

**Appendix J The sequence information of the conserved motifs in different families of sorghum sugar transporters**

Gene Family	Motif Name	Motif Length	Motif Sequence
SUT_motif	MEME-1	50	QYGWALQLSLTPYVQTLGISHAYVSLTWLCPIAGLVVQPLVGYYSDRC
	MEME-2	46	FKSLKNLPPGMPSVLIVTALTWLSWFPFILYDTDWMGREIYHGEPD
	MEME-3	44	TKEHCSTYTGSRWHAASAVYIVGFWLDFANNTVQGPARAMMADL
	MEME-4	50	HGPNVANAIFSLWMALGNILGYSAGATAKWHFWFPFLKTAACCEACANLK
	MEME-5	50	YBEGVREGAFGLLNSVVLGVTSFLIEPLCRKLGARVVWSISNFMVFIAM
	MEME-6	50	VTAZAAEEGGGQGLATGVLNIAIVLPQLIIALGAGPWDGLFGKGNIPAF
	MEME-7	29	SKLGRRRPFILAGCIICLAVJVIGFSAD
	MEME-8	29	PDKTIKSAALVIFALLGIPLAILYSVPFA
	MEME-9	29	AFLVAVIFIITMSVTWFAGEZPLDPAB
	MEME-10	21	SRKPPIGIVRLFLACMVAGGV
	MEME-11	18	EEGNNKQRLEWATMNLER
	MEME-12	24	GFALIAGVLAJLLPKTRGVSNAS
	MEME-13	14	NNEEFPNGNVDGDN
	MEME-14	17	TAMVVLGIVSMKGYKPS
	MEME-15	7	WSLKDH
	MEME-16	7	PVKDRDQ
	MEME-17	6	DGELEL
	MEME-18	6	NPGEEQ
	MEME-19	6	PYRFJR
	MEME-20	6	MDGGDG
SWEET_motif	MEME-1	29	GJLGNVFSFLMFLAPLPTFRRVIKTKSVE
	MEME-2	29	FVATPNGLGFVFELVQJVLYLLYAPKKAK

	MEME-3	15	YLATLLNAMLWFLYG
	MEME-4	41	EGKDAGGKLPSAADEHVLVNIAKLSPALPERSSGVHRATQM
	MEME-5	6	YMPFSL
	MEME-6	11	AHTHERRSMVV
	MEME-7	15	FTAKILLLNNGVFG
	MEME-8	11	MAGLSLQHPWA
	MEME-9	20	MLPNRDVVDVFVSRQSPA VH
	MEME-10	8	PVVHPNSI
	MEME-11	16	IIEARKRKADQVAMTE
	MEME-12	6	GFQSVP
	MEME-13	15	ILLLTLLFKGDKRV
	MEME-14	11	MVSPDTIRTAI
	MEME-15	6	LLIKDK
	MEME-16	6	QYSPIP
	MEME-17	6	LIRFDL
	MEME-18	6	DDEEEP
	MEME-19	14	AVPAKSCAAEAAAP
	MEME-20	6	LIKSNE
TMT_motif	MEME-1	29	PIYISETAPTEIRGLLNTJPQFTFWIGMI
	MEME-2	41	MKGAVLVAIAASIGNLLQGWWDNATIAGAVLYIKKEFHLZSZ
	MEME-3	50	SYCMVFGMTLMPSPDWRJMLGVLSJPSLIYFALTIFYLPESPRWL VSKGR
	MEME-4	50	TYSLPVMLNAIGLAGVFGIYAVVCCCLALVFVYLKV PETKGMPLEVITEFF
	MEME-5	29	LMLWSPNILLARLVEGLGIGLATTJV
	MEME-6	49	AKGPRWKDLFEPGVRRALFVGVGIQILQQFAGINGVLYYTPQILEQAGV
	MEME-7	29	EGLJVATSLIGATIITFSGPVADWVGRR

	MEME-8	21	GETVSSMGIGGGWQLAWKWTE
	MEME-9	15	IVYFCCFVMGFGPIP
	MEME-10	22	SQYKPLVDPVVTLFGSVHEKMP
	MEME-11	13	KEGGFKRMYLHEE
	MEME-12	19	RRSTLFPNFGSMFSVAEQH
	MEME-13	26	DEGLGDKEQITLYGPEEGLSWVARP
	MEME-14	19	GEFVHAAALVSQSALYSKD
	MEME-15	29	YASDGGGGDIEDNLQSPLJSRQATSVEGK
	MEME-16	11	DWDEENQHPND
	MEME-17	7	RCRPGQH
	MEME-18	11	PMLIASSILYF
	MEME-19	8	MKEAKAVL
	MEME-20	6	EYIIGP
VGT_motif	MEME-1	48	YVGCYQLSFGPIGWLMISEIFPLRLRGJGLAVLVNFGSNALVTFAF
	MEME-2	14	AYTIVDDLGRRPEL
	MEME-3	35	PSSPRWLLCAIQGKGKNLPDNKEKAIRCLCRLRGR
	MEME-4	45	PNFVILIIGRFLYGIGIGLAMHGAPLYIAETAPSQIRGMLISLKE
	MEME-5	49	YIGQEKGZGNFWEIFZGKCLKAFIIGCGLVFFQQITGQPSVLYYAASIFQ
	MEME-6	43	PFFFPALEGGLLFGYDIGATSGATISLKSPDFSGTDWFNLSSLQ
	MEME-7	19	WRYMFGFSAPLCLIMGIM
	MEME-8	13	HIVPETKGLSLEE
	MEME-9	7	RQRPHVR
	MEME-10	6	KLJMTG
	MEME-11	6	YYKJLD
	MEME-12	6	DLEDLI

	MEME-13	7	ASDAARV
	MEME-14	10	RAPAPAECYS
	MEME-15	20	FIVLGILLGYFVGNLEIENV
	MEME-16	6	EEKILK
	MEME-17	6	FGVIAV
	MEME-18	6	SWVPVI
	MEME-19	6	SGSLYG
	MEME-20	6	AAAEGD
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EDR_motif	MEME-1	50	PCLLJPGLFFIPESPRWLAKMGKMEEFETSLQVLRGFDTDISEEVNEIK
	MEME-2	50	IPNIIGWLAISFAKDASFLYMGRLLEGFGVGIJSYVVPVYIAEISPKNLR
	MEME-3	50	RRLPKIRFQDLFQKKYITPLIVGIGLLVLQLQQLGGINGILFYASSIFKAAG
	MEME-4	50	TMTANLLSWSSGGTFFIYAAVSAFTVVVFILWVPETKGRTLEEIQWSFR
	MEME-5	50	GYSSPTQDGIVRDLNLSJSEFSVFGSJLNVGAMVGAIASGQMAEYIGRKG
	MEME-6	41	AFSLGMGAIPWVIMSEILPVNIKSLAGSLATLANWLTSFAI
	MEME-7	41	TSGNLGTFALGAIQVPATGVGTLLMDRAGRILLISSSGT
	MEME-8	29	LGTVNQLSITFGISLAYVLGLFVPWRLLA
	MEME-9	40	RRQSLLAPGGSSMAVLRESHVSAFLCTLIVALGPIQFGFT
	MEME-10	29	FYIKDNISQSDSDLYNILSMVSLGVVVAFV
	MEME-11	15	GSDHDGALQKPLLPT
	MEME-12	21	FLGCFLVGLSFLAKEQHWERD
	MEME-13	6	GSWYRM
	MEME-14	8	DCGKEEGD
	MEME-15	15	TAVAVAGSFEFGISV
	MEME-16	6	LPPFHK
	MEME-17	6	MANNRA

	MEME-18	6	DFTEKL
	MEME-19	7	MEREGQE
	MEME-20	6	EYIESJ
INT_motif	MEME-1	40	TGVIAGALLYIRDDFVGINTVMYLSPTIVSMAGFGANVGA
	MEME-2	29	NGLLITGGQFLAYLINLAFTKVPGTWRWM
	MEME-3	50	YIVFYSPGMGTVPWIVNSEIYPLRYRGVCGGIAAVANWVSNLIVAQTFLS
	MEME-4	46	PAJVQFVLMALPESPRWLYRKGRKEEAELRKIYPAEEVEEEIE
	MEME-5	41	PPVJIVGRVFVGLGVGMASMTAPLYISEASPARIRGALVST
	MEME-6	19	VGGWFNDRFGRRRLILIAL
	MEME-7	41	TFLJFCGVSVLAFIFVFLLVPETKGLQFEEVEQMLERKDYK
	MEME-8	41	CAGGGDKLLPGACLVSNDAASRHACRADRREWYTRGCPSNFG
	MEME-9	29	ECLYLSWSNPYILRLAFLSAGIGGLFGYD
	MEME-10	15	WSCTRCLKAASSCFG
	MEME-11	21	SHSPPVSDAETALFGANGTCP
	MEME-12	6	HEFDGN
	MEME-13	6	PWKKFN
	MEME-14	6	NNGNCQ
	MEME-15	15	ALSLVTSGLNAJGSI
	MEME-16	6	MEGGIH
	MEME-17	6	NEPGKN
	MEME-18	25	RASVEEEMAQEWSIGEGGLIGKLK
	MEME-19	6	DKFEFK
	MEME-20	6	IMAFAP
PLT_motif	MEME-1	41	MPESPRWLVMQGRLADARAVLLRTSDTPAEAEERLAEIKAA
	MEME-2	41	SARGFLTSFPEVFINVGILLGYVSNYAFAGLPVHLGWRVML
	MEME-3	50	KPRRNKYAFACATLASMTSILLGYBJGVMSGAQLFIKEDLGJTDVQVEVL

	MEME-4	50	HFFQQASGIDAVVLYSPRVFKKAGITSBSALLGATVAVGVVKTLFILVAT
	MEME-5	50	FVAFFSIGLPIAWVYSSEIFPLRLRAQGAALGVAVNRVTSGVVSMTFJS
	MEME-6	50	AGRRTSDWJGRRRTVVLAAAFFAGALAMGLAPSYAALMAGRIVAGVGVGF
	MEME-7	29	FFLYAGIAAAAWFVFYTRLPETKGRSLED
	MEME-8	30	FLLDRVGRRPLLLASTGGMAVSLVGLGVTL
	MEME-9	15	ALMVAPVYTAEISPA
	MEME-10	15	GGGGVWKELLRPTP
	MEME-11	15	GIGAVPPVFLAAGVL
	MEME-12	11	GIJNVYSLLGSL
	MEME-13	11	VRRILLAVLGL
	MEME-14	15	GIPHDLGDVVAVPK
	MEME-15	15	HHPDAKIPWAVALCI
	MEME-16	8	DAITMPGC
	MEME-17	21	GGEDVDEDEEDGTPAKEKSTE
	MEME-18	31	HPDGLVYLGCILGSGVYSMGFLRIPAHAWR
	MEME-19	8	SKAITIGG
	MEME-20	18	KVFQQASGKGSILQYVQQ
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	MEME-1	50	PLYISEVSPTEIRGTLGSLVQIATCLGIIVALLJGJPVEGBPRWWRTMFW
	MEME-2	36	AFFGSLVASSLMDKFGRKRLILSYLPMAIGAFLSA
	MEME-3	49	HWIVNFFVGLYFLELVNKFGVGAVYAGFASVCVLAIFVRGHVVTKGR
	MEME-4	50	KALPHVCVASLASFLFGYHJGVVNGPLEDIAKDLGFAGNPLLQGLVVSIF
SGB/pGlcT_motif	MEME-5	41	WSDLFYGRHWKVFIGASLFFLQQLAGINAVLYFSSSVFRS
	MEME-6	40	GMQFAPESPWRWLKYVGRIDEAEKVVEKLWGPEHVEEAMYE
	MEME-7	28	YVLSFALGAGPVPGLLPEIFPSRIRAK
	MEME-8	15	EIEMEPDVETPGKQE
	MEME-9	6	WCGGRR

	MEME-10	11	DSLEEMLFGRF
	MEME-11	11	DPPDPPLKEKPZ
	MEME-12	9	NNPCYKRMP
	MEME-13	6	QEIEVM
	MEME-14	6	NJCMGI
	MEME-15	6	GDDGEG
	MEME-16	6	RALPRR
	MEME-17	8	RPRPGPVR
	MEME-18	6	ANRQAL
	MEME-19	11	SFPWDEGVPHS
	MEME-20	6	WPPRLP
STP_motif	MEME-1	45	QAVPLYLSEMAPARWRGALNIGFQLFITIGILAANLINYGTNKIP
	MEME-2	39	SEIFPLEIRSAGQSITVAVNLLTFVIAQAFSLSMCHLK
	MEME-3	39	IPFFQQLTGINVIMFYAPVLFRVGFGSDASLMSAVITG
	MEME-4	21	VMTAFVALFLPETKGVPIEEM
	MEME-5	29	NNYCKFDSQLTAFTSSLYLAGLVASLVA
	MEME-6	29	TDRVGRRALFLIGGVQMJAGQVVNGAAVN
	MEME-7	41	SAGGGKDYGGKLTAFVVLCLVAASGLIFGYDIGISGGVT
	MEME-8	21	LICVYVAGFAWSWGPLGWLP
	MEME-9	21	AVWARHWYWKRKVKKDDADKHE
	MEME-10	15	GWGWRLSLGLAAVPA
	MEME-11	15	MLIVGRILLGVGVGF
	MEME-12	15	RRJLRRRYRPQLVMA
	MEME-13	21	DVDAEFDDJVAASEEARAVEH
	MEME-14	15	PDEARAVLQRIRGTD

MEME-15	21	SMDSFLKKFFPSVYRRMKSAK
MEME-16	11	FGIFFFFAGWV
MEME-17	21	AVIVVGALLIPDTPSSLVLRG
MEME-18	15	KFGKSGAATMARSYA
MEME-19	11	LVNVFSTLVSI
MEME-20	29	TRVFGRKWSMFAGGVAFLAGAAJGGAATB

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