

Supplementary Table S1. *Rhododendron* samples and outgroups collected for this study.

Taxon	Collection locality	Herbarium voucher (Herbarium)
<i>R. beyerinckianum</i> Koord.	Rhododendron Species Botanical Garden, Federal Way, WA, USA, accession 1985/047	Soza et al. 1926 & 1933 (WTU)
<i>R. camtschaticum</i> Pall.	Rhododendron Species Botanical Garden, Federal Way, WA, USA, accession 1977/080	Soza & Ramage 1934 (WTU)
<i>R. edgeworthii</i> Hook. f.	Rhododendron Species Botanical Garden, Federal Way, WA, USA, accession 2001/229	Soza 1958 (WTU)
<i>R. meliphagidum</i> J.J.Sm.	Royal Botanic Garden Edinburgh, UK, accession 19880517	Conlon C114 (E)
<i>R. taxifolium</i> Merr.	Rhododendron Species Botanical Garden, Federal Way, WA, USA, accession 2013/241	Soza & Ramage 1954 (WTU)
<i>Empetrum nigrum</i> L.	University of Washington Medicinal Herb Garden, Seattle, WA, USA	Soza 1957 (WTU)
<i>Erica scoparia</i> L.	University of Washington Botanic Gardens, Washington Park Arboretum, Seattle, WA, USA, accession 303-81	N/A
<i>Kalmia latifolia</i> L.	University of Washington Botanic Gardens, Washington Park Arboretum, Seattle, WA, USA, accession 1054-40	Herbarium Committee 1935 (WTUH)

Supplementary Table S2. Sources of DNA sequences used in this study.

GenBank accessions numbers indicated below unless otherwise noted by footnotes.

Taxon	CYC1	CYC2	CYC3	RAD1/3*	RAD2	DIV1	DIV2	DIV3	ACT5
<i>R. beyerinckianum</i>	N/A	CYC2.1: MZ208772; CYC2.2: MZ208773; CYC2.3: MZ208774; CYC2.4: MZ208775; CYC2.5: MZ208776	N/A	N/A	RAD2.1: MZ209225; RAD2.2: MZ209233	DIV1.1: MZ209241; DIV1.2: MZ209249	N/A	N/A	
<i>R. camtschaticum</i>	N/A	CYC2.1: MZ208777; CYC2.2: MZ208778; CYC2.3: MZ208779	N/A	N/A	RAD2.1: MZ209227; RAD2.2: MZ209235	DIV1.1: MZ209243; DIV1.2: MZ209251	N/A	N/A	N/A
<i>R. delavayi</i> Franch. ¹	CYC1.1: scaffold387	CYC2.1: scaffold376	scaffold247 8	scaffold571 0	RAD2.1: scaffold9	DIV1.1: scaffold119	scaffold2 143	scaffold287 210	scaffold420 8

	7 (DUH02393 2.1); CYC1.2: scaffold107 8 (DUH00097 8.1); CYC1.3: scaffold660 5 (DUH02912 0.1)	1 (DUH02354 4.1); CYC2.2: scaffold376 1 (DUH02354 5.1); CYC2.3: scaffold376 1 (DUH02354 6.1); CYC2.4: scaffold376 1 (DUH02354 7.1); CYC2.5: scaffold225 92	(DUH00884 0.1)	(DUH02755 5.2, DUH02754 8.1), scaffold682 3 (DUH02944 9.1), scaffold287 816 (DUH02005 1.1), scaffold600 3 (DUH02787 0.1), scaffold571 0	(DUH032037. 1); RAD2.2: scaffold314 (DUH022018. 1)	9 (DUH00188 1.1); DIV1.2: scaffold218 4 (DUH00769 5.1)	(DUH00 7400)	(DUH01316 8.2), scaffold287 745 (DUH01883 3.1)	(DUH02526 9.1)
<i>R. edgeworthii</i>	N/A	CYC2.1:	N/A	N/A	RAD2.1:	DIV1.1:	N/A	N/A	N/A

		MZ208780; CYC2.2: MZ208781; CYC2.3: MZ208782; CYC2.4: MZ208783; CYC2.5: MZ208784; CYC2.6: MZ208785			MZ209228; RAD2.2: MZ209236	MZ209244; DIV1.2: MZ209252			
<i>R. meliphagidum</i>	N/A	CYC2.1: MZ208786; CYC2.2: MZ208787; CYC2.3: MZ208788; CYC2.4: MZ208789	N/A	N/A	RAD2.1: MZ209229; RAD2.2: MZ209237	DIV1.1: MZ209245; DIV1.2: MZ209253	N/A	N/A	N/A
<i>R. simsii</i> Planch. ²	CYC1.1: CM024964. 1	CYC2.1: CM024962. 1	CM024961. 1 (Rhsim09G	CM024958. 1 (Rhsim06G	RAD2.1: CM024963.1 (Rhsim11G017	DIV1.1: CM024953. 1	CM0249 57.1(Rhsi m05G02	CM024961. 1 (Rhsim09G	N/A

	(Rhsim12G 0144800); CYC1.2: CM024960. 1 (Rhsim08G 0137600)	(Rhsim10G 0063600); CYC2.2: CM024962. 1; CYC2.3: CM024962. 1 (Rhsim10G 0063800); CYC2.4: CM024962. 1 (Rhsim10G 0063900); CYC2.5: CM024962. 1 (Rhsim10G 0064000)	0112900)	0128900), CM024958. 1 (Rhsim06G 0032200), CM024959. 1 (Rhsim07G 0240600), CM024959. 1 (Rhsim07G 0239900)	7900); RAD2.2: CM024957.1 (Rhsim05G007 3900	(Rhsim01G 0235000); DIV1.2 CM024965. 1 (Rhsim13G 0072600	06600)	0172100), CM024955. 1 (Rhsim03G 0139800)	
<i>R. taxifolium</i>	N/A	CYC2.1: MZ208790;	N/A	N/A	RAD2.1: MZ209226;	DIV1.1: MZ209242;	N/A	N/A	

		CYC2.2: MZ208791; CYC2.3: MZ208792; CYC2.4: MZ208793			RAD2.2: MZ209234	DIV1.2: MZ209250			
<i>R. williamsianum</i> Rehder & E.H. Wilson ³	CYC1.2: LG01_order ed_scaffold _52 (C3L33_00 958-RA); CYC1.1: unclustered _scaffold_7 97 (C3L33_23 136-RA)	CYC2.1: LG11_order ed_scaffold _106 (C3L33_18 671-RA); CYC2.2: LG11_order ed_scaffold _106 (C3L33_18 672-RA); CYC2.3: LG11_order ed_scaffold _107	LG10_order ed_scaffold _29 (C3L33_17 041-RA)	LG06_order ed_scaffold _66, LG06_order ed_scaffold _126 (C3L33_11 058-RA), LG05_order ed_scaffold _118 (C3L33_09 508-RA), LG05_order ed_scaffold _118	RAD2.1: LG13_ordered _scaffold_4 (C3L33_20823 -RA); RAD2.2: LG12_ordered _scaffold_33 (C3L33_19524 -RA)	DIV1.1: LG03_order ed scaffol_14 (C3L33_04 512-RA); DIV1.2: LG04_order ed_scaffold _90 (C3L33_07 065-RA)	LG12_or dered_sc affold_11 0 (C3L33_ 20406-R A)	LG10_order ed_scaffold _14 (C3L33_16 627-RA), LG02_order ed_scaffold _91 (C3L33_02 859-RA)	LG02_order ed_scaffold _83 (C3L33_02 818-RA)

		(C3L33_18 673-RA)		(C3L33_09 514-RA)					
<i>Actinidia chinensis</i> Planch. ⁴	N/A	Contig0117 7 (Actinidia24 782), Lachesis_gr oup4 (Actinidia36 307), Lachesis_gr oup11 (Actinidia18 122)	N/A	N/A	Lachesis_grou p7, Lachesis_grou p12 (Actinidia0052 9)	Lachesis_gr oup15 (Actinidia3 4447), Lachesis_gr oup9 (Actinidia2 3898), Lachesis_gr oup24 (Actinidia3 8831), Lachesis_gr oup20 (Actinidia2 5144)	N/A	N/A	N/A
<i>Antirrhinum majus</i> L. ⁵	TCP5: Chr5 (Am05g302 60)	CYC: Y16313; DICH:	TCP1: Chr3 (Am03g341	RADLI: AJ791699.1 ;	RAD: AY954971.1	DIV: AY077453. 1;	N/A	N/A	N/A

		AF199465	20)	<i>RADL2:</i> Am05g0229 0 <i>RADL3:</i> DQ375227. 1; <i>RADL4:</i> Am07g1081 0 <i>RADL5:</i> AJ793240.1		<i>DIVL1:</i> AY077454. 1			
<i>Aquilegia caerulea</i> E.James ⁶	<i>CYC1:</i> Aqcoe3G39 5500.1; <i>CYC2:</i> Aqcoe3G04 8600.1	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
<i>Arabidopsis thaliana</i> (L.) Heynh.	<i>TCP18:</i> NM_11274 1	<i>TCP1:</i> NM_00116 0982	<i>TCP12:</i> NM_10555 4	<i>RL3:</i> NM_11982 0; <i>RL4:</i> NM_00108	<i>RL1:</i> NM_120086; <i>RL2</i> (NM_127736)	N/A	N/A	N/A	N/A

				4443; <i>RL5</i> : NM_10180 8; <i>RL6</i> : NM_00108 4356					
<i>Empetrum nigrum</i>	N/A	MZ208769	N/A	N/A	RAD2.1: MZ209230; RAD2.2: MZ209238	DIV1.1: MZ209246; DIV1.2: MZ209254	N/A	N/A	N/A
<i>Erica scoparia</i>	N/A	MZ208770	N/A	N/A	RAD2.1: MZ209231; RAD2.2: MZ209239	DIV1.1: MZ209247; DIV1.2: MZ209255	N/A	N/A	N/A
<i>Kalmia latifolia</i>	N/A	MZ208771	N/A	N/A	RAD2.1: MZ209232; RAD2.2: MZ209240	DIV1.1: MZ209248; DIV1.2: MZ209256	N/A	N/A	N/A
<i>Magnolia grandiflora</i> L. ⁷	N/A	N/A	N/A	<i>RAD1</i> : WBOD-208 6252;	N/A	<i>DIV1</i> : WBOD-202 2953; <i>DIV2</i> :	N/A	N/A	N/A

				<i>RAD2</i> : WBOD-201 9537; <i>RAD3</i> : WBOD-200 6094		WBOD-202 4364			
<i>Solanum lycopersicum</i> L. ⁶	<i>CYC1A</i> : Solyc03g11 9770.2.1; <i>CYC1B</i> : Solyc06g06 9240.1.1	<i>CYC2A</i> : Solyc02g08 9830.1.1; <i>CYC2B</i> : Solyc03g04 5030.1.1	<i>CYC3A</i> : Solyc05g00 9900.1.1; <i>CYC3B</i> : Solyc04g00 6980.1.1	<i>RADL5</i> : Solyc10g08 0920.1.1; <i>RADL3</i> : Solyc04g08 0500.2.1; <i>RADL4</i> : Solyc12g08 9190.1.1; <i>RADL1</i> : Solyc01g10 9690.1.1	<i>RAD</i> : Solyc01g1096 70.2.1; <i>RADL2</i> : Solyc10g0524 70.1.1	<i>DIV</i> : Solyc06g07 6770.2.1	<i>DIVL</i> : Solyc09g 014250.2 .1; <i>DIVL2</i> : Solyc10g 076820.1 .1	<i>DIVL4</i> : Solyc03g09 6350.2.1; <i>DIVL5</i> : Solyc05g05 2610.2.1	N/A
<i>Vaccinium corymbosum</i> L. ⁸	N/A	VaccDscf 7-snap-gene -330.28,	N/A	N/A	VaccDscf14- gene-372.36, VaccDscf2-s	VaccDscf 19-augustus -gene-360.1	N/A	N/A	N/A

		VaccDscf 16-snap-gen e-95.39, VaccDscf 31-snap-gen e-5.36			nap-gene-426. 30, VaccDscf13- snap-gene-273. 47, VaccDscf30- snap-gene-127. 34, VaccDscf32- processed-gene -84.20, VaccDscf42- processed-gene -185.4	9, VaccDscf 15-augustus -gene-332.3 1, VaccDscf 15-augustus -gene-315.3 3, VaccDscf 24-augustus -gene-73.38			
<i>Vitis vinifera</i> L. ⁶	GSVIVT01 008234001	GSVIVT01 036449001	GSVIVT01 011962001	<i>RADL4</i> : GSVIVT01 009723001; <i>RADL2</i> :	<i>RAD</i> : GSVIVT01031 975001	<i>DIV</i> : GSVIVG01 024794001	<i>DIVL2</i> : GSVIVG 0103400 1001	<i>DIVL3</i> : GSVIVG01 016370001	N/A

				GSVIVT01 018944001; <i>RADLI</i> : GSVIVT01 031982001; <i>RADL3</i> : GSVIVT01 009716001					
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*RAD1 and RAD 3 are not supported as distinct groups.

¹All *R. delavayi* sequences obtained from Zhang et al. 2017 at <http://gigadb.org/dataset/100331>. Genomic scaffold and gene ID, if predicted, given.

²All *R. simsii* sequences obtained from Yang et al. 2020 at <http://bioinfor.kib.ac.cn/RPGD/index.html>. Genomic scaffold and gene ID, if predicted, given.

³All *R. williamsianum* sequences obtained from Soza et al. 2019 at <https://genomevolution.org/coge/GenomeInfo.pl?gid=59084>. Genomic scaffold and gene ID, if predicted, given.

⁴All *A. chinensis* sequences obtained from Wu et al. 2019 at <http://kiwifruitgenome.org/organism/5>. Genomic scaffold and gene ID, if predicted, given.

⁵*A. majus* sequences obtained from GenBank or Li et al. 2019 at <http://bioinfo.sibs.ac.cn/Am>. Genomic scaffold and gene ID, if predicted, given.

⁶All sequences obtained from Phytozome at <https://phytozome.jgi.doe.gov/pz/portal.html>.

⁷All *M. grandiflora* sequences obtained from 1,000 Plants (Carpenter et al. 2019, Leebens-Mack et al. 2019) at China National Gene Bank, <https://db.cngb.org>.

⁸All *V. corymbosum* sequences obtained from Colle et al. 2019 at <https://www.vaccinium.org>. Genomic scaffold and gene ID, if predicted, given.

Supplementary Table S3. Primer sequences and thermal cycling conditions used in this study.

Primer	Sequence	Annealing Temperature (C)	Extension Time (s)	Purpose
CYC2				
RhCYC2A_StartF2	5'-ATGWTCTCTTCAACCAMYAAYGS-3'	62	60	Ingroup PCR
RhCYC2A_StopR	5'-GTTACCAYTGGCTGWAGATGTTGC-3'	62	60	Ingroup PCR
RhCYC2_TCPF	5'-GCACAAGCACAGYAAGATYT-3'	52	30	Outgroup PCR
RhCYC2_RR	5'-CTCTCTHGCYYTTTRCCCTAGA-3'	52	30	Outgroup PCR
IDT ReadyMade™ Anchored Oligo dT (20)	5'-TTTTTTTTTTTTTTTTTTTTTV-3'	45/55	180	3' RACE
Rbey_CYC2_3RACE_F1	5'-TTCTTCSTCCAGTACCACTC-3'	45/55	180	3' RACE
Rbey_CYC2_3RACE_F2	5'-YAWGCTAGGGTTCGAGAAAG-3'	45/55	180	3' RACE
<i>RhCYC2.1</i>				
Rbey_CYC2_3RACE_intF	5'-TCTACAGCCAATGGTGACAT-3'	50	240	3' RACE sequencing
Rbey_CYC2.1B_RT_F	5'-CGCTGGCAAGTTCTTCGATCTT-3'	68	30	RT-PCR
Rbey_CYC2.1B_RT_F2	5'-GGTGAACCCAATGGTGAAA-3'	60	90	3' UTR PCR
Rbey_CYC2.1_RT_R	5'-GGCCGGCTCAAGAGTTTT-3'	68, 60	30, 90	RT-PCR, 3' UTR PCR
Rbey_CYC2.1_intF	5'-GAGTGACGTGGATCAAGTAT-3'	50	240	3' UTR sequencing
Rbey_CYC2.1_intF2	5'-GCTATTGAGCCAAAGGCCTC-3'	50	240	3' UTR sequencing
Rbey_CYC2.1_intR	5'-TCCTAGGGAGAGAGAGAGAG-3'	50	240	3' UTR sequencing
Rbey_CYC2.1_intR2	5'-TCACAACCGTAAACACGATC-3'	50	240	3' UTR sequencing

Rtax_CYC2.1_RT_F2	5'-AAGCCGGTGAACCCAATGGT-3'	64	30	RT-PCR
Rtax_CYC2.1_RT_R2	5'-GACTTTACACCACCACTYGAG-3'	64	30	RT-PCR
<i>RhCYC2.2</i>				
Rbey_CYC2.2_F	5'-ATGGTGTAAGGGGAGTACTCT-3'	64	90	3' UTR PCR
Rbey_CYC2.2_RT_F2	5'-CAACTTGGAGGATGGAGCAT-3'	65	30	RT-PCR
Rbey_CYC2.2_RT_R2	5'-GCCTACCCGTAACCCAAAA-3'	65, 64	30, 90	RT-PCR, 3' UTR PCR
Rtax_CYC2.2_RT_F	5'-CTTTTCGGCATGGTGGTTTC-3'	64	30	RT-PCR
Rtax_CYC2.2_RT_R	5'-GCTGATACCACTTGATCACTTCC-3'	64	30	RT-PCR
<i>RhCYC2.3</i>				
Rbey_CYC2.3_RT_F	5'-CCTGACCGACACCCTTTT-3'	65	30	RT-PCR
Rbey_CYC2.3_RT_R	5'-CAGCAGCCCTATCTTTAAGT-3'	65	30	RT-PCR
Rtax_CYC2.3_RT_F	5'-GTCGATCGAAACGGCTCGCAAGTTC-3'	66	30	RT-PCR
Rtax_CYC2.3_RT_R	5'-ATGCAGCAGCCCTATCTTTAAGTAA-3'	66	30	RT-PCR
<i>RhCYC2.4</i>				
Rbey_CYC2.4a_RT_F	5'-TCCAAGTTGAAGCGATCTCC-3'	67	90	3' UTR PCR
Rbey_CYC2.4c_RT_F	5'-AGGTTCTGTTGTGGGCATTA-3'	67	30	RT-PCR
Rbey_CYC2.4c_RT_R	5'-TAGCCAGAGAGCCAAACAAA-3'	67	30, 90	RT-PCR, 3' UTR PCR
Rtax_CYC2.4_3utrF	5'-GACACAGAAAGATAGGACTGCT-3'	58	90	3' UTR PCR
Rtax_CYC2.4_3utrR	5'-CAAGAGGTAATATTGCGGCAG-3'	58	90	3' UTR PCR
Rtax_CYC2.4_RT_F	5'-AAGAAGGCCGCGAAGAAG-3'	66	30	RT-PCR
Rtax_CYC2.4_RT_R	5'-AGCAGTCCTATCTTTCTGTGTC-3'	66	30	RT-PCR

<i>RhCYC2.5</i>				
Rbey_CYC2.5_3RACE_F2	5'-TCAGGGACCAATATTGAAGGT-3'	45/55, 66	180, 90	3' RACE, 3' UTR PCR
Rbey_CYC2.5c_3RACE_R	5'-ATCATGGTACATCGGCACTA-3'	66	90	3' UTR PCR
Rbey_CYC2.5_intF	5'-ATACGAAAATGGCAGTGTCT-3'	50	240	3' UTR sequencing
Rbey_CYC2.5_intR	5'-CCAAGACAACAAAACACCTC-3'	50	240	3' UTR sequencing
Rbey_CYC2.5_RT_F	5'-CGAGAAACCAAGAAGCCAG-3'	65	30	RT-PCR
Rbey_CYC2.5_RT_R	5'-ACCTTCAATATTGGTCCCTGA-3'	65	30	RT-PCR
RAD2				
<i>RhRAD2.1</i>				
RhRADcopy1_F1	5'-ACGTCCTCCCAAGGCTCTG-3'	67	35	PCR
RhRADcopy1_R1	5'-GGTCTTGTAGTCAGGAAAGGG-3'	67	35	PCR
RhRADcp1_fwd_rtPCR	5'-ACCATCTACTCTACTTTCCG-3'	56 (Rtax) or 61 (Rbey)	30	RT-PCR
RhRADcp1_rev2_rtPCR	5'-CCTTTGCTTCTCTTCACTAG-3'	56 (Rtax) or 61 (Rbey)	30	RT-PCR
<i>RhRAD2.2</i>				
RhRADcopy2_F1	5'-ATGGCATCAATGTCTTCCG-3'	67	35	PCR
RhRADcopy2_R1	5'-AGTTCTTGTAGTTTGGATAGG-3'	67	35	PCR
RhRADcp2_fwd1_rtPCR	5'-CCTTCTCACTCTACCGAAACAT-3'	56 (Rtax) or 61 (Rbey)	30	RT-PCR
RhRADcp2_rev1_rtPCR	5'-CCTTGGTTCATCACTTCATCT-3'	56 (Rtax) or 61 (Rbey)	30	RT-PCR
DIV1				
<i>RhDIV1.1</i>				
RhDIV_LG03_F1	5'-ATGAGGTGGGGAATGGAGATTC-3'	64	35	PCR
RhDIV_LG03_R1	5'-CTGACTTGTGCTCTTCTTCAG-3'	64	35	PCR

RhDIVlg03_fwd2	5'-GCTCCTCTGCCTTCTCTTG-3'	61 (Rtax) or 63 (Rbey)	30	RT-PCR
RhDIVlg03_rev1	5'-GGAAGAAGCACTATTATACCACG-3'	61 (Rtax) or 63 (Rbey)	30	RT-PCR
<i>RhDIV1.2</i>				
RhDIV_LG04_F1	ATGGAAATTCTGTCGCCTGCATC	62	35	PCR
RhDIV_LG04_R1	CCAACTTACTTATGCTCTTCTTCTG	62	35	PCR
RhDIVlg04_fwd1	5'-GCTGTGAGGTGGGTTTTCC-3'	63 (Rbey), 66 (Rtax)	30	RT-PCR
RhDIVlg04_rev1	5'-CGGGAACCACTGTACCAAG-3'	63 (Rbey), 66 (Rtax)	30	RT-PCR
<i>ACT5</i>				
DN129728_c6_g2_i3_Fwd_primer3	5'-CGGGGTTGGATGAAATGGCT-3'	63 (Rtax) or 65 (Rbey)	30	RT-PCR
DN129728_c6_g2_i3_Rev_primer3	5'-GCCAATCCTCACCTTCTCA-3'	63 (Rtax) or 65 (Rbey)	30	RT-PCR
<i>EF1A</i>				
RhEF1a_Yi_FWD	5'-TGTCATCGATGCTCCTGGAC-3'	62	30	RT-PCR
RhEF1a_REV	5'-AGGGCCTCTTGGGTTCATAA-3'	62	30	RT-PCR
M13				
M13*F	5'-GTAAAACGACGGCCAGTGAAT-3'	55	30 or 60	Clone screening
M13*R	5'-CAGGAAACAGCTATGACCATG-3'	55	30 or 60	Clone screening