Plant & Animal Genome Conference XXIV
Computer Demo 1 (C05) January 09, 2016

National Institute of Agrobiological Sciences

TENOR

Database for Comprehensive mRNA-Seq Experiments in Rice

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TENOR development team

Sample & library preparation

- Youko Oono
- Jun Ogata
- Takashi Matsumoto

DB & software development

- Yoshihiro Kawahara
- Hironobu Wakimoto
- Takeshi Itoh

mRNA-Seq sequencing

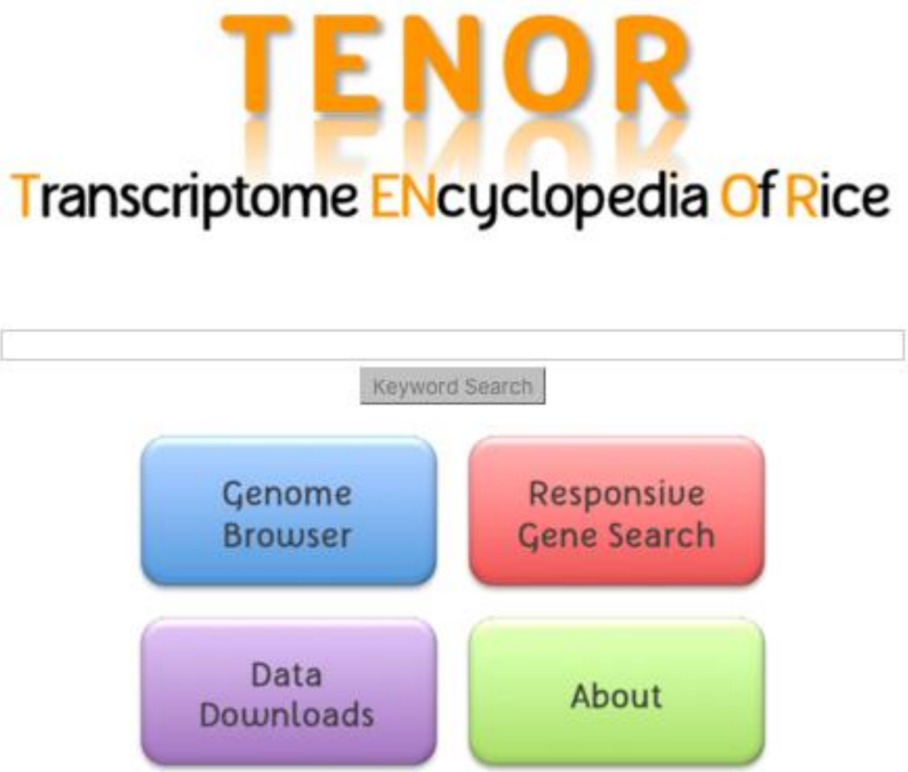
- Harumi Sasaki
- Satomi Mori
- Hiroyuki Kanamori

Funding

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

What is TENOR?

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. 2015 Nov 16
doi: 10.1093/pcp/pcv179

TENOR provides rice transcriptome information

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

×

of **Shoot** and **Root** tissues

(seedlings 14 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 stress and **2 plant hormone** treatment conditions (+ no treatment)

Salinity [a]

Low Pi [b]

High Pi [b]

High Cd [c]

Low Cd

Very-low Cd

Drought

Flood

Osmotic

ABA

JA

No treatment

[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***

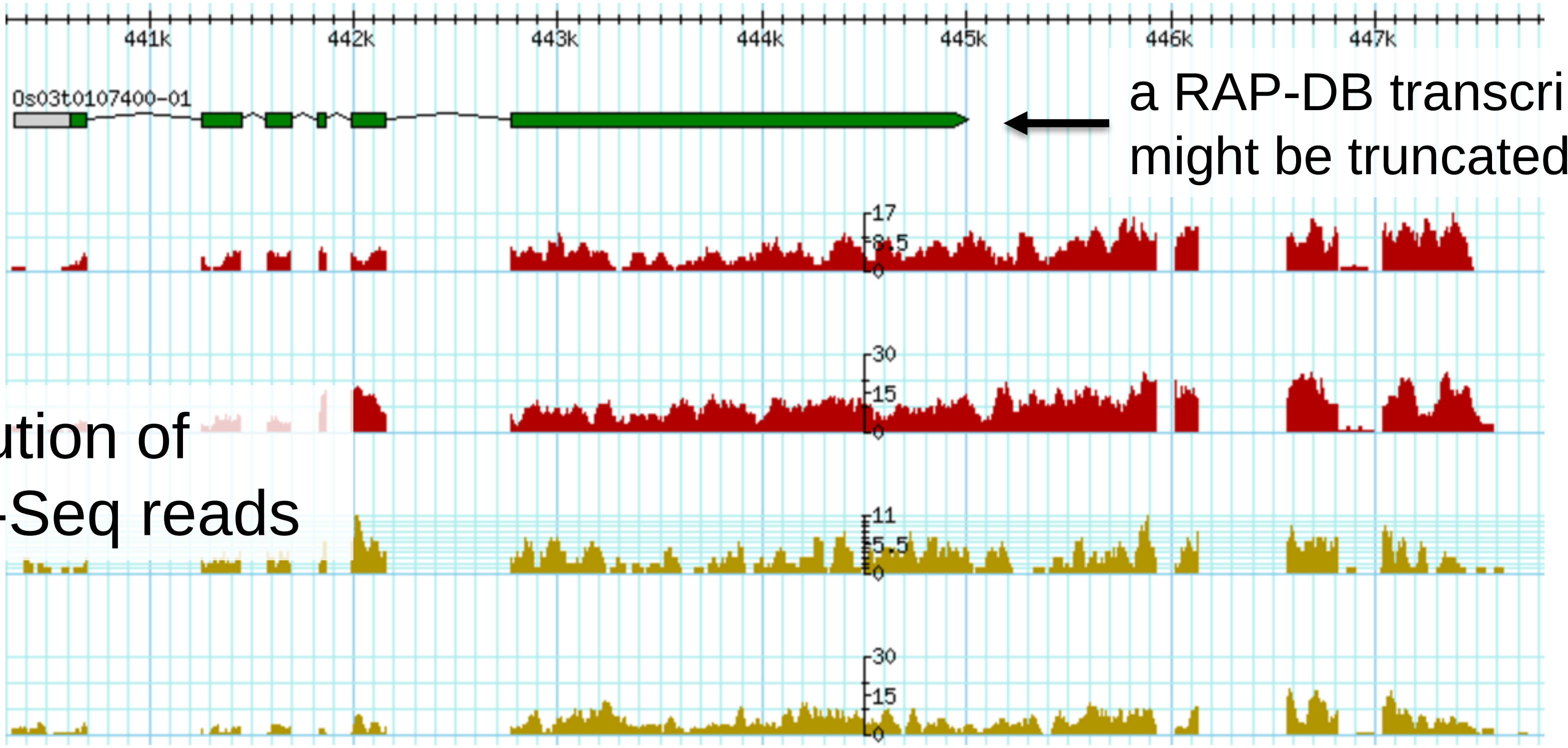
All experiments were performed
at **a single laboratory**
under **standardized conditions**
using **a single analysis platform (mRNA-Seq)**

- a highly reliable resource
- a standard data set

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

Use of **mRNA-Seq technique** provides

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

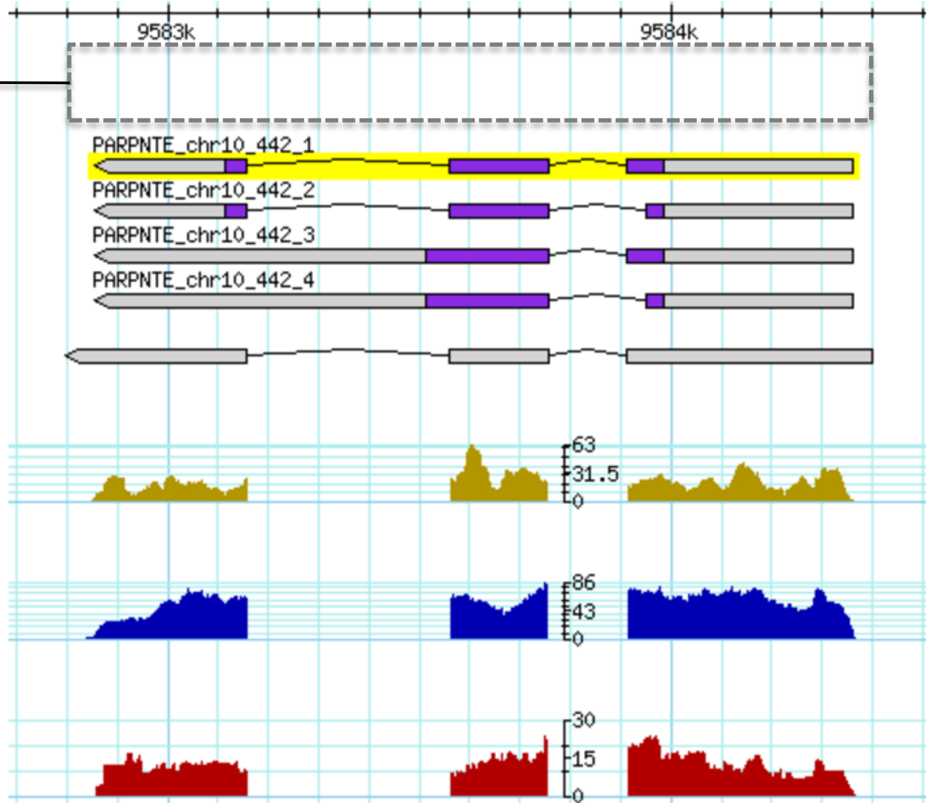


a RAP-DB transcript might be truncated

Distribution of mRNA-Seq reads

Use of **mRNA-Seq technique** provides

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



No transcripts in RAP-DB

RNA-Seq based predicted transcripts (Cufflinks & PARPNTE)

Distribution of RNA-Seq reads

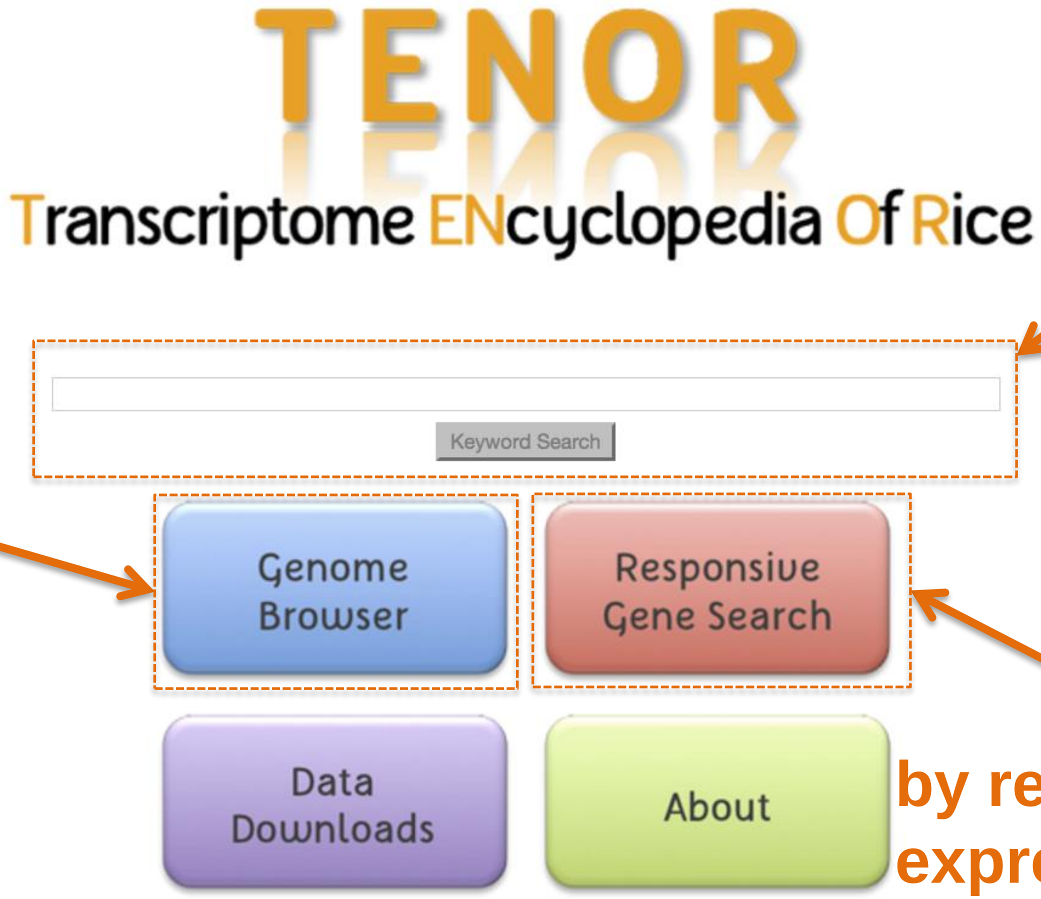
Low P, 5d, Root

Cold, 1d, Root

Drought, 1d, Root

Functions in TENOR

Three entrances on the top page

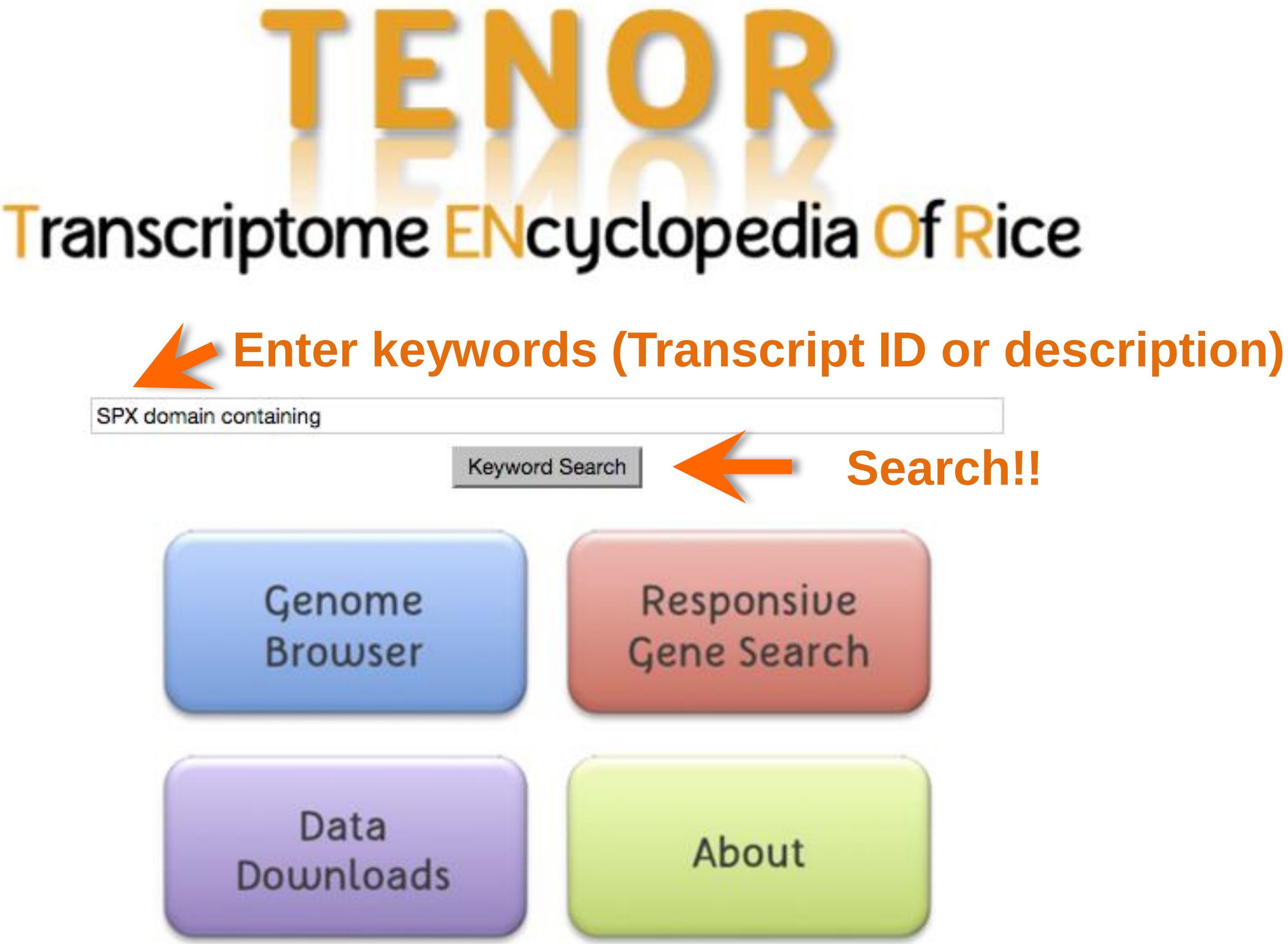


by Keywords

by genomic coordinates

by responsive expression profiles

Search by Keywords



SPX domain containing

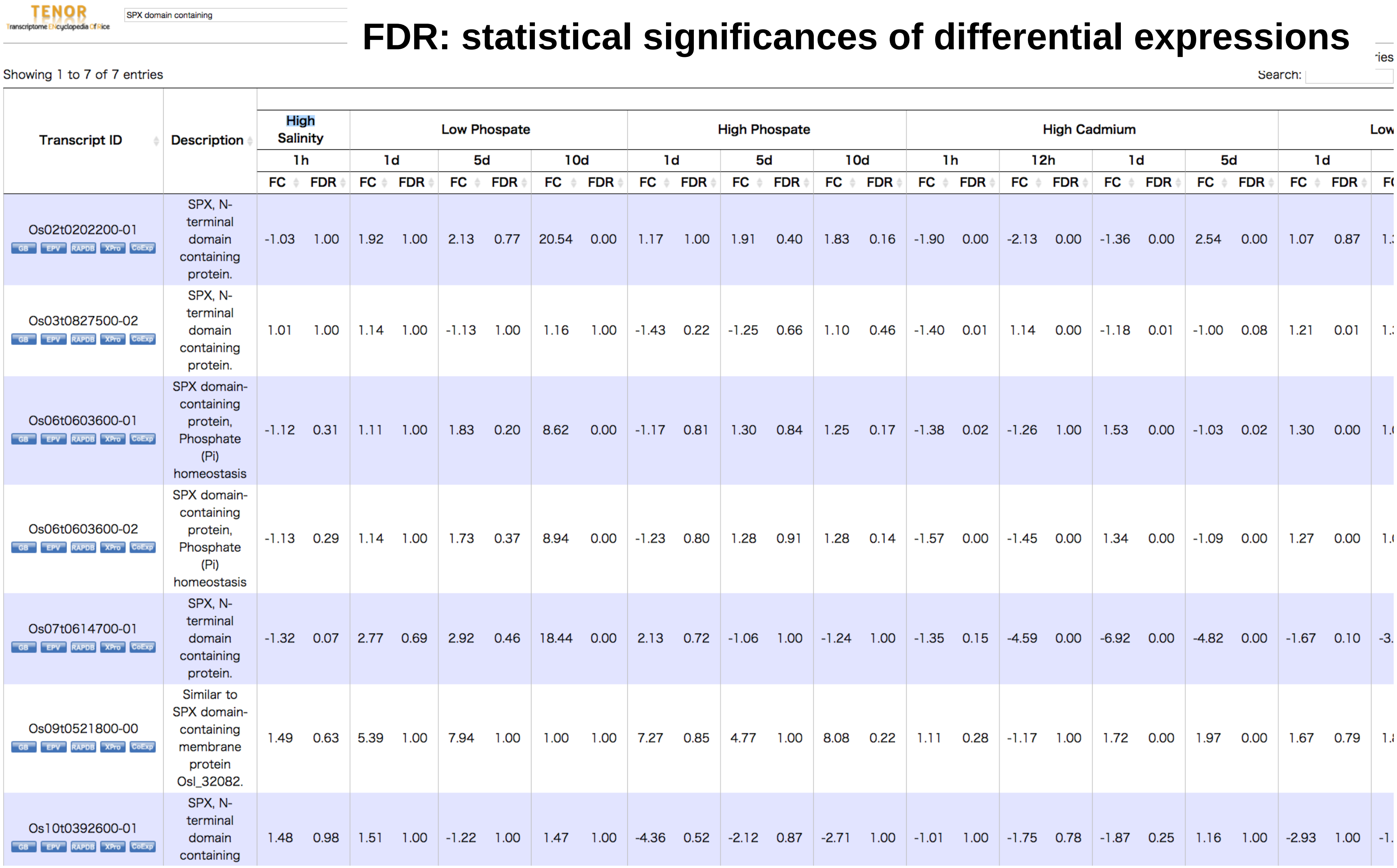
Enter keywords (Transcript ID or description)

Search!!

Search results in a table

FC: fold-changes relative to the control samples

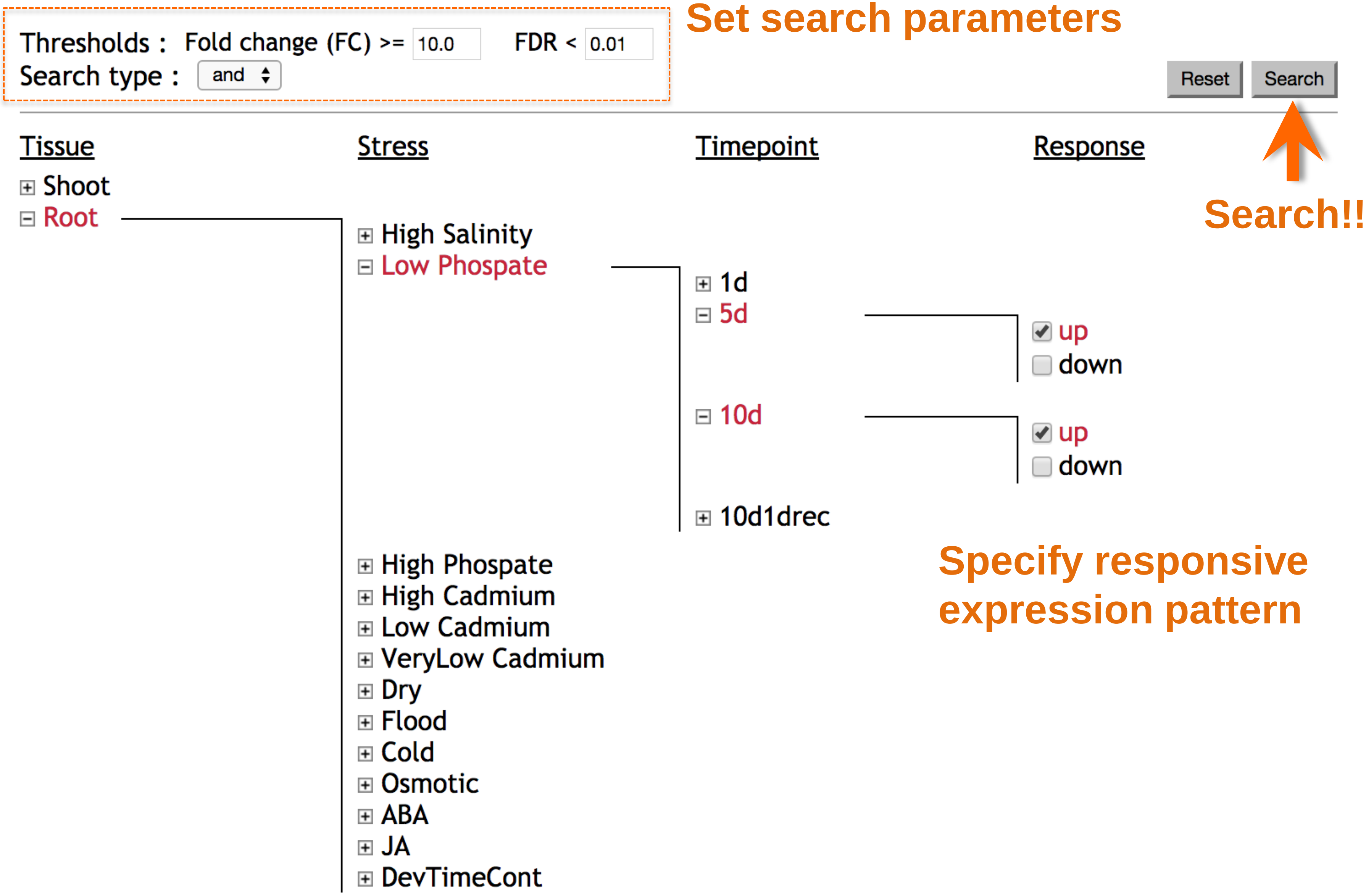
FDR: statistical significances of differential expressions



Showing 1 to 7 of 7 entries

Transcript ID	Description	High Salinity		Low Phospate						High Phospate						High Cadmium								Low		
		1h		1d		5d		10d		1d		5d		10d		1h		12h		1d		5d		1d		
		FC	FDR	FC	FDR	FC	FDR	FC	FDR	FC	FDR	FC	FDR	FC	FDR	FC	FDR	FC	FDR	FC	FDR	FC	FDR	FC	FDR	F
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	-1.36	0.00	2.54	0.00	1.07	0.87	1.
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	-1.18	0.01	-1.00	0.08	1.21	0.01	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	1.53	0.00	-1.03	0.02	1.30	0.00	1.
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	1.34	0.00	-1.09	0.00	1.27	0.00	1.
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	-6.92	0.00	-4.82	0.00	-1.67	0.10	-3.
Os09t0521800-00 GB EPV RAPDB XPro CoExp	Similar to SPX domain-containing membrane protein Osl_32082.	1.49	0.63	5.39	1.00	7.94	1.00	1.00	1.00	7.27	0.85	4.77	1.00	8.08	0.22	1.11	0.28	-1.17	1.00	1.72	0.00	1.97	0.00	1.67	0.79	1.
Os10t0392600-01 GB EPV RAPDB XPro CoExp	SPX, N-terminal domain containing	1.48	0.98	1.51	1.00	-1.22	1.00	1.47	1.00	-4.36	0.52	-2.12	0.87	-2.71	1.00	-1.01	1.00	-1.75	0.78	-1.87	0.25	1.16	1.00	-2.93	1.00	-1.

Search by Responsive expression profile



Set search parameters

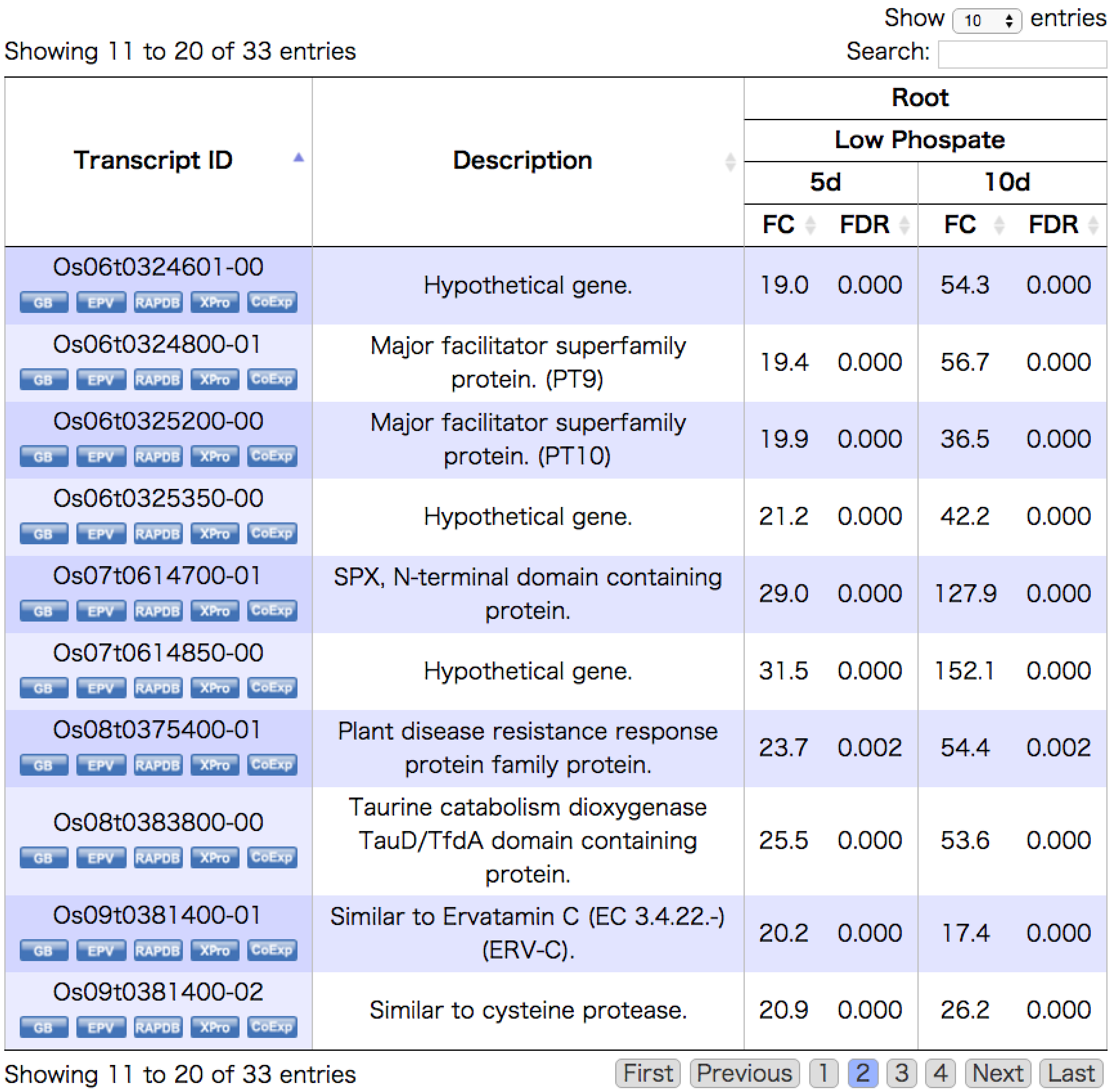
Thresholds : Fold change (FC) >= 10.0 FDR < 0.01
Search type : and

Search!!

- ⊞ 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

Specify responsive expression pattern

Search results in a table

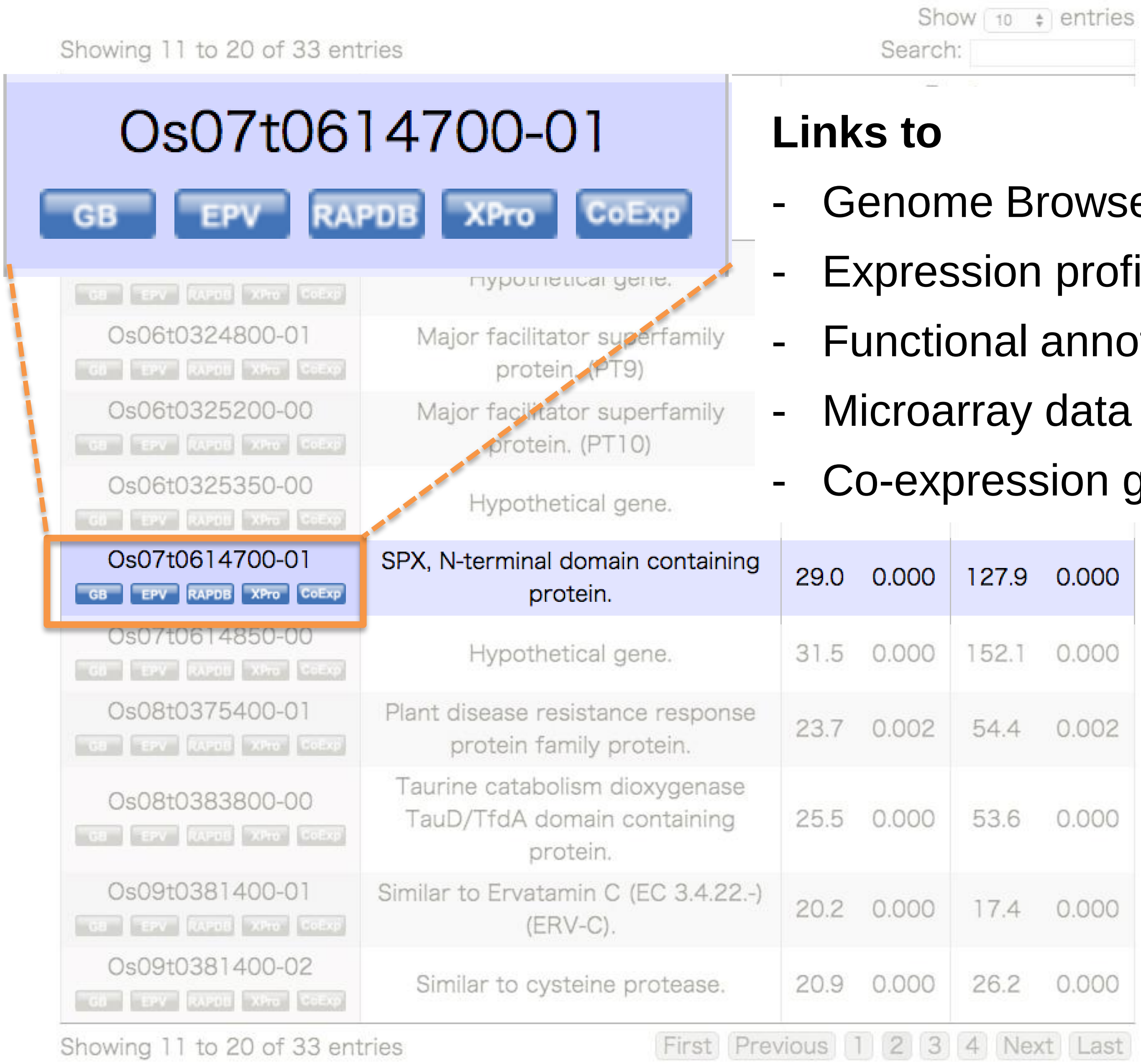


Showing 11 to 20 of 33 entries

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

Showing 11 to 20 of 33 entries

Links to other viewers and database



Show 10 entries

Search:

Showing 11 to 20 of 33 entries

	Hypothetical gene.				
Os06t0324800-01	Major facilitator superfamily protein. (PT9)				
Os06t0325200-00	Major facilitator superfamily protein. (PT10)				
Os06t0325350-00	Hypothetical gene.				
Os07t0614700-01	SPX, N-terminal domain containing protein.	29.0	0.000	127.9	0.000
Os07t0614850-00	Hypothetical gene.	31.5	0.000	152.1	0.000
Os08t0375400-01	Plant disease resistance response protein family protein.	23.7	0.002	54.4	0.002
Os08t0383800-00	Taurine catabolism dioxygenase TauD/TfdA domain containing protein.	25.5	0.000	53.6	0.000
Os09t0381400-01	Similar to Ervatamin C (EC 3.4.22.-) (ERV-C).	20.2	0.000	17.4	0.000
Os09t0381400-02	Similar to cysteine protease.	20.9	0.000	26.2	0.000

Showing 11 to 20 of 33 entries

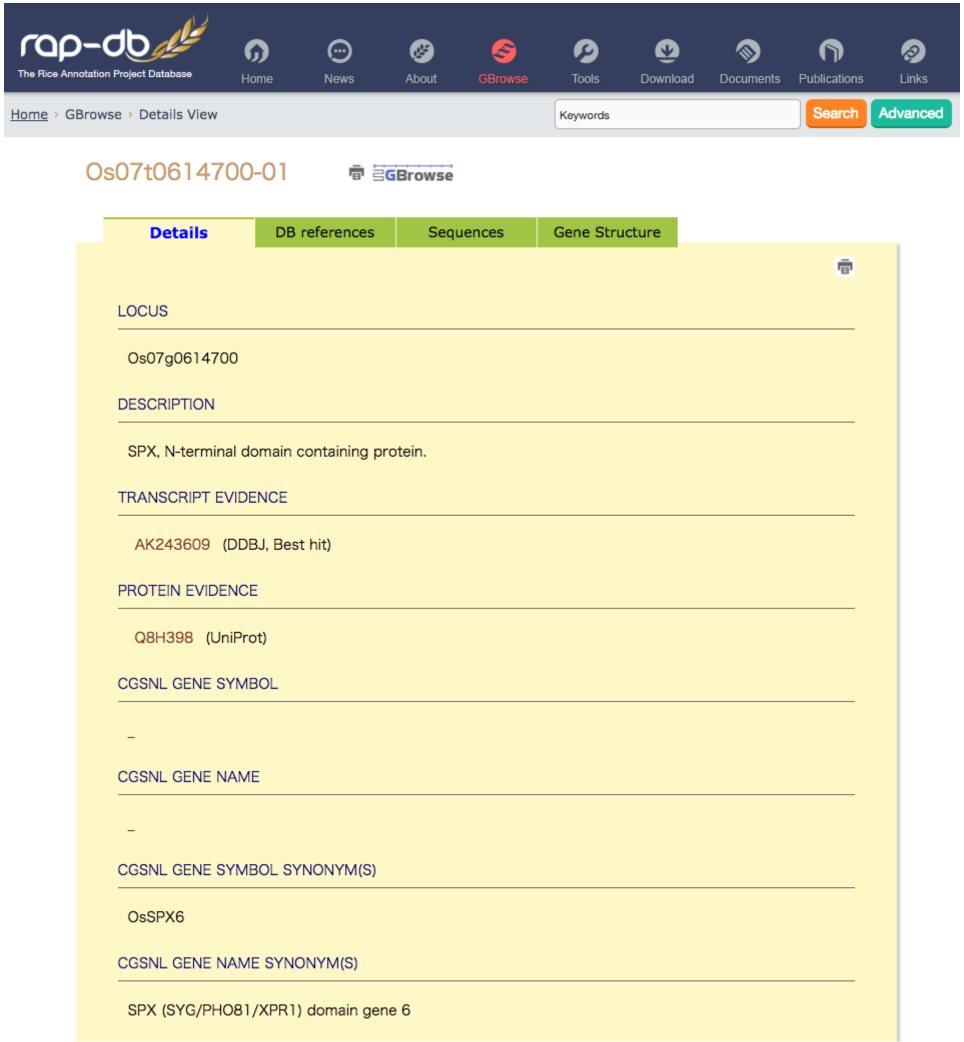
First Previous 1 2 3 4 Next Last

Links to

- Genome Browser (GB: GBrowse)
- Expression profile view (EPV)
- Functional annotation (RAP-DB)
- Microarray data (XPro: RiceXPro)
- Co-expression gene list (CoExp)

RAP-DB:

Functional annotation



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)

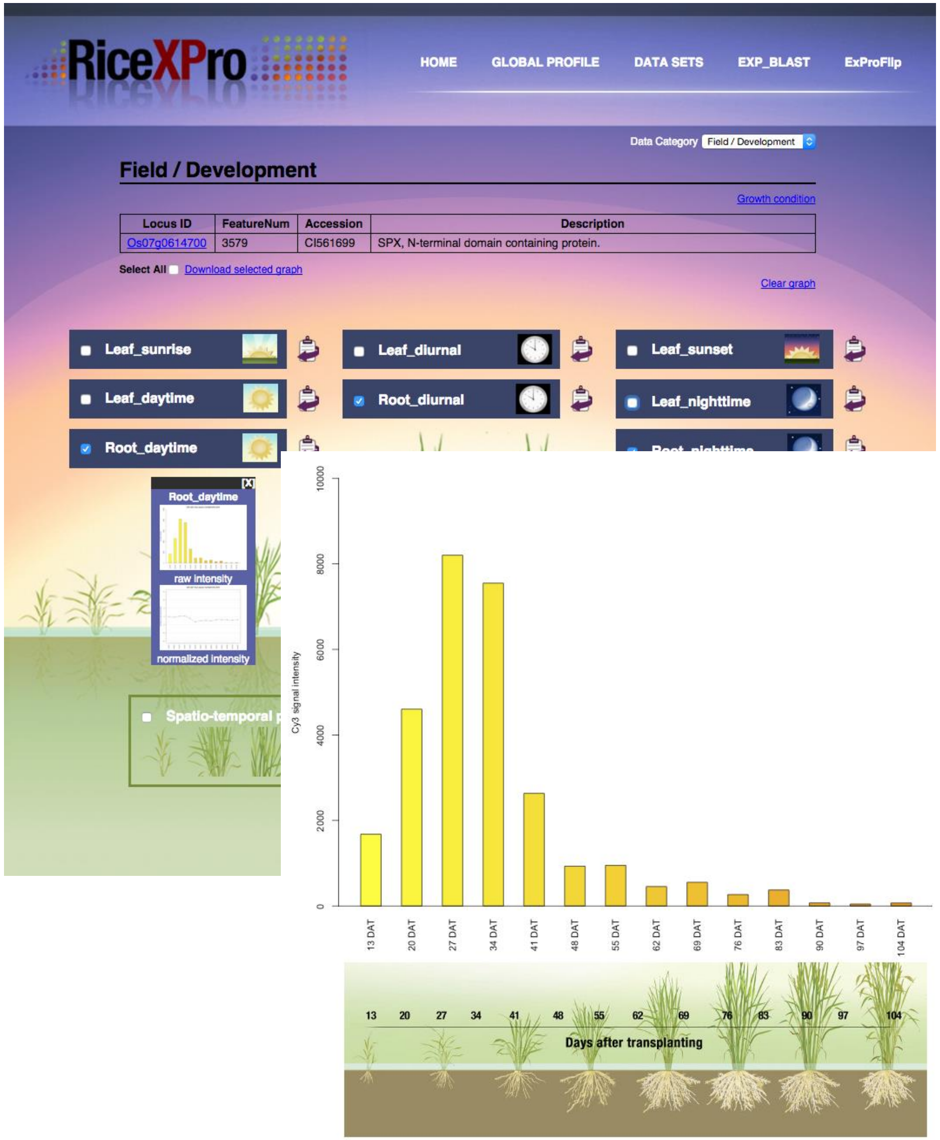
OsSPX6

CGSNL GENE NAME SYNONYM(S)

SPX (SYG/PHO81/XPR1) domain gene 6

RiceXPro:

Expression data by Microarray

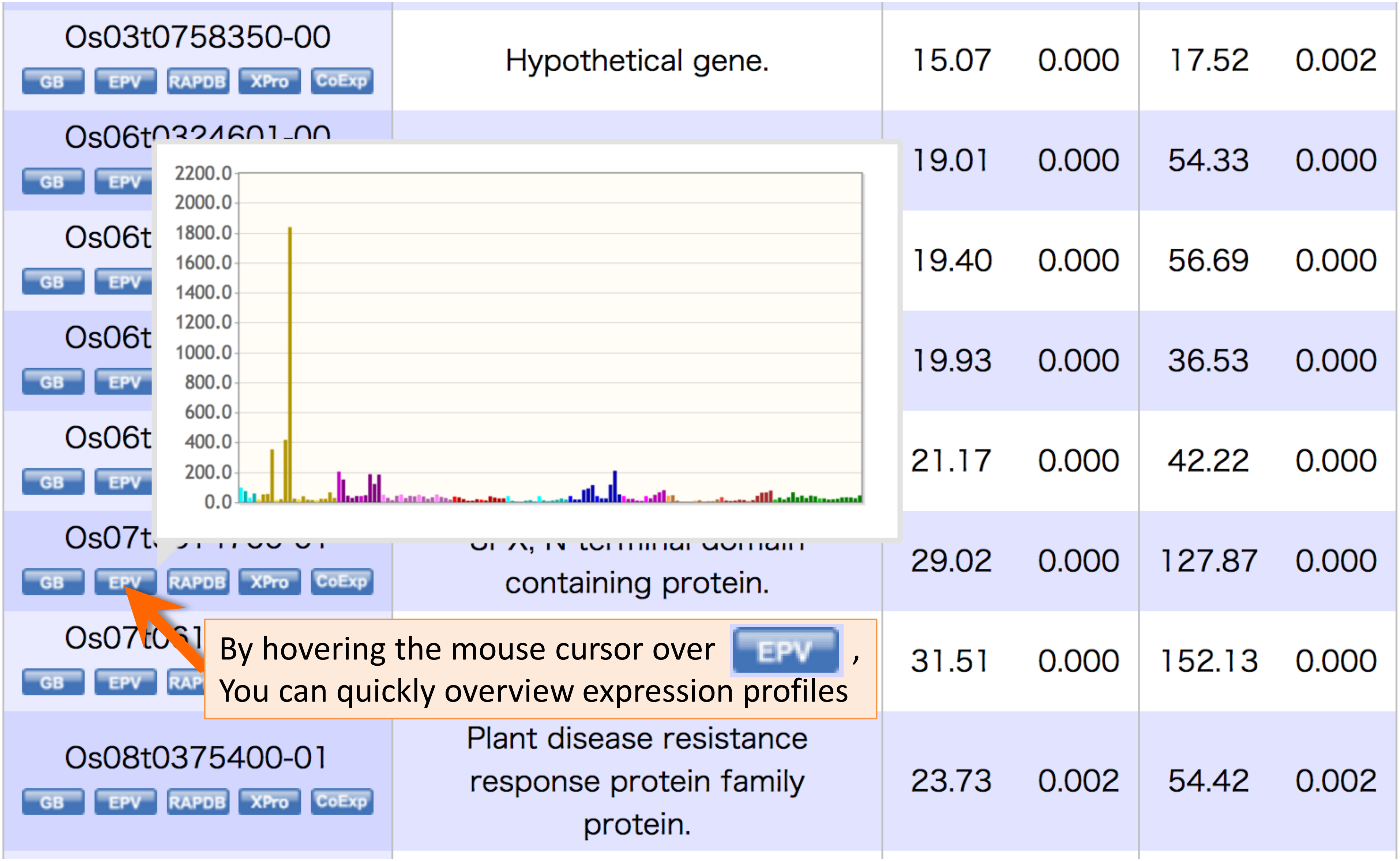


Data Category: Field / Development

Field / Development

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

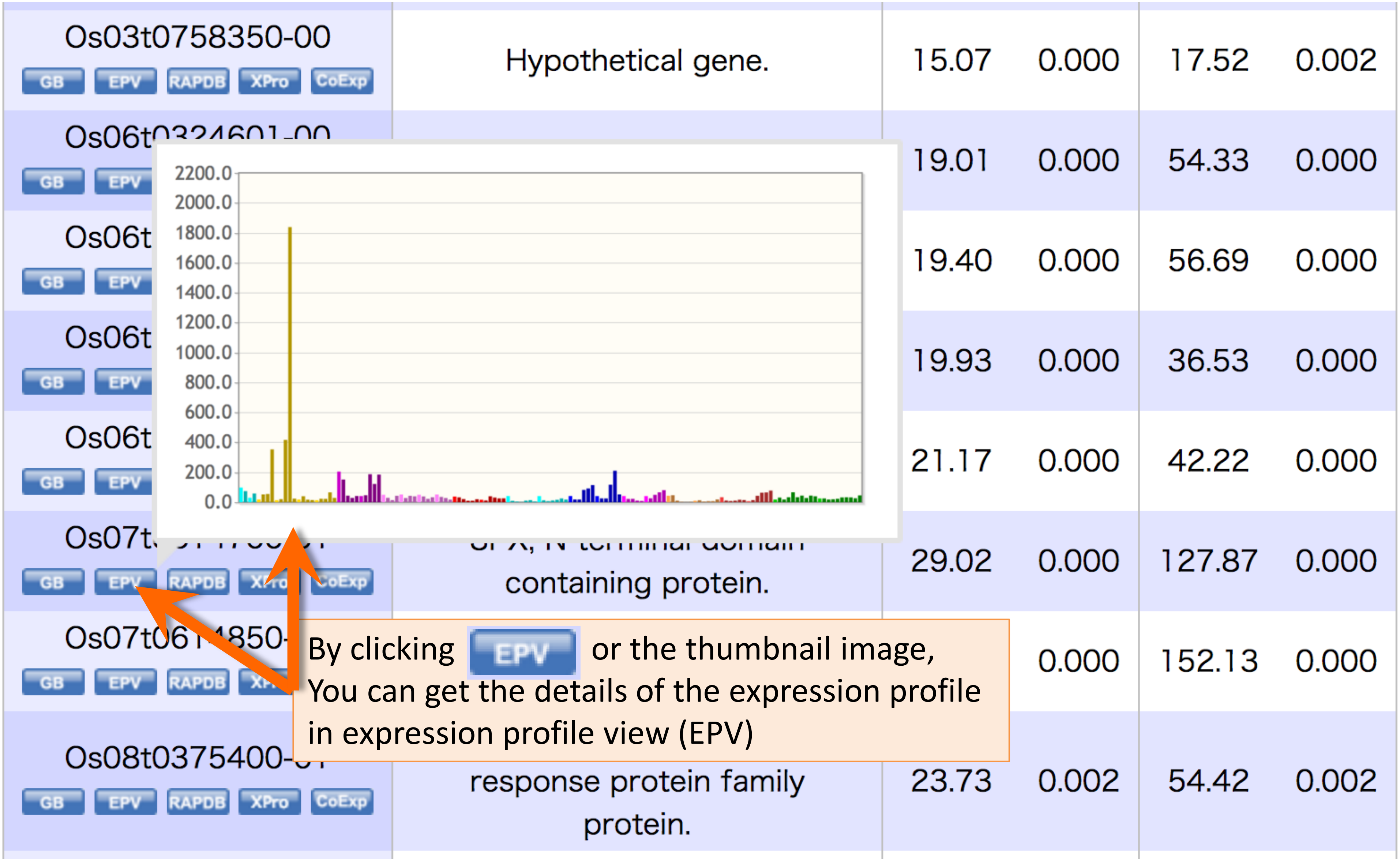
Quick overview of expression profiles



Os03t0758350-00 GB EPV RAPDB XPro CoExp	Hypothetical gene.	15.07	0.000	17.52	0.002
Os06t0324601-00 GB EPV		19.01	0.000	54.33	0.000
Os06t GB EPV		19.40	0.000	56.69	0.000
Os06t GB EPV		19.93	0.000	36.53	0.000
Os06t GB EPV		21.17	0.000	42.22	0.000
Os07t GB EPV RAPDB XPro CoExp	containing protein.	29.02	0.000	127.87	0.000
Os07t0 GB EPV RAP		31.51	0.000	152.13	0.000
Os08t0375400-01 GB EPV RAPDB XPro CoExp	Plant disease resistance response protein family protein.	23.73	0.002	54.42	0.002

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

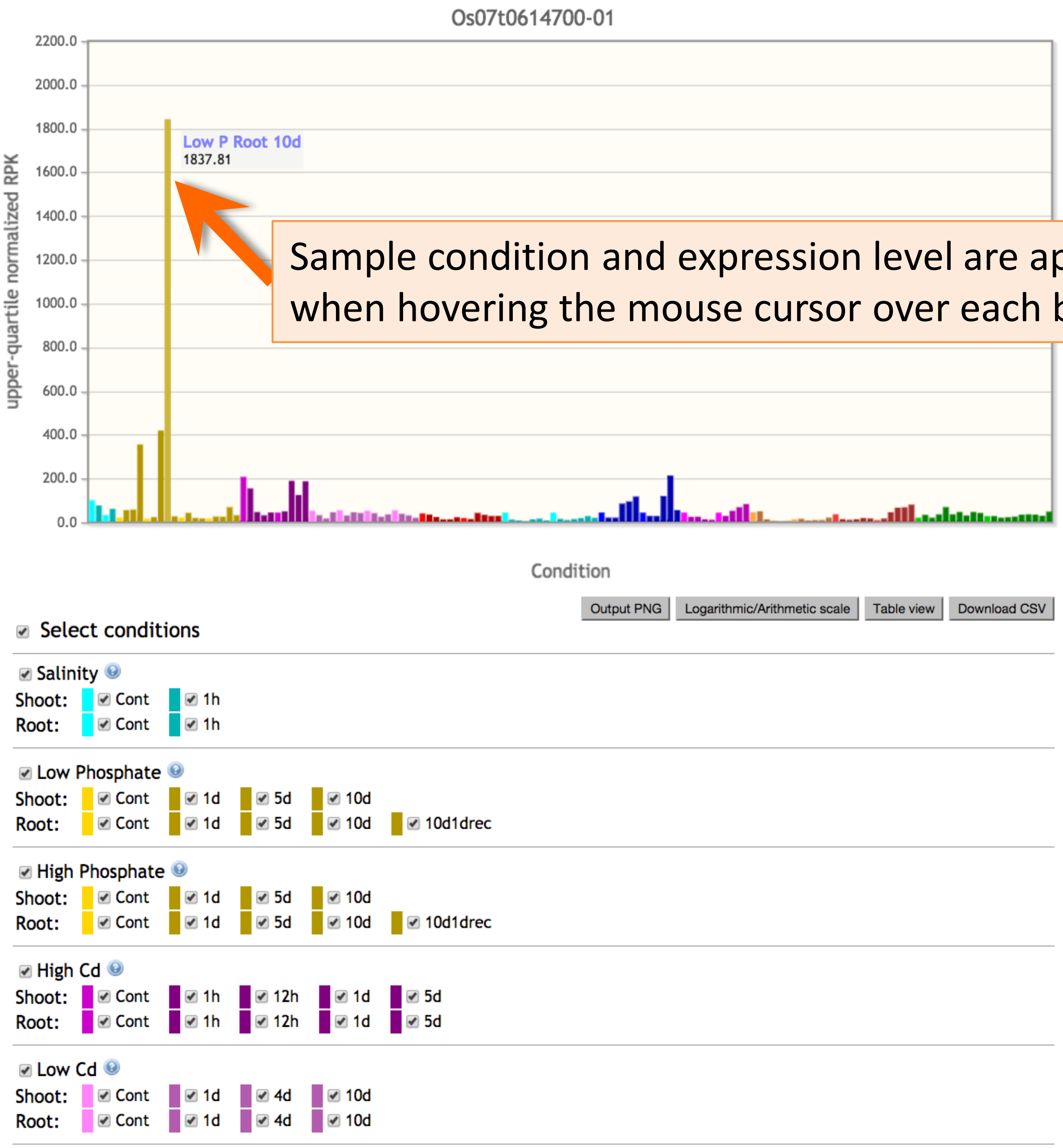
Quick overview of expression profiles



Os03t0758350-00 GB EPV RAPDB XPro CoExp	Hypothetical gene.	15.07	0.000	17.52	0.002
Os06t0324601-00 GB EPV		19.01	0.000	54.33	0.000
Os06t GB EPV		19.40	0.000	56.69	0.000
Os06t GB EPV		19.93	0.000	36.53	0.000
Os06t GB EPV		21.17	0.000	42.22	0.000
Os07t GB EPV RAPDB XPro CoExp	containing protein.	29.02	0.000	127.87	0.000
Os07t06 850- GB EPV RAPDB			0.000	152.13	0.000
Os08t0375400- GB EPV RAPDB XPro CoExp	response protein family protein.	23.73	0.002	54.42	0.002

By clicking EPV or the thumbnail image,
You can get the details of the expression profile
in expression profile view (EPV)

Expression profile view (EPV)



Sample condition and expression level are appeared, when hovering the mouse cursor over each bar

☑ Select conditions

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

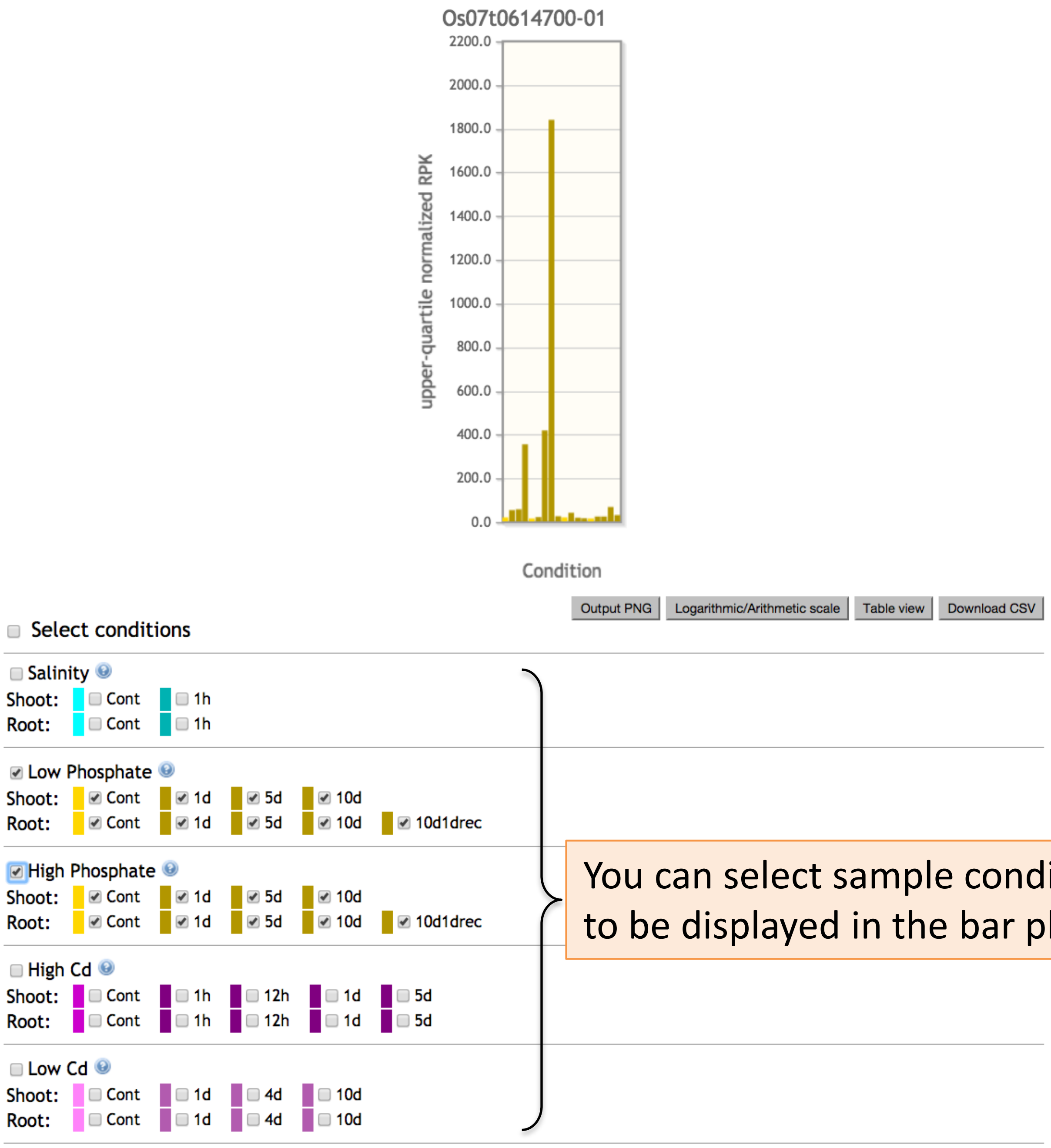
☑ Low Phosphate
Shoot: ■ ☑ Cont ■ ☑ 1d ■ ☑ 5d ■ ☑ 10d
Root: ■ ☑ Cont ■ ☑ 1d ■ ☑ 5d ■ ☑ 10d ■ ☑ 10d1drec

☑ 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

☑ Low Cd
Shoot: ■ ☑ Cont ■ ☑ 1d ■ ☑ 4d ■ ☑ 10d
Root: ■ ☑ Cont ■ ☑ 1d ■ ☑ 4d ■ ☑ 10d

Functions in Expression profile view



☐ Select conditions

☐ Salinity
Shoot: ■ ☐ Cont ■ ☐ 1h
Root: ■ ☐ Cont ■ ☐ 1h

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

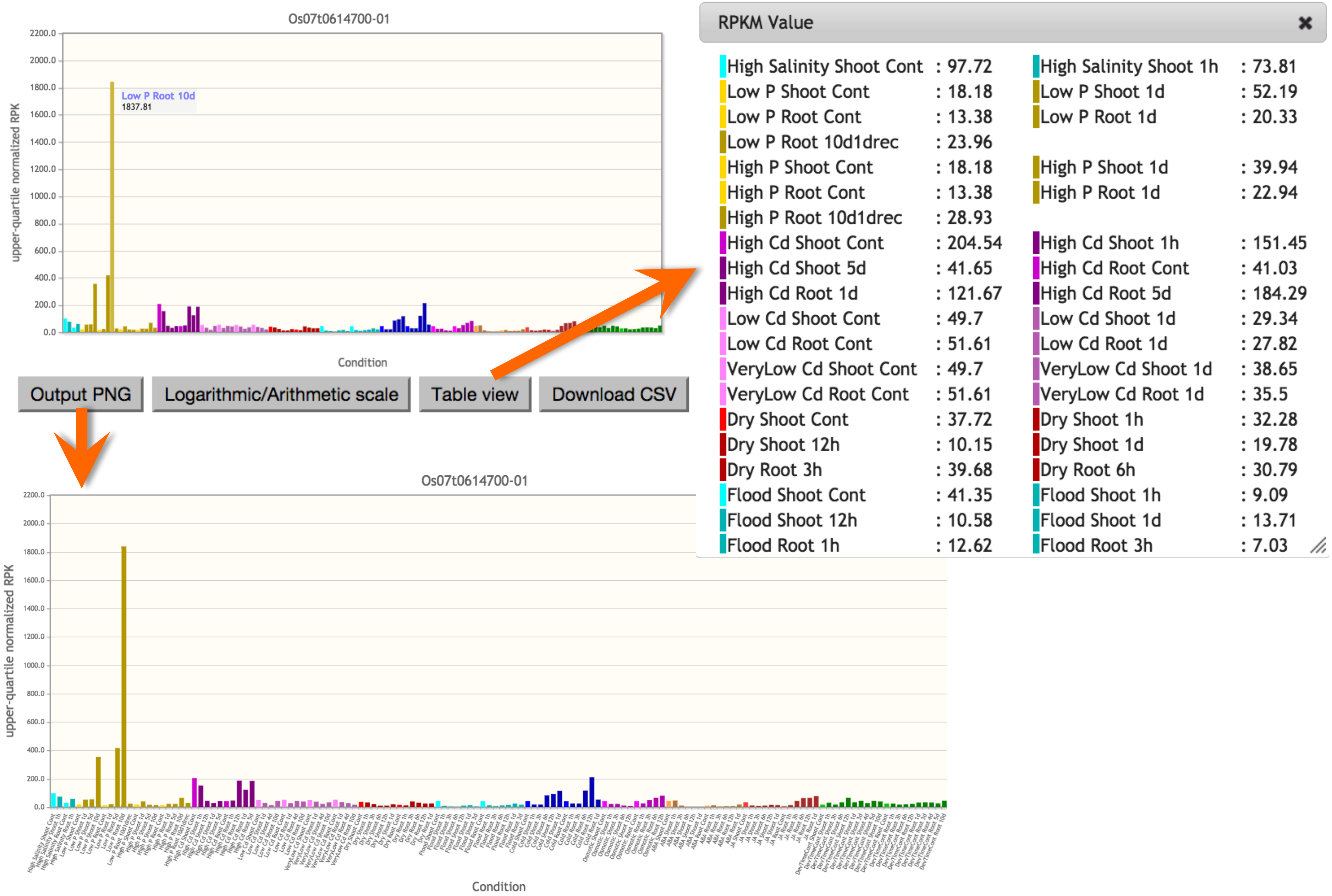
☑ High Phosphate
Shoot: ■ ☑ Cont ■ ☑ 1d ■ ☑ 5d ■ ☑ 10d
Root: ■ ☑ Cont ■ ☑ 1d ■ ☑ 5d ■ ☑ 10d ■ ☑ 10d1drec

☐ High Cd
Shoot: ■ ☐ Cont ■ ☐ 1h ■ ☐ 12h ■ ☐ 1d ■ ☐ 5d
Root: ■ ☐ Cont ■ ☐ 1h ■ ☐ 12h ■ ☐ 1d ■ ☐ 5d

☐ Low Cd
Shoot: ■ ☐ Cont ■ ☐ 1d ■ ☐ 4d ■ ☐ 10d
Root: ■ ☐ Cont ■ ☐ 1d ■ ☐ 4d ■ ☐ 10d

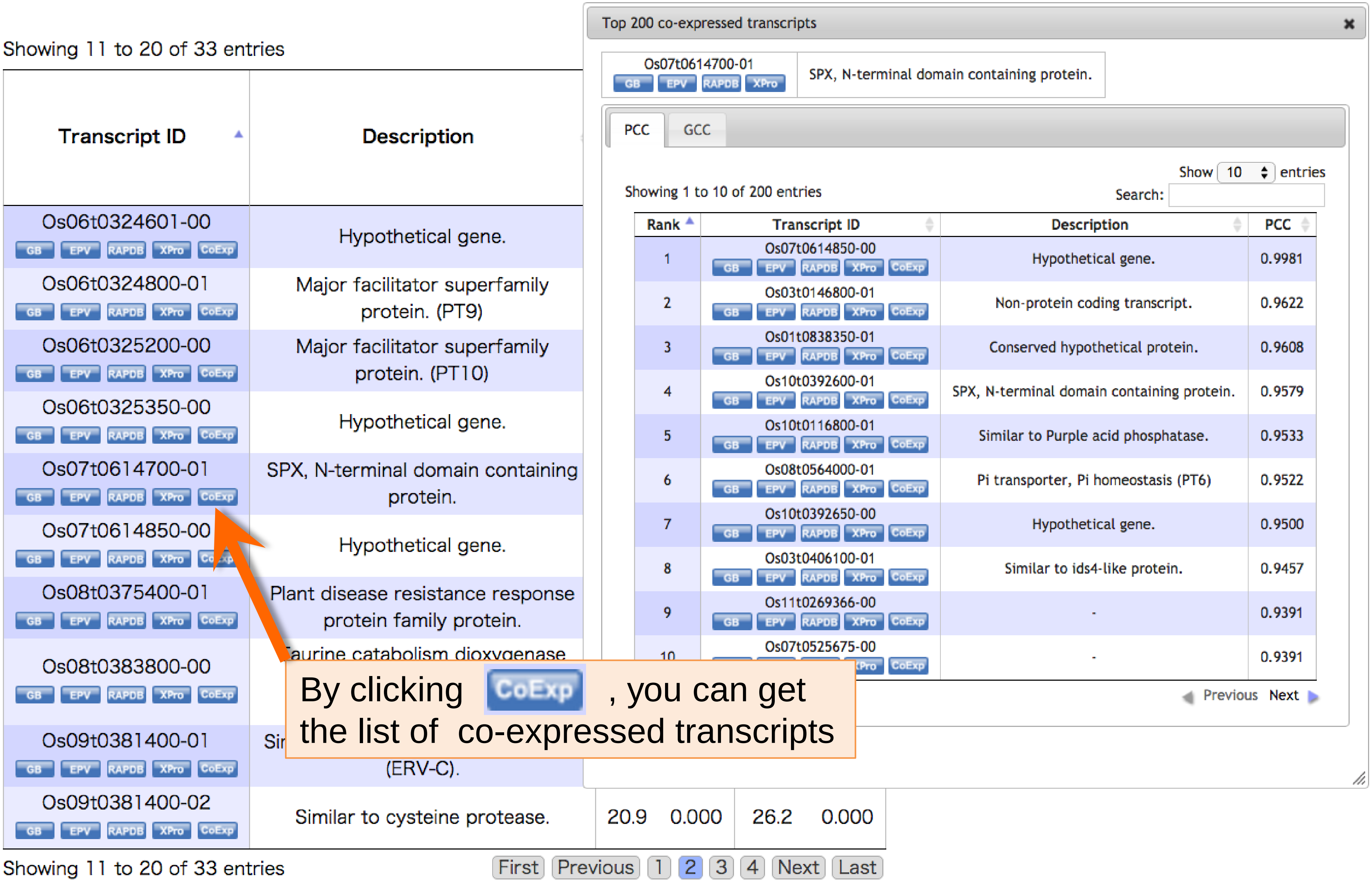
You can select sample conditions to be displayed in the bar plot

Functions in Expression profile view



High Salinity Shoot Cont	: 97.72	High Salinity Shoot 1h	: 73.81
Low P Shoot Cont	: 18.18	Low P Shoot 1d	: 52.19
Low P Root Cont	: 13.38	Low P Root 1d	: 20.33
Low P Root 10d1drec	: 23.96		
High P Shoot Cont	: 18.18	High P Shoot 1d	: 39.94
High P Root Cont	: 13.38	High P Root 1d	: 22.94
High P Root 10d1drec	: 28.93		
High Cd Shoot Cont	: 204.54	High Cd Shoot 1h	: 151.45
High Cd Shoot 5d	: 41.65	High Cd Root Cont	: 41.03
High Cd Root 1d	: 121.67	High Cd Root 5d	: 184.29
Low Cd Shoot Cont	: 49.7	Low Cd Shoot 1d	: 29.34
Low Cd Root Cont	: 51.61	Low Cd Root 1d	: 27.82
VeryLow Cd Shoot Cont	: 49.7	VeryLow Cd Shoot 1d	: 38.65
VeryLow Cd Root Cont	: 51.61	VeryLow Cd Root 1d	: 35.5
Dry Shoot Cont	: 37.72	Dry Shoot 1h	: 32.28
Dry Shoot 12h	: 10.15	Dry Shoot 1d	: 19.78
Dry Root 3h	: 39.68	Dry Root 6h	: 30.79
Flood Shoot Cont	: 41.35	Flood Shoot 1h	: 9.09
Flood Shoot 12h	: 10.58	Flood Shoot 1d	: 13.71
Flood Root 1h	: 12.62	Flood Root 3h	: 7.03

A list of co-expressed transcripts



Showing 11 to 20 of 33 entries

Transcript ID	Description				
Os06t0324601-00	Hypothetical gene.				
Os06t0324800-01	Major facilitator superfamily protein. (PT9)				
Os06t0325200-00	Major facilitator superfamily protein. (PT10)				
Os06t0325350-00	Hypothetical gene.				
Os07t0614700-01	SPX, N-terminal domain containing protein.				
Os07t0614850-00	Hypothetical gene.				
Os08t0375400-01	Plant disease resistance response protein family protein.				
Os08t0383800-00	aurine catabolism dioxygenase				
Os09t0381400-01	Si (ERV-C).				
Os09t0381400-02	Similar to cysteine protease.	20.9	0.000	26.2	0.000

Showing 11 to 20 of 33 entries

Top 200 co-expressed transcripts

Os07t0614700-01 SPX, N-terminal domain containing protein.

Show 10 entries

Showing 1 to 10 of 200 entries

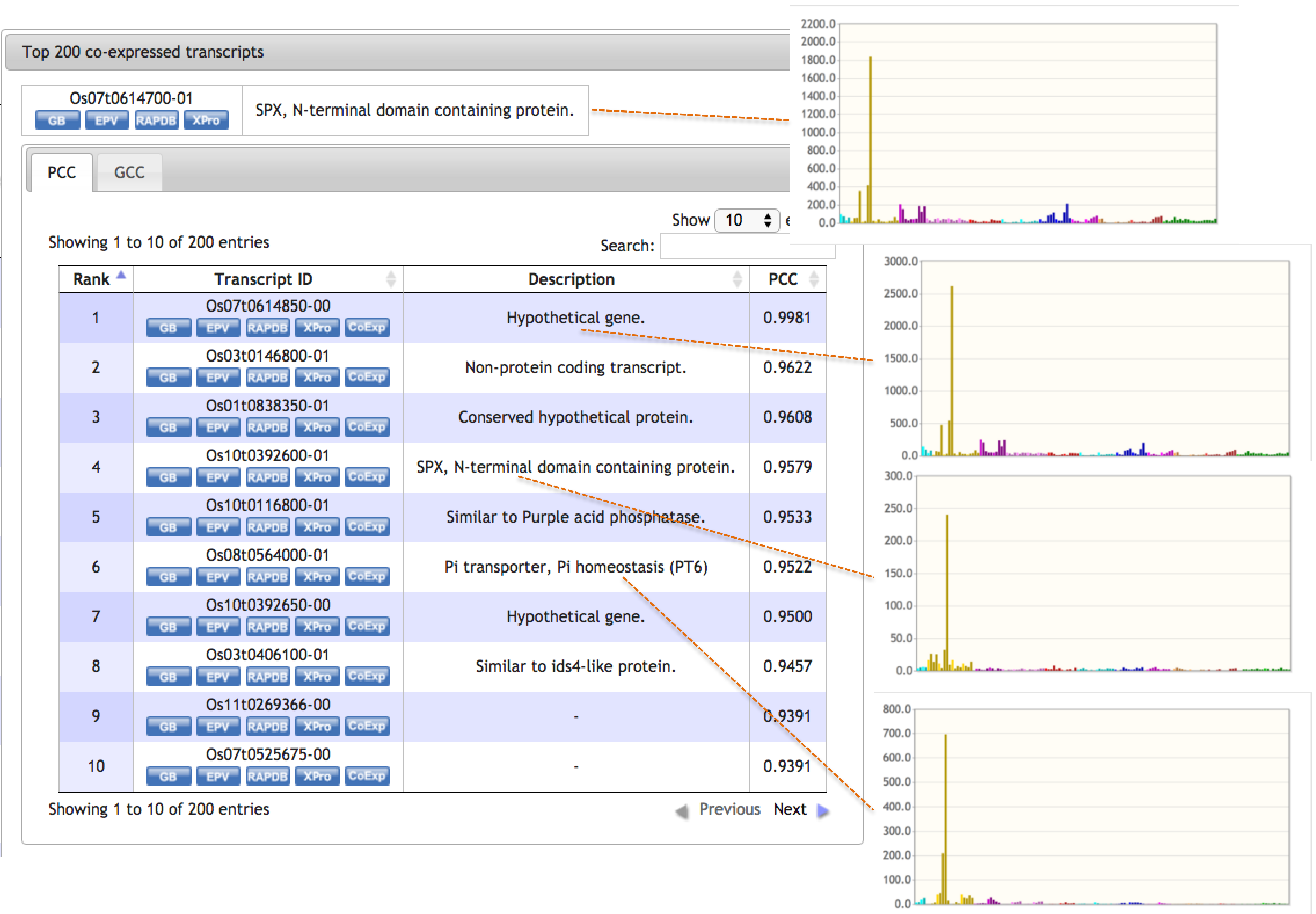
Search:

Rank	Transcript ID	Description	PCC
1	Os07t0614850-00	Hypothetical gene.	0.9981
2	Os03t0146800-01	Non-protein coding transcript.	0.9622
3	Os01t0838350-01	Conserved hypothetical protein.	0.9608
4	Os10t0392600-01	SPX, N-terminal domain containing protein.	0.9579
5	Os10t0116800-01	Similar to Purple acid phosphatase.	0.9533
6	Os08t0564000-01	Pi transporter, Pi homeostasis (PT6)	0.9522
7	Os10t0392650-00	Hypothetical gene.	0.9500
8	Os03t0406100-01	Similar to ids4-like protein.	0.9457
9	Os11t0269366-00	-	0.9391
10	Os07t0525675-00	-	0.9391

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

PCC: Pearson's correlation of coefficient

A list of co-expressed transcripts



Top 200 co-expressed transcripts

Os07t0614700-01 GB EPV RAPDB XPro	SPX, N-terminal domain containing protein.

Showing 1 to 10 of 200 entries

Rank	Transcript ID	Description	PCC
1	Os07t0614850-00 GB EPV RAPDB XPro CoExp	Hypothetical gene.	0.9981
2	Os03t0146800-01 GB EPV RAPDB XPro CoExp	Non-protein coding transcript.	0.9622
3	Os01t0838350-01 GB EPV RAPDB XPro CoExp	Conserved hypothetical protein.	0.9608
4	Os10t0392600-01 GB EPV RAPDB XPro CoExp	SPX, N-terminal domain containing protein.	0.9579
5	Os10t0116800-01 GB EPV RAPDB XPro CoExp	Similar to Purple acid phosphatase.	0.9533
6	Os08t0564000-01 GB EPV RAPDB XPro CoExp	Pi transporter, Pi homeostasis (PT6)	0.9522
7	Os10t0392650-00 GB EPV RAPDB XPro CoExp	Hypothetical gene.	0.9500
8	Os03t0406100-01 GB EPV RAPDB XPro CoExp	Similar to ids4-like protein.	0.9457
9	Os11t0269366-00 GB EPV RAPDB XPro CoExp	-	0.9391
10	Os07t0525675-00 GB EPV RAPDB XPro CoExp	-	0.9391

Showing 1 to 10 of 200 entries

Genome Browser (GBrowse)

Annotated transcripts in RAP-DB

and **unannotated transcripts** predicted by RNA-Seq data

cis-regulatory elements within the 1kb promoter regions

Transcriptional activity at single nucleotide resolution under the 140 conditions

GBrowse

Genome Browser (GBrowse)

By hovering the mouse cursor over the transcript structures,
you can quickly overview expression profiles along the chromosome.

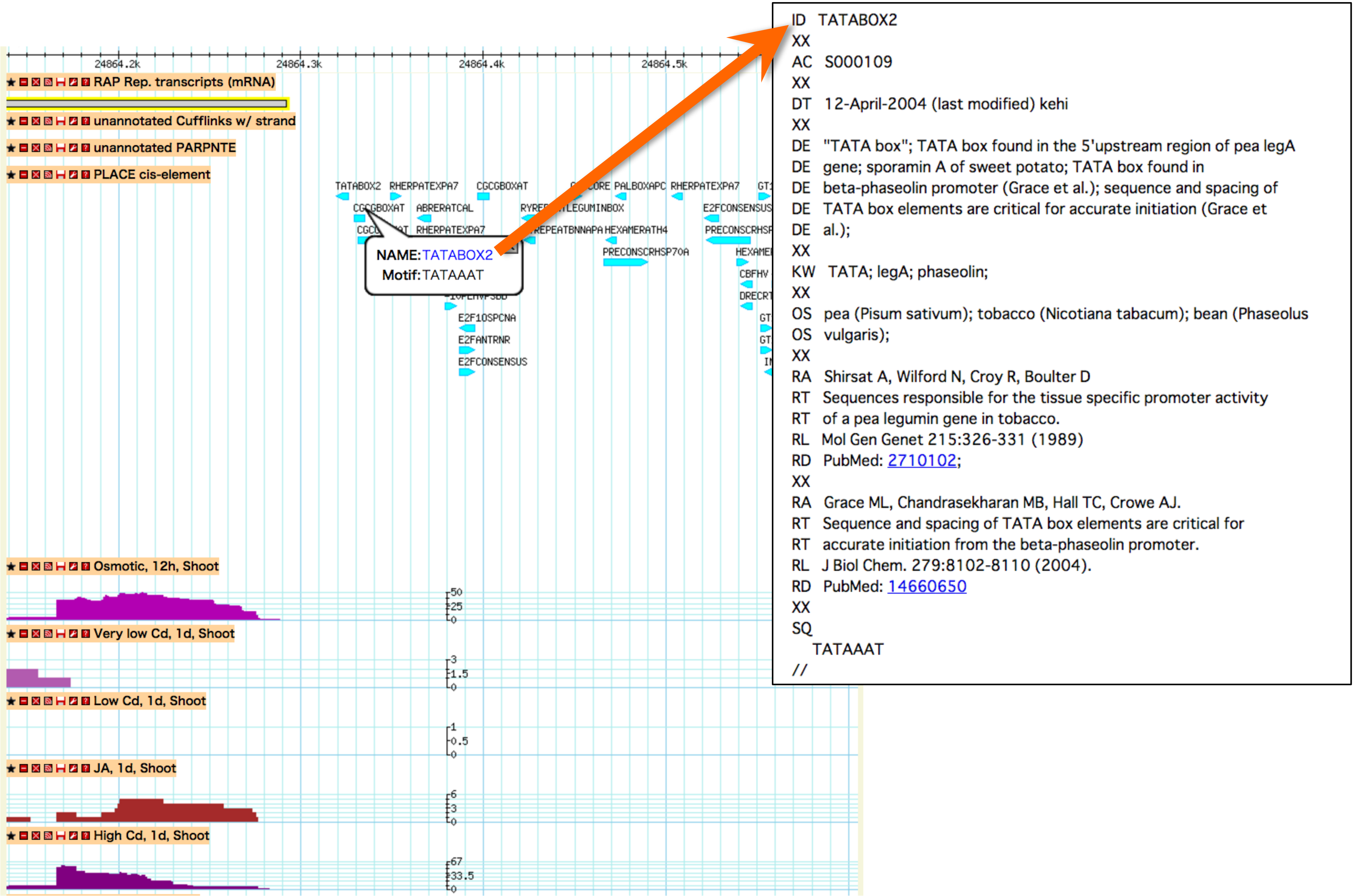
ID: Os01t0621900-01 (-) RAP-DB RiceXPro
Desc: Similar to OSIGBa0097P08.1 protein.

ID: Os01t0622300-01 (-) RAP-DB RiceXPro
Desc: Similar to Plastid uroporphyrinogen decarboxylase (Fragment).

ID: Os01t0622600-01 (-) RAP-DB RiceXPro
Desc: Similar to calcium-dependent protein kinase isoform 2.

ID: Os01t0623200-01 (-) RAP-DB RiceXPro
Desc: Similar to C4-dicarboxylate transporter/malic acid transport protein.

cis-regulatory elements within 1kb promoter regions



```
ID  TATABOX2
XX
AC  S000109
XX
DT  12-April-2004 (last modified) kehi
XX
DE  "TATA box"; TATA box found in the 5'upstream region of pea legA
DE  gene; sporamin A of sweet potato; TATA box found in
DE  beta-phaseolin promoter (Grace et al.); sequence and spacing of
DE  TATA box elements are critical for accurate initiation (Grace et
DE  al.);
XX
KW  TATA; legA; phaseolin;
XX
OS  pea (Pisum sativum); tobacco (Nicotiana tabacum); bean (Phaseolus
OS  vulgaris);
XX
RA  Shirsat A, Wilford N, Croy R, Boulter D
RT  Sequences responsible for the tissue specific promoter activity
RT  of a pea legumin gene in tobacco.
RL  Mol Gen Genet 215:326-331 (1989)
RD  PubMed: 2710102;
XX
RA  Grace ML, Chandrasekharan MB, Hall TC, Crowe AJ.
RT  Sequence and spacing of TATA box elements are critical for
RT  accurate initiation from the beta-phaseolin promoter.
RL  J Biol Chem. 279:8102-8110 (2004).
RD  PubMed: 14660650
XX
SQ
    TATAAAT
//
```

Download data

◆ **Expression profile data** (tab-delimited text file)

Normalized RPK values for annotated and unannotated transcripts under various conditions.

◆ **mRNA-Seq based unannotated transcripts** (GFF, GTF and FASTA files)

Exon-Intron structures and sequences of Cufflinks and PARPNTE predicted transcript that are not annotated in RAP-DB.

◆ **cis-regulatory elements** (GFF file)

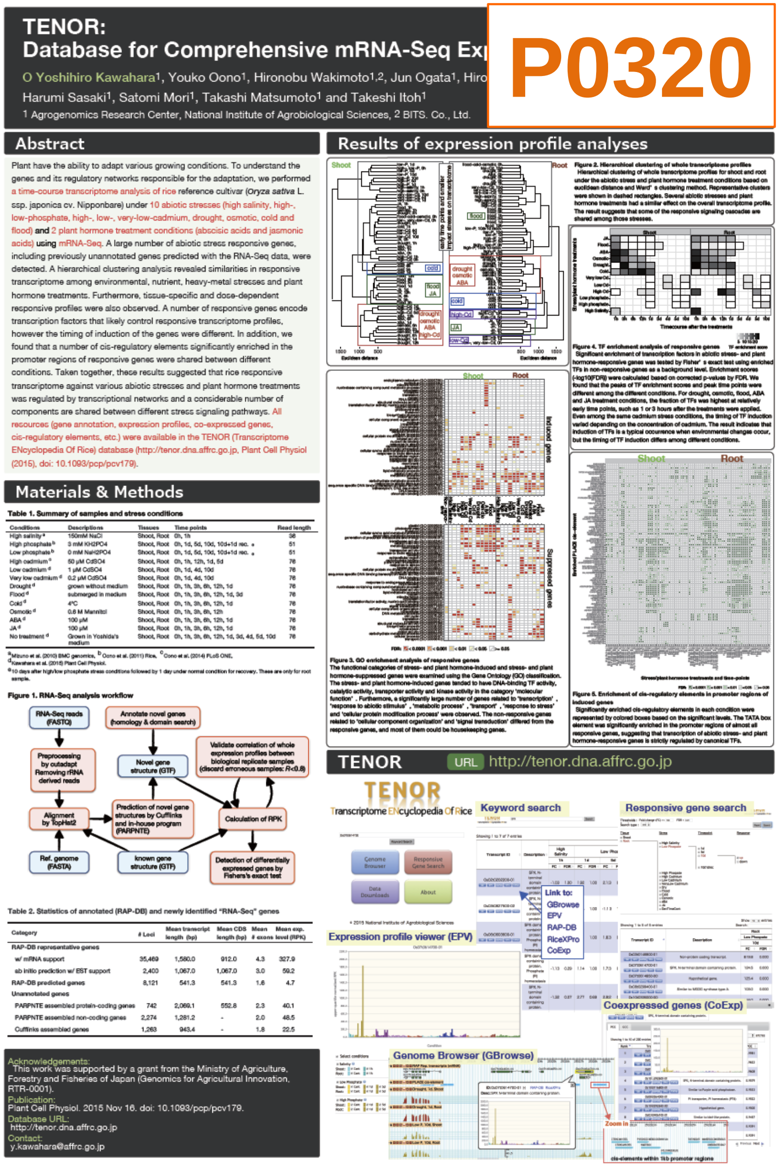
PLACE cis-regulatory elements in 1-kb promoter regions of each transcript.

◆ **Gene prediction program PARPNTE** (JAR file)

mRNA-Seq and HMM based gene prediction program written in Java

Poster@PAG

MONDAY, JANUARY 11
10:00 AM - 11:30 AM



P0320

TENOR:
Database for Comprehensive mRNA-Seq Exp

O Yoshihiro Kawahara[1], Youko Oono[1], Hironobu Wakimoto[1,2], Jun Ogata[1], Hiro
Harumi Sasaki[1], Satomi Mori[1], Takashi Matsumoto[1] and Takeshi Itoh[1]
[1] Agrogenomics Research Center, National Institute of Agrobiological Sciences, [2] BITS. Co., Ltd.

Abstract

Plant have the ability to adapt various growing conditions. To understand the genes and its regulatory networks responsible for the adaptation, we performed a time-course transcriptome analysis of rice reference cultivar (*Oryza sativa* L. ssp. japonica cv. Nipponbare) under 10 abiotic stresses (high salinity, high-, low-phosphate, high-, low-, very-low-cadmium, drought, osmotic, cold and flood) and 2 plant hormone treatment conditions (abscisic acids and jasmonic acids) using mRNA-Seq. A large number of abiotic stress responsive genes, including previously unannotated genes predicted with the RNA-Seq data, were detected. A hierarchical clustering analysis revealed similarities in responsive transcriptome among environmental, nutrient, heavy-metal stresses and plant hormone treatments. Furthermore, tissue-specific and dose-dependent responsive profiles were also observed. A number of responsive genes encode transcription factors that likely control responsive transcriptome profiles, however the timing of induction of the genes were different. In addition, we found that a number of cis-regulatory elements significantly enriched in the promoter regions of responsive genes were shared between different conditions. Taken together, these results suggested that rice responsive transcriptome against various abiotic stresses and plant hormone treatments was regulated by transcriptional networks and a considerable number of components are shared between different stress signaling pathways. All resources (gene annotation, expression profiles, co-expressed genes, cis-regulatory elements, etc.) were available in the TENOR (Transcriptome ENcyclopedia Of Rice) database (http://tenor.dna.affrc.go.jp, Plant Cell Physiol (2015), doi: 10.1093/pcp/pcv179).

Materials & Methods

Table 1. Summary of samples and stress conditions

Conditions	Descriptions	Tissues	Time points	Read length
High salinity [a]	150mM NaCl	Shoot, Root	0h, 1h	38
High phosphate [b]	3 mM KH2PO4	Shoot, Root	0h, 1d, 5d, 10d, 10d+1d rec. [e]	51
Low phosphate [b]	0 mM NaH2PO4	Shoot, Root	0h, 1d, 5d, 10d, 10d+1d rec. [e]	51
High cadmium [c]	50 μM CdSO4	Shoot, Root	0h, 1h, 12h, 1d, 5d	76
Low cadmium [d]	1 μM CdSO4	Shoot, Root	0h, 1d, 4d, 10d	76
Very low cadmium [d]	0.2 μM CdSO4	Shoot, Root	0h, 1d, 4d, 10d	76
Drought [d]	grown without medium	Shoot, Root	0h, 1h, 3h, 6h, 12h, 1d	76
Flood [d]	submerged in medium	Shoot, Root	0h, 1h, 3h, 6h, 12h, 1d, 3d	76
Cold [d]	4°C	Shoot, Root	0h, 1h, 3h, 6h, 12h, 1d	76
Osmotic [d]	0.6 M Mannitol	Shoot, Root	0h, 1h, 3h, 6h, 12h	76
ABA [d]	100 μM	Shoot, Root	0h, 1h, 3h, 6h, 12h, 1d	76
JA [d]	100 μM	Shoot, Root	0h, 1h, 3h, 6h, 12h, 1d	76
No treatment [d]	Grown in Yoshida's medium	Shoot, Root	0h, 1h, 3h, 6h, 12h, 1d, 3d, 4d, 5d, 10d	76

[a] Mizuno et al. (2010) BMC genomics, [b] Oono et al. (2011) Rice, [c] Oono et al. (2014) PLoS ONE, [d] Kawahara et al. (2015) Plant Cell Physiol.
[e] 10 days after high/low phosphate stress conditions followed by 1 day under normal condition for recovery. These are only for root sample.

Figure 1. RNA-Seq analysis workflow

Table 2. Statistics of annotated (RAP-DB) and newly identified "RNA-Seq" genes

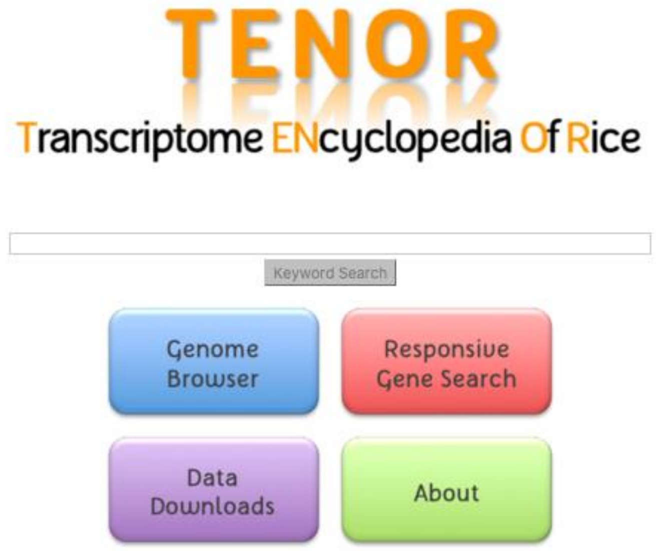
Category	# Loci	Mean transcript length (bp)	Mean CDS length (bp)	Mean # exons	Mean exp. level (RPK)
RAP-DB representative genes					
w/ mRNA support	35,469	1,580.0	912.0	4.3	327.9
ab initio prediction w/ EST support	2,400	1,067.0	1,067.0	3.0	59.2
RAP-DB predicted genes	8,121	541.3	541.3	1.6	4.7
Unannotated genes					
PARPNTE assembled protein-coding genes	742	2,069.1	552.8	2.3	40.1
PARPNTE assembled non-coding genes	2,274	1,281.2	-	2.0	48.5
Cufflinks assembled genes	1,263	943.4	-	1.8	22.5

Acknowledgements:
This work was supported by a grant from the Ministry of Agriculture, Forestry and Fisheries of Japan (Genomics for Agricultural Innovation, RTR-0001).
Publication:
Plant Cell Physiol. 2015 Nov 16. doi: 10.1093/pcp/pcv179.
Database URL:
http://tenor.dna.affrc.go.jp
Contact:
y.kawahara@affrc.go.jp

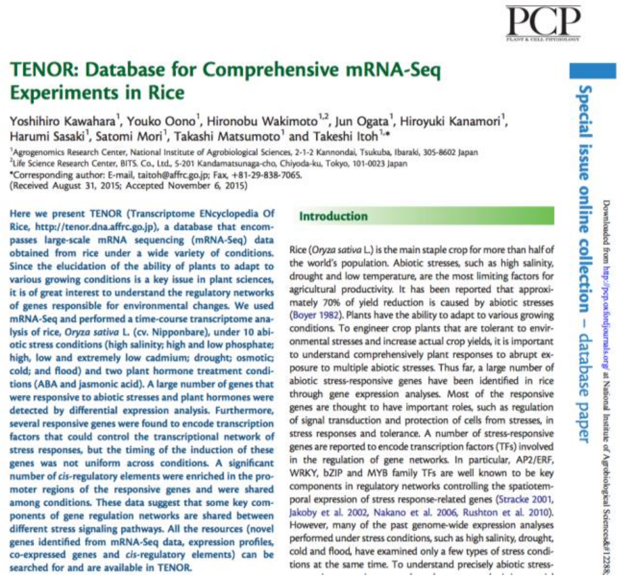
Results of expression profile analyses

TENOR URL http://tenor.dna.affrc.go.jp

URL http://tenor.dna.affrc.go.jp



Paper Kawahara Y. et al.
Plant Cell Physiol. 2015



PCP
PLANT & CELL PHYSIOLOGY

TENOR: Database for Comprehensive mRNA-Seq Experiments in Rice

Yoshihiro Kawahara[1], Youko Oono[1], Hironobu Wakimoto[1,2], Jun Ogata[1], Hiroyuki Kanamori[1], Harumi Sasaki[1], Satomi Mori[1], Takashi Matsumoto[1] and Takeshi Itoh[1,*]
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(Received August 31, 2015; Accepted November 6, 2015)

Here we present TENOR (Transcriptome ENcyclopedia Of Rice, http://tenor.dna.affrc.go.jp), a database that encompasses large-scale mRNA sequencing (mRNA-Seq) data obtained from rice under a wide variety of conditions. Since the elucidation of the ability of plants to adapt to various growing conditions is a key issue in plant sciences, it is of great interest to understand the regulatory networks of genes responsible for environmental changes. We used mRNA-Seq and performed a time-course transcriptome analysis of rice, *Oryza sativa* L. (cv. Nipponbare), under 10 abiotic stress conditions (high salinity; high and low phosphate; high, low and extremely low cadmium; drought; osmotic; cold; and flood) and two plant hormone treatment conditions (ABA and jasmonic acid). A large number of genes that were responsive to abiotic stresses and plant hormones were detected by differential expression analysis. Furthermore, several responsive genes were found to encode transcription factors that could control the transcriptional network of stress responses, but the timing of the induction of these genes was not uniform across conditions. A significant number of *cis*-regulatory elements were enriched in the promoter regions of the responsive genes and were shared among conditions. These data suggest that some key components of gene regulation networks are shared between different stress signaling pathways. All the resources (novel genes identified from mRNA-Seq data, expression profiles, co-expressed genes and *cis*-regulatory elements) can be searched for and are available in TENOR.

Introduction

Rice (*Oryza sativa* L.) is the main staple crop for more than half of the world's population. Abiotic stresses, such as high salinity, drought and low temperature, are the most limiting factors for agricultural productivity. It has been reported that approximately 70% of yield reduction is caused by abiotic stresses (Boyer 1982). Plants have the ability to adapt to various growing conditions. To engineer crop plants that are tolerant to environmental stresses and increase actual crop yields, it is important to understand comprehensively plant responses to abrupt exposure to multiple abiotic stresses. Thus far, a large number of abiotic stress-responsive genes have been identified in rice through gene expression analyses. Most of the responsive genes are thought to have important roles, such as regulation of signal transduction and protection of cells from stresses, in stress responses and tolerance. A number of stress-responsive genes are reported to encode transcription factors (TFs) involved in the regulation of gene networks. In particular, AP2/ERF, WRKY, bZIP and MYB family TFs are well known to be key components in regulatory networks controlling the spatiotemporal expression of stress response-related genes (Stracke 2001, Jakoby et al. 2002, Nakano et al. 2006, Rushton et al. 2010). However, many of the past genome-wide expression analyses performed under stress conditions, such as high salinity, drought, cold and flood, have examined only a few types of stress conditions at the same time. To understand precisely abiotic stress-

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