

	Domain topology	HGNC* Subfamily	Number of TMHs	GI Number	Name	C motif	AA	mW	pI
1	TMD-NBD	ABCB (TAP/HMT)	5	241920289	SbABCB1	LSGGQKQRIAIARAL	648	69880.5	8.82
2	(TMD-NBD)2	ABCB (MDR/PGP)	9	992273154	SbABCB37	LSGGQKQRIAIARAI	1269	137315.8	6.35
3	(TMD-NBD)2	ABCB (MDR/PGP)	9	992272203	SbABCB33	LSGGQKQRVAIARAI LSGGQKQRIAIARAI	1280	137864.6	8.6
4	(TMD-NBD)2	ABCB (MDR/PGP)	9	992276819	SbABCB40	LSGGQKQRVAIARAI LSGGQKQRIAIARAI	1255	135678.3	6.38
5	(TMD-NBD)2	ABCB (MDR/PGP)	9	242044206	SbABCB10	LSGGQKQRVAIARAI LSGGQKQRIAIARAI	1284	139049.2	6.52
6	(TMD-NBD)2	ABCB (MDR/PGP)	11	38049160	SbABCB25	LSGGQKQRVAIARAI LSGGQKQRIAIARAM	1402	151039	8.93
7	(TMD-NBD)2	ABCB (MDR/PGP)	12	992273149	SbABCB35	LSGGQRQRIAIARAL LSGGQKQRIAIARAI	1274	138319.3	7.11
8	(TMD-NBD)2	ABCB (MDR/PGP)	12	242054103	SbABCB12	LSGGQKQRVAIARAI LSGGQKQRIAIARAI	1237	135191.3	8.01
9	(TMD-NBD)2	ABCB (MDR/PGP)	9	992273150	SbABCB36	LSGGQKQRVAIARAI LSGGQKQRIAIARAI	1261	136485.3	6.67
1	(TMD-NBD)2	ABCB (MDR/PGP)	8	241942016	SbABCB8	LSGGQKQRVAIARAI LSGGQKQRIAIARAM	1683	181393.5	8.84
1	(TMD-NBD)2	ABCB (MDR/PGP)	10	241939807	SbABCB6	LSGGQRQRIAIARAL LSGGQRQRIAIARAL LSGGQKQRIAIARAM	1266	137347.8	8.31
1	(TMD-NBD)2	ABCB (MDR/PGP)	11	241944525	SbABCB9	LSGGQKQRIAIARAV LSGGQKQRIAIARAI	1285	137733.6	6.81
1	(TMD-NBD)2	ABCB (MDR/PGP)	8	992272545	SbABCB34	LSGGQKQRVAIARAI LSGGQKQRIAIARAI	1164	126627.9	7.55
1	(TMD-NBD)2	ABCB (MDR/PGP)	8	242053189	SbABCB11	LSGGQKQRVAIARAI LSGGQKQRIAIARAI	1161	126310.6	7.9
1	(TMD-NBD)2	ABCB (MDR/PGP)	10	241939142	SbABCB5	LSGGQKQRVAIARAI LSGGQKQRIAIARAM	1262	136867.2	8.57
1	(TMD-NBD)2	ABCB (MDR/PGP)	9	242054109	SbABCB13	LSGGQKQRIAIARAV LSGGQKQRIAIARAI	1241	134429.3	6.27
1	(TMD-NBD)2	ABCB (MDR/PGP)	10	992163816	SbABCB27	LSGGQKQRVAIARAI LSGGQKQRIALARAI	1548	165621.7	8.88
1	(TMD-NBD)2	ABCB (MDR/PGP)	10	242075048	SbABCB21	LSGGQKQRIAIARAI LSGGQKQRIALARAI	1568	168017.6	8.83
1	(TMD-NBD)2	ABCB (MDR/PGP)	11	992169235	SbABCB31	LSGGQKQRIAIARA MSGGQKQRIAIARAI	1248	135595.5	8.12
2	(TMD-NBD)2	ABCB (MDR/PGP)	11	242064316	SbABCB19	LSGGQKQRIAIARA MSGGQKQRIAIARAI	1236	134496.3	8.12
2	(TMD-NBD)2	ABCB (MDR/PGP)	9	242058427	SbABCB16	LSGGQKQRIAIARAI LSGGQKQRIAIARAI	1219	131875.9	6.38
2	(TMD-NBD)2	ABCB (MDR/PGP)	9	241930399	SbABCB2	LSGGQKQRVAIARAI LSGGQKQRIAIARAI	1235	134876.7	8.77
2	(TMD-NBD)2	ABCB (MDR/PGP)	11	241932543	SbABCB4	LSGGQKQRIAIARAI LSGGQKQRIAISRAI	1260	137922.9	9.35
2	TMD-NBD-TMD	ABCB	11	992170642	SbABCB32	LSGGQKQRIAIARAI LSGGQKQRIAISRAI	936	102463.6	9.33
2	(TMD-NBD)2	ABCB (MDR/PGP)	11	992164650	SbABCB28	LSGGQKQRIAIARAL	1305	141841.6	8.83
2	(TMD-NBD)2	ABCB (MDR/PGP)	12	992169232	SbABCB29	LSGGQRQRIALARAI MSGGQKQRIAIARAI	1251	136511.8	7.3

2	(TMD-NBD)2	ABCB (MDR/PGP)	11	992161948	SbABCB26	LSGGQKQRIAIARAI LSGGQKQRIAIARAM	1237	136104.3	7.12
2	(TMD-NBD)2	ABCB (MDR/PGP)	11	242078191	SbABCB22	LSGGQKQRIAIARTI LSGGQKQRIAIARAM	1237	136064.2	7.12
2	(TMD-NBD)2	ABCB (MDR/PGP)	9	242064314	SbABCB18	LSGGQKQRIAIARTI MSGGQKQRIAIARAI	1237	135091.6	8.77
3	(TMD-NBD)2	ABCB (MDR/PGP)	9	242088693	SbABCB24	LSGGQKQRIAIARAI LSGGQKQRIAIARAI	1255	135363.9	6.57
3	TMD-NBD-TMD	ABCB	9	242064312	SbABCB17	LSGGQKQRIAIARAI MSGGQKQRIAIARAI	999	109700.5	7.12
3	(TMD-NBD)2	ABCB (MDR/PGP)	9	241932084	SbABCB3	MSGGQKQRIAIARAI	1244	133515.1	7.3
3	(TMD-NBD)2	ABCB (MDR/PGP)	9	242073482	SbABCB20	LSGGQKQRIAIARAI LSGGQKQRIAIARAL	1286	139805.1	8.86
3	(TMD-NBD)2	ABCB (MDR/PGP)	7	241940215	SbABCB7	LSGGQKQRIALARAI LSGGQKQRIAIARAI	1260	138517.7	6.11
3	(TMD-NBD)2	ABCB (MDR/PGP)	8	992169233	SbABCB30	LSGGQKQRIAIARAI MSGGQKQRIAIARAI	1211	132301	8.51
3	(TMD-NBD)2	ABCB (MDR/PGP)	6	242057593	SbABCB15	LSGGQKQRIAIARAI LSGGQKQRIQLSRAL	946	105751.5	6.21
3	TMD-NBD	ABCB (TAP/HMT)	3	992274009	SbABCB38	LSGGQKQRVAIARAL	1064	116059.3	9.76
3	TMD-NBD	ABCB (TAP/HMT)	3	992274010	SbABCB39	LSGGQKQRVAIARAL	634	69562.6	9.43
3	TMD-NBD	ABCB (TAP/HMT)	6	242057337	SbABCB14	LSGGQKQRIQLARAV	779	87110.1	5.44
4	(TMD-NBD)2	ABCC (MRP)	14	241939733	SbABCC3	ISGGQKQRVSMARAV FSVGQRQLLSLARAL	1627	183005.3	6.49
4	(TMD-NBD)2	ABCC (MRP)	13	992155414	SbABCC16	LSGGQRARLALARAL FSVGQRQLLCLARAI	1465	163415.4	6.73
4	(TMD-NBD)2	ABCC (MRP)	10	992282114	SbABCC26	LSGGQKQRIQIARAL	1511	166076.3	5.98
4	TMD-NBD-TMD	ABCC (MRP)	15	992281625	SbABCC25	LSGGQKQRIQIARAL	1289	141743	7.97
4	TMD-NBD-TMD	ABCC (MRP)	15	242041335	SbABCC5	LSGGQKQRIQIARAL	1300	143009.4	8.25
4	(TMD-NBD)2	ABCC (MRP)	13	992164152	SbABCC21	MSGGQKQRIQIARSM	1488	167326.7	8.78
4	(TMD-NBD)2	ABCC (MRP)	11	242072762	SbABCC9	MSGGQKQRIQIARSM	1335	149588.7	8.31
4	(TMD-NBD)2	ABCC (MRP)	14	992271552	SbABCC23	LSGGQKQRIQIARAL	1512	165364.4	6.18
4	(TMD-NBD)2	ABCC (MRP)	14	242056227	SbABCC7	LSGGQKQRIQIARAL	1498	164034.9	6.18
4	(TMD-NBD)2	ABCC (MRP)	16	241922382	SbABCC1	LSGGQKQRVQLARAL	1512	166545.9	8.31
5	(TMD-NBD)2	ABCC (MRP)	11	241944702	SbABCC4	MSGGQKQRIQLARAV	1312	145782.2	6.15
5	(TMD-NBD)2	ABCC (MRP)	15	992156168	SbABCC17	MSGGQKQRIQLARAV	1497	163892.6	8.04
5	(TMD-NBD)2	ABCC (MRP)	15	242093342	SbABCC13	MSGGQKQRIQLARAV	1483	162534	8.26
5	(TMD-NBD)2	ABCC (MRP)	12	992155260	SbABCC15	LSGGQKQRVQLARAL	1484	165365.5	8.35
5	(TMD-NBD)2	ABCC (MRP)	12	242094756	SbABCC14	LSGGQKQRVQLARAL	1475	164269.3	8.35
5	(TMD-NBD)2	ABCC (MRP)	13	992163867	SbABCC20	LSGGQKQRIQLARAV	1520	164700.6	7
5	(TMD-NBD)2	ABCC (MRP)	8	242072374	SbABCC8	LSGGQKQRIQLARAV	1520	164752.6	7.01
5	(TMD-NBD)2	ABCC (MRP)	12	992163217	SbABCC18	LSGGQKQRVQLARAL	1482	164832.5	8.25

5	(TMD-NBD) ₂	ABCC (MRP)	12	242080007	SbABCC11	LSGGQKQRVQLARAL	1474	163968.6	8.25
5	(TMD-NBD) ₂	ABCC (MRP)	4	242074148	SbABCC10	MSGGQKQRIQIARSV	1367	153088.5	8.32
6	(TMD-NBD) ₂	ABCC (MRP)	15	992272364	SbABCC24	LSGGQKQRIQLARAV	1512	166540.5	6.97
6	(TMD-NBD) ₂	ABCC (MRP)	13	241937307	SbABCC2	LSGGQKQRIQLARAV	1549	169000.4	5.61
6	(TMD-NBD) ₂	ABCC (MRP)	12	992163218	SbABCC19	LSGGQKQRVQLARAL	1466	163730.7	8.07
6	(TMD-NBD) ₂	ABCC (MRP)	5	242092242	SbABCC12	LSGGQARLALARAL FSVGQRLLCLARAI	1265	141245.4	6.78
6	(TMD-NBD) ₂	ABCC (MRP)	6	242042087	SbABCC6	LSGGQKQRIQIARAL	1412	155090.2	5.69
6	(TMD-NBD) ₂	ABCC (MRP)	13	992165132	SbABCC22	MSGGQKQRIQIARSV	1595	178730.9	8.49
6	(TMD-NBD) ₂	ABCD (PMP)	0	241928977	SbABCD1	LSLGEQQRLGMARLF LSLGEQQRLGMARLF	1324	148003.4	9.14
6	(TMD-NBD) ₂	ABCD (PMP)	2	992157631	SbABCD3	LSLGEQQRLGMARLF LSLGEQQRLGMARLF	1317	147320.6	9.32
6	(TMD-NBD) ₂	ABCD (PMP)	3	242086563	SbABCD2	LSLGEQQRLGMARLF LSLGEQQRLGMARLF	1264	141479.8	9.26
6	NBD-NBD	ABCE1 (RLI)	13	992167635	SbABCE1	ISGGQKKRVTIGEML	1435	162120	6.48
7	NBD-NBD	ABCE2 (RLI)	0	242071667	SbABCE2	ISGGQKKRVTIGEML	1438	162375.3	6.48
7	NBD-NBD	ABCE3 (RLI)	12	992163020	SbABCE3	ISGGQKKRATVIGEML	1380	156596.1	8.45
7	NBD-NBD	ABCE4 (RLI)	13	992170503	SbABCE4	ISGGQKKRRTIGEML	1375	155514.3	7.33
7	NBD-NBD	ABCF1 (GCN)	13	241935658	SbABCF1	FSGGWKMRMSLGKIL LSGGEKARLAFCKFM	703	78649.8	8
7	NBD	ABCI (NAP)	5	241930348	SbABCI7	VSGGERRRVSIGVDI	732	80737.9	9.04
7	NBD	ABCI (NAP)	6	241921920	SbABCI2	VSGGERRRVSIGVDI	796	88083.6	9.36
7	NBD	ABCI (NAP)	5	992277385	SbABCI25	ISGGQRRRVVICMEI	734	79463.4	8.69
7	NBD	ABCI (NAP)	6	242090379	SbABCI18	VSGGERKRVIAVDI	673	72645.9	9.41
7	NBD	ABCI (NAP)	5	242072059	SbABCI17	ISGGQRKRLSICIEM	699	76712.7	8.85
7	NBD	ABCI (NAP)	5	242045026	SbABCI15	ISGGQRRRVVICMEI	699	76712.7	8.85
8	NBD	ABCI (NAP)	6	992155906	SbABCI20	ISGGQRKRLSICLEI	728	79707.7	8.12
8	NBD	ABCI (NAP)	6	241945778	SbABCI12	VSGGERRRVSIGTDI	714	77311.3	9.1
8	NBD	ABCI (NAP)	6	242095718	SbABCI19	ISGGQRKRLSICLEI	728	79749.8	8.09
8	NBD	ABCI (NAP)	7	241940270	SbABCI10	LSGGERKRVSIGLEM	749	79497.4	9.69
8	NBD	ABCI (NAP)	7	241927257	SbABCI3	ISGGEKKRLSLACEL	664	72783.1	8.73
8	NBD	ABCI (NAP)	6	241944469	SbABCI11	VSGGERRRVSIGTDI	710	76535.5	9.26
8	NBD	ABCI (NAP)	7	241928573	SbABCI4	VSGGERRRVSIGTDI	745	80210.8	9.59
8	NBD	ABCI (NAP)	6	992276420	SbABCI24	ISGGQRRRVVICVEL	699	76465.1	8.95
8	NBD	ABCI (NAP)	5	242043694	SbABCI14	ISGGQRRRVVICVEL	615	67511.7	9.1
8	NBD	ABCI (NAP)	6	992158560	SbABCI21	VSGGERKRVIAVDI	698	75343.9	9.11
9	NBD	ABCI (NAP)	6	241938010	SbABCI8	VSGGEKRRVSIALEL	724	79596.2	8.96
9	NBD	ABCI (NAP)	6	992280143	SbABCI26	ISGGEKRRVSIALEI	714	78770.2	8.71
9	NBD	ABCI (NAP)	7	241946103	SbABCI13	ISGGEKKRLSIALEI	688	76501.1	9.31
9	NBD	ABCI (NAP)	6	24194 b n=6103	SbABCI9	ISGGEKKRLSIALEI	688	76501.1	9.31
9	NBD	ABCI (NAP)	5	242066134	SbABCI16	ISGGQKKRRTIGEML	712	80465	6.35
9	NBD	ABCI (NAP)	5	241928752	SbABCI5	LSGGERRRVSIGVEA	673	72500.9	9.14
9	NBD	ABCI (NAP)	6	992276419	SbABCI23	ISGGQRRRVVICVEL	512	56825.9	8.86
9	TMD	ABCI (NAP)	6	241930131	SbABCI6	VSGGERRRVSIGMDL	612	65312.7	9.45

9	TMD	ABCI (NAP)	7	241919688	SbABCI1	VSGGERKRVCI GNEI TSGLDSTTALRIVQLL	763	83764.7	9.13
9	TMD	ABCI (NAP)	4	992169231	SbABCI22	MSGGQKQRIAIARAI LSGGQKQRIAIACAI	647	71063.2	6.06
1	Not available		6	992164873		VSGGEKRRVSIALEL	539	61011	9.05

**S. bicolor* ABC proteins have been named according to HGNC (Human Gene Nomenclature Committee) (Verrier et al., 2008); TMs: transmembrane helices.

Table S1: Inventory of *Sorghum bicolor* ABC Transporters

<i>S. bicolor</i> ABC transporters	Ortholog	Identity	Accession	Function of ortholog	Involvement	PUB MED ID	Function of <i>S. bicolor</i> ABC protein	Involvement
SbABCB1	ABC transporter B family member 27 [Arabidopsis thaliana]	77%	NP_19 8720.2	ATPase activity, coupled to transmembrane movement of substances, transporter activity	Response to aluminium ion		ATPase activity, coupled to transmembrane movement of substances, transporter activity	Response to aluminium ion
SbABCB4	P-glycoprotein 2 [Arabidopsis thaliana]	76%	NP_19 4326.2	ATPase activity, coupled to transmembrane movement of substances	Transport, transmembrane transport	1061 7198	ATPase activity, coupled to transmembrane movement of substances	Transport, transmembrane transport
SbABCB5	ABC transporter B family member 19 [Arabidopsis thaliana]	83%	NP_18 9528.1	ATPase activity, coupled to transmembrane movement of substances, auxin efflux transmembrane transporter activity	14 processes	1113 0713	ATPase activity, coupled to transmembrane movement of substances, auxin efflux transmembrane transporter activity	
SbABCB6	ABC transporter B family member 27 [Arabidopsis thaliana] TAP	77%	NP_19 8720.2	ATPase activity, coupled to transmembrane movement of substances, transporter activity	Response to aluminium ion		ATPase activity, coupled to transmembrane movement of substances, transporter activity	Response to aluminium ion
SbABCB8	ABC transporter B family member 1 [Arabidopsis thaliana] PGP1	77%	NP_18 1228.1	ATPase activity, coupled to transmembrane movement of substances, calmodulin binding, auxin efflux transmembrane transporter activity	10 processes		ATPase activity, coupled to transmembrane movement of substances, calmodulin binding, auxin efflux transmembrane transporter activity	
SbABCB9	auxin efflux transmembrane transporter MDR4 [Arabidopsis thaliana] PGP4	96%	NP_18 2223.1	Xenobiotic-transporting ATPase activity, ATPase activity, coupled to transmembrane movement of substances	8 processes		Xenobiotic-transporting ATPase activity, ATPase activity, coupled to transmembrane movement of substances	
SbABCB19	ABC transporter B family member 15 [Arabidopsis thaliana]	70%	NP_18 9475.1	ATPase activity, coupled to transmembrane movement of substances	Transport, transmembrane transport	1113 0713	ATPase activity, coupled to transmembrane movement of substances	Transport, transmembrane transport

SbABCB25 (PGP 1)	ABC transporter B family member 1 [Arabidopsis thaliana]	77%	NP_18 1228.1	ATPase activity, coupled to transmembrane movement of substances, calmodulin binding, auxin efflux transmembrane transporter activity	10 processes	1061 7197	ATPase activity, coupled to transmembrane movement of substances, calmodulin binding, auxin efflux transmembrane transporter activity	
SbABCB31	ABC transporter B family member 15 [Arabidopsis thaliana]	70%	NP_18 9475.1	ATPase activity, coupled to transmembrane movement of substances	Transport, transmembrane transport	1113 0713	ATPase activity, coupled to transmembrane movement of substances	Transport, transmembrane transport
SbABCB32	P-glycoprotein 2 [Arabidopsis thaliana]	76%	NP_19 4326.2	ATPase activity, coupled to transmembrane movement of substances	Transport, transmembrane transport	1061 7198	ATPase activity, coupled to transmembrane movement of substances	Transport, transmembrane transport
SbABCB33	ABC transporter B family member 21 [Arabidopsis thaliana]	70%	NP_19 1774.2	ATPase activity, coupled to transmembrane movement of substances	Transport, transmembrane transport	1113 0713	ATPase activity, coupled to transmembrane movement of substances	Transport, transmembrane transport
SbABCC1	TPA: low phytic acid 1 [Zea mays]	97%	DAA4 3317.1	ATPase activity, coupled to transmembrane movement of substances	Accumulation of phytic acid in seeds		ATPase activity, coupled to transmembrane movement of substances	Accumulation of phytic acid in seeds
	inositol hexakisphosphate transporter [Arabidopsis thaliana] (alias AtABCC5)	72%	NP_1 71908.1	ATPase activity, coupled to transmembrane movement of substances, sulfonyleurea receptor activity	Response to salt stress, cellular potassium ion homeostasis	1113 0712	ATPase activity, coupled to transmembrane movement of substances, sulfonyleurea receptor activity	Response to salt stress, cellular potassium ion homeostasis
SbABCC3	ABC transporter C family member 2 [Arabidopsis thaliana]	74%	NP_18 1013.1	ATPase activity, coupled to transmembrane movement of substances	Response to cyclopentenone	1061 7197	ATPase activity, coupled to transmembrane movement of substances	Response to cyclopentenone
SbABCI3	ABC transporter G family member 7 [Arabidopsis thaliana]	75%	NP_84 9921.1	ATPase activity, coupled to transmembrane movement of substances		1061 7197	ATPase activity, coupled to transmembrane movement of substances	
SbABCI8	ABC transporter G family member 11 [Arabidopsis thaliana]	77%	NP_17 3226.2	ATPase activity, coupled to transmembrane movement of substances, fatty acid transport activity	Cutin transport, fatty acid transport	1113 0712	ATPase activity, coupled to transmembrane movement of substances, fatty acid transport activity	Cutin transport, fatty acid transport
SbABCI26	ABC transporter G family member 11 [Arabidopsis thaliana]	77%	NP_17 3226.2	ATPase activity, coupled to transmembrane movement of substances, fatty acid transport activity	Cutin transport, fatty acid transport	1113 0712	ATPase activity, coupled to transmembrane movement of substances, fatty acid transport activity	Cutin transport, fatty acid transport

SORBI_00 6G155700	ABC transporter G family member 11 [Arabidopsis thaliana]	78%	NP_17 3226.2	ATPase activity, coupled to transmembrane movement of substances, fatty acid transport activity	Cutin transport, fatty acid transport	1113 0712	ATPase activity, coupled to transmembrane movement of substances, fatty acid transport activity	Cutin transport, fatty acid transport
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Table S2: Orthologs of *Sorghum bicolor* ABC Transporters

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