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Genome assembly PAV_r1.0

reference



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Actions

NCBI RefSeq assembly	
GCF_002207925.1	
Submitted GenBank assembly	
GCA_002207925.1	
Taxon	
Prunus avium (sweet cherry)	
Cultivar	
Satonishiki	
WGS project	
BDGV01	
Assembly type	
haploid	
Submitter	
Kazusa DNA Research Institute	
Date	
Jun 12, 2017	



View annotated genes



See in Genome Data Viewer




BLAST the reference genome

Assembly statistics

	RefSeq	GenBank
Genome size	272.4 Mb	272.4 Mb
Total unapped length	246.8 Mb	246.8 Mb

	RefSeq	GenBank
Number of scaffolds	10,148	10,148
Scaffold N50	219.6 kb	219.6 kb
Scaffold L50	316	316
Number of contigs	32,310	32,310
Contig N50	28.8 kb	28.8 kb
Contig L50	2,191	2,191
GC percent	37.5	37.5
Genome coverage	327x	327x
Assembly level	Scaffold	Scaffold
View sequences	view RefSeq sequences	

Sample details

BioSample ID	SAMD00052827
Description	Prunus avium Genome
Comment	Keywords: GSC:MixS;MIGS:6.0
Submitter	Kazusa DNA Research Institute
Sample name	Genome
Biomaterial provider	Yamagata Integrated Agricultural Research Center and Hokkaido Research Organization
Collection date	2015
View more 	

Assembly methods

Sequencing technology	Illumina HiSeq 2000
Assembly method	SOAPdenovo v. 2-rev240; GapCloser v. 1.10

Additional genomes

[Browse all Prunus avium genomes \(5\)](#)

BioProject

[PRJDB4877](#)

Publications

Showing 5 of 11

DNA Res

2017

[The genome sequence of sweet cherry \(Prunus avium\) for use in genomics-assisted breeding](#)

K Shirasawa, et al.

Plants (Basel)

2025

[Pseudomonas syringae Pathovar syringae Infection Reveals Different Defense Mechanisms in Two Sweet Cherry Cultivars](#)

C Carreras, et al.

Mol Hortic

2025

[Population sequencing of cherry accessions unravels the evolution of Cerasus species and the selection of genetic characteristics in edible cherries](#)

Y Lei, 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 Spiraeaeae](#)

L Laczkó, et al.

[View all 11 in PubMed](#)

Publication list limited to 400 entries

Annotation details

[See full annotation report](#)

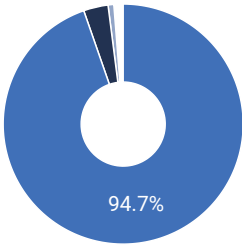
	RefSeq
Provider	NCBI RefSeq
Name	NCBI Prunus avium Annotation Release 100
Date	Jul 25, 2017
Genes	30,405
Protein-coding	25,841
Software version	7.4

[View RefSeq annotation](#)

Quality analysis

BUSCO analysis (4.0.2)

- Single_copy 94.7%
- Duplicated 3.3%
- Fragmented 0.8%
- Missing 1.2%



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Note: This scaffold-level genome assembly includes 10,148 scaffolds and no assembled chromosomes.

Revision history

This record has not been revised

GenBank	RefSeq	Name	Level	Date	Action
GCA_002207925.1	GCF_002207925.1	PAV_r1.0	Scaffold	Jun 12, 2017	<div></div>

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