66	27.76	19.12	37.08	Rna-Binding Family Protein With Retrovirus Zinc Finger-Like Domain, Putative
F01.PB18278	83.43	67.07	2.72	14.66	30.90	Bzip Transcription Factor Bzip124
F01.PB1833	38.69	38.84	30.53	46.83	23.70	Nac Domain-Containing Protein 78-Like Isoform X2
F01.PB18393	134.53	192.00	86.99	36.92	38.97	Homeobox-Leucine Zipper Protein Hat5
F01.PB18559	0.10	7.55	128.57	7.86	21.04	Gata Transcription Factor 21
F01.PB18592	0.31	0.17	0.18	0.23	675.10	Late Embryogenesis

					Abundant Protein D-34
F01.PB18668	4.58	1.98	6.41	5.78	13.80
					Nuclear Transcription Factor Y Subunit A-7
F01.PB18696	0.00	0.00	1.50	0.00	14.14
					Nac Domain-Containing Protein 2-Like
F01.PB187	1708.02	930.11	765.44	4164.14	80.79
					Putative Late Embryogenesis Abundant Protein
F01.PB18702	0.58	4.83	0.00	3.37	13.21
					Trihelix Transcription Factor Gtl2-Like Isoform X1
F01.PB18724	8.56	9.80	8.79	0.55	24.81
					Zinc-Finger Homeodomain Protein 9-Like
F01.PB18751	1.88	4.99	3.75	6.18	11.18
					Zinc Finger Protein Zat4
F01.PB18914	5.78	6.63	10.70	5.52	10.88
					Homeobox Protein Luminidependens
F01.PB19012	0.18	2.00	1.19	104.61	295.28
					Mads Box Protein M8
F01.PB19296	0.06	0.35	0.14	4.86	17.65
					Protein Yabby 4
F01.PB19338	32.24	38.03	27.52	27.79	17.43
					Zinc Transporter Ztp29 Isoform X1
F01.PB19415	6.21	36.81	23.68	33.52	14.04
					Myb-Related Transcription Factor
F01.PB19453	326.51	331.89	80.68	13.10	17.51
					Homeobox Protein,

						Putative Isoform 2
F01.PB19594	10.02	15.02	21.94	2.93	11.11	B-Box Type Zinc Finger Family Protein
F01.PB19638	23.95	27.77	21.14	22.17	19.25	Alcohol Dehydrogenase Transcription Factor Myb/Sant-Like Family Protein
F01.PB19690	51.53	36.22	5.62	12.96	31.92	Homeobox-Leucine Zipper Protein Revoluta
F01.PB1975	80.94	41.38	12.20	12.10	10.80	Probable Wrky Transcription Factor 32 Isoform X1
F01.PB19780	19.67	14.52	10.00	10.88	12.25	Zinc Finger Ccch Domain-Containing Protein 13
F01.PB20184	35.70	22.13	4.48	34.40	10.03	Zinc Finger Protein Constans-Like Protein
F01.PB2029	57.55	57.35	18.07	14.94	23.39	Protein Auxin Signaling F-Box 2-Like, Partial
F01.PB20390	146.00	93.00	38.92	23.29	58.58	Homeobox-Leucine Zipper Protein 4 / Hd-Zip Protein
F01.PB20463	17.66	42.18	51.21	25.42	28.93	Zinc Finger Protein Constans-Like 13-Like
F01.PB20618	91.17	84.81	35.72	18.88	17.63	Homeobox-Leucine

					Zipper Protein Hat5
F01.PB20902 10.53	10.82	6.46	4.05	11.61	Gata Transcription Factor 24
F01.PB21142 20.33	17.38	3.61	10.56	62.74	Transcription Factor Bhlh93
F01.PB21330 62.70	85.14	25.99	14.87	20.26	Transcription Factor Lhw
F01.PB21339 109.79	145.21	43.80	77.54	58.22	Nuclear Transcription Factor Y Subunit C-9
F01.PB21351 70.42	58.27	21.96	16.66	23.44	Wrky Transcription Factor 32
F01.PB21364 15.69	4.98	0.57	4.86	18.69	Auxin Response Factor 5
F01.PB21549 330.10	291.35	11.89	152.82	41.40	Auxin-Responsive Protein Iaa16-Like
F01.PB21596 122.07	75.72	42.49	125.74	11.55	Transcription Factor Bhlh14
					Zinc Finger Ccch
F01.PB21671 35.28	27.41	19.10	17.44	12.19	Domain-Containing Protein 17
F01.PB21869 128.24	97.97	45.81	24.94	18.86	Wrky Protein Isoform 1
F01.PB21888 51.54	42.36	26.17	34.07	26.74	Tcp-1/Cpn60 Chaperonin Family Protein Isoform 1
F01.PB22021 33.62	16.85	5.93	24.24	12.56	Gata Transcription Factor 8-Like Isoform X2
F01.PB22694 19.80	27.93	2.29	14.75	13.45	Dof Zinc Finger Protein

					Dof2.1-Like	
					K-Box Region And	
					Mads-Box Transcription	
F01.PB22777	0.11	0.03	0.00	6.04	24.48	Factor Family Protein
						Isoform 1
						Zinc Finger Ccch
						Domain-Containing
F01.PB22985	28.13	50.89	100.25	126.61	14.88	Protein Zfn-Like
						Isoformx2
F01.PB23062	761.96	380.30	104.36	215.56	26.19	Nac Domain Protein
F01.PB23090	199.40	131.53	78.54	107.93	17.38	Transcription Factor C2H2
F01.PB23106	36.45	25.12	33.36	32.06	24.35	Zinc Finger Protein 622
						Squamosa
F01.PB2315	118.27	100.61	60.21	98.30	42.22	Promoter-Binding-Like
						Protein 12
F01.PB23201	641.64	238.87	115.06	229.13	21.23	Zinc Finger Protein
						Nuclear Transcription
F01.PB2321	38.71	39.77	32.07	24.79	14.46	Factor Y Subunit C-1
						Zinc Finger Ccch
F01.PB23270	38.80	20.73	27.65	16.14	21.47	Domain-Containing
						Protein 1
						Late Embryogenesis
F01.PB23372	17.56	37.73	60.92	84.08	73.82	Abundant Protein
						Lea14-A, Putative

F01.PB2363	86.35	37.26	28.86	26.92	35.96	Bzip Transcription Factor Bzip78
F01.PB23633	11.96	29.04	43.58	14.85	15.44	Auxin Response Factor
F01.PB23645	58.70	37.93	20.52	24.88	16.25	Gras Family Transcription Factor
F01.PB23665	67.46	62.14	52.91	47.98	15.25	Transcription Factor Bhlh143
F01.PB23723	13.36	21.01	37.39	39.25	29.89	Atp-Dependent Zinc Metalloprotease Ftsh 10, Mitochondrial
F01.PB23739	16.12	19.77	25.36	19.99	11.72	Nac Domain-Containing Protein 78
F01.PB23919	15.43	15.29	22.18	39.74	30.11	Tcp-1/Cpn60 Chaperonin Family Protein
F01.PB2405	350.74	121.41	125.47	105.58	52.66	Nac Domain-Containing Protein 2
F01.PB24072	34.54	1.00	0.33	20.59	220.58	Auxin-Responsive Gh3 Family Protein
F01.PB24083	35.67	29.94	20.88	19.78	17.86	Zinc Finger Cchc Domain-Containing Protein 7
F01.PB2410	183.60	33.59	24.46	46.58	29.92	Lob Domain-Containing Protein 38
F01.PB24154	8.36	24.69	177.73	48.32	12.39	Atp-Dependent Zinc

						Metalloprotease Ftsh 2
						Zinc Finger
F01.PB24253	15.95	16.33	12.80	37.87	24.87	C-X8-C-X5-C-X3-H Type Family Protein
F01.PB24376	34.95	31.46	19.96	23.19	29.11	Transcription Factor Bhlh3
F01.PB24488	6.57	6.49	3.68	11.77	14.74	Zinc Finger Ccch Domain-Containing Protein
F01.PB24648	18.68	32.85	32.95	28.02	28.12	Nac Transcription Factor 044
F01.PB24858	1.63	9.63	26.15	2.18	10.94	Zinc Finger Protein Magpie
F01.PB25741	0.97	4.09	16.80	1.67	15.25	Zinc Finger Protein Magpie-Like Isoform X1
F01.PB25934	141.52	21.05	14.45	128.65	13.82	Ring Finger And Chy Zinc Finger Domain-Containing Protein 1
F01.PB27486	27.49	46.66	20.31	11.42	14.03	Zinc Finger Protein Constans-Like 9
F01.PB27782	26.46	25.72	21.09	16.56	15.27	Zinc Finger Ccch Domain-Containing Protein 13
F01.PB2811	143.07	118.02	34.64	31.14	26.55	Homeobox-Leucine

						Zipper Protein Hat5
						Homeobox-Leucine
F01.PB28873	43.75	20.90	5.54	35.52	35.47	Zipper Protein Glabra 2
						Homeobox-Leucine
F01.PB28873	43.75	20.90	3.78	35.52	35.47	Zipper Protein Glabra 2, Partial
F01.PB2934	11.60	19.76	12.85	11.83	14.00	Transcription Factor C2H2
F01.PB2975	57.82	48.30	28.43	32.37	23.91	Transcription Factor Hbp-1A
F01.PB29862	26.66	31.53	62.70	54.71	36.74	Nac Domain-Containing Protein 78-Like Isoform X1
F01.PB30023	23.23	14.75	14.83	16.96	16.85	C2H2-Like Zinc Finger Protein
F01.PB30023	23.23	14.75	14.83	16.96	16.85	C2H2-Like Zinc Finger Protein
F01.PB30072	28.20	16.24	5.42	18.00	26.34	Zinc Finger Protein Nutcracker
F01.PB30173	16.58	11.10	0.98	4.75	11.34	Homeobox-Leucine Zipper Protein Revoluta
F01.PB30194	3.52	19.03	23.20	17.46	16.11	Transcription Factor Bhlh3-Like Isoform X1
F01.PB303	64.50	115.95	0.61	18.10	13.44	Auxin-Responsive Protein Iaa27

					Zinc Finger Ccch	
F01.PB30557	22.81	13.00	15.22	18.95	18.41	Domain-Containing Protein
F01.PB30997	13.24	10.06	7.95	7.33	14.62	Myb-Like Protein X-Like Isoform X1
F01.PB31220	18.29	13.71	10.45	10.88	13.31	Ankyrin Repeat And Zinc Finger Domain-Containing Protein 1-Like Isoform X2
F01.PB31450	18.34	9.79	12.08	9.64	31.39	Nuclear Transcription Factor Y Subunit A-1
F01.PB31483	22.35	8.02	6.18	35.67	22.94	Ring Finger And Chy Zinc Finger Domain-Containing Protein 1
F01.PB31676	9.31	11.99	8.82	10.27	12.88	Zinc Finger Ccch Domain-Containing Protein 53-Like Isoform X1
F01.PB3189	32.53	31.10	14.05	24.77	25.57	Late Embryogenesis Abundant Protein Lea14-A
F01.PB32560	60.01	25.27	10.18	12.11	14.00	Low Quality Protein: Transcription Factor Tcp8
F01.PB33011	13.44	8.82	1.48	9.83	14.15	Predicted: Auxin Response Factor 9

F01.PB33304	13.78	15.55	49.67	27.46	72.58	Trihelix Transcription Factor Gt-2
F01.PB33839	1.75	17.64	7.03	14.60	15.52	Trihelix Transcription Factor Gtl2-Like Isoform X1
F01.PB34396	44.43	40.20	8.40	22.66	16.40	Putative Wrky Transcription Factor 21
F01.PB34408	3.88	10.39	123.53	43.47	12.00	Atp-Dependent Zinc Metalloprotease Ftsh 2
F01.PB35492	2.54	17.63	100.49	24.03	14.58	Atp-Dependent Zinc Metalloprotease Ftsh 2
F01.PB35614	14.38	19.51	24.72	17.16	15.02	Zinc-Metallopeptidase, Peroxisomal-Like Isoform X2
F01.PB35640	16.47	10.95	8.88	14.08	21.66	Ring Finger And Chy Zinc Finger Domain-Containing Protein 1
F01.PB35768	29.49	15.06	16.53	23.40	16.46	Atp-Dependent Zinc Metalloprotease Ftsh 10
F01.PB3605	4.57	5.54	0.78	2.81	10.17	Gata Transcription Factor 16
F01.PB36117	39.73	28.09	15.06	17.15	19.10	Zinc Finger Protein 598
F01.PB36157	12.87	20.22	23.94	19.57	13.82	Squamosa Promoter-Binding-Like

					Protein 12
F01.PB36406	15.05	12.52	3.55	12.50	15.75
					Homeobox-Leucine Zipper Protein Revoluta
F01.PB36694	28.11	21.44	2.40	14.54	18.08
					Homeobox-Leucine Zipper Protein Revoluta
F01.PB37055	12.83	10.50	7.65	9.61	11.20
					Bromodomain Adjacent To Zinc Finger Domain Protein 1A
F01.PB3780	174.17	343.68	396.55	270.25	24.59
					Myb Transcription Factor Myb156
F01.PB3829	0.00	0.00	0.00	0.02	22.20
					Myb-Related Protein Myb4
F01.PB38904	18.71	18.30	4.58	93.08	38.41
					Ring Finger And Chy Zinc Finger Domain-Containing Protein 1
F01.PB39154	10.50	26.63	18.09	27.36	14.79
					Squamosa Promoter-Binding-Like Protein 12
F01.PB3944	26.00	39.60	33.73	29.76	21.35
					Transcription Factor Bhlh1 13-Like Isoform X2
F01.PB3952	34.61	43.78	15.10	12.80	10.02
					14 Kda Zinc-Binding Protein
F01.PB40141	2.46	2.34	4.53	9.98	10.21
					Atp-Dependent Zinc Metalloprotease Ftsh 2

F01.PB4026	790.68	204.97	87.88	58.54	10.56	Putative Zinc-Binding Protein
F01.PB40675	64.13	28.56	19.19	23.80	35.10	Auxin Response Factor 1-Like Isoform X1
F01.PB409	0.17	0.18	0.12	13.20	157.06	Agamous-Like Mads-Box Protein Agl11 Isoform X3
F01.PB41445	16.91	13.16	9.65	6.51	12.94	Zinc Ion-Binding Protein
F01.PB41678	7.18	11.00	12.30	9.98	21.72	Zinc Finger Ccch Domain-Containing Protein 53-Like Isoform X1
F01.PB42383	3.99	3.21	0.63	3.21	15.46	Wrky Transcription Factor 32
F01.PB42544	19.80	17.36	5.73	11.13	11.73	Homeobox Protein Luminidependens
F01.PB42615	24.51	33.57	16.57	7.95	12.79	Auxin Response Facto
F01.PB43929	34.64	58.44	42.43	39.84	31.43	Zinc Finger Ccch Domain-Containing Protein 30
F01.PB44833	146.77	50.13	1.75	18.36	19.31	Putative Cadmium/Zinc-Transporting Atpase Hma4
F01.PB46103	18.45	30.80	48.65	32.26	17.52	Auxin Response Factor
F01.PB46224	9.54	9.03	19.70	14.11	10.57	Squamosa Promoter-Binding-Like

					Protein 12-Like	
F01.PB46433	19.18	25.67	12.82	6.03	31.53	Zinc/Ring Finger Protein
						Late Embryogenesis
F01.PB46565	0.40	0.64	1.41	19.30	890.58	Abundant Protein Group 3, Putative
F01.PB46590	41.70	94.76	13.20	74.40	18.51	Ring-H2 Zinc Finger Protein Rha1A
F01.PB46762	78.48	108.54	12.95	55.33	17.67	Auxin-Responsive Protein Iaa9
F01.PB46839	11.63	18.84	25.27	16.52	22.68	Myb-Like Protein X-Like Isoform X6
F01.PB46867	134.40	90.92	14.91	7.11	12.15	Homeobox-Leucine Zipper Protein Hat22
F01.PB46923	12.60	33.91	36.83	18.67	24.95	Zinc Transporter 6, Chloroplastic
F01.PB47101	3.25	9.73	2.53	7.72	14.17	Gata Transcription Factor
F01.PB4739	325.45	217.24	316.31	269.01	96.73	Nac Domain-Containing Protein 2
F01.PB47406	5.35	18.88	0.84	2.99	12.23	Transcription Factor Myb86
F01.PB4743	695.97	350.20	48.57	169.29	17.17	Auxin-Responsive Protein Iaa16
F01.PB47777	32.76	30.30	16.74	20.07	11.72	Wrky Transcription Factor

					15 Family Protein
F01.PB47802 45.21	41.70	3.18	13.57	18.56	Dof Zinc Finger Protein Dof2.1
F01.PB47802 45.21	41.70	3.18	13.57	18.56	Dof Zinc Finger Protein Dof2.1
F01.PB48100 0.04	2.16	0.00	0.27	13.76	Transcription Factor Myb86
F01.PB48118 34.84	22.42	21.26	15.88	19.85	Zinc Finger Ccch Domain-Containing Protein 48
F01.PB48170 50.83	40.50	38.02	72.43	44.78	Atp-Dependent Zinc Metalloprotease Ftsh 10
F01.PB4830 263.42	401.09	168.21	89.48	59.11	Homeobox Protein, Putative Isoform 1
F01.PB48499 54.51	47.35	20.67	16.78	21.85	Auxin Signaling F-Box Protein 2
F01.PB48544 0.66	1.10	0.65	12.11	16.69	Transcription Factor Tcp4
F01.PB4856 106.85	104.01	49.01	50.61	63.21	Zinc Finger Ccch Domain-Containing Protein 43
F01.PB48668 37.13	32.53	25.71	40.48	20.92	Nac Domain-Containing Protein 78
F01.PB48794 125.24	36.05	12.89	25.44	14.57	Homeobox-Leucine Zipper Protein Athb

					Zinc Finger Ccch	
F01.PB48807	9.30	17.65	13.88	12.58	18.64	Domain-Containing Protein 56
F01.PB48908	0.22	0.13	0.08	0.74	465.30	Late Embryogenesis Abundant Protein D-34
F01.PB48947	25.13	17.85	1.02	2.43	15.77	Nac Domain-Containing Protein 8
F01.PB49035	14.23	16.62	2.91	9.88	11.66	Gata Transcription Factor 5
F01.PB49074	0.00	0.02	54.20	0.32	11.72	Putative Gata Transcription Factor 22
F01.PB49173	0.09	1.15	0.13	47.70	34.68	Zinc Finger Homeodomain Protein Szf-Hd1
F01.PB49352	105.48	152.55	96.74	81.10	37.32	Transcription Factor Bhlh144
F01.PB49546	89.88	102.01	94.08	29.84	16.69	Nuclear Transcription Factor Y Subunit B-2
F01.PB50180	193.66	113.66	53.70	23.35	22.71	Gata Transcription Factor 24-Like Isoformx1
F01.PB5076	32.47	211.72	271.38	66.33	22.80	B-Box Zinc Finger Protein 32
F01.PB5085	38.23	16.62	18.77	17.35	63.26	Zinc Finger C-X8-C-X5-C-X3-H Type Family Protein, Putative

F01.PB51016	15.18	15.31	20.21	20.08	19.69	Transcription Factor Bhlh49-Like Isoform X2
F01.PB51097	14.76	12.88	8.16	8.72	11.26	Zinc Finger Ccch Domain-Containing Protein 64
F01.PB5125	340.99	296.27	142.28	75.26	91.15	Trihelix Transcription Factor Asil1
F01.PB52031	9.78	4.96	9.25	14.59	18.42	Atp-Dependent Zinc Metalloprotease Ftsh 2
F01.PB52040	39.84	51.28	26.97	24.59	16.10	Transcription Factor Bhlh143
F01.PB5266	24.37	13.25	3.45	9.60	179.88	Nuclear Transcription Factor Y Subunit A-9
F01.PB54457	2.53	3.44	8.32	4.55	11.22	Trihelix Transcription Factor Gt-2
F01.PB54738	10.11	6.25	5.39	27.27	11.75	Ring Finger And Chy Zinc Finger Domain-Containing Protein 1
F01.PB5579	58.42	34.93	46.79	22.56	15.09	Myb Domain Protein 3, Putative
F01.PB55961	12.24	11.19	8.27	6.81	12.84	Zinc Finger Ccch Domain-Containing Protein 69
F01.PB56112	20.60	11.79	8.11	9.07	13.30	Myb Transcription Factor

F01.PB5631	0.00	5.05	2.77	0.00	11.04	Nac Domain-Containing Protein 2
F01.PB5633	59.43	54.24	45.97	30.77	16.84	Nuclear Transcription Factor Y Subunit A-7
F01.PB5638	186.62	57.74	39.17	30.24	21.08	Gata Transcription Factor 5-Like Isoform X1
F01.PB5671	302.52	244.13	163.43	112.43	87.47	Transcription Factor Myb1R1
F01.PB5683	55.66	54.86	56.15	20.46	39.66	Putative Myb-Related Protein 23
F01.PB5689	101.54	83.49	99.17	23.25	15.18	Nac Domain-Containing Protein 2
F01.PB5702	34.20	23.86	10.24	7.03	12.21	Putative R2R3 Myb Protein 5
F01.PB57075	3.73	5.39	8.58	10.46	17.19	Atp-Dependent Zinc Metalloprotease Ftsh 2
F01.PB5808	194.20	245.74	14.97	82.31	143.61	Bzip Transcription Factor Bzip124
F01.PB5815	146.82	330.39	60.35	121.63	40.62	Bzip Transcription Factor Bzip124
F01.PB5974	0.00	0.00	0.00	0.00	19.69	Mads-Box Transcription Factor 18
F01.PB5984	10.48	10.67	27.31	16.86	26.91	Predicted: Transcription Factor Myb44

F01.PB6021	59.10	27.39	18.86	12.90	10.61	Auxin Response Factor
F01.PB6125	18.85	16.02	16.56	20.03	16.33	Zinc Finger Protein Zpr1 Homolog Isoformx1
F01.PB6309	36.38	28.91	10.70	8.09	12.38	Zinc Finger Protein Constans-Like 9
F01.PB6426	47.81	34.83	19.63	34.89	19.53	Predicted: Transcription Factor Tcp7
F01.PB6443	49.95	27.12	24.83	22.27	24.07	Zinc Finger Protein 830
F01.PB652	230.14	64.07	33.26	66.74	29.83	Lob Domain-Containing Protein 37
F01.PB6521	17.58	40.32	240.36	142.07	17.71	Atp-Dependent Zinc Metalloprotease Ftsh 2
F01.PB6572	51.75	37.48	34.58	40.83	27.28	Zinc Finger Ccch Domain-Containing Protein 11
F01.PB6578	0.05	1.40	0.00	0.52	16.38	Transcription Factor Myb86-Like
F01.PB6621	4.06	6.75	1.47	11.62	28.54	Gata Transcription Factor 5-Like
F01.PB6711	56.37	121.23	108.18	115.94	12.95	Myb Transcription Factor Myb62 Isoform X1
F01.PB6716	41.16	21.79	3.76	16.49	23.02	Zinc Finger Protein Nutcracker
F01.PB6777	29.38	18.34	28.15	19.07	25.62	Zinc Finger Protein

						Gis2-Like Isoform X1
F01.PB6853	38.97	31.46	34.00	21.49	26.16	Nac Domain-Containing Protein 78
F01.PB7074	7.53	16.28	26.70	10.60	64.95	Nuclear Transcription Factor Y Subunit A-1
F01.PB7319	110.43	23.58	28.82	11.64	11.04	Zinc Finger Ccch Domain-Containing Protein 49
F01.PB755	101.68	143.80	7.33	11.51	12.58	Auxin-Responsive Protein Iaa27
F01.PB7641	20.32	51.17	82.64	16.09	24.92	Nuclear Transcription Factor Y Subunit C-3
F01.PB7772	19.26	13.73	9.70	18.40	14.45	Transcription Factor Bhlh49-Like Isoform X2
F01.PB7782	189.33	35.33	16.28	158.78	29.30	Ring Finger And Chy Zinc Finger Domain-Containing Protein 1-Like Isoform X1
F01.PB7839	1.72	7.79	0.00	16.93	37.36	Agamous-Like Mads-Box Protein Agl11
F01.PB7863	61.72	68.07	19.48	33.84	18.93	Myb Family Transcription Factor Apl-Like Isoform X4

F01.PB798	125.70	116.16	84.71	118.10	40.89	Zinc Finger A20 And An1 Domain-Containing Stress-Associated Protein 1
F01.PB80	558.98	402.61	230.82	259.68	56.27	Zinc Finger A20 And An1 Domain-Containing Stress-Associated Protein 5
F01.PB8040	73.74	86.54	81.15	252.89	16.57	Nac Domain-Containing Protein 72
F01.PB8196	35.88	33.21	17.76	22.03	10.36	Squamosa Promoter-Binding-Like Protein 12
F01.PB8218	58.25	12.28	5.82	3.18	10.91	Gata Transcription Factor 24
F01.PB8265	10.10	48.33	17.75	7.91	13.97	Transcription Factor Myb1R1
F01.PB8316	16.19	7.81	31.12	7.79	34.35	Auxin Response Factor
F01.PB8332	10.96	32.66	5.08	13.44	16.76	Auxin-Responsive Protein Iaa9
F01.PB835	20.32	24.55	21.84	49.40	45.86	Nuclear Transcription Factor Y Subunit B-8, Partial
F01.PB8399	145.89	109.46	23.57	14.34	17.79	Transcription Factor Bhlh145

						Predicted: Zinc Finger
F01.PB8473	33.18	28.96	32.57	15.96	30.42	Ccch Domain-Containing Protein 20
F01.PB8557	0.00	0.00	0.10	86.15	21.45	Mads-Box Transcription Factor 12
F01.PB8670	22.20	19.59	9.82	15.52	12.61	Zinc-Metallopeptidase, Peroxisomal-Like Isoform
F01.PB8684	75.02	69.06	56.73	53.45	28.70	Glabra2 Expression Modulator
F01.PB8701	18.40	26.53	23.78	15.48	26.88	Trihelix Transcription Factor Gt-1
F01.PB8823	1.49	3.66	20.17	7.28	56.04	Zinc Finger Protein Magpie-Like Isoform X1
F01.PB8965	44.98	30.78	15.15	12.99	18.75	Gamyb-Binding Protein Family Protein
F01.PB8983	84.97	56.49	25.09	50.05	23.55	Transcription Factor Tcp7-Like
F01.PB9224	0.04	0.19	2.47	85.70	19.73	K-Box Region And Mads-Box Transcription Factor Family Protein Isoform 1
F01.PB9253	43.93	34.75	11.62	128.96	58.61	Ring Finger And Chy Zinc Finger Domain-Containing Protein 1

F01.PB9260	27.02	27.86	30.36	96.20	35.87	Bzip Transcription Factor Bzip68
F01.PB9276	12.64	13.55	6.42	14.04	15.98	Zinc Finger Protein-Like 1
						Zinc Finger Ccch
F01.PB9305	29.43	23.54	16.16	13.34	10.11	Domain-Containing Protein 69
F01.PB9343	128.62	50.04	1.31	9.39	12.87	Auxin-Responsive Protein Iaa13, Putative
F01.PB9552	60.58	43.75	33.98	29.75	20.04	Zinc Finger, C3Hc4 Type (Ring Finger) Protein
F01.PB9572	76.52	46.14	30.16	23.22	27.91	Transcription Factor Bhlh148-Like
F01.PB9609	44.31	38.98	32.68	27.53	19.19	Zinc Finger Protein Gis2-Like Isoform X1
F01.PB9796	69.67	46.72	94.91	13.74	35.17	Nuclear Transcription Factor Y Subunit A-3-Like Isoform X1

Table S3. Putative genes involved in anthraquinone biosynthesis identified in the root, stem, leaf, flower and seed of *C. obtusifolia*.

Pathway	Gene	Symbol	Number in root	Number in stem	Number in leaf	Number in flower	Number in seed
Mevalonate pathway	Acetyl-CoA C-acetyltransferase	ACAT	20	19	23	23	19
	Hydroxymethylglutar yl-CoA synthase	HMGS	3	3	3	3	3
	Hydroxymethylglutar yl-CoA reductase	HMGR	9	10	9	13	10
	Mevalonate kinase	MK	3	3	3	3	3
	Phosphomevalonate kinase	PMK	3	3	3	3	3
	Diphosphomevalonate decarboxylase	MPD	2	2	2	2	2
	1-deoxy-D-xylulose-5 -phosphate synthase	DXS	9	9	9	9	9
	1-deoxy-D-xylulose-5 -phosphate reductoisomerase	DXR	7	11	18	14	6
MEP pathway	2-C-methyl-D-erythrit ol 4-phosphate cytidyltransferase	ISPD	2	3	2	2	3
	4-diphosphocytidyl-2- C-methyl-D-erythritol kinase	CDPMEK	4	4	4	4	3
	2-C-methyl-D-erythrit ol 2, 4-cyclodiphosphate Synthase	ISPF	1	1	1	1	1
	(E)-4-hydroxy-3-me thylbut-2-enyl-diphos	HDS	3	3	3	3	3

	phase synthase						
	4-hydroxy-3-methylbut-2-enyl-diphosphate reductase	HDR	11	10	10	9	10
	Isopentenyl-diphosphate delta-isomerase	IPP	11	10	9	12	11
	3-deoxy-7-phosphoheptulonate synthase	DAHPS	8	8	8	8	8
	3-dehydroquinate synthase	DHQS	4	4	4	4	4
Shikimate pathway	3-dehydroquinate dehydratase/shikimate dehydrogenase	SDH/DH QD	1	1	1	2	1
	Shikimate kinase	SMK	6	6	7	6	6
	3-phosphoshikimate 1-carboxyvinyltransferase	EPSP synthase	7	7	7	7	7
	Chorismate synthase	CS	8	8	6	6	7
	Menaquinone-specific isochorismate synthase	ICS	2	2	2	2	2
	Isochorismate synthase	ICS					
Menaquinone pathway	2-succiny-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase/O-succinylbenzoate synthase	menC/PH YLLO	3	3	2	2	3
	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase	MenH					
	2-succinyl-5-enolpyruvate synthase	menD					

	vyl-6-hydroxy-3-cycl ohexene-1-carboxylat e synthase						
	Acyl-activating enzyme	menE	40	40	40	41	37
	Naphthoate synthase	menB	2	2	2	2	2
Polyketide pathway	Polyketide synthaseIII	PSKIII	9	10	10	10	9
	Polyketide cyclase/dehydratase	PKC	3	3	3	3	3
Glycosylation	UDP-Glucosyl transferase	UDPG	90	96	96	99	82
	Cytochrome p450	CYP	112	126	120	127	109
CYPs	Cytochrome p450 Monooxygenase	—	4	5	5	6	5
	NADPH-cytochrome p450 reductase	—	19	20	19	19	21

Table S4. List of CYPs of different plant species used for phylogenetic analysis

CYP name	Species	Accesssion id	Length
NADPH-cytochrome p450 reductase	Arachis duranensis	XP_015934960.1	692
CYP714A1	Arachis duranensis	XP_015946736.1	533
CYP71A1	Arachis duranensis	XP_015954538.1	522
CYP716B1	Arachis duranensis	XP_015956144.1	473
CYP85A	Arachis duranensis	XP_015962617.1	468
CYP71A26	Arachis duranensis	XP_015964672.1	505
CYP83B1	Arachis duranensis	XP_015969861.1	514
CYP98A2	Arachis duranensis	XP_015970644.1	508
NADPH-cytochrome p450 reductase	Arachis ipaensis	XP_016163722.1	692
CYP71A1	Arachis ipaensis	XP_016187643.1	527

CYP71A26	Arachis ipaensis	XP_016189615.1	505
CYP85A	Cajanus cajan	KYP49608.1	466
CYP716B2	Cajanus cajan	KYP76833.1	468
NADPH-cytochrome p450 reductase	Cajanus cajan	XP_020211814.1	691
CYP71A1	Cajanus cajan	XP_020216626.1	522
CYP714A1	Cajanus cajan	XP_020229038.1	532
CYP97B2	Cajanus cajan	XP_020230175.1	580
CYP98A2	Cicer arietinum	XP_004493325.1	527
CYP734A1	Cicer arietinum	XP_004495852.1	518
CYP71A1	Cicer arietinum	XP_004499226.1	513
CYP714A1	Cicer arietinum	XP_004502797.1	530
CYP71A26	Cicer arietinum	XP_004505028.1	500
CYP71A26	Cicer arietinum	XP_004515856.1	504
CYP97B1	Cicer arietinum	XP_012574398.1	580
CYP51	Corchorus olitorius	OMO51606.1	486
CYP709B2	Durio zibethinus	XP_022769769.1	523
CYP89H3	Glycine max	ABC68408.1	373
CYP51G1	Glycine max	ABC68412.1	475
CYP97B2	Glycine max	NP_001235534.2	576
CYP85A	Glycine max	NP_001241912.2	464
NADPH-cytochrome p450 reductase	Glycine max	XP_003526551.1	691
CYP714A1	Glycine max	XP_003526785.1	532
CYP71A1	Glycine max	XP_003526991.1	519
CYP85A	Glycine max	XP_003544008.2	496
CYP71A1	Glycine max	XP_003549825.1	514
CYP85A	Glycine max	XP_003554965.1	465
CYP89A2	Glycine max	XP_003556183.1	500
CYP89A2	Glycine max	XP_003556196.1	512
CYP714A1	Glycine max	XP_014630399.1	532
CYP734A1	Glycine soja	KHN02133.1	532
CYP89A2	Glycine soja	KHN08060.1	319
CYP85A	Glycine soja	KHN08349.1	464
CYP71A1	Glycine soja	KHN10452.1	437

NADPH-cytochrome p450 reductase	Glycine soja	KHN39959.1	689
CYP89A2	Glycine soja	KHN42995.1	364
CYP716B2	Glycine soja	KHN48077.1	425
CYP716B1	Hevea brasiliensis	XP_021636104.1	492
CYP89A2	Hevea brasiliensis	XP_021673274.1	516
CYP709B2	Hevea brasiliensis	XP_021676114.1	522
CYP98A2	Juglans regia	XP_018843655.1	564
CYP714A1	Lupinus angustifolius	XP_019417080.1	537
CYP85A	Lupinus angustifolius	XP_019442760.1	465
CYP71A1	Lupinus angustifolius	XP_019457306.1	514
CYP71A26	Lupinus angustifolius	XP_019463598.1	505
CYP51	Macleaya cordata	OVA07832.1	461
CYP51	Macleaya cordata	OVA17354.1	488
CYP709B2	Manihot esculenta	XP_021620148.1	523
NADPH-cytochrome p450 reductase	Medicago truncatula	XP_003602898.1	692
CYP98A37	Medicago truncatula	ABC59086.1	509
CYP83B1	Medicago truncatula	XP_003589391.2	515
CYP71B37	Medicago truncatula	XP_003589394.2	514
CYP714A1	Medicago truncatula	XP_003602453.1	524
CYP97B1	Medicago truncatula	XP_003610974.1	574
CYP71A26	Medicago truncatula	XP_013457072.1	522
CYP71A3	Medicago truncatula	XP_013457073.1	521
CYP71A23	Medicago truncatula	XP_013457721.1	495
CYP71A26	Medicago truncatula	XP_013457724.1	500
CYP709B2	Medicago truncatula	XP_013469137.1	518
CYP51	Pisum sativum	BAR45707.1	489
CYP89A2	Populus euphratica	XP_011015670.1	512
CYP89A2	Populus trichocarpa	XP_002306325.2	507
CYP98A2	Populus trichocarpa	XP_002308860.2	508
CYP709B2	Quercus suber	XP_023876027.1	518
CYP71A1	Quercus suber	XP_023886322.1	515
CYP714A1	Theobroma cacao	XP_007011424.1	523
CYP85A	Theobroma cacao	XP_007032850.2	465

CYP709B2	Theobroma cacao	XP_017969771.1	522
CYP71A26	Trifolium pratense	PNX77318.1	439
CYP734A6	Trifolium pratense	PNX93612.1	436
CYP71A26	Trifolium pratense	PNX96961.1	521
CYP71A26	Trifolium pratense	PNY10523.1	434
CYP97B2	Vigna angularis	XP_017407829.1	576
CYP71A1	Vigna angularis	XP_017420230.1	528
NADPH-cytochrome p450 reductase	Vigna angularis	XP_017422031.1	691
NADPH-cytochrome p450 reductase	Vigna radiata	NP_001304239.1	690

Table S5. The expression pattern of differentially spliced isoforms of transcriptional factors involved in seed formation and development.

Gene ID	Expression in (FPKM)	nr_annotation
F01.PB1652	24.23	Zinc finger protein 207
F01.PB2367	7.52	C2H2-type zinc finger protein
F01.PB1740	37.08	RNA-binding family protein with retrovirus zinc
F01.PB1355	2.99	serine/arginine-rich splicing factor RS2Z33 isoform
F01.PB1978	12.25	zinc finger CCCH domain-containing protein 13-like
F01.PB4108	0.53	zinc finger CCCH domain-containing protein 13-like
F01.PB2425	24.87	Zinc finger C-x8-C-x5-C-x3-H type family protein
F01.PB1403	5.03	Zinc finger C-x8-C-x5-C-x3-H type family protein
F01.PB2593	13.82	RING finger and CHY zinc finger domain-containing
F01.PB2608	5.67	RING finger and CHY zinc finger domain-containing
F01.PB3148	22.94	RING finger and CHY zinc finger domain-containing
F01.PB4436	0.20	RING finger and CHY zinc finger domain-containing
F01.PB5109	11.26	zinc finger CCCH domain-containing protein 64-like
F01.PB2932	0.80	zinc finger CCCH domain-containing protein 64-like
F01.PB3615	13.82	squamosa promoter-binding-like protein 12-like
F01.PB5467	0.00	squamosa promoter-binding-like protein 12-like
F01.PB4935	37.32	transcription factor bHLH144-like

Supplementary Data.

The nucleotide sequences of DXSand DXR in the transcriptome of *C. obtusifolia*

>F01.PB17587(DXR)

ATACACATTTAGTTTCTGATTCTTTTCCCCTCTTCCAATTGAAGTGGGTTGAGTCTATTGTTTCTTGCGAT
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>F01.PB29801(DXS)

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CGTGGAGGAAGGATCGATCGGAGGATTGGGTCTCATGTTGCTCAATTCATGGCCCTTGATGGTCTTCTTGA
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Amino acid sequence of CYPs used to phylogenetic analysis from *C. obtusifolia*

>F01.PB16738_Co-CYP450-1

LYNKGNRVAQELDQFFDEVIEQHINRRVKQDLCLVNDDDDGEEQSDDFVDVLLRIQKR
NITGFPVDITTIKALILDMFAAGTDTTSTVVEWAMTELLRHPRVMKKLQDDMRKVVGSR
THITEEDLVEMHYLKAVLKETLRTHSPVPLLVPRESMQDMKLNQYDIKAGTQVIVNAWAI
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HQFDWALPAGKELDMAETAGLTIHRKFPLIAIPSPRKA*

>F01.PB25462_Co-CYP450-2

MATAAISHLSTFPNANSHPKHNRGFSPLSSCVSHFPISIHFRSSMPRGCPVRCQSIDTNERK
SDRNLLDNASNLLTQLLSGGSIGSMPTAEGAVTDLFDRPLFFSLYDWFLEHGSVYKLAFGP
KAFVVVSDPIVARHILRENAFCYDKGVLADILEPIMGKGLIPADLDTWKQRRRVIA PGFHT
SYLEAMIKIFTDCSERTILKFNKLLEGESPNDQKSIELDLEAEFSSLALDIIGLGVFN YDFGS
VTKESPVIAVYGTLF EA EHRSTFYIPYWKIPLARWIVPRQRKFQSDLKIIN SCLDGLIRNA
KESRQETDVEKLQQRDYLNLKDASLLRFLVDMRGADVDDRQLRDDLMTMLIAGHETTA
AVLTWAVFLLAQNPTKMKKAQAEVDSVLGEGRP TFESLKKLQYIRLIVIEALRLYPQPPLL
IRRALKSDVLPGGYKGD KDGYAIPAGTDVFISVYNLHRSPYFWDSPNDFEPERFMVQRKN
EDIEGWAGFDPSRSPGALYPNEVISDFAFLPFGGGPRKCVGDQFALMESTVALALLLQKFD
VQLKGTPQSVELVTGATIHTKNGLWCKLSKRSNLHH*

>F01.PB15276_Co-CYP450-3

EERGKKFRKLLVELGEVIGKFVVGDYIPWLQWLNQISGFYNRGNRVAQELDQFLNEVIEE
HMSTNGEGQSDDFVDVLLRIQKTNITGFPIDTTIHKALILNMFTAGTDTTSTLLEWEMTEL
LRHPRVMKKLQDEMVRKVVGSRTHITEEDLVEMHYLKAVLKETLRTHPPVPLLVPRESMQ
DINLNGYDIKAGTHVIVNAWAIAHDASIWDHPPEFKPERFLNSSIDFKGQDFELIPFGAGR
RGCPGTAFAMAVNEMVVANLVHYFDWALPAGKELDMAETAGVIIIHRKFPLTAIPSPRKA*

>F01.PB19520_Co-CYP450-4

AHTAFGSSFAQGKEVFIAQRQLQQHCVASASDIFIPGTQYLPTRSNLKTWQLDWKIKKSL
KQIMESRLNSQSSSYGDDLLGVMLEAAETEKLNNGPKFRMEEIIIECKTFFAGHETTSN
LLTWTVFLLSIHKEWQERLRQEVLNNGMEIPDAEVLKSKLMVMNMLLEALRLYCPAIQ
LIRETSEDMKLGNLRIKHTCVTIPVATIHRKREYWGEDANEFKPERFMNGVSKAASHPN
AMIAFSIGPRACIGQNFAMLEAKTVMVLILQRFWSLSPHYKHAPANNTLQPPQFGLPVIL
KPLHS*

>F01.PB13542_Co-CYP450-5

MEVVIEFVKLVSVVGVVGLSWLVYGYSSVWVKSERVRRKLRMQGIRGPSFLYGNLP
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VNEAELVREMNCITLNLGKPSYVTNKLAPLLGNGILRANGLSWAHQRKLVAAEFYMDK
VKGMVGLMIESAQPLLTKWEQLIEAHEGGSSDNGTEVKVDADLRGFSADVISRVCFGHS
YSKGKEVFSKLRSIQKAMSTQGGFQLFGVSGIRGMLHYLWSTKKQNQISSLEKEVESIHW
ELVEERRRKQSEYSSAAAEKDLMQLLLEAAESDQSSDHEGKEFSKRSFIVDNCKNIYFAG
HETTAVAASWCLMLLALHPQWQTSIRNEVAQLCPNGIPDADSLPHLKTVMVIQETLRLY
PPAAFVSREAYEDVQIGNIKVPKGVCLWTLIPTLHRDPEIWGADANEFKPERFSEGVSKAC
KFPQAYVPFGLGTRLCLGKNFAMVQLKVVLAIIISNFSLSLSPSYTHSPAYRMIVEPGHGV
YILIRKI*

>F01.PB15419_Co-CYP450-6

IKFEVSEAEGGRIHFKKNDNFSGNFETSRNLLLLVITNTCTSNLTHLPFQCHFQMVVFQFK
NHQQLTSFSSKIPVIGNLHQLGTCPHRALQSLAQKYGPMMLLHFGKVPVLVSSADGAC

DVMKTHDLVFSNRPRRRVADILLYASKDIASAQYGEYWRQIRSIGVLHLLSNKRVQSLRG
VREEETKIMMESLEHSASRNLEVNLSSEFSKVTNDIICRVALGRKYSGGERGKKFQKLLV
DFGEVLGTFDVGDIYIPWLEWLSNMSGLYNKGNRVAQELDQFFDEVIEQHINRRVKQDLD
CLVNDDDDGEEQSDDFVDVLLRIQKRNTGFPVDITTIKALILDMFAAGTDTTSTVVEWA
MTELLRHPRVMKKLQDDMRKVVGSRTHITEEDLVEMHYLKAVLKETLRTHSPVPLLVR
ESMQDMKLNKYDIKAGTQVIVNAWAIAHDASIWDHPPEFKPERFLNNSIDFKGQDFELIP
FGAGRRGCPGTAFAMAVNEVVVANLVHQFDWALPAGKELDMAETAGLTIHRKFPLIAIPS
PRKA*

>F01.PB11581_Co-CYP450-7

MGVLMAMHIGVLFLLCFCSALLRWNQLRFSQKGLPPGTMGWPIFGETTEFLKQGSPFMKN
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THKYMARGALLSIISPSMMKHLLPKIDHFMRRHLSNWDNQVINIQHKTQMAFLSSLKQI
AGIESTSPISHNFMSEFFKLVLGTISLPIDLPGANYYRRGVQARKNIVSIVRDLVEERRRVS
GE
NHQDMLGFLMGKDDDDDDGGGRRYKLNDEEIIDLIITIIYSGYETVSTTSMMAVKYLHDHP
KVLQQLRKEHMAIRERKKPEDPIDCEDLKSMMKFTRAVIFETSRLATIVNGVLRKTTQDME
LNGYLIPKGWRIYVYTREINYDPFLYPDPLTFNPWRWLDKSIESQSYFLIFGGGTRQCPGK
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>F01.PB20786_CO-CYP450-8

ALLVILYSSIILLLLLLIIHTRKRRGTSVPPGPPGLPFIGNFHQLHNSAPHHLILCQLSKHYGPL
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MKKLCVLHLFNPRRIHSFCPIREDEVLRMITKISQSHGLINLSETSMSFTSSLICRIAFGKRY
EEDQGSRFHIGLLTEAQALLAEFYLSYIPWLGWVDRLTGKLWRLDQIFNKLDMPYQQVI
NDHLDQSNQQQRDIIDIFLQIIHSHNSTPFHLTMDHIKALLMNIFIAGTDTSAATIVWAMTS
LIKNPGLVMKKAQDEIRSVYGEKDFIREEDIQRLPYLKAIVKETLRLFPSPLLVPRESMQK
CNIEGYEIQPKTLVFNNAWAIGRDPETWEEAEQFNPDRFFKCEIDFKGQDFELIPFGAGRR
MCPGMQMGVVTVELALVNLLHSFDWDLPGIHKHDIDTQIKPGITTHKKIDLCLVAHSHT
KTR*

>F01.PB47552_CO-CYP450-9

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VSFTRYGEEWRQKRKICVLQLLSPKRVQSFQFIREEEVAELVHNIRQKCGGGGSVINLTQM
TIEATNNIVSRCVLGRKYDAPSGSGSFGDVARKVLSQFSDFSVGDFFPSLGWIDFLTGLISK
LKGTLGELDAVFDDVIAQHKKKSNIIEDEERKDFVDILLEIQKNGMLDFELTNDHIKGV
MDLFLGGSDTSSATIEWAMAELMRSPTEMRKVQDEVRRVVGHKSKVEEADVKQMKYL
GFVVKEALRLHPPNLIIPREARSSVKLGGYDIPSKATVFINVWAIQRDPQVWERAEFIPER
FENSEIDFKGQDFEFIPFGSGRKGCPGMTFGVTMVEYVLANVLYWFDWKLPPTAQDVDM
NEGYGLTVTKKEPLLLQPSIFSFSFSP*

>F01.PB20158_CO-CYP450-10

MALFLIPIAILALLCFNLYHRLRFRLPPGPRWPVIVGNLYDIKPVRFRCAEWAQSYGPIIS
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VRKVCTLELFSPKRLEALRPIREDEVTAMVESVFRDSTNPENEGKSILVKKYLGAVAFNNI
TRLAFGKRFVNEEGVMDEQGVFEKAIVSNGCLKLGASLAMA EHIPWLRWMFPLEEEAFA
KHGARRDRLTRAIMEEHTQARNLSGGAKQHFVDALLTLQDKYDLSEDTHIGLLWDMITA
GMDTTAISTEWAMAELIKNPRVQQKAQEEMDRVIGFERVMTETDFSSLPYLQCVAKEALR
LHPPTPLMLPHRANANVKVGGYDIPKGSNVHVNVAIARDPAVWKDPLEFRPERFLEED
VDMKGHDFRLLPFGAGRRVCPGAQLGINLVTSMLGHLLHHFCWAPPEGMKPEEIDMSEN
PGLVTYMRTPQLQAVATPRLPSQLYKRVPADM*

>F01.PB15287_CO-CYP450-11

EEAFPALLALLFLLLSLHFITKIIVKTTRKHQNLPPGSLGWPIVGETLEFMRCGGEGNHERF
IRERMEKYDWRVFKTSM LG EAMIVFCGPAGNKLLFSNENKNVQVWWPSSVRKLLRSS
VTKVGSEAKTMKRLTTFLNPEALKNYLSKMDAIAHTHIH THWQGKEQVLVYPTVKKY
TFELACSLFASIEDSIHISKLSSQFDEFLKGVISFPVNFPGSRFHCAMRAANAI RQELKLIKK
RRVDLEDKSASPTQDLLSHLLLTSDTTGRFLTEMEIIDNILLLLFAGHDTSRSVISSIFKYL
QFPQVYQQVCKNN*

>F01.PB2613_Co-CYP450-12

RKEQDDVLIPLIRARKKAREERLSKSEEDRCKVVENDVVVPYVDTLFDLELPEEKRLLEE
SELVSVTSEFINAGTDTTATALQWIMANLVKYPEIQERVFEIKEVMGNKIGEDNEEVKEE
DLNKLGYLKAVILEGLRRHPPGHFLLPHAVSEDVVLNDYLVPKNGTINVMVAEMGWDPK
VWENPMEFKPERFLRSEGEEAFDITGSKEIKMMPFGAGRRICPGYNLAMLHLEYFVANLV
WNFEWKAGNGDVDLSEKQEFTVVMANPLQVQLTRRR*

>F01.PB9468_Co-CYP450-13

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TYPHRTLHSLAQKYGPLMLLHFGKVPVLVVSSADAARDVTKTHDLVFSNRPRRRVADILT
YGSIDIAFSGYGEYWRQIRSIGVLHLLSNKKVQSIRGVREEETKILMENINHSASTNLQVN
LSEEFFRLANDIICRVALGNKYSGEERGKKFRKLLVELGEVIGKFVVGDYIPWLQWLNQIS
GFYNRGNRVAQELDQFLNEVIEEHMSTNGEGQSDDFVDVLLRIQKTNITGFPIDTTIIKALI
LNMFTAGTDTTSTLLEWEMTELLRHPRVMKKLQDEMRRKVVGSRTHITEEDLVEMHYLK
AVLKETLRTHPPVPLLVPRESMQDINLNGYDIKAGTHVIVNAWAIAHDASIWDHPPEEFKPE
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>F01.PB11533_Co-CYP450-14

GEEWRQKRKICVLELLSLKRVRSFQFIREEEASDLVTKIRESCENNIINGSPALINLTPMLIA
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LKATSVELDTFFDEIIAQHKMAKTNDDESEKKDFVDILLQLQDDDMLEFKLTHQDLKGM
ADMFGVGGDTTSTALEWTFAELLKNPIAMKKVQEEVRRVVGHKSKIDENDVRQMKYLE
CVVKESLRRLHPPLLLVPRETRSIKLG EYDIPPQTSVFLNAWAIQRDPPELWEKPEEFIPERF
ENSEVDFKGQDFQLVPFGFGRRGCPGMSFGVASVEYFLAVLLFWFDWKLPSGTTTTSSQD
IDMSEIYGLTVNKKVPILVEPIPYSGPQL*

>F01.PB22595_Co-Monooxygenase-1

LTASRCLLGREVRDKLFDDVSALFHDLNGLPISVLPYLPPIAHRRRDQARKKLSEIFA
SIITSRKSTGKSENDMLQC FIDSKYKDGRPTTESEVTGLLIAALFAGQHTSSITSTWTGAYL
LCNKQYLSAVMEEQKELMGKHGDRVDHDILAEMDVLYRCIKEALRLHPPLIMLLRSSHS

DFSVKTREGIEYDIPKGHIVATSLLLRTAYLIFSRILIVMILIGLP*

>F01.PB4860 _Co-Monooxygenase-2

MFCLLVFMCFGERLDEKQIREIEFVQRLLLLNFNKYSMNLNIMPRITRILFRKLWEELLQVR
KEQDDVLIPLIRARKKAREERLSKSEEDRCKVVENDVVVPYVDTLFDLELPEEKRKLEES
ELVSVTSEFINAGTDTTATALQWIMANLVKYPEIQERVFEEIKEVMGNKIGEDNEEVKEED
LNKLGYLKAVILEGLRRHPPGHFLLPHAVSEDVVLNDYLPKNGTINVMVAEMGWDPKV
WENPMEFKPERFLRSEGEEAFDITGSKEIKMMPFGAGRRICPGYNLAMLHLEYFVANLV
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>F01.PB24506 _Co-reductase -1

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DYAADDEYEEKKKETLAFFMLATYGDGEPTDNAARFYKWFTEGKEEGASWLQQLTY
GVFGLGNRQYEHFNKIGKVIDQKLSAQKRLVPVGLGDDDDQSIEDDFSARKESLWPEL
DQLLRDEDDMNTVSTPYTAAIAEYRLVIHDPITITSCYDRNLSMTNGNALFDIHHPCRVDV
AVQRELHKPESDRSCIHFEDISGTGITYETGDHVGVAENCDVVEEAGKLLGQNLDLL
FSLHTDNEDGASLGGSLPPFPGPCTLRAALARYADLLNPPRKAALVALAAHASEPSESER
LKFLTSPQGKDEYSKWVVGSRSLLEVMAEFPSAKPPLGVFFAAVAPRLQPRYYSSSSPK
FAPQRVHVTCALVYGPTPTGRIHKGVCSTWMKNAVPSKSRDCSWAPIFIRPSNFKLPADH
LTPIMVGPGTGLAPFRGFLQERLALKEEGVELGPALLFFGCRNRQMDFIYEDELTFNVEQ
SALSELVVAFSREGPEKEYVQHKMMDKSEYLVSLISQGGYLYVCGDAKGMARDVHRTL
HTIVQQQENVDSKAEIVKKLQMDGRYL RDVW*

