



Information

非モデル植物のための 遺伝子ネットワーク情報活用基盤

All words

Search

» Help

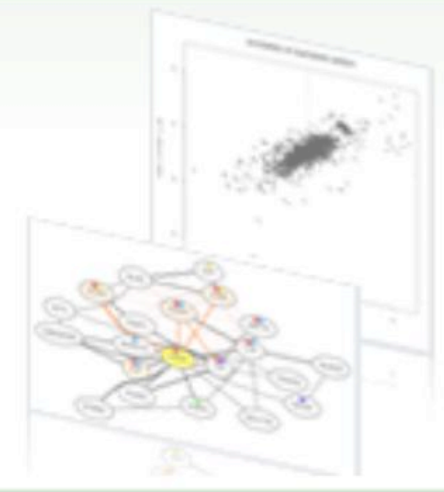
Search

- GeneTable
- EdgeAnnotation
- CoExSearch
- etc.



Draw

- NetworkDrawer
- HCluster
- CoexViewer
- etc.



What's new

2022.09.15

» [Bug fix] The coexpression z-score of a guide gene was incorrectly duplicated in the reference column(s) of a paralog gene(s) in the same as been fixed. We for any inconvenience.

Browse

東北大学 大学院情報科学研究科 大林武

Target sp

2023-10-05 トーゴの日シンポジウム2023 (日本科学未来館)

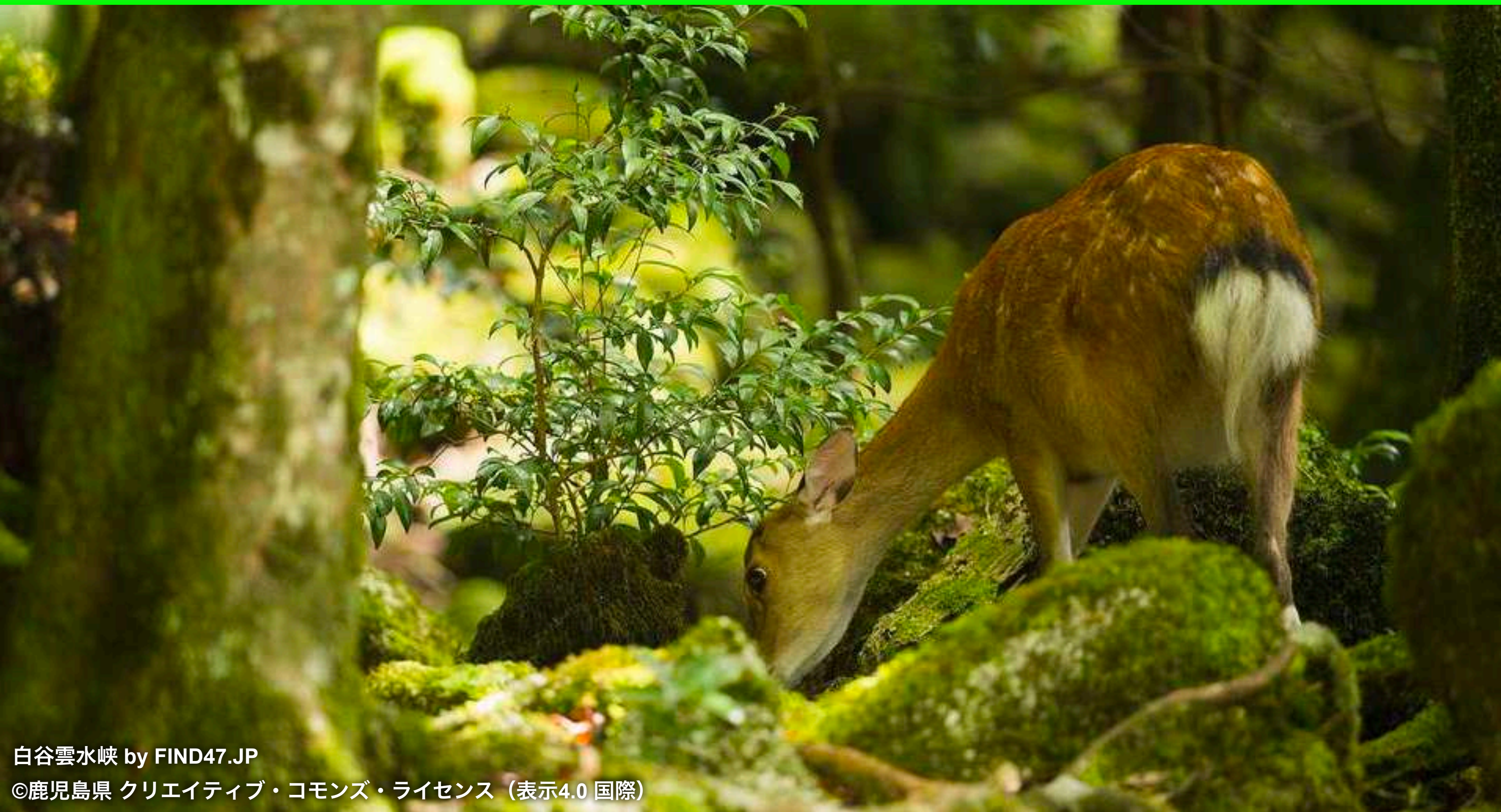
Arabidopsis

Field mustard

Soybean

have revised the calculation method of the union

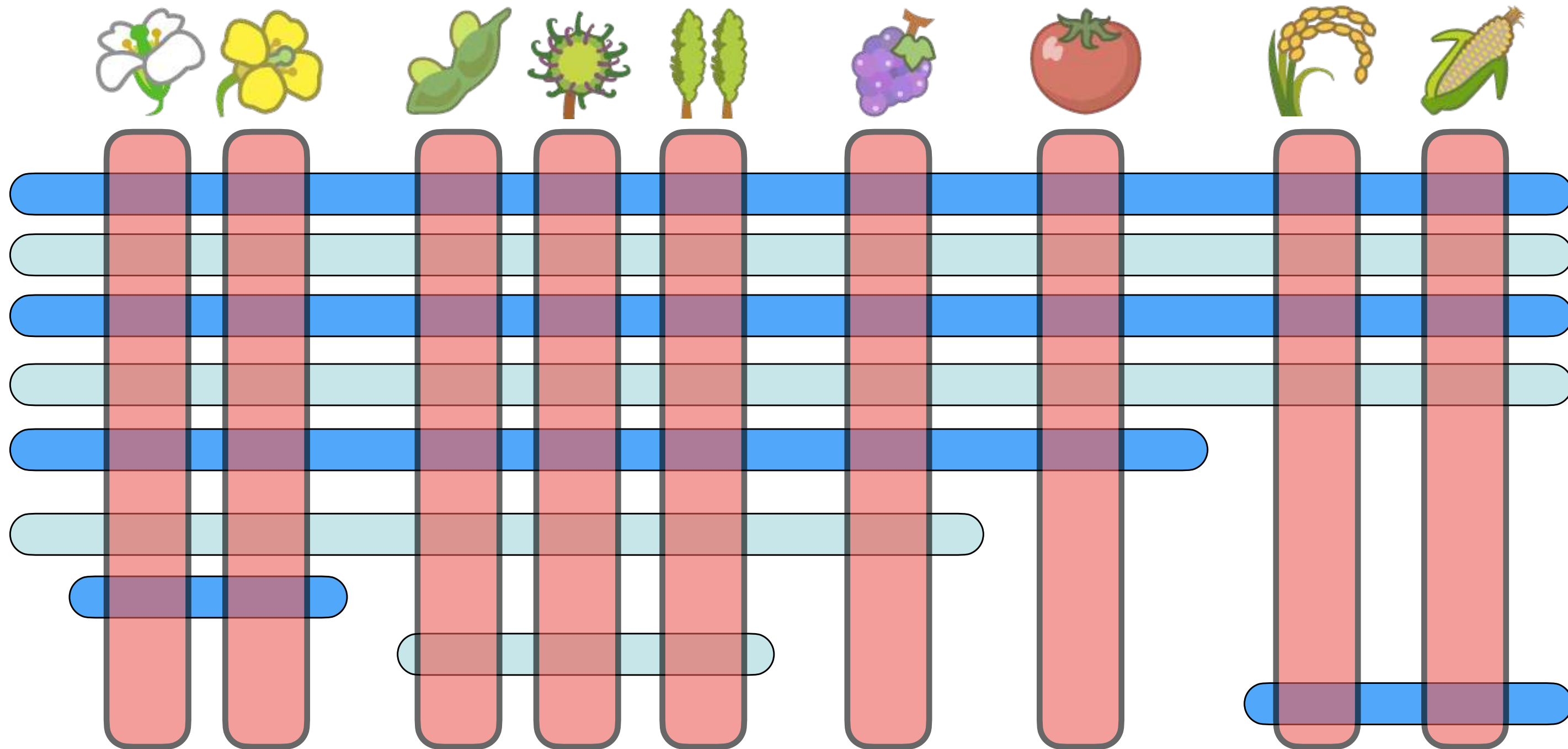
植物の多様性は宝の山



縦横無尽な遺伝子探索

遺伝子共発現による遺伝子の探索

モデル植物

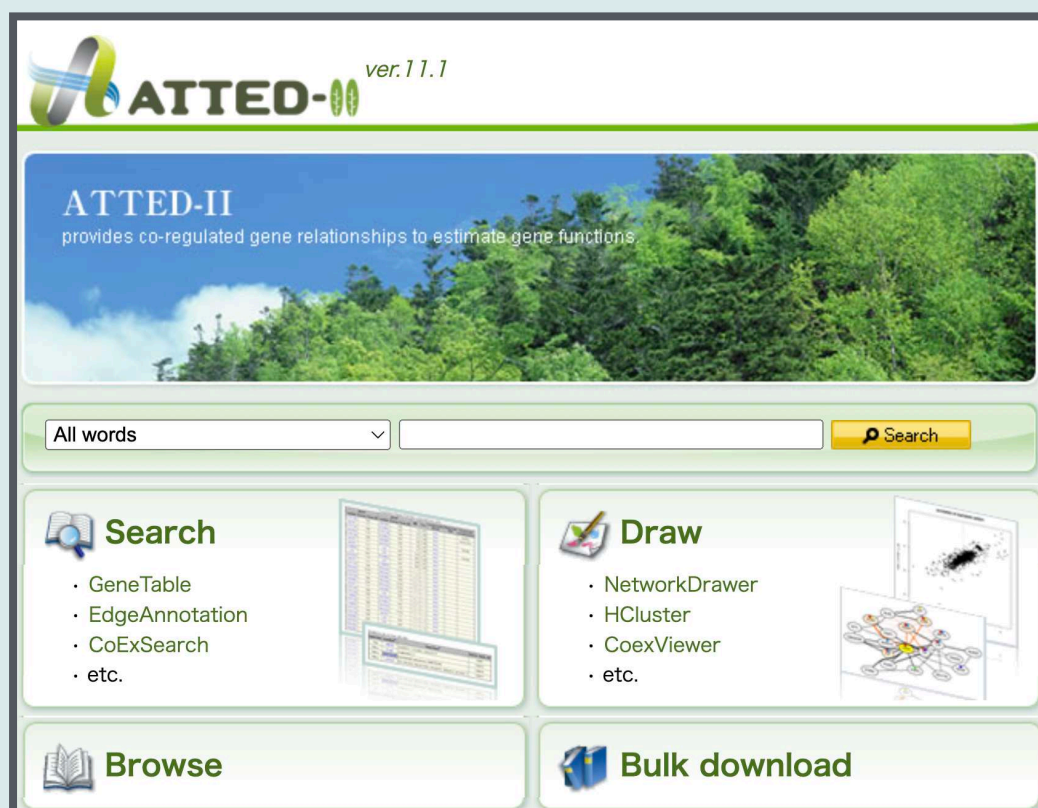


配列相同性による探索

非モデル植物研究はデータ駆動型アプローチが必須

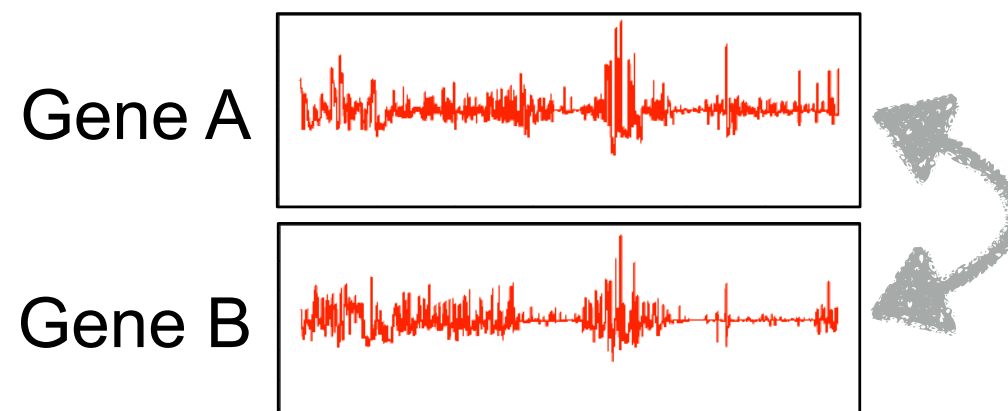
ゲノムにコードされた基盤的情報

遺伝子共発現データベース ATTED-II

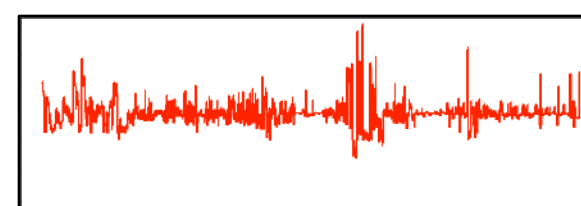
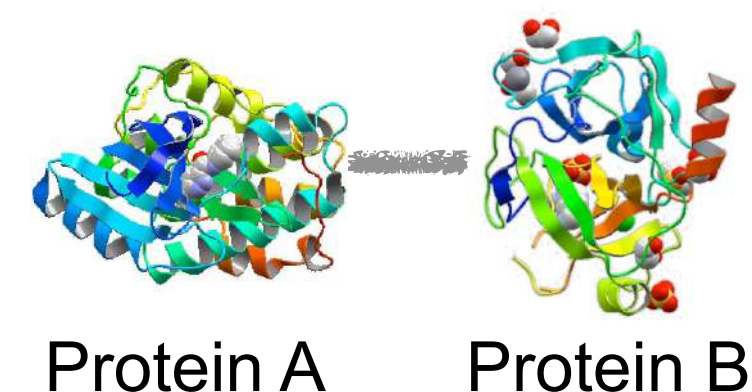



- 利用者：月間1300ユーザー
- 引用数：1700報

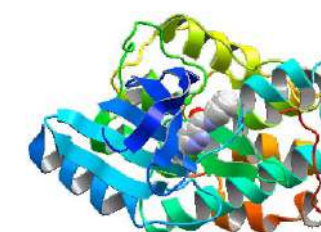
遺伝子共発現



タンパク質間相互作用



Expression



Protein structure

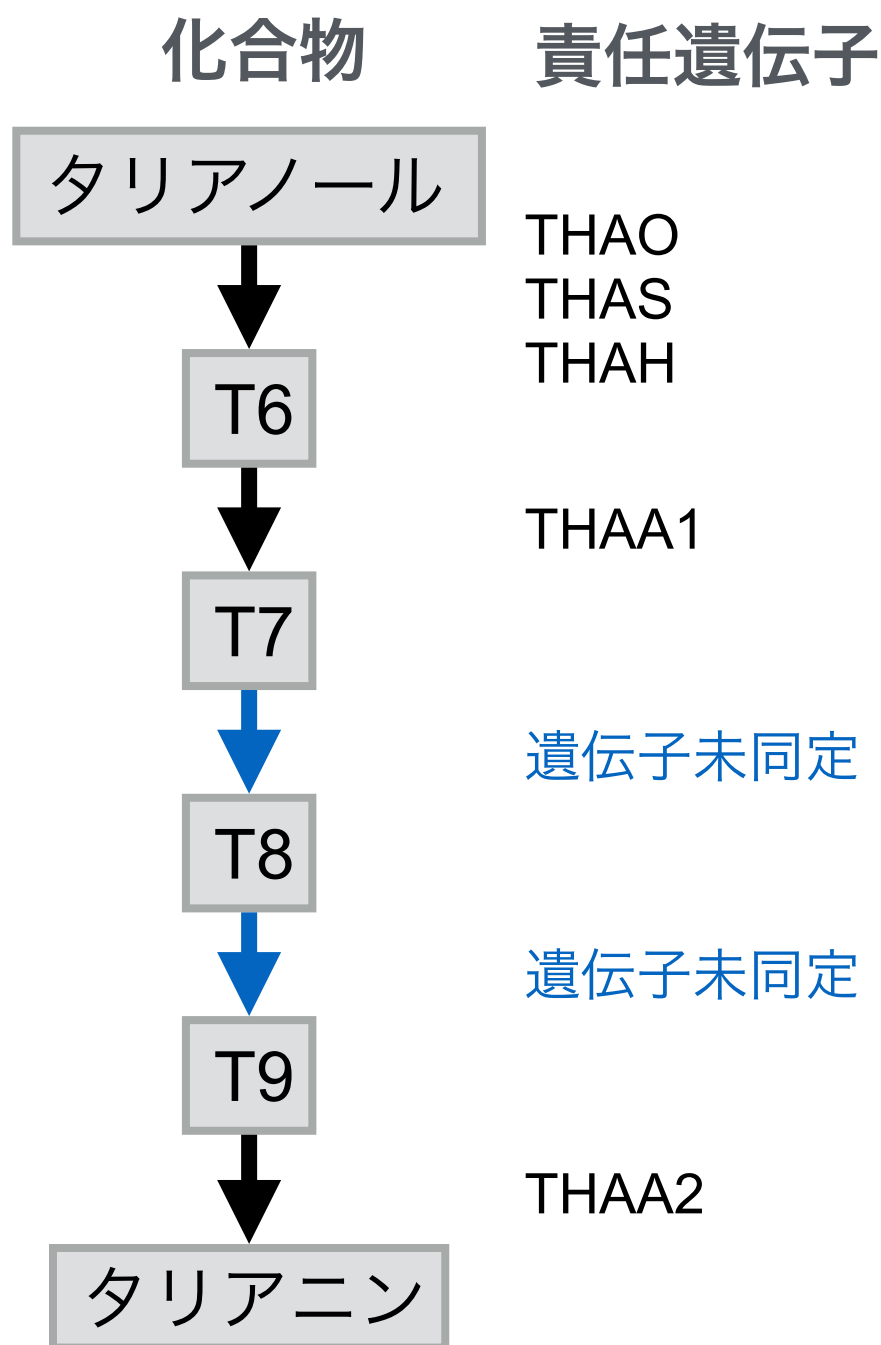
制御領域

タンパク質コード領域



根圏化合物の生合成

Huang+ (*Science* 2019)
A specialized metabolic network selectively modulates Arabidopsis root microbiota.

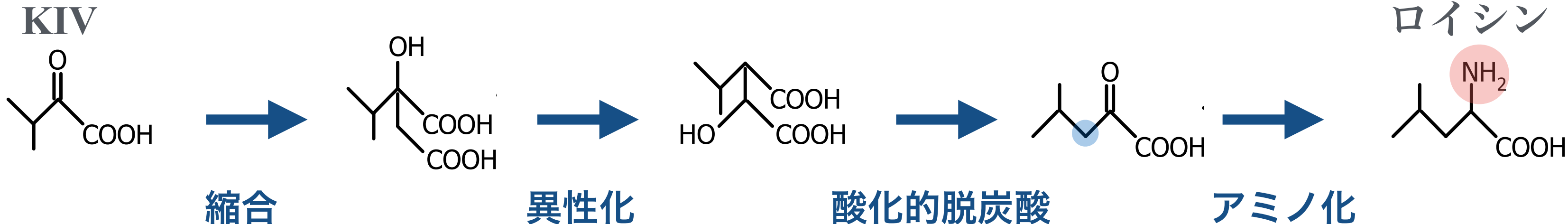


Supplementary Table 3 (一部改変)

Rank	AGI code	Gene annotations
1	At5g47990 (THAO)	Cytochrome P450, family 705, subfamily A
2	At5g48010 (THAS)	Thalianol synthase 1
3	At5g48000 (THAH)	Cytochrome P450, family 708, subfamily A
4	At5g47980 (THAA1)	HXXXD-type acyl-transferase family protein
5	At1g66800	NAD(P)-binding Rossmann-fold superfamily
6	At1g14960	Polyketide cyclase/dehydrase and lipid transport superfamily protein
7	At5g42590 (MRO)	Cytochrome P450, family 71, subfamily A
8	At2g01880	Purple acid phosphatase 7
9	At3g29250	NAD(P)-binding Rossmann-fold superfamily
10	At3g45710	Major facilitator superfamily
11	At5g23840	MD-2-related lipid recognition domain-containing
12	At5g38030	MATE efflux family
13	At4g22610	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily
14	At5g42580	Cytochrome P450, family 705, subfamily A
15	At2g16005	MD-2-related lipid recognition domain-containing
16	At3g46700	UDP-Glycosyltransferase superfamily
17	At5g38020	S-adenosyl-L-methionine-dependent methyltransferase superfamily
18	At5g47950 (THAA2)	HXXXD-type acyl-transferase family
19	At1g50560	Cytochrome P450, family 705, subfamily A
20	At4g12550	Auxin-Induced in Root cultures 1



パスウェイの機能分化

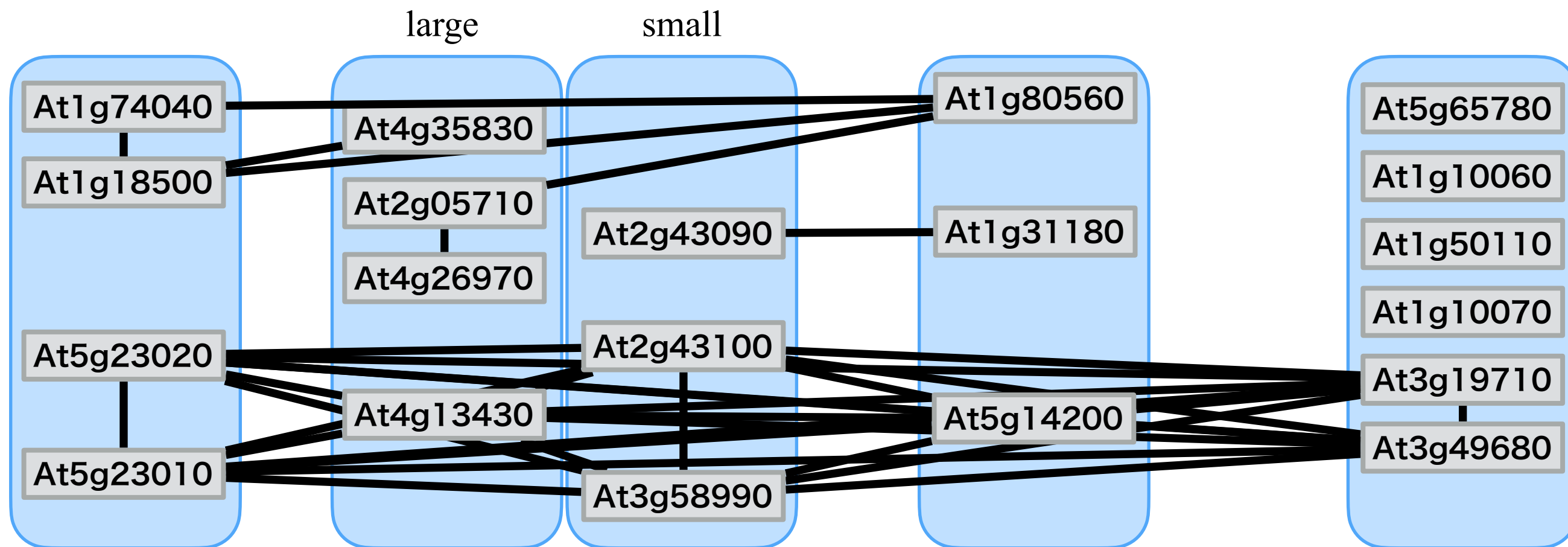
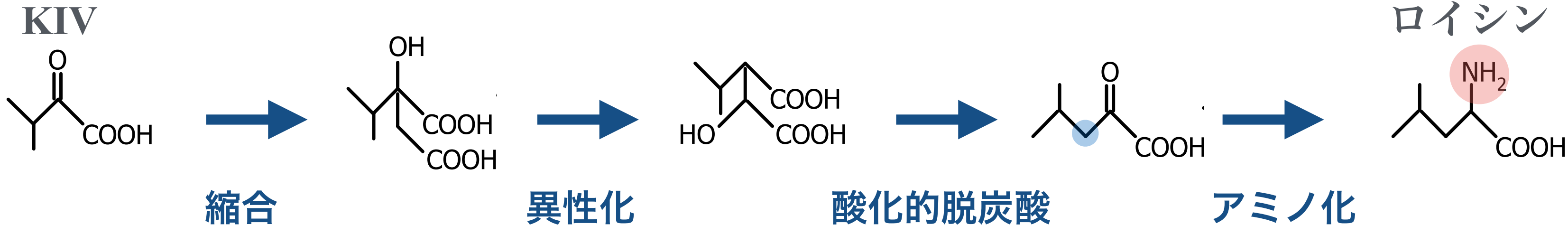


- | | large | small | | |
|---|---|--|--|---|
| <div style="border: 1px solid #ccc; padding: 2px; margin-bottom: 5px;">At1g74040</div> <div style="border: 1px solid #ccc; padding: 2px; margin-bottom: 5px;">At1g18500</div> <div style="border: 1px solid #ccc; padding: 2px; margin-bottom: 5px;">At5g23020</div> <div style="border: 1px solid #ccc; padding: 2px; margin-bottom: 5px;">At5g23010</div> | <div style="border: 1px solid #ccc; padding: 2px; margin-bottom: 5px;">At4g35830</div> <div style="border: 1px solid #ccc; padding: 2px; margin-bottom: 5px;">At2g05710</div> <div style="border: 1px solid #ccc; padding: 2px; margin-bottom: 5px;">At4g26970</div> <div style="border: 1px solid #ccc; padding: 2px; margin-bottom: 5px;">At4g13430</div> | <div style="border: 1px solid #ccc; padding: 2px; margin-bottom: 5px;">At2g43090</div> <div style="border: 1px solid #ccc; padding: 2px; margin-bottom: 5px;">At2g43100</div> <div style="border: 1px solid #ccc; padding: 2px; margin-bottom: 5px;">At3g58990</div> | <div style="border: 1px solid #ccc; padding: 2px; margin-bottom: 5px;">At1g80560</div> <div style="border: 1px solid #ccc; padding: 2px; margin-bottom: 5px;">At1g31180</div> <div style="border: 1px solid #ccc; padding: 2px; margin-bottom: 5px;">At5g14200</div> | <div style="border: 1px solid #ccc; padding: 2px; margin-bottom: 5px;">At5g65780</div> <div style="border: 1px solid #ccc; padding: 2px; margin-bottom: 5px;">At1g10060</div> <div style="border: 1px solid #ccc; padding: 2px; margin-bottom: 5px;">At1g50110</div> <div style="border: 1px solid #ccc; padding: 2px; margin-bottom: 5px;">At1g10070</div> <div style="border: 1px solid #ccc; padding: 2px; margin-bottom: 5px;">At3g19710</div> <div style="border: 1px solid #ccc; padding: 2px; margin-bottom: 5px;">At3g49680</div> |

Hirai+ (PNAS 2007) Omics-Based Identification of Arabidopsis Myb Transcription Factors Regulating Aliphatic Glucosinolate Biosynthesis.
 Sawada+ (PCP 2009) Omics-Based Approaches to Methionine Side Chain Elongation in Arabidopsis: Characterization of the Genes Encoding Methylthioalkylmalate Isomerase and Methylthioalkylmalate Dehydrogenase.



パスウェイの機能分化

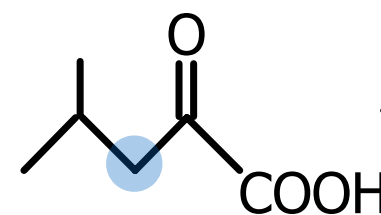
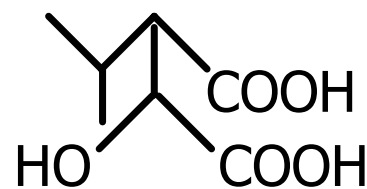
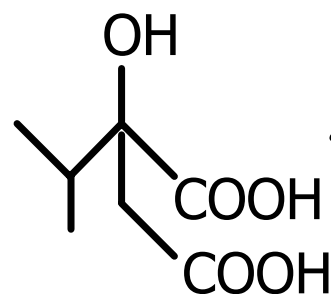
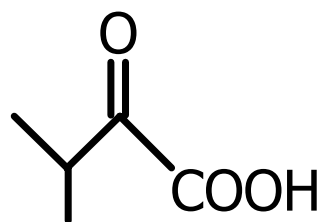


Hirai+ (PNAS 2007) Omics-Based Identification of Arabidopsis Myb Transcription Factors Regulating Aliphatic Glucosinolate Biosynthesis.
 Sawada+ (PCP 2009) Omics-Based Approaches to Methionine Side Chain Elongation in Arabidopsis: Characterization of the Genes Encoding Methylthioalkylmalate Isomerase and Methylthioalkylmalate Dehydrogenase.

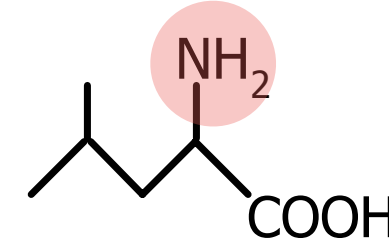


パスウェイの機能分化

KIV



ロイシン

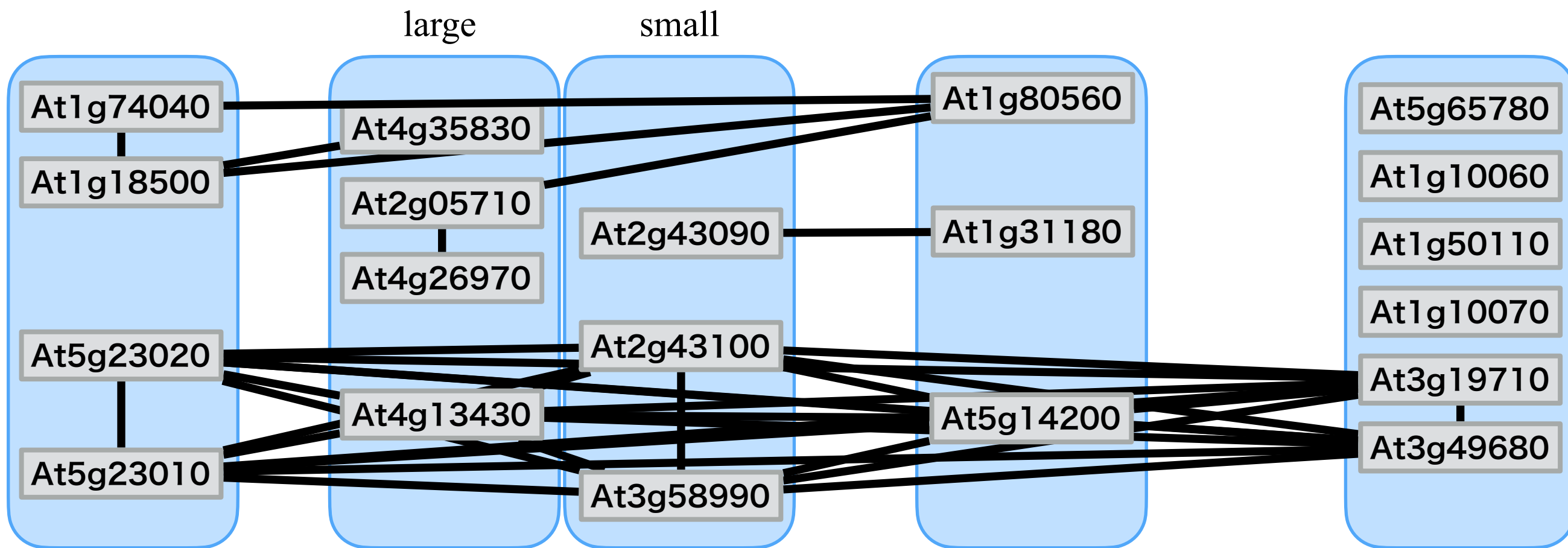


縮合

異性化

酸化的脱炭酸

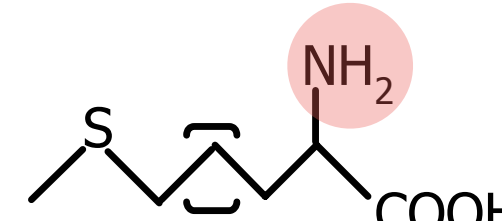
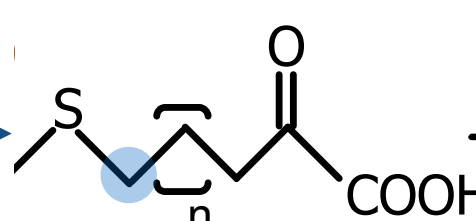
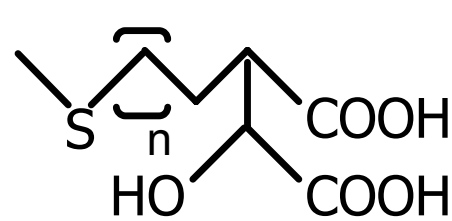
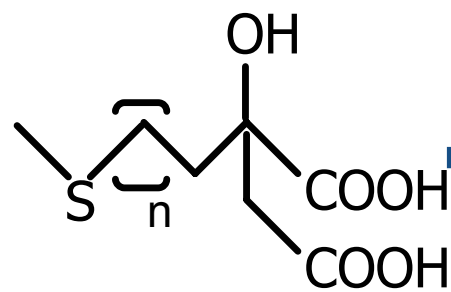
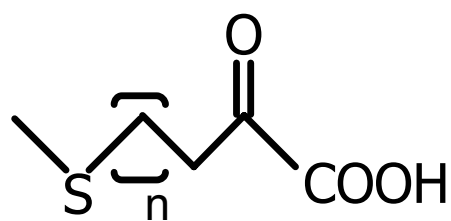
アミノ化



Glucosinolates



メチオニン



メチオニン誘導体

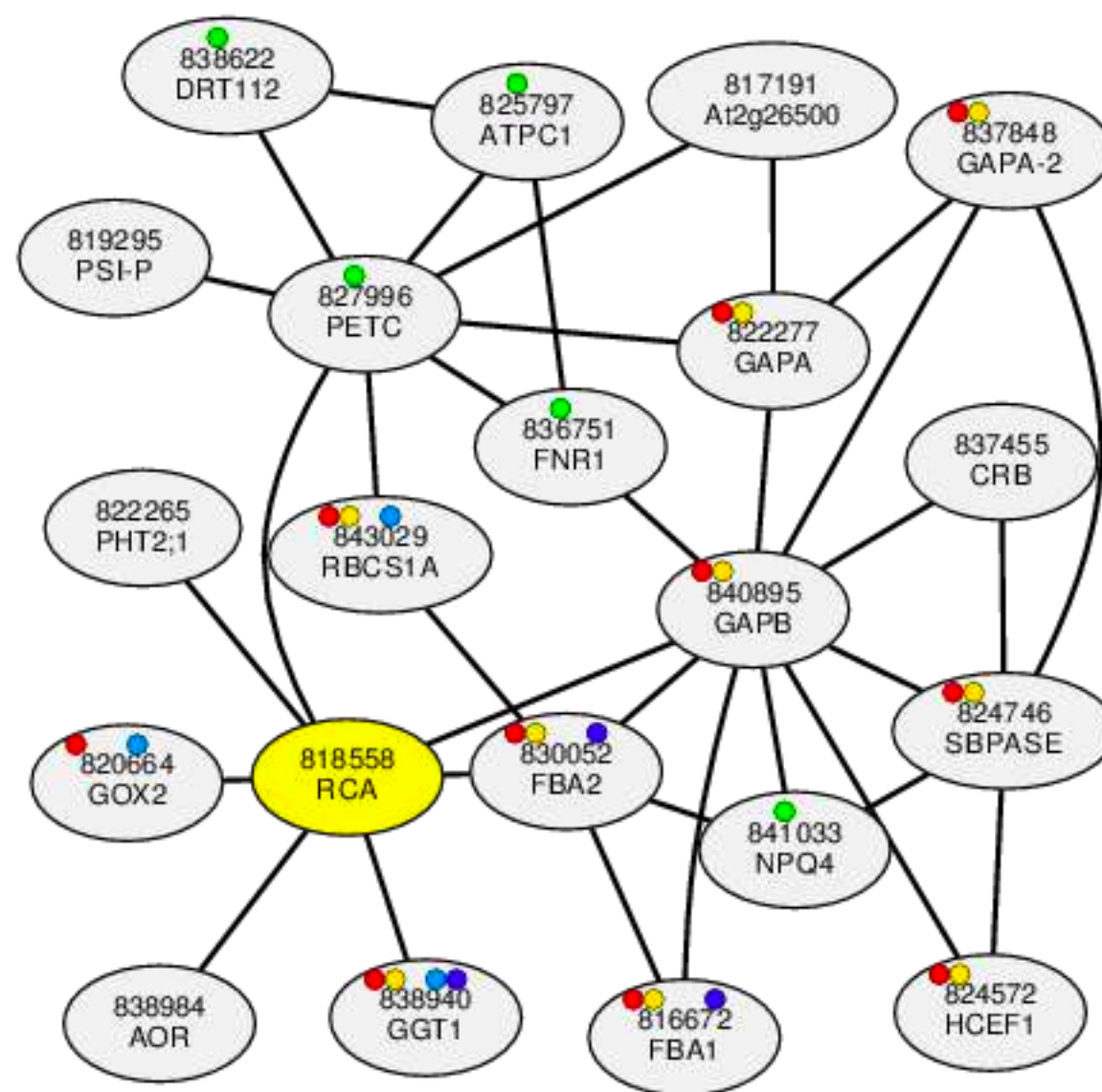
共発現情報を理解する

ターゲット：Rubisco Activase (RCA)

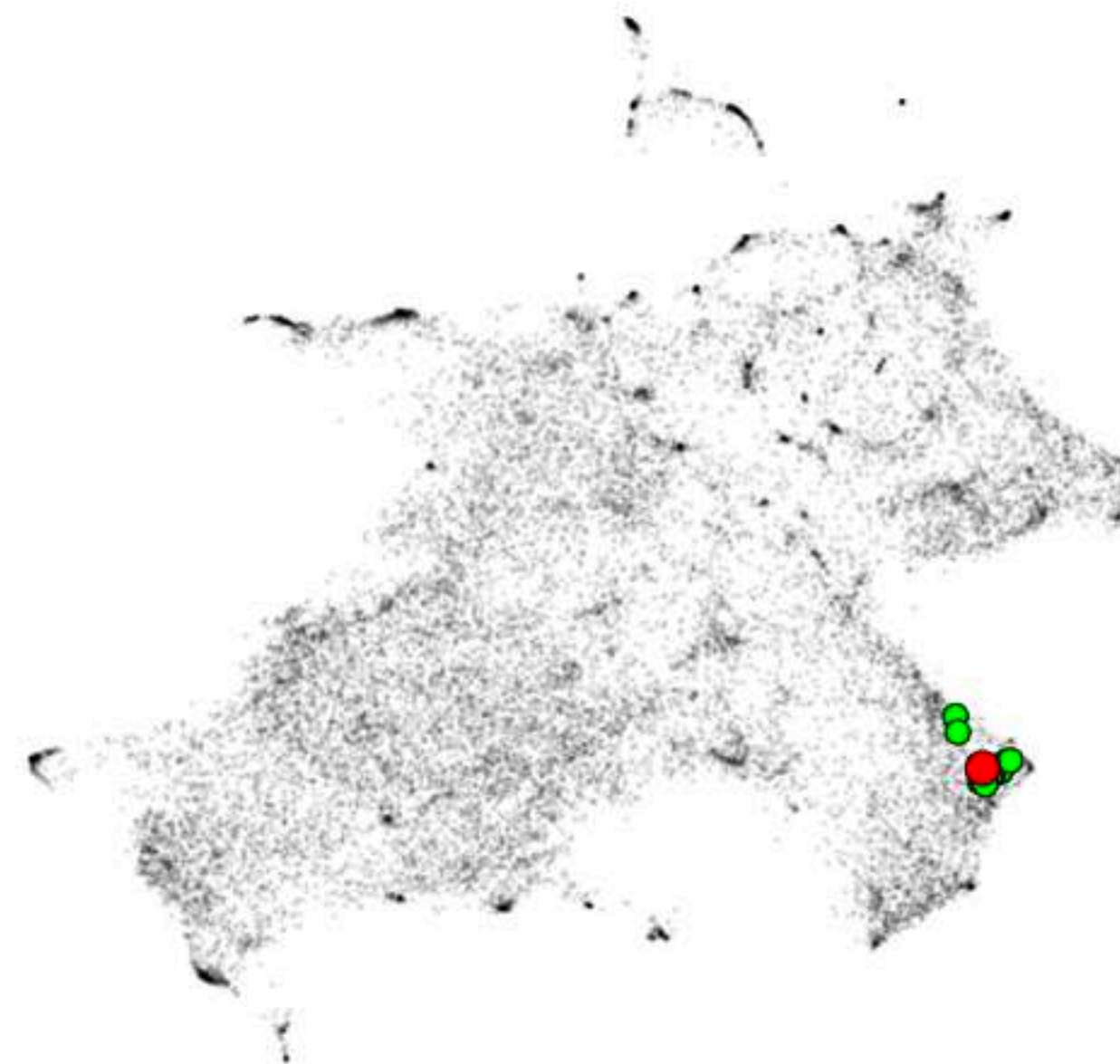
List

	coexpressed genes	z
1	FBA2	15.6
2	GAPB	12.4
3	PETC	12.2
4	DRT112	11.0
5	GGT1	10.9
6	SBPASE	10.6
7	CRB	10.6
8	FBA1	10.5
9	GAPA	10.4
10	GOX1	10.2

Network



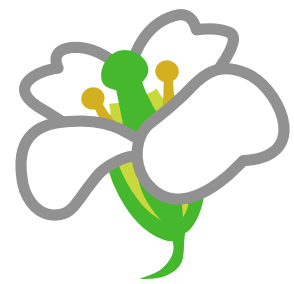
Map



- 正確な共発現度
- 局所的

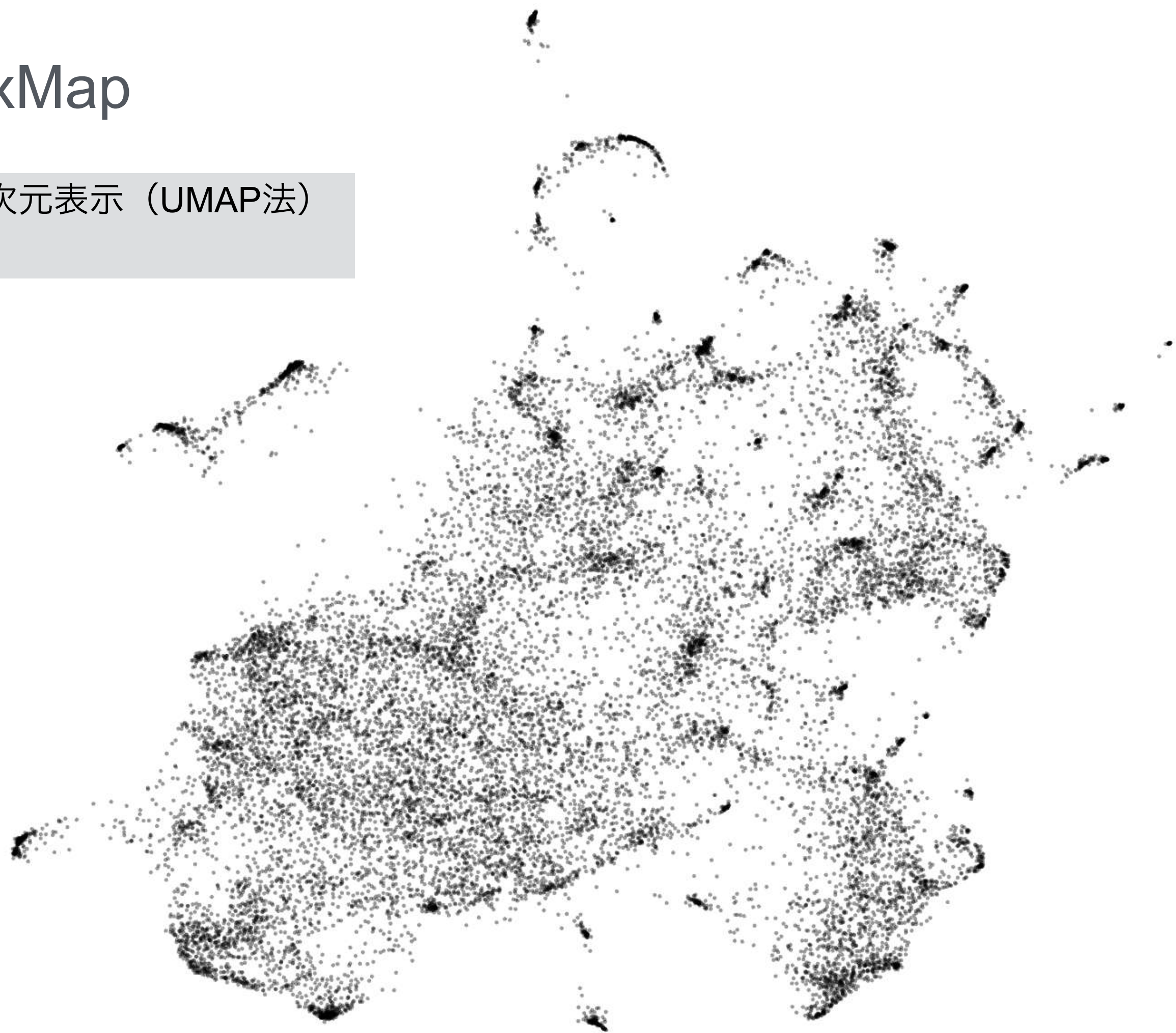
- 近似 (二値化)
- 局所的

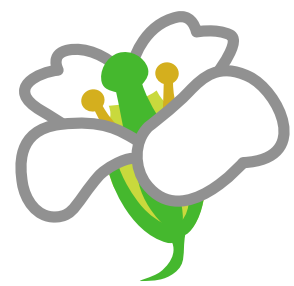
- 近似 (2次元)
- 全ゲノム



CoexMap

- 共発現情報の2次元表示 (UMAP法)
- 点は遺伝子





CoexMap

Pollen Tube

Seed Germination

Seed coat

Xyloglucan syn

Phenylpropanoid syn

Phragmoplast

Cyanoamino acid

DNA Replication
Base excision repair
Nucleosome

Sulfur
metabolism

N-Glycan Biosynthesis

Plant-pathogen
interaction

chloroplast/
mitochondrial
RNA modification

Galactose metabolism

Mitochondrial Matrix

Glycolysis

Photosynthesis

ER lumen

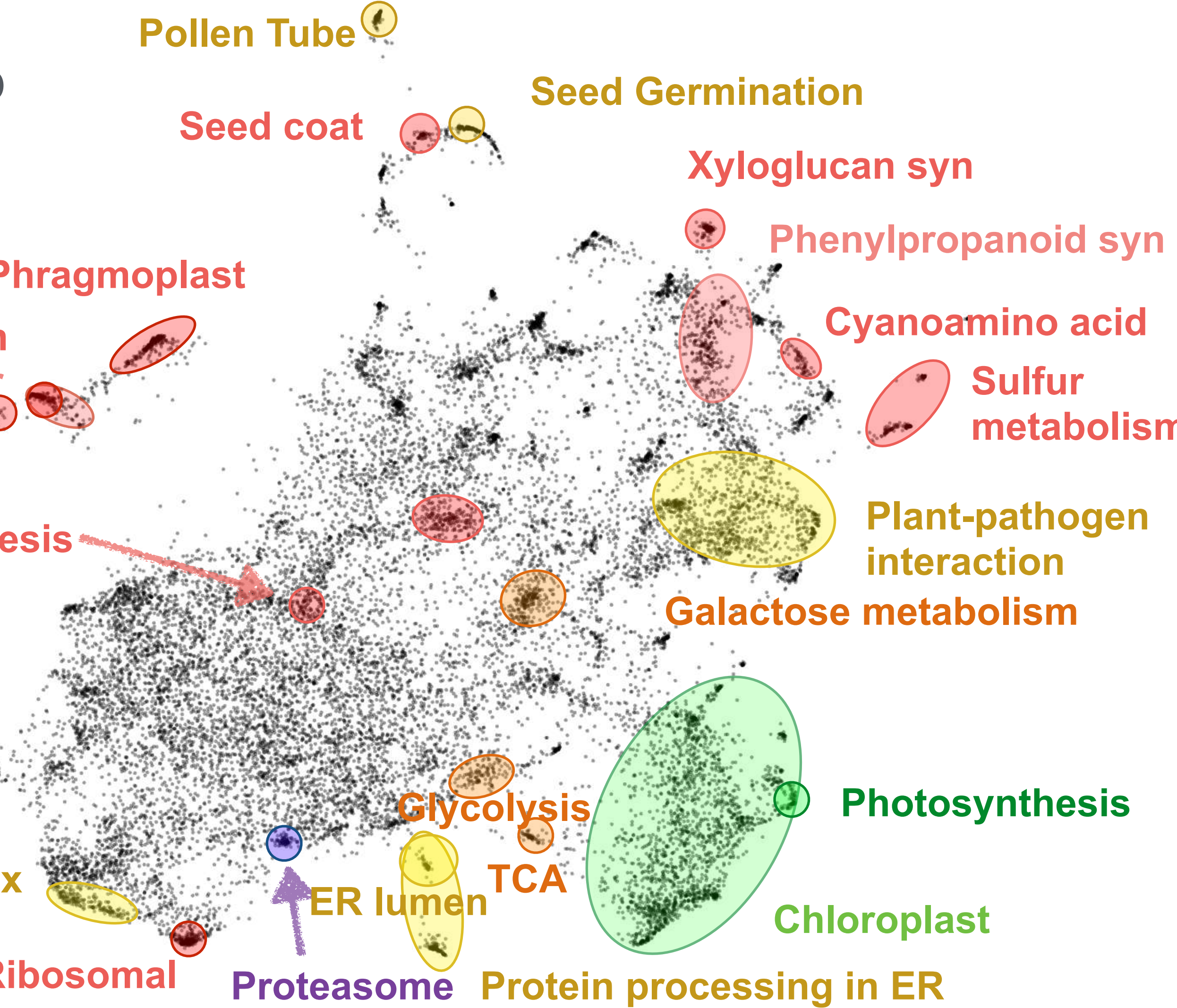
TCA

Chloroplast

Ribosomal

Proteasome

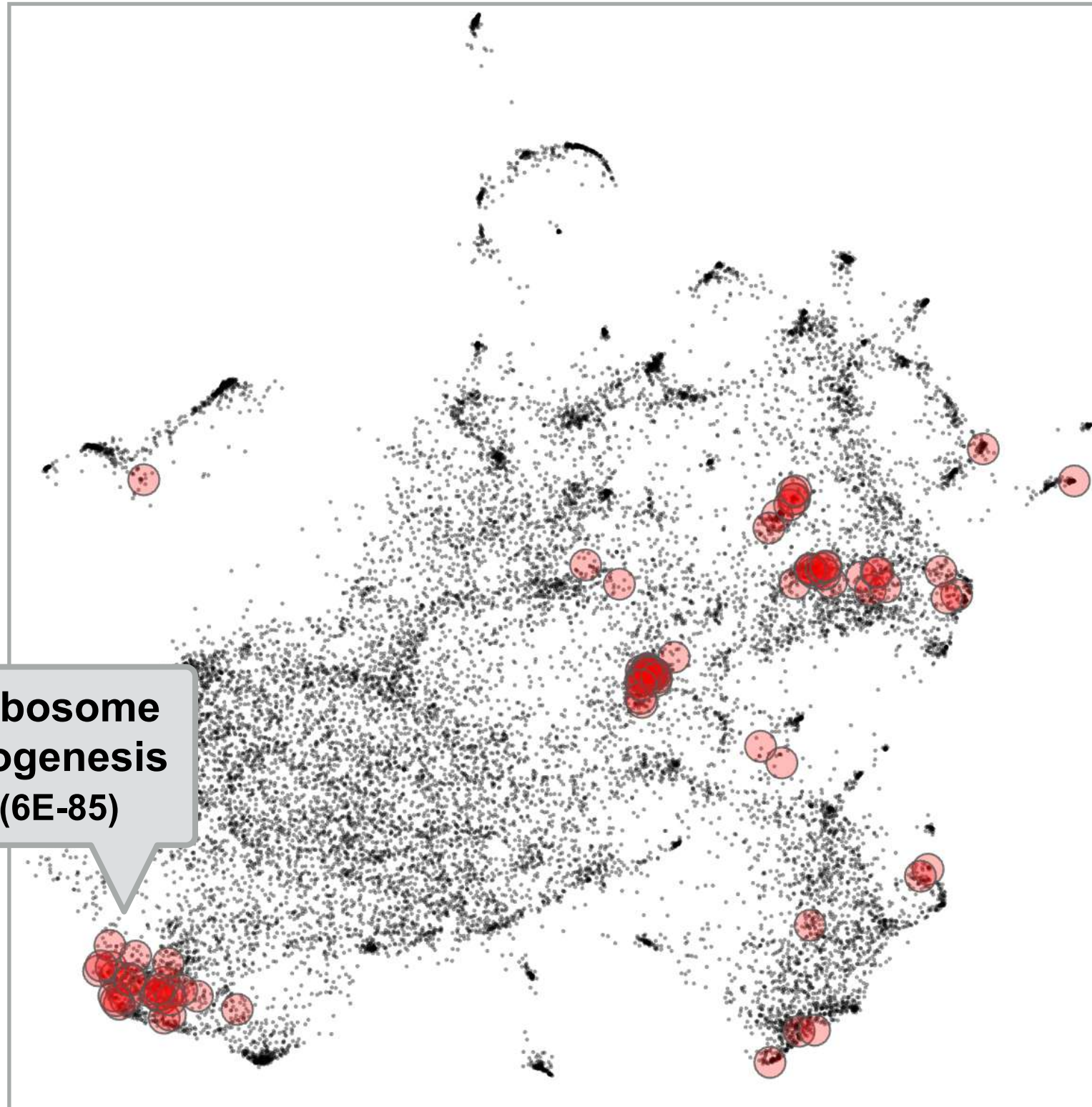
Protein processing in ER



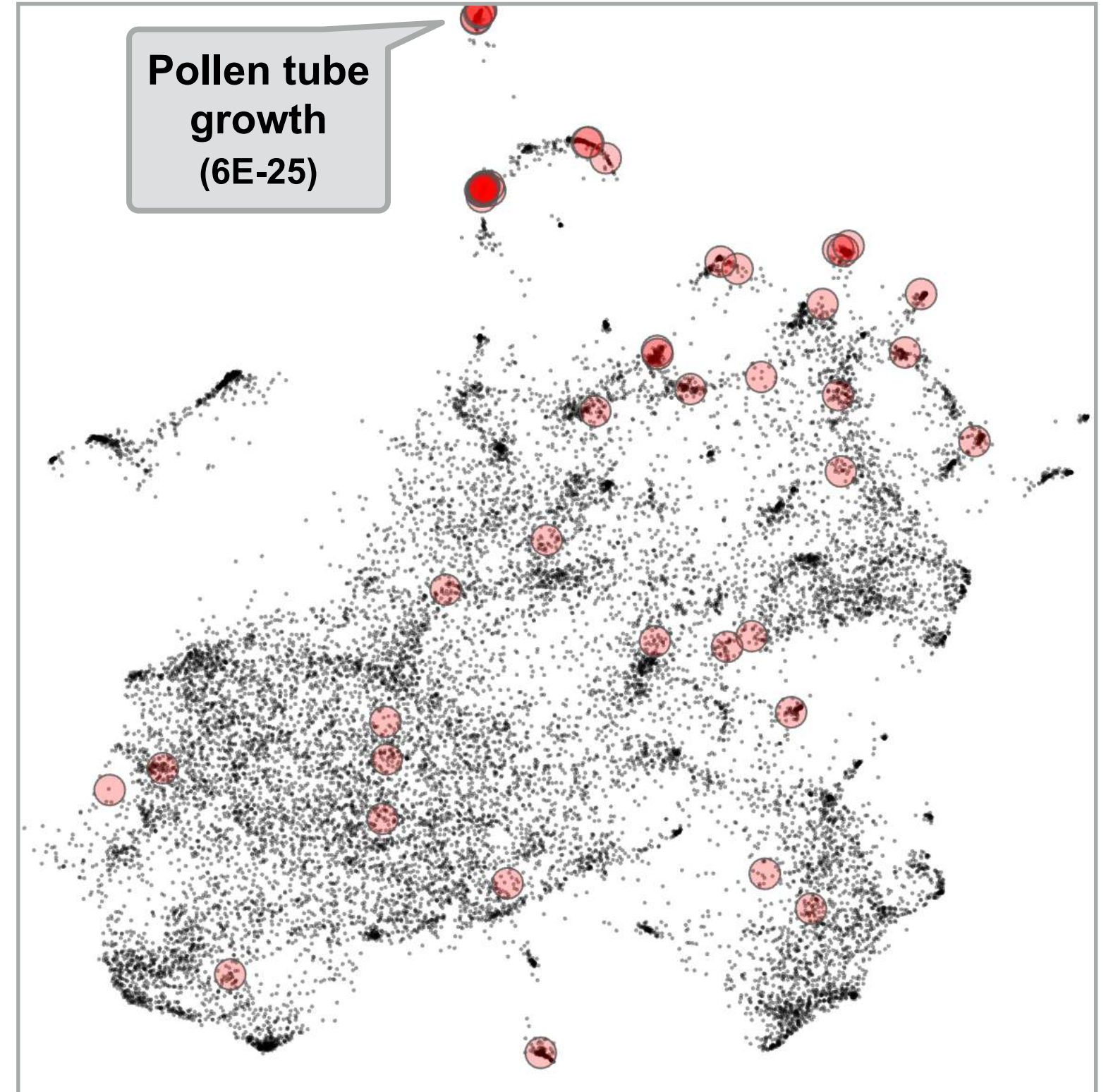


rdp1-3 変異体の発現変動遺伝子

100 Up-regulated genes



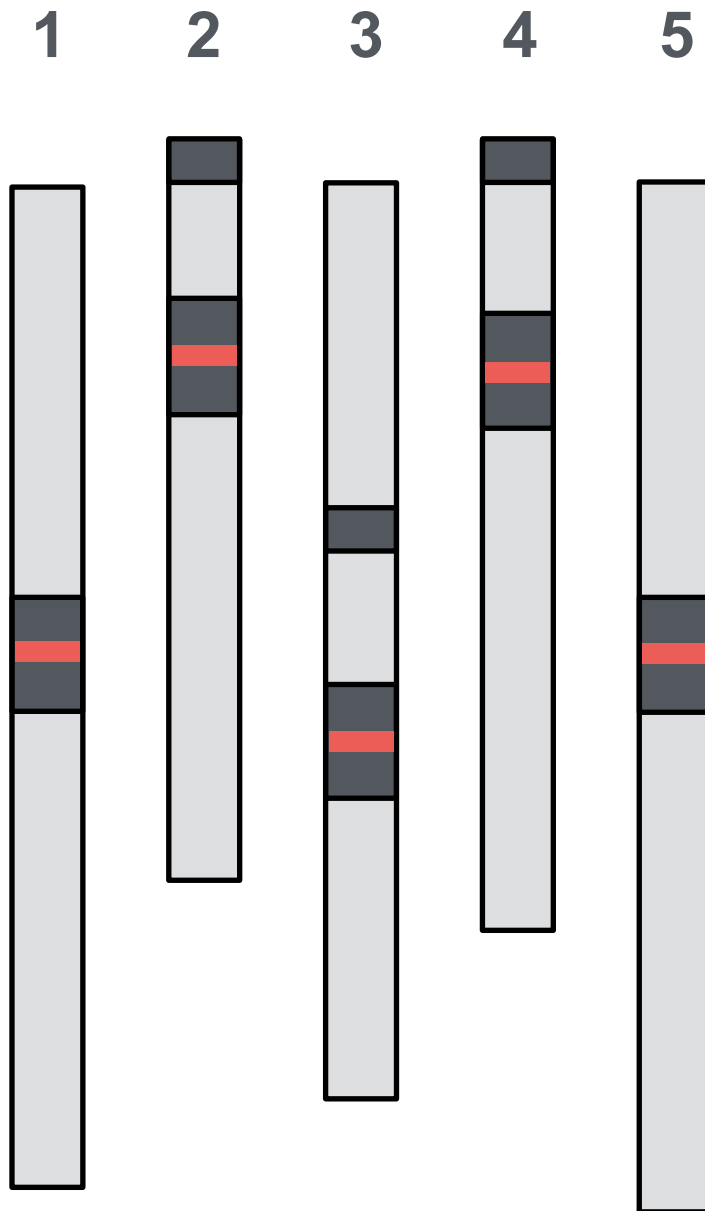
100 Down-regulated genes





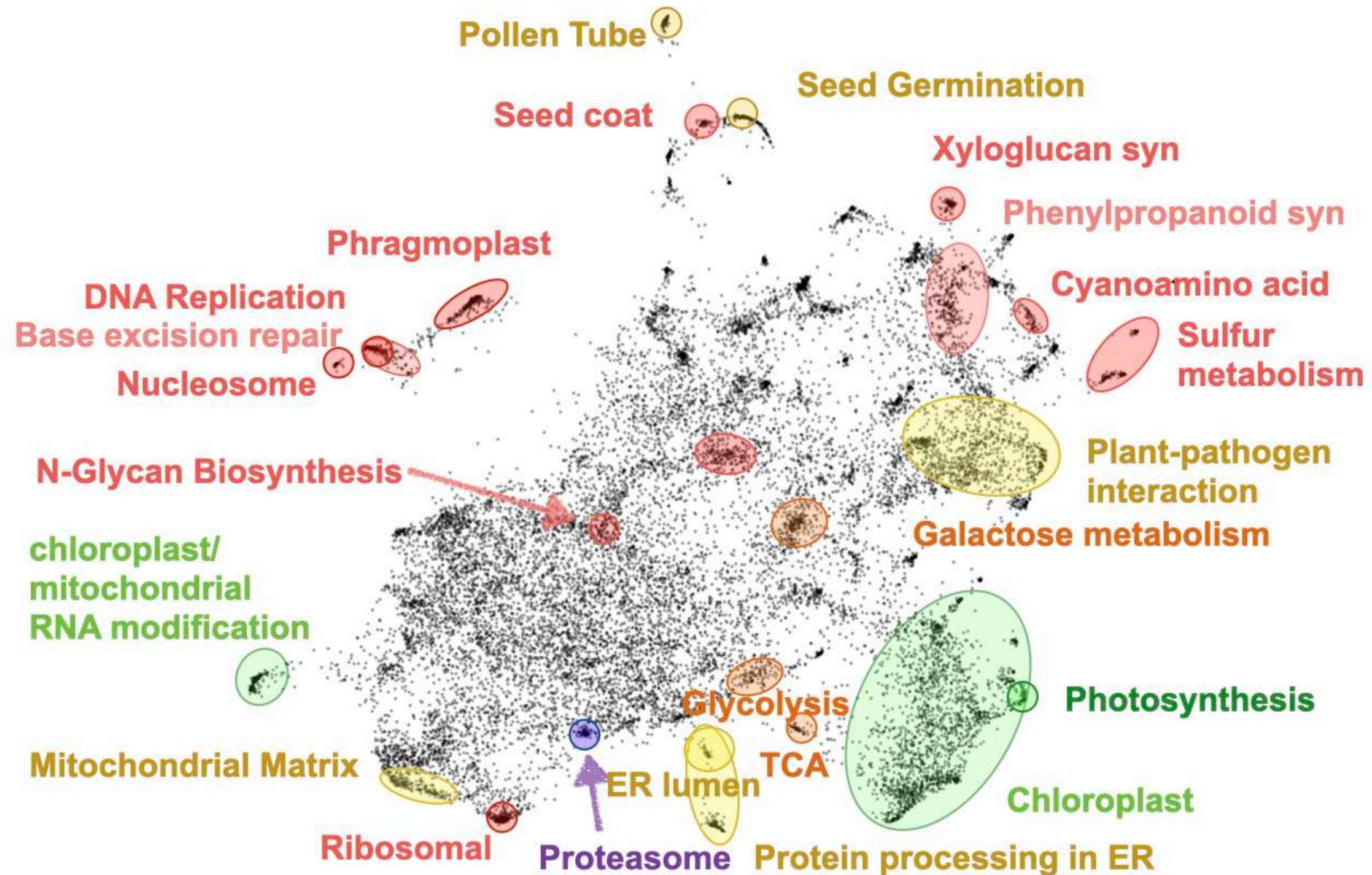
システムの可視化

遺伝子の物理マップ



Zapata+ (PNAS 2016) Chromosome-Level Assembly of *Arabidopsis Thaliana* Ler Reveals the Extent of Translocation and Inversion Polymorphisms.

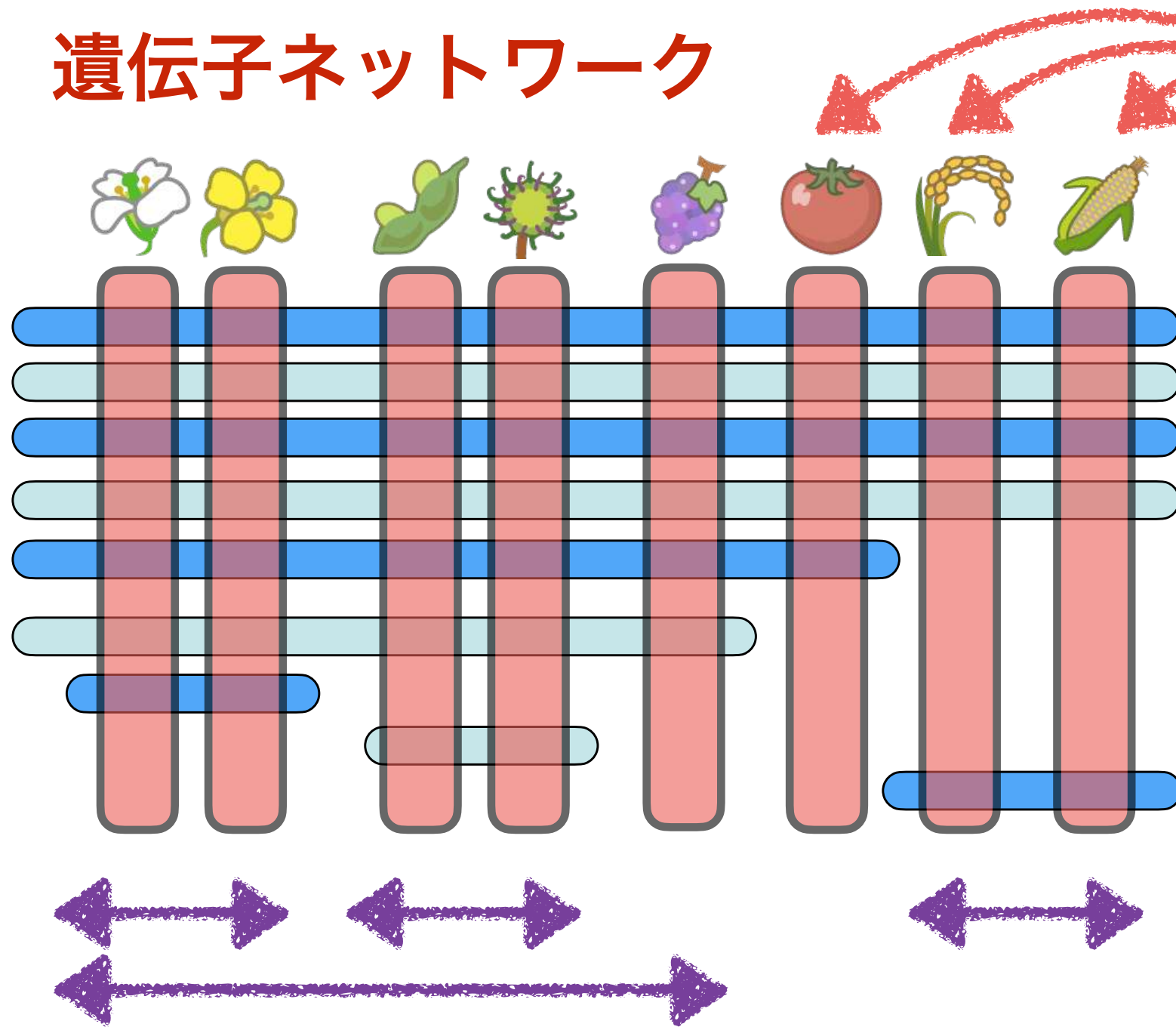
遺伝子の機能マップ (ATTED-II v11)



遺伝子ネットワーク基盤の非モデル植物への展開

遺伝子ネットワーク

配列相同性



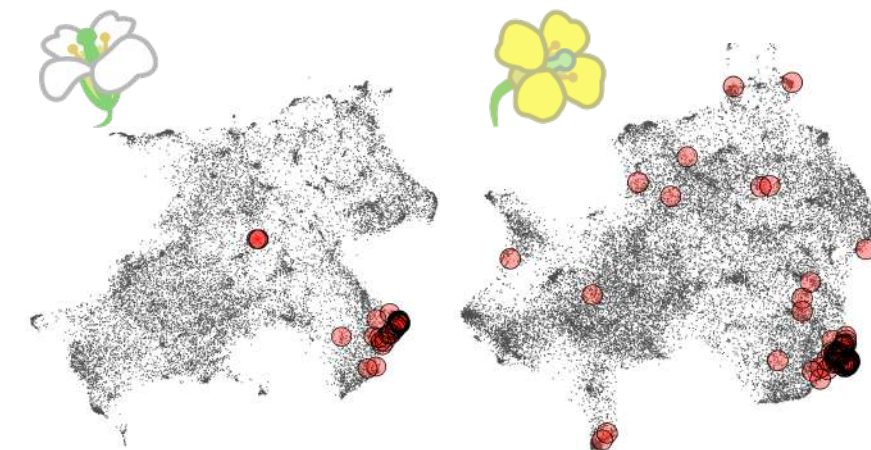
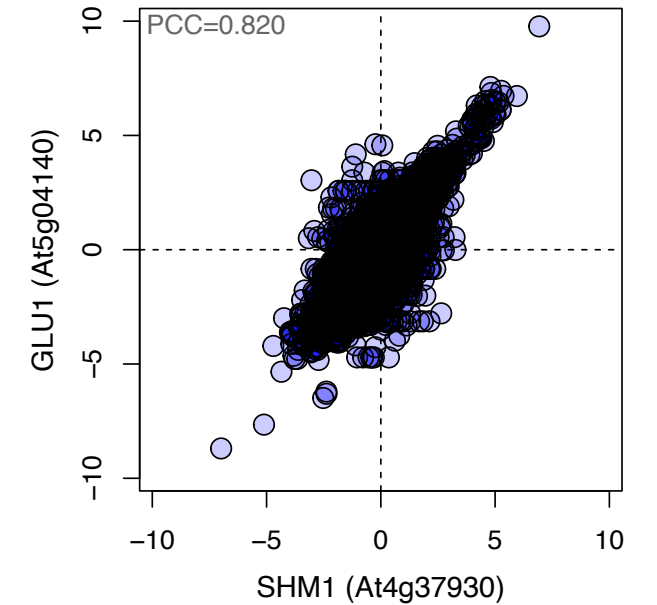
テーマ 1

共発現情報の深化

- 対象生物種の拡大
- サンプルの偏り
- データ連携

テーマ 2

種間比較と統合



植物ゲノムポータル Plant GARDEN、知識データベース KEGG Pathwayの機能を補完し、植物科学の自由な発展を推進する。