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PPGV: a comprehensive database of peach population genome variation

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Abstract
Peach tree is one of the most important fruit trees in the world, and it has been cultivated for more than 7,500 years. In recent years, the genome and population resequencing of peach trees have been published continuously, which has effectively promoted the research of peach tree genetics and breeding. In order to promote the further mining and utilization of these data, we integrated and constructed a comprehensive peach genome and variation database (PPGV, http://peachtree.work/home). The PPGV contains 10 sets of published peach tree genome data, as well as genomic variation information for 1,378 peach tree samples (the resequencing data of 1,378 samples were aligned with the high-quality genomes of Lovell, CN14 and Chinesecling, respectively, for mutation detection). A variety of useful and flexible tools, such as BLAST, Gene ID Convert, KEGG/GO Enrichment, Primer Design and Gene function, were also specially designed for searching data and assisting in breeding.

Keywords Peach tree, Genome, Variation, Database, Tools module

Introduction

Peach tree (*Prunus persica*) is one of the most representative and widely cultivated crops of the rose family that originated in China [1]. Its fruit has a wonderful flavor and rich nutrients, thus giving the peach fruit high economic and health value. Peach trees were already planted in China at least 7,500 years ago and spread to most of the world over the millennia since. Today, peach is the fourth largest fruit after apples, pears and grapes, with 1,527,052 hectares harvested worldwide [2, 3].

The advancement of sequencing technology and the rapid reduction of sequencing costs have greatly promoted the research process of plant genome and population evolution. Up to now, more than 1,300 plant genomes have been published and are still growing rapidly (https://www.plabipd.de/index.ep). For peach trees, at least five more peach tree genomes have been released since the first genome was published in 2013 [1, 2, 4–6]. Studies have shown that the genomes of different peach tree varieties have significant differences, such as “LHSM” and “124 Pan” with genome sizes of 257.2 Mb and 206 Mb, respectively [4, 6]. To reveal the genetic diversity and evolutionary history of peach trees, many population resequencing studies have been widely carried out based on the above reference genomes. For example, Cao et al. [7] identified 409 selected genes based on resequencing analysis of 10 wild and 74 cultivated peach, and proved that human breeding activities led to a sharp decline in the heterozygosity proportion of SNPs;

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Guan et al. [8] identified a 1.67 Mb structural variation controlling the shape of peach fruit through genome and resequencing analysis of 149 peach trees; Li et al. [9] and Yu et al. [6] analyzed the domestication patterns and the biochemical basis of fruit flavor in the breeding process of peach trees through resequencing data analysis of 480 and 564 peach accessions, respectively. Extensive large-scale resequencing not only greatly promoted the research progress of peach trees, but also released a large amount of raw sequencing data. Effectively integrating and utilizing these data is undoubtedly quite challenging [10, 11].

For many food and cash crops, various functional databases have been successfully constructed [12–14]. For example, Gui et al. [15] constructed a comprehensive maize multiomics database; based on thousands of soybean germplasm resources, Zheng et al. [16] built a large database containing 65,374,688 SNPs and 10,952,749 InDels. In addition, databases of genetic variation of species such as *Brassica napus*, sorghum and tea plants have been successfully published [17–19]. In the previous research, although some databases of *Rosaceae* plants have been reported (https://www.rosaceae.org/), the database dedicated to the genetic variation of peach tree population has not been constructed.

Materials and methods

Retrieval of genome and resequencing data resources

Before constructing the database, we first obtain peach tree genome sequences, gff files, protein sequences, and a large amount of resequencing data from public databases such as NCBI (https://www.ncbi.nlm.nih.gov/), CNCB (https://www.cncb.ac.cn/) and GDR (https://www.rosaceae.org/). In addition to the ten sets of genomic data (including 'Lovell', 'CN14', 'Chinesecling', 'Pfe', 'Pka', 'Pmi', 'Pda', 'LHSM', 'RYP1', '124Pan'), another 1,378 samples of resequencing data were downloaded for analysis. For the resequencing data, detailed information can be found in the Overview section of this database (http://peachtree.work/overview).

Identification of the peach tree genome and population genetic variation

In this study, we chose the 'Lovell' (about 220 Mb), 'CN14' (about 222 Mb), and 'Chinesecling' (about 236 Mb) peach tree genomes as reference genomes and used the BWA software to build indexes for each of them [19]. The downloaded sequences were filtered using the following parameters of the fastp software: --length_required=25 --cut_front --cut_window_size 4 --cut_mean_quality 15 [20]. High quality reads of all samples were aligned to the reference genome with BWA software under the default reference. Following that, use the samtools software to convert the SAM file to the BAM format, then sort and build an index. PCR duplicates were removed using the Picard software [21]. Subsequently, the HaplotypeCaller mode of GATK software is used to identify SNP/INDEL mutation sites with default parameters, and finally the original mutation data set is obtained. Due to differences in the depth of resequencing among populations, we used the --minQ parameter to filter SNPs (--minQ 180) and INDELs (--minQ 50) rseparately, and annotated all the mutation sites by snpEFF software [22]. At the same time, structural variations were identified using the default parameters of the LUMPY software [23].

Genomic and protein sequence analysis

We first used EDTA software to perform a preliminary identification of transposons in each genome, and TEsorter software was used to classify unknown types of transposons based on the above identification results, and then further identification was performed using EDTA software to ensure the reliability of the results [24, 25]. The MISA software was used to identify SSR (Simple Sequence Repeat) loci on different genomes, with the specific definition (unit_size, min_repeats) parameters as follows: 2–6, 3–6, 4–5, 5−4, 6−4. At the same time, we annotate the protein sequence with eggNOG online website (http://eggnog5.embl.de/#/app/home) and pfamscan software respectively. In addition, transcription factors were further identified and annotated by iTAK website (http://itak.feilab.net/cgi-bin/itak/index.cgi).

Integration of other biological analysis tools

On this website, we offer several practical bioinformatics tools such as get sequence, blast, primer design, and enrichment analysis. These tools are primarily implemented by utilizing bioinformatics software and R packages such as seqtk, blast, primer3, and clusterProfiler. In addition, some softwares such as ORFfinder, SSRMMD and TBtools are also used for data analysis or to provide support for this site [26, 27].

Database construction

We used Flask (a web package encoded by Python) and Dash (a fast Python web framework package) to build the basic framework of this website, and used Hypertext Markup Language (HTML) and Cascading Style Sheets (CSS) to refine the web layout. All interactive functions were implemented through the third-party plugin feffery-antd-components, which provides rich UI components and interactive functions to help developers quickly build interactive web applications. At the same time, we also used the cacheout caching technology to enhance the response speed of the website. All the data were imported into the MySQL database to improve the query speed. Finally, the website was deployed on Ubuntu 22.04 LTS system provided by Tencent Cloud.

Results

Summary of the PPGV database

In this study, we constructed a comprehensive peach genome and population variation database, which includes genetic variation information for 1,378 peach samples aligned to the "Lovell", "CN14", and "Chinese-cling" genomes, as well as genome information from 10 publicly available peach genomes. Apart from the Home and Overview pages, PPGV mainly consists of five functional modules: Variation, Genome, JBrowse, Tools, and Download. In the following, we will provide a detailed introduction to these modules (Fig. 1). However, it is particularly important to note that due to some studies only publishing genome sequences without accompanying protein sequences, gff files, or accompanying files that cannot be used, it is difficult to perform transcript factor, collinearity, and other analyses.

Variation module

In the current module, users can choose any one of the three reference genomes, "CN14", "Lovell", and "Chinese-cling", and then search for SNP, INDEL, or SV variations in different samples (Fig. 2A). According to the different types of mutations, we provide diverse search modes. For SNP and INDEL, after selecting the reference genome, further selection of the sample name and chromosome information is required, and the range interval of the starting and ending positions of the variant site needs to be entered (Fig. 2B). After that, clicking the "Submit" button will submit the query conditions and view the corresponding results (Fig. 2C). At the same time, users can enter the gene ID to further filter the above search results to view specific gene-related mutation sites. They can also query specific types of mutations based on SnpEff annotation results, such as "splice acceptor variant" and "MODERATE" (Fig. 2D). For INDEL and SV, users can also filter the query results based on the mutation type and length (Fig. 2E).

Genome module

In the Genome module, PPGV provides three search functions including TE/SSR/Synteny, Function search, and Transcription factor (Fig. 3A). Taking the TE/SSR/Synteny sub-module as an example, when users enter the interactive interface, they need to select the genome first, and then click the submit button to get the corresponding results (Fig. 3B). Based on the result list, users can further filter the results based on chromosome or the type of transposon/SSR (Fig. 3C). Meanwhile, through the Genomic Synteny function, users can query the tandem duplicated genes within different peach tree genomes and the collinear gene pairs between genomes (Fig. 3D). In the Function search sub-module, users can easily obtain the GO, KEGG and Pfam annotation information of different peach tree genomes, and visualize the gene structure of specific genes (Fig. 3E). In addition, we provide a transcription factor search function. Users can not only quickly download all the sequences of specific transcriptome factors in each genome, but also observe the quantitative characteristics of transcription factors in different peach genomes through column charts (Fig. 3F).

Tools module

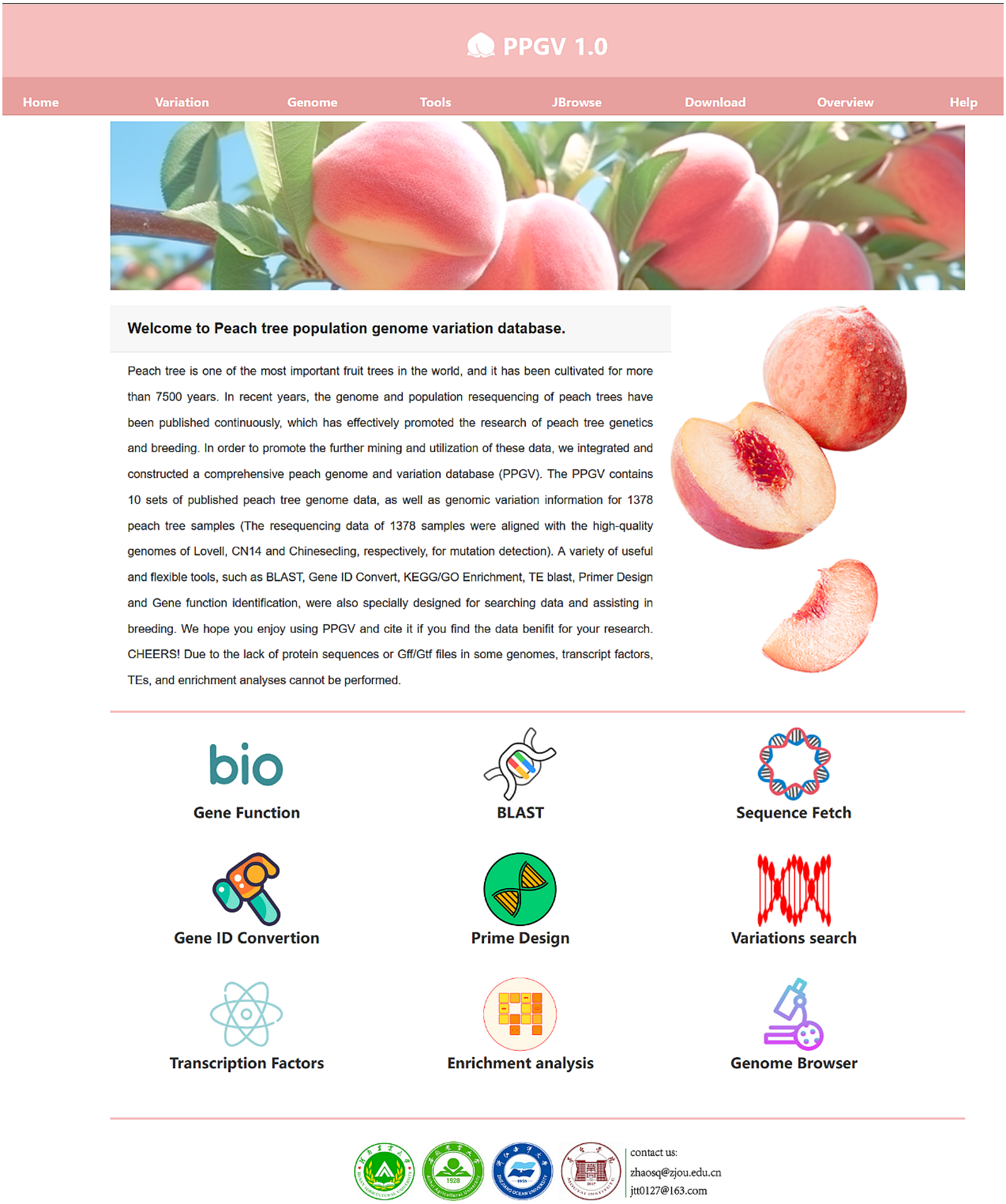
To enhance the functionality of the PPGV site, we have configured several commonly used biology tools in the Tools module, including GetSequence, BLAST, IDConvert, orfFinder, Primerdesign, PolySSR, and EnrichmentAnalysis. In this module, users can not only obtain the corresponding sequences according to the input location information or gene ID (Fig. 4A), but also perform blastn, blastp and TEblast analysis through the alignment function (Fig. 4B). At the same time, through the gene ID converter, homologous genes of different genes can be obtained (Fig. 4C). In addition, primer design and identification of polymorphic SSR sites are also built into the Tools module, and users can enter sequences and parameters and click the submit button to obtain the corresponding results (Fig. 4D, E). It should be noted that for PPGV, all input sequences need to be in Fasta format. Moreover, PPGV can also perform orffinder and KEGG/GO enrichment analysis. As shown in Fig. 5A, after selecting the GO/KEGG enrichment analysis, the user can upload the target gene set or paste it directly into the input box, and then select the more detailed analysis parameters on the right side of the page and click submit, and wait for a short time to download the corresponding analysis results (Fig. 5B).

JBrowse, download and overview module

Due to the volume of population variation data obtained based on three different reference genomes exceeding 1 Tb, therefore, in the JBrowse module, we only provide the browsing function for genome and GFF files to ensure a good user interaction experience. The Overview module displays a list of all samples and density and quantity statistics graphs related to variations (Fig. 5C). Especially through the download module, users can not only download SNP/SV and INDEL mutation files of all samples, but also obtain genome sequences, protein sequences, gff files, and SSR locus file (Fig. 5D). All these genomic data sets and resources promote the rapid and simple genetic analysis of peach crops.

Discussion

In recent years, the explosive growth of genome and other sequencing data has promoted the progress of plant database research. More and more databases are being released that integrate massive amounts of data [28–30].



Welcome to Peach tree population genome variation database.

Peach tree is one of the most important fruit trees in the world, and it has been cultivated for more than 7500 years. In recent years, the genome and population resequencing of peach trees have been published continuously, which has effectively promoted the research of peach tree genetics and breeding. In order to promote the further mining and utilization of these data, we integrated and constructed a comprehensive peach genome and variation database (PPGV). The PPGV contains 10 sets of published peach tree genome data, as well as genomic variation information for 1378 peach tree samples (The resequencing data of 1378 samples were aligned with the high-quality genomes of Lovell, CN14 and Chinesecling, respectively, for mutation detection). A variety of useful and flexible tools, such as BLAST, Gene ID Convert, KEGG/GO Enrichment, TE blast, Primer Design and Gene function identification, were also specially designed for searching data and assisting in breeding. We hope you enjoy using PPGV and cite it if you find the data benifit for your research. CHEERS! Due to the lack of protein sequences or Gff/Gtf files in some genomes, transcript factors, TEs, and enrichment analyses cannot be performed.

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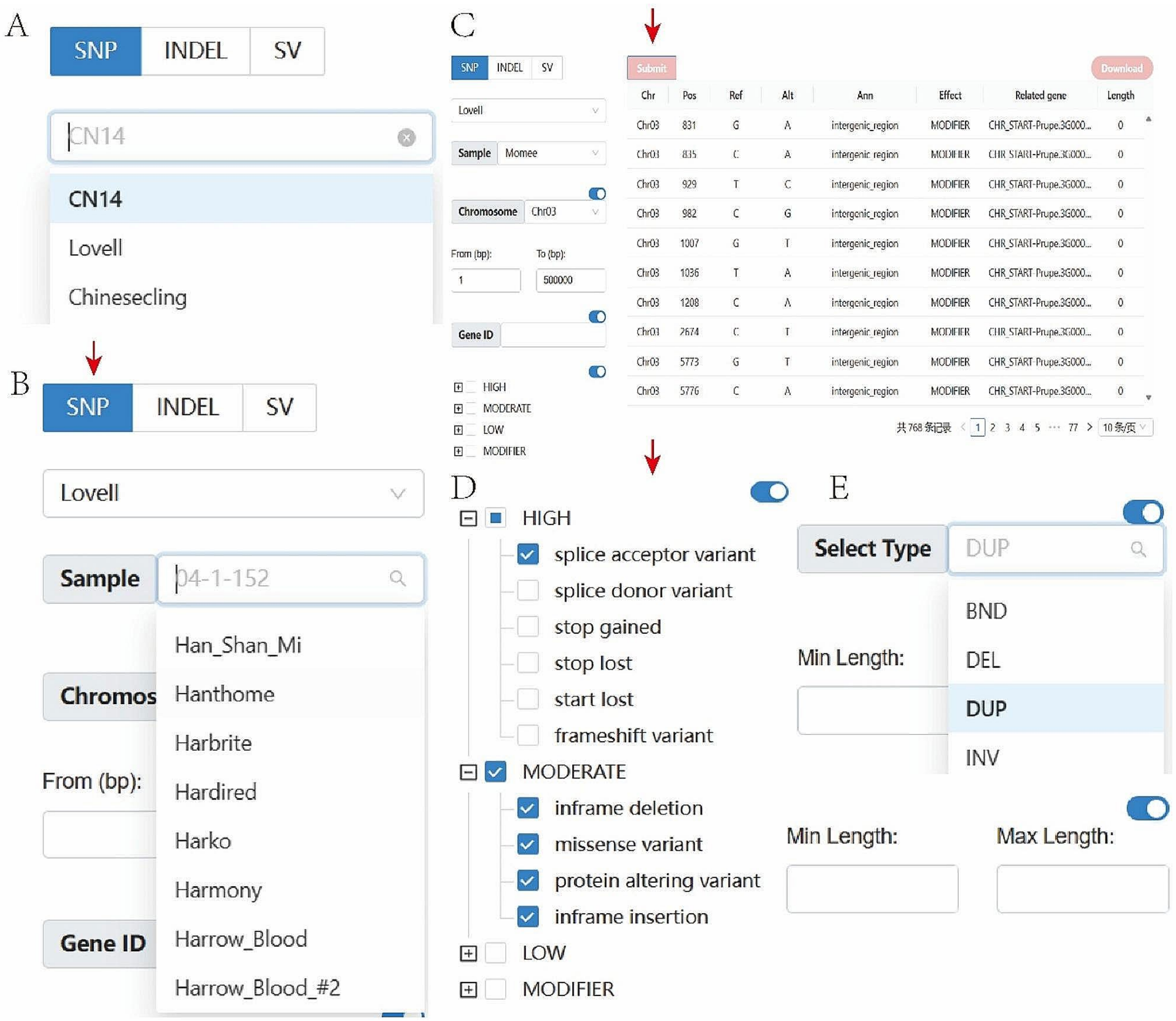
Fig. 1 Screenshot of the homepage of PPGV database, showing a subset of available genome sequences, search and analysis tools



Lovell

Sample: Momee

Chromosome: Chr03

From (bp): 1 To (bp): 500000

Gene ID:

⊞ □ HIGH
⊞ □ MODERATE
⊞ □ LOW
⊞ □ MODIFIER

Chr	Pos	Ref	Alt	Ann	Effect	Related gene	Length
Chr03	831	G	A	intergenic_region	MODIFIER	CHR_START-Prupe.3G000...	0
Chr03	835	C	A	intergenic_region	MODIFIER	CHR_START-Prupe.3G000...	0
Chr03	929	T	C	intergenic_region	MODIFIER	CHR_START-Prupe.3G000...	0
Chr03	982	C	G	intergenic_region	MODIFIER	CHR_START-Prupe.3G000...	0
Chr03	1007	G	T	intergenic_region	MODIFIER	CHR_START-Prupe.3G000...	0
Chr03	1036	T	A	intergenic_region	MODIFIER	CHR_START-Prupe.3G000...	0
Chr03	1208	C	A	intergenic_region	MODIFIER	CHR_START-Prupe.3G000...	0
Chr03	2674	C	T	intergenic_region	MODIFIER	CHR_START-Prupe.3G000...	0
Chr03	5773	G	T	intergenic_region	MODIFIER	CHR_START-Prupe.3G000...	0
Chr03	5776	C	A	intergenic_region	MODIFIER	CHR_START-Prupe.3G000...	0

共 768 条记录 < 1 2 3 4 5 ··· 77 > 10 条/页

⊟ ■ HIGH
- ☑ splice acceptor variant
- □ splice donor variant
- □ stop gained
- □ stop lost
- □ start lost
- □ frameshift variant

⊟ ☑ MODERATE
- ☑ inframe deletion
- ☑ missense variant
- ☑ protein altering variant
- ☑ inframe insertion

⊞ □ LOW

⊞ □ MODIFIER

Select Type: DUP

BND
DEL
DUP
INV

Min Length:

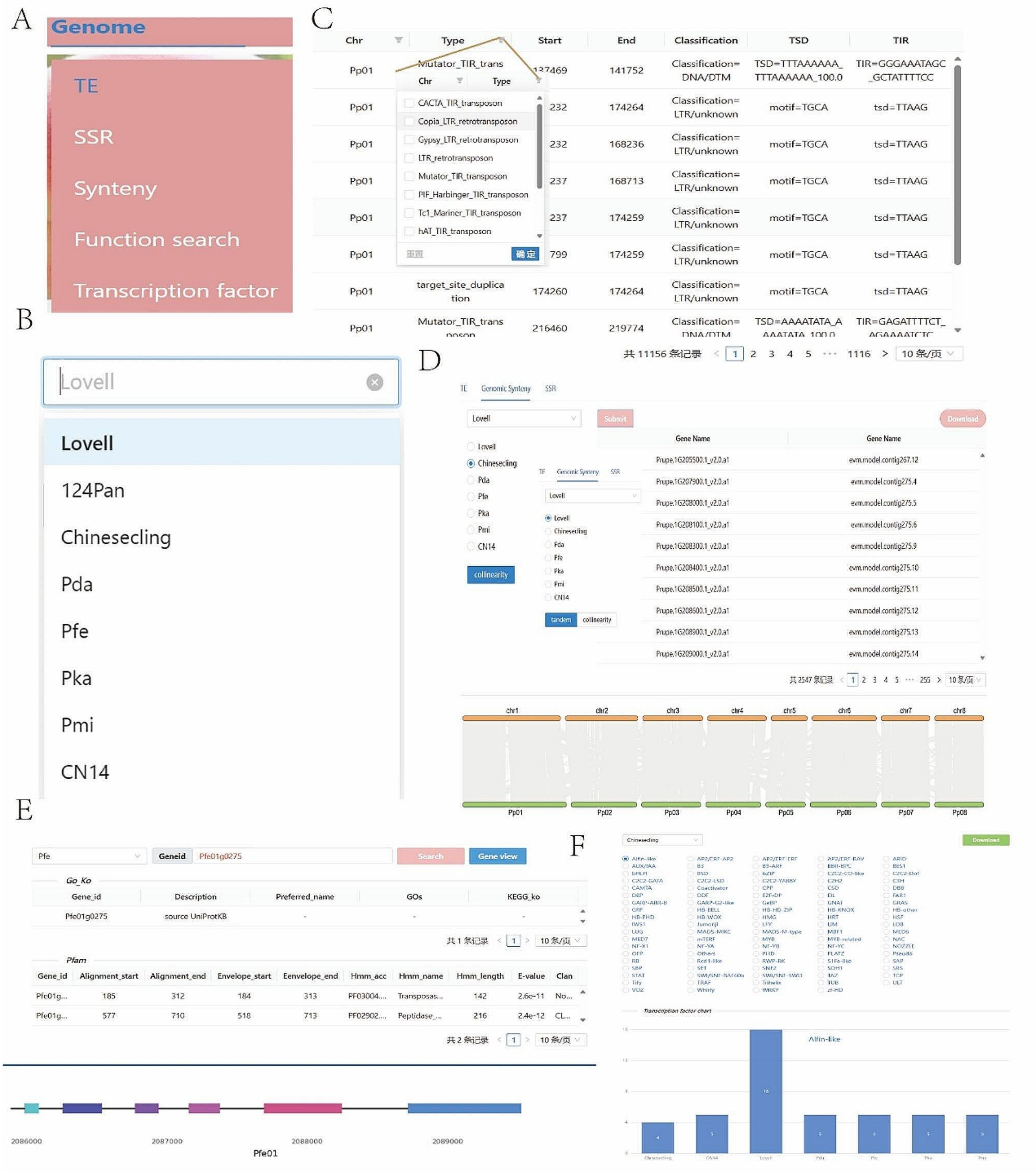
Min Length: Max Length:

Fig. 2 Flow chart of mutation search module. (**A**) Select reference genome. (**B**) Selection of samples. (**C**) Display of search results. (**D**) Search according to the annotation results. (**E**) Filter the results according to mutation type or length

At present, ten peach tree genomes and thousands of resequencing data have been published, however, these data are not yet effectively integrated for deep utilization.

Although some published *Rosaceae* databases contain some peach tree data, these databases are still not comprehensive enough. Such as the famous GDR (https://www.rosaceae.org/) database, which only contains a small amount of peach tree population variation information. The newly released ROFT database contains the transcription and expression information of four Rosaceae plants, including peach trees [31]. In this study, we collected 10 sets of peach genome and 1, 378 samples of resequencing data, and through multiple analysis strategies, tens of millions of variation information including SNP/INDEL/SV were integrated into the PPGV database. At the same time, users can not only easily obtain tandem repeat genes, collinear genes and transposon sequences on the genome, but also query SSR loci and transcription factor sequences through the interactive interface. At the same time, PPGV is equipped with a variety of bioinformatics tools, such as Blast, primer design, and enrichment analysis, which enhance the practicality of the database and will contribute to the genetic breeding research of peach trees.

However, it needs to be acknowledged that some of the genomic protein data and GFF files in this database still need to be supplemented. At present, the genome quality of peach trees still needs to be improved, and a large number of resequencing data are still dominated by next-generation sequencing. In the future, we will continue to update this site with the release of peach tree T2T genome and long-read population sequencing data



Chr	Type	Start	End	Classification	TSD	TIR
Pp01	Mutator_TIR_trans	137469	141752	Classification=DNA/DTM	TSD=TTTAAAAAA_TTTAAAAAA_100.0	TIR=GGGAAATAGC_GCTATTTTCC
Pp01		232	174264	Classification=LTR/unknown	motif=TGCA	tsd=TTAAG
Pp01		232	168236	Classification=LTR/unknown	motif=TGCA	tsd=TTAAG
Pp01		237	168713	Classification=LTR/unknown	motif=TGCA	tsd=TTAAG
Pp01		237	174259	Classification=LTR/unknown	motif=TGCA	tsd=TTAAG
Pp01		799	174259	Classification=LTR/unknown	motif=TGCA	tsd=TTAAG
Pp01	target_site_duplication	174260	174264	Classification=LTR/unknown	motif=TGCA	tsd=TTAAG
Pp01	Mutator_TIR_transposon	216460	219774	Classification=DNA/DTM	TSD=AAAATATA_AAAATATA_100.0	TIR=GAGATTTTCT_AGAAAATCTC

共 11156 条记录 < 1 2 3 4 5 ··· 1116 > 10 条/页

Gene Name	Gene Name
Prupe.1G205500.1_v2.0.a1	evm.model.contig267.12
Prupe.1G207900.1_v2.0.a1	evm.model.contig275.4
Prupe.1G208000.1_v2.0.a1	evm.model.contig275.5
Prupe.1G208100.1_v2.0.a1	evm.model.contig275.6
Prupe.1G208300.1_v2.0.a1	evm.model.contig275.9
Prupe.1G208400.1_v2.0.a1	evm.model.contig275.10
Prupe.1G208500.1_v2.0.a1	evm.model.contig275.11
Prupe.1G208600.1_v2.0.a1	evm.model.contig275.12
Prupe.1G208900.1_v2.0.a1	evm.model.contig275.13
Prupe.1G209000.1_v2.0.a1	evm.model.contig275.14

共 2547 条记录 < 1 2 3 4 5 ··· 255 > 10 条/页

Go_Ko

Gene_id	Description	Preferred_name	GOs	KEGG_ko
Pfe01g0275	source UniProtKB	-	-	-

共 1 条记录 < 1 > 10 条/页

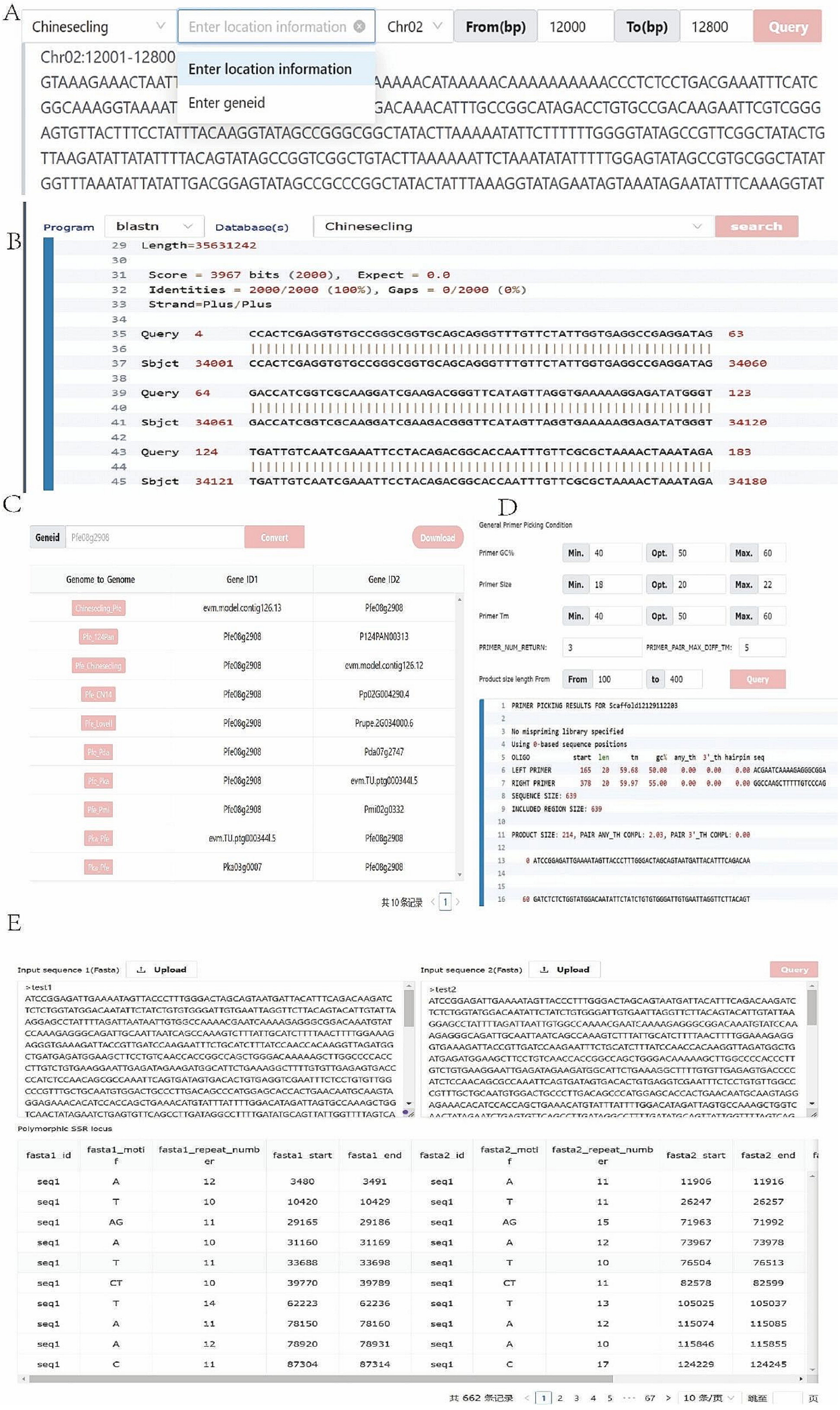
Pfam

Gene_id	Alignment_start	Alignment_end	Envelope_start	Eenvelope_end	Hmm_acc	Hmm_name	Hmm_length	E-value	Clan
Pfe01g...	185	312	184	313	PF03004....	Transposas...	142	2.6e-11	No...
Pfe01g...	577	710	518	713	PF02902....	Peptidase_...	216	2.4e-12	CL...

共 2 条记录 < 1 > 10 条/页

Fig. 3 Functional schematic of Genome module. (**A**) Select the submodule. (**B**) Select the genome. (**C**) Example of transposon search results. (**D**) Example plot of tandem repeat and genomic collinearity results (**E**) Examples of gene function search results. (**F**) Transcription factor submodule

(this database will integrate the newly released genome and resequencing data every 12 months until a more complete database is released). In conclusion, PPGV will promote the study of peach tree genome and population genome, and contribute to peach tree breeding and fruit improvement.



```
Chr02:12001-12800
GTAAAGAAACTAATT                         AAAAACATAAAAACAAAAAAAAAACCCTCTCCTGACGAAATTTCATC
GGCAAAGGTAAAAT                          GACAAACATTTGCCGGCATAGACCTGTGCCGACAAGAATTCGTCGGG
AGTGTTACTTTCCTATTTACAAGGTATAGCCGGGCGGCTATACTTAAAAATATTCTTTTTTGGGGTATAGCCGTTCGGCTATACTG
TTAAGATATTATATTTTACAGTATAGCCGGTCGGCTGTACTTAAAAAATTCTAAATATATTTTTGGAGTATAGCCGTGCGGCTATAT
GGTTTAAATATTATATTGACGGAGTATAGCCGCCCGGCTATACTATTTAAAGGTATAGAATAGTAAATAGAATATTTCAAAGGTAT
```

```
Length=35631242

 Score = 3967 bits (2000),  Expect = 0.0
 Identities = 2000/2000 (100%), Gaps = 0/2000 (0%)
 Strand=Plus/Plus

Query  4      CCACTCGAGGTGTGCCGGGCGGTGCAGCAGGGTTTGTTCTATTGGTGAGGCCGAGGATAG  63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  34001  CCACTCGAGGTGTGCCGGGCGGTGCAGCAGGGTTTGTTCTATTGGTGAGGCCGAGGATAG  34060

Query  64     GACCATCGGTCGCAAGGATCGAAGACGGGTTCATAGTTAGGTGAAAAAGGAGATATGGGT  123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  34061  GACCATCGGTCGCAAGGATCGAAGACGGGTTCATAGTTAGGTGAAAAAGGAGATATGGGT  34120

Query  124    TGATTGTCAATCGAAATTCCTACAGACGGCACCAATTTGTTCGCGCTAAAACTAAATAGA  183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  34121  TGATTGTCAATCGAAATTCCTACAGACGGCACCAATTTGTTCGCGCTAAAACTAAATAGA  34180
```

Genome to Genome	Gene ID1	Gene ID2
Chinesecling_Pfe	evm.model.contig126.13	Pfe08g2908
Pfe_124Pan	Pfe08g2908	P124PAN00313
Pfe_Chinesecling	Pfe08g2908	evm.model.contig126.12
Pfe_CN14	Pfe08g2908	Pp02G004290.4
Pfe_Lovell	Pfe08g2908	Prupe.2G034000.6
Pfe_Pda	Pfe08g2908	Pda07g2747
Pfe_Pka	Pfe08g2908	evm.TU.ptg000344l.5
Pfe_Pmi	Pfe08g2908	Pmi02g0332
Pka_Pfe	evm.TU.ptg000344l.5	Pfe08g2908
Pka_Pfe	Pka03g0007	Pfe08g2908

共 10 条记录 < 1 >

General Primer Picking Condition

Primer GC%	Min.	40	Opt.	50	Max.	60
Primer Size	Min.	18	Opt.	20	Max.	22
Primer Tm	Min.	40	Opt.	50	Max.	60

PRIMER_NUM_RETURN: 3 PRIMER_PAIR_MAX_DIFF_TM: 5

Product size length From From 100 to 400

```
PRIMER PICKING RESULTS FOR Scaffold12129112203

No mispriming library specified
Using 0-based sequence positions
OLIGO            start  len     tm     gc%  any_th  3'_th hairpin seq
LEFT PRIMER        165   20  59.68   50.00    0.00   0.00    0.00 ACGAATCAAAAGAGGGCGGA
RIGHT PRIMER       378   20  59.97   55.00    0.00   0.00    0.00 GGCCAAGCTTTTTGTCCCAG
SEQUENCE SIZE: 639
INCLUDED REGION SIZE: 639

PRODUCT SIZE: 214, PAIR ANY_TH COMPL: 2.03, PAIR 3'_TH COMPL: 0.00

    0 ATCCGGAGATTGAAAATAGTTACCCTTTGGGACTAGCAGTAATGATTACATTTCAGACAA



   60 GATCTCTCTGGTATGGACAATATTCTATCTGTGTGGGATTGTGAATTAGGTTCTTACAGT
```

Input sequence 1(Fasta)

```
>test1
ATCCGGAGATTGAAAATAGTTACCCTTTGGGACTAGCAGTAATGATTACATTTCAGACAAGATC
TCTCTGGTATGGACAATATTCTATCTGTGTGGGATTGTGAATTAGGTTCTTACAGTACATTGTATTA
AGGAGCCTATTTTAGATTAATAATTGTGGCCAAAACGAATCAAAAGAGGGCGGACAAATGTAT
CCAAAGAGGGCAGATTGCAATTAATCAGCCAAAGTCTTTATTGCATCTTTTAACTTTTGGAAAG
AGGGTGAAAGATTACCGTTGATCCAAGAATTTCTGCATCTTTATCCAACCACAAGGTTAGATGG
CTGATGAGATGGAAGCTTCCTGTCAACCACCGGCCAGCTGGGACAAAAAGCTTGGCCCCACC
CTTGTCTGTGAAGGAATTGAGATAGAAGATGGCATTCTGAAAGGCTTTTGTGTTGAGAGTGACC
CCATCTCCAACAGCGCCAAATTCAGTGATAGTGACACTGTGAGGTCGAATTTCTCCTGTGTTGG
CCCGTTTGCTGCAATGTGGACTGCCCTTGACAGCCCATGGAGCACCACTGAACAATGCAAGTA
GGAGAAACACATCCACCAGCTGAAACATGTATTTATTTTGGACATAGATTAGTGCCAAAGCTGG
TCAACTATAGAATCTGAGTGTTCAGCCTTGATAGGCCTTTTGATATGCAGTTATTGGTTTTAGTCA
```

Input sequence 2(Fasta)

```
>test2
ATCCGGAGATTGAAAATAGTTACCCTTTGGGACTAGCAGTAATGATTACATTTCAGACAAGATC
TCTCTGGTATGGACAATATTCTATCTGTGGGATTGTGAATTAGGTTCTTACAGTACATTGTATTAA
GGAGCCTATTTTAGATTAATTGTGGCCAAAACGAATCAAAAGAGGGCGGACAAATGTATCCAA
AGAGGGCAGATTGCAATTAATCAGCCAAAGTCTTTATTGCATCTTTTAACTTTTGGAAAGAGG
GTGAAAGATTACCGTTGATCCAAGAATTTCTGCATCTTTATCCAACCACAAGGTTAGATGGCTG
ATGAGATGGAAGCTTCCTGTCAACCACCGGCCAGCTGGGACAAAAAGCTTGGCCCCACCCTT
GTCTGTGAAGGAATTGAGATAGAAGATGGCATTCTGAAAGGCTTTTGTGTTGAGAGTGACCCC
ATCTCCAACAGCGCCAAATTCAGTGATAGTGACACTGTGAGGTCGAATTTCTCCTGTGTTGGCC
CGTTTGCTGCAATGTGGACTGCCCTTGACAGCCCATGGAGCACCACTGAACAATGCAAGTAGG
AGAAACACATCCACCAGCTGAAACATGTATTTATTTTGGACATAGATTAGTGCCAAAGCTGGTC
AACTATAGAATCTGAGTGTTCAGCCTTGATAGGCCTTTTGATATGCAGTTATTGGTTTTAGTCAG
```

Polymorphic SSR locus

fasta1_id	fasta1_motif	fasta1_repeat_number	fasta1_start	fasta1_end	fasta2_id	fasta2_motif	fasta2_repeat_number	fasta2_start	fasta2_end	fa
seq1	A	12	3480	3491	seq1	A	11	11906	11916	
seq1	T	10	10420	10429	seq1	T	11	26247	26257	
seq1	AG	11	29165	29186	seq1	AG	15	71963	71992	
seq1	A	10	31160	31169	seq1	A	12	73967	73978	
seq1	T	11	33688	33698	seq1	T	10	76504	76513	
seq1	CT	10	39770	39789	seq1	CT	11	82578	82599	
seq1	T	14	62223	62236	seq1	T	13	105025	105037	
seq1	A	11	78150	78160	seq1	A	12	115074	115085	
seq1	A	12	78920	78931	seq1	A	10	115846	115855	
seq1	C	11	87304	87314	seq1	C	17	124229	124245	

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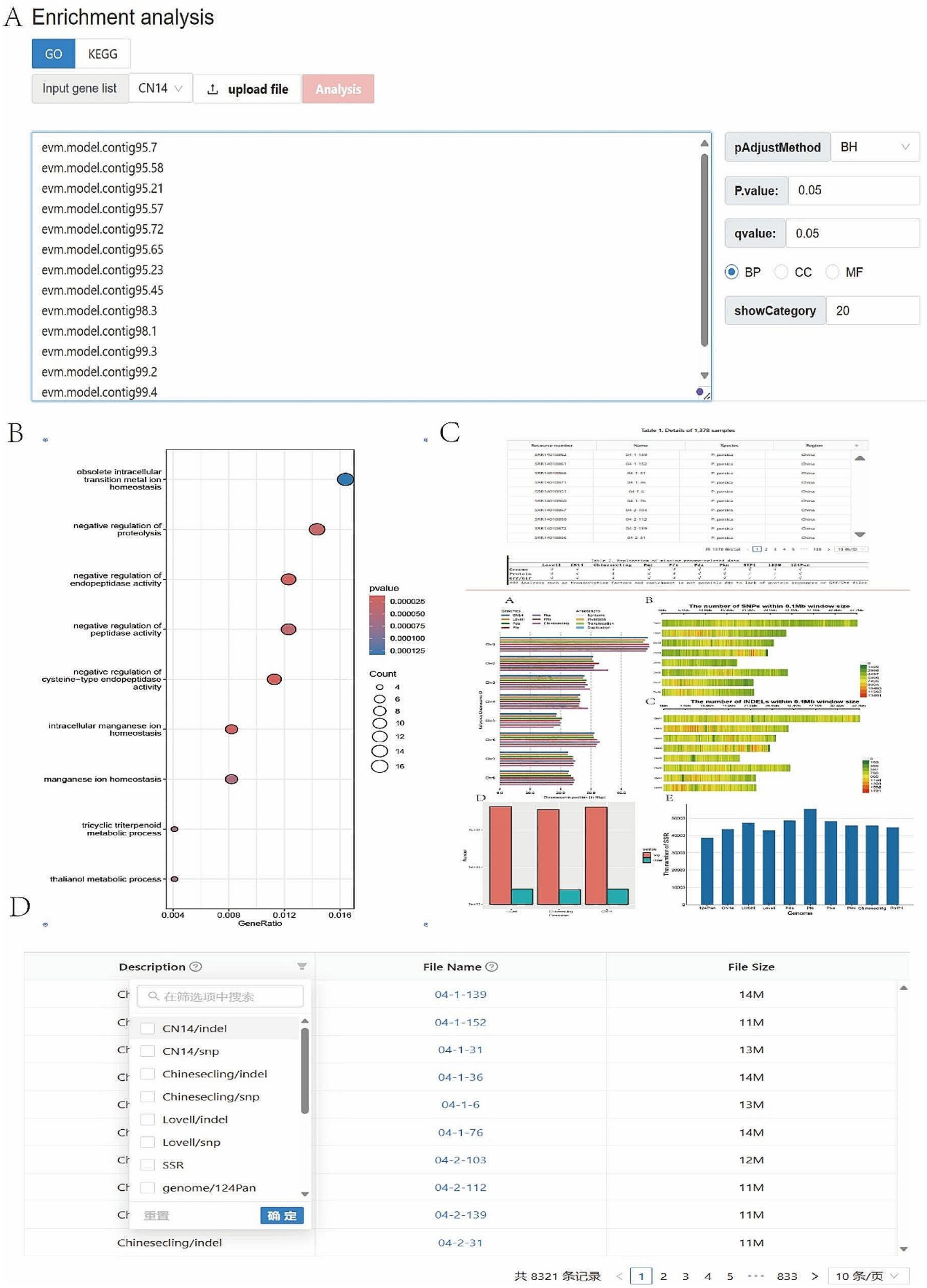
Fig. 4 Tools built-in biology tool example. (**A**) Sequence fetch function. (**B**) Sequence alignment function. (**C**) Gene ID conversion. (**D**) Primer design. (**E**) Polymorphism SSR site identification



A
Enrichment analysis
GO
KEGG
Input gene list
CN14
upload file
Analysis

evm.model.contig95.7
evm.model.contig95.58
evm.model.contig95.21
evm.model.contig95.57
evm.model.contig95.72
evm.model.contig95.65
evm.model.contig95.23
evm.model.contig95.45
evm.model.contig98.3
evm.model.contig98.1
evm.model.contig99.3
evm.model.contig99.2
evm.model.contig99.4

pAdjustMethod: BH

P.value: 0.05

qvalue: 0.05

● BP ○ CC ○ MF

showCategory: 20

B
obsolete intracellular transition metal ion homeostasis
negative regulation of proteolysis
negative regulation of endopeptidase activity
negative regulation of peptidase activity
negative regulation of cysteine−type endopeptidase activity
intracellular manganese ion homeostasis
manganese ion homeostasis
tricyclic triterpenoid metabolic process
thalianol metabolic process
0.004
0.008
0.012
0.016
GeneRatio
pvalue
0.000025
0.000050
0.000075
0.000100
0.000125
Count
4
6
8
10
12
14
16

Table 1. Details of 1,378 samples

Resource number	Name	Species	Region
SRR14010862	04-1-139	P. persica	China
SRR14010861	04-1-152	P. persica	China
SRR14010866	04-1-31	P. persica	China
SRR14010871	04-1-36	P. persica	China
SRR14010851	04-1-6	P. persica	China
SRR14010860	04-1-76	P. persica	China
SRR14010867	04-2-103	P. persica	China
SRR14010850	04-2-112	P. persica	China
SRR14010872	04-2-139	P. persica	China
SRR14010856	04-2-31	P. persica	China

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Table 2. Explanation of missing genome-related data

	Lovell	CN14	Chinesecling	Pmi	Pfe	Pdu	Pku	SYP1	LHSW	124Pan
Genome	√	√	√	√	√	√	√	√	√	√
Protein	√	√	√	√	√	√	√	/	/	√
Gff/Gtf	√	√	√	√	√	√	√	/	/	√

*** Analysis such as transcription factors and enrichment is not possible due to lack of protein sequences or Gff/Gtf files

Description	File Name	File Size
Ch	04-1-139	14M
Ch	04-1-152	11M
Ch	04-1-31	13M
Ch	04-1-36	14M
Ch	04-1-6	13M
Ch	04-1-76	14M
Ch	04-2-103	12M
Ch	04-2-112	11M
Ch	04-2-139	11M
Chinesecling/indel	04-2-31	11M

在筛选项中搜索
□ CN14/indel
□ CN14/snp
□ Chinesecling/indel
□ Chinesecling/snp
□ Lovell/indel
□ Lovell/snp
□ SSR
□ genome/124Pan
重置 确定

共 8321 条记录 < 1 2 3 4 5 ··· 833 > 10 条/页

Fig. 5 Examples of enrichment analysis and other functional modules. (**A**) and (**B**) represent the enrichment analysis input page and the result display, respectively. (**C**) Overview page. (**D**) Download page

Abbreviations

PPGV	Peach Population Genome Variation
SNP	Single nucleotide polymorphism
INDEL	Insertion-deletion
SV	Structure Variantion
TE	Transposable element

Author contributions

S.Z. and T.J. conceived the project and was responsible for project initiation. Y.A. and Q.B. supervised and managed the project and research. The data collection and bioinformatics analyses were led by Y.A., Q.B., L.L., F.Z., and S.Y. The construction of the database and the writing of the manuscript were mainly done by Y.A. All authors read and approved the manuscript.

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Data availability

All materials and related data in this study are provided in the PPGV database.

Declarations

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Conflict of interest

The authors declare that they have no conflict of interest.

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