

4466	aquaporin.1	transport	255	contig	14	EG974583	GAACCTTCTCATTAGACATTTTCACAAACACTTCTCTACTCTCTCTCAATATGACTAAAGAC GTTGAAAGTAAACCGAGCGCGAGTTTCGGCCCAAGGACTACCAGACCCACTCCACTCCCTT CTTCGACCCGATGAACTAAACAAATGTTCTTCTACAGAGCTTAATCGCGAATTCATCGCA CACTCCTCTCTACATACTGTCTTAACAGTCAATCGGCTACAAAGCCAAACCGATCCAAAC AATCGAGCGTCCAGAGTCCGGCGGTTCGGAAATCTCGAAATCTCGGATCTTGGTGGAAAT GATCTCATCTGTTTACTGACCGCTGGAATCTCTGTGGACATATTAATCCGGCGGTGACAT TCGGACTGTCTTGGCGAGAAAAGTGTCTTTTATTAGAGCTGTGTGTATATGGTGGCTCAGTGT TTGGTGGCGAT	83756	3707.06275	15409.18844	10036.26557-1.4	-1.8	-0.3	0
3855	aquaporin.1	transport	255	contig	14	EG974581	AGACATTTTCACAAACACTTCTCTACTCTCTTCAATACCCTAAAGACGTTGAAAGTAAACCGA AGCCGGGAGTTTCGGCCCAAGGACTACACAGACCCACTCCACTCCCTCTTCGACCCCGATG AATCAACAAATGGTCTTCTACAGAGCTTAATCGCGAATTCATCGCCACACTCCTCTCTCCTC TACATACTGTAAACAGTCAATCGGCTACAAAGCCAAACCGATCCAAAC CGAGTCCGCGGTTCGGAATCTCGGAATCGTGGCTTTGGTGGAAATCTCTCAATCCTCGG TTACTGACCCGCTGGAATCTCTGGTGGACATATTAATCCGGCGGTGACATTCGGACTGTCTTG CGGAAAAGTGTCTTTTATTAGAGCTGTGTGTATATGGTCTCAGTGTGGTGGCGATTTG TGGAGTGGATTGGT	85354.25	3962.480663	16755.9418	10057.834 -1.5	-1.9	-0.4	0
2994	aquaporin.1	transport	255	contig	14	EG974579	AACCTTCTAATCAGACATTTTCACACTACTTCTCTACTCTCTCTCAATATGACTAAAGACG TTGAAAGTAAACCGAAGCGCGAGTTTCGGCCCAAGGACTACCAGACCCACTCCACTCCCTTC TTCGAGGGGATGAACTAAACAAATGGTCTTCTACAGAGCTTAATCGCGAATTCATCGCCAC ACTCTCTCTCTACATACTGTGTAAACAGTCAATCGGCTACAAAGCCAAACCGATCCAAAC AATCTCAATCTGTTTACTGACCGCTGGAATCTCTGTGGACATATTAATCCGGCGGTGACAT TGGAGTGGATTGGT	115640.125	7169.858095	27089.70226	14021.22097 -1	-1.5	-0.5	0
3818	aquaporin.1	transport	255	contig	14	EG974574	AATCTCAATCTGTTTACTGACCGCTGGAATCTCTGGTGGACATATA TCAATATGACTAAAGCTTGAAGTAAACCGAAGCGCGAGTTTCGGCCCAAGGACTACCAGAC CCACTCCACTCCCTTCTCGACCCGATGAACTAAACAAATGGTCTTCTACAGAGCTTAAT CGCGAATTCATCGCCACACTCTCTCTCTACATACTGTGTAAACAGTCAATCGGCTACAAAC GCCAAAACCGATCCAAACATCGAAGCGTTCGAGAGTGGCGGTGTCGGAAATCTCGGAATCGC TTGGCTTTTGGTGGAAATGATCTTCTCTGGTGTACTGACCGCTGGAAATCTCTGGTGGACATA TAAATCCGGCGGTGACATTCGGACTGTCTTGGCGAGAAAAGTGTCTTGTATTAGAGCTGTGTG TATATGGTGGCTCAGTGTGGTGGCGAATTTGGAGTTGGATTTGGTTAAAGCTTTTTCAGAGCTC GTATTAC	146861	90364.125	26693.80721	12048.20142-0.7	-1.4	-0.7	0
6361	aquaporin.1	transport	255	contig	14	EG974578	CTTCAACAACACTTCTCTACTCTCTCTCAATATGACTAAAGAGCTTGAAGTAAACCGAAGCGCG CGAATTTCCGGCAAGGACTACCAGACCCACTCCCTCTCTTTCGACCCCGATGAACTAA CCAAATGTCTTCTACAGAGCTCTAATCGCGAATTCATCGCCACTCTCTCTCTCTACATA ACTGTCTTAAAGTCAATCGGCTACAAAGCCAAACCGATCCAAACAGTCAATCGGCTACAGAGTG CGCGGTGTGGAAATCTCGGAATCGTGGCTTTGGTGGAAATCTCTCTGGTGTACT GCACCGTGGAAATCTCTGGTGGACATATTAATCGCGCGGTGACATTCGGACTGTCTTGGCGAGA AAAGTGTCTTTGATTAGAGCTGTGTGTATTATGGTGGCTCAGTGTGGTGGCGAATTTGGGAGT TGGATTGGTTAAAGCTTTTCAGAGCT	141913.4583	10318.52582	30717.20244	18923.52396-0.9	-1.4	-0.6	0
224	aquaporin.2	transport	257	singleton	1	EG974587	GCTTCTTAICTAICTAICTTCTTCT CATTAAGCGGAACCTACAGCTTAAAGCTTAAACTTAAACAAAGAACAGCTAAAGACTACCAT GACCAAAGACATAGAAGTAAACAGGACTCAACAGGATTAACAGACCCACTCCGGCGCAATCT TCGATACCGCGGAGCTCGGAAATGGTCTTCTACAGAGCTTAAATAGAGCTTAAATAGAGCTT CTTCTCTCTCTACACTGTTTAACTGTTTACAGGTTTACAAATCCCAATCGACCTTAAAGC CGCGCGGACAGTGGTGGAGTTGGTATCTCGGATCTTGGGCTTTGGAGGCAATTTGGG TCGTTCTGTTTACTGCACTGCCGAAATTCAGGGGCTCATATAAACCCCGCGGTGACATTTGGG TTGTTGGG	28821.20833	3845.356161	8134.780517	5127.403926-0.3	-1	-0.7	0.1
980	arabinogalactan protein.01	other cell wall proteins	70	contig	10	EG974748	GAAACCTTAACAACCCCTGACGGACACAAGCAATATCTCTTAATATTTTGGTCCGAAGTATG TTGGTTACATATCCACTGAGTTGTATGCAACAATTAATGCAACAATTAATGAGGATAATC AGTTGGCTATTTACAGGTGGATAAGGTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT AAAAGGGGTGGTGGCGACCGGCTCCATCAAGTATGTTGTTAAAGCTGATGAGTT TCCAACATCTGTTGATGCT GTCCCTTTGCTTGTAGTGGAAATGGATTTGAGCTTTGGAAATGCTGTGGTTTACGTGGTACTA CTTCTCTTTTGGTTG	181915	125321.4583	22294.74222	15557.96567-2.5	-3.1	-0.5	0
1045	arabinogalactan protein.01	other cell wall proteins	70	contig	10	EG974743	CATCTCACGGTCCGAGTAAATCTCAAAGAAAAGCAAGCAATATCTCTTAATATTTTGGTCCGAAGTATG TCTCCCTTCT ACCCAAACCTAGCCCAAGCAATATACATCAACAACACTCAACAGGCTCAATCCAAACCCCAAGCTCA CGCGGCTGGCAACCTTACAAAAGCCCGAGATCTCGGAAAGAGTGGGATTCAGTGTCT TCATCATCTCTCAAAAACATCAGTAAATATTAATCGAAAATCAACTCAATACATCA AACAGTTGACAATCTAGCCCAATCAACAAGCAATTTCCAAATCTCAACAACCAACTCAAA CTCACTCACCAAAAAGAAAACCTCAACTATACATAATACCACATCATCTCTCTCTCTCTCTCTCTCA TCCAAAATTTCCAAACCTCAAAA	252803.5417	144698.7917	33031.95973	14550.43367-2.9	-3.7	-0.8	0
6332	arabinogalactan protein.01	other cell wall proteins	70	contig	10	EG974741	GCTAGCTAATAATCTCAAAGAAAACAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA CTTCAATTCATTTCTCCATAGCCCTAGTCTAATCTCAACCCAGCTCAACCCCAAGCTCA TAGCCCAAGCACAATATACATCAACACACTCCGAGGCGCACTAGTCCAAACCCCGCGGCGCTG GCAACCTTACAACCGCCACCGAGTCTCGAAAAGTGGGGATTCAGTGTCTTGTCCACCT CTCAAAAACATCAGAAATTTCAAATCGAAAACCAACTCAAAATCAATCTCAACAACCAACTCAAA CAATCTTAGCCCATCAACAAGCAATTTCCAAATCTCAACAACCAACTCAAACTCAACTCA ACAAAAGAAAACCTCAACTATACAAAACCAACTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT CCAAAACCTCAAT	475151.5417	250007.125	48820.86451	23056.77677-3.8	-4.8	-0.9	0
693	arabinogalactan protein.01	other cell wall proteins	70	contig	10	EG974733	GTAGCTAATAATCTCAAAGAAAACAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA CATTTCCATCTTTCTCAATAGCCCTAGTCTAATCTCAACCCAGCTCAACCCCAAGCTCA CCCAAGCACAAATATACATCAACACACTCCGAGGCGCACTAGTCCAAACCCCGCGGCGCTGGGG AACCTACAAGCCACCGAGATCTCGAAAAGTGGGGATTCAGTGTCTTCAATCCATCTCT CAAAAACATCAGTAAATFATTCAAAATCGAAAATCAATCAATCAATCAATCAATCAATCAATCA TCTTAGCCCATCAACAAGCAATTTCCAAATCTCAACAACCAACTCAAACTCAACTCAACTCA AAAGAAAACCTCAACTATACAAAACCAACTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCA AACCCCTCAAT	104147.4583	131798.2083	30104.95362	30106.86563-5.2	-4.9	0.3	0
169	arabinogalactan protein.01	other cell wall proteins	70	contig	10	EG974742	GCTCAAGAAAACAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA TTTTTCTCAATAGCCCTAGTCTAATCTCAACCCAGCTCAACCCCAAGCTCAACCCCAAGCTCA AATATACCAACAACCACTCCGAGGCGCACTAGTCCAAACCCCGCGGCGCTGGAAAACCCCTACA AGCCACCGAGATCTCGAAAAGTGGGGATTCAGTGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT TCAGAAATATTCAAATCGAAAACCAACTCAATATCAATCAATCAATCAATCAATCAATCAATCA ATCAACAAGCAATTTCCAAATCTCAACAACCAACTCAATCAATCAATCAATCAATCAATCAATCA TCCAACTATACAAAACCAACTCATCT AACCTGTACCG	83082.79167	1028.976148	20871.49686	8241.508172-5	-5.8	-0.8	0

5343	arabinogalactan protein_04	other cell wall proteins	72	singleton	1	EG974154	GACAAAATGGGAAAATCACAAAGATTAGCTCTACTATAAACCACAGCCATTTTCCTCTTTCGAAAACCTATCTAGGCCAAAGTCCGGGAAAGTCCAGGGCCAGGAGGCCCTGTGACATAATAGCTGTCTTAAAAAAGCAGGCCAAATACACCAATTCATCAAGCTTCTGAAAGGTGACCCAAAGTATCTGACCAAATCAATCCCAACTTAGTGGTTCAAGTCAAGGCAATACAGTCTTTCGACCCACCGACTCAGCCTTCTAGCTCAAGACAGGCACTCAACTCTTGGACAGTGAACAACAACCTTCACTAGTTCAGTACATGTCTCCAGCTTTTATACACTCTCCAAATTCAAACTCTCCAAACCAATTCACACCAAGCTGGTATAGCGAA.AATGGCCAGTACCCACTTAATGTAAACAACCTCGACTAGTAAACCAAGTCAACATA	37176.54167	146758.75	124324.75	4567.954107	21191.15917	12481.11403-1.7	-2	-0.2	0
4536	arabinogalactan protein_05	other cell wall proteins	76	contig	1	EG974155	GCTCTAAGCTATTTCTCAGTGGCCACTTTAAAGCAAGAGAGTGGCCAGATTAATCTCATCATCATC ATGGATCTAAAATGTCAICTTAATCGGCTTTCTTTAGCCATTTGGCTTCAAGTCTGGGCTCA ATCTCTGCAAGTTCTCTTGGCTTACACCCGGGCTCAAGCTCCACCAAGCCACCAACTCCCT CAGCGCGCGGACCAAFACCTAGCCACCAACTCCAGTCCGCTACTCCACCCCAACCAAC CAGCCACCACCACTCCGGTGGCTCTCTCTGCTCTCACCACCGGCAAGCCCAACCCCTAAGCCA TCCTCTCCGGTCCGGCCACTCTCCACCGGTAAAGTGTCCACTCCGGCTACTCTCTCCAG CCACCCCAACAGCCACTCTCCACTCCAGTAAAGCCACCCACCCAGCCACCCACCGCCACT CCTCTCCGG	317705.875	826312.25	717979.5	35464.78765	98951.25982	76114.01857-1.2	-1.4	-0.2	0
3991	arabinogalactan protein_06	other cell wall proteins	64	contig	4	EG974159	CATTCAGCGTCCGTAGTCTAGATCCGGAGCGGGCGGCTTTTTTTTTTTTTTTTTTTTCTTTC TCTTCTTACTTTTACTCAATCTCCAGCTCACTCCCAACTCCCAACTCAAAACCAATTCCTAA AGCTAATCGCTACTATAA.CCCGCTCTTCTCAACCGCATCTCAAGCCATCTCAAGCAGTACTACCGGCTC CTTCTAAGCTCAACCAAAAGCCCTCTCCCTCAACCCCAAGCCGGAAGCCAAACCCCTAAGCCA GCCCGCTAATGTCACTGAGATCTTGCACAAAGCTGGAGGCTTCAAGTCTCTGGTCCGCTCTCT TAAAAACTCAAGTGTCAATCAGATCGAAATCAACTCAACTTCCACAGCTTAAACCAACTAACC TGGCCCAACCAAGCGGATCTCTAGTCTAAAGCCGGCTCTCAACGGCTTACCCCTGAG CAAAAAGTCCACTCTCAAT	9383.041667	532524.625	403355.9583	1217.846354	60429.12399	39761.98353-5.4	-5.8	-0.4	0
3643	arabinogalactan protein_06	other cell wall proteins	64	contig	4	EG974156	GCAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAATTTT TCTTGTCTTCTCATTTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT TCCCAACTCAGCTCAAAAACCAATTTCTAAAGCTCAATCGCTACTATAAACCCGCTCTTGC TCAACGCCATCTCAAGCAGTACTACCGCTCTCTCAAGCTCCAAACCCCAAAAGCCCTCCCTC ACACCCACCGGAAAGCCAACTAAACAGCCGGCTAATGCTACTGAGTCTTGCACAAA GCTGGAGGTTCAAGTCTCTGCTCCGCTCTTAAAGAACACTAAGTCTCAACTCAAGTCAAGTCA TCAACTCAACTTCCAAAGCTTAAACCAATTTGGCCCAACCAACCGGGGATCTCTAGTCTAA AAGCCGGCTC	5432.833333	499687.75	311640.6667	957.8760163	59234.69313	32784.92756-5.8	-6.5	-0.7	0
5051	arabinogalactan protein_06	other cell wall proteins	64	contig	4	EG974158	TACGGCTCCGCAATCCACACTTATAACAACCAACCAAGAAAAGAAAAGAAAAGAAAAGAAAATTTT ACTACAAGAAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT TCTTACTTTTACTCAATCTCCAGCTCACTCCCAACTCAAGCTCAAAAACCAATTCCTAAAGC TCAATCGCTACTATAAACCGCTCTTGTCAACCGCATCTCAAGCCATCTCAAGCAGTACTACCGGCTCTT CTAAGCTCAACCAAAAGCCCTCTCTCAACCCCAAGCCGGAAGCCAAACCCCTAAGCCAGCC CCGCTAATGTCAGTGAATCTTGCACAAAGCTGGAGGCTTCAAGTCTCTGCTCCGCTCTTAA AAACTCAAGTCTCAATCAGATCGAAAATCAACTCAACTCAACTCAACTCAACTCAACTCAACT CCCCAACCAAGCGGGAT	3113.125	299884.25	217474.8333	480.0745576	33941.06983	25141.88569-6.1	-6.6	-0.5	0
6155	arabinogalactan protein_06	other cell wall proteins	64	contig	4	EG974157	GATCAATCCACACTTCTTAAACAACCAACCAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAATTTT AAATGATGAAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT TTTAGCTCAATCTCAGCTCACTCCCAACTAGCTCAAAACCAAAACCAAAAGCTCAATCGC CTACTAAACCCGCTCTTGTCAACCGCATCTCAAGCCATCTCAAGCCATCTCAAGCAGTACTACCGGCTCTT CCAATCACATCGACACCACTAAAGATCACTCTTCAAGCTCAAGCCATCTCAAGCAGTACTACCGGCTCTT CCAACCAAAAGCTCTCCCTCAACCCCAAGCCGGAAGCCAAACCCCTAAGCCAGCCGCTTAA TGTCACTGAGTCTTGACAAGCTGGAGGCTTCAAGTCTCTGCTCCGCTCTTAAACCAACTC AAGTCTCAATCAGATCGAAAATCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACT AAGCCGGGAT	7987	87231.70833	58030.20833	1215.202633	12864.34186	6738.854847-2.9	-3.4	-0.6	0.1
4847	arabinogalactan protein_07	other cell wall proteins	65	singleton	1	EG974160	GATTAATCAAAATAGTCTTTCTAGAGAAAGTGAAGTCAACACTCAAAATCTCAACAA TAAATAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA GTTTTCT CCAATCACATCGACACCACTAAAGATCACTCTTCAAGCTCAAGCCATCTCAAGCAGTACTACCGGCTCTT CGGATCAGCCATAGTGGAGCCCAACAGCGAAATCCAGAGAAAGGACAACCCCAACCA ATAACAATCTAGAGAAAGCCGGGCTTCAAGTCTCTGCTCCGCTCTTAAACCAACTC GTGATCAGTCCCGTGAATGATCAACTTCAACTTCAACTTCAACTTCAACTTCAACTTCAACTTCA ATGAGGATCT	2700.041667	129927.75	102717.625	609.5776558	20416.78994	9815.229494-5.2	-5.6	-0.3	0.1
1092	arabinogalactan protein_08	other cell wall proteins	67	singleton	1	EG974734	CATTCAGCGTCCGGGATCTTCTGTCAACATCACTGAGGATGTC AACACAACCAATCTGG AACCAATTTCCGATAACCACTTGTATTTATCGAGTTGATAGTGTCTTCTCTCTCTCTCTCTCTCT TTTTTGTCTTAAAGGTTGGTCACTGGCCAGCTCCAGCCAGCCCAAGCCCAAGCCCAAGCCCAAG CTTAAAGAAATCGACAGATCAGCTCCATGTTGGTCCGCTCACTCTCTCTCTCTCTCTCTCTCTCT TTTAACTACATCACCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT CAGATACATCTGGTGAACGACGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT TTGTTCTTATGATACATATCTTCCGATCGAGACGGTACTTACTTCACTTCACTTCACTTCACTTCACT AACTAAAATATGTTTTTGAATA	4725	143621.7917	187460.6667	582.1324305	19689.41019	25193.77262-5.3	-4.9	0.4	0.1
1935	arabinogalactan protein_09	other cell wall proteins	66	singleton	1	EG974161	CACCCAGCGTCCGAAACCAATTTCCATCAACATAATTTTTTTCTAGCTAAGAAAATCCAGCATAT ATCAGTTAATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA TTTATCT CAACAACCAATAAAGAATAATTCATCCGTCATCACTCACTCACTCACTCACTCACTCACTCACT CAGCCATTGGTGAAGCCCAAGCCGCTTTCAGAGAAAAGGACAATCCCAACCAACTTCA AGAAATCTGGAGAAAGCCGGGATTTCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT TCACTCCATCGAAAATGATCTCAACTTCCAAACCCGTCACCAATTTTGGTCCCAACCAATGGA GATTTCTAGCCCTTAAAG	4768.625	174545.0417	127898.9583	835.6480645	30522.03361	15723.36395-4.7	-5.2	-0.4	0
1127	arabinogalactan protein_10	other cell wall proteins	71	contig	3	EG974753	CTTCTCAITCTGTTTTTGGTTTTTTTACTGCAAAAGGAGCCCAATATAGCTCACTCTC CAGCCCAACTCCCTCAAAAGGTTGCTGTGAGCCCAACTAAAGTAAAGGCTTAAACCCCA ACGAAAGCCCAACAGCTTTGCCAGTCCCGGGTGGAGCCGCCATCTCAAGTCCACTCGTCCA AGCCG	41296.08333	95955.75	73524.5	6370.967912	16107.80057	11279.6259-0.8	-1.2	-0.4	0
6482	arabinogalactan protein_10	other cell wall proteins	71	contig	3	EG974751	GAGAAAACATCATTTCTTACTTAAGTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT ACAAGATGACAACAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA GGGCAACTTTAGCTCACTCCAGCCCAAGCTCCAAACCAATGAGCTATAGCCCGGCTAA GGCTAAGGATAGCCCAACCAAGCCCAACATCTTTGGCAGTGTCCGGTGGAGCCACCGT CTCAAGTGCATTTGCGCCGCAACCCCAAGCCCTTCAACACCAAGAGCTCAACCA ATCTCGAAAAGCGGATCTTCAAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT TCAGATAGAAAATCAGCTCAATGTATCAACAACATGACCAATTTTGGCCCAACAATGGGCTT TTGGTCTTTGA	7452.791667	177294.5	116693.0417	1035.292637	24891.52911	12051.63141-4	-4.6	-0.6	0

1123	arabinogalactan protein_10	other cell wall proteins	71	contig	3	EG974752	<p>TCACGGCTCCGTTCATAAACAATTAGTAAATTAATACACTAAGTAGCCCTTGGTACGAAATCCATTCT CATATAGTAAAAAAGAAAAAAGAAAATGAAAGCAAGCAAGCAAGCAAGCAATCTTACTTCTCATITCTTGT TTTTGTTTTTACCACTGCAAGAGCCACATATAGTCACTCCTCCAGCCCAACTCCAT CAAAACATGTAAGCTGAGCCCAAAAGTAAGCTAAAGCCCTAAACCCCACCTAAAGCCCAACA GCTTCCAGTCCCGGTGGAGCCCACTCAGTGGCCACTCCAGCCGCAAGCCCAAA AGCCCTTTACACACCAACCGAGTCAACAAATCTCAGAAAGCCGATCTCAGTGTCTTCA TCCGCTCTTAAGAGTACTCTGAAGCAITCAAGATTAGAAATCAACTGAATGTATCCCAACA TTGACCAITTTGCCCA</p>	7571.875	334329.2083	251342.2917	1042.752561	40962.5579	24299.54926-5.1	-5.5	-0.4	0
4464	arabinogalactan protein_11	other cell wall proteins	79	singleton	1	EG974747	<p>CGTCCGCTCTATAAAACCTCTTCATITTTCTCTCTAATAATCCTCCACACAAATCGAGTCCGT CCGGCTTACCGGGACACTGGTCTAGTATGCGCTCATTCTCCTCCGGCACCGG TGCTATGCTAGGGCATCACAGAAATTCAGAAATCCGAGGTTCTTCTTCTTCAACCAT TACCTAACTAACTCCTCGCTCAGAAATCAACAGCGGACGATTAAGTCTGCTGGCGGT TGATAAGCCGCTATGGGGATTTCTCGAAGCATCCGAAATATATCTAGTGAAGAATTC TCTCGATTCAITTTCTCAGTTTCTGATTTCTGGGCCAAGAGTCCACCAGATCACTAAGCGTACT GCTCTGCTAGTATTTTCAAGCTACCGGTTCCCGCTCCGATCTTACTGGATTCTTAATAT CACAGATTACACCGGTGGAAGGT GGCCTCAATCTCCAGTGTGCTATCAACCTGGGGAAGTATTTACTTATAGATTTCTTACTGATGATA AGCCGGGAACAATTTTTACCATGGACAACGAAATGCAAGAAATACAGAGGCTATACGGGTCA TAAATTTGGGTGGCAGAGGAGAGGAGGAGCCCTTCCACTACGATGGGAGCTCAACCTTT ACTCAGCAATTTGGTGGCAAAAGTGTTCAGAGCAAGAGTGGTCTCTTCCGGGCCAATGC GTTGGATCGGTGACCACAGAGCTTTGTTACTGAATGTTAGAGGACAAATATAAAGTCTCATTTGGCA GGCAATATAGCAACTCTCTCTAAGCAGTCAAGTAAAGGGTGGAAAAGTGGCACCCAT GATTATGACGTTGCAACAAAAAGACAATACAGGCTAAGAATCCGCTAGTACACTGCACTAGCTT CCCTCAAC</p>	111690.5	43011	37541.79167	15186.54928	6721.343572	5791.791443 1.6	1.4	-0.2	0
1003	ascorbate oxidase	miscellaneous	153	singleton	1	EG974204	<p>28475.125</p>	12265.29167	10988.20833	3086.597165	1664.234474	1683.651377 1.4	1.2	-0.2	0.1	
6768	ATP sulfurylase	miscellaneous	128	contig	1	EG974551	<p>51975.75</p>	105385.5	66550.54167	6718.153411	14836.05514	8998.677932 0.4	-1	-0.7	0	
428	auxin growth promoter protein	miscellaneous	151	singleton	1	EG974326	<p>97868.75</p>	46673.08333	43339.66667	19196.55627	11601.53311	6419.174779 1.2	1.1	-0.1	0	
3123	auxin-repressed protein	miscellaneous	104	contig	3	EG974362	<p>25064.04167</p>	178141.6667	84777	3489.599379	20134.64627	9951.680318-1.8	-2.8	-1.1	0	
3826	auxin-repressed protein	miscellaneous	104	contig	3	EG974360	<p>22970.04167</p>	168606.0417	71250.25	2805.774964	20040.68814	9091.308971-1.6	-2.9	-1.2	0	
3794	auxin-repressed protein	miscellaneous	104	contig	3	EG974359	<p>21161.375</p>	168157.5	69217.375	2997.110012	22785.13031	8104.38486-1.7	-3	-1.3	0.1	
109	B12D protein	miscellaneous	129	contig	2	EG974363	<p>34266.83333</p>	68892.04167	35310.375	5500.562805	11628.86013	3448.610514 0	-1	-1	0	
5451	B12D protein	miscellaneous	129	contig	2	EG974364	<p>27370.58333</p>	54768.125	29613.16667	5915.018986	10465.75165	2893.122395-0.1	-1	-0.9	1.9	

3225	beta-D-galactosidase	glycosylhydrolases	46	singleton	1	EG974152	GGATCCATCAAGAATTACTTTGTCAAGCGGGAAGTAACTGGCCCTCTGTGCTCTTTGTCAGAGG ATCATCTTCTATAAGACCTGAGCTTTGGAGAAAGAAAGAAAGTGGAAACAGAAATGTTCCA ACTGTCTACTTGCATGCTCAGTAATACCCCTTGTATCTGCTGTAAATAATTTGCTAGCTTTGGAAC TCCTTCAGAAACTGTGGATCTTAFACCAAGGAGATGCCCCAGCATCTAAATTTAGTTGG TTGAAAGTTTCTGCCCGAATAAGAACAACTGCGCTATCGAATGAGTGAAGAAGAAATTTCCAGCACT AGTACGTGCTCCTGTTGTAGCAAAGGCTTTCAGTAGAGCAGATCGCCGATGAAACTTTGAAGT TCATCAGTGTGGAAATGATATACACAAAGTGAAGAAAGAAACGCCCTTTGTGAGCTTTTGAGAA AATTTGTTTAACT	45314.5	5494.083333	4784.666667	9574.293764	996.2834867	1006.905349	3	-0.2	0	
3591	beta-glucosidase	glycosylhydrolases	40	contig	3	EG974163	ATATGCCATTAGCTAGTGAATGCCATTTACTCAACCCCCTCTTATTTGTTTTCTCATTTGGCTCT CTCCCAGCCACATCTTCCAGCTACATAAAGCTGTCCCTATGCCCAGCTTTCAATAAGACA GTTTTCCAAAAGGCTTCATTTTTGGAGCTGGGACAGCTTCTTACCAGTCTGAAGGAGGACATCC TTAGATGGAAGGGTCCGAAATATGGAATCTTTACTCGTACATCCAGCAATCCAGAAAAATATGGA TCGAAATATGGAATGATGCTGAGTTTATCATGTTTAAAGGATGACATCAATTTGATGA AGAAAGTTGTTTTGGACTCTTCAGATTTTTCCATCGGATGTCAGAAATATCCCAAAGGGAACA CTCAGAGGAGGCATCATCTAGGGCTTAATACTAGCTATGATCTGATCAACGAGCTTCTAGC CAATGGA	44193.08333	16992.16667	8303	8198.512318	3717.061155	1305.791314	2.4	1.4	-1	0
5554	beta-glucosidase	glycosylhydrolases	40	contig	3	EG974174	GGTACAATAGCCATTAGCTAGTGAATGGCAATTTACTCAACCTTCTGCTATTTGTTTTCTCATTTG GCTCTCCCCAGCCACATCTTCCAGCTACATAAAGCTGTCCCTATGCCCAGCTTTCAATAAGACA GACAAGTTTTTCCAAAAGGCTTCATTTTTGGAGCTGGGACAGCTTCTTACCAGTCTGAAGGAGGAG CATCTTAGATGGAAGGGTCCGAAATATGGAATCTTTACTGTCGTGAACATCCAGAAATATA TGGATCAGAAATGGAATGATGCTGAGTTTATCATGTTTAAAGGATGACATCAATTTGATGA AGAAAGTTGTTTTGGACTCTTCAGATTTTTCCATCGGATGTCAGAAATATCCCAAAGGGAACA CTCAGAGGAGGCATCATCTAGGGCTTAATACTAGCTATGATCTGATCAACGAGCTTCTAGC CAATGGA	82347.41667	29174.95833	15472.16667	18416.82398	6471.593316	2494.269199	2.4	1.5	-0.9	0
1117	beta-glucosidase	glycosylhydrolases	40	contig	3	EG974185	ATAGCCATTAGCTAGTGAATGGCAATTTACTCAACCTTCTGCTATTTGTTTTCTCATTTG GCTCTCCCCAGCCACATCTTCCAGCTACATAAAGCTGTCCCTATGCCCAGCTTTCAATAAGACA GACAAGTTTTTCCAAAAGGCTTCATTTTTGGAGCTGGGACAGCTTCTTACCAGTCTGAAGGAGGAG CATCTTAGATGGAAGGGTCCGAAATATGGAATCTTTACTGTCGTGAACATCCAGAAATATA TGGATCAGAAATGGAATGATGCTGAGTTTATCATGTTTAAAGGATGACATCAATTTGATGA AGAAAGTTGTTTTGGACTCTTCAGATTTTTCCATCGGATGTCAGAAATATCCCAAAGGGAACA CTCAGAGGAGGCATCATCTAGGGCTTAATACTAGCTATGATCTGATCAACGAGCTTCTAGC CAATGGA	41428.70833	17756.95833	11586.5	4837.771183	2900.593663	1722.910322	1.8	1.2	-0.6	0.1
966	beta-mannan endolydrolase.1	glycosylhydrolases	33	contig	2	EG974162	CGTTCACCGCTCGGATTTGAAATAAAGCTGAAATACCTCTCAAGTGGATGCTATCCCAAT GAGATGGTAAACAAGAGCTGAAGAAGCCAGTGTGTCTCTGAATTCGGCTTGTCAAACTGAA CAAGGATTTCAAGCCAGAGCCGGGATATATTTACAAAGTATTTAGCACATAATTTACAAAT CTGCCAAAAGGCGGTCTGTGCGGGTGGCTGATCTGGCAAGTATTTGGTTGGATGGATGGAG GTATACAACGATTTTGGAAATGGTACATGGAAAGTGGCTTCATTTGCAACATTTGGTGGTAA ACAATATGCAGTTTCCAGTTCCAGGTGAGGGAGTGGCTCAACAACAGCCGACTCAAAAGCCTCT GTATGCAAAAAAGCTGATATTTCTGAGTCCATTTGAGAGGGGGAAGAAAGCTTTCTTTTTTTG GGTGTGGTATATAGTCAATTG	18492.29167	77649.20833	41498.91667	2655.259843	11931.9503	4493.151213	-1.2	-2.1	-0.9	0
999	beta-mannan endolydrolase.1	glycosylhydrolases	33	contig	2	EG974164	CGTTCACCGCTCGGATTTGAAATAAAGCTGAAATACCTCTCAAGTGGATGCTATCCCAAT GAGATGGTAAACAAGAGCTGAAGAAGCCAGTGTGTCTCTGAATTCGGCTTGTCAAACTGAA CAAGGATTTCAAGCCAGAGCCGGGATATATTTACAAAGTATTTAGCACATAATTTACAAAT CTGCCAAAAGGCGGTCTGTGCGGGTGGCTGATCTGGCAAGTATTTGGTTGGATGGATGGAG GTATACAACGATTTTGGAAATGGTACATGGAAAGTGGCTTCATTTGCAACATTTGGTGGTAA ACAATATGCAGTTTCCAGTTCCAGGTGAGGGAGTGGCTCAACAACAGCCGACTCAAAAGCCTCT GTATGCAAAAAAGCTGATATTTCTGAGTCCATTTGAGAGGGGGAAGAAAGCTTTCTTTTTTTG GGTGTGGTATATAGTCAATTG	17871.83333	69029.33333	42818	2199.158372	8153.609329	4275.734209	1.3	-1.9	-0.7	0.1
5093	beta-mannan endolydrolase.2	glycosylhydrolases	47	singleton	1	EG974449	CGTTCACCGCTCGGATTTGAAATAAAGCTGAAATACCTCTCAAGTGGATGCTATCCCAAT TCTATATAGCAGGAGTGGCTATGATTTGGAAGCACTCATTTGATGAGTGGATGATGCT TTCATATTTCTGGCACAATGATGGGGTTGATGAGTGGATGAAAGTAAAGTCAATGGG AAATGGTGCAAAAGAAAGAAACCATTTGATGATCAATGATCAACCTTTTATGTAATGGTTC AACACTATGGTGTATGGTGTCTGGGATCAATCCACAAGAGGAAAAGTCTCTGAGGTTTT CAAGAGGCACTCTCTGCAAGTTTTGACAGTTTTGCGGACTTGTAAACGATGGTCAAGGCTCTT GAGCTCTCAAAGTCCCCATCACTTATGATGAAGATTTTTCAAGGGCTTTAGATTTGTGTGA AGTGAAGCAA	23969.83333	2655	4457.625	3847.960893	553.5602883	1598.660609	2.4	3.2	0.7	0.1
3273	beta-mannosidase.2	glycosylhydrolases	43	singleton	1	EG974196	CGTCCGGATGAGAGAAATAAGTACTTTTTCTGTTAGCAATTTGCTTTTTAGTAGTAAATTTGATCC ACCAACAATTTGTAGAAGCAAAAAATGGTTTTATGGAAGCACTCATTTGATGAGTGGCACCATTTATG CTGAATGGTAAATCGGTACTATGCAATGATGATCAATGCTACTGTTAAATGATGATGCTCTGA CCATCTCAGAGTTCAAAGTTTCACTGCTTTCAAGAAAGTCTTAGCCATGGCCTACTGTAG CAAGAACTTGGCTTTTCAGTAGTGGATTAAGACCCTTTCAGTATGCTCCTGGCTCATATAAT GACCAAGCTTTTAAAGGGCTGATTTTGTGATGCTGAGCCAGAAAGCATGGGATTAAGCTTAT ACTGATTTGGTTAAACAATATGAGAGCTTTGGTGGGAAAAAAGCAGTACGTGAAATTTGGGCTAGAA ATCAAGGCAGTATTTCACATCT	17441.5	5672.208333	2946.041667	3186.085741	1201.531194	492.6664232	6	1.6	-0.9	0
6253	beta-mannosidase.3	glycosylhydrolases	35	singleton	1	EG974207	GTACTACTAGCATACTCGTATGATCAGCTAGCGGCCTGGTGCAGTGGAGCTAGTGAGG AAGCTCCCATTTTTCGGGCCGAAATAATGGTTGATGAGAGCCCAAGTTTTCCGATGGGCTTT GTGTTGGAACGGCCAGCTCTGCTTACCAAGTCGAAGCATGGCCATAAAGATGGTCTGGGCC CAGCAATTTGGGATGCTTCAAAAAATCCGGAATTTAGCAAATAATGTTACTGGAGAGGTTTT CAGTAGCAAAATACCCGTTCAAAAGAAAGATATCAGCATATGAAAAAGCTAAAATTTTATGCT TATCGATTTTCAATTCATGGTCTCGTATTTTCCAGAGGGAACCTGAAAAGTAAATTGGAAAAGG AGTTGCAICTATAACAGATTTGATCA	27341.45833	14928.83333	8582.833333	4888.382759	2649.341145	1472.409837	1.7	0.9	-0.8	0
910	beta-tubulin	miscellaneous	119	contig	2	EG974398	GCAAAATGCGGTGAAATTTCTCACATCCAGGCTGGCCAGTGGCCAAACCAGATCGGCCCAAAGTTTC TGGGAAGTGGTATGCGCTGAACTGGAATGACCTGAGCAGAGTCTGATGAGGAGGCAAGCAAGCACT CCAACTGAGGCTGTCATGTTGTTACTTACAAAGGAGGTTGGGTGGTGGTCTGTACCGGCGGAG TCTCTATGGATCTGAGCCCGGAACTATGGACAGCCTTATGATCTGTCGTTAGCAGACATATC AGCCGGAGCAACTTTTGGCTTGGGCAGCCGCGGAAACAATTTGGGCTAAAGGTTCTACTAC TGAGGGGCTGAGTTGATTGACTCGGTTCTTGATGTTGAGTGGTGGTGAAGGAGGCTGAGAAATTGATT GCTTACAAAGGATTTCAAGGTTCTGCTACTTTAGGAGTGGTACTGGAATCAGGAATGGGAACACTT CTTATTTCAA	49797.66667	104609	109441.6667	5936.416757	15032.92742	14539.95242	-1.1	-1.1	0.1	0
5573	beta-tubulin	miscellaneous	119	contig	2	EG974404	GGTGTCTCTCAAGCCCTCAATCTCTTCTTCAAAGCTACTTTCCTACTTCTCTTCAAAAC TCAATTTCTCCGATCATAAATGGCTGAAAATTTCTCACATCCAGGTTGGCCAGTGGCGGAAAC CAGATCGGCCCAAGTTCTGGGAAGTGTATGCCCTGAACTGGAATTTGACTCGACAGTCTGTTA CCAGGGAGACAAGCAACTCCACTGACCGCTGCATAATGTACTACACAAGCAGGAGGTTTTGCCGTG GGTTCTACCCGGCGGAGCTCATGATCTTGAGCCCGGAACTATGACACAGCTTAGATCTGGT CCGTACGGTCAAGATTTAGGCCGCAACTTTTGTCTTGGCAGTCCGGAGCCGAAACAATTTG GGCTAAGGGTCACTACACTGAGGGCGGCTGAGTTGATGTTGACTCGGTTCTTATGTGAGGAAAG AGGCTGAGAA	44711.25	104377.9167	73017.125	6066.069328	15237.56329	6943.424656	-0.7	-1.2	-0.5	0

2353	blue copper protein	oxidoreductases	181	contig	4	EG974446	7699.916667	14697.75	15935.625	1189.433881	2242.264816	2720.092461	-1	-0.9	0.1	0
							6699.916667	14697.75	15935.625	1189.433881	2242.264816	2720.092461	-1	-0.9	0.1	0
678	blue copper protein	oxidoreductases	181	contig	4	EG974447	12000.29167	55835.625	63257.58333	1922.33969	7663.387969	7304.522014	2.4	-2.2	0.2	0.1
							12000.29167	55835.625	63257.58333	1922.33969	7663.387969	7304.522014	2.4	-2.2	0.2	0.1
1567	blue copper protein	oxidoreductases	181	contig	4	EG974445	127284.6667	654680.9167	663815.875	16912.15913	85558.51622	79327.45627	-2.4	-2.4	0	0.1
							127284.6667	654680.9167	663815.875	16912.15913	85558.51622	79327.45627	-2.4	-2.4	0	0.1
1647	blue copper protein	oxidoreductases	181	contig	4	EG974444	55757.04167	289540.6667	290922.125	5903.607495	37975.91527	29572.22276	-2.4	-2.4	0	0.1
							55757.04167	289540.6667	290922.125	5903.607495	37975.91527	29572.22276	-2.4	-2.4	0	0.1
3040	brassinosteroid receptor	regulation	231	singleton	1	EG974540	103083.125	25320.875	22745.91667	17346.21519	4098.719966	4206.61442	2.2	-0.2	-0.2	0.1
							103083.125	25320.875	22745.91667	17346.21519	4098.719966	4206.61442	2.2	-0.2	-0.2	0.1
2928	bZIP DNA binding protein	regulation	223	singleton	1	EG974556	13232.04167	32970.95833	28138.33333	1751.854549	4869.751924	4450.681459	1.1	-1.3	-0.2	0
							13232.04167	32970.95833	28138.33333	1751.854549	4869.751924	4450.681459	1.1	-1.3	-0.2	0
2213	caffeic acid O-methyltransferase.1	secondary metabolism	248	contig	3	EG974504	232351.9167	94648.83333	63470.95833	29654.29926	13917.3121	5955.606996	1.9	1.3	-0.6	0.1
							232351.9167	94648.83333	63470.95833	29654.29926	13917.3121	5955.606996	1.9	1.3	-0.6	0.1
2496	caffeic acid O-methyltransferase.1	secondary metabolism	248	contig	3	EG974506	40798.66667	15463.79167	11124	6915.798651	2336.658464	1298.03356	1.9	1.4	-0.5	0
							40798.66667	15463.79167	11124	6915.798651	2336.658464	1298.03356	1.9	1.4	-0.5	0
127	caffeic acid O-methyltransferase.1	secondary metabolism	248	contig	3	EG974507	130873.4167	48991.54167	38575.70833	18249.72641	7014.362415	3499.648398	1.8	1.4	-0.3	0.1
							130873.4167	48991.54167	38575.70833	18249.72641	7014.362415	3499.648398	1.8	1.4	-0.3	0.1
4901	caffeic acid O-methyltransferase.2	secondary metabolism	247	contig	4	EG974508	146122	70443.29167	34224.70833	26074.55412	11352.54135	3393.299636	2.1	1.1	-1	0
							146122	70443.29167	34224.70833	26074.55412	11352.54135	3393.299636	2.1	1.1	-1	0
6381	caffeic acid O-methyltransferase.2	secondary metabolism	247	contig	4	EG974510	111219.1667	57279.04167	40642.83333	15734.90885	6243.37868	3590.399314	1.5	1	-0.5	0
							111219.1667	57279.04167	40642.83333	15734.90885	6243.37868	3590.399314	1.5	1	-0.5	0

5025	caffeic acid O-methyltransferase.2	secondary metabolism	247	contig	4	EG974509	79991.83333	36294.5	22947.29167	13473.46397	4724.302664	2737.387827	1.8	1.1	-0.7	0
GGCTATTCTAGAGAGGGGAAAGAAAACAATGGTGTGCTGAGTGAAGAGGACAAATACTAG CAATAGACAACGAAGTTCACAGATCAAGCAGAGATCTGGAAATATGCTCAACTTCCGGA GACTCATGGCCATAATGGCCGTGGAGCTCAGACTCCCGACATCTCCACTGACAGCGG CCCAATACACTCAGAAATCGTCCCAATCCCTGACGCGCCGCCCCACAGCGTCAACCC TCTCAGAGTCTGGTCTACTCTGCTGCAAAATTTTCACTCCCAAGAGACAAAGTGTCA GGTAAACCCCTTACGGGCCCAAAAGCTGTGAGCTGGCTCTCCAGAGCCAGCTCCCAACATC TGACTCAGATCTCAATATGACACTGGCTCCATGTTAATAGTGAAGAAACCCCGTGGCAGC CAAACCCGTGG																
976	caffeic acid O-methyltransferase.2	secondary metabolism	247	contig	4	EG974511	110862.875	45163.375	35444.66667	14629.95973	5774.136581	3768.75145	1.6	1.3	-0.3	0.1
GCTCCGGAATAAATGCTGCTGCAAGTGAAGAGCAACCCCCCAATAGACAACGAAGCAA GTTTCCAAGATCAAGCAGAGATCTGAAATACATGCTCACTCCAGAGACTCCATGGCGTAA TGGCCGTGGAGTGGACTCCCGACATCTCCACTGACAGCGCCCAATGACACTCAGAA AATCGCTCGCAATCCCTGACGCGTCCACAGCGTCCACAGCTCTCAAGAGTCTCGCTC TACTGCTCGCAAAATTTTCACTTCCCAAGAGACAAAGTGTCAAGAGTCCAGTAAACCC CCCAAGCTCTCGAGTGGCTCTCCAGAGCCAGCTCCCAACATCTGACTCAGATGCTCAAT CATGACACTG																
4307	caffeic acid O-methyltransferase.3	secondary metabolism	250	contig	6	EG974514	62036.91667	25246.91667	20640.16667	8263.817995	3935.148378	2692.385643	1.6	1.3	-0.3	0.1
CTTTTTTTTTTTTTAAGGACACAATACTTCAACTAATAATAAGGCAATAATAATAA CATGATAATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA GAATAACTAAGAGTAATGGCTAAACATTAATAATAATAATAATAATAATAATAATA AATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA AATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA TTTT																
5017	caffeic acid O-methyltransferase.3	secondary metabolism	250	contig	6	EG974517	155609.375	53117.125	47185.54167	26841.23905	9483.266625	5255.987403	1.7	1.6	-0.2	0
CACTCAGCTCCGATGTTTCAAGAGTCTTCTGCTGACGCTGTTGTCACCAAGTGGTAT GCATGATGGGAGATGACATGTTGTAAGCTAATGAAGAAATGCAAGAAAGCAATCCAGAA AAGAGGAAAGTGAATAAGTGGATGATGATGTTGAGGCTGATGGGAAAGAGTGTGATG CTGGAGAAATCTCTGTACATAAATGCTTCAACACGCGGATGGCTGACGCGCAAAATACG ATAAGACATACTGATGATGGTGAATGATTTTTCAATGGGGTGGATGCTGCTGATGAT TGTTGGGACTGGGAGATTAATTCAGAAATGAAATCATATCTCATATAAAGGGATTA ATTTGATGATCTATGATTTCTACTGCTCAGCTTACTGGTCTACTCATATGGGGGT GACATGTTTCAAGAGGTTCTTCTGCTGATGCTGTTGTCACCAAGTGGGATGCTGACTGGG AGATGAC																
2433	caffeic acid O-methyltransferase.3	secondary metabolism	250	contig	6	EG974512	53636.5	20653.625	16532.83333	8941.930605	3610.467474	2861.497383	1.7	1.4	-0.3	0
GCATGGCTCCCATGTAATCATGGAGAACCCCGTGGCAGTGGACCCGTCGACAAACTGAG CGAGTTCAAGAGAGTGGACTGCTCCGTTGAGAAAGAACCGGTAACATGTTGATTTG CTGGAGAAATCTCTGTACATAAATGCTTCAACACGCGGATGGCTGACGCGCAAAATACG ATAAGACATACTGATGATGGTGAATGATTTTTCAATGGGGTGGATGCTGCTGATGAT TGTTGGGACTGGGAGATTAATTCAGAAATGAAATCATATCTCATATAAAGGGATTA ATTTGATGATCTATGATTTCTACTGCTCAGCTTACTGGTCTACTCATATGGGGGT GACATGTTTCAAGAGGTTCTTCTGCTGATGCTGTTGTCACCAAGTGGGATGCTGACTGGG AGATGAC																
2974	caffeic acid O-methyltransferase.3	secondary metabolism	250	contig	6	EG974513	197385.6667	66403.75	54091.95833	34538.41893	10622.1896	7614.262412	1.9	1.6	-0.3	0
GCAAGAGTTCCTTCTGCTGATGCTGTTGCCACCAGTGGGCCCGCATGATGGGAGATGAAT TATGTTGAGATGATTAATAAATGCAAGAAAGCAATCCAGAAAGAGTGGAAAGTGTGAT GTTGACATAGGGGTGAGCTGATGGGAAGGATGTTGATGACACTGGTGTGCTTGTGATG TCTATGCTTTCATAAAGTGGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG ACCAATGCTTCCCTGTTACAAAATCACCAAAATCCCTGCTTGCATCTGCTCAATGAAACC TATCCAAATACTTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA ATACTATAAGTATAATCTTCTCAAGAGTGAATTAATGATGATGTTGAT																
5588	caffeic acid O-methyltransferase.3	secondary metabolism	250	contig	6	EG974518	618273.2917	220990.4583	204750.0417	78356.57205	27869.93126	22829.82907	1.6	1.5	-0.1	0.1
GGAACATGTGGAAGTGAATAAATGCAAGAAAGCAATCCAGAAAGTGGGAAAGTGA TAATGTTGACATAGTTGAGAGCTGATGGGAAAGAGTGTGTTGATGACACTGGTGTGCT GATGTTTATGCTGCTCACACTGGTGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG GTTGGACCAATCTGGTTCCCTGTTACAAAATCACCAAAATCCCTGCTTGCATCTGCTA AAGCTATCCAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA AATACTATAAGTATAATCTTCTCAAGAAAGTGAATTAATGATGATGTTGATGATGTTG TAAGTTTATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA GTCTTAAT																
3009	caffeic acid O-methyltransferase.3	secondary metabolism	250	contig	6	EG974515	437858	148314.5833	123430.625	64306.18523	17228.45777	12899.71643	1.8	1.6	-0.3	0.1
GAAAGGATTAATTTGAPAGATCTCATGATGATTTCTACTGCTCCCGTTCCTGCTGCTC ATGTTGGGGTGACATGTTTCAAGAGGTTCTCTGCTGATGCTGTTGTCACAAAGTGGTATG CATGATGGGAGATGACTATGTTGAAGCTATGAAAGTGAAGAAATGCAAGAAAGCAAA AGTGGGAAAGTGAATAAGTGTGATGTTGAGGCTGATGGGAAAGAGTGTGTTGATGACA CTGGTGTCTTGTATTTCTATGCTGCTCATAACACTGGTGGAAAGAAAGAAAGAAAGAA GAGTGGAAATCTGTTGGACCAATCTGCTTCCCTGTTACAAAATCACCAAAATCCCTGCT GCAATCTGCTATGAAAGCTTCCAAATAATAATAATAATAATAATAATAATAATAATAATA AATAATAATGTT																
5751	caffeic acid O-methyltransferase.1	secondary metabolism	233	contig	5	EG974526	3280.25	13526.66667	10667.625	1002.657867	1831.662444	1595.105658	1.7	-2	-0.3	0
GAGGAAAGGAAAGTGGAGAGGCTTATGGGTTGGCTCGGTGAGTAAATCTGACGAAGAATGA AGATGGAGTCCATGCTCCTTGTCTCATGAAACAGGATAAGTTCTTATGGAGTGGT TTCATGAAAGATGACTTATGTTGGGGAATACCTTCAACAAAGATGAAATGACAGCA TTTGAATCATGGAACCGATCAAGGTTCAATAAATCTTAAATAGAGGAATGCTCCGACACT GACTATACC																
2395	caffeic acid O-methyltransferase.1	secondary metabolism	233	contig	5	EG974525	2839.333333	13882.41667	10585.83333	517.3148225	1776.826894	1319.083477	1.9	-2.3	-0.4	0
GGGGGCTCCAGGCGGTTCTCACCTCCAGATAGCCCAACAGCTTCCGACTCAGAACCCA GACGCCCTGTGATGCTGGACCGGATGAGACTGTTGGTAGCTACAACTGGTGGAGCTACT GCTGCTGAGACGGGGAAGGGAAGGGAAGTGGAGAGGCTTATGGGTTGGCTCCGGTAGTA AATACTGACGAAGAATGAAGTGGAGTCTCATGCTCCTTCTGCTCATGAACAGGATAAG GTTCTAATGGAGTGGTATCTTGAAGATGCAAGTCTGATGGGGAATACTTTCAACA AGCATGATGATGACAGCATTTGATATCATGAAAGCTTCAAAAGTTCAAATAAATCTTAA GAGAAATGTCGACACTGACTATACCATGAAAATAAATCTCGAAAACCTTCAAGGGTTT GGTCTTAACCT																
2996	caffeic acid O-methyltransferase.1	secondary metabolism	233	contig	5	EG974524	20709.25	101262.4167	71615.20833	2475.343834	11365.70196	6566.230248	1.8	-2.3	-0.5	0
GCTTCTTCTCCATTTTCTATATATATAGAGAGATCTGAAATTTGAAATAATAATA ATAATAAGATAAAATGGGTTCAACGAAATAGAGACCCAAATGACCCCAATATCCGAC GAAGAAAGCAACCTTTCGCTCATGATAGCCAGTGGCTCATGCTTACCCATGGTCTCAAGC AGCTTGGAGCTGACTTGGAGATCAGCAAGGGGGTCCAGGGCGGTTCTCTCACCTT CCGACATAGCCCAACAGCTTCCGACTCAGAACCAAGCCCTGATGCTGACCCGATGCTG AGACTTGGTAGCTACAAGTGGTACGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG GGTGGAGGCTTTATGGGTTGGCTCCGGTGAATAATCTGACGAAGAATGAGATGGAGTCT CCATTGCTCT																
6271	caffeic acid O-methyltransferase.1	secondary metabolism	233	contig	5	EG974528	14323.125	165108.3333	139409.5833	1455.854267	16747.56412	13484.06733	-3.3	-3.5	-0.2	0
GAGAGATCTGAAATGAAATAATAATAATAATAAGATAAATAAATGGGTTCAACAGGAATAG ACCCAAATGACCCCAACCAATATCCGACGAAGAAAGCAACCTTCCGCTTCCGCAATAGCCAG TGCTCAGCTTACCATGGTCTCAAGCAGCTTGGAGCTGCACTTGGAGATCAGCCA AGGGCGTCCAGGGCGGTTTCTCCTCCTCCAGATAGCCCAACAGCTTCCGACTCAGAACCA GACGCCCTGTGATGCTGACCGGATGCTGACTGTTGGTGGTGGTGGTGGTGGTGGTGGTGG GCTGCTGACGCGGGAAGAGGAAGGGAAGTGGAGAGGCTTATGGGTTTGGCTCCGCTGAGTA AATACTGACGAAGAATGAAGATGGAGTCTCCTTCTGCTCCTTCTGCTCATGAAACAGGATAAG GTTCTTAT																

4933	caffeic O-methyltransferase.1	secondary metabolism	233	contig	5	EG974523	<p>CATCCACGGTCCGGACCGGATGCTGAGACTGTTGGCTAGCTACACGCTGGTACGACTCGCT CGGTGAGAGCGGGAAGAGGAAGGAAGGAGGAGGCTTATGGGTTGGCTCCGGTGAGTAAAT ATCTGACGAGAAGTGAAGATGGAGTCTCCATGCTCTCTTTGCTCATGAAACCAGGATAAGGTT CTTATGGAGAGTTGGTATCACTTGAAGATGCACTACTTATGGGGGGAATACCTTCAACAAGC ATATGGAATGACACTTGAATATCAATGGAACCGCATCAAGGTTCAATAAAATCTTAAATAGAG GATGTCGCCACCTCAGACTATACCATGAAAAAATCCTCGAAACTTACAAGGGTTTCGAGGGT CTTACTCGAATGTTGATGTTGGTGGTGGTACTGGAGCTGTTGTTAACATGATCGTCTCTAAAGTA CCCTACTTAAAGGGTAAATA</p>	14065.79167	192451.125	123737.7917	1779.627331	22045.68479	12986.54174-3.1	-3.8	-0.6	0
3161	caffeic O-methyltransferase.2	secondary metabolism	242	singleton	1	EG974520	<p>GTACATGTTGAGCTTCGAGATCCATGGCTTACCGCGGGTGGAGCTTCAATTAGCCGACA TAATCCACTCTCACACCTCTCAATCACTTGTCCAAATAAGTTCCTGGCTATCTTGGCGCTACC TCGCCAGACTCTCTTGGCTTGGCCCGCATATGGCGCTACTCGTCCGCGGTGGATATCCACCA ACACCAAAACAAATCGGACGGGAGAAGAAGCCGCTTACGGGCCACACACTTCCCA GATGGCTGTGACCAAAACGACGATCAGATCACTAACTAATCACTAGCTCCAATGATTTGATGGAG AACGATCTAGACTGATGGCTCCATGGCAATGCTTACGGCGTTGTTAAGGAAGGTGGCGTGGC TTTTAAGAAGGCCAATAACGGCCAAAGATAATGAGGTTTGGGGCGGAGAATCCGG GGGTGATCAATGGCACTAGGCCGAAACATTCGAAAGATCCTTCCGAAAGCAAGTGAAGTCTTTGG AATGTGCTACTCTGGATGGGGCTGTGTAAGATAAAGAACTTGAATGGACTTGGACACAGTTG AAGTATAGCGGAGCTTCTTAACCCAGATCGAATTCATGCTGATATGCTGCCATGAAGAAGGG AATGAAGATAGACATTCATGAATGATGATGATGACAATGGTCTCACCCAGCTTAAGG AGCTGTAGATGAGACAGATTTCTTTGGCTGAAAGCTTGTGAGATTAACGCAAGATGATTTTC TATGAAGTGAAAAGAAGAGGTTTACAGTGATAACAGATGCTTTTGGCCACCAAGTCGACTGAGAC AGAAATAGCACAAAACTAGGCTAICTAGGTGTTGCTCCAGCAIACAAGCGTGTGGATACTTGTG CTGCTGAGTT</p>	7789.958333	20994.70833	4574.791667	1779.908861	4216.161146	933.18586110.8	-1.4	-2.2	0
3064	carbamoyl phosphate synthase	miscellaneous	141	singleton	1	EG974519	<p>GGGTGATCAATGGCACTAGGCCGAAACATTCGAAAGATCCTTCCGAAAGCAAGTGAAGTCTTTGG AATGTGCTACTCTGGATGGGGCTGTGTAAGATAAAGAACTTGAATGGACTTGGACACAGTTG AAGTATAGCGGAGCTTCTTAACCCAGATCGAATTCATGCTGATATGCTGCCATGAAGAAGGG AATGAAGATAGACATTCATGAATGATGATGACAATGGTCTCACCCAGCTTAAGG AGCTGTAGATGAGACAGATTTCTTTGGCTGAAAGCTTGTGAGATTAACGCAAGATGATTTTC TATGAAGTGAAAAGAAGAGGTTTACAGTGATAACAGATGCTTTTGGCCACCAAGTCGACTGAGAC AGAAATAGCACAAAACTAGGCTAICTAGGTGTTGCTCCAGCAIACAAGCGTGTGGATACTTGTG CTGCTGAGTT</p>	45241.66667	26822.75	19916.95833	6911.295401	4416.660874	2788.6380671.2	0.8	-0.4	0
1406	casein kinase II	miscellaneous	112	singleton	1	EG974468	<p>GAAATAGCGCACGTTAACGGGAGTGGTGTGCTGCTTATGACCCATGCGCCAACTCATCTACTA CTCTAGCTTCTGTAGTGTGCACCTGTGTGTGCTGCTGGCGGATTTGATACACTCTCTAT CGTGGCACCTTGGGCTCTCCAAATCGCTAATAACAATAACAAACCATCCACCTTCTGTAGCCACT CTAATAAAGGCTCATCATCACAGACGCCAACGAGATCTTGGGTCCAAAGCTCCAAAGCTATG TCCAAAGCTGTGTACACAGATGTCAAATGCTTGGCTTAAAGAGTACTGGGATGAGTACGAGTCC CCTGGCTGTTCAATGGGGTGTCAAGATGATGAGGTTGTTCCGAAAGTAGGAAGGGGGA.AAT ACAGTGAAGT</p>	19296.79167	61739.08333	36636.5	2091.63016	7123.657141	3670.530271+0.9	-1.7	-0.8	0.1
2396	catalase	oxidoreductases	195	singleton	1	EG974439	<p>CACCCACGGTCCGCTCACTACTCTTTCTCTCTA.AAATCTTGATCCAACTTTCGCTCCATC TTCAAACATGGATCTTACAGTATCGACCATCGAGTGTCTACACGCACGTTTATGACTACAA ATGCCGAGCTCCGGTTTACAACAATGAGTGGCTTAACTGCGGACCCAGAGGTTCCAACTCTG TTGGAGGATATCATCTGGTGGAGAAGATTGCTAAGTCCACAGGGAAGGATGCCAGAGCGTAT TGTCCATGCCAGGGAGCCAGTGTAAAGGTTTCTTTGAGGTGACTCATGATGTTTCAAACTCA CCTGTGCTACTTCTCGAGCTCTGGGGTTCAGACCTGTCTAGTGTCTGTTCTCCACTGTC ATCCACGAAGCGTGTAGTCTCGAAACTATCAGAGACCTCGTGGTTTTGACGTAAGTTTTACAC CAGAGGGTAAATTCGATAT</p>	76218.25	4988.33333	15025.45833	14079.11323	873.9260848	3861.4232392.3	3.9	1.6	0
4780	cellulase	glycosylhydrolases	30	contig	4	EG974167	<p>CACCCACGGTCCGCAAAATCGAGGTGGATTGTGAACGAGAGTGGGATAGAGTGAAGCTGGCCT GGTGAATTTGGCTTCTCATTTGATGGTGGTGGCGGAGGCTTAGAAGCCAAAGCCCAACGAA GCAATTGCAGCCCAATCATCATTTGGTTAATACTGGTTCATCTCAATTTGGCTACTACTT GGTCAACCAAGCGCTTTCCTCCCAAGCGCCGAGACTCTTCAAAAGTCTTGGCTCACCC AAGCATTGTGGGTGAGAGCCATAAACCCTCCATAATCGATTTCTCACTGTTTGAAGCTTTC AAGGCTGTGGTATCTGCTTGGAGACAAGAATGTTAAGTGTGATTTGGATAATCAGTAAAGCAA ACCCAGTTGGTGTGACAGTGAATCAGATGGGAATGGATTTTTGGGGACATAACTTGGACCCTA ACGCTGGATTAAGGGCCATTAC</p>	9122.25	130915.375	86982.875	1323.616968	14699.59226	7475.538218-3.3	-3.8	-0.6	0
4451	cellulase	glycosylhydrolases	30	contig	4	EG974168	<p>TCACGGTCCGGCCAGGGCTTGTACACTGAGTACAAAATCGAGGTGGATTGTGAACGAGAGTGGG CATAGAGTGAAGCTGGCTGGCTGAAATGGGCTTCTCATCTGATGCGGGTGCAGCCGAAGGCGT TAGCAAGCAGCCATCGAAGCAATTCAGCCCAAACTCATCATTTGGGTTAATACTGGCTGTCAATC TCAATGGCTTACCTACTTGTTCACAAAGCGCTTCTGCTCCCTAACCCTCGAGACTCTTC AAAAGTCTGGCTCACCAAGCCATTTGGGGTAGAGCCATAACCCCTCCATAATCGATTTC TTCATGTTTGAAGCTTCAAGGCTGTGGTATGCTCTTGGAGACAAGAATGTTAAGTGTGATTT TGGATAATCAGTAAAGCAAACCCAGTTGGTGTGAGTATCAGATGGGAATGGATTTTTGGG GACATACTTCGACCCCT</p>	3305.791667	63955.375	36766.29167	936.9256153	9318.503548	4906.140317-3.5	-4.3	-0.8	0.1
5760	cellulase	glycosylhydrolases	30	contig	4	EG974165	<p>TCGAGGTGGATTGTGAACGAGGTGGCATAAGAGTGAAGCTGGCTCGTGAATTTGGCTTCTCA TCTGTATGGTGTGGTGGCCGAAGCCCTTAGCAAGCAGCCCATCGAAGCAATTCAGCCCAAACT CATCATTTGGGTTAFAACTGGTTCATCTCAATTTGGCTACTTGTTCACCAACGACTCTT GCCTCCTAACCGTCCGAGACTCTCAAAAGTCTTGGCTCACCAAGCCATTGCTGGGTAGA GGCAATAACCCCTCAATAATGATTTCTCACTGTTGAAGCTTTCAAGGCTGTGGTATCGCTC TTGGAGACAAGAATGTTAAGTGTGATTTGGATAATCAGTAAAGCAAACCCAGTTGGTGTGCAAGT GATTCAGATGGGAATGATTTTTGGGGACAT</p>	3305.791667	63955.375	36766.29167	936.9256153	9318.503548	4906.140317-3.5	-4.3	-0.8	0.1
3008	cellulase	glycosylhydrolases	30	contig	4	EG974166	<p>GCCAAAACCTCACAAAAA.AAAAAA.AAAAAA.AAAAAA.AAAAAA.AAAAAA.AAAAAA.AAAAAA GTGTCAGCTTAGTATATGATGCTCAATCGTCAATTCATCCAAACTGGCCAGCCAGCCAGGGC TTTTGACACTGATAAATAATCGAGGTGGATTGTGAACGAGAGTGGGCTAGAGTGAAGCTGGCC CGGTGAATTTGGCTTCTCATTTGATGGTGGTGGCCGAAAGCCCTTAGCAAGCCCAACCGAA GCAATTCAGCCCAAACTCATCATTTGGGTTAATACTGGGTTCAATTCATTTGGCCCTACTACT GGTCAACCAAGCGCTTTCCTCCCAAGCCCTGAGACTCTTCAAAAGTCTTGGCCCTCACCC AAGCCATTGCTGGGTAGAGCCCAATAACCCCTCCATAATCGATTCTTCACTGTTGAAGCTTTC AAGGCTGTGGTA</p>	17194.33333	212970.375	124522.4583	3313.696628	27524.0615	13929.23232-2.9	-3.6	-0.8	0
6708	cellulose synthase.1	glycosyltransferases	50	singleton	1	EG974169	<p>GTGAACCCAGTTGAGGATTCATTTGGCTTATGTTGACTTCTGTGATATGTGAGATTTGGTTGG GTTTTATGATTTGATCAGTTTTCCAAATGGTTCCCAATGACCCGAGACCTAICTTGAIC GTCTTTCAATCAGGTATGAGAGAGAGGAGCCAAACATGCTTCCCGCCAGTGTGATGTTGTTG AGTACAGTGGATCCATGAAGAACCTCTATTTGACTGCCCAACAAATCTTTCGATCTAGC AATGGACTCCAGTTGACAAGACTCTTGTACTATTTTGTGATGAGGAGTTCCTCATGTGCACAT TCGAAGCCTTATCGAAACTGCAGAGTTTGTAGGAAATGGGTTCTTTTGGCAAGAAGTTTTCC ATAGACCCAGAGCTCCTGACATGACTTTTTGTGAGAAGATGATTAACCTCAAGGCAAAAGTGCA ACCTACTTTT</p>	8960.875	52981.08333	42247.625	1134.972255	7756.66489	5688.53735-2.2	-2.6	-0.3	0.1
1914	cellulose synthase.2	glycosyltransferases	51	singleton	1	EG974170	<p>GGGAAAATTCATCCCAACACTTAAACAATCTGGCAGTATAGGTTCTTAGCTCTTTTCTTTT CCATCATGCCACCGGCAATTCGAGCTTCGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG AATGAGCAATTTGGTCAITGGTGTCTCAGCACATCTTTCCCGCTTCCAGGCTTCCAAAGGCTTCT CAAAGTCTTGGAGGATGACATAATTTAAGTACATCAAAAGGAGCCAGCCAGCCAGGAGT TTGGAGAACTTACCTTCAATGGACTACTACTATCCCAACCACTCTTATAATAATA AACATGGTGGAGTTGACTGGAGTTCTGATGCCAATAACAAATGGCTATGTTCAITGGGGTCC TCTTTCCGTTAAGTTGTTTTCCGCTTTTGGGTCATTTCCATCTCAACCTTCTCTTAAAGGTT TAATGGGAAG</p>	12270	71922.04167	56419.375	1386.323764	9348.291409	5185.309594-2.2	-2.6	-0.4	0.1

3898	chlorophyll a/b-binding protein_4	photosynthesis	213	contig	8	EG974270	GTATATCC AAGGAGAAC AAAAGTCTCTCTCC AITGAAAATTCCTTCTTAATAATGGCTTCTTCA ACAATGGCTCTCTCTCCATCTTTTGCAGGCCAAGCTGTGAGGCTTGTCTCTTCCCAATCTAA ACTCATGGGTGAGAGCGGAACACCATGAGAAAGCCGCAAGTAAACCCAAAGAAATTCATCTT CAAGCCATGTTAGCGCCAGACGGCCCAAGTACTTTGGGCCATTCTCAGGTGAGGCTCCATCT TACCTACCGGAGAAATCCCTGGGCAITATGGCTGGGATACAGCTGGGCTTTTCAAGTATCCCGA AACCTTCGCCAAGAACCGTGTAGCTGAGTCCATCCACTCAGGTGGGCCATGCTCGGGCCCTGG GCTGTCTTCCCGAACTTTGGCCCAATGGGTC AAGTTCGGTAGAGCAAGTTCGGTAGAGTATGGTTC AAG CCCGGTCTC	276349.2917	152400.1667	115262.375	46635.47647	27917.96359	24661.86426	1.3	0.9	-0.4	0
2945	chlorophyll a/b-binding protein_4	photosynthesis	213	contig	8	EG974304	GGGGAAACA AAGTCTCTCCATGAAAATCTCTTCTATAACCGCTTCTTCAACAATGGCTC TCTCTCTCCATCTTTTGCAGGCCAAGCTGTGAGGCTTCTCTTCCCAATCAAACATCAIAGGCG GAGCGGAAGCGCATGAGAAAGCGCCAGCTAAACCCAAAGAAAGTTCATCTTCAAAGCCCATG GTAGGCCAGACCGGCCAAGTACTTTGGGCCAATCTCAGGTGAGGCTCCATCTTACCTCACCG GAAATTCCTGTGGATATGGTTGGGATACAGCTGGGTTTCAGGTATCCCGAAACCTTCCGCC AAGAACCGTGTAGCTGAGGTCATCCACTCAGGTGGCCATGCTCGGGCCCTGGGGCTGTGCTT CCCGAACTTTGGCCCAATGGGTC AAGTTCGGTAGAGCAAGTTCGGTAGAGTATGGTTC AAGGCCGGGTCTC AAATATACGGATG	276349.2917	152400.1667	115262.375	46635.47647	27917.96359	24661.86426	1.3	0.9	-0.4	0
2128	chlorophyll a/b-binding protein_4	photosynthesis	213	contig	8	EG974271	GATTCAGGAGAAC AAGTCTCTCTCC AITGAAAATTCCTTCAACAATGGGCTTCTTCAACA TGGCTCTCTCTCTCCATCTTTTGCAGGCCAAGCTGTGAGGCTTCTCTTCCCAATCAAACATC GTAGGCCAGACCGGCCAAGTACTTTGGGCCAATCTCAGGTGAGGCTCCATCTTACCTCACCG GAAATTCCTGTGGATATGGTTGGGATACAGCTGGGTTTCAGGTATCCCGAAACCTTCCGCC AAGAACCGTGTAGCTGAGGTCATCCACTCAGGTGGCCATGCTCGGGCCCTGGGGCTGTGCTT CCCGAACTTTGGCCCAATGGGTC AAGTTCGGTAGAGCAAGTTCGGTAGAGTATGGTTC AAGGCCGGGTCTC AAATATACGGATG	276349.2917	152400.1667	115262.375	46635.47647	27917.96359	24661.86426	1.3	0.9	-0.4	0
91	chlorophyll a/b-binding protein_4	photosynthesis	213	contig	8	EG974274	CTCTCTCCATGAAAATTCCTTCTATAAGTGGCTTCTTCAACAATGGGCTTCTCTCTCTCCATCT TTTGCAGGCCAAGCTGTGAGGCTTGTCTCTCTTCCCAATCAAACATCAAGTGGCGAGAGCCGAACCC CATGAAAAGGCCGCAAGTAAACCCAAAGAAAGTTCATCTTCAAGCCATGTTAGGCTCCAGACC GGCCAAAGTACTTTGGCCCATCTCAGGTGAGGCTCCATCTTACCTCACCGGAAATTCCTGTGG GATATGTTGGATACAGCTGGGCTTTCAGCTGATCCCGAAACCTTCGCCAAGAACCGTGTAGCT GGAGTCAATCCACTCAGGTGGCCATGCTCGGGCCCTTGGGCTGTGCTTCCCGAACTTCTGG CCGTAATGGGTC AAGTTCGGTAGAGCAAGTTCGGTAGAGCAAGTTCGGTAGAGTATGGTTC AAGGCCGGGTCTC GGTCTCAA	276349.2917	152400.1667	115262.375	46635.47647	27917.96359	24661.86426	1.3	0.9	-0.4	0
281	chlorophyll a/b-binding protein_4	photosynthesis	213	contig	8	EG974272	GATGGGAGAGCCG AACCATGAGAAAAGCCGACGCTTAAACCCAAAGAAAGTTCATCTTCAA GCCATGTAGGCCAGACCGGCCAAGTACTTTGGGCCAATCTCAGGTGAGGCTCCATCTTAC CTCAGCGGAAATTCCTGGGCAITATGGTGGGATACAGCTGGGCTTTCAGCTGATCCCGAAAC CTTCCGCAAGAACCGTGTAGCTGGAGTCTCCACTCAGGTGGCCATGCTCGGGCCCTGGGCT GTGCTTCCCGAACTTTGGCCCAATGGGTC AAGTTCGGTAGAGCAAGTTCGGTAGAGTATGGTTC AAGGCCGGGTCTC GGGTC AATATATCAGCGATGGGCTGACTTATGGGAAACCCCTAAGTTCGCTCCAGCAAGTTC AAGCATTTAGCAATTTGGGCCACACAAGTATCTTAATGGGAGCAGTTG AAGGTTACAGAATG GAGGTGGCCACT	276349.2917	152400.1667	115262.375	46635.47647	27917.96359	24661.86426	1.3	0.9	-0.4	0
3714	chloroplast ferredoxin I	photosynthesis	215	singleton	1	EG974275	GCAGTTCAGTTC AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA TGCCATGGTAGACACCTCTGTGGAGGAGACACCCACAGGCTTCTAGAGGCTTCTAGAGGCTTCTTCCCA ACGTTGGTCAAGCCACTTTTCGGGCTCAAGGCCAGCACAGAAAGCCGAGGAGGCGGTGTGACTGCC ATGGCAGCTACAAGGTGAAGTAAATCACCCGAGGGGAGACTGAGTTCGAATGCCCTGACGA GTGACGTGCTCGAACAAAGCCGAGGAAATGGGCTGGACTTGGCTTACTCTGGCCGAGCAGGGT CTTGTCTCTCGTGGGAAAGTGTGAGTGGAGATGTAGACAGCTTGACACAAGTTCCTC GATGATGATCAGATTTGGTGAAGGTTGGTTCACATGTTGGTTCACCCCTAGCTGTGATGTTG CATTTAGACT	276349.2917	152400.1667	115262.375	46635.47647	27917.96359	24661.86426	1.3	0.9	-0.4	0
97	cinnamic acid 4-hydroxylase	secondary metabolism	241	singleton	1	EG974529	GCATCTCTAATTTAATCTGTTCTCTTATGTGTGGCCACTTTTCCCTTATCCAACGGCATGG ATCTCTCTCTTGGAGAAAGCCCTCATAGCTCTTCTTAGCTGTGGTGTGTCGAATAGTCAATC GCAAGCTCAAAGAAAGAATTC AAGCTCCACCCGACCCATCCCTGACCCGTAATTTGGAAA CTGGCTCCAGTGGGAGTGTGAACACCGCAACTTAAACCCGACTTACCCCAAAATTCGGCG ACATTTCTTGTGTAGAAITGGGACAAAGAAATCTCGTGTGGTTTCATCACCGGAGCTAGCTAA GAGGTGCTCACACCCAGGAGTTGAATTCGGATTCAGAACCCGAAACCGTGTATTCGATCTT CACTGTGAAGGTCAGGATATGGTGTTCAGTGTAGCGGTGAGCAATGGAGAAAGATGAGGAGAA TCATGACCGTT	276349.2917	152400.1667	115262.375	46635.47647	27917.96359	24661.86426	1.3	0.9	-0.4	0
2425	crambin_1	miscellaneous	175	contig	2	EG974392	GTAATAATTTTGAAGAAGATATATAGTAGAGTGAACCTAAATAAATAAATAAATAAATAA GGCAAACTAGGTTATGTGAGTGTCTGTAGTGTAGGCTTGTTTGGGACAAATTC AAGTTGA GGCAAGAAGTGTGTCCAAACCGCTGTAGAAATATACGATCGATGCTGTTTGGCCGAG GCTCCAGAAATTTGTGCAAACTCAGCGGATCAAAATATTTCTGGGACACATGTCGCCGAC GGTTAAACAGACTTCAAATAATGGTGGTGTATCTGTCAATGATTTGAAGTTGGG GTGTACATCCCTCGGTGGGATCCCTTAACCACTTCCAAAGACTTTCAGCAAGTGAAGTGTGA AGGAAGCTTGTGAATAATGTATCAAGGCTGTTTGCATTTTGCATTAAGGTTCCATTTGCACT ACTCAGTTGA	276349.2917	152400.1667	115262.375	46635.47647	27917.96359	24661.86426	1.3	0.9	-0.4	0
3224	crambin_1	miscellaneous	175	contig	2	EG974393	GCAAAAGTCTCTATAATAAATAATTTTGAAGAAGATATATATAGTAGAGTGAACCTAAATAA TAGAAGATCAATGAAAGGCAAACTAGGTTATGTGAGTGTCTGTAGTAGAGGCTTGTGTTG AGGCAAAATTC AAGTTGAGGCGAAGAGTGTGTCCAAACACCCACTGTAGAAATATACGATG CATGCTGTTTACGGGAGGCTCAAGAAATTTGTGCAAACTCAGCGGATGCAAAATCAATTTCT GGAAATACATGTCGCCAGGTTAAGCAATGACATCTCGAAACAAAGTGGTGTGATTTGGCCAA TGAATACTGAAATTTGGGTTGACATCTCTGTGCGATCCCTTAAACCCACTCCCAAGACTCTG ACGCAAGTGAAGTGTGAAGGAGCTGTTGAAAATAATGACGAAAGGCAATGTTTGTCTATTTGCACT AAGGTTCCAT	276349.2917	152400.1667	115262.375	46635.47647	27917.96359	24661.86426	1.3	0.9	-0.4	0
373	crambin_2	miscellaneous	176	contig	3	EG974396	CCATTCAGCGTCCGCTATAATAAATAATTTTGAAGAAGATATATAGTAGAGTGAACCTAA TAATAAGGATCAATGAAAGGCAAACTAGGTTATGTGAGTGTCTGTAGTAGAGGCTTGTGTTG TTTTGGCAAAATTC AAGTTGAGGCGAAGAGTGTGTCCAAACACCCACTGTAGAAATATACGATG ATGATGCTGTTAAACGGGAGACTCAGAAATTTGTGATCATGATCAGCGGATGCAAAATAT TCTGGAAATACATGTCGCCAGCTTATGTCAATGAATACGTGAAGTGGGTTGATCTCTCTCT GTGGATCCCTTAAACACTCCAAAGACTCTGATGCAAGTGGTGTGGAAGGAGCTGTTGAAA AATGACCAAGGCAATGTTTGTGATTTTACACTAAGGTTTCCATTAAGTGTGACTTCCAGTTGAAAT GCTATGAAGGATAAATTTGTCAATC	276349.2917	152400.1667	115262.375	46635.47647	27917.96359	24661.86426	1.3	0.9	-0.4	0
1373	crambin_2	miscellaneous	176	contig	3	EG974395	CCCCTTTACGGCTCCGATATTTTGAAGAAGATATATAGTAGACTTAATAAATAAATAA GATCAATGTGAAGGCAAACTAGGTTATGTGAGTGTCTGTAGTAGAGGCTTGTGTTGGGAC AAATTCAGTTGAGGCAAGAGTGTGTGCAACCAACCCACTGTAGAAATATCTACAAATGATG CGTTAACGGGAGACTCCAATAATTTGTGCAATGATCAGCGGATGCAAAATATTTCTGGGAA TAGATGTCGCCAGCTTATGTCAATGAATACGTGAAGTGGGTTGATCCTCTCTGTGGCATC CCTTAAACCACTTCCAAAGACTCTGATGCAAGTGGTGTGGAAGGAGCTGTTGAAAATGTAC AAGGCAATGTTTGTATTTACACTAAGGTTTCCATTAAGTGTGACTTCCAGTTGAAATGCAAGG GGAGTAAATTTGTCACTAAGG	276349.2917	152400.1667	115262.375	46635.47647	27917.96359	24661.86426	1.3	0.9	-0.4	0

913	crambin_2	miscellaneous	176	contig	3	EG974397	271411.875	11369.58333	60159.54167	26223.3764	1645.419825	8588.670626	2.2	4.6	2.4	0
GCTATAATAAATATTTTGTAGAAGATATATAGTAGAGTGGAAGTAATAAATAAATAAATTAAGATCAAT ATGGAAGCATAAACTATGTTATGTAGTGTGTTTGTAGTGGCTTTGTTGGGACAATAATCA AGTTGAGCGGAAGAGTTGTTGTTCCAAACACCAGCTGTAGAGAATATCTACAAATGCATGCTGTTTAA CGGAGACTCCAGAAAATTTTGTGCATCGAATAGCGGATGCAAAATATTTTCTGGGAAATACATGT CCGACCCTTATGTCAATGAAATGTTAAAGTTGGGTGTGACATCCCTCTGTCGGATCCCTAAAC CACTCCAGACTGTATGCAAGTGGTTGTGAAGGAGCTGTGAATAATGTTACCAAGGCAT GTTTGGCTATTTACACTAAGGGTTCCATTAAGTGTGCAAGTGTGAAATGTTGAAATGTTGAAAGGATTA TATTTGTCA																
1601	CYP78A3	oxidoreductases	188	singleton	1	EG974432	15386.16667	8994.75	7634.583333	1765.44776	1154.420138	1042.4853	1	0.8	-0.2	0.3
GTAACCTTTTATCTTTCATAAATGACCGACCCACTTCTCAATATCTCTGTTCTCTCTCTCTCT TCTGGCTTCGCTCGCTCCAAACATGCAAGAGCTTCTCCAAAGAACCTTTCGATGGTTG CTTCTGGGGGGGCTCACTGGCTGCTAGTCTTAGTTTATTTGGGCACATCCGGAGGCC AGCTGGGCAAGCAAAAATGGATGAAAACCCATTAACACGTTAAGACTGCAAGCTGCAATTC CAGGCCAAGAGGCTTCCCTCTCGGACAGTGGCTTATGGCTTCTGGCTACCCGCCG TTAGCCCAATGGCTACAGATGCAAGCCAAAGCTCAITGGCTTTTCTTTGGGGACACTCC TCTTATGGTACGTTGCACCTGACGTGCCAAAGAAATACTCAACAGCCCTGTTTCGCTGACC GTCCGATCAAGGAA																
137	cystein proteinase.1	amino acid & protein metabolism	11	contig	3	EG974480	29066.75	57260.45833	32501.375	3274.285302	6722.8657	2116.189657	-0.2	-1	-0.8	0
GCAACATCTCTTCCAAAATGACCGACCCACTTCTCAATATCTCTGTTCTCTCTCTCTCTCT ATCTACGGTGTGCCCTCCGCGTGAATCGAAGGAGGTCAAGAGCAAGCAAGATCTTCTGATCCGCTC AGTTTGTTCGGAAGGAGATGATATATTTCAACCGCGCACACTTCAACCGCTTCAAGCAACACTT AATTTGGGAAGACCTATGCTACCCCGAGGAACACGACTACCGCTTGACTCTTAAAGGCTAA TCTTGGCCGCAAGGAGGACCAGAGCTTGAACCTACCGCCGTTCATGGAGCTACTAAGTTTT CCGATCTGACTCCAGTGAATTCACAGGAGCTTCTCGGCTCAAGCTCTCCGCTACCTAC GACGCTCAAAGGCTCCGATCTTCTACTAAGGATCTTCCAGGACTTCCAGAGACTTGTGACTGGCAGATCA TGTGCGCTCAC																
3128	cystein proteinase.1	amino acid & protein metabolism	11	contig	3	EG974481	34552.5	69617.45833	39967.33333	5400.358428	9132.045872	4085.198147	-0.2	-1	-0.8	0
CTTCTCTACTACGGTGTGCCCTCCGCGTGAATCGAAGGAGGTCAAGAGCAAGATCTTCT GATCCGTAGGTTGTTTGGGAAGGAGATGATCAIATTTCAAGCGCCAGCAACACTTCCAGAGCT TCAAGCAACACTTTGGGAAGACTATGCTACCCCGAGGAACACGACTACCGCTTGACTCTTAAAGGCTAA AAGGCTAATCTTCCGCGCAAGGAGGACCAGAAAGCTTGAACCTACCGCCGTTCATGGAGTCA TAAATTTTCCGATCTGACTCCAGTGAATTCACCGGAGCTTCTCGGCTCAAGCTCTCCGCTCCGCT TACCTACGACGCTCAAAGGCTCCGATCTTCTACTAAGGATCTTCCAGGACTTCCAGAGACTTGTGACTGG CGAGATATGGTGGCTCACGGAG																
1916	cystein proteinase.1	amino acid & protein metabolism	11	contig	3	EG974484	18282.25	38024	23224.75	2363.594804	4672.059781	2268.247197	-0.3	-1.1	-0.7	0
GTCTTCCAAAATGACCGACCCACTTCTCAATATCTCTCTCTCTCTCTCTCTCTCTCTCTCT GTGCTGCCCTCCGCTGAAATCGAAGGAGGTCAAGAGCAAGATCTTCTGATCCGCTCAGGTTGT TTCGGAAGGAGATGATATATTTCAACCGCGCACACTTCAACCGCTTCAAGCAACACTTTCG GGAAGACTATGCTACCCCGAGGAACACGACTACCGCTTGACTCTTAAAGGCTAATCTTCG CGGCAAGGAGGCCAGAGCTTGAACCTACCGCCGTTCATGGAGTCACTAAGTTTTCCGATCT GACTCCAGTGAATTCACAGGAGCTTCTCGGCTCAAGCTCTCCGCTTACCTACCGGCTC AAAAGGCTCCGATCTTCTACTAAGGATCTTCCAGGACTTGTGACTGGGAGATCATGTTGGTCC GTACAGGAGTTA																
3882	cystein proteinase.2	amino acid & protein metabolism	3	singleton	1	EG974485	22462	63208.79167	47966.20833	2874.3007	7874.932689	5032.973237	-1.1	-1.5	-0.4	0
GAAAATATCTCTTCCCGGGAAAGCTCATGGCCACCGCACCTCACCTCCTCTCTCTCTCTCTCT TCTGCTCTCTGTAATCGCTCCGGTAGCGGGAACTAGTCGGAGATGTTCTCCGATTTGCCCTC TCAAGCTTCCAGATTTTCCGACTTAATCTGCTCGGAGCTTCCGAGCTTCCGATCCGCTGGGACCA GATGGCTGTTCTGATTTGCTGATGAGTGGATGGAATACAGGCAATGAGGCTGACATATGT CATGCTTACCACTTGAAGAAAGGTTTAAAGGATGAGCAATTTGTTGTTATGATGA TGATATAGCTTCCAATGAAGAACCCAGGCTGAGTCAITTAATTAACCACCCACATGGGGTG ATGTATAAAGGTTTCCAAAAGGATTAATCTGTTGGAAGTCACTGTGGAACTTTTTTCCGCT GCCATCTCGA																
2000	cytochrome b5	oxidoreductases	183	singleton	1	EG974450	60200.625	217922.25	113363.7083	8984.952397	68435.99465	10939.01632	-0.9	-1.9	-0.9	3.4
GCTTCTCTCTCTTTTGAITTAAGCTTCTGGAGTGGCGGGGACAAACTCAGATCAAT AGTATGGAGAGAGAAAAAAGTTTACACCTTCTGAGTGTCTGAGTCAACAAACCGGCACAA ATGTTGGCTGTCATCCGGGAAAGGATATGATGACAAAATCTTGGATGACCATCTGGTG GTGATGATGTCATATCTAGCAAGGAAAGGATGCAACTAATGATTTGACAGATGGGCAAT AGTACAACTGCTACTATGATGGATGATTTTACATAGGAGATATTGACAAACAATTTCC TCTAAGGTTGACATACACACCACAAACAGCCCTCATTAACAGGACAAAGACACCAAGAGTTCA TCATCAAGATCTCCAAAGTACTTCTCTCTTCTAAATTTTGGGTGTAGCCGTCCGAAATTCGCTTC TACACCAAGTC																
2748	Cytochrome c	oxidoreductases	178	singleton	1	EG974451	3732	70227.75	47744.41667	587.6884712	9093.812388	5639.13809	-3.7	-4.2	-0.6	0
GCCAGCTGGCAGGACACCAGAAAGCCCTGATGGCCCTACCGGCAGTCCCTGACGAGCGGTT GCCGATCGAGCAGTGCAGCGCCCTGGACGTGGCAAGGCAAGCTCACCGAGTCCGCGCGCC TGTGGGAGCGGATGGCTTGGCTGCTCCTGATGATACATCTCCGGTTTGGTATCTGCTGGCC GAGGCTGGAAGCTGCTGGGCTGGGCGATCTCCGCTTCCGTTAACACCGCCAGCA ATCGGGTGGCAGGCTAACGTCGGCTGGGCGCTGGGCTATTGGCCGGCTTGGCCACCTGGG CGTTGGCGCTTATGATGACGCTAGCGGCGCCAGCGGAGTTGCTGGAAGGCTGCACGGCC CTGTTGCCAGTGTGATGGCTGGCTGGGCTGATGACAGC																
850	dehydrin	miscellaneous	132	contig	3	EG974424	63245.66667	138103.875	91847.33333	8446.762921	18620.39903	10529.08675	-0.5	-1.1	-0.6	0
CGCACTTACATACAGTTAAGCCAAAGTTTCTTCTAGTCAACCCTGAGGAGAAACAAGA GCCAGATACGGGTTTCCTGGTGAACAAAGATCGTGACTTGGATTTGATTTCTTGAAGAAA GATGATCGGGGAGGAGAAAGAAAGGCTGATCCACATCATGATGCTGTATAAGTCCGA GTTCACTGAGAGGTTCAAGGTTCTGAACAACACGACCTGTAAAGTCTTCTCATGACCACTCA ACTATTTCAACGCTGAAGAAGCTTAAAGAAAGAAAAGATGAACCCAACTCCAGTAAACTC CACCCTTCTCAGAGTACTAGCTCTTAGCGATGAGGAAGAATGTTGAAGGAGGAGAGAAAA GAAGAAGAAGAAAGGG																
1866	dehydrin	miscellaneous	132	contig	3	EG974423	74445.04167	171886.625	95369.375	9608.506918	23524.28432	7753.334188	-0.4	-1.2	-0.8	0
GCCACGGTCCGACACTCTAATACAAAAAACHTTCTTCTTCAACTCTCCTTACTTACATA TCAGTTAAACCAGGTTCTTTCTAGTTAACATGGCTGAGAGAGAAAGAGCCAGATACAGAG GGTTCATCCGTGGAGCAAGATCGTGGACTATTTGATTTCTTGAAGAAAGATGATCAAGAA GGAGAAAAGAGGCTGATCAACATATCAGTGTGTATAAGCTCCGAGTTCCTGAGAAAG TCAAGGTGTCTGAACAACAGCTTGAAGTCTCTCATGACCCAGCTCAACTATTTCAACGCT GAAGAAGTTTAAAGAAAGAAAGATGAACCCAAATCCAGCTAACTCCACCGTTCACAG TAGCTTAGCTCTTAGCGATGAGGAGATGTTGAAGGAGAGAAAAGAAAGAAAGAAAGAA AGGAAATTAAGG																
2948	dehydrin	miscellaneous	132	contig	3	EG974425	205088.7083	434210.6667	298682.2917	23074.91035	64232.47228	32698.83475	-0.5	-1.1	-0.5	0
GCAAAAAAACHTTCTTTCAAACTCTCCTCTTATCATCTTCTCTCTCTCTCTCTCTCTCTCT TTAACCATGGCTGAAGAGAACAGGCTCAGGATTTACGGGTTTCTCCGTGGAGCCAAAGATCG TGGACTATTGATTTCTTGAAGAAAGATGATCAAGGAGGAGGAAAAGAGGCTGATCACCATC ATCATGATGCTGTATAAGCTCCGAGTTCACTGAGAGGTTCAAAAGTGTCTGAAACAACAGACT GTTAAGTCTTCAAGACCAGTCAACTATTCAAGGCTGAAGAACTTAAATGAAAGAAAGAA GATGACCCAAATCCAGCTAAACTCCAGGTTCTCACAGTACTGACTTAGCTTCTTAGCGATGAGG AAGAATGAAAGGAGAAAGAAAAGAAAGAAAGAAAGAAAGGAAATTAAGGAGACACTAAAGGAA AAATCTCAGGT																

682	dessication-related_1	169	contig	2	EG974390	CGCTAATAATAATAATAAAAGTAAGTATAGAGAAATCAATACCGGACACTCAATTGTTGCTC TTACATAGTCCCTCTTTCAAAATCTGACCAGTGTGGTACCAATTGATATCTCCA AATGACTAGTATGATGTAATCGTTGGAAATTTCTTGAATCTTGGATTTTGGCAGCTGAAT CTTCTGTAGCGATCATTTGGGTATGTTGGACAGAGTTGATCCACAACATGGCCAAAGGTTGGCC CACCTCCATTGGTTACAAAGGGCCAATTTGGTAATCTACAGCAAGATATATACAAATTC GGATATCAGCAAGTTGGAACAATCAGAGCTATTTGCAATACAGTGAAGGGTTCCCAAGGCCACT ATTGGATAAGTTCAGCAGTATTTGCAGCAAAATAGACATTGCATTTGGAGAGACATAAGAC CACCTTTAATCTTACGGAAATAGCAATA GCTAATAATAATAATAAAAGTAAGTATAGAGAAATCAATATGGACACTCCAATTGTTGCTCT TACATTAGTCCCTCTTTTCAAAATCTGACCAAGTGTGTGTACCAATTAATCTTCCA TTAGCTAATATGATGATCGCTTGGAAATTTCTTGAATCTTGGATTTTGGCAGCTGAATTC TTCTTGGCAGATCATTTGGGTATGTTGGACAGAGTTGATCCACAACAGTGGCCAAAGGTTGGCC ACCTCCATTGGTTGACAAAGGGCCAATTTGGATAATCTACAGATATATACACAAATTCG GATATCAGCAAGTTGGAACAATCAGAGCTATTTGCAATACAGTGAAGGGTTCCCAAGGCCACTA TTGGATAAAGTTTACAGCAATTTTGCAGCAAAATAGACATTTGCAATTTGGAGAGACATAAGACC ACCCTTAATCTTAC	4086.625	11289.83333	3715.793798	754.7124028	7219.937871	1.1	2.5	1.5	0
4206	dessication-related_1	169	contig	2	EG974389	GCTAATAATAATAATAAAAGTAAGTATAGAGAAATCAATATGGACACTCCAATTGTTGCTCT TACATTAGTCCCTCTTTTCAAAATCTGACCAAGTGTGTGTACCAATTAATCTTCCA TTAGCTAATATGATGATCGCTTGGAAATTTCTTGAATCTTGGATTTTGGCAGCTGAATTC TTCTTGGCAGATCATTTGGGTATGTTGGACAGAGTTGATCCACAACAGTGGCCAAAGGTTGGCC ACCTCCATTGGTTGACAAAGGGCCAATTTGGATAATCTACAGATATATACACAAATTCG GATATCAGCAAGTTGGAACAATCAGAGCTATTTGCAATACAGTGAAGGGTTCCCAAGGCCACTA TTGGATAAAGTTTACAGCAATTTTGCAGCAAAATAGACATTTGCAATTTGGAGAGACATAAGACC ACCCTTAATCTTAC	4567.625	7532.958333	9696.434179	761.0168036	1746.85239	2.7	3.5	0.7	0.1
6744	dessication-related_2	174	singleton	1	EG974391	GAAGAAGACCCCTTAATCTTACCGAAATAGCAATTAATTTCTTATAGCATATATATATG CCTTATACAGTACTCTGGTACGTTGAGCAAAACCCCAACCCCTGATGGATCTTCCAAAGC ACTTGTGGCAGGCTTTTGGGTGTGAAGCAGGGCAAGATGGTGTATTAGAGCATTTGTGTACC AGCGTAGATACAAAGAGTGAAGTATATAAACAAGTGGCGGAGTTCCAAATCGAAATTTCT GAGCTAAGGAACACCTTGGCAGGTTGGTGAAGAAGAAGAGGGCTTATAAAGCTCACAGATC TTTAGGGTTGGCGAATTAGGTTTCCACCGGAAATGTTGTGTCTGCAAAAGATGACTCAGTTC CGTATGGAAAGGACACAGCTGAGATATCTGAAATTTTATGGAAGCTGTAACGAAACCGTAGGCCT GGGGCTTCT	8752.458333	20945.66667	29961.50863	1575.774804	4261.852325	3.1	4.4	1.3	0
1028	dihydroipoamide dehydrogenase	87	singleton	1	EG974244	AAAGAAGAGGGTTACCTTCTTATAGAACTCTCCCGCACCTCCGAAGCTCTCAGGTACTC GCTTCTTACCTCATTTTCCAGGGGTTTTCAGGCTATCCGAGTCTGATGAGCGCATGAGTG GGGGGGGGTGTCTGGCGGCTAGTGGCCGCAATCAAGGGCCGCTAGCTTGGACTTAAAGACC ACCTGATCGAAGAACAGTGGACTCTGGGTGACTTGGCTTAATTTGGTGTGCATACCTTCAA GGCACTTCTATCTCCCAATGATACCATGAAGTATGCAATCTTTTGGCAATCATGGAGTGA AGTTTGCATCTGTGAAATGATTTACCCTGCATGATGGTCCAGAGGATAAAGCTGTCTTGAAC CTTACCGGAGTATTGAAGGCTTATCAAGAAGAATAAGTGTGACTATGTC AAGGGGT GATAAGAAAGATTAATTTAGTGGTGTGGTGGTAAATCAAGATGGAAGTGTGAATTAACG AGGCTTGAATAATCTGGTTCCTTCAATTTCTGATGCCACCAATAAATGGCCAAACCGCCG CCTACTCAGGTTGCACCTCAAGGAGGGTTTAACTTACTGCTAGAAAATAACAAGAGTACTT GCTCAGAAATTAATCAATGCTGCTCAATGAGGAGCTTTTTTCAAGATAGCCGCCCAAGTCA CAGTTGCGAAGTTGATGCTGTCTACACCAACCCCTCAAACTGACACCTTTGATAGCCCT GGTCAACAACAACGCTCATCTCCACGCCGCGCAATGTTGGCAAGTATGCTGCTGCTCAATC TCCATCATGATGCTCTCGGATGCTGTGATAACAAGACCCCGCACCTTTGCAATACT CGGGAACC	62859.875	36087.75	3235.578677	11038.68908	4889.884848	0.6	-1.4	-0.8	0
1351	diphenol oxidase_1	186	singleton	1	EG974350	AAAGAAGAGGGTTACCTTCTTATAGAACTCTCCCGCACCTCCGAAGCTCTCAGGTACTC GCTTCTTACCTCATTTTCCAGGGGTTTTCAGGCTATCCGAGTCTGATGAGCGCATGAGTG GGGGGGGGTGTCTGGCGGCTAGTGGCCGCAATCAAGGGCCGCTAGCTTGGACTTAAAGACC ACCTGATCGAAGAACAGTGGACTCTGGGTGACTTGGCTTAATTTGGTGTGCATACCTTCAA GGCACTTCTATCTCCCAATGATACCATGAAGTATGCAATCTTTTGGCAATCATGGAGTGA AGTTTGCATCTGTGAAATGATTTACCCTGCATGATGGTCCAGAGGATAAAGCTGTCTTGAAC CTTACCGGAGTATTGAAGGCTTATCAAGAAGAATAAGTGTGACTATGTC AAGGGGT GATAAGAAAGATTAATTTAGTGGTGTGGTGGTAAATCAAGATGGAAGTGTGAATTAACG AGGCTTGAATAATCTGGTTCCTTCAATTTCTGATGCCACCAATAAATGGCCAAACCGCCG CCTACTCAGGTTGCACCTCAAGGAGGGTTTAACTTACTGCTAGAAAATAACAAGAGTACTT GCTCAGAAATTAATCAATGCTGCTCAATGAGGAGCTTTTTTCAAGATAGCCGCCCAAGTCA CAGTTGCGAAGTTGATGCTGTCTACACCAACCCCTCAAACTGACACCTTTGATAGCCCT GGTCAACAACAACGCTCATCTCCACGCCGCGCAATGTTGGCAAGTATGCTGCTGCTCAATC TCCATCATGATGCTCTCGGATGCTGTGATAACAAGACCCCGCACCTTTGCAATACT CGGGAACC	19732.20833	16217.33333	1405.943695	4654.693875	1882.023431	-1	-1.2	-0.3	1.6
1875	diphenol oxidase_2	185	singleton	1	EG974531	GCAATCCCCAAGTCAATGATTAAGCTTCAAAACAAGTAGCTCAATACTCAAGTGTAGCA AGCGAATTAAGATGGGGCTTCTTGATGATCAAGCGGTGTTCCTCTAGCCCTTGGGCTTCTC TTTGTTCAGCATTAATGCTTGGCCAAATGCCATCCAAAACCTCAACAACTCAAGATTTGTTAT TCAAGCAACACCAGTGAAGAGGCTGCAAAACCCATAACAGCATCAAGCTTAAACGGTCAATATC CTGGCCCAACCTTGAAGTGAACAGGTCACCTTCTGCTCAAGTCAACCAACAAGCTAGA TATAATGTCACCATCTGCTGATCGCATAGCAAAATGAGGACTGGTGGGCTGATGGGCTGA GTTGTGACTCAATGCCAATCCGACCGAGGAGGAGCTACTACCTATCGATTCAACAATCAAGGCC AAGAAGGACTC GCAAAACCTTCTTCTCTCTCCTCCCAACTTTTCGCCAAATCTCTTCTGCTCTCTCTGCTC GTCCTCTACTTCTCCCTCGGTGAGATTCCGCAACACAGCCGCGCCGCGCAGCAACAGCTT CAACATCTTAGCCCTCAGCGAGCGAAACACCAAGCAAGAGCTGCTCTCAACAACAAC ACCGCTCGAAGAAACGTCGCTCTCTCTAGAGATCTTGGGATCTCCGCAATCCCTACCGCCGACGTTG TCAGGATCAAAAGCCGCTACGGAGATGAGTGGGTTTGTCTCTGATGAGCGAGGATCG ATCGGAAGGATTCTTCCGGATGATTTAAGAATACAGCTGCTTACTCTTCTCCGAT CCGACTAAACCGGCGACTTATGATCGGAGATTTCTGAGGGGTCGAGTCCGTTACTATGGCTTC TGGATTTCT	28332.75	14716.375	2058.885396	4881.61682	1693.119227	0.2	-1.1	-0.9	0
6772	DUF_231_1	106	singleton	1	EG974366	CCGCATATGAGTTTGCATGGCTCCACTCTTGTAGAGCCCAAGAAAGATCTGGGAAGAAG AGAAATTAAGATTTGGATTCATTTGAAGATAATCAAGATCCGCAACAGCCGCGCCGCGCAGCAACAGCTT TTTTACTCTGCTCATTTGGTGGACTCACAGACAATGGAGTTCGTGGACTATTAATCTGGAAG GTAGTCTCTCAAAAGATGAATCCAATGATTCATFAAAGGACTACTACTACTAGTGGGCT AAATGGGTAGATTGATCTAGCCCTCAAACTGACTTTTTCAGGAGCATGTCACCTAG GCATACAGGAAATGGTGGAAATGCTACAATCAGAGCCCTCAACTGCTTTCAGTCAATC CATATGTTCTCAACAATAATAGTACTGCAAGGGGTTTAAAGAGGATGGATTTCTCTGTATAT CTACAGAGGTACTA	347824.4583	142801.6667	10131.09232	53293.44572	23472.0606	-1.2	-2.4	-1.3	0
621	DUF_231_2	99	singleton	1	EG974367	CACTACCGGCTCCGCAAGATTCGATGGAGCAAAATTTCTTGACAAGGTTTGAAGGAAAAGCAATA ATGTTTTGGGGACTATGAGCTTAAACCAATGCAATCTCTTACTTCTGATGTTCAATACAGC TAACCCATTGGTCAATAACAATCGGTAGGGTGGAGACTCTGTATTTTCAATTTCCGGCAT CAAAATTTGAGATAAATCCATAGAAATGCAATCTAGAGAAATATCTTCAAAATTTGATGCC GGAAATGAAAATAATGTTCTAGGAATGCTTCTAGTGGATATTGTAGGCCAAGTGTGGAC GAGTTCTTCAACTGACTCAGTTGGAGTTGCAACATTTGGAAAACCGTCGAGCTTTGATCTTC AACACTGGCAGCTGGCTTCACACTGGCAAAAACAGCCATGGGATTTGATTCAAGATGGGCA AGTCTAGTGAAGACATGAAT	65376.375	58288.5	873.8611377	11281.64756	12246.19902	-3.8	-4	-0.2	0
6757	DUF567_Contig114	164	contig	2	EG974329	TGTTTTGGTTTGATAATTAATAATAATGGAAACGAAAGTTCCTTGACAAGTGGTGAAGGAAAAGCAATA GGTGGCTATCCGGTGGAGTGGTGGGTCAGAATTCATGGCGCTATCCGGTGGAGTGGTGA TGACGGAGAAGAGCTTGACTCGAGAGAAGGTACTTTTACGGTAAACAGACACTCAAGAGAATCTC ATCTTAAAGTCAAAGGCTCCATTTACGCTCCATGTCGCGACTCTCTGTGATGATGCTGCA AAAGCCATCTCTTAGCCCAAAAGATAATGACAATGCAACAAAGATGG GCTTCTGATGTTTTGTTGATAATTAATAATAATGGAAAGTGGAAAGTTCACGGCACCGG GTTTTACTCCGGTGGCTCATCCGGTGGAGTGGTGGGTGAGATTCATGGCGCTATCCGGTGTG GAGTTGGTATGACGGAGAAGAGCTTGACTCGAGAGAAGTACTTTTACGGTAAACAGACTCA AGAGAATCATCTTAAAGTCAAAAGGCTCATTTCAGCTCCATGTCAGCTCCATGCTGCGACTCTTG ATGCCACTGAAAAGCCACTCTCTTAGCCCAAAAGATAATGACAATGACAAGAGATGGCAT GTATACAAAGGAGAAGCTCAGATGCAAAAGACTTACTTTTACAGCCAAAAGACTCTCAATCAT TCAAATCAATACAGATTTAGAAAGTGTCTTAGGTGGAATAACAAAGCAAGAAAATTCCTGATTTA AGTCAAAAGGG	67769.91667	59780.91667	30467.91005	11486.94715	11758.23154	2	1.8	-0.2	0.1
1318	DUF567_Contig114	164	contig	2	EG974327	AAAGCCATCTCTTAGCCCAAAAGATAATGACAATGCAACAAAGATGG GCTTCTGATGTTTTGTTGATAATTAATAATAATGGAAAGTGGAAAGTTCACGGCACCGG GTTTTACTCCGGTGGCTCATCCGGTGGAGTGGTGGGTGAGATTCATGGCGCTATCCGGTGTG GAGTTGGTATGACGGAGAAGAGCTTGACTCGAGAGAAGTACTTTTACGGTAAACAGACTCA AGAGAATCATCTTAAAGTCAAAAGGCTCATTTCAGCTCCATGTCGCGACTCTCTGTGATGCTC ATGCCACTGAAAAGCCACTCTCTTAGCCCAAAAGATAATGACAATGACAAGAGATGGCAT GTATACAAAGGAGAAGCTCAGATGCAAAAGACTTACTTTTACAGCCAAAAGACTCTCAATCAT TCAAATCAATACAGATTTAGAAAGTGTCTTAGGTGGAATAACAAAGCAAGAAAATTCCTGATTTA AGTCAAAAGGG	16368.08333	12176.29167	15113.19198	2464.134603	1490.180367	3.3	2.9	-0.4	0

Accession	Category	Region	Type	Length	Start	End	Score	E-value	Other							
4480	DUF642 containing	miscellaneous	singleton	107	1	1	9354.75	48027.79167	38383.54167	1422.828419	6275.253109	3818.36521	-2	-2.4	-0.3	0
4145	DUF642 containing_1	miscellaneous	contig	170	16	16	19924.83333	10303.04167	9919.583333	2966.151519	2213.193207	2408.471602	1	1	-0.1	0
6071	DUF642 containing_1	miscellaneous	contig	170	16	16	219556.0833	11002.04167	29754.29167	26039.99417	2418.359093	6743.031963	2.9	4.3	1.4	0
6033	DUF642 containing_1	miscellaneous	contig	170	16	16	11774.5	3110.75	3149.416667	2150.522143	615.5143167	750.486573819	1.9	1.9	0	0
4335	DUF642 containing_1	miscellaneous	contig	170	16	16	11126.95833	2071.875	2909.583333	1532.604139	417.7477626	732.610989619	2.4	2.4	0.5	0
3080	DUF642 containing_1	miscellaneous	contig	170	16	16	450946.875	75123.79167	104619.25	52482.44593	12793.69316	22380.18761	2.1	2.6	0.5	0
5006	DUF642 containing_1	miscellaneous	contig	170	16	16	76416.54167	4957.333333	12955.83333	9318.630415	882.3290832	3043.729517	2.6	3.9	1.4	0
665	DUF642 containing_1	miscellaneous	contig	170	16	16	67424.04167	4097.833333	14209.45833	9064.093959	1118.232391	3986.958335	2.2	4	1.8	0
834	DUF642 containing_1	miscellaneous	contig	170	16	16	190732.375	9573.375	36736.20833	25550.95526	1679.11228	9654.852479	2.4	4.3	1.9	0
2214	DUF642 containing_1	miscellaneous	contig	170	16	16	500668.3333	26684.91667	66665	63818.99964	5042.027947	14892.39653	3.1	4.4	1.3	0
5634	DUF642 containing_1	miscellaneous	contig	170	16	16	182310.3333	7844.833333	20004.29167	27079.9383	1951.500507	3598.057996	3.2	4.5	1.4	0

3271	endo-1,4-beta-glucanase.2	glycosylhydrolases	38	singleton	1	EG974284	CGTCCACGGCTCCGTTAATGTCACAAAACCCACATACTCTCACACTTATTTACAGCATGCCAAA CAGTATTTGAAATTTGGAGACAAGTACAGGGGAAAGATGATGATGGTAGTGTGGAGTAGTGAAGAA TTACTATGCTCGGTGAGTGGATATGATGAATTTATTTGAGGAGCTGCTGTGGCTATACAAAG CCACGGACAATGAAGTACTTGAATATGATGATGACAGGCTCATTTCTTTGGGGTACTGTG TGGCCATATCTGAGTTCCAGCTGGGATGTTAAAGTATGCTGGCCCTTCATTTACTAGCCACTAAGTT ATTATGGAAGAAAACACAGATCATAGAGTGAACAATTCTAGAGCAATATCGATGATCAAAAAG CAGAATACTACTATTGCTCAAGCCATAACAAGAACAAATGGGAGCAACAAGTAGAAGAAACCCCG GGTGGCTTACTCTATATCCGCCAAATGGAAACAAT CCGCTTTCGCTTATGAAAAGCTTTAGCTGGCAATTTGAGTACACCCACACCCTTCCGATCAAC AATTTCAAGTTCCACACCCAAAAGTGGCCACTAAAGCATTATCTCATCTCTGCTTCTTAITCG CCCTAAAAGCGCGGCTTCAGCCCAACATACAGAAAATCTCTCCGGATTCAGGATTCAGAGTACAGT GATTACAAATCTTTTATCCCAAACAAAAGCTCAGGGATGAAATCAATAAGCCGCCAAACACTAAC CGTCTTGTCTGAGTAAGC CCGCTCCACGGTCCGCCCACCTCTCTCTCTATTTATTTATCTCTTTGCTTATCGCAAAAG CTTTAGTCCGATATTTGAGTATACAAAACACCCTGTCATCAACAATTTAGTTCCACACCCCA AAATGTCGCTCAATAAACCATATCTCATCTCTCTCTCTCTATTCGCTTAAACCGCCGTGCTTTCA GCCACAACATCACAGAAATCTCTCCGGATTCACAGATCCAGAGTACAGTATACATAAATCTTTATC CCAAAACAAGCTCAGCGATGAAATCAATAGCGCCAAAACACTAACGCTCTGCTGAGTAAGC GAGCTCTTCTCCCTTACGCCAAAACACCCCTCTCCGCTTATCAAGAAAGCCCTTAGCCCTCAC GTGCTTCTGGACTTTCAGCCGAAAAGCTCACCATCTCAGGGAGCCACTTATCCACTA CTCTTACCAGACTTCGGAAATGC CTCCCTCTCTCTATTTATTTATCTCTTTGCTTATGCAAAAGCTTTAGCTGCCATTTATTCGAG TATACAAAACACCGGTTCCGATCAACAATTTAGTTCCACACCCCAAAAATGTCGCACTAAACCATT AICTCATCTCTCTCTCTATTCGCCATAACCGCCGCTGTTTCAGCCCAACATCACAGAAATC CTCTCCGATTCAGAGTACAGTATACATAACTTTTATCCAAAACAAAGCTCAGCGATGA AATCAATAGCCGCAACAACACTAACCTCTGCTGAGTACAGGAGCTCTTCTCCCTTACAG CCAAACACCCCTCTCTCCGTTATCAAGAAAAGCCCTTAGCCCTCACGTCGTTCTGGACTACTCGAC TTCGACCCGAAAAGCTCCACAGATCTCTCAGGGAAAGCACTTATCCACTACTCTTACAGACTCCGG AAATGCCCC GAGTATACAAAACACCGGTTCCGATCAACAATTTAGTTCCACACCCCAAAAATGTCGCACTAAACC ATTATCTATCT GAAATCTCTCTCCGATTCAGAGTACAGTATACATAACTTTTATCCAAAACAAAGCTCAGCGATGA CGATGAAATCAATAGCCGCAACAACACTAACCTCTGCTGAGTACAGGAGCTCTTCTCCCTTACAG TTACAGCCAAAACACCCCTCTCTCCGTTATCAAGAAAAGCCCTTAGCCCTCACGTCGTTCTGGACTAC TTCGACCCGAAAAGCTCCACAGATCTCTCAGGGAAAGCACTTATCCACTACTCTTACAGACTCCGG TTCGGAAAATGCCCCCTGAAAATCTTGGCTTCTGTCACAATCACCCGACCTTAAAGGGGCGCAAAAGTTG GCTTCCGTTCCG TGTGACCATGTCTTTAACCTTGTGCTGATATCCCTGGGATGGGTTTCAATCCAGTCCAAATCAC TCTGTATCATGTAACAAACAATGATCAGTATTCACATGTTTCAACATGTTGAAGCTCCAGGATCAGCGG TGTAAAAGGTTTTCTATGCTCTAGTGTCTGTATTTACCTGAGTTCAAGCAGCTGGAACAATA AIGTAGCTTGAAGAAGAGCTGTGCTGAGCCCTCAGATGCTTATGGGTTAGAAAAG CTTGCCACTGAGGAGTAT GCTCTCCCAATCTCTCTCAGCCTAGCAACACTTGAAGTTTCAACTTTCAACTTTACAGATTAC AGAAATGGAGTAGTGTGAGCCAGCTATGCTTACACTATGAGGCTTTGAGAGAGAGCC TTACTGCCATCGGAGAAGCTTCGCATTTCCATTACCGGGCAGGCTGCTTATGCAATCACACA TTGCTCGACTTGAAGAGGCAATACATTTGCTCTGATTTGGAAGAAGAATGAGCAT ATGACAGAAGACATGTTCTGCCATGATTTCACTTGTGACCTAAAGGGTATGATAATTTGCTT GAAGTTACTAAAGATTTGACATGTTTAACTTAACTTCTGCTGATGATGGGTGGGTTTCA TCCAGTCCAATCACTGTTATCATGTAACAAACACAATGATCAAGTTTCAACATGCTTGAAGCT GCCAGGATCAGC ACATCTGCTCTCTGAGGTTGCTGGTGAACCTCAGCAACACTAGCAACACTGATAAAGAAAATT GGTTGGCTCTTCCATCGGTTGAAAGGATGGTTGAGATCACTCTGATCAAAAGAAACA AAGTTGGAGAGAAAACAAGTATGACTTATTTATTTGAGTTTGGTCAATCAAAGGTGGTGGGA ACCCAAAGCCCGTTCACTTGGCTCTGCTGCTGATGGCAAAGAGTAAAGCTGGTCAATC CTAAGATGATGTTTTTGAAGAACTCCAAATATAGTAAAGAAAGGAGTCTGCTTATTTGTT TTCTCAGTCAATCAATTTATGATTTGAAAATAAATAGTTTGGAGAGTAAAGTTCTTATCTTGT TTCGCATGTATAAGGGAG TCTCTCATTTGGGTTTTCCGCTGTAAGCCCGATCTCCGTTGTTACGGTGTGACACTGACCGGCGC CCGCTCCGGAGTCTTACAGTTTTTACACATCTGCTGGACCTGATCCGCTTCTGGACCATCT GGTATCAACCAAGTCTTGTGGTGGCCATGATGGGAGCTTCACTGCTT TCCGATCCGGGTCGCAAAAATTAATCTCAGCCAAACCCAGCCTTAAAGATGAAAGAAACAAGAG GGCACTCCCTCGGAAGAATGGCAACACTCCCAAAATGTTAAAGCATGAAAGGAAACAAGAAAG AAGAACTTTGCTATACAGCAGCAGGTTGTGAATCAACTCACTGCTCTCCATGCTCTTGCATCT GCCATGAGCTTGGAGTTTTTGTATCATAGCAAGGATGGTGTGATGAGCCTCCCGC GGACATCGTGGCCAGATGCCACTACCAACCCCTGATGCCCTAGAAATGTTAGCCCGATCCCTCA GAATGCTGGCCCACTGACTTCTCATTTCTCTGGAAATGAGGATCTAAGGGGTACTGT CTTATGATGTTTTCCAAAGTTATTTGTCTACTAATGAAGATGGTTTCTTACAGTATGCTGATGTC TTTTGTGCA GCAAAAATTAATCTCAAGCACCAAAACAATAAGTTAGTACGTTTCTATGCCACTCCCTCGGAAAG AATGGCAACTCCCAATTTTACGATGAAAGGAAACAAGAAAGAAAGAAACTTTGCATAC GCAGCACAGTTTGGAACTCTCACTGCT TTTTGATATATAGCCAAAGCTGTTGATGCAGCCAAAGCTCTCCGGCAGGACATCGTGGCCGAGA TGCCTACCAACCCGTGATGAGTGTAGACCGCATCTCAGAAATGCTGGCCAGCCAC TCTGACTTCTATGTTCTGGAATGAGGATTAAGGCTGACTGCTTAAATGATGTTCCAA GTATTTGCTACTAATGAAAGTGGTGTCTAATGGTCCACTGATGCTTTGTTGCAAGATAAGG TCTTCTTGGAT	54063.41667	24960.625	22257.66667	7030.998843	4114.38969	4559.767575	1.1	-0.2	0
1119	endosperm-specific protein	miscellaneous	159	contig	5	EG974348	143354.4167	58060.125	59607.375	18143.77748	8057.117738	1.3	0	0		
2095	endosperm-specific protein	miscellaneous	159	contig	5	EG974331	76716.16667	29788.33333	29495.79167	10460.74315	3586.300476	1.4	0	0		
6044	endosperm-specific protein	miscellaneous	159	contig	5	EG974351	91971.79167	38728.91667	47125	11940.61192	8880.217035	1	1.2	0.3	0	
4284	endosperm-specific protein	miscellaneous	159	contig	5	EG974349	134565.4167	51879.375	61364.875	15217.90534	7471.684994	1.4	0.2	0		
3654	endosperm-specific protein	miscellaneous	159	contig	5	EG974330	79321.625	31006.20833	24495.66667	13885.91737	3282.253695	1.7	1.4	-0.3	0	
16	epimerase.1	other cell wall enzymes	29	contig	2	EG974306	99895.83333	44140.33333	28933.83333	15157.69573	3479.664991	1.8	1.2	-0.6	0	
5037	epimerase.1	other cell wall enzymes	29	contig	2	EG974295	45410.20833	24861.91667	10174.58333	11586.52473	3169.199382	2.2	0.9	-1.3	0	
131	epimerase.2	other cell wall enzymes	28	singleton	1	EG974317	43904.375	22067.58333	16401.04167	6077.090404	1885.24303	1.4	1	-0.4	0	
6291	epoxide hydrolase	miscellaneous	120	singleton	1	EG974369	13610.08333	30027.70833	16119.08333	1839.96294	2373.371406	0.2	-1.1	-0.9	0	
5499	eugenol O-methyltransferase	secondary metabolism	237	contig	2	EG974532	4570.041667	23960.91667	10683.45833	593.709029	1314.148785	1.2	-2.4	-1.2	0	
3771	eugenol O-methyltransferase	secondary metabolism	237	contig	2	EG974533	8438.958333	28680.375	16897.58333	1368.372076	3997.140495	-1	-1.8	-0.8	0.3	

3122	expansin	81	singleton	1	EG974328	CATTCACGGCTCGGAAAAAAGGAAAAAATGGGATTAATGATGGGCATAAATCTCCCTCATCA TAAGCTTTGCTCAGTAATTCATACGCCAAAGGCTCCTACTATGCCGATCGGACAAACGGCTCAT GCCATTTTACGGTGGCGGATGCTTCGGGCAAAATGGCGGGCTTCGGGATGGGAAACCT GTACAGCCAAAGGATGGGACAAACACAGCAGCAAGCAGCAATATTAACAGGAGGATTA GTTGGGTGCATGTTTTCCAAATAGGTGGCCCAAGAACCTCAATGGTGGCCCTCCCGGACCAIT GTGTAAAGGCCTAATTTCTTCCACGGTGTGGTGGACCCCTCCAACCTCCACTTCCG TCTGTCAACCCGCTTTTCCCGAATGGCCAATACAGAGCCGGAATAGTACTGTTGTTTACA GAAGGTTCCGTTGTAAGAAAG	17939.73832	4915.195803	3781.785213	2.9	2.7	-0.2	0.1
3010	F-box protein: EIN3-binding	225	singleton	1	EG974545	GGTCATGTCTTGCTTGGCTAAGTTTCCAGGAGAACAGTAGAGTCCCTGAATCTTGACGGATGCAGGA AGATCACCGGATGCAGAGTTTCCGAGCAATTCAGCAAGTTCAGCTGTACTCAGAGACTAGACCTT TCTAAATGTGCAATCTCAATTTCCAGATTTCCAGCCCTTCTAATGCAAAACAGATCAATTTGCA AGTCTCTCTTTCTGGCTGCTGATGTGTCAACAAGAGCCATTTTTCTTAAAGAAATGG GTAGACTCTAGTTGGTGTGAAATCTCCAACTTCAATTCACAGCAGCAGAACCCGTGAGGCTG CTTGTGGAGAGCTTGTGGAGATGTATATCTTTGGCCATAAAGAGATTGAACAGAAACAATGC TCTTATCTCTAAAGAGAGGCATATATAGAGATGCTGGAGATAGCAGAGTCCCTGAAATTTCTGGCT AAAGGTTCCGTTGTAAGAAAG	3572.427832	8856.800886	4690.739299	0.3	-1	-0.7	0
3056	ferulate 5-hydroxy lase.1	232	singleton	1	EG974534	GCCCCGATTCGTTTAAACCCTCGGTTTATGAAGGAAGGTGTGCTGATTTTAAAGGAGTAAT TTTGGATTTATCCATTCCGGTGGGCTGGAGGTCTTCCCGGATGCAAACTTGGGCTTTACGC GCTTGAATGGCGGTTGGACACCTTCCATGTTTCACGTGGGAATACCCTGATGGTATGAAAC CGAGTGAATCTCATATGAGTGAACCTGTTGGACTCACGCGCCGAGAGAGTCGAGCTCATGGCT GTACCGAGTAAAGCGTGTGGCTGCTCCATCTCATATCTCTTTTGAAAATTTGGACACATGTG AATTTGGAGTTTTAATAGGCTTTTAATTAICATTAATAATTAATAATAATAATAATAATAATAATA TCCTTTTTCTTTAATTTTGAATTCCTTTTTGAAAAAATAAATAATAATAATAATAATAATAATAATA AAGGAAAGGA	5161.62604	23642.01926	12007.16823	-2.4	-3.3	-0.9	0.1
4481	ferulate 5-hydroxy lase.2	239	singleton	1	EG974535	GATPAACATGTACTTATATAATTTCCCTGTGTTTTGTTACTGGGATAATAATTTCCGATTCGCGGA CGCGACTTCCATTTCCCGCGGACCAAAGGGTTACCAATAATCGGAACAATGCTCAATGATGGA CCAAATAACTCACCGTGGATAGGAAATAGCCGAGAAATACCGAGGCGTTTTTCCCATGAA TGGGTATCTTCACATGGTGGCAATCTCACCCTGAAACAGCTCGTCAAGTCTTCAAGTTCAA GATAACATTTTTCAAATCGACCGGCCACATAGCCATAGCTACTCACATACGACCCTGCTGA CATGGCTTTTCTCCTACTACGAGCCCTTTTGGAGACAGATGAAAGCTCTGTTGTTAGAAAGCTTT TTAGCCGTAAGAAGCAGATCATGGAACTCTGTTAGAGATGAAGTTGATAAGACTATTCGAACACT GTGGCTAA	1965.091702	6218.571395	3049.56513	-1.2	-1.9	-0.7	0.1
3570	fiber protein Fb34	127	singleton	1	EG974370	GAGCGAGCAGAAGAAGAAGATGTGATGATCTCGAGAGGAAAGCTTTGAAGCTTTCTAGAAA TGGCTCAAAGCTGCTTTTGAATGGGTATCACTTAGACATAITAGCTTTTGGTCTGGCTGTT GGGCTGAGCAGAGAAAGCACAAGGGTGGGTTTTCAAGATGCTGATGAAGAACTACAACTACTG CGTTAATTCAGACATTCACACTGGCTAGGTTGGTGCATCTTGTTCTTATGGTAAGTC AGATCATTATAATGGTGGCAAGCCGATGCTTGTGTTGGGAAAGCCTTAAAGTTCTGGAGGATCA AGGCTGGGCAGTGGTTTTTTCATATCTGCTGGTATTTTCATGCTGGAGGCATGCTT ATTAGCTGTTTCAAGTGGATGGCTACATACCAGTACAGGAACCTTCTCAGTATAGACAACC CTCCATCTGTGA	6066.404123	10795.78517	4124.13851	7.03	-1	-0.8	0
454	fructokinase	89	singleton	1	EG974179	GCAAGGTGACGTCAACAGTCAAGCAGGATGTTGAGCTTGTATCTCTAATAAGAAATGACAAAATC GAGATGCTCCGCGCATGCTTTTGGGCAACCACAACTCAAGCTTCTCTGTGCTACTGTGGCGA GATGGCTGACAGATACTACAAAAGGTAATAACTAAGAAATATAATATATCTATGAACAATCTC TTTTTAATTAATGTTAATGTTTTTATTAAGAAATAAGTTTTAATGATGATGCTGTT TTTTGACGTTTAGCTGTTAATGAAATGGTTGGTGGGGTTTTTTAAAGAAATAGTGAAATA TGCTGACAAATCTCGCTGCTCAGTAGCACTTGGCCACAATGAAGTTGGGCTGGTAGGAAGTA GTAGGCCCCTTTCTAATTTTATTTTACTTTTTTTTTGGTGGATTAATAATGCTAGTTTTTA GGCTAGCTGAA	3041.362547	8080.997694	6196.960848	1.2	-1.3	-0.1	0
5747	fructose-bisphosphate aldolase	90	singleton	1	EG974180	GAGTATTTCTCTCCTCAAATTTCAATGAAAATGTCTTGTTCAGAGCAAATGAGAAAT GAGCTATTTGCCAAGCTCTTACATCGTACCCTGGAAAGGTTATTTGCCGCTGATGAGTC AACTGGTACCATTGGCAAGCGTCTTTCAGCAATCAATGATGAGAATGTCGAGTCCAACAGGCGTG CTTCTGGAGCTCTTTTTCACACTCTGGAGCCCTTGAATGCCTCAGTGGTGATTTCTTTT GAGGAACTCTCAACAAGCAGTCTGCTGGTAAACCTTTTGTGTGTTGATGGTGAAGGAGGGTGG AGTCTGCCAGGAAATTAAGGTTGACAAGGGTACAGTTGAGCTTGTGGAACAACCGGTGAAACCA CCACTAGGGTCTTGACGGCTTGCTCAAAGATGCCAAGAACTATGAAAGCTGATGAAAGCGGTGCTGA GCTAAGTGGCGTGC	18799.08451	38400.75276	17777.11947	-0.3	-1.1	-0.8	0
4249	galactinol synthase	49	singleton	1	EG974181	GGGCTCTCAGTGTGTCTAATTTACTTCTTCAATATGCTCCCTCACAATCTCATCAATA AAATGGGTTCCAGAGTTGGTGGAGGTGATCAATAATGGTAAGCTGGTCTCAGCTCATCCAGTG ATAATAATGATAATAATAAAAGGCTTACGTAATTTTTTGGCCGGTAAATGGTGGTACGTTGAA AGGGTAGTAGGATTGGCCAAAGCTTGAAAAAGTAAGAGTGGTTCCTTCTTGGTGGCA TACTGCCGATGTGCCCTGAAGAACCCGCTCAATTTGAAAGTCTAGGGTTGCATGCCCCGTGAG AITGAACCCATCTATCCACTGAAAATCAGATTCAGTTTGCCATGGCTTATATGCTCATCACTA CTCAAGCTCCGATTTGGAAATTTGAGGAGTACAGGAAGATGATGATTTGGATGCTGATATCC AAGTGTTCGAA	867.6342741	7952.986548	3254.441947	2.5	-3.2	-0.7	0.1
3342	GDSL-motif lipase/hydrolyase-like protein.1	162	singleton	1	EG974387	GATTTATTGGAGAGTTTTTATGGTATTTTTCCATATACACTAGTCTCTTGGTCTCTCAAT CGAGCGAAGAAGAAAATTTGCAAATCTAGCTAATAATAAGATTATGATGAGATGAGG GTGTGGCAGTTGAGTTGTTAGTCAACAATGATGGTATGTTTGGTAGAGTCTGGAGTTGTA AGTGGGTTTAATGTTGATGATGATGATCATATAACTCATGAGAACAAGATGATTTAATAATTG ACTAGGGTCGAGTACGAAAGTGCAGCTGAATAAGTCTTGGTGGTGGTTTCCGGTGGAGAT TCCAGTGGATCCAGCAATAATAAGTTCTTCCACCAATGAAGAAAGGAAATTTCCCTCCCTTA TGGTAAAGACTTCTTGGTGGCCCTACTGCGAGGTTCAGCGATGGTAGACTTGGCCACTGATT TTATAGCCGAAGCA	5263.374921	1796.894689	3616.763085	1.3	1.8	0.4	0.1
6659	GDSL-motif lipase/hydrolyase-like protein.2	166	singleton	1	EG974386	GTAATATGATATGGATTTTCATCTCCACCCCTCAGCAATGGAATTTGAAACATCAAAGATTGGC TGCTGTGGACAAGGACATTAAATGGAATAGGTCTTTGCAACCCAGTCTCAAACTTGTGTCAAA CAGAGATGCTTATGTTCTGGATCCCTCCACCATCAGAGGGCCAAAAGAAATAATTGTGC AGCAAATCTGGAGGTTCTAACAAGTACATGCCCAATGAAATCTCAGCAATATGATGGCATG GACTCAGCTAGGACCTAGAGAGGAGTCTTTTACTACTTCTCATATATACATATATATACACTT TCTTTTTTTTTTATTTTTATTTTACGTGGCCAGTTTGTACAGTCCATATATTTAC ACTTAAAGCCATTGTAAAATTTCAATATGATAITTCAAATAAGGTAATATTAGTTTTCAGTGTGCA CTTTTTTTAAA	19680.69358	3754.61687	3797.55205	2.5	2.3	-0.2	0.1

Gene ID	Gene Name	Category	Length	Structure	EG	Strain	Gene Type	Genomic Location	Coordinates	Score	Value			
5511	glutamate decarboxylase	amino acid & protein metabolism	13	singleton	EG974319	1	singleton	20	6780.089264	3104.164042	1.1	0.3	-0.8	0
2039	glutamine synthetase	amino acid & protein metabolism	20	singleton	EG974320	1	singleton	98	4675.719101	3753.71691	1.7	1.3	-0.4	0
3256	glyceraldehyde-3-phosphate dehydrogenase.1	glycolysis & respiration	98	singleton	EG974234	1	singleton	94	5460.677518	3198.373907	2.2	1.8	-0.4	0.1
5029	glyceraldehyde-3-phosphate dehydrogenase B-subunit precursor.3	glycolysis & respiration	94	contig	EG974236	2	contig	97	1653.387749	1355.2113	1	1	0	0.5
5338	glyceraldehyde-3-phosphate dehydrogenase B-subunit precursor.3	glycolysis & respiration	94	contig	EG974235	2	contig	94	2567.186052	1843.895218	1.2	0.7	-0.5	0
1044	glyceraldehyde-3-phosphate dehydrogenase.2	glycolysis & respiration	97	contig	EG974242	4	contig	97	3724.780819	3787.551041	1.4	1.5	0.1	0.1
4059	glyceraldehyde-3-phosphate dehydrogenase.2	glycolysis & respiration	97	contig	EG974239	4	contig	97	5379.305912	4153.365233	2	1.6	-0.3	0
2056	glyceraldehyde-3-phosphate dehydrogenase.2	glycolysis & respiration	97	contig	EG974237	4	contig	97	41191.23298	19812.76297	1	0.6	-0.4	0
1770	glyceraldehyde-3-phosphate dehydrogenase.2	glycolysis & respiration	97	contig	EG974238	4	contig	97	5004.975358	2329.244254	2.2	1.8	-0.4	0
4237	glycerophosphoryl diester phosphodiesterase	miscellaneous	139	singleton	EG974332	1	singleton	21	29745.85846	18074.41123	1	0.5	-0.4	0
2489	glycine decarboxylase H-protein.1	amino acid & protein metabolism	21	contig	EG974228	2	contig	21	2132.967959	1995.761968	1.7	1.7	0	0
6	glycine decarboxylase H-protein.1	amino acid & protein metabolism	21	contig	EG974227	2	contig	21	1170.323537	686.73366491	5	1	-0.4	3.6

5385	LIM transcription factor	regulation	218	contig	4	EG974558	14989.66667	68130.16667	42853.04167	2027.272634	9612.80293	4407.214064	1.5	-2.2	-0.7	0.1
<p>CTGCTTGTAACAAGACTGTGTACTGTTGATAAGTTAAACAGCTGATACAGGATTTACCACAAG GCCTGCTCCGATGCCATCAGCAAGCAACCCCTTAAGCTTAGCAACTATTGTTCCGATTTGAAAGG GGTCTTACTGCAGGCTCACATGATCAACTCTTCAAGAGAACTGCGCAGCCTAGCAAGAGTT TTGAAGGACTCCTAAGATCTTGAACACAGAAAGACCACTAGTGAGAATGCAAGACAGTCTCG AATATGTTGGGGACCAAGATAAGTGTGTGGGA CCTTTACGGCTCCGGAGGCTCAACCAATGCAATTTGCTTCTAGCTTTCTTGTAAATCCCGG GATCAATGAGCTGATTTGACGGTTCATGGGCTGTGAGTGTGGGAAACTTCTACTAACCTGAC AAGAGGCTTTCAAGCTAGCACCATGTGCATATGCAGCCAGAGATGAGAAACCGCTTCCAGTTCCAG CCGATGCTGCTCAGGTGAAAGAGCTTGGCCAGAACCCAGCTGCTTGGCTGTCCATGCTTT CCAACTGCAAGAGTTCGGGGTAAAGCAGAAAGTGGCTGTGACCAATCCAAAGCGAIGCAAC ATTGATAGCCGCTGTTGTTACAAGTGGAGGTGACATTTGCTTGAAGACATTTCAACCCT ACGCTGTTTGTAGTGTGTGGCAGTTTGTAGTAAAGAAATGCTAAATTTGTGTGTTT TTAGCCAGTTCTAGTTTTTACTTGGGA GAAAATCTTCTTATCTACTGTGACCCTTCTTCACTATTTACCAACAAACAGAAAATA AGATGAAGAACACAGCTCTTTTGAACAGTGTGGGATGGGATGGGCGGACAGTGTGTTG TCGGAAGCCGAGTGCAGAGCAGTGCAGCTCAGCCAGCTGAGATGAGCTATGCTGCTGCGG CATCACTAGTGGATCCCGCTCGAGTCAATGCTGGCCAGCTCAAGGAAACAGAGCCCTGGC TCTGTGGTATCTAAGGACCTAATCTTCCGCAAGTATGTCAACTCTCTAATGCTAGAAATGTT GCTGCCAAGTGTGTTTCTTACCCAAATGTTGATCCACTACTAGTGTGAAACATCCTT CCATATTATTAATAAATAAGACACTTGTTCACCTCTTCACTACTGCTTACGGAAAATAAAA TATATATTA</p>																
4885	lipid binding	miscellaneous	167	singleton	1	EG974353	42468.04167	7351.833333	22576.16667	6605.198479	1583.916611	3856.123838	0.9	2.5	1.6	0
<p>CTTTACGGCTCCGGAGGCTCAACCAATGCAATTTGCTTCTAGCTTTCTTGTAAATCCCGG GATCAATGAGCTGATTTGACGGTTCATGGGCTGTGAGTGTGGGAAACTTCTACTAACCTGAC AAGAGGCTTTCAAGCTAGCACCATGTGCATATGCAGCCAGAGATGAGAAACCGCTTCCAG CCGATGCTGCTCAGGTGAAAGAGCTTGGCCAGAACCCAGCTGCTTGGCTGTCCATGCTTT CCAACTGCAAGAGTTCGGGGTAAAGCAGAAAGTGGCTGTGACCAATCCAAAGCGAIGCAAC ATTGATAGCCGCTGTTGTTACAAGTGGAGGTGACATTTGCTTGAAGACATTTCAACCCT ACGCTGTTTGTAGTGTGTGGCAGTTTGTAGTAAAGAAATGCTAAATTTGTGTGTTT TTAGCCAGTTCTAGTTTTTACTTGGGA GAAAATCTTCTTATCTACTGTGACCCTTCTTCACTATTTACCAACAAACAGAAAATA AGATGAAGAACACAGCTCTTTTGAACAGTGTGGGATGGGATGGGCGGACAGTGTGTTG TCGGAAGCCGAGTGCAGAGCAGTGCAGCTCAGCCAGCTGAGATGAGCTATGCTGCTGCGG CATCACTAGTGGATCCCGCTCGAGTCAATGCTGGCCAGCTCAAGGAAACAGAGCCCTGGC TCTGTGGTATCTAAGGACCTAATCTTCCGCAAGTATGTCAACTCTCTAATGCTAGAAATGTT GCTGCCAAGTGTGTTTCTTACCCAAATGTTGATCCACTACTAGTGTGAAACATCCTT CCATATTATTAATAAATAAGACACTTGTTCACCTCTTCACTACTGCTTACGGAAAATAAAA TATATATTA</p>																
5917	lipid transfer protein.1	other cell wall proteins	77	singleton	1	EG974217	46423.16667	99191.83333	67363.375	6382.039002	16072.09649	11030.27074	-0.5	-1.1	-0.6	0
<p>AGATGAAGAACACAGCTCTTTTGAACAGTGTGGGATGGGATGGGCGGACAGTGTGTTG TCGGAAGCCGAGTGCAGAGCAGTGCAGCTCAGCCAGCTGAGATGAGCTATGCTGCTGCGG CATCACTAGTGGATCCCGCTCGAGTCAATGCTGGCCAGCTCAAGGAAACAGAGCCCTGGC TCTGTGGTATCTAAGGACCTAATCTTCCGCAAGTATGTCAACTCTCTAATGCTAGAAATGTT GCTGCCAAGTGTGTTTCTTACCCAAATGTTGATCCACTACTAGTGTGAAACATCCTT CCATATTATTAATAAATAAGACACTTGTTCACCTCTTCACTACTGCTTACGGAAAATAAAA TATATATTA</p>																
606	lipid transfer protein.2	other cell wall proteins	69	contig	2	EG974220	7794.916667	78435.41667	45852.91667	1444.795238	11704.62438	12564.74459	-2.6	-3.3	-0.8	0
<p>CGGTTCCGGAATTCGGGGGCTTTCAGGGGTCGGAAGAAAATAAGGATAAGAAATATCCTC TTTGGCGTGTGATGGTGTGAGGCTGCAGTAGTACTGGTGTGTCGGAAGCACCAGTAG CAGAGCAGTGACTTCCAGGATGAGGATGAGCTGCTTCTGCCAGCATTCCAGTGGGCA AATCCATCGACCAATGCTGCAAGCAAGCTCAAGCAAGCAAGCTTGGCTTTTGGGTACTCA AGATCCAAAGCTGGCTAGTATGAAACTGCTAATGCCAAGAGAGTGGCTCTCACTGTGGG TGCTACCCCAATGCTGATCAATGCTCGCTCGCTACTACTACTACTACTACTACTACTACT GTATCTACTAT TGATATATCATCATTTGAATCCAGAAAAGATAAGAAATGATTAC CATTCAGCGCTCGAATAAAGATAAAGAAAATAAGGTAAGAAAGTATCTCTTTGGCGTGG GTGATGGTGGTGTAGCCGCTGCAGTAGTACTGGTGTGCGGAAGCACCAGTAGCAGGCA GACTTCCAGCTGATGAGTGCCTGCTGCTGCCAGCCTACACAGTGGGGCAAATCCATCGA CCAAATGCTGCAGCAAGCTCAAGCAAGAGCCTTGTCTTGGGTACTCAAAAGATCCAAAGC CTGGTCAATATGAACTCTGTAATGCCAAGAGAGTGGCTCTCAATGGGCTGTCTTACCC CAATGCTGATCAATGCTCGCTACTACTACTACTACTACTACTACTACTACTACTACTACT CTAT ATCAATTAATAAATAAGAAAGAAAT</p>																
3150	lipid transfer protein.2	other cell wall proteins	69	contig	2	EG974219	27160.54167	369249	113106.5417	3894.570657	47859.53635	8870.86225	2.1	-3.8	-1.7	0
<p>CATTCAGCGCTCGAATAAAGATAAAGAAAATAAGGTAAGAAAGTATCTCTTTGGCGTGG GTGATGGTGGTGTAGCCGCTGCAGTAGTACTGGTGTGCGGAAGCACCAGTAGCAGGCA GACTTCCAGCTGATGAGTGCCTGCTGCTGCCAGCCTACACAGTGGGGCAAATCCATCGA CCAAATGCTGCAGCAAGCTCAAGCAAGAGCCTTGTCTTGGGTACTCAAAAGATCCAAAGC CTGGTCAATATGAACTCTGTAATGCCAAGAGAGTGGCTCTCAATGGGCTGTCTTACCC CAATGCTGATCAATGCTCGCTACTACTACTACTACTACTACTACTACTACTACTACTACT CTAT ATCAATTAATAAATAAGAAAGAAAT</p>																
5042	lipid transfer protein.3	other cell wall proteins	82	singleton	1	EG974212	28221.95833	3891.958333	4791.666667	4009.230903	532.6510008	933.006917	0.6	2.9	0.3	0.1
<p>AATTTCTTGTGGCAATATGGTGTGATGGTATFAGCGCACAGCTGCTFAAATGGCGACATTA TGTTCAAGATTAATACTCTCTTCAATGTA.AACTACTTAGAATGGTGGTCTGTCTC GTGGATTTGTTCAACAGGTGCAATGCTAAAGCTCAGGCGAACACATCAATCAACCAGCAAT CCATGCAAAATGCTTGAAGGATTTATAAAGTGTCAAGGAAATCAATCTGATCTGCTTCT GGATGCTCTAAATGCAAGCTCAAACTCTTCCCACTCTTCCCAATGCTTCTGCAATGGCCAA TTTTGCTGATCAAGTTTTGGTGTGGTGTGATTTCCAGCATATAATATATATATATATAT ATATATATATATAT</p>																
2466	lipid transfer protein.4	other cell wall proteins	85	contig	5	EG974211	18985.20833	3999.791667	2280.583333	2870.812149	902.8169622	498.1214308	1	2.2	-0.8	0
<p>GAAAACCAAAATCTATACACTACTACTACTACTACTACTACTACTACTACTACTACTACT AGAAAATGGCAATGCTTAGTATGAAGTCA.CCACTTGTGTGACTACTACTACTACTACTACT TGTTGACCCCTTTGAGAGAAATGGCAATGCTTAGCTAGTAAAGCTCACACTTGTGTGGTACT CATGTGCATGTTGTGGTGCACCGTCCAGCCAGCCATAAATGTTGGTCCGTAAGCACCATGCTCG TAGCACCATGCTTCCCTACTTGAATCTGGGGTGTCTCCGACGGGATGCTGTAATGGGGTT CAGGCTGGAACACAGCAACCGTCAAGCTGTGTGCAAGTGTGGTGTAGTGTGCAAGGCAATTT TCCCGACTAAACCTAATCTGTTTCTGGCTCCCTTCCGCTTGGGGTTCCTTCCCTTCTTA AAATCAGCACCTCCACCACTGCAACAGCATCAAGTGAATGAAGTGTGAGAAAGAAAGAGAGT ATATATATATATAT</p>																
5105	lipid transfer protein.4	other cell wall proteins	85	contig	5	EG974214	43859.17458	101377.7917	190496.9583	3411.709248	21306.39955	46730.07527	4.5	5.4	0.9	0
<p>GAAAACCAAAATCTATACACTACTACTACTACTACTACTACTACTACTACTACTACTACT AGAAAATGGCAATGCTTAGTATGAAGTCA.CCACTTGTGTGACTACTACTACTACTACTACT TGTTGACCCCTTTGAGAGAAATGGCAATGCTTAGCTAGTAAAGCTCACACTTGTGTGGTACT CATGTGCATGTTGTGGTGCACCGTCCAGCCAGCCATAAATGTTGGTCCGTAAGCACCATGCTCG TAGCACCATGCTTCCCTACTTGAATCTGGGGTGTCTCCGACGGGATGCTGTAATGGGGTT CAGGCTGGAACACAGCAACCGTCAAGCTGTGTGCAAGTGTGGTGTAGTGTGCAAGGCAATTT TCCCGACTAAACCTAATCTGTTTCTGGCTCCCTTCCGCTTGGGGTTCCTTCCCTTCTTA AAATCAGCACCTCCACCACTGCAACAGCATCAAGTGAATGAAGTGTGAGAAAGAAAGAGAGT ATATATATATATAT</p>																
176	lipid transfer protein.4	other cell wall proteins	85	contig	5	EG974213	953297.875	17423.08333	31358.5	116094.1151	2243.636255	6692.401069	4.9	5.8	0.8	0
<p>GAAAATCTATACACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT TGCAATGCTTAGCTAGTATGAGCTACCTTGTCTGGTACTACTACTACTACTACTACTACTACT CCGCTAGCCAGCCATAAATGTTGGCAAGTGGCTAGCTGGTAGCACCATGCAATGCCATCCCTACT GAGATCTGGGGTGTCTCCGACGGGATGCTGTAATGGGGTTCGAAGGCTAAATAGTCAAGGCT CGAACACAGAAACCGTCAAGCTGTGTGCAAGTGTGGTGTAGTGGTGCAGGCAATTTCCCGGA CTTAACTAAATCTGTTCTGGCTCCCTTCCGCTTGGGGTTCCTTCCCTTTTAAAAATCAG CACTCCCAACTGCAACAGCATCAAGTGAATGAAGTGTGAGAAAGAAAGAGAGATTAATA ATAAAGTGTATC</p>																
5954	lipid transfer protein.4	other cell wall proteins	85	contig	5	EG974216	239341.6667	3185	11983.75	33292.39066	509.3319118	3507.782943	4.3	6.2	1.9	0
<p>GAAAATCTATACACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT TTTTGGCCCTTTGAGAGAAATGGCAATGCTTAGCTAGTAAAGCTCACACTTGTGGTACTCA TGTCATGTTTGTGGTGCACCGTCCAGCCAGCCATAAATGTTGGCCAAAGTGGCTAGCTCGTAGC GCCATGCTCCCTACTTGAATCTGGGGTGTCTCCGACGGGATGCTGTAATGGGGTTCCGAA AAGCCTAAATAGTAGCCCTCGAACACAGCAACCGTCAAGCTGTGTGCAAGTGTGGTGTAGTG CTGAGGCAATTTCCCGACTTAAACCTAATCTGTTTCTGGCTCCCTTCCGCTTGTGGGGTT TCCCTCTTTTAAATCAGCACCTCCCAACTGCAACAGCATCAAGTGAATGAAGTGAATGAAGTGTAGAA AGAAAGTGTATC</p>																
1339	lipid transfer protein.4	other cell wall proteins	85	contig	5	EG974215	972492.8333	11278.20833	28825	100619.2489	2181.29019	6443.218006	5.1	6.4	1.4	0
<p>TCACGGTCCGCAAAAACCAAACTATACACTACTACTACTACTACTACTACTACTACTACT TTGGCCCTTTGAGAGAAATGGCAATGCTTAGCTAGTAAAGCTCACACTTGTGGTACTCATG TGCATGTTGTTGGTGCACCGTCCAGCCAGCCATAAATGTTGGCCAAAGTGGCTAGCTCGTAGC ACCATGCTCCCTACTTGAATCTGGGGTGTCTCCGACGGGATGCTGTAATGGGGTTCCGAA GCCTAAATAGTAGCCCTCGAACACAGCAACCGTCAAGCTGTGTGCAAGTGTGGTGTAGTGCT GCAGCAATTTCCCGACTTAAACCTAATCTGTTTCTGGCTCCCTTCCGCTTGTGGGGTTTCC CCTTCTTTTAAATCAGCACCTCCCAACTGCAACAGCATCAAGTGAATGAAGTGAATGAAGTGTAGAAAG AAAGAGAGATTAATAA</p>																

207	mitochondrial 2-oxoglutarate/malate carrier protein	glycolysis & respiration	93	singleton	1	EG974241	GCCAAAACATCTTAAGCAAGATGGTATTGGTTCCTTACAAAGGGACCTCTCCTGCTGCTGCTGCT	39187.125	32959.45833	18553.875	5630.784008	5033.37981	1515.745013	1.1	0.2	-0.8	0
5421	MYB transcription factor	regulation	219	singleton	1	EG974562	GGAATTCCTCGGGTCGACCCACGGCTCCGAAGAGGCCCTCCCTCATCAGCTCGAGGTTCTGACCA	14638.875	41116.54167	21470.125	2550.527529	6600.097272	2861.24088	-0.6	-1.5	-0.9	0
4850	myo-inositol 1-phosphatase synthase	secondary metabolism	251	contig	3	EG974339	CGAAAAGAAAAGGGTCTCTGGACCAAGAGATAGACACAGAGGTTTTGTTGGGCTGATGA	63168.33333	13688.45833	11434.83333	10405.95724	2013.598246	1484.853822	2.5	2.2	-0.3	0.1
6308	myo-inositol 1-phosphatase synthase	secondary metabolism	251	contig	3	EG974627	AATATGGTAAGGGGATTGGAGAAATATCTCAAGGAGTTTTGTTATCCTAAGACCCCAACAAA	55372.875	5971.833333	6564.625	9178.63507	899.20329	1223.829976	3.1	3.2	0.1	0.1
5572	myo-inositol 1-phosphatase synthase	secondary metabolism	251	contig	3	EG974350	GGAITCAACACTCACCTCTTCTGAGCCTTTTTCTAATCCTTTCCTTAACAAAGAGCTTTTTCCCTT	48661.625	5173.375	4494.083333	9337.912417	1101.479445	684.4469123	4	3.2	-0.2	0.1
5052	nicotinate-nucleotide adenyltransferase	miscellaneous	101	singleton	1	EG974245	TCCATCACTATCGAGAAAATGTTTATGAGAGCTTAAAGTGCAGATAGCCCAACGTACGTAC	14312.79167	148111.875	104112.5417	1825.582862	19586.5122	12104.90427	-2.9	-3.4	-0.5	0.1
396	nodulin.1	miscellaneous	123	contig	2	EG974408	TGAGAGTGAAGATTCTGTFACAACTATGACACCACTGAGCTTGCCCTGACATAAATAAGAA	33403.91667	68111.29167	58952	5023.594576	9439.995745	6847.314218	-0.8	-1	-0.2	0
4946	nodulin.1	miscellaneous	123	contig	2	EG974407	AGCTCCAGCTGATGCTGAGCAGGCTCCAGCTCCCGGAGCCATGTTGGCTTGCAGTTTGTTA	57469.66667	122630.2083	96421.20833	8415.061793	16440.32497	10328.98968	-0.7	-1.1	-0.3	0
1007	nodulin.2	miscellaneous	131	contig	2	EG974410	TGCTGGTTCAGTTGTTTCAAGAGCTGCCCTTAATGAGCTTAGAAGCTGCTGTCTCCAG	62286.91667	120555.125	103309.2083	7629.544204	15510.97541	10952.37259	-0.7	-1	-0.2	0
6582	nodulin.2	miscellaneous	131	contig	2	EG974409	TTAGAAATATAAGATTATGTTGATCAATGAGAGGATCAATGAGCTTAGAAGCTGCTTCCAG	28404.33333	59331.79167	43267.33333	4141.777661	9078.629897	5007.111847	-0.6	-1.1	-0.5	0
1565	nodulin.3	miscellaneous	102	singleton	1	EG974411	GCCCTTAATAGGGCATAGTCCGTTCCAGTTTACAGGAACAATAGCCCTGTCTTTC	24412.91667	212934.625	158476.0833	2932.514658	27101.13861	14308.16802	-2.7	-3.1	-0.4	0

951	nucleoid DNA binding protein.1	miscellaneous	103	contig	3	EG974414	11612.16667	80738	76469.04167	1527.379635	11581.92518	7801.322822.2.7	-2.8	-0.1	0.1	
							TTCCAGCGTCCGCCGGCGGCTGCTTACGCTCTCCAAAGTTCTGCCATAAGCGTAGGCCGGA AAGAAGTTCCTGATTCAGCTTCCCTTTCAGACAGCCGGCACGATCAGTCCGATTCGGGACAGT CAITACTCGCTTCGGCGAGTCTAGCGGCTAGAGTCTAGAGTTCAGAAACACAGATAGTA GCTTGGTTATCCGACGGCTCGGCTCTATCGAATTTGGACAGGTGTAGATCTGAGTAAGTAT AAGATGTGACGATTCCTAAGATTGGAATCTTTCGGGAGGAACGCGGTGGATCTTGTATGC GACGGGATCTTTACGCTCGAAGATTTCTAGTGTGTTGGCGTTCGGCGCAACGGAGACG ATGGTAGCTGGCAAFATTTGGGAATTTTCAACAGAAAGACTTTGCAAGTGTGTTAIGATAFAGGA GGAGGAAATTTGGGTTGG									
2862	nucleoid DNA binding protein.1	miscellaneous	103	contig	3	EG974415	18201.91667	183997	179149.875	2660.591033	27558.79267	17485.00868-3.3	-3.3	0	0.1	
							CAITTAAGCTCCGAGNCTTTTGGTGGTCCGGGGCCCATTTGGGCTGGGCCGAAACAAACT CTCAATAATCGAACAAACGGCCAAAATAATACATGCTACTTCTCATATTGACCCAGCACAG CCAGCAAAACCGGTACTAACCTTAGAAAGGGCGGCTGGCTTCAATCAGTCAAGTACACGCC ACTCTCCACATATCCGGGGCGGCTGTCTACGCTCTCCAAAGTCTTGGCCAFAGAGTAAAGGG GAAGAAGCTTCCGATTTCCAGTCTCCCTTCCAGACAGCGGACGATCATCCGATCCGGGACA GTCAITACTCGGCTTCCCGCAGCGGCTACGGGCTAGGCTGAGCTCCGAGTTCAAGAAACAGATGAG TAGCTTGGTTATCCGACGGCTCCGGCTATGCTATTTGGACACGCTGGCTTGTATTAATAATAA ATAATAATTGATTAATAATTGAGCTATAATAATAAAGAAAGAGAAAGGGGATGATGATTA TTATAGCTCAAGCT									
831	nucleoid DNA binding protein.1	miscellaneous	103	contig	3	EG974413	3277.33333	12905.45833	11450.08333	796.2574771	2304.991543	1850.762695-1.8	-2	-0.2	0	
							TCCGGGACAGTCAATACTCGGCTTCCGGCAGCGGCTTACGGGCTATGAGTCCGAGTTC AAGA AACAGATGAGTAGCTTGGGTTATCCGACGGCTCCGGCTCTATCGATTTGGACAGTGTACGAT CTGAGTAAGTATGAGAGTGTGACGATTTCTAAGATTGGATTCTTTCGCGGGAGAAACGCGGT GGATCTTGATCGGACGGGATTTTACGCTTCGAAGATTTCTCAGGTTGTTGGGCTTCGGCG GCAAGGAGAGATGGTACGTGGCAATATTTGGAAATTTCCACAGAGACTTTGCAAGTGGTTT ATGATAGGAGGAGGAGAAATTTGGTTTGGACACGCTGGCTTGTATTAATAATAATAA ATAATAATTGATTAATAATTGAGCTATAATAATAAAGAAAGAGAAAGGGGATGATGATTA TTATAGCTCAAGCT									
4254	nucleoid DNA binding protein.2	miscellaneous	124	singleton	1	EG974412	15041.79167	31539.83333	13100.25	2511.845754	5702.542938	2075.224449-0.2	-1.1	-1.3	0	
							GAACATAGTATATACATTAGAGTCCATCACACTTTGTCTTACACAGAGATAATTTTACG CATGATAAGGCTTCTAATCTCCACACTAGCTGTGGTACTTATACTACTAAGTACAGCCC AAGCATCAATAAACAATAACTACTGTTGGAAAGAAAGAGCAAGGCTCAACCTTAGAGGTG TTCCAGGTGTACAGCACGTGCTACCATTTCCGACCACTGAGGCCACCTATGGGAGGAGATGT CTTCAAATGACAAAGGCAAGCCAGCCAGGCTTACCTCCAGCTTGGTGGTGGTGGTGGTGGT CTGTGTTGCCATTGCTCAGGAGCGGTTGTCAGAGCCCAACATACATTTGTCAGAGCCAG ATCGGTACACTCCACAGACCATGCTCTAGCCATGGATAACCAGCAACGACGCCCTGGATTCC ATCGACGGT									
6233	nucleotide-sugar dehydratase.1	other cell wall enzymes	26	contig	3	EG974184	31199.54167	86173.08333	78171.08333	3896.818052	14019.67175	11146.64444-1.3	-1.5	-0.1	0	
							GATTCAACTCAAGGAATTCAGTACCAGACAGGATTTGAGCCAGATCGGCAATGGCGAAGAA GCTTCAATACCAATGGAGTGTGACGACAAACACCTCCATCCCATCTCTTTAAGAANAATGC CAAGTCTTCCAGGCCAATATGAGAACTTTGGTAACCTGGAGGCTGGATTTACTGGCTCTCACT TGGTAGACAGTTGATGGAATATGAAAGAAATGAAAGATGAGTGTGGGGAATAATTTTACCTGGC TCAAAAGGACATCTGAAGAAATGGATTGGTCAATCCAAAGATTTGAGCTTTCCTCATGATGTGAC AGAGACTTGTGTTGAGTGTGATCAATAATACCAATTTGCTTGTCTCCCTCCCGATCTCT ACAAATACAAACCCCTGTAAAGACTATAAAGACAAATATGATCGGTACATGATAATGTTGGACTT GCCAAGCGTGTGGTGGCA									
4948	nucleotide-sugar dehydratase.1	other cell wall enzymes	26	contig	3	EG974187	101613.875	201708.4167	185364	23297.76338	28415.47379	20279.12523-0.9	-1	-0.1	0	
							CCGTCCACGGCTCCGAAAGGAATTCGAGTACCAGACAGGATTTGAGCAAGATCTGCGCAATGGC GAGGAAAGCTCTAATACCATGGCAGTGTGAGCAAAAACCCCTCCATCCCATCTCTTTAA GAAATGCCAAGTCTCCAGGCCAATATGAGAATCTTTGTAACCTGGAGGCTGGATTTATTTGGC TCTCATTTGTAGACAGGTGTGAGGAATATGAAAGAAATGAAAGATGAGTGTGGGGAATAATTT CACTGGCTCAAAGGACAATCGAAGAATGGATTGGTCAATCCAGATTTGAGCTTATCCGTCATG ATGTGACAGACATTTGCTGTTGAGTGTGATCAATAATACCATTTGCTTGTCTCCCTCCCG ATCTTCTACAAATACAAACCCCTGTAAAGACTATAAAGACAAATATGATCGGTACATGATAATGTT GGGACTTCCAAAGCGTGTGGTGGCA									
5615	nucleotide-sugar dehydratase.1	other cell wall enzymes	26	contig	3	EG974186	117451.8333	236686.2917	216751.4167	13471.26874	33541.09161	29641.11345-0.9	-1	-0.1	0	
							TCCACGGCTCCGAAAGGAATTCGAGTACCAGACAGGATTTGAGCAAGATCTGCGCAATGGCGAAG AAGCTTAATACCAATGGCAGTGTGACGACAAACCCCTCCATCCCATCTCTTTAAGAANAAT GCCAAGTTCTCCAGGCCAATATGAGAATCTTTGTAACCTGGAGGCTGGATTTATTTGGCTCTCA CTTGGTAGACAGTTGTGAGAAATGAAAGAAATGAGTGTGGGATAATAATTTTCACTG GCTCAAAGGACAATCTGAAGATGGATTGGTCAATCCAGATTTGAGCTTATCCGTCATGATGTG ACAGACATTTGCTGTTGAGTGTGATCAATAATACCATTTGCTTGTCTCCCTCCCGATCTT CTCAAATACAAACCCCTGTAAAGACTATAAAGACAAATATGATCGGTACATGATAATGTTGGAC TTGCCAAGCGTGTGGTGGCAGG									
1202	nucleotide-sugar dehydratase.2	other cell wall enzymes	25	singleton	1	EG974188	14887.33333	32073.41667	20755.75	2114.19677	5507.778396	2712.601958-0.5	-1.1	-0.6	0	
							GTCTCTCAGATCCATCCATTTCTTCCATCTCTAGCTTCCATCACACAAATTCACCTAGGCG CATATCGTGTATGGCAATTAACATTTGAAATAAGGACATGCTCGAGTGTGATCTCTCTC CTCAGAGCTTGGAGTTGAGGAGCTCAAATCTGTATATTCAGAACCCGCAAAATCTAAGAAATG AAGCAGTTACATAAGCAATCGAGCTGATCACAGAGGGATGAGGAGATGGCGCAACAGGCTC GACATCTCACTCACTAAACCCCTAAACCCAGATCCAGATCCAGATCCAGATCCAGATCCAG TCTTCAAAGAACAGAGCTTCTTATCTTGTGGTATTTGGTGGTCCACATTTCTCATT CTCAGCCGACCTGTCTGAAATGGACCCCTCCGACCCCAATTCGGGTATAGCAGATCTTTTCA GGCAAGCTAGGGA									
3293	O-acetyltransferase-related	miscellaneous	110	singleton	1	EG974378	15349.16667	66376.20833	41640.58333	2098.816246	22360.47895	4960.940017-1.4	-2.1	-0.7	3.4	
							TGATCTTATATGATCGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG TGGAAAATTTGGAGGAATCAGAAACAAAGAGAGATTTCAATCAAAGAGCCATAGTTGCTGTT TCTGATTTTGGTTATTTGTTTGGATGATGATGATGATGATGATGATGATGATGATGATGATG GCTCCACCCCTACACCTATGGATCCATAACGGTGTATATGATTTTGGCGGAACTTCCACCCAGC AGTTCGAAATTTCCATGACTCTTTGATGGTAGGCAAGGTTACTCTGAAACCTACATT TCCAGTTCCACATCTGTTGAGATCAAACATCCCAATGGACCCCAATTCGGGTATAGCAGATCTTCT GATCCCGGAAT									
6893	oxygen evolving complex 33 kDa photosystem II protein [Nicotiana tabacum]	photosynthesis	207	contig	8	EG974281	315182.1667	151613.8333	137512.125	57814.89946	31109.12631	22580.461	1.2	1.1	-0.1	0
							CCCCCGGCTCGGTCTAACCCTTGGACGATGCGAAGGACCTTTGAGGCTTCGAGCG ACGGACAGTCAAGTTCGAGGAGAAAGCGGCATAGACTACCGCGCATCCCGTCCAGCTCCCG GGAGTGAACCGGTGCCATCTTATTCACAAATCAAGCAACTTGGGCTTCTGGCAACCCGAAAG CTTACCGGTGATGTTTTTGTCCCGTTCACCTGGTTCGCTGTTTTGGACCCAAAGGGCAGAG GTGGTCCACTGGTATGACAAATGCTGATGATGACAGTGGGGGACAGAGTGTAGGAGGAA CTTCAAAGGAGAAATGAAAGAAACTCTTCAACTGGCAAAATTAATCTTAGTGTACTTAA GACTAAGCTGAGACTGGTGGTGTATGGTGTGTTTGGAGTGTTCAGCCATCTGATGACTGAT TGGTGTAAAGTCTCTAAAGATG									
3368	oxygen evolving complex 33 kDa photosystem II protein [Nicotiana tabacum]	photosynthesis	207	contig	8	EG974282	160063.625	70186.625	70029.20833	28869.82965	14757.44403	10848.54581	1.2	1.2	0	0
							GCAATCGACGGGTGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG TTTGGACCAACTTCAATTCACAGTGAAGCAAGAGAGTGAAGCAAGCAAGCAAGCAAGCAAGTCC AAAACCAAGCTCATGACAGCTTAACTTACACTTGGACGAGATCGAAGGACCTTTTCGAGGTC TCGACCGACGGGACAGTCAAGTTCGAGGAGAAAGCGGCATAGACTACCGCCGATCCCGTCCA GCTCCCGGAGGTGAAGCGGTGCCATCTTATTCACAATCAAGCAACTTGGGCTTCTGGCAAC CCGAAAGCTTCAGCGGTGATTTCTTCCCGTTCAGCGGTGCTGTTTTTGGACCCAAAG GGCAGAGGTGGTGGACTGGGTATGACAAATGCTGATGATGATGATGATGATGATGATGATGATG GGGGAACCTCAAAAGGAGA									

3807	oxygen evolving complex 33 kDa photosystem II protein [Nicotiana tabacum]	photosynthesis	207	contig	8	EG974276	GTGGAAGTGAAGGAACAGCAAGCAAGCAAAATGCCCCAACATCGACGCGCGGTGTCGAGTCAATT CGCTTCAAAGCGGGAAATACAAACGCGAAAGAAAGTTCTGTTGGAGCCAACCTTCACTACAGTGA AAGCAAGAGATTAGCAAGAACAGCCAGCAAGATTCAAAACACCAAGCTCAGTACAGCTCA ACTTACACTTTGACGAGATCGAAAGGACCTTTGAGAGTTTGGAGTTTGGAGGACAGGCTCACTTG GGAAAGAGCGGCATAGACTAGCCGCACTCAGCTCAGCTCCCGGAGGTGAATGCGTGCAT TCATTAACAATCAAGCAACTTTGGCTTCTGGCAAAACCCAAAGCTTCAAGCGGTGAGTTTCT GTCCGTCTAACCGTGGTCTGCTGTTTTGGACCAAGGCAAGGCGAGAGTGGTCCACTGGGTATGA CAATGCTGTAG	335410.9167	245538.0833	156914.375	56089.95445	41831.12316	20078.10685	1.1	0.4	-0.6	0.5
6934	oxygen evolving complex 33 kDa photosystem II protein [Nicotiana tabacum]	photosynthesis	207	contig	8	EG974280	CATTACGCGTCCGGAAGAAGAAAGAGTGTAACTAATGCTGAGTCCGCTCGCTACAAAG CAGCGCCACTAATGACGCCACTAAGATGGGTCTAATGCTAGCCAGGTGGTTCGAACCTG AGTCTCTCAGAGTTTCAAAGGCTTTGGTGTGGAGTTTGGAGTTTGGAGGACAGGCTCACTTG CTCACTCAAAGTACTTAAAGGATTTGGCCAAAAGTGGCTTGAATGCTACTAAGATCCGTGGCT TTGCTTTGGCCACTTCTGCTTCTGCTCGGGAGCAAGTGCAGAGGAGCAACAAACAGCTCA ACATTCGACAAATCAAAGACATACATGGAAGTGAAGCAAGCAAGCAAGCAAGCAAGCAATG CCCAACATCGAGCGGTGTGAGTCAATCGCCTTCAAAGCGGGGAAATACAAAGCGGAAAAAGT TCTGTTGGAGCCAACTCACTT	221193.0417	122924	100296.3333	29581.93725	17848.96056	13872.50372	1.1	0.8	-0.3	0
3260	oxygen evolving complex 33 kDa photosystem II protein [Nicotiana tabacum]	photosynthesis	207	contig	8	EG974277	CCCCCTGCGTCCGCTCTCTCTCTGCCACTTTTCAATTAATTAATCTGTTTTTTCAGTTAGG ACAATAGAAAACAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGCTT CGTACAAGAGCGGCCACTTAANTGCAGCCACTAAGATGGGTCTAATGCTAGCCGAGGTGGG TTGCACTGAGGCTTCTCAGAGTTTCAAAGGCTTTCGACAGTGTTCAAAGGCTTTTGGTGTGAG AGTTTGGTGGAGCCAGGCTTCTGCTACTCCTCAAACTGCTTAAAGGATTTGGTGTGAGAGTTG GCTCACTTCTCACTCAAAGTAAAGGATTTGGCCAAAAGTGCCTTTGATGCTACTAAGA TCGCTGGCTTCTCTGCCACTTCTGCTTCTGCTCGGGAGCAAGTGCAGAAAGGAGCACCA AAAGCTTAACATTCGAGAAATCCAAAAGCAAGCATATGGAAGTGAAGAAAAGCAAGCAAGCA AAACCAATGCCCAACATCGA	442333.7083	263349.3333	197978	59734.02694	39599.22115	28095.77902	1.2	0.7	-0.4	0
240	oxygen evolving complex 33 kDa photosystem II protein [Nicotiana tabacum]	photosynthesis	207	contig	8	EG974279	GATTACTCTGTTTTTTCAGTTAGGACAAATAGAAAACAAGAAAAGAAAAGAAAAGAAAAGTGA ACCAATATGGGAGCCTCGTACAGCAGCGGCCACTCTAATGCAAGCCACTAAGATGGGTCTA ATGTAGCGGAGGTGGTGGCACTGAGTCTTCGACAGTGTTCAAAGGCTTTTGGTGTGAG AGTTTGGTGGAGCCAGGCTTCTGCTACTCCTCAAACTGCTTAAAGGATTTGGGCTTAAAGT CCTTGTACTAAGATCGCTGGCTTCTGCTGCCACTTCTGCTCGGGAGCAAGTGCAGAAAGG GTGCAAGGAGCAACAAAGCTTAACATTCGACAAAATCCAAAGCAAGCAATATGGAAGTGA AAAGAAACAGAACAGCAAAACCAATGCCCAACATCGACGCGGTGTGCGATCAATCGCCTTCAA AGCGGGAAAT	225194.0833	113745.9583	90499.66667	31168.57335	17319.7827	12779.42028	1.3	1	-0.3	0
4583	oxygen evolving complex 33 kDa photosystem II protein [Nicotiana tabacum]	photosynthesis	207	contig	8	EG974278	GAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA TGCAGCCACTAAGATGGGTCTAATGCTAGCCGAGTGGTTCGCACTGAGGCTTCCGACAGG GTTTTAAAGGTTTTGGTGTGAGAGTTTGGTGGAGCCAGGCTCACTTGTCTCACTCAAAGTGA CTTAAAGGATTTGGCCAAAAGTGGCTTGAATGCTACTAAGATCGCTGGCTTTGCTTTGGCCACTT CTGCTTGTGCTCGGGAGCAAGTGCAGAAAGGAGCAACAAAGCTTAACATTCGACGAAATC CAAAGCAAGCAATACATGGAAGTGAAGAAAGCAAGCAAGCAACCAATGCCCAACAAAGTCCG CGGTGCGAGTCAATCGCTTCAAAGCGGGAAATACAAAGCAAGCAAGCAAGCAAGCAAGCAAG CTTCAATCACAGT	116256.2083	62562.625	48699.25	15342.71108	9370.143161	6140.305395	1.3	0.9	-0.4	0
6788	oxygen evolving complex 33 kDa photosystem II protein [Nicotiana tabacum]	photosynthesis	207	contig	8	EG974322	GCTCTCTCTCTGCCCACCTTTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA AAGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA GCCACTCTAATGACGCCACTAAGATGGGTCTAATGCTAGCCGAGTGGTTCGCACTGAGGCTTCCGACAGC CTTCTCAGAGTGTTCAAAGGCTTTTGGTGTGAGAGTTTGGTGGAGCCAGGCTCACTTGTCTCACTCAAAGTGA CTCCAACCTGACTTAAAGGATTTGGCCAAAAGTGGCTTGAATGCTACTAAGATCGCTGGCTTTG TCITGCCACTTCTGCTTCTGCTCGGGAGCAAGTGCAGAAAGGAGCAACAAAGCTTAACAT TCGAGCAATCAAAGCAAGCAATATGGAAGTGAAGAAAGCAAGCAAGCAAGCAAGCAAGCAAG GGAAGAAAGTGGCCCAAGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG GCAGACCAGCGGTTGTTTACCGTTTCAATCTCGGATACCAAGCAACTGTACGTTGCTGACGTTATC	16174.91667	46145.25	29516.04167	1934.871075	5866.224898	4128.030605	0.9	-1.5	-0.6	0
320	pectinesterase_1	glycosylhydrolases	36	contig	3	EG974638	CAATCGCCAGGTTCCCGGAGTGGAAATACGGAACCAAGCCAGTCCGCTCGCTCGGCTGATC GCAGACCAGCGGTTGTTTACCGTTTCAATCTCGGATACCAAGCAACTGTACGTTGCTGATC CAATCGCCAGGTTCCCGGAGTGGAAATACGGAACCAAGCCAGTCCGCTCGCTCGGCTGATC CTGTGTTTTCCAAAAGTGTCAACTACGCAAGCAAGCCAGTCCGCTCGCTCGGCTGATC ACGGCCAAAACCCGAAAGCCGAAACAAATACGGGTATTCGATCCAGCTTACGGATCCT TGCCAGTCAATCTTGAAGCCTCGAAGGTTAGTTCGCGGATCTCGGCTGCTCGGCTGCTG TGACGCTAGAACCGTGTACATGATGACGTTACATGGTGTATCATCCATCCAGTGGATGGCTA GAATGGAAAC	175613.5	80905.16667	80931	18083.72344	11090.6693	11480.39734	1.1	1.1	0	0
5590	pectinesterase_1	glycosylhydrolases	36	contig	3	EG974372	GGGAGGATCAACCAACCATGACGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG CTGTGGAGAAAGGTTTCAAGAAAGTGGGCCCAAGGTTGACCGGAAACGTTGAGACTCAAGTGGCCG AGAATTTGAAGGACTTATCTGAACCTGAGTAAATGCTGGGCTATTTCTGGAGTGGAAAGTGAAT GACGATTTCCGGGATCCGATTCAGAACAGAGGAGTTTGGGCTGAGATGAAAGGAA GGCAATATCTGGGAGATTTCCCGAGTGGTGAAGCAAGTGAAGGAGGCTATGGGTTTAC CTGTCCGGGATCAAGCCGATCTGTGTCAAAAGACGGAAATGGACTTACAAGACTATT ACTGAAGCAATTAAGAAAGCAACCGGATACAGTGTGCTCGGACTATTAATACGTTGAGGGCAGG AAGTTACGAA	142904.7917	74488.29167	65808.91667	15983.09971	12322.92342	12113.46166	1.1	0.9	-0.2	0
3722	pectinesterase_1	glycosylhydrolases	36	contig	3	EG974361	GGAAAGCAGCGGAGTACAGTATCGTGGACTATTAATTAATTAATTAATTAATTAATTAATTA AATAATTTGAAGGTAAGAAAGAAAGAAAGAAAGTGTGATTTTATTTGGAGTGGAAAGGCGCAAAAC AGTCAATTCAGGAGAAAGAGGTTGGGAGAACATGACAACATTTCCACAGCACTTTCCGCTG CAACTGGGCTGGTTTCAATAGCTGGGACATCACTTTGTAAGTGGGCTGGCCAGCTAGACAC CAAGCCGCTGCACTCCGGGTAGTGCAGCAACCGGTTTGTACCGTTGTCAAAATCTCGGATA CCAAGACTCTAGTGCATCCATCGCCAGTCTCCCGAGTGGGAAAGTTACGGAACAG TCGACTCAATTCGAAACCGCTGTTGTTTTCCAAAAGTGTTCATTAATACGCAAGAAAGCC AAGTTACGAA	77537.375	41247.41667	30578.5	10694.89101	7618.8362	4293.051142	1.3	0.9	-0.4	0
3919	pectinesterase_2	glycosylhydrolases	34	contig	2	EG974394	GCTTACTTTTTTTTTTTTGGTGTGTTTTTCAAACCAAAAACAACACTAATTTGTTAAAGTAA CAAACGAACTGAACAATTTTATCTAGTTTCTATGGCGCTAATAAGCTTACGAGAGTTAAACTCT CGCTCTGATGATCACTACTTCTGTTCCGCAATGTTAGGCTGAGATCTTACGATTCTC TTTGACTGGAAATGCACTTATGAGCAATTTACCGCTCGGCTTCCGCAACAGGAAATTTAT CAATGGCAATTTCTGGCCCGCAATTCATTCGGTTACTACAGCAATCTCAATCAATGCTC ACAAGCTTGGACGAGCTTTTCTCTATCTTGGAAATGGAATTCAAAACAGGAGAAATCTTTT GAAAGTGGTATGGGAACCAACATGCCAATACCCCAAGCAAGAAATTCACCTTACTTCTCCA AGTGAAGGATC	55056.08333	32436.29167	27315	6955.366566	4884.004559	4281.131844	1	0.8	-0.2	0

2985	pectinesterase.2	34	contig	2	EG974383	glycosylhydrolases	63068.20833	33409.875	26033.91667	9243.765809	5233.140841	3403.925381	1.3	0.9	-0.4	0
2096	pectinesterase.3	37	singleton	1	EG974649	glycosylhydrolases	73888.75	34128.25	35967.25	9650.382265	6039.731649	7244.050706	1	1.1	0.1	0
6647	pectinesterase.4	32	contig	2	EG974735	glycosylhydrolases	7511	42822.91667	48498.91667	1197.124824	7744.76347	5424.449294	2.7	-2.5	0.2	0
4775	pectinesterase.4	32	contig	2	EG974737	glycosylhydrolases	6088.75	25484.33333	31145.875	2269.613543	3131.681547	3689.853399	2.4	-2.1	0.3	0
5583	peptidase	22	singleton	1	EG974476	amino acid & protein metabolism	130479.625	10018.33333	5719.458333	30401.95285	2386.459028	1325.104055	4.5	3.7	-0.8	0
2834	peroxidase.1	184	contig	3	EG974456	oxidoreductases	9923.166667	47491.25	32746.41667	1163.967165	7140.744095	4544.688466	1.7	-2.3	-0.5	0.1
6595	peroxidase.1	184	contig	3	EG974455	oxidoreductases	27731.25	60225.875	41301.875	4147.822396	10674.2545	7407.605987	0.6	-1.1	-0.5	0
5372	peroxidase.1	184	contig	3	EG974454	oxidoreductases	11907.45833	38421.66667	25328.75	1703.149322	7275.382908	3621.521555	1.1	-1.7	-0.6	0
1987	peroxidase.2	180	singleton	1	EG974457	oxidoreductases	13618.04167	79777.45833	49629.54167	1862.392264	14919.84672	4153.659108	1.9	-2.6	-0.7	0
4320	peroxidase.3	182	singleton	1	EG974458	oxidoreductases	3095.833333	13034.04167	4868.333333	503.9659548	2028.712191	702.28994607	0.7	-2.1	-1.4	0.8
4884	peroxidase.4	192	singleton	1	EG974433	oxidoreductases	94166.83333	28063.25	9548.458333	17297.81893	5712.435102	1725.361467	3.3	1.7	-1.6	0

5033	peroxidase.5	194	singleton	1	EG974440	194	oxidoeductases	GCTAGCTTCCCTTGGTTATATAGAAATATACCTAATCATGAGGAGAAATACACATT AATCTTGGCAITGATCTTTTAAATAAGCTTTGGTATTTGAGTACTCCTTATGGTTTT GGTCAACTAAACCTAATTTCTACAAAAGAGTTGGCCTAATGCGGAGCAAAATGTAACAAAGT TGTCAAAAGAGCAATTTGGAAAGATCTTACCATTACCGTGGCTTACTCTGTAIGCATTTCCAG ATTGCTTTGTAGAGTTGGGATGCATCATACTAATCAATCTACATCAACAAAGCCCTCTGAA AAAACAGAGCAAAATCACTAGAGGGTATGAGCTCATGATGAGGCCAAAAGAAAGGCT CGAAGCAGCATGCCCTTCAAAGTCTATGTGACAGACATCAACCCCTAGCAACTCGAGACTCTG TCATCTTCCA	101489.375	23242.95833	31538.91667	16225.05788	4383.505178	6893.080085	1.7	2.1	0.4	0
2773	peroxidase.6	190	contig	3	EG974443	190	oxidoeductases	CTGGGCAACACAAATATGGGAAAGCAAGATGTACACTTTTCAGAGACAGAATATACAAATGAGAG CAACATTGATAGTTTATTCGCAAAAAGGCAAAAAGAGTGTCCACGTAAGGCTCTCTGAGGCTCTCTGGAG ATAACAGGTGGCAGATCTGATGTTAACTCAACTCCAAAGATTTGATAATCTACTTCAAAA TCTTTGAGCCAAAAGGGTCTTTTACACTCTGATCAGATCTTGTTCACCGTGGATCCACTGATT CTGTTTAAAGGTTACAGTTTCAAGCCCTAGTACTTCTGAGGACTTTGTTA TTGGAAGAAAGACTCAAGACCGCCCTTAAATGGCCCAATAAGTGGAGTCAATCCCTCTCC ACTTCCACCCTAAGCAACTATAATAGATTCAAGTAAAGTCTCTGCAAAAGACATGGT TGCTATCTGGGACACACAATGGGAAAGCAAGATGTACAACCTTCAGAGACAGAATATACA ATGAGACCAACATTGATAGTTTCTGCTAAACAAGGCAAAAACAAGTGTCCAGTAAGGCTCTT TCTGGAGATAACAATGTGGTAGATCTGATGTACAACTCCAAACAAGATTTGATAATCTACTT CAAAAATCTGTTGAGCCAAAAGGTTCTTTTACACTCTGATCAGATCTTGTTCATGTTGATCCA CTGATCTG	80255.04167	31091.625	70089.70833	13126.6325	5302.446705	10596.62034	0.2	1.4	1.2	0
3227	peroxidase.6	190	contig	3	EG974441	190	oxidoeductases	TTGGAAGAAAGACTCAAGACCGCCCTTAAATGGCCCAATAAGTGGAGTCAATCCCTCTCC ACTTCCACCCTAAGCAACTATAATAGATTCAAGTAAAGTCTCTGCAAAAGACATGGT TGCTATCTGGGACACACAATGGGAAAGCAAGATGTACAACCTTCAGAGACAGAATATACA ATGAGACCAACATTGATAGTTTCTGCTAAACAAGGCAAAAACAAGTGTCCAGTAAGGCTCTT TCTGGAGATAACAATGTGGTAGATCTGATGTACAACTCCAAACAAGATTTGATAATCTACTT CAAAAATCTGTTGAGCCAAAAGGTTCTTTTACACTCTGATCAGATCTTGTTCATGTTGATCCA CTGATCTG	502664.4583	220825.4583	314391.7083	70198.21558	37668.57455	35177.77912	0.7	1.2	0.5	0
2780	peroxidase.6	190	contig	3	EG974442	190	oxidoeductases	GGGAAGAGAGACTCAAGACCGCAAGCTTAAATGATGCCAATGATGGAGTCAATCCCTCTCCCA CTTCCACCCTAAGCAACTATAATAGATTCAAGTAAAGTCTCTGCAAAAGACATGGT GCCTATCTGGGACACACAATGGGAAAGCAAGATGTACAACCTTCAGAGACAGAATATACA TGAGAGCAACATTGATAGTTTCTGCTAAACAAGGCAAAAACAAGTGTCCAGTAAGGCTCTT CTGGAGATAACAATGTGGTAGATCTGATGTACAACTCCAAACAAGTGTTCATAATCTACTT AAAAATCTGTTGAGCCAAAAGGTTCTTTTACACTCTGATCAGATCTTGTTCACCGTGGATCCAC TGATCTGTTTAAACCGGTACAGTTTCAAGCTTAGTAGCTTGTGAGGACTTTGTTAAAGGCA TGATCAAG	124660.7917	45546.95833	98339.58333	18651.07438	6293.189809	13199.3761	0.3	1.5	1.1	0
2692	peroxidase.7	191	contig	2	EG974434	191	oxidoeductases	GAAAGTCTACCATGGTTAAGGCTAGTTCATCACTCTTCCCTTCTTACTAGTAATAAAAAT CTGGTTTGTATAATCTGTTGTTACTAATTTGATAGTATATAGTGTGTCAGTGTCAAAA TTTTGAAAGCCAGCTGAGAAAACAGTTTCTTAAACCAAGGCTCTCAATGGCAATCTATGCAA AATATGCTCTCTGCTGATATACCGCTCTTGGCTGATGATGATGATGATGATGATGATGATG GCCAAGCTGCTGGCTTCTGCTCTCCATTTCCATGATGCTTGTTCAGGGTGTGATGGTTTC AGTGTGTAGATGGTCAAGAAAGTGTGAGCAAGTGTGAGAAAGTGTGACCACTAATCTACCTTGA GAGCCACTGCATCAAGATCATTAATGATCTTCGAGCCCTAATTCACAAGAAAGTGTGGAAGAGTT GTTCTTGGCT	16410.08333	5444.5	2890.125	4096.907721	894.7941975	637.90353025	1.6	1.6	-0.9	0
1266	peroxidase.7	191	contig	2	EG974435	191	oxidoeductases	GAAAGCAATCATTGAAATGGAGCAAGCAAGTGGACCAAGTGGAAAGATGCACCACTAATC TCACCTTGAGGCCACTGGATCAAGATCATTAATGATCTTCGAGCCCTAATTCACAAGAAAGTGT GGAAGTGTGTTTCTTGGCTGATATACCGCTCTTGGCTGATGATGATGATGATGATGATGATG TGCCAGACTAGCCGTACCAATGGGAAAGCAAGAGCGGCTTAGCAATTCGCAACCCAAACGAAA CCAAATCCACTTCCACCAAGTGTGAGTGGCCCAAGCCATTCACAACAACCTGCGGCAAC CAAACTCCGACAGATGCTGCTCTACCCCAACCAAGATCAGTCAATGGACCAACCTTCGCCAAGA CGGATCTTCGACAAACCGTCTCTACCCCAACCAAGATCAGTCAATGGACCAACCTTCGCCAAGA ATCTAAATCCA	61867	18712	11179.25	7922.555213	3028.839529	1638.356557	2.5	1.7	-0.7	0
1321	peroxidase.8	189	singleton	1	EG974436	189	oxidoeductases	AAATAATAATAATAGTTAAAGTAAAGTAAATATATATATATATATATATATATATATATAT ACAGAGAAAGAGAGAGAGAAATGGTGTCTCAATCCGTATCTGAGAAATCCATTCACGAATTC ACAGTCAAGGATGCCAGAGGTAAGATGTCAACTTAGCAGTTACAAAGGGAAGTCTTCTTGT GGTAAATGTTCTTAAATGTTGCTTACGATTCGAAATATACACAGTGTGAGCTTAC ACAAATACAGGCAAAAGGTTTGAAGTATGGCATTTCCCTTCCATCAATCTTAAAGCAAGAG CTGGGTGAGGATGCTCAAAAATTTGTTGTGAACGATACAGGCGCAATATATCCGATAT TCAAAAGTACGAGTCAATGGCC	28473.75	13242.95833	10446.875	5733.693317	2542.031042	1517.146833	1.4	1.1	-0.3	0
3331	peroxidase.9	196	singleton	1	EG974453	196	oxidoeductases	GTGTTCTTCCAGATGCTTGTCAATGGATGTGATGATGATGATGATGATGATGATGATGATGAT TTTGTGGGCGAGAAAACCTGTAATGCTAATCAAGCAAGTCAAGAGGTTTGTGCTGTTGATG ACATCAATCCGAGTGGAGTGTGCTGGTGTCTTCAATGCTGATATATGGCCATT ACTGTAGAGACTCCGTTTACAAATTCGGGGGTTCAAATGGAAAGTGAATGGAAGAAAGGGA GGGAAAACCTAGCAGAGCTGCAACAATGGCATCCACAGCAATCTTCAACTTAAACA GGCTCTCTAGATCAATGCTTGGCCCTTCCAACTGACTTGGTGTCTTACTGCTGAGGAGCC CATACAATGGGTGAGCAAGATGCACATCTAGGGCTCACATATACAAACGAGCAACATCGA TGGTTCAATCCG	3044.583333	16723.375	5713.416667	618.333129	2710.226186	919.71686509	-2.5	-1.5	-0.1	0
3186	peroxidoxin Q [Populus balsamifera subsp. trichocarpa x Populus deltoides]	193	singleton	1	EG974437	193	oxidoeductases	GTCTCTTCCCTAAGCACTACTCCACCTGCTCCCTCCCAAACTCGTAAAGACTTATTTTC CAAACTCAAAATCTTCCAAATCACTCACTCAGTTTATGGCACCAGCTCTCCTATTC TACATCTACTACTCCACTTCTCCACCAAGAAAGTGTGTTTCGCCAAGGTGAAAAGG GTTCCACCCACCCCTTACCTTGAAGATCAGGATGGAAGAAAGTGTGAGCTTCCAAATTC AAAGGAAAACCTGTGATGCTATTTTACCCTGCTGATGAGACTCCGGCTGTACTAAACAGGC TTGTCTTTCAGGGATCTTATGAGAAATTAAGAAAGCTGGAAGGCTGAGCTGGTATGATG GTGATGATGTAACCTCACAAAGGCTTCGCAAAAGAAATAAACTTCTTACACATTAAGCC GATGAAGTAAAC	29287.5	7317.416667	6847.833333	5407.168027	1473.177142	1352.884548	2.1	2	-0.1	0
290	phenylalanine ammonia-lyase	238	singleton	1	EG974536	238	secondary metabolism	AGTAGTTAGTTCTTGTATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG GCAGAAAACGAGCTGTGGAGTTCTGTGTGAGAGTATCCCTCACTCACTCACTCACTCACTCACT CAGCTGATCGATGATGGAGTCACTTGGACGAGTCAAGAAAGTGTGCTGATACCGAAAA CCGGTAGTCAGGCTAGTGTGAGACTTTCAGGATATCTCAGGTGGCTGCCATCCCGCTGTGGA TGGGTGAAAGTGGAGCTGTCTGAGTCTCCAGGCGGGGTGTTAAAGTAGTAGTGGGTTA TGG	5307.458333	19338.04167	14094.75	899.6181114	2741.734446	1503.495572	1.4	-1.9	-0.5	0
228	phosphatase.1	171	contig	2	EG974467	171	miscellaneous	GCATAATAATCTCTCTTTTTTCT AAGATGAAATTTGTAGGAAAAATAAGAGATGGTGGGGTTTATTCAGTATATATTTTGT GTTGTTTTGGGATAAGTGTGTGGATCATATGGAGATGATTAATAGCACCATTGTGAG TAATAGCCATFACAAAACCCAGTTGCTTTCATATCTGCCCTATAGAGAGTAAACCCAGCT CTTCTGGCTTGAAGGGTGAAGATCCCAATGGTAAACAGTGGAGTTAGAACCCCTGAACCCATC TCCGGAGATTGGGTTGGAGTTTCTCCCTGCAAAATTTCAACTCAACTCAACTCAACTCAACTCA ACCCGATAATTTGAAAAATCGGAAAACCTTACTATGTGTACTGCCCAATCAAGTTCAAGTAGCT AATAATCCAAAC	64286.33333	4890.458333	20376.625	10621.40509	771.2447073	16298.47612	1.7	3.7	2.1	0

4980	polygalacturonase.1	glycosylhydrolases	45	contig	3	EG974671	129972.2917	22604.25	34163.29167	16806.81669	4310719404	13272.15154	1.9	2.5	0.6	0.1
TTTTATCTTATTTAGCTTCCATCAATAAAGTAGTAGGAGCCAGAAATACTGTAGTAATCAAT AGTGAAGATATCGTTAATTAATTAATAGATAGTGGTTTGGGTTAGTGTAGTATTAATTTGGTGGC CGCTAGGTTGGCCCGCCAGGCGCTGTCCACCGTCGGACAGGCGCGCTTATGGCTTCAAA CTGCTATGGAGTATGATGATCAAGGAACCGTGGTCCGGATATAAATCTCCGTGGGAGT CCGAAGACCCGATTTTGAAGGGCTCGCCGAACCGGGTATAATGACCGGT GTCCTATTTAGCTTCCATCAATAAAGTAGTAGGAGAAAGATACTGTAGTAATCAATAAGTG AAGATTATCGTTAATTAATTAATAGATAGTGGTTGGGCTAGTAGTATTAATTTGGTGGCCGCT ACTTTGGCCCGCCAGGCGCTGCCACCGTCGGACAGGCGCGCTCTATGGCTTCAAGACCGC TCTCCAGGCGCTATTTGGGAATCTCAACTCTGACCGGAAACCGACTGCTGFAAAACTGTT ATGGAGTAGTTGTATCAGGAAACCGTGGTCCGGTCCGGAATAAATCTCCGTGGGAGTCCGAA GACCGATTTTGAAGGGCTCACGAAACCGGATATAGCCGGTACATTTCTCCCGCCATTTG CAAGTCTCCGGACTCTCCAGCATCAATCGCCGACTGGAAGGAATACCGGAGTCAATCTC AATGATAACAGC																
3694	polygalacturonase.1	glycosylhydrolases	45	contig	3	EG974660	45956.79167	7342.583333	8003.083333	6986.620896	1355.882027	1301.040115	2.5	2.6	0.1	0.1
GTCCTATTTAGCTTCCATCAATAAAGTAGTAGGAGAAAGATACTGTAGTAATCAATAAGTG AAGATTATCGTTAATTAATTAATAGATAGTGGTTGGGCTAGTAGTATTAATTTGGTGGCCGCT ACTTTGGCCCGCCAGGCGCTGCCACCGTCGGACAGGCGCGCTCTATGGCTTCAAGACCGC TCTCCAGGCGCTATTTGGGAATCTCAACTCTGACCGGAAACCGACTGCTGFAAAACTGTT ATGGAGTAGTTGTATCAGGAAACCGTGGTCCGGTCCGGAATAAATCTCCGTGGGAGTCCGAA GACCGATTTTGAAGGGCTCACGAAACCGGATATAGCCGGTACATTTCTCCCGCCATTTG CAAGTCTCCGGACTCTCCAGCATCAATCGCCGACTGGAAGGAATACCGGAGTCAATCTC AATGATAACAGC																
6002	polygalacturonase.2	glycosylhydrolases	44	contig	1	EG974682	186744.4583	46154.66667	51476.20833	22169.51004	7702.281805	11977.13381	1.9	2	0.2	0.1
TGCTAGTATTAICTCAAAATTTGAGAAAGATAAAGAAATAAATAAATAAGGAGGAGAGG AATGACTTTTGTGATGTTCAAGTTAACAATGATGACCATAATCTCGGCCGCTAATCTCGCCCGC CGTCGGACAGGCGCTGATGGCATTCAAGCGGCCCTCTCTGAACCTTACTGGGCACTTTC CAGTCTGTGCTGGAACCGACTGCTCAACAATGTTACGGCTCAGCTGCGATCCGACCACTGG CCGGTCTGTGACATAAACCTCCGGGAGAGTCCGAGGACCGGATAATAGCCAAAGGCGAG GTCAGGACTGTGCTGTGGGATTTGCTTTTGGTTTCTTCCAGTTCTTGGTGGGACTTCTGGTG TCTTGAAGGATTTCTGCAATGGCCAAATTTGCTGGTGAATTTGATTTGCAATTTAGCTGTTTTG TCAATGATCTCGACTGCTCCCTTGGTTACTAATAATGATGATAGCTATCGTCTCAGAC CAATGAATCTATCAATTTGGCAATGAGGCAATTTCTGTTACTCTGTTAGCTGTAGTGAATG TGGACTAAGTCTAGAGCTGGTTCTGTTGCTGCTGTTGATGATATCCAAACCGATCTTGA CCACTACTCTTGAACAATTTGAGCCCATTCGAAATCTTCCGCTCTTTTCTTGGCAGCAT TGGGATGTTGATCCATGTTCTATGGAATCACGTAGACATATTTGCTTGCATCCGTTATAT TGGTCAIC																
2767	prephenate dehydratase	secondary metabolism	243	singleton	1	EG974569	5160.458333	28904.33333	20739.33333	602.0815793	4249.359888	2691.567734	-2	-2.5	-0.5	0
GGTCTCGCTCAGCAATAAGGGAATTCGGTCTTTTCAAGGTTCTTTCGGCTTCCGCTTTCAGAA ACATAAGTCTGACGAGATGGAATCGAGCGCCACCGTAACCGTCCGATTAGTGGTGGATGAT GTAACGTCGGTACCGTAAGCAATTTGAGTACATGTTCTTAATGATTTTGAAGCTTCAATGG GCACTTAGGCTCAGATGCTGATGCTAGGTTTCAAGGTTTCACTCATTTTGGGTTATGG GAAGTATCAATGGCAATGAGCCCTTGGTGGCCGTCACGGGAGATAGCAAAACCCATCTTT TTTTTATTTTCTTATTTTAAATAAAGGAGTAAATAAATAATTTCTTACTCATCTCTTCT TTTTTTTTT																
2629	profilin	miscellaneous	135	contig	2	EG974380	9691.25	18773.75	14697.29167	1629.977751	3315.471202	2238.675618	0.6	-1	-0.4	3.4
CCGAAATTCACAGGAAAATCTTGTAGTAGTACACCCCCAGAAGAAGAAGAAGATGCTGGC AAGCTTAGATGACCAATCTGATGGGAAATCCATGGCAATCTCTCAGTCTGCGGCTATC CTCGGCGTGTGGGAGCGTTTGGGCTCCGAGCGCTAATTTCCCTCAGTCCAGCCGAAAGAAAT AAGTGGCAATGATGATGATTTGAAGAACTTGAAGAACTTGCACCTACTGGCTCATGATG GCACCAATATTTGGTATCCAAAGGGAGCCAGGTGCTGTATCAGAGAAAGAGGGTGTGGT GGTGTACTGTTAAAGACTAGCCAGGCTTTGATCATTTGTTGATGATGACCAATGACGCC AGGCAATGCAACATGATTTGGTGGAGGCTTGGAGACTATCTCGTTGAGCAGGGTCTCTAATGG CTTGT																
148	profilin	miscellaneous	135	contig	2	EG974340	196166.0417	166904.5833	98086.95833	26190.39085	24286.44835	15260.77144	1	0.2	-0.8	0
CTTCCAGCGTCCGAAGAGTAGACACAGCTATTTTCCACCATCCAAACAGCAAGAAATTCACAG GAAAATCTTGTAGTAGTACTACTAGAAGAAGAAGAAGATGTCGTGGCAGCAGTACATGAGA TGACCATCTGATGTGGAAATCGATGGCAATCATCTACTGTCGGCTATCATCGTCTCATGATG GTAGCTTTGGGCTCAGAGCGCTAATTTCCCTCAGTTCAAGCCGAAAGAAATACTGGCATG AATGACTTTGAAGAACTTGGACACTTGGACCTTGGTGTATCTTGGTGGCAAAAATATAT GGTATCCAGGGGAGCCAGTGTGTATCAGAGGAAAGAAGGGTGTGGTGGTGTACTGTTA AAAGACTAGCCAGGCTTTGATCATTTGTTGATGATGACCAATGACCCAAATGACCAATGCAAC ATGATTTGTGAGGCTTGGAG																
4194	proline rich protein.1	other cell wall proteins	83	contig	2	EG974493	20945.75	3531.291667	5790.083333	4363.953149	934.3917643	1700.143756	1.9	2.6	0.7	0
ATAIATTTCAATGGAGAGTCTTCAAAATCAATATATTGCTTCTTATACTACTAGTAC TACTACTGTACTTGTAAATGGGTTTGGGCAACAACAGCTGAGCAAGAGCTTCTTTGTGTTT GGAGATCTCTTGTGGCAATGGCAATA																
3774	proline rich protein.1	other cell wall proteins	83	contig	2	EG974492	50793.375	4966.166667	7706.916667	6823.037638	900.5683645	1751.702951	2.7	3.4	0.6	0
GATCCCTTCTTAATGAGTACTAGTATATATTTCTTAGTAAAGTTTTTGTACTAGTTA TATATCTCAATGGAACTCTTCTCAATCATCATATTTCTTCTATACTACTAGTACT ACTACTTTGTTGTAATGATTTTTGGGCAACAACAGCTGAGGCAAGAGCTTCTTTGTGTTG GAGATCTTGTGGCAATGGCAATAACAATTTTAGCCACACAGCAAGACTGACTCTCTCT CCTATGGGATGACTACCTACTATAGACCCACTGGCCGTTTCTTAATGGCCCTCAACATGCC TGACCTTATCAGTGGCAAAATTTGGTCCAGAGCCACATGCTGATGATGTCGGGCTCACTG GAGAAAGGCTACTAGTTGGTGGCAACTTTGCTTCAAGTGGATAGGAATACTCAATGACACTGGA TTTTAGTTTC																
3237	proline rich protein.2	other cell wall proteins	80	singleton	1	EG974490	34447	10941	9324.041667	5684.447651	2443.208932	1339.0098	1.9	1.7	-0.2	0
CCCATTCACCGCTCCGCTCTCTAAGTCTGTTTTGACTTGAATATATATGAACTTTGTCT TTGCTAAGTCTCTACTGCCATCCACTGTTAAAGAAAGAAGAAGAAAGATAAATGCAATAACA GAGGAGGACTAGCATGTTTGAACCTTGGTGTGTTGTTATTAATTAATTTTATTTATTTGGTGG AATGCTCAGGACTTGTCCAGGGTCAATTTTTGGTACTCTGTAGTTGATGGGCA CAACACTCTCTCACTTTTAAAGGTAATTTCTCTTATGGAAGGGACTTCCGTAATC ACCAACCCACAGGATTTGCAATGAAACTAGCCACTGACCTCCTGCTGAGACTTTAGGC TTCAAGACTTACCAGCGCAATCTTAGCCCAAGAGCAATGAGGAAACCTTCTCAITGGAGC CACTTTGCTTCACTGATCTGGT																
4446	proline rich protein.3	other cell wall proteins	84	singleton	1	EG974491	39291.20833	3776.916667	3168.375	5404.85436	655.5625859	608.829772	15.6	3.4	-0.3	0
GATCTCTTCTCTTATAGCCAAAACAATAATAAATAAATAATATAGCTAGTCAATGGCTT CTTCTGGTAAACAAGTTTTTGGCCATTTGAAATGATCCATCTTAAATTTGACACTTGTCTAC GCTTGTCAAAATACATAAGTGAAGCCAAACACCGGCTCAGTCCCGCCGGAATATG CCAAAGACACTTGAAGCTAGGAGTGTGTGGAGCTGGGATTTGGTGAATAATAGTGGTGG GTAGCCCTCAACTACCAATGCTGTGCTCTCCAAAGGATTTAGAGGCAAGCCCTG TGCTCTGACAGCTTAAAGCCAAATGACTTGGTATCAACATCAATACAGTGTCTCTTAG TGTCTCTAAATGCTTGGCAAAAACACTTCCACCAGGCTTCAATGCCAATAAATAAATGATGA CCACCTTACC																

1393	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit_1	photosynthesis	216	contig	8	EG974313	537082.7917	90711.70833	102187.5833	68883.87103	16488.67823	14498.45734	2.4	2.6	0.2	0
6657	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit_1	photosynthesis	216	contig	8	EG974298	246814.7917	45531.20833	37383.45833	48579.5988	10908.26685	6269.084389	2.7	2.4	-0.3	0
3072	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit_1	photosynthesis	216	contig	8	EG974312	595425.4583	102657.2917	115513.1667	91885.36098	20790.36104	20132.30417	2.4	2.5	0.2	0.1
4086	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit_1	photosynthesis	216	contig	8	EG974314	132801.5417	61444.91667	72221	23632.07593	10826.97012	14655.44226	0.9	1.1	0.2	0
1867	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit_1	photosynthesis	216	contig	8	EG974311	239504.7083	42927.375	47190.33333	47500.78128	9884.007382	7627.8843	2.3	2.5	0.1	0
5505	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit_1	photosynthesis	216	contig	8	EG974310	579739.5417	116864.4583	121892.1667	89725.36761	23954.26171	18583.95243	2.2	2.3	0.1	0.1
1605	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit_1	photosynthesis	216	contig	8	EG974316	864840.6667	153568.875	198496	129665.4572	34953.48975	36085.46288	2.1	2.5	0.4	0.1
5064	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit_1	photosynthesis	216	contig	8	EG974315	755130.125	163851.9167	208648.9583	103553.4806	32382.8184	39412.86659	1.9	2.2	0.3	0.1
6621	ribulose-1,5-bisphosphate carboxylase/oxygenase small sub-unit2	photosynthesis	199	singleton	1	EG974299	234081.2917	156599.4583	111203.7083	34000.5581	27407.77649	17338.77892	1.1	0.6	-0.5	0
171	RING domain	miscellaneous	100	singleton	1	EG974381	8486.125	97646.04167	62573.125	1445.761903	15344.53777	5997.824256	2.9	-3.5	-0.6	0.1
2660	ripening-related protein	miscellaneous	147	contig	2	EG974343	39135.625	23864.08333	10792.16667	4018.699882	3341.234751	1261.507896	1.9	0.7	-1.1	0.1

233	ripening-related protein	miscellaneous	147	contig	2	EG974342	CCCGTCCGGCGTCCGGTGGTTGATCCAAAACAATAAGGTAAGCTTATTAACCTCTTGGCTTTCTTCTAGCTTTCTTATCTGGGTGCGGTCCACAGGTTACAAAAGCCCAAGCAACCAACCAACCAATTTGTAAATGGGCTTGTAGTTCCAGCATATCCAGGCTCTGCATCAGAACCCACCTTACTTCCATTTTCAGATAFAAAGATGGAGACCTTCTTATTAACCTCCGAGTCCG	111885.9583	56286.91667	25393.79167	13963.06983	9258.615228	2270.431876	2.1	1	-1.1	0.1
3747	S-adenosyl-L-methionine decarboxylase	secondary metabolism	240	singleton	1	EG974503	CCCGTCCGGCGTCCGGTGGTTGATCCAAAACAATAAGGTAAGCTTATTAACCTCTTGGCTTTCTTCTAGCTTTCTTATCTGGGTGCGGTCCACAGGTTACAAAAGCCCAAGCAACCAACCAATTTGTAAATGGGCTTGTAGTTCCAGCATATCCAGGCTCTGCATCAGAACCCACCTTACTTCCATTTTCAGATAFAAAGATGGAGACCTTCTTATTAACCTCCGAGTCCG	4041.791667	13084.25	7696.875	699.3184777	1981.521172	1104.417017	0.9	-1.7	-0.8	3.7
3815	S-adenosyl-L-methionine synthetase.1	secondary metabolism	249	singleton	1	EG974498	CCCGTCCGGCGTCCGGTGGTTGATCCAAAACAATAAGGTAAGCTTATTAACCTCTTGGCTTTCTTCTAGCTTTCTTATCTGGGTGCGGTCCACAGGTTACAAAAGCCCAAGCAACCAACCAATTTGTAAATGGGCTTGTAGTTCCAGCATATCCAGGCTCTGCATCAGAACCCACCTTACTTCCATTTTCAGATAFAAAGATGGAGACCTTCTTATTAACCTCCGAGTCCG	50487.83333	18864.58333	12884.75	8221.943869	3190.902546	1646.804389	2	1.4	-0.6	0
799	S-adenosyl-L-methionine synthetase.2	secondary metabolism	234	singleton	1	EG974502	CCCGTCCGGCGTCCGGTGGTTGATCCAAAACAATAAGGTAAGCTTATTAACCTCTTGGCTTTCTTCTAGCTTTCTTATCTGGGTGCGGTCCACAGGTTACAAAAGCCCAAGCAACCAACCAATTTGTAAATGGGCTTGTAGTTCCAGCATATCCAGGCTCTGCATCAGAACCCACCTTACTTCCATTTTCAGATAFAAAGATGGAGACCTTCTTATTAACCTCCGAGTCCG	53396.04167	324371.375	325024.7083	9784.135442	48921.6085	41956.58158	-2.6	-2.6	0	0
3726	SAM_DC	secondary metabolism	245	contig	3	EG974501	CCCGTCCGGCGTCCGGTGGTTGATCCAAAACAATAAGGTAAGCTTATTAACCTCTTGGCTTTCTTCTAGCTTTCTTATCTGGGTGCGGTCCACAGGTTACAAAAGCCCAAGCAACCAACCAATTTGTAAATGGGCTTGTAGTTCCAGCATATCCAGGCTCTGCATCAGAACCCACCTTACTTCCATTTTCAGATAFAAAGATGGAGACCTTCTTATTAACCTCCGAGTCCG	140707.375	282387.2917	122751.5417	20018.94137	41319.02896	20179.52501	0.2	-1	-1.2	0
5328	SAM_DC	secondary metabolism	245	contig	3	EG974500	CCCGTCCGGCGTCCGGTGGTTGATCCAAAACAATAAGGTAAGCTTATTAACCTCTTGGCTTTCTTCTAGCTTTCTTATCTGGGTGCGGTCCACAGGTTACAAAAGCCCAAGCAACCAACCAATTTGTAAATGGGCTTGTAGTTCCAGCATATCCAGGCTCTGCATCAGAACCCACCTTACTTCCATTTTCAGATAFAAAGATGGAGACCTTCTTATTAACCTCCGAGTCCG	34954.04167	71510.5	27542.16667	7292.593647	11742.21324	3708.6761	0.3	-1	-1.4	0
6680	SAM_DC	secondary metabolism	245	contig	3	EG974499	CCCGTCCGGCGTCCGGTGGTTGATCCAAAACAATAAGGTAAGCTTATTAACCTCTTGGCTTTCTTCTAGCTTTCTTATCTGGGTGCGGTCCACAGGTTACAAAAGCCCAAGCAACCAACCAATTTGTAAATGGGCTTGTAGTTCCAGCATATCCAGGCTCTGCATCAGAACCCACCTTACTTCCATTTTCAGATAFAAAGATGGAGACCTTCTTATTAACCTCCGAGTCCG	62240.58333	137818.25	52064.45833	9785.030654	21390.68162	9076.770371	0.3	-1.1	-1.4	0
5746	serine carboxypeptidase	amino acid & protein metabolism	16	singleton	1	EG974477	CCCGTCCGGCGTCCGGTGGTTGATCCAAAACAATAAGGTAAGCTTATTAACCTCTTGGCTTTCTTCTAGCTTTCTTATCTGGGTGCGGTCCACAGGTTACAAAAGCCCAAGCAACCAACCAATTTGTAAATGGGCTTGTAGTTCCAGCATATCCAGGCTCTGCATCAGAACCCACCTTACTTCCATTTTCAGATAFAAAGATGGAGACCTTCTTATTAACCTCCGAGTCCG	28221.54167	16338.875	10982.70833	4570.561622	3284.595027	2201.401619	1.4	0.8	-0.6	0
17	spermidine synthase	secondary metabolism	244	singleton	1	EG974539	CCCGTCCGGCGTCCGGTGGTTGATCCAAAACAATAAGGTAAGCTTATTAACCTCTTGGCTTTCTTCTAGCTTTCTTATCTGGGTGCGGTCCACAGGTTACAAAAGCCCAAGCAACCAACCAATTTGTAAATGGGCTTGTAGTTCCAGCATATCCAGGCTCTGCATCAGAACCCACCTTACTTCCATTTTCAGATAFAAAGATGGAGACCTTCTTATTAACCTCCGAGTCCG	12705.04167	32767.625	14850.54167	2703.40004	7430.136771	1587.87314	-0.2	-1.4	-1.1	0.4
39	squamosa promoter binding protein	regulation	228	singleton	1	EG974553	CCCGTCCGGCGTCCGGTGGTTGATCCAAAACAATAAGGTAAGCTTATTAACCTCTTGGCTTTCTTCTAGCTTTCTTATCTGGGTGCGGTCCACAGGTTACAAAAGCCCAAGCAACCAACCAATTTGTAAATGGGCTTGTAGTTCCAGCATATCCAGGCTCTGCATCAGAACCCACCTTACTTCCATTTTCAGATAFAAAGATGGAGACCTTCTTATTAACCTCCGAGTCCG	20478.66667	12261	7539.958333	3407.664108	2435.946252	1293.079027	1.4	0.7	-0.7	0
706	starch synthase, granule bound	miscellaneous	149	singleton	1	EG974427	CCCGTCCGGCGTCCGGTGGTTGATCCAAAACAATAAGGTAAGCTTATTAACCTCTTGGCTTTCTTCTAGCTTTCTTATCTGGGTGCGGTCCACAGGTTACAAAAGCCCAAGCAACCAACCAATTTGTAAATGGGCTTGTAGTTCCAGCATATCCAGGCTCTGCATCAGAACCCACCTTACTTCCATTTTCAGATAFAAAGATGGAGACCTTCTTATTAACCTCCGAGTCCG	172441.8333	83989.875	55265.625	25209.18772	17350.61496	8134.896402	1.6	1	-0.6	0

3199	unk_Contig22	269	EG974701	1	singleton	no blast match	269	EG974701	1	EG974701	103748.0833	90107.25	5129.69431	16191.7196	15199.98245-1.4	-1.6	-0.2	0
6340	unk_Contig24	262	EG974670	2	contig	no blast match	262	EG974670	2	EG974670	462665.9167	300236.375	5911.351057	66596.17839	39306.01984-2.9	-3.6	-0.6	0.1
4859	unk_Contig24	262	EG974672	2	contig	no blast match	262	EG974672	2	EG974672	217541.5417	174205.0833	808.4825224	28618.68173	16564.64397-5.6	-6	-0.3	0
5729	unk_Contig26	290	EG974673	1	contig	no blast match	290	EG974673	1	EG974673	353271.9167	244496.0833	25331.17486	50774.58216	40361.2291-0.6	-1.1	-0.5	0
205	unk_Contig37	267	EG974674	1	singleton	no blast match	267	EG974674	1	EG974674	29057.875	25100.79167	1227.223536	4934.614263	3500.086514-1.5	-1.7	-0.2	0
2408	unk_Contig40	286	EG974675	1	singleton	no blast match	286	EG974675	1	EG974675	304397.625	208010.5	19945.52533	65584.19033	29129.31057-0.6	-1.1	-0.5	3.3
4245	unk_Contig46	277	EG974676	1	singleton	no blast match	277	EG974676	1	EG974676	39221.5	26024.58333	2642.065599	5697.898461	3868.358729-0.7	-1.3	-0.6	0
4606	unk_Contig63	292	EG974705	2	contig	no blast match	292	EG974705	2	EG974705	391264.7083	231392.7083	19794.35044	44882.42467	21202.66776-0.3	-1	-0.8	0
6782	unk_Contig63	292	EG974702	2	contig	no blast match	292	EG974702	2	EG974702	317589.9583	171132.4583	16509.60339	41532.23761	18593.95444-0.3	-1.2	-0.9	0
1098	unk_Contig65	270	EG974706	1	singleton	no blast match	270	EG974706	1	EG974706	57153.125	47565.83333	3018.581976	9046.975444	5501.987166-1.3	-1.6	-0.3	0
1162	unk_Contig66	288	EG974707	1	singleton	no blast match	288	EG974707	1	EG974707	109426.2083	74368.83333	9576.766134	22992.52886	13100.17647-0.6	-1.1	-0.6	4.8

TCCACGGCTCCGGTATCATGTCACATGAAATGAACCTCTTGGCTTCCCAACGACATATCCTTTG
TTTACTTACATATCTTTGGAATCAAAATTTAAATCAAAGGTGTTTTTCCAAAGTACATAAAAAA
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GCTCAGATGGGAGTGTGTACAAACCAATGAGTACAGTACAGTACAGTACAGTACAGTACAG
CGGAGTCCGGTGGGGTGTATGTTCCAGGGTGGGCTATGTTCTCTCTCTCTCTCTCTCTCT
ACATGAACAAACATGAGTATGGGTAGTG

Accession	Length	Score	Expect	Ident	Query Start	Query End	Subject Start	Subject End	Subject Accession				
1597	unkl_UID1597	305	singleton	1	EG974589	no blast match	305	singleton	1	EG974589	1.1	-0.2	0.2
1604	unkl_UID1604	261	singleton	1	EG974680	no blast match	261	singleton	1	EG974680	4.6	-6.1	-1.5
1844	unkl_UID1844	284	singleton	1	EG974667	no blast match	284	singleton	1	EG974667	0	-1.2	-1.2
2094	unkl_UID2094	264	singleton	1	EG974681	no blast match	264	singleton	1	EG974681	1.6	-1.9	-0.3
245	unkl_UID245	304	singleton	1	EG974590	no blast match	304	singleton	1	EG974590	1.5	0.9	-0.6
2655	unkl_UID2655	303	singleton	1	EG974591	no blast match	303	singleton	1	EG974591	1.3	0.9	-0.4
3102	unkl_UID3102	317	singleton	1	EG974592	no blast match	317	singleton	1	EG974592	3.3	2.1	-0.2
440	unkl_UID440	294	singleton	1	EG974683	no blast match	294	singleton	1	EG974683	0.3	-1	-0.7
4908	unkl_UID4908	289	singleton	1	EG974668	no blast match	289	singleton	1	EG974668	0.1	-1.1	-1.2
5061	unkl_UID5061	275	singleton	1	EG974684	no blast match	275	singleton	1	EG974684	0.6	-1.3	-0.7
5832	unkl_UID5832	268	singleton	1	EG974685	no blast match	268	singleton	1	EG974685	-1	-1.6	-0.7
6427	unkl_UID6427	300	singleton	1	EG974595	no blast match	300	singleton	1	EG974595	1.1	0.6	-0.5

6389	unknownContig2:207	no blast match	306	singleton	1	EG974642	39472	5047.819336	2635.094092	4748.81064	0.2	1	0.8	0
<p>GCTCATTTAGTGTCTGCGCTTTTGAATCTTAGTAGGGGCCCTTATGTTCTTTTGGATTAGAGTAGG GTCGAGAGAGAGGCTAGCCGCTCCCAATGCTGGAGTTGTATTATAGTGGACTGTG TCATAGCGACAAGGTTGAAACTTCCAGGAAAAAACTTCAATTTGGAGGGGATCCCGCCGGT AACTGACCCTACCCAAACCACAGGTTGAACAAAGTAGGATTAAGGAGGCTTGGAGAACCC ATGTGGAAGAACTCGCAAAAATGACCCGTAATCTCGGAGAGGAGGCTTCTTCTTTG ATTAGAAAGCGGCACATACAGGGGTAGGACTTTTAAAAAACACAGGACTCTGTAAGT GGAACACAGATGTATAGATCTACACCTGCCCCGTTGGAAAGGTCGGAAGGAGGTTATA AGCTTTGAA</p>														
3060	unknownContig2:16	no blast match	323	contig	3	EG974643	116990	17636.59598	2972.219189	2219.0982	3	3	0	0
<p>GGCTTAGCCATCTCTAGTTATAATATAGCTTAAATATGTTTGGTAGTCTTCTAAT TACTTTACACACAAACACTAGATCTCTGTTTGTATCTTGAATAATGTTGAGCCTAGCT CAAAATGGCGTTTCAAAGTGGGATGTCCTTCAGGTAGCAACAAGCAATCGAAGGCGAGGT CAGCTTGTTCCTCATTCGAAAGAAATCACTGACTTACGTAACACTATGTCCACGCG ATGACACATTCGACGAGACTCTTTTGCATCGTGGAAATATTCCTACTCGTGCACACTCAG TCCATTGAAAATTTGTTAGGGAGGCCAAGTTCATCTGGAGACATAGAGACAGAGCCCTGC AAAAGTAACTCAATGTTCCCTTATGCACCCTCAAGTCGATATFAGCGAGCTGTTTGCAGG CTCGGGAGAG</p>														
247	unknownContig2:16	no blast match	323	contig	3	EG974644	98805.08333	10398.691	1503.629448	1853.313829	2.9	3.3	0.4	0
<p>GGGGTGTTTAAAGTTCATCTAGTTTATAATATAGCTTAAATATGTTTGGTAGTCTTCTAAT CTAGTCTCTAATTAACACACACAAACACTAGATCTCTGTTTGTGAICTTGAAAA TGTGAGCTTAGCTCAAAAATGTCCTTCCAAAGTGGGATTTGTTCAGGAGAGCAACAGCC ATCGAAGCGGAGTCAAGTCTTCCATCTCCGATAAGAAGACTCTAGACCTTATCTAGCCTAC TCATGCCACGCGATGACATTCGACGAGACTACTTTCGTCATCTCGTGGAAAAATATCTCA CTGTGCAACTCAGTCCATGAAAACCTGTTCCAGGAAAGCAAGTTCATCTGGAGAACATAGA GACAGAGCCCTGCAAAAGCTAATCTTCAATGTTCCCTTATGACCCTCAAGTCAATATAGCA GCTGTGTGAAG</p>														
3865	unknownContig2:16	no blast match	323	contig	3	EG974645	64570.91667	11345.21727	1649.450656	1749.170363	2.6	3.1	0.5	0.1
<p>GATCAAGGTTGTTAATGCTTAGCCATCTCTAATTTATAATATAGCTTAAATATGTTT GCTAGCTTCTAATACTTAACACACAAACACTAGATCTCTGTTTGTGAICTTGAAAA ATGTTGAGCCCTAGCTCAAAAATGTCCTTCCAAAGTGGGATTTGTTCAGGAGAGCAACAGCC CATCGAAGGCGAGTCAAGTCTTCCATCTCCGATAAGAAGACTCTAGACCTTATCTAGCCTA CTCATGTCCAGCCGATGACATTCGACGAGACTACTTTCGTCATCTCGTGGAAAAATATCTC ACTGTGCAACTCAGTCCATGAAAACCTGTTCCAGGAAAGCAAGTTCATCTGGAGAACATAGA AGACAGGCCCTGCAAAAGCTAATCTTCAATGTTCCCTTATGACCCTCAAGTCAATATAGCG AGCTGTGTGCA</p>														
1927	unknownContig2:17	no blast match	313	contig	5	EG974602	68887.04167	11934.74256	7078.728938	3239.300658	1.4	1.3	-0.1	0
<p>CTTACACAACATATAGTTCTAATAATCTCTTCTCTCTATAATATCTTTCAATAATATATA TATAATATAATGATGATAATTTAGTGTATGATGATACTATGTTGGTGGCTTGG TCGAAATAAGGATGAGCCATTTTATGAATCCAACTCAAAATAGGTTTACATACCTGGTGAAT ATTTGGTCAATTAATGAAGACTGCTGTGAAGACTTTACATGTAAGGAGGTTGCCTTCAAT GGTACTGTGTTCCTGTTCTATGATGATAATGCGAAATCGGGGGTTCGGGTGCGAAATCGG AGCTCCTCATGTTGCTACCACAACTTGCCATGTTGAAGGATTTGGAATTCAAAGGACAT GTCTGCCCCAACACTTTGCCCCCTTCTGAATAATAGAGGACTTCTAGAAAGTCACTATT CTAGTAGC</p>														
3635	unknownContig2:17	no blast match	313	contig	5	EG974601	113985.1667	17594.64076	11228.05824	8983.729286	1.4	1.2	-0.2	0
<p>GATTACGAGGACTTCTAGAAAGTCCATTTAGTACTAATAATATTTACTATAAATGATTAGT ATACTAGTATAATAATATGTTTGGCTGTGTGTCAAAATAATAAAGAAATAAT TAAGTAGGGTGGATTAATAATTTCCCTGTGTAATACATTTACACACCACACTATACACTA CTGTGTAGTTGTGTATGTTTAAATGTTGTTACTAGTCTACTTCTTTTAAATAAAGT TGTATTCTATTACTTAAAAAATAAAAGAGG GCACAACATATAATGTTAAATAATCTTCTTCTTACTATCTTTCATATAATATATAAT AATAATGAAAGTCAATAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG AATAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG GTCTCAATTAATGAATGAAAGACTGTGAAGACTTTACATGTAAGGAGGTTCACTCTGTGAAT ACCTGTTTCTGTTCTCATTTGCAATTCGAAATCGGGCGGTTTGGGCTGTTGAAATCGGAGC TCTCCATGTGTGACCCCAACACTTGGTGAAGGATTTGGACTATCAACGGACATTTGTG CTGCCCAACACTTTGCCCGCTCTGATAATAATAGAGGACTTCTAGAAAGTCACTATTCTA GTACTAATAATTT</p>														
4983	unknownContig2:17	no blast match	313	contig	5	EG974600	107859	19524.28332	12407.39937	5981.911531	1.5	1.1	-0.4	0
<p>GGTCAATAATGTAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT GTAGCCATTTATGAATCCACTCCAAATAGGTTTACATACCTGGTAATAATGTGCTACAT TGAATGAAGAAGCTGTGGAAGACTTACATGTAAGGAGGTTGCTTCAATGTGTTT CTGTTTCTCATTTGCAATTCGGAAATCGGGCGGTTTGGGCTGGAAATCGAGCTCCCATGT TGTACCCAAACACTTGCTGTGAAGGATTTGGACTATCAACGGACTTTGCGTCCGCGGCTG CACTTGCCTCTGATAATAATAGAGACTTCTAGAAAGTCTTGGACTATCAACGGACATTTGT TTTACTATAATCAATTAATAGTAGTATAATAATAATAATAATAATAATAATAATAATAATA TAAAAATAAAG</p>														
1165	unknownContig2:17	no blast match	313	contig	5	EG974646	147151.375	20131.74572	12861.78443	13481.16029	1	1.2	0.1	0
<p>GATCAATAATGTAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT GTAGCCATTTATGAATCCACTCCAAATAGGTTTACATACCTGGTAATAATGTGCTACAT TGAATGAAGAAGCTGTGGAAGACTTACATGTAAGGAGGTTGCTTCAATGTGTTT CTGTTTCTCATTTGCAATTCGGAAATCGGGCGGTTTGGGCTGGAAATCGAGCTCCCATGT TGTACCCAAACACTTGCTGTGAAGGATTTGGACTATCAACGGACTTTGCGTCCGCGGCTG CACTTGCCTCTGATAATAATAGAGACTTCTAGAAAGTCTTGGACTATCAACGGACATTTGT TTTACTATAATCAATTAATAGTAGTATAATAATAATAATAATAATAATAATAATAATAATA TAAAAATAAAG</p>														
4287	unknownContig2:17	no blast match	313	contig	5	EG974647	77808.20833	14749.15846	9144.516035	9201.783701	0.8	1.3	0.4	0
<p>TATAATGAAGTCAATAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT TAAATGATGAGCCATTTTATGAATCCAACTCCAAATAGGTTTACATACCTGGTAATAATGT GCTCAATTAATGAATGAAAGACTGTGAAAGACTTACATGTAAGGAGGTTGCTTCAATGTGTT CTGTTTCTCATTTGCAATTCGGAAATCGGGCGGTTTGGGCTGGAAATCGAGCTCCCATGT TGTACCCAAACACTTGCTGTGAAGGATTTGGACTATCAACGGACTTTGCGTCCGCGGCTG CACTTGCCTCTGATAATAATAGAGACTTCTAGAAAGTCTTGGACTATCAACGGACATTTGT TTTACTATAATCAATTAATAGTAGTATAATAATAATAATAATAATAATAATAATAATAATA TAAAAATAAAG</p>														
3604	unknownContig2:36	no blast match	309	contig	6	EG974607	175647.6667	22156.61496	18450.53168	19093.50011	1	1	-0.1	0
<p>GTCTTTATAAAACCCAAAAAGAGAAAGAGAGAAACACACAAATGGATTCCTCAAAGCTTT CAGCTTTCTTCATTTCCATTTTCTTCAGCACCTCCCAATTTGGGATGCACCTAC TGTGGCAAAACCCCTTCAAAGGAGTAAAGGAAAAGGAGGAGGAAAAGGTACCCAGTTAAGCC ATCTCCAGGGTCCAAATTTTCCCTCCGTTAAAGTTTCTCCAACTCCCAATCACACACAG TTGTACCCAACTCCTCCACAGTAAACCTCCACAGTTTGGCCAACTCCAACTCCCTCTC CCTCAGTGACACTCTCCACAGTTGTAACCCAAACTCTCCTCTCCCTCCAGTTAAGTCCCTCC AGTTACTCCTCACTCCACAGTCAACCCCTCTCTCCTCCCTCCCTCCAGTTGCTGGTGGG GCAGCCCTCTT</p>														
2004	unknownContig2:36	no blast match	309	contig	6	EG974608	335118.5	45021.93292	34183.28301	31731.62648	1.2	1.2	0	0
<p>GCTCACTCTCTTTATTAACCCAAAAAGAGAAAGAGAGAAACACACAAATGGATTCCTCAA AAGCTTTCTAGCTTCTCTCATTTCCATTTCTTCTATTTCTCCAGCCACTCCCATTTGGGATG CAACCTGTGGCAACCCCTTCAAAGGAGGTAAGGAAAAGGAGGAGGAAAAGGTACCCAG TTAAGCCATCTCCAAAGGTTTCAATTTCCCTCCGTTAAAGTTTCCCTCCAGTAACTCCAAATC ACACAGTTGTACCCAACTCCCTCTCCACAGTAAACACTCTCCACAGTTGTGCCAAAAT CCCTCCTCCAGTGACCACTCTCCAGCTTGTACCCAACTCCCTCCTCCCTCCAGTTAAGG TCCCTCCAGTTACTTCCACTCCACAGTCAACCCCTCTCTCCCTTCTCCCTCTCCCTTTCGGT GGTGGCGGAGC</p>														

Query ID	Contig ID	Match Type	Score	Start	End	Fragment						
4489	unknownContig248	no blast match	318	contig	2	EG974661						
4426	unknownContig59	no blast match	315	contig	2	EG974663						
282	unknownContig59	no blast match	315	contig	2	EG974617						
99	unknownContig64	no blast match	308	contig	2	EG974618						
6375	unknownContig64	no blast match	308	contig	2	EG974619						
1004	unknownUID_1004	no blast match	325	singleton	1	EG974664						
158	unknownUID_158	no blast match	312	singleton	1	EG974665						
1963	unknownUID_1963	no blast match	299	singleton	1	EG974620						
1975	unknownUID_1975	no blast match	311	singleton	2	EG974621						
858	unknownUID_1975	no blast match	311	singleton	2	EG974622						
2118	unknownUID_2118	miscellaneous	168	singleton	1	EG974357						
1			153006.875	25908.41667	76114.875	18306.99496	4539.058248	12456.21067	1	2.6	1.6	0.1
0.1			25586.75	12118.95833	16863.70833	4027.182512	2619.137444	3728.052038	0.6	1.1	0.5	0.9
0.9			641578.875	254976.3333	248156.375	79618.2334	39612.10209	34598.82313	1.4	1.3	0	0
0			26579.66667	12368.41667	6109.625	7383.082309	3225.865913	1091.080957	2.1	1.1	-1	0
0			58490.66667	28228	14903.125	16432.23928	6713.423117	2893.602642	2	1.1	-0.9	0.5
0.5			121516.6667	7881.875	79892.08333	13859.81314	1331.488904	17867.07402	0.6	3.9	3.3	0.1
0.1			42169.75	15770.20833	18170.91667	7571.220611	3020.070606	2840.458523	1.2	1.4	0.2	0
0			90550.79167	61100.41667	37751.875	14663.12194	9270.738447	3713.175107	1.3	0.6	-0.7	0
0			178590.3333	79447.66667	49839.91667	26064.42848	13057.82932	7373.168654	1.8	1.2	-0.7	0
0			28652.25	18152.91667	12713.66667	4223.58559	3064.339817	1789.548766	1.2	0.7	-0.5	0
0			36275.66667	4851.5	7494.791667	5706.284119	1072.172785	1154.701428	2.3	2.9	0.6	0.1

Accession	Gene	Protein	CD	Contig	Size (bp)	GC Content (%)	GC Content (bp)	GC Content (G)	GC Content (C)	GC Content (T)	GC Content (A)	GC Content (N)	GC Content (S)	GC Content (O)	GC Content (M)	GC Content (I)	GC Content (U)	
3587	xyloglucan endotransglycosylase.2	glycosyltransferases	63	contig	11	EG974723	197128.4583	33068	105291.125	21921.11691	5147.73825	17709.15408	0.9	2.6	1.7	0.1		
1913	xyloglucan endotransglycosylase.2	glycosyltransferases	63	contig	11	EG974730	158890.125	26847.45833	105474.25	16324.27905	4057.363443	18660.17825	0.6	2.6	2	0.1		
2776	xyloglucan endotransglycosylase.2	glycosyltransferases	63	contig	11	EG974724	134845.4167	26693.33333	85668.5	20819.27743	7555.29048	17138.34111	0.7	2.3	1.7	0		
4338	xyloglucan endotransglycosylase.3	glycosyltransferases	61	contig	2	EG974731	13396.625	4204	6282	1869.456337	739.7263497	1128.936459	1.1	1.7	0.6	0		
4250	xyloglucan endotransglycosylase.3	glycosyltransferases	61	contig	2	EG974732	214118.4583	50968.875	115625.7083	28573.28925	10128.09372	28191.03435	0.9	2.1	1.2	0		
5035	xyloglucan endotransglycosylase.4	glycosyltransferases	58	singleton	1	EG974203	28689.45833	74767.91667	73409.08333	4721.189343	16789.94226	15464.75341	-1.4	-1.4	0	1.4		
2894	zinc finger-like	regulation	229	singleton	1	EG974554	131818.2083	69304.625	57639.95833	18762.53748	9391.823206	5894.600654	1.2	0.9	-0.3	-0.3	0	
2170	zinc transporter	transport	252	singleton	1	EG974570	9541.375	73689.29167	57212.08333	1091.784064	9853.443638	5792.945956	2.6	-2.9	-0.4	-0.4	0	
4528	-	-	-	-	-	-	23713.125	17843.25	27820.91667	3073.584295	3084.755296	4044.682644	0.2	0.4	0.6	0		
6528	-	-	-	-	-	-	242403.9167	298022.9167	179748.2917	28048.51389	30880.06989	16014.58695	0.4	-0.3	-0.7	0		
6786	-	-	-	-	-	-	811699.5417	1024270.792	608873.4167	98123.03927	110176.4338	70560.54791	0.4	-0.3	-0.8	0		
5342	-	-	-	-	-	-	81736.75	109644.6667	62171.16667	10672.61838	13899.90424	6587.777494	0.4	-0.4	-0.8	0		
2980	-	-	-	-	-	-	113099.7917	154102.5	89491.83333	14161.08381	19149.72808	9945.878149	0.3	-0.4	-0.8	0		
6451	-	-	-	-	-	-	30695.875	21126.79167	24972	2659.140144	2351.888419	2195.217478	0.3	0.5	0.2	0		
6380	-	-	-	-	-	-	721193	510332.125	494338.75	66964.62439	60402.04102	43697.69176	0.5	0.5	0	0		
1085	-	-	-	-	-	-	91990.54167	65822.25	62945.20833	8574.038469	8075.301698	6435.524512	0.5	0.5	-0.1	0		
3832	-	-	-	-	-	-	38545.20833	40078.625	54418.79167	4037.577486	5794.582573	6096.023108	0.5	-0.1	0.4	0		
225	-	-	-	-	-	-	365638.9583	430270.1667	252542.8333	41776.6683	40897.34385	19986.81826	0.5	-0.2	-0.8	0		
1457	-	-	-	-	-	-	341070.625	404388.7083	236086.875	39900.14131	44217.14162	19337.22713	0.5	-0.2	-0.8	0		
6826	-	-	-	-	-	-	257653.9167	404388.7083	145896.2917	29276.24512	29575.79856	12021.334	0.5	-0.3	-0.8	0		
5582	-	-	-	-	-	-	13681.62917	170645.625	95699.45833	17584.30983	21745.35887	9258.169265	0.5	-0.3	-0.8	0		
3731	-	-	-	-	-	-	36990.22917	518128.2917	30423.17083	43639.38566	59972.44317	37210.9941	0.3	-0.5	-0.8	0		
4486	-	-	-	-	-	-	74216.08333	104674.0417	51034.25	11239.83895	16232.49485	6838.689097	0.5	-0.5	-1	0		
1991	-	-	-	-	-	-	44053.16667	62349.125	31403.20833	5425.534401	9931.79485	2689.160052	0.5	-0.5	-1	0		
4684	-	-	-	-	-	-	55169.04167	79649.16667	52467.79167	5812.41904	8756.286109	4669.686107	0.1	-0.5	-0.6	0		
5340	-	-	-	-	-	-	31844.95833	46434.33333	27856.66667	4276.748792	5611.319147	3028.191064	0.2	-0.5	-0.7	0		

2184	152605.375	20513.08333	28576.58333	19116.46248	3793.588624	5363.594428	2.4	2.9	0.5	0
2838	92339.625	9821.125	18238.5	20757.46563	1938.494791	5088.970831	2.3	3.2	0.9	0
5015	7080.541667	80789.75	4156.333333	950.848494	17498.64787	824.09510690	8	-3.5	-4.3	0
6797	4520.166667	104466.5833	74370.41667	794.0090047	14298.34305	8431.128481	-4	-4.5	-0.5	0
707	23917.6625	48750.95833	94813.41667	28843.05677	9582.535413	19470.61594	1.3	2.3	1	0.1
4909	9019.208333	69739.08333	41094.08333	1294.098354	9634.93247	4466.748829	2.2	-3	-0.8	0.1
6275	107837.2917	9399.875	20500.29167	17232.76357	1573.511809	5301.887403	2.4	3.5	1.1	0.1
4173	14501.79167	7387.5	11904.45833	2334.100034	1468.063823	2274.441206	0.3	1	0.7	0.8
1900	91261.58333	57010.125	33794.91667	19879.98368	13583.09311	5971.30247	1.4	0.7	-0.8	1.3
6213	86424.875	35135.29167	34780.79167	22346.68447	8918.526133	10547.82376	1.3	1.3	0	1.8
5863	43911.25	111382.4167	57246.20833	12771.73176	27175.49795	13074.90974	-0.4	-1.3	-1	4.7
6732	49530.83333	25683.45833	21969.70833	7318.209111	4161.751692	3208.822798	1.2	0.9	-0.2	0
6175	163262.875	383172.125	226662.0833	18332.84108	51359.36963	26750.79671	-0.5	-1.2	-0.8	0
4118	122905.2917	36647	47175.91667	23723.15884	7252.118846	11975.69308	1.4	1.7	0.4	0
3857	16403.58333	6635.916667	4085.958333	4002.241306	1467.871829	673.6780546	2	1.3	-0.7	0.4
1961	206361.625	118154	102614.25	29892.98955	25895.70047	19964.84023	1	0.8	-0.2	0
323	534698.0417	258817.7917	180959.4167	78396.34483	43476.16494	30535.10186	1.6	1	-0.5	0
2543	18907.70833	8177.041667	5921.916667	3429.522535	1493.187963	1010.201338	1.7	1.2	-0.5	0
5058	36223.79167	16318.41667	20852.75	4929.927736	2284.640003	2893.975935	0.8	1.2	0.4	0
2136	7994.208333	556455.8333	335083.2083	1856.760162	73463.82369	36169.38304	-5.4	-6.1	-0.7	0
2217	59535.45833	186244.7917	71781.08333	8287.561324	29735.78938	10390.37408	-0.3	-1.6	-1.4	0
6502	23235.29167	120615.2917	67510.79167	3647.034616	17198.595	9594.034265	1.5	-2.4	-0.8	0
4873	145447.0417	37728	32863.79167	20918.32678	6171.397339	5040.399431	2.1	1.9	-0.2	0.1
5661	244313.7917	61160.29167	46369.08333	52570.40459	14765.96592	6922.026181	2.4	2	-0.4	0
2870	25776.20833	51199.04167	38101.375	3895.982832	8139.088934	5292.08475	-0.6	-1	-0.4	0
3285	180196.375	28289.08333	142435.125	23659.64386	4270.500625	28635.27526	0.3	2.7	2.3	0
2053	8043.583333	22894.91667	12571.95833	1201.866893	3434.521222	1691.406866	0.6	-1.5	-0.9	0
6536	9968.333333	3614.375	3102.25	1508.950201	590.32924	622.83050781	7	1.5	-0.2	2.2
4675	22467.08333	51699.875	33044.79167	3118.203594	7669.336532	4694.334552	-0.6	-1.2	-0.6	0
2480	26991.04167	8599.333333	5811.083333	3657.617487	1473.335784	1111.683243	2.2	1.7	-0.6	0.1
2874	51504.33333	119997.25	17057.04167	10953.78699	18359.67241	3438.866535	1.6	-1.2	-2.8	0
3213	485275.3333	21539.95833	87076.66667	64820.80037	4568.872153	21419.6764	2.5	4.5	2	0
4665	6948.416667	19365.33333	12388.54167	948.7837064	3098.122405	1645.44049	-0.8	-1.5	-0.6	0

279	unk_Contig76	1	no blast match	92584.25	15081.45489	217365	31354.31072	105205.125	9390.257998	-1.2	-0.2	1
280	unk_UID1090	1	no blast match	11129.25	2734.6879	26012.625	4330.272658	16146.70833	2886.648811	-1.2	-0.5	0.7
281	unk_Contig141	2	no blast match	126617.375	20465.75014	295879.0526	48625.59971	174677.7708	31640.74887	-1.2	-0.5	0.8
282	unk_Contig98	1	no blast match	68914.33333	12025.91751	158463.5417	28765.45529	100943.9583	15461.35696	-1.2	-0.6	0.7
283	unk_Contig137	1	no blast match	25555.54167	3178.997063	58701.91667	7493.121524	34105.375	3779.685215	-1.2	-0.4	0.8
284	unk_UID1844	1	no blast match	7950.5	1280.523688	18197.58333	3431.775436	7791.208333	1206.577693	-1.2	0	1.2
285	unk_Contig73	2	no blast match	70514.79167	157489.5789	157489.5789	16602.1226	89930.5625	9024.478766	-1.2	-0.4	0.8
286	unk_Contig40	1	no blast match	137399.125	19945.52533	304397.625	65584.19033	208010.5	29129.31057	-1.1	-0.6	0.5
287	unk_Contig178	1	no blast match	41304.04167	5699.910814	90052.91667	10988.535	50998.375	5622.056591	-1.1	-0.3	0.8
288	unk_Contig66	1	no blast match	50538.625	9576.766134	109426.2083	22992.52686	74368.83333	13100.17647	-1.1	-0.6	0.6
289	unk_UID4908	1	no blast match	92402	21527.91375	197745.9167	47858.34751	88891.91667	15974.88018	-1.1	0.1	1.2
290	unk_Contig226	1	no blast match	165247.2917	25331.17486	353271.9167	50774.58216	244496.0833	40361.2291	-1.1	-0.6	0.5
291	unk_Contig79	1	no blast match	10616.75	1998.243471	22392.70833	3091.592031	16083.54167	2201.800039	-1.1	-0.6	0.5
292	unk_Contig63	2	no blast match	164633.875	13253.17987	334475	27970.65881	201262.5833	14625.56742	-1	-0.3	0.7
293	unk_UID1108	1	no blast match	97748.91667	11753.83568	196731.375	22796.66496	110645.7917	11699.98431	-1	-0.2	0.8
294	unk_UID440	1	no blast match	40067.25	6919.054619	79222	11826.94646	49883.70833	6897.722364	-1	-0.3	0.7
295	unk_Contig103	2	no blast match	359168.3958	33946.14891	700465.6842	68357.75655	478768.4792	49924.52504	-1	-0.4	0.5
296	unk_Contig143	1	no blast match	7856.958333	999.9796347	15303.54167	1763.463391	10186.83333	1310.841512	-1	-0.4	0.6
297	unk_Contig82	2	no blast match	11482.89583	1519.750195	22013.92105	2315.944406	15376.45833	1456.998304	-0.9	-0.4	0.5
298	unknownUID_5670	1	no blast match	27493.625	4888.418048	25508.375	5166.991462	11307.20833	1316.232248	0.1	1.3	1.2
299	unknownUID_1963	1	no blast match	90550.79167	14663.12194	61100.41667	9270.738447	37751.875	3713.175107	0.6	1.3	0.7
300	unk_UID6427	1	no blast match	69507.625	11504.8535	45409.875	7846.227928	31795.625	6555.449862	0.6	1.1	0.5
301	unknownContig106	1	no blast match	184293.0417	30069.40356	113228.625	20321.47231	78670.79167	11928.28071	0.7	1.2	0.5
302	unknownContig16	1	no blast match	95244.20833	9578.447099	51835.58333	7683.778819	46154.70833	5543.746794	0.9	1	0.2
303	unk_UID2655	1	no blast match	28933.54167	5305.867194	15480	3390.22441	11616.91667	2072.30962	0.9	1.3	0.4
304	unk_UID245	1	no blast match	22087.75	3604.665837	11458.16667	1719.461137	7680	1222.20805	0.9	1.5	0.6
305	unk_UID1597	1	no blast match	16500.5	3482.199092	8435.375	1496.801879	7566.875	1655.152602	1	1.1	0.2
306	unknownContig207	1	no blast match	44147.375	5047.819336	22315.16667	2635.094092	39472	4748.81064	1	0.2	-0.8
307	unknownUID_4235	1	no blast match	47774.33333	7623.31762	22161.16667	4228.763381	15783.375	2098.755774	1.1	1.6	0.5
308	unknownContig64	2	no blast match	42535.16667	9209.90966	18179.28947	3259.747518	10506.375	1658.700083	1.2	2	0.8
309	unknownContig236	6	no blast match	191436.8611	14591.89618	76632.65789	8290.247478	83620.06944	8877.455408	1.3	1.2	0.1
310	unknownContig244	11	no blast match	628873.178	36659.71327	248954.1722	16843.10717	276592.2652	19141.42019	1.3	-0.1	-0.2
311	unknownUID_1975	2	no blast match	103625.7917	17034.85331	39220.18421	5828.624308	31276.79167	4627.85224	1.4	1.7	0.3
312	unknownUID_158	1	no blast match	42169.75	7571.220611	15770.20833	3020.070606	18170.91667	2840.458523	1.4	1.2	-0.2
313	unknownContig217	5	no blast match	109470.6458	8153.167057	39422.57895	3814.114637	44929.88542	4157.947364	1.5	1.3	-0.2
314	unknownUID_4679	1	no blast match	91174.91667	12663.94705	30896.54167	4696.21475	30658	4782.617263	1.6	1.6	0
315	unknownContig59	2	no blast match	333582.8125	59777.4791	109717.3684	19939.48909	132510.0417	24100.98839	1.6	1.3	-0.3
316	unknownContig131	3	no blast match	98423.65278	8297.086302	25934	3347.828604	43225.23611	3579.870912	1.9	1.2	-0.7
317	unk_UID3102	1	no blast match	21968.20833	2892.389599	4989.708333	703.136002	4331.583333	791.6009391	2.1	2.3	0.2
318	unknownContig248	2	no blast match	117646.8125	11776.36497	18535.97368	2041.986227	68099.35417	8855.231071	2.7	0.8	-1.9
319	unknownUID_2215	1	no blast match	150354.125	35852.95926	23625.66667	5421.021808	29892.125	6295.88395	2.7	2.3	-0.3
320	unknownContig238	6	no blast match	726282.9792	59179.47536	84462.05263	9755.552674	359587.5208	41142.46106	3.1	1	-2.1
321	unknownContig196	3	no blast match	175987.0208	15886.11588	18140.18421	1627.138284	31656.76042	3489.572169	3.3	2.5	-0.8
322	unknownContig112	2	no blast match	139214.7292	13788.08476	13293.65789	1697.995248	22988.77083	3267.552459	3.4	2.6	-0.8
323	unknownContig216	3	no blast match	93455.33333	8112.594848	8883.210526	808.8823009	13039.625	1131.340159	3.4	2.8	-0.6
324	unknown function, similar to AT3G01680	1	no blast match	126470.7083	22082.80153	8251.291667	1819.402159	10164.75	1986.475873	3.9	3.6	-0.3
325	unknownUID_1004	1	no blast match	121516.6667	13859.81314	7881.875	1331.488904	79892.08333	17867.07402	3.9	0.6	-3.3
326	unknownUID_5423	1	no blast match	142007.7083	22791.0357	6658.958333	1217.388854	3305.458333	783.8373786	4.4	5.4	1
327	unknownContig170	3	no blast match	123120.3611	13221.65949	4806.526316	555.2229524	8065.819444	1253.698706	4.7	3.9	-0.7