

Additional file 4 for Joo et al.

Article title: Evolution of heterodimerizing TALE homeobox transcription factors as a developmental mechanism for the haploid-to-diploid transition.

Authors: Sunjoo Joo, Ming Hsiu Wang, Gary Lui, Jenny Lee, Andrew Barnas, Eunsoo Kim, Sebastian Sudek, Alexandra Z. Worden, and Jae-Hyeok Lee.

Supplemental Data S1-S2

Data S1. HMM-motif search result

Query: KNA_JW2 [M=31]

Scores for complete sequences (score includes all domains):

--- full sequence ---			--- best 1 domain ---			-#dom-		
E-value	score	bias	E-value	score	bias	exp	N	Sequence
2.1e-12	41.2	0.0	8.6e-12	39.4	0.0	2.1	1	RCC809_56605_KNOX
2.3e-12	41.2	0.2	1.1e-11	39.0	0.0	2.3	1	Ostlu_5313_KNOX
3.5e-12	40.6	0.5	2.6e-11	37.9	0.1	2.5	2	Ostta_04g04290_KNOX
2.7e-10	34.7	1.3	5.5e-10	33.7	0.0	2.2	1	Picsa_04387_KNOX
8.3e-10	33.1	0.8	2e-09	31.9	0.0	2.1	1	Aceac_AAD51632_KNOX1
8.7e-10	33.1	1.1	2.9e-09	31.4	0.2	2.4	1	AT1G62360_STM
1.8e-09	32.1	1.1	5.4e-09	30.6	0.1	2.5	1	RCC299_62285_KNOX
1.9e-09	32.0	0.2	7.3e-09	30.2	0.0	2.1	1	AT4G08150_BP
2.8e-09	31.5	0.0	5.3e-08	27.5	0.0	2.9	2	Pp3c21_10320_MKN5
6.1e-09	30.4	0.0	2.3e-08	28.6	0.0	2.0	1	Pp3c18_18720_MKN2
1.3e-08	29.4	0.0	3.9e-08	27.9	0.0	1.8	1	Pp3c6_1550_MKN6v2
1.5e-08	29.2	0.3	6e-08	27.3	0.3	2.1	1	CCMP1545_69285_KNOX
1.5e-08	29.2	0.0	4.6e-08	27.7	0.0	1.9	1	Pp3c5_26440_MKN1
1.9e-08	28.9	0.3	8.3e-08	26.9	0.3	2.2	1	Cre08.g375400_KNOX/GSM1
2.1e-08	28.8	0.8	9.1e-08	26.7	0.0	2.4	2	AT5G25220_KNAT3
2.3e-08	28.6	0.5	1.7e-07	25.9	0.0	2.7	1	Cymte_Sc9672_1_KNOX
1.2e-07	26.4	0.2	6.6e-07	24.1	0.1	2.3	1	Cz15g18055v2_KNOX
3e-07	25.1	0.9	8.7e-05	17.4	0.0	3.8	3	Klefl00118_0070_KNOX2
5e-07	24.5	0.0	1.8e-06	22.7	0.0	2.0	1	Cymte_Sc2807_10_KNOX
1.6e-06	22.9	0.0	5e-06	21.3	0.0	1.9	1	CCMP726_01361191_KNOX
2.6e-06	22.2	0.1	1.3e-05	20.0	0.1	2.3	1	Klefl00113_0180_KNOX1
4e-06	21.6	0.0	1.7e-05	19.6	0.0	2.0	1	Cyagl_026930_TALE
4.7e-06	21.4	0.0	1.2e-05	20.1	0.0	1.7	1	CCMP720_03114_KNOX
8.6e-06	20.6	0.0	2.9e-05	18.9	0.0	2.0	1	Bathy08g03820_KNOX
1e-05	20.3	0.1	0.00014	16.8	0.0	2.5	2	Dunsa_0012s00032v2_KNOX
1.7e-05	19.6	2.0	1.9e-05	19.5	0.1	2.1	1	Pycno_01672_KNOX
3.1e-05	18.8	0.0	8.9e-05	17.4	0.0	1.8	1	CCMP720_035111_KNOX
4.5e-05	18.3	0.2	0.00014	16.8	0.2	1.9	1	Gonpe_2g991_KNOX
0.00024	16.1	0.8	0.0014	13.7	0.0	2.8	1	Cyapa_21179.70_KNOX
0.00047	15.1	0.0	0.0015	13.6	0.0	2.0	1	Klefl00157_0150_TALE2
0.0019	13.2	0.0	0.0059	11.7	0.0	1.9	1	CCMP726_01351541_KNOX
0.0019	13.2	0.0	0.0059	11.7	0.0	1.9	1	CCMP726_01357749_KNOX

Query: KNB_JW2 [M=22]

Scores for complete sequences (score includes all domains):

--- full sequence ---			--- best 1 domain ---			-#dom-		
E-value	score	bias	E-value	score	bias	exp	N	Sequence
3.1e-08	27.5	0.9	3.9e-07	24.2	0.2	3.2	2	Aceac_AAD51632_KNOX1
2.5e-07	24.8	0.7	2.1e-06	22.0	0.4	2.7	1	AT4G08150_BP
4.2e-07	24.1	0.6	2e-06	22.1	0.2	2.4	1	AT1G62360_STM
8.1e-07	23.3	0.2	3.4e-06	21.4	0.2	2.2	1	Pp3c5_26440_MKN1
2.1e-06	22.0	0.2	1.1e-05	19.8	0.1	2.3	1	CCMP726_01361191_KNOX
1.3e-05	19.6	3.4	2e-05	19.1	0.2	3.0	2	Ostlu_5313_KNOX
2.3e-05	18.8	0.0	0.00012	16.7	0.0	2.2	1	CCMP720_029342_KNOX
2.6e-05	18.7	0.0	0.00024	15.8	0.0	2.6	2	Pp3c18_18720_MKN2
3.5e-05	18.3	0.2	0.00015	16.4	0.2	2.1	1	Ostta_04g04290_KNOX
8.6e-05	17.1	0.2	0.00044	15.0	0.2	2.3	1	AT5G25220_KNAT3
9.2e-05	17.0	0.5	0.00043	15.0	0.5	2.3	1	Cz15g18055v2_KNOX
0.0001	16.9	0.1	0.0012	13.6	0.0	2.7	2	Picsa_0325_TALE-R1
0.00024	15.8	0.3	0.0014	13.4	0.2	2.5	1	RCC809_56605_KNOX
0.00027	15.6	2.6	0.00042	15.0	0.2	2.6	2	Galsu_EME30635_TALE
0.00035	15.3	0.0	0.0014	13.4	0.0	2.2	1	Pp3c6_1550_MKN6v2
0.00038	15.2	0.0	0.0014	13.5	0.0	2.0	1	Cyapa_21179.70_KNOX
0.0004	15.1	0.2	0.01	10.8	0.0	3.0	2	Porpu_2271.2_TALE
0.00043	15.0	0.1	0.0014	13.4	0.1	2.0	1	Pp3c21_10320_MKN5
0.00046	14.9	0.1	0.0027	12.6	0.1	2.3	1	Pp3c19_5620V_MKN4
0.00046	14.9	0.8	0.0026	12.6	0.1	2.8	1	RCC299_62285_KNOX
0.00084	14.1	0.0	0.0047	11.9	0.0	2.4	1	Bathy08g03820_KNOX
0.00086	14.1	0.6	0.0044	11.9	0.0	2.5	1	Klefl00118_0070_KNOX2
0.0014	13.5	0.1	0.0087	11.1	0.1	2.5	1	CCMP726_01351541_KNOX
0.0014	13.4	1.9	0.0035	12.3	0.2	2.5	1	Porum_0247s0008_RKNOX1
0.0014	13.4	0.5	0.023	9.8	0.1	2.9	2	Picsa_04387_KNOX
0.0014	13.4	0.1	0.0086	11.1	0.1	2.5	1	CCMP726_01357749_KNOX
0.0015	13.4	2.2	0.0044	11.9	0.2	2.7	2	Pyrye_g7505_TALE
0.0017	13.2	0.1	0.011	10.7	0.1	2.4	1	CCMP1545_69285_KNOX
----- inclusion threshold -----								
0.021	9.9	3.5	0.016	10.2	0.1	2.7	1	Gonpe_2g991_KNOX

Query: PBC_JW [M=67]

Scores for complete sequences (score includes all domains):

--- full sequence ---			--- best 1 domain ---			-#dom-		
E-value	score	bias	E-value	score	bias	exp	N	Sequence
2.7e-24	79.4	0.3	5.6e-24	78.4	0.3	1.6	1	Cyame_CMR176C_TALE
1.2e-19	64.5	0.4	3.3e-18	60.0	0.3	2.3	2	Galsu_EME32651v2_TALE
1.9e-17	57.5	0.3	4.8e-17	56.2	0.3	1.7	1	Chocr_41034_TALE
3e-17	56.9	1.0	6e-17	55.9	1.0	1.5	1	Picsa_04995_TALE-R2
3.4e-17	56.7	1.7	7.9e-17	55.5	1.7	1.6	1	Porpu_4416.19_TALE
4.2e-17	56.4	1.1	6.6e-17	55.8	1.1	1.3	1	Glowi_03052_TALE
5.6e-17	56.0	0.8	5.6e-17	56.0	0.8	1.8	2	HsPBX1
6.2e-17	55.9	4.8	6.2e-17	55.9	4.8	1.8	1	Porpu_3495.4_TALE
9e-17	55.3	3.6	1.8e-16	54.4	3.6	1.5	1	Porpu_2282.2_TALE
1.1e-16	55.1	6.8	2.2e-16	54.1	6.8	1.5	1	Cyapa_20927.63_PBC1
2.6e-16	53.8	2.6	5.4e-16	52.9	2.6	1.6	1	Porpu_3495.3_TALE

7.4e-16	52.4	0.7	1.5e-15	51.4	0.7	1.5	1	Porpu_677.2_TALE?
5e-15	49.7	0.4	5e-15	49.7	0.4	1.9	2	Accas_4342337_PBX
7.7e-15	49.2	0.6	4.4e-14	46.7	1.1	2.1	2	Porpu_2095.1_TALE?
1.1e-14	48.6	1.0	2.6e-14	47.5	1.0	1.6	1	Caltu_18607_PBX
1.3e-14	48.4	1.0	3.5e-14	47.0	1.0	1.8	1	Caltu_g18607v2_PBX
2.1e-13	44.5	0.1	5.4e-13	43.2	0.1	1.7	1	Klefl00021_0250_TALE1
2.5e-06	21.9	1.6	5.4e-06	20.8	1.6	1.6	1	Cyapa_20927.64_PBC2
4.4e-06	21.1	0.3	7.3e-06	20.4	0.3	1.3	1	Porum_1010s0003_RPBX
2.5e-05	18.7	0.2	5.3e-05	17.6	0.2	1.5	1	Pyrye_con7264

Data S2. Domain alignment in fasta format.

KN-A domain

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>Calliarthron_tuberculosis_g2262_extraction
MLPHPALALVIRFAFDA--RDADQVELREGD-----GTAEALR
>Cyanidizyon_merolae_CMH049C_extraction
VRSHSFFGKLASGVQDV-----VVAPPAD-----SSAEELQ
>Galdieria_sulfuraria_EME32194_extraction
IQQHESFVYSFLKALEA-----WKQIGWNT-----NHAVIQ
>Picocystis_salinarum_0325_extraction
LTSHPLFPSLLKQF-----RKNAE-----LLEELD
>Klebsormidium_flaccidum_00157_0150_extraction
ASKRRESKERDKQQVECGHNQEQEASKGAKKKRERKGGGRQAVSS
>Micromonas_commoda_62285_extraction
VRANPRYPKLLDAYFAC-----RRVGADAT-----SKASLA
>Micromonas_pusilla_69285_extraction
MRVHTMYPALLRAYFAC-----RSAGADRA-----TELALR
>Ostreococcus_tauri_04g04290_extraction
IRAHPMYARLVEAYYEC-----RKIGAHGD-----AAVALE
>Ostreococcus_lucimarinus_g5313_extraction
VRAHPMPRLVEAYYEC-----RQIGAEGD-----VLEALD
>Ostreococcus_sp_RCC809_56605_extraction
IRAHPMYSRLVEAYYEC-----RKIGADSE-----TADALE
>Bathycoccus_prasinus_08g03820_extraction
VRTHEKFREYVEIMMTC-----RKLTAQTK-----RERESLE
>Gonium_pectorale_KXZ56109_extraction
LLHHPRLRELVDVAVGC-----RKVVVRSR-----EAADELD
>Chlamydomonas_reinhardtii_GSM1_extraction
VQQHEAYPAVVRGTLDV-----RKACLPRFPLVAREQAEELQ
>Volvox_carteri_0053s0055_extraction
FLWHPQKADALLAVFEA-----KMAVTPVN-----AATNFT
>Chromochloris_zofingiensis_15g18055v2_extraction
VACHPLYPKIMDAICSC-----MKVAQPVE-----VTQQLD
>Pyramimonas_parkeae_01351541_extraction
IGSHPEFKRVVQLYGNL-----MRLDGHIT-----SMPPDME
>Pyramimonas_parkeae_01361191_extraction
IQKHRLYSRMDTAYLLGKHDNAMRFGENAD----GDFPLATTQ
>Cymbomonas_tetramitiformis_Sc2807_10_extraction
IITHPLYQRLVKANFER-----LKLGAEE-----AKAGID
>Cymbomonas_tetramitiformis_Sc9672_1v2_extraction

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VMRHPLFPRLVQANFDS-----LRIGQLPS-----QVETLN
>Pycnococcus_sp_01672_extraction
VAYHALYLRLVEAHFNV-----RRLSEKDS-----SDSVLE
>Picocystis_salinarum_04387_extraction
ICAHPLYPKLLTAHFEC-----KMGVGLNEE-----EKASLQ
>Acetabularia_acetabulum_AAD51632_extraction
VIMHPLYPDLVKAIMDC-----RKVGGMDE-----SRHHIQ
>Pyramimonas_amylifera_03114_extraction
AYTLQLFCRIVHAYSRSQQNDDSRQMGLLAD-----SEDLLE
>Pyramimonas_amylifera_035111_extraction
AHTLQLFCQNIHKYMRCLQVDGRLWSSSFSS-----SDRLF

>Arabidopsis_thaliana_STM_extraction
IMAHPHYHRLLAAYVNC-----QKVGAPPE-----VVARLE
>Arabidopsis_thaliana_BP_extraction
IIAHPHYSTLLQAYLDC-----QKIGAPPD-----VVDRIT
>Physcomitrella_patens_MKN5_extraction
IIDHPFYPEMVLAHVRV-----FKIGAPRR-----LINKLD
>Physcomitrella_patens_MKN2_extraction
IIDHPFYPEMVLAHVRV-----FKIGAPRR-----LRRKLD
>Klebsormidium_flaccidum_00113_0180_extraction
IRRHDRYPELVGRLMDC-----LKVGASEN-----EIRRLD
>Arabidopsis_thaliana_KNAT3_extraction
ILSHPLYEQLLSAHVAC-----LRIATPVD-----QLPRID
>Physcomitrella_patens_MKN1_extraction
IVAHPPLYPDLLNAHASC-----LRVGTPVD-----QLPHIE
>Physcomitrella_patens_MKN6v2_extraction
IVNHPLYPEMLMNAAC-----LRVGTPVD-----QLPSIE
>Klebsormidium_flaccidum_00118_0070_extraction
IECNQSYPKLIAAHVAC-----VQMDTSSP-----RLYQLE
>Cyanoptycha_gloeocystis_026930_extraction
IRKHPLWPSVMTMFRDA-----EKSGIKKI-----QLSELP
>Cyanophora_paradoxa_21179.70_extraction
VRSHPSFPLIAEGVRAV-----ELAGLLSR-----GHPAAAFP

KN-B domain

>Calliarthron_tuberculosis_g14488_extraction
NSDLLDVFFAALS----AALDQLRQTN
>Calliarthron_tuberculosis_g2262_extraction
QSSSLDIFLSALC----SALREANSAS
>Cyanidizyon_merolae_CMH049C_extraction
ILTILDTLAAAVCYV--RNLQAWVALQ
>Picocystis_salinarum_0325_extraction
DFPELDEFYCINYI----ARLKAQREAV
>Klebsormidium_flaccidum_00157_0150_extraction
LQSEGPSFLPPDFL---TDLGGLDANL
>Pyropia_yezoensis_g7505_extraction
D-AAKMEFVSAYM----ALMDVYEARC
>Chondrus_crispus_c1808_extraction
S-VERARFFDTYE----RLIKEYEARC
>Porphyra_umbilicalis_0247s0008_extraction
D-ASKMAFVSSYM----QLMDVYEARC
>Cyanidizyon_merolae_CM153C_extraction
E-PSRNGFDGRST----GRLGTAETTP
>Galdieria_sulfuraria_EME30635_extraction
N-EDFQHFLITYV----ELLEKEYEQR
>Porphyridium_purpureum_3408.5_extraction
A-LAFRMQSAEYA----ELGMYESRL
>Porphyridium_purpureum_2271.2_extraction
P-GSSDEWFHTYI----SLIESYKNRL

>Porphyridium_purpureum_4494.3_extraction
G-LGLKLSSGVAP----QTMDVFQQRL
>Micromonas_commoda_62285_extraction
G-AELDEFMDNVT----DELTAYAEEL
>Micromonas_pusilla_69285_extraction
G-EEMDDFIARCT----AELRAYSVEL
>Ostreococcus_tauri_04g04290_extraction
S-CDLDEFMRDCT----HELETYVKEL
>Ostreococcus_lucimarinus_g5313_extraction
Q-RDLDRFMRECT----HELESYVKEL
>Ostreococcus_sp_RCC809_56605_extraction
A-LDLDDYMRECT----HELESYVKEL
>Bathycoccus_prasinus_08g03820_extraction
K-QELNAFMEHSC----ENARKFQKEL
>Gonium_pectorale_KXZ56109_extraction
D-PALDLAVNQYI----DLCEAYQAEI
>Chlamydomonas_reinhardtii_GSM1_extraction
N-PGLDEAMGAYV----RVAALYGDEA
>Volvox_carteri_0053s0055_extraction
K-IDPMSFMERAV----GRLNMAHNLH
>Chromochloris_zofingiensis_15g18055v2_extraction
D-EDLDAFMQRYL----QVLASYLREL
>Tetraselmis_astigmatica_021027_extraction
EMEGCRHFVSKAA----EALD---QTL
>Pyramimonas_parkeae_01351541_extraction
C-PELDEFMVLFR----QALERHWVDR
>Pyramimonas_parkeae_01361191_extraction
P-SELDFMEDCC----KLEETWDEL
>Cymbomonas_tetramitiformis_Sc2807_10_extraction
D-EELDAFMLEYC----STVETQCGEM
>Cymbomonas_tetramitiformis_Sc9672_1v2_extraction
D-DDLDDFMLNYC----SILESHEET
>Pycnococcus_sp_01672_extraction
D-HFLNEFMFKYV----MIVDSLHLEL
>Picocystis_salinarum_04387_extraction
E-QEIRKFIQDYC----CTLESLRSDL
>Acetabularia_acetabulum_AAD51632_extraction
D-PELDQFLRQYI----QVLDELHAEL
>Pyramimonas_amylifera_029342_extraction
N-PELQRWRYQDIFGTWKEMESCDRNF
>Pyramimonas_amylifera_03114_extraction
--RNIHGFLASDI-----ALLEVDSSI
>Pyramimonas_amylifera_035111_extraction
E-GEVSDILEKFS----DTWREIESNT
>Pyramimonas_amylifera_094156_extraction
E-KEVSDTCKSMI----STLEDFDFNT
>Arabidopsis_thaliana_STM_extraction
D-PGLDQFMEAYC----EMLVKYEQEL
>Arabidopsis_thaliana_BP_extraction
D-PELDQFMEAYC----DMLVKYREEL

>Physcomitrella_patens_MKN5_extraction
D-PALDHFMRYSYV----DMLTKFAEDL
>Physcomitrella_patens_MKN2_extraction
D-PELDHFMRYSYV----GVLTKFAEDL
>Klebsormidium_flaccidum_00113_0180_extraction
E-PGLDKVMLIEK----QQLVALKQQL
>Arabidopsis_thaliana_KNAT3_extraction
D-KELDQFMTHYV----LLLCSFKEQL
>Physcomitrella_patens_MKN1_extraction
EKTELDQFMAQYI----MLLCSFKDHL
>Physcomitrella_patens_MKN6v2_extraction
EKVELDRFMTEYT----ALLGDFKDVL
>Klebsormidium_flaccidum_00118_0070_extraction
A-PEVDAFMAECL----AQLGRLKAAL
>Cyanoptycha_gloeocystis_026930_extraction
P-PSVQEFLLKMA----QLLQMQUIAAS
>Cyanophora_paradoxa_21179.70_extraction
G-SQLDALVSQYIAALQQVLRFSFHGTL
>Gloeochaete_wittrockiana_014496_extraction
P-PETNAGAYNSL---QRALRVQQQTS

PBL-Red domain

>HsPBX1_extraction
KLSQI-RQIYHTELEKYEQACNEFTTH-----VMNLLREQSRTR-PIS-----
PKEIERMVSIIHRKFS-----SIQMQLKQS
>Accas_4342337_extraction
KVKKL-QEAYEVELGQLNLVADQYASH-----VMSLLKAQAATR-PIT-----
DKEQSMKLAVLQERFD-----YLRTQLRQS
>Guith_137502_extraction
QIKLI-ENQFNSEKCKVDQVCEDVCQR-----MRTILNSQRKTR-HVS-----
EQEENVHCQAIQAKFQ-----YQEYVNDCL
>Naegr_78561_extraction
RFKEL-QKQYRVECSYIDDALKKWQET-----FERVLNNQSSFR-VVS-----
FEEKHRCKKSLEARFG-----LMKQLLKDK
>Cyapa_20927.63_extraction
KRAAL-ESWYNTQHRKIEVAEAEYRSK-----IEQELLAQRAFR-TIT-----
PQEERTRLMKVENAFK-----TVRAELERK
>Glowi_03052_extraction
QRQQL-RVWYDAQLQKIDTAASDYTRQ-----VRAALEKQASLR-PVT-----
PSEVAARVDKIQGYFR-----AVRLNLRRK
>Caltu_g18607_extraction
NVYKVLQANLSSRLKEVRDSAIMVEDV-----LERRLHRQLHFR-PVP-----
VEEVDRRMEYIKIKFL-----RARLVIVEK
>Chocr_41034_extraction
NFVAL-KNSLMESLANVRHMAQDAVAE-----METNLAQQLHFR-IVP-----
PEEVHNRRLRYIVSRFS-----KTRKEILHK
>Porpu_2282.2_extraction
HEAEF-EE-FKKRLQLMRARCVAYSFY-----LTEEELQKDFR-LVP-----

DVEIHERRREIVMTFL-----RARQKLIRS
>Porpu_3495.3_extraction
DDPRL-QE-LLEKLHALRQRCEIYTSI-----VSHELELQSKFR-LVP-----
ELEAREREGEVVKAFI-----RARQTLIRL
>Porpu_4416.19_extraction
GDELM-NS-LIERLQMMRQRCELLSAG-----VVEELLLQSKFR-LVT-----
PEEILERRARIVQLFL-----DARNRLVEN
>Porpu_3495.4_extraction
E-RAVFQQ-IRNVLQRLREVHGKWMKK-----VQHEICAQREFR-PVS-----
KVEVMFWHNRITAICR-----AERVRIMQL
>Porpu_2095.1_extraction
ENPGTAKASSQTVMQMEEIRTVFQAA-----IIEELQEQSKCR-IIS-----
PGEEKERLLAVAAIARAH-----AVRGENVRK
>Porpu_677.2_extraction
GHLELSESLDHHVQKLLKEIRLRYHYL-----MEHELRLQAEFR-IVR-----
DAEKHGRLHAITALTADY-----KARGEALEA
>Galsu_EME32651v2_extraction
Q-KVMWKNWLIDLKTRWSDTVHHYMSL-----MLEELKQRRFR-TIT-----
EEEVQSWIHPMMQTFE-----NIW-NIIRQ
>Cyame_CM176C_extraction
RNLALEYDGPYKDLVRLQAHCLANQVEQLWAESP-CRHEARAPVATRHSVSASASLATAS-
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