Supplementary Information

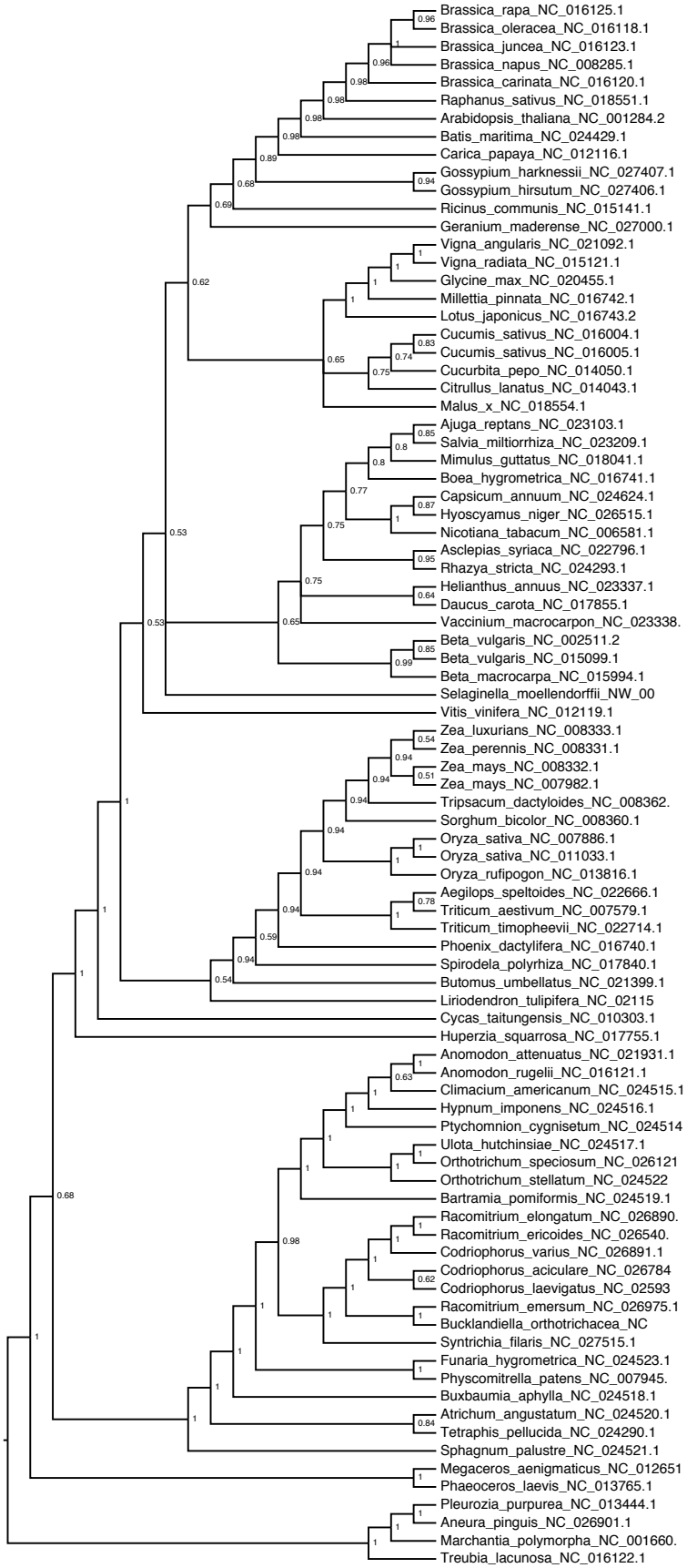
Homology-aware phylogenomics at gigabase scales

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SUPPLEMENTARY TABLE 1: The five longest inter-chromosomal transfers identified with runs of *k*-mer blocks in the *Oryza* data set

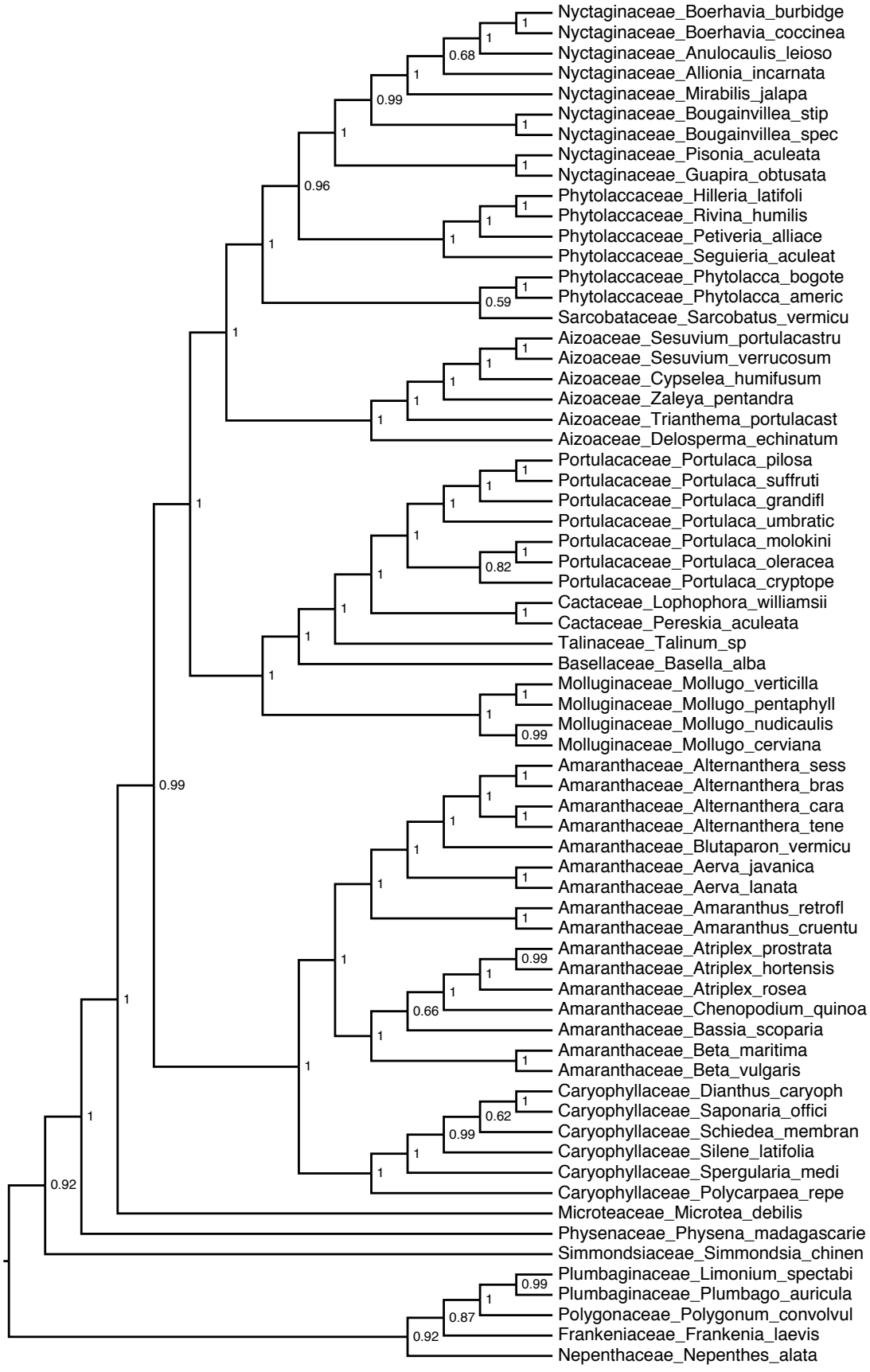
Start coordinate of *k*-mer (in *Leersia*)	#contiguous *k*-mer blocks	Span (nt in *Leersia*)	Taxon and chromosome with transferred run of *k*-mer blocks	All other taxa have run of blocks on chromosome
7456994	23	253183	*O. nivara*: 5	2
5669440	11	280899	*O. glumipatula*: 5	7
1913131	31	308921	*O. nivara*: 10	6
22247671	84	360939	*O. nivara*: 6	2
12107651	87	414864	*O. meridionalis*: 7	9


Brassica_rapa_NC_016125.1
Brassica_oleracea_NC_016118.1
Brassica_juncea_NC_016123.1
Brassica_napus_NC_008285.1
Brassica_carinata_NC_016120.1
Raphanus_sativus_NC_018551.1
Arabidopsis_thaliana_NC_001284.2
Batis_maritima_NC_024429.1
Carica_papaya_NC_012116.1
Gossypium_harknessii_NC_027407.1
Gossypium_hirsutum_NC_027406.1
Ricinus_communis_NC_015141.1
Geranium_maderense_NC_027000.1
Vigna_angularis_NC_021092.1
Vigna_radiata_NC_015121.1
Glycine_max_NC_020455.1
Millettia_pinnata_NC_016742.1
Lotus_japonicus_NC_016743.2
Cucumis_sativus_NC_016004.1
Cucumis_sativus_NC_016005.1
Cucurbita_pepo_NC_014050.1
Citrullus_lanatus_NC_014043.1
Malus_x_NC_018554.1
Ajuga_reptans_NC_023103.1
Salvia_miltiorrhiza_NC_023209.1
Mimulus_guttatus_NC_018041.1
Boea_hygrometrica_NC_016741.1
Capsicum_annuum_NC_024624.1
Hyoscyamus_niger_NC_026515.1
Nicotiana_tabacum_NC_006581.1
Asclepias_syriaca_NC_022796.1
Rhazya_stricta_NC_024293.1
Helianthus_annuus_NC_023337.1
Daucus_carota_NC_017855.1
Vaccinium_macrocarpon_NC_023338.
Beta_vulgaris_NC_002511.2
Beta_vulgaris_NC_015099.1
Beta_macrocarpa_NC_015994.1
Selaginella_moellendorffii_NW_00
Vitis_vinifera_NC_012119.1
Zea_luxurians_NC_008333.1
Zea_perennis_NC_008331.1
Zea_mays_NC_008332.1
Zea_mays_NC_007982.1
Tripsacum_dactyloides_NC_008362.
Sorghum_bicolor_NC_008360.1
Oryza_sativa_NC_007886.1
Oryza_sativa_NC_011033.1
Oryza_rufipogon_NC_013816.1
Aegilops_speltoides_NC_022666.1
Triticum_aestivum_NC_007579.1
Triticum_timopheevii_NC_022714.1
Phoenix_dactylifera_NC_016740.1
Spirodela_polyrhiza_NC_017840.1
Butomus_umbellatus_NC_021399.1
Liriodendron_tulipifera_NC_02115
Cycas_taitungensis_NC_010303.1
Huperzia_squarrosa_NC_017755.1
Anomodon_attenuatus_NC_021931.1
Anomodon_rugelii_NC_016121.1
Climacium_americanum_NC_024515.1
Hypnum_imponens_NC_024516.1
Ptychomnion_cygnisetum_NC_024514
Ulota_hutchinsiae_NC_024517.1
Orthotrichum_speciosum_NC_026121
Orthotrichum_stellatum_NC_024522
Bartramia_pomiformis_NC_024519.1
Racomitrium_elongatum_NC_026890.
Racomitrium_ericoides_NC_026540.
Codriophorus_varius_NC_026891.1
Codriophorus_aciculare_NC_026784
Codriophorus_laevigatus_NC_02593
Racomitrium_emersum_NC_026975.1
Bucklandiella_orthotrichacea_NC
Syntrichia_filaris_NC_027515.1
Funaria_hygrometrica_NC_024523.1
Physcomitrella_patens_NC_007945.
Buxbaumia_aphylla_NC_024518.1
Atrichum_angustatum_NC_024520.1
Tetraphis_pellucida_NC_024290.1
Sphagnum_palustre_NC_024521.1
Megaceros_aenigmaticus_NC_012651
Phaeoceros_laevis_NC_013765.1
Pleurozia_purpurea_NC_013444.1
Aneura_pinguis_NC_026901.1
Marchantia_polymorpha_NC_001660.
Treubia_lacunosa_NC_016122.1

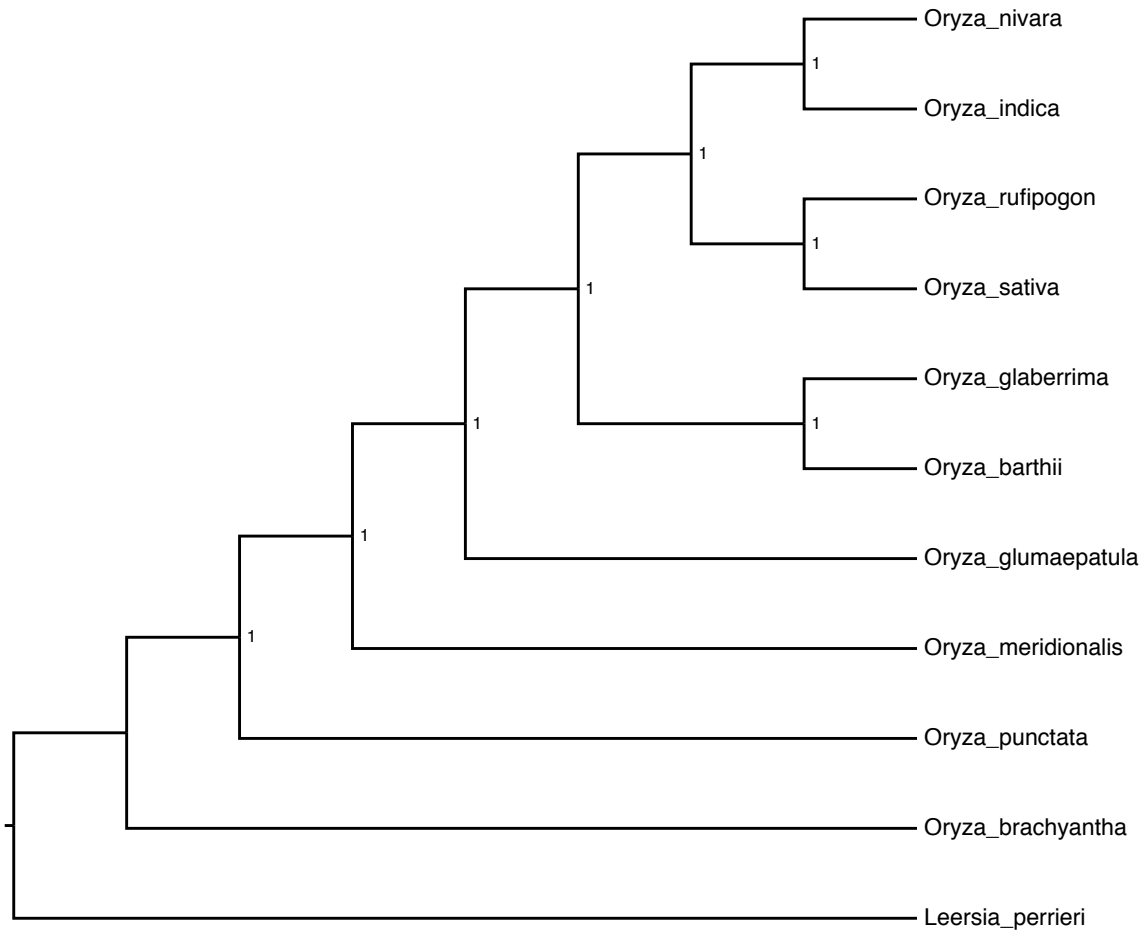
SUPPLEMENTARY FIGURE 1. Land plant mitochondrial genome tree. Tree is bootstrap majority rule tree constructed from 100 replicate maximum likelihood runs. Bootstrap support values are indicated at each clade above 50%.



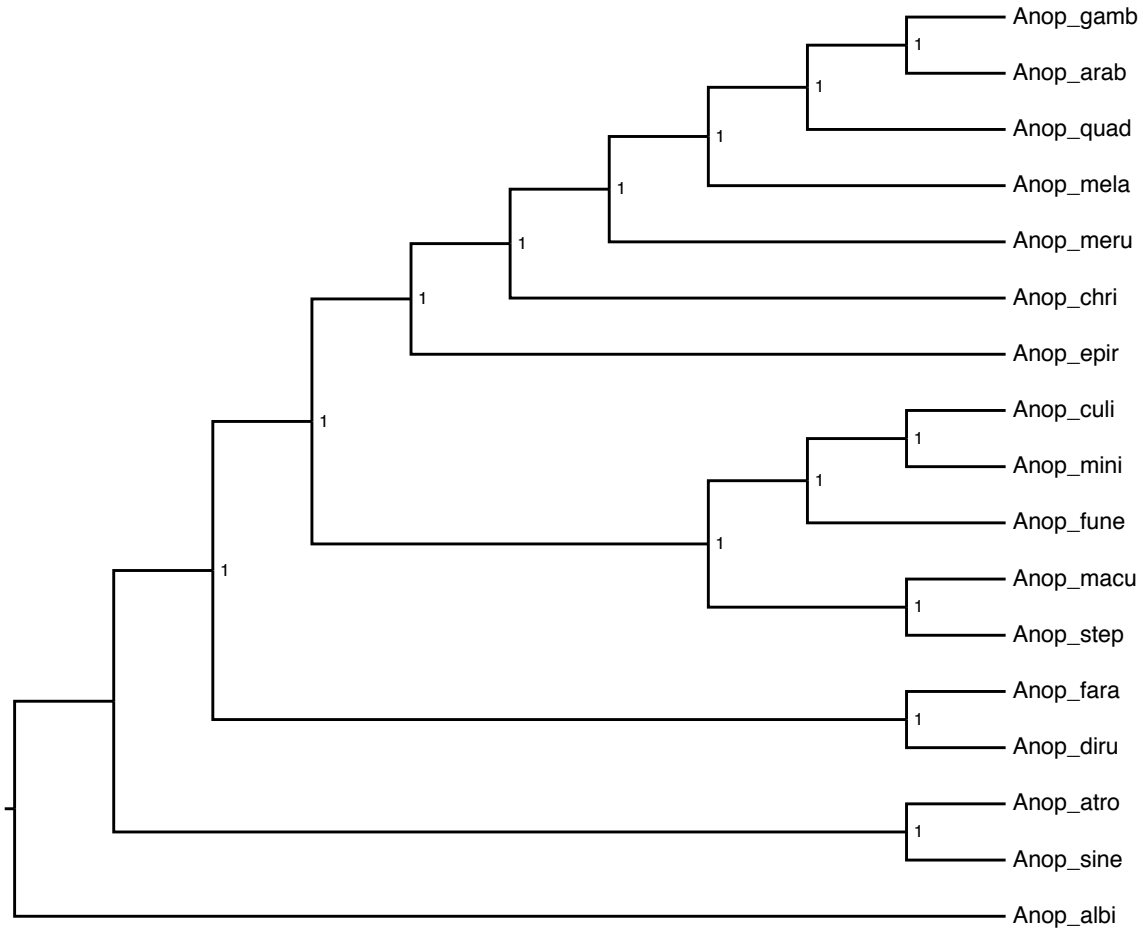
SUPPLEMENTARY FIGURE 2. Angiosperm plastid genome tree. Tree is bootstrap majority rule tree constructed from 100 replicate maximum likelihood runs. Bootstrap support values are indicated at each clade above 50%.


Nyctaginaceae_Boerhavia_burbidge
Nyctaginaceae_Boerhavia_coccinea
Nyctaginaceae_Anulocaulis_leioso
Nyctaginaceae_Allionia_incarnata
Nyctaginaceae_Mirabilis_jalapa
Nyctaginaceae_Bougainvillea_stip
Nyctaginaceae_Bougainvillea_spec
Nyctaginaceae_Pisonia_aculeata
Nyctaginaceae_Guapira_obtusata
Phytolaccaceae_Hilleria_latifoli
Phytolaccaceae_Rivina_humilis
Phytolaccaceae_Petiveria_alliace
Phytolaccaceae_Seguieria_aculeat
Phytolaccaceae_Phytolacca_bogote
Phytolaccaceae_Phytolacca_americ
Sarcobataceae_Sarcobatus_vermicu
Aizoaceae_Sesuvium_portulacastru
Aizoaceae_Sesuvium_verrucosum
Aizoaceae_Cypselea_humifusum
Aizoaceae_Zaleya_pentandra
Aizoaceae_Trianthema_portulacast
Aizoaceae_Delosperma_echinatum
Portulacaceae_Portulaca_pilosa
Portulacaceae_Portulaca_suffruti
Portulacaceae_Portulaca_grandifl
Portulacaceae_Portulaca_umbratic
Portulacaceae_Portulaca_molokini
Portulacaceae_Portulaca_oleracea
Portulacaceae_Portulaca_cryptope
Cactaceae_Lophophora_williamsii
Cactaceae_Pereskia_aculeata
Talinaceae_Talinum_sp
Basellaceae_Basella_alba
Molluginaceae_Mollugo_verticilla
Molluginaceae_Mollugo_pentaphyll
Molluginaceae_Mollugo_nudicaulis
Molluginaceae_Mollugo_cerviana
Amaranthaceae_Alternanthera_sess
Amaranthaceae_Alternanthera_bras
Amaranthaceae_Alternanthera_cara
Amaranthaceae_Alternanthera_tene
Amaranthaceae_Blutaparon_vermicu
Amaranthaceae_Aerva_javanica
Amaranthaceae_Aerva_lanata
Amaranthaceae_Amaranthus_retrofl
Amaranthaceae_Amaranthus_cruentu
Amaranthaceae_Atriplex_prostrata
Amaranthaceae_Atriplex_hortensis
Amaranthaceae_Atriplex_rosea
Amaranthaceae_Chenopodium_quinoa
Amaranthaceae_Bassia_scoparia
Amaranthaceae_Beta_maritima
Amaranthaceae_Beta_vulgaris
Caryophyllaceae_Dianthus_caryoph
Caryophyllaceae_Saponaria_offici
Caryophyllaceae_Schiedea_membran
Caryophyllaceae_Silene_latifolia
Caryophyllaceae_Spergularia_medi
Caryophyllaceae_Polycarpaea_repe
Microteaceae_Microtea_debilis
Physenaceae_Physena_madagascarie
Simmondsiaceae_Simmondsia_chinen
Plumbaginaceae_Limonium_spectabi
Plumbaginaceae_Plumbago_auricula
Polygonaceae_Polygonum_convolvul
Frankeniaceae_Frankenia_laevis
Nepenthaceae_Nepenthes_alata

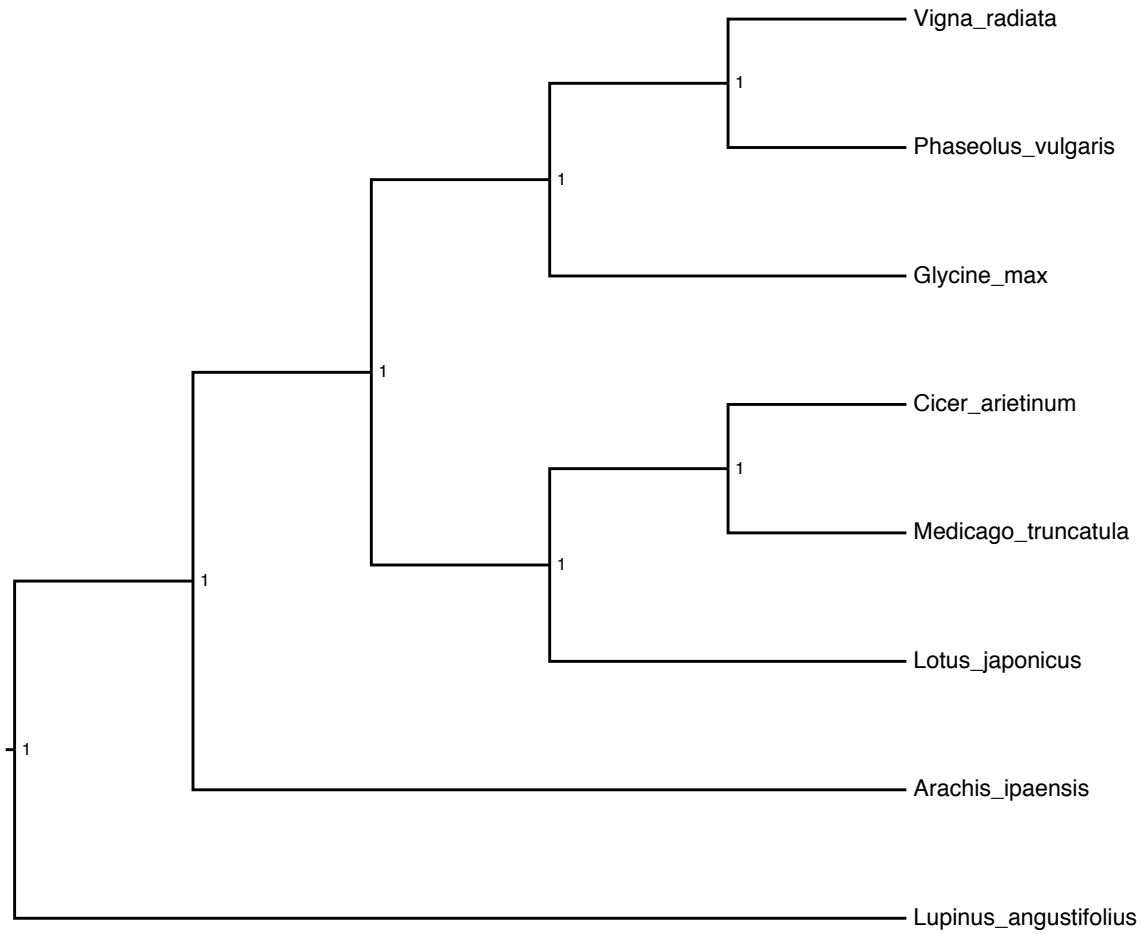
SUPPLEMENTARY FIGURE 3. Caryophyllales transcriptome tree. Tree is bootstrap majority rule tree constructed from 100 replicate maximum likelihood runs. Bootstrap support values are indicated at each clade above 50%.



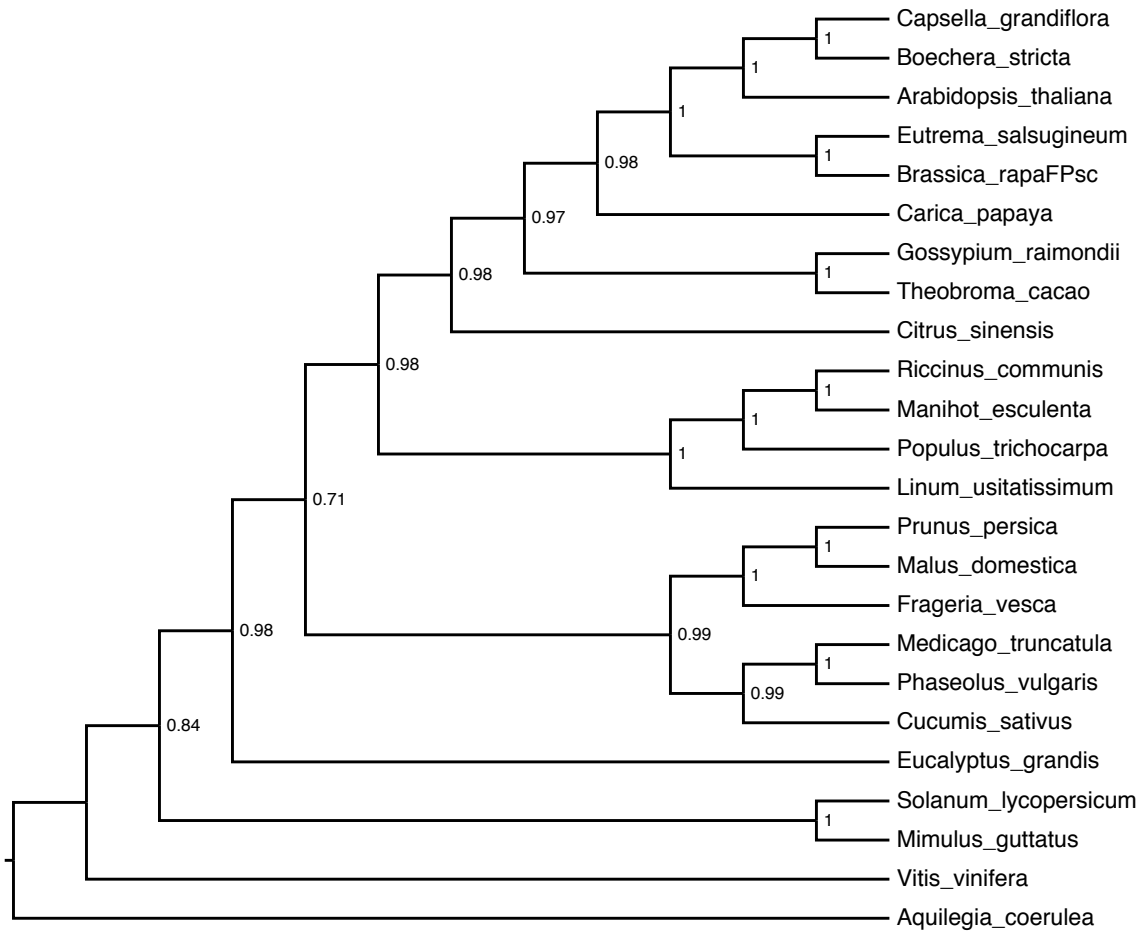
SUPPLEMENTARY FIGURE 4. *Oryza* whole genome tree. Tree is bootstrap majority rule tree constructed from 100 replicate maximum likelihood runs. Bootstrap support values are indicated at each clade above 50%.



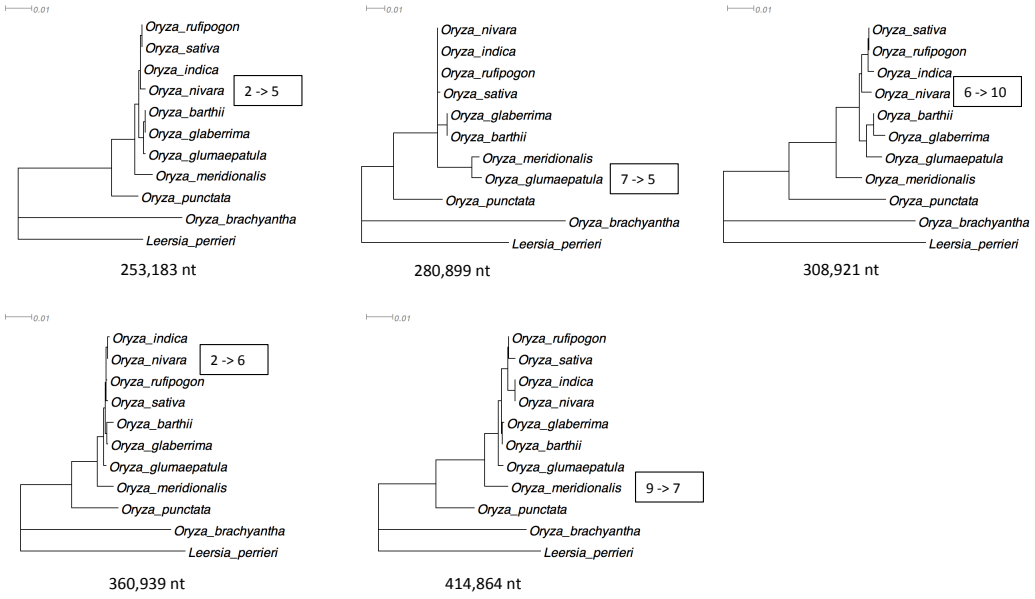
SUPPLEMENTARY FIGURE 5. *Anopheles* whole genome tree. Tree is bootstrap majority rule tree constructed from 100 replicate maximum likelihood runs. Bootstrap support values are indicated at each clade above 50%.



SUPPLEMENTARY FIGURE 6. Fabaceae whole genome tree. Tree is bootstrap majority rule tree constructed from 100 replicate maximum likelihood runs. Bootstrap support values are indicated at each clade above 50%.



SUPPLEMENTARY FIGURE 7. Eudicot whole genome tree. Tree is bootstrap majority rule tree constructed from 100 replicate maximum likelihood runs. Bootstrap support values are indicated at each clade above 50%.



SUPPLEMENTARY FIGURE 8. Phylogenies of orthologous regions involving 5 inter-chromosomal transfers. Size of regions is indicated underneath each panel, and chromosome source and destination is indicated next to taxon name (each transfer occurs in only a single taxon in these instances). Scale bar is in units of substitutions per site.