

Campbell and others, BMC Microbiology

Additional file 1A

		1	50
Ago2.aae	(1)	-----	
Ago2.agam	(1)	-----	
Ago2b.dm	(1)	MGKKDKNKKGGQDSAAAPQPQQQKQQQQRQQQPQQQLQQPQQQLQQPQQQLQ	
		51	100
Ago2.aae	(1)	-----	
Ago2.agam	(1)	-----	
Ago2b.dm	(51)	QPQQQQQQQPHQQQQQSSRQQPSTSSGGSRASGFQQGGQQQKSQDAEGWT	
		101	150
Ago2.aae	(1)	-----	
Ago2.agam	(1)	-----	
Ago2b.dm	(101)	AQKKQGKQQVQGWTKQGQQGGHQQGRQGDGGYQQRPPGQQQGGHQQGRQ	
		151	200
Ago2.aae	(1)	-----MILNARYLYIPCRQKQ-----QQQQQPQQQQHQQKQQSQQQ	
Ago2.agam	(1)	-----FLAQLGKRYQGHYSNNS-----HRNNNNHNNHNNHNNSSSLNNG	
Ago2b.dm	(151)	GQEGGYQQRPPGQQQGGHQQGRQGGYQQRPSGQQQGGHQQGRQGGYQQRPSG	
		201	250
Ago2.aae	(39)	QQQQQQQQRSKQGSQ-----QQQRPQQQAQQQQPSQQQQQSQKQ	
Ago2.agam	(39)	RNSSSSHSLNKGHSSSSHKVHCSDRPNRSKGMHRSSNSRRAHNSSSSRG	
Ago2b.dm	(201)	GYQQRPPGQQQGGHQQGRQGGYQQRPSGQQQGGHQQGRQGGYQQRPSG	
		251	300
Ago2.aae	(79)	QHPQQQQQQRPKQQQQFQQDQRPQQQQQQQLQKQQQQQGQSWRPQSHDPS	
Ago2.agam	(89)	IRRKSKRSSRNREVSISRD LHNNSSNMNRKNSMNRSSNSNSHSAHSSS	
Ago2b.dm	(251)	RPPGQQQGGHQQGRQGGYQQRPPGQQQGGHQQGRQGGYQQRPSG	
		301	350
Ago2.aae	(129)	PASGSHSHSSS-----P-----	
Ago2.agam	(139)	SSSNNSAHSSSNSSSRAPHNSSSNNSA--HGSSNTNRRFLLPPGSAV-	
Ago2b.dm	(301)	QQQGGHQQGRQGGYQQRPSGQQQGGHQQGRQGGYQQRPSGQQQGG	
		351	400
Ago2.aae	(141)	-----SHAAALERVEEDFSKIKIDKQKIHSSALLPV	
Ago2.agam	(185)	-----HRDASVASTKSSSGDGTLTIEENLGAMRIAKEKIRRTDLRPV	
Ago2b.dm	(351)	GHQGRQGGYQQRPPGQPNQTQSQGQYQSRGPPQQQAAPLPLPPQ	
		401	450
Ago2.aae	(172)	LMRPNAHGTRGRAIKVEVNYIQLLLERLIPTAYHYDVDIQPAASRKWQRL	
Ago2.agam	(229)	LVRGAHGKRGKPVSVANFFRLLLDKLKGTAYHYDVATIEPDRPKKFYRP	
Ago2b.dm	(401)	PAGSIKRGTIKPGQVGINYLDLDLSKMPSVAYHYDVKIMPERPKKFYRP	
		451	500
Ago2.aae	(222)	AFSEFTKQMFPNHGFAFDGHKNAYAAARRLQADVYEQEVKVRDE-GRERRF	
Ago2.agam	(279)	VFAQFCRENYPGAMLAFDGQKNAYTTRKLSDKKAKVVFQPDG-GKQREY	
Ago2b.dm	(451)	AFEQFRVDQLGGAVLAYDGKASCYSVDKLLPLNSQNPEVTVTDRNGRTLRY	
		501	550
Ago2.aae	(271)	KVAMKEAAVLDMTCLKTYMN-NGSTLDKPMASIQCLDIVLRTAYENNPRF	

Ago2.agam	(328)	TVQVKEAAQLDLGVLKTYMKSNEETMAKPMSAIQCLDVVLSAYENNNPNF	
Ago2b.dm	(501)	TIEIKETGDSTIDLKSLTTYMNDRIFDKPMRAMQCVEVVLASPCHNKAIR	
		551	600
Ago2.aae	(320)	IKFKKSIYVKPDRPDDIGSNHELWYGLFQSALLGARPFNLIDVSHKAFPT	
Ago2.agam	(378)	VRFKRAVYAVPRQSIDIGRGHELWFGLFQSALLGSRPYLNVDSHKAFPM	
Ago2b.dm	(551)	VGRSFFKMSPNNRHLEDDGYEALVGLYQAFMLGDRPFNLNVDISHKSFP	
		601	650
Ago2.aae	(370)	GGPVLRLIVDMNRGQ--VPDRVTDWMSRDLHDFLKGMELSYTGPDG--V	
Ago2.agam	(428)	GAPVLKVIGDFNRG---QVDQVSGWVQQLHSFLKGMDVVYTNPTTR--M	
Ago2b.dm	(601)	SMPMIEYLERFSLKAKINNTTNLDYSRRFLEPFRLRGINVVYTPPQSFQSA	
		651	700
Ago2.aae	(415)	SKLFKYNISIKSPANQQKFKLENGTEMTIDQYFR-SKNKQLRYPSPVLHV	
Ago2.agam	(473)	AKRMRCNGLREPASQQMFKLEDGTRLVADYFARKLNFRRLRYPNLPVLHV	
Ago2b.dm	(651)	PRVYRVNGLSRAPASSETFEHDGKKVTIASYFH-SRNYPLKFPQLHCLNV	
		701	750
Ago2.aae	(464)	GSLVRNVMLPIELCSIPPGQALNKKHPDQCTQFIIRKSATDTATRKRKIM	
Ago2.agam	(523)	GSTVRSVYVPAELCDIPAGQALNKNNPEECTRDIIRYAATSAPERKRKIL	
Ago2b.dm	(700)	GSSIKSILLPIELCSIEEGQALNRKDGATQVANMIKYAATSTNVRKRKIM	
		751	800
Ago2.aae	(514)	DLFNQIGYNNAPTIKEFGVSVGNFETVDGRILDPPPELSYRNDRRVKPMR	
Ago2.agam	(573)	DLASQIQYNKCPDLLDFGITVGNFEKVPARIIDAPPIEYARGEKIPPQR	
Ago2b.dm	(750)	NLLQYFQHNLDPTISRFGIRIANDFIVVSTRVLSPPQVEYHSKRFTMVKN	
		801	850
Ago2.aae	(564)	GVWRADNMNFIIPSTEITRRELSWTILNLDGRTRPDAIDFGRNIYQMSL	
Ago2.agam	(623)	GVWRAEGKNFIVPSTELSKRPLRWIRILNLDSTNEATVKKFGEMLQSQAM	
Ago2b.dm	(800)	GSRMDGMKFLEPKPKAHKCAVLYCDPRSGRKMNYTQLNDFGNLIISQ GK	
		851	900
Ago2.aae	(614)	KQGVQLQQFSMKNNFYEPDRMRFVAVKDLNIFDELKKRKIDLVFVVIPSP	
Ago2.agam	(673)	RCNVQMEPFDMAKTYVLVRDMRNCLRDIGTLLQNIKREEPAVTIVVLP SR	
Ago2b.dm	(850)	AVNISLSDSDVTYRPFDTDDERS-----LDTIFADLKRSQHDLAIVII PQF	
		901	950
Ago2.aae	(664)	GRDGDVYAKVKQKAELC---VGLLTQCIKSFTLDKKRGDMSTISNIWLKI	
Ago2.agam	(723)	---GDAYAKVKQKAELASERIGLLTQCVKGMTVAKKGTDMSTLNNIMLKI	
Ago2b.dm	(894)	R--ISYDTIKQKAELQH---G-ILTQCIKQFTVER-KCNNQTIGNILLKI	
		951	1000
Ago2.aae	(711)	NAKTNGSNHVLAKNFKPPIARKTVMYVGADVTHPSPEQTNIPSVVGVAAS	
Ago2.agam	(770)	NAKTNGTNHCISQVAVPPLGRGKVMYIGADVTHPLSE--NEPSVVGVAAL	
Ago2b.dm	(937)	NSKLNGINHKIKDDPRLPMMKN-TMYIGADVTHPSPDQREIPSVVGVAAS	
		1001	1050
Ago2.aae	(761)	YDLEGFRYNCCYRLQGPKDEMIRDLQNIIVIKQLRQFKQTNQSLPELIMYY	
Ago2.agam	(818)	YDLTGFRYNCSVRLQGARDEMIRDLQNIIVQRQLLLYKQYNGALPERIMYY	
Ago2b.dm	(986)	HDPYGASYNMQYRLQRGALKEETEDMFSITLEHLRVYKEYRNAYPDHIIYY	
		1051	1100
Ago2.aae	(811)	RDGVSEGQFQEVLTIELRAMQAAAASVQQGYKPNITFIVVQKRHHARFFP	
Ago2.agam	(868)	RDGVSDGQFAEILTIELQALHAAIARVEPGYKPAVTFIVVQKRHHTRFFP	
Ago2b.dm	(1036)	RDGVSDGQFPKIKNEELRCIKQACDKVG--CKPKICCVIVVKRHHTRFFP	

		1101		1150
Ago2.aae	(861)	TANCPTEGRNNNV	QPGTIVDRYITAPNQYQFFLVSHA	QGVAKPTKYCV
Ago2.agam	(918)	QPGCPTEGKNGNV	PPGTIVDSEITTPDRYEFYLVSHA	AVQGVAKPTKYVV
Ago2b.dm	(1084)	SGDVTTSNKFNNVD	PGTIVVDRTIVHPNEMQFFMVSHQAI	QGTAKPTRYNV
		1151		1200
Ago2.aae	(911)	LYDDENCNP	DQLQALTYYLCHMFTRCNRAVSYPAP	TYAHLAAYRGRVYI
Ago2.agam	(968)	LYDDSNCHP	DSLQALTYNLCHLFARCNRAVSYPAP	TYAHLAAYRGRVYI
Ago2b.dm	(1134)	IENTGNLDI	DLQLQALTYNLCHMFP	RCNRSVSYPAPAYLAHLVAARGRVYL
		1201		1232
Ago2.aae	(961)	KDRPLNMNNLT	KEYERMQIRTEIQDGH	PMFFV
Ago2.agam	(1018)	KDRRINMNDMEN	AYRDIQIIDTVNNST	PMFFV
Ago2b.dm	(1184)	TG-TNRFLDLK	KEYAKRTIVPEFMKKN	PMYFV

Additional file 1B

		1		50
Dcr2.aae	(1)	MDMIMPQQDDFI	PRDYQRTMKTICMQKNTIIYLP	TGAGKTHIALMVIKEM
Dcr2agam	(1)	-SQNKEPMEDF	APRNYQVQMKEICLAKNTII	IFLPTGSGKTYIALMVMKEI
Dcr2.dm	(1)	-----MEDVEIK	PRGYQLRLVDHLTKSNGI	VYLP
		51		100
Dcr2.aae	(51)	GKDLDKPLTE	GGKRTFFVNTVALAKQQA	EFLSHNLTYDTSIYTSDRNVD
Dcr2agam	(50)	SHQLRNTVHE	GGKRTFFLANTVALAKQQA	QFFARHMPFNVR
Dcr2.dm	(46)	SQDFDKPIES	GGKRALFMCNTVELARQQA	MAVRRCTNFKVGFYVGEQGV
		101		150
Dcr2.aae	(101)	AWKQDKWLEEF	AKYQVIVCTCQIILLDVLKHGYL	SVKHINLLIFDECHHGV
Dcr2agam	(100)	AWKSDRWHEEF	SEGVIICTAQIILLDVLRHGYM	SPANINLIVFDECHRAV
Dcr2.dm	(96)	DWTRGMWSDEI	KKNQVLVGTAQVFLDMVTQT	YVALSSLSVVIIDECHHGT
		151		200
Dcr2.aae	(151)	GEHPMHGIMEQ	FLRPVPSDHPRVIGLSGMLLYKQIK	SVALVSPELERLEN
Dcr2agam	(150)	GQHPMHAIMKEI	VAAPASERPRVLGLSGTLLFKEL	KMASQVPDELERLEN
Dcr2.dm	(146)	GHHPFREFMRL	FTIANQTKLPRVVG	LTGVLIK--GNEITNVATKLKELEI
		201		250
Dcr2.aae	(201)	TFNATIIATVGS	YDAFTEVCKFSTD	PNELLVSYST--LRLSPVMADIVNNI
Dcr2agam	(200)	TFSSIIATVANY	DDYATVASFSTNP	NEVLVTYSKPAVHLMPLVKEMWPRI
Dcr2.dm	(194)	TYRGNIIITVSD	TKEMENVMLYATK	PTVMSFPH-QEQVLTVTRLISAEI
		251		300
Dcr2.aae	(249)	NAFSQTIEEFH	LPKYLNQ-NKALLKDRP-KPLKEIR	KLFTELIYQLGDTG
Dcr2agam	(250)	DAFVEWLLQVY	LPEYSTQSTRTLQKSFC-KPLKEV	KRALTEFKHQLEEHG
Dcr2.dm	(243)	EKFYVSLDLMN	IGVQPIRRSKSLQCLRDPSKKS	SVKQLFNDFLYQMKEYG
		301		350
Dcr2.aae	(297)	LFGGSIALGL	LIVQFELDKRQSDSSMLRLAL	RSCITFCESLRHQIEKLMS
Dcr2agam	(299)	MYAGSLAILAV	LIVQLEVSKRQSPCDKARQVY	RSATSFCEIRHELVEAMS
Dcr2.dm	(293)	IYAASIAIISL	LIVEFDIKRRQAETLSVKLMH	RALTLCCKIRHLLVQKLG
		351		400

Dcr2.aae	(347)	-----GLDMKTKLTKFSSSLKVRQLIDQLEKLYEENRDKKAKTLLIFV	
Dcr2agam	(349)	-----GLRGTHQILSFSSDQARKLLKYLED SYRTAEDKKNQALV FV	
Dcr2.dm	(343)	DMTYDDDDDNVNTEEVIMNFSTPKVQRFLMSLKV SFADKDPK DICCLV FV	
		401	450
Dcr2.aae	(388)	QRRFSAKVLYHLLKIYFAETEDANLIVPDFMVGNNGSMPE SIEQILSAKK	
Dcr2agam	(390)	KRRFTAKVLYHLIRIYFHYELVEPIVKPDFIVGANAALEESIDAILV VRE	
Dcr2.dm	(393)	ERRYTCKCIYGLLLNYIQSTPELRNVLT PQFMVGRNNISPDFESVLERKW	
		451	500
Dcr2.aae	(438)	DRRVLERFKKNETNVIVTTNVLEEGIDLQMCNTVVKYDHPQTFAS YQSK	
Dcr2agam	(440)	DRRVLENFRKRKINVLCATNVLEEGIDLQMCNMVIMYDAPLSYASF MQSK	
Dcr2.dm	(443)	QKSAIQQFRDGNANLMICSSVLEEGIDVQACNHVF ILDPVKTFNMVYQSK	
		501	550
Dcr2.aae	(488)	GRARMKNSQYMVMLDNENRHIFLEKYRLYKSIEEELRRCLIGKTINRPDP	
Dcr2agam	(490)	GRARMKTSTYLMMPAADLQQFAKRMKLYRDIENRLKEELVGKTINRPEP	
Dcr2.dm	(493)	GRARTTEAKFVLFTADKEREKTIQQIYQYRKAHNDIAEY LKDRVLEKTEP	
		551	600
Dcr2.aae	(538)	LDADVHKELYNEIIPPFFTAKGAKLDALSAIQLLNRYCMGMPRDAFTNTN	
Dcr2agam	(540)	LENDVRKELLDDLIPPFYTPFKAKLDALSAIQLLNRYCMSMPRDLFTGSN	
Dcr2.dm	(543)	ELYEIKGHFQDDIDP--FTNENGAVLLPNNALAILHRYCQTIPTDAFGFVI	
		601	650
Dcr2.aae	(588)	VTWERIDLKD-----GRIIVEVLLPLQSTVREKISGNPMRNIKLA	
Dcr2agam	(590)	VTWERIDRSP-----TEIIVTVKLPLQSTVREV IHGQTMKNL KLA	
Dcr2.dm	(592)	PWFHVLQEDERDRIFGVSAKGKHVISINMPVNCMLRDTIYSDPMDNVKTA	
		651	700
Dcr2.aae	(628)	KRSAAFNACRKLYENKELNEHLIPIDCKYQLNNLKDVYFRHWKDFDADLG	
Dcr2agam	(630)	KQSAAFNACKRLFVGEELNMYLLPIATKDKVEELSEQYFKLWRKMSDEPN	
Dcr2.dm	(642)	KISAAFKACKVLYSLGELNERFVPKTLKERVASIADVHFEHWNKYGDSVT	
		701	750
Dcr2.aae	(678)	--KLAGTQKCI RTHAIQYPKQTTECF P QPG-KPCYIYVLRIAAGFAQDPT	
Dcr2agam	(680)	P-KQAGTMKYVRGHKIVYPEETVGCTP QADGEQCYVYIVRMRAHF DANTH	
Dcr2.dm	(692)	ATVNKADKSKDRTYKTECPLEFYDALPRVG-EICYAYE IFLEPQFESCEY	
		751	800
Dcr2.aae	(725)	NDNVNIFHSLYSEN NFGLMTTKPLPALAKMKFFVTLGLINVHIEETPIV	
Dcr2agam	(729)	LENVRIFQELYSSAN NFGLTRKRLPRLARMKLFVTLGAIGVEIVPEPVC	
Dcr2.dm	(741)	TEHMYLNLQTP---RNYAILLRNKLPRLAEMPLFSNQGKLHVVRVANAPLE	
		801	850
Dcr2.aae	(775)	LPNGGSEIELALLRQFHVTVFRDVLKLWKEFLCCDYDNEENSFLV VPLKN	
Dcr2agam	(779)	ITLAPDSGELQRLKRFHLLLF RDLLKVWKPFVTLDALPEENGFLIVPMLR	
Dcr2.dm	(788)	VIIQ-NSEQLELLHQFHGMVFRDILKIWHPPFFVLDRRSKENSYL VVPLIL	
		851	900
Dcr2.aae	(825)	STH----LDWKLIREFQNLSEPPSEISTIARNKMEFEADKYRHKVILPWY	
Dcr2agam	(829)	SQS----IDWELMGKFPYLR-PAAETSTRARQHLRFETE QYLLRVVHPWY	
Dcr2.dm	(837)	GAGEQKCFDWELMTNFRRLPQSHGSNVQQREQQAPRPEDFEGKIVTQWY	
		901	950
Dcr2.aae	(871)	KNNKEQPYVVTMVHEHLTPESFPFNPEYGSYANYFSQAYHLAVVK-PDQF	
Dcr2agam	(874)	KNDPDQNYVVVRVRRDDL RPTSPFPNAKYDSYEQYFAQEHQVVRHEDQF	

Dcr2.dm	(887)	AN-YDKPMLVTKVHRELTPLSYMEKNQQDKTYIEFTMSKYGNRIGDVVHK	
		951	1000
Dcr2.aae	(920)	LIEVKGITSYLNRLNPGVEDDG-KSTRSKHWRFNELIPELCHNYQFPAD	
Dcr2agam	(924)	LIEVKGITTSLNRLHPGAEADGGASTRSRYWEFQELIPELVHNFEPAD	
Dcr2.dm	(936)	DKFMIEVRDLTEQLTFYVHNRG-KFNAKSKAKMKVLIPELCFNFNFPGD	
		1001	1050
Dcr2.aae	(969)	YWLKATLLPSALHRLHYLLLAENIRVDLATGANVGLENHTIEDVDVEYK	
Dcr2agam	(974)	YWLKATLLPSALHRVHYLLLAEGIRVDLARNAGVGSEHCERVEDVIIDRV	
Dcr2.dm	(985)	LWLKLIFLPSILNRMFYLLHAEALRKRFNTYLNHLLPFNGTDYMPRPLE	
		1051	1100
Dcr2.aae	(1019)	ERKGKQLEELQLMEFEDEDEDEDEFDLEEAKRSLVAPEN-----LSELA	
Dcr2agam	(1024)	LSIEHQKSTALYGGEDDDDEDEDEDEDEEKDSDEEGARSMQLLQVLNQI	
Dcr2.dm	(1035)	IDYSLKRNVDPLGNVIPTEDIIEPKSLLEPMPTKSIEAS-----VAN	
		1101	1150
Dcr2.aae	(1063)	RNQMCSTITGDIPLPWQEEDEEPVDIERNWDQVSKLDLDYYNVFVNKFSDSL	
Dcr2agam	(1074)	HSDSISLADRVQYPWEENEQPKDLERNWDTVSKIDIDYYASFVKKYEQQA	
Dcr2.dm	(1077)	LEIT-----EFENPWQKYMEPVDLSRNLLSTYPVELDYYYHFSVGNVCEM	
		1151	1200
Dcr2.aae	(1113)	MREKAAERISTAYTSAVYRR-----AAGSPKREPMAILDVPVDQK	
Dcr2agam	(1124)	VTITNIDRMLANLNMNKNE-----AEASPVKALPALEDGHGPV	
Dcr2.dm	(1122)	NEMDFEDKEYWAKNQFHMPTGNIYGNRTPAKTNANVPALMPSKPTVRGKV	
		1201	1250
Dcr2.aae	(1153)	FAIKLLQLTPANTVNVNLOQKNIIKALTTKSSSDVFDLERYELLGDAFLK	
Dcr2agam	(1162)	AQIAMLRITMDNTANVALQOSDLLQALTTKSSADVFNLERFEVLGDAFLK	
Dcr2.dm	(1172)	KPLLILQKTVSKEHITPAEQGEFLAAITASSAADVFDMERLEILGDSFLK	
		1251	1300
Dcr2.aae	(1203)	FSISLYLVKYHKEWHEGFLTAVKGQIVSNRNLVYCAIKYGLPGMLKIHKF	
Dcr2agam	(1212)	FAVSVYILFRHTSWHEGYLTTCGRMVSNRNLLYCAMGYGLPGKIKAHFP	
Dcr2.dm	(1222)	LSATLYLASKYSDWNEGTLTEVKSKLVSNRNLFLCLIDADIPKTLNTIQF	
		1301	1350
Dcr2.aae	(1253)	DPKNDWQPPLATVPKNIKRTMQSVN-----HSARVLYRLTLTEEEIKTG	
Dcr2agam	(1262)	DPKNDWVPPLSTVPGAVRRAMVDAN-----ESPALLYNLKLTEEEIQSG	
Dcr2.dm	(1272)	TPRYTWLPPGISLPHNVLALWRENPEFAKIIIGPHNLRDLALGDEESLVKG	
		1351	1400
Dcr2.aae	(1297)	VVTAKNSDDFIAQLELHGN-----MPDPSPMANYLSQQTMGDKTPADAME	
Dcr2agam	(1306)	VVAQATVDKFLPLIEQAP-----APSQSTLHTVLQQVQIRDKVVADVTE	
Dcr2.dm	(1322)	NCSIDINYNRFVEGCRANGQSFYAGADFSSEVNFCVGLVTIPNKVIADTLE	
		1401	1450
Dcr2.aae	(1342)	ALLGVCVQSVGIERSFKLLPHFGILPKTHNVLRLLADKIEHQ--RLKTHI	
Dcr2agam	(1350)	ALLGVCVKTVGYERSFRFLSHLGIIPKGADVPMLLRTTTTFP---IGDYFP	
Dcr2.dm	(1372)	ALLGVIVKNYGLQHAFKMLEYFKICRADIDKPLTQLLNLELGKKMRANV	
		1451	1500
Dcr2.aae	(1390)	DIREVDAFLKNYRRIEGLGYKFKDRTYLLQALTHASYPTNRRITGSYQQL	
Dcr2agam	(1397)	VRHKVDQLLCNPERIEATLGYRFRNRTYLLQAFTHTSYTSNSLTGSYQQL	
Dcr2.dm	(1422)	NTTEIDGFLINHYYLEKNLGYTFKDRRYLLQALTHPSYPTNRRITGSYQEL	

		1501		1550
Dcr2.aae	(1440)	EFLGDAVLDFLI	SMYIFEQNPTMSPGQLTDLRSALVNNVT	LACILVRHGL
Dcr2.agam	(1447)	EFLGDAVLDFLV	SMYIYERNPSMSPGQLTDLRSALVNNVN	LACVLVRNEL
Dcr2.dm	(1472)	EFIGDAILDFLI	SAYIFENNTKMNP	GALTDLRSALVNNNTLACICVRHRL
		1551		1600
Dcr2.aae	(1490)	HLYILAESASFT	DTVSKFVLFQEQHKHEITDQVNLL	VEESDRK-----
Dcr2.agam	(1497)	HRHILSQSPMLT	DAIGKFVAVHRCHRNQGSNWVRL	LTEESDTP-----
Dcr2.dm	(1522)	HFFILAENAKLSE	IISKFVNFQESQGHRVTNYVRIL	LEEADVQPTPLDLD
		1601		1650
Dcr2.aae	(1533)	-----	MAEFVDVPKALGDVF	ESLVA
Dcr2.agam	(1540)	-----	MAEYVDVPKVLGDV	LEALIG
Dcr2.dm	(1572)	DELDMTELPHANK	CISQEAKEGVPPKGEFNMSTN	VDVPKALGDVLEALIA
		1651		1700
Dcr2.aae	(1553)	AVFLDSGNDFAAT	WQVIYGMGNELTFTENTPIQIVRQ	LYEFKPSCKPT
Dcr2.agam	(1560)	AIYLDSGNDLAAT	WEVCFRLLRDEIADFTRKTPIQVVRQ	LYEHP-EASPH
Dcr2.dm	(1622)	AVYLCR-DLQRT	TWEVIFNLFEP	ELQEFTRKVPINHIRQLVEHK-HAKPV
		1701		1750
Dcr2.aae	(1603)	FSRAIPDEDTV	LVKLRYEIRNQQHEAYGFGQNKDDAKRAA	AKAALQVLRK
Dcr2.agam	(1609)	FSAPFVEEEVV	YVVKLSYTHRSQRQTVYGFQNKDDAKRAA	AKIALSKIM-
Dcr2.dm	(1670)	FSSPIVEGETV	VMVSCQFTCMEKTIKVYGFQSNKDQAKLS	AAKHALQQLSK
		1751		
Dcr2.aae	(1653)	HYRSAK-		
Dcr2.agam	(1658)	-----		
Dcr2.dm	(1720)	CDA----		

Additional file 1C

		1		50
TSN.aae	(1)	-----MSAAP	AASAPAPAPVLKR	GIVKQVLSGDSVIIRGQPKGGPPP
TSN.agam	(1)	-----MSAANV	PAAAAANPAPPPVLKK	GIVK-ILSGDSLILRDKPVNGPPR
TSN.dm	(1)	MATAANTATAAG	AAKDAPPAPT	KSLSGIVKQVLSGDTVIR-ATKGAPP
		51		100
TSN.aae	(43)	EKQINFSGVI	APKLARRPTNNSTEITKDEPYAWEAREYLRQRL	IGQEVYF
TSN.agam	(45)	EKQLNFAGIV	APKLARRPTNGSSDGSRDQPYAWESREYLRQRL	IGQEVWF
TSN.dm	(50)	EKQITFSHVL	APKLARRPG-AGGDETKDEPWAWESREFLRKK	LIGVEVTF
		101		150
TSN.aae	(93)	YSERPPNATR	DYGYVCLGKDPATS	ENIVESIVSEGLVSVRREGVROTPEL
TSN.agam	(95)	YSEKPPNANR	EYGYVKLGKEPN-AENIVESIVSEGLVTVRRDNVROTPEH	
TSN.dm	(99)	TFDKPANSNR	EYGFVWIGKDKETGENV	VESIVREGLVSVRRE-GRPTAEQ
		151		200
TSN.aae	(143)	TRLCELEDAAKA	ARKGKWSDSP-SSDHVRNITWNIENPKAFFD	HNHGKPI
TSN.agam	(144)	ARLIELEDAARR	ARKGLWSDAP-EGEHVRNIVWNIDNPKQFVDQ	HAGQLI
TSN.dm	(148)	QTLIELEDQARA	AGRGKWSPTASAADKVRNIKWSHENPAHLVDI	YGGNPV
		201		250
TSN.aae	(192)	KATIEHVRDGS	TVRAFLLP---EFQHVTLMMSGIRCPGF	KLDVDGKPDIT

TSN.agam	(193)	KAIIEHVVDGSTVRAFLMPNPRVFQHVTLMMSGIRCPGFKLDAGEPRDNT	
TSN.dm	(198)	KAIIEHVVDGSTVRAFLLP---DFHYITLMISGIRCPGVKLDADGKPDLS	
		251	300
TSN.aae	(239)	AEVPFAEEARYFVESRLLQRDVEIRLESVNNSNFVGTIIFPKGNIAEALL	
TSN.agam	(243)	TEVPYADEARFHVECRLLQREVVKVRLESNSNTNFLTGTILCPEGNIAESLL	
TSN.dm	(245)	VKVPFADAEARYYVETRLLQRDVEIRLESVNNSNFI GTILY PKGNIAESLL	
		301	350
TSN.aae	(289)	KEGFAKCVIEWSMPYVKEGVDRRLRAAEKHAAGNRLRLWKDYQAPTAAYNTK	
TSN.agam	(293)	RNGFAKCVIEWSIPYVKEGIDRLRACEREAKAARLRLWKDYKPPAALANTK	
TSN.dm	(295)	REGLAKCVDWSMAVMKGTGDKLRAAERFAKEKRLRQWQDYQAKTPAFNSK	
		351	400
TSN.aae	(339)	DKDFTGTVVEVFNGDAVMVKISNTVSKKVFLSSIKPPREA----ARTADE	
TSN.agam	(343)	DKELVGTVMVEVYNGDAVLVKVG-TVSKKVFFSSIRPP-----RPKED	
TSN.dm	(345)	EKDFSGTVVEVFNGDAINVRLSNGQVKKVFFSSIRPPRDQRAVVGTDGEE	
		401	450
TSN.aae	(385)	EGNLP RP PKGSRPLYDVPWMFEAREFLRKKLIGKKVHCSLDYVTPARDNF	
TSN.agam	(384)	DG---PRAKNSRPLYDIPYMF EAREFLRKKLIGKRVTCTLDYVAPARDNY	
TSN.dm	(395)	IVKAPPRGKNYRPLYEIPHMF DAREFLRKKLINKKVQC NL DYI SP PRENF	
		451	500
TSN.aae	(435)	PEKCCYTVTLSGANVAEALVAKGLATVIKYRQDDQORSVHYDELRSAETQ	
TSN.agam	(431)	PEKYCYTVRLDDQNI AEAMLERGLATVINYRQDDEQRSPEYDKLRAAQEQ	
TSN.dm	(445)	PEKYCYTVSIGGQNVAEAMVAKGLATCVRYRQDDQORSSAYDQLIAAEQQ	
		501	550
TSN.aae	(485)	AMKQLKGVHAKDDIPSHRINDLTVDHSRIKHQYLPWQRALRTEAIVEFV	
TSN.agam	(481)	AIKGQKGMHAKKQTPSHRINDLTTDHSRIKHHYLPWQRALRTEALVEFV	
TSN.dm	(495)	AIKGLKGLHAKKDNATLRVNDLTVDHSRIKVQYLPWQRALRTEAIVEFV	
		551	600
TSN.aae	(535)	ASGSRFRIYCPKDSCLVTFLLAGISCPRSSRPALSGVPAQEGEPFGDEAL	
TSN.agam	(531)	ASGSRLRLYCPKESCLVTFLLAGISCRSSRP AIGGAPAQEAEPY GDEAL	
TSN.dm	(545)	ASGSRLRIFVPKDSCLVTFLLAGISCPRSSRPALNGVPAQEGEPFGDEAL	
		601	650
TSN.aae	(585)	QFSKERILQRDVSVKIETTDKAATSVIGWLWTENNVLNSVALVEEGLASV	
TSN.agam	(581)	QFTREKVLQRDVSVKIETTDKQATSVIGWLFTDHNVLNSVALVEEGLAEV	
TSN.dm	(595)	TFTRERVLQRDVSVHIDTTDKAGSVIGWLWTDSGANLSVALVEEGLAEV	
		651	700
TSN.aae	(635)	HFTA E KTEHFRALSEAEARAKAKRKNIWKDYVEKVEEDN-KENEDEKDDP	
TSN.agam	(631)	HFTA E KSDYYRVLRDAEARAKAQRKNIWKDYVEKAAAE E E K D E I E D T P D V	
TSN.dm	(645)	HFSAEKSEYYRQLKIAEDRAKAAKNIWTNYVEEVPKEK--TVTEEEKED	
		701	750
TSN.aae	(684)	AAPADRKVKYENVVVT E VTPELHFY AQHADQGAKLEELMTKLRQEF RAMP	
TSN.agam	(681)	NTPVERKVKYESVVVT E VTPELQFY AQHTDQGAKLEELMTKLRQDFKAMP	
TSN.dm	(693)	KVVAERKVNYENVIVTEITETLTFFAQSVESGSKLESLSMSKLHADFQSNP	
		751	800
TSN.aae	(734)	PVTGAYNPRRGDMCAAKFSEDNEWYRAKVEKIEKGGNASILYVDYGNRET	
TSN.agam	(731)	PVTGSYAPKRGDMCAAKFSEDNEWYRAKVEKVEKGGNVTILYIDYGNRET	
TSN.dm	(743)	PIAGSYTPKRGDLVAAQFTLDNQWYRAKVERVQ-GSNATVLYIDYGNKET	

		801		850
TSN.aae	(784)	VPTTRLAMLPPAFISDKPYAHEYSLALVVLPTDEEDKADALKAFQAQDALN		
TSN.agam	(781)	VPSTRLAMIPPFTFISEKPFahLYVPALLLLPTDADDRAEAVKAFSQDVLN		
TSN.dm	(792)	LPTNRLAALPPAFSSSEKPYATEYALALVALPTDNEDKEEALRAFSEDEVLN		
		851		900
TSN.aae	(834)	KTLMNVEYRVSG-AEHVTLVDPATKVDIGKELVSDGFLIAEKNKKDRRL		
TSN.agam	(831)	RTLNMNVEYRISG-TEYVTLTDPATKADIAEDLIADGYLIADKNKKDRRL		
TSN.dm	(842)	HKVQLNVELKVTGSPNLATLRDPTTKVDFGKQLVAEGLVLAEQ-RGERKL		
		901		939
TSN.aae	(883)	QKLINDYKEAEQSARKNRNGIWQYGDSTEDQAGEFGLSR		
TSN.agam	(880)	TKLIADYKDAE-----		
TSN.dm	(891)	KELVDQYKAAQEAARVAHLAIWKYGDITQDDAPEFR---		

Additional file 1. Amino acid conservation of Ago2, Dcr2, and TSN across

species. (A) Ago2. (B) Dcr2. (C) TSN. Black shaded sequence indicates a.a.

identity; gray shaded sequence indicates a.a. similarity. *Ae. aegypti*, Ago2. aae,

[Vectorbase: SUPP_AEDES003395]; *An. gambiae*, Ago2.agam, [Genbank:

XM_559969]; *D. melanogaster*, Ago2.dm isoform B, [Genbank: NP_648775]. Dcr2.aae,

[Genbank: AY713296]; Dcr2.agam, [Genbank: XM_320248]; Dcr2.dm, [Genbank:

NM_079054]. TSN.aae, Genbank: [AAEL000293], Genbank: [NP_612021], Genbank:

[XM_315689].