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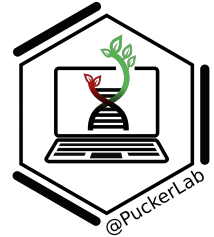

Prof. Dr. Boas Pucker

Long Read Genomics

- Read Mapping and Variant Calling

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Availability of slides

- All materials are freely available (CC BY) - after the lectures:
  - GitHub: https://github.com/bpucker/LRG

- Questions: Feel free to ask at any time

- Feedback, comments, or questions: pucker[a]uni-bonn.de

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Repetition

- Genome sequence assembly
- Assembly quality evaluation (completeness, contiguity, correctness)
- Structural annotation (GeMoMa, BRAKER3)
  - ab initio
  - hint-based
- Functional annotation (KIPEs, InterProScan5)

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Read Mapping & Variant Calling

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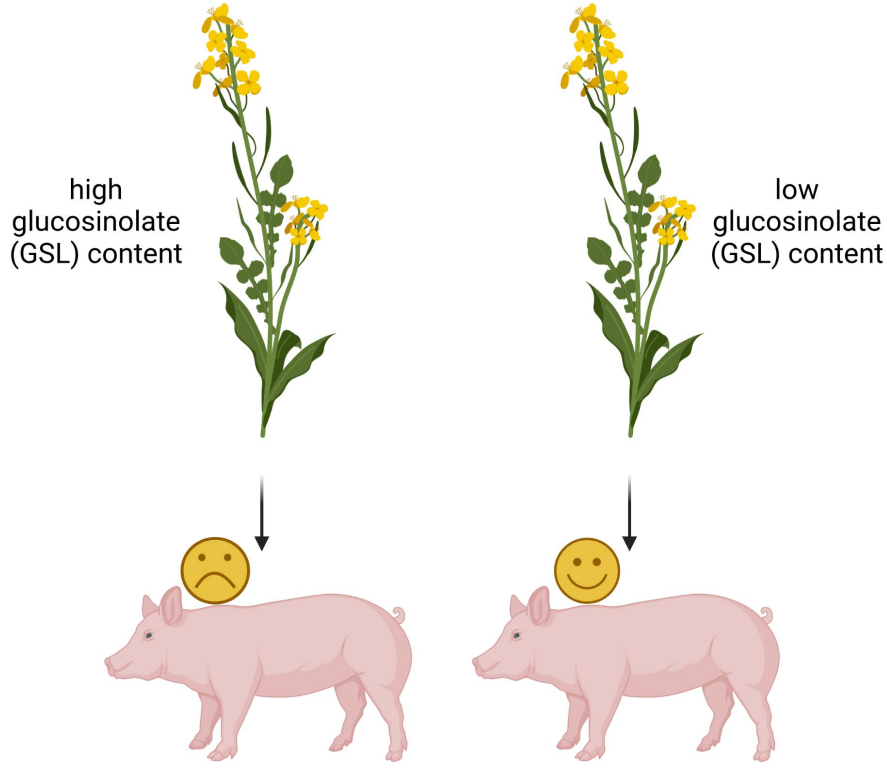
Question: What determines differences between plants?



Intraspecific variation

- Different accessions of the same species have genomic differences
- Genotype determines phenotype (traits)
- Specific traits are relevant for breeding or biotechnological/agronomical applications

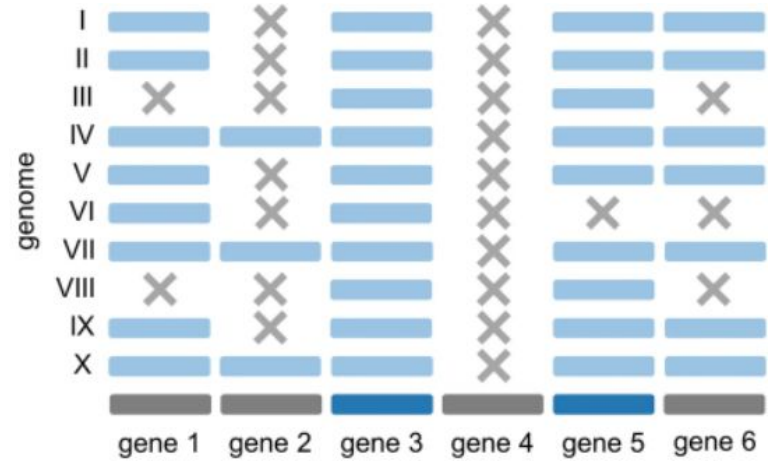


Figure source: 10.1186/s13007-021-00718-5

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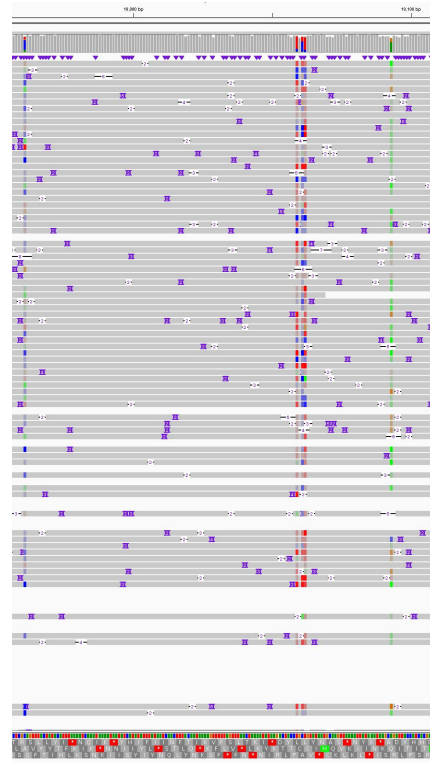
Differences between samples and reference

- Differences are identified against a reference genome sequence (classic approach)
- Reads of a sample are aligned against the reference (mapping)
- Differences are identified by tools (variant calling)



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Types of sequence variants

- SNVs vs. SNPs
  - Single Nucleotide Variants = no information about their effect
  - Single Nucleotide Polymorphisms = no detrimental impact
- MNVs
  - Multiple Nucleotide Variants
- InDels
  - Insertions: additional bases in sample compared to reference
  - Deletions: loss of bases in sample compared to reference
- Inversions
  - Orientation of sequence differs between sample and reference
- Tandem duplications

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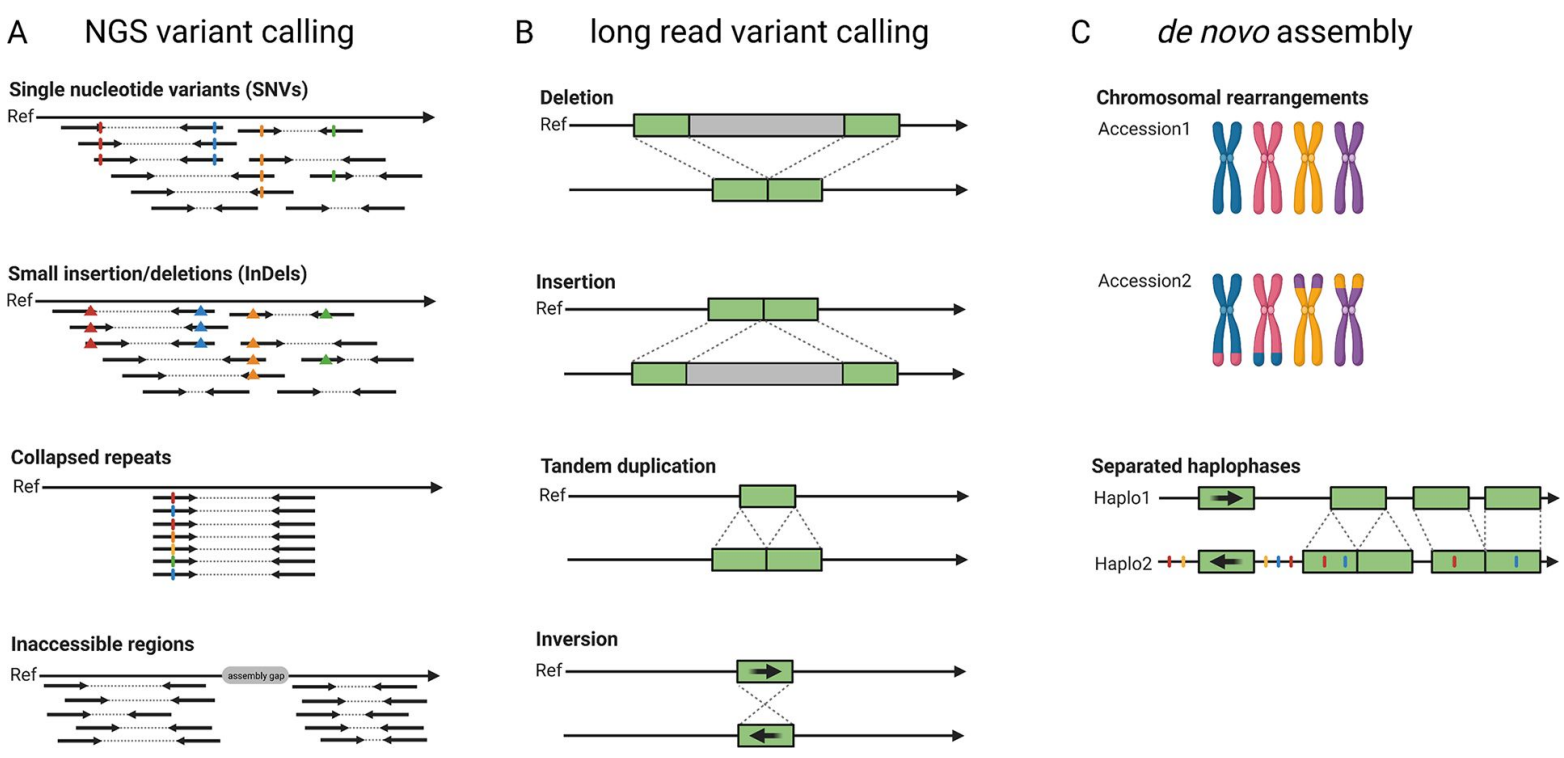
Read mapping vs. de novo genome sequence assembly



Pucker et al., 2022: 10.1017/qpb.2021.18

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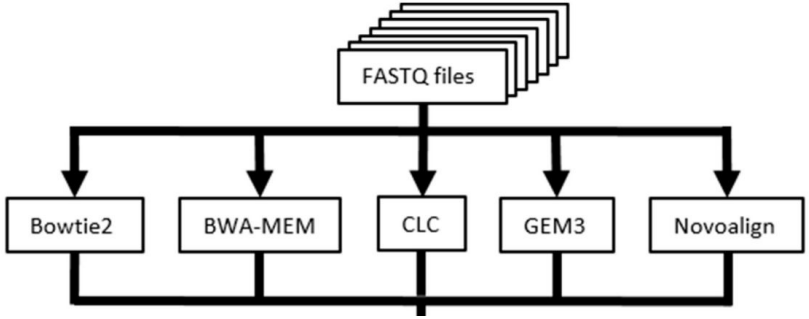
Challenges of read mappings

- Speed / computational costs
  - BLAST would be too slow
- Specific assignment of reads / repeats
  - (especially challenging in polyploid species)
- Splitting around InDels or across introns

Short read mappings

- Large number of tools for mappings
- DNA seq read mappers: BWA MEM, bowtie2
- RNA-seq read mappers (split read): STAR, HiSAT2



Li, 2013: 10.48550/arXiv.1303.3997; Langmead & Salzberg, 2012: 10.1038/nmeth.1923
Dobin et al., 2013: 10.1093/bioinformatics/bts635; Kim et al., 2015: 10.1038/nmeth.3317
Schilbert et al., 2020: 10.3390/plants9040439

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Coverage analysis: genomic copy numbers

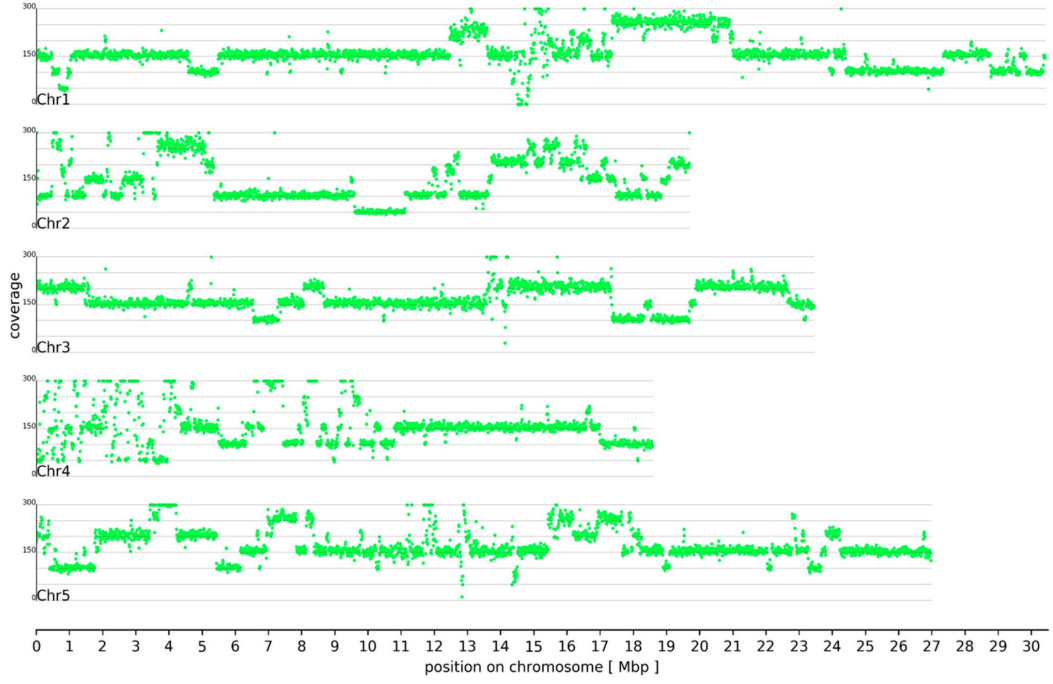

Figure source: 10.3390/genes10090671

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Coverage analysis: segmental duplication

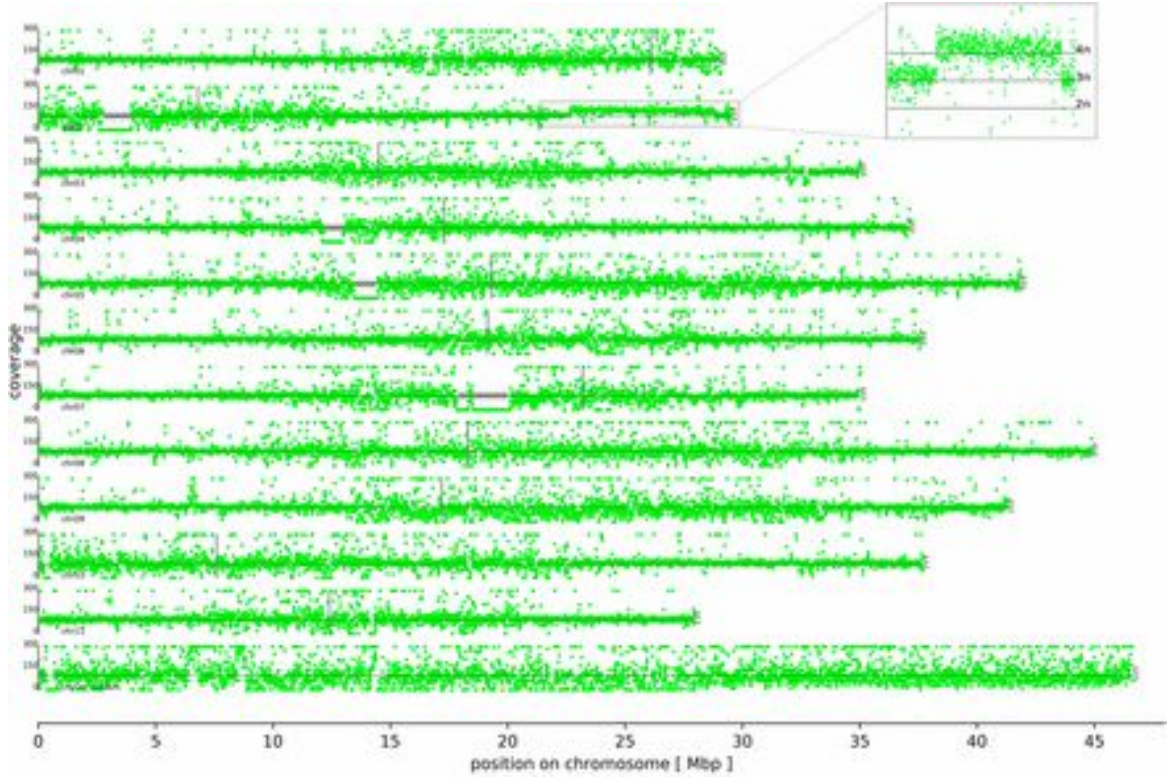
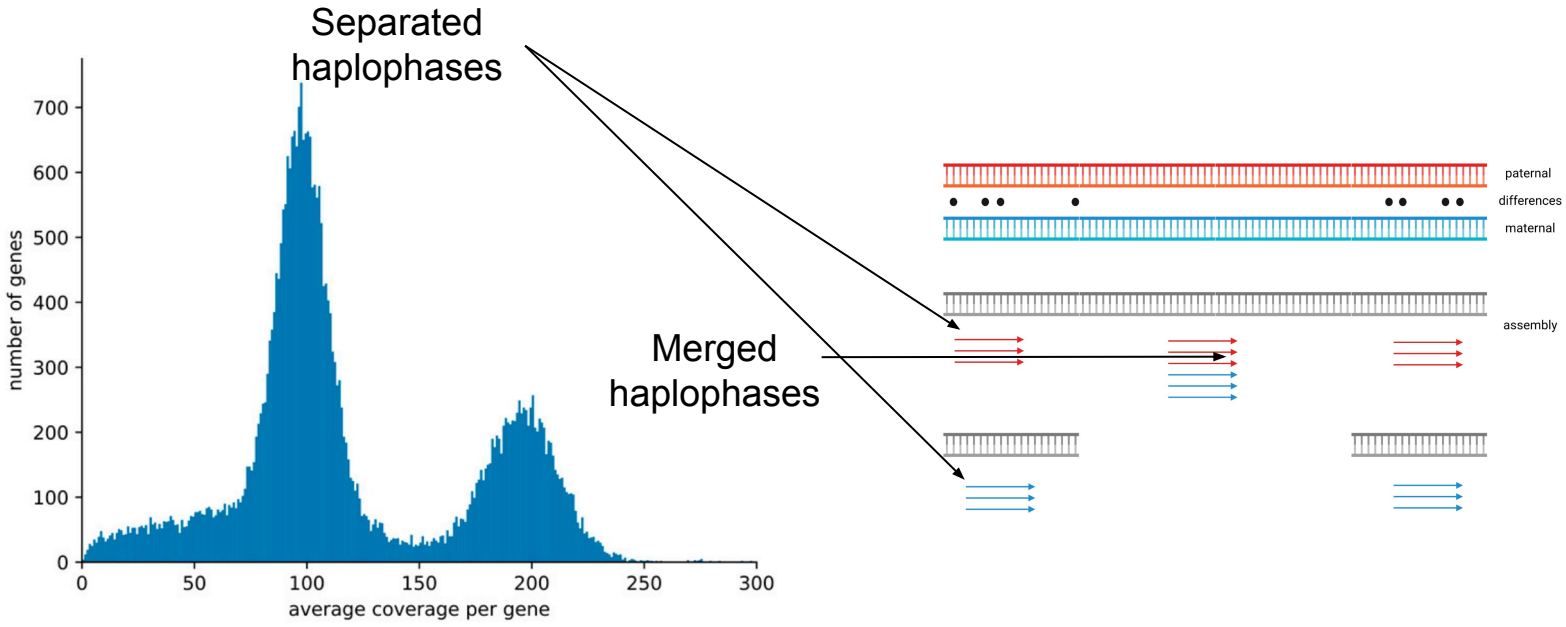


Figure source: 10.1534/g3.119.400847

Coverage analysis: haplotype phasing / ploidy



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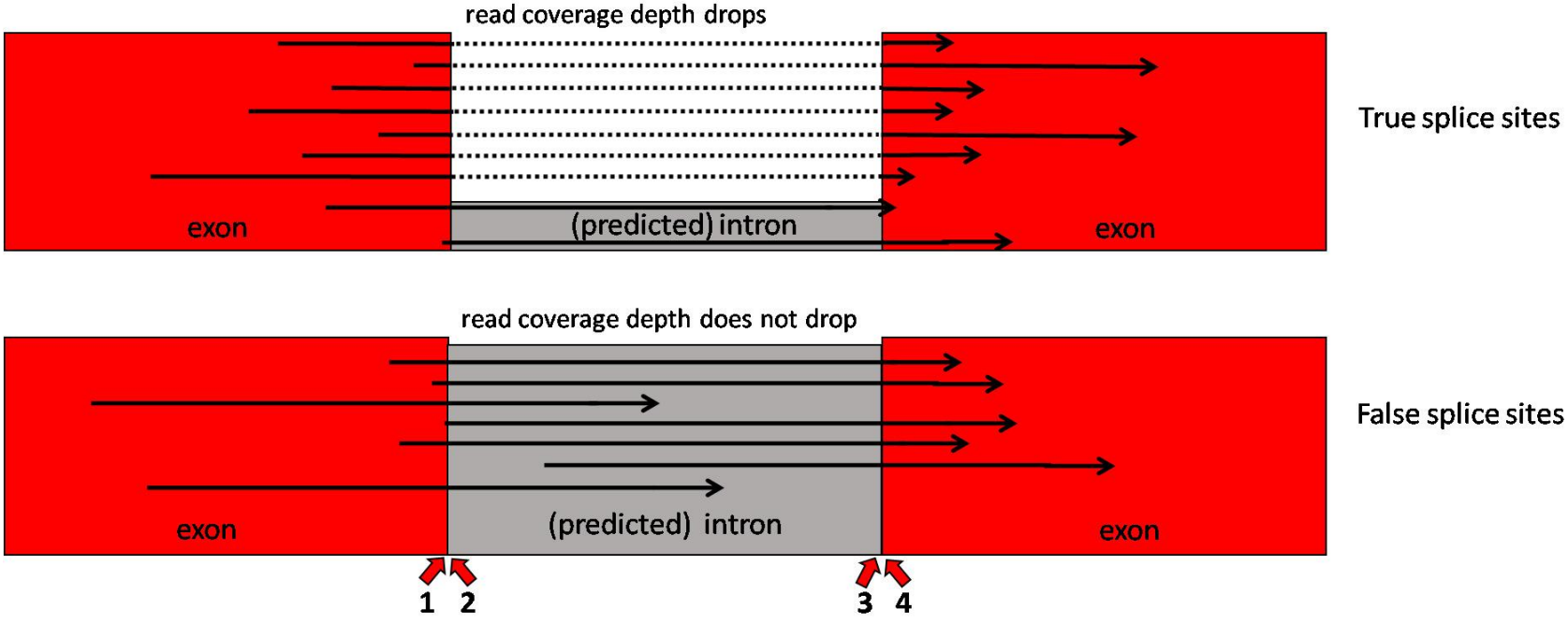
Coverage analysis: splice sites



Pucker & Brockington, 2018: 10.1186/s12864-018-5360-z

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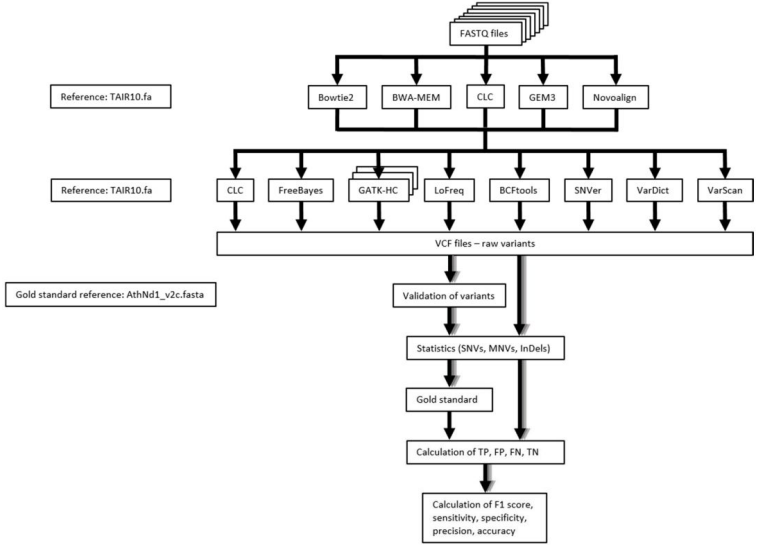
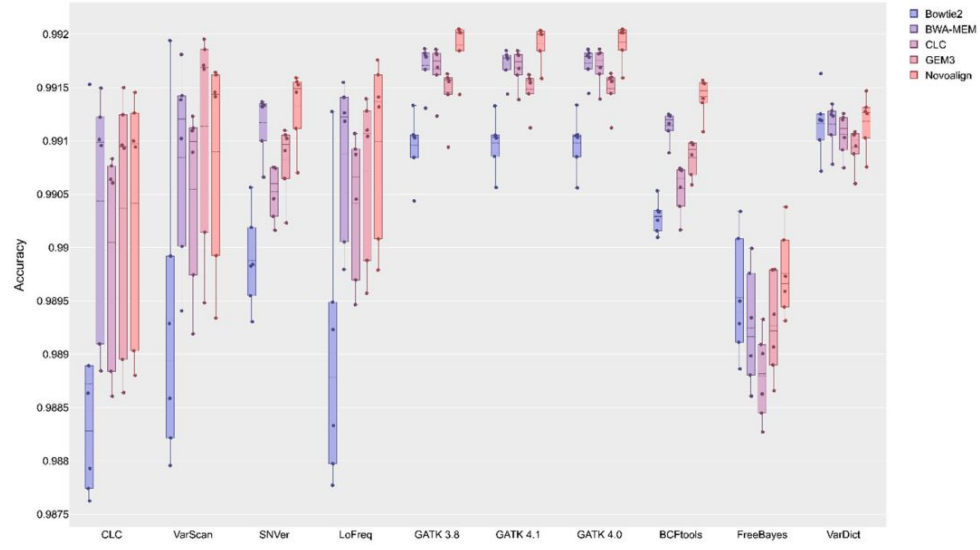
Short read variant callers

- Millions of differences between samples and reference
- Automatic detection with tools required
- Tools:
  - Genome Analysis Tool Kit (GATK): https://gatk.broadinstitute.org/hc/en-us
  - Samtools: http://www.htslib.org/
  - VarDict: https://anaconda.org/bioconda/vardict
  - VarScan: https://github.com/dkoboldt/varscan
  - SNVer: http://snver.sourceforge.net/
  - FreeBayes: https://github.com/freebayes/freebayes

McKenna et al., 2010: 10.1101/gr.107524.110; Li et al., 2009: 10.1093/bioinformatics/btp352
Lai et al., 2016: 10.1093/nar/gkw227; Koboldt et al., 2009: 10.1093/bioinformatics/btp373
Wei et al., 2011: 10.1093/nar/gkr599; Garrison & Marth, 2012: 10.48550/arXiv.1207.3907

Benchmarking of variant callers





Schilbert et al., 2020: 10.3390/plants9040439

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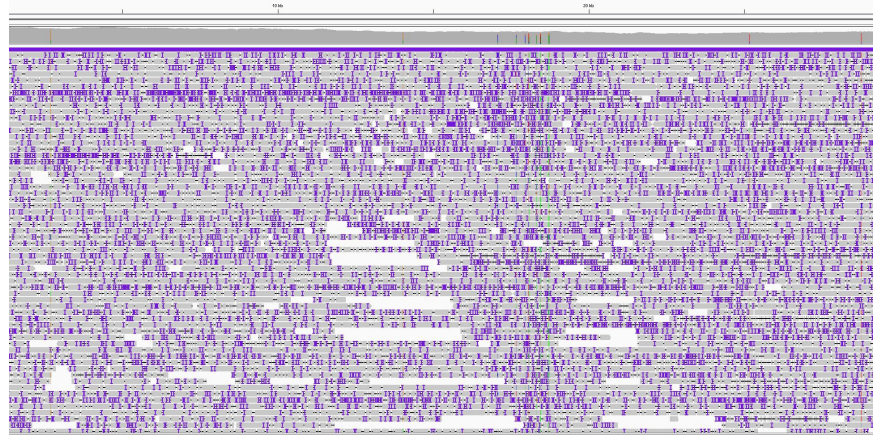
Long read mapping

- Noisy alignments due to high rate of sequencing errors; InDels are particularly abundant (purple ticks)
- Rapid development of new tools
- Benchmarking studies are missing and would require frequent updates



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Long read mapping tools

- Collection of long read tools: https://long-read-tools.org/

- Over 600 tools available

- Examples:
  - BWA-SW: http://bio-bwa.sourceforge.net/
  - Minimap2: https://github.com/lh3/minimap2
  - GraphMap: https://github.com/isovic/graphmap
  - NGMLR: https://github.com/philres/ngmlr
  - Winnowmap2: https://github.com/marbl/Winnowmap

Amarasinghe et al., 2021: 10.1093/gigascience/giab003; Li & Durbin, 2010: 10.1093/bioinformatics/btp698
Li, 2018: 10.1093/bioinformatics/bty191; Sovic, 2016: 10.1038/ncomms11307
Sedlazeck et al., 2018: 10.1038/s41592-018-0001-7; Jain et al., 2022: 10.1038/s41592-022-01457-8

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Long read variant calling

- Rapid development of new tools and lack of benchmarking studies

- Tools:
  - SVIM2: https://github.com/eldariont/svim
  - Longshot: https://github.com/pjedge/longshot
  - NanoCaller: https://github.com/WGLab/NanoCaller
  - Sniffles2: https://github.com/fritzsedlazeck/Sniffles

Heller & Vingron, 2019: 10.1093/bioinformatics/btz041; Edge & Basal, 2019: 10.1038/s41467-019-12493-y
Ahsan et al., 2021: 10.1186/s13059-021-02472-2; Smolka et al., 2022: 10.1101/2022.04.04.487055

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Variant Call Format (VCF)

- Chromosome: name of sequence in the reference
- Position: position on the specified sequence
- ID (not relevant in plant biology): variants in humans have IDs
- Reference allele: nucleotide(s) in the reference sequence at the specified position
- Alternative allele: nucleotide(s) in the sample at the same position
- Quality: tool specific value that can be used for filtering
- Filter status: specifies filter name if variant was filtered out
- Info: collection of information
- Format: explains the fields in the following sample columns
- DATA_SET1, DATA_SET2, DATA_SET3, …: one column per sample

#CHROM	POS	ID	REF	ALT	QUAL	FILTER	INFO	FORMAT	DATA_SET
R105	10929	.	A	G	58.64	PASS	AC=1;AF=0.500;AN=2;BaseQRankSum=-1.242;DP=8;ExcessHet=3.0103;FS=0.000;MLEAC=1;MLEAF=0.500;MQ=44.01;MQRankSum=-2.100;QD=7.33;ReadPosRankSum=0.619;SOR=0.307	GT:AD:DP:GQ:PL	0/1:6,2:8:66:66,0,230
R105	10944	.	A	G	58.64	PASS	AC=1;AF=0.500;AN=2;BaseQRankSum=-1.068;DP=8;ExcessHet=3.0103;FS=0.000;MLEAC=1;MLEAF=0.500;MQ=44.01;MQRankSum=-2.100;QD=7.33;ReadPosRankSum=-1.465;SOR=0.307	GT:AD:DP:GQ:PL	0/1:6,2:8:66:66,0,230
R105	10955	.	G	T	61.64	PASS	AC=1;AF=0.500;AN=2;BaseQRankSum=-1.068;DP=7;ExcessHet=3.0103;FS=0.000;MLEAC=1;MLEAF=0.500;MQ=46.16;MQRankSum=-1.981;QD=8.81;ReadPosRankSum=-1.465;SOR=0.446	GT:AD:DP:GQ:PL	0/1:5,2:7:69:69,0,204
R105	10962	.	A	G	61.64	PASS	AC=1;AF=0.500;AN=2;BaseQRankSum=-1.068;DP=8;ExcessHet=3.0103;FS=0.000;MLEAC=1;MLEAF=0.500;MQ=48.11;MQRankSum=-1.981;QD=8.81;ReadPosRankSum=-1.465;SOR=0.446	GT:AD:DP:GQ:PL	0/1:5,2:7:69:69,0,204
R105	13234	.	T	C	32.64	MQ_filter;QD_filter	AC=1;AF=0.500;AN=2;BaseQRankSum=-1.962;DP=35;ExcessHet=3.0103;FS=2.782;MLEAC=1;MLEAF=0.500;MQ=37.70;MQRankSum=-1.106;QD=1.31;ReadPosRankSum=-0.209;SOR=1.911	GT:AD:DP:GQ:PL	0/1:22,3:25:40:40,0,706
R105	13260	.	T	G	72.64	MQ_filter	AC=1;AF=0.500;AN=2;BaseQRankSum=-0.172;DP=36;ExcessHet=3.0103;FS=11.698;MLEAC=1;MLEAF=0.500;MQ=38.68;MQRankSum=-1.349;QD=2.50;ReadPosRankSum=0.243;SOR=3.442	GT:AD:DP:GQ:PL	0/1:23,6:29:80:80,0,695
R105	13395	.	T	A	183.64	PASS	AC=1;AF=0.500;AN=2;BaseQRankSum=1.979;DP=19;ExcessHet=3.0103;FS=8.929;MLEAC=1;MLEAF=0.500;MQ=43.94;MQRankSum=-1.631;QD=9.67;ReadPosRankSum=1.186;SOR=3.126	GT:AD:DP:GQ:PL	0/1:13,6:19:99:191,0,413
R105	13538	.	T	C	61.64	PASS	AC=1;AF=0.500;AN=2;BaseQRankSum=1.359;DP=27;ExcessHet=3.0103;FS=0.000;MLEAC=1;MLEAF=0.500;MQ=46.51;MQRankSum=-1.847;QD=2.47;ReadPosRankSum=1.188;SOR=0.760	GT:AD:DP:GQ:PL	0/1:21,4:25:69:69,0,660
R105	14511	.	C	T	39.64	PASS	AC=1;AF=0.500;AN=2;BaseQRankSum=-0.563;DP=13;ExcessHet=3.0103;FS=2.522;MLEAC=1;MLEAF=0.500;MQ=43.42;MQRankSum=-2.771;QD=3.05;ReadPosRankSum=0.217;SOR=1.546	GT:AD:DP:GQ:PL	0/1:9,4:13:47:47,0,352
R105	14542	.	G	A	51.64	PASS	AC=1;AF=0.500;AN=2;BaseQRankSum=-1.825;DP=15;ExcessHet=3.0103;FS=0.000;MLEAC=1;MLEAF=0.500;MQ=42.30;MQRankSum=-2.843;QD=3.44;ReadPosRankSum=-0.919;SOR=1.022	GT:AD:DP:GQ:PL	0/1:10,5:15:59:59,0,390
R105	15681	.	A	G	116.64	PASS	AC=1;AF=0.500;AN=2;BaseQRankSum=1.897;DP=43;ExcessHet=3.0103;FS=4.187;MLEAC=1;MLEAF=0.500;MQ=40.84;MQRankSum=-2.008;QD=2.92;ReadPosRankSum=0.303;SOR=1.721	GT:AD:DP:GQ:PL	0/1:34,6:40:99:124,0,1161
R105	15712	.	C	T	70.64	MQ_filter	AC=1;AF=0.500;AN=2;BaseQRankSum=1.307;DP=35;ExcessHet=3.0103;FS=2.026;MLEAC=1;MLEAF=0.500;MQ=39.58;MQRankSum=-2.129;QD=2.08;ReadPosRankSum=-0.994;SOR=1.230	GT:AD:DP:GQ:PL	0/1:30,4:34:78:78,0,1247
R105	15719	.	C	T	64.64	MQ_filter;QD_filter	AC=1;AF=0.500;AN=2;BaseQRankSum=0.166;DP=37;ExcessHet=3.0103;FS=2.037;MLEAC=1;MLEAF=0.500;MQ=38.62;MQRankSum=-2.020;QD=1.80;ReadPosRankSum=-1.360;SOR=1.251	GT:AD:DP:GQ:PL	0/1:32,4:36:72:72,0,1310
R105	16037	.	C	A	50.64	MQ_filter	AC=1;AF=0.500;AN=2;BaseQRankSum=0.000;DP=7;ExcessHet=3.0103;FS=0.000;MLEAC=1;MLEAF=0.500;MQ=34.75;MQRankSum=0.303;QD=7.23;ReadPosRankSum=-0.712;SOR=1.802	GT:AD:DP:GQ:PL	0/1:5,2:7:58:58,0,171
R105	16582	.	CATTGTAAG	C	58.60	PASS	AC=1;AF=0.500;AN=2;BaseQRankSum=0.712;DP=8;ExcessHet=3.0103;FS=3.680;MLEAC=1;MLEAF=0.500;MQ=38.22;MQRankSum=0.319;QD=7.33;ReadPosRankSum=0.366;SOR=2.236	GT:AD:DP:GQ:PL	0/1:6,2:8:66:66,0,246
R105	17718	.	A	G	79.64	MQ_filter	AC=1;AF=0.500;AN=2;BaseQRankSum=-0.722;DP=18;ExcessHet=3.0103;FS=7.656;MLEAC=1;MLEAF=0.500;MQ=29.01;MQRankSum=-0.858;QD=4.42;ReadPosRankSum=0.099;SOR=0.041	GT:AD:DP:GQ:PL	0/1:13,5:18:87:87,0,392
R105	37909	.	A	G	51.64	MQ_filter	AC=1;AF=0.500;AN=2;BaseQRankSum=-0.431;DP=9;ExcessHet=3.0103;FS=10.792;MLEAC=1;MLEAF=0.500;MQ=37.28;MQRankSum=0.549;QD=5.74;ReadPosRankSum=-0.549;SOR=2.206	GT:AD:DP:GQ:PL	0/1:7,2:9:59:59,0,254
R105	45724	.	C	CTTATA	61.60	PASS	AC=1;AF=0.500;AN=2;BaseQRankSum=0.210;DP=7;ExcessHet=3.0103;FS=0.000;MLEAC=1;MLEAF=0.500;MQ=43.83;MQRankSum=0.967;QD=8.80;ReadPosRankSum=-0.210;SOR=0.446	GT:AD:DP:GQ:PL	0/1:5,2:7:69:69,0,204

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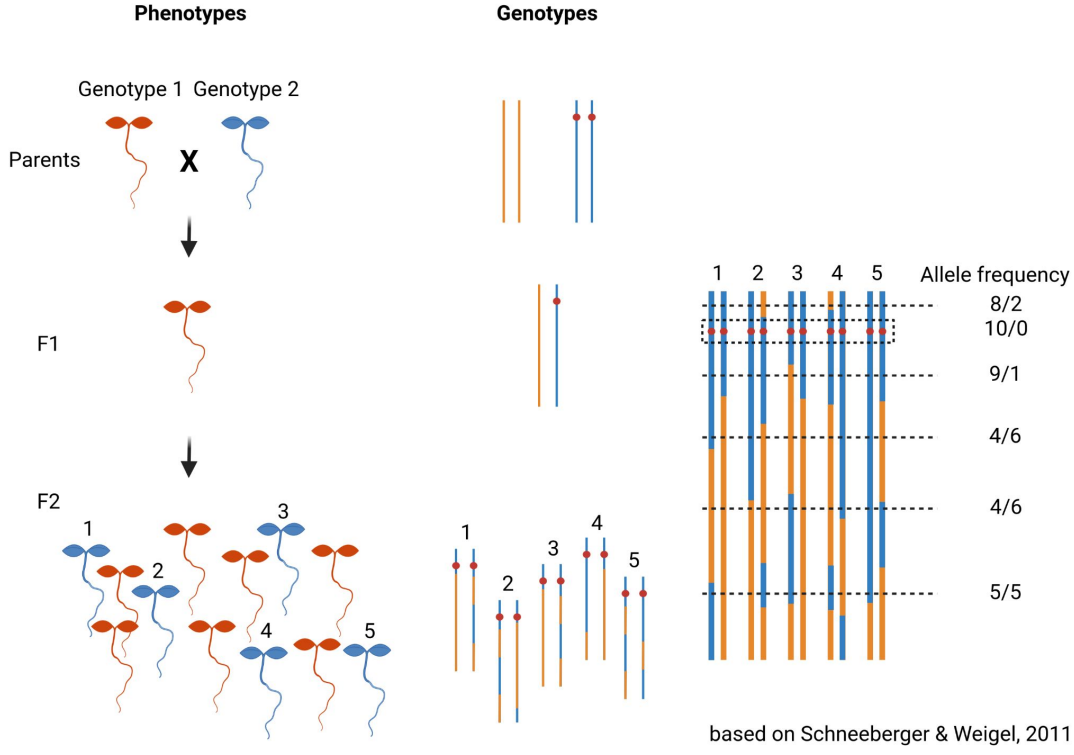
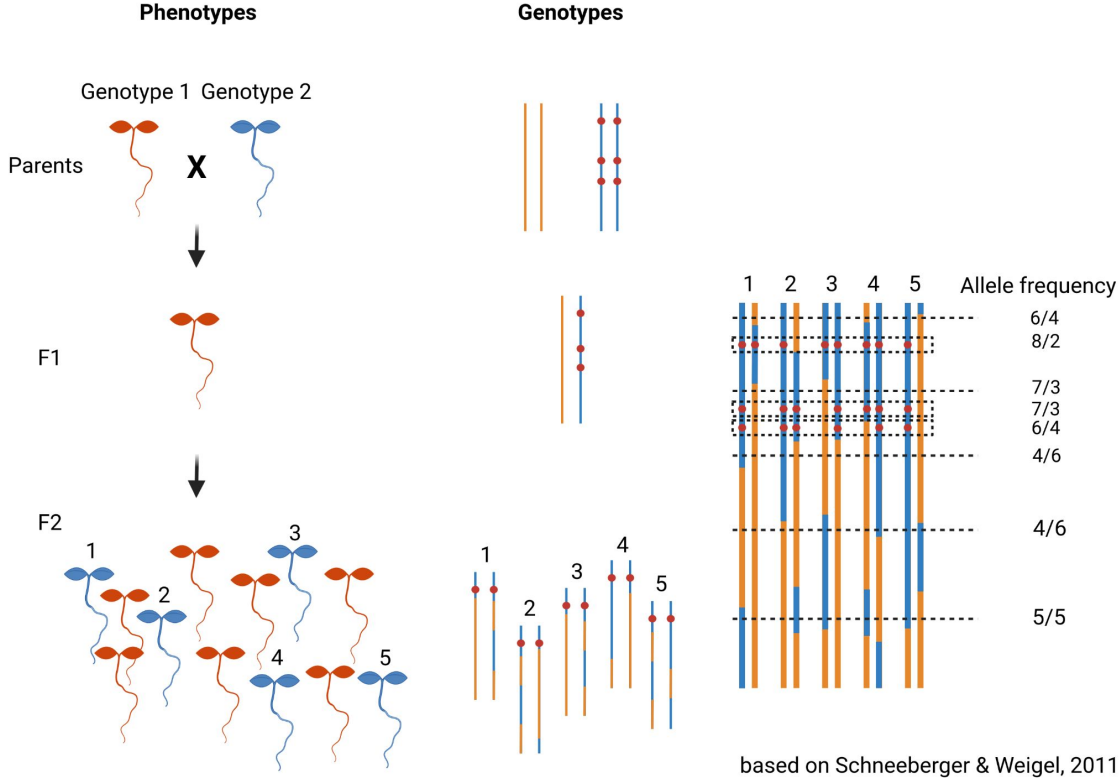
genomic Variant Call Format (gVCF)

- Generally similar to VCF file
- One entry for each position in the reference
- Not just variants, but also non-variants are listed

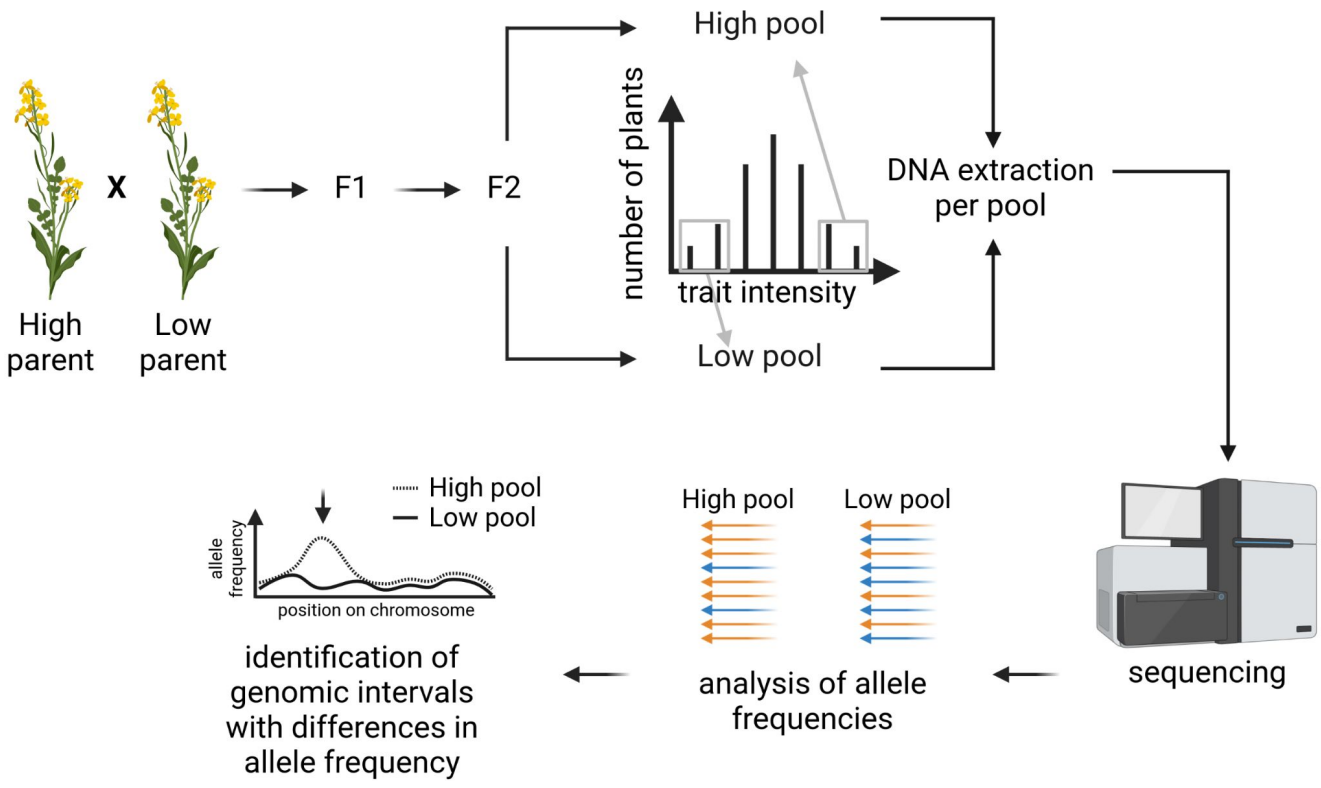
Mapping-by-sequencing (1)



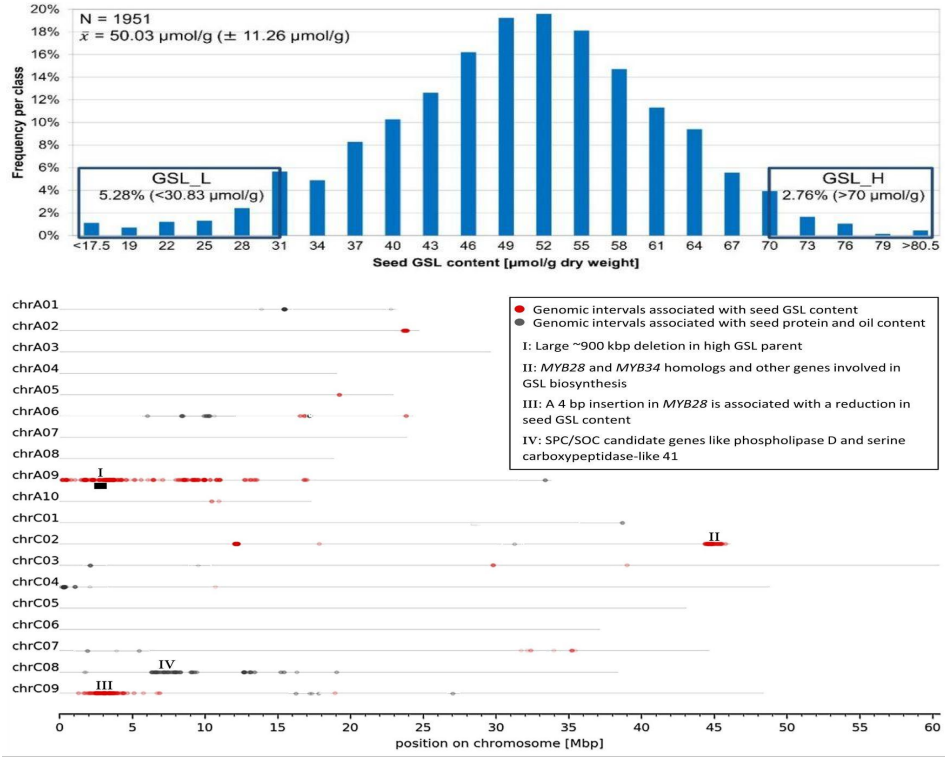
Mapping-by-sequencing (2)



Mapping-by-sequencing (3)



Mapping-by-sequencing (4)



Schilbert et al., 2022: 10.1101/2022.06.01.494149

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Variant annotation

- Variants can have functional consequences
- Variants in coding sequences can change amino acids
- Variants outside CDS can have regulatory consequences

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Variant Annotation - SnpEff

- High throughput annotation of SNVs and larger variants
- Reference sequence (FASTA) and structural annotation (GFF) required
- Freely available software: http://pcingola.github.io/SnpEff/
- Addition of one annotation field to VCF file

```
chrA01  179964  .  T  A  .  PASS  GSL_Hlgh,GSL_Low;ANN=A|stop_gained|HIGH|Gene_BnaA01g00340D|Gene_BnaA01g00340D|transcript|BnaA01g00340D|Coding|5/9|c.863T>A|p.Leu288*|863/1834|863/1834|288/610|   GT:AD:DP:GQ:PL
chrA01  179967  .  T  C  .  PASS  GSL_Hlgh,GSL_Low;ANN=C|missense_variant|MODERATE|Gene_BnaA01g00340D|Gene_BnaA01g00340D|transcript|BnaA01g00340D|Coding|5/9|c.866T>C|p.Phe289Ser|866/1834|866/1834|289/610|       GT:AD:DP:GQ:PL
chrA01  179979  .  C  T  .  PASS  GSL_Low;ANN=T|missense_variant|MODERATE|Gene_BnaA01g00340D|Gene_BnaA01g00340D|transcript|BnaA01g00340D|Coding|5/9|c.878C>T|p.Thr293Met|878/1834|878/1834|293/610|         GT:AD:DP:GQ:PL
chrA01  179988  .  A  T  .  PASS  GSL_Low;ANN=T|missense_variant|MODERATE|Gene_BnaA01g00340D|Gene_BnaA01g00340D|transcript|BnaA01g00340D|Coding|5/9|c.887A>T|p.Tyr296Phe|887/1834|887/1834|296/610|         GT:AD:DP:GQ:PL
chrA01  180003  .  G  A  .  PASS  GSL_Low;ANN=A|missense_variant|MODERATE|Gene_BnaA01g00340D|Gene_BnaA01g00340D|transcript|BnaA01g00340D|Coding|5/9|c.902G>A|p.Gly301Asp|902/1834|902/1834|301/610|         GT:AD:DP:GQ:PL
chrA01  180024  .  A  G  .  PASS  GSL_Hlgh,GSL_Low;ANN=G|missense_variant|MODERATE|Gene_BnaA01g00340D|Gene_BnaA01g00340D|transcript|BnaA01g00340D|Coding|5/9|c.923A>G|p.His308Arg|923/1834|923/1834|308/610|       GT:AD:DP:GQ:PL
chrA01  180039  .  T  C  .  PASS  GSL_Hlgh,GSL_Low;ANN=C|missense_variant|MODERATE|Gene_BnaA01g00340D|Gene_BnaA01g00340D|transcript|BnaA01g00340D|Coding|5/9|c.938T>C|p.Ile313Thr|938/1834|938/1834|313/610|       GT:AD:DP:GQ:PL
chrA01  180048  .  G  A  .  PASS  GSL_Hlgh,GSL_Low;ANN=A|stop_retained_variant|LOW|Gene_BnaA01g00340D|Gene_BnaA01g00340D|transcript|BnaA01g00340D|Coding|5/9|c.947G>A|p.Ter316Ter|947/1834|947/1834|316/610|       GT:AD:DP:GQ:PL
```


Cingolani et al., 2012: 10.4161/fly.19695

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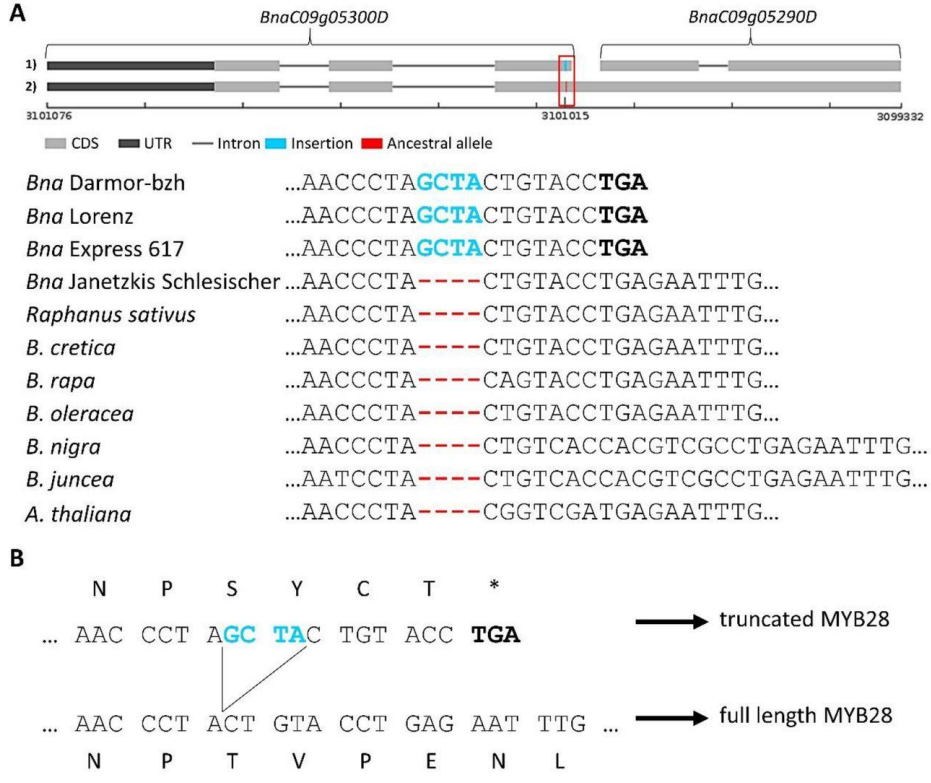
SnpEff predictions

Type	Meaning	Example
SNP	Single Nucleotide Polymorphism	Reference = ‘A’, Sample = ‘C’
Ins	Insertion	Reference = ‘A’, Sample = ‘AGT’
Del	Deletion	Reference = ‘AC’, Sample = ‘C’
MNP	Multiple Nucleotide Polymorphism	Reference = ‘ATA’, Sample = ‘GTC’
MIXED	MNP and InDel	Reference = ‘ATA’, Sample = ‘GTCAGT’

http://pcingola.github.io/SnpEff/se_introduction/

Example: Glucosinolate biosynthesis in rapeseed



Schilbert et al., 2022: 10.1101/2022.06.01.494149

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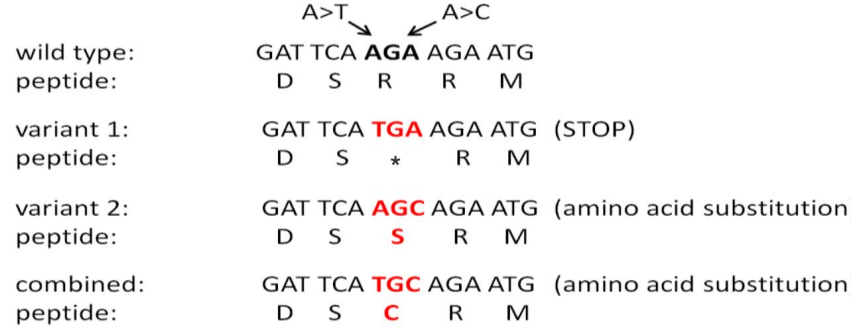
Is there something that SnpEff might miss?

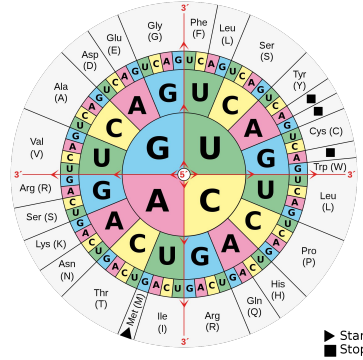
Variant Annotation - NAVIP

- NAVIP = Neighborhood-Aware Variant Impact Predictor
- Variants can have interacting effects e.g. compensate each other
- Considering multiple variants while predicting effects
- Tool freely available: https://github.com/bpucker/NAVIP



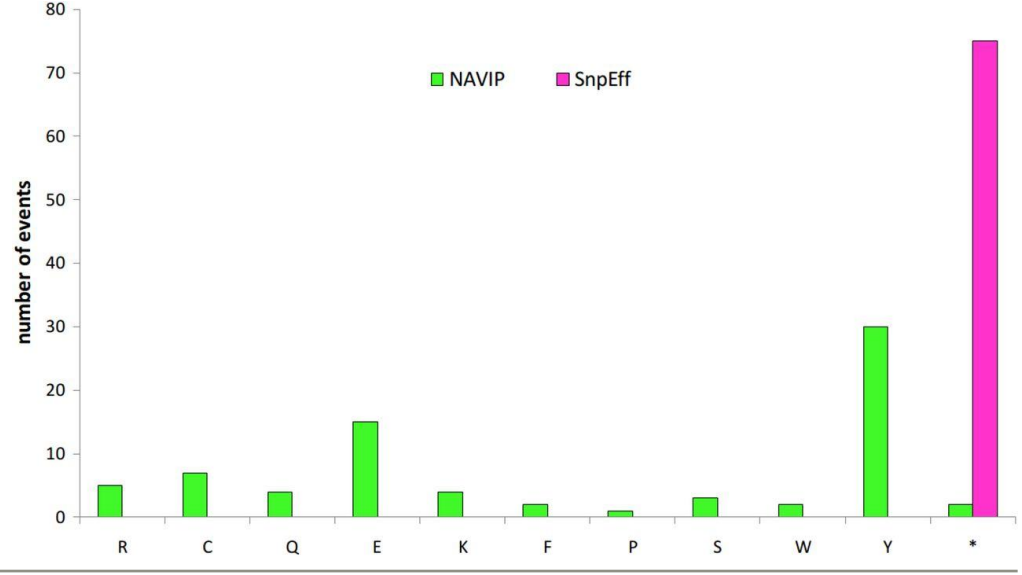
Baasner et al., 2025: 10.1371/journal.pcbi.1012732

Connected SNVs



A>T A>C

wild type:	GAT TCA **AGA** AGA ATG
peptide:	D S R R M
variant 1:	GAT TCA **TGA** AGA ATG (STOP)
peptide:	D S * R M
variant 2:	GAT TCA **AGC** AGA ATG (amino acid substitution)
peptide:	D S **S** R M
combined:	GAT TCA **TGC** AGA ATG (amino acid substitution)
peptide:	D S **C** R M



Baasner et al., 2025: 10.1371/journal.pcbi.1012732

Compensating InDels

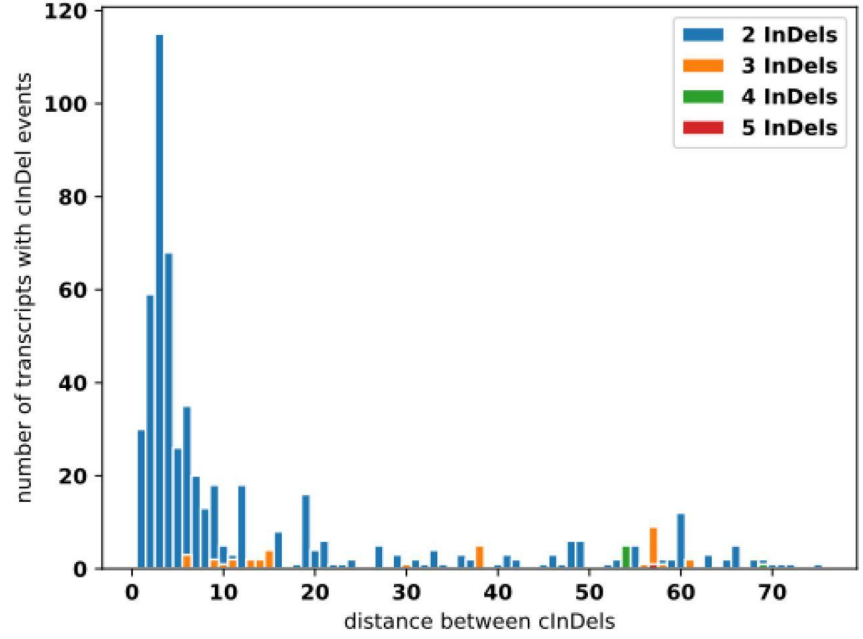
T>TA C>CGC

wild type: GTG TA**T** CTG **C**GC ATT
peptide: V Y L R I

variant 1: GTG TA**T** **A**CT GCG CAT T (frameshift)
peptide: V Y **T** **A** **H**

variant 2: GTG TAT CTG **C**GC GCA TT (frameshift)
peptide: V Y L **R** **A**

combined: GTG TA**T** **A**CT G**C**G **C**GC ATT
peptide: V Y **L** **A** R I



Baasner et al., 2025: 10.1371/journal.pcbi.1012732

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Evolutionary Genomic

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“Nothing in biology makes sense except in the light of evolution”

Theodosius Dobzhansky

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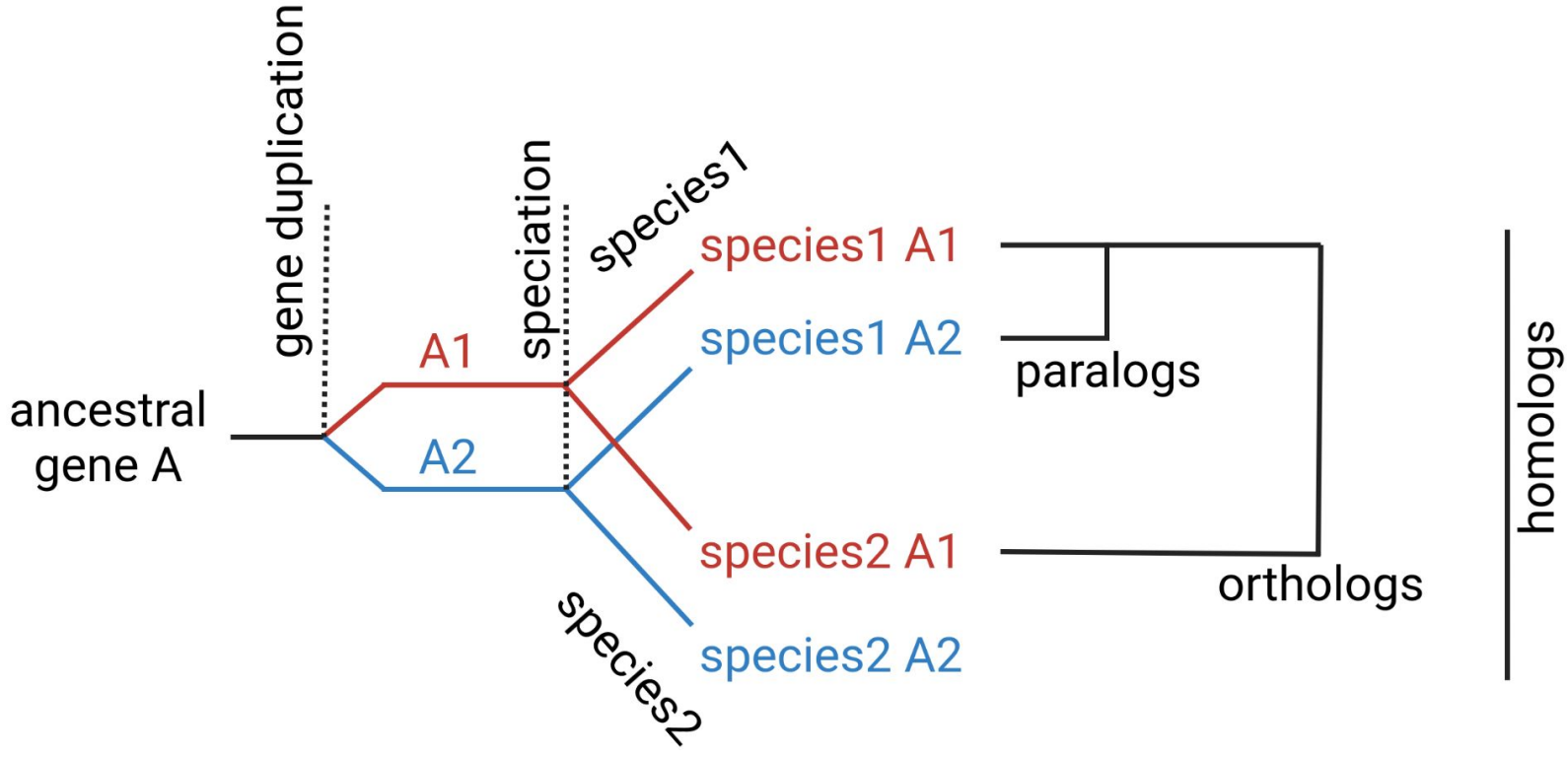
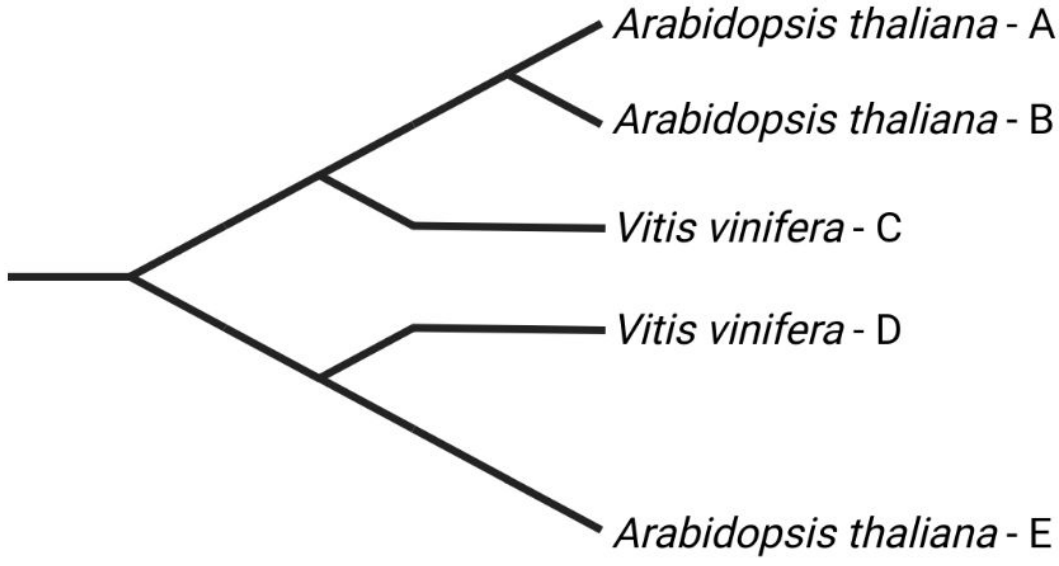
Paralogs & orthologs



Which are orthologs/paralogs?



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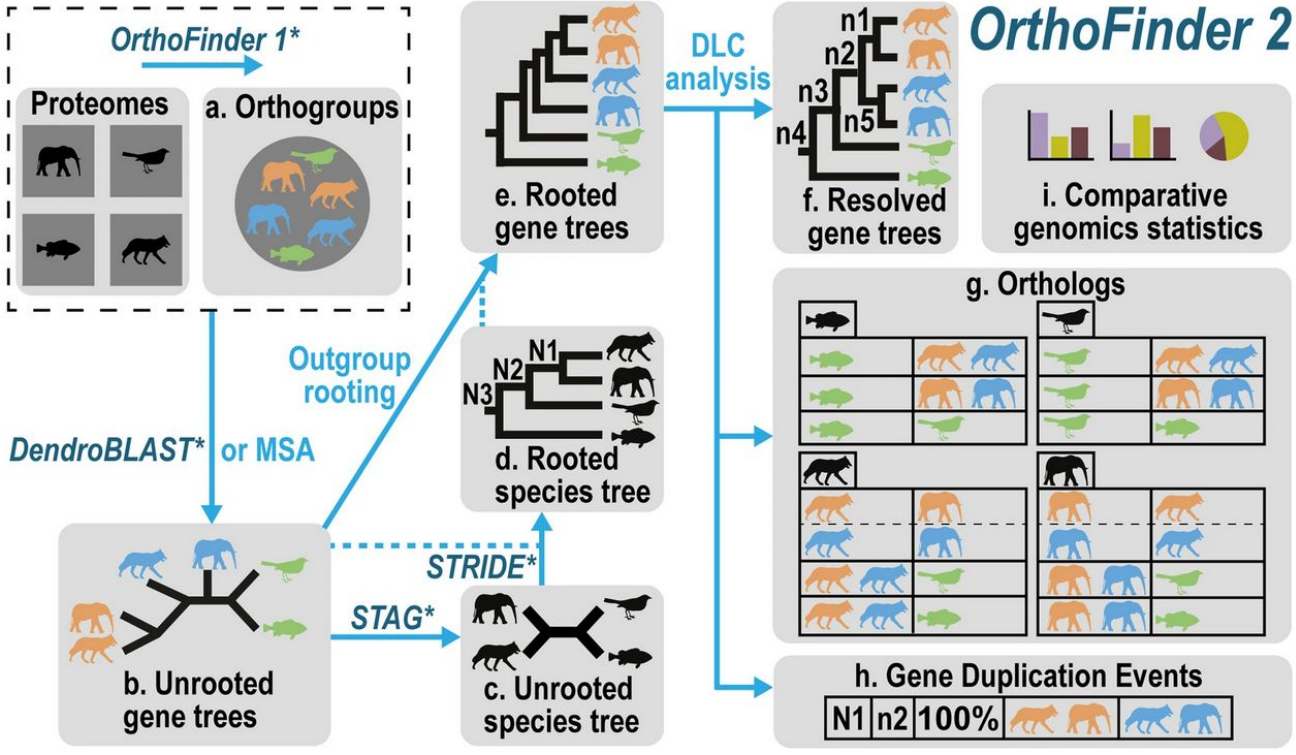
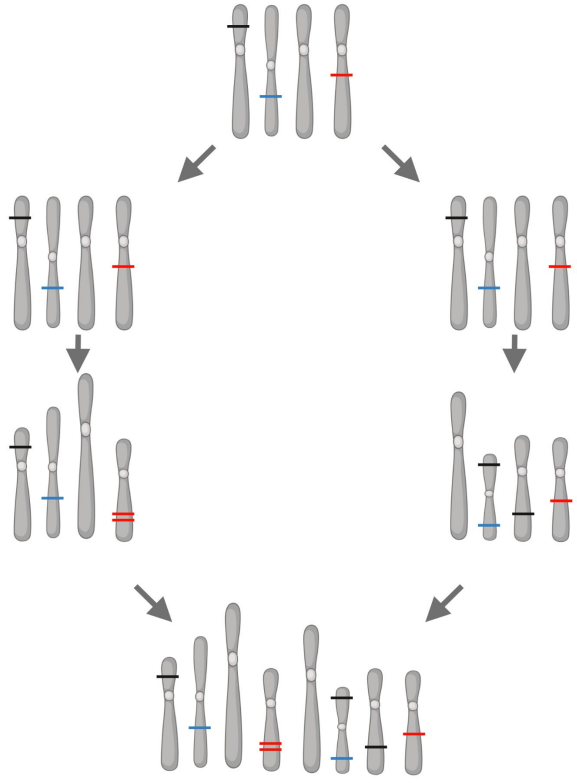
OrthoFinder2



Emms et al., 2019: 10.1186/s13059-019-1832-y

Homeologs



Speciation

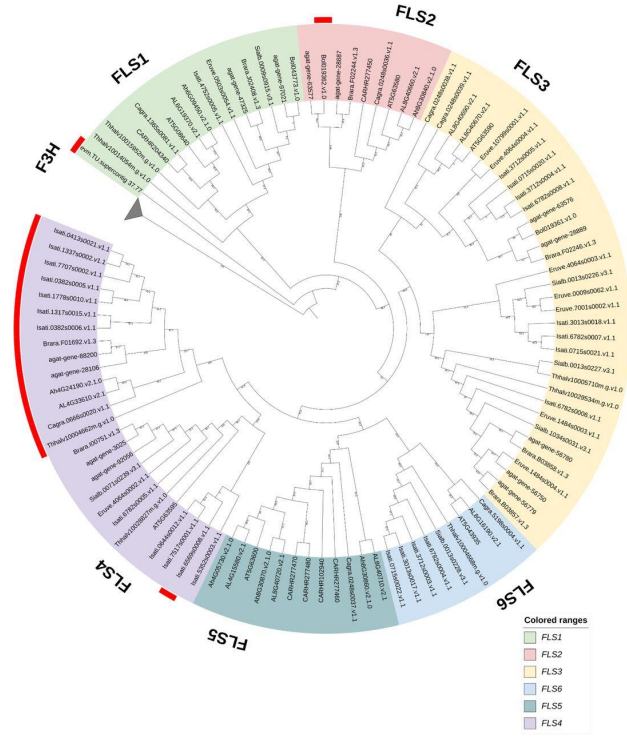
Gene duplications, translocations, and rearrangements

Hybridization leads to polyploidization

Glover et al., 2016: 10.1016/j.tplants.2016.02.005

DupyliCate - investigation of gene duplications

- Python tool for investigation of gene copies
- Classification of duplicates
- Investigation of sub-/neofunctionalization at expression level



Natarajan & Pucker, 2025: 10.1101/2025.10.10.681656

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Comparative Genomics

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Comparative genomics

- Compare genome sizes
- Compare chromosome numbers
- Compare gene sets
- Compare gene positions & chromosome structures

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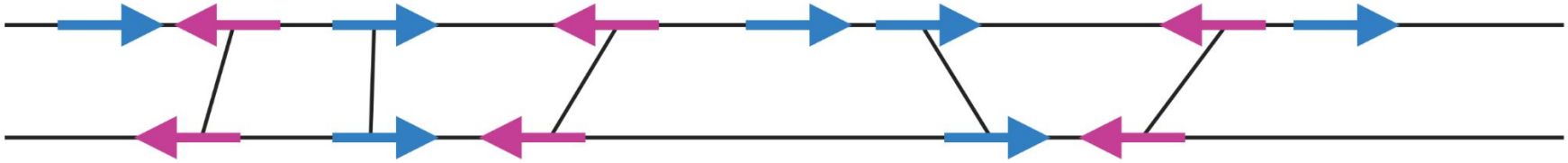
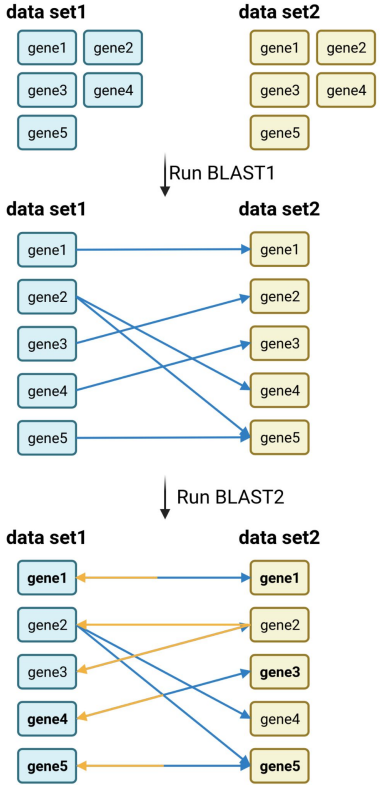
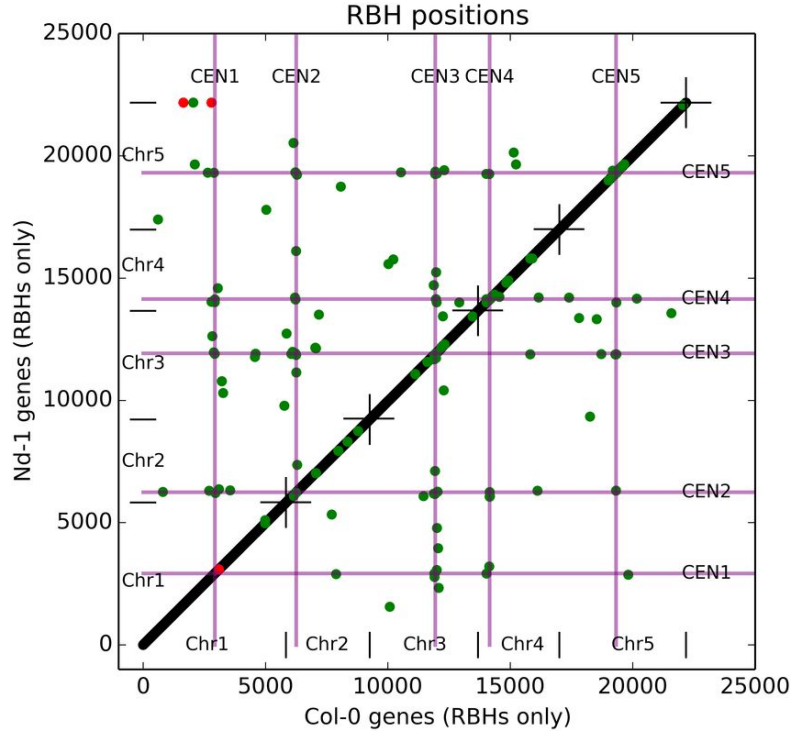
Synteny

Synteny = Same order of genes in different genomes



Reciprocal Best BLAST hits (RBHs)





Pucker et al., 2016: 10.1371/journal.pone.0164321

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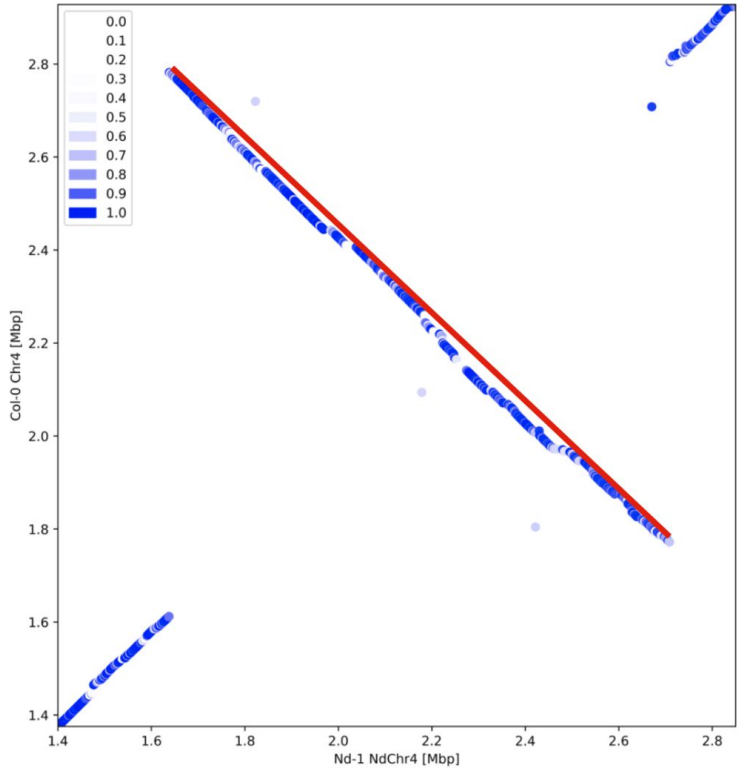
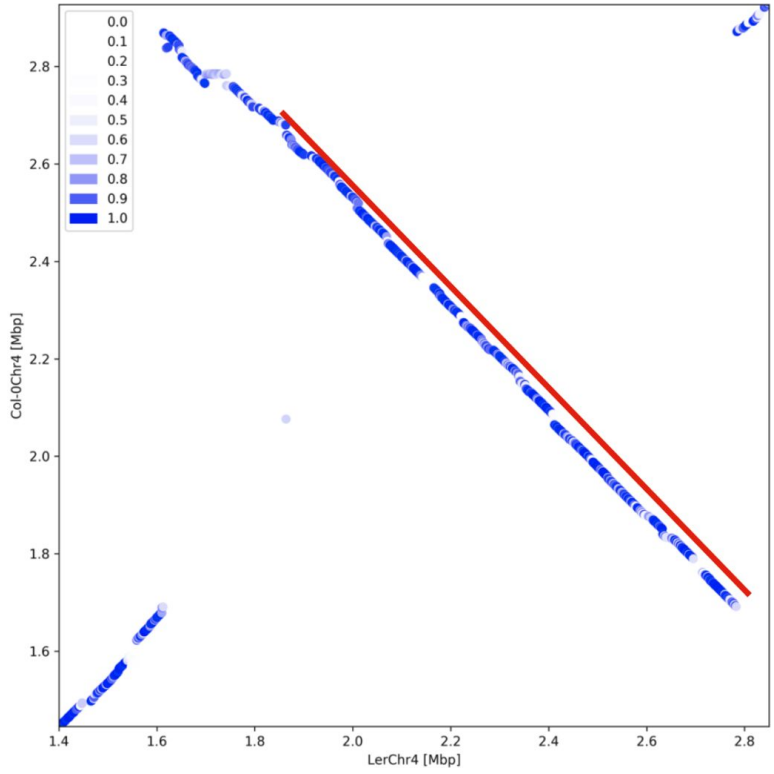
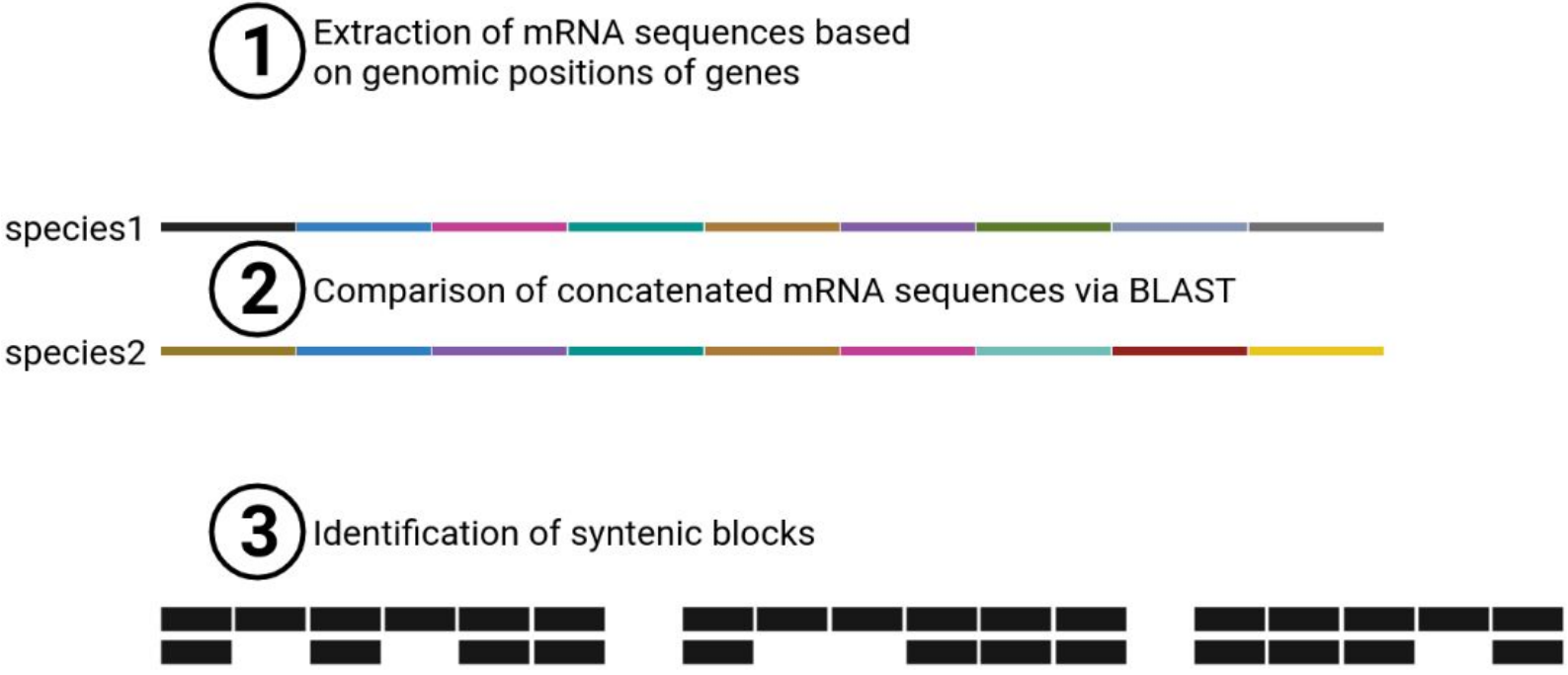
Dot plots





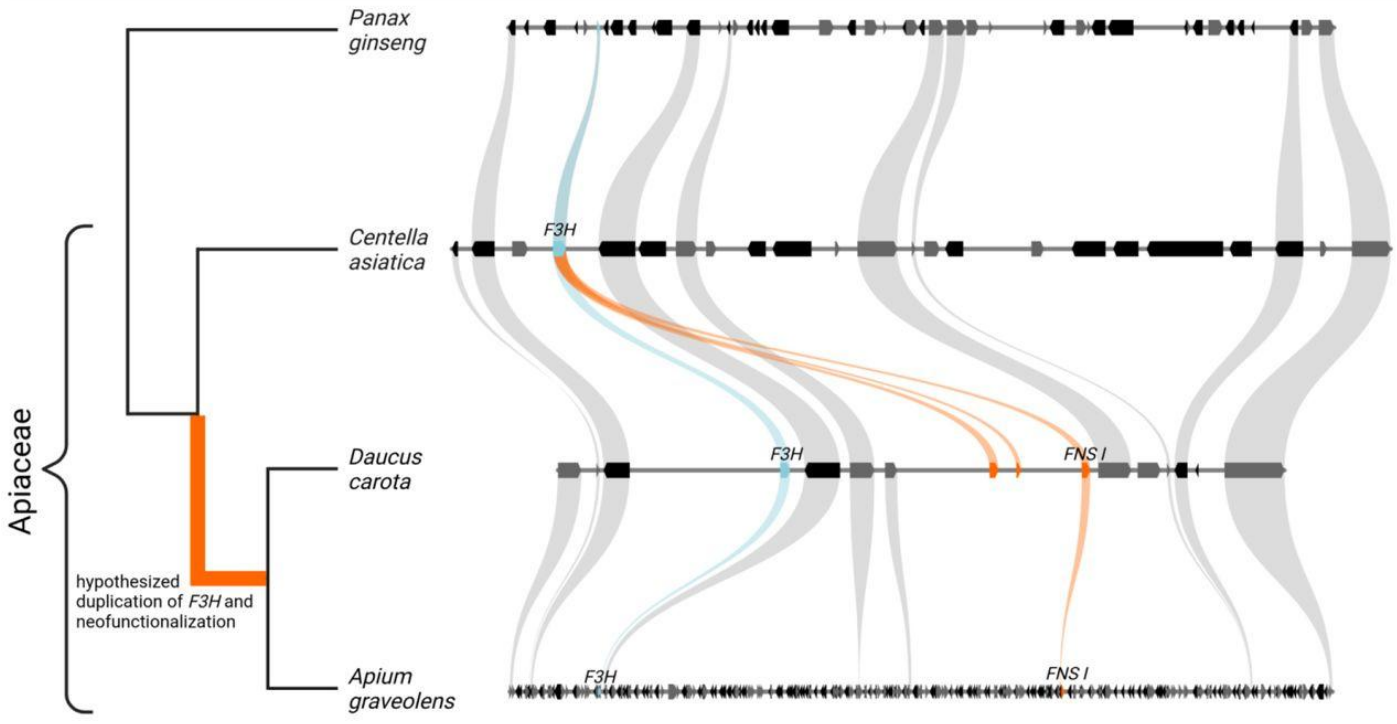
Pucker et al., 2019: 10.1371/journal.pone.0216233

JCVI/MCscan



https://github.com/tanghaibao/jcvi/wiki/MCscan-(Python-version)

Evolution of FNS I in the Apiaceae



Pucker & Iorizzo, 2022: 10.1101/2022.02.16.480750

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Recent Genomic Studies - Examples

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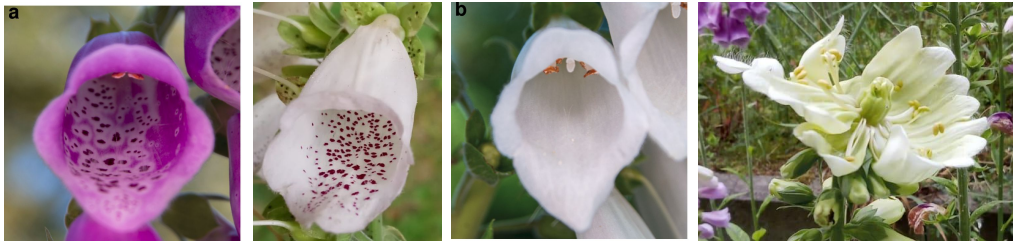
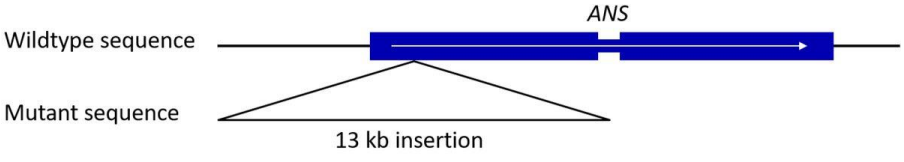
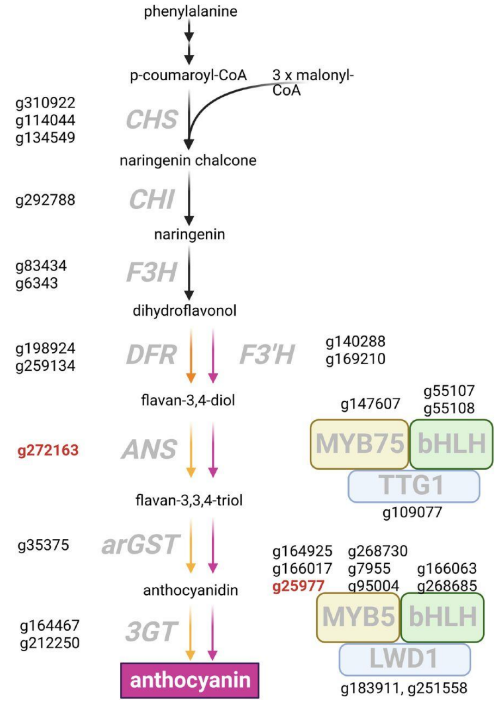
Flower diversity in *Digitalis purpurea* I



Horz *et al.*, 2024: 10.1101/2024.02.14.580303

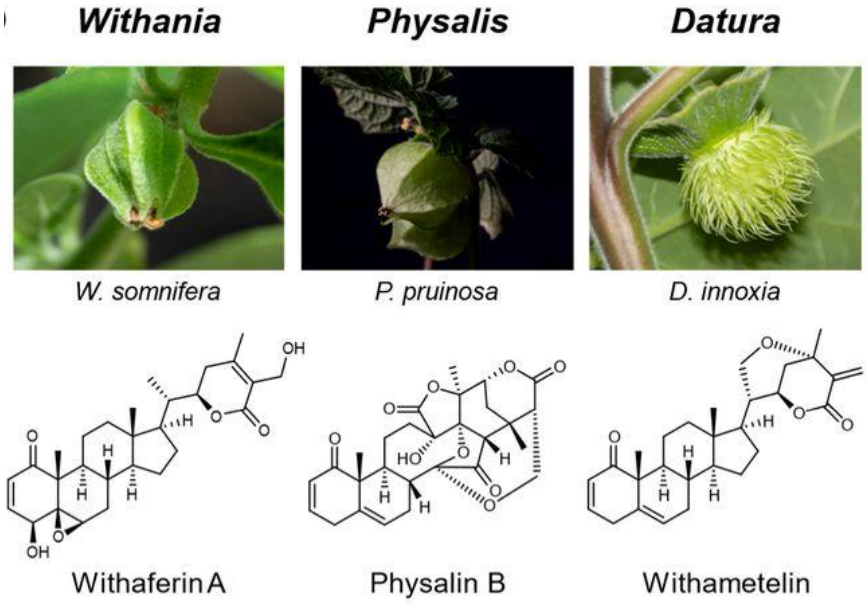
Flower diversity in *Digitalis purpurea* II

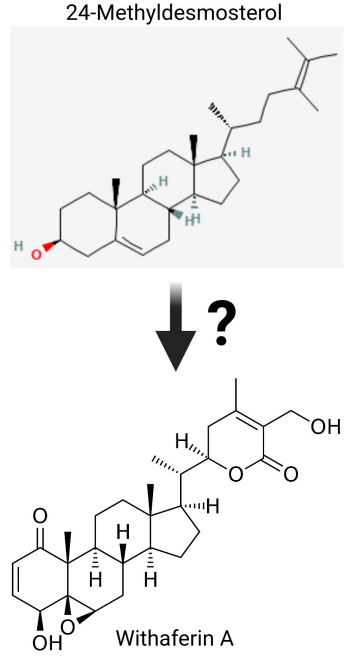




Horz *et al.*, 2024: 10.1101/2024.02.14.580303

Discovery of the withanolide biosynthesis I

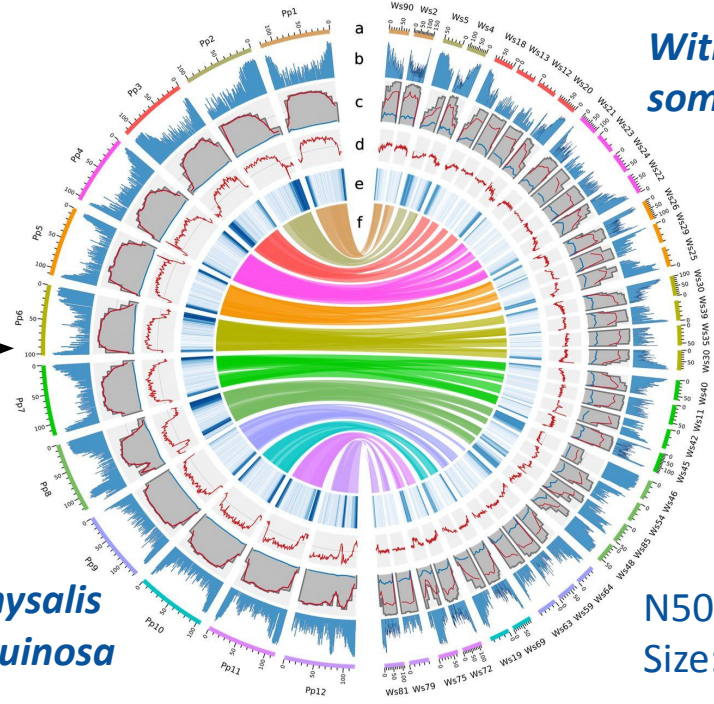




Hakim, Choudhary, Malhotra, Peng *et al.*, 2024: 10.1101/2024.09.27.614867

Discovery of the withanolide biosynthesis II

Withania produces especially interesting withanolides



N50: 71 Mb
Size: 2.8 Gbp

Hakim, Choudhary, Malhotra, Peng *et al.*, 2024: 10.1101/2024.09.27.614867

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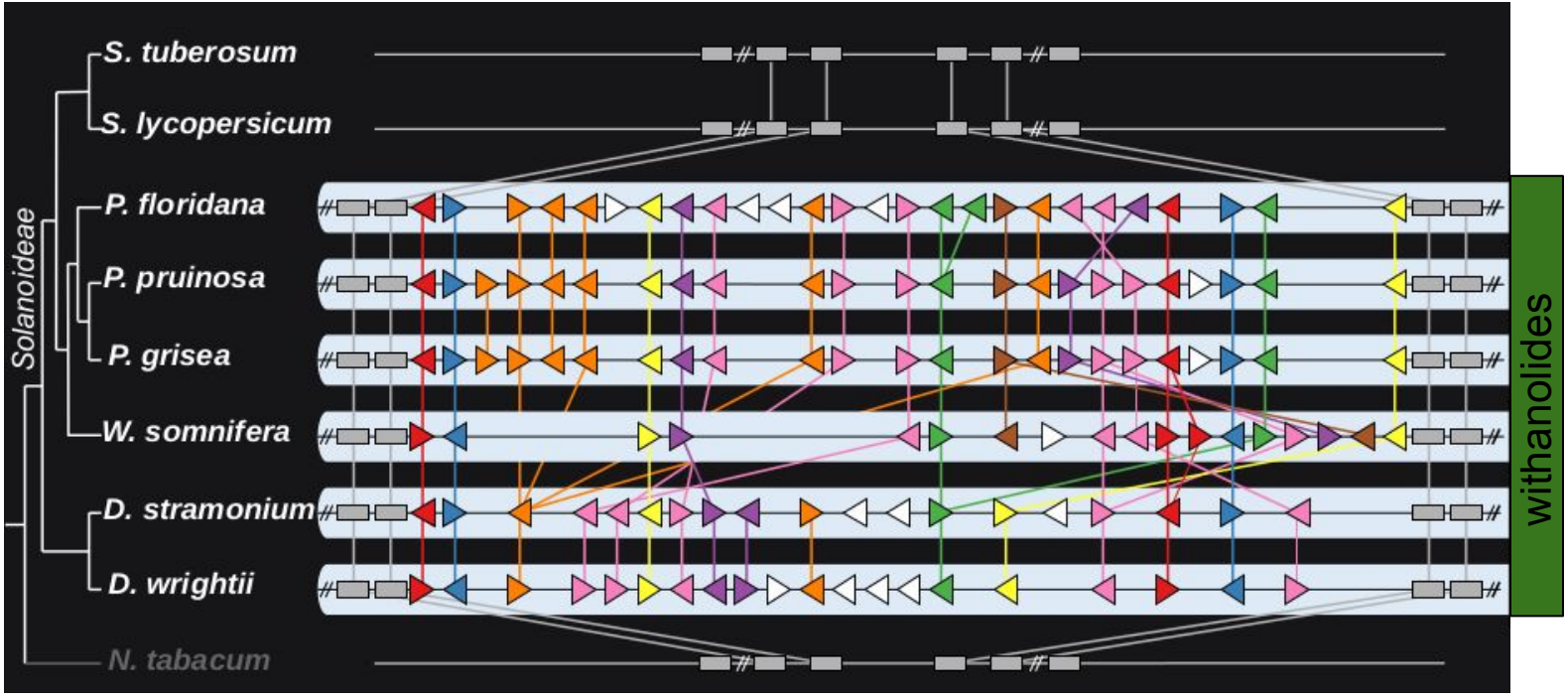
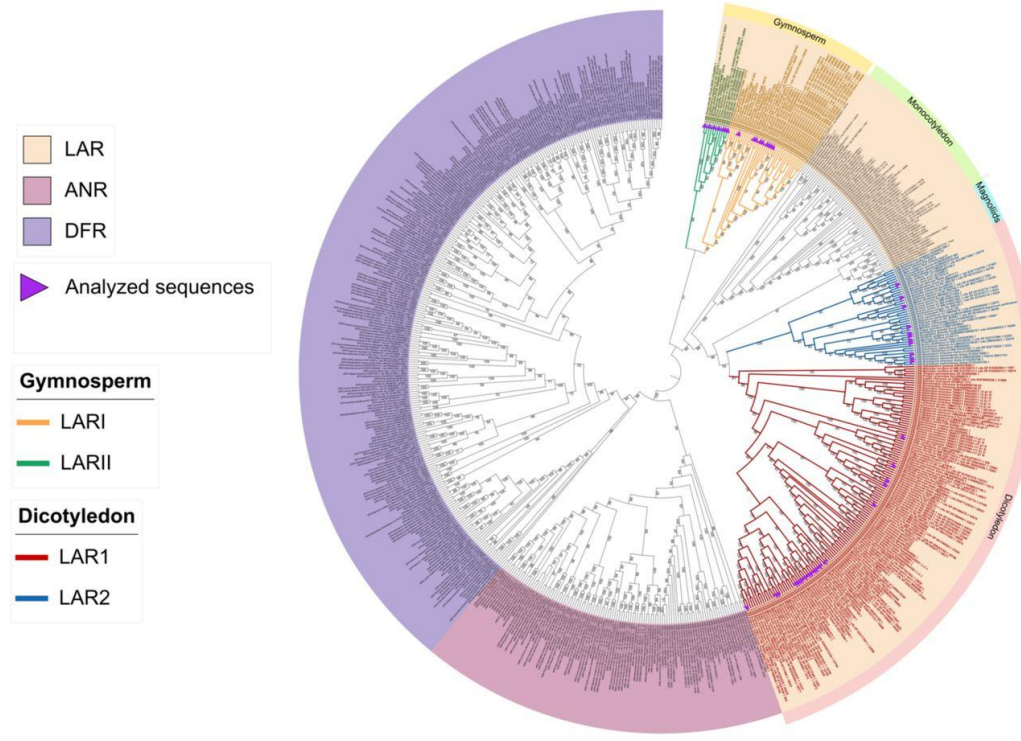
Discovery of the withanolide biosynthesis III



Hakim, Choudhary, Malhotra, Peng *et al.*, 2024: 10.1101/2024.09.27.614867

LAR evolution I

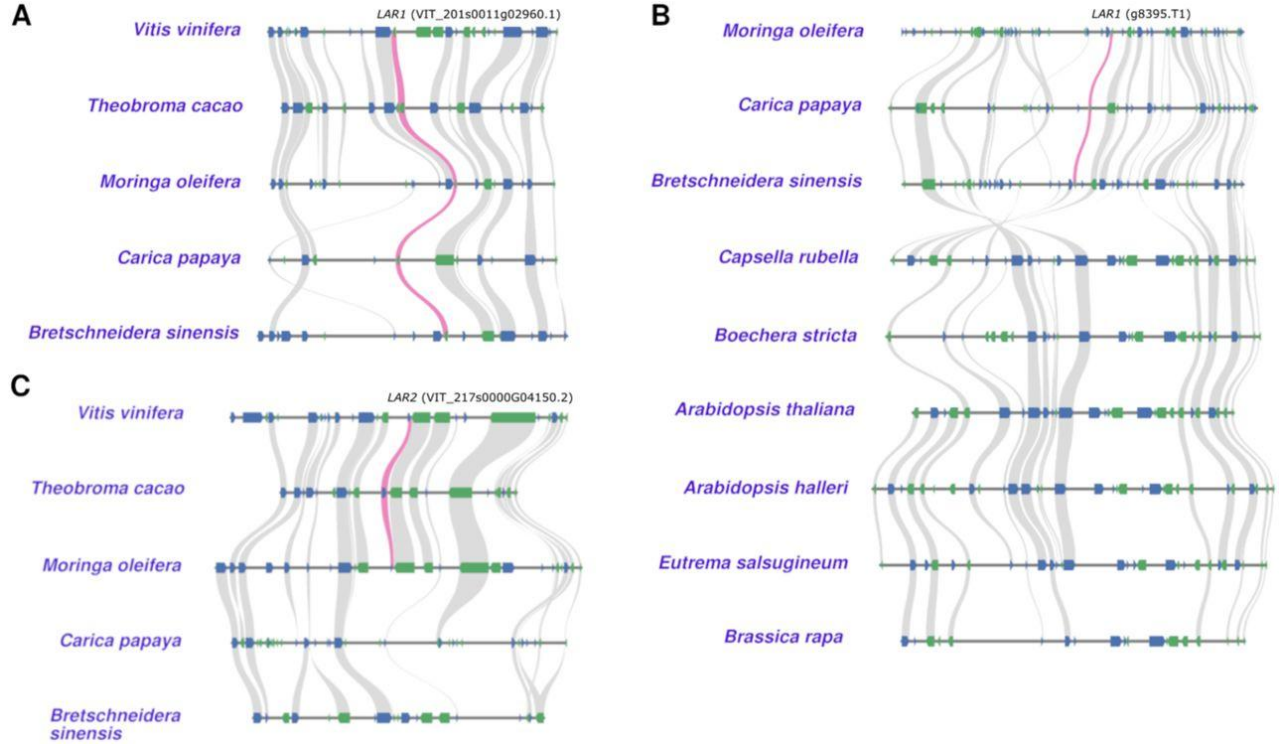
- Leucoanthocyanidin reductase (LAR)
- LAR was duplicated at basis of angiosperms
- Large numbers of genome sequences enables such large scale analyses



Recinos & Pucker, 2025: 10.1101/2025.08.06.668978

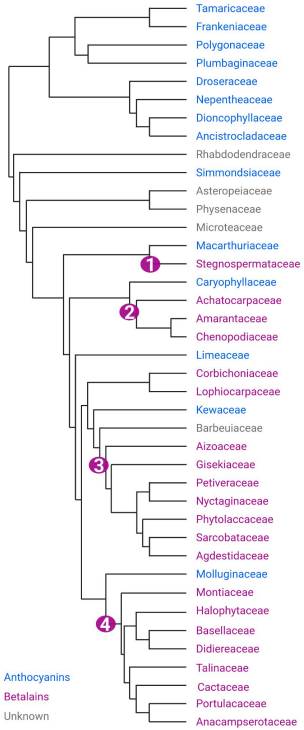
LAR evolution II

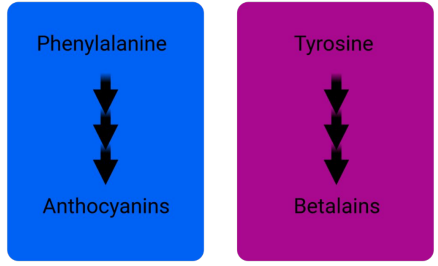
- LAR appears lost in Brassicales
- Synteny analyes allow to confirm this



Recinos & Pucker, 2025: 10.1101/2025.08.06.668978

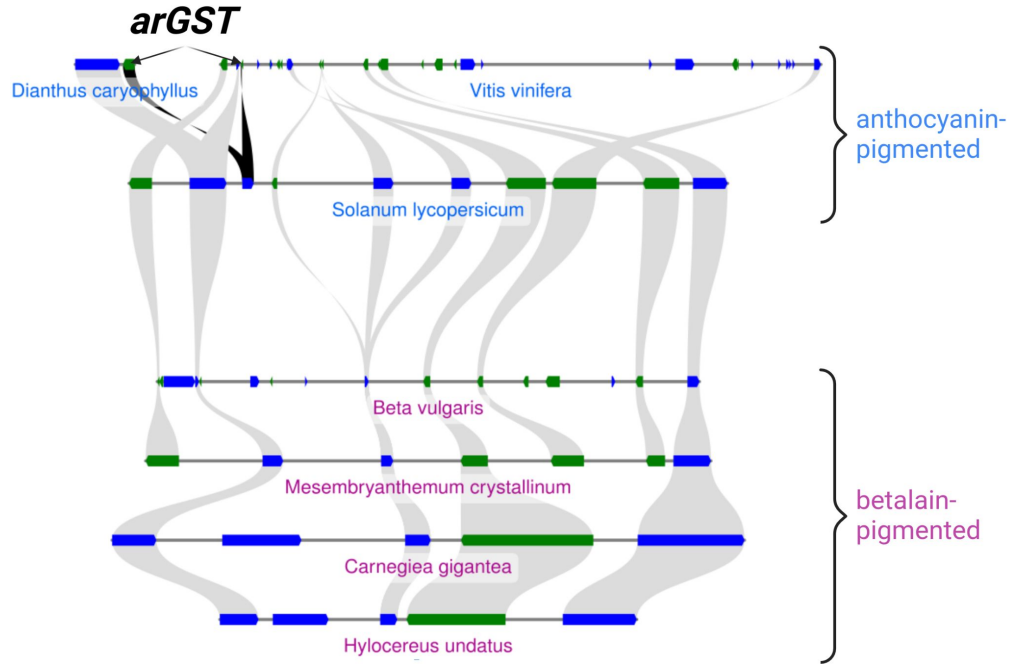
Anthocyanin loss in Caryophyllales





Antirrhinum majus

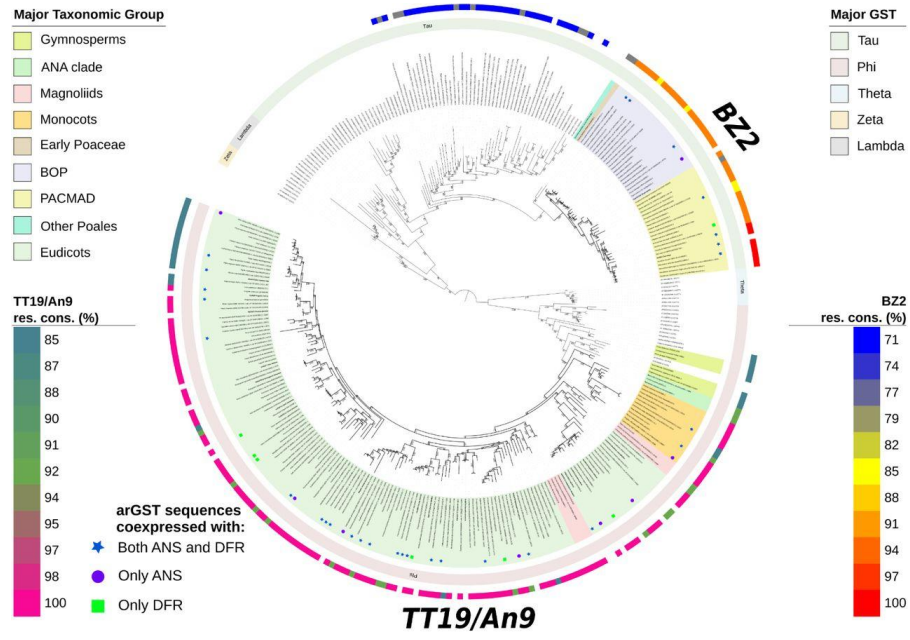
Mirabilis jalapa



Pucker *et al.*, 2024: 10.1111/nph.19341

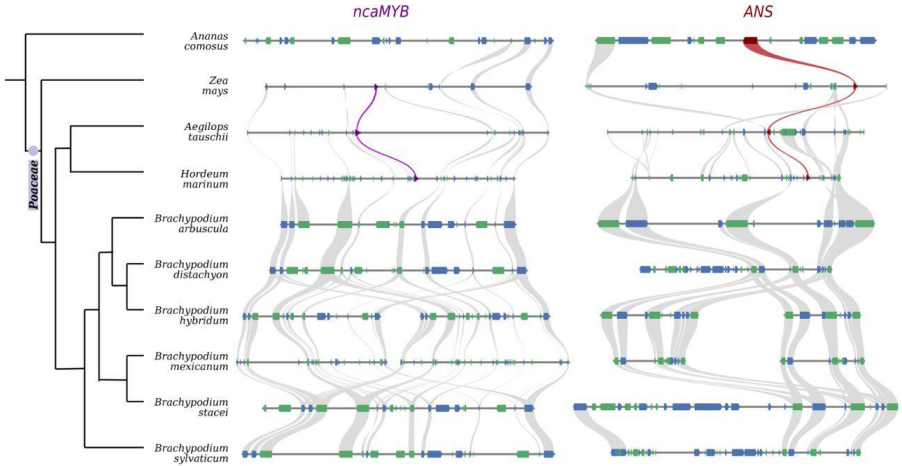
Anthocyanin loss in Poaceae I

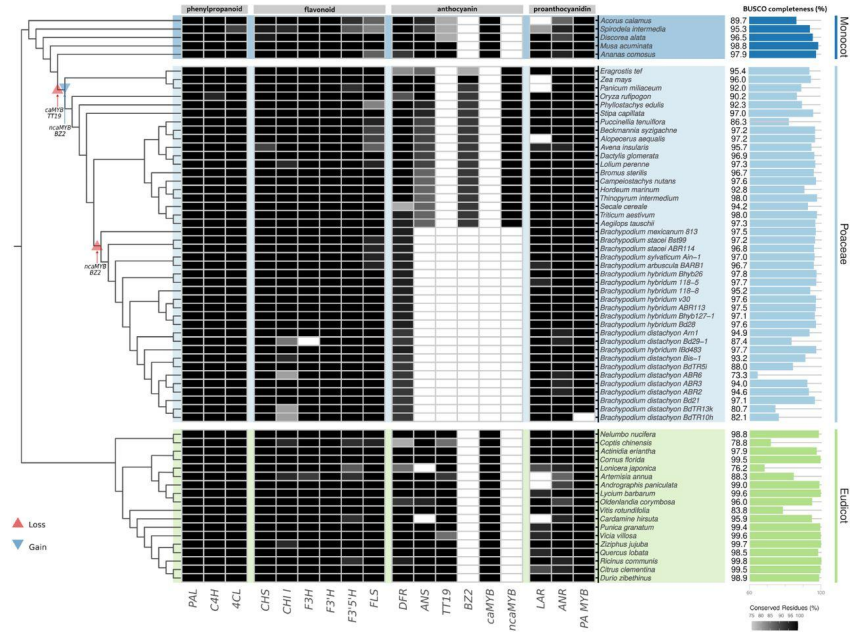
- Poaceae (true grasses) harbour numerous crops
- Anthocyanin biosynthesis gene arGST (TT19/An9) was lost
- Independent recruitment of a novel arGST in Poaceae (BZ2)



Khatun et al., 2025: 10.1101/2025.09.21.677584

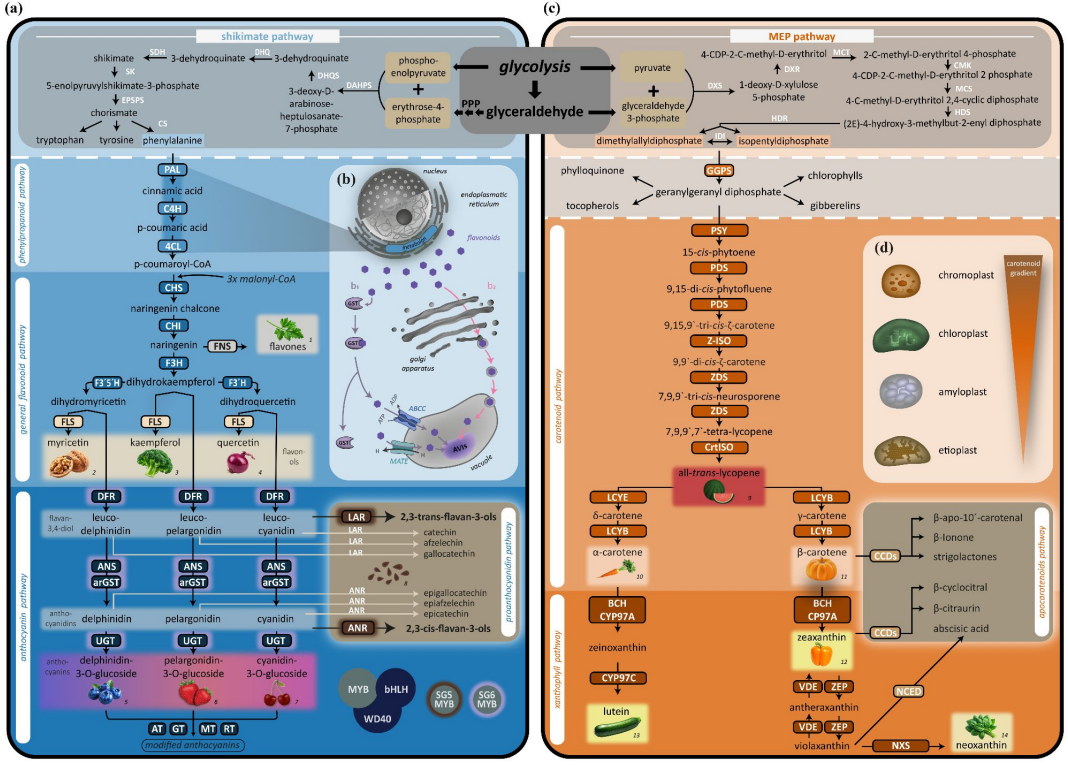
Anthocyanin loss in Poaceae II





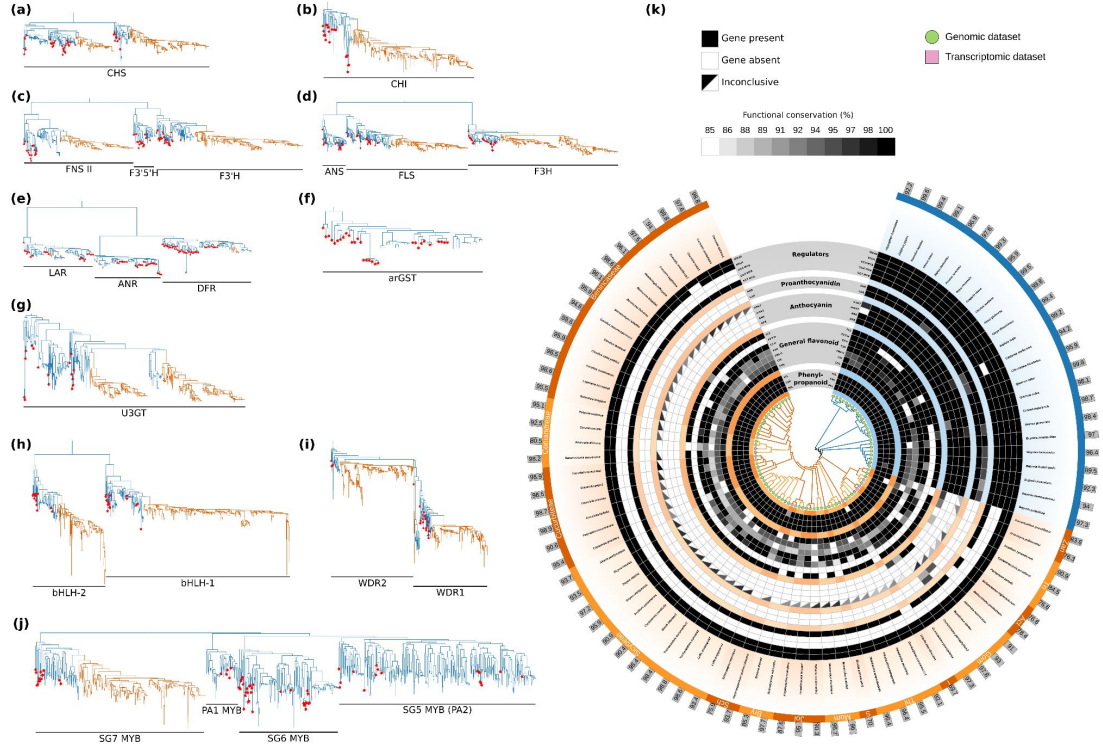
Khatun et al., 2025: 10.1101/2025.09.21.677584

Anthocyanin loss in Cucurbitaceae I



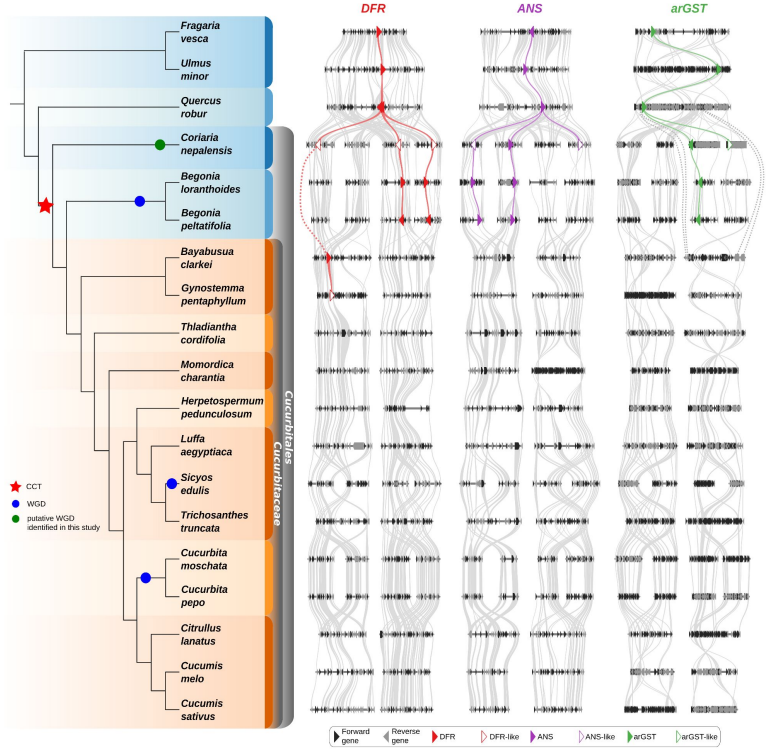
Choudhary et al., 2025: 10.1101/2025.10.06.680802

Anthocyanin loss in Cucurbitaceae II



Choudhary et al., 2025: 10.1101/2025.10.06.680802

Anthocyanin loss in Cucurbitaceae III



Choudhary et al., 2025: 10.1101/2025.10.06.680802

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Summary

- Read mapping (short reads vs. long reads)
- Variant calling (short reads vs. long reads)
- Evolutionary genomics
- Comparative genomics & synteny analysis
- Application examples

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Time for questions!

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Literature

- de Oliveira, J. A. V. S.; Choudhary, N.; Meckoni, S. N.; Nowak, M. S.; Hagedorn, M.; Pucker, B. (2025). Cookbook for Plant Genome Sequences. doi: 10.20944/preprints202508.1176.v2.

- Wolff, K.; Friedhoff, R.; Schwarzer, F.; Pucker, B. (2023). Data Literacy in Genome Research. Journal of Integrative Bioinformatics, 2023, pp. 20230033. doi: 10.1515/jib-2023-0033.

- Pucker B, Irisarri I, de Vries J and Xu B (2022). Plant genome sequence assembly in the era of long reads: Progress, challenges and future directions. Quantitative Plant Biology, 3, E5. doi: 10.1017/qpb.2021.18.