Table S1. Drought and salinity stress and development related microarray data used in this study.

S. No.	GEO accession	No. of samples	Description
Stress data			
1	GSE26280	36	Genome-wide temporal-spatial gene expression profiling of drought responsiveness in rice
2	GSE24048	12	Expression data from field droughted rice plants
3	GSE13735	11	Expression data from rice genotypes FL478 and IR29
4	GSE16108	8	Transcription profiling of parental lines and bulked salt sensitive and salt tolerant RILs derived from 2 rice varieties
5	GSE14403	23	Root-specific transcriptional profiling of contrasting rice genotypes in response to salinity stress
6	GSE6901	9	Expression data for stress treatment in rice seedlings
Development data			
1	GSE6893	45	Expression data for reproductive development in rice
2	GSE19024	190	Dissecting the developmental transcriptome of rice
3	GSE13988	26	Rice expression atlas (1): Anther development
4	GSE14298	20	Rice expression atlas (2): Pollination-fertilization
5	GSE14299	27	Rice expression atlas (3): Early embryogenesis
6	GSE14300	25	Rice expression atlas (4): Vegetative tissues
7	GSE27988	24	Genome-wide gene expression profiling of rice pollen in different developmental stages

Table S2. Summary of rice TFs classified in different families and showing differential expression under drought and salinity conditions.

TF family	Total	Differentially expressed	Salinity	Drought	Drought and salinity	No change
ABI3VP1 (ABA Insensitive 3 like/Viviparous 1)	55	19	1	10	8	36
Alfin-like	9	7	1	5	1	2
AP2-EREBP (APETALA2/Ethylene-responsive Element Binding Proteins)	165	96	11	25	60	69
ARF (Auxin Response Factors)	27	16	0	10	6	11
ARR-B (Type-B phospho-accepting Response Regulators)	10	4	0	3	1	6
Aux/IAA (Auxin/Indole-3-Acetic Acid proteins)	29	27	2	6	19	2
BES1 (BRI1-EMS-SUPPRESSOR 1) *alias* BZR2 (BRASSINAZOLE-RESISTANT 2)	6	4	0	1	3	2
bHLH (Basic helix-loop-helix) *alias* MYC	160	88	5	27	56	72
BSD (domain conserved in BTF2-like transcription factors, Synapse-associated proteins and DOS2-like proteins)	10	5	0	0	5	5
bZIP (Basic Leucine Zipper)	96	65	1	21	43	31
C2C2-CO-like (Constans-like Zinc finger)	17	14	1	3	11	3
C2C2-Dof (DNA-binding with One Finger)	30	18	1	5	12	12
C2C2-GATA (GATA Zinc finger domain containing proteins)	25	17	4	6	10	8
C2C2-YABBY	8	7	0	2	5	1
C2H2 (Cys2His2 zinc finger)	102	53	0	16	33	49
C3H (Cys3His zinc finger)	70	44	5	15	24	26
CAMTA (Calmodulin binding Transcription Activators)	6	4	0	4		2
CCAAT (cytidine-cytidine-adenosine-adenosine-thymidine)	46	24	4	6	14	22
CPP (Cystein-rich Polycomb-like Proteins)	11	7	0	2	5	4
DBB (Double B-box zinc finger)	10	10	0	2	8	0
DBP (DNA Binding protein Phosphatases)	6	6	1	1	4	0
DDT (DNA-binding homeobox and Different Transcription factors)	6	3	0	1	2	3

E2F-DP (E2F-Dimerization Partner)	9	7	0	3	4	2
EIL (Ethylene-insensitive3 like)	9	5	0	3	2	4
FAR1 (Far-red-impaired Response)	124	28	10	10	8	96
FHA (Forkhead-associated Domain)	18	14	0	8	6	4
G2-like (Golden 2-like)	46	31	0	14	17	15
GeBP (GLABRA1 enhancer Binding Proteins)	13	7	1	4	2	6
GNAT (GCN5-related N-acetyltransferases)	37	25	4	6	15	12
GRAS (GIBBERELLIN-INSENSITIVE, REPRESSOR of ga1-3, SCARECROW)	60	27	1	12	14	33
GRF (Growth Regulating Factors)	12	9	1	4	4	3
HB (HomeoBox)	98	59	0	23	36	39
HMG (High Mobility Group proteins)	9	8	0	4	4	1
HSF (Heat Shock transcription Factors)	25	20	1	3	16	5
Jumonji	14	9	2	2	5	5
LIM (Lin11, Isl-1 & Mec-3)	6	3	0	2	1	3
LOB (Lateral Organ Boundaries) *alias* AS2 (Asymmetric Leaves 2)	36	20	0	8	12	16
LUG (LEUNIG)	6	3	0	1	2	3
MADS (MCM1, AGAMOUS, DEFICIENS and SRF (Serum Response Factor))	70	23	3	13	7	47
mTERF (mitochondrial Transcription Termination Factors)	30	21	0	7	14	9
MYB (MYeloBlastosis)	122	87	5	27	55	35
MYB-related (MYeloBlastosis-related)	80	48	6	9	33	32
NAC (NAM (no apical meristem); ATAF (Arabidopsis transcription activation factor); CUC (cup-shaped cotyledon))	144	71	3	22	46	73
OFP (Ovate Family Proteins)	31	18	2	8	8	13
Orphans	58	29	1	8	20	29
PHD (Plant HomeoDomain)	49	31	2	14	15	18
PLATZ (Plant AT-rich sequence and Zinc binding proteins)	15	7	0	4	3	8
RWP-RK (Arginine Tryptophan Proline - Arginine Lysine)	13	6	0	1	5	7
SBP (Squamosa-promoter Binding Proteins)	19	13	1	5	7	6

SET (Su(var)3-9, Enhancer-of-zeste and Trithorax)	32	23	3	7	13	9
Sigma70-like	6	5	0	1	4	1
SNF2 (Sucrose NonFermentable 2)	37	21	4	4	13	16
SWI/SNF-BAF60b (SWItch/Sucrose NonFermentable)	11	6	1	2	3	5
TCP (TB1, CYC and PCFs)	22	12	0	3	9	10
TIFY	17	14	1	3	10	3
TRAF (TNF (Tumor necrosis factor) Receptor-Associated Factors) *alias* BTB (BR-C, ttk and bab)/ POZ (Pox virus and Zinc finger)	71	17	1	7	9	54
Trihelix	29	19	1	5	13	10
TUB (TUBBY-like proteins)	14	10	0	4	6	4
WRKY	103	71	6	20	45	32
zf-HD (Zinc Finger HomeoDomain proteins)	15	7	0	2	5	8
ARID (AT-Rich Interaction Domain)	5	3	0	3	0	2
LSD (Lesion Stimulating Disease zinc finger)	5	4	0	2	2	1
Pseudo_RR (Pseudo Response Regulator)	5	5	0	2	3	0
Rcd1-like (Retinoic acid-induced Cell Differentiation 1 like)	5	3	0	3	0	2
SRS (SHI (Short Internodes) Related Sequence)	5	2	0	0	2	3
BBR/BPC (Barley b Recombinant proteins/ Basic Pentacysteine1)	4	3	2	0	1	1
SWI/SNF-SWI3 (SWItch/Sucrose NonFermentable-SWItch 3)	4	1	0	0	1	3
Coactivator_p15	3	1	0	0	1	2
CSD (Cold Shock Domain)	3	1	0	0	1	2
MBF1 (Multiprotein bridging factor 1)	2	1	0	0	1	1
NF-X1 (NF-X1 zinc finger)	2	2	0	1	1	0
PBF-2-like (PR-10a Binding Factor 2 like) *alias* Whirly	2	1	0	1	0	1
RB (Retinoblastoma-associated protein B domain)	2	1	0	0	1	1
S1Fa-like (Spinach leaf site 1 binding Factor a-like)	2	1	0	1	0	1
SOH1 (Suppressors of hpr1) *alias* MED31	2	1	0	0	1	1
TAZ (Transcription Adaptor putative Zinc finger)	2	2	1	1	0	0

ULT (ULTRAPETALA)	2	1	0	0	1	1
VOZ (Vascular plant One Zinc finger proteins)	2	2	0	2	0	0
HRT (Hordeum Repressor of Transcription)	1	1	0	0	1	0
IWS1 (Interact With SPT6)	1	0	0	0	0	1
MED6 (Mediator complex subunit 6)	1	0	0	0	0	1
MED7 (Mediator complex subunit 7)	1	0	0	0	0	1
LFY (LEAFY)	2	0	0	0	0	2
STAT (Signal Transducers and Activators of Transcription)	1	0	0	0	0	1
Total	**2478**	**1408**	**100**	**470**	**838**	**1070**

‘No change’ represents genes showing no significant change in expression under drought and/or salinity stress conditions.

Figure S1. Number of *Tos17* mutant lines and TFs with the corresponding phenotypes are given. A and B represent the mutant lines identified in the genomic and promoter regions, respectively.

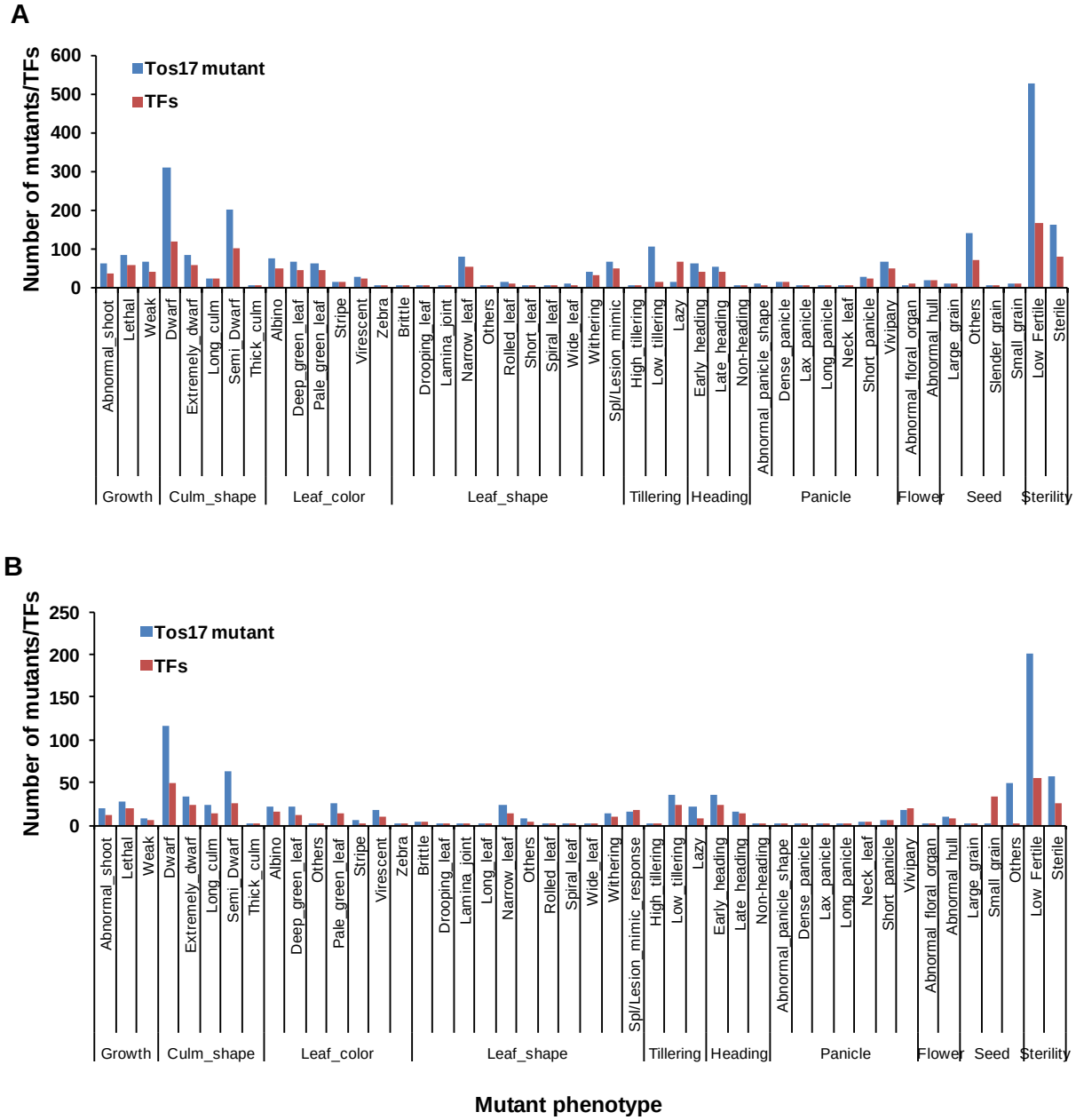
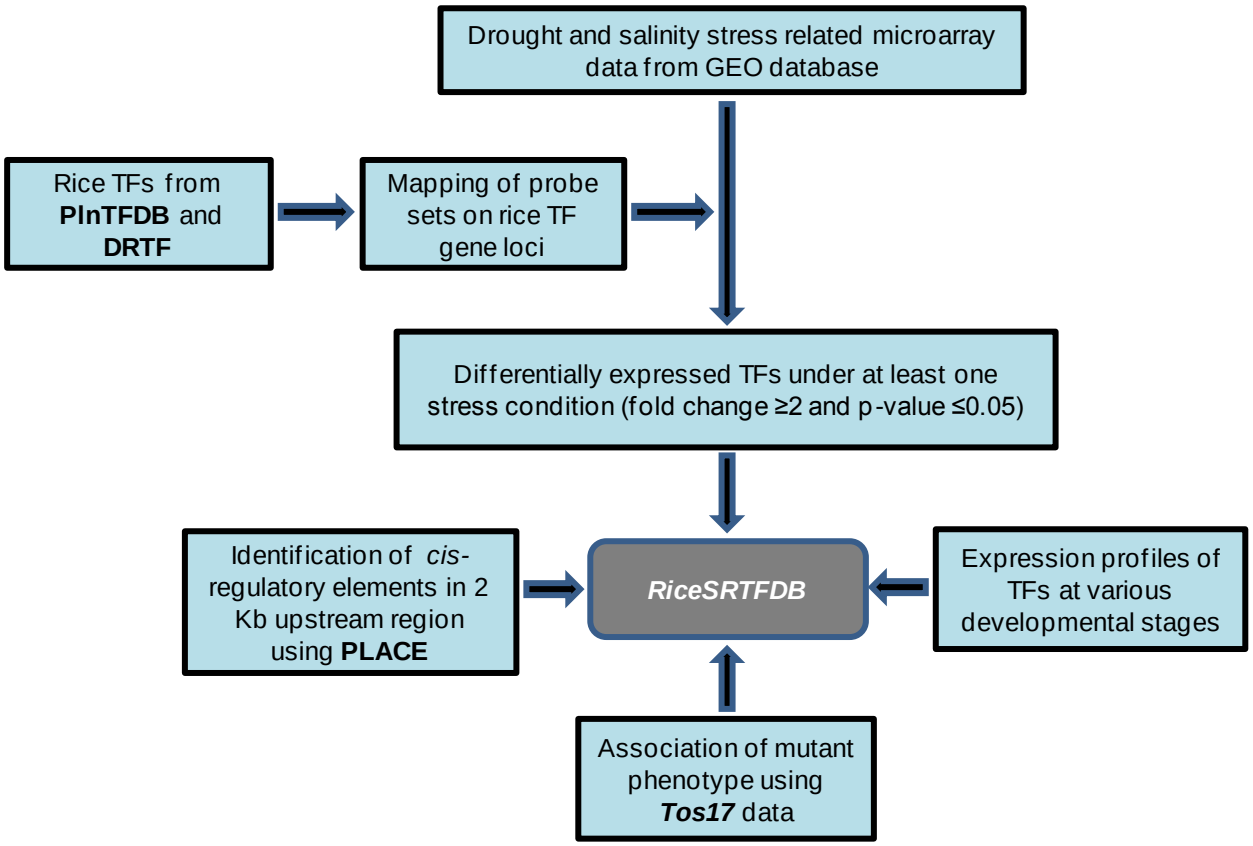
Figure S2. Diagrammatic representation of information/data integrated in the RiceSRTFDB.