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Genome assembly ALMONDv2   (reference)

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Actions

NCBI RefSeq assembly
GCF_902201215.1 (sequences differ from GenBank assembly)   ⋮

Submitted GenBank assembly
GCA_902201215.1   ⋮

Taxon
Prunus dulcis (almond)

WGS project
CABIKO01

Assembly type
haploid

Submitter
CNAG

Date
Oct 10, 2019

View annotated genes

See in Genome Data Viewer

BLAST the reference genome

Assembly statistics

	RefSeq	GenBank
Genome size	227.6 Mb	227.6 Mb
Total ungapped length	223.7 Mb	223.7 Mb
Number of chromosomes	8	8

	RefSeq	GenBank
Number of organelles	1	0
Number of scaffolds	691	691
Scaffold N50	24.4 Mb	24.4 Mb
Scaffold L50	4	4
Number of contigs	4,395	4,395
Contig N50	115.2 kb	115.2 kb
Contig L50	511	511
GC percent	37.5	37.5
Genome coverage	800x	800x
Assembly level	Chromosome	Chromosome
View sequences	view RefSeq sequences	view GenBank sequences

Sample details

BioSample ID
SAMEA5704668

Description
Texas DNA

Comment
Genomic DNA from Texas

Submitter
EBI

ENA-CHECKLIST
ERC000037

ENA-FIRST-PUBLIC
2019-09-09T17:03:57Z

ENA-LAST-UPDATE
2019-06-11T16:01:18Z

View more ⌄

Assembly methods

Sequencing technology
Illumina, ONT

Comment
The Prunus dulcis whole genome shotgun (WGS) project has the project accession CABIKO000000000. This version of the project (01) has the accession number CABIKO010000000, and consists of sequences CABIKO010000001-CABIKO010001699.

Assembly method
MASURCA,Redundans,SSPACE-LongRead,AMOS,ALLMAPS

Additional genomes

Browse all Prunus dulcis genomes (5)

BioProject

[PRJEB32994](#)

Transposons played a major role in the diversification between the closely related almond (Prunus dulcis) and peach (P. persica) genomes: Results from the almond genome sequence.

Publications

Showing 5 of 14

Genes (Basel) 2024
[Genome-Wide Identification and Characterization of *TCP* Genes in Eight *Prunus* Species and Their Expression Patterns Under Cold Stress in *P. tenella* var. *tenella*](#)
Q Zhang, et al.

BMC Genomics 2024
[Genomic exploration of Iranian almond (Prunus dulcis) germplasm: decoding diversity, population structure, and linkage disequilibrium through genotyping-by-sequencing analysis](#)
S Khojand, et al.

Sci Data 2024
[Chromosome-level genome assembly and annotation of Flueggea virosa (Phyllanthaceae)](#)
BZ Chen, et al.

J Integr Bioinform 2024
[Auto-phylo v2 and auto-phylo-pipeliner: building advanced, flexible, and reusable pipelines for phylogenetic inferences, estimation of variability levels and identification of positively selected amino acid sites](#)
H López-Fernández, et al.

Sci Data 2024
[The draft genome of Spiraea crenata L. (Rosaceae) - the first complete genome in tribe Spiraeeae](#)
L Laczkó, et al.

[View all 14 in PubMed](#)

Publication list limited to 400 entries

Annotation details

[See full annotation report](#)

	RefSeq	GenBank
Provider	NCBI RefSeq	CNAG
Name	NCBI Prunus dulcis Annotation Release 100	Annotation submitted by CNAG
Date	May 13, 2020	Jul 6, 2022
Genes	26,936	109,390
Protein-coding	23,151	27,984
Software version	8.4	
	[View RefSeq annotation](#)	[View GenBank annotation](#)

Quality analysis

BUSCO analysis (4.0.2)

- Single_copy 92.2%
- Duplicated 5.6%
- Fragmented 0.3%
- Missing 2.0%

92.2%
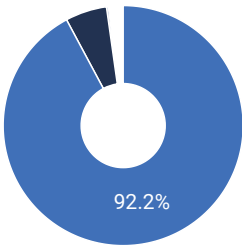
C:97.8%[S:92.2%,D:5.6%],F:0.3%,M:2.0%,n:2326
eudicots_odb10 (2326)

Chromosomes

1 2 3 4 5 6 7 8

View chromosomes from: **GenBank sequence** | RefSeq sequence

Download

Chromosome	GenBank	RefSeq	Size (bp)	GC content (%)	Unlocalized count	Action
1	LR694006.1	NC_047650.1	43,996,934	37.5	0	⋮
2	LR694007.1	NC_047651.1	26,138,581	37.5	0	⋮
3	LR694008.1	NC_047652.1	24,073,526	37.5	0	⋮
4	LR694009.1	NC_047653.1	24,375,383	37.5	0	⋮
5	LR694010.1	NC_047654.1	18,233,718	37.5	0	⋮
6	LR694011.1	NC_047655.1	29,596,931	37.5	0	⋮
7	LR694012.1	NC_047656.1	21,340,587	37.5	0	⋮
8	LR694013.1	NC_047657.1	20,428,636	37.5	0	⋮

Note: This genome assembly includes 683 unplaced scaffolds.

RefSeq and GenBank assembly differences

The NCBI RefSeq assembly differs from the submitted assembly in the following ways:

Added chromosome Pltd

Revision history

This record has not been revised

GenBank	RefSeq	Name	Level	Date	Action
GCA_902201215.1	GCF_902201215.1	ALMONDv2	Chromosome	Oct 10, 2019	⋮