ABC transporters coordinately expressed during lignification of Arabidopsis stems include a set of ABCB's associated with auxin transport

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Supplementary Material

Supplementary Tables S1-S4

Supplementary Figures S1-S4

Supplemental table 1. TDNA insertion lines and a RNAi list nd their polymorphism sites.

MIPS locus	ABC transporter	Synonyms	mutant name	Salk/SAIL TDNA insertions	Polymorphism site
At1g02520	***ABCB11***	*MDR8/PGP11*	*abcb11*	Salk_094249	exon
At1g28010	***ABCB14***	*MDR12/PGP14*	*abcb14-1*	Salk_016005	exon
			abcb14-2	Salk_026876	exon
			abcb14RNAi		
At3g28345	***ABCB15***	*MDR13/PGP15*		Salk_121099	promoter
			abcb15-1	WiscDsLox501E11	exon
			abcb15-2	SAIL1187-C04 (CS843941)	exon
				Salk_036868	intron
				Salk_034562	intron
At3g16340	***ABCG29***	*PDR1*	*abcg29*	Salk_113825	exon
At2g37280	***ABCG33***	*PDR5*	*abcg33*	Salk_002380	exon

Supplemental table 2. Primer list

salk_016005/abcb14-1		
	Left primer	5'-TGGTCAAGTTAGGGAAACCGGA-3’
	Right primer	5’-GCCCTTGTGAATCTCCTCCAAA-3
salk_026876/abcb14-2		
	Left primer	5'-CGAGTTTCAGCCGGGAAGAGT-3’
	Right primer	5'-CCACCCAAGAGTTCTTAATGCGA-3'
salk_121099		
	Left primer	5’-TTTTCTTTTGTGGATTCCTTTG-3’
	Right primer	5’-TTGTTGTGCGGTGTGGCTTTA-3’
WiscDslox501E11/abcb15-1		
	Left primer	5’-GAGTCTAGAGCAAATGGC-3’
	Right primer	5’-AATGGCTACGAAACTCAG-3’
sail_1187-C04/abcb15-2		
	Left primer	5’-GGACAAGAACAGGGGAGAGAC-3’
	Right primer	5’-TGTTCAGACTGTTTCATTGTAGACAC-3’
salk_036868		
	Left primer	5’-ATTAGAGGCTTTGGCAGCTTC-3’
	Right primer	5’-TACTGTCTTTGCAGTTGCTGC-3’
salk_034562		
	Left primer	5’-ATTAGAGGCTTTGGCAGCTTC-3’
	Right primer	5’-TACTGTCTTTGCAGTTGCTGC-3’
salk_113825/abcb29		
	Left primer	5’-CAACGCTGCTTTAAACATTGC-3’
	Right primer	5’-TCGGACTATTGGGGTTGTTC-3’
salk_002380/abcb33		
	Left primer	5’-TTCCTGGAGTTGCTAAGATCAGAGA-3’
	Right primer	5’-AGCTGCGACCATGAAGTTTGG-3’
TDNA specific primer		
	LBa1	5'-TGGTTCACGTAGTGGGCCATCG-3'
	LBb1	5’-GCGTGGACCGCTTGCTGCAACT-3’
	sail Lb1	5'-GCCTTTTCAGAAATGGATAAATAGCC-3'
RNAi vector primers		
	Agri 51	5’-CAACCACGTCTTCAAAGCAA-3’
	Agri 56	5’-CTGGGGTACCGAATTCCTC-3’
	Agri 64	5’-CTTGCGCTG CAGTTATCATC-3’
	Agri 69	5’-AGGCGTCTCGCATATCTCAT-3’
ABCG33/PDR5		
	forward primer	5’-TTTGAATTCGAATTGGACACAGTTTGGCTA-3’
	reverse primer	5’-CCAGGATCCTTTCCAATCTCTGCAAGCTC-3’
	* underlined are BamHI and EcoRI recognition sites, respectively	
ABCB11/MDR8		
	forward primer	5’-CGGGAATTCGGGAATCGCAAGAAGGTAAG-3’
	reverse primer	5’-CGTGGATCCTTCGGCGCTGACAAAAAT-3’
	*underlined are BamHI and EcoRI sites, respectively	
ABCB14/MDR12		
	forward primer	5’-TGTGGATCCTTATCACTTTAGCACTGTG-3’
	reverse primer	5’-TTAGGATCCATGGATGGGAATTGATGC-3’
	*underlined are BamHI sites	
ABCB15/MDR13		
	forward primer	5’-TGTGGATCCGCCTATAAATAAAGTACGTAAGAC-3’
	reverse primer	5’-CCCGGATCCTTGTGTGTGTTTAAAGAGACAG-3’
	*underlined are BamHI sites	

ABCB13_RT_F	5'-CGTCTTACTTCTAGGGTTCG-3'
ABCB13_RT_R	5'-GCCACTGAAGTTGCCCTAGA-3'
ABCB14_RT_F	5'-ATCCATGCTGAGACCGAAGT-3'
ABCB14_RT_R	5'-AAGATTGCGTCGCTTGAGAT-3'
ABCB14_RT_F2	5'-TGGTCAAGTTAGGGAAACCGGA-3'
ABCB14_RT_R2	5'-GCGTTCTCGTTCCCATAC-3'
ABCB15_RT_F	5'-GAGTCTAGAGCAAATGGC-3'
ABCB15_RT_R	5'-AATGGCTACGAAACTCAG-3'
ABCG33_RT_F	5'-AACATCGGCATATATAAGTC-3'
ABCG33_RT_R	5'-CCTCACAGCTTTGTCTCA-3'
ACTIN8_RT_F	5'-ATTAAGGTCGTGGCA-3'
ACTIN8_RT_R	5'-TCCGAGTTTGAAGAGGCTAC-3'

Supplemental table 3: Nucleotides matrix in the boxes P, A and L

BOX P

POS	1	2	3	4	5	6	7	8	9	10	11	12	13	14
A	2	1	1	2	17	16	0	11	20	13	0	4	4	2
T	8	16	14	6	1	0	0	1	3	1	0	1	0	3
G	0	0	0	0	0	0	0	0	0	0	0	0	0	0
C	13	6	8	15	5	7	23	11	0	9	23	18	19	18

Number of elements used to build matrix: 23

BOX L

POS	1	2	3	4	5	6	7	8	9	10	11
A	2	0	1	1	21	0	0	7	20	1	1
T	11	3	17	7	0	2	0	14	0	0	0
G	2	0	0	0	0	0	0	0	0	0	0
C	6	18	3	13	0	19	21	0	1	20	20

Number of elements used to build matrix: 21

BOX A

POS	1	2	3	4	5	6
A	1	0	1	0	0	1
T	0	2	0	19	4	3
G	0	1	15	0	2	0
C	18	16	3	0	13	15

Number of elements used to build matrix: 19

Supplemental Table 4. Locus information and gene names used in this study for ABC transporter candidate genes

Description	MIPS locus	Synonyms [a]	ABC transporter nomen-clature [b]	Correlation with phenyl-propanoid gene expression [c]	Epidermal expression pattern [d]	Targeting prediction [e]	P/L/A box [f]	Pattern of expression in stem [g]
1 ABC transporter	At3g28345	*MDR13*	*ABCB15*	positive	Stem >Epi	Other	P	High from 3cm to base
2 ABC transporter	At1g02520	*MDR8*	*ABCB11*	positive	ND	Other	P	High from 3cm to base
3 ABC transporter	At5g06530	*WBC23*	*ABCG22*	positive	Stem = Epi	Other	ND	Increasing towards base
4 ABC transporter	At1g59870	*PDR8/PEN3*	*ABCG36*	positive	Epi >Stem	Chl	ND	Increase towards base
5 ABC transporter	At5g61690	*ATH15*	*ABCA11*	positive	ND	Mit	ND	High in 7-9cm segment
6 ABC transporter	At1g66950	*PDR13*	*ABCG39*	positive	Epi >Stem	Other	A	Stem apex only
7 ABC transporter	At3g16340	*PDR1*	*ABCG29*	positive	Stem > Epi	Chl	P	High at 3-5 cm segment
8 ABC transporter	At2g37280	*PDR5*	*ABCG33*	positive	Stem>Epi	Other	LP	Stem apex only
9 ABC transporter	At1g28010	*MDR12*	*ABCB14*	positive	Stem >Epi	Other	AP	Stem apex only
10 ABC transporter	At2g26910	*PDR4*	*ABCG32*	negative	Epi>stem	Other	ND	Decreasing towards base
11 ABC transporter	At5g61730	*ATH11*	*ABCA9*	negative	ND	Mit	ND	High between 2-5 cm
12 ABC transporter	At4g15230	*PDR2*	*ABCG30*	negative	low	Other	A	Negative in 3-5cm stem
13 ABC transporter	At4g25960	*MDR2*	*ABCB2*	negative	Epi >Stem	Other	AL	Negative at base
14 ABC transporter	At2g13610	*WBC5*	*ABCG5*	negative	low	Other	ND	Negative at base

[a] Arabidopsis ABC protein system by Sanchez-Fernandez et al. 2001

[b] Plant ABC proteins updated nomemclature by Verrier et al. 2008

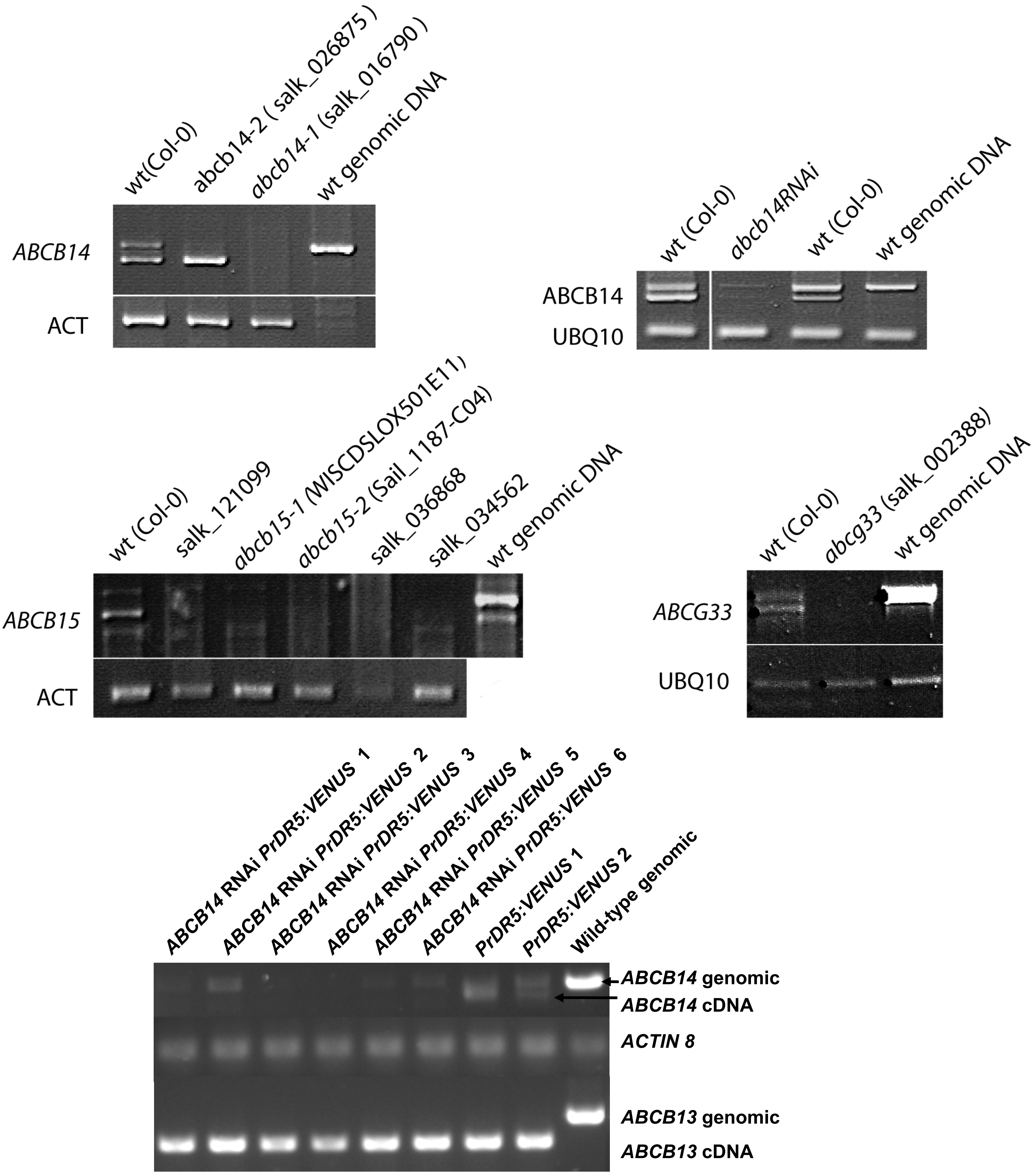
[c] Expression relative to phenylpropanoid genes.

[d] Data from Suh et al. (2005) Affymetrix "full genome" microarray study of Arabidopsis stem epidermal peel with reference to whole stems.

[e] Aramemnon: web-based targeting prediction program (http://aramemnon.botanik.uni-koeln.de)

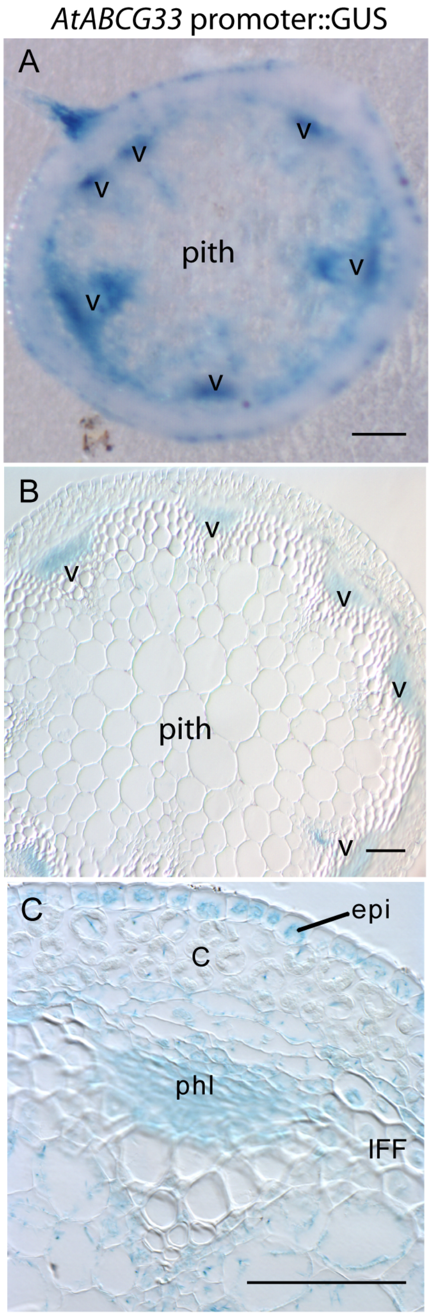
[f] Presence of P/L and A promoter elements was determined using MotifMapper, presence of motifs is indicated if the motif was present in the 1000 bp promoter region of candidate genes.

[g] Data from Ehlthing et al. (2005) Operon 'longmer' microarray study of Arabidopsis whole stems over a developmental gradient from stem apex to base, with reference to the o-2 cm apex region prior to lignification.

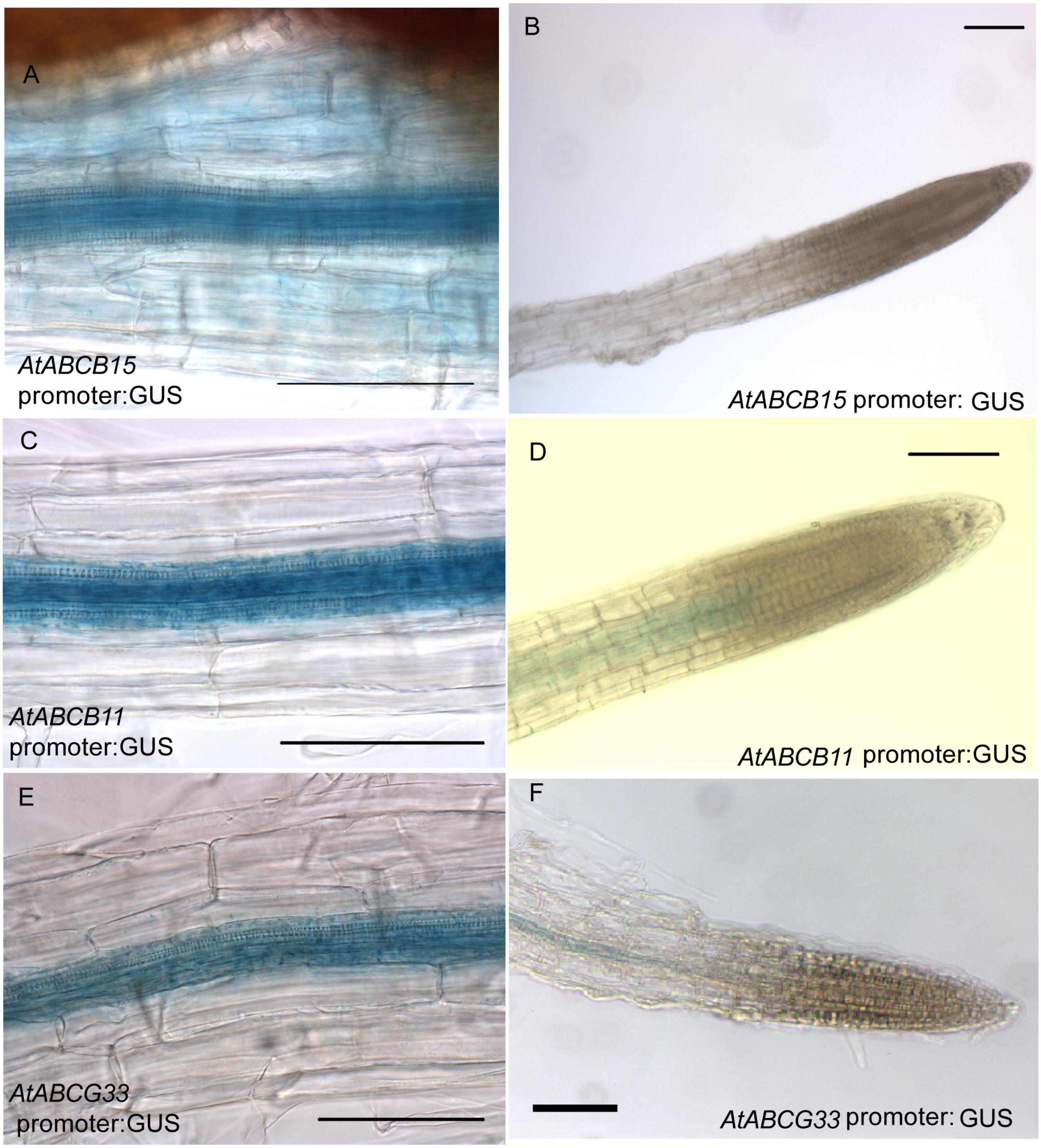


Supplemental figure 1. Transcriptional level by RT-PCR in ABC transporter candidate gene mutants.

Transcriptional level of *ABCB14*, *ABCB15* and *ABCG33* were very low or not detected either in *abcb14* RNAi, *abcb14-1, abcb15-1, abcb15-2* and *abcg33* compared to wild-type Columbia. *ABCB13* amplification in *abcb14* RNAi compared to wild-type plants showed the specificity of the RNAi effect to *ABCB14* transcripts. Actin (ACT) and ubiquitin (UBQ10) amplifications were used as control.



Supplemental figure 2. Gene expression profiles of candidate ABC transporter genes, *pABCG33*::GUS in stem vasculatures. A) Young stem sections, and B) and C) mature stem sections showed constant vasculature (V) specific GUS expression. cortex, epi: epidermal cells, IFF: interfascicular fiber, phl: phloem tissue. Scale bar = 50 um.



Supplemental figure 3. GUS expression profiles of candidate ABC transporter gene in seedling root tissue A) to F) Seedling root of promoter::GUS showed vascular cylinder specific GUS activity but no root tip in all three transporters. Bar = 250 m

Supplemental figure 4 Protein Alignment used for phylogenetic reconstruction

MDR protein sequences from Arabidopsis were retrieved from 'TAIR' (v9) and aligned using Dialign2 (Morgenstern et al., 2006). Only amino acid positions with more than 40% diagonal similarity are shown, which were used for further analyses. Identical and similar amino acids in more than 50% of all sequences are shaded in dark and light grey, respectively.

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                      10        20        30        40        50        60
              ....|....|....|....|....|....|....|....|....|....|....|....|
MDR1  ABCB1   ELFRFADGLDYVLMGIGSVGAFVHGCSLPLFLRFFADLALYFLVVGAAIWASSWAEISCW
MDR11 ABCB19  KLFSFADKFDYLLMFVGSLGAIVHGSSMPVFFLLFGQMSLYFVYLGLVVCFSSYAEIACW
MDR10 ABCB10  KLFSFADFYDCVLMALGSIGACIHGASVPVFFIFFGKLSLDFVYLSVVILFSSWLEVACW
MDR2  ABCB2   KLFSFADFYDCVLMTLGSVGACIHGASVPIFFIFFGKLSLDFVYLSVAILFSSWLEVACW
MDR12 ABCB14  GLFSAADNVDYFLMFLGGLGTCIHGGTLPLFFVFFGGMALYLVYLGLVNLVSAWIGVACW
MDR15 ABCB13  GLFSAADKLDYFLMLLGGLGACIHGATLPLFFVFFGKMALYLVYLGLVNFVSAWIGVSCW
MDR14 ABCB20  QLFACADRFDWVLMIVGSVAAAAHGTALIVYLHYFAKISLTIVYIAGGVFISGWIEVSCW
MDR6  ABCB6   QLFACADRFDWVLMVFGSVAAAAHGTALIVYLHYFAKISLTIVYIAGGVFISGWIEVSCW
MDR3_ ABCB3   KLFSFSDSTDVLLMIVGSIGAIGNGVGFPLMTLLFGDLCLKFVYLGLGTLGAAFLQVACW
MDR5¯ ABCB5   KLFFFSDSTDVLLMIVGSIGAIANGVCSPLMTLLFGELCLSLVYLGLGALGAAFLQVACW
MDR16 ABCB12  KLFAFADSFDVFLMICGSLGAIGNGVCLPLMTLLFGDLCLKFVYLGLGRLGAAFLQVACW
MDR8  ABCB11  KLFAFADSSDVLLMICGSIGAIGNGMSLPFMTLLFGDLCLKFVYLGLGTLGAAFLQVACW
MDR17 ABCB21  KLFAFADSFDIILMILGTIGAVGNGLGFPIMTILFGDVALKFVYLGLGTLVAALLQVSGW
MDR4  ABCB4   KLFAFADSFDFLLMILGTLGSIGNGLGFPLMTLLFGDLALKFVWLGIGTFAAAFLQLSGW
MDR9  ABCB9   KLFSFADKTDVVLMTVGTIAAAGNGLTQPFMTLIFGQLAVKFIYLAVYSCVVAFLQVSCW
MDR7  ABCB7   KLFTFADRYDIVLMVIGTLSAMANGLTQPFMSILMGQLAVKFLYLAAYAGVVSFLQVSCW
MDR19 ABCB17  SIFMHADGVDWILMALGLIGAVGDGFITPVVVFIFNTLVVALLYVACGSWVICFLEGYCW
MDR20 ABCB18  SIFMHADGVDWMLMALGLIGAVGDGFITPIIFFICSKLAVALVYVACASWVICFIEGYCW
MDR18 ABCB16  SIFMHADGVDWMLMGLGLIGAVGDGFITPILFFITAMLALAMLYVACASWVICFLEGYCW
MDR13 ABCB15  SIFMHADGVDWLLMGLGLIGAVGDGFTTPLVLLITSKLSVALLYVACGSWVVCFLEGYCW

                      70        80        90       100       110       120
              ....|....|....|....|....|....|....|....|....|....|....|....|
MDR1  ABCB1   MWSGERQTTKMRIKYLEAALNQDIQFFDTEVRTSDVVFAINTDAVMVQDAISEKLGNFIH
MDR11 ABCB19  MYSGERQVAALRKKYLEAVLKQDVGFFDTDARTGDIVFSVSTDTLLVQDAISEKVGNFIH
MDR10 ABCB10  MHTGERQAAKIRKAYLRSMLSQDISLFDTEISTGEVISAITSEILVVQDAISEKVGNFMH
MDR2  ABCB2   MHTGERQAAKMRRAYLRSMLSQDISLFDTEASTGEVISAITSDILVVQDALSEKVGNFLH
MDR12 ABCB14  MQTGERQTARLRINYLKSILAKDITFFDTEARDSNFIFHISSDAILVQDAIGDKTGHVLR
MDR15 ABCB13  MQTGERQTARLRINYLKSILAKDITFFDTEARDSNLIFHISSDAILVQDAIGDKTDHVLR
MDR14 ABCB20  ILTGERQTAVIRSKYVQVLLNQDMSFFDTYGNNGDIVSQVLSDVLLIQSALSEKVGNYIH
MDR6  ABCB6   ILTGERQTAVIRSKYVQVLLNQDMSFFDTYGNNGDIVSQVLSDVLLIQSALSEKVGNYIH
MDR3_ ABCB3   MITGERQAARIRSLYLKTILRQDIGFFDVETSTGEVVGRMSGDTVLILEAMGEKVGKFIQ
MDR5¯ ABCB5   MITGERQAARIRSLYLKTILRQDIGFFDVEMTTGEVVGRMSGDTVLILDAMGEKVGKFIQ
MDR16 ABCB12  MITGERQAAKIRSNYLKTILRQDIGFFDVETNTGEVVGRMSGDTVHIQDAMGEKVGKFIQ
MDR8  ABCB11  MITGERQAARIRSTYLKTILRQDIGFFDVETNTGEVVGRMSGDTVLIQDAMGEKVGKFIQ
MDR17 ABCB21  MISGERQAGRIRSLYLQTILRQDIAFFDVETNTGEVVGRMSGDTVLIQDAMGEKVGKAIQ
MDR4  ABCB4   MISGERQAARIRSLYLKTILRQDIAFFDIDTNTGEVVGRMSGDTVLIQDAMGEKVGKAIQ
MDR9  ABCB9   MVTGERQSATIRGLYLKTILRQDIGYFDTETNTGEVIGRMSGDTILIQDAMGEKVGKFTQ
MDR7  ABCB7   MVTGERQSTRIRRLYLKTILRQDIGFFDTETNTGEVIGRMSGDTILIQDSMGEKVGKFTQ
MDR19 ABCB17  TRTGERQAARMREKYLRAVLRQDVGYFDLHVTSSDVITSISSDSLVIQDFLSEKLPNFLM
MDR20 ABCB18  TRTGERQAAKMREKYLKAVLRQDVGYFDLHVTSSDVITSVSSDSLVIQDFLSEKLPNFLM
MDR18 ABCB16  TRTGERQAAKMRERYLRAVLRQDVGYFDLHVTSSDIITSVSSDSLVIQDFLSEKLPNILM
MDR13 ABCB15  TRTGERQTARMREKYLRAVLRQDVGYFDLHVTSSDVITSVSSDSFVIQDVLSEKLPNFLM

                     130       140       150       160       170       180
              ....|....|....|....|....|....|....|....|....|....|....|....|
MDR1  ABCB1   YMATFVSGFIVGFTAVWQLALVTLAVVPLIAVIGSQESLSQAGNIVEQTVVQIRVVMAFV
MDR11 ABCB19  YLSTFLAGLVVGFVSAWKLALLSVAVIPGIAFAGSRESYANAGVIAEQAIAQVRTVYSYV
MDR10 ABCB10  FISRFIAGFAIGFASVWQISLVTLSIVPFIALAGVRKSYVKANEIAEEVIGNVRTVQAFT
MDR2  ABCB2   YISRFIAGFAIGFTSVWQISLVTLSIVPLIALAGVRKSYIKAGEIAEEVIGNVRTVQAFT
MDR12 ABCB14  YLCQFIAGFVIGFLSVWQLTLLTLGVVPLIAIAGSEAAYADAGKVAEEVMSQVRTVYAFV
MDR15 ABCB13  YLSQFIAGFVIGFLSVWQLTLLTLGVVPLIAIAGSETAYADAGKVAEEVMSQVRTVYAFV
MDR14 ABCB20  NMATFISGLVIGFVNCWEIALITLATGPFIVAAGIQDAYAEAAGIAEQAISYIRTLYAFT
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MDR6  ABCB6    NMATFISGLIIGFVNCWEIALITLATGPFIVAAGIQDAYAEAASIAEQAVSYVRTLYAFT
MDR3_ ABCB3    LIATFVGGFVLAFVKGWLLTLVMLVSIPLLAIAGEQAAYAKASTVVEQTLGSIRTVASFT
MDR5  ABCB5    LISTFVGGFVIAFLRGWLLTLVMLTSIPLLAMSGEQAAYAKASNVVEQTLGSIRTVASFT
MDR16 ABCB12   LVSTFVGGFALAFAKGWLLTLVMLTSIPFLAMAGGQAAYAKAATVVEQTIGSIRTVASFT
MDR8  ABCB11   LVSTFVGGFVLAFIKGWLLTLVMLTSIPLLAMAGGQAAYAKAATVVEQTIGSIRTVASFT
MDR17 ABCB21   LVSTFIGGFVIAFTEGWLLTLVMVSSIPLLVMSGGQTSYAKAAVVVEQTVGSIRTVASFT
MDR4  ABCB4    LLATFVGGFVIAFVRGWLLTLVMLSSIPLLVMAGGQTAYAKAATVVEQTIGSIRTVASFT
MDR9  ABCB9    LLCTFLGGFAIAFYKGPLLAGVLCSCIPLIVIAGGQVAYAEAGNVVEQTVGAIRTVVAFT
MDR7  ABCB7    LVSSFVGGFTVAFIVGMKLTLALLPCVPLIVGTGVQLAYTEAGNVVQQAVGSIRTVVAFT
MDR19 ABCB17   NASAFVASYIVSFILMWRLTIVGFPFIILLLVPGIHEQYNEAGSIAEQAISSVRTVYAFG
MDR20 ABCB18   NTSAFVASYIVGFLLLWRLTIVGFPFIILLLIPGIREEYNEAGSIAEQVISSVRTVYAFG
MDR18 ABCB16   NASAFVGSYIVGFMLLWRLTIVGFPFIILLLIPGIREEYNEAGSIAEQAISSVRTVYAFV
MDR13 ABCB15   SASTFVGSYIVGFILLWRLAIVGLPFIVLLVIPGIREEYNEAGFVAEQAISSVRTVYAFS

                      190       200       210       220       230       240
               ....|....|....|....|....|....|....|....|....|....|....|....|
MDR1  ABCB1    GESRASQAYSSALKIAQKLGYKTGLAKGMGLGATYFVVFCCYALLLWYGGYLVRHHLTNG
MDR11 ABCB19   GESKALNAYSDAIQYTLKLGYKAGMAKGLGLGCTYGIACMSWALVFWYAGVFIRNGQTDG
MDR10 ABCB10   GEEKAVSSYQGALRNTYNYGRKAGLAKGLGLGSLHFVLFLSWALLIWFTSIVVHKGIANG
MDR2  ABCB2    GEERAVRLYREALENTYKYGRKAGLTKGLGLGSMHCVLFLSWALLVWFTSVVVHKDIADG
MDR12 ABCB14   GEEKAVKSYSNSLKKALKLSKRSGLAKGLGVGLTYSLLFCAWALLFWYASLLVRHGKTNG
MDR15 ABCB13   GEEKAVKSYSNSLKKALKLGKRSGLAKGLGVGLTYSLLFCAWALLLWYASLLVRHGKTNG
MDR14 ABCB20   NETLAKYSYATSLQATLRYGILISLVQGLGLGFTYGLAICSCALQLWIGRFFVHNGRANG
MDR6  ABCB6    NETLAKYSYATSLQATLRYGILISLVQGLGLGFTYGLAICSCAMQLWIGRFFVIHHRANG
MDR3_ ABCB3    GEKQAMKSYREFINLAYRASVKQGFSMGLGLGVVFFVFFCSYALAIWFGGEMILKKGYTG
MDR5  ABCB5    GEKQAMSSYKELINLAYKSNVKQGFVTGLGLGVMFLVFFSTYALGTWFGGEMILRKGYTG
MDR16 ABCB12   GEKQAINSYKKYITSAYKSSIQQGFSTGLGLGVMIYVFFSSYALAIWFGGKMILEKGYTG
MDR8  ABCB11   GEKQAINSYKKFITSAYKSSIQQGFSTGLGLGVMFFVFFSSYALAIWFGGKMILEKGYTG
MDR17 ABCB21   GEKQAISNYNKHLVSAYRAGVFEGASTGLGLGTLNIVIFCTYALAVWYGGKMILEKGYTG
MDR4  ABCB4    GEKQAISNYNKHLVTAYKAGVIEGGSTGLGLGTLFLVVFCSYALAVWYGGKLILDKGYTG
MDR9  ABCB9    GEKQATEKYESKLEIAYKTVVQQGLISGFGLGTMLAVIFCSYGLAVWYGAKLIMEKGYNG
MDR7  ABCB7    GEKQSMGKYEKKLEIAYKSMVKQGLYSGLGIGIMMVVVYCTYGFAIWYGARQIIEKGYTG
MDR19 ABCB17   SENKMIGKFSTALRGSVKLGLRQGLAKGITIGSN-GVTHAIWAFLTWYGSRLVMNHGSKG
MDR20 ABCB18   SEKKMIEKFSTALQGSVKLGLRQGLAKGIAIGSN-GITYAIWGFLTWYGSRMVMNHGSKG
MDR18 ABCB16   SEKKMIEKFSDALQGSVKLGLRQGLAKGIAIGSN-GIVYAIWGFLTWYGSRMVMNYGYKG
MDR13 ABCB15   GERKTISKFSTALQGSVKLGIKQGLAKGITIGSN-GITFAMWGFMSWYGSRMVMYHGAQG

                      250       260       270       280       290       300
               ....|....|....|....|....|....|....|....|....|....|....|....|
MDR1  ABCB1    GLAIATMFAVMIGGLALGQSAPSMAAFAKAKVAAAKIFRIIDHKPTIERNSESGVELDSV
MDR11 ABCB19   GKAFTAIFSAIVGGMSLGQSFSNLGAFSKGKAAGYKLMEIINQRPTIIQDPLDGKCLDQV
MDR10 ABCB10   GESFTTMLNVVIAGLSLGQAAPDISTFMRASAAAYPIFQMIER----NTEDKTGRKLGNV
MDR2  ABCB2    GKSFTTMLNVVIAGLSLGQAAPDISAFVRAKAAAYPIFKMIERNTVTKTSAKSGRKLGKV
MDR12 ABCB14   AKAFTTILNVIYSGFALGQAVPSLSAISKGRVAAANIFKMIGN----NNLLENGTTLQNV
MDR15 ABCB13   AKAFTTILNVIFSGFALGQAAPSLSAIAKGRVAAANIFRMIGN----NNSLDEGTTLQNV
MDR14 ABCB20   GEIIAALFAVILSGLGLNQAATNFYSFDQGRIAAYRLFEMITRSSSVA--NQEGAVLASV
MDR6  ABCB6    GEIITALFAVILSGLGLNQAATNFYSFDQGRIAAYRLFEMISR----S--NQEGIILSAV
MDR3_ ABCB3    GEVVNVMVTVVASSMSLGQTTPCLTAFAAGKAAAYKMFETIERKPSIDAFDLNGKVLEDI
MDR5  ABCB5    GAVINVMVTVVSSSIALGQASPCLTAFTAGKAAAYKMFETIEREPLIDTFDLNGKVLEDI
MDR16 ABCB12   GSVINVIIIVVAGSMSLGQTSPCVTAFAAGQAAAYKMFETIKRKPLIDAYDVNGKVLGDI
MDR8  ABCB11   GAVINVIIIVVAGSMSLGQTSPCVTAFAAGQAAAYKMFETIKRKPLIDAYDVNGKVLEDI
MDR17 ABCB21   GQVLIIIFAVLTGSMSLGQASPCLSAFAAGQAAAYKMFEAIKRKPEIDASDTTGKVLDDI
MDR4  ABCB4    GQVLNIIIAVLTGSMSLGQTSPCLSAFAAGQAAAYKMFETIERRPNIDSYSTNGKVLDDI
MDR9  ABCB9    GQVINVIFAVLTGGMSLGQTSPSLNAFAAGRAAAFKMFETIKRSPKIDAYDMSGSVLEDI
MDR7  ABCB7    GQVMNVITSILTGGMALGQTLPSLNSFAAGTAAAYKMFETIKRKPKIDAYDMSGEVLEEI
MDR19 ABCB17   GTVFVVISCITYGGVSLGQSLSNLKYFSEAFVAWERILEVIKRVPDIDSNKKEGQILERM
MDR20 ABCB18   GTVSSVIVCVTFGGTSLGQSLSNLKYFSEAFVVGERIMKVINRVPGIDSDNLEGQILEKT
MDR18 ABCB16   GTVSTVTVCVTFGGTALGQALSNLKYFSEAFVAGERIQKMIKRVPDIDSDNLNGHILETI
MDR13 ABCB15   GTVFAVAAAIAIGGVSLGGGLSNLKYFFEAASVGERIMEVINRVPKIDSDNPDGHKLEKI

                      310       320       330       340       350       360
               ....|....|....|....|....|....|....|....|....|....|....|....|
MDR1  ABCB1    TGLVELKNVDFSYPSRPDVKILNNFCLSVPAGKTIALVGSSGSGKSTVVSLIERFYDPNS
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MDR11 ABCB19        HGNIEFKDVTFSYPSRPDVMIFRNFNIFFPSGKTVAVVGGSGSGKSTVVSLIERFYDPNS
MDR10 ABCB10        NGDILFKDVTFTYPSRPDVVIFDKLNFVIPAGKVVALVGGSGSGKSTMISLIERFYEPTD
MDR2  ABCB2         DGHIQFKDATFSYPSRPDVVIFDRLNLAIPAGKIVALVGGSGSGKSTVISLIERFYEPIS
MDR12 ABCB14        VGKIEFCGVSFAYPSRPNMV-FENLSFTIHSGKTFAFVGPSGSGKSTIISMVQRFYEPRS
MDR15 ABCB13        AGRIEFQKVSFAYPSRPNMV-FENLSFTIRSGKTFAFVGPSGSGKSTIISMVQRFYEPNS
MDR14 ABCB20        QGNIEFRNVYFSYLSRPEIPILSGFYLTVPAKKAVALVGRNGSGKSSIIPLMERFYDPTL
MDR6  ABCB6         QGNIEFRNVYFSYLSRPEIPILSGFYLTVPAKKAVALVGRNGSGKSSIIPLMERFYDPTL
MDR3_ ABCB3         RGEIELRDVCFSYPARPMEEVFGGFSLLIPSGATAALVGESGSGKSSVISLIERFYDPSS
MDR5  ABCB5         RGEIELRDVCFSYPARPKEEVFGGFSLLIPSGTTTALVGESGSGKSTVISLIERFYDPNS
MDR16 ABCB12        RGDIELKDVHFSYPARPDEEIFDGFSLFIPSGATAALVGESGSGKSTVINLIERFYDPKA
MDR8  ABCB11        RGDIELKDVHFSYPARPDEEIFDGFSLFIPSGATAALVGESGSGKSTVISLIERFYDPKS
MDR17 ABCB21        RGDIELNNVNFSYPARPEEQIFRGFSLSISSGSTVALVGQSGSGKSTVVSLIERFYDPQS
MDR4  ABCB4         KGDIELKDVYFTYPARPDEQIFRGFSLFISSGTTVALVGQSGSGKSTVVSLIERFYDPQA
MDR9  ABCB9         RGDIELKDVYFRYPARPDVQIFAGFSLFVPNGKTVALVGQSGSGKSTVISLIERFYDPES
MDR7  ABCB7         KGDIELRDVYFRYPARPDVQIFVGFSLTVPNGMTVALVGQSGSGKSTVISLIERFYDPES
MDR19 ABCB17        KGEVEFNHVKFTYLSRPETTIFDDLCLKIPAGKTVALVGGSGSGKSTVISLLQRFYDPIA
MDR20 ABCB18        RGEVEFNHVKFTYPSRPETPIFDDLCLRVPSGKTVALVGGSGSGKSTVISLLQRFYDPIA
MDR18 ABCB16        RGEVEFNNVKCKYPSRPETLIFDDLCLKIPSGKTVALVGGSGSGKSTVISLLQRFYDPNE
MDR13 ABCB15        RGEVEFKNVKFVYPSRLETSIFDDFCLRVPSGKTVALVGGSGSGKSTVISLLQRFYDPLA

                            370       380       390       400       410       420
                    ....|....|....|....|....|....|....|....|....|....|....|....|
MDR1  ABCB1         GQVLLDGQDLKTLKLRWLRQQIGLVSQEPALFATSIKENILLGRPDADQVEIEEAARVAN
MDR11 ABCB19        GQILLDGVEIKTLQLKFLREQIGLVNQEPALFATTILENILYGKPDATMVEVEAAASAAN
MDR10 ABCB10        GAVMLDGNDIRYLDLKWLRGHIGLVNQEPVLFATTIRENIMYGKDDATSEEITNAAKLSE
MDR2  ABCB2         GAVLLDGNNISELDIKWLRGQIGLVNQEPALFATTIRENILYGKDDATAEEITRAAKLSE
MDR12 ABCB14        GEILLDGNDIKNLKLKWLREQMGLVSQEPALFATTIASNILLGKEKANMDQIIEAAKAAN
MDR15 ABCB13        GEILLDGNDIKSLKLKWFREQLGLVSQEPALFATTIASNILLGKENANMDQIIEAAKAAN
MDR14 ABCB20        GEVLLDGENIKNLKLEWLRSQIGLVTQEPALLSLSIRENIAYGRD-ATLDQIEEAAKNAH
MDR6  ABCB6         GEVLLDGENIKNLKLEWLRSQIGLVTQEPALLSLSIRENIAYGRD-ATLDQIEEAAKKAH
MDR3_ ABCB3         GSVLIDGVNLKEFQLKWIRGKIGLVSQEPVLFSSSIMENIGYGKENATVEEIQAAAKLAN
MDR5  ABCB5         GQVLIDGVDLKEFQLKWIRGKIGLVSQEPVLFSSSIMENIGYGKEGATVEEIQAASKLAN
MDR16 ABCB12        GEVLIDGINLKEFQLKWIRSKIGLVCQEPVLFSSSIMENIAYGKENATLQEIKVATELAN
MDR8  ABCB11        GAVLIDGVNLKEFQLKWIRSKIGLVSQEPVLFSSSIMENIAYGKENATVEEIKAATELAN
MDR17 ABCB21        GEVRIDGINLKEFQLKWIRSKIGLVSQEPVLFTSSIKENIAYGKENATVEEIRKATELAN
MDR4  ABCB4         GDVLIDGINLKEFQLKWIRSKIGLVSQEPVLFTASIKDNIAYGKEDATTEEIKAAAELAN
MDR9  ABCB9         GQVLIDNIDLKKLQLKWIRSKIGLVSQEPVLFATTIKENIAYGKEDATDQEIRTAIELAN
MDR7  ABCB7         GEVLIDGIDLKKFQVKWIRSKIGLVSQEPILFATTIRENIVYGKKDASDQEIRTALKLAN
MDR19 ABCB17        GEILIDGVSIDKLQVNWLRSQMGLVSQEPVLFATSITENILFGKEDASLDEVVEAAKASN
MDR20 ABCB18        GEILIDGLPINKLQVKWLRSQMGLVSQEPVLFATSIKENILFGKEDASMDEVVEAAKASN
MDR18 ABCB16        GDILIDSVSINNMQVKWLRSQMGMVSQEPSLFATSIKENILFGKEDASFDEVVEAAKASN
MDR13 ABCB15        GEILIDGVSIDKLQVKWLRSQMGLVSQEPALFATTIKENILFGKEDASMDDVVEAAKASN

                            430       440       450       460       470       480
                    ....|....|....|....|....|....|....|....|....|....|....|....|
MDR1  ABCB1         AHSFIIKLPDGFDTQVGERGLQLSGGQKQRIAIARAMLKNPAILLLDEATSALDSESEKL
MDR11 ABCB19        AHSFITLLPKGYDTQVGERGVQLSGGQKQRIAIARAMLKDPKILLLDEATSALDASSESI
MDR10 ABCB10        AISFINNLPEGFETQVGERGIQLSGGQKQRISISRAIVKNPSILLLDEATSALDAESEKI
MDR2  ABCB2         AISFINNLPEGFETQVGERGIQLSGGQKQRIAISRAIVKNPSILLLDEATSALDAESEKS
MDR12 ABCB14        ADSFIKSLPNGYNTQVGEGGTQLSGGQKQRIAIARAVLRNPKILLLDEATSALDAESEKI
MDR15 ABCB13        ADSFIKSLPNGYNTQVGEGGTQLSGGQKQRIAIARAVLRNPKILLLDEATSALDAESEKI
MDR14 ABCB20        AHTFISSLEKGYETQVGRAGLAMTEEQKIKLSIARAVLLNPTILLLDEVTGGLDFEAERI
MDR6  ABCB6         AHTFISSLEKGYETQVGKTGLTLTEEQKIKLSIARAVLLDPTILLLDEVTGGLDFEAERV
MDR3_ ABCB3         AANFIDKLPRGLETLVGEHGTQLSGGQKQRIAIARAILKDPRILLLDEATSALDAESERV
MDR5  ABCB5         AAKFIDKLPLGLETLVGEHGTQLSGGQKQRIAIARAILKDPRILLLDEATSALDAESERV
MDR16 ABCB12        AAKFINNLPQGLDTKVGEHGTQLSGGQKQRIAIARAILKDPRVLLLDEATSALDTESERV
MDR8  ABCB11        AAKFIDKLPQGLDTMVGEHGTQLSGGQKQRIAIARAILKDPRILLLDEATSALDAESERV
MDR17 ABCB21        ASKFIDKLPQGLDTMVGEHGTQLSGGQKQRIAVARAILKDPRILLLDEATSALDAESERI
MDR4  ABCB4         ASKFVDKLPQGLDTMVGEHGTQLSGGQKQRIAVARAILKDPRILLLDEATSALDAESERV
MDR9  ABCB9         AAKFIDKLPQGLDTMVGEHGTQMSGGQKQRLAIARAILKNPKILLLDEATSALDAESERI
MDR7  ABCB7         ASNFIDKLPQGLETMVGEHGTQLSGGQKQRIAIARAILKNPKILLLDEATSALDAESERI
MDR19 ABCB17        AHTFISQFPLGYKTQVGERGVQMSGGQKQRIAIARAIIKSPKILLLDEATSALDSESERV
MDR20 ABCB18        AHSFISQFPNSYQTQVGERGVQLSGGQKQRIAIARAIIKSPIILLLDEATSALDSESERV
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MDR18 ABCB16   AHNFISQFPHGYQTQVGERGVHMSGGQKQRIAIARALIKSPIILLLDEATSALDLESERV
MDR13 ABCB15   AHNFISQLPNGYETQVGERGVQMSGGQKQRIAIARAIIKSPTILLLDEATSALDSESERV

                       490       500       510       520       530       540
               ....|....|....|....|....|....|....|....|....|....|....|....|
MDR1  ABCB1    VQEALDRFMIGRTTLIIAHRLSTIRKADLVAVLQQGSVSEIGTHDELFSKGENGVYAKLI
MDR11 ABCB19   VQEALDRVMVGRTTVVVAHRLCTIRNVDSIAVIQQGQVVETGTHEELIAKS--GAYASLI
MDR10 ABCB10   VQEALDRVMVGRTTVVVAHRLSTVRNADIIAVVGGGKIIESGSHDELISNP-DGAYSSLL
MDR2  ABCB2    VQEALDRVMVGRTTVVVAHRLSTVRNADIIAVVHEGKIVEFGNHENLISNP-DGAYSSLL
MDR12 ABCB14   VQQALDNVMEKRTTIVIAHRLSTIRNVDKIVVLRDGQVRETGSHSELISRG--GDYATLV
MDR15 ABCB13   VQQALDNVMEKRTTIVVAHRLSTIRNVDKIVVLRDGQVRETGSHSELMLRG--GDYATLV
MDR14 ABCB20   VQEALDLLMLGRSTIIIARRLSLIKNADYIAVMEEGQLVEMGTHDELINLG--GLYAELL
MDR6  ABCB6    VQEALDLLMLGRSTIIIARRLSLIRNADYIAVMEEGQLLEMGTHDELINLG--NLYAELL
MDR3_ ABCB3    VQEALDRVMMSRTTVIVAHRLSTVRNADMIAVIHRGKIVEEGSHSELLKDH-EGAYAQLI
MDR5  ABCB5    VQEALDRIMVNRTTVIVAHRLSTVRNADIIAVIHRGKIVEEGSHSELLKDH-EGAYSQLL
MDR16 ABCB12   VQEALDRVMVNRTTVVVAHRLSTVRNADMIAVIHSGKMVEKGSHSELLKDS-VGAYSQLI
MDR8  ABCB11   VQEALDRVMVNRTTVIVAHRLSTVRNADMIAVIHRGKMVEKGSHSELLKDS-EGAYSQLI
MDR17 ABCB21   VQEALDRIMVNRTTVVVAHRLSTVRNADMIAVIHQGKIVEKGSHSELLRDP-EGAYSQLI
MDR4  ABCB4    VQEALDRIMVNRTTVVVAHRLSTVRNADMIAVIHQGKIVEKGSHTELLKDP-EGAYSQLI
MDR9  ABCB9    VQDALVNLMSNRTTVVVAHRLTTIRTADVIAVVHQGKIVEKGTHDEMIQDP-EGAYSQLV
MDR7  ABCB7    VQDALVKLMLSRTTVVVAHRLTTIRTADMIAVVQQGKVIEKGTHDEMIKDP-EGTYSQLV
MDR19 ABCB17   VQESLDNASIGRTTIVIAHRLSTIRNADVICVIHNGQIVETGSHEELLKRI-DGQYTSLV
MDR20 ABCB18   VQEALDNASIGRTTIVIAHRLSTIRNADVICVVHNGRIIETGSHEELLEKL-DGQYTSLV
MDR18 ABCB16   VQEALDNASVGRTTIVIAHRLSTIRNADIICVLHNGCIVETGSHDKLMEID--GKYTSLV
MDR13 ABCB15   VQEALENASIGRTTILIAHRLSTIRNADVISVVKNGHIVETGSHDELMENI-DGQYSTLV

                       550       560       570       580       590       600
               ....|....|....|....|....|....|....|....|....|....|....|....|
MDR1  ABCB1    KMQMNSPEWKYALLGSVGSVICGSLSAFFAYVIDKYCYLLIGLSSAALVFNTLQHSFWDI
MDR11 ABCB19   RFQLNSPEWPYSIMGAVGSILSGFIGPTFAIVTKEYVFIYIGAGLYAVGAYLIQHYFFSI
MDR10 ABCB10   RIQMIRPDWKYGLCGTLGSFIAGSQMPLFALGVKRISILFCCGSVITVIVHTIEHTTFGI
MDR2  ABCB2    RLQMIRPDWMYGVCGTICAFIAGSQMPLFALGIKKIAILFCCASVITLIVYTIEHICFGT
MDR12 ABCB14   NCQLNAPEWLYALLGSIGAVLAGSQPALFSMGVDKVAIIFVGAGIVTAPIYILQHYFYTL
MDR15 ABCB13   NCQLNSPEWPYALLGSIGAVLAGAQTPLFSMGVEKVAIIFAGAGIVTAPIYLLQHYFYTL
MDR14 ABCB20   KCELSFPEWLYAVLGSLGAAIFGSFNPLLAYVVDKWCLIIACMGIVTVVANFLQHFYFGI
MDR6  ABCB6    KCELSFPEWLYAVLGSIGAAIFGSFNPLLAYVVDKWCLIIACMGIVTVVANFLQHFYFGI
MDR3_ ABCB3    RLQLNKPETTILILGTLLGAVNGTIFPIFGILSRFWSMIFVLLGVASLIVYPMHTYLFAV
MDR5  ABCB5    RLQLNKPEIPILILGTLVGAVNGTIFPIFGILSRFWSMIFVLLGVAAVIVYPTTNYLFAI
MDR16 ABCB12   RCQLNKPEIPVLLLGTVVAAINGAIFPLFGILSRFWAIIFVALGVTSLIVSPSQMYLFAV
MDR8  ABCB11   RLQLNKPEIPVLLLGTVAAAINGAIFPLFGILSRFWAIIFVALGVTSLIVSPTQMYLFAV
MDR17 ABCB21   RLQLNKPEIPMLILGSIAAVLNGVILPIFGILTRFWAIIFMLLGVASMVVFPAQTIFFSI
MDR4  ABCB4    RLQLNKPEIPVLILGSISAAANGVILPIFGILTSFWAIIFMVLGFASIIAYPAQTFFFAI
MDR9  ABCB9    RLQLNKPEIPVLVLGSIAAMVHGTVFPIFGLLSHFWALIYIALGLTNFVMIPVQNYFFGI
MDR7  ABCB7    RLQLNKPEISVLLLGSLAAVIHGIVFPVQGLLSLFWALIFVALGLTDLIVIPLQNYLFAI
MDR19 ABCB17   SLQMNRPEWKHALYGCLSAALVGVLQPVSAYSTRIYVLLFVGLAIFSFLVNISQHYGFAY
MDR20 ABCB18   RLQMNRPEWKHALYGCLGAALFGAVQPIYSYSTRIYVLLFVGLALFTFLSNISQHYGFAY
MDR18 ABCB16   RLQMNRPEWKHALCGCLSASLGGAVQPIYAYSTRIYVLLFFGLALFTFFTSISQQYSFSY
MDR13 ABCB15   HLQMNLPEWKQALYGCISATLFGAIQPAYAYSTRIYALSFVGLAVLSFLINISQHYNFAY

                       610       620       630       640       650       660
               ....|....|....|....|....|....|....|....|....|....|....|....|
MDR1  ABCB1    VGENLTKRVREKMLSAVLKNEMAWFDQEENESARIAARLALDANNVRSAIGDRISVIVQN
MDR11 ABCB19   MGENLTTRVRRMMLSAILRNEVGWFDEDEHNSSLIAARLATDAADVKSAIAERISVILQN
MDR10 ABCB10   MGERLTLRVRQKMFSAILRNEIGWFDKVDNTSSMLASRLESDATLLRTIVVDRSTILLEN
MDR2  ABCB2    MGERLTLRVRENMFRAILKNEIGWFDEVDNTSSMLASRLESDATLLKTIVVDRSTILLQN
MDR12 ABCB14   MGERLTSRVRLSLFSAILSNEIGWFDLDENNTGSLTSILAADATLVRSAIADRLSTIVQN
MDR15 ABCB13   MGERLTSRVRLSLFSAILSNEIGWFDLDENNTGSLTSILAADATLVRSALADRLSTIVQN
MDR14 ABCB20   MGEKMTERVRRMMFSAMLRNEVGWFDDEENSPDTLSMRLANDATFVRAAFSNRLSIFIQD
MDR6  ABCB6    MGEKMTERVRRMMFSAMLRNEVGWYDEEENSPDTLSMRLANDATFVRAAFSNRLSIFIQD
MDR3_ ABCB3    AGGRLIQRIRVMCFEKVVHMEVGWFDDPENSSGTIGSRLSADAALIKTLVGDSLSLSVKN
MDR5  ABCB5    AGGRLIRRIRSMCFEKVVHMEVGWFDEPGNSSGAMGARLSADAALIRTLVGDSLCLSVKN
MDR16 ABCB12   AGGKLIRRIQSMCFEKAVHMEVSWFDEPENSSGTMGARLSTDAALIRALVGDALSLAVQN
MDR8  ABCB11   AGGKLIRRIRSMCFEKAVHMEVAWFDEPQNSSGTMGARLSADATLIRALVGDALSLAVQN
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MDR17 ABCB21   AGCKLVQRIRSMCFEKVVRMEVGWFDETENSSGAIGARLSADAATVRGLVGDALAQTVQN
MDR4  ABCB4    AGCKLVQRIRSMCFEKVVHMEVGWFDEPENSSGTIGARLSADAATIRGLVGDSLAQTVQN
MDR9  ABCB9    AGGKLIKRIRSMCFDKVVHQEISWFDDTANSRSLV---------------GDALALIVQN
MDR7  ABCB7    AGAKLIKRIRSLSFDRVLHQDISWFDDTKNSSGVIGARLSTDASTVKSIVGDVLGLIMQN
MDR19 ABCB17   MGEYLTKRIREQMLSKILTFEVNWFDIDDNSSGAICSRLAKDANVVRSMVGDRMSLLVQT
MDR20 ABCB18   MGEYLTKRIRERMLGKILTFEVNWFDKDENSSGAICSRLAKDANMVRSLVGDRMSLLVQT
MDR18 ABCB16   MGEYLTKRIREQMLSKILTFEVNWFDEEENSSGAICSRLAKDANVVRSLVGERMSLLVQT
MDR13 ABCB15   MGEYLTKRIRERMLSKVLTFEVGWFDRDENSSGAICSRLAKDANVVRSLVGDRMALVVQT

                       670       680       690       700       710       720
               ....|....|....|....|....|....|....|....|....|....|....|....|
MDR1  ABCB1    TALMLVACTAGFVLQWRLALVLVAVFPVVVAATVLQKMFMTGFSGDLEAAHAKGTQLAGE
MDR11 ABCB19   MTSLLTSFIVAFIVEWRVSLLILGTFPLLVLANFAQQLSLKGFAGDTAKAHAKTSMIAGE
MDR10 ABCB10   LGLVVTAFIISFILNWRLTLVVLATYPLIISGHISEKIFMQGYGGNLSKAYLKANMLAGE
MDR2  ABCB2    LGLVVTSFIIAFILNWRLTLVVLATYPLVISGHISEKLFMQGYGGDLNKAYLKANMLAGE
MDR12 ABCB14   LSLTITALALAFFYSWRVAAVVTACFPLLIAASLTEQLFLKGFGGDYTRAYSRATSLARE
MDR15 ABCB13   LSLTVTALALAFFYSWRVAAVVTACFPLLIAASLTEQLFLKGFGGDYTRAYSRATSVARE
MDR14 ABCB20   SFAVIVALLIGLLLGWRLALVALATLPILTLSAIAQKLWLAGFSKGIQEMHRKASLVLED
MDR6  ABCB6    SFAVIVAILIGLLLGWRLALVALATLPVLTLSAIAQKLWLAGFSKGIQEMHRKASLVLED
MDR3_ ABCB3    AAAAVSGLIIAFTASWKLAVIILVMIPLIGINGYLQIKFIKGFTADAKAKYEEASQVAND
MDR5  ABCB5    VASLVTGLIIAFTASWEVAIIILVIIPFIGINGYIQIKFMKGFSADAKAKYEEASQVAND
MDR16 ABCB12   AASAASGLIIAFTASWELALIILVMLPLIGINGFLQVKFMKGFSADAKSKYEEASQVAND
MDR8  ABCB11   VASAASGLIIAFTASWELALIILVMLPLIGINGFVQVKFMKGFSADAKSKYEEASQVAND
MDR17 ABCB21   LASVTAGLVIAFVASWQLAFIVLAMLPLIGLNGYIYMKFMVGFSADA----KEASQVAND
MDR4  ABCB4    LSSILAGLIIAFLACWQLAFVVLAMLPLIALNGFLYMKFMKGFSADAKKMYGEASQVAND
MDR9  ABCB9    IATVTTGLIIAFTANWILALIVLALSPFIVIQGYAQTKFLTGFSADAKAMYEEASQVAND
MDR7  ABCB7    MATIIGAFIIAFTANWLLALMALLVAPVMFFQGYYQIKFITGFGAKARGKYEEASQVASD
MDR19 ABCB17   ISAVIIACIIGLVIAWRLAIVMISVQPLIVVCFYTQRVLLKSLSEKASKAQDESSKLAAE
MDR20 ABCB18   ISAVSITCAIGLVISWRFSIVMMSVQPVIVVCFYTQRVLLKSMSRNAIKGQDESSKLAAE
MDR18 ABCB16   ISTVMVACTIGLVIAWRFTIVMISVQPVIIVCYYIQRVLLKNMSKKAIIAQDESSKLAAE
MDR13 ABCB15   VSAVTIAFTMGLVIAWRLALVMIAVQPVIIVCFYTRRVLLKSMSKKAIKAQDESSKLAAE

                       730       740       750       760       770       780
               ....|....|....|....|....|....|....|....|....|....|....|....|
MDR1  ABCB1    AIANVRTVAAFNSEAKIVRLYTANLEPPLKRFLMVSANGAAETLTLAPDFIKGGQAMRSV
MDR11 ABCB19   GVSNIRTVAAFNAQSKILSLFCHELRVPQKRFLVITANSVAETVSLAPEIIRGGEAVGSV
MDR10 ABCB10   SISNIRTVVAFCAEEKVLDLYSKELLEPSERFLIVTALVMGEVLALAPDLLKGNQMVVSV
MDR2  ABCB2    SVSNIRTVAAFCAEEKILELYSRELLEPSKSFLIVTALAMGETLALAPDLLKGNQMVASV
MDR12 ABCB14   AISNIRTVAAFSAEKQISEQFTCELSKPTKSFLLVTAYSVAETLALTPDIVKGTQALGSV
MDR15 ABCB13   AIANIRTVAAYGAEKQISEQFTCELSKPTKNFLIVTAFSVSETLALTPDIVKGTQALGSV
MDR14 ABCB20   AVRNIYTVVAFCAGNKVMELYRMQLQRILRQYFSFATFALVEPFGLAPYILKRRKSLISV
MDR6  ABCB6    AVRNIYTVVAFCAGNKVMELYRLQLQRILRQYFSFATFALVEPFGLAPYILKRRRSLASV
MDR3_ ABCB3    AVGSIRTVASFCAEEKVMEMYKKRCEDTIKSFLTMTAIGISQASSFAPDSSKAKGAAASI
MDR5  ABCB5    AVGSIRTVASFCAEEKVMEMYKKRCEDTIKSFLTLTAVGISQASSFAPDSSKGKGAAVSI
MDR16 ABCB12   AVGSIRTVASFCAEEKVMQMYNKQCEGPIKDFLTMAAIGISQSSTFAPDSSKAKVAAASI
MDR8  ABCB11   AVGSIRTVASFCAEEKVMQMYKKQCEGPIKDFLTMAAIGISQSSTFAPDSSKAKVAAASI
MDR17 ABCB21   AVGSIRTVASFCAEEKVMKMYKKKCEGPMRTFLTMAAVAISQSSSLSPDSSKASNAAASI
MDR4  ABCB4    AVGSIRTVASFCAEDKVMNMYSKKCEGPMKNFLTMAAMAISQSSSLSPDSSKADVAAASI
MDR9  ABCB9    AVSSIRTVASFCAEEKVMDLYQQKCDGPKKNFLTIMAIGVSQTSAMAPDSNKAKDSAASI
MDR7  ABCB7    AVSSIRTVASFCAEDKVMDLYQEKCDEPKQQFLTLTAVGVTQTSTMAPDINKAKDSAASI
MDR19 ABCB17   AVSNIRTITAFSSQERIIKLLKKVQEGPRREFFVTTGRVIADAGTMTTDLARGLDAVGSV
MDR20 ABCB18   AVSNIRTITAFSSQERIINLLKMVQEGPRKDFFASTGRVIAEAGTMTKDLVKGSDAVASV
MDR18 ABCB16   AVSNIRTITTFSSQERIMKLLERVQEGPRREFFKTTGRAIAEAGTMTTDLAKGSNSVDSV
MDR13 ABCB15   AVSNVRTITAFSSQERIMKMLEKAQESPRREFLVSTGRVIADAGSMTTDLAKGSDAVGSV

                       790       800       810       820       830       840
               ....|....|....|....|....|....|....|....|....|....|....|....|
MDR1  ABCB1    FELLDRKTEIEPDDPDTTPVPDRLRGEVELKHIDFSYPSRPDIQIFRDLSLRARAGKTLA
MDR11 ABCB19   FSVLDRQTRIDPDD-ADADPVETIRGDIEFRHVDFAYPSRPDVMVFRDFNLRIRAGHSQA
MDR10 ABCB10   FELLDRRTQVVG---DTGEELSNVEGTIELKGVHFSYPSRPDVTIFSDFNLLVPSGKSMA
MDR2  ABCB2    FEILDRKTQIVG---ETSEELNNVEGTIELKGVHFSYPSRPDVVIFRDFDLIVRAGKSMA
MDR12 ABCB14   FRVLHRETEIPPDQ-PNSRLVTHIKGDIEFRNVSFAYPTRPEIAIFKNLNLRVSAGKSLA
MDR15 ABCB13   FRVLHRETKISPDQ-PNSRMVSQVKGDIEFRNVSFVYPTRPEIDIFKNLNLRVSAGKSLA
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MDR14 ABCB20   FEIVDRVPTIEPDD-NSALKPPNVYGSIELKNVDFCYPTRPEILVLSNFSLKISGGQTVA
MDR6  ABCB6    FEIIDRVPTIEPDD-TSALSPPNVYGSIELKNIDFCYPTRPEVLVLSNFSLKVNGGQTVA
MDR3_ ABCB3    FGIIDGKSMIDSRD-ESGLVLENVKGDIELCHISFTYQTRPDVQIFRDLCFAIRAGQTVA
MDR5  ABCB5    FRIIDRISKIDSRD-ESGMVLENVKGDIELCHISFTYQTRPDVQVFRDLCLSIRAGQTVA
MDR16 ABCB12   FAIIDRKSKIDSSD-ETGTVLENVKGDIELRHLSFTYPARPGIQIFRDLCLTIRAGKTVA
MDR8  ABCB11   FAIIDRKSKIDSSD-ETGTVLENVKGDIELRHLSFTYPARPDIQIFRDLCLTIRAGKTVA
MDR17 ABCB21   FAVIDRESKIDPSD-ESGRVLDNVKGDIELRHISFKYPSRPDVQIFQDLCLSIRAGKTIA
MDR4  ABCB4    FAIMDRESKIDPSV-ESGRVLDNVKGDIELRHVSFKYPARPDVQIFQDLCLSIRAGKTVA
MDR9  ABCB9    FDILDSTPKIDSSS-DEGTTLQNVNGDIEFRHVSFRYPMRPDVQIFRDLCLTIPSGKTVA
MDR7  ABCB7    FDILDSKPKIDSSS-EKGTILPIVHGDIELQHVSFRYPMRPDIQIFSDLCLTISSGQTVA
MDR19 ABCB17   FAVLDRCTTIEPKN-PDGYVAEKIKGQITFLNVDFAYPTRPDVVIFENFSIEIDEGKSTA
MDR20 ABCB18   FAVLDRNTTIEPEN-PDGYVPKKVKGQISFSNVDFAYPTRPDVIIFQNFSIDIEDGKSTA
MDR18 ABCB16   FTVLDRRTTIEPEN-PDGYILEKIKGQITFLNVDFAYPTRPNMVIFNNFSIEIHEGKSTA
MDR13 ABCB15   FAVLDRYTSIDPED-PDGYETERITGQVEFLDVDFSYPTRPDVIIFKNFSIKIEEGKSTA

                       850       860       870       880       890       900
               ....|....|....|....|....|....|....|....|....|....|....|....|
MDR1  ABCB1    LVGPSGCGKSSVISLIQRFYEPSSGRVMIDGKDIRKYNLKAIRKHIAIVPQEPCLFGTTI
MDR11 ABCB19   LVGASGSGKSSVIAMIERFYDPLAGKVMIDGKDIRRLNLKSLRLKIGLVQQEPALFAATI
MDR10 ABCB10   LVGQSGSGKSSVLSLVLRFYDPTAGIIMIDGQDIKKLKLKSLRRHIGLVQQEPALFATTI
MDR2  ABCB2    LVGQSGSGKSSVISLILRFYDPTAGKVMIEGKDIKKLDLKALRKHIGLVQQEPALFATTI
MDR12 ABCB14   VVGPSGSGKSTVIGLIMRFYDPSNGNLCIDGHDIKSVNLRSLRKKLALVQQEPALFSTSI
MDR15 ABCB13   VVGPSGSGKSTVIGLIMRFYDPSNGNLCIDGQDIKTLNLRSLRKKLALVQQEPALFSTTI
MDR14 ABCB20   VVGVSGSGKSTIISLVERYYDPVAGQVLLDGRDLKLYNLRWLRSHMGLVQQEPIIFSTTI
MDR6  ABCB6    VVGVSGSGKSTIISLIERYYDPVAGQVLLDGRDLKSYNLRWLRSHMGLIQQEPIIFSTTI
MDR3_ ABCB3    LVGESGSGKSTVISLLQRFYDPDSGHITLDRVELKKLQLKWVRQQMGLVGQEPVLFNDTI
MDR5  ABCB5    LVGESGSGKSTVISLLQRFYDPDSGHITLDGVELKKLRLKWLRQQMGLVGQEPVLFNDTI
MDR16 ABCB12   LVGESGSGKSTVISLLQRFYDPDSGQITLDGVELKKLQLKWLRQQMGLVGQEPVLFNDTI
MDR8  ABCB11   LVGESGSGKSTVISLLQRFYDPDSGHITLDGVELKKLQLKWLRQQMGLVGQEPVLFNDTI
MDR17 ABCB21   LVGESGSGKSTVIALLQRFYDPDSGQITLDGVEIKTLQLKWLRQQTGLVSQEPVLFNETI
MDR4  ABCB4    LVGESGSGKSTVIALLQRFYDPDSGEITLDGVEIKSLRLKWLRQQTGLVSQEPILFNETI
MDR9  ABCB9    LVGESGSGKSTVISMIERFYNPDSGKILIDQVEIQTFKLSWLRQQMGLVSQEPILFNETI
MDR7  ABCB7    LVGESGSGKSTVISLLERFYDPDSGKILLDQVEIQSLKLSWLREQMGLVSQEPVLFNETI
MDR19 ABCB17   IVGTSGSGKSTIIGLIERFYDPLKGTVKIDGRDIRSYHLRSLRKYISLVSQEPMLFAGTI
MDR20 ABCB18   IVGPSGSGKSTIISLIERFYDPLKGIVKIDGRDIRSCHLRSLRQHIALVSQEPTLFAGTI
MDR18 ABCB16   IVGPSRSGKSTVIGLIERFYDPLQGIVKIDGRDIRSYHLRSLRQHMSLVSQEPTLFAGTI
MDR13 ABCB15   IVGPSGSGKSTIIGLIERFYDPLKGIVKIDGRDIRSYHLRSLRRHIALVSQEPTLFAGTI

                       910       920       930       940       950       960
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MDR1  ABCB1    YENIAYGHATEAEIIQAATLASAHKFISALPEGYKTYVGERGVQLSGGQKQRIAIARALV
MDR11 ABCB19   FDNIAYGKATESEVIDAARAANAHGFISGLPEGYKTPVGERGVQLSGGQKQRIAIARAVL
MDR10 ABCB10   YENILYGKASESEVMEAAKLANAHSFISSLPEGYSTKVGERGIQMSGGQRQRIAIARAVL
MDR2  ABCB2    YENILYGNASQSEVVESAMLANAHSFITSLPEGYSTKVGERGVQMSGGQRQRIAIARAIL
MDR12 ABCB14   HENIKYGNASEAEIIEAAKAANAHEFISRMEEGYMTHVGDKGVQLSGGQKQRVAIARAVL
MDR15 ABCB13   YENIKYGNASEAEIMEAAKAANAHEFIIKMEEGYKTHAGDKGVQLSGGQKQRVAIARAVL
MDR14 ABCB20   RENIIYARASEAEMKEAARIANAHHFISSLPHGYDTHIGMRGVELTPGQKQRIAIARVVL
MDR6  ABCB6    RENIIYARASEAEMKEAARIANAHHFISSLPHGYDTHIGMRGVELTQGQKQRIAIARVVL
MDR3_ ABCB3    RSNIAYGKASEAEIIAAAELANAHGFISSIQQGYDTVVGERGIQLSGGQKQRVAIARAIV
MDR5  ABCB5    RANIAYGKATEAEIIAASELANAHRFISSIQKGYDTVVGERGIQLSGGQKQRVAIARAIV
MDR16 ABCB12   RANIAYGKATESEIIAAAELANAHKFISSIQQGYDTVVGEKGIQLSGGQKQRVAIARAIV
MDR8  ABCB11   RANIAYGKATESEIIAAAELANAHKFISSIQQGYDTVVGERGIQLSGGQKQRVAIARAIV
MDR17 ABCB21   RANIAYGKATETEIVSAAELSNAHGFISGLQQGYDTMVGERGVQLSGGQKQRVAIARAIV
MDR4  ABCB4    RANIAYGKASESEIVSSAELSNAHGFISGLQQGYDTMVGERGIQLSGGQKQRVAIARAIV
MDR9  ABCB9    RSNIAYGKATEEEIIAAAKAANAHNFISSLPQGYDTSVGERGVQLSGGQKQRIAIARAIL
MDR7  ABCB7    GSNIAYGKATEEEIITAAKAANVHNFISSLPQGYETSVGERGVQLSGGQKQRIAIARAIL
MDR19 ABCB17   RENIMYGGIDESEIIEAAKAANAHDFITSLSNGYDTNCGDKGVQLSGGQKQRIAIARAVL
MDR20 ABCB18   RENIMYGGIDESEIIEAAKAANAHDFITSLSNGYDTCCGDRGVQLSGGQKQRIAIARAVL
MDR18 ABCB16   RENIMYGRIDESEIIEAGKTANAHEFITSLSDGYDTYCGDRGVQLSGGQKQRIAIARTIL
MDR13 ABCB15   RENIIYGGIDEAEIIEAAKAANAHDFITSLTEGYDTYCGDRGVQLSGGQKQRIAIARAVL

                       970       980       990      1000      1010      1020
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MDR1  ABCB1    RKAEIMLLLDEATSALDAESERSVQEALDQACS-GRTSIVVAHRLSTIRNAHVIAVIDDGK
MDR11 ABCB19   KNPTVLLLDEATSALDAESECVLQEALER-LMRGRTTVVVAHRLSTIRGVDCIGVIQDGR
MDR10 ABCB10   KNPEILLLDEATSALDVESERVVQQALDR-LMRDRTTVVVAHRLSTIKNSDMISVIQDGK
MDR2  ABCB2    KNPAILLLDEATSALDVESERVVQQALDR-LMANRTTVVVAHRLSTIKNADTISVLHGGK
MDR12 ABCB14   KDPSVLLLDEATSALDTSAEKQVQEALDK-LMKGRTTILVAHRLSTIRKADTIVVLHKGK
MDR15 ABCB13   KDPSVLLLDEATSALDTSSEKLVQEALDK-LMKGRTTVLVAHRLSTIRKADTVAVLHKGR
MDR14 ABCB20   KNAPIILIDEASSSIESESSRVVQEALDTLIMGNKTTILIAHRAAMMRHVDNIVVLNGGR
MDR6  ABCB6    KNAPILLIDEASSSIESESSRVVQEALDTLIMGNKTTILIAHRVAMMRHVDNIVVLNGGK
MDR3_ ABCB3    KEPKILLLDEATSALDAESERVVQDALDR-VMVNRTTVVVAHRLSTIKNADVIAVVKNGV
MDR5  ABCB5    KEPKILLLDEATSALDAESERVVQDALDR-VMVNRTTIVVAHRLSTIKNADVIAVVKNGV
MDR16 ABCB12   KEPKILLLDEATSALDAESERLVQDALDR-VIVNRTTVVVAHRLSTIKNADVIAIVKNGV
MDR8  ABCB11   KEPKILLLDEATSALDAESERVVQDALDR-VMVNRTTIVVAHRLSTIKNADVIAVVKNGV
MDR17 ABCB21   KDPKVLLLDEATSALDAESERVVQDALDR-VMVNRTTVVVAHRLSTIKNADVIAVVKNGV
MDR4  ABCB4    KDPKVLLLDEATSALDAESERVVQDALDR-VMVNRTTIVVAHRLSTIKNADVIAVVKNGV
MDR9  ABCB9    KDPKILLLDEATSALDAESERVVQDALDR-VMVNRTTVVVAHRLTTIKNADVIAVVKNGV
MDR7  ABCB7    KDPKILLLDEATSALDAESERVVQDALDQ-VMVNRTTVVVAHLLTTIKDADMIAVVKNGV
MDR19 ABCB17   KNPSVLLLDEATSALDSKSERVVQDALER-VMVGRTSIMIAHRLSTIQNCDMIVVLGKGK
MDR20 ABCB18   KNPSVLLLDEATSALDSQSESVVQDALER-LMVGRTSVVIAHRLSTIQKCDTIAVLENGA
MDR18 ABCB16   KNPSILLLDEATSALDSQSERVVQDALEH-VMVGKTSVVIAHRLSTIQNCDTIAVLDKGK
MDR13 ABCB15   KNPSVLLLDEATSALDSQSERVVQDALER-VMVGRTSVVIAHRLSTIQNCDAIAVLDKGK

                       1030
               ....|....|.
MDR1  ABCB1    VAEQGSHSHLL
MDR11 ABCB19   IVEQGSHSELV
MDR10 ABCB10   IIEQGSHNILV
MDR2  ABCB2    IVEQGSHRKLV
MDR12 ABCB14   VVEKGSHRELV
MDR15 ABCB13   VVEKGSHRELV
MDR14 ABCB20   IVEEGTHDSLA
MDR6  ABCB6    IVEEGTHDCLA
MDR3_ ABCB3    IVEKGTHETLI
MDR5  ABCB5    IAEKGTHETLI
MDR16 ABCB12   IAENGTHETLI
MDR8  ABCB11   IAEKGTHETLI
MDR17 ABCB21   IVEKGKHETLI
MDR4  ABCB4    IVEKGKHDTLI
MDR9  ABCB9    IAEKGRHETLM
MDR7  ABCB7    IAESGRHETLM
MDR19 ABCB17   IVESGTHSSLL
MDR20 ABCB18   VVECGNHSSLL
MDR18 ABCB16   VVESGTHASLL
MDR13 ABCB15   LVERGTHSSLL
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