

[NCBI Datasets](#)[Taxonomy](#)[Genome](#)[Gene](#)[Command-line tools](#)[Documentation](#)

Genome assembly ASM211411v1

[Download](#)[datasets](#)[URL](#)[FTP](#)

Status: RefSeq GCF_002114115.1 is suppressed

This record was removed as a result of standard genome annotation processing. Please see www.ncbi.nlm.nih.gov/genome/annotation_euk/process/ for more information.

Actions

NCBI RefSeq assembly

GCF_002114115.1 (suppressed) (sequences differ from GenBank assembly)



Submitted GenBank assembly

GCA_002114115.1



Taxon

[Malus domestica](#) (apple)

Cultivar

Golden Delicious

Isolate

X9273 #13

WGS project

[MJAX01](#)

Assembly type

haploid

Submitter

IRHS

Date

May 3, 2017

Genome notes

NCBI has noted the following for this genome assembly. [View definitions](#)

- superseded by newer assembly for species

[View annotated genes](#)[See in Genome Data Viewer](#)



BLAST the genome



Compare genomes

Assembly statistics

	RefSeq	GenBank
Genome size	703 Mb	703 Mb
Total ungapped length	625.3 Mb	625.3 Mb
Number of chromosomes	17	17
Number of organelles	1	0
Number of scaffolds	806	806
Scaffold N50	37.6 Mb	37.6 Mb
Scaffold L50	9	9
Number of contigs	7,496	7,496
Contig N50	588.9 kb	588.9 kb
Contig L50	329	329
GC percent	38	38
Genome coverage	700x	700x
Assembly level	Chromosome	Chromosome
View sequences		view GenBank sequences

Sample details

BioSample ID	SAMN05603590
Description	Plant sample from Malus domestica
Submitter	IRHS
Isolate	X9273 #13
Cultivar	Golden Delicious
Development stage	Adult
Geographic location	France: Angers

[View more](#) 

Assembly methods

Sequencing technology
Illumina; PacBio; BioNano

Assembly method
DBG2OLC v. May-2016; SOAPdenovo2 v. May-2016; BESST v. May-2016; BioNano hybrid assembly v. May-2016

Additional genomes

[Browse all Malus domestica genomes \(41\)](#)

BioProject

[PRJNA339703](#)
Malus domestica isolate:X9273 #13 | cultivar:Golden Delicious Genome sequencing and assembly

Publications

Showing 5 of 27

Data Brief

2025

[New coastal records in northern Brittany \(Plouescat, NW France\): Sedimentological, palynological and paleogenomic data over the last 7.3 ka BP](#)
O David, et al.

Sci Data

2024

[Chromosome-level Haploid Assembly of Cannabis sativa L. cv. Pink Pepper](#)
BR Ryu, et al.

Evol Appl

2024

[Evolutionary Genomics Provides Insights Into Endangerment and Conservation of a Wild Apple Tree Species, *Malus sieversii*](#)
J Zhang, et al.

Sci Data

2024

[Telomere-to-telomere Genome Assembly of two representative Asian and European pear cultivars](#)
Y Qi, et al.

Mob DNA

2024

[Accelerating de novo SINE annotation in plant and animal genomes](#)
H Liao, et al.

View all 27 in PubMed

Publication list limited to 400 entries

Annotation details

[See full annotation report](#)

	RefSeq
Provider	NCBI RefSeq
Name	NCBI Malus domestica Annotation Release 102
Date	Apr 26, 2019

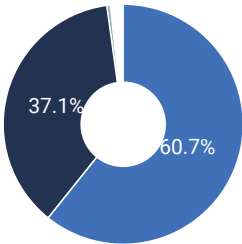
	RefSeq
Genes	45,408
Protein-coding	35,926
Software version	8.2

[View RefSeq annotation](#)

Quality analysis

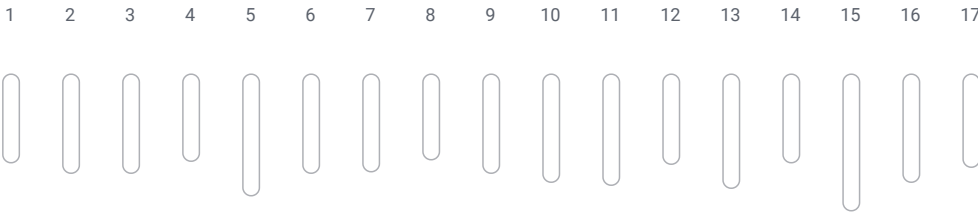
BUSCO analysis (4.0.2)

- Single_copy 60.7%
- Duplicated 37.1%
- Fragmented 0.5%
- Missing 1.7%



C:97.8%[S:60.7%,D:37.1%],F:0.5%,M:1.7%,n:2326
eudicots_odb10 (2326)

Chromosomes



View chromosomes from:

GenBank sequence

RefSeq sequence

Download

Chromosome	GenBank	RefSeq	Size (bp)	GC content (%)	Unlocalized count	Action
1	CM007867.1	NC_041789.1	32,709,648	38.5	0	<div></div>
2	CM007868.1	NC_041790.1	37,631,755	38	0	<div></div>
3	CM007869.1	NC_041791.1	37,690,471	38	0	<div></div>
4	CM007870.1	NC_041792.1	32,357,154	38	0	<div></div>
5	CM007871.1	NC_041793.1	48,068,851	38	0	<div></div>
6	CM007872.1	NC_041794.1	37,231,166	38	0	<div></div>
7	CM007873.1	NC_041795.1	36,738,692	38	0	<div></div>
8	CM007874.1	NC_041796.1	31,666,303	38	0	<div></div>
9	CM007875.1	NC_041797.1	37,676,754	38	0	<div></div>
10	CM007876.1	NC_041798.1	41,841,605	38	0	<div></div>
11	CM007877.1	NC_041799.1	42,925,075	38	0	<div></div>

Chromosome	GenBank	RefSeq	Size (bp)	GC content (%)	Unlocalized count	Action
12	CM007878.1	NC_041800.1	33,134,071	38	0	⋮
13	CM007879.1	NC_041801.1	44,437,459	38.5	0	⋮
14	CM007880.1	NC_041802.1	32,560,231	38	0	⋮
15	CM007881.1	NC_041803.1	55,080,361	38	0	⋮
16	CM007882.1	NC_041804.1	41,441,581	38.5	0	⋮
17	CM007883.1	NC_041805.1	34,817,048	38	0	⋮

Note: This genome assembly includes 789 unplaced scaffolds.

RefSeq and GenBank assembly differences

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

Added chromosome MT

Revision history

This record has not been revised

GenBank	RefSeq	Name	Level	Date	Action
GCA_002114115.1	GCF_002114115.1	ASM211411v1	Chromosome	May 3, 2017	⋮

FOLLOW NCBI











Connect with NLM



National Library of Medicine
8600 Rockville Pike
Bethesda, MD 20894

- Web Policies
- FOIA
- HHS Vulnerability Disclosure
- Help
- Accessibility
- Careers