Transcriptomics insights into the genetic regulation of root apical meristem exhaustion and determinate primary root growth in *Pachycereus pringlei* (Cactaceae)

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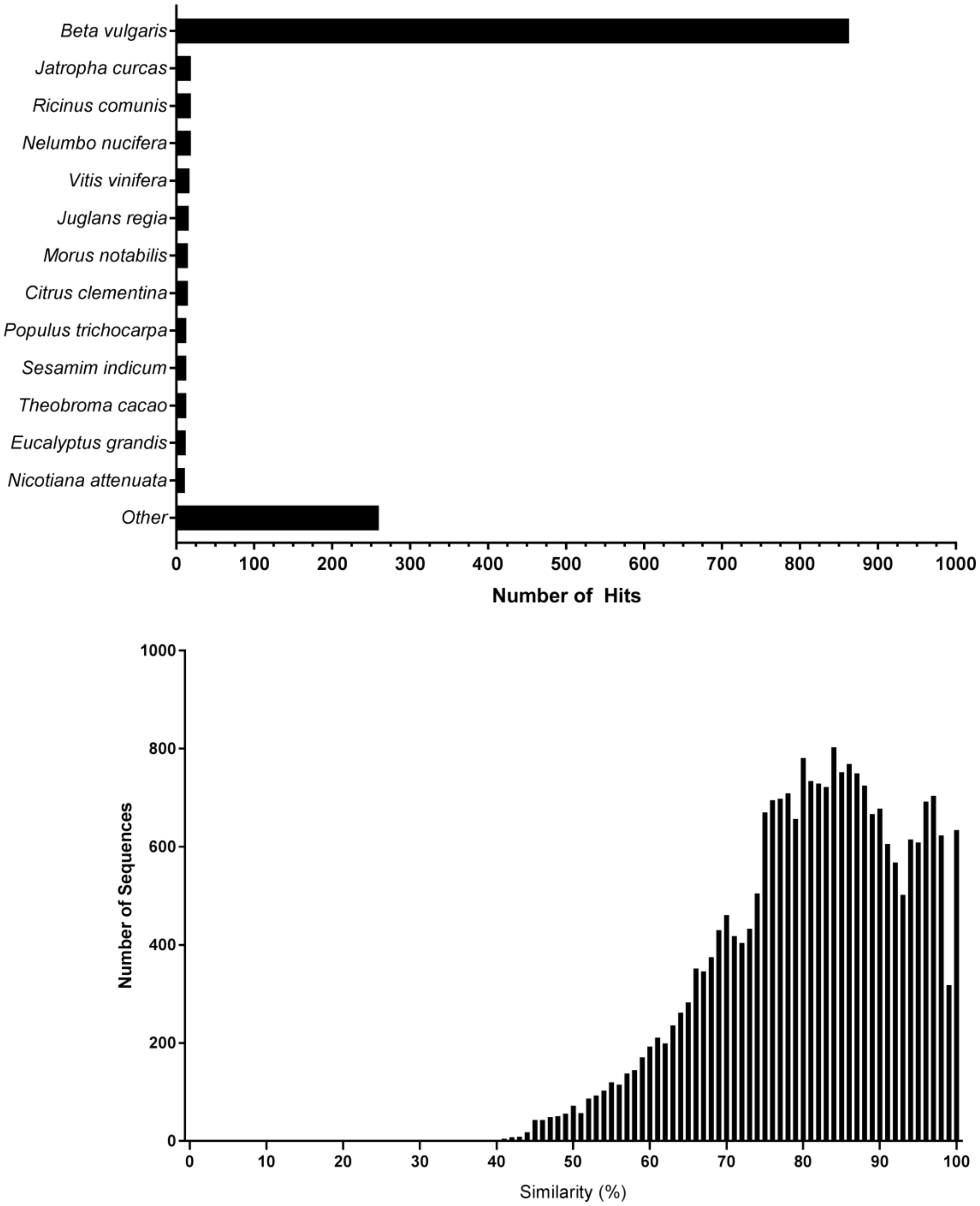
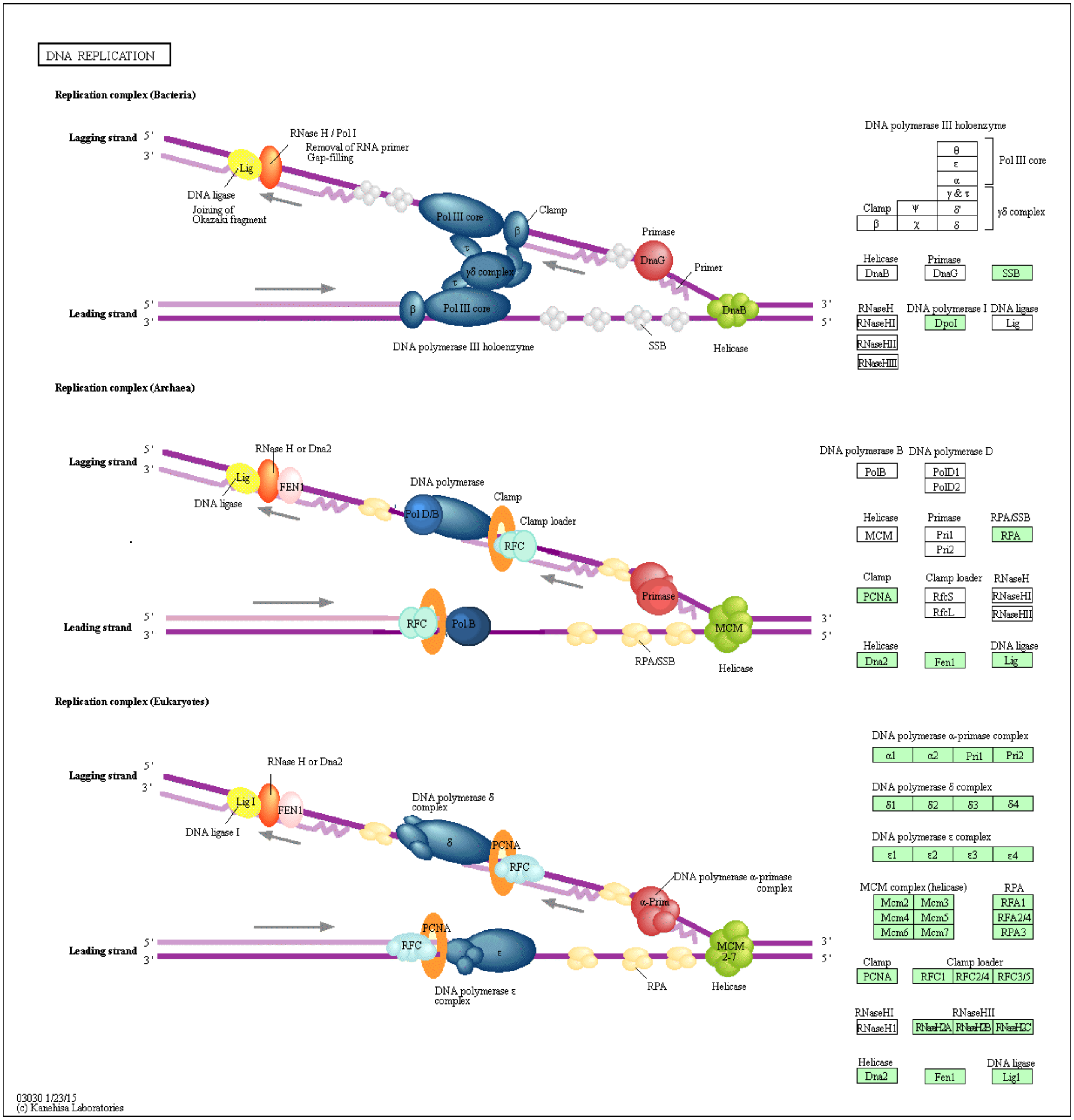
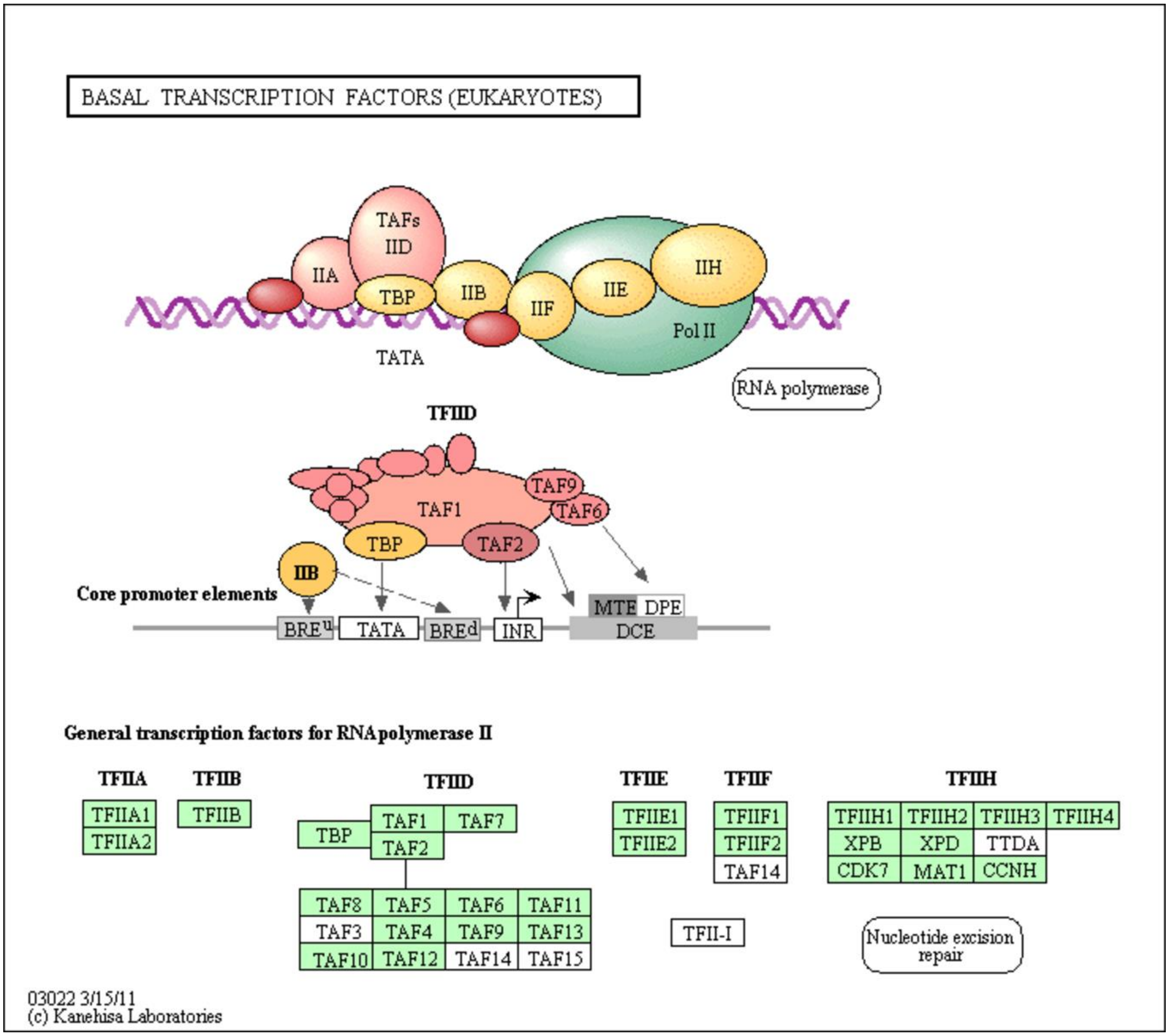
Supplementary Figure S1. B2GO annotation statistics for the *de novo* assembled transcriptome of the *Pachycereus pringlei* primary root apex. Note: the following stats are from a representative subset of the total contigs. Upper panel: top hit species during the B2GO annotation; lower panel: distribution of similarity values between *P. pringlei* translated contigs and the top hit sequences during B2GO annotation.



Supplementary Figure S2. The *Pachycereus pringlei* transcriptome is comprehensive. KEGG Automatic Annotation Server mapping of the *de novo* assembled primary root apex transcriptome of *P. pringlei* to some biological processes and pathways. The boxes in each process or pathway represent enzymes or structural proteins. Green boxes: at least one *P. pringlei* putative ortholog was identified in the transcriptome; white boxes: no *P. pringlei* putative ortholog was identified. Permission to use the schemes was kindly granted by Kanehisha Laboratories. Schemes were generated by the KAAS mapping tool (Moriya *et al.*, 2007, DOI:10.1093/nar/gkm321). Reference: Kanehisa M., Furumichi M., Tanabe M., Sato Y., Morishima K. KEGG: new perspectives on genomes, pathways, diseases and drugs. Nuc. Ac. Res. 45, D353-D361 (2017).




BASAL TRANSCRIPTION FACTORS (EUKARYOTES)
TAFs
IID
IIA
TBP
IIB
IIF
IIE
IIH
Pol II
TATA
RNA polymerase
TFIID
TAF9
TAF6
TAF1
TBP
TAF2
IIB
Core promoter elements
BRE u
TATA
BRE d
INR
MTE
DPE
DCE
General transcription factors for RNA polymerase II
TFIIA
TFIIA1
TFIIA2
TFIIB
TFIIB
TFIID
TBP
TAF1
TAF7
TAF2
TAF8
TAF5
TAF6
TAF11
TAF3
TAF4
TAF9
TAF13
TAF10
TAF12
TAF14
TAF15
TFIIE
TFIIE1
TFIIE2
TFIIF
TFIIF1
TFIIF2
TAF14
TFII-I
TFIIH
TFIIH1
TFIIH2
TFIIH3
TFIIH4
XPB
XPD
TTDA
CDK7
MAT1
CCNH
Nucleotide excision repair
03022 3/15/11
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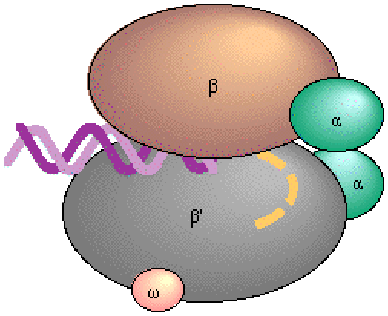
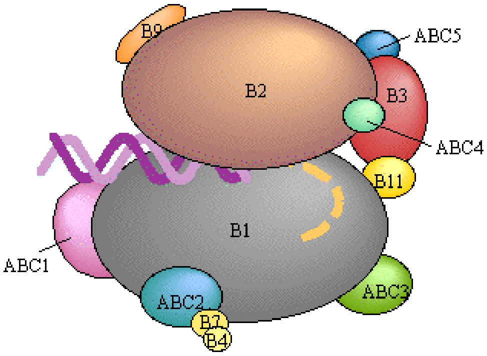
RNA POLYMERASE



RNA polymerase (Thermus aquaticus)



RNA polymerase II (Saccharomyces cerevisiae)

Bacterial

β	α	ω	δ
β'			

Archaeal

B	D	F	H	K	E
A	G		N	L	P

Eukaryotic Pol II

Core subunits

B2	B3
B1	B11

Pol II specific subunits

B4	B7	B9

Pol I, II, and III common subunits

ABC1	ABC2	ABC3
ABC4	ABC5	

Eukaryotic Pol III

Core subunits

C2	AC2
C1	AC1

Pol III specific subunits

C3	C4	C11	
C25	C31	C34	C37

Eukaryotic Pol I

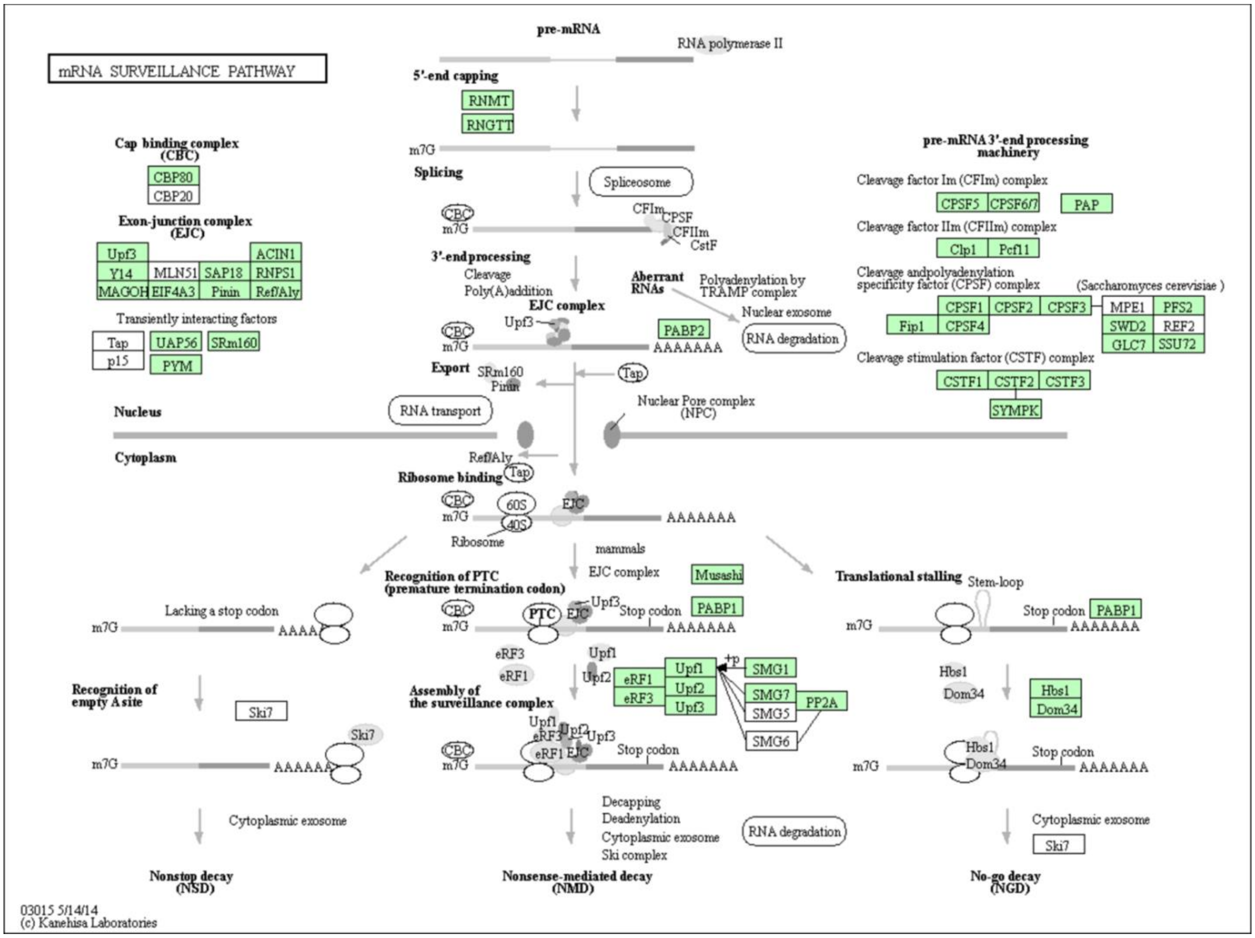
Core subunits

A2	AC2
A1	AC1

Pol I specific subunits

A12	A14	A34
A49	A43	

03020 3/25/11


mRNA SURVEILLANCE PATHWAY
pre-mRNA
RNA polymerase II
5'-end capping
RNMT
RNGTT
m7G
Splicing
Spliceosome
CBC
CFIm
CPSF
CFIIm
CstF
3'-end processing
Cleavage
Poly(A)addition
Aberrant RNAs
Polyadenylation by TRAMP complex
Nuclear exosome
RNA degradation
EJC complex
Upf3
PABP2
AAAAAAA
Export
SRm160
Pinin
Tap
RNA transport
Nuclear Pore complex (NPC)
Nucleus
Cytoplasm
Ref/Aly
Ribosome binding
60S
40S
EJC
Ribosome
Cap binding complex (CBC)
CBP80
CBP20
Exon-junction complex (EJC)
Upf3
ACIN1
Y14
MLN51
SAP18
RNPS1
MAGOH
EIF4A3
Pinin
Ref/Aly
Transiently interacting factors
Tap
p15
UAP56
SRm160
PYM
pre-mRNA 3'-end processing machinery
Cleavage factor Im (CFIm) complex
CPSF5
CPSF6/7
PAP
Cleavage factor IIm (CFIIm) complex
Clp1
Pcf11
Cleavage and polyadenylation specificity factor (CPSF) complex
(Saccharomyces cerevisiae)
CPSF1
CPSF2
CPSF3
MPE1
PFS2
Fip1
CPSF4
SWD2
REF2
GLC7
SSU72
Cleavage stimulation factor (CSTF) complex
CSTF1
CSTF2
CSTF3
SYMPK
mammals
EJC complex
Musashi
Recognition of PTC (premature termination codon)
PTC
Stop codon
PABP1
Lacking a stop codon
AAAA
Translational stalling
Stem-loop
eRF3
eRF1
Upf1
Upf2
Upf1
Upf2
Upf3
eRF1
eRF3
+p
SMG1
SMG7
SMG5
SMG6
PP2A
Assembly of the surveillance complex
Hbs1
Dom34
Recognition of empty A site
Ski7
AAAAAA
Decapping
Deadenylation
Cytoplasmic exosome
Ski complex
Cytoplasmic exosome
Nonstop decay (NSD)
Nonsense-mediated decay (NMD)
No-go decay (NGD)
03015 5/14/14
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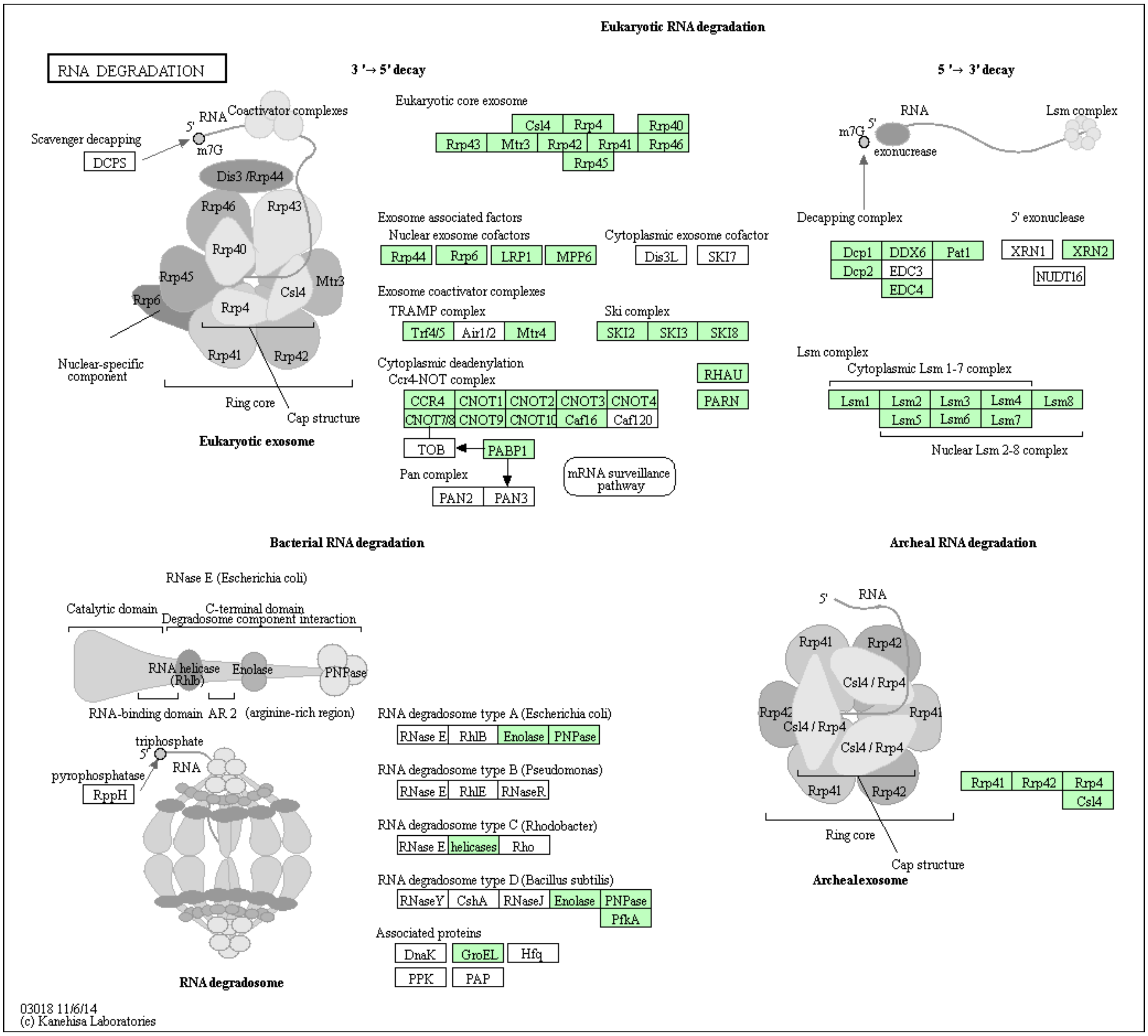
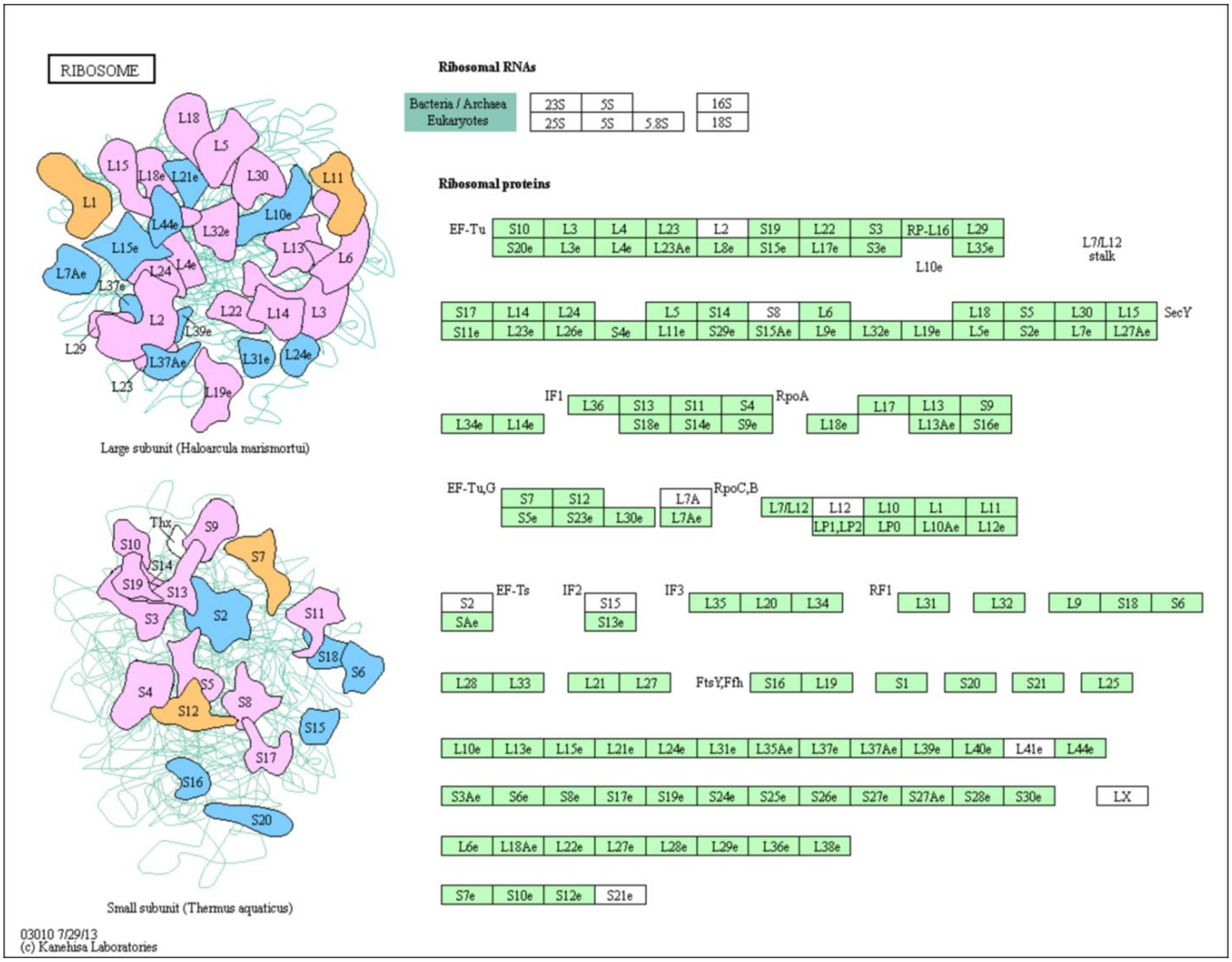

RNA DEGRADATION
Eukaryotic RNA degradation
3 '→ 5' decay
5 '→ 3' decay
Scavenger decapping
DCPS
5'
RNA
m7G
Coactivator complexes
Dis3 /Rrp44
Rrp46
Rrp43
Rrp40
Rrp45
Rrp6
Mtr3
Csl4
Rrp4
Rrp41
Rrp42
Nuclear-specific component
Ring core
Cap structure
Eukaryotic exosome
Eukaryotic core exosome
Csl4
Rrp4
Rrp40
Rrp43
Mtr3
Rrp42
Rrp41
Rrp46
Rrp45
Exosome associated factors
Nuclear exosome cofactors
Rrp44
Rrp6
LRP1
MPP6
Cytoplasmic exosome cofactor
Dis3L
SKI7
Exosome coactivator complexes
TRAMP complex
Trf4/5
Air1/2
Mtr4
Ski complex
SKI2
SKI3
SKI8
Cytoplasmic deadenylation
Ccr4-NOT complex
CCR4
CNOT1
CNOT2
CNOT3
CNOT4
CNOT7/8
CNOT9
CNOT10
Caf16
Caf120
RHAU
PARN
TOB
PABP1
Pan complex
PAN2
PAN3
mRNA surveillance pathway
RNA
Lsm complex
m7G
5'
exonuclease
Decapping complex
Dcp1
DDX6
Pat1
Dcp2
EDC3
EDC4
5' exonuclease
XRN1
XRN2
NUDT16
Lsm complex
Cytoplasmic Lsm 1-7 complex
Lsm1
Lsm2
Lsm3
Lsm4
Lsm8
Lsm5
Lsm6
Lsm7
Nuclear Lsm 2-8 complex
Bacterial RNA degradation
RNase E (Escherichia coli)
Catalytic domain
C-terminal domain
Degradosome component interaction
RNA helicase (Rhlb)
Enolase
PNPase
RNA-binding domain
AR 2
(arginine-rich region)
triphosphate
5'
RNA
pyrophosphatase
RppH
RNA degradosome
RNA degradosome type A (Escherichia coli)
RNase E
RhlB
Enolase
PNPase
RNA degradosome type B (Pseudomonas)
RNase E
RhlE
RNaseR
RNA degradosome type C (Rhodobacter)
RNase E
helicases
Rho
RNA degradosome type D (Bacillus subtilis)
RNaseY
CshA
RNaseJ
Enolase
PNPase
PfkA
Associated proteins
DnaK
GroEL
Hfq
PPK
PAP
Archeal RNA degradation
5'
RNA
Rrp41
Rrp42
Csl4 / Rrp4
Rrp42
Csl4 / Rrp4
Rrp41
Csl4 / Rrp4
Rrp41
Rrp42
Ring core
Cap structure
Archeal exosome
Rrp41
Rrp42
Rrp4
Csl4

03018 11/6/14



03010 7/29/13
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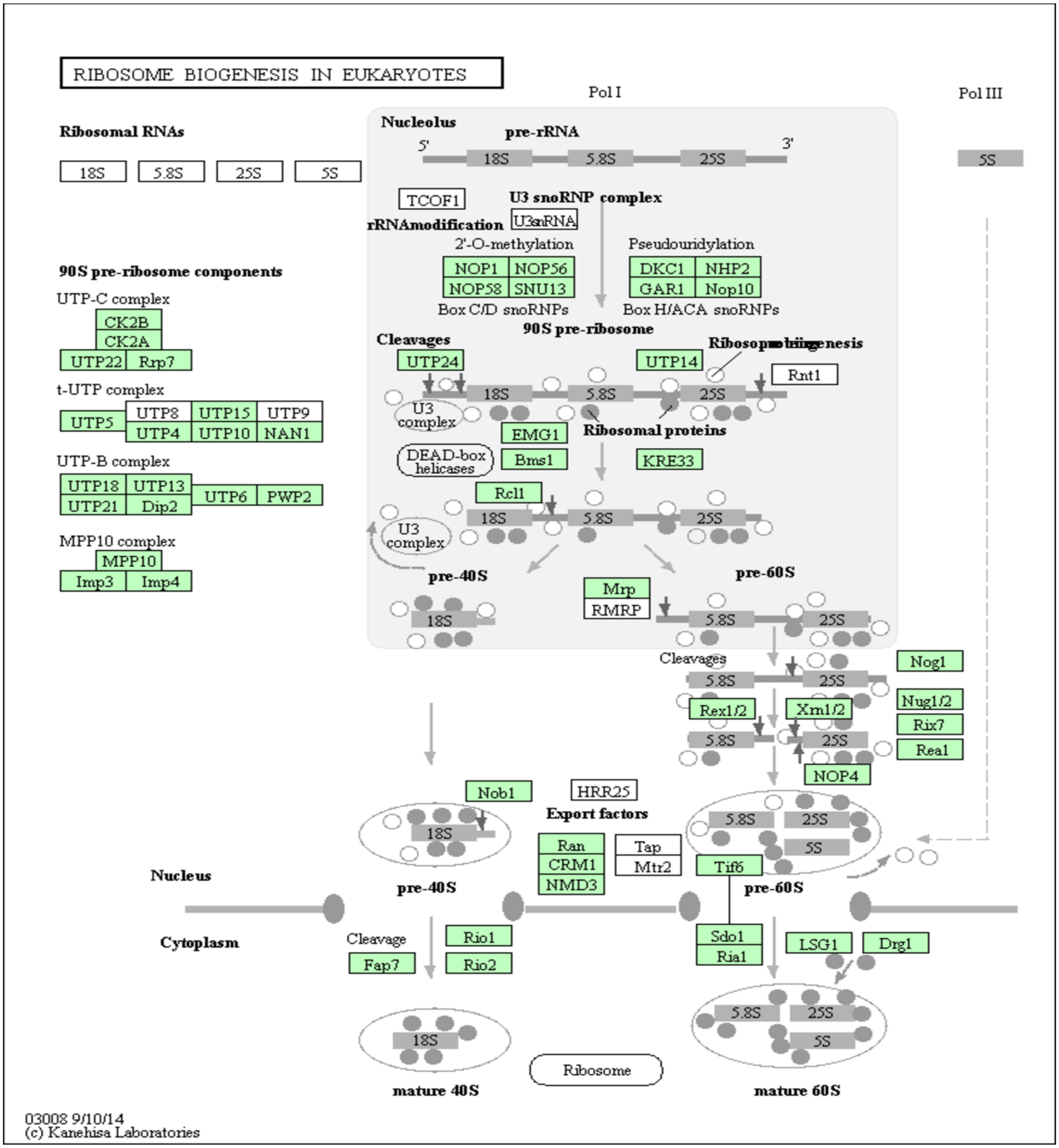
RIBOSOME BIOGENESIS IN EUKARYOTES
Pol I
Pol III
Nucleolus
pre-rRNA
5'
3'
18S
5.8S
25S
5S
Ribosomal RNAs
18S
5.8S
25S
5S
TCOF1
rRNAmodification
U3 snoRNP complex
U3 snoRNA
2'-O-methylation
NOP1
NOP56
NOP58
SNU13
Box C/D snoRNPs
Pseudouridylation
DKC1
NHP2
GAR1
Nop10
Box H/ACA snoRNPs
90S pre-ribosome components
UTP-C complex
CK2B
CK2A
UTP22
Rrp7
t-UTP complex
UTP5
UTP8
UTP15
UTP9
UTP4
UTP10
NAN1
UTP-B complex
UTP18
UTP13
UTP21
Dip2
UTP6
PWP2
MPP10 complex
MPP10
Imp3
Imp4
90S pre-ribosome
Cleavages
UTP24
UTP14
Ribosome biogenesis
Rnt1
U3 complex
EMG1
Ribosomal proteins
DEAD-box helicases
Bms1
KRE33
Rcl1
U3 complex
pre-40S
pre-60S
Mrp
RMRP
Cleavages
Nog1
Rex1/2
Xrn1/2
Nug1/2
Rix7
Rea1
NOP4
Nob1
HRR25
Export factors
Ran
CRM1
NMD3
Tap
Mtr2
Tif6
pre-40S
pre-60S
Nucleus
Cytoplasm
Cleavage
Fap7
Rio1
Rio2
Sdo1
Ria1
LSG1
Drg1
Ribosome
mature 40S
mature 60S
03008 9/10/14
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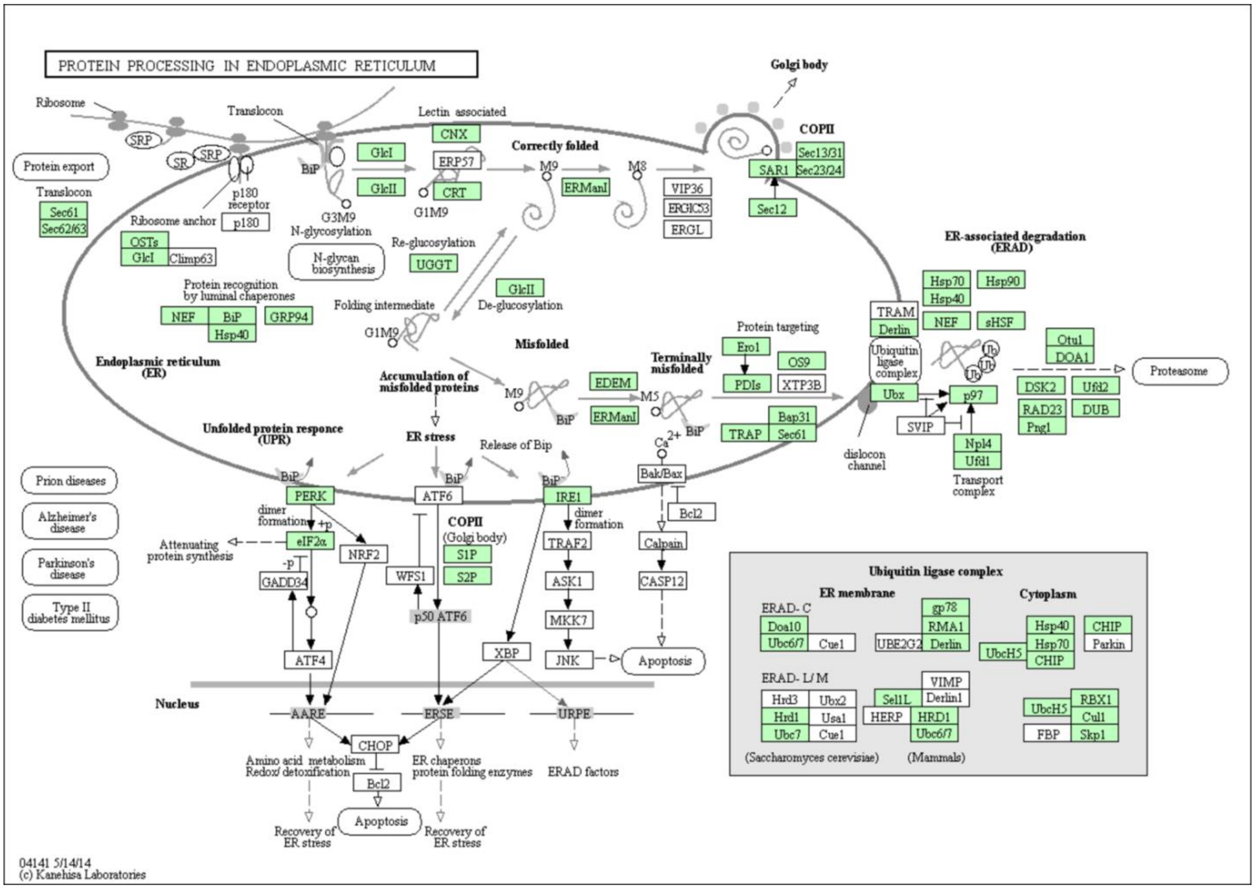
PROTEIN PROCESSING IN ENDOPLASMIC RETICULUM
Ribosome
Translocon
SRP
SR
SRP
Protein export
Translocon
Sec61
Sec62/63
p180 receptor
Ribosome anchor
p180
OSTs
GlcI
Climp63
BiP
G3M9
N-glycosylation
N-glycan biosynthesis
Lectin associated
CNX
GlcI
GlcII
ERP57
CRT
G1M9
Re-glucosylation
UGGT
Correctly folded
M9
M8
ERManI
VIP36
ERGIC53
ERGL
Golgi body
COPII
SAR1
Sec13/31
Sec23/24
Sec12
Protein recognition by luminal chaperones
NEF
BiP
Hsp40
GRP94
GlcII
De-glucosylation
Folding intermediate
G1M9
Endoplasmic reticulum (ER)
Misfolded
Accumulation of misfolded proteins
M9
EDEM
M5
ERManI
BiP
Terminally misfolded
Protein targeting
Ero1
PDIs
OS9
XTP3B
Bap31
TRAP
Sec61
ER-associated degradation (ERAD)
TRAM
Derlin
Hsp70
Hsp40
Hsp90
NEF
sHSF
Ubiquitin ligase complex
Ubx
Ub
Ub
Ub
p97
SVIP
Npl4
Ufd1
Transport complex
dislocon channel
Otu1
DOA1
Proteasome
DSK2
Ufd2
RAD23
DUB
Png1
Unfolded protein responce (UPR)
ER stress
Release of Bip
Ca2+
BiP
BiP
BiP
BiP
PERK
ATF6
IRE1
Bak/Bax
Bcl2
dimer formation
+p
eIF2α
Attenuating protein synthesis
-p
GADD34
NRF2
WFS1
COPII (Golgi body)
S1P
S2P
p50 ATF6
dimer formation
TRAF2
ASK1
MKK7
JNK
Apoptosis
Calpain
CASP12
ATF4
XBP
Nucleus
AARE
ERSE
URPE
CHOP
Bcl2
Amino acid metabolism
Redox/ detoxification
ER chaperons
protein folding enzymes
ERAD factors
Apoptosis
Recovery of ER stress
Recovery of ER stress
Prion diseases
Alzheimer's disease
Parkinson's disease
Type II diabetes mellitus
Ubiquitin ligase complex
ER membrane
Cytoplasm
ERAD- C
Doa10
Ubc6/7
Cue1
gp78
RMA1
UBE2G2
Derlin
Hsp40
CHIP
UbcH5
Hsp70
Parkin
CHIP
ERAD- L/ M
Hrd3
Ubx2
Hrd1
Usa1
Ubc7
Cue1
VIMP
Sel1L
Derlin1
HERP
HRD1
Ubc6/7
UbcH5
RBX1
Cul1
FBP
Skp1
(Saccharomyces cerevisiae)
(Mammals)
04141 5/14/14
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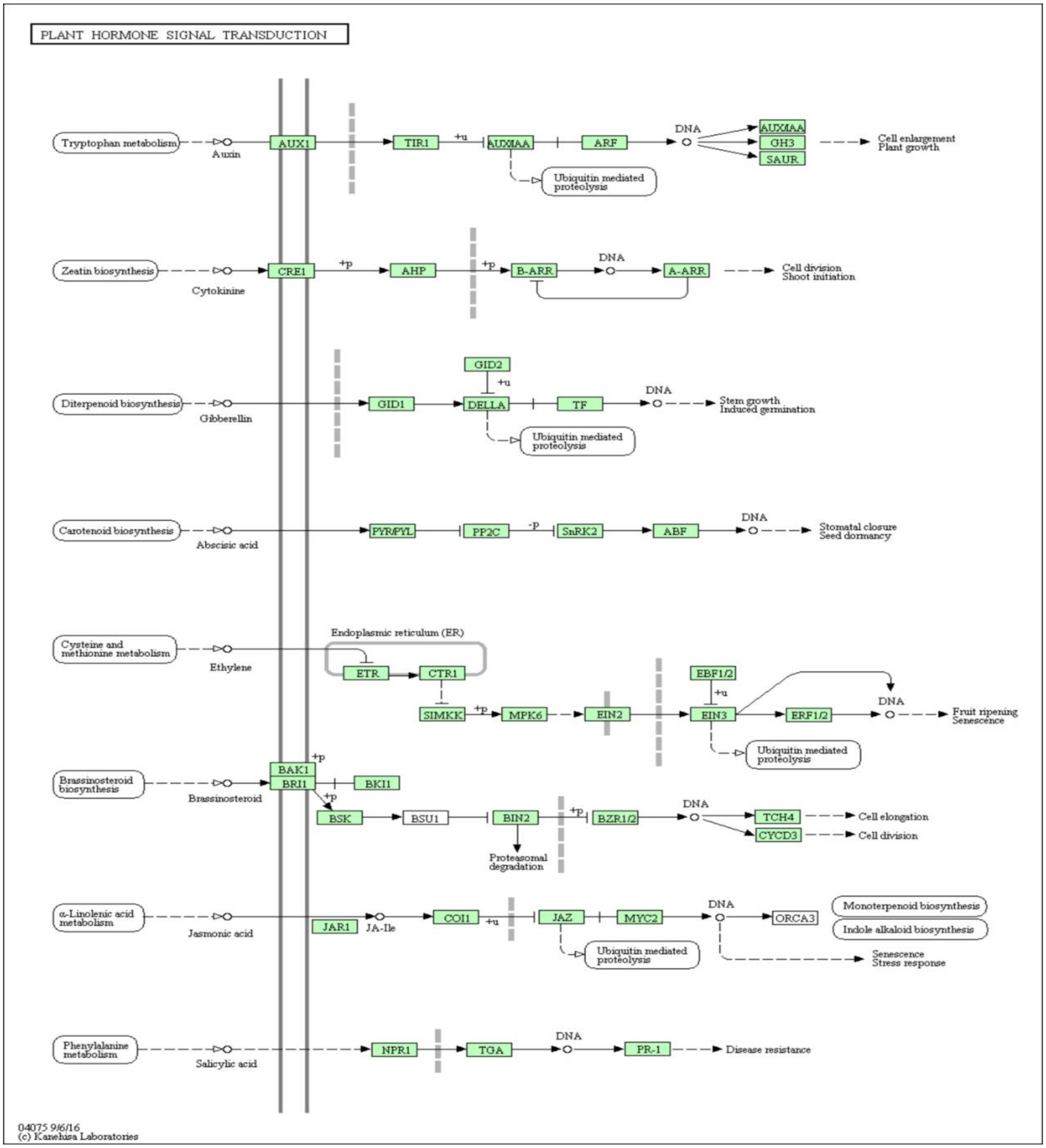
PLANT HORMONE SIGNAL TRANSDUCTION
Tryptophan metabolism
Auxin
AUX1
TIR1
+u
AUX/IAA
ARF
DNA
AUX/IAA
GH3
SAUR
Cell enlargement
Plant growth
Ubiquitin mediated proteolysis
Zeatin biosynthesis
Cytokinine
CRE1
+p
AHP
+p
B-ARR
DNA
A-ARR
Cell division
Shoot initiation
GID2
+u
Diterpenoid biosynthesis
Gibberellin
GID1
DELLA
TF
DNA
Stem growth
Induced germination
Ubiquitin mediated proteolysis
Carotenoid biosynthesis
Abscisic acid
PYR/PYL
PP2C
-p
SnRK2
ABF
DNA
Stomatal closure
Seed dormancy
Cysteine and methionine metabolism
Ethylene
Endoplasmic reticulum (ER)
ETR
CTR1
SIMKK
+p
MPK6
EIN2
EBF1/2
+u
EIN3
ERF1/2
DNA
Fruit ripening
Senescence
Ubiquitin mediated proteolysis
Brassinosteroid biosynthesis
Brassinosteroid
BAK1
BRI1
+p
BKI1
+p
BSK
BSU1
BIN2
Proteasomal degradation
+p
BZR1/2
DNA
TCH4
CYCD3
Cell elongation
Cell division
α-Linolenic acid metabolism
Jasmonic acid
JAR1
JA-Ile
COI1
+u
JAZ
MYC2
DNA
ORCA3
Monoterpenoid biosynthesis
Indole alkaloid biosynthesis
Ubiquitin mediated proteolysis
Senescence
Stress response
Phenylalanine metabolism
Salicylic acid
NPR1
TGA
DNA
PR-1
Disease resistance
04075 9/6/16
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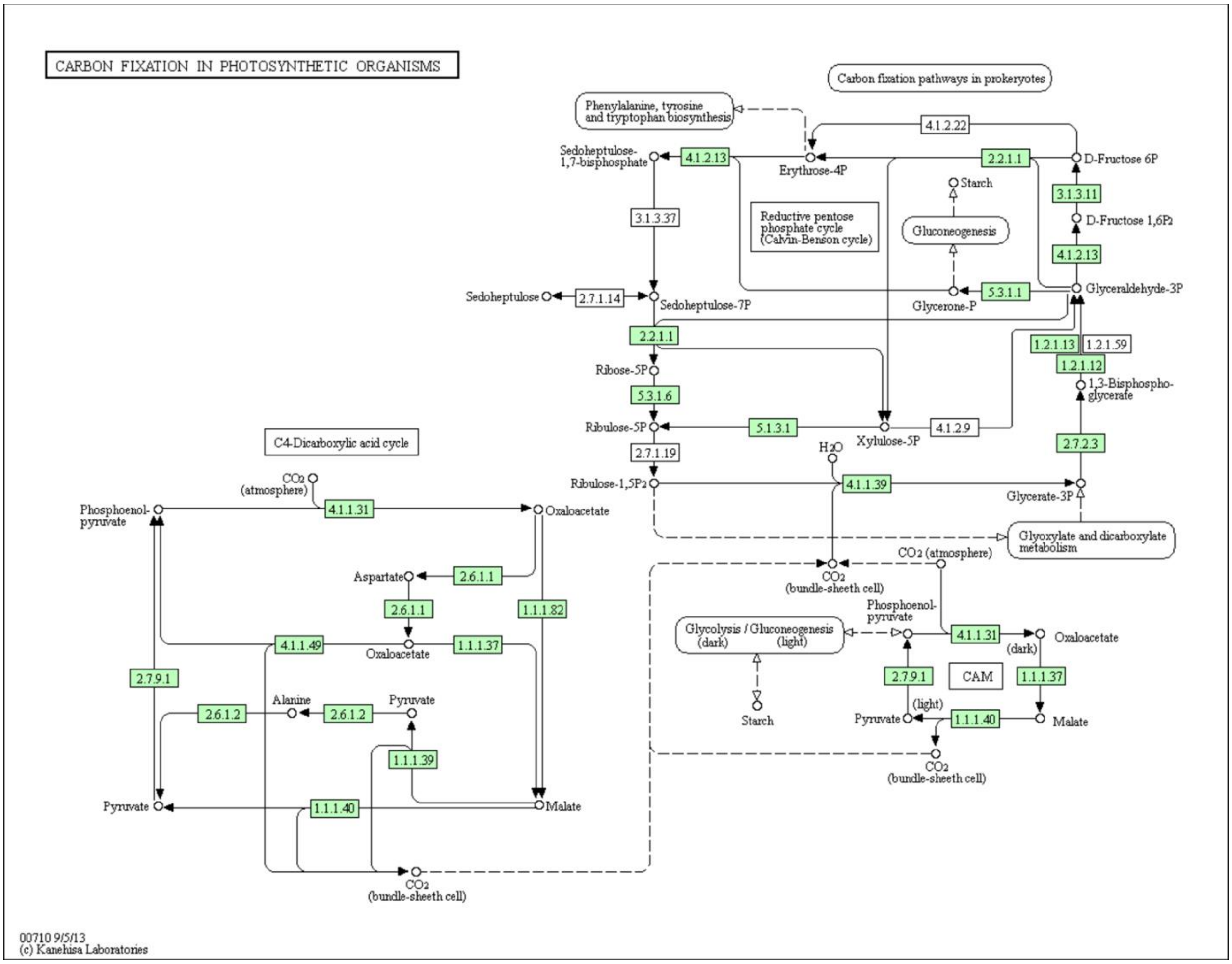
CARBON FIXATION IN PHOTOSYNTHETIC ORGANISMS
Carbon fixation pathways in prokeryotes
Phenylalanine, tyrosine and tryptophan biosynthesis
4.1.2.22
Sedoheptulose-1,7-bisphosphate
4.1.2.13
Erythrose-4P
2.2.1.1
D-Fructose 6P
Starch
3.1.3.11
3.1.3.37
Reductive pentose phosphate cycle (Calvin-Benson cycle)
Gluconeogenesis
D-Fructose 1,6P2
4.1.2.13
Sedoheptulose
2.7.1.14
Sedoheptulose-7P
Glycerone-P
5.3.1.1
Glyceraldehyde-3P
2.2.1.1
1.2.1.13
1.2.1.59
1.2.1.12
Ribose-5P
1,3-Bisphospho-glycerate
5.3.1.6
Ribulose-5P
5.1.3.1
Xylulose-5P
4.1.2.9
2.7.1.19
H2O
2.7.2.3
C4-Dicarboxylic acid cycle
Ribulose-1,5P2
4.1.1.39
Glycerate-3P
CO2 (atmosphere)
Phosphoenol-pyruvate
4.1.1.31
Oxaloacetate
Glyoxylate and dicarboxylate metabolism
CO2 (atmosphere)
CO2 (bundle-sheeth cell)
Aspartate
2.6.1.1
2.6.1.1
1.1.1.82
Phosphoenol-pyruvate
Glycolysis / Gluconeogenesis (dark) (light)
4.1.1.31
Oxaloacetate
(dark)
4.1.1.49
Oxaloacetate
1.1.1.37
2.7.9.1
2.7.9.1
CAM
1.1.1.37
Starch
(light)
Alanine
Pyruvate
Pyruvate
1.1.1.40
Malate
2.6.1.2
2.6.1.2
CO2 (bundle-sheeth cell)
1.1.1.39
Pyruvate
1.1.1.40
Malate
CO2 (bundle-sheeth cell)
00710 9/5/13
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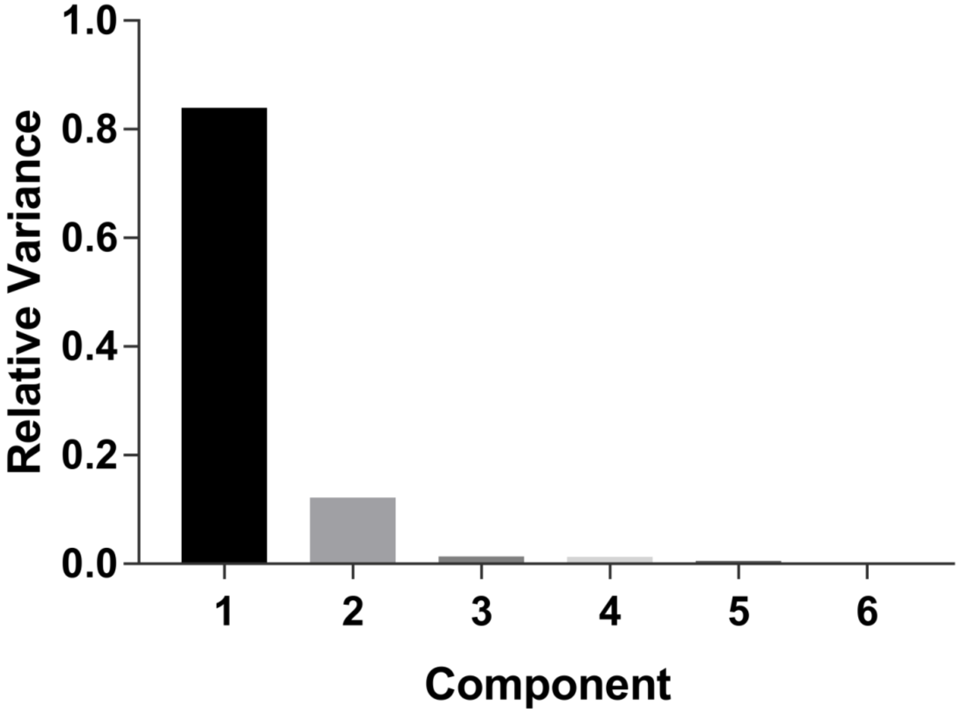
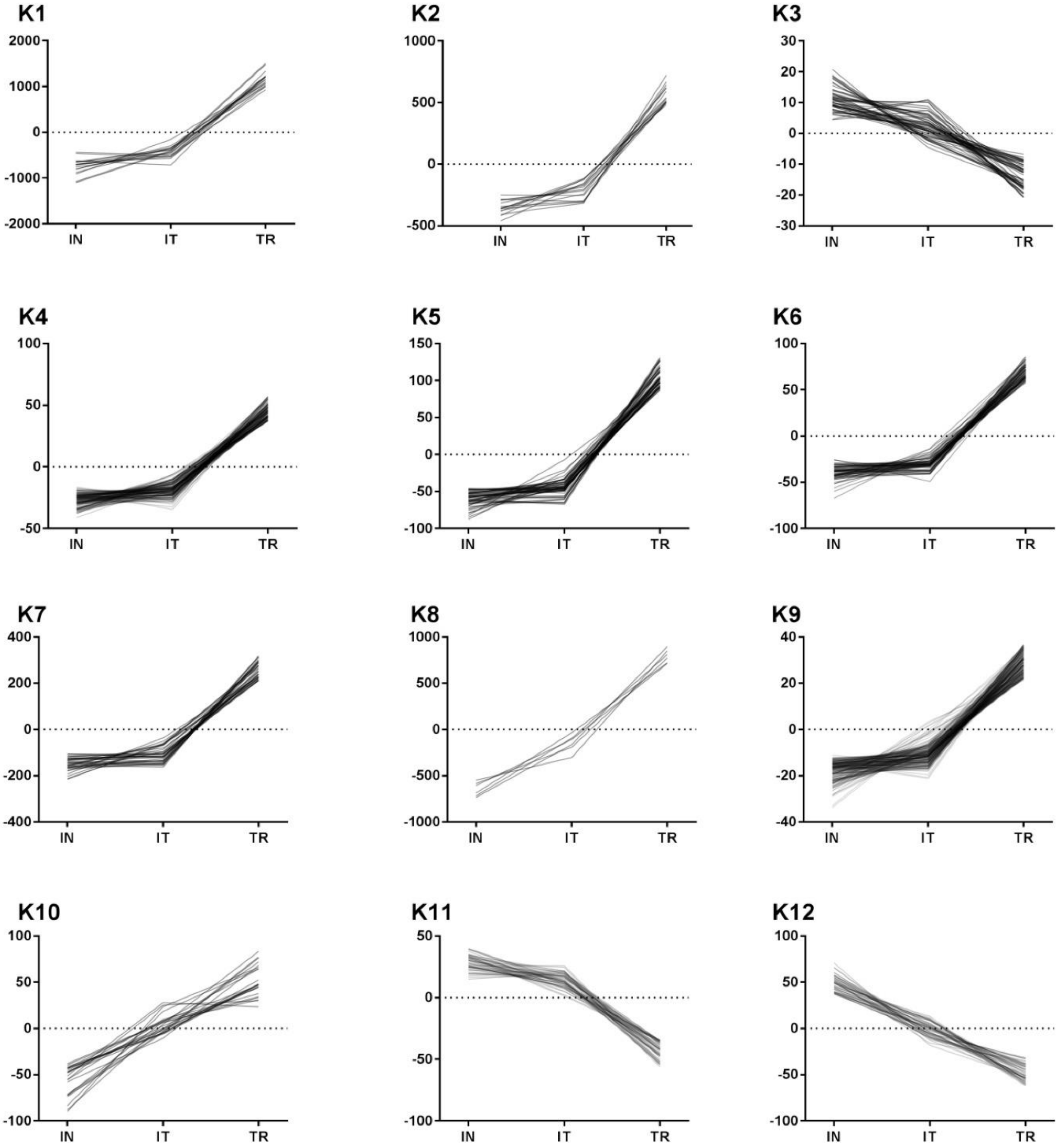
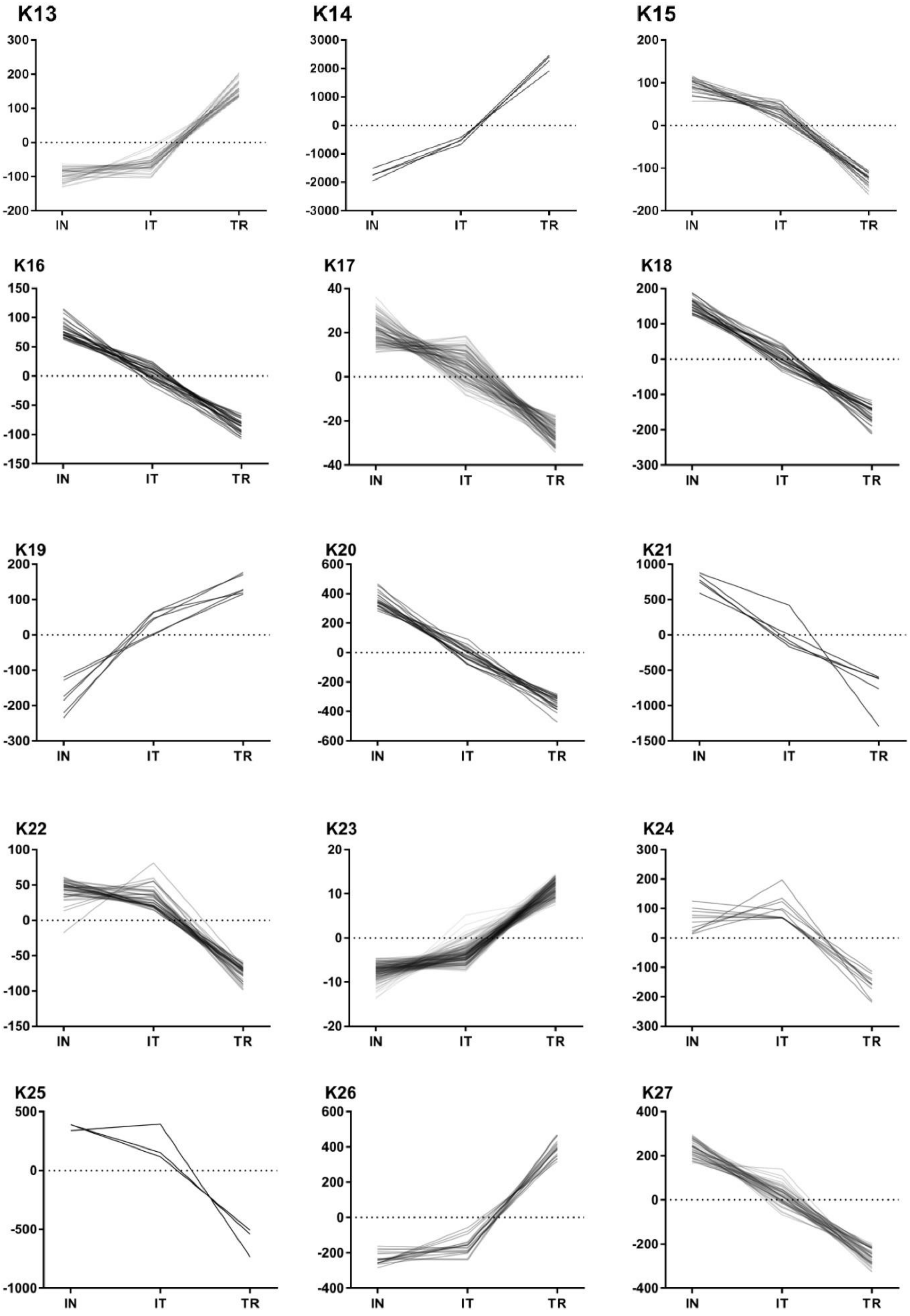
Supplementary Figure S3. Scree plot of the principal components for the *Pachycereus pringlei* samples used in this study. The cumulative variance of the two first principal components is 96.2%.

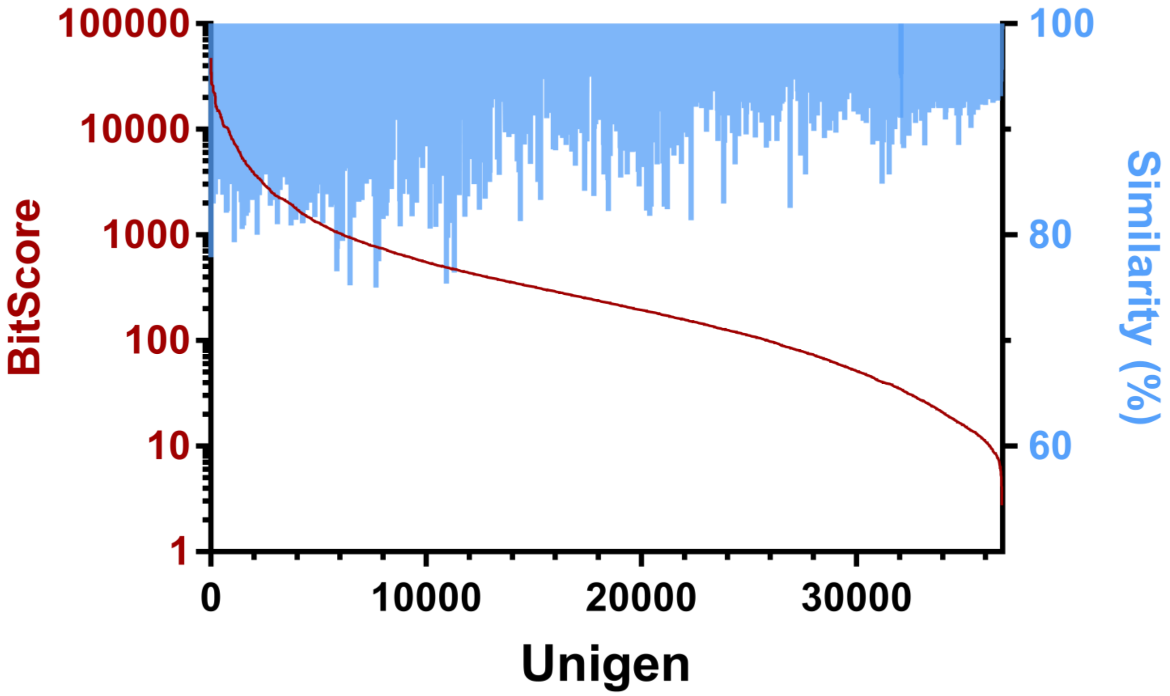


Supplementary Figure S4. Transcriptional profiles identified by *k*-mean clustering of the differentially expressed transcripts (DETs). Each plot depicts the normalized and centered expression level of the DETs at the three developmental stages of the *Pachycereus pringlei* primary root apex: IN, initial; IT, intermediate; TR, terminal.

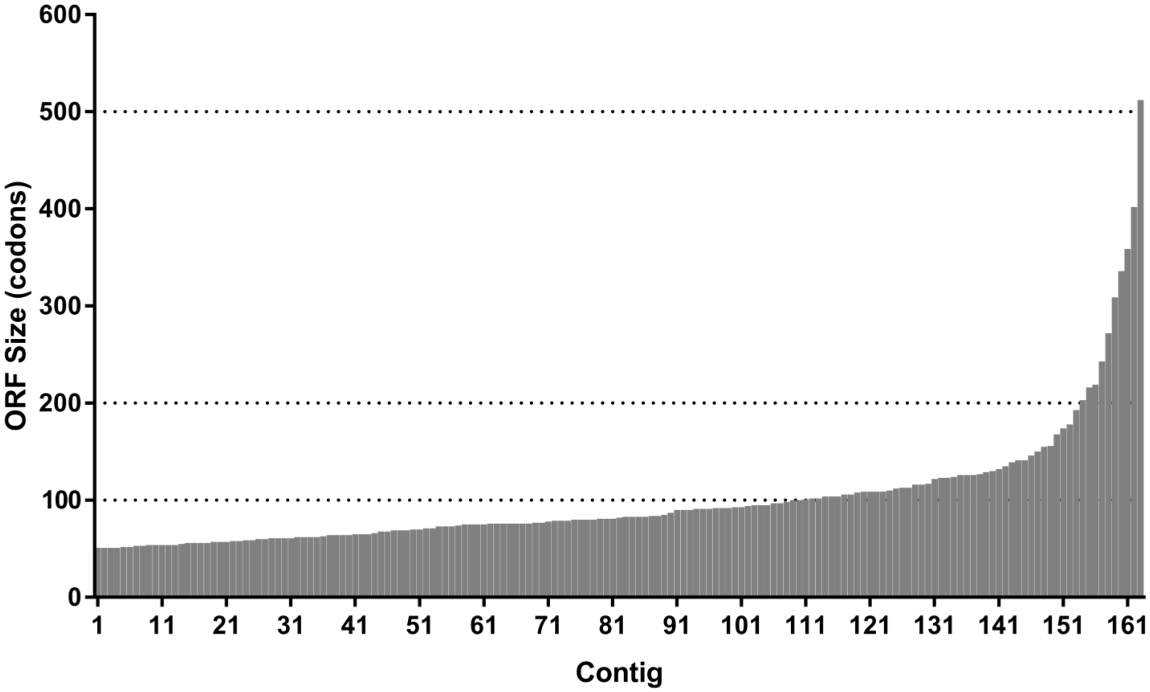



K13
300
200
100
0
-100
-200
IN
IT
TR
K14
3000
2000
1000
0
-1000
-2000
-3000
IN
IT
TR
K15
200
100
0
-100
-200
IN
IT
TR
K16
150
100
50
0
-50
-100
-150
IN
IT
TR
K17
40
20
0
-20
-40
IN
IT
TR
K18
200
100
0
-100
-200
-300
IN
IT
TR
K19
200
100
0
-100
-200
-300
IN
IT
TR
K20
600
400
200
0
-200
-400
-600
IN
IT
TR
K21
1000
500
0
-500
-1000
-1500
IN
IT
TR
K22
100
50
0
-50
-100
-150
IN
IT
TR
K23
20
10
0
-10
-20
IN
IT
TR
K24
300
200
100
0
-100
-200
-300
IN
IT
TR
K25
500
0
-500
-1000
IN
IT
TR
K26
600
400
200
0
-200
-400
IN
IT
TR
K27
400
200
0
-200
-400
IN
IT
TR

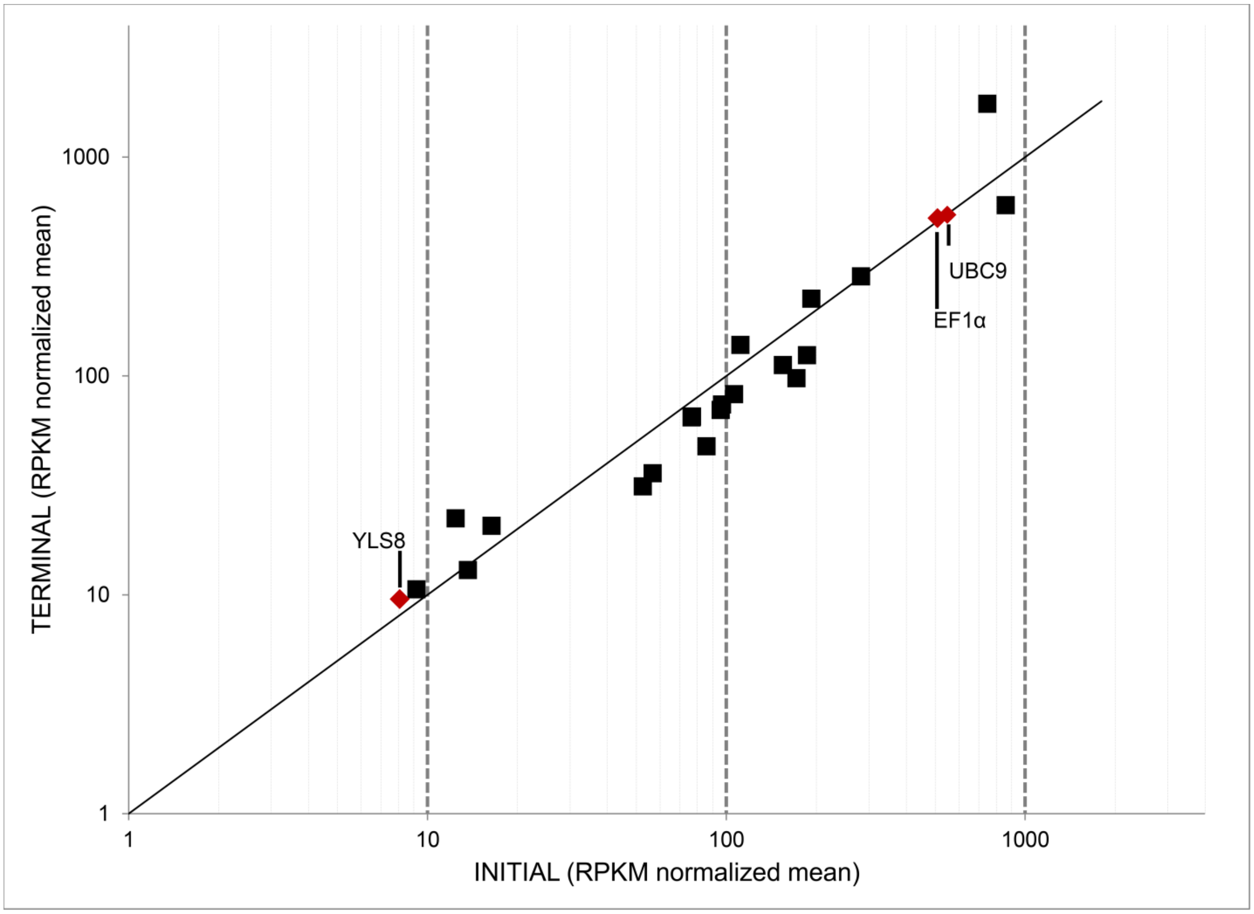
Supplementary Figure S5. Summary plot of the BlastN of the *Lophophora williamsii* shoot+root transcriptome against the *de novo* assembled transcriptome of the primary root apex of *Pachycereus pringlei*.



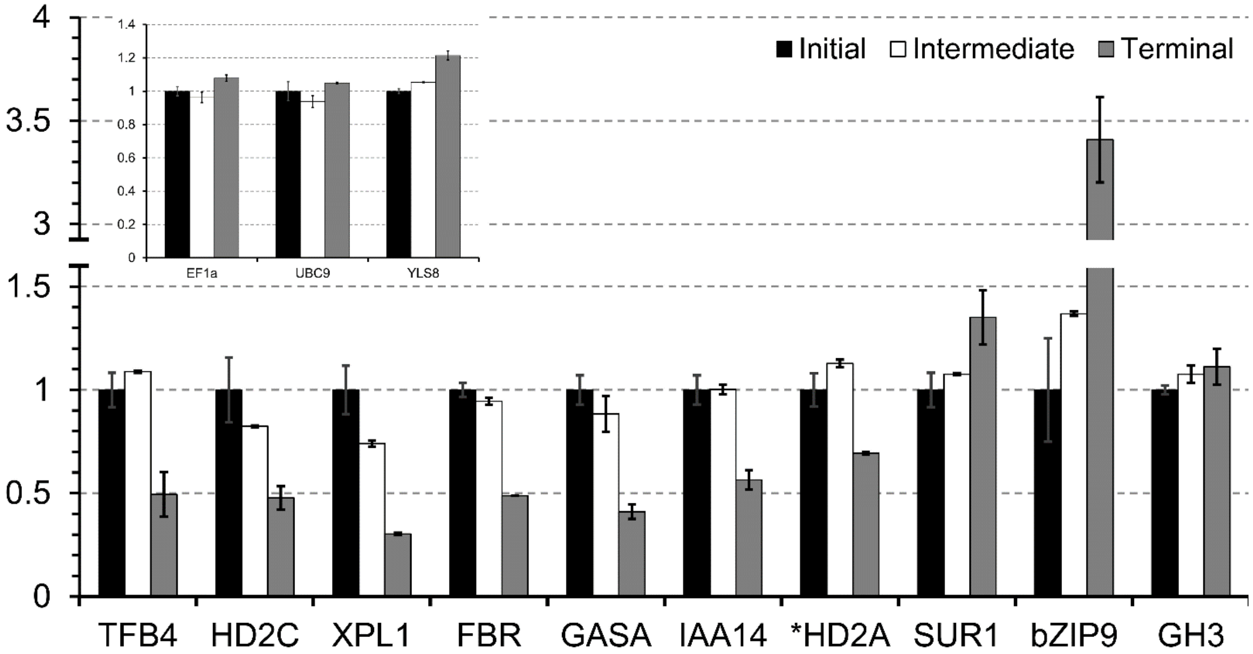
Supplementary Figure S6. Length distribution of the putative open reading frames identified in the un-annotated *Pachycereus pringlei* differentially expressed transcripts.



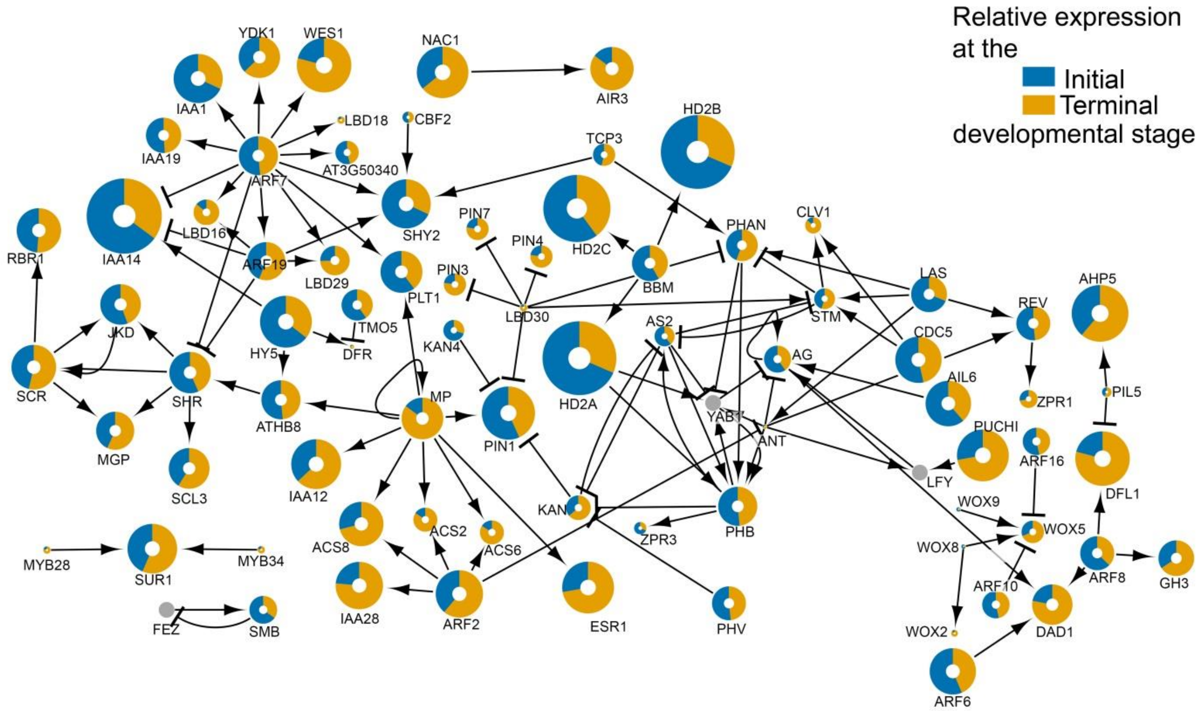
Supplementary Figure S7. Expression levels (RPKM values) of the *Pachycereus pringlei* candidate reference genes in the primary root apex at the initial and terminal developmental stages. Red diamonds correspond to the selected reference genes for this study.



Supplementary Figure S8. Average RPKM values of the *Pachycereus pringlei* transcripts quantified by RT-qPCR. * the trend for RPKM values and transcript abundance evaluated by qRT-PCR between initial and terminal development stages was different for this transcript.



Supplementary Figure S9. Inferred transcriptional regulatory network for the *Pachycereus pringlei* primary root apex. The node size is proportional to the average expression level (log$_2$(RPKM)) of the transcript in the *P. pringlei* transcriptome.



Supplementary Table S1. Number of differentially expressed genes for developmental zones of the primary root of six angiosperm species.

	EDGE MZ vs EZ		EDGE MZ vs DZ	
Species	MZ	EZ	MZ	DZ
Arabidopsis thaliana	2,683	4,432	3,734	8,947
Cucumis sativus	601	380	1,341	301
Glycine max	1,357	4,159	3,866	7,685
Oryza sativa	772	1,655	3,084	7,743
Solanum lycopersicum	2,905	3,542	4,125	5,661
Zea mays	2,018	3,285	8,012	8,563

* With the exception of *Cucumis sativus*, the number of up-regulated genes at the meristematic zone is lower in comparison to the up-regulated genes at the elongation or differentiation zone. This exception may arise from the fact that in *C. sativus*, unlike all the other species included in this table, new lateral root primordia are developed within meristematic zone (moreover, *C. sativus* develops the first lateral root primordia since the embryo development) (Dubrovsky & Rost, 2003).

Row data taken from Huang & Schiefelbein, 2015.

Dubrovsky J.G. & Rost T.L. 2003. Lateral root initiation. Encyclopedia of Applied Plant Sciences. Ed. by Thomas B., Murphy D.J., and Murray B.G. Academic Press (ISBN:0122270509) pp: 1101-1107.

Supplementary Table S2. Comparison of *Lophophora williamsii* and *Pachycereus pringlei de novo* assembled transcriptomes.

		*Lophophora**	*Pachycereus*
Sequencing	Platform	IonTorrent / 454	Illumina HiSeq
	Reads:	Single End	Paired End
	Total Reads	$6x10^6$	$280x10^6$
	Read Size (nt)	50-150	100 (x2)
Assembly	Min. contig Length (nt)	200	400
	Max. contig Length (nt)	4,170	14,583
	Av. contig Length (nt)	572	1,081
	Median contig Length (nt)	454	728
	Total contigs	40,436	49,045

* Data taken from Ibarra-Laclette *et al.*, 2015.

Supplementary Table S3. BlastN statistics from the comparison of *Lophophora williamsii* shoot+root transcriptome and *Pachycereus pringlei* root tip transcriptome.

	Minimum	Maximum	Average	Median
Identity	75	100	99.26	100
Bit Score	20.02	47,628.06	1,054.18	261.38
HSP*	1	270	21.6	21
E-value	0	9.75	0.02	0

* HSP: High-scoring significant pair.

Supplementary Table S4. *Pachycereus pringlei* putative orthologs of the *Arabidopsis* superior reference genes (Czechowski *et al*., 2005). The less variable contigs are included in the box. The asterisks indicate the reference genes used in this study.

Arabidopsis name	*P. pringlei* Contig	INITIAL		INTERMEDIATE		TERMINAL	
		RPKM 1	RPKM 2	RPKM 1	RPKM 2	RPKM 1	RPKM 2
AcylCoA BP	03269	73.21	58.6	66.48	66.63	38.02	38.08
PP2A	05248	142.42	121.42	123.2	123.98	77.23	78.74
AcylCoA BP	02079	43.93	36.76	39.08	40.8	24.55	25.43
CLA	09503	44.57	42.57	45.06	40.6	26.73	30.67
PP2A	09902	149.25	136.93	142.45	131.55	99.33	99.38
E2Fα	05001	717.61	604.83	684.04	727.78	545	415.74
PP2A	08913	112.74	124.83	112.59	100.72	88.43	90.68
CLA	12003	76.83	70.33	70.34	74.13	51.9	55.87
PP2A	07793	73.44	75.34	66.15	55.63	53.3	65.22
PP2A	04543	84.65	78.54	76.9	77.21	61.8	70.07
UBC	22624	59.02	58.65	56.54	54.67	48.15	55.25
KOR1	03527	58.84	59.27	64.18	72.66	54.75	49.39
KOR1	22902	10.52	10.46	14.94	17.09	10.13	10.62
UBC	**24691**	**414.88**	**427.47**	**396.49**	**377.1**	**402.53**	**470.79**
UBC9*	**15035**	**229.12**	**204.45**	**210.96**	**195.78**	**226.4**	**228.57**
E1Fα*	**06759**	**401.27**	**379.59**	**363.6**	**388.22**	**428.72**	**413.51**
GalaOx	***03600***	***7.44***	***6.67***	***8.34***	***8.38***	***9.1***	***7.8***
YLS8*	**17282**	**145.98**	**150.19**	**156.32**	**155.68**	**183.81**	**175.92**
AGL31	***07058***	***5.9***	***6.49***	***5.29***	***7.16***	***7.85***	***7.45***
UBC	17222	80.47	90.87	89.78	90.51	100.3	121.37
PTB	48438	12.67	12.51	16.71	20.22	16.55	16.46
YLS8	30952	9.48	9.62	7.07	7.67	19.24	16.42
UBC	35678	525.63	622.83	655.12	672.13	1,546.79	1,249.75

Supplementary Table S5. Interaction of the *Arabidopsis* nodes used for the *Pachycereus pringlei* transcriptional regulatory network.

Node A	Interaction type	Node B
AT1G30330	Activation	AT2G44810
AT1G30490	Repression	AT5G16560
AT5G16560	Repression	AT1G65620
AT5G16560	Repression	AT1G73590
AT1G09770	Activation	AT1G62360
AT1G09770	Activation	AT1G75820
AT1G62360	Repression	AT2G37630
AT1G62360	Repression	AT1G65620
AT1G62360	Activation	AT1G75820
AT2G45190	Repression	AT4G18960
AT2G45190	Activation	AT2G34710
AT4G18960	Activation	AT2G44810
AT4G18960	Activation	AT4G18960
AT2G34710	Activation	AT1G65620
AT2G34710	Repression	AT5G16560
AT2G34710	Activation	AT2G45190
AT2G34710	Activation	AT3G52770
AT2G37630	Activation	AT2G34710
AT2G37630	Repression	AT2G45190
AT1G65620	Repression	AT2G45190
AT1G65620	Activation	AT2G34710
AT1G65620	Repression	AT1G62360
AT1G65620	Repression	AT5G16560
AT4G37750	Activation	AT5G61850
AT4G37750	Activation	AT5G60690
AT4G37750	Repression	AT4G18960
AT4G37750	Activation	AT2G45190
AT4G37750	Activation	AT2G34710
AT5G42630	Repression	AT1G73590
AT5G45980	Activation	AT5G59340
AT5G45980	Activation	AT3G11260
AT5G62000	Activation	AT1G01480
AT5G62000	Activation	AT4G11280
AT5G62000	Repression	AT4G37750
AT5G62000	Activation	AT4G37770
AT5G62000	Activation	AT5G25890
AT2G28350	Repression	AT3G11260
AT5G61850	Activation	AT4G18960

AT5G60690	Activation	AT2G45450
AT3G44750	Activation	AT2G34710
AT3G44750	Activation	AT2G45190
AT1G55580	Activation	AT1G62360
AT1G55580	Activation	AT2G37630
AT1G55580	Activation	AT5G60690
AT1G55580	Activation	AT4G37750
AT1G79580	Repression	AT1G26870
AT1G26870	Activation	AT1G79580
AT1G56010	Activation	AT2G04160
AT3G25710	Repression	AT5G42800
AT4G30080	Repression	AT3G11260
AT4G25470	Activation	AT1G04240
AT4G37650	Activation	AT5G03150
AT4G37650	Activation	AT3G54220
AT4G37650	Activation	AT1G03840
AT4G37650	Activation	AT1G50420
AT5G03150	Activation	AT3G54220
AT3G54220	Activation	AT1G03840
AT3G54220	Activation	AT3G12280
AT3G54220	Activation	AT5G03150
AT5G11260	Activation	AT4G32880
AT5G11260	Activation	AT4G14550
AT5G11260	Activation	AT5G42800
AT4G32880	Activation	AT4G37650
AT5G10510	Activation	AT4G18960
AT1G19850	Activation	AT3G20840
AT1G19850	Activation	AT4G11280
AT1G19850	Activation	AT4G32880
AT1G19850	Activation	AT4G37770
AT1G19850	Activation	AT1G04550
AT1G19850	Activation	AT1G12980
AT1G19850	Activation	AT1G19850
AT1G19850	Activation	AT1G73590
AT1G19850	Activation	AT1G01480
AT5G61420	Activation	AT2G20610
AT2G33880	Activation	AT3G11260
AT1G53230	Activation	AT2G37630
AT1G53230	Activation	AT1G04240
AT1G19220	Repression	AT4G14550
AT1G19220	Repression	AT4G37650
AT1G19220	Activation	AT2G42430
AT1G19220	Activation	AT3G58190

AT1G19220	Activation	AT1G04240
AT2G20180	Activation	AT1G03430
AT2G20180	Repression	AT5G54510
AT5G20730	Activation	AT3G20840
AT5G20730	Activation	AT3G15540
AT5G20730	Activation	AT3G58190
AT5G20730	Activation	AT3G50340
AT5G20730	Activation	AT1G19220
AT5G20730	Activation	AT1G04240
AT5G20730	Activation	AT2G45420
AT5G20730	Activation	AT2G42430
AT5G20730	Repression	AT4G37650
AT5G20730	Activation	AT4G14560
AT5G20730	Repression	AT4G14550
AT5G20730	Activation	AT4G37390
AT5G20730	Activation	AT4G27260
AT5G17430	Activation	AT3G44750
AT5G17430	Activation	AT5G03740
AT5G17430	Activation	AT5G22650
AT5G18560	Activation	AT5G61850
AT5G37020	Activation	AT1G28130
AT5G37020	Activation	AT2G44810
AT5G37020	Activation	AT5G54510
AT5G60890	Activation	AT2G20610
AT4G00220	Repression	AT2G37630
AT4G00220	Repression	AT2G01420
AT4G00220	Repression	AT1G73590
AT4G00220	Repression	AT1G70940
AT4G00220	Activation	AT1G62360
AT4G00220	Repression	AT1G23080

Supplementary Table S6. Properties of the nodes included in the *Pachycereus pringlei* transcriptional regulatory network of the primary root apex. NSH=No significant hit; NHF=No hit found; Y= Yes; N=No; Interm.=Intermediate.

Node	*Arabidopsis* name	*P. pringlei* contig	*P. pringlei* annotation	E-value	BBH	RPKM Initial	RPKM Interm.	RPKM Term.
AT1G30330	ARF6	0001038	auxin response factor 6-like	0	Y	24.12	27.34	18.65
AT2G44810	DAD1	0005103	phospholipase a1-chloroplastic-like	2.52E-75	N	7.27	9.93	25.76
AT1G30490	PHV	0001618	homeobox-leucine zipper protein revoluta	0	Y	7.93	9.77	7.39
AT5G16560	KAN	0005141	probable transcription factor kan2-like	4.24E-47	N	2.62	4.36	4.6
AT1G09770	CDC5	0000721	cell division cycle 5-like isoform x1	0	Y	23.08	26.9	20.04
AT1G62360	STM	0009327	homeobox protein knotted-1-like 6	3.66E-72	N	2.52	2.83	3.05
AT1G75820	CLV1	0001781	receptor protein kinase clavata1-like	0	Y	0.6	1.5	3.68
AT2G45190	YAB1	NSH	NSH	3.51	NSH	0.001	0.001	0.001
AT4G18960	AG	0032278	mads-box transcription factor 27-like isoform x1	2.62E-44	N	6.33	3.48	4.25
AT2G34710	PHB	0000849	homeobox-leucine zipper family protein	0	Y	12.14	14.87	11.42
AT2G37630	PHAN	0008775	transcription factor as1	1.94E-118	Y	5.7	8.01	7.17
AT1G65620	AS2	0027369	lob domain-containing protein 6	1.71E-62	Y	2.89	3.22	1.86
AT1G73590	PIN1	0002874	auxin efflux carrier component 1-like	0	Y	44.07	46	33.59
AT3G52770	ZPR3	0030394	PREDICTED: uncharacterized protein LOC101514572	1.15E-08	Y	1.74	1.66	0.78
AT4G37750	ANT	0014765	ap2-like ethylene-responsive transcription factor ant-like	1.99E-113	Y	0.53	0.34	1.28
AT5G42630	KAN4	0013106	probable transcription factor kan2-like	6.47E-35	N	3.3	3.75	1.42
AT5G45980	WOX8	0045416	wuschel-related homeobox 11-like	7.83E-16	N	1.15	0.48	0.54
AT5G59340	WOX2	0033393	wuschel-related homeobox 4	1.52E-21	N	0.33	0.39	1.91
AT3G11260	WOX5	0019483	wuschel-related homeobox 5-like	2.28E-51	Y	1.77	3.98	3.94
AT5G62000	ARF2	0001054	auxin response factor 2	0	N	19.42	26.39	30.43
AT1G01480	ACS2	0006764	1-aminocyclopropane-1-carboxylate synthase-	0	Y	1.28	2.89	6.82

			like					
AT4G11280	ACS6	0006764	1-aminocyclopropane-1-carboxylate synthase-like	0	Y	1.28	2.89	6.82
AT4G37770	ACS8	0007505	1-aminocyclopropane-1-carboxylate synthase-like	0	Y	9.92	25.33	24.34
AT5G25890	IAA28	0005636	auxin-responsive protein iaa26-like	5.59E-35	N	13.32	20.16	43.38
AT2G28350	ARF10	0001279	auxin response factor 18-like	0	Y	5.09	5.04	4.42
AT5G61850	LFY	0000040	dna polymerase theta	4.14	NSH	0.001	0.001	0.001
AT5G60690	REV	0001618	homeobox-leucine zipper protein revoluta	0	Y	7.93	9.77	7.39
AT3G44750	HD2A	0027114	histone deacetylase isoform 2	8.55E-30	Y	286.77	270.64	131.72
AT2G45450	ZPR1	0041901	PREDICTED: uncharacterized protein LOC101244019	0.03	N	1.46	1.48	3.71
AT1G55580	LAS	0001820	scarecrow-like protein 28	2.58E-50	N	10.83	13.6	4.89
AT1G79580	SMB	0015551	no apical meristem family protein	1.04E-80	Y	5.84	6.09	3.13
AT1G26870	FEZ	NSH	NSH	NSH	NSH	0.1	0.1	0.1
AT1G56010	NAC1	0016854	nac domain-containing protein 21 22-like	2.92E-70	Y	26.76	33.91	47.81
AT2G04160	AIR3	0002155	subtilisin-like protease-like	0	N	6.59	10.36	37.91
AT3G25710	TMO5	0015249	transcription factor bhlh30-like	1.25E-64	N	7.38	6.47	4.98
AT5G42800	DFR	0031589	dihydroflavonol reductase	4.90E-104	Y	0.38	0.36	1.38
AT4G30080	ARF16	0001279	auxin response factor 18-like	0	Y	5.09	5.04	4.42
AT4G25470	CBF2	0025501	dehydration-responsive element-binding protein	1.90E-45	N	1.11	1.73	1.02
AT1G04240	SHY2 (IAA3)	0014302	auxin-induced protein 22b	1.21E-70	N	35.46	36.07	16.64
AT4G37650	SHR	0003271	protein short-root	5.85E-172	Y	15.86	18.57	12.14
AT5G03150	JKD	0003299	zinc finger protein jackdaw-like isoform x1	3.80E-96	Y	15.2	16.09	12.09
AT3G54220	SCR	0003217	protein scarecrow-like	0	Y	16.24	26.26	18.73
AT1G03840	MGP	0005022	zinc finger protein magpie-like	8.02E-127	Y	9.11	14.27	11.97
AT1G50420	SCL3	0003587	scarecrow-like protein 3	0	Y	12.54	13.71	17.92
AT5G11260	HY5	0015206	transcription factor hy5-like	1.04E-46	Y	49.43	33.1	27.33
AT4G32880	ATHB8	0000849	homeobox-leucine zipper family protein	0	Y	12.14	14.87	11.42
AT4G14550	IAA14	0018103	auxin-induced protein aux28	6.06E-99	Y	343.11	351.74	185.48

AT5G10510	AIL6	0003496	ap2-like ethylene-responsive transcription factor ail6-like	5.36E-115	Y	23.18	27.88	14.55
AT1G19850	MP	0000685	transcriptional factor b3 family protein auxin-responsive factor aux iaa-related	0	Y	5.84	8.35	33.42
AT3G20840	PLT1	0004605	ovule development family protein	0	Y	15.14	23.61	9.93
AT1G04550	IAA12	0009934	auxin-responsive protein iaa11-like	6.86E-58	N	22.94	32.12	39.07
AT1G12980	ESR1	0012720	ethylene-responsive transcription factor 4-like	1.54E-16	N	21.46	33.81	55.6
AT5G61420	MYB28	0035249	transcription factor myb35	3.00E-68	N	0.41	0.73	1.62
AT2G20610	SUR1	0007195	tyrosine aminotransferase-like	7.98E-165	N	27.15	29.93	35.17
AT3G12280	RBR1	0001201	retinoblastoma-related protein	0	Y	18.44	21.99	19.38
AT2G33880	WOX9	0045416	wuschel-related homeobox 11-like	1.43E-22	N	1.15	0.48	0.54
AT1G53230	TCP3	0003653	transcription factor tcp4-like	4.30E-70	N	2.99	3.01	3.47
AT1G19220	ARF19	0000777	auxin response factor 19-like	0	Y	9.5	13.97	12.13
AT2G42430	LBD16	0023003	lob domain-containing protein 16	4.33E-65	Y	1.6	1.25	9.77
AT3G58190	LBD29	0010011	lob domain-containing protein 29-like	9.93E-63	N	3.23	4.69	9.43
AT2G20180	PIL5	0021486	transcription factor pif3-like	1.29E-26	N	0.85	1.33	1.16
AT1G03430	AHP5	0018863	histidine-containing phosphotransfer	2.51E-56	N	47.56	43.54	74.89
AT5G54510	DFL1	0006889	indole-3-acetic acid-amido synthetase	0	Y	22.05	32.66	83.56
AT5G20730	ARF7	0000777	auxin response factor 19-like	0	Y	12.14	14.87	11.42
AT3G15540	IAA19	0015499	auxin-induced protein aux22	3.88E-50	Y	8.92	10.69	8.52
AT3G50340		0010064	PREDICTED: uncharacterized protein LOC100262755	3.12E-165	Y	3.36	4.24	2.85
AT2G45420	LBD18	0044113	lob domain-containing protein 18-like	3.58E-67	N	0.36	0.68	1.73
AT4G14560	IAA1	0014302	auxin-induced protein 22b	6.76E-53	N	35.46	36.07	16.64
AT4G37390	YDK1	0004749	probable indole-3-acetic acid-amido synthetase	0	Y	10.5	18.51	17.66
AT4G27260	WES1	0006889	indole-3-acetic acid-amido synthetase	0	Y	22.05	32.66	83.56

AT5G17430	BBM	0002613	ap2-like ethylene-responsive transcription factor bbm-like	1.34E-122	Y	9.55	13.02	6.82
AT5G03740	HD2C	0009674	histone deacetylase hdt1-like	1.02E-24	N	139.84	161.42	92.97
AT5G22650	HD2B	0027114	histone deacetylase isoform 3	8.21E-26	N	286.77	270.64	131.72
AT5G18560	PUCHI	0012720	ethylene-responsive transcription factor 4-like	3.71E-23	N	21.46	33.81	55.6
AT5G37020	ARF8	0001138	auxin response factor 8-like	0	Y	9.71	9.76	5.8
AT1G28130	GH3	0004939	indole-3-acetic acid-amido synthetase -like	0	Y	7.5	7.25	14.31
AT5G60890	MYB34	0035249	transcription factor myb34	1.30E-67	N	0.41	0.73	1.62
AT4G00220	LBD30	0044113	lob domain-containing protein 18-like	5.91E-59	Y	0.36	0.68	1.73
AT2G01420	PIN4	0002917	auxin efflux carrier component 3-like	0	Y	1.66	2.17	5.65
AT1G70940	PIN3	0002917	auxin efflux carrier component 3-like	0	Y	1.66	2.17	5.65
AT1G23080	PIN7	0002917	auxin efflux carrier component 3-like	0	Y	1.66	2.17	5.65

Supplementary Table S7. List of primers used in this work.

Primer Name	Sequence
PpUBC9_fw	GGTGTTCCAGGTATTGAGCTG
PpUBC9_rv	AGCCATCCTCACAAAAGCAACC
PpYLS8_fw	ACCGTTCAGGTTGAGGCGAAG
PpYLS8_rv	GATACCCCAAACTAAGCATAGGC
PpEF1a_fw	GAGGTCTGAAGTTATGGGTCGTG
PpEF1a_rv	AGCACACCGACGCTACTAATG
* PpTFB4_fw	GCAATGCCTATAGCTCCTCCG
* PpTFB4_rv	GTTGTTGCCCGAGTCACCTTG
* PpHD2C_fw	GGTGGAAAGACTCCTGGTGGAG
* PpHD2C_rv	GTGCTTGGCCTTTGTGTGAGAC
* PpXPL1_fw	GGCCAGATGCTTAGAGATGCTG
* PpXPL1_rv	CTCGGATGAACTGATCAGTCC
* PpFBR_fw	CTGCAGCAAGACCAGTTCAAGC
* PpFBR_rv	CTGCTTCTTAGGCATGCGGTAAC
* PpGASA_fw	GCTCTCATTGCCATTTCCATGC
* PpGASA_rv	GAAGGCTTGACGCTGCCAGG
* PpHD2A_fw	GGTTTTGGAGTCTAGCGAGGAATG
* PpHD2A_rv	TTCCCTGTCTGCCTGTTCTGTTTC
PpSUR1_fw	TGTTAGATGTCACCCGTTGCTG
PpSUR1_rv	CATGACCATTGTGCCTGATTAGC
PpZIP9_fw	TCTGAACTGTGGTCTTGGGAATC
PpZIP9_rv	TCACAATCAACTCAACTAGCACC
PpIAA14_fw	CTGGGCAAGATGTTCAGTTCCT
PpIAA14_rv	AAGATCAGCGGAACAACATCAGC
PpGH3_fw	TCAACCAAACACCCCAAAGAGC
PpGH3_rv	TCAACCAAACACCCCAAAGAGC

* primers reported in Shishkova *et al.* (2013), designed for regions with 100% homology between *Stenocereus gummosus* and *Pachycereus pringlei* genes.