

Table S1. Plant genomes analyzed in this study.

Plant species	Depository	Literature References
<i>Actinidia chinensis</i>	NCBI Genome	
<i>Aegilops tauschii</i>	Phytozome	
<i>Aethionema arabicum</i>	Brassica Database	
<i>Amaranthus hypochondriacus</i>	Phytozome	
<i>Amborella trichopoda</i>	Phytozome	
<i>Ammopiptanthus nanus</i>		(Gao et al., 2018)
<i>Anacardium occidentale</i>	Phytozome	
<i>Ananas comosus</i>	Phytozome	
<i>Apostasia shenzhenica</i>		(Zhang et al., 2017)
<i>Antirrhinum majus</i>		(Li et al., 2019)
<i>Aquilegia coerulea</i>	Phytozome	
<i>Arabidopsis halleri</i>	Phytozome	
<i>Arabidopsis lyrata</i>	Phytozome	
<i>Arabidopsis thaliana</i>	Phytozome	
<i>Arachis duranensis</i>		(Bertioli et al., 2015)
<i>Arachis ipaensis</i>		(Bertioli et al., 2015)
<i>Arachis monticola</i>		(Yin et al., 2018)
<i>Artemisia annua</i>		(Lin et al., 2017)
<i>Artocarpus camansi</i>		(Gardner et al., 2016)
<i>Asparagus officinalis</i>	Phytozome	
<i>Atalantia buxifolia</i>		(Wang et al., 2017)
<i>Avicennia marina</i>		http://evolution.sysu.edu.cn/Sequences.html
<i>Azolla filiculoides</i>		(Li et al., 2018)
<i>Barbarea vulgaris</i>		(Byrne et al., 2017)
<i>Beta vulgaris</i>	Phytozome	
<i>Dorcoceras hygrometricum</i>		(Xiao et al., 2015)
<i>Bombax ceiba</i>		(Gao et al., 2018)
<i>Boechera retrofracta</i>		(Kliver et al., 2018)
<i>Boechera stricta</i>	Phytozome	
<i>Boehmeria nivea</i>		(Luan et al., 2018)
<i>Brachypodium distachyon</i>	Phytozome	
<i>Brachypodium hybridum</i>	Phytozome	
<i>Brachypodium stacei</i>	Phytozome	
<i>Brachypodium sylvaticum</i>	Phytozome	
<i>Brassica napus</i>	Brassica Database	

<i>Brassica oleracea</i>	Brassica Database	
<i>Brassica rapa</i>	Brassica Database	
<i>Cajanus cajan</i>		(Varshney et al., 2012)
<i>Calamus jenkinsianus</i>		(Zhao et al., 2018)
<i>Calamus simplicifolius</i>		(Zhao et al., 2018)
<i>Calotropis gigantea</i>		(Hoopes et al., 2018)
<i>Camelina sativa</i>	Brassica Database	
<i>Camellia sinensis</i>		(Wei et al., 2018)
<i>Camptotheca acuminata</i>		(Zhao et al., 2017)
<i>Cannabis sativa</i>		(van Bakel et al., 2011)
<i>Capsella grandiflora</i>		(Slotte et al., 2013)
<i>Capsella rubella</i>	Brassica Database	
<i>Capsicum annuum</i>		(Kim et al., 2014)
<i>Capsicum baccatum</i>		(Kim et al., 2017)
<i>Capsicum chinense</i>		(Kim et al., 2017)
<i>Cardamine hirsuta</i>		(Gan et al., 2016)
<i>Carica papaya</i>	Phytozome	
<i>Castanea mollissima</i>	HWG	
<i>Catharanthus roseus</i>		(Kellner et al., 2015)
<i>Cephalotus follicularis</i>		(Fukushima et al., 2017)
<i>Chenopodium quinoa</i>	Phytozome	
<i>Chrysanthemum indicum</i>		(Song et al., 2018)
<i>Cicer arietinum</i>	Phytozome	
<i>Cicer reticulatum</i>		(Gupta et al., 2016)
<i>Cinnamomum micranthum</i>	NCBI Genome	
<i>Citrullus lanatus</i>		(Guo et al., 2013)
<i>Citrus clementina</i>	Phytozome	
<i>Citrus maxima</i>	Citrus Genome Database	
<i>Citrus cavaleriei</i>	Citrus Genome Database	
<i>Citrus medica</i>	Citrus Genome Database	
<i>Citrus reticulata</i>		(Wang et al., 2018)
<i>Citrus sinensis</i>	Phytozome	
<i>Citrus unshiu</i>		(Shimizu et al., 2017)
<i>Cocos nucifera</i>		(Xiao et al., 2017)
<i>Coffea arabica</i>	NCBI Genome	
<i>Coffea canephora</i>	Phytozome	
<i>Corchorus capsularis</i>	Phytozome	

<i>Corchorus olitorius</i>		(Sarkar et al., 2017)
<i>Cucumis melo</i>	CuGenDB	
<i>Cucumis sativus</i>	Phytozome	
<i>Cucurbita pepo</i>	CuGenDB	
<i>Cynara cardunculus</i>		(Scaglione et al., 2016)
<i>Daucus carota</i>	Phytozome	
<i>Dendrobium officinale</i>		(Yan et al., 2015)
<i>Dianthus caryophyllus</i>		(Yagi et al., 2013)
<i>Dichantheium oligosanthes</i>		(Studer et al., 2016)
<i>Dioscorea rotundata</i>	Phytozome	
<i>Durio zibethinus</i>		(Teh et al., 2017)
<i>Echinochloa crus-galli</i>		(Guo et al., 2017)
<i>Elaeis guineensis</i>		(Jin et al., 2016)
<i>Eragrostis tef</i>		(Cannarozzi et al., 2014)
<i>Erigeron breviscapus</i>		(Yang et al., 2017)
<i>Eschscholzia californica</i>		(Hori et al., 2017)
<i>Eucalyptus camaldulensis</i>	NCBI Genome	
<i>Eucalyptus grandis</i>	Phytozome	
<i>Eutrema salsugineum</i>	Brassica Database	
<i>Fagopyrum esculentum</i>	NCBI Genome	
<i>Fagopyrum tataricum</i>	NCBI Genome	
<i>Fagus sylvatica</i>	NCBI Genome	
<i>Faidherbia albida</i>		(Chang et al., 2018)
<i>Fragaria vesca</i>	Phytozome	
<i>Fraxinus excelsior</i>	NCBI Genome	
<i>Genlisea aurea</i>	NCBI Genome	
<i>Ginkgo biloba</i>		(Guan et al., 2016)
<i>Glycine max</i>	Phytozome	
<i>Glycine soja</i>		(Qi et al., 2014)
<i>Glycyrrhiza uralensis</i>		(Mochida et al., 2017)
<i>Gnetum montanum</i>		(Wan et al., 2018)
<i>Gossypium arboreum</i>	NCBI Genome	
<i>Gossypium barbadense</i>	NCBI Genome	
<i>Gossypium hirsutum</i>	Phytozome	
<i>Gossypium raimondii</i>	Phytozome	
<i>Handroanthus impetiginosus</i>	NCBI Genome	
<i>Helianthus annuus</i>	Phytozome	

<i>Hevea brasiliensis</i>	NCBI Genome	
<i>Hordeum vulgare</i>	Phytozome	
<i>Humulus lupulus</i>	NCBI Genome	
<i>Ipomoea batatas</i>	NCBI Genome	
<i>Ipomoea nil</i>	NCBI Genome	
<i>Ipomoea trifida</i>	NCBI Genome	
<i>Jatropha curcas</i>	NCBI Genome	
<i>Juglans regia</i>	NCBI Genome	
<i>Kalanchoe fedtschenkoi</i>	Phytozome	
<i>Kalanchoe laxiflora</i>	Phytozome	
<i>Lablab purpureus</i>		(Chang et al., 2018)
<i>Lactuca sativa</i>	Phytozome	
<i>Lagenaria siceraria</i>	CuGenDB	
<i>Leavenworthia alabamica</i>	Brassica Database	
<i>Leersia perrieri</i>	Phytozome	
<i>Linum usitatissimum</i>	Phytozome	
<i>Liriodendron chinense</i>	NCBI Genome	
<i>Lolium perenne</i>	NCBI Genome	
<i>Lotus japonicus</i>	Phytozome	
<i>Lupinus angustifolius</i>	Phytozome	
<i>Macleaya cordata</i>	NCBI Genome	
<i>Malania oleifera</i>		(Xu et al., 2019)
<i>Malus domestica</i>	Phytozome	
<i>Manihot esculenta</i>	Phytozome	
<i>Marchantia polymorpha</i>	Phytozome	
<i>Medicago truncatula</i>	Phytozome	
<i>Erythranthe guttata</i>	NCBI Genome	
<i>Miscanthus sinensis</i>	Phytozome	
<i>Momordica charantia</i>	NCBI Genome	
<i>Moringa oleifera</i>		(Chang et al., 2018)
<i>Morus notabilis</i>	NCBI Genome	
<i>Musa itinerans</i>	NCBI Genome	
<i>Musa acuminata</i>	Phytozome	
<i>Musa balbisiana</i>		(Davey et al., 2013)
<i>Musa schizocarpa</i>	NCBI Genome	
<i>Nelumbo nucifera</i>	NCBI Genome	
<i>Nicotiana attenuata</i>	Phytozome	
<i>Nicotiana benthamiana</i>	NCBI Genome	
<i>Nicotiana obtusifolia</i>	NCBI Genome	

<i>Nicotiana sylvestris</i>	NCBI Genome	
<i>Nicotiana tabacum</i>	NCBI Genome	
<i>Nicotiana tomentosiformis</i>	NCBI Genome	
<i>Ocimum tenuiflorum</i>	NCBI Genome	
<i>Olea europaea</i>	Phytozome	
<i>Oropetium thomaeum</i>	Phytozome	
<i>Oryza barthii</i>	Phytozome	
<i>Oryza brachyantha</i>	Phytozome	
<i>Oryza glaberrima</i>	Phytozome	
<i>Oryza longistaminata</i>	Phytozome	
<i>Oryza meridionalis</i>	Phytozome	
<i>Oryza sativa f. spontanea</i>	Phytozome	
<i>Oryza meyeriana var. granulata</i>		(Wu et al., 2018)
<i>Oryza punctata</i>	Phytozome	
<i>Oryza rufipogon</i>	Phytozome	
<i>Oryza sativa</i>	Phytozome	
<i>Panax ginseng</i>		(Kim et al., 2018)
<i>Panicum hallii</i>	Phytozome	
<i>Panicum virgatum</i>	Phytozome	
<i>Parasponia andersonii</i>	NCBI Genome	
<i>Cenchrus americanus</i>	NCBI Genome	
<i>Petunia axillaris</i>		(Bombarely et al., 2016)
<i>Petunia integrifolia subsp. inflata</i>		(Bombarely et al., 2016)
<i>Phalaenopsis aphrodite</i>	NCBI Genome	
<i>Phalaenopsis equestris</i>	NCBI Genome	
<i>Phaseolus vulgaris</i>	Phytozome	
<i>Phoenix dactylifera</i>	NCBI Genome	
<i>Phyllostachys edulis</i>		(Fei et al., 2018)
<i>Physcomitrella patens</i>	Phytozome	
<i>Picea abies</i>	NCBI Genome	
<i>Pinus lambertiana</i>	NCBI Genome	
<i>Pinus taeda</i>	NCBI Genome	
<i>Pogostemon cablin</i>	NCBI Genome	
<i>Populus deltoides</i>	Phytozome	
<i>Populus euphratica</i>	NCBI Genome	
<i>Populus pruinosa</i>		(Wang et al., 2017)
<i>Populus tremula</i>		(Lin et al., 2018)

<i>Populus tremuloides</i>		(Lin et al., 2018)
<i>Populus trichocarpa</i>	Phytozome	
<i>Potentilla micrantha</i>		(Giongo et al., 2017)
<i>Primula veris</i>	NCBI Genome	
<i>Primula vulgaris</i>	NCBI Genome	
<i>Prunus avium</i>	NCBI Genome	
<i>Prunus mume</i>	NCBI Genome	
<i>Prunus persica</i>	Phytozome	
<i>Pseudotsuga menziesii</i>	NCBI Genome	
<i>Punica granatum</i>	NCBI Genome	
<i>Pyrus x bretschneideri</i>	NCBI Genome	
<i>Pyrus communis</i>		(Chagné et al., 2014)
<i>Quercus lobata</i>	NCBI Genome	
<i>Quercus robur</i>	NCBI Genome	
<i>Quercus suber</i>	NCBI Genome	
<i>Raphanus raphanistrum</i>	NCBI Genome	
<i>Raphanus sativus</i>	NCBI Genome	
<i>Rhizophora apiculata</i>		http://evolution.sysu.edu.cn/Sequences.html
<i>Rhododendron delavayi</i>		(Yan et al., 2017)
<i>Ricinus communis</i>	Phytozome	
<i>Rosa chinensis</i>	NCBI Genome	
<i>Rosa multiflora</i>	NCBI Genome	
<i>Rubus occidentalis</i>		(Wai et al., 2018)
<i>Saccharum spontaneum</i>	NCBI Genome	
<i>Salix purpurea</i>	Phytozome	
<i>Salvia miltiorrhiza</i>		(Zhang et al., 2015)
<i>Salvia splendens</i>		(Dong et al., 2018)
<i>Salvinia cucullata</i>		(Li et al., 2018)
<i>Schrenkiella parvula</i>	Brassica Database	
<i>Sclerocarya birrea</i>		(Chang et al., 2018)
<i>Secale cereale</i>	NCBI Genome	
<i>Selaginella moellendorffii</i>	Phytozome	
<i>Sesamum indicum</i>	NCBI Genome	
<i>Setaria italica</i>	Phytozome	
<i>Setaria viridis</i>	Phytozome	
<i>Siraitia grosvenorii</i>		(Xia et al., 2018)
<i>Sisymbrium irio</i>	Brassica Database	
<i>Solanum lycopersicum</i>	Phytozome	
<i>Solanum melongena</i>	NCBI Genome	

<i>Solanum pennellii</i>	NCBI Genome	
<i>Solanum pimpinellifolium</i>	NCBI Genome	
<i>Solanum tuberosum</i>	Phytozome	
<i>Sonneratia alba</i>		http://evolution.sysu.edu.cn/Sequences.html
<i>Sonneratia caseolaris</i>		http://evolution.sysu.edu.cn/Sequences.html
<i>Sorghum bicolor</i>	Phytozome	
<i>Sphagnum fallax</i>	Phytozome	
<i>Spinacia oleracea</i>	NCBI Genome	
<i>Spirodela polyrhiza</i>	Phytozome	
<i>Taraxacum kok-saghyz</i>		(Lin et al., 2017)
<i>Tarenaya hassleriana</i>	NCBI Genome	
<i>Tectona grandis</i>		(Zhao et al., 2019)
<i>Theobroma cacao</i>	Phytozome	
<i>Thinopyrum intermedium</i>	Phytozome	
<i>Thlaspi arvense</i>		(Dorn et al., 2015)
<i>Trema orientale</i>		(van Velzen et al., 2018)
<i>Trifolium pratense</i>	Phytozome	
<i>Trifolium subterraneum</i>		(Hirakawa et al., 2016)
<i>Triticum aestivum</i>	Phytozome	
<i>Triticum turgidum</i>		(Avni et al., 2017)
<i>Triticum urartu</i>	Phytozome	
<i>Utricularia gibba</i>		(Ibarra-Laclette et al., 2013)
<i>Vaccinium corymbosum</i>		(Gupta et al., 2015)
<i>Vigna angularis</i>		(Kang et al., 2015)
<i>Vigna radiata</i>		(Kang et al., 2014)
<i>Vigna subterranea</i>		(Chang et al., 2018)
<i>Vigna unguiculata</i>	Phytozome	
<i>Vitis vinifera</i>	Phytozome	
<i>Zea mays</i>	Phytozome	
<i>Zizania latifolia</i>		(Guo et al., 2015)
<i>Ziziphus jujuba</i>		(Liu et al., 2014)
<i>Zostera marina</i>	Phytozome	
<i>Zostera muelleri</i>		(Lee et al., 2016)
<i>Zoysia japonica</i>		(Tanaka et al., 2016)
<i>Zoysia matrella</i>		(Tanaka et al., 2016)
<i>Zoysia pacifica</i>		(Tanaka et al., 2016)

Table S2. Number of putative GA2ox genes in flowering plants.

Plant species	Total number of GA2ox genes	C ₁₉ -GA2ox number	C ₂₀ -GA2ox number
<i>Actinidia chinensis</i>	14	10	4
<i>Aegilops tauschii</i>	3	1	2
<i>Aethionema arabicum</i>	5	5	0
<i>Amaranthus hypochondriacus</i>	5	3	2
<i>Amborella trichopoda</i>	2	1	1
<i>Ammopiptanthus nanus</i>	10	7	3
<i>Anacardium occidentale</i>	16	11	5
<i>Ananas comosus</i>	7	4	3
<i>Apostasia shenzhenica</i>	7	6	1
<i>Antirrhinum majus</i>	13	7	6
<i>Aquilegia coerulea</i>	8	5	3
<i>Arabidopsis halleri</i>	5	4	1
<i>Arabidopsis lyrata</i>	8	6	2
<i>Arabidopsis thaliana</i>	8	5	3
<i>Arachis duranensis</i>	9	7	2
<i>Arachis ipaensis</i>	10	7	3
<i>Arachis monticola</i>	15	11	4
<i>Artemisia annua</i>	11	7	4
<i>Artocarpus camansi</i>	4	2	2
<i>Asparagus officinalis</i>	6	4	2
<i>Atalantia buxifolia</i>	17	5	12
<i>Avicennia marina</i>	12	9	3
<i>Barbarea vulgaris</i>	4	3	1
<i>Beta vulgaris</i>	3	2	1
<i>Dorcoceras hygrometricum</i>	5	5	0
<i>Bombax ceiba</i>	18	13	5
<i>Boechera retrofracta</i>	8	6	2
<i>Boechera stricta</i>	8	6	2
<i>Boehmeria nivea</i>	6	2	4
<i>Brachypodium distachyon</i>	17	13	4
<i>Brachypodium hybridum</i>	24	16	8
<i>Brachypodium stacei</i>	10	7	3
<i>Brachypodium sylvaticum</i>	9	6	3
<i>Brassica napus</i>	26	22	4
<i>Brassica oleracea</i>	14	10	4

<i>Brassica rapa</i>	14	11	3
<i>Cajanus cajan</i>	15	9	6
<i>Calamus jenkinsianus</i>	10	8	2
<i>Calamus simplicifolius</i>	7	6	1
<i>Calotropis gigantea</i>	5	4	1
<i>Camelina sativa</i>	18	15	3
<i>Camellia sinensis</i>	6	4	2
<i>Camptotheca acuminata</i>	13	8	5
<i>Cannabis sativa</i>	7	4	3
<i>Capsella grandiflora</i>	7	6	1
<i>Capsella rubella</i>	8	6	2
<i>Capsicum annuum</i>	11	6	5
<i>Capsicum baccatum</i>	8	5	3
<i>Capsicum chinense</i>	10	7	3
<i>Cardamine hirsuta</i>	7	5	2
<i>Carica papaya</i>	5	4	1
<i>Castanea mollissima</i>	8	5	3
<i>Catharanthus roseus</i>	4	3	1
<i>Cephalotus follicularis</i>	4	3	1
<i>Chenopodium quinoa</i>	4	3	1
<i>Chrysanthemum indicum</i>	10	6	4
<i>Cicer arietinum</i>	9	5	4
<i>Cicer reticulatum</i>	7	5	2
<i>Cinnamomum micranthum</i>	10	7	3
<i>Citrullus lanatus</i>	8	5	3
<i>Citrus clementina</i>	8	4	4
<i>Citrus maxima</i>	8	4	4
<i>Citrus cavaleriei</i>	12	5	7
<i>Citrus medica</i>	8	4	4
<i>Citrus reticulata</i>	7	4	3
<i>Citrus sinensis</i>	10	4	6
<i>Citrus unshiu</i>	9	4	5
<i>Cocos nucifera</i>	8	6	2
<i>Coffea arabica</i>	14	6	8
<i>Coffea canephora</i>	6	4	2
<i>Corchorus capsularis</i>	5	4	1
<i>Corchorus olitorius</i>	8	4	4
<i>Cucumis melo</i>	8	5	3
<i>Cucumis sativus</i>	6	3	3

<i>Cucurbita pepo</i>	15	10	5
<i>Cynara cardunculus</i>	13	7	6
<i>Daucus carota</i>	20	13	7
<i>Dendrobium officinale</i>	10	6	4
<i>Dianthus caryophyllus</i>	2	2	0
<i>Dichantherium oligosanthes</i>	10	7	3
<i>Dioscorea rotundata</i>	5	2	3
<i>Durio zibethinus</i>	17	11	6
<i>Echinochloa crus-galli</i>	18	13	5
<i>Elaeis guineensis</i>	9	5	4
<i>Eragrostis tef</i>	5	4	1
<i>Erigeron breviscapus</i>	5	3	2
<i>Eschscholzia californica</i>	2	2	0
<i>Eucalyptus camaldulensis</i>	4	3	1
<i>Eucalyptus grandis</i>	6	4	2
<i>Eutrema salsugineum</i>	8	6	2
<i>Fagopyrum esculentum</i>	7	6	1
<i>Fagopyrum tataricum</i>	5	4	1
<i>Fagus sylvatica</i>	8	5	3
<i>Faidherbia albida</i>	12	8	4
<i>Fragaria vesca</i>	5	4	1
<i>Fraxinus excelsior</i>	22	18	4
<i>Genlisea aurea</i>	6	5	1
<i>Glycine max</i>	33	19	15
<i>Glycine soja</i>	22	13	9
<i>Glycyrrhiza uralensis</i>	9	7	2
<i>Gossypium arboreum</i>	16	11	5
<i>Gossypium barbadense</i>	42	27	15
<i>Gossypium hirsutum</i>	32	19	13
<i>Gossypium raimondii</i>	22	15	7
<i>Handroanthus impetiginosus</i>	10	7	3
<i>Helianthus annuus</i>	11	8	3
<i>Hevea brasiliensis</i>	15	8	7
<i>Hordeum vulgare</i>	23	19	4
<i>Humulus lupulus</i>	2	2	0
<i>Ipomoea batatas</i>	6	3	3
<i>Ipomoea nil</i>	11	8	3
<i>Ipomoea trifida</i>	6	5	1
<i>Jatropha curcas</i>	7	3	4

<i>Juglans regia</i>	18	7	11
<i>Kalanchoe fedtschenkoi</i>	9	6	3
<i>Kalanchoe laxiflora</i>	14	8	6
<i>Lablab purpureus</i>	10	6	4
<i>Lactuca sativa</i>	12	8	4
<i>Lagenaria siceraria</i>	7	4	3
<i>Leavenworthia alabamica</i>	10	9	1
<i>Leersia perrieri</i>	11	7	4
<i>Linum usitatissimum</i>	11	4	7
<i>Liriodendron chinense</i>	3	2	1
<i>Lolium perenne</i>	9	7	2
<i>Lotus japonicus</i>	5	4	1
<i>Lupinus angustifolius</i>	5	4	1
<i>Macleaya cordata</i>	4	2	2
<i>Malania oleifera</i>	6	4	2
<i>Malus domestica</i>	12	9	3
<i>Manihot esculenta</i>	12	7	5
<i>Medicago truncatula</i>	14	8	6
<i>Erythranthe guttata</i>	11	8	3
<i>Miscanthus sinensis</i>	19	13	6
<i>Momordica charantia</i>	8	4	4
<i>Moringa oleifera</i>	6	4	2
<i>Morus notabilis</i>	7	4	3
<i>Musa itinerans</i>	12	8	4
<i>Musa acuminata</i>	13	8	5
<i>Musa balbisiana</i>	13	8	5
<i>Musa schizocarpa</i>	11	8	3
<i>Nelumbo nucifera</i>	8	4	4
<i>Nicotiana attenuata</i>	8	5	3
<i>Nicotiana benthamiana</i>	19	14	5
<i>Nicotiana obtusifolia</i>	8	5	3
<i>Nicotiana glauca</i>	12	9	3
<i>Nicotiana tabacum</i>	19	14	5
<i>Nicotiana tomentosiformis</i>	11	7	4
<i>Ocimum tenuiflorum</i>	9	8	1
<i>Olea europaea</i>	19	13	6
<i>Oropetium thomaeum</i>	6	4	2
<i>Oryza barthii</i>	4	2	2
<i>Oryza brachyantha</i>	6	3	3

<i>Oryza glaberrima</i>	7	4	3
<i>Oryza longistaminata</i>	4	3	1
<i>Oryza meridionalis</i>	10	8	2
<i>Oryza meyeriana</i> var. <i>granulata</i>	10	7	3
<i>Oryza punctata</i>	9	6	3
<i>Oryza rufipogon</i>	9	6	3
<i>Oryza sativa</i>	9	5	4
<i>Oryza sativa</i> f. <i>spontanea</i>	10	7	3
<i>Panax ginseng</i>	12	6	6
<i>Panicum hallii</i>	11	8	3
<i>Panicum virgatum</i>	18	12	6
<i>Parasponia andersonii</i>	7	4	3
<i>Cenchrus americanus</i>	2	1	1
<i>Petunia axillaris</i>	10	8	2
<i>Petunia integrifolia</i> subsp. <i>inflata</i>	9	7	2
<i>Phalaenopsis aphrodite</i>	8	5	3
<i>Phalaenopsis equestris</i>	10	5	5
<i>Phaseolus vulgaris</i>	13	8	5
<i>Phoenix dactylifera</i>	10	7	3
<i>Phyllostachys edulis</i>	5	4	1
<i>Pogostemon cablin</i>	0	0	0
<i>Populus deltoides</i>	19	9	10
<i>Populus euphratica</i>	24	7	17
<i>Populus pruinosa</i>	14	6	8
<i>Populus tremula</i>	26	11	15
<i>Populus tremuloides</i>	14	9	5
<i>Populus trichocarpa</i>	21	10	11
<i>Potentilla micrantha</i>	6	4	2
<i>Primula veris</i>	5	3	2
<i>Primula vulgaris</i>	6	4	2
<i>Prunus avium</i>	14	5	9
<i>Prunus mume</i>	8	4	4
<i>Prunus persica</i>	12	4	8
<i>Punica granatum</i>	7	4	3
<i>Pyrus x bretschneideri</i>	20	9	11
<i>Pyrus communis</i>	11	7	4
<i>Quercus lobata</i>	8	3	5
<i>Quercus robur</i>	5	4	1

<i>Quercus suber</i>	8	4	4
<i>Raphanus raphanistrum</i>	11	8	3
<i>Raphanus sativus</i>	11	10	1
<i>Rhizophora apiculata</i>	9	5	4
<i>Rhododendron delavayi</i>	5	4	1
<i>Ricinus communis</i>	7	3	4
<i>Rosa chinensis</i>	7	4	3
<i>Rosa multiflora</i>	8	4	4
<i>Rubus occidentalis</i>	7	4	3
<i>Saccharum spontaneum</i>	11	7	4
<i>Salix purpurea</i>	16	10	6
<i>Salvia miltiorrhiza</i>	3	2	1
<i>Salvia splendens</i>	24	16	8
<i>Schrenkiella parvula</i>	7	6	1
<i>Sclerocarya birrea</i>	7	5	2
<i>Secale cereale</i>	4	2	2
<i>Sesamum indicum</i>	9	6	3
<i>Setaria italica</i>	18	10	8
<i>Setaria viridis</i>	13	11	2
<i>Siraitia grosvenorii</i>	9	6	3
<i>Sisymbrium irio</i>	5	4	1
<i>Solanum lycopersicum</i>	10	7	3
<i>Solanum melongena</i>	10	8	2
<i>Solanum pennellii</i>	15	10	5
<i>Solanum pimpinellifolium</i>	10	7	3
<i>Solanum tuberosum</i>	16	11	5
<i>Sonneratia alba</i>	14	11	3
<i>Sonneratia caseolaris</i>	14	11	3
<i>Sorghum bicolor</i>	12	9	3
<i>Spinacia oleracea</i>	9	2	7
<i>Spirodela polyrhiza</i>	5	3	2
<i>Taraxacum kok-saghyz</i>	3	3	0
<i>Tarenaya hassleriana</i>	8	5	3
<i>Tectona grandis</i>	12	8	4
<i>Theobroma cacao</i>	11	5	6
<i>Thinopyrum intermedium</i>	66	37	19
<i>Thlaspi arvense</i>	7	5	2
<i>Trema orientale</i>	7	4	3
<i>Trifolium pratense</i>	11	6	5

<i>Trifolium subterraneum</i>	5	5	0
<i>Triticum aestivum</i>	17	9	8
<i>Triticum turgidum</i>	33	20	13
<i>Triticum urartu</i>	4	1	3
<i>Utricularia gibba</i>	6	6	0
<i>Vaccinium corymbosum</i>	4	3	1
<i>Vigna angularis</i>	11	7	4
<i>Vigna radiata</i>	13	8	5
<i>Vigna subterranea</i>	12	7	5
<i>Vigna unguiculata</i>	14	9	5
<i>Vitis vinifera</i>	8	5	3
<i>Zea mays</i>	12	9	3
<i>Zizania latifolia</i>	10	7	3
<i>Ziziphus jujuba</i>	8	4	4
<i>Zostera marina</i>	4	3	1
<i>Zostera muelleri</i>	0	0	0
<i>Zoysia japonica</i>	10	6	4
<i>Zoysia matrella</i>	15	8	7
<i>Zoysia pacifica</i>	12	7	5

Table S3. Full-length *SABATH* genes in *Brachypodium distachyon*.

Gene name	Gene ID
<i>BdSABATH1</i>	<i>Bradi1g44620</i>
<i>BdSABATH2</i>	<i>Bradi1g43080</i>
<i>BdSABATH3</i>	<i>Bradi1g42760.1</i>
<i>BdSABATH4</i>	<i>Bradi2g47550</i>
<i>BdSABATH5</i>	<i>Bradi2g60180</i>
<i>BdSABATH6</i>	<i>Bradi2g60170.1</i>
<i>BdSABATH7</i>	<i>Bradi3g05550</i>
<i>BdSABATH8</i>	<i>Bradi3g57790</i>
<i>BdSABATH9</i>	<i>Bradi4g16077</i>
<i>BdSABATH10</i>	<i>Bradi4g16110</i>

Table S4. Selected *GA2ox* genes for HMM profile construction.

Gene Name	Class
<i>AtGA2ox1</i>	C19
<i>AtGA2ox2</i>	C19
<i>AtGA2ox3</i>	C19
<i>AtGA2ox4</i>	C19
<i>AtGA2ox6</i>	C19
<i>AtGA2ox7</i>	C20
<i>AtGA2ox8</i>	C20
<i>OsGA2ox1</i>	C19
<i>OsGA2ox3</i>	C19
<i>OsGA2ox4</i>	C19
<i>OsGA2ox5</i>	C20
<i>OsGA2ox6</i>	C20
<i>OsGA2ox7</i>	C19
<i>OsGA2ox8</i>	C19
<i>OsGA2ox9</i>	C20
<i>SoGA2ox1</i>	C19
<i>SoGA2ox2</i>	C19
<i>SoGA2ox3</i>	C20
<i>CmGA2ox</i>	C19
<i>LsGA2ox1</i>	C19
<i>NtGA2ox1</i>	C19
<i>NtGA2ox3</i>	C19
<i>NtGA2ox5</i>	C19
<i>PcGA2ox1</i>	C19
<i>PaGA2ox1</i>	C19
<i>PsGA2ox1</i>	C19
<i>PsGA2ox2</i>	C19

At: *Arabidopsis thaliana*; *Os*: *Oryza sativa*; *So*: *Spinacia oleracea*; *Cm*: *Cucurbita maxima*; *Ls*: *Lactuca sativa*; *Nt*: *Nicotiana sylvestris*; *Pc*: *Phaseolus coccineus*; *Pa*: *Populus alba*; *Ps*: *Pisum sativum*.

Table S5. Primers used in this study.

Gene name and ID	Primers	Sequence (5'→3')
<i>GbGAMT1</i> (<i>Gb 37441</i>)	Gb1-F Gb1-R	ATGGATTGCTCGACTAGCGTGGTGTCA CTATTTTCTGACAGCAAACACAACAATAACGCCA
<i>GbGAMT2</i> (<i>Gb 37750</i>)	Gb2-F Gb2-R	ATGGATGGTCCTACCATAGCTGCATC TTATTCCTCAGCAAATCTGGTCATTACATC
<i>BrGAMT1</i> (<i>Bra026440</i>)	Br1-F Br1-R	ATGGATTCTTCTCGGAGCCTC TCAAACCCTAATCGCTGAGACAG
<i>BrGAMT2</i> (<i>Bra028937</i>)	Br2-F Br2-R	ATGGAGTCACCAAGTCTTCCAGTAAC TCATTCAATTCGGATGGCAGA
<i>BrGAMT3</i> (<i>Bra010433</i>)	Br3-F Br3-R	ATGCAAGGCGGAGACGGTGACGTCAG TTAATACCAAACCCGAATCGCTGAAAC

Gb: *Ginkgo biloba*; *Br*: *Brassica rapa*.

Reference

- Avni R, Nave M, Barad O, Baruch K, Twardziok SO, Gundlach H, Hale I, Mascher M, Spannagl M, Wiebe K (2017)** Wild emmer genome architecture and diversity elucidate wheat evolution and domestication. *Science* **357**: 93-97
- Bertioli DJ, Cannon SB, Froenicke L, Huang G, Farmer AD, Cannon EK, Liu X, Gao D, Clevenger J, Dash S (2015)** The genome sequences of *Arachis duranensis* and *Arachis ipaensis*, the diploid ancestors of cultivated peanut. *Nature Genetics* **47**: 438
- Bombarely A, Moser M, Amrad A, Bao M, Bapaume L, Barry CS, Bliet M, Boersma MR, Borghi L, Bruggmann R, Bucher M, D'Agostino N, Davies K, Druege U, Dudareva N, Egea-Cortines M, Delledonne M, Fernandez-Pozo N, Franken P, Grandont L, Heslop-Harrison JS, Hintzsche J, Johns M, Koes R, Lv X, Lyons E, Malla D, Martinoia E, Mattson NS, Morel P, Mueller LA, Muhlemann J, Nouri E, Passeri V, Pezzotti M, Qi Q, Reinhardt D, Rich M, Richert-Pöggeler KR, Robbins TP, Schatz MC, Schranz ME, Schuurink RC, Schwarzacher T, Spelt K, Tang H, Urbanus SL, Vandebussche M, Vijverberg K, Villarino GH, Warner RM, Weiss J, Yue Z, Zethof J, Quattrocchio F, Sims TL, Kuhlemeier C (2016)** Insight into the evolution of the Solanaceae from the parental genomes of *Petunia hybrida*. *Nature Plants* **2**: 16074
- Byrne SL, Erthmann PØ, Agerbirk N, Bak S, Hauser TP, Nagy I, Paina C, Asp T (2017)** The genome sequence of *Barbarea vulgaris* facilitates the study of ecological biochemistry. *Scientific reports* **7**: 40728
- Cannarozzi G, Plaza-Wüthrich S, Esfeld K, Larti S, Wilson YS, Girma D, de Castro E, Chanyalew S, Blösch R, Farinelli L (2014)** Genome and transcriptome sequencing identifies breeding targets in the orphan crop tef (*Eragrostis tef*). *BMC genomics* **15**: 581

Chagné D, Crowhurst RN, Pindo M, Thrimawithana A, Deng C, Ireland H, Fiers M, Dzierzon H, Cestaro A, Fontana P, Bianco L, Lu A, Storey R, Knäbel M, Saeed M, Montanari S, Kim YK, Nicolini D, Llarger S, Stefani E, Allan AC, Bowen J, Harvey I, Johnston J, Malnoy M, Troggio M, Percepied L, Sawyer G, Wiedow C, Won K, Viola R, Hellens RP, Brewer L, Bus VGM, Schaffer RJ, Gardiner SE, Velasco R (2014) The Draft Genome Sequence of European Pear (*Pyrus communis* L. ‘Bartlett’). *PLOS ONE* **9**: e92644

Chang Y, Liu H, Liu M, Liao X, Sahu SK, Fu Y, Song B, Cheng S, Kariba R, Muthemba S (2018) The draft genomes of five agriculturally important African orphan crops. *GigaScience* **8**: giy152

Davey MW, Gudimella R, Harikrishna JA, Sin LW, Khalid N, Keulemans J (2013) “A draft *Musa balbisiana* genome sequence for molecular genetics in polyploid, inter- and intra-specific Musa hybrids”. *BMC Genomics* **14**: 683

Dong A-X, Cui R-F, Zhao Z-N, Li Z-J, Cong R-C, Xin H-B, Liu H, Nie S, Sun Y-Q, Mao J-F, Yun Q-Z, Zhang R-G, Wang X-N, Maghuly F, Porth I (2018) High-quality assembly of the reference genome for scarlet sage, *Salvia splendens*, an economically important ornamental plant. *GigaScience* **7**

Dorn KM, Fankhauser JD, Wyse DL, Marks MD (2015) A draft genome of field pennycress (*Thlaspi arvense*) provides tools for the domestication of a new winter biofuel crop. *DNA Research* **22**: 121-131

FAIRsharing.org: HWG; Hardwood Genomics Project; DOI:

<https://doi.org/10.25504/FAIRsharing.srgkaf>; Last edited: Jan. 8, 2019, 1:24 p.m.; Last accessed: Apr 16 2019 6:24 p.m.

- Fei B, Zhao H, Xu H, Sun H, Wang J, Chen L, Li L, Wang S, Yang Y, Lou Y, Gao Z, Jiang Z, Zhang C, Chen C, Zhang H, Yang H, Gao Q, Yang W, Zhou X, Wei Y, Wang L, Wang S, Zhao S, Shi C, Liu X** (2018) Chromosome-level reference genome and alternative splicing atlas of moso bamboo (*Phyllostachys edulis*). *GigaScience* **7**
- Fukushima K, Fang X, Alvarez-Ponce D, Cai H, Carretero-Paulet L, Chen C, Chang T-H, Farr KM, Fujita T, Hiwatashi Y** (2017) Genome of the pitcher plant *Cephalotus* reveals genetic changes associated with carnivory. *Nature ecology & evolution* **1**: 0059
- Gan X, Hay A, Kwantes M, Haberer G, Hallab A, Ioio RD, Hofhuis H, Pieper B, Cartolano M, Neumann U** (2016) The *Cardamine hirsuta* genome offers insight into the evolution of morphological diversity. *Nature plants* **2**: 16167
- Gao F, Wang X, Li X, Xu M, Li H, Abila M, Sun H, Wei S, Feng J, Zhou Y** (2018) Long-read sequencing and de novo genome assembly of *Ammopiptanthus nanus*, a desert shrub. *GigaScience*
- Gao Y, Wang H, Liu C, Chu H, Dai D, Song S, Yu L, Han L, Fu Y, Tian B** (2018) De novo genome assembly of the red silk cotton tree (*Bombax ceiba*). *GigaScience* **7**: giy051
- Gardner EM, Johnson MG, Ragone D, Wickett NJ, Zerega NJ** (2016) Low- coverage, whole- genome sequencing of *Artocarpus camansi* (Moraceae) for phylogenetic marker development and gene discovery. *Applications in plant sciences* **4**: 1600017
- Giongo L, Šurbanovski N, Velasco R, Sargent DJ, Buti M, Brillì M, Cestaro A, Engelen K, Moretto M, Sonogo P, Cavallini A, Barghini E, Mascagni F, Natali L, Borodovsky M, Lomsadze A, Ward JA, Alonge M, Varotto C** (2017) The genome sequence and transcriptome of *Potentilla micrantha* and their comparison to *Fragaria vesca* (the woodland strawberry). *GigaScience* **7**

- Guan R, Zhao Y, Zhang H, Fan G, Liu X, Zhou W, Shi C, Wang J, Liu W, Liang X (2016)**
Draft genome of the living fossil *Ginkgo biloba*. *Gigascience* **5**: 49
- Guo L, Qiu J, Han Z, Ye Z, Chen C, Liu C, Xin X, Ye CY, Wang YY, Xie H (2015)** A host plant genome (*Zizania latifolia*) after a century- long endophyte infection. *The Plant Journal* **83**: 600-609
- Guo L, Qiu J, Ye C, Jin G, Mao L, Zhang H, Yang X, Peng Q, Wang Y, Jia L (2017)**
Echinochloa crus-galli genome analysis provides insight into its adaptation and invasiveness as a weed. *Nature communications* **8**: 1031
- Guo S, Zhang J, Sun H, Salse J, Lucas WJ, Zhang H, Zheng Y, Mao L, Ren Y, Wang Z (2013)** The draft genome of watermelon (*Citrullus lanatus*) and resequencing of 20 diverse accessions. *Nature genetics* **45**: 51
- Gupta S, Nawaz K, Parween S, Roy R, Sahu K, Kumar Pole A, Khandal H, Srivastava R, Kumar Parida S, Chattopadhyay D (2016)** Draft genome sequence of *Cicer reticulatum* L., the wild progenitor of chickpea provides a resource for agronomic trait improvement. *Dna Research* **24**: 1-10
- Gupta V, Estrada AD, Blakley I, Reid R, Patel K, Meyer MD, Andersen SU, Brown AF, Lila MA, Loraine AE (2015)** RNA-Seq analysis and annotation of a draft blueberry genome assembly identifies candidate genes involved in fruit ripening, biosynthesis of bioactive compounds, and stage-specific alternative splicing. *Gigascience* **4**: 5
- Hirakawa H, Kaur P, Shirasawa K, Nichols P, Nagano S, Appels R, Erskine W, Isobe SN (2016)** Draft genome sequence of subterranean clover, a reference for genus *Trifolium*. *Scientific reports* **6**: 30358

Hoopes GM, Hamilton JP, Kim J, Zhao D, Wiegert-Rininger K, Crisovan E, Buell CR

(2018) Genome assembly and annotation of the medicinal plant *Calotropis gigantea*, a producer of anticancer and antimalarial cardenolides. *G3: Genes, Genomes, Genetics* **8**: 385-391

Hori K, Yamada Y, Purwanto R, Minakuchi Y, Toyoda A, Hirakawa H, Sato F (2017)

Mining of the uncharacterized cytochrome p450 genes involved in alkaloid biosynthesis in *California poppy* using a draft genome sequence. *Plant and Cell Physiology* **59**: 222-233

Ibarra-Laclette E, Lyons E, Hernández-Guzmán G, Pérez-Torres CA, Carretero-Paulet L,

Chang T-H, Lan T, Welch AJ, Juárez MJA, Simpson J (2013) Architecture and evolution of a minute plant genome. *Nature* **498**: 94

Jin J, Lee M, Bai B, Sun Y, Qu J, Alfiko Y, Lim CH, Suwanto A, Sugiharti M, Wong L

(2016) Draft genome sequence of an elite *Dura* palm and whole-genome patterns of DNA variation in oil palm. *DNA research* **23**: 527-533

Kang YJ, Kim SK, Kim MY, Lestari P, Kim KH, Ha B-K, Jun TH, Hwang WJ, Lee T, Lee

J (2014) Genome sequence of mungbean and insights into evolution within *Vigna* species. *Nature communications* **5**: ncomms6443

Kang YJ, Satyawan D, Shim S, Lee T, Lee J, Hwang WJ, Kim SK, Lestari P, Laosatit K,

Kim KH (2015) Draft genome sequence of adzuki bean, *Vigna angularis*. *Scientific reports* **5**: 8069

Kellner F, Kim J, Clavijo BJ, Hamilton JP, Childs KL, Vaillancourt B, Cepela J,

Habermann M, Steuernagel B, Clissold L (2015) Genome-guided investigation of plant natural product biosynthesis. *The Plant Journal* **82**: 680-692

- Kim N-H, Jayakodi M, Lee S-C, Choi B-S, Jang W, Lee J, Kim HH, Waminal NE, Lakshmanan M, van Nguyen B, Lee YS, Park H-S, Koo HJ, Park JY, Perumal S, Joh HJ, Lee H, Kim J, Kim IS, Kim K, Koduru L, Kang KB, Sung SH, Yu Y, Park DS, Choi D, Seo E, Kim S, Kim Y-C, Hyun DY, Park Y-I, Kim C, Lee T-H, Kim HU, Soh MS, Lee Y, In JG, Kim H-S, Kim Y-M, Yang D-C, Wing RA, Lee D-Y, Paterson AH, Yang T-J (2018) Genome and evolution of the shade-requiring medicinal herb *Panax ginseng*. *Plant Biotechnology Journal* **16**: 1904-1917**
- Kim S, Park J, Yeom S-I, Kim Y-M, Seo E, Kim K-T, Kim M-S, Lee JM, Cheong K, Shin H-S (2017) New reference genome sequences of hot pepper reveal the massive evolution of plant disease-resistance genes by retroduplication. *Genome biology* **18**: 210**
- Kim S, Park M, Yeom S-I, Kim Y-M, Lee JM, Lee H-A, Seo E, Choi J, Cheong K, Kim K-T (2014) Genome sequence of the hot pepper provides insights into the evolution of pungency in *Capsicum* species. *Nature genetics* **46**: 270**
- Kliver S, Rayko M, Komissarov A, Bakin E, Zhernakova D, Prasad K, Rushworth C, Baskar R, Smetanin D, Schmutz J (2018) Assembly of the *Boechera retrofracta* Genome and Evolutionary Analysis of Apomixis-Associated Genes. *Genes* **9**: 185**
- Lee H, Golicz AA, Bayer P, Jiao Y, Tang H, Paterson AH, Sablok G, Krishnaraj RR, Chan C-KK, Batley J (2016) The genome of a southern hemisphere seagrass species (*Zostera muelleri*). *Plant physiology*: pp. 00868.02016**
- Li F-W, Brouwer P, Carretero-Paulet L, Cheng S, De Vries J, Delaux P-M, Eily A, Koppers N, Kuo L-Y, Li Z (2018) Fern genomes elucidate land plant evolution and cyanobacterial symbioses. *Nature plants* **4**: 460**

Li M, Zhang D, Gao Q, Luo Y, Zhang H, Ma B, Chen C, Whibley A, Zhang Ye, Cao Y
(2019) Genome structure and evolution of *Antirrhinum majus* L. *Nature plants*: 1

Lin T, Xu X, Cheng Z, Yu H, Li J, Xiong G, Ruan J, Huang S, Wu S, Wang X, Shao X, Qin B, Gan L, Liu S, Yang Y, Yang S, Zhang Z (2017) Genome analysis of *Taraxacum kok-saghyz* Rodin provides new insights into rubber biosynthesis. *National Science Review* **5**: 78-87

Lin T, Xu X, Ruan J, Liu S, Wu S, Shao X, Wang X, Gan L, Qin B, Yang Y (2017) Genome analysis of *Taraxacum kok-saghyz* Rodin provides new insights into rubber biosynthesis. *National Science Review* **5**: 78-87

Lin Y-C, Wang J, Delhomme N, Schiffthaler B, Sundström G, Zuccolo A, Nystedt B, Hvidsten TR, de la Torre A, Cossu RM, Hoepfner MP, Lantz H, Scofield DG, Zamani N, Johansson A, Mannapperuma C, Robinson KM, Mähler N, Leitch IJ, Pellicer J, Park E-J, van Montagu M, van de Peer Y, Grabherr M, Jansson S, Ingvarsson PK, Street NR (2018) Functional and evolutionary genomic inferences in *Populus* through genome and population sequencing of American and European aspen. *Proceedings of the National Academy of Sciences* **115**: E10970-E10978

Liu M-J, Zhao J, Cai Q-L, Liu G-C, Wang J-R, Zhao Z-H, Liu P, Dai L, Yan G, Wang W-J
(2014) The complex jujube genome provides insights into fruit tree biology. *Nature communications* **5**: 5315

Luan MB, Jian JB, Chen P, Chen JH, Chen JH, Gao Q, Gao G, Zhou JH, Chen KM, Guang XM (2018) Draft genome sequence of ramie, *Boehmeria nivea* (L.) Gaudich. *Molecular ecology resources* **18**: 639-645

Mochida K, Sakurai T, Seki H, Yoshida T, Takahagi K, Sawai S, Uchiyama H, Muranaka

T, Saito K (2017) Draft genome assembly and annotation of *Glycyrrhiza uralensis*, a medicinal legume. *The Plant Journal* **89**: 181-194

Qi X, Li M-W, Xie M, Liu X, Ni M, Shao G, Song C, Kay-Yuen Yim A, Tao Y, Wong F-L,

Isobe S, Wong C-F, Wong K-S, Xu C, Li C, Wang Y, Guan R, Sun F, Fan G, Xiao Z,

Zhou F, Phang T-H, Liu X, Tong S-W, Chan T-F, Yiu S-M, Tabata S, Wang J, Xu

X, Lam H-M (2014) Identification of a novel salt tolerance gene in wild soybean by whole-genome sequencing. *Nature Communications* **5**: 4340

Sarkar D, Mahato AK, Satya P, Kundu A, Singh S, Jayaswal PK, Singh A, Bahadur K,

Pattnaik S, Singh N (2017) The draft genome of *Corchorus olitorius* cv. JRO-524

(Navin). *Genomics data* **12**: 151-154

Scaglione D, Reyes-Chin-Wo S, Acquadro A, Froenicke L, Portis E, Beitel C, Tirone M,

Mauro R, Monaco AL, Mauromicale G (2016) The genome sequence of the

outbreeding globe artichoke constructed de novo incorporating a phase-aware low-pass sequencing strategy of F1 progeny. *Scientific Reports* **6**: 19427

Shimizu T, Tanizawa Y, Mochizuki T, Nagasaki H, Yoshioka T, Toyoda A, Fujiyama A,

Kaminuma E, Nakamura Y (2017) Draft Sequencing of the Heterozygous Diploid

Genome of Satsuma (*Citrus unshiu* Marc.) Using a Hybrid Assembly Approach.

Frontiers in genetics **8**: 180

Slotte T, Hazzouri KM, Ågren JA, Koenig D, Maumus F, Guo Y-L, Steige K, Platts AE,

Escobar JS, Newman LK (2013) The *Capsella rubella* genome and the genomic

consequences of rapid mating system evolution. *Nature genetics* **45**: 831

- Song C, Liu Y, Song A, Dong G, Zhao H, Sun W, Ramakrishnan S, Wang Y, Wang S, Li T** (2018) The *Chrysanthemum nankingense* genome provides insights into the evolution and diversification of chrysanthemum flowers and medicinal traits. *Molecular plant* **11**: 1482-1491
- Studer AJ, Schnable JC, Weissmann S, Kolbe AR, McKain MR, Shao Y, Cousins AB, Kellogg EA, Brutnell TP** (2016) The draft genome of the C₃ panicoid grass species *Dichanthelium oligosanthes*. *Genome biology* **17**: 223
- Tanaka H, Hirakawa H, Kosugi S, Nakayama S, Ono A, Watanabe A, Hashiguchi M, Gondo T, Ishigaki G, Mugerza M** (2016) Sequencing and comparative analyses of the genomes of zoysiagrasses. *DNA Research* **23**: 171-180
- Teh BT, Lim K, Yong CH, Ng CCY, Rao SR, Rajasegaran V, Lim WK, Ong CK, Chan K, Cheng VKY** (2017) The draft genome of tropical fruit durian (*Durio zibethinus*). *Nature genetics* **49**: 1633
- van Bakel H, Stout JM, Cote AG, Tallon CM, Sharpe AG, Hughes TR, Page JE** (2011) The draft genome and transcriptome of *Cannabis sativa*. *Genome biology* **12**: R102
- van Velzen R, Holmer R, Bu F, Rutten L, van Zeijl A, Liu W, Santuari L, Cao Q, Sharma T, Shen D** (2018) Comparative genomics of the nonlegume *Parasponia* reveals insights into evolution of nitrogen-fixing rhizobium symbioses. *Proceedings of the National Academy of Sciences*: 201721395
- Varshney RK, Chen W, Li Y, Bharti AK, Saxena RK, Schlueter JA, Donoghue MT, Azam S, Fan G, Whaley AM** (2012) Draft genome sequence of pigeonpea (*Cajanus cajan*), an orphan legume crop of resource-poor farmers. *Nature biotechnology* **30**: 83

- Wai CM, Colle M, Edger PP, VanBuren R, Wang J, Childs K, Liachko I, Sullivan S, Bushakra JM, Bassil NV, Vining KJ, Dossett M, Finn CE, Chagné D, Jibrán R, Mockler TC (2018)** A near complete, chromosome-scale assembly of the black raspberry (*Rubus occidentalis*) genome. *GigaScience* 7
- Wan T, Liu Z-M, Li L-F, Leitch AR, Leitch IJ, Lohaus R, Liu Z-J, Xin H-P, Gong Y-B, Liu Y, Wang W-C, Chen L-Y, Yang Y, Kelly LJ, Yang J, Huang J-L, Li Z, Liu P, Zhang L, Liu H-M, Wang H, Deng S-H, Liu M, Li J, Ma L, Liu Y, Lei Y, Xu W, Wu L-Q, Liu F, Ma Q, Yu X-R, Jiang Z, Zhang G-Q, Li S-H, Li R-Q, Zhang S-Z, Wang Q-F, van de Peer Y, Zhang J-B, Wang X-M (2018)** A genome for gnetophytes and early evolution of seed plants. *Nature Plants* 4: 82-89
- Wang K, Yang W, Ma T, Liu J, Zhang J, Ma J (2017)** The draft genome sequence of a desert tree *Populus pruinosa*. *GigaScience* 6
- Wang L, He F, Huang Y, He J, Yang S, Zeng J, Deng C, Jiang X, Fang Y, Wen S (2018)** Genome of wild mandarin and domestication history of mandarin. *Molecular Plant* 11: 1024-1037
- Wang X, Xu Y, Zhang S, Cao L, Huang Y, Cheng J, Wu G, Tian S, Chen C, Liu Y (2017)** Genomic analyses of primitive, wild and cultivated citrus provide insights into asexual reproduction. *Nature genetics* 49: 765
- Wei C, Yang H, Wang S, Zhao J, Liu C, Gao L, Xia E, Lu Y, Tai Y, She G (2018)** Draft genome sequence of *Camellia sinensis* var. *sinensis* provides insights into the evolution of the tea genome and tea quality. *Proceedings of the National Academy of Sciences*: 201719622

- Wu Z, Fang D, Yang R, Gao F, An X, Zhuo X, Li Y, Yi C, Zhang T, Liang C** (2018) De novo genome assembly of *Oryza granulata* reveals rapid genome expansion and adaptive evolution. *Communications biology* **1**: 84
- Xia M, Cheng B, Zhen G, He H, Yu R, Han X, Deng XW, Jia X** (2018) Improved de novo genome assembly and analysis of the Chinese cucurbit *Siraitia grosvenorii*, also known as monk fruit or luo-han-guo. *GigaScience* **7**
- Xiao L, Yang G, Zhang L, Yang X, Zhao S, Ji Z, Zhou Q, Hu M, Wang Y, Chen M** (2015) The resurrection genome of *Boea hygrometrica*: A blueprint for survival of dehydration. *Proceedings of the National Academy of Sciences*: 201505811
- Xiao Y, Xu P, Fan H, Baudouin L, Xia W, Bocs S, Xu J, Li Q, Guo A, Zhou L** (2017) The genome draft of coconut (*Cocos nucifera*). *GigaScience* **6**: 1-11
- Xu C-Q, Liu H, Zhou S-S, Zhang D-X, Zhao W, Wang S, Chen F, Sun Y-Q, Nie S, Jia K-H** (2019) Genome sequence of *Malania oleifera*, a tree with great value for nervonic acid production. *GigaScience*
- Yagi M, Kosugi S, Hirakawa H, Ohmiya A, Tanase K, Harada T, Kishimoto K, Nakayama M, Ichimura K, Onozaki T** (2013) Sequence analysis of the genome of carnation (*Dianthus caryophyllus* L.). *DNA Research* **21**: 231-241
- Yan H, Song J, Zou L, Zhang L, Ma L, Peng L, Li S, Li S, Xie W, Cai Y, Wang J, Xu P, Gao Q, Ma Y, Zhang C** (2017) The draft genome assembly of *Rhododendron delavayi* Franch. var. *delavayi*. *GigaScience* **6**
- Yan L, Wang X, Liu H, Tian Y, Lian J, Yang R, Hao S, Wang X, Yang S, Li Q** (2015) The genome of *Dendrobium officinale* illuminates the biology of the important traditional Chinese orchid herb. *Molecular plant* **8**: 922-934

- Yang J, Zhang G, Zhang J, Liu H, Chen W, Wang X, Li Y, Dong Y, Yang S** (2017) Hybrid de novo genome assembly of the Chinese herbal fleabane *Erigeron breviscapus*. *GigaScience* **6**: 1-7
- Yin D, Ji C, Ma X, Li H, Zhang W, Li S, Liu F, Zhao K, Li F, Li K** (2018) Genome of an allotetraploid wild peanut *Arachis monticola*: a de novo assembly. *GigaScience* **7**: giy066
- Zhang G, Tian Y, Zhang J, Shu L, Yang S, Wang W, Sheng J, Dong Y, Chen W** (2015) Hybrid de novo genome assembly of the Chinese herbal plant danshen (*Salvia miltiorrhiza* Bunge). *GigaScience* **4**
- Zhang G-Q, Liu K-W, Li Z, Lohaus R, Hsiao Y-Y, Niu S-C, Wang J-Y, Lin Y-C, Xu Q, Chen L-J** (2017) The *Apostasia* genome and the evolution of orchids. *Nature* **549**: 379
- Zhao D, Hamilton JP, Buell CR, Hamberger B, Johnson SR, Bhat WW, Godden GT, Soltis PS, Soltis DE, Kinser TJ, Boachon B, Dudareva N** (2019) A chromosomal-scale genome assembly of *Tectona grandis* reveals the importance of tandem gene duplication and enables discovery of genes in natural product biosynthetic pathways. *GigaScience* **8**
- Zhao D, Hamilton JP, Pham GM, Crisovan E, Wiegert-Rininger K, Vaillancourt B, DellaPenna D, Buell CR** (2017) De novo genome assembly of *Camptotheca acuminata*, a natural source of the anti-cancer compound camptothecin. *GigaScience* **6**: 1-7
- Zhao H, Wang S, Wang J, Chen C, Hao S, Chen L, Fei B, Han K, Li R, Shi C** (2018) The chromosome-level genome assemblies of two rattans (*Calamus simplicifolius* and *Daemonorops jenkinsiana*). *GigaScience* **7**: giy097