

RAP-DB : イネゲノムアノテーションデータベースと
TENOR : 12種類の非生物学的ストレスおよび植物ホルモン処理
条件下におけるイネのトランスクリプトームデータベース

川原 善浩^{1,2}、**脇本 泰暢**³、**坂井 寛章**²、**岸川 (広実) 朋子**²、
松本 隆¹、**伊藤 剛**²

¹ 農研機構 次世代作物開発研究センター

² 農研機構 高度解析センター

³ ビッツ株式会社

イネの参照ゲノムおよびアノテーション情報を提供するデータベース

rap-db
The Rice Annotation Project Database

Home News About GBrowse Tools Download Documents Publications Links

The Rice Annotation Project (RAP) was conceptualized in 2004 upon the completion of the *Oryza sativa ssp. japonica* cv. Nipponbare genome sequencing by the **International Rice Genome Sequencing Project** with the aim of providing the scientific community with an accurate and timely annotation of the rice genome sequence. One of the major objectives of this project is to facilitate a comprehensive analysis of the genome structure and function of rice on the basis of the annotation.

More

GBrowse
Browse rice genome and genes
★★★★★

BLAST
Execute NCBI BLAST against rice genome or genes
★★★★★

BLAT
Align your sequence with rice genome
★★★★★

ID Converter
Convert IDs between RAP and MSU
★★★★★

Keyword search
Keywords
Search Advanced

Batch Retrieval
★★★★★

Build5 -> IRGSP-1.0 History(Search)
★★★★

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09/Mar/2016

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More

Links
Oryza sativa
riceXPro
Q-TARO
SALAD Database
GRAMENE
More

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Previous version | Disclaimer | FAQ | Contact

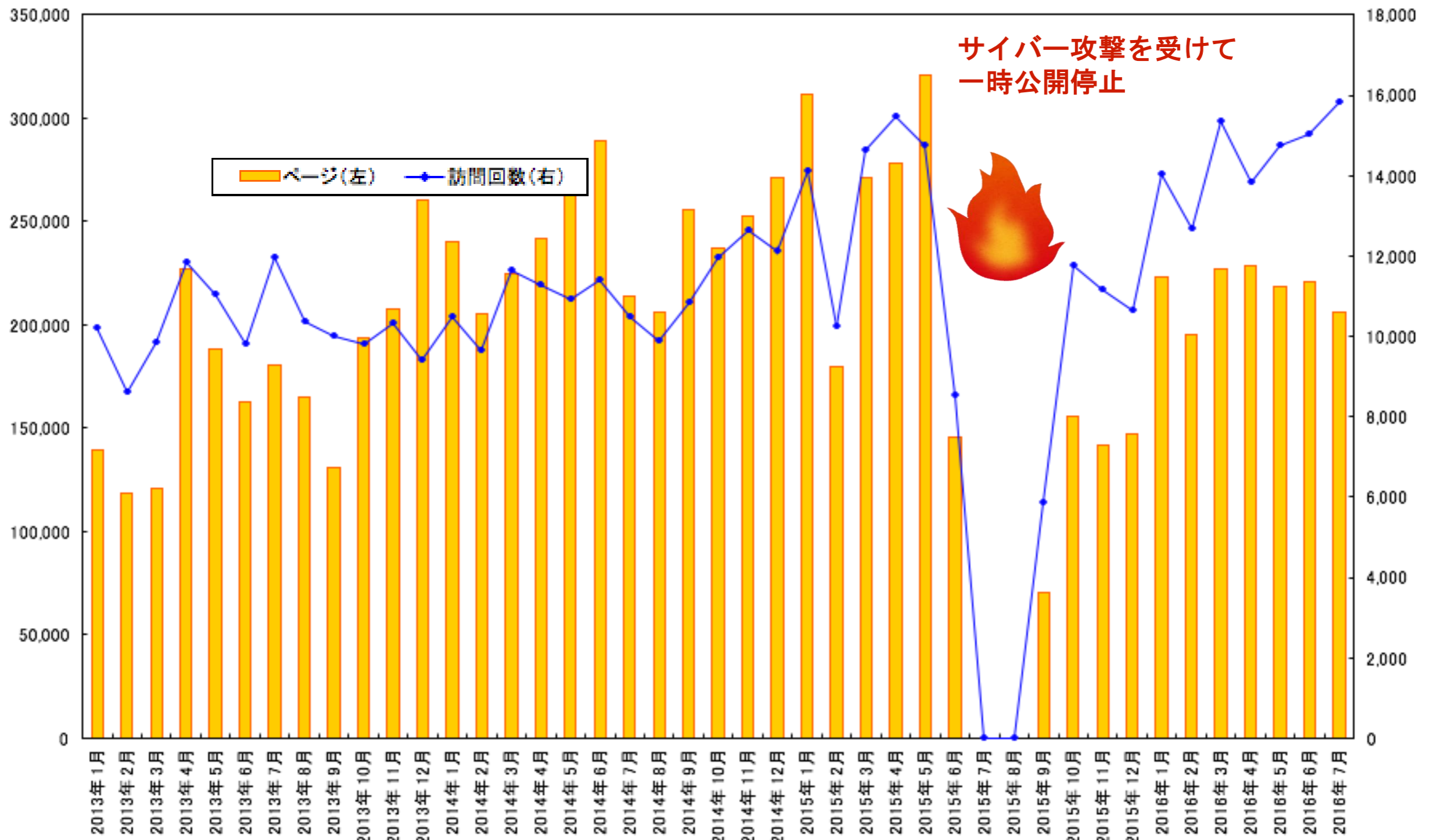
<http://rapdb.dna.affrc.go.jp/>

2006年1月に論文発表、DB公開（実は10周年）

2013年1月にメジャーアップデート、今年の8月にマイナー更新

月間 20万 ページビュー、1万5千 訪問回数

昨年の夏にサイバー攻撃を受けて一時停止。
再開後、アクセスは回復、増加しつつある



2013年、2種類存在したイネゲノムが統一された、が・・

Kawahara Y *et al.* *Rice* 2013, 6:4

RESEARCH

Open Access

Improvement of the *Oryza sativa* Nipponbare reference genome using next generation sequence and optical map data

Yoshihiro Kawahara¹, Melissa de la Bastide², John P Hamilton³, Hiroyuki Kanamori¹, W Richard McCombie², Shu Ouyang⁴, David C Schwartz⁵, Tsuyoshi Tanaka¹, Jianzhong Wu¹, Shiguo Zhou⁵, Kevin L Childs³, Rebecca M Davidson^{3,6}, Haining Lin^{3,7}, Lina Quesada-Ocampo³, Brieanne Vaillancourt³, Hiroaki Sakai¹, Sung Shin Lee¹, Jungsok Kim¹, Hisataka Numa¹, Takeshi Itoh^{1*}, C Robin Buell³ and Takashi Matsumoto¹

正式名称は、
Os-Nipponbare-Reference-
IRGSP-1.0 pseudomolecules

しかしながら、依然としてゲノムアノテーションを提供するDBは2つ

RAP-DB

MSU Rice Genome Annotation
Project Database

The Rice Annotation Project (RAP) was conceptualized in 2004 upon the completion of the *Oryza sativa* ssp. *japonica* cv. Nipponbare genome sequencing by the International Rice Genome Sequencing Project with the aim of providing the scientific community with an accurate and timely annotation of the rice genome sequence. One of the major objectives of this project is to facilitate a comprehensive analysis of the genome structure and function of rice on the basis of the annotation.

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Rice Genome Annotation Project
Funded by the NSF

Home Rice Gene Annotation Analyses/Tools Genome Browser Downloads

RGAP 7 Summary	
Gene Annotation	
Total loci	55,986
Non-TE Loci	
Number	39,045
Gene models	49,066
Gene size	2,853 bp
Exons/gene	4.9
Introns/gene	3.9
TE Loci	
Number	16,941
Gene models	17,272
Gene size	3,223 bp
Exons/gene	4.2
Introns/gene	3.2
Genome Browser	
83 tracks of annotation	
Popular Tools	
BLAST	
Locus Name Search	
Functional Term Search	
All Tools	

Introduction to the Rice Genome Annotation Project

Feb 6, 2013 - A paper describing the unified **Os-Nipponbare-Reference-IRGSP-1.0 pseudomolecules** and MSU Rice Genome Annotation Project Release 7 has been published in the journal *Rice*.

The MSU Rice Genome Annotation Project Database and Resource is a National Science Foundation project and provides sequence and annotation data for the rice genome.

This website provides genome sequence from the Nipponbare subspecies of rice and annotation of the 12 rice chromosomes. These data are available through search pages and our Genome Browser that provides an integrated display of annotation data.

Release 7 - Unified Rice Pseudomolecules

In cooperation with researchers at the **Agrogenomics Research Center at the National Institute of Agrobiological Sciences**, Tsukuba, Japan, we have prepared a final assembly of the rice pseudomolecules. These pseudomolecule sequences are now common to both the MSU Rice Genome Annotation Project and the **Rice Annotation Project Database (RAP-DB)/International Rice Genome Sequencing Project**. This effort was undertaken in order to allow researchers to easily compare annotations from both the MSU and RAP-DB projects. Gene loci, gene models and associated annotation data are available in the RAP-DB. The pseudomolecules derived by the pseudomolecules used by the rice genome annotation projects to generate those annotations are now identical and can be easily compared. A manuscript describing the generation of the final rice pseudomolecule assembly is in preparation.

RGAP Updates

- February 6, 2013**
- A paper describing the unified **Os-Nipponbare-Reference-IRGSP-1.0 pseudomolecules** and MSU Rice Genome Annotation Project Release 7 has been published.
- February 7, 2012**
-The GFF3 and brief info files were updated on the FTP site. The update corrects issues with the UTR feature type and several cases where the mRNA coordinates were incorrect. The sequence files and other features in the GFF3 files were not changed.
- October 31, 2011**
-Release 7 of the MSU Rice Genome Annotation Project is available.
-This release is based on a new pseudomolecule assembly (Os-Nipponbare-Reference-IRGSP-1.0) made in collaboration with the Agrogenomics Research Center at the National Institute of Agrobiological Sciences, Tsukuba, Japan. This set of pseudomolecules unifies the previous MSU with the IRGSP/RAP effort.
-Genome browser has been updated with 8 filtered gene models.
-In 2010, the IRGSP-1.0 assembly was updated to include 200,000 new release 50 filtered gene models.

<http://rapdb.dna.affrc.go.jp/>

<http://rice.plantbiology.msu.edu/>

2つのアノテーションデータベースの違い

RAP-DB

MSU Rice Genome Annotation Project Database

Gene Annotation	
Total loci	55,986
Non-TE Loci	
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最新バージョン

IRGSP-1.0 annotation
(release 2016-08-05)

RGAP Release 7
(release 2013-02-06)

更新頻度

年2回ぐらいのデータ更新

更新なし

登録遺伝子数

45,990 loci
 - 33,279 タンパク質コード遺伝子
 - 2,190 タンパク質非コード遺伝子
 - 10,521 予測遺伝子

55,986 loci
 - 39,045 Non-TE
 - 16,941 TE

遺伝子名の扱い

CGSNL Gene Symbol/Name

遺伝子名等の情報なし

遺伝子名、シンボルの検索や閲覧が可能になり、より使いやすく

Rice (2008) 1:72-84

Gene Nomenclature System for Rice

Susan R. McCouch •

CGSNL (Committee on Gene Symbolization, Nomenclature and Linkage, Rice Genetics Cooperative)

遺伝子名の登録、管理、公開



CGSNL 遺伝子シンボル	遺伝子シンボルシノニム	CGSNL 遺伝子名	遺伝子名シノニム	染色体番号	形質クラス	Gene Ontology	Trait Ontology	Plant Ontology
PI6	Pi6(t)* Pi6 Pi-6(t) pi6(t)	PYRICULARIA ORYZAE RESISTANCE 6	いもち病抵抗性6	12	耐性、抵抗性 - 病気抵抗性	GO:0009620 - response to fungus	TO:0000477 - panicle blast disease resistance TO:0000468 - leaf blast disease resistance TO:0000503 - leaf rolling time	PO:0009025 - vascular leaf _維管束のある葉, または維管束植物の葉
PI62	Pi62(t)*(=Pita?) Pi62(t)* Pi62 Pi62(t) Pi-62(t)	PYRICULARIA ORYZAE RESISTANCE 62	いもち病抵抗性62	12	耐性、抵抗性 - 病気抵抗性	GO:0009620 - response to fungus	TO:0000477 - panicle blast disease resistance TO:0000468 - leaf blast disease resistance TO:0000479 - acid sensitivity	PO:0009025 - vascular leaf _維管束のある葉, または維管束植物の葉
PRO1	Pro1* Pro1	PROLAMIN 1	Prolamin1 Prolamin 1 Prolamin-1	12	種子 - 生理的な特色 - 貯蔵物質	GO:0045735 - nutrient reservoir activity	TO:0000490 - protein composition related trait	PO:0009010 - seed _種子
S15	S15(S10) S10	HYBRID STERILITY 15	F1不稔性15	12	生殖器官 - 受粉、受精、稔性 - 雑種不稔	GO:0007275 - multicellular organismal development	TO:0000042 - f1-hybrid incompatibility TO:0000358 - female sterility	PO:0009046 - flower _花
SDH1	Sdh1 Skd	SHIKIMATE DEHYDROGENASE 1	シキミ酸デヒドロゲナーゼ1	12	生化学的性質	GO:0004764 - shikimate 5-dehydrogenase activity		

Os06g0275000, Os08g0174500,
Os06g0157700, Os06g0142600,
Os03g0762000, Os03g0793500,
Os07g0695100, Os07g0261200,
Os07g0261200

Hd1, Hd5, Hd3a, Hd17, Hd6,
Hd16, Hd2, Hd4, Ghd7

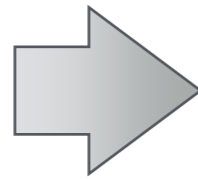
出穂期関連遺伝子



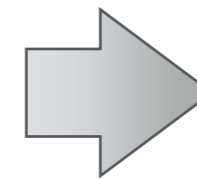
マニュアルキュレーションによるアノテーションの高度化と更新

文献精査、遺伝子の構造・機能情報等の抽出

検証、確定



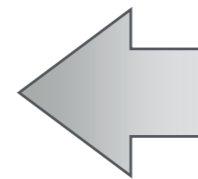
キュレータ



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Curation - transcript

User ID: torikai Dataset: IRGSP-1.0_2015-03-31

chr04: 3934628 - 3934748 Search

Transcript ID: O0440612000-01 Strand: + Version: 2

Oryzabase_ID = 3132
CGSNL_Gene_Symbol = K52
CGSNL_Gene_Name = ENT-4ALRENE SYNTHASE 2
CGSNL_Gene_Symbol_Synonym(s) = OAKS1, K52, K50.3, OAKS1.2, OAKS1.1
CGSNL_Gene_Name_Synonym(s) = rice ent-4alrene synthase2, ENT-4A
Transcript_Evidence = LC331788 (Yakuhikari) [E]
Protein_Evidence = BAB72396

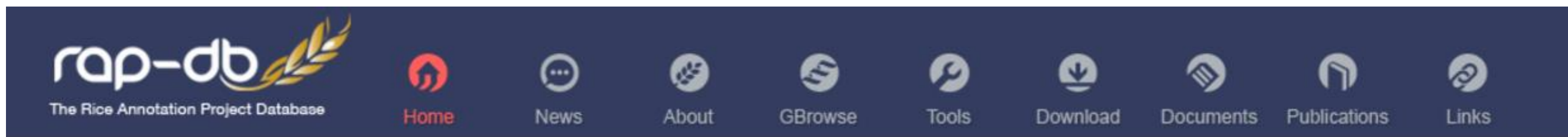
Type: 5'UTR
Start: 3934090 End: 3934271
Score: Phase

Type: CDS
Start: 3934272 End: 3934410
Score: Phase

データ更新は年2回ほど、年間約300遺伝子について




キュレーションシステムによる遺伝子構造や機能、遺伝子名の編集

RAP-DBの機能の紹介



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➔ More

GBrowse Browse rice genome and genes ★★★★★	BLAST Execute NCBI BLAST against rice genome or genes ★★★★★		BLAT Align your sequence with rice genome ★★★★★
ID Converter Convert IDs between RAP and MSU ★★★★★		Keyword search Keywords <input type="text"/> Search Advanced	
Batch Retrieval ★★★★★	Build5 -> IRGSP-1.0 History(Search) ★★★★	Build5 -> IRGSP-1.0 History(List) ★★★★	

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➔ More

様々なキーワードで遺伝子情報を検索する



- Home
- News
- About
- GBrowse
- Tools
- Download
- Documents
- Publications
- Links

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Build5 -> IRGSP-1.0 History(List)
★★★★

Advanced keyword search

Search string

Search all words (AND search):

Search exact phrase (Phrase search):

Search any words (OR search):

Exclude words (NOT search):

Search attributes

- Gene identifier (e.g. Os01g0100600, Os01t0100600-01, AK121362)
- Gene description
- CGSNL Gene Symbol
- CGSNL Gene Name
- CGSNL Gene Symbol Synonym(s)
- CGSNL Gene Name Synonym(s)
- Gene ontology (e.g. nucleic acid binding, GO:0003676)
- Functional domain (InterPro) (e.g. Single-stranded nucleic acid binding R3H, IPR001374)

Output options

Results per page:

Search

Reset

遺伝子ID、遺伝子名、遺伝子シンボル、機能情報、Gene Ontology、機能ドメインなどで検索が可能。

検索結果と遺伝子情報ページ (Details View)

Os04t0670900-00

Keyword Search Result

Sh4

Hits (Search results 1 - 4 of 4)

ID	Description	Position
Os03g0449200	Similar to Protein argonaute 7. (Os03t0449200-00)	chr03:19244015
Os03t0449200-00	Similar to Protein argonaute 7.	chr03:19244015
Os04g0670900	Homeodomain-like containing protein. (Os04t0670900-00)	chr04:34231186
Os04t0670900-00	Homeodomain-like containing protein.	chr04:34231186

Details **DB references** Sequences Gene Structure

LOCUS
Os04g0670900

DESCRIPTION
Homeodomain-like containing prot

TRANSCRIPT EVIDENCE
DQ383374 (DDBJ, Best hit)

PROTEIN EVIDENCE
Q258Z1 (UniProt)

CGSNL GENE SYMBOL
SH4

CGSNL GENE NAME
SHATTERING 4

CGSNL GENE SYMBOL SYNONYM(S)
sh4, SH4, SHAT2, SHA1, qSH4, OsSh4, Sh4, Osh4

CGSNL GENE NAME SYNONYM(S)
grain shattering quantitative trait locus on chromosome 4, SHATTERING ABORTION2, shattering abortion 2, shattering 4, Shattering1

Details **DB references** Sequences Gene Structure

INTERPRO
MYB-like (IPR017877)

KEGG
Os04t0670900-00

ORYZABASE
8737

EXPRESSION DATABASES
TENOR

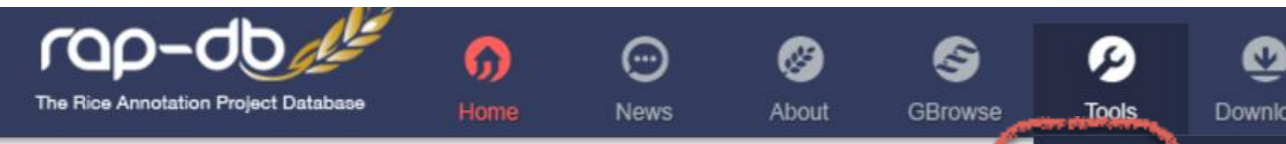
外部DB

- InterProの機能ドメイン
- KEGGの代謝マップ
- Oryzabaseの遺伝子情報
- TENORの遺伝子発現情報

などへのリンク

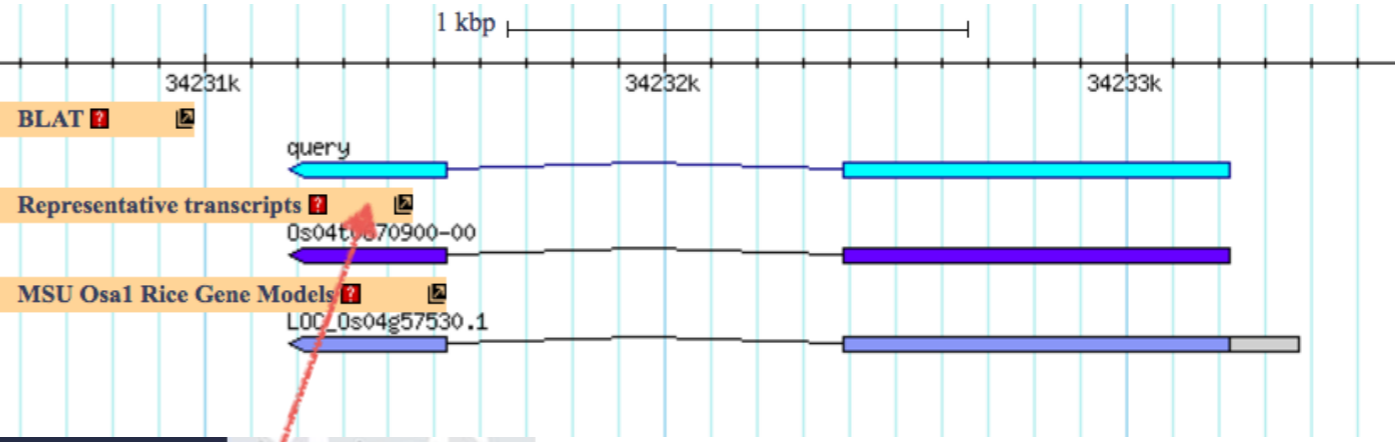
- 遺伝子ID
- 遺伝子機能情報
- 転写産物のエビデンス情報
- タンパク質のエビデンス情報
- 遺伝子名・シンボル
- 文献情報

ホモロジー検索 (BLAST/BLAT)



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- BLAST
- BLAT
- ID Converter
- Keyword Search
- Batch Retrieval
- History (Search)
- History (List)



BLAT

Query sequence

Enter query sequence in FASTA format

```

gggcggggagccg
gagcgaagcggcggcggctgagccggctggggtcgagcgtggtgaggagcgcga
cggtg
gtggcgAGGACGCTGGTGGCGTGCGAGGAGAAGCGGGAGCGCCGGC
ACCGGGAGCTGCTG
CAGCTGGAGGAGCGGCGGCTGCGCCTCGAGGAGGAGCGCACCGA
GGTCCGCCCGCCAGGGC
TTCGCCGGCCTCATCGCCGCCGTCAACAGCCTCTCCTCCGCCATCC
ACGCCCTCGTCTCC
GACCACCGCAGCGGCGACTCCTCCGGCCGATGA
    
```

Upload FASTA file 選択されていません

Target sequence

Rice genome sequence (Os-Nipponbare-Reference-IRGSP-1)

BLAT result

Query: Os04t0670900-00 (1173 letters)
Hit #1: chr04

Alignment	Query			Hit		Identity (%)
	Start	End	Strand	Start	End	
	1	338	-	34231186	34231523	100

```

Query: 1      tcatcgccggaggagtcgcccgtcggtggtcgagacgagggcgtggatggcggagga 60
              |||
Hit : 34231186 tcatcgccggaggagtcgcccgtcggtggtcgagacgagggcgtggatggcggagga 34231245

Query: 61     gaggctgttagcggcgatgagccggcgaagccctggcggcgacacctcggtcgctc 120
              |||
Hit : 34231246 gaggctgttagcggcgatgagccggcgaagccctggcggcgacacctcggtcgctc 34231305

Query: 121    ctctcaggcgcagccgctctccagctcagcagctcccgggtccggcgctccc 180
              |||
Hit : 34231306 ctctcaggcgcagccgctctccagctcagcagctcccgggtccggcgctccc 34231365

Query: 181    cttctctcgcacccaccagctcctcgccaccaccgtcgctcctcaccagctcga 240
              |||
Hit : 34231366 cttctctcgcacccaccagctcctcgccaccaccgtcgctcctcaccagctcga 34231425

Query: 241    cccagccggtcagccgcccgttcgctccggctccccgccgacctcctcctc 300
              |||
Hit : 34231426 cccagccggtcagccgcccgttcgctccggctccccgccgacctcctcctc 34231485

Query: 301    ctccccgactccgacgacccgacatctcctcctccg 338
              |||
Hit : 34231486 ctccccgactccgacgacccgacatctcctcctccg 34231523
    
```

その他のツール

BLAST

BLAT

ID Converter

Keyword Search

Batch Retrieval

ID Converter

Input Os ID:

Convert

Reset

Convert ID From: MSU to RAP RAP to MSU

(You can submit multiple IDs. Either space or comma is acceptable as delimiter.)

RAP (Os ID)

MSU (LOC_Os ID)

[Os04g0670900](#)

[LOC_Os04g57530.1](#)

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GBrowse

BLAST

BLAT

Batch Retrieval

Data type you want to retrieve

Sequence data

Annotation data

Gene description (gene function and accession number)

Genomic location (chromosome, start, end and strand)

Gene ontology (GO) annotation

Functional domain (InterPro domain)

Gene IDs or genomic segment

List of IDs separated by commas, spaces or returns

Chromosome and coordinates*

Dump genes located on

in the range between -

Marker names*

Dump genes in the region between two markers,

and

(* The maximum length of the region is 10,000,000 bp.)

Output type

View

Save as FASTA file

Save as tab-delimited file

Save as Excel file

抽出したい情報
(例：遺伝子機能情報)

対象の遺伝子、領域
(例：遺伝子IDリスト、座標やDNAマーカーによるゲノム領域指定)

出力フォーマット (FASTA、txt、Excel)

GBrowse: 遺伝子などのゲノム上の様々な領域の位置情報

rap-DB The Rice Annotation Project

The Rice Genome Sequencing Project
Oryza sativa ssp. indica
Genome Sequencing Project
accurate and timely genome annotation
project is to facilitate the use of the genome data on the basis of the annotation

Browser | Select Tracks | Snapshots | Custom Tracks | Preferences

検索

ランドマークまたは領域:
chr01:1..50,000
例: ABC transporter, chr1, chr02:1..105000, Os03g0100300, AK060852, LOC_Os01g54390.
データソース: IRGSP-1.0

filter Genes 設定... 実行
Save Snapshot Load Snapshot

スクロール/ズーム: << < - 表示 50 kbp + > >> 反転

オーバービュー
chr01
0k 10M 20M 30M 40M

領域
0k 10k 20k 30k 40k 50k 60k 70k 80k 90k 100k 110k 120k 130k 140k 150k 160k 170k 180k 190k 200k

詳細ビュー
10 kbp
20k 30k 40k 50k

遺伝子構造 (RAP-DB)
Representative transcripts
Os01t0100100-01 Os01t0100400-01 Os01t0100600-01 Os01t0100800-01 Os01t0100900-01
Os01t0100200-01 Os01t0100650-00
Os01t0100300-00 Os01t0100700-01
Os01t0100466-00

遺伝子構造 (MSU)
LOC_Os01g01010.1 LOC_Os01g01030.1 LOC_Os01g01050.1 LOC_Os01g01070.1 LOC_Os01g01090.1
LOC_Os01g01010.2 LOC_Os01g01019.1 LOC_Os01g01050.2 LOC_Os01g01070.2 LOC_Os01g01090.1
LOC_Os01g01040.4 LOC_Os01g01060.1 LOC_Os01g01080.1
LOC_Os01g01040.1 LOC_Os01g01070.3
LOC_Os01g01040.2 LOC_Os01g01080.2
LOC_Os01g01040.3 LOC_Os01g01080.3

リピート配列

GBrowse
Browse rice genome
and genes
★★★★★

ID Converter
Convert IDs between
RAP and MSU
★★★★★

Batch Retrieval
★★★★★

遺伝子発現データベースとの相互リンク

Os10t0392600-01



Details

DB references

Sequences

Gene Structure

遺伝子情報ページ (Details View)

LOCUS

Os10g0392600

DESCRIPTION

SPX domain-containing protein,

TRANSCRIPT EVIDENCE

AK108539

PROTEIN EVIDENCE

Q7XEY9

CGSNL GENE SYMBOL

CGSNL GENE NAME

CGSNL GENE SYMBOL SYNONYM

OsSPX3

CGSNL GENE NAME SYNONYM(S)

SPX (SYG/PHO81/XPR1) domain

Details

DB references

Sequences

Gene Structure

GO

Biological Process: cellular response to phosphate starvation (GO:001

INTERPRO

SPX domain-containing protein (IPR031142)

SPX, N-terminal (IPR004331)

KEGG

Os10t0392600-01

KOME

002-144-C12 (Online Clone Ordering)

ORYZABASE

11154

EXPRESSION DATABASES

TENOR

RiceXPro (AK108539)

TENOR

Transcriptome ENcyclopedia Of Rice

Keywords

SEARCH



Genome Browser



Responsive Gene Search



Data Download



About TENOR

What's New

November 16, 2015

A paper about TENOR was published.

TENOR: Database for Comprehensive mRNA-Seq Experiments in Rice. Kawahara Y. et al.

Plant Cell Physiol (2016) 57 (1):e7

RiceXPro

Version 3.0



HOME

RICE 44K ARRAY

QUICK GUIDE

EXP_BLAST

ExProFlip

DISCLAIMER

PUBLICATIONS

LINKS

CONTACT

The Rice Expression Profile Database (RiceXPro) is a repository of gene expression profiles derived from microarray analysis of tissues/organs encompassing the entire growth of the rice plant under natural field conditions, rice seedlings treated with various phytohormones, and specific cell types/tissues isolated by laser microdissection (LMD). This database is part of a project on rice transcriptome analysis using microarray technology aimed at characterizing the expression profile of all predicted genes in rice and providing reference information that can be used in functional genomics. All expression profiles were generated using a single microarray platform with probes based on manually curated gene models in RFP-DB and rice full-length cDNA sequence information in KOME database. This project is supported by a grant from the Ministry of Agriculture, Forestry and Fisheries of Japan.

GLOBAL PROFILE

DATA SETS

VEGETATIVE

REPRODUCTIVE

RIPENING

TENORとはどんなデータベース？

TENOR (Transcriptome ENcyclopedia Of Rice)

様々な条件下でサンプリングされたmRNA-Seq法によるイネの遺伝子発現プロファイルデータベース

TENOR
Transcriptome ENcyclopedia Of Rice

Keywords

SEARCH



Genome Browser



Responsive Gene Search



Data Download



About TENOR

URL

<http://tenor.dna.affrc.go.jp>

Publication

Kawahara Y. et al.
Plant Cell Physiol. 2016 57 (1):
doi: 10.1093/pcp/pcv179

Funding

This work was supported by a grant from the Ministry of Agriculture, Forestry and Fisheries of Japan (Genomics for Agricultural Innovation, RTR1001).

サンプリング条件

10種 of 非生物学的ストレスと2種 of 植物ホルモン処理条件、
(と、無処理のコントロール)



発芽後10日目の日本晴の幼苗の葉と根

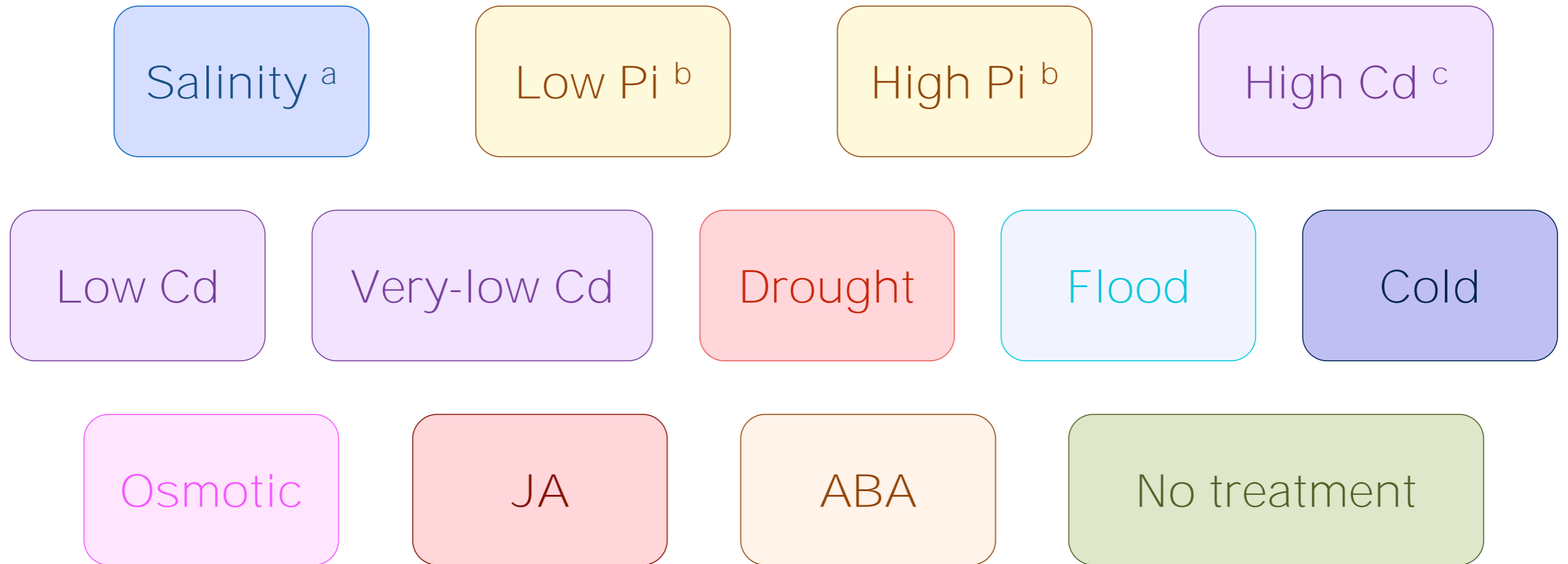


ストレスやホルモン処理後、複数のタイムポイント
(0h, 1h, 3h, 6h, 12h, 1d, 3d, 4d, 5d, 10d)



合計、140条件 (ちなみに、2,500億塩基、35億リード)

10種の非生物学的ストレスと2種の植物ホルモン処理条件

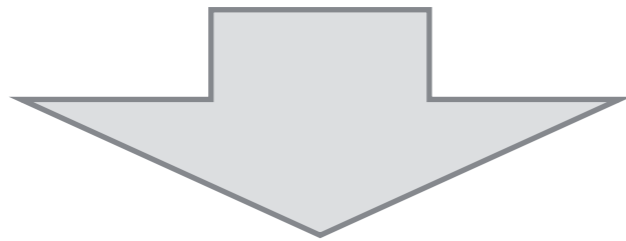


Previous studies published from our group
a. Mizuno H, Kawahara Y et al. (2010) *BMC Genomics*
b. Oono Y, Kawahara Y et al. (2011) *Rice*
c. Oono Y, Yazawa T, Kawahara Y et al. (2014) *PLoS One*

Hydroponic cultivation in growth chamber
(at 28°C temperatures, 16h-light/8h-dark cycle
with the light period from 6:00 A.M. to 10:00 P.M.,
and 70-80% relative humidity)

全てのサンプルで実験や解析手法が統一されている

All experiments were performed
at a single laboratory
under standardized conditions
using a single analysis platform (mRNA-Seq)



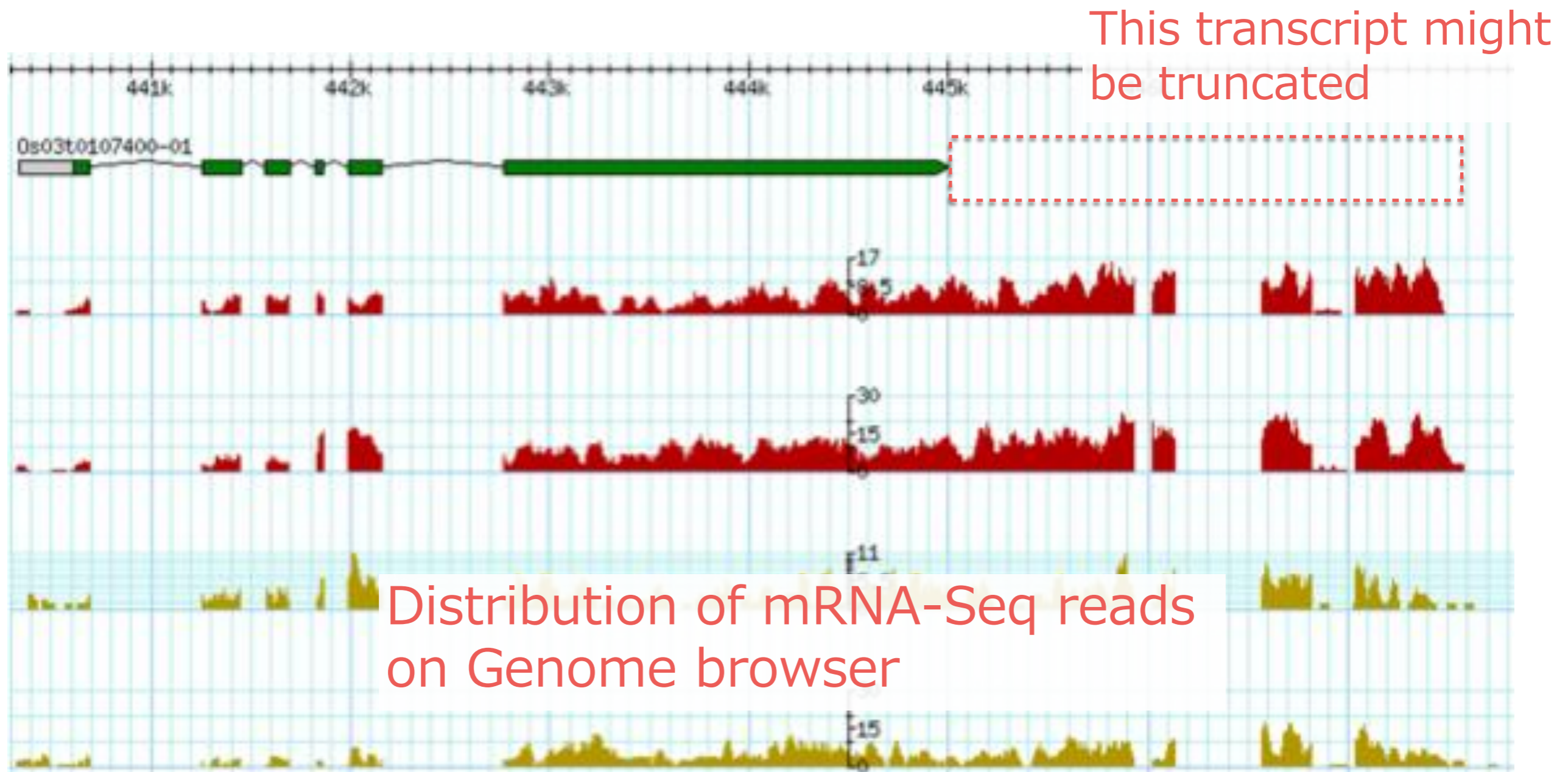
- a highly reliable resource
- a standard data set

for comprehensive understanding of genome-wide gene expression under the various conditions

1塩基レベルでの転写活性情報を提供

Use of mRNA-Seq technique provides

- transcriptional activity at single nucleotide resolution
- expression profile of unannotated transcripts



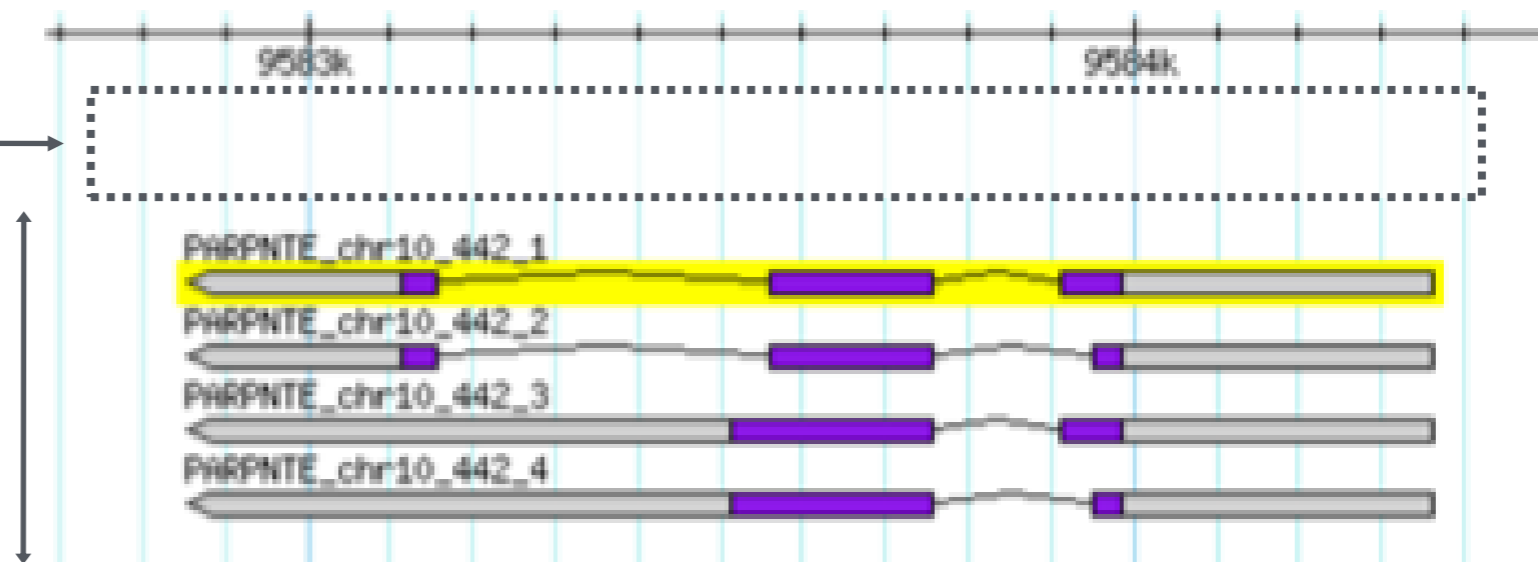
データベースに未登録の転写産物も明らかに

Use of mRNA-Seq technique provides

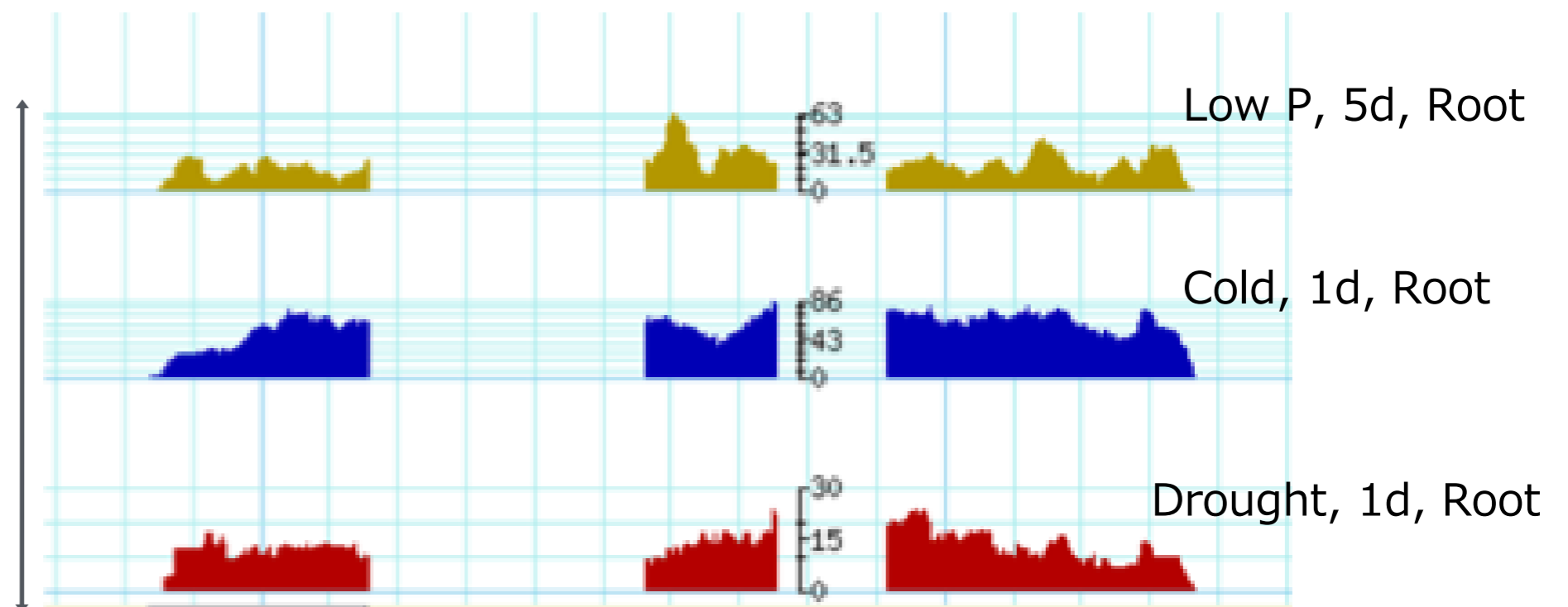
- transcriptional activity at single nucleotide resolution
- expression profile of unannotated transcripts

No RAP-DB
transcript

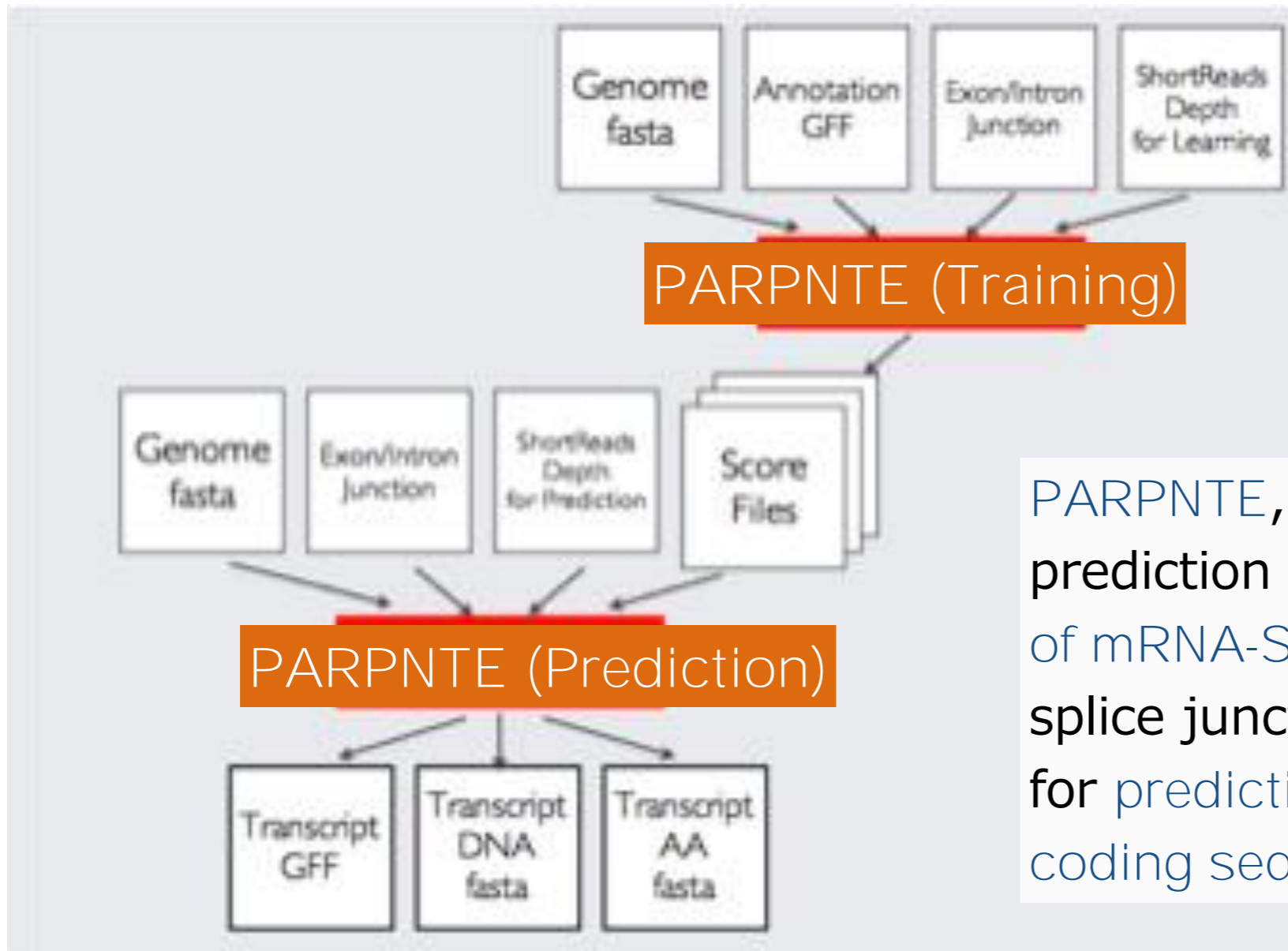
mRNA-Seq-based
predicted transcripts



Distribution of
mRNA-Seq reads



遺伝子予測プログラム PARPANTE とは



PARPANTE, which is our in-house gene prediction program, integrates alignments of mRNA-Seq reads (depth of coverage and splice junction) and a HMM-based algorithm for prediction of transcript structures and coding sequences.

Program	Transcripts	Loci	Multi-exon transcripts	Base		Exon		Intron	
				Sn	Sp	Sn	Sp	Sn	Sp
PARPANTE	48,366	38,228	30,293	51.2	64.1	52.4	58.9	70.1	80.6
Cufflinks	45,415	30,617	30,249	59.0	50.8	49.1	54.2	69.3	79.5

新規遺伝子の構造や発現量

Category	No. of loci	Mean transcript length (bp)	Mean CDS length (bp)	Mean no. of exons	Mean exp. level (RPK)
RAP-DB representative genes					
- with mRNA evidence	35,469	1,580.0	912.0	4.3	327.9
- ab initio pred. with EST	2,400	1,067.0	1,067.1	3.0	59.2
RAP-DB predicted genes					
	8,121	541.3	541.3	1.6	4.7
Unannotated genes					
- PARPNTTE protein-coding	742	2,069.1	552.8	2.3	40.1
- PARPNTTE non-coding	2,274	1,281.2	-	2.0	48.5
- Cufflinks genes	1,263	943.4	-	1.8	22.5

実際の発現情報に基づいているため、ab initio遺伝子予測によって予測された遺伝子よりも信頼度が高そう。

URL入力でもGoogle検索でも



tenor rice



すべて

画像

動画

ショッピング

ニュース

もっと見る ▾

検索ツール

約 527,000 件 (0.47 秒)

TENOR - Transcriptome ENcyclopedia Of Rice | Home

tenor.dna.affrc.go.jp/ ▾ このページを訳す

What's New. November 16, 2015. A paper about **TENOR** was published. **TENOR**: Database for Comprehensive mRNA-Seq Experiments in **Rice**. Kawahara Y. et al. Plant Cell Physiol (2016) 57 (1):e7. disclaimer | faq | contact. © 2016 National ...

TENOR: Database for Comprehensive mRNA-Seq ...

www.ncbi.nlm.nih.gov/pubmed/26578693 - このページを訳す

Y Kawahara 著 - 2016 - 引用元 2 - 関連記事

Plant Cell Physiol. 2016 Jan;57(1):e7. doi: 10.1093/pcp/pcv179. Epub 2015 Nov 16.

TENOR: Database for Comprehensive mRNA-Seq Experiments in **Rice**. Kawahara Y(1), Oono Y(1), Wakimoto H(2), Ogata J(1), Kanamori H(1), Sasaki H(1), ...

URL

<http://tenor.dna.affrc.go.jp>

遺伝子発現情報への3つのアクセス方法

TENOR

Transcriptome Encyclopedia Of Rice

by Keywords



Keywords

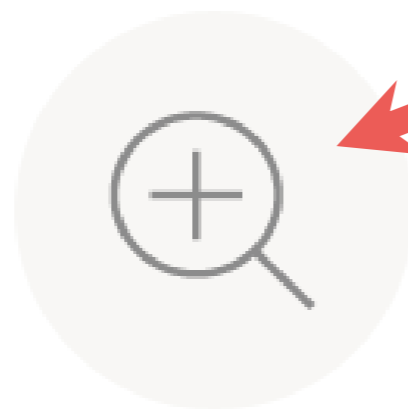
by Genomic
coordinates



Genome Browser

SEARCH

by Responsive
expression
profiles



Responsive Gene Search



Data Download



About TENOR

1. キーワード検索

SPX genes play important roles in phosphorus signaling network regulating root growth and phosphorus homeostasis

TENOR

Transcriptome ENyclopedia Of Rice

SPX domain containing protein



Enter keywords
(transcript ID/description)

SEARCH



Genome Browser



Responsive Gene Search



Data Download



About TENOR

キーワード検索の結果

Showing 1 to 7 of 7 entries

Show 10 entries

Search:

Conditions

Transcript ID	Description	High Salinity		Low Phosphate				High Phosphate				High Cadmium								
		1h		1d		5d		10d		1d		5d		10d		1h		12h		
		FC	FDR	FC	FDR	FC	FDR	FC	FDR	FC	FDR	FC	FDR	FC	FDR	FC	FDR	FC		
Os02t0202200-01 GB EPV RAPDB XPro CoExp	SPX, N-terminal domain containing protein.	-1.03	1.00	1.92	1.00	2.13	0.77	20.54	0.00	1.17	1.00	1.91	0.40	1.83	0.16	-1.90	0.00	-2.13	0.00	-1.3
Os03t0827500-02 GB EPV RAPDB XPro CoExp	SPX, N-terminal domain containing protein.	1.01	1.00	1.14	1.00	-1.13	1.00	1.16	1.00	-1.43	0.22	-1.25	0.66	1.10	0.46	-1.40	0.01	1.14	0.00	-1.1
Os06t0603600-01 GB EPV RAPDB XPro CoExp	SPX domain-containing protein, Phosphate (Pi) homeostasis	-1.12	0.31	1.11	1.00	1.83	0.20	8.62	0.00	-1.17	0.81	1.30	0.84	1.25	0.17	-1.38	0.02	-1.26	1.00	1.5
Os06t0603600-02 GB EPV RAPDB XPro CoExp	SPX domain-containing protein, Phosphate (Pi) homeostasis	-1.13	0.29	1.14	1.00	1.73	0.37	8.94	0.00	-1.23	0.80	1.28	0.91	1.28	0.14	-1.57	0.00	-1.45	0.00	1.3
Os07t0614700-01 GB EPV RAPDB XPro CoExp	SPX, N-terminal domain containing protein.	-1.32	0.07	2.77	0.69	2.92	0.46	18.44	0.00	2.13	0.72	-1.06	1.00	-1.24	1.00	-1.35	0.15	-4.59	0.00	-6.9

FC: fold-changes relative to the control samples

FDR: statistical significances of differential expressions

2. 発現プロファイルによる検索

TENOR

Transcriptome Encyclopedia Of Rice

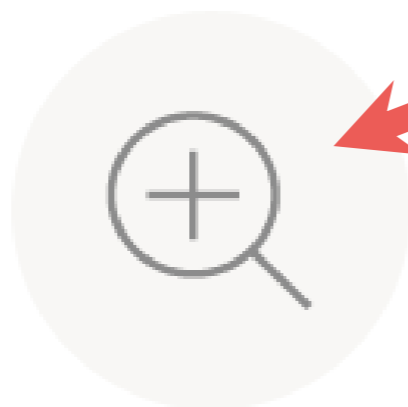
Keywords

SEARCH

by Responsive
expression
profiles



Genome Browser



Responsive Gene Search



Data Download



About TENOR

「リン酸欠乏の5日目と10日目で誘導される」遺伝子の検索

Thresholds : Fold change (FC) \geq FDR $<$

Search type :

Set search parameters

RESET

SEARCH

Tissue Stress Timepoint Response

Shoot

Root

High Salinity
 Low Phospate

1d

5d

10d

10d1drec

High Phospate
 High Cadmium
 Low Cadmium
 VeryLow Cadmium
 Dry
 Flood
 Cold
 Osmotic
 ABA
 JA
 DevTimeCont

up
 down

up
 down

Specify responsive expression patterns

リン酸欠乏によって誘導される遺伝子群

Showing 11 to 20 of 33 entries

Show entries

Search:

Transcript ID ▲	Description	Root			
		Low Phosphate			
		5d		10d	
		FC ▲	FDR ▲	FC ▲	FDR ▲
Os06t0324601-00 GB EPV RAPDB XPro CoExp	Hypothetical gene.	19.0	0.000	54.3	0.000
Os06t0324800-01 GB EPV RAPDB XPro CoExp	Major facilitator superfamily protein. (PT9)	19.4	0.000	56.7	0.000
Os06t0325200-00 GB EPV RAPDB XPro CoExp	Major facilitator superfamily protein. (PT10)	19.9	0.000	36.5	0.000
Os06t0325350-00 GB EPV RAPDB XPro CoExp	Hypothetical gene.	21.2	0.000	42.2	0.000
Os07t0614700-01 GB EPV RAPDB XPro CoExp	SPX, N-terminal domain containing protein.	29.0	0.000	127.9	0.000
Os07t0614850-00 GB EPV RAPDB XPro CoExp	Hypothetical gene.	31.5	0.000	152.1	0.000
Os08t0375400-01 GB EPV RAPDB XPro CoExp	Plant disease resistance response protein family protein.	23.7	0.002	54.4	0.002
Os08t0383800-00 GB EPV RAPDB XPro CoExp	Taurine catabolism dioxygenase TauD/TfdA domain containing protein.	25.5	0.000	53.6	0.000
Os09t0381400-01 GB EPV RAPDB XPro CoExp	Similar to Ervatamin C (EC 3.4.22.-) (ERV-C).	20.2	0.000	17.4	0.000
Os09t0381400-02 GB EPV RAPDB XPro CoExp	Similar to cysteine protease.	20.9	0.000	26.2	0.000

Showing 11 to 20 of 33 entries

First Previous 1 2 3 4 Next Last

Pi transporters

SPX genes

外部データベースや発現プロファイルビューアへのリンク

Showing 11 to 20 of 33 entries

Show 10 entries

Transcript ID					FDR	
Os06t0324601-00	GB	EPV	RAPDB	XPro	CoExp	0.000
Os06t0324800-01	GB	EPV	RAPDB	XPro	CoExp	0.000
Os06t0325200-00	GB	EPV	RAPDB	XPro	CoExp	0.000
Os06t0325350-00	GB	EPV	RAPDB	XPro	CoExp	0.000
Os07t0614700-01	GB	EPV	RAPDB	XPro	CoExp	0.000
Os07t0614850-00	GB	EPV	RAPDB	XPro	CoExp	0.000

Os07t0614700-01

GB EPV RAPDB

XPro CoExp

Hypothetical gene.	21.2	0.000	42.2	0.000
SPX, N-terminal domain containing protein.	29.0	0.000	127.9	0.000
Hypothetical gene.	31.5	0.000	152.1	0.000

GB: Genome Browser
EPV: Expression Profile Viewer
RAPDB: Rice Annotation Project DB (RAP-DB)
XPro: RiceXPro
CoExp: List of co-expressed genes



Expression Profile Viewer

Showing 10 entries

Search:

Show 10 entries

		Root		Low Phosphate	
		5d		10d	
		FC	FDR	FC	FDR
Os06t0324601-00	Major facilitator superfamily protein. (PT9)	19.0	0.000	54	
Os06t0324601-00	Hypothetical gene.	19.4	0.000	56	
Os06t0325200-00	Major facilitator superfamily protein. (PT10)	19.9	0.000	36	
Os06t0325200-00	in. (PT9)	19.0	0.000	54.3	0.000
Os06t0325200-00	Major facilitator superfamily protein. (PT10)	19.4	0.000	56.7	0.000
Os06t0325200-00	Hypothetical gene.	19.9	0.000	36.5	0.000
Os06t0325200-00	Hypothetical gene.	21.2	0.000	42.2	0.000
Os07t0614700-01	SPX, N-terminal domain containing protein.	29.0	0.000	127.9	0.000
Os07t0614700-01	Hypothetical gene.	31.5	0.000		

Transcript ID

Description

5d

FC

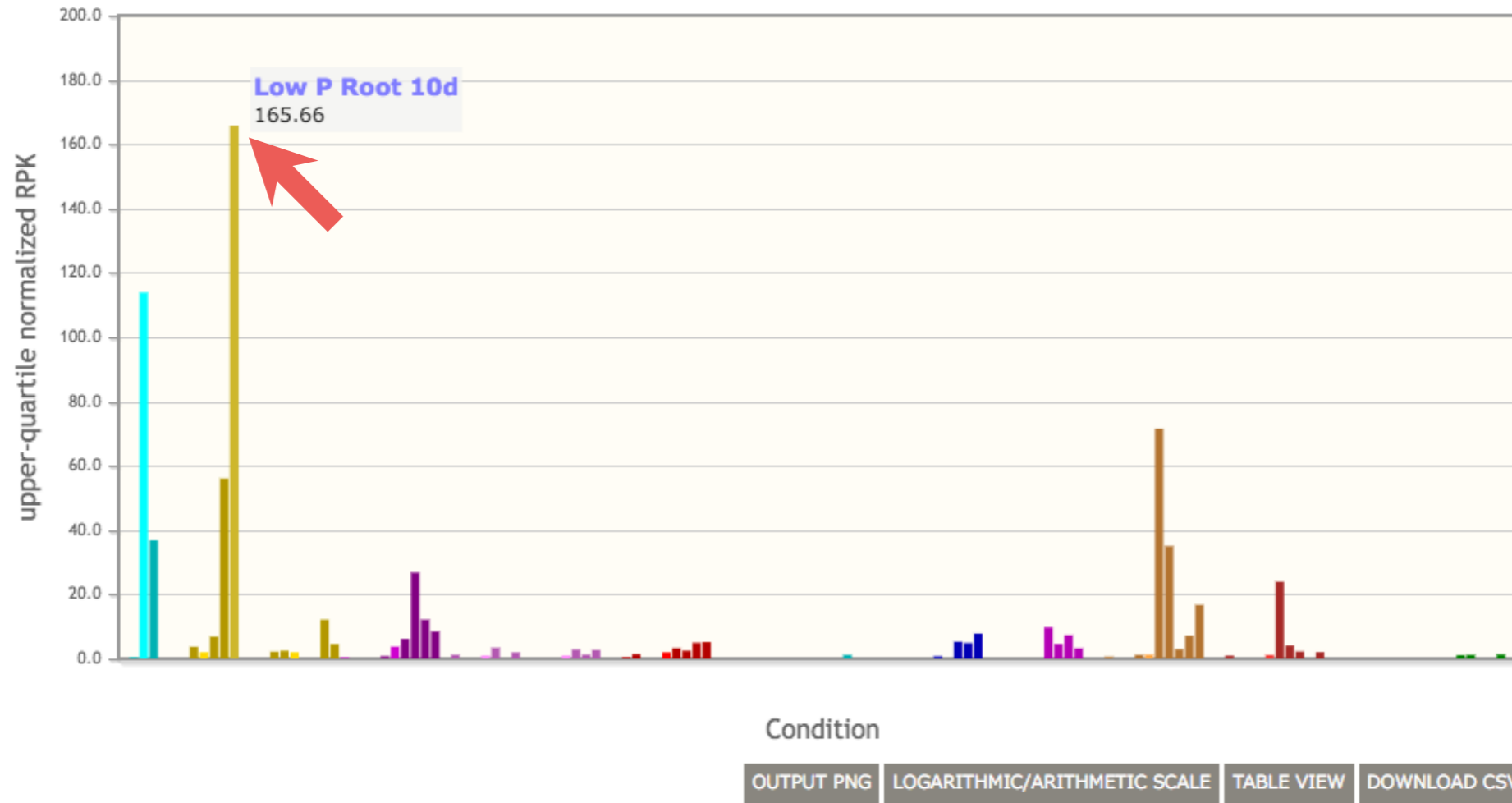
FDR

GB EPV XPro RAPDB CoExp

By hovering the mouse cursor over **EPV**,
You can quickly overview expression profiles

Os06t0324800-01

Major facilitator superfamily protein. (PT9)



Select conditions

Salinity

Shoot: Cont 1h
 Root: Cont 1h

Low Phosphate

Shoot: Cont 1d 5d 10d
 Root: Cont 1d 5d 10d 10d1drec

High Phosphate

Shoot: Cont 1d 5d 10d
 Root: Cont 1d 5d 10d 10d1drec

High Cd

Shoot: Cont 1h 12h 1d 5d
 Root: Cont 1h 12h 1d 5d

Output: PNG, Table View and CSV
 Change scale: logarithmic/arithmetric

3. ゲノム位置情報から発現情報へ

TENOR

Transcriptome Encyclopedia Of Rice

Keywords

SEARCH

by Genomic
coordinates



Genome Browser



Responsive Gene Search



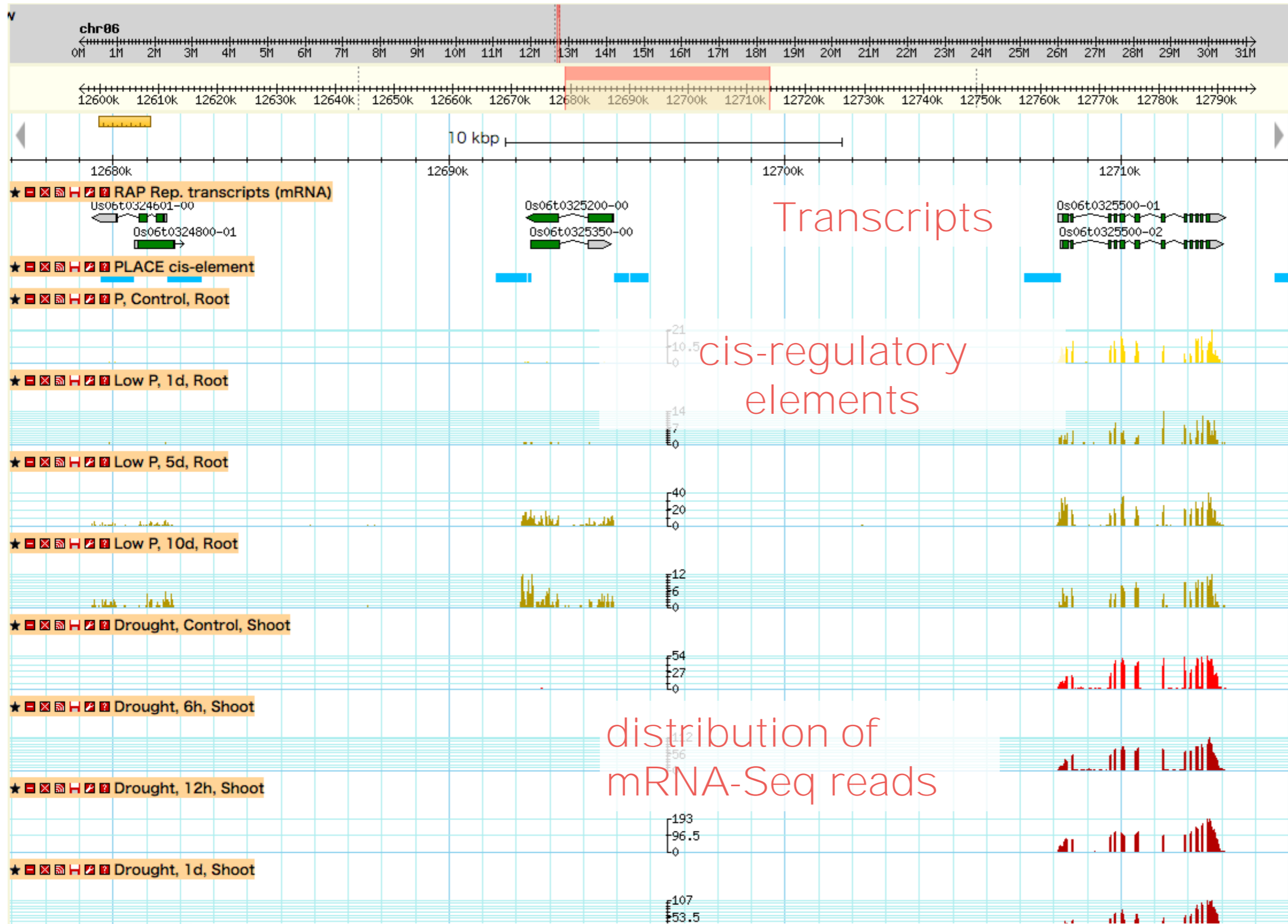
Data Download



About TENOR



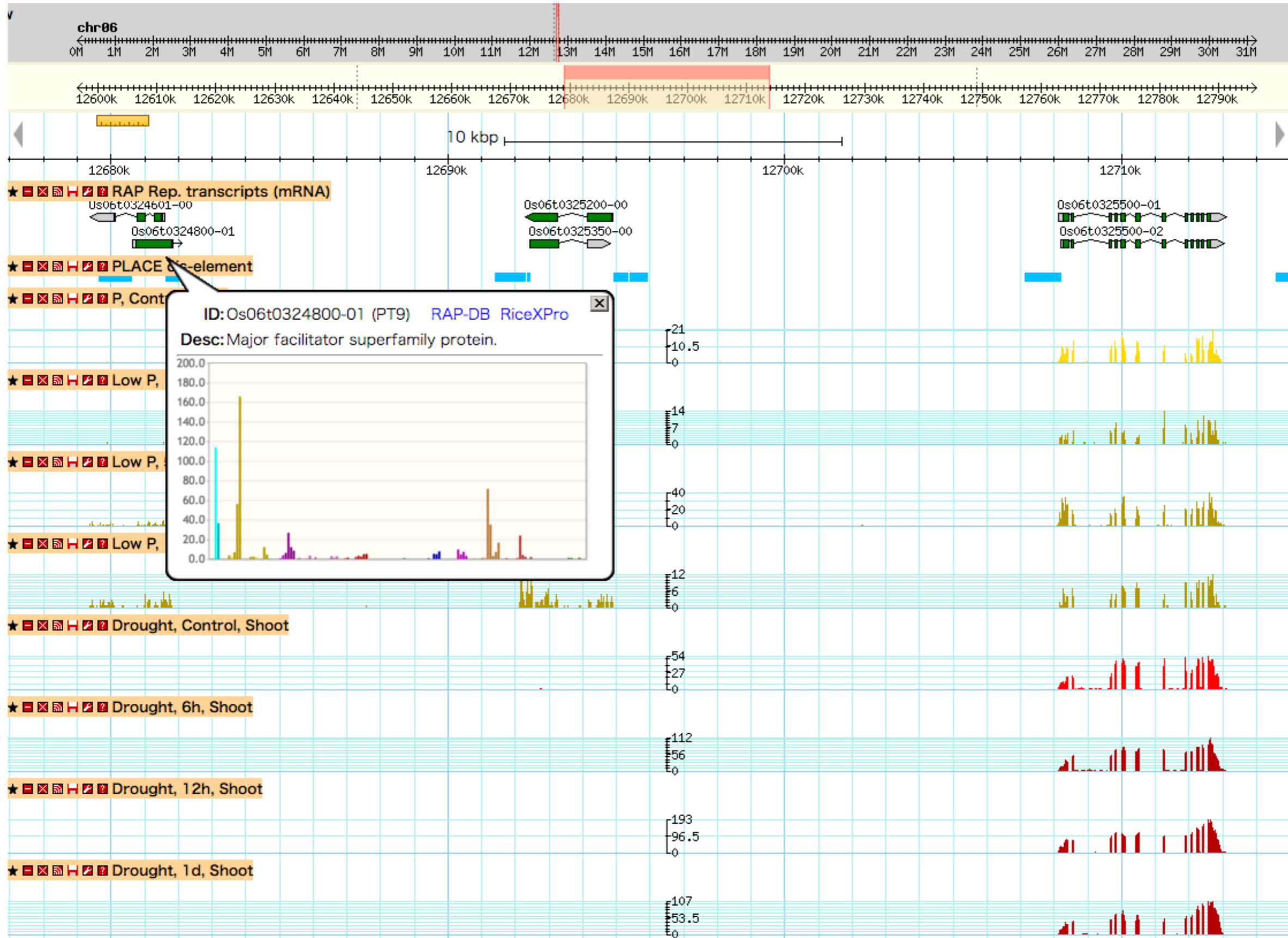
Genome Browser (GBrowse)



Link to GBrowse: http://tenor.dna.affrc.go.jp/gb2/gbrowse/rnaseq_db/?chr06:12,679,000..12,713,999

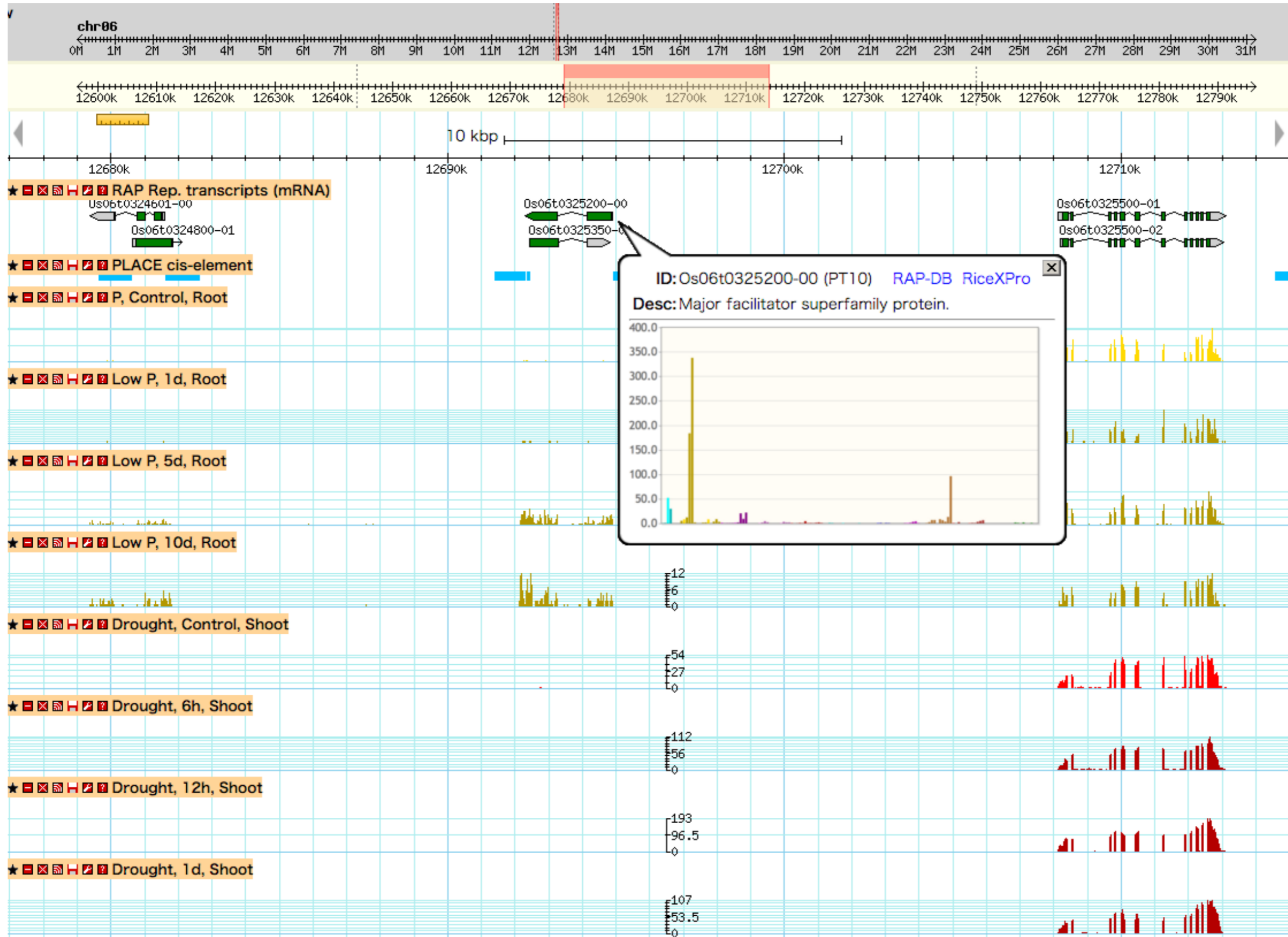


Genome Browser (GBrowse)



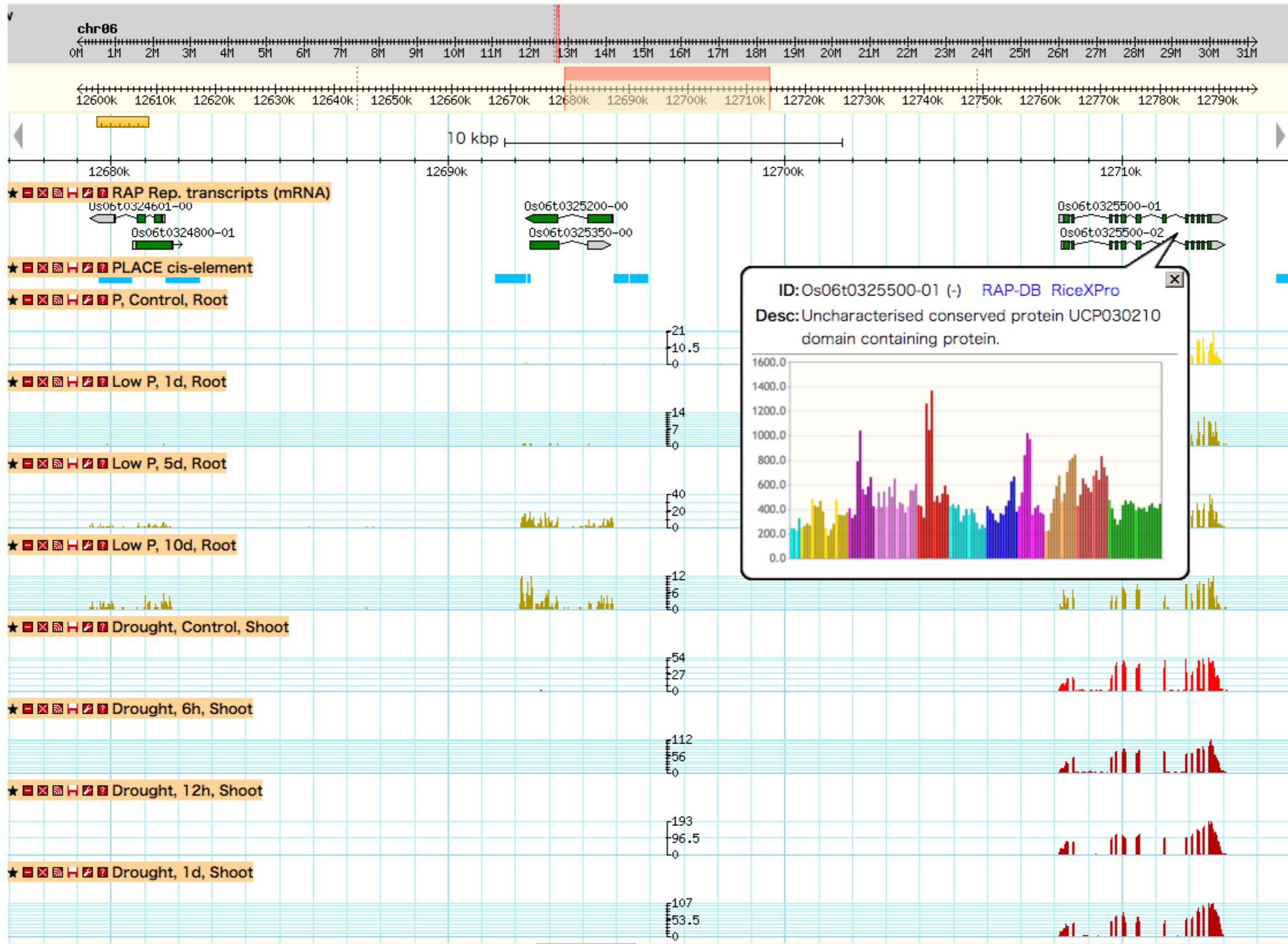


Genome Browser (GBrowse)

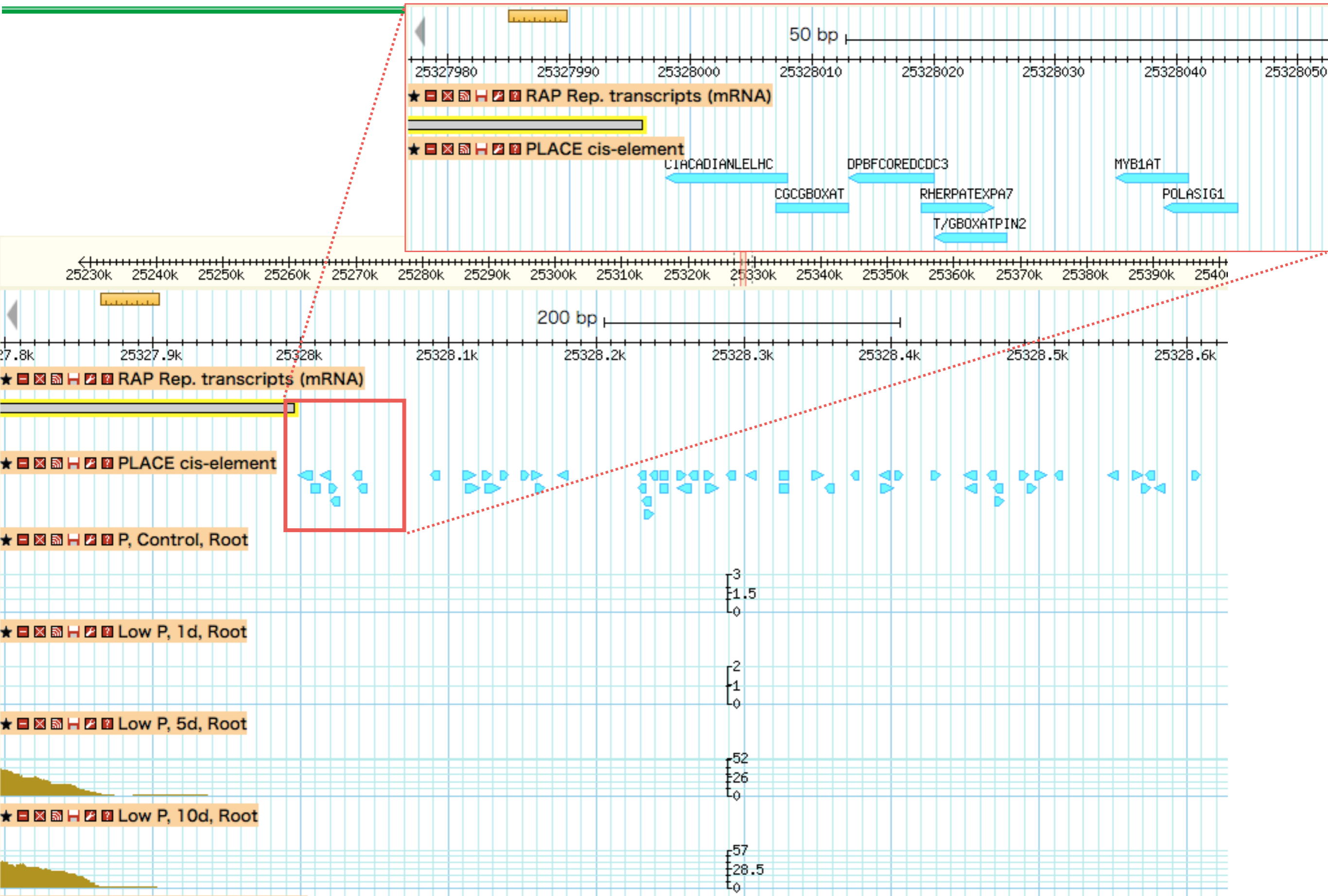




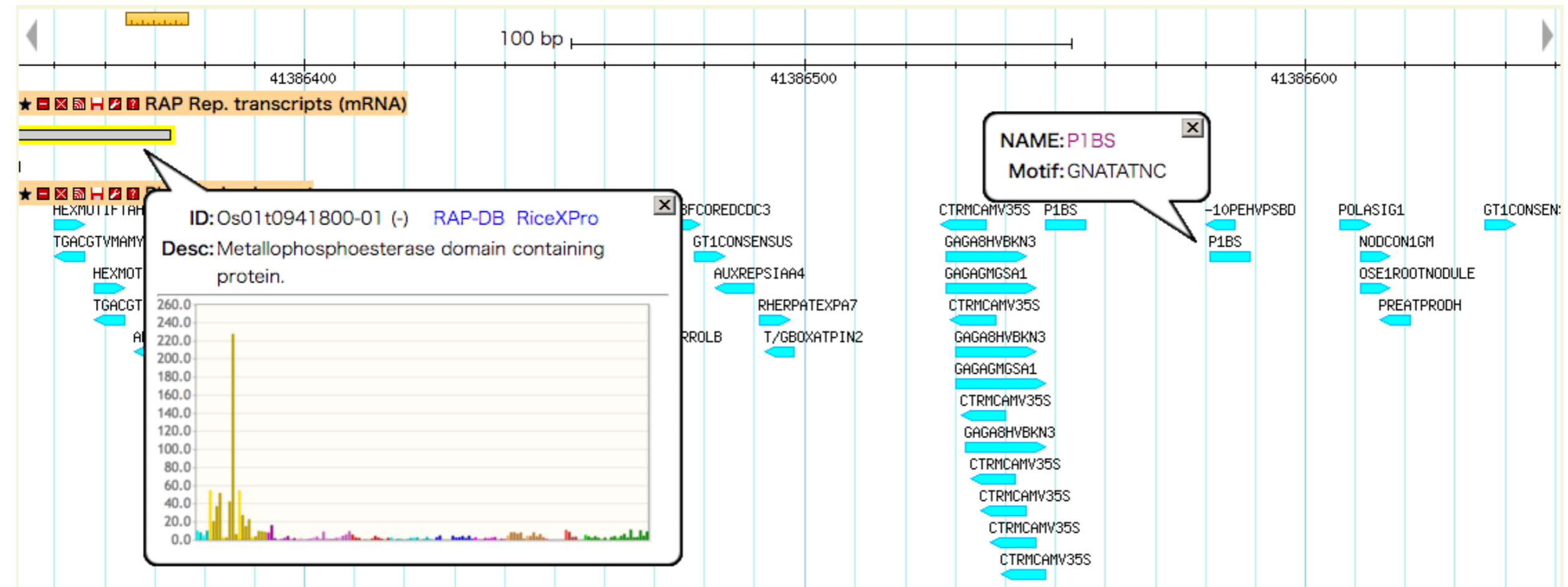
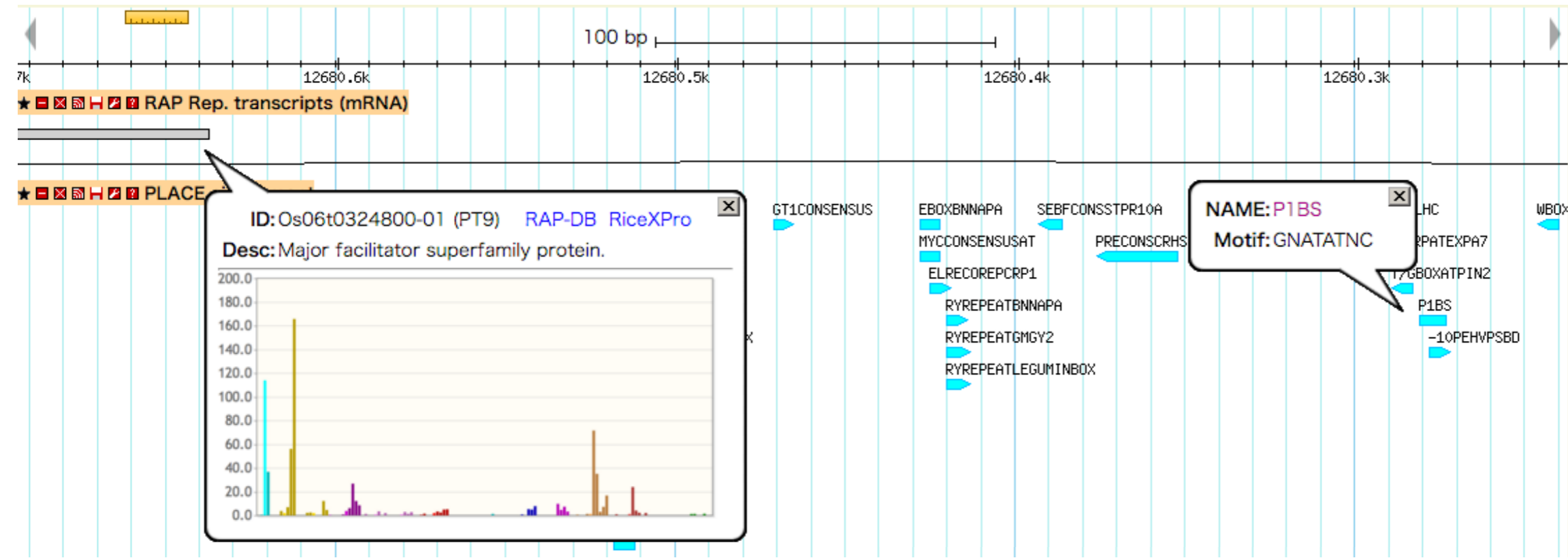
Genome Browser (GBrowse)

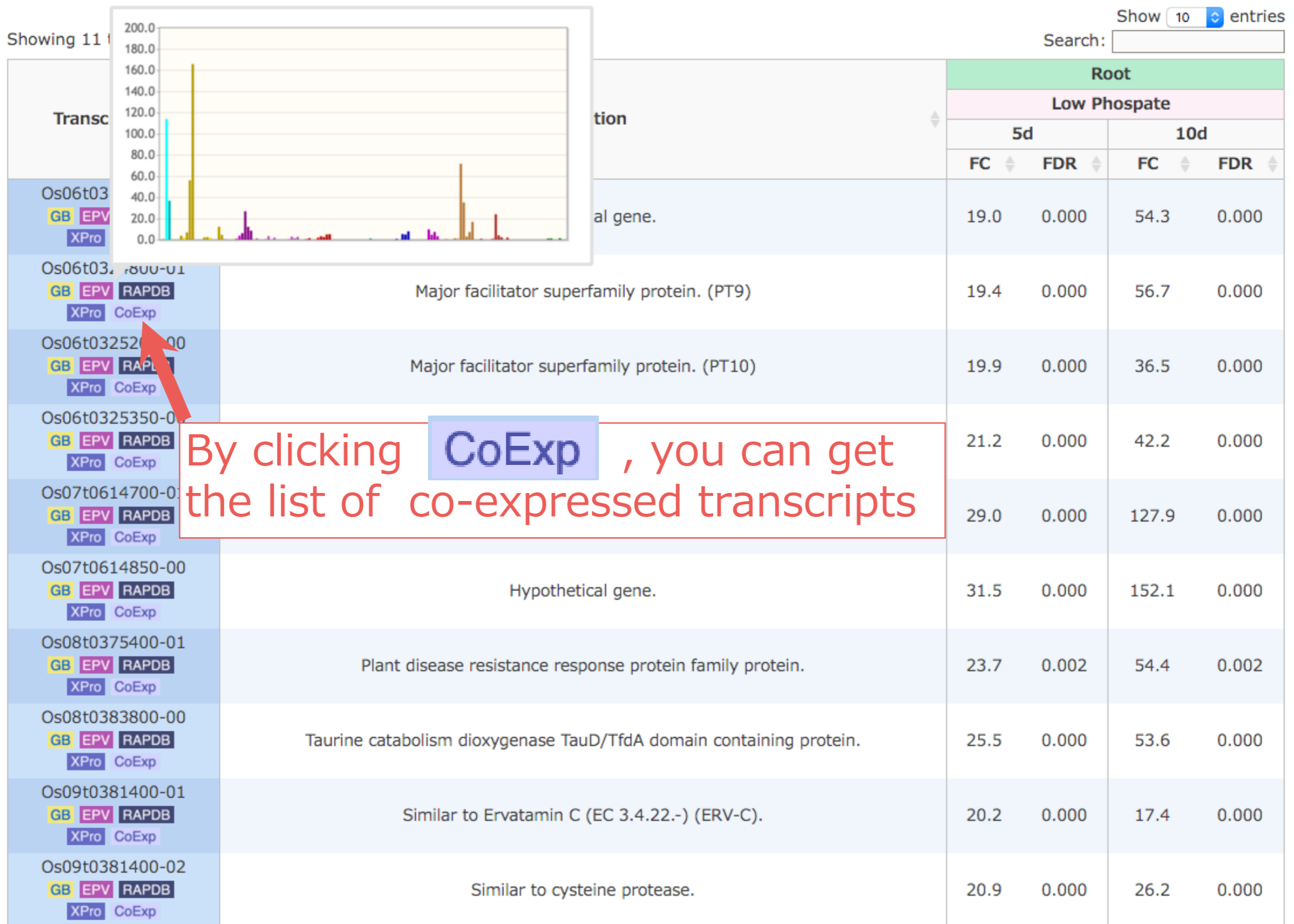


各遺伝子の上流1kbのシス転写調節配列 (PLACE)



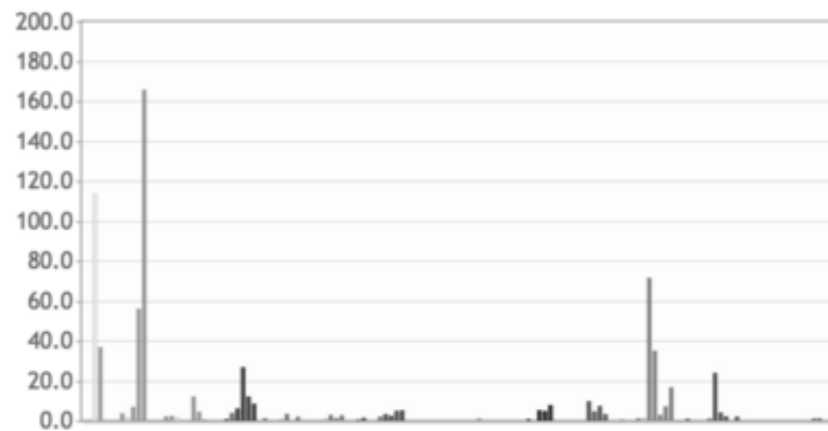
リン酸欠乏で誘導される遺伝子の上流を並べてみると





Showing 11

Transcript ID	Description
Os06t0324800-01	Major facilitator su
Os06t0324601-00	Hypothetical gene.
Os03t0408600-00	
Os03t0260000-00	
Os03t0260000-00	
Os06t0325200-00	Major facilitator su
Os06t0325350-00	Hypot
Os07t0614700-01	SPX, N-terminal do
Os07t0614850-00	Hypot
Os08t0375400-01	Plant disease resistance r
Os08t0383800-00	Taurine catabolism dioxygenase
Os09t0381400-01	Similar to Ervatamir
Os09t0381400-02	Similar to c



Top 200 co-expressed transcripts

Os06t0324800-01 (PT9)

Major facilitator superfamily protein.

GB EPV RAPDB XPro

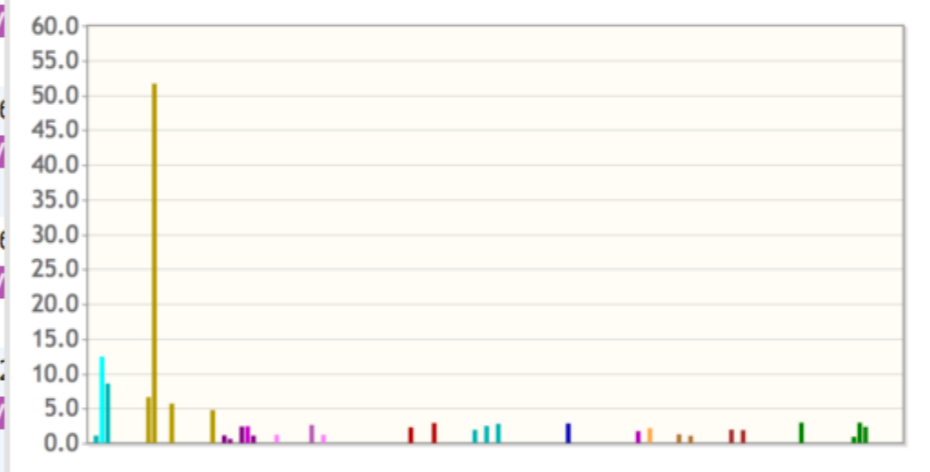
PCC GCC

Show 10 entries

Showing 1 to 10 of 200 entries

Search:

Rank	Transcript ID	Description	PCC
1	Os06t0324601-00 GB EPV RAPDB XPro CoExp	Hypothetical gene.	0.9594
2	Os03t0408600-00 GB EPV XPro		0.9011
3	Os03t0260000-00 GB EPV XPro		0.8527
4	Os03t0260000-00 GB EPV XPro		0.8451
5	Os06t0324800-01 GB EPV XPro		0.8306
6	Os04t0643401-00 GB EPV RAPDB XPro CoExp	Non-protein coding transcript.	0.8280
7	Os04t0545700-00 GB EPV RAPDB XPro CoExp	Transferase family protein.	0.8237
8	Os09t0409100-01 GB EPV RAPDB XPro CoExp	Conserved hypothetical protein.	0.8234
9	PARPNT_ chr04_1623_2 GB EPV RAPDB XPro CoExp	ID: gi 125583105 gb EAZ24036.1 ,DESC: hyp othetical protein OsJ_07767 [Oryza sativa Japo nica Group],ID: 0.467,COV: 0.513,TYPE: best hit	0.8192
10	Os04t0643500-00 GB EPV RAPDB XPro CoExp	Similar to H0306F03.8 protein.	0.8170



Showing 1 to 10 of 200 entries

Previous Next

PCC: Pearson's correlation of coefficient

RAP-DBやRiceXProへのリンク

Os07t0614700-01



Details

DB references

Sequences

Gene Structure

LOCUS

Os07g0614700

DESCRIPTION

SPX, N-terminal domain containing protein.

TRANSCRIPT EVIDENCE

AK243609 (DDBJ, Best hit)

PROTEIN EVIDENCE

Q8H398 (UniProt)

CGSNL GENE SYMBOL

CGSNL GENE NAME

CGSNL GENE SYMBOL SYNONYM(S)

OsSPX6

CGSNL GENE NAME SYNONYM(S)

SPX (SYG/PHO81/XPR1) domain gene 6

Os07t0614700-01

GB EPV RAPDB

XPro CoExp

RiceXPro HOME GLOBAL PROFILE DATA SETS EXP_BLAST ExProFlip

Data Category: Field / Development

Field / Development

Locus ID	FeatureNum	Accession	Description
Os07g0614700	3579	CI561699	SPX, N-terminal domain containing protein.

Select All [Download selected graph](#) [Clear graph](#)

- Leaf_sunrise
- Leaf_daytime
- Root_daytime
- Leaf_diurnal
- Leaf_sunset
- Leaf_nighttime
- Root_nighttime

raw intensity

normalized intensity

様々なデータをまとめてダウンロード可能

TENOR [GBrowse](#) [Responsive Gene Search](#) [Data Downloads](#) [About](#)



[Home](#) > [Data Downloads](#)

Data Downloads

TENOR Data

RNA-Seq transcripts

- Unannotated PARPNTTE protein-coding transcripts that do not overlap with any RAP-DB transcripts.
[\[GFF\]](#) [\[exonwise GTF\]](#) [\[FASTA \(transcript\)\]](#) [\[FASTA \(CDS\)\]](#) [\[FASTA \(protein\)\]](#)
- Unannotated PARPNTTE non protein-coding transcripts that do not overlap with any RAP-DB transcripts.
[\[GFF\]](#) [\[exonwise GTF\]](#) [\[FASTA \(transcript\)\]](#)
- Unannotated Cufflinks transcripts with strand information that do not overlap with any RAP-DB and PARPNTTE transcripts.
[\[GFF\]](#) [\[exonwise GTF\]](#) [\[FASTA \(transcript\)\]](#)

mRNA-Seq-based predicted transcripts
(GFF/GTF/FASTA)

Other annotation

- cis-regulatory elements in the 1-kb promoter regions of all transcripts predicted by the PLACE database.
[\[GFF\]](#)

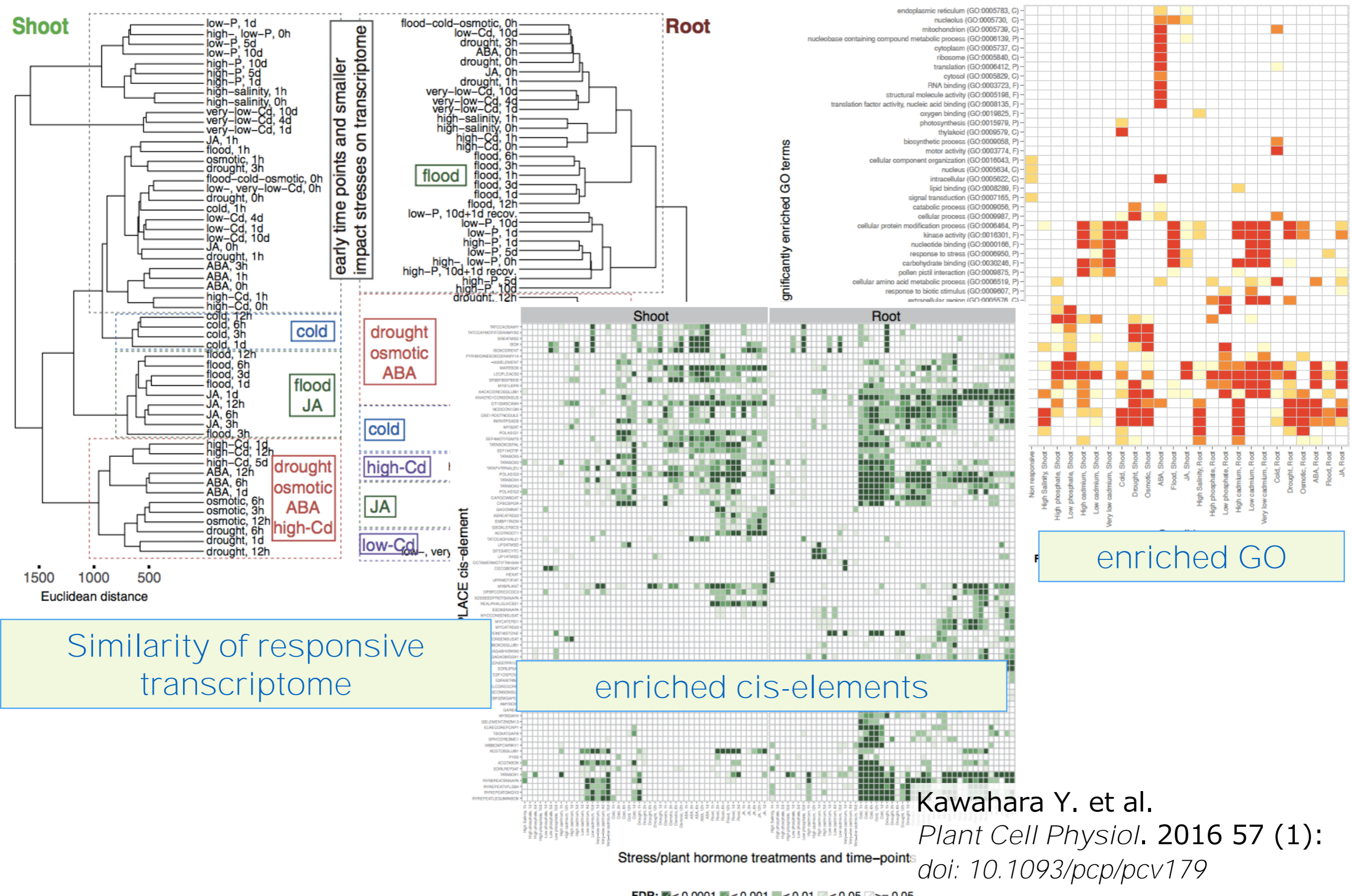
cis-regulatory elements (GFF)

Expression profile data

- Gene expression levels (RPK) for each transcript
[\[normalized RPK\]](#)

normalized expression profiles (tab-delimited txt)

TENOR論文



Similarity of responsive transcriptome

enriched cis-elements

enriched GO

Kawahara Y. et al.
Plant Cell Physiol. 2016 57 (1):
 doi: 10.1093/pcp/pcv179

TENORの概要

TENOR

Transcriptome ENcyclopedia Of Rice

Keywords

SEARCH

Search by Keywords/responsive expression profiles

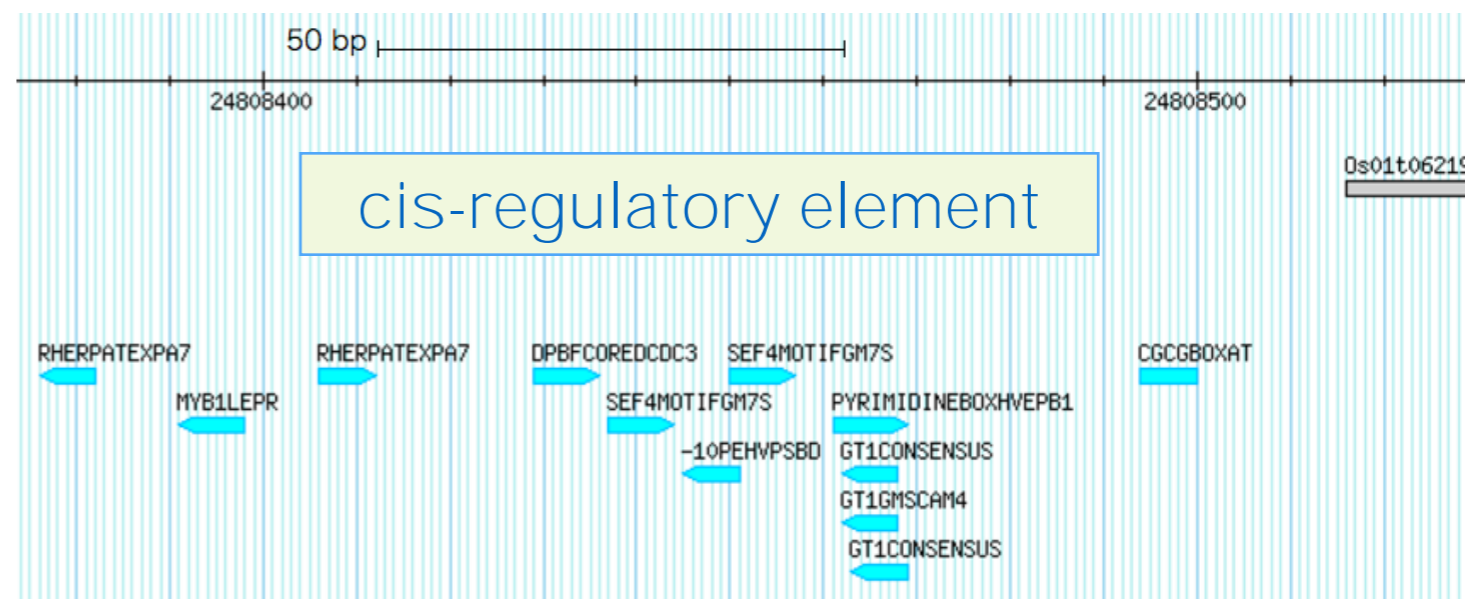
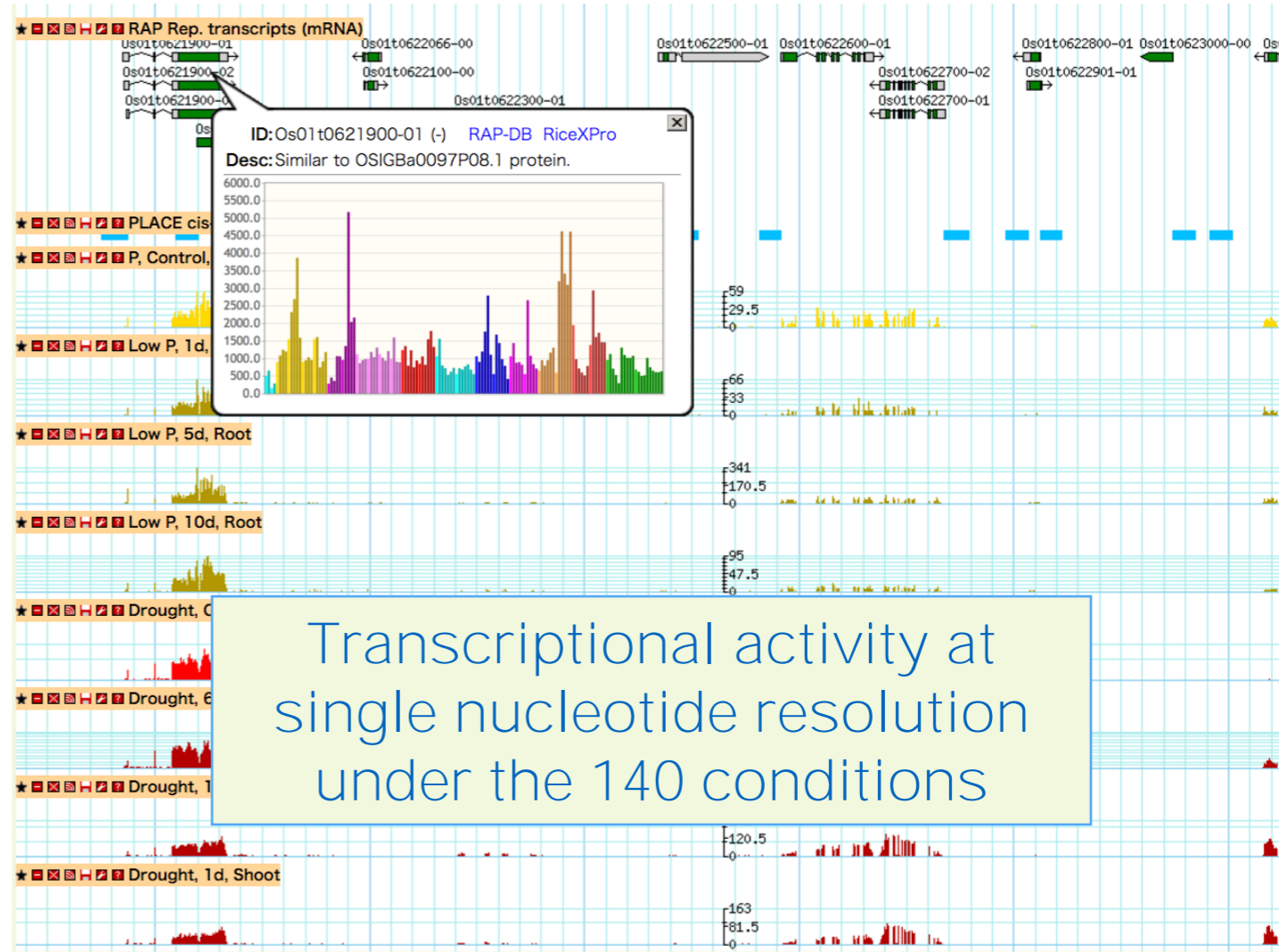
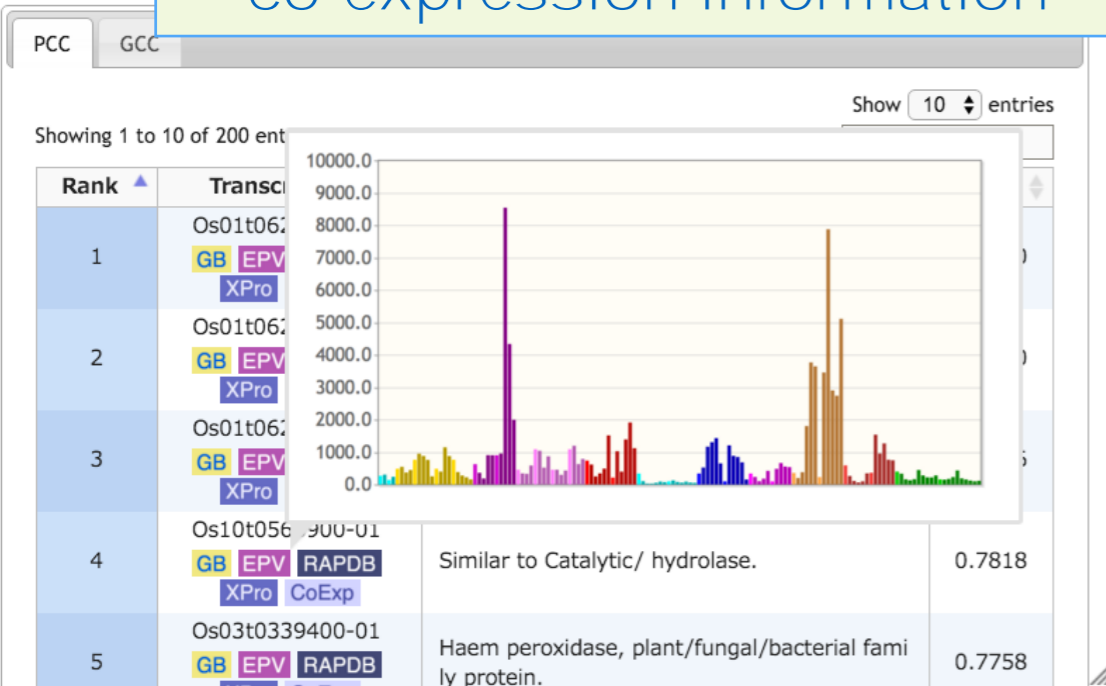
Genome Browser

Responsive Gene Search

Data Download

About TENOR

Expression profiles & co-expression information



ご質問やご意見等ありましたらご連絡下さい。

The screenshot shows the RAP-DB website homepage. At the top is a navigation bar with icons for Home, News, About, GBrowse, Tools, Download, Documents, Publications, and Links. Below the navigation bar is a main heading: "The Rice Annotation Project (RAP) was conceptualized in 2004 upon the completion of the *Oryza sativa* ssp. *japonica* cv. Nipponbare genome sequencing by the International Rice Genome Sequencing Project with the aim of providing the scientific community with an accurate and timely annotation of the rice genome sequence. One of the major objectives of this project is to facilitate a comprehensive analysis of the genome structure and function of rice on the basis of the annotation." Below this is a "More" link. The main content area is a grid of tool tiles: GBrowse (Browse rice genome and genes, 5 stars), BLAST (Execute NCBI BLAST against rice genome or genes, 5 stars), BLAT (Align your sequence with rice genome, 5 stars), ID Converter (Convert IDs between RAP and MSU, 5 stars), Keyword search (with a search input field and Search/Advanced buttons), Batch Retrieval (5 stars), Build5 -> IRGSP-1.0 History(Search) (3 stars), and Build5 -> IRGSP-1.0 History(List) (3 stars). To the right is a "What's New" section with a "NEWS" icon, listing updates from 05/Aug/2016, 09/Mar/2016, and 21/Dec/2015, each with a "More" link.

rapdb@ml.affrc.go.jp

The screenshot shows the TENOR website homepage. At the top is the logo "TENOR Transcriptome ENcyclopedia Of Rice". Below the logo is a search bar with the placeholder text "Keywords" and a "SEARCH" button. Below the search bar are four circular icons representing different features: Genome Browser (DNA double helix), Responsive Gene Search (magnifying glass with plus sign), Data Download (download arrow), and About TENOR (musical note with 'R'). Below these icons is a "What's New" section with a heading "What's New" and a date "November 16, 2015". The text in this section reads: "A paper about TENOR was published. TENOR: Database for Comprehensive mRNA-Seq Experiments in Rice. Kawahara Y. et al. Plant Cell Physiol (2016) 57 (1):e7".

tenor@ml.affrc.go.jp

遺伝子アノテーションや構造の誤り、アノテーション情報がついていない遺伝子についての論文を出した（出ている）なども是非お願いします！