

Table 1 Suppl. The list of primers used in real-time PCR. The efficiency for each primer pair was calculated using the *LightCycler® Software 4.1* (Roche, Basel, Switzerland).

Forward primers	Sequences (5'-3')	Reverse primers	Sequences (5'-3')
CsPDR8	CTTCCCTTCTTGAATCTG	CsPDR8	ATTTCACCTCTAGGAATGATA
CsPDR12	AGATTCTAGGACTTGAAATCTGTGC	CsPDR12	TAAGTTGTCGAACTGTCGAATCCTG
CsCACS	GTGCTTTCTTTCTGGAATGC	CsCACS	TGAACCTCGTCAAATTTACACA

CsPDR8	MERRTSRNFSSRSISRSFSRASWSMEDVFANGNPSRRSSRVDEDEEALRWAAIEKLPPTYDR	60
CsPDR12	MDSGEIYRVSSARINSSSIWRNSAMEVFS-----RSSRDDDEEALKWASIERLPTYLR	54
CsPDR8	LRTSILQSVNEPDPRIAGNLPLHKEVDVRKLGVSQDFIDRIFKVAEEDNEKFLRKQKN	120
CsPDR12	VRRGILNLDGES-----AREIDVQNLGLLERNILERLVKIAEDDNERFLLLKKN	104
CsPDR8	RIDRVGIRLPTVEVRFEHLTMEADCHVGNRALPTLPNVARNMAESAISLVGVKLAKQTKL	180
CsPDR12	RMERVGLDLPAIEVRFEHLEVEAEAHAGRALPTMFNFSLNMLEGFLSYFHIIPNRKKQL	164
CsPDR8	TILKDASGIVKPSRMTLLGLPSSGKTTLLLAGLAKGLDPSLKVKGEVSYNGHKLKEFVPQ	240
CsPDR12	SILHDVSGI IKPGRMTLLGLPSSGKTTLLKTLAGLKGDLKFSGRVITYNGHGMNEFVPQ	224
CsPDR8	KTSAYISQNDVHMGIMTVKETLDFSARCQGVGTRYELLESELARREKDAKIKPEAEVDLFM	300
CsPDR12	RTSAYISQQDLHIGEMTVRETLSFSARCQGVGPRYDMLTELSRREKAANIKPDPDLDIIM	284
CsPDR8	KATAMEGVESSLITDYTLKILGLDICKDTIVGDEMIRGISGGQKRKRVTTGEMIVGPTKTL	360
CsPDR12	KAAALGGQETNVVTDYVLKILGLEICADTMVGDEMFRGISGGQKKRVTTGEMLVGPSRAL	344
CsPDR8	FMDEISTGLDSSTTYQIVKCLQQIVHLTEGTILMSLLQPAPETFDLFDIILVSEGQIVY	420
CsPDR12	FMDEISTGLDSSTTYQIVNSMRQYIHI LN GTALISLLQPAPETYELFDIILISDGQVY	404
CsPDR8	QGPRDHVVEFFESCCKPERKGTADFLQEVTSRKDQEQYWADRRKPYRVVPVSEFASRF	480
CsPDR12	QGPRENVLFFFQHMGTCPQRKGADFLQEVTSRKDQEQYWKTRDEVYRFVSVVEEFSEAF	464
CsPDR8	KRFHVGLRLENELSI SYDKSRGHKAALVSENVVPMKELLKACFKDEWLLMKRNSFVYIF	540
CsPDR12	QSFHVGKGLGDELATPFDKSKSHAALTEKYGASKELLKACISRELLMKRNSFVYIF	524
CsPDR8	KTVQIIIVAI IASTVFLTRMHRTRDQSDGAVFIGALLFSLISNMLNGFSELAMTISRLPV	600
CsPDR12	KLIQLILMAFVTMTLFFRTEMHRRTVDDGSVYMGALFFAIITMFNGFSELALTILKLPV	584
CsPDR8	FYKQRDLKFHPWPWTYTIPTVILGIPTSLLESVVVLVVTYITIGFAPEASRFFKQLLIFL	660
CsPDR12	FYKQRDLFFPPWAYSIFPTWILKIPITFEVGVIVVMTYVYVGFDPNAGREFKHFLMLLF	644
CsPDR8	VQQMAAGVFRLIAGICRSMTIANTGGSLLILLIFLLGGFIIPRGEIPKWWIWGYWISPLT	720
CsPDR12	VNQMASALFRLIGALGRNIIVANTFGSFALLTVLVLGGFVLARDDVHPWWIWGYWISPM	704
CsPDR8	YGFNAIAVNEMFAPRWKLIPTNTVTTLGVKVLNFDFVPKNWYWGIAAILGFAILFNI	780
CsPDR12	YAQNGIAVNEFLGHKWRHPAPNSNESLGVLLKSRGIFPQASWYWGIVGATIGYILLNF	764
CsPDR8	LFTIALTYLNPLTKHQAIMSEETASEMEANQ-EDSQEPRLR-RPMSKKDSFPRSLASDG	838
CsPDR12	LFTIALQYLDPFEPKQAI VSKETSTD KSVKKSQDVQELLSKKGKSSSERTENQISLSSR	824
CsPDR8	NNTREVNMQRMSSKSEANGVAACKGMILPFSPLAMSFDTVNYVDMPPMKEQGVTEDRL	898
CsPDR12	TSS-----ARVGSFSEANQNKRGMLVPFEPHSITFDEIRYAVDMPQEMKSQGVTEDRL	879
CsPDR8	QLLRGVTGAFRPGILTALMGVSGAGKTTLMDVLAGRKTGGYIEGDVRISGFPKKQETFAR	958
CsPDR12	ELLKGVS GSRPGVLTALMGVSGAGKTTLMDVLAGRKTGGYIEGNITISGYPKKQETFAR	939
CsPDR8	ISGYCEQNDIHSPQVTIRESLIYSAFLRLPKEVSKEEKMVFVDEVMDELVDNLKDAIVG	1018
CsPDR12	IAGYCEQTDIHSPHVTVYESLVYSAWLRLPD VDSATRKMFVEEVMELIELNPLRDAIVG	999
CsPDR8	LPGVTGLSTEQRKRLTIAVELVANPSIIFMDEPTSGLDARAAAIVMRAVRNTVDTGRTVV	1078
CsPDR12	LPGVSGLSTEQRKRLTIAVELVANPSIIFMDEPTSGLDARAAAIVMRTVRNTVDTGRTVV	1059
CsPDR8	CTIHQPSIDIFEAFDELLMKRGGQVIYFGPLGRNSQKII EYFESIPGVPKIKEKYNPAT	1138
CsPDR12	CTIHQPSIDIFDAFDELFLLRGGEEIYVGPVGRHSSQLIEYFESIEGVPKIKDGYNPAT	1119
CsPDR8	WMLEVSSVAAEVR LGMDFAEHYKSSSLKRKNELVTDLTSPPPGAKDLYFESQYSQSTWG	1198
CsPDR12	WMLEITTAQETT LGVNFNTLYKDSELYRRNKALIKELSVPNENSNELYFPTKYSQSFFI	1179
CsPDR8	QLKCCLWKQWWTYWRS PDYNLVRYFFTLAAALMIGTVFVKVGT KRDSSTDLTMIIGAMYA	1258
CsPDR12	QCIACLWKQHLSYWRNP PYSAVRFLFTTFI ALMFGTIFWDLGSKRGTKQDLFNAMGSMYA	1239
CsPDR8	AVLFVGINNCOTVOPIVSVERTVFYRERAA GMYSAFFYVLAOVLVEIPFILVOTTYTTLI	1318

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CsPDR12      AVLFIGVQNATSVQPVVAIERTVFYRERAAGMYSALPYAFGQVVIELPYIFIQTVVYGVI 1299
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CsPDR8      VYSMVSFQWTAPKFFWFYFINFFSFLYFTYYGMMTVSITPNHHVAAIFAAAFYALFNLF 1378
CsPDR12      VYGMIGFEWTAAKFFWYIFFMYFTLLYFTFYGMMTVAVTPNHNIAAIVSSAFYGFWNLF 1359
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CsPDR8      GFFVPRPRIPKWWVWYIWICPIAWTVYGLIISQYGDVEKKISVPGLSDPISIKSYIESHF 1438
CsPDR12      GFIVPRTRIPWWRWYIWICPVAWTLYGLVTSQFGDINDPMDSN-----QTVAEFVSNYF 1414
            **:***.*** ** *****:***:***: **:*:*:*.*.*:.*:***:***
CsPDR8      GYDPNFMGPVAGVLVGFAAFFAFMFAYCIKTLNFQLR 1475
CsPDR12      GYKYDFLGVVAAVHVGITVLFGFIFAFSIKVFNFQKR 1451
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Fig. 1 Suppl. *ClustalW* alignment of CsPDR8/CsABCG36 and CsPDR12/CsABCG40. *Asterisks* indicate identical amino acid residues. The sequences of peptides used to generate specific antibodies for CsPDR8/CsABCG36 and CsPDR12/CsABCG40 are marked in *yellow* and *green*, respectively. The transmembrane helices predicted by the *TMHMM 2.0* server are marked in *grey*.