The 57th Annual Meeting of the Japanese Society of Plant Physiologists
@Iwate University, Morioka, Japan
The 12th Database Workshop (March 19, 2016)

TENOR :
Database for Comprehensive mRNA-Seq Experiments in Rice

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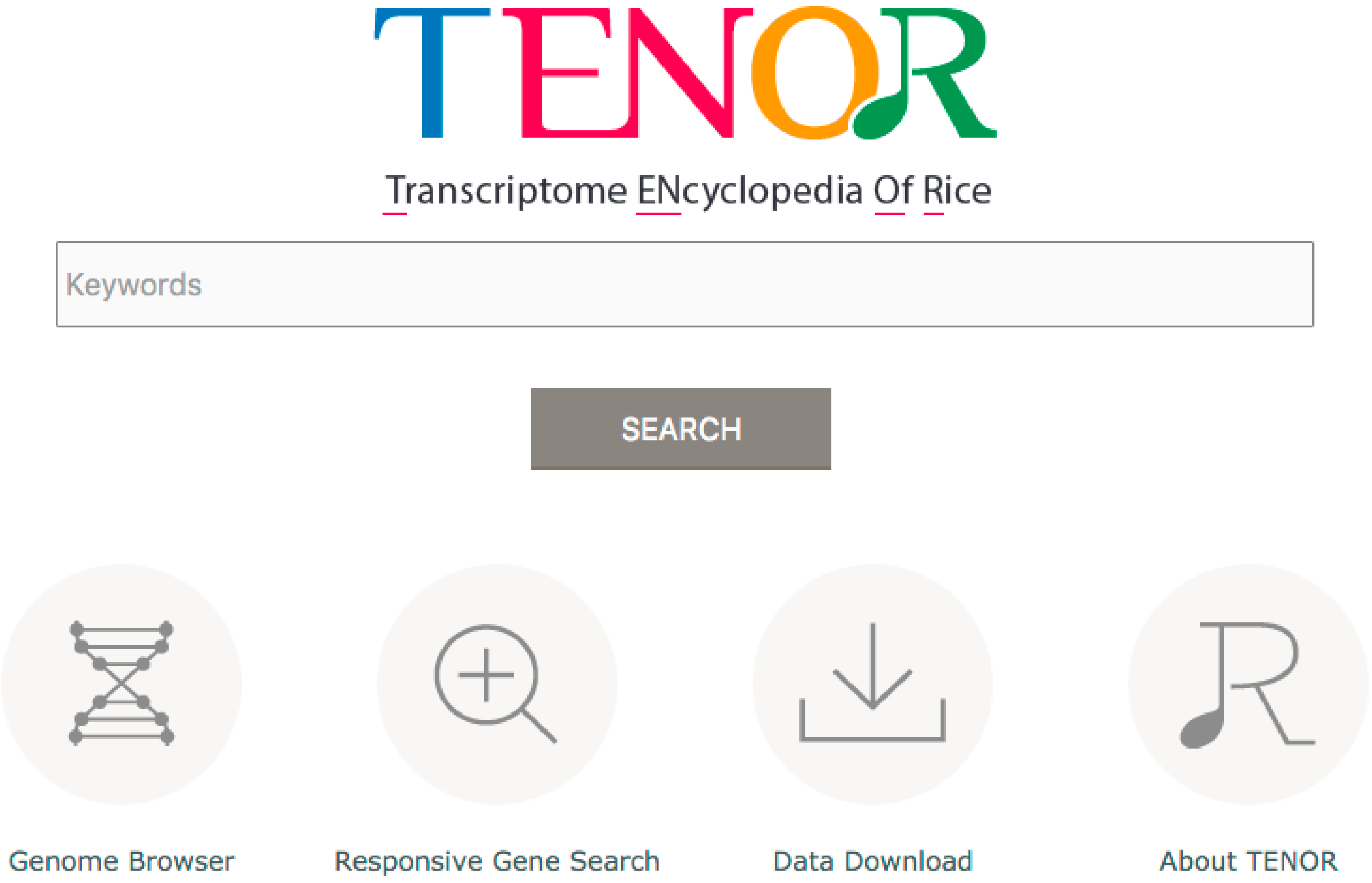
What is TENOR?

TENOR (**T**ranscriptome **EN**cyclopedia **O**f **R**ice)
A database that contains large-scale mRNA sequencing (mRNA-Seq) data obtained from rice under a wide variety of conditions.



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).

TENOR provides rice transcriptome data

under **10 abiotic stress** and **2 plant hormone**
treatment conditions (+ no treatment)

×

Shoot and **Root** tissues of *Oryza sativa* L. ssp. japonica
cv. **Nipponbare** (seedlings 10 days after germination)

×

at **Multiple timepoints**
(0h, 1h, 3h, 6h, 12h, 1d, 3d, 4d, 5d, 10d after treatments)

×

Total **140** conditions (250 billion bp from 3.5 billion reads)

10 abiotic stresses and 2 plant hormones

Salinity [a]

Low Pi [b]

High Pi [b]

High Cd [c]

Low Cd

Very-low Cd

Drought

Flood

Cold

Osmotic

JA

ABA

No treatment

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 28ºC 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)

Features of transcriptome data in TENOR

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

The TENOR development team

Sample & library preparation

- Youko Oono
- Jun Ogata
- Takashi Matsumoto

mRNA-Seq sequencing

- Harumi Sasaki
- Satomi Mori
- Hiroyuki Kanamori

DB & software development

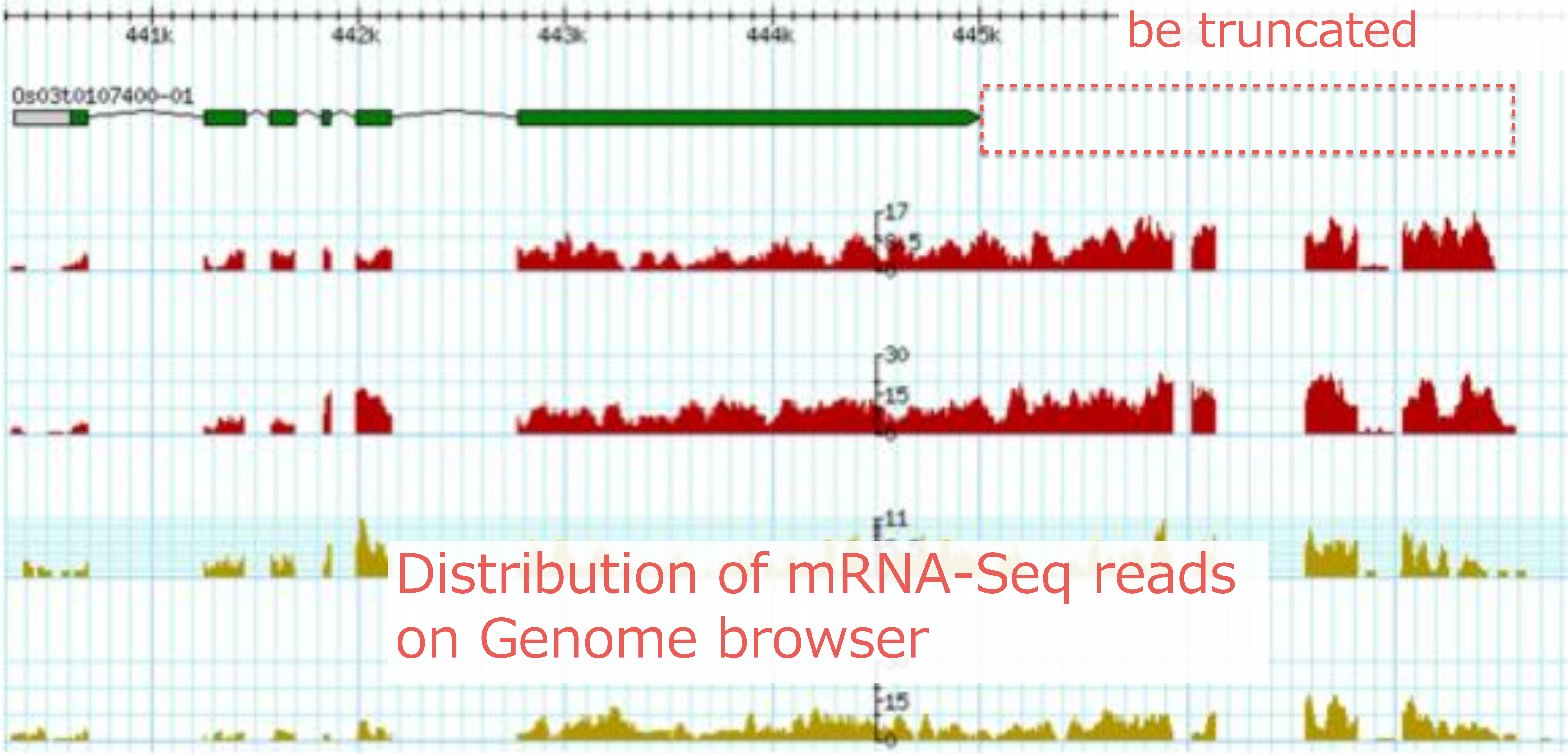
- Yoshihiro Kawahara
- Hironobu Wakimoto
- Takeshi Itoh

National Institute of Agrobiological Sciences (NIAS)
Agrogenomics Research Center

Features of transcriptome data in TENOR

Use of **mRNA-Seq technique** provides

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



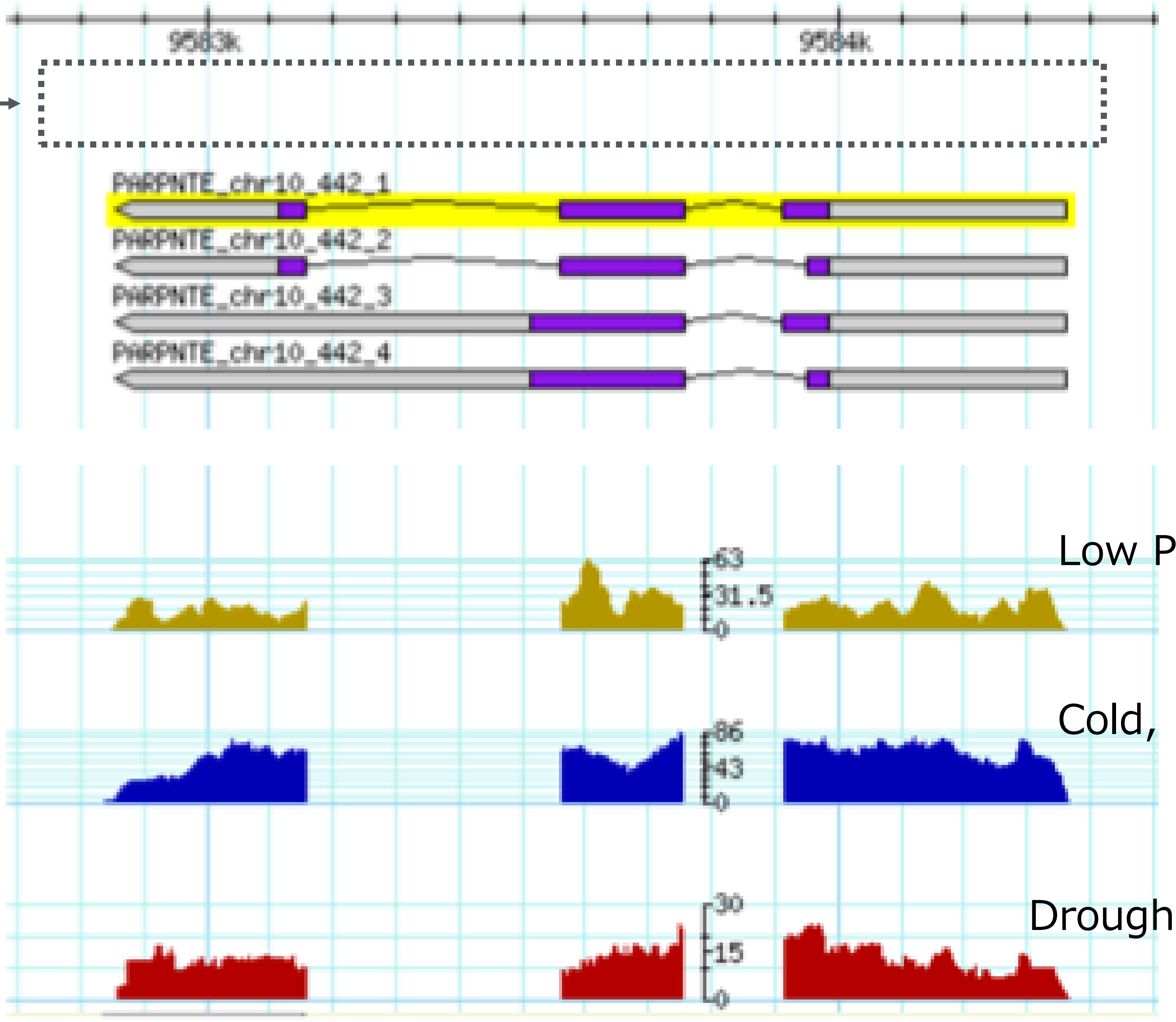
This transcript might be truncated

Distribution of mRNA-Seq reads on Genome browser

Features of transcriptome data in TENOR

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

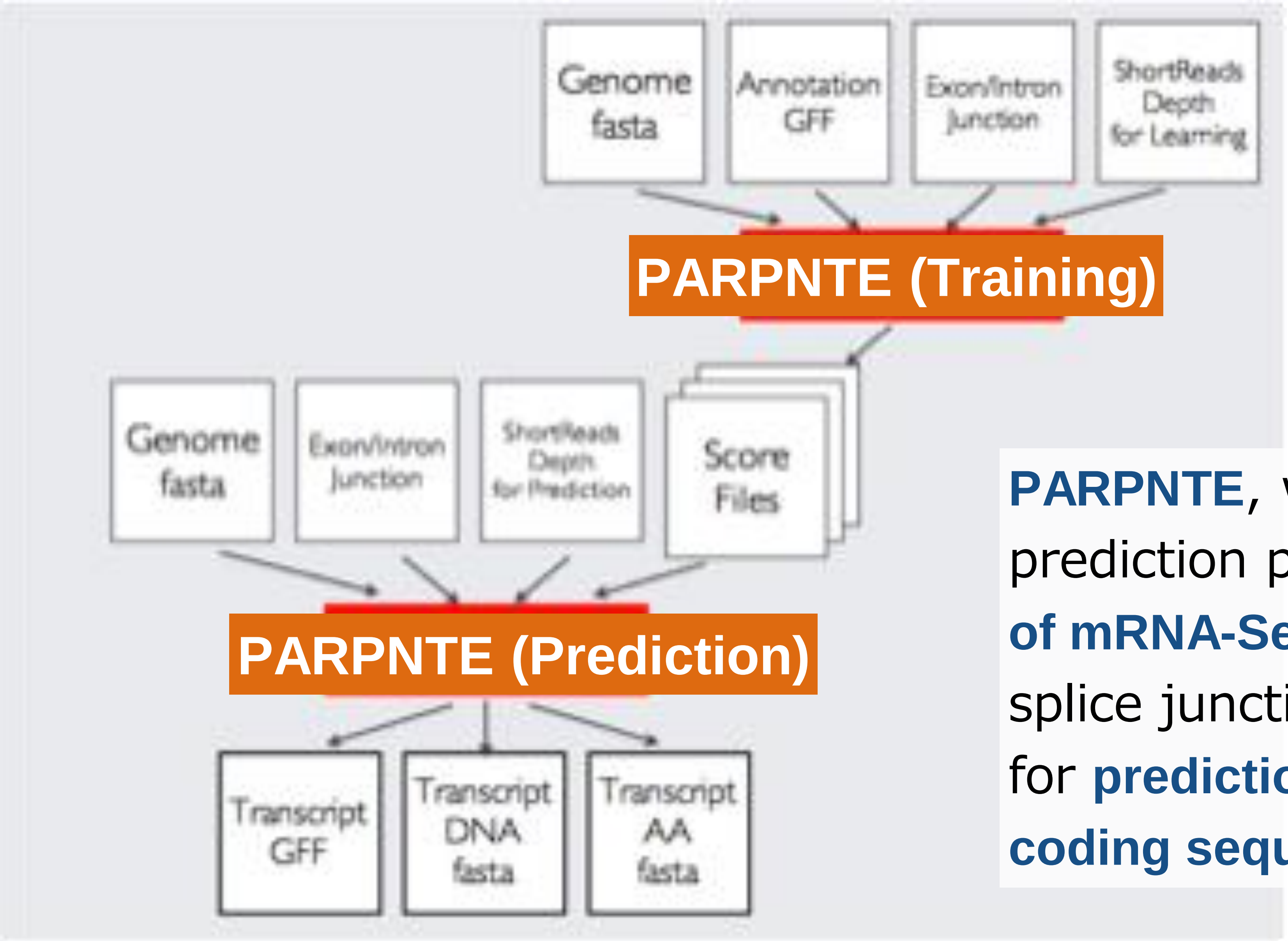
Distribution of mRNA-Seq reads

Low P, 5d, Root

Cold, 1d, Root

Drought, 1d, Root

What is PARPNTE



PARPNTE, 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**.

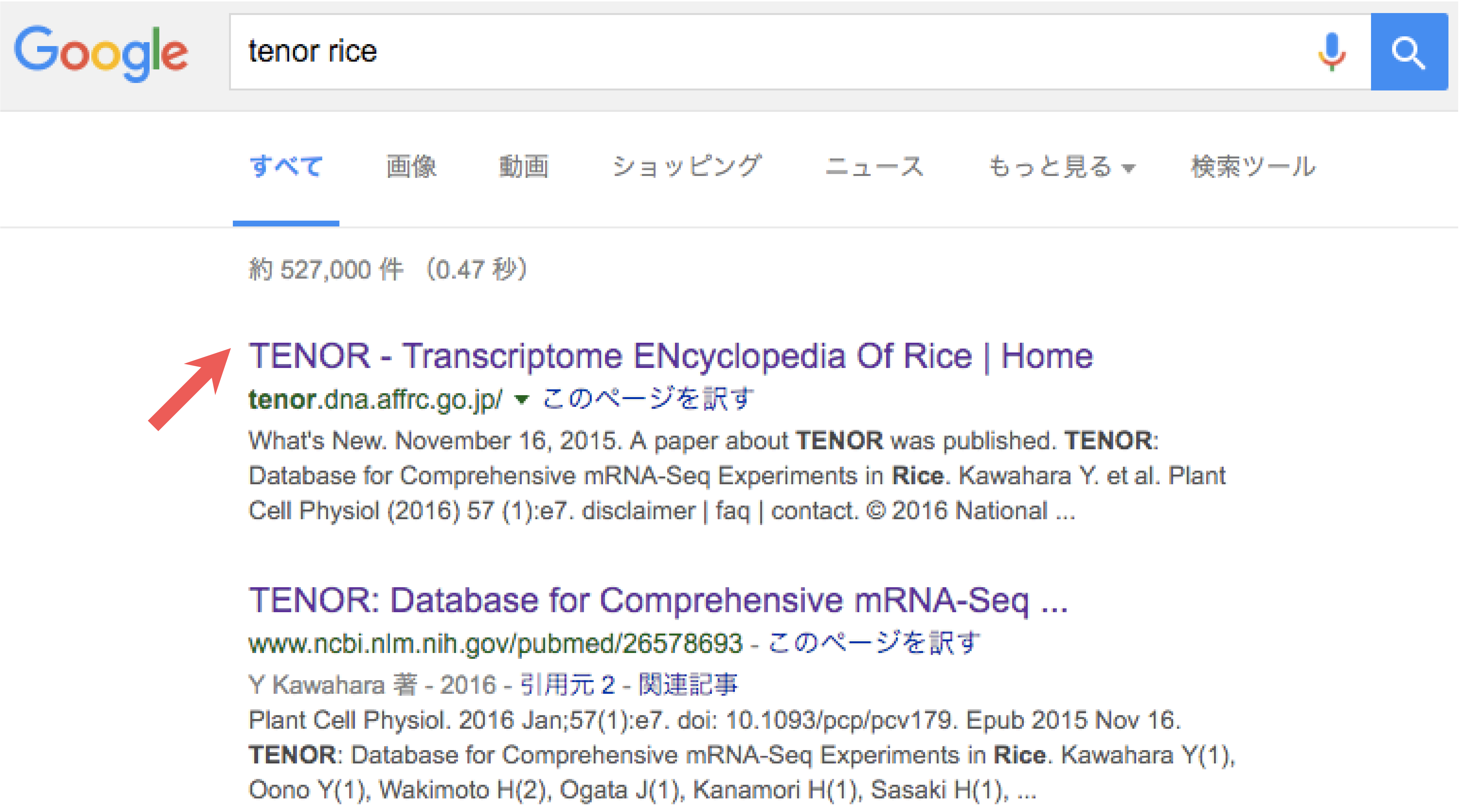
Program	Transcripts	Loci	Multi-exon transcripts	Base Sn	Base Sp	Exon Sn	Exon Sp	Intron Sn	Intron Sp
PARPNTE	48,366	38,228	30,293	51.2	64.1	52.4	58.9	70.1	80.6
Cufflinks	45,415	30,617	30,249	59.0	50.8	49.1	54.2	69.3	79.5

Statistics of annotated and unannotated genes

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					
- PARPNTE protein-coding	742	2,069.1	552.8	2.3	40.1
- PARPNTE non-coding	2,274	1,281.2	–	2.0	48.5
- Cufflinks genes	1,263	943.4	–	1.8	22.5

Functions in TENOR

Google search for TENOR



tenor rice

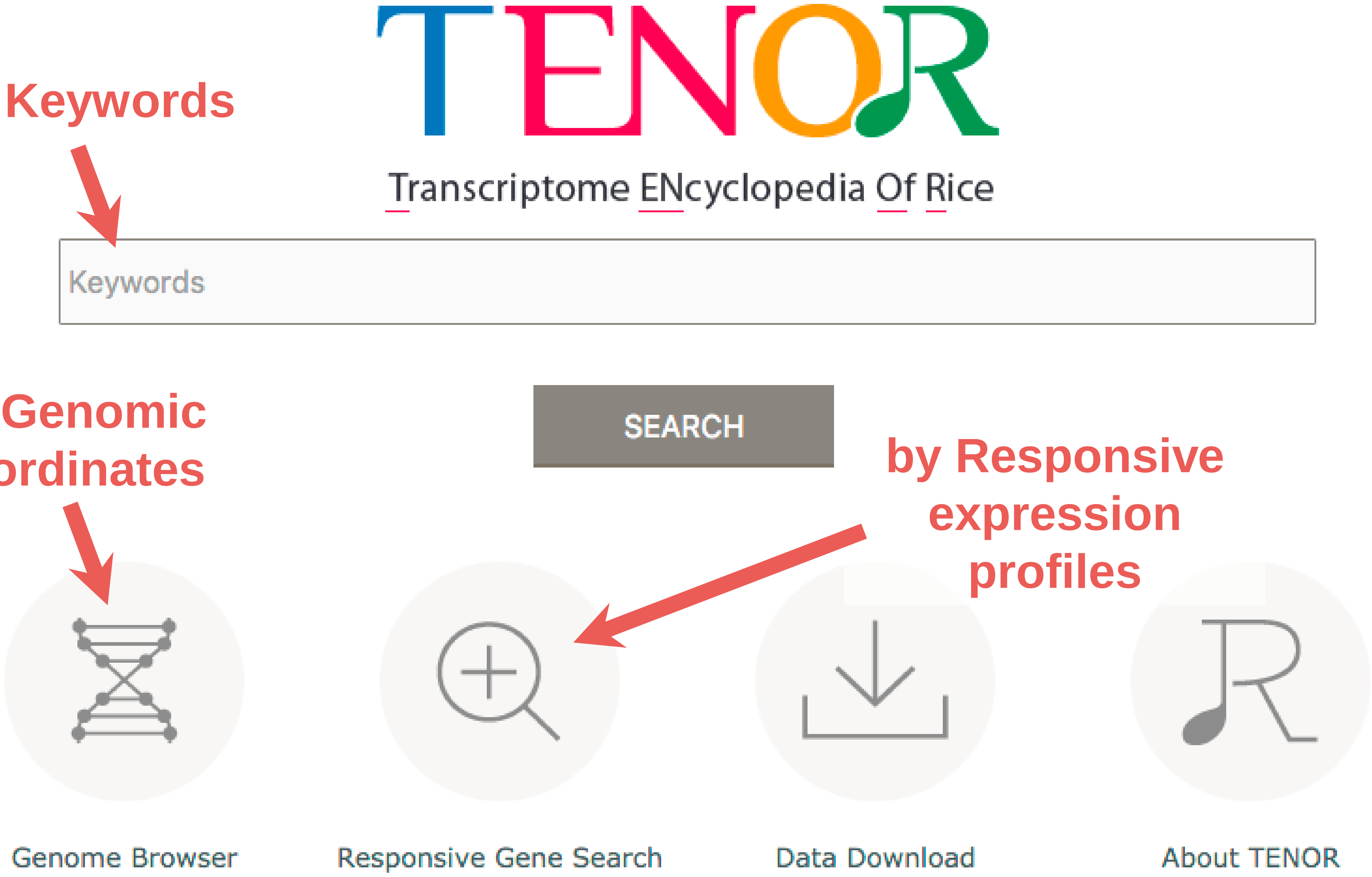
約 527,000 件 （0.47 秒）

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

Three entrances on the top page



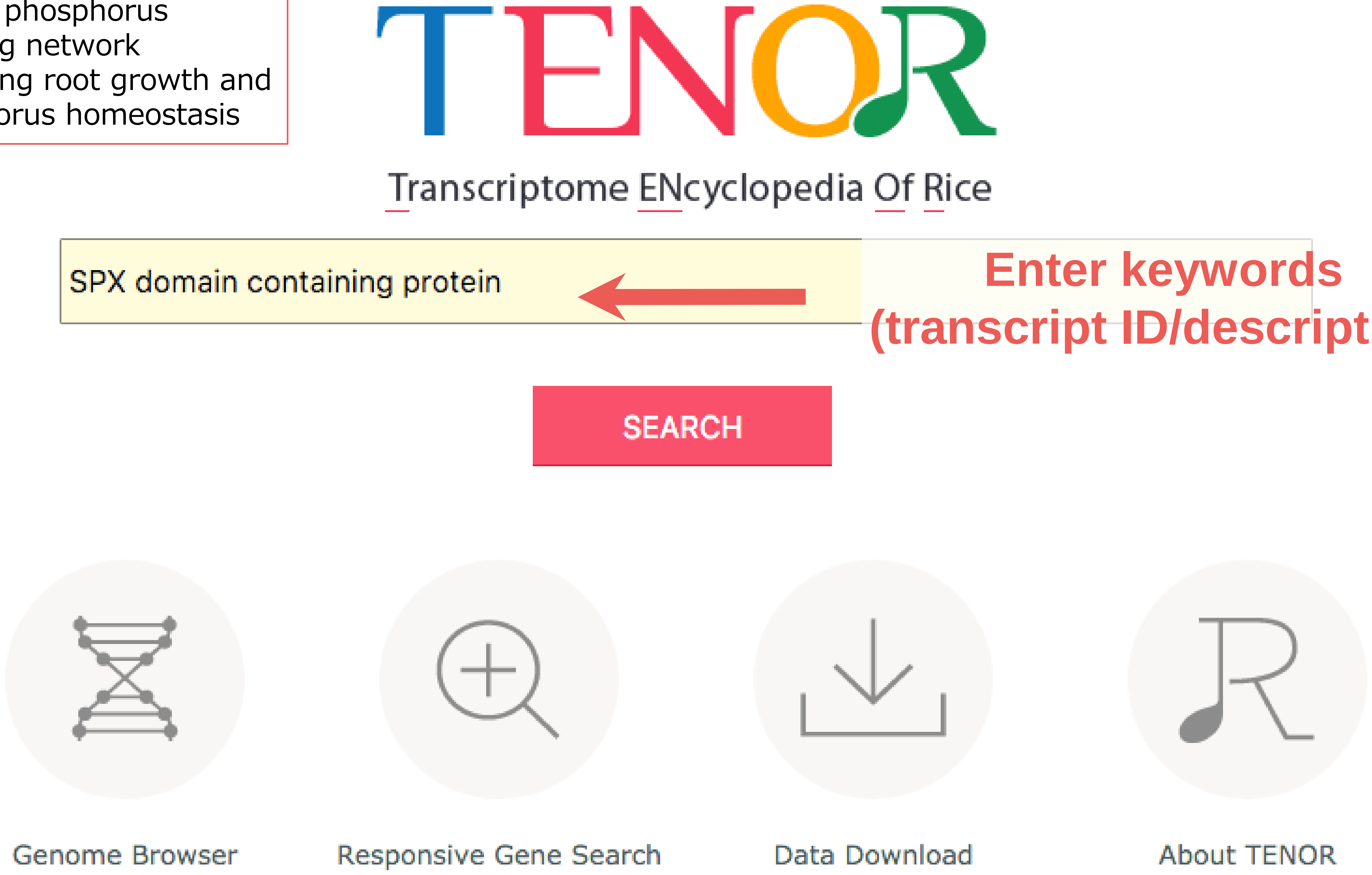
by Keywords

by Genomic coordinates

by Responsive expression profiles

Search by Keywords

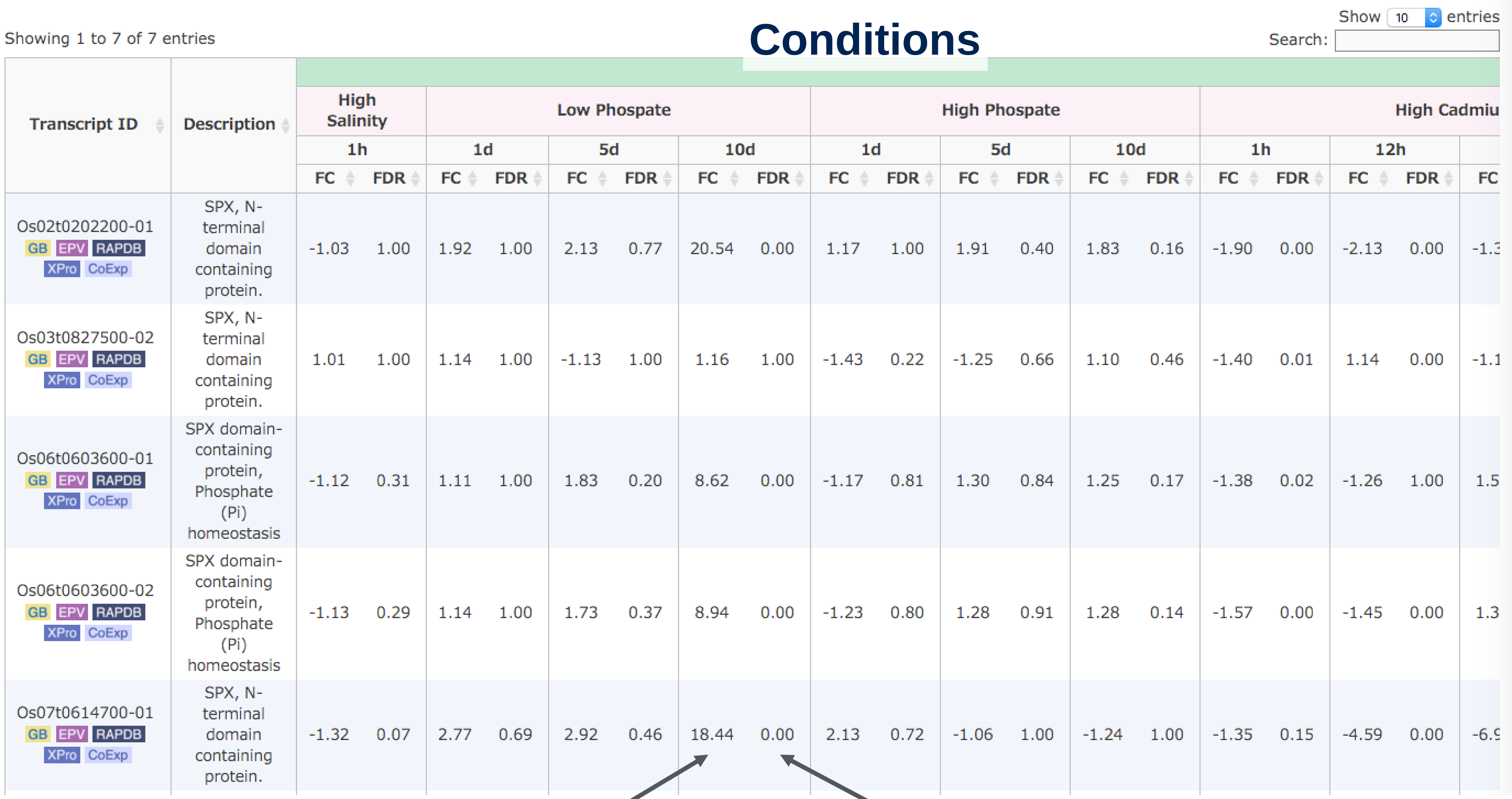
SPX genes play important roles in phosphorus signaling network regulating root growth and phosphorus homeostasis



SPX domain containing protein

Enter keywords (transcript ID/description)

Search results



Show 10 entries

Search:

Showing 1 to 7 of 7 entries

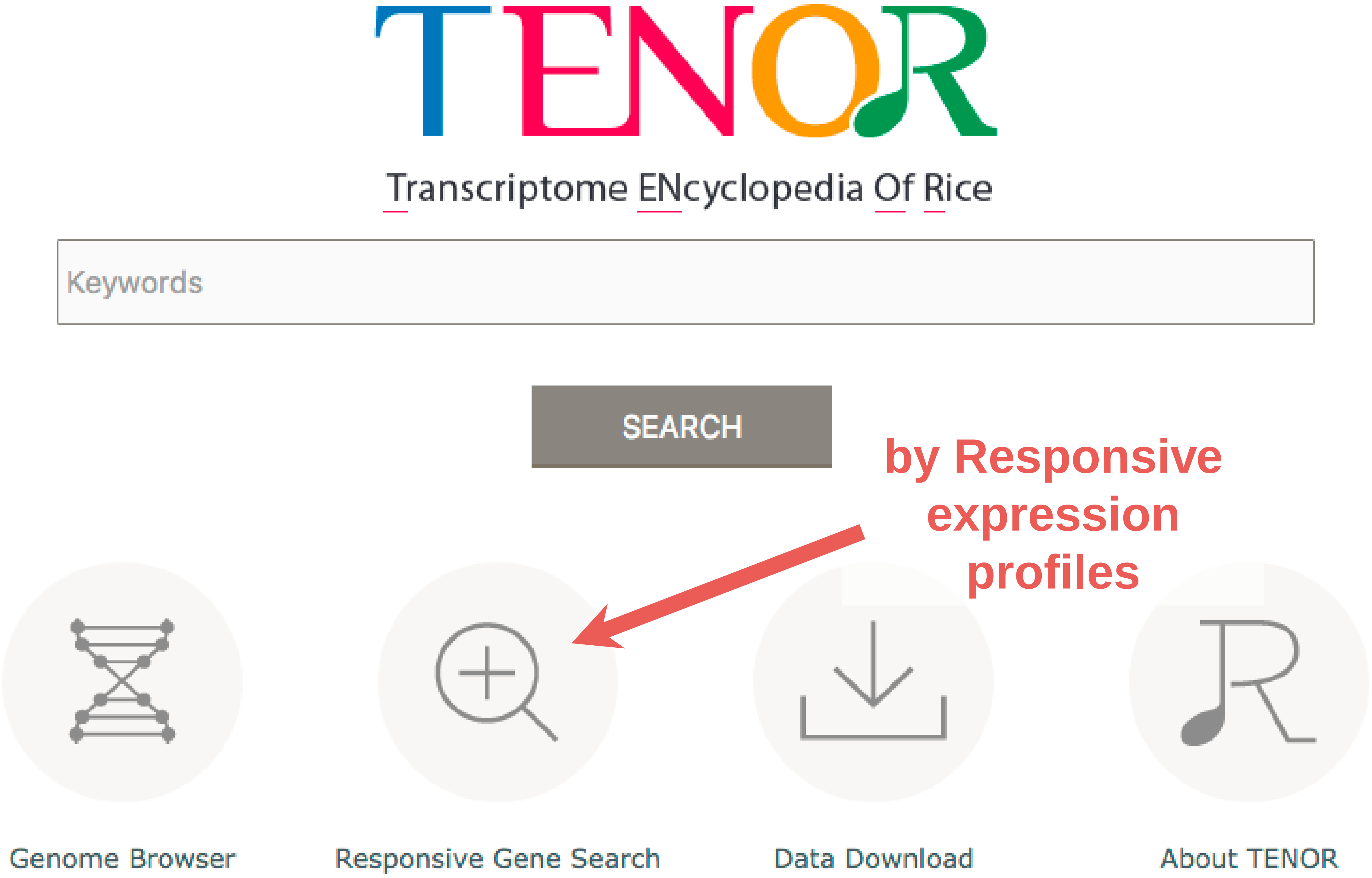
Conditions

Transcript ID	Description	High Salinity		Low Phospate						High Phospate						High Cadmiu				
		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	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

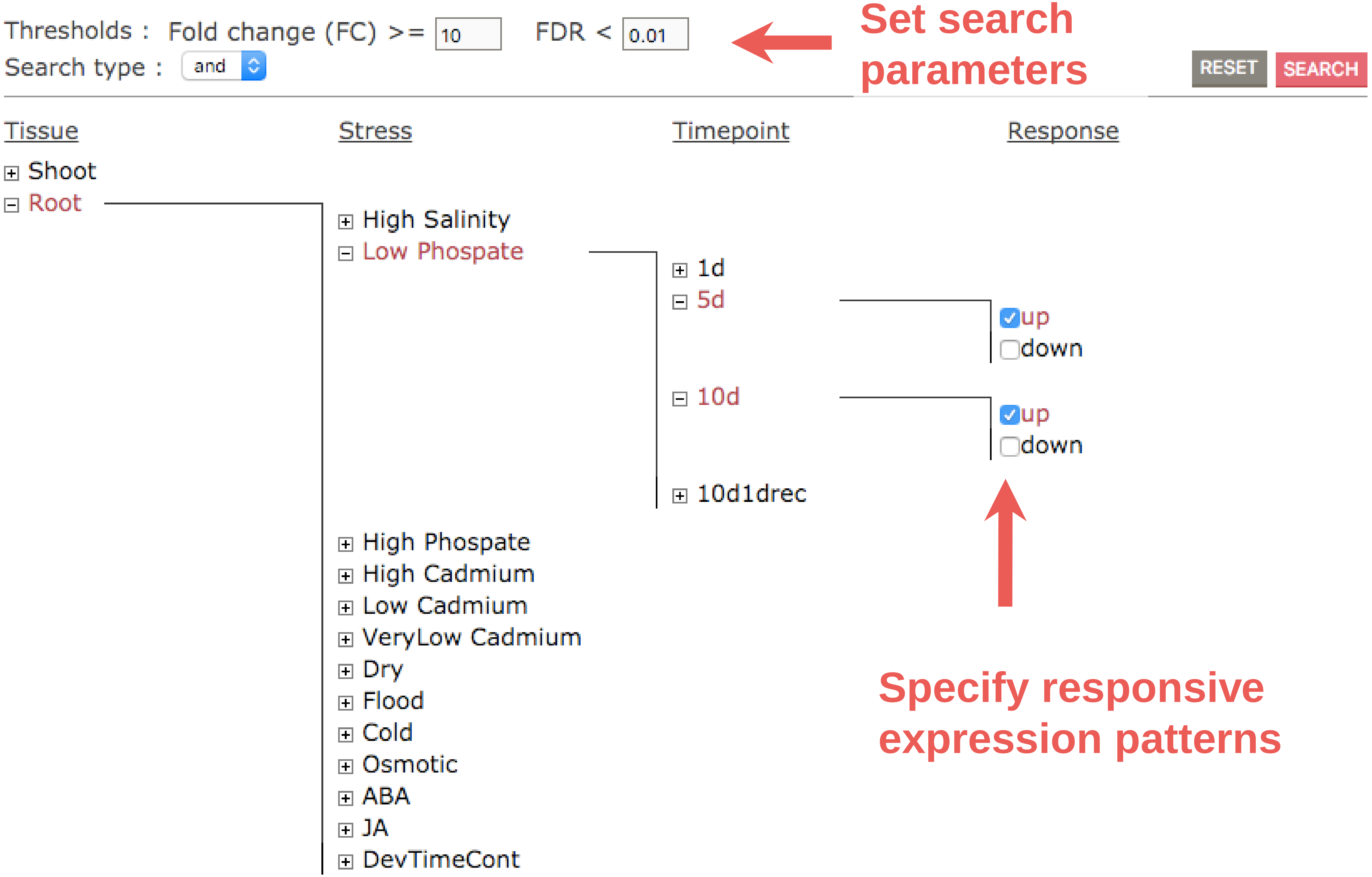
FDR: statistical significances of differential expressions

Three entrances on the top page



by Responsive expression profiles

Search by responsive expression profile



Thresholds : Fold change (FC) >= 10 FDR < 0.01

Search type : and

Tissue | Stress | Timepoint | Response

- ⊞ Shoot
- ⊟ Root
  - ⊞ High Salinity
  - ⊟ Low Phospate
    - ⊞ 1d
    - ⊟ 5d
      - ☑ up
      - ☐ down
    - ⊟ 10d
      - ☑ up
      - ☐ down
    - ⊞ 10d1drec
  - ⊞ High Phospate
  - ⊞ High Cadmium
  - ⊞ Low Cadmium
  - ⊞ VeryLow Cadmium
  - ⊞ Dry
  - ⊞ Flood
  - ⊞ Cold
  - ⊞ Osmotic
  - ⊞ ABA
  - ⊞ JA
  - ⊞ DevTimeCont

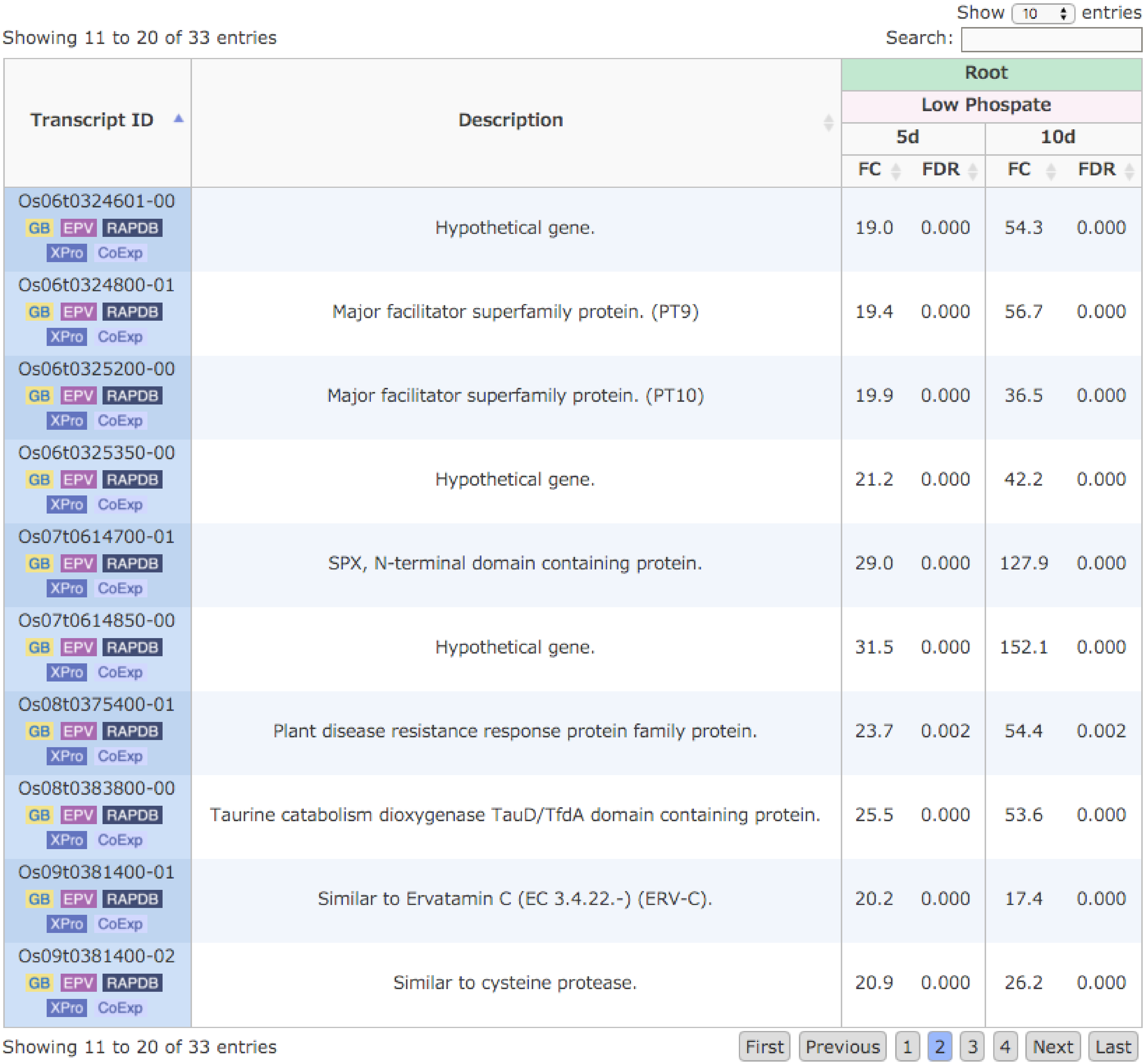
Set search parameters

Specify responsive expression patterns

Phosphate starvation induced genes

Pi transporters

SPX genes



Show 10 entries

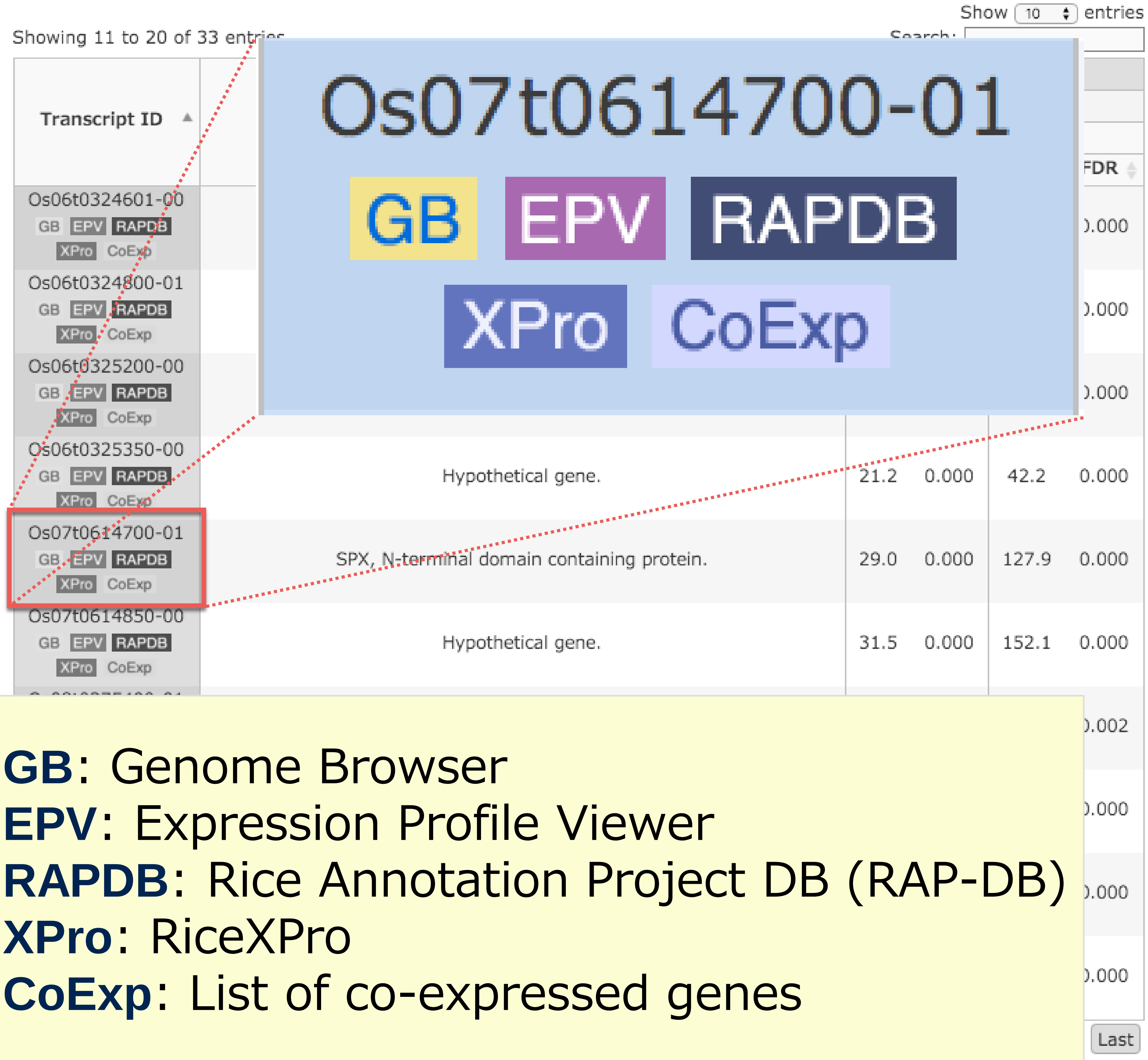
Search:

Showing 11 to 20 of 33 entries

Transcript ID	Description	Root			
		Low Phospate			
		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

Links to other DB & viewer



Showing 11 to 20 of 33 entries

Show 10 entries

Search:

Transcript ID					FDR
Os06t0324601-00 GB EPV RAPDB XPro CoExp					.000
Os06t0324800-01 GB EPV RAPDB XPro CoExp					.000
Os06t0325200-00 GB EPV RAPDB XPro CoExp					.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
					.002
					.000
					.000
					.000

GB: Genome Browser

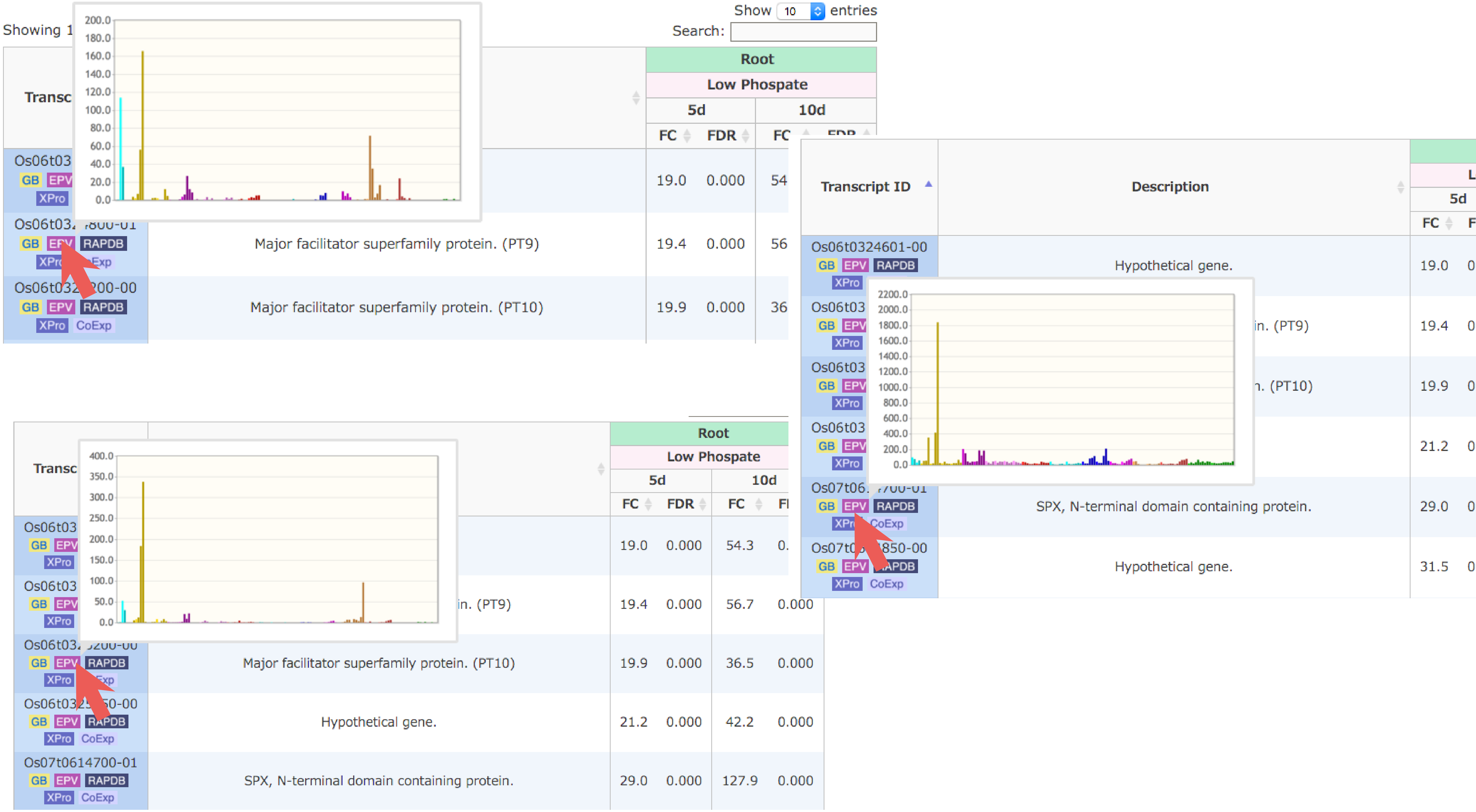
EPV: Expression Profile Viewer

RAPDB: Rice Annotation Project DB (RAP-DB)

XPro: RiceXPro

CoExp: List of co-expressed genes

Expression Profile Viewer (EPV)



Show 10 entries

Showing 1

Search:

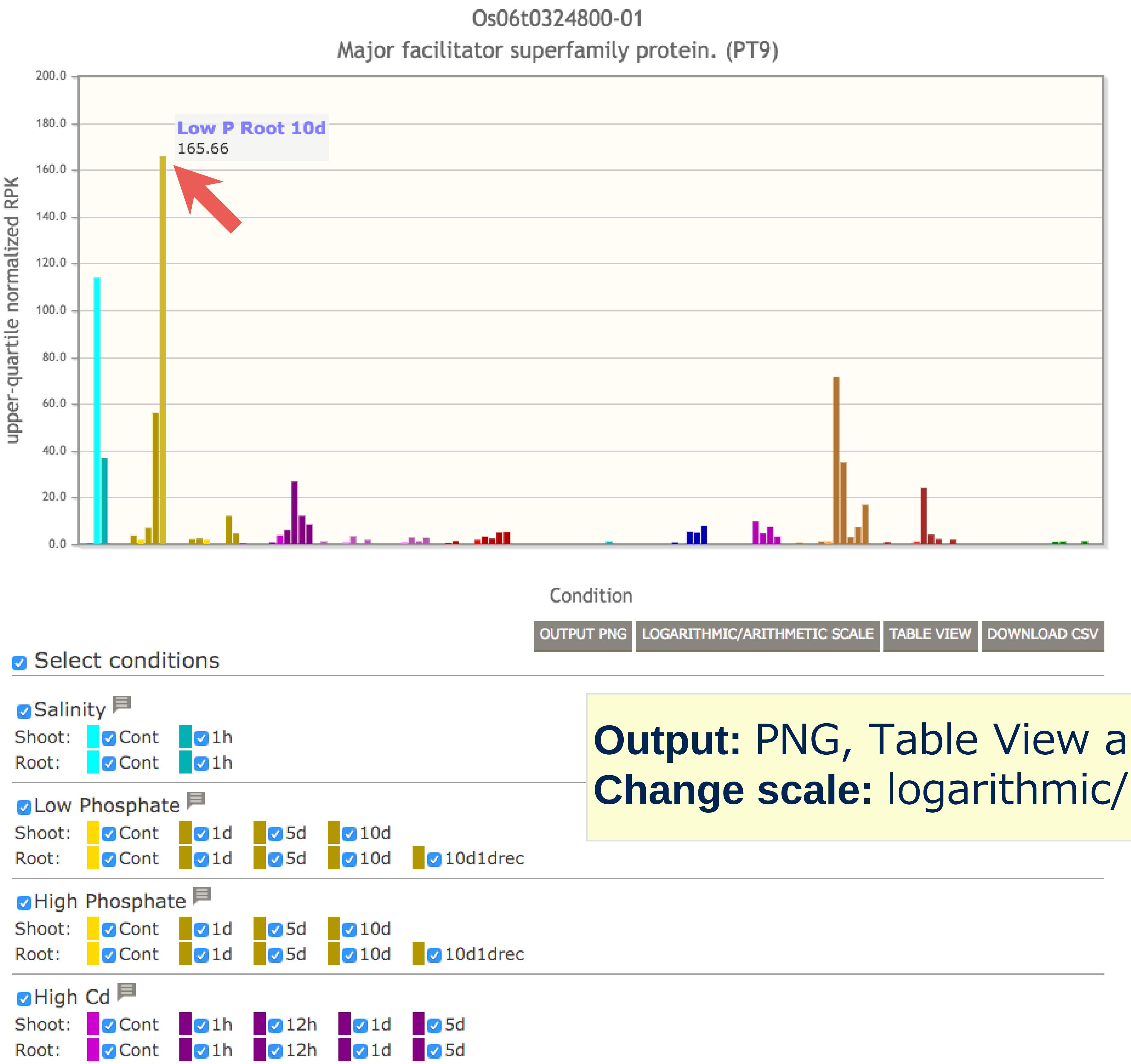
Transc		Root			
		Low Phospate			
		5d		10d	
		FC	FDR	FC	FDR
Os06t03 GB EPV XPro		19.0	0.000	54	
Os06t03 800-01 GB EPV RAPDB XPro Exp	Major facilitator superfamily protein. (PT9)	19.4	0.000	56	
Os06t032 200-00 GB EPV RAPDB XPro CoExp	Major facilitator superfamily protein. (PT10)	19.9	0.000	36	

Transcript ID	Description	L	
		5d	
		FC	F
Os06t0324601-00 GB EPV RAPDB XPro	Hypothetical gene.	19.0	0
Os06t03 GB EPV XPro	in. (PT9)	19.4	0
Os06t03 GB EPV XPro	n. (PT10)	19.9	0
Os06t03 GB EPV XPro		21.2	0
Os07t06 700-01 GB EPV RAPDB XPr CoExp	SPX, N-terminal domain containing protein.	29.0	0
Os07t0 850-00 GB EPV APDB XPro CoExp	Hypothetical gene.	31.5	0

Transc		Root			
		Low Phospate			
		5d		10d	
		FC	FDR	FC	FI
Os06t03 GB EPV XPro		19.0	0.000	54.3	0.
Os06t03 GB EPV XPro	in. (PT9)	19.4	0.000	56.7	0.000
Os06t03 200-00 GB EPV RAPDB XPro Exp	Major facilitator superfamily protein. (PT10)	19.9	0.000	36.5	0.000
Os06t032 50-00 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

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

Expression Profile Viewer (EPV)



☑ Select conditions

☑ Salinity
Shoot: 🟦 ☑ Cont 🟦 ☑ 1h
Root: 🟦 ☑ Cont 🟦 ☑ 1h

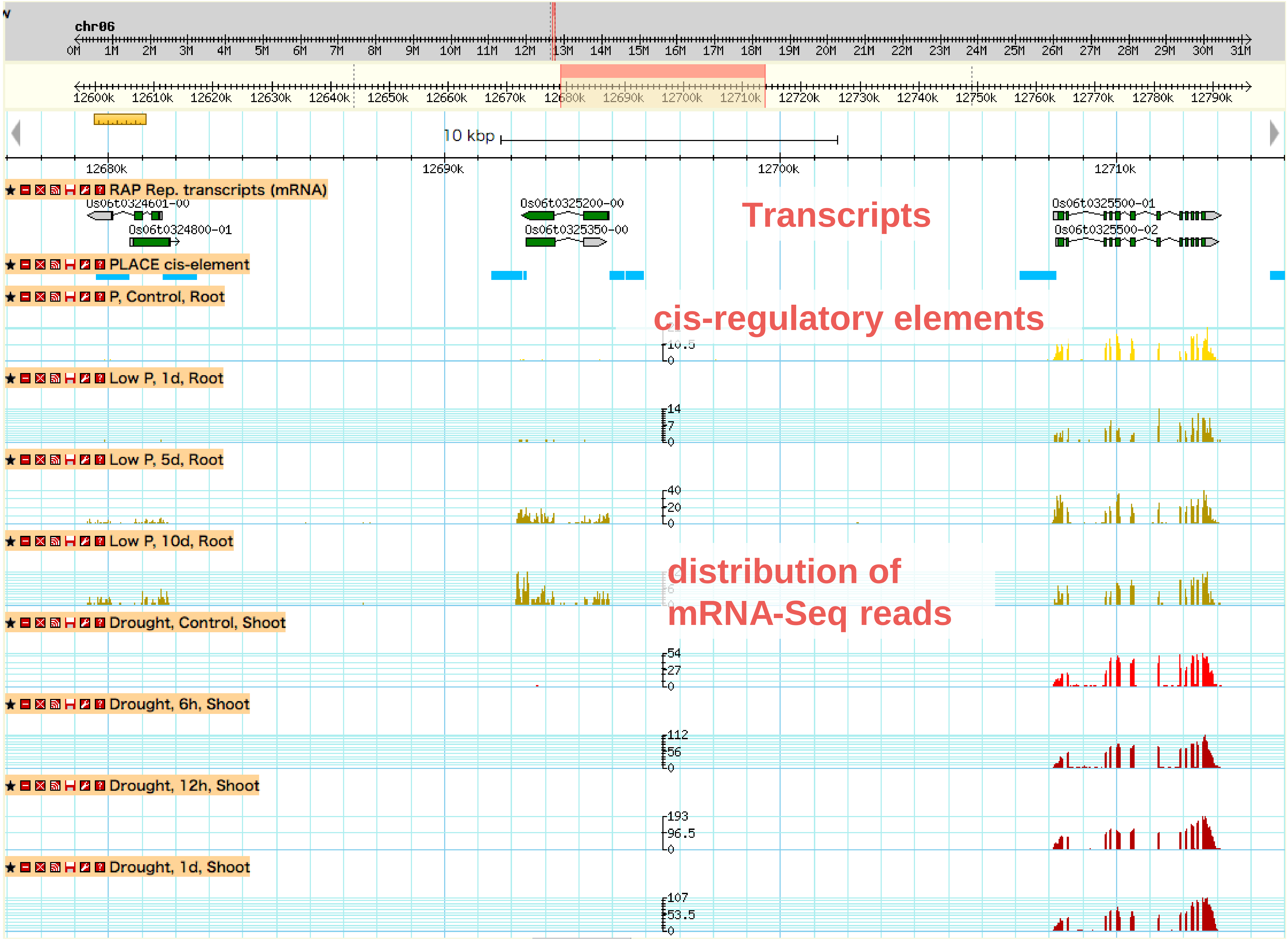
☑ Low Phosphate
Shoot: 🟨 ☑ Cont 🟫 ☑ 1d 🟫 ☑ 5d 🟫 ☑ 10d
Root: 🟨 ☑ Cont 🟫 ☑ 1d 🟫 ☑ 5d 🟫 ☑ 10d 🟫 ☑ 10d1drec

☑ 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/arithmetic

Genome Browser (GBrowse)

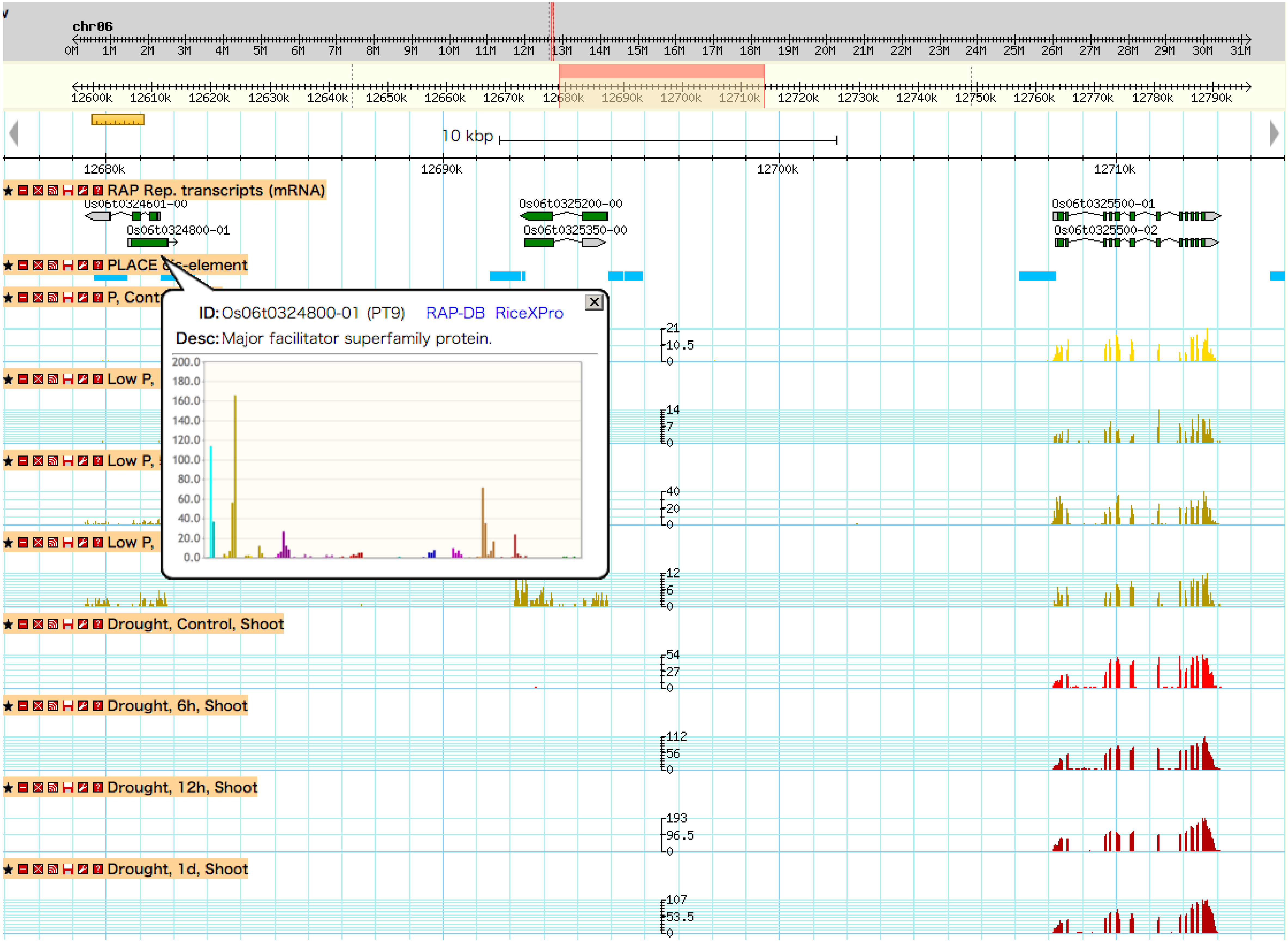


Transcripts

cis-regulatory elements

distribution of mRNA-Seq reads

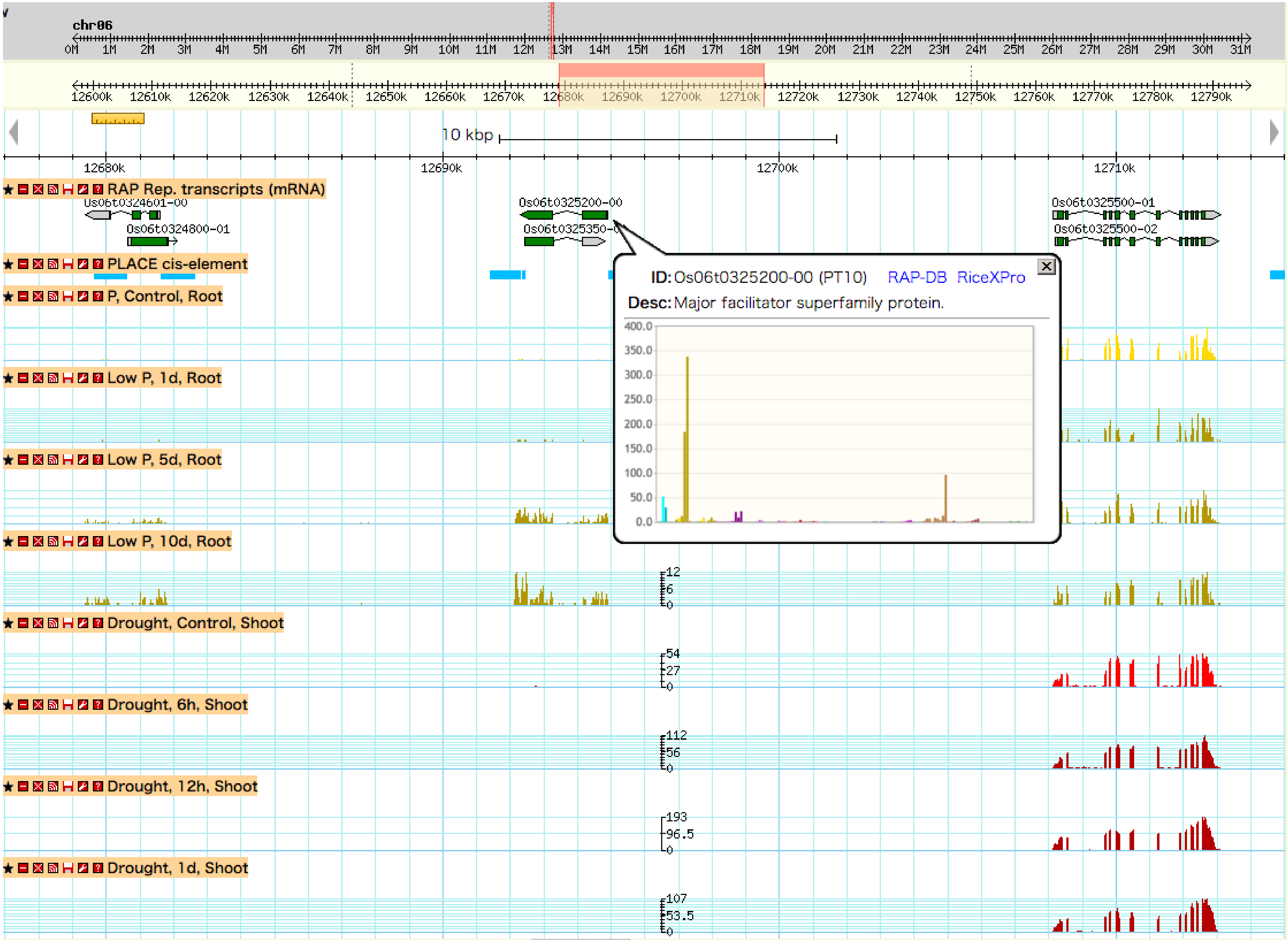
Genome Browser (GBrowse)



ID: Os06t0324800-01 (PT9)

Desc: Major facilitator superfamily protein.

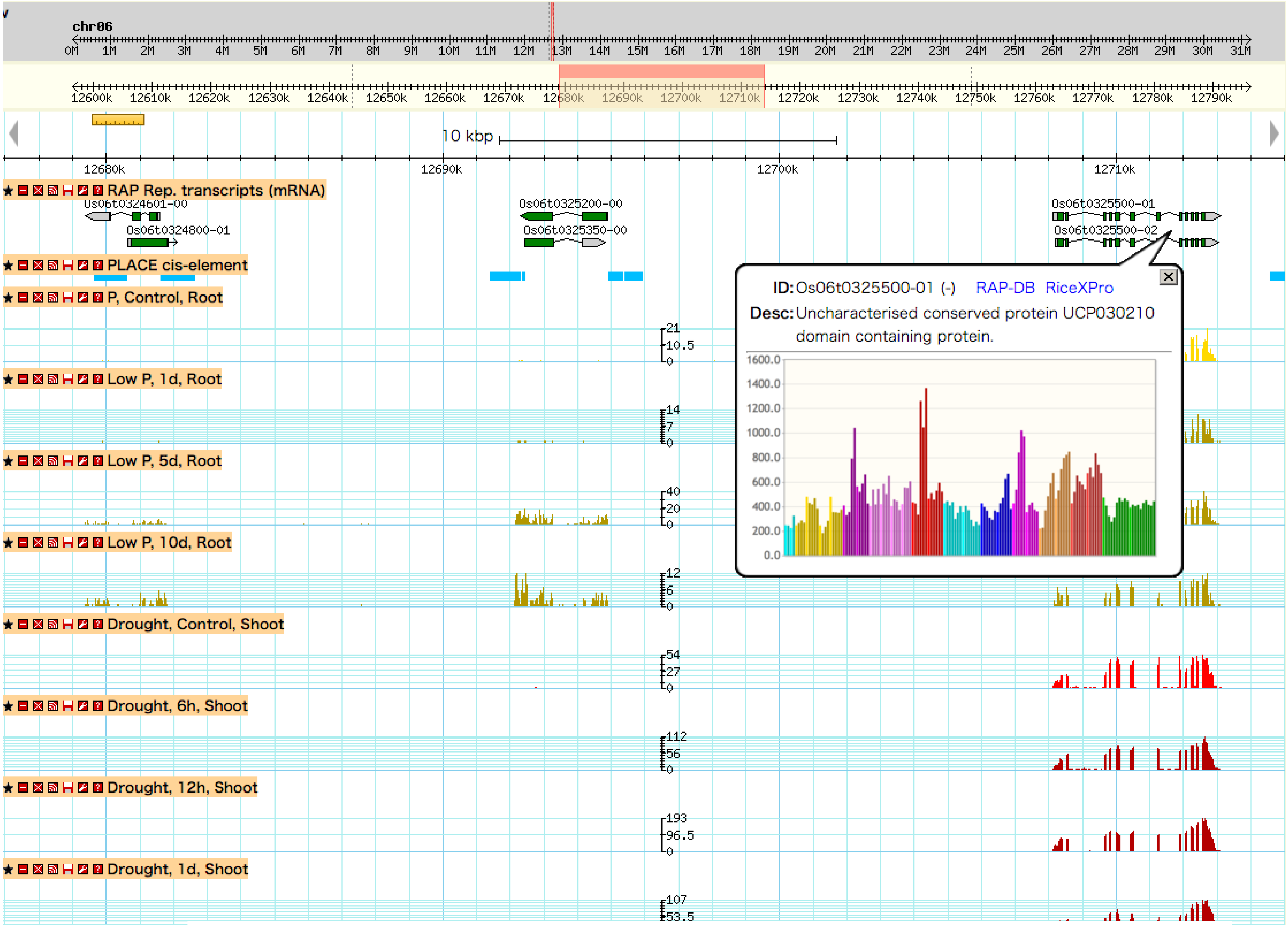
Genome Browser (GBrowse)



ID: Os06t0325200-00 (PT10)

Desc: Major facilitator superfamily protein.

Genome Browser (GBrowse)



ID: Os06t0325500-01 (-) RAP-DB RiceXPro

Desc: Uncharacterised conserved protein UCP030210 domain containing protein.

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

cis-regulatory elements in 1kb upstream regions

New PLACE

A Database of Plant Cis-acting Regulatory DNA Elements

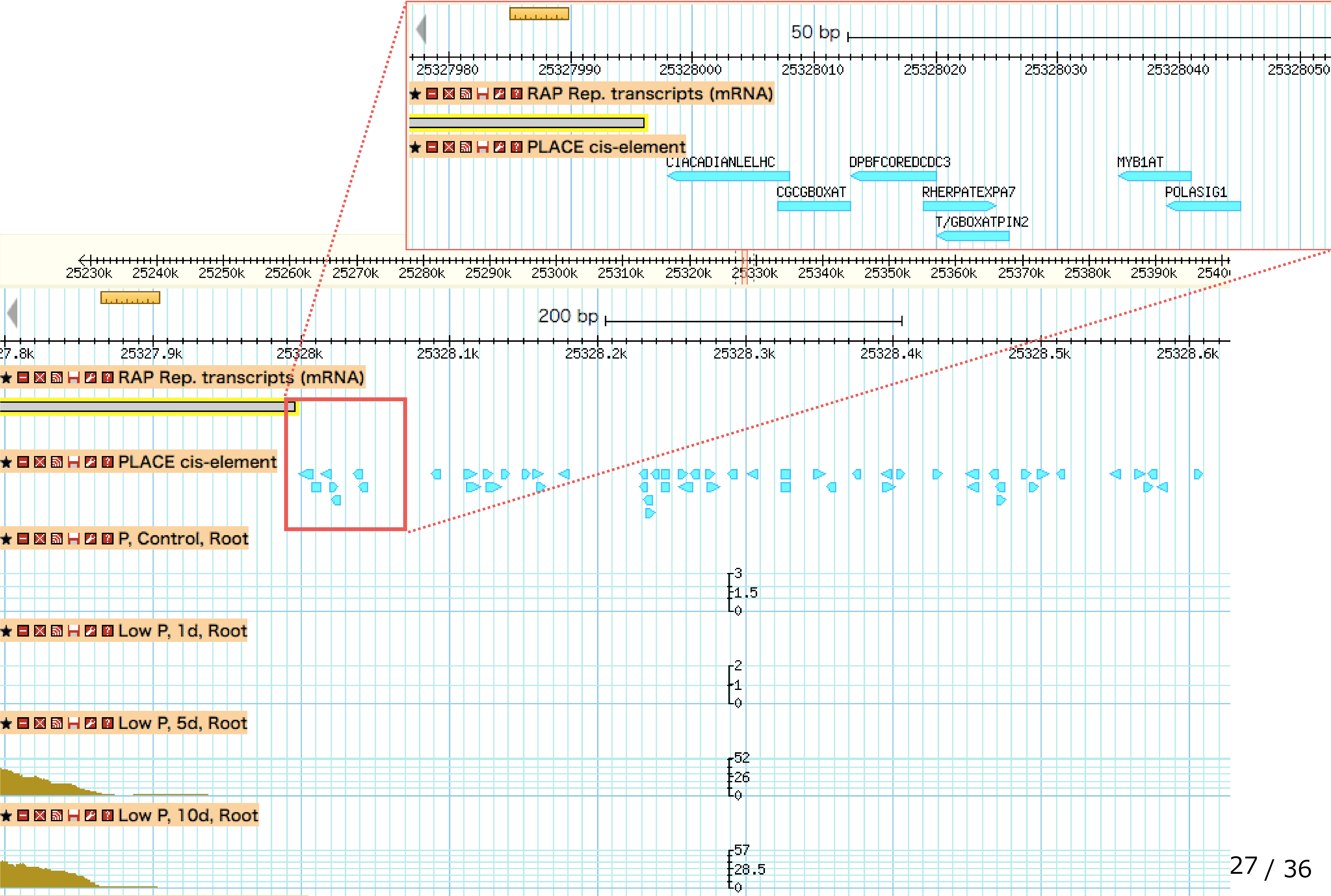
PLACE is a database of motifs found in plant cis-acting regulatory DNA elements, all from previously published reports. It covers vascular plants only (But since April 2006, we changed the policy. See the release note for PLACE 26.0). In addition to the motifs originally reported, their variations in other genes or in other plant species reported later are also compiled. The PLACE database also contains a brief description of each motif and relevant literature with PubMed ID numbers. DDBJ/EMBL/GenBank nucleotide sequence databases accession numbers will be also included. See 'sample record'. List of entries can be found in 'place.dat'.

Paste a FASTA format sequence, please.
Upper limit of multi FASTA is 20 sequences.

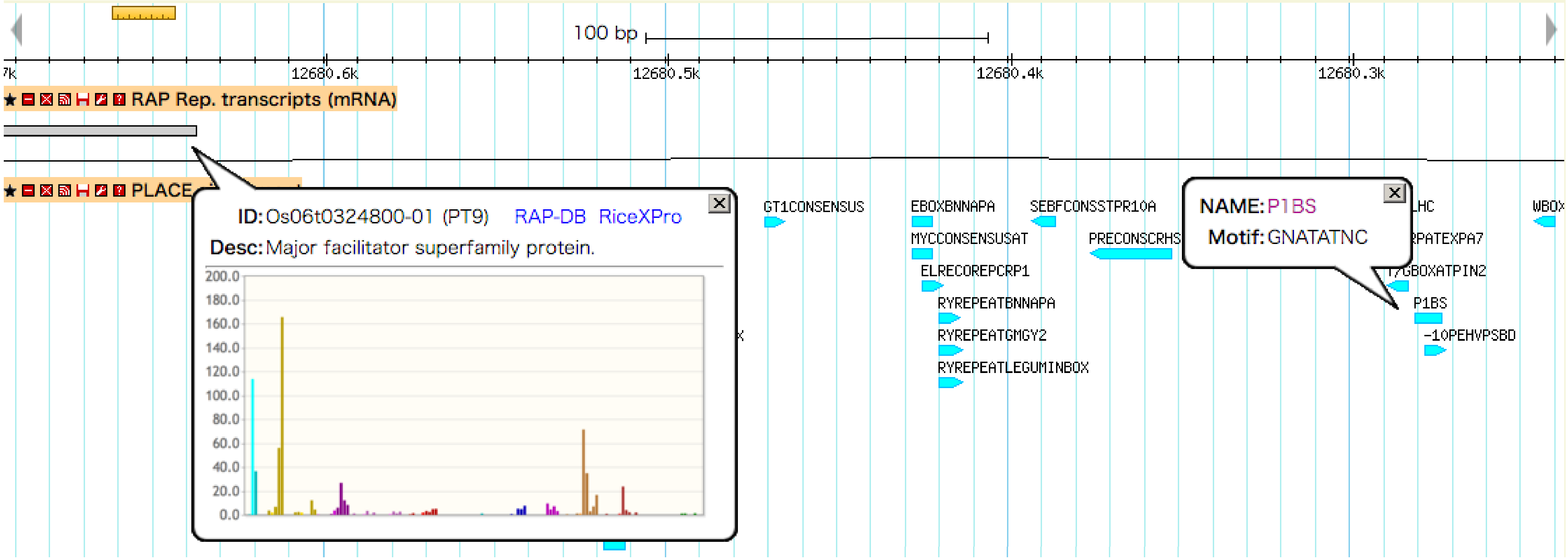
Data file of Plant Cis-acting Regulatory DNA Elements:
place.dat place.seq (30.0, 469 entries, Jan.8, 2007, © Kenichi Higo)

If you use this data file in published research, please cite:
Higo, K., Y. Ugawa, M. Iwamoto and T. Korenaga (1999) Plant cis-acting regulatory DNA elements (PLACE) database. Nucleic Acids Res. 27 (1): 297-300.

cis-regulatory elements in 1kb upstream regions



cis-regulatory elements in 1kb upstream regions

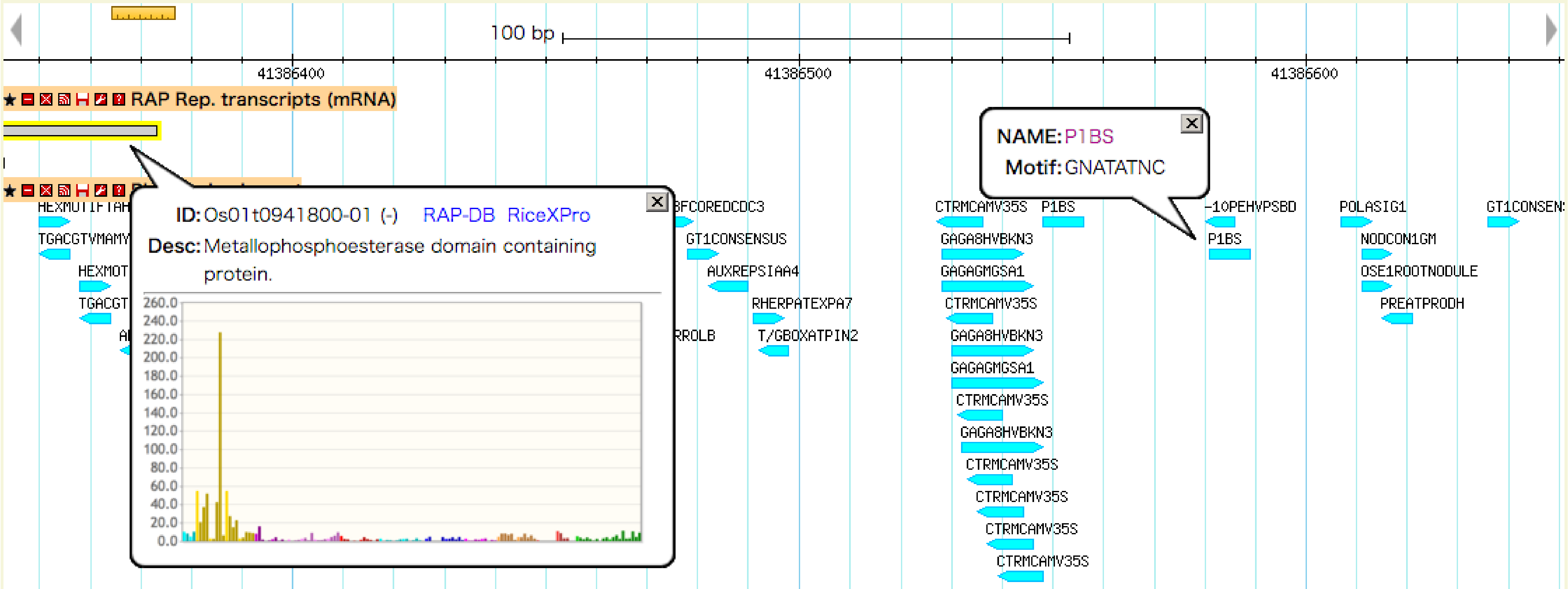


ID: Os06t0324800-01 (PT9) RAP-DB RiceXPro

Desc: Major facilitator superfamily protein.

NAME: P1BS

Motif: GNATATNC



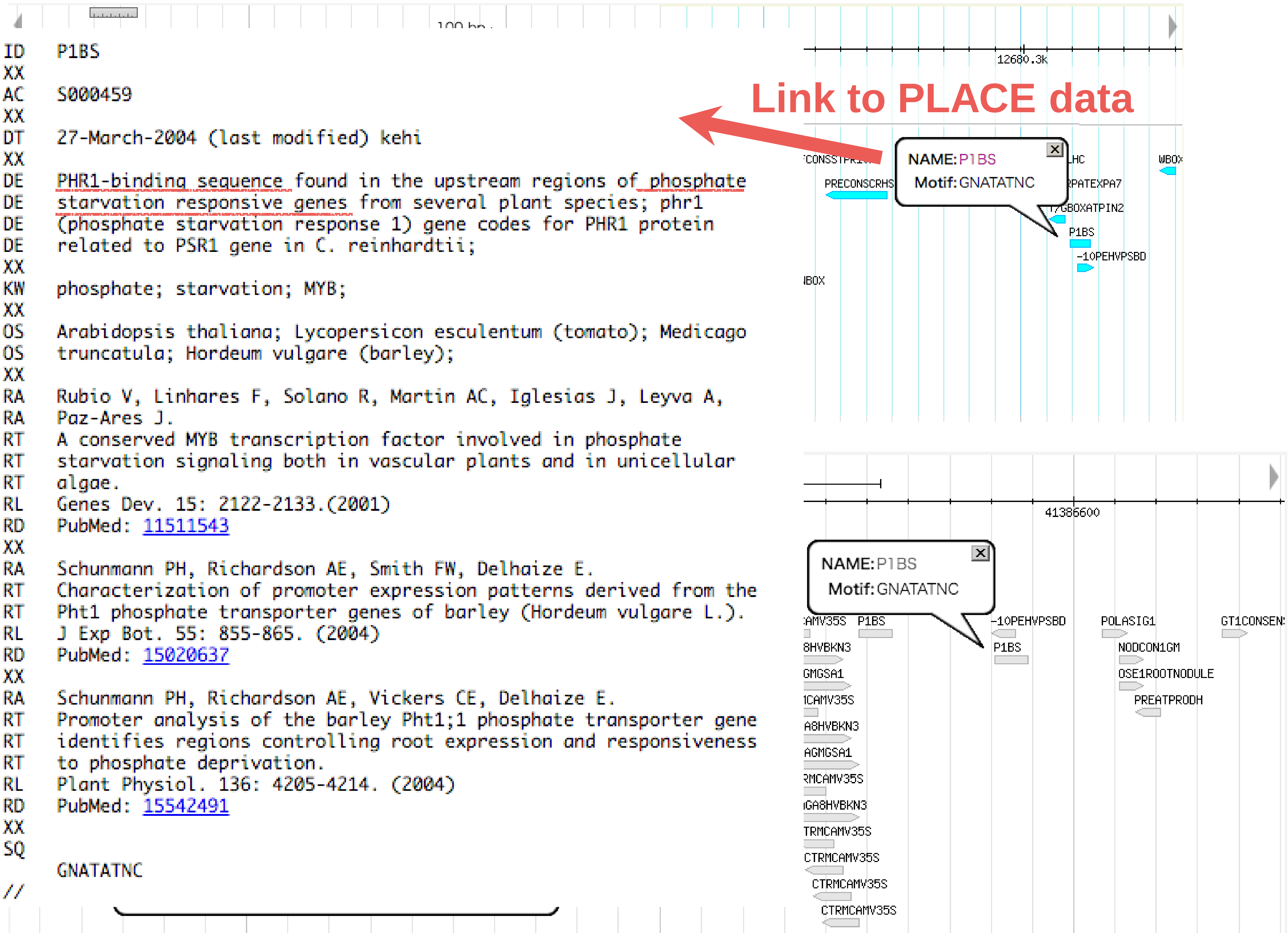
ID: Os01t0941800-01 (-) RAP-DB RiceXPro

Desc: Metallophosphoesterase domain containing protein.

NAME: P1BS

Motif: GNATATNC

cis-regulatory elements in 1kb upstream regions



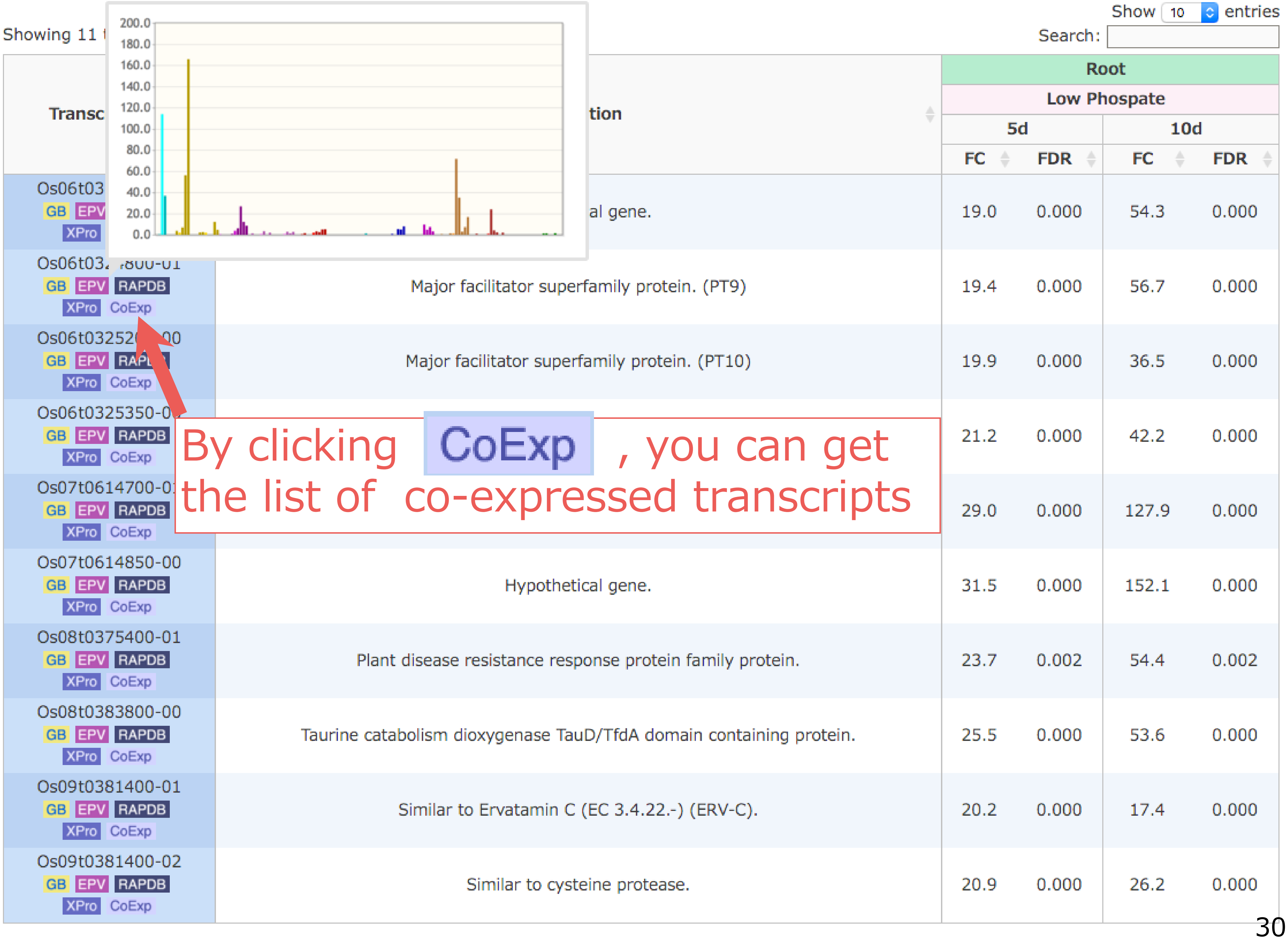
```
ID   P1BS
XX
AC   S000459
XX
DT   27-March-2004 (last modified) kehi
XX
DE   PHR1-binding sequence found in the upstream regions of phosphate
DE   starvation responsive genes from several plant species; phr1
DE   (phosphate starvation response 1) gene codes for PHR1 protein
DE   related to PSR1 gene in C. reinhardtii;
XX
KW   phosphate; starvation; MYB;
XX
OS   Arabidopsis thaliana; Lycopersicon esculentum (tomato); Medicago
OS   truncatula; Hordeum vulgare (barley);
XX
RA   Rubio V, Linhares F, Solano R, Martin AC, Iglesias J, Leyva A,
RA   Paz-Ares J.
RT   A conserved MYB transcription factor involved in phosphate
RT   starvation signaling both in vascular plants and in unicellular
RT   algae.
RL   Genes Dev. 15: 2122-2133.(2001)
RD   PubMed: 11511543
XX
RA   Schunmann PH, Richardson AE, Smith FW, Delhaize E.
RT   Characterization of promoter expression patterns derived from the
RT   Pht1 phosphate transporter genes of barley (Hordeum vulgare L.).
RL   J Exp Bot. 55: 855-865. (2004)
RD   PubMed: 15020637
XX
RA   Schunmann PH, Richardson AE, Vickers CE, Delhaize E.
RT   Promoter analysis of the barley Pht1;1 phosphate transporter gene
RT   identifies regions controlling root expression and responsiveness
RT   to phosphate deprivation.
RL   Plant Physiol. 136: 4205-4214. (2004)
RD   PubMed: 15542491
XX
SQ

     GNATATNC
//
```

NAME: P1BS
Motif: GNATATNC

NAME: P1BS
Motif: GNATATNC

Link to PLACE data

co-expressed genes



Showing 11 t

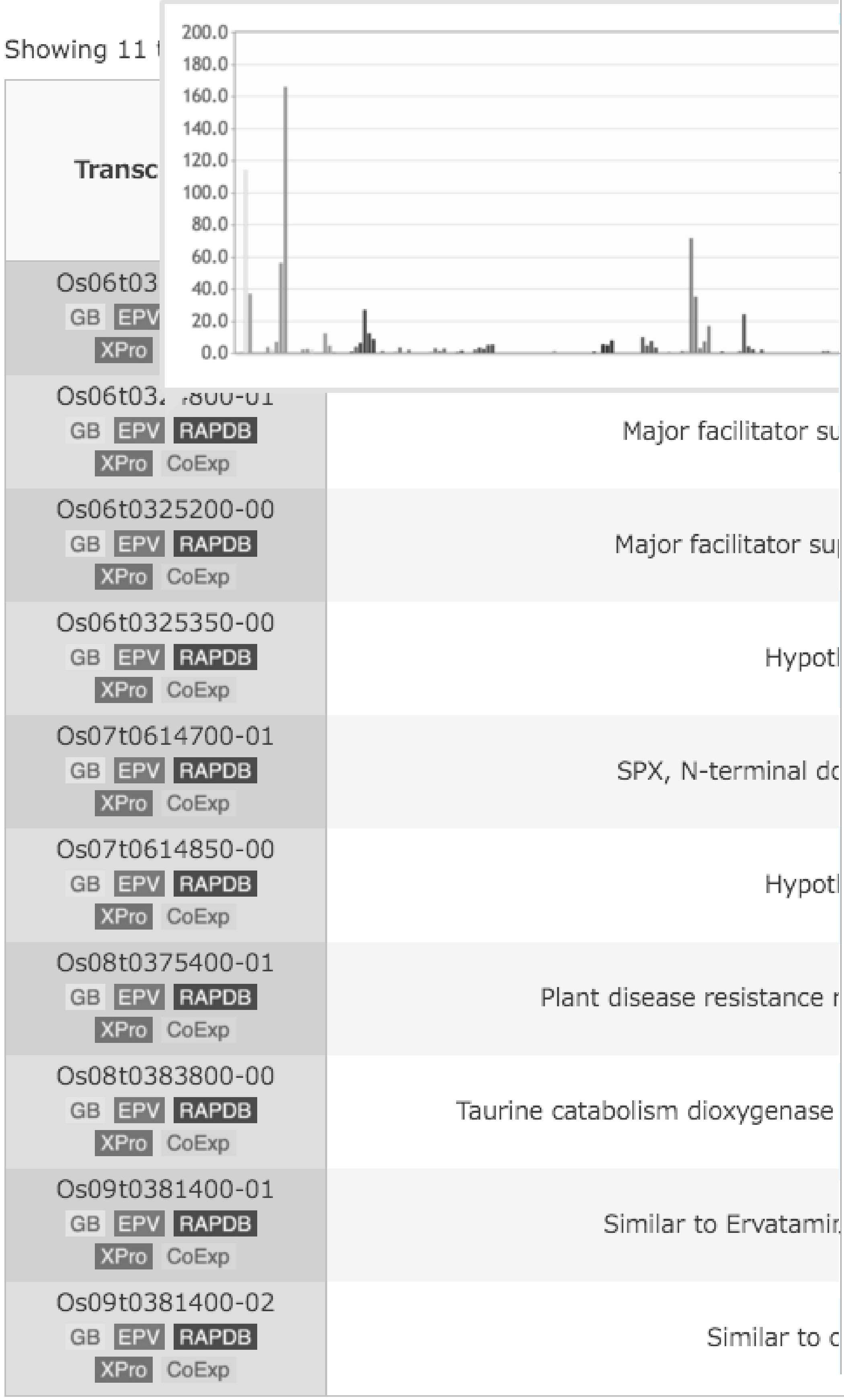
Show 10 entries

Search:

Transc	tion	Root			
		Low Phospate			
		5d		10d	
		FC	FDR	FC	FDR
Os06t03 GB EPV XPro	al gene.	19.0	0.000	54.3	0.000
Os06t03 800-01 GB EPV RAPDB XPro CoExp	Major facilitator superfamily protein. (PT9)	19.4	0.000	56.7	0.000
Os06t03252 00 GB EPV RAP XPro CoExp	Major facilitator superfamily protein. (PT10)	19.9	0.000	36.5	0.000
Os06t0325350-0 GB EPV RAPDB XPro CoExp		21.2	0.000	42.2	0.000
Os07t0614700-0 GB EPV RAPDB XPro CoExp		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

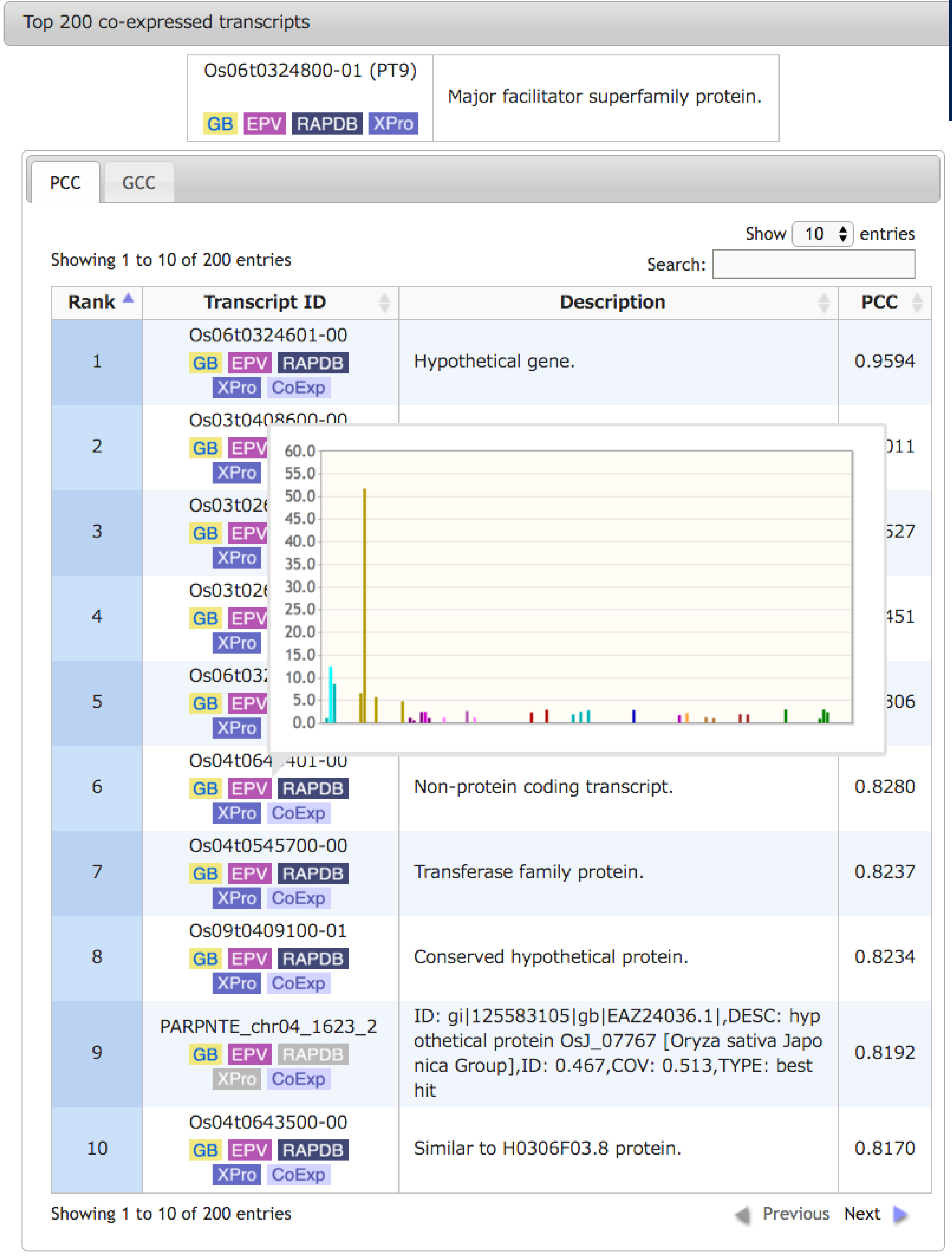
By clicking **CoExp** , you can get the list of co-expressed transcripts

co-exp



Showing 11 t

Transc	
Os06t03 GB EPV XPro	
Os06t03 800-01 GB EPV RAPDB XPro CoExp	Major facilitator su
Os06t0325200-00 GB EPV RAPDB XPro CoExp	Major facilitator su
Os06t0325350-00 GB EPV RAPDB XPro CoExp	Hypot
Os07t0614700-01 GB EPV RAPDB XPro CoExp	SPX, N-terminal dc
Os07t0614850-00 GB EPV RAPDB XPro CoExp	Hypot
Os08t0375400-01 GB EPV RAPDB XPro CoExp	Plant disease resistance r
Os08t0383800-00 GB EPV RAPDB XPro CoExp	Taurine catabolism dioxygenase
Os09t0381400-01 GB EPV RAPDB XPro CoExp	Similar to Ervatamir
Os09t0381400-02 GB EPV RAPDB XPro CoExp	Similar to c



Top 200 co-expressed transcripts

Os06t0324800-01 (PT9) GB EPV RAPDB XPro	Major facilitator superfamily protein.

Show 10 entries

Showing 1 to 10 of 200 entries

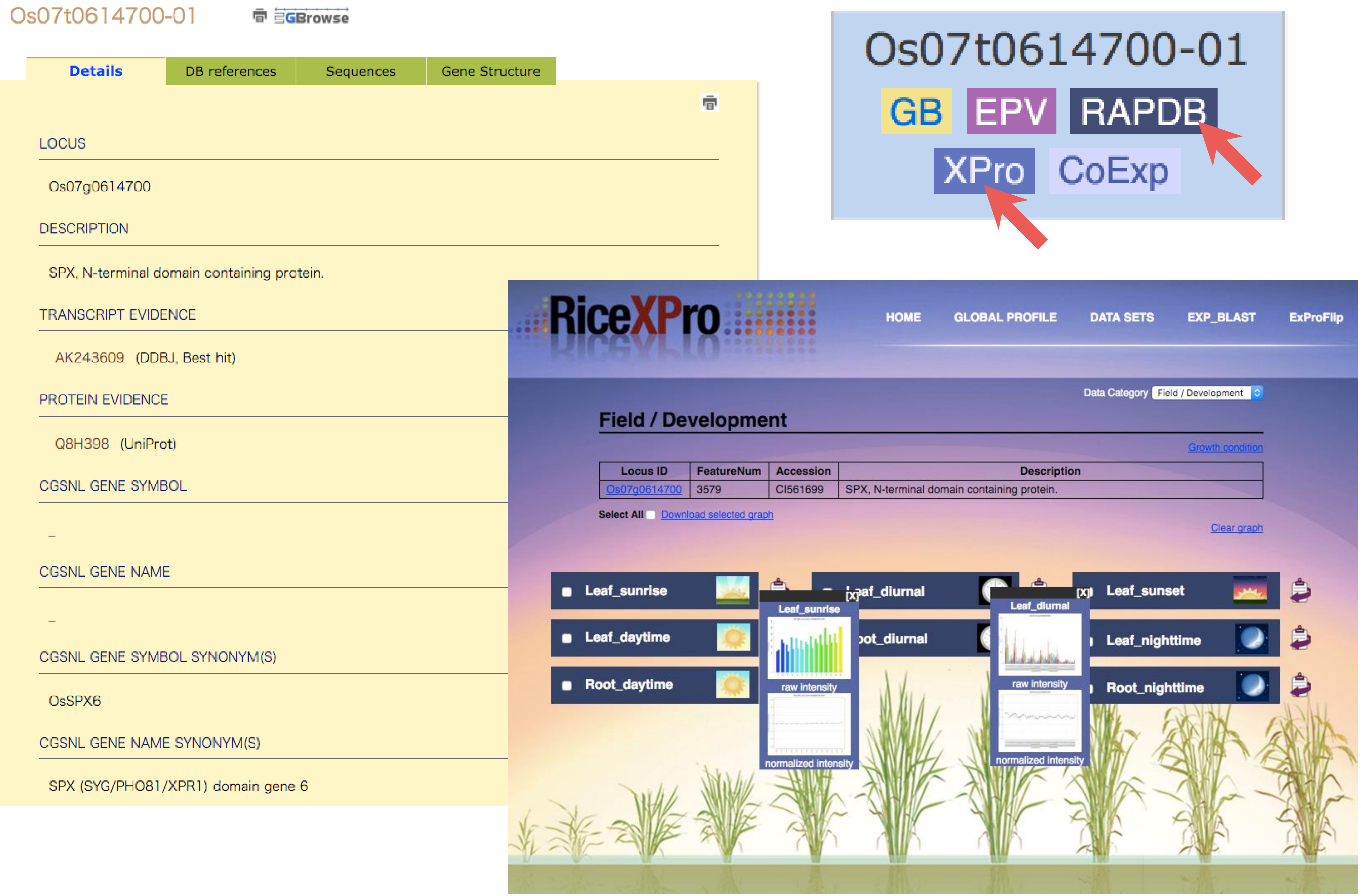
Search:

Rank	Transcript ID	Description	PCC
1	Os06t0324601-00 GB EPV RAPDB XPro CoExp	Hypothetical gene.	0.9594
2	Os03t0408600-00 GB EPV XPro		011
3	Os03t02 GB EPV XPro		527
4	Os03t02 GB EPV XPro		451
5	Os06t03 GB EPV XPro		306
6	Os04t064 401-00 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	PARPNTE_chr04_1623_2 GB EPV RAPDB XPro CoExp	ID: gi|125583105|gb|EAZ24036.1|,DESC: hypothetical protein OsJ_07767 [Oryza sativa Japonica 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

PCC: Pearson’s correlation of coefficient

Links to external databases



Os07t0614700-01

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

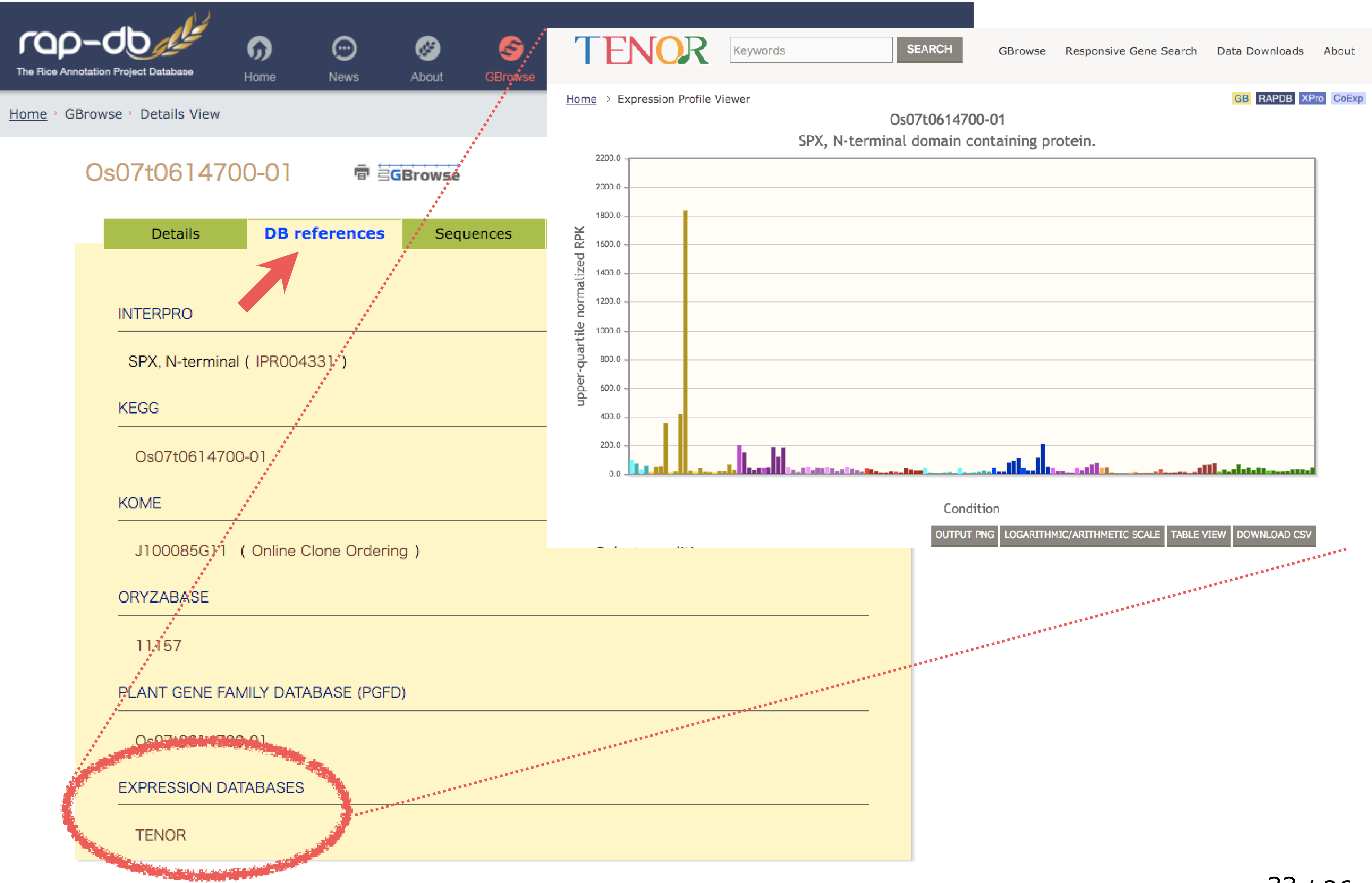
Os07t0614700-01

Data Category: Field / Development

Field / Development

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

Link to TENOR in RAP-DB



Home › GBrowse › Details View

Os07t0614700-01

INTERPRO

SPX, N-terminal (IPR004331)

KEGG

Os07t0614700-01

KOME

J100085G11 (Online Clone Ordering)

ORYZABASE

11157

PLANT GENE FAMILY DATABASE (PGFD)

Os07t0614700-01

EXPRESSION DATABASES

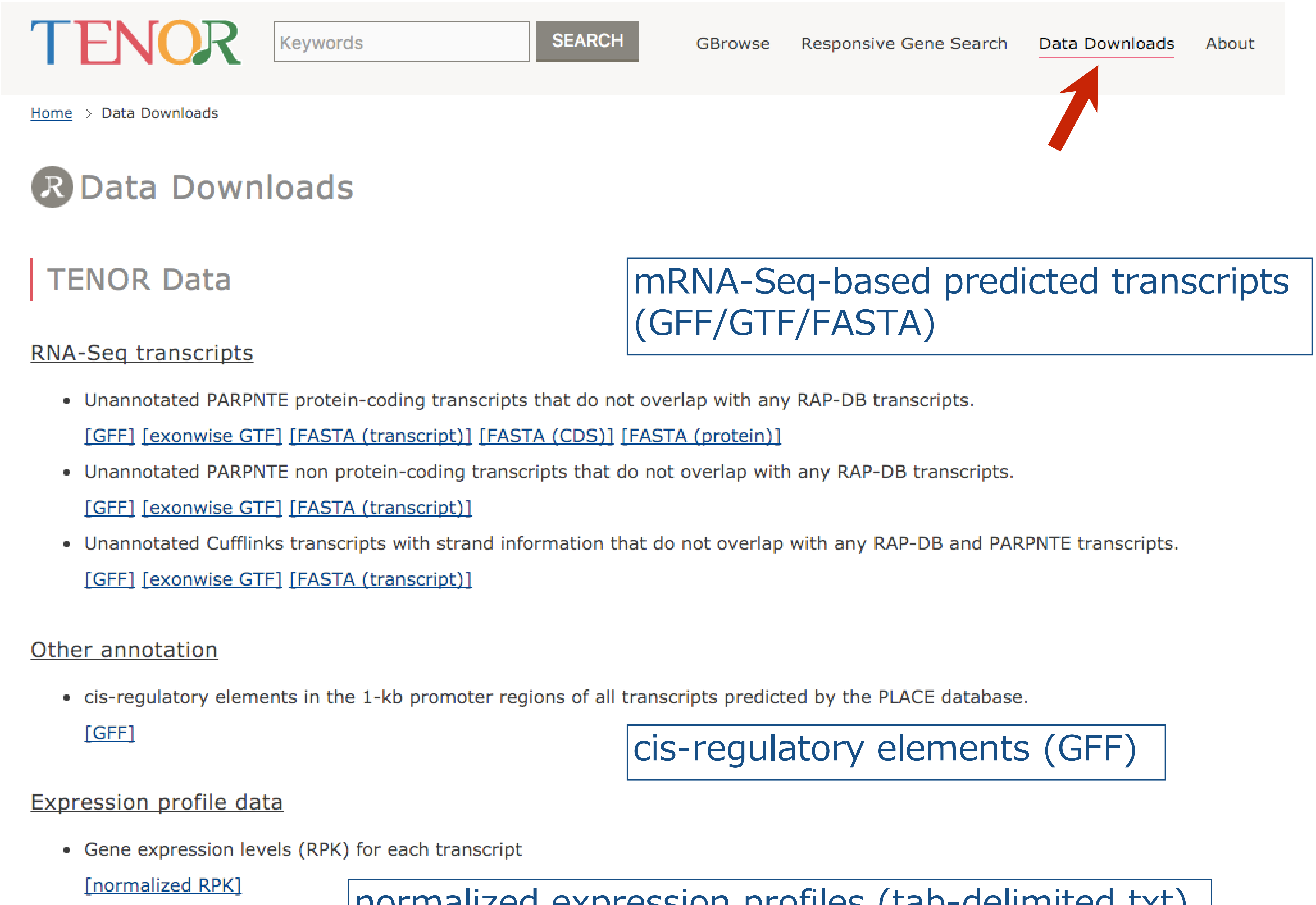
TENOR

Home › Expression Profile Viewer

Os07t0614700-01

SPX, N-terminal domain containing protein.

Downloadable data files



Home > Data Downloads

Data Downloads

TENOR Data

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

RNA-Seq transcripts

- Unannotated PARPNTE protein-coding transcripts that do not overlap with any RAP-DB transcripts.
  [GFF] [exonwise GTF] [FASTA (transcript)] [FASTA (CDS)] [FASTA (protein)]
- Unannotated PARPNTE 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 PARPNTE transcripts.
  [GFF] [exonwise GTF] [FASTA (transcript)]

Other annotation

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

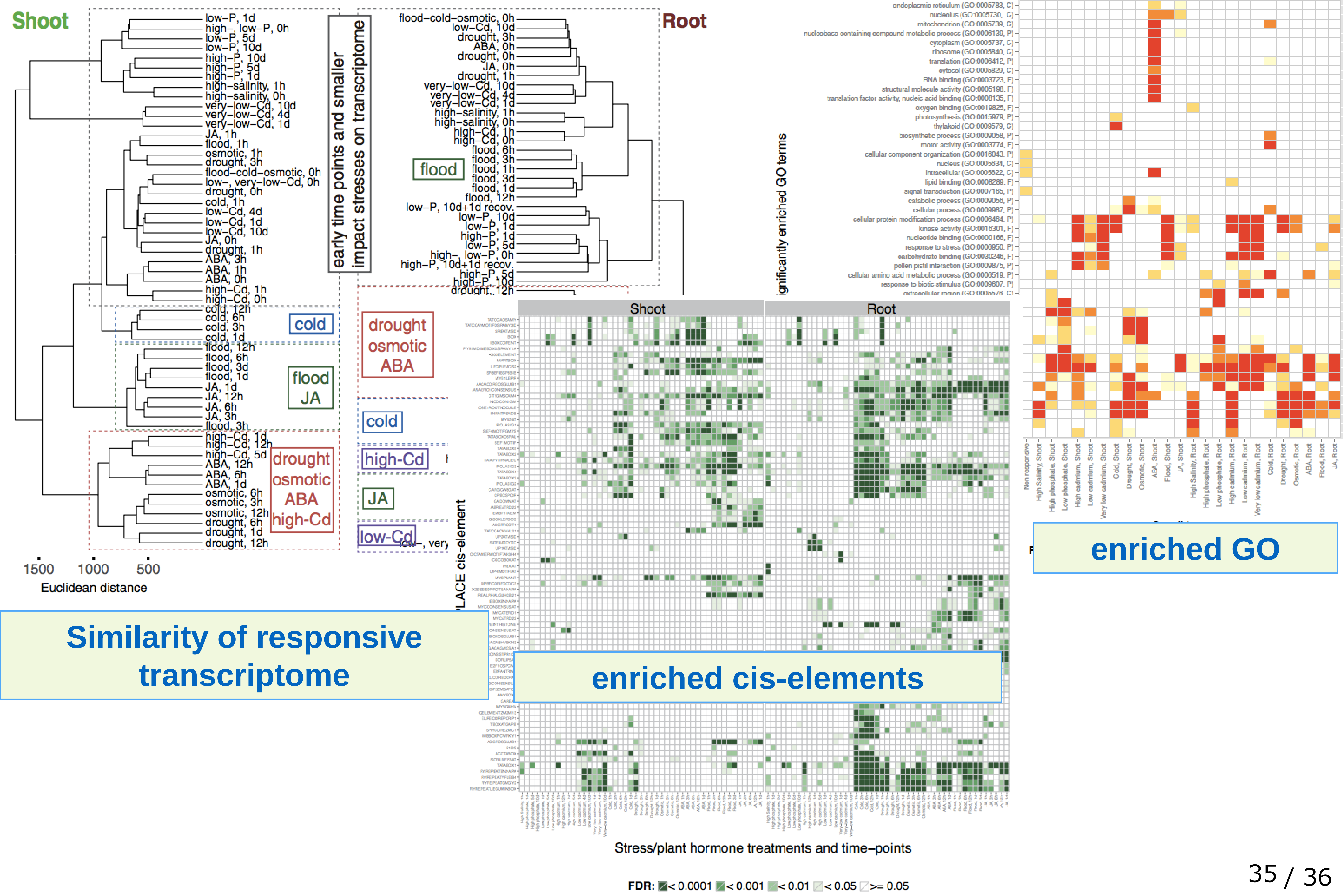
cis-regulatory elements (GFF)

Expression profile data

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

normalized expression profiles (tab-delimited txt)

TENOR paper

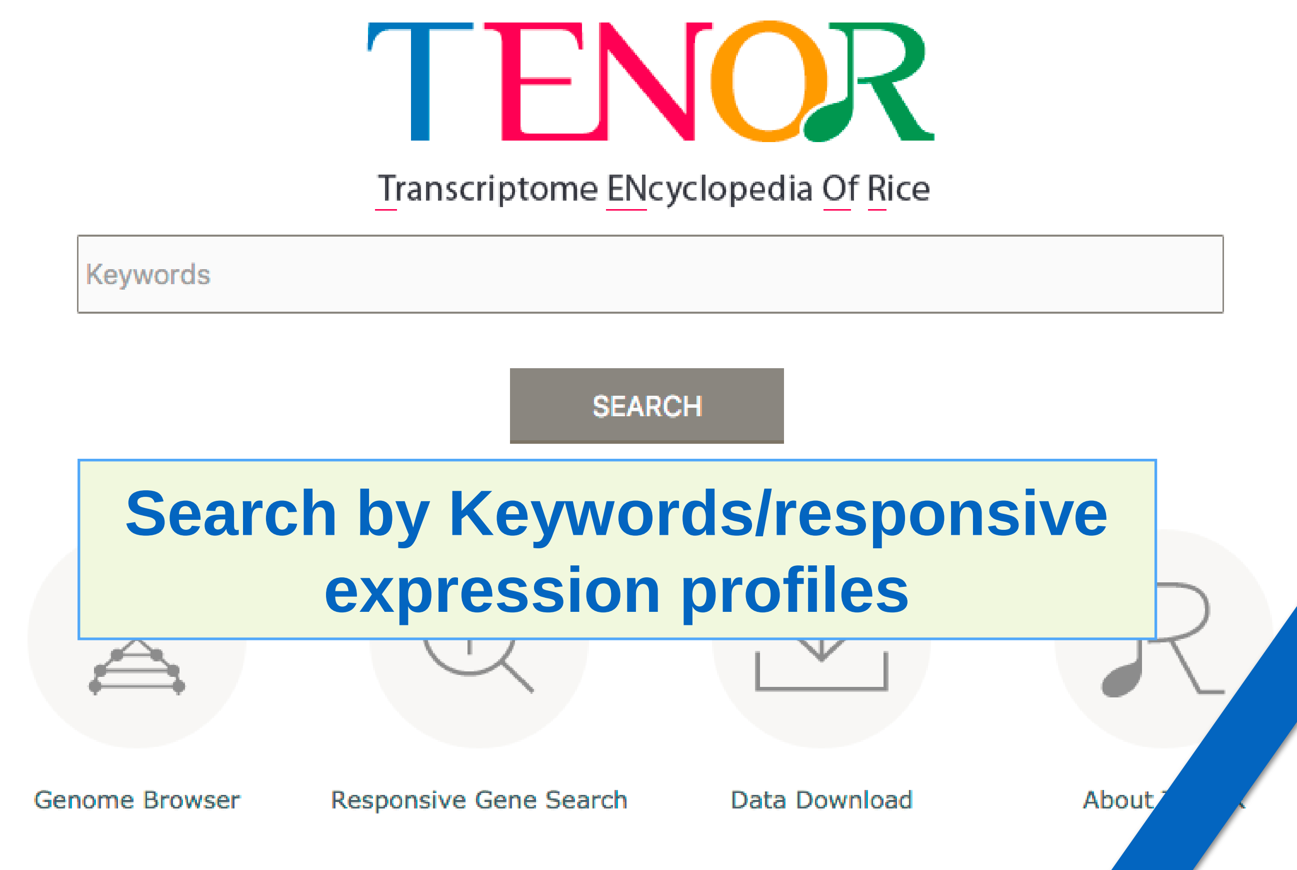


Similarity of responsive transcriptome

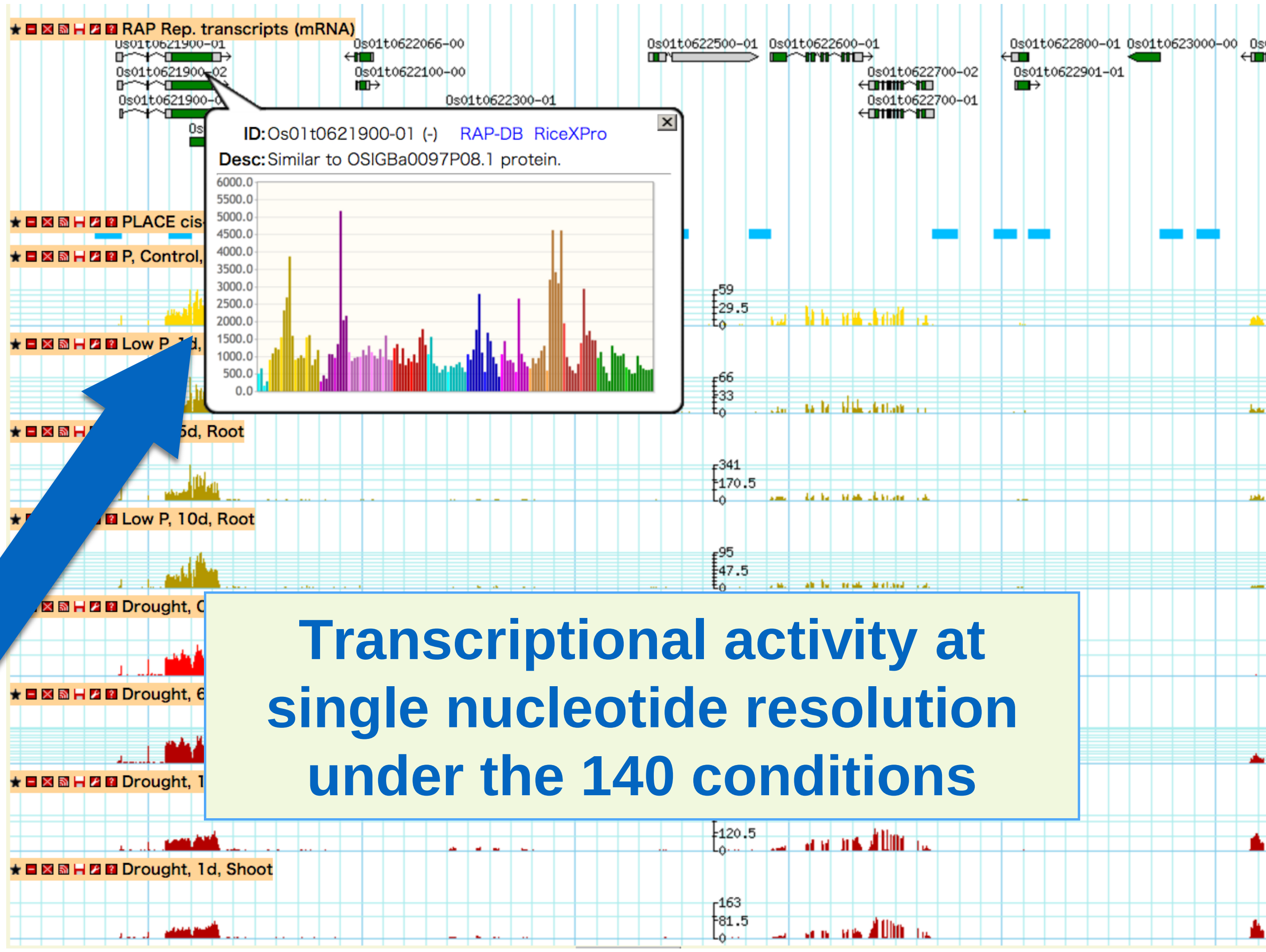
enriched cis-elements

enriched GO

Summary



Search by Keywords/responsive expression profiles

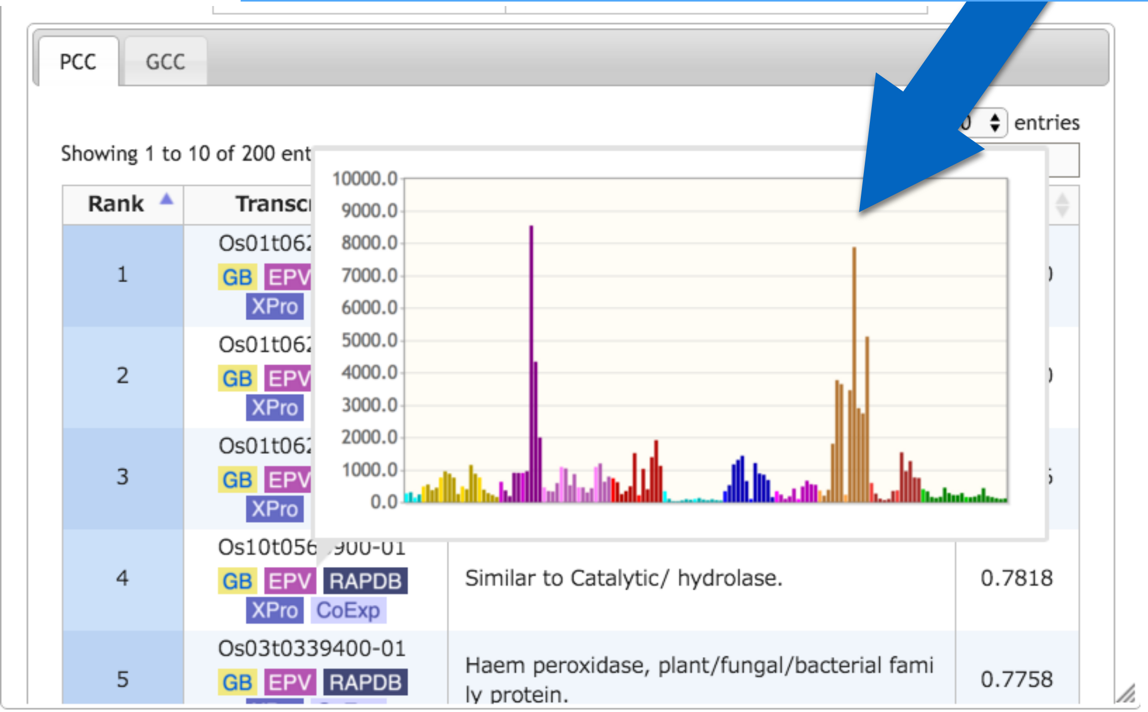


ID:Os01t0621900-01 (-) RAP-DB RiceXPro

Desc:Similar to OSIGBa0097P08.1 protein.

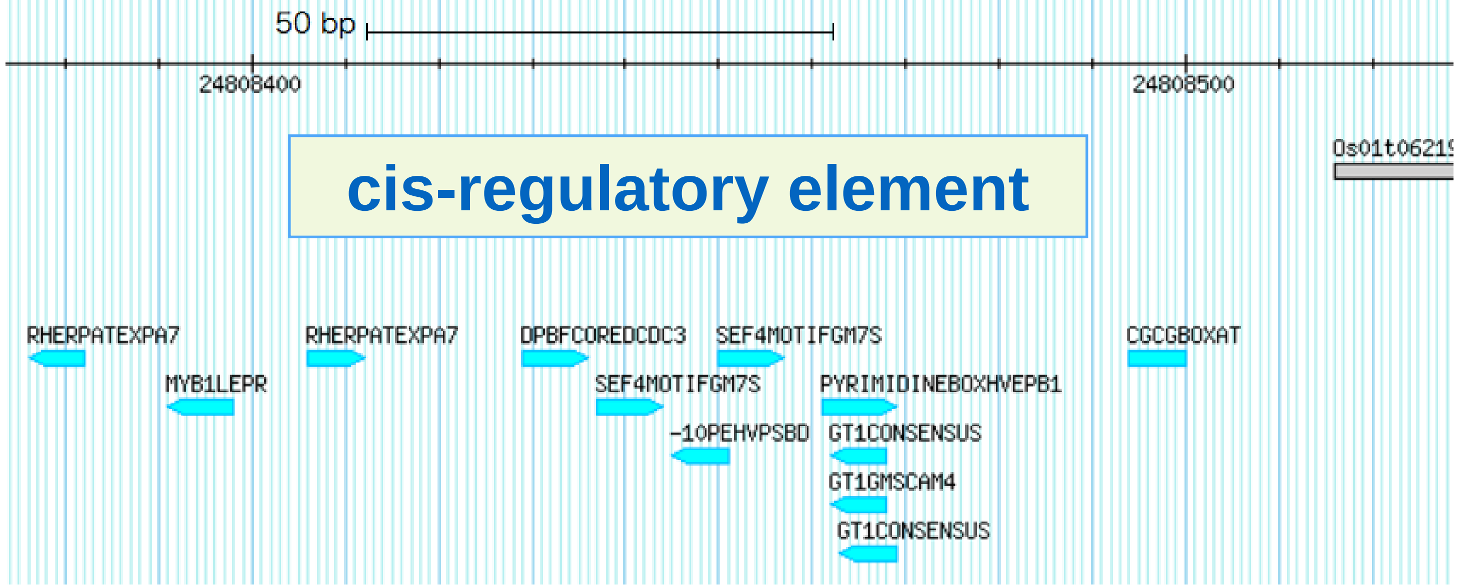
Transcriptional activity at single nucleotide resolution under the 140 conditions

Expression profiles & co-expression information



Showing 1 to 10 of 200 ent

Rank	Transc		
1	Os01t062 GB EPV XPro		)
2	Os01t062 GB EPV XPro		)
3	Os01t062 GB EPV XPro		5
4	Os10t056 900-01 GB EPV RAPDB XPro CoExp	Similar to Catalytic/ hydrolase.	0.7818
5	Os03t0339400-01 GB EPV RAPDB	Haem peroxidase, plant/fungal/bacterial family protein.	0.7758



cis-regulatory element