

ID	bp	No. of VGT	No. of mapped gDNA read	No. of intron	Prog	Top hit Species	Top hit accession	E-value	Cov	Ident	Vitis rank	Vitis chromosome	Top annotated hit
333189	177	0	0	-	DMB	<i>Vitis vinifera</i>	XM_002279638.1	4e-36	99%	80%	1	chr9	<i>Arabidopsis thaliana</i> putative bZIP protein
333651	381	1	1	1	DMB	<i>Vitis vinifera</i>	FQ382796.1	2e-100	95%	82%	1	chr2	<i>Ricinus communis</i> acetylornithine deacetylase, putative
333728	105	1	0	-	DMB	<i>Vitis vinifera</i>	XM_002275068.1	3e-27	99%	87%	1	chr9	<i>Ricinus communis</i> ubiquitin carboxyl-terminal hydrolase, putative
333838	123	0	1	0	BN	<i>Vitis vinifera</i>	AK336366.1	1e-8	65%	78%	1	chr16	Unknown
333872	780	0	0	-	DMB	<i>Populus trichocarpa</i>	XM_002321104.1	8e-85	96%	69%	3	chr12	<i>Ricinus communis</i> ubiquitin fusion degradation protein, putative
333882	351	0	1	1	DMB	<i>Populus trichocarpa</i>	XM_002325436.1	9e-61	75%	80%	2	chr4	<i>Ricinus communis</i> riboflavin-specific deaminase, putative
334054	141	0	0	-	DMB	<i>Hordeum vulgare</i>	AK362737.1	2e-24	92%	80%	14	chr4	<i>Ricinus communis</i> UDP-sugar transporter, putative
334144	558	0	5	3	DMB	<i>Vitis vinifera</i>	XM_002284850.1	3e-19	33%	73%	1	chr3	Unknown
334652	267	0	0	-	DMB	<i>Vitis vinifera</i>	XM_002283726.1	7e-48	94%	77%	1	chr6	<i>Ricinus communis</i> glucosidase II beta

334656	672	0	7	0	MB	<i>Vitis vinifera</i>	FQ381335.1	0	97%	92%	1	chr6	subunit, putative <i>Ricinus communis</i> catalytic, putative
334660	327	3	2	0	MB	<i>Vitis vinifera</i>	XM_002282932.1	1e-29	73%	77%	1	chr18	<i>Ricinus communis</i> kinesin heavy chain, putative
334741	417	0	1	0	DMB	<i>Vitis vinifera</i>	XM_002270744.1	3e-35	50%	83%	1	chr2	Unknown
335786	177	0	3	0	DMB	<i>Vitis vinifera</i>	XM_002270742.1	1e-10	48%	81%	1	chr19	Unknown
335857	126	0	2	0	DMB	<i>Vitis vinifera</i>	XM_002279944.1	1e-21	100%	79%	1	chr14	<i>Arabidopsis thaliana</i> HEAT repeat-containing protein (SWEETIE)
336256	129	0	1	1	DMB	<i>Vitis vinifera</i>	XM_002266735.1	1e-15	77%	80%	1	chr14	Unknown
336539	108	0	2	1	DMB	<i>Vitis vinifera</i>	XM_002284768.1	2e-4	66%	76%	1	chr18	Unknown
336659	105	1	0	-	BN	No hits							
336802	375	0	0	-	MB	<i>Rafflesia pricei</i>	EU281020.1	0	100%	99%	>120	Mitochondrial	<i>Rafflesia pricei</i> cytochrome oxidase subunit I ( <i>cox1</i> ) gene, partial cds; mitochondrial
336940	474	0	2	2	DMB	<i>Populus trichocarpa</i>	XM_002320805.1	5e-91	99%	76%	22	Unknown	<i>Arabidopsis thaliana</i> hexaprenyldihydr oxybenzoate methyltransferase (COQ3)
337488	162	0	1	0	BN	No hits							
338097	147	1	0	-	DMB	<i>Vitis vinifera</i>	XM_002266364	7e-44	100%	87%	1	chr13	<i>Ricinus communis</i> beta- galactosidase, putative
338243	156	0	1	1	DMB	<i>Populus</i>	XM_002319618.1	7e-19	82%	77%	2	chr14	<i>Arabidopsis</i>

<i>trichocarpa</i>													<i>thaliana</i>
													transcription factor jumonji and C5HC2 type zinc finger domain-containing protein
339075	639	0	0	-	MB	<i>Vitis vinifera</i>	XM_002271943.1	0	98%	87%	1	chr1	<i>Ricinus communis</i> ankyrin repeat-containing protein, putative
340728	534	1	4	0	DMB	<i>Vitis vinifera</i>	FQ381717.1	1e-11	88%	64%	1	chr13	<i>Populus trichocarpa</i> f-box family protein (FBL9)
341676	282	0	74	0	MB	<i>Vitis vinifera</i>	GQ220326.1	2e-110	99%	93%	1	Mitochondrial	<i>Platanus occidentalis</i> mitochondrial ribosomal protein S7 ( <i>rps7</i> )
342353	201	1	2	0	BN	<i>Triticum aestivum</i>	AK334693.1	6e-15	58%	76%	2	chr18	<i>Oryza sativa</i> PHD finger family protein
342556	765	0	6	2	MB	<i>Vitis vinifera</i>	XM_002274635.1	0	99%	86%	1	chr15	<i>Ricinus communis</i> oxidoreductase, putative
343080	171	0	0	-	DMB	<i>Glycine max</i>	BT091661.1	9e-31	89%	80%	3	chr1	Unknown
343101	174	1	2	0	BN	<i>Glycine max</i>	AK286903.1	9e-06	68%	92%	(2)		Unknown
345350	147	1	0	-	DMB	<i>Populus trichocarpa</i>	XM_002330916.1	7e-25	95%	79%	2	chr14	<i>Arabidopsis thaliana</i> regulator of chromosome condensation domain-containing protein (AT3G02300)

345865	852	0	4	0	DMB	<i>Vitis vinifera</i>	FQ385727.1	2e-124	90%	79%	1	chr7	<i>Arabidopsis thaliana</i> prenylcysteine oxidase (FCLY)
347162	657	0	0	-	MB	<i>Vitis vinifera</i>	XM_002269195.1	0	97%	87%	1	chr19	<i>Ricinus communis</i> cytochrome C oxidase assembly protein <i>cox15</i> , putative
347814	213	0	0	-	DMB	<i>Vitis vinifera</i>	FQ387635.1	9e-39	94%	78%	1	chr11	<i>Arabidopsis thaliana</i> NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 1 (AT3G08610)
348124	543	0	5	1	BN	<i>Oryza sativa</i>	NM_001062124.1	1e-4	22%	71%	(3)		Unknown
348250	168	0	0	-	BN	No hits							
348974	573	0	4	1	MB	<i>Vitis vinifera</i>	XM_002270094.1	3e-176	97%	87%	1	chr15	<i>Ricinus communis</i> glutamyl-tRNA(Gln) amidotransferase subunit A, putative
349164	354	0	9	0	MB	<i>Vitis vinifera</i>	FQ382494.1	1e-138	97%	92%	1	chr19	<i>Gossypium hirsutum</i> rhamnose synthase (RHM2)
349228	558	0	0	-	DMB	<i>Vitis vinifera</i>	FQ381933.1	2e-84	94%	73%	1	chr2	<i>Ricinus communis</i> ATP binding protein, putative
349578	561	0	4	2	MB	<i>Vitis vinifera</i>	XM_002283781.1	0	95%	88%	1	chr17	<i>Ricinus communis</i> deoxycytidylate deaminase,

349697	486	0	2	0	DMB	<i>Vitis vinifera</i>	XR_077894.1	6e-39	52%	74%	1	chr9	putative <i>Arabidopsis thaliana</i> polygalacturonase QRT3 (QRT3)
349718	732	0	0	-	DMB	<i>Populus trichocarpa</i>	XM_002305552.1	6e-168	99%	78%	3	chr10	<i>Ricinus communis</i> derlin-2, putative
349768	321	1	1	1	DMB	<i>Vitis vinifera</i>	FQ382715.1	3e-54	70%	81%	1	chr7	<i>Ricinus communis</i> casein kinase II, putative
350313	414	0	4	2	DMB	<i>Vitis vinifera</i>	FQ393633.1	2e-115	100%	82%	1	chr18	<i>Ricinus communis</i> glycerophosphoryl diester phosphodiesterase , putative
351354	327	0	3	1	DMB	<i>Vitis vinifera</i>	XM_002283439.1	2e-56	99%	75%	1	chr5	<i>Ricinus communis</i> aspartyl aminopeptidase, putative
352143	243	0	2	1	DMB	<i>Vitis vinifera</i>	XM_002271948.1	2e-36	69%	80%	1	chr11	<i>Arabidopsis thaliana</i> diacylglycerol kinase 3 (DGK3)
352578	327	0	0	-	DMB	<i>Vitis vinifera</i>	XM_002282519.1	7e-62	99%	76%	1	chr8	Unknown
352590	117	0	1	1	DMB	<i>Vitis vinifera</i>	XM_002266054.1	2e-23	100%	82%	1	Unknown	<i>Ricinus communis</i> XPA-binding protein, putative
352635	690	1	3	0	DMB	<i>Vitis vinifera</i>	XM_002263874.1	3e-70	47%	78%	1	chr5	<i>Arabidopsis thaliana</i> ankyrin repeat-containing protein (AT3G24210)

Notes: **ID** = *Rafflesia* sequence ID from this study; **bp** = number of base pairs in the transcript; **No. of VGT** = number of vertically inherited *Rafflesia* transcripts in the same gene cluster; **No. of mapped gDNA reads** = number of *Rafflesia* genomic DNA (gDNA) Illumina read (150bp) mapped onto cDNA transcript; **No. of intron** = number of intron based on the mapped gDNA read; **Prog** = BLAST algorithm used: **MB** = high similarity Megablast, **DMB** = Somewhat dissimilar discontinuous megablast, and **BN** = Somewhat similar blastn; **Top hit species** = species with highest confidence BLAST hit; No hits indicates that no sequence was identified in any of the three BLAST searches with an e-value <0.0001. **Top hit Accession** = Genbank accession number of top hit; **E-value** = E-value from BLAST of top hit; **Cov** = percent coverage; **Ident** = percent identity with top hit; **Vitis rank** = position of *Vitis* sequence among BLAST hits in Genbank, numbers in parentheses indicate number of sequences on list if *Vitis* was not present; **Vitis chromosome** = chromosomal location of *Vitis* sequence; **Top annotated hit** = top hit with some indication or inference of gene function.