

**Supplementary Table 16. GO enrichment of significantly expanded ( $p < 0.05$ ) gene families of the *C. goeringii* genome.**

GO_ID	GO_Term	GO_Class	Pvalue	AdjustedPv	x1	x2	n	N	GOlevl
GO:1900057	positive regulation of leaf senescence	BP	9.82E-10	6.87E-07	10	13	2499	34243	4
GO:0031307	integral component of mitochondrial outer membrane	CC	9.82E-10	6.87E-07	10	13	2499	34243	5
GO:0022836	gated channel activity	MF	2.77E-08	1.94E-05	11	20	2499	34243	6
GO:0008308	voltage-gated anion channel activity	MF	5.08E-08	3.56E-05	10	17	2499	34243	8
GO:0004402	histone acetyltransferase activity	MF	1.08E-07	7.53E-05	8	11	2499	34243	8
GO:0033178	proton-transporting two-sector ATPase complex, catalytic domain	CC	1.37E-07	9.60E-05	12	27	2499	34243	3
GO:0005215	transporter activity	MF	3.88E-07	0.00027184	49	314	2499	34243	2
GO:0006479	protein methylation	BP	8.21E-07	0.00057438	9	17	2499	34243	5
GO:0045261	proton-transporting ATP synthase complex, catalytic core F(1)	CC	1.20E-06	0.00084188	10	22	2499	34243	4
GO:0005216	ion channel activity	MF	2.05E-06	0.0014333	11	28	2499	34243	6
GO:0006914	autophagy	BP	2.78E-06	0.00194291	7	11	2499	34243	5
GO:0016831	carboxy-lyase activity	MF	3.18E-06	0.00222935	10	24	2499	34243	5
GO:0019253	reductive pentose-phosphate cycle	BP	1.16E-05	0.00813603	5	6	2499	34243	5
GO:0048518	positive regulation of biological process	BP	1.86E-05	0.01299538	17	74	2499	34243	2
GO:0006564	L-serine biosynthetic process	BP	2.83E-05	0.01981111	4	4	2499	34243	8
GO:0004617	phosphoglycerate dehydrogenase activity	MF	2.83E-05	0.01981111	4	4	2499	34243	6
GO:0006529	asparagine biosynthetic process	BP	2.83E-05	0.01981111	4	4	2499	34243	7
GO:0004066	asparagine synthase (glutamine-hydrolyzing) activity	MF	2.83E-05	0.01981111	4	4	2499	34243	6
GO:0046933	proton-transporting ATP synthase activity, rotational mechanism	MF	3.25E-05	0.02275546	10	30	2499	34243	8
GO:0032041	NAD-dependent histone deacetylase activity (H3-K14 specific)	MF	3.82E-05	0.02675069	5	7	2499	34243	8
GO:0016984	ribulose-bisphosphate carboxylase activity	MF	3.82E-05	0.02675069	5	7	2499	34243	6

GO:0046034	ATP metabolic process	BP	5.17E-05	0.03622132	12	44	2499	34243	8
GO:0022857	transmembrane transporter activity	MF	5.43E-05	0.03800088	35	237	2499	34243	3
GO:1902600	hydrogen ion transmembrane transport	BP	6.59E-05	0.04612968	12	45	2499	34243	6

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