Supplementary material Table S1. List of Plant species used in this study, their taxonomy (according to NCBI Taxonomy: http://www.ncbi.nlm.nih.gov/taxonomy) and results of *in silico* mining of chromodomains by LTR retrotransposons clades.

Class	Order	Family	Tribe	Species	EST			GSS/WGS		
					Chlamyvir	other		Chlamyvir	other	
Bangiophyceae	Bangiales	Bangiaceae		*Porphyra yezoensis*	--	--		ND	ND	
	Cyanidiales	Cyanidiaceae		*Galdieria sulphuraria*	--	--		ND	ND	
				Cyanidioschyzon merolae	ND	ND		--	--	
Trebouxiophyceae	Chlorellales	Chlorellaceae		*Chlorella vulgaris*	--	--		7	--	
Chlorophyceae	Chlamydomonadales	Chlamydomonadaceae		*Chlamydomonas reinhardtii*	--	--		13	3	
				Volvox carteri f nagariensis	3	--		241	20	
Prasinophyceae		Mamiellaceae		*Micromonas pusilla*	ND	ND		--	--	
				Ostreococcus lucimarinus	ND	ND		--	--	
				Ostreococcus tauri	ND	ND		--	--	
					Reina	Tekay	Galadriel	Reina	Tekay	Galadriel
Lycopodiopsida	Lycopodiales	Lycopodiaceae		*Huperzia serrata*	--	--	--	ND	ND	ND
Polypodiopsida	Polypodiales	Pteridaceae		*Adiantum capillus-veneris*	--	1	--	ND	ND	ND
Coniferopsida	Coniferales	Pinaceae		*Picea glauca*	6	2	--	--	--	--
				Picea sitchensis	5	5	--	ND	ND	ND
				Pinus taeda	4	5	--	18	2	--
				Pinus banksiana	9	3	--	--	--	--
				Pinus contorta	2	3	--	ND	ND	ND
				Pseudotsuga menziesii var. menziesii	2	1	--	ND	ND	ND
				Pseudotsuga menziesii	1	--	--	ND	ND	ND
				Cryptomeria japonica	2	--	--	ND	ND	ND
Monocotyledons	Alismatales	Araceae		*Wolffia arrhiza*	--	--	--	ND	ND	ND
	Poales	Poaceae	Poeae	*Agrostis stolonifera*	1	6	--	ND	ND	ND
				Festuca arundinacea	19	4	--	1	10	--
				Festuca pratensis	20	7	--	ND	ND	ND
				Puccinellia tenuiflora	--	--	--	ND	ND	ND
			Triticeae	*Hordeum vulgare*	--	2	--	--	3	--
				Hordeum vulgare subsp. vulgare	5	5	--	--	--	--
				Leymus cinereus x Leymus triticoides	1	--	--	ND	ND	ND
				Triticum aestivum	37	5	--	10	91	--
				Triticum monococcum	--	--	--	--	--	--
				Triticum turgidum subsp durum	2	2	--	--	--	--
				Pseudoroegneria spicata	--	--	--	ND	ND	ND
			Brachypodieae	*Brachypodium distachyon*	11	--	--	46	371	--
			Oryzeae	*Oryza sativa*	2	1	--	--	8	--
				Oryza sativa Indica Group	5	1	--	64	239	--
				Oryza sativa Japonica Group	55	6	--	23	78	--
			Paniceae	*Panicum virgatum*	11	1	--	ND	ND	ND
				Pennisetum glaucum	--	1	--	--	--	--
			Andropogoneae	*Saccharum hybrid cultivar CP72 2086*	1	--	--	ND	ND	ND
				Saccharum officinarum	12	6	--	ND	ND	ND
				Sorghum bicolor	14	--	--	18	>1000	--
				Zea mays	53	105	--	600	>10000	--
			Cynodonteae	*Cynodon dactylon*	--	--	--	--	--	--

Supplementary material Table S1 (continued). List of Plant species used in this study, their taxonomy (according to NCBI Taxonomy: http://www.ncbi.nlm.nih.gov/taxonomy) and results of *in silico* mining of chromodomains by LTR retrotransposons clades.

	Order	Family	Tribe	Species	EST			GSS/WGS		
					Reina	Tekay	Galadriel	Reina	Tekay	Galadriel
Monocotyledons	Poales	Poaceae	Eragrostideae	*Eragrostis curvula*	--	--	--	ND	ND	ND
	Zingiberales	Zingiberaceae		*Zingiber officinale*	--	--	--	ND	ND	ND
Eudicotyledons	Caryophyllales	Amaranthaceae		*Beta vulgaris*	--	--	1	7	39	--
		Aizoaceae		*Mesembryanthemum crystallinum*	--	--	--	ND	ND	ND
		Tamaricaceae		*Tamarix hispida*	--	--	--	ND	ND	ND
	Ericales	Actinidaceae		*Actinidia chinensis*	--	1	--	ND	ND	ND
				Actinidia deliciosa	2	9	--	--	--	--
		Theaceae		*Camellia sinensis*	--	--	--	--	--	--
	Asterales	Asteraceae	Anthemideae	*Artemisia annua*	--	14	--	--	--	--
			Heliantheae	*Helianthus annuus*	5	2	3	1	4	--
				Zinnia violacea	--	3	--	ND	ND	ND
			Mutisieae	*Gerbera hybrid cultivar*	--	--	1	ND	ND	ND
			Cichorieae	*Lactuca sativa*	--	1	--	--	--	--
				Lactuca serriola	--	--	1	ND	ND	ND
	Solanales	Solanaceae	Capsiceae	*Capsicum annuum*	11	4	--	--	--	--
			Solaneae	*Solanum habrochaites*	--	2	--	ND	ND	ND
				Solanum lycopersicum	--	11	--	17	>1000	80
				Solanum melongena	--	4	--	--	1	--
				Solanum torvum	--	3	3	ND	ND	ND
				Solanum tuberosum	2	8	1	11	>1000	12
			Nicotianeae	*Nicotiana benthamiana*	14	--	--	18	>1000	--
				Nicotiana tabacum	23	39	2	185	2973	297
	Lamiales	Phrymaceae		*Mimulus guttatus*	2	--	1	16	370	13
				Mimulus lewisii	--	--	--	4	--	--
		Orobanchaceae	Buchnereae	*Striga hermonthica*	--	2	--	10	34	1
			Rhinantheae	*Triphysaria versicolor*	--	--	--	ND	ND	ND
	Gentianales	Apocynaceae	Vinceae	*Catharanthus roseus*	--	--	--	1	--	--
		Rubiaceae	Coffeeae	*Coffea arabica*	--	--	--	1	6	--
	Apiales	Araliaceae		*Eleutherococcus sessiliflorus*	--	--	--	ND	ND	ND
				Panax ginseng	--	--	--	--	5	--
	Brassicales	Brassicaceae		*Arabidopsis thaliana*	2	6	--	14	23	--
				Brassica napus	2	3	--	5	99	2
				Brassica oleracea	--	--	--	53	101	90
				Brassica rapa	--	--	2	2	7	2
				Raphanus sativus	--	1	--	--	--	--
				Raphanus raphanistrum subsp. raphanistrum	--	--	--	ND	ND	ND
				Tropaeolum majus	--	--	--	ND	ND	ND
	Sapindales	Rutaceae		*Citrus clementina*	--	--	1	11	8	35
				Citrus sinensis	2	5	3	ND	ND	ND
				Citrus trifoliata	--	1	--	ND	ND	ND
				Citrus unshiu	--	--	1	ND	ND	ND

Supplementary material Table S1 (continued). List of Plant species used in this study, their taxonomy (according to NCBI Taxonomy: http://www.ncbi.nlm.nih.gov/taxonomy) and results of *in silico* mining of chromodomains by LTR retrotransposons clades.

	Order	Family	Tribe	Species	EST			GSS/WGS		
					Reina	Tekay	Galadriel	Reina	Tekay	Galadriel
Eudicotyledons	Malvales	Malvaceae		*Gossypium arboreum*	--	6	--	--	--	--
				Gossypium hirsutum	3	17	3	3	406	17
				Gossypium raimondii	1	2	--	1	91	4
				Theobroma cacao	--	3	--	--	--	--
	Myrtales	Myrtaceae		*Eucalyptus gunnii*	--	--	--	ND	ND	ND
	Fabales	Fabaceae	Dalbergieae	*Arachis hypogaea*	3	3	1	--	9	--
			Phaseoleae	*Glycine max*	1	2	--	22	252	--
				Glycine soja	--	--	--	17	306	--
				Vigna unguiculata	3	--	--	7	99	--
				Cajanus cajan	--	--	--	11	113	--
			Loteae	*Lotus japonicus*	2	3	--	8	62	--
			Trifolieae	*Medicago sativa*	1	1	--	--	--	--
				Medicago truncatula	--	2	--	3	322	--
				Trifolium pratense	--	--	--	1	8	--
			Phaseoleae	*Phaseolus vulgaris*	--	2	--	--	--	--
				Phaseolus angustissimus	--	--	--	ND	ND	ND
			Fabeae	*Pisum sativum*	1	--	--	--	--	--
			Cicereae	*Cicer arietinum*	--	--	--	12	309	--
			Galegeae	*Glycyrrhiza uralensis*	--	--	--	ND	ND	ND
	Cucurbitales	Cucurbitaceae		*Cucumis sativus*	--	--	1	1	2	--
	Rosales	Rosaceae	Potentilleae	*Fragaria vesca*	--	--	4	ND	ND	ND
			Pyreae	*Malus x domestica*	3	1	--	--	--	--
			Amygdaleae	*Prunus persica*	--	1	--	1	18	4
		Cannabaceae		*Humulus lupulus*	1	--	--	ND	ND	ND
				Cannabis sativa	--	--	--	ND	ND	ND
	Fagales	Juglandaceae		*Juglans hindsii x Juglans regia*	1	--	--	ND	ND	ND
		Fagaceae		*Quercus robur*	1	--	--	ND	ND	ND
		Betulaceae		*Betula platyphylla*	--	--	--	ND	ND	ND
	Malpighiales	Euphorbiaceae	Manihoteae	*Manihot esculenta*	--	2	2	1	31	--
		Salicaceae	Saliceae	*Populus tremula x Populus tremuloides*	--	1	--	ND	ND	ND
				Populus trichocarpa x Populus deltoides	3	1	--	ND	ND	ND
	Vitales	Vitaceae		*Vitis vinifera*	--	4	4	18	59	327
	Ranunculales	Ranunculaceae		*Aquilegia formosa x Aquilegia pubescens*	5	--	--	ND	ND	ND
		Papaveraceae		*Papaver somniferum*	7	3	2	ND	ND	ND
	Malvales	Malvaceae		*Gossypium arboreum*	--	6	--	--	--	--
				Gossypium hirsutum	3	17	3	3	406	17
				Gossypium raimondii	1	2	--	1	91	4

Supplementary material Table S2. List of species genomes of which were analyzed *in silico* in present study and the sources of the ESTs and/or genomic sequences.

Class	Order	Family	Species	Organization: Web link
Bangiophyceae		Bangiaceae	*Porphyra yezoensis*	KDRI: http://est.kazusa.or.jp/en/plant/porphyra/EST/
		Cyanidiaceae	*Galdieria sulphuraria*	MSU: http://genomics.msu.edu/galdieria/
			Cyanidioschyzon merolae	http://merolae.biol.s.u-tokyo.ac.jp/
Trebouxiophyceae	Chlorellales	Chlorellaceae	*Chlorella vulgaris*	JGI: http://genome.jgi-psf.org/Chlvu1/Chlvu1.home.html
Chlorophyceae		Chlamydomonadaceae	*Chlamydomonas reinhardtii*	KDRI: http://est.kazusa.or.jp/en/plant/chlamy/EST/ PlantGDB: http://www.plantgdb.org/prj/ESTCluster/ JGI Phytozome: http://www.phytozome.net/
Prasinophyceae		Mamiellaceae	*Micromonas pusilla*	JGI: http://genome.jgi-psf.org/MicpuC1/MicpuC1.home.html
			Ostreococcus lucimarinus	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Ostreococcus tauri	JGI: http://genome.jgi-psf.org/Ostta4/Ostta4.home.html
			Volvox carteri f nagariensis	JGI Phytozome: http://www.phytozome.net/ JGI: http://genome.jgi-psf.org/Volca1/Volca1.home.html PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
Lycopodiopsida	Lycopodiales	Lycopodiaceae	*Huperzia serrata*	NCBI SRA: http://www.ncbi.nlm.nih.gov/sra/SRX010999
Polypodiopsida	Polypodiales	Pteridaceae	*Adiantum capillus-veneris*	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
Coniferopsida	Coniferales	Pinaceae	*Picea glauca*	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Picea sitchensis	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Pinus taeda	MGEL: http://www.pine.msstate.edu/seq.htm PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Pinus banksiana	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Pinus contorta	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Pseudotsuga menziesii var. menziesii	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Pseudotsuga menziesii	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Cryptomeria japonica	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
Monocotyledons	Alismatales	Araceae	*Wolffia arrhiza*	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
	Poales	Poaceae	*Agrostis stolonifera*	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Festuca arundinacea	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Festuca pratensis	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Hordeum vulgare	PlantGDB: http://www.plantgdb.org/HvGDB/
			Hordeum vulgare subsp. vulgare	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Leymus cinereus x Leymus triticoides	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Triticum aestivum	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Triticum monococcum	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Triticum turgidum subsp durum	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Pseudoroegneria spicata	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Brachypodium distachyon	JGI Phytozome: http://www.phytozome.net/ PlantGBD: http://www.plantgdb.org/BdGDB/ PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Oryza sativa	JGI Phytozome: http://www.phytozome.net/ PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Oryza sativa Indica Group	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Oryza sativa Japonica Group	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Panicum virgatum	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/

Supplementary material Table S2 (continued). List of species genomes of which were analyzed *in silico* in present study and the sources of the ESTs and/or genomic sequences.

Class	Order	Family	Species	Organization: Web link
			Saccharum hybrid cultivar CP72 2086	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Saccharum officinarum	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Sorghum bicolor	JGI Phytozome: http://www.phytozome.net/ PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Zea mays	JGI Phytozome: http://www.phytozome.net/ PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Cynodon dactylon	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Eragrostis curvula	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
	Zingiberales	Zingiberaceae	*Zingiber officinale*	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
Eudicotyledons	Caryophyllales	Amaranthaceae	*Beta vulgaris*	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
		Aizoaceae	*Mesembryanthemum crystallinum*	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
		Tamaricaceae	*Tamarix hispida*	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
	Ericales	Actinidaceae	*Actinidia chinensis*	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Actinidia deliciosa	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
		Theaceae	*Camellia sinensis*	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
	Asterales	Asteraceae	*Artemisia annua*	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Helianthus annuus	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Zinnia violacea	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Gerbera hybrid cultivar	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Lactuca sativa	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Lactuca serriola	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
	Solanales	Solanaceae	*Capsicum annuum*	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Solanum habrochaites	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Solanum lycopersicum	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Solanum melongena	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Solanum torvum	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Solanum tuberosum	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Nicotiana benthamiana	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Nicotiana tabacum	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
	Lamiales	Phrymaceae	*Mimulus guttatus*	JGI Phytozome: http://www.phytozome.net/ PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Mimulus lewisii	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
		Orobanchaceae	*Striga hermonthica*	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Triphysaria versicolor	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
	Gentianales	Apocynaceae	*Catharanthus roseus*	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
		Rubiaceae	*Coffea arabica*	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
	Apiales	Araliaceae	*Eleutherococcus sessiliflorus*	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Panax ginseng	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
	Brassicales	Brassicaceae	*Arabidopsis thaliana*	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Brassica napus	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Brassica oleracea	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Brassica rapa	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Raphanus sativus	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/

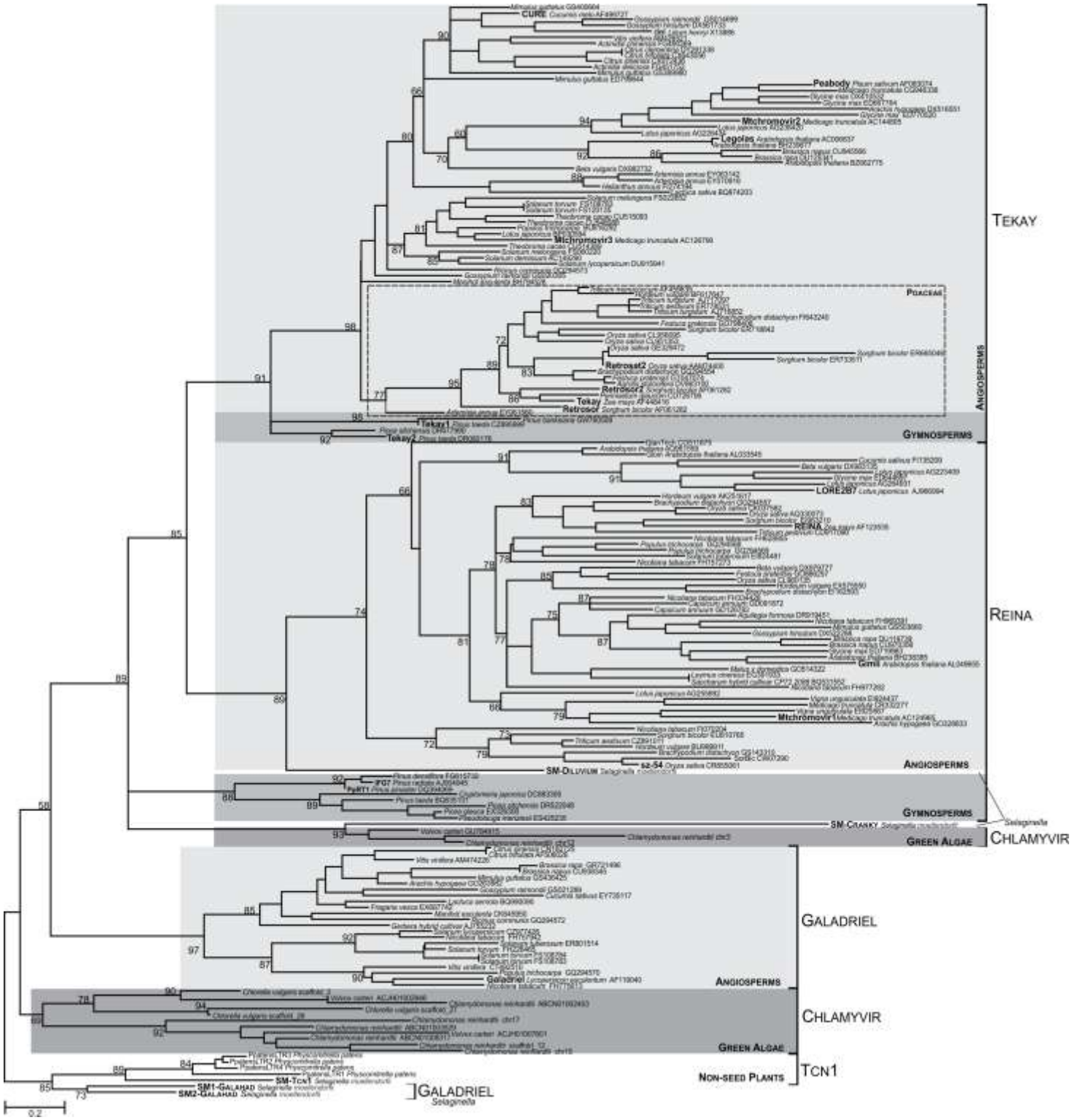
Supplementary material Table S2 (continued). List of species genomes of which were analyzed *in silico* in present study and the sources of the ESTs and/or genomic sequences.

Class	Order	Family	Species	Organization: Web link
Eudicotyledons			*Raphanus raphanistrum subsp. raphanistrum*	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Tropaeolum majus	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
	Sapindales	Rutaceae	*Citrus clementina*	JGI Phytozome: http://www.phytozome.net/ PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Citrus sinensis	JGI Phytozome: http://www.phytozome.net/ PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Citrus trifoliata	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Citrus unshiu	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
	Myrtales	Myrtaceae	*Eucalyptus gunnii*	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
	Fabales	Fabaceae	*Arachis hypogaea*	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Glycine max	JGI Phytozome: http://www.phytozome.net/ PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Glycine soja	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Vigna unguiculata	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Cajanus cajan	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Lotus japonicus	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Medicago sativa	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Medicago truncatula	JGI Phytozome: http://www.phytozome.net/ PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Trifolium pratense	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Phaseolus vulgaris	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Phaseolus angustissimus	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Pisum sativum	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Cicer arietinum	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Glycyrrhiza uralensis	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
	Cucurbitales	Cucurbitaceae	*Cucumis sativus*	JGI Phytozome: http://www.phytozome.net/ PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
	Rosales	Rosaceae	*Fragaria vesca*	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Malus x domestica	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Prunus persica	JGI Phytozome: http://www.phytozome.net/ PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
		Cannabaceae	*Humulus lupulus*	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Cannabis sativa	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
	Fagales	Juglandaceae	*Juglans hindsii x Juglans regia*	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
		Fagaceae	*Quercus robur*	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
		Betulaceae	*Betula platyphylla*	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
	Malpighiales	Euphorbiaceae	*Manihot esculenta*	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
		Salicaceae	*Populus tremula x Populus tremuloides*	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Populus trichocarpa x Populus deltoides	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
	Vitales	Vitaceae	*Vitis vinifera*	JGI Phytozome: http://www.phytozome.net/ PlantGDB: http://www.plantgdb.org/prj/ESTCluster/

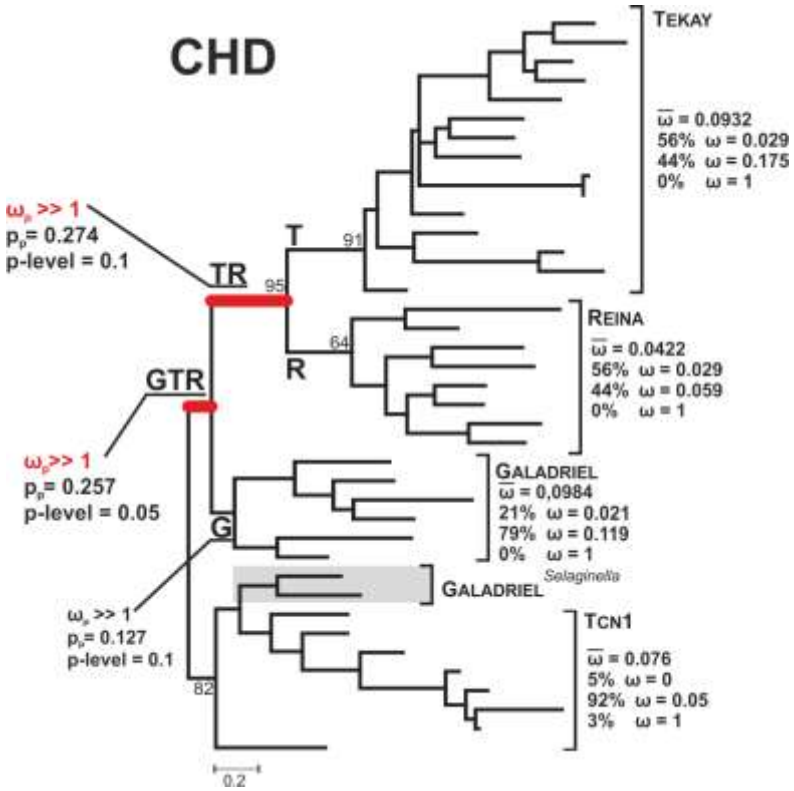
Supplementary material Table S2 (continued). List of species genomes of which were analyzed *in silico* in present study and the sources of the ESTs and/or genomic sequences.

Class	Order	Family	Species	Organization: Web link
Eudicotyledons	Ranunculales	Ranunculaceae	*Aquilegia formosa x Aquilegia pubescens*	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
		Papaveraceae	*Papaver somniferum*	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
	Malvales	Malvaceae	*Gossypium arboreum*	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Gossypium hirsutum	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Gossypium raimondii	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/
			Theobroma cacao	PlantGDB: http://www.plantgdb.org/prj/ESTCluster/

Supplementary Material Figure S1



Supplementary Material Dataset S1
Analysis of CHD tree



Branch-site tests.

(2.71 (0.05 level); 5.41 (0.01 level) – Null 2 vs Positive

3.84 (0.05 level); 6.63 (0.01 level) – Null 1 vs Null 2)

Branch-site test for positive selection at the base of T clade.

Model	lnL	Significant	Class 0	Class 1	Class 2a	Class 2b
Null 1 (M1a)	-5994.608301		p = 0.96436 ω = 0.07057	p = 0.03564 ω = 1.00000		
Null 2 (neutral)	-5993.232546	2.75151	p = 0.73553 ω_b = 0.06950 ω_f = 0.06950	p = 0.02732 ω_b = 1.00000 ω_f = 1.00000	p = 0.22865 ω_b = 0.06950 ω_f = 1.00000	p = 0.00849 ω_b = 1.00000 ω_f = 1.00000
Positive Selection	-5992.415185	1.634722	p = 0.71854 ω_b = 0.07183 ω_f = 0.07183	p = 0.02675 ω_b = 1.00000 ω_f = 1.00000	p = 0.24557 ω_b = 0.07183 ω_f = 999.00000	p = 0.00914 ω_b = 1.00000 ω_f = 999.00000

Naive Empirical Bayes (NEB) analysis; positive sites for foreground lineages Prob(w>1):

```
 6 E 0.656
14 I 0.894
16 R 0.975*
24 E 0.974*
26 L 0.997**
28 K 0.900
31 G 0.592
45 L 0.651
53 E 0.954*
```

Bayes Empirical Bayes (BEB) analysis [73]; positive sites for foreground lineages Prob(w>1):

1 * 0.600	12 R 0.588	23 T 0.605	34 E 0.607	45 L 0.806	56 R 0.600
2 D 0.600	13 V 0.600	24 E 0.811	35 S 0.612	46 W 0.588	57 A 0.600
3 K 0.620	14 I 0.868	25 Y 0.589	36 E 0.577	47 Q 0.634	58 E 0.600
4 E 0.594	15 R 0.582	26 L 0.948	37 A 0.584	48 F 0.590	59 G 0.600
5 V 0.591	16 R 0.897	27 V 0.588	38 S 0.586	49 Q 0.595	60 A 0.600
6 E 0.783	17 R 0.590	28 K 0.785	39 W 0.588	50 E 0.591	61 T 0.600
7 I 0.602	18 G 0.611	29 W 0.588	40 E 0.575	51 Q 0.593	62 R 0.600
8 I 0.583	19 V 0.595	30 K 0.628	41 P 0.591	52 I 0.642	63 T 0.600
9 L 0.589	20 P 0.596	31 G 0.676	42 A 0.595	53 E 0.760	64 S 0.600
10 A 0.575	21 P 0.611	32 L 0.590	43 G 0.584	54 R 0.585	65 A 0.600
11 D 0.591	22 A 0.600	33 P 0.710	44 A 0.581	55 F 0.600	66 A 0.600

Branch-site test for positive selection at the base of R clade.

Model	lnL	Significant	Class 0	Class 1	Class 2a	Class 2b
Null 1 (M1a)	-5994.608301		p = 0.96436 ω = 0.07057	p = 0.03564 ω = 1.00000		
Null 2 (neutral)	-5993.469959	2.276684	p = 0.73773 ω_b = 0.06975 ω_f = 0.06975	p = 0.02736 ω_b = 1.00000 ω_f = 1.00000	p = 0.22651 ω_b = 0.06975 ω_f = 1.00000	p = 0.00840 ω_b = 1.00000 ω_f = 1.00000
Positive Selection	-5992.910964	1.11799	p = 0.69307 ω_b = 0.07074 ω_f = 0.07074	p = 0.02571 ω_b = 1.00000 ω_f = 1.00000	p = 0.27116 ω_b = 0.07074 ω_f = 19.50879	p = 0.01006 ω_b = 1.00000 ω_f = 19.50879

Naive Empirical Bayes (NEB) analysis; positive sites for foreground lineages Prob(w>1):

```
 3 K 0.885
 7 I 0.776
17 R 0.509
18 G 0.655
20 P 0.513
32 L 0.765
41 P 0.969*
42 A 0.967*
46 W 0.655
49 Q 0.557
51 Q 0.812
54 R 0.970*
55 F 0.722
```

Bayes Empirical Bayes (BEB) analysis [73]; positive sites for foreground lineages Prob(w>1):

```
 3 K 0.945
 7 I 0.619
17 R 0.685
18 G 0.847
20 P 0.666
21 P 0.628
27 V 0.594
32 L 0.857
41 P 0.990**
42 A 0.990**
```

```
46 W 0.792
49 Q 0.727
51 Q 0.874
53 E 0.558
54 R 0.988*
55 F 0.833
56 R 0.600
```

Branch-site test for positive selection at the base of G clade.

Model	lnL	Significant	Class 0	Class 1	Class 2a	Class 2b
Null 1 (M1a)	-5994.608301		p = 0.96436 ω = 0.07057	p = 0.03564 ω = 1.00000		
Null 2 (neutral)	-5993.843327	1.529948	p = 0.83878 ω_b = 0.06896 ω_f = 0.06896	p = 0.03114 ω_b = 1.00000 ω_f = 1.00000	p = 0.12542 ω_b = 0.06896 ω_f = 1.00000	p = 0.00466 ω_b = 1.00000 ω_f = 1.00000
Positive Selection	-5991.460278	4.766098	p = 0.84189 ω_b = 0.07093 ω_f = 0.07093	p = 0.03127 ω_b = 1.00000 ω_f = 1.00000	p = 0.12229 ω_b = 0.07093 ω_f = 999.00000	p = 0.00454 ω_b = 1.00000 ω_f = 999.00000

Naive Empirical Bayes (NEB) analysis; positive sites for foreground lineages Prob(w>1):

```
21 P 0.660
46 W 0.854
48 F 0.971*
49 Q 0.923
```

Bayes Empirical Bayes (BEB) analysis [73]; positive sites for foreground lineages Prob(w>1):

```
2 D 0.539
20 P 0.529
21 P 0.651
23 T 0.553
24 E 0.506
46 W 0.834
48 F 0.831
49 Q 0.782
51 Q 0.530
52 I 0.561
58 E 0.509
```

Branch-site test for positive selection at the base of TR clade.

Model	lnL	Significant	Class 0	Class 1	Class 2a	Class 2b
Null 1 (M1a)	-5994.608301		p = 0.96436 ω = 0.07057	p = 0.03564 ω = 1.00000		
Null 2 (neutral)	-5992.115488	4.985626	p = 0.71615 ω_b = 0.06855 ω_f = 0.06855	p = 0.02664 ω_b = 1.00000 ω_f = 1.00000	p = 0.24798 ω_b = 0.06855 ω_f = 1.00000	p = 0.00923 ω_b = 1.00000 ω_f = 1.00000
Positive Selection	-5990.255016	3.720944	p = 0.70023 ω_b = 0.07199 ω_f = 0.07199	p = 0.02601 ω_b = 1.00000 ω_f = 1.00000	p = 0.26395 ω_b = 0.07199 ω_f = 999.00000	p = 0.00981 ω_b = 1.00000 ω_f = 999.00000

Naive Empirical Bayes (NEB) analysis; positive sites for foreground lineages Prob(w>1):

```
 5 V 0.998**
11 D 0.836
25 Y 0.805
48 F 0.992**
49 Q 0.665
50 E 0.996**
52 I 0.533
53 E 0.871
```

Bayes Empirical Bayes (BEB) analysis [73]; positive sites for foreground lineages Prob(w>1):

```
 1 * 0.599
 2 D 0.599
 3 K 0.695
 4 E 0.582
 5 V 0.995**
 6 E 0.527
 7 I 0.616
 8 I 0.527
 9 L 0.551
11 D 0.926
12 R 0.549
13 V 0.599
14 I 0.561
15 R 0.528
16 R 0.551
17 R 0.557
18 G 0.610
19 V 0.553
20 P 0.686
21 P 0.681
22 A 0.599
23 T 0.667
24 E 0.726
25 Y 0.932
26 L 0.574
27 V 0.548
28 K 0.725
29 W 0.548
30 K 0.659
31 G 0.550
32 L 0.579
33 P 0.609
34 E 0.538
35 S 0.648
36 E 0.514
37 A 0.533
38 S 0.554
39 W 0.548
41 P 0.581
42 A 0.567
43 G 0.574
44 A 0.520
45 L 0.566
46 W 0.589
47 Q 0.564
48 F 0.966*
49 Q 0.677
50 E 0.990*
51 Q 0.736
52 I 0.805
53 E 0.815
54 R 0.541
55 F 0.633
56 R 0.697
57 A 0.592
58 E 0.621
59 G 0.550
60 A 0.599
61 T 0.599
62 R 0.599
63 T 0.599
64 S 0.599
65 A 0.599
66 A 0.599
```

Branch-sites test for positive selection at the base of GTR clade.

Model	lnL	Significant	Class 0	Class 1	Class 2a	Class 2b

Null 1 (M1a)	-5994.608301		p = 0.96436 ω = 0.07057	p = 0.03564 ω = 1.00000		
Null 2 (neutral)	-5992.166788	4.883026	p = 0.72582 ω_b = 0.06740 ω_f = 0.06740	p = 0.02699 ω_b = 1.00000 ω_f = 1.00000	p = 0.23832 ω_b = 0.06740 ω_f = 1.00000	p = 0.00886 ω_b = 1.00000 ω_f = 1.00000
Positive Selection	-5989.340762	5.652052	p = 0.71684 ω_b = 0.07097 ω_f = 0.07097	p = 0.02660 ω_b = 1.00000 ω_f = 1.00000	p = 0.24738 ω_b = 0.07097 ω_f = 999.00000	p = 0.00918 ω_b = 1.00000 ω_f = 999.00000

Naive Empirical Bayes (NEB) analysis; positive sites for foreground lineages Prob(w>1):

```
 3 K 0.969*
19 V 0.665
21 P 0.514
23 T 0.853
32 L 0.943
46 W 0.986*
47 Q 0.928
48 F 0.999**
49 Q 0.967*
51 Q 0.932
```

Bayes Empirical Bayes (BEB) analysis [73]; positive sites for foreground lineages Prob(w>1):

1 * 0.612	19 V 0.785	37 A 0.610	55 F 0.574
2 D 0.824	20 P 0.688	38 S 0.573	56 R 0.586
3 K 0.972*	21 P 0.696	39 W 0.572	57 A 0.697
4 E 0.530	22 A 0.612	40 E 0.528	58 E 0.623
5 V 0.569	23 T 0.814	41 P 0.572	59 G 0.612
6 E 0.533	24 E 0.549	42 A 0.588	60 A 0.612
7 I 0.624	25 Y 0.574	43 G 0.578	61 T 0.612
8 I 0.556	26 L 0.575	44 A 0.584	62 R 0.612
9 L 0.574	27 V 0.563	45 L 0.575	63 T 0.612
10 A 0.531	28 K 0.556	46 W 0.960*	64 S 0.612
11 D 0.621	29 W 0.572	47 Q 0.964*	65 A 0.612
12 R 0.574	30 K 0.547	48 F 0.996**	66 A 0.612
13 V 0.612	31 G 0.556	49 Q 0.907	
14 I 0.585	32 L 0.932	50 E 0.579	
15 R 0.577	33 P 0.627	51 Q 0.963*	
16 R 0.561	34 E 0.571	52 I 0.825	
17 R 0.584	35 S 0.572	53 E 0.603	
18 G 0.596	36 E 0.577	54 R 0.588	

Corrections for Multiple Testing

Foreground branch	base of T clade	base of R clade	base of G clade	base of TR clade	base of GTR clade
$2\Delta l$	1.634722	1.11799	4.766098	3.720944	5.652052
$p_{\chi^2_1}$	.201051	.290352	.029026	.053734	.017435
Hommel procedure $\alpha = 0.1$	TRUE	TRUE	TRUE	TRUE	**FALSE**

Hommel procedure $\alpha = 0.05$	TRUE	TRUE	TRUE	TRUE	TRUE
Hommel procedure $\alpha = 0.01$	TRUE	TRUE	TRUE	TRUE	TRUE
$p_{1/2\chi_0^2+1/2\chi_1^2}$	0.10053	0.14518	0.01451	0.02687	0.00872
Hommel procedure $\alpha = 0.1$	TRUE	TRUE	**FALSE**	**FALSE**	FALSE
Hommel procedure $\alpha = 0.05$	TRUE	TRUE	TRUE	TRUE	**FALSE**
Hommel procedure $\alpha = 0.01$	TRUE	TRUE	TRUE	TRUE	TRUE

Clade tests with several branch types (Yang's Model C).

Model	lnL	Significant	Class 0	Class 1	Class 2
Null 1 (M1a) (np=77)	-5994.608301		p = 0.96436 ω = 0.07057	p = 0.03564 ω = 1.00000	
Model C (np=84)	-5940.930269	Yes (vs Null1)	p = 0.04666 ω_{ALL} = 0.00000	p = 0.03336 ω_{ALL} = 1.00000	p = 0.91999 $\omega_{TCN, REINA, GALADRIEL, TEKAY}$ = 0.08036 ω_{GTR} = 999.00000 ω_{G} = 0.02933 ω_{TR} = 999.00000 ω_{T} = 999.00000 ω_{R} = 999.00000

Clade-sites test (Yang's Model C). (df = 3; 7.81 (0.05 level); 11.34 (0.01 level))

Clade-sites test (Yang's Model C) comparing TEKAY to REINA

Model	lnL	Significant	Class 0	Class 1	Class 2
Null 1 (M1a) (np = 46)	-3517.498312		p = 0.63068 ω = 0.15566	p = 0.36932 ω = 1.00000	
Model C (np = 49)	-3444.092199	Yes	p = 0.55513 ω_{TEKAY} = 0.02851 ω_{REINA} = 0.02851	p = 0.00000 ω_{TEKAY} = 1.00000 ω_{REINA} = 1.00000	p = 0.44487 ω_{TEKAY} = 0.17503 ω_{REINA} = 0.05868

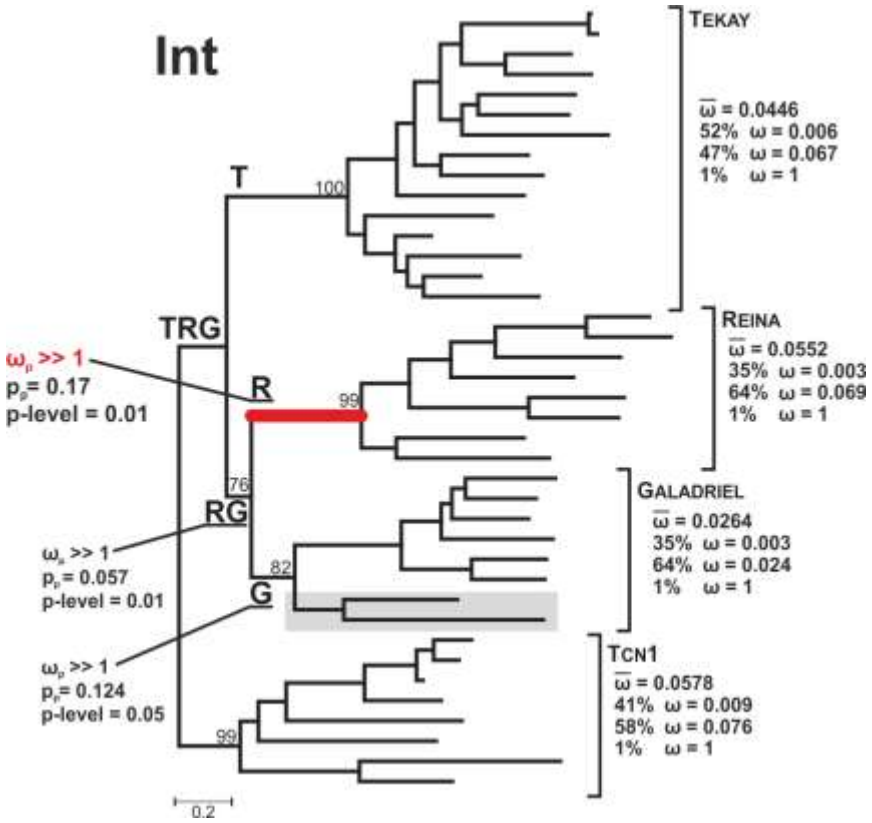
Clade-sites test (Yang's Model C) comparing GALADRIEL to TEKAY/REINA

Model	lnL	Significant	Class 0	Class 1	Class 2
Null 1 (M1a) (np = 58)	-4631.687679		p = 0.96823 ω = 0.07746	p = 0.03177 ω = 1.00000	
Model C (np = 61)	-4567.327157	Yes	p = 0.20856 $\omega_{TEKAY/REINA}$ = 0.02110 $\omega_{GALADRIEL}$ = 0.02110	p = 0.00000 $\omega_{TEKAY/REINA}$ = 1.00000 $\omega_{GALADRIEL}$ = 1.00000	p = 0.79144 $\omega_{TEKAY/REINA}$ = 0.10610 $\omega_{GALADRIEL}$ = 0.11909

Clade-sites test (Yang's Model C) comparing TCN to GALADRIEL/TEKAY/REINA

Model	lnL	Significant	Class 0	Class 1	Class 2
Null 1 (M1a)	-5994.608301		p = 0.96436 ω = 0.07057	p = 0.03564 ω = 1.00000	
Model C (np =80)	-5940.757189	Yes	p = 0.04667 ω_{TCN} = 0.00000 $\omega_{GALADRIEL/TEKAY/REINA}$ = 0.00000	p = 0.03243 ω_{TCN} = 1.00000 $\omega_{GALADRIEL/TEKAY/REINA}$ = 1.00000	p = 0.92091 ω_{TCN} = 0.04987 $\omega_{GALADRIEL/TEKAY/REINA}$ = 0.08886

Analysis of int tree



Branch-site tests.
(2.71 (0.05 level); 5.41 (0.01 level) – Null 2 vs Positive
3.84 (0.05 level); 6.63 (0.01 level) – Null 1 vs Null 2)

Branch-site test for positive selection at the base of T clade.

Model	lnL	Significant	Class 0	Class 1	Class 2a	Class 2b
Null 1 (M1a)	-13195.288420		p = 0.96147 ω = 0.04686	p = 0.03853 ω = 1.00000		
Null 2 (neutral)	-13187.570487	15.435866	p = 0.80915 ω_b = 0.04588 ω_f = 0.04588	p = 0.03326 ω_b = 1.00000 ω_f = 1.00000	p = 0.15136 ω_b = 0.04588 ω_f = 1.00000	p = 0.00622 ω_b = 1.00000 ω_f = 1.00000
Positive Selection	-13186.968977	1.20302	p = 0.83657 ω_b = 0.04723 ω_f = 0.04723	p = 0.03492 ω_b = 1.00000 ω_f = 1.00000	p = 0.12336 ω_b = 0.04723 ω_f = 2.72294	p = 0.00515 ω_b = 1.00000 ω_f = 2.72294

Naive Empirical Bayes (NEB) analysis; positive sites for foreground lineages Prob(w>1):

```
  5 V 0.978*
 22 F 0.529
 28 M 0.534
 43 L 0.573
 87 F 0.941
 89 M 0.858
118 Y 0.998**
121 C 0.977*
124 F 0.968*
127 P 0.933
133 A 0.787
```

Bayes Empirical Bayes (BEB) analysis [73]; positive sites for foreground lineages Prob(w>1):

```
  5 V 0.975*
 28 M 0.505
 43 L 0.551
 87 F 0.933
 89 M 0.842
118 Y 0.998**
121 C 0.975*
124 F 0.964*
127 P 0.920
133 A 0.785
```

Branch-site test for positive selection at the base of R clade.

Model	lnL	Significant	Class 0	Class 1	Class 2a	Class 2b
Null 1 (M1a)	-13195.288420		p = 0.96147 ω = 0.04686	p = 0.03853 ω = 1.00000		
Null 2 (neutral)	-13186.728575	17.11969	p = 0.80964 ω_b = 0.04324 ω_f = 0.04324	p = 0.03186 ω_b = 1.00000 ω_f = 1.00000	p = 0.15250 ω_b = 0.04324 ω_f = 1.00000	p = 0.00600 ω_b = 1.00000 ω_f = 1.00000
Positive Selection	-13181.218118	11.020914	p = 0.79655 ω_b = 0.04839 ω_f = 0.04839	p = 0.03335 ω_b = 1.00000 ω_f = 1.00000	p = 0.16326 ω_b = 0.04839 ω_f = 999.00000	p = 0.00684 ω_b = 1.00000 ω_f = 999.00000

Naive Empirical Bayes (NEB) analysis; positive sites for foreground lineages Prob(w>1):

```
  3 E 0.598
  8 D 0.615
 10 T 0.532
 37 Y 0.959*
 43 L 0.976*
 45 A 1.000**
 46 D 0.751
 55 A 0.998**
 69 S 0.994**
 77 V 0.999**
 80 S 0.586
 85 H 0.536
114 C 0.999**
117 M 0.990*
122 F 0.872
123 T 0.532
124 F 0.748
127 P 0.969*
129 T 0.955*
133 A 0.988*
```

Bayes Empirical Bayes (BEB) analysis [73]; positive sites for foreground lineages Prob(w>1):

```
  1 I 0.525
  2 P 0.533
  3 E 0.822
  4 Q 0.637
  5 V 0.539
  6 W 0.536
  7 D 0.683
  8 D 0.673
  9 V 0.530
 10 T 0.714
 11 M 0.505
 12 D 0.516
 13 F 0.520
 14 I 0.520
 15 T 0.558
 16 G 0.530
 17 L 0.533
```

18 P 0.533
19 L 0.556
20 S 0.534
21 * 0.558
22 F 0.541
23 G 0.530
24 F 0.531
25 T 0.519
26 V 0.558
27 I 0.519
28 M 0.537
29 V 0.525
30 V 0.533
31 V 0.525
32 D 0.516
33 R 0.538
34 L 0.526
35 S 0.532
36 K 0.521
37 Y 0.725
38 A 0.527
39 H 0.523
40 F 0.519
41 M 0.539
42 P 0.533
43 L 0.874
44 K 0.555
45 A 0.998**
46 D 0.803
47 Y 0.526
48 S 0.538
49 N 0.527
50 R 0.706
51 T 0.625
52 V 0.538
53 A 0.527
54 E 0.526
55 A 0.979*
56 F 0.520
57 V 0.566
58 N 0.558
59 Y 0.622
60 V 0.526
61 V 0.526
62 K 0.598
63 L 0.539
64 H 0.523
65 G 0.530
66 M 0.577
67 P 0.533
68 K 0.624
69 S 0.919
70 I 0.520
71 I 0.527
72 S 0.533
73 D 0.516
74 R 0.536
75 D 0.534
76 K 0.623

```
 77 V 0.976*
 78 F 0.520
 79 T 0.540
 80 S 0.629
 81 K 0.535
 82 F 0.520
 83 W 0.535
 84 Q 0.644
 85 H 0.601
 86 L 0.533
 87 F 0.520
 88 Q 0.525
 89 M 0.545
 90 Q 0.540
 91 G 0.534
 92 T 0.530
 93 T 0.522
 94 L 0.534
 95 S 0.571
 96 M 0.561
 97 S 0.525
 98 T 0.528
 99 T 0.528
100 Y 0.530
101 H 0.524
102 P 0.533
103 Q 0.531
104 T 0.528
105 D 0.516
106 G 0.531
107 Q 0.531
108 S 0.528
109 E 0.521
110 A 0.543
111 V 0.540
112 N 0.516
113 K 0.539
114 C 0.986*
115 L 0.540
116 E 0.521
117 M 0.912
118 Y 0.529
119 L 0.533
120 R 0.532
121 C 0.534
122 F 0.821
123 T 0.632
124 F 0.708
125 K 0.521
126 N 0.532
127 P 0.975*
128 K 0.577
129 T 0.932
130 W 0.535
131 F 0.547
132 K 0.551
133 A 0.935
134 L 0.533
135 T 0.533
```

136 W 0.535
137 V 0.528
138 E 0.521
139 L 0.519
140 W 0.714
141 Y 0.529
142 N 0.516

Branch-site test for positive selection at the base of G clade.

Model	lnL	Significant	Class 0	Class 1	Class 2a	Class 2b
Null 1 (M1a)	-13195.288420		p = 0.96147 ω = 0.04686	p = 0.03853 ω = 1.00000		
Null 2 (neutral)	-13191.650894	7.275052	p = 0.85179 ω_b = 0.04515 ω_f = 0.04515	p = 0.03371 ω_b = 1.00000 ω_f = 1.00000	p = 0.11014 ω_b = 0.04515 ω_f = 1.00000	p = 0.00436 ω_b = 1.00000 ω_f = 1.00000
Positive Selection	-13188.845227	5.611334	p = 0.84166 ω_b = 0.04762 ω_f = 0.04762	p = 0.03405 ω_b = 1.00000 ω_f = 1.00000	p = 0.11946 ω_b = 0.04762 ω_f = 999.00000	p = 0.00483 ω_b = 1.00000 ω_f = 999.00000

Naive Empirical Bayes (NEB) analysis; positive sites for foreground lineages Prob(w>1):

```
  8 D 0.634
 35 S 0.919
 43 L 0.761
 46 D 0.677
 57 V 0.559
 69 S 0.614
 77 V 0.715
 80 S 0.593
 84 Q 0.533
113 K 0.988*
114 C 0.669
123 T 0.913
124 F 0.569
125 K 0.685
128 K 0.671
135 T 1.000**
```

Bayes Empirical Bayes (BEB) analysis [73]; positive sites for foreground lineages Prob(w>1):

```
 35 S 0.799
 77 V 0.531
113 K 0.610
123 T 0.537
125 K 0.577
135 T 0.898
```

Branch-site test for positive selection at the base of RG clade.

Model	lnL	Significant	Class 0	Class 1	Class 2a	Class 2b
Null 1 (M1a)	-13195.288420		p = 0.96147 ω = 0.04686	p = 0.03853 ω = 1.00000		
Null 2 (neutral)	-13193.336471	3.903898	p = 0.89858 ω_b = 0.04498 ω_f = 0.04498	p = 0.03528 ω_b = 1.00000 ω_f = 1.00000	p = 0.06364 ω_b = 0.04498 ω_f = 1.00000	p = 0.00250 ω_b = 1.00000 ω_f = 1.00000
Positive Selection	-13189.089754	8.493434	p = 0.90584 ω_b = 0.04717 ω_f = 0.04717	p = 0.03729 ω_b = 1.00000 ω_f = 1.00000	p = 0.05461 ω_b = 0.04717 ω_f = 999.00000	p = 0.00225 ω_b = 1.00000 ω_f = 999.00000

Naive Empirical Bayes (NEB) analysis; positive sites for foreground lineages Prob(w>1):

```
 22 F 0.511
 37 Y 0.837
 80 S 0.999**
128 K 0.543
140 W 0.947
```

Bayes Empirical Bayes (BEB) analysis [73]; positive sites for foreground lineages Prob(w>1):

```
 75 D 0.518
 80 S 0.912
140 W 0.620
```

Branch-sites test for positive selection at the base of TRG clade.

Model	lnL	Significant	Class 0	Class 1	Class 2a	Class 2b
Null 1 (M1a)	-13195.288420		p = 0.96147 ω = 0.04686	p = 0.03853 ω = 1.00000		
Null 2 (neutral)	-13193.759756	3.057328	p = 0.87726 ω_b = 0.04592 ω_f = 0.04592	p = 0.03625 ω_b = 1.00000 ω_f = 1.00000	p = 0.08306 ω_b = 0.04592 ω_f = 1.00000	p = 0.00343 ω_b = 1.00000 ω_f = 1.00000
Positive Selection	-13192.774806	1.9699	p = 0.87443 ω_b = 0.04676 ω_f = 0.04676	p = 0.03702 ω_b = 1.00000 ω_f = 1.00000	p = 0.08495 ω_b = 0.04676 ω_f = 75.85586	p = 0.00360 ω_b = 1.00000 ω_f = 75.85586

Naive Empirical Bayes (NEB) analysis; positive sites for foreground lineages Prob(w>1):

```
8 D 0.945
37 Y 0.843
43 L 0.699
117 M 0.587
126 N 0.584
128 K 0.822
132 K 0.826
140 W 0.677
```

Bayes Empirical Bayes (BEB) analysis [73]; positive sites for foreground lineages Prob(w>1):

```
8 D 0.907
37 Y 0.762
43 L 0.622
117 M 0.532
126 N 0.522
128 K 0.746
132 K 0.758
140 W 0.601
```

Corrections for Multiple Testing

Foreground branch	base of T clade	base of R clade	base of G clade	base of RG clade	base of TRG clade
$2\Delta l$	1.20302	11.020914	5.611334	8.493434	1.9699
$p_{\chi_1^2}$	0.272719	0.000901	0.017845	0.003564	0.160458
Hommel procedure $\alpha = 0.1$	TRUE	FALSE	**FALSE**	FALSE	TRUE
Hommel procedure $\alpha = 0.05$	TRUE	FALSE	TRUE	**FALSE**	TRUE
Hommel procedure $\alpha = 0.01$	TRUE	**FALSE**	TRUE	TRUE	TRUE
$p_{1/2\chi_0^2+1/2\chi_1^2}$	0.13636	0.00045	0.00892	0.00178	0.08023
Hommel procedure $\alpha = 0.1$	TRUE	FALSE	FALSE	FALSE	TRUE
Hommel procedure $\alpha = 0.05$	TRUE	FALSE	**FALSE**	FALSE	TRUE
Hommel procedure $\alpha = 0.01$	TRUE	**FALSE**	TRUE	**FALSE**	TRUE

Clade tests with several branch types (Yang's Model C).

Model	lnL	Significant	Class 0	Class 1	Class 2
Null 1 (M1a) (np=77)	-13195.288420		p = 0.96147 ω = 0.04686	p = 0.03853 ω = 1.00000	
Model C (np=84)	-12812.406941	Yes	p = 0.40931 ω_{ALL} = 0.00947	p = 0.01283 ω_{ALL} = 1.00000	p = 0.57786 $\omega_{TCN, REINA, GALADRIEL, TEKAY}$ = 0.06924 ω_{TRG} = 0.12593 ω_{G} = 0.06454 ω_{RG} = 0.00010 ω_{T} = 0.06671 ω_{R} = 999.00000

Clade-sites test (Yang's Model C). (df = 3; 7.81 (0.05 level); 11.34 (0.01 level))

Clade-sites test (Yang's Model C) comparing REINA to GALADRIEL

Model	lnL	Significant	Class 0	Class 1	Class 2
Null 1 (M1a)	-5856.502483		p = 0.98481 ω = 0.01125	p = 0.01519 ω = 1.00000	
Model C (np = 36)	-5699.488755	Yes	p = 0.35473 $\omega_{GALADRIEL}$ = 0.00302 ω_{REINA} = 0.00302	p = 0.00724 $\omega_{GALADRIEL}$ = 1.00000 ω_{REINA} = 1.00000	p = 0.63803 $\omega_{GALADRIEL}$ = 0.02378 ω_{REINA} = 0.06898

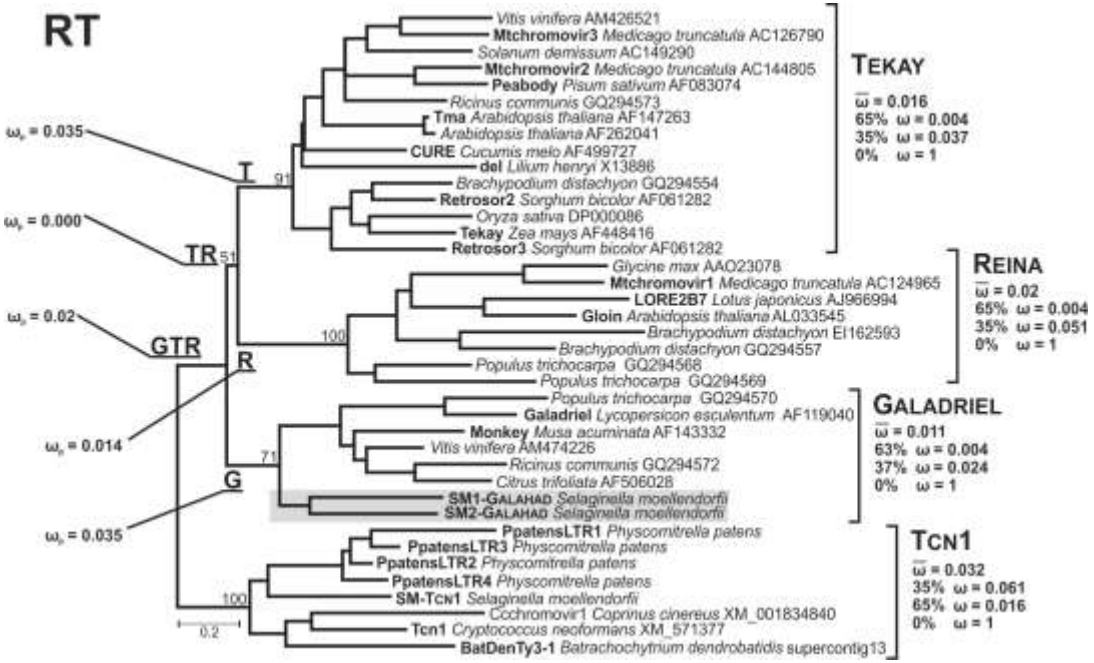
Clade-sites test (Yang's Model C) comparing TEKAY to REINA/GALADRIEL

Model	lnL	Significant	Class 0	Class 1	Class 2
Null 1 (M1a)	-10538.466732		p = 0.97776 ω = 0.02219	p = 0.02224 ω = 1.00000	
Model C (np = 65)	-10221.715021	Yes	p = 0.51611 $\omega_{REINA/GALADRIEL}$ = 0.00616 ω_{TEKAY} = 0.00616	p = 0.00902 $\omega_{REINA/GALADRIEL}$ = 1.00000 ω_{TEKAY} = 1.00000	p = 0.47488 $\omega_{REINA/GALADRIEL}$ = 0.02813 ω_{TEKAY} = 0.06715

Clade-sites test (Yang's Model C) comparing TCN to TEKAY/REINA/GALADRIEL

Model	lnL	Significant	Class 0	Class 1	Class 2
Null 1 (M1a)	-13195.288420		p = 0.96147 ω = 0.04686	p = 0.03853 ω = 1.00000	
Model C (np =80)	-12819.241300	Yes	p = 0.41059 ω_{TCN} = 0.00934 $\omega_{TEKAY/REINA/GALADRIEL}$ = 0.00934	p = 0.01281 ω_{TCN} = 1.00000 $\omega_{TEKAY/REINA/GALADRIEL}$ = 1.00000	p = 0.57660 ω_{TCN} = 0.07643 $\omega_{TEKAY/REINA/GALADRIEL}$ = 0.06668

Analysis of rt tree



Clade tests with several branch types (Yang's Model C).

Model	lnL	Significant	Class 0	Class 1	Class 2
Null 1 (M1a) (np=77)	-12681.467466		p = 0.96420 ω = 0.02376	p = 0.03580 ω = 1.00000	
Model C (np=84)	-12301.725739	Yes	p = 0.64927 ω_{ALL} = 0.00898	p = 0.00000 ω_{ALL} = 1.00000	p = 0.35073 $\omega_{TCN, REINA, GALADRIEL, TEKAY}$ = 0.06463 ω_{TR} = 0.00010 ω_{G} = 0.03462 ω_{GTR} = 0.02032 ω_{T} = 0.03451 ω_{R} = 0.01397

Clade-sites test (Yang's Model C). (df = 3; 7.81 (0.05 level); 11.34 (0.01 level))

Clade-sites test (Yang's Model C) comparing TEKAY to REINA

Model	lnL	Significant	Class 0	Class 1	Class 2
Null 1 (M1a) (np = 46)	-7442.407249		p = 0.93598 ω = 0.00893	p = 0.06402 ω = 1.00000	
Model C (np = 49)	-7203.037533	Yes	p = 0.64828 ω_{TEKAY} = 0.00447 ω_{REINA} = 0.00447	p = 0.00000 ω_{TEKAY} = 1.00000 ω_{REINA} = 1.00000	p = 0.35172 ω_{TEKAY} = 0.03678 ω_{REINA} = 0.05055

Clade-sites test (Yang's Model C) comparing GALADRIEL to TEKAY/REINA

Model	lnL	Significant	Class 0	Class 1	Class 2
Null 1 (M1a) (np = 62)	-10080.622888		p = 0.97356 ω = 0.01050	p = 0.02644 ω = 1.00000	
Model C (np = 65)	-9754.644094	Yes	p = 0.62908 $\omega_{TEKAY/REINA}$ = 0.00432 $\omega_{GALADRIEL}$ = 0.00432	p = 0.00000 $\omega_{TEKAY/REINA}$ = 1.00000 $\omega_{GALADRIEL}$ = 1.00000	p = 0.37092 $\omega_{TEKAY/REINA}$ = 0.03791 $\omega_{GALADRIEL}$ = 0.02403

Clade-sites test (Yang's Model C) comparing TCN to GALADRIEL/TEKAY/REINA

Model	lnL	Significant	Class 0	Class 1	Class 2
Null 1 (M1a)	-12681.467466		p = 0.96420 ω = 0.02376	p = 0.03580 ω = 1.00000	
Model C (np =80)	-12305.690695	Yes	p = 0.34595 ω_{TCN} = 0.06136 $\omega_{GALADRIEL/TEKAY/REINA}$ = 0.06136	p = 0.00000 ω_{TCN} = 1.00000 $\omega_{GALADRIEL/TEKAY/REINA}$ = 1.00000	p = 0.65405 ω_{TCN} = 0.01572 $\omega_{GALADRIEL/TEKAY/REINA}$ = 0.00835