

S8 Table. Genes selected for q-PCR validation

Gene ID	Functional description	Swissprot ID	Bitscore	E-value	RPKM		
					Con	Wat6	Wat24
comp37254	Auxin response factor 2, ARF2	sp Q94JM3	952	0	89.852	37.954	50.760
comp35374	Auxin response factor 18, ARF18	sp Q653H7	816	0	26.952	16.698	14.999
comp35831	Auxin response factor 1, ARF1	sp Q8L7G0	885	0	29.128	15.349	16.768
comp29470	Auxin response factor 3, ARF3	sp O23661	450	1E-142	32.138	10.622	12.376
comp13756	Auxin response factor 6, ARF6	sp Q9ZTX8	376	2E-114	40.028	15.658	13.549
comp36957	Auxin response factor 19, ARF19	sp Q8RYC8	734	0	57.040	24.402	29.694
comp24483	Auxin response factor 8, ARF8	sp Q9FGV1	278	3E-82	13.053	8.386	8.696
comp23260	Auxin transporter-like protein 4	sp Q8L884	851	0	159.520	73.881	49.185
comp34322	LOB domain-containing protein 41, LBD41	sp Q9M886	185	3E-53	55.243	121.677	134.119
comp39013	LOB domain-containing protein 21, LBD21	sp Q9SRL8	188	1E-54	94.987	84.197	46.743
comp40540	LOB domain-containing protein 29, LBD29	sp Q9M2J7	186	3E-54	3.714	26.745	12.554
comp38129	Sodium/hydrogen exchanger 2, NHX2	sp Q56XP4	333	5E-103	381.908	429.401	472.443
comp40252	NAC domain-containing protein 72, NAC72	sp Q93VY3	350	2E-114	73.946	21.275	61.914
comp44893	NAC domain-containing protein ,NAC1	sp Q84TE6	339	5E-112	24.715	17.499	19.606
comp56348	NAC transcription factor , NAC2	sp Q8GY42	303	3E-97	7.724	1.993	6.702
comp34452	NAC transcription factor NAM-B2, NAMB2	sp A0SPJ6	188	9E-53	105.389	35.786	100.297
comp32636	Auxin-responsive protein IAA9, IAA9	sp Q38827	404	8E-132	167.645	180.603	152.081
comp13386	Auxin-responsive protein IAA26, IAA26	sp Q8LAL2	227	9E-67	95.846	129.343	104.800
comp32189	Auxin-responsive protein IAA14, IAA14	sp Q38832	337	7E-111	630.691	551.345	220.222
comp13709	Auxin-responsive protein IAA8, IAA8	sp Q38826	207	1E-58	112.586	79.588	82.916
comp38087	Alcohol dehydrogenase 1, ADH1	sp P13603	618	0	7170.197	7091.752	3678.503
comp13399	Alcohol dehydrogenase 1, ADH1	sp P13603	307	5E-101	52.076	202.286	151.123
comp33063	Histidine kinase 1, AHK1	sp Q9SXL4	847	0	28.731	1.089	5.825
comp33358	Histidine kinase 2, AHK2	sp Q9C5U2	1275	0	20.795	12.318	11.801
comp40153	Histidine kinase 3, AHK3	sp Q9C5U1	1351	0	49.501	35.556	34.619
comp38180	Dehydration-responsive protein RD22, RD22	sp Q08298	310	2E-99	1249.984	356.157	738.560
comp34639	Auxin-induced protein 22E, AUX22E	sp O24543	379	8E-129	52.651	50.996	26.642
comp31234	Auxin-induced protein 22B ,AUX22B	sp P32294	279	3E-88	58.082	58.968	37.863
comp39198	Auxin-induced protein 22C ,AUX22C	sp O24541	268	5E-89	6.366	43.768	4.778
comp47043	Auxin-induced protein 15A, AUX15A	sp P33081	85.9	8E-20	1.261	39.716	2.638
comp22610	Cationic peroxidase 1, PER1	sp P22195	324	2E-107	0.193	139.508	372.845
comp21159	Auxin efflux carrier component 1, PIN1	sp Q9C6B8	464	2E-156	0.317	15.078	10.054
comp39799	Protein LHY ,LHY	sp Q6R0H1	122	2E-28	249.382	5.232	112.908
comp40489	Protein LHY, LHY	sp Q6R0H1	118	5E-28	223.864	4.108	94.885
comp31128	Cationic peroxidase 2 , PER2	sp P22196	485	1E-168	4.195	169.179	226.783
comp36822	Quinone oxidoreductase-like protein	sp Q9ZUC1	378	1E-124	7.085	40.927	4.776
comp39707	Peptidyl-prolyl cis-trans isomerase CYP20, CYP20	sp Q9ASS6	289	9E-94	58.173	62.356	58.411
comp38164	Eukaryotic translation initiation factor 5A, eIF5A	sp Q9AXJ4	313	4E-105	606.853	602.711	602.154
comp31451	Actin-related protein 4, ACTIN	sp Q84M92	712	0	18.727	19.322	20.725

Primers for q-PCR verification

comp39707 F: 5' TCCCCAAACAGCCGAAAA 3' 59.5
comp39707 R: 5' CCCCTTGAATCATGAAATCCTT 3' 59.9 107bp
comp38164 F: 5' ACCTTAGGCTTCCAACCGAT 3' 58.0
comp38164 R: 5' CTCCCATTGCAGACATAACAGA 3' 57.8 99bp
comp31451 F: 5' CGTGTTTCCTTCTGTTGTTGG 3' 58.1
comp31451 R: 5' CCTCTTCCCTTAGCCTTGTC 3' 57.7 142bp
comp37254 F: 5' ATCTCTCATCCGCAACTCCT 3' 60.3
comp37254 R: 5' TTCACCCCACTTCTCTTACCTC 3' 61.4 123bp
comp35374 F: 5' ACCTTGTCGCTGTCTTCGTGG 3' 62.4
comp35374 R: 5' GTGGCGGCTGTAAATTCCTC 3' 61.4 110bp
comp35831 F: 5' CCGCAGCCAACACAAAGAAAC 3' 63
comp35831 R: 5' GGTGATGGATAGAGGCCACGTC 3' 63.1 155bp
comp29470 F: 5' CTTGTTCTAAGTGCCCTTGTGG 3' 59.3
comp29470 R: 5' GCTTGCGTTTGCCTTTCCT 3' 61.3 175bp
comp13756 F: 5' AAGGTTGGCTGGGATGAAT 3' 58.7
comp13756 R: 5' TAAGGGGAAATGGAGATGGAT 3' 57.1 109bp
comp36957 F: 5' GCTGGCTATTCTGCTGTACCTG 3' 59.5
comp36957 R: 5' TCCCTTACTATTGGAGTCGGC 3' 58.7 96bp
comp24483 F: 5' TTGAGGGAAAGTTGGAAGACC 3' 58.3
comp24483 R: 5' CCTGAACCTAGAGCAAGGGATT 3' 59.5 196bp
comp23260 F: 5' ACTCCAACGCCTTCTCTCCTC 3' 63.1
comp23260 R: 5' ATCCAATCACCTTCTCCACA 3' 62.9 136bp
comp34322 F: 5' CAATGGATAAGTTGCCCTCAC 3' 57.2
comp34322 R: 5' ACCGCTGGTTGGAGATGG 3' 58.5 119bp
comp39013 F: 5' CAAGGCTCAGAGACCCCG 3' 58.4
comp39013 R: 5' TAGCAGCAGCGTGACATCG 3' 58.8 126bp
comp40540 F: 5' ATCTCAGGGAACAGGCAGGTC 3' 60.4
comp40540 R: 5' TCCGTCTGGAACCAACTCTGA 3' 60.2 121bp
comp38129 F: 5' CTGAACTGCGAACCAATGC 3' 57.1
comp38129 R: 5' TTCTTGCGTTTAGGAGGTGG 3' 58.0 136bp
comp40252 F: 5' AGACCCTCTTGCCAGTTG 3' 57.1
comp40252 R: 5' CCGAAAATCGCCTTGCTT 3' 58.7 180bp
comp44893 F: 5' AGGGTTCAGGTTCCATCAA 3' 59.0
comp44893 R: 5' GAATATCCCAAGGTTGCACT 3' 58.5 125bp
comp56348 F: 5' ATTCAACCTCAAAACCCCT 3' 57.6
comp56348 R: 5' CACAACACCAATCATCAAGC 3' 58.5 76bp
comp34452 F: 5' CCGACGAGGAATTGGTTGTG 3' 61.0
comp34452 R: 5' GAGCGGTTGCCGTTAGGATA 3' 60.4 181bp
comp32636 F: 5' GACTGTAGCGTCTGGTTCTTCG 3' 59.3
comp32636 R: 5' CCTCAACTCCGTAGCCTTCAA 3' 61.3 181bp
comp13386 F: 5' ACCCCACCAAGAGAAAGGAAG 3' 59.8
comp13386 R: 5' CCCACTAAGCGTGCAAATAAAA 3' 60.2 128bp
comp32189 F: 5' GTGGAAACACCAAGGGCTACTG 3' 61.2
comp32189 R: 5' CCAACCAACCACTTGAGCCT 3' 59.7 171bp

comp13709 F: 5' TGGGCATAGGAGAGGAGGA 3' 57.5
 comp13709 R: 5' GAGAAAGACGGAACGGAGC 3' 57.0 163bp
 comp38087 F: 5' AGAATCCGCTGTTTCCTCGT 3' 58.8
 comp38087 R: 5' ACAGTTGCTCTCTCCGATT 3' 58.1 162bp
 comp13399 F: 5' AGGCTGGTGAAGTGCCTTT 3' 57.9
 comp13399 R: 5' TATGCGAGGAAACAATGGAGT 3' 57.4 101bp
 comp33063 F: 5' ACAAGAGCACCCCAAAA 3' 60.2
 comp33063 R: 5' TGTGTAAATCTTCGTGAAATGCC 3' 59.7 194bp
 comp33358 F: 5' GCATCAGGGGGGGTGTGTTG 3' 62.9
 comp33358 R: 5' GCCTCAGCACGGCTTTTCAG 3' 63.2 125bp
 comp40153 F: 5' CAAATCGTCTGGGGGTTATCC 3' 60.8
 comp40153 R: 5' GAAGCAGTTTCTCCACCAATGAC 3' 60.5 144bp
 comp38180 F: 5' CCCGAGTCAGAGGAGGCTAA 3' 59.3
 comp38180 R: 5' CCCCCTTTCTTTGTCAACTTCT 3' 60.2 177bp
 comp34639 F: 5' AACTCTGATTCTTCGGACTCCACAAC 3' 64.3
 comp34639 R: 5' TCGCCCTGCTCCACCTTTTT 3' 64.3 143bp
 comp31234 F: 5' GCTCCAGGAACAGAAGAAA 3' 56.8
 comp31234 R: 5' ATAAATCCAGCACCCCTCAT 3' 56.1 199bp
 comp39198 F: 5' TGGCCTCCGGTTTGCTCCTA 3' 65.1
 comp39198 R: 5' CCGCATCCTTCAACGCTTCG 3' 66.1 193bp
 comp47043 F: 5' TCAAGTTTTGGCAAGAAGCA 3' 57.0
 comp47043 R: 5' GTTCTCCCAACATAGACAGC 3' 56.2 90bp
 comp22610 F: 5' CAAGAATCTCATCAACAAAAGGG 3' 62.1
 comp22610 R: 5' GGGCTAAGGTTTCCATTTTG 3' 60.5 156bp
 comp21159 F: 5' ATGCGGAGATTTACTCGCTTCA 3' 61.7
 comp21159 R: 5' CCCCCAAAATACTACTCTGC 3' 61.0 132bp
 comp39799 F: 5' AAAAGGAAGAGCCCAACAAAG 3' 58.2
 comp39799 R: 5' CTGGAGAATAGCGCCTGAAA 3' 58.2 145bp
 comp40489 F: 5' GGACCTGCTTCATCTGTACTG 3' 60.5
 comp40489 R: 5' TGTTTGTGGTCTCCGTCATCTAA 3' 59.8 164bp
 comp31128 F: 5' CCTAGACACGGGTAGTCAAAGAGC 3' 61.6
 comp31128 R: 5' TCATCGTTCCAGAGGGCTTG 3' 60.7 102bp