## SUPPLEMENTAL FIGURE LEGENDS

**FIGURE S1.** Clustal W alignment of BLM orthologs was performed using default parameters (<u>http://www.ebi.ac.uk/Tools/clustalw2/index.html</u>). Note that highlighting identifies similar residues. Sequence names include the aa residues used in the alignment: *Hs, human; Dr, Danio rerio; Ol, Oryzias latipes; Xl, Xenopus laevis, Gg, Gallus gallus; Dm, Drosophila melanogaster; Kl, Kluvermyces lactis; Sc, Saccharomyces cerevisiae.* (A) RecQ domains. (B) N-terminal domains. The BDHCT domain is underlined.

**FIGURE S2.** The indicated GST fusion proteins were subjected to EMSA but the reaction products were incubated for 30 min on ice with or without  $\alpha$ -GST prior to gel electrophoresis.

**FIGURE S3.** (A) SDS-PAGE analysis of purified recombinant proteins. Proteins were expressed and purified from bacteria with either an N-terminal GST-tag (GST) or a C-terminal V5-His6 tag (V5). Approximately 1.5 µg of each recombinant protein was resolved by 15% SDS-PAGE and the gel was stained with Coomassie blue. Molecular weight standards are shown in kDa. (B) V5-His6-tagged N-terminal domains of BLM orthologs bind d(T)174. The indicated V5-His6-tagged proteins were assayed by EMSA as described in Fig.1D.

**FIGURE S4.** The SE domain lacks meltase and nuclease activity. (A) A SE reaction (1) was carried out using 1 nM of a <sup>32</sup>P-labeled donor DNA with flush ends plus 5 nM of recipient oligo (lanes 1-9, 14). In reaction (2) the substrate consisted of 1 nM <sup>32</sup>P-labeled oligo 6 alone (lanes 10-13). Both reactions were performed as described in the standard SE assay except that oligo 11 (25 nM final concentration) was added with the stop buffer in lanes 7-14 and incubated at 37°C for 30 min (3). (B) One nM of <sup>32</sup>P-labeled oligo 6 or 1 nM of <sup>32</sup>P-labeled oligo 6 plus 14) was incubated with the indicated amount of protein at 37°C for 30 min and analyzed as described in SE reaction.

**FIGURE S5.** (A) A SE reaction was carried out in the presence of  $Sgs1_{103-322}$  and the indicated concentrations of  $Mg^{2+}$ . (B) A SE reaction containing two potential recipient ssDNAs was carried out in the presence or absence of  $Mg^{2+}$ . (C)  $Sgs1_{103-322}$  was titrated into a SE reaction employing 10 nM flush-ended duplex as donor and 50 nM ssDNA as recipient. The products of the indicated reactions were quantified and its efficiency is presented as the percent of total signal present in the slower migrating band. Shown below these values is the ratio of molecules of ssDNA (in nucleotides) to molecules of protein used in the reaction.

 Table S1. Oligonucleotides used in this study.

		10	20	30	40	50	60	70	80	90	100	110	120	130	
HSBLM/651-1417 DrBLM/662-1261 OIBLM/630-1393 XIBLM/630-1364 GBBLM/422-1183 DmBLM/721-1487 KIBLM/579-1367 SCSgs1/662-1447	651 HT K EMMK 662 HS P EMMK 630 HS Q EMMK 633 HS K EMMK 422 HS E EMLK 721 HS T R LMH 579 WT S EMY H 662 WS D E V L Y	I F <mark>H K K</mark> F G L H I F H K K F G L H I F H K K F G L H I F H K K F G L H I F H <b>R K</b> F G L H G L S Y S F G L K K L R H V F G L D R L H E V F K L P	N F RT NQ LEAIN Q F R F NQ LEAIN Q F R F NQ LEAIN R F RT NQ LEAIN S F R T NQ LEAIN S F R P NQ LEAVN G F R P NQ LEAVN G F R P NQ LEAVN	AALLGEDC ASLLGEDT AALLGEDA ACLCGEDC AALLGEDC ATLLGNDC ATLLGNDA ATLQGKDV	FILMPTGGGK FVLMPTGGGK FVLMPTGGGK FILMPTGGGK FILMPTGGGK FVLMPTGGGK FVLMPTGGGK	SLCYQLPACV SLCYQLPACV SLCYQLPACV SLCYQLPACV SLCYQLPACV SLCYQLPATU SLCYQLPATU SLCYQLPATV SLCYQLPATV	S P G VT V V S A G VT V V S P G VT V V S A G VT V V S A G VT I V K S G R T S GTT I V K S G K T H GTT I V	YISPERSEIN YISPERSEIN YISPERSEIN YISPERSEIN YISPERSEIN YISPERSEIN YISPEISEMO	/DQVQKLTSLD /DQVQKLTTLD /DQIQKLTTLD /DQVQKLTSLD IDQVQKLKTLD FDQINKLASLD 2DQVEHLLAKD 2DQVEHLLAKD	PATYLTGD CATSLSGD PATSLSGD PATYLTGD ASTYLTGD CAESLSGE KASMFSSK KASMFSSR	KTDSEATNIY KKDSEAARIY KSDSEAGRIY KTDAEAASIY ITDADASKTY QKMADVMAIY GTAEQRRMTF GTAEQRRATF	LQLSKKDPI MQLSRKDPA MQLSRKDPL LQLSKKDPI MQLSKKDPI RDLESQPPM NLFMNGL NLFINGL	I KLLYVT PE IKLLYVT PE IKLLYVT PE IKLLYVT PE IKLLYVT PE IKLLYVT PE LELVYIS PE LDLVYIS PE	KICASNRLIS KVCASGRMIS KVSASGRLIS KVCASTRLIS KVCASTRLIS KISSSARFQD MIKASVQCKK MISASEQCKR	T L EN LY E 785 A L Q N LY E 796 A L Q N LY E 764 T M EN LY E 737 A L EN LY E 737 A L EN LY N 556 T L D T L N S 855 A I S K LY E 715 A I S R LY A 798
	140	150	1,60	1,70	180	190	200	210	220	230	240	250	260	270	
HSBLM/651–1417 DrBLM/662–1261 OIBLM/630–1393 XIBLM/603–1364 GBBLM/422–1183 DmBLM/721–1487 KIBLM/579–1367 S(Sgs1/662–1447	786 RKLLARF 797 RGLLARF 765 RGLLARF 738 RQLLARF 557 RKLARF 856 NNYISRF 716 HGKLARI 799 DGKLARI	VIDEAHCVS VIDEAHCVS VIDEAHCVS VIDEAHCVS VIDEAHCVS VIDEAHCVS VVDEAHCVS VVDEAHCVS	QWGHDFRQDY QWGHDFRPDYK QWGHDFRPDYK QWGHDFRPDYK QWGHDFRPDYK QWGHDFRPDYK NWGHDFRPDYK NWGHDFRPDYK	R M N M L R Q K R L H E L R R M R L H E L R Q K R L N V L R Q K R L N M L R K K K L G V L K K E L S F F K Q E E L K F F K R E	F P S V P V M A L T F P N V P I M A L T F P S V R M M A L T F Q S V P M M A L T F Q S V P M M A L T F P N V P T I A L T Y P D I P M I A L T Y P D I P M I A L T	AT AN PR VQ KD AT AT PR VQ KD AT AT PR VQ KD AT AN PR VQ KD AT AN PR VQ KD AT AN PR VQ KD AT AS EQ VRMD AT AS EQ VRMD	I LTQLKIL <b>R</b> PC I LNQLAMT <b>R</b> PC I LNQLNMM <b>R</b> PC I LNQLKMTKPC I QNQLEML <b>K</b> PC I LAQLNLKNCK I I HNLQLNNPV I I HNLELK <mark>P</mark> PV	V F S MS F N R F V F T MS F N R N V F T MS F N R S L I F T MS F N R D V F T MS F N R F V F T MS F N R T V F L KQS F N R T V F L KQS F N R T	4 N L K Y Y V L P K K F N N L K Y S V L P K K F S N L K Y S V L P K K F D N L K Y S V L P K K F S N L R Y R V L P K K K F N L F Y Q V L - K K F F N L Y Y E V N - K K F	KKVAFDCL KKVDEECI KKVDEDCI KKVALDCV KKVAMDCL VSTLDDI <mark>S</mark> KNSIFQMC KNTIFEIC	EWIRKHPYD QWIKKYYPRD GWIKKHYPRD EWIKKHPDD EWIKKYHPHD RYIRSKPQHF DMIRTKFKNO DAVKSRFKNO	0 S G I I Y C L S R 0 S G I VY C L S R 0 S G I VY C L S R 0 S G I I Y C L S R 0 S G I I Y C L S R 0 S G I I Y C L S R 1 S G I I Y C L S R 1 G I I Y C H S K	R E C D T M A D T N D C D T L A D S N D C D A MA E S H E C D T M A D T H E C D T T A A I K E C D E T S K K N S C E Q T S A L K S C E Q T S A Q	LQRDGLAALA LQRAGIAALA LKRAGIQALS LQKEGLAALA LQKEGLAALA MCKDGVRAVS MQKNGVKCAF MQRNGIKCAY	Y HAGLSD 924 Y HAGLSD 935 Y HAGLSD 903 Y HAGLAD 876 Y HAGLAD 876 Y HAGLTD 994 Y HAGLTD 994 Y HAGMDP 853 Y HAGMEP 936
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HSBLM/651-1417 DrBLM/652-1261 OIBLM/670-1393 XIBLM/603-1394 GgBLM/422-1183 DmBLM/721-1487 KIBLM/579-1367 SCSgS1/662-1447 HSBLM/651-1417 DMBLM/651-1261 OIBLM/650-1393 XIBLM/603-1364 GgBLM/422-1487 KIBLM/579-1367 SCSgS1/662-1447	420 1064 DN C CKT K 1075 DN C AK PN 1043 DN C AK PN 1043 DN C AK PN 1016 DN C L GKK 835 DN C S RKK 1132 DN C I NKR 987 DN C KN S S 1070 DN C RN SA 560 1195 S S S V KQ 1205 AS S I RKQ 1173 AS S I RKQ 1166 AS S I RKQ 1173 AS S I RKQ 1174 AS S I RKQ 1175 AS S I RKQ 1175 AS S I RKQ 1176 AS S I RKQ 1177 AS S I RKQ 1177 AS S I RKQ 1178 AS S I RKQ 1178 AS S I RKQ 1178 AS S I RKQ 1178 AS S I RKQ 1179 AS S I RKQ 1179 AS S I RKQ 1170 AS S I RK	430 - DYKT RDV - KYKS RDV - QYQM QNV - NYKS RDV - NYKS RDV - NYKS RDV - NYKS RDV - YKS VDA - YKS VDA - YSDKNG SSSFQA	440 T DD VK S I VR FV T DD VK KI AR FV T DD VK KI AR FV T DD VG NI VR FV T D VG NI VR FV T D EVK SI I R FV L EHAR KAAR AV T E E S N DI ANLI T E P AK KI VK LV 580 AL VAK - VS QR E AS VC EKVS KR E AAVS KS VS QR D AS VT NT SQR E AS VT K-MSQR E SS T AD GQS GMR K E GP AHNHS AR N E D N I P	450 Q EHS S S Q Q Q N C E K V G Q E N C S L V Q Q M C S L V Q Q M C G Q V G Q M C G Q V G Q M C G Q V G Q M C G Q V G S I Q N E S I Q N E	460 MRNIKHVGP SRFGKSAQQN SRFGKTAQQN GR-GKGRSNN GRGKGRSNN GINGNRNTGS GR 600 ELTEVCKSLG ELNDLCKLLG ELVDLCKELG ELVDLCKELG ELTDTCKTLG DLLDLCKTLA DKSNMAVLST IGGNVAANPP	LEGYYQET GN/ 470 - RLTLNMLVD - RLTLNMLVD - RLTLNMLVD - RLTLNMLVD GRYTLNMMVD GRYTLNMVD - RVTLIHCQD - RVTIIYCQD - RVTII - RVTII	4 GROGNIST C 480 I F L GS KS A KIC I F L GA S A KIC V K GS K V QK I V K GS K V QK I V F K GS R S K I V F K GS R S K I V F K GS R S K K V F K S K K K K K K K K K K K K K K K K K	490 5 G	STMQTMIQKDK 500 FGKGSAYSKH AFGVGAAYSKH AFGMGAYSKH AFGKGAAYSKH FGKGAAYSKH HGVLKDWDKN HGVLKDWDKN HGVLKDWDKN HGVLKDWDKN CHGMGKDWKKA FGKS KKIAESLSS LKKIAESLSS LKKIAESLSS LKKIAESLSS LKKIAESLSS LKKIAESLSP LKKIAESLSP LKKIAESLSP ILKKIAESLS	A ER LF KK L AER LF KK L AER LF KK L AER LF KK L AER LF KK L VER LF KK L F ER IFF L F EV LQ ID P EV LQ ID F EV		Y CDNVT DCR Y ITNANDQAY Y ITNS GQAY Y ITNS GQAY Y ITANDQAY Y ITANDQAY Y ITANDQAY IFT - ND FPQ VST GR G FFS IMNNS G FAS 60 GAEVI SVLQ GAELI DVLQ GAELI DVLQ GAELI KVMD GAKLLE ITS FNLLKDIAI Y ER LRELS L	AY UNLGNKA AY ISAGPKA SY ISAGPKA AY VKMGERA AY VKMGERA AY VKUGPNA SY VKUGPNA SY VKUGPNA 670 KYSEWTSPA KYSEWTSPA KYSEWTPP NYASEKLLM NYSSKFNFP NLGNRWVPP	540 (QT VLN GN LKV MS VLN G CMQV (MNV LS GY MQV QAVLN G FLKV QAVLN G FLKV SK LM EGT PN F KD L FK GK LKV KK LLT GKMEI 680 ED EE DA DA NDTMLISDAI VG - N FMPDSI	K N C 1069 550 D F M ET EN 1194 E F H ET EN 1204 D F Y ET ES 1172 D F Q DT ES 1145 E F A VT K N 1256 E F A VT K N 1256 E F A VT K N 1256 E F A VT K N 1256 F A VT K N 1256 E J R F V AT 1112 K Q F I S 1300 1261 - Q A E G - 1277 - I C Q K S G 1257 - A C Q S V D 1071 - V L D E E 1371 L WKAAN K 1249 L KKMAA I 1312
HSBLM/651-1417 DrBLM/652-1261 OIBLM/650-1393 XIBLM/603-1394 GgBLM/422-1183 DmBLM/721-1487 KIBLM/579-1367 SCSgs1/662-1447 HSBLM/651-1417 DMBLM/650-1393 XIBLM/603-1364 GgBLM/422-1183 DmBLM/721-1487 KIBLM/579-1367 SCSgs1/662-1447	420 1064 DN C CKT K 1075 DN CAR PN 1043 DN CAKPN 1043 DN CAKPN 1016 DN CLGKK 835 DN CS RKK 1132 DN CINKR 987 DN CKNSS 1070 DN CRNSA 560 1195 SS SVKQ 1205 ASSIRKQ 966 ASAIRKQ 146 ASSIRKQ 966 ASAIRKQ 1257 AKEAKAA 1113 EET GSN 1196 APNS PS 700	430 - DYKT RDV - KYKS RDV - QYQM QNV - QYKS RDV - DYKS RDV - NYKS RDV - NYKS RDV - YKSVD - YKSVD - YSD 	440 T DD VK S I VR FV T DD VK KI AR FV T DD VK KI AR FV T DD VG NI VR FV T D VG NI VR FV T D EVK SI I R FV L EHAR KAARAV T E E S N DI ANLI T E P AK KI VK LV S80 AL VAK - VS QR E AS VC EKVS KR QR AS VC EKVS KR QR AS VT NT SQR E AS VT K-MSQR E S T AD GQS GMR K E GP AHNHS AR N E D N I P 720	450 QEHSSSQQ QENCEKVG QENCEKVG QENCEKVG QENCEKVG QDNCSLVQ QQHCGQVG QQHCCQVG QQHCQQCQ QQHCQQVG QQHCQQVG QQHCQQQ QQHCQQVG QQUG QQUG QQUG QQUG QQUG QQUG QQUG	460 MRNIKHVGPS SRFGKAQQN GR-GKGRSNN GR-GKGRSNN GINGNRNTGS CHARCE	LEGYYQET GN/ 470 GR FTMNMLVD - R LT LNMLVE - R LT LNMLVD GR YT LNMMVD GR YT LNMVD SR FT LLH LQD - R VT I IY CQD' 610 KVF G	4 GROGNIST C 480 IFLGSKSARIC IFLGSKSARIC IFLGSKSARIC IFLGSKSAKIC IFLGACSAKIC VKGSKYQCIN VKGSKYQCIN VFKGSSSKIK 620 	490 5 G	STMOT MIQKDK 500 FGKGSAYSKH AFGVGAAYSKH AFGWGAYSKH FGKGAAYSKH FGKGAAYSKH HGVLKDWDKN HGVLKDWDKN HGVLKDWDKN CHGMGKDWKKA EHGIGKSMQKS 0 640 LKKLAELSSC LKKLAELSSC LKKLAELSSC LKKLAELSSC LKKLAELSSC JRKLAELSSC	A ER LF KK L AAR LF KK L F ER LF KL F ER LF KK F ER LF KK F ER LF KK F ER LF KK F ER LF KK F ER LF KK F ER	HLNKLQQVMA         520           VLDNVLMEDI         VLDNUWEDI           VLDNILVEDI         VLDNILVEDI           VLDNILVEDI         VLDRILVEDI           VLDRILVEDI         VTERLUNEY           S0         6           GVTEDKLEKY         6           GVTEDKLEKY         6           GVTEDKLEKY         6           GVTEDKLEKY         7           GVTEDKLEKY         790	Y ICDNVTDCR Y ITNANDQAY Y ITNSGQAY Y ITNSGQAY Y ITNSGQAY Y ITANDQAY Y ITANDQAY IFT ANDAY VSTGRGFFS IMNNSGFAS 60 GAEVISVLQ GAELIDVLQ GAELIDVLQ GAELIKVMD GAKLLEITS FNLLKDIAI Y ERLRELSL 800	AY UNLGNKA AY ISAGPKA SY ISAGPKA AY UKAGPKA AY UKAGPKA AY UKUGPKA AY UKUGPNA AY UKUGPNA SY UKUGPNA 670 KYSEWTSPA 670 KYSEWTSPA KYSEWTSPA KYSEWTPP NYASEKLLM NYSSKFNFP NLGNRMUPP 810	540 QT V LN G N LKV MS V LN G C MQV MN V LS G Y MQV QA V LN G F LKV QA V LN G F LKV QA V LN G L LQV SK LM EGT PN F KD L FK G K LKV KK L LT G KM EI 680 ED DA DA ND TM L I S DA I V G - N FM PD S I 820	K N C 1069 550 D FM ET EN 1194 EF H ET EN 1204 D FY ET ES 1172 D FQ DT ES 1145 EF AUT KN 1256 E F AVT KN 1256 E F AVT KN 1256 E F AVT KN 1256 F AVT KN 1256 F AVT KN 1256 C A C A C A C A C A C A C A C A C A C A
HSBLM/651-1417 DrBLM/652-1261 OIBLM/652-1261 OIBLM/653-1364 GgBLM/422-1183 DmBLM/721-1487 KIBLM/579-1367 SSGs1/662-1447 HSBLM/651-1417 DrBLM/653-1364 GgBLM/422-1183 DmBLM/721-1487 KIBLM/651-1417 DrBLM/651-1417 DrBLM/651-1417 DrBLM/651-1417 DrBLM/651-1417 GIBLM/651-1364 GgBLM/422-1183 GgBLM/422-1183	420 1064 DN C C KT K 1075 DN C AR PN 1043 DN C AK PN 1043 DN C AK FN 1043 DN C AK FN 1075 DN C AR FN 1075 DN C KNS 1070 DN C NS R 1070 DN C KNS S 1070 DN C KNS S 107	430 - DYKT RDV - VYKT RDV - VYKS RDV - VYKS RDV - VYKS RDV - YKS RDV - YKS RDV - YKS RDV - YKS RDV	440 T D D V K S I V R F V T D D V K S I V R F V T D D V K I A R F V T D D V K I A R F V T D D V K I A R V T E V K I A R V T E V K I V K I V K V L E H A K A A R A V T E E S K D I A N I I T E P A K I V K L V S V C K V S Q R A V V K S V S Q R A V V K S V S Q R A V V T K S V S Q R A V V T K S V S Q R A S V T K - MS Q R S T A D G Q S G M R K E G P A H N H S A R N E D N I P 720 E E I P V S S H Y F S D E S C K S Y F S A D V V T S S Y F G	450 Q EHS S S Q G Q D N C E K V G Q D N C E K V G Q D N C S L V Q Q H C G Q V G K D L C S K S I Q D S E S I Q N E - S I Q N E - S I Q N E - S I Q N E - E S I Q N E - S I Q N E - E S I Q N E - S I Q N	460 MRNIKHVGPS MRNIKHVGPS NRYGKSAQQN SRFGKTAQQN GR-GKGRSNN GINGNRNTGS GR 600 ELTEVCKSLG ELNDLCKKLG ELND	LEGYYQET GN/ 470 GR FTMNMLVD - RLTLNMLVD - RLTLNMLVD GR YTLNMLVD GR YTLNMLVD GR YTLNMVD SR FTLLHIAD - KVTIIKCQD - KVTIIKCQD - KVTIIKCQD - KVTIIKCQD - KVTI KAFG	480 G N I S T C I 480 G N I S T C I 480 G N I S T C I 480 G N I S N I N I 480 G N I S N I 480 G	490 5 G	ST MQ T M I Q K D K 500 F G K G S A Y S R H AF G V G A Y S R H F G M G G A Y S R H F G K G A A Y S R H F G K G A Y S R H H G V L K D W K K A I F G K G A Y S R H H G V L K D W K K A I C K K I A S S I L K K I A S S I S T M G S H P I T S T M G S K K S S R S S S S S S S S S S S S S S S S S S S	A E R         510           A E R         L F KK           A D R         L F KK           A E R         L F KK           I E R         I F F H           I E R         I F F H           I E R         I F F H           I E V         L Q I D           P E V         L Q I D           P E V         L Q I D           K N T D         L RS           S S I I G S S S         S           S S T S         S RAA	HILNKLQQVMA         521           ILDKILDEDI         VIDNVMEDI           VLDNVMEDI         VENVEDI           VTERILNEY         S           GVTEDKLEY         S           GVTEQ         S           SQEQAHITNG         S           GSRNSAGOPT         S           GSRNSAGOPT         S           SSY IS         S           SSY IS         S           APAQSSAL         S	Y CDNVT DCR Y INANDQA Y ITNNGQAV Y ITNNGQAV Y ITNNGQAV Y ITFNDQAV Y ITANDQAV VSTGRGFFS IMNNSGFAS GAEVISVLQ GAELIDVLQ GAELIDVLQ GAELIVKVD GAELISVLQ GAELIKVMD GAKLLEITS FNLLKDIAI Y FRLRELS ANSKLGIMA ADKRPGFMA	RKLVLSTFN           30           AY WLGNKA           AY ISAGPKA           AY USAGPKA           AY VKMGERA           AY VKLGPNA           AY VKLGPNA           AY VKLGPNA           AY VKLGPNA           AY VKLGPNA           AY VKLGPNA           SY VKLGPNA           SY VKLGPNA           KY SERQLPV           KY SERQLPV           KY SEWT TPE           NY ASEKLLPV           KY SEWT TPE           NY ASEKLLPV           SKFNFP           NLGNRWYP           810           PPKP           PPMQP           PPMQP           AP TPQS	\$40           \$40           QT VLNGNLKV           MS VLNGCNQV           MNVLSGYMQV           QAVLNGFLKV           QAVLNGLQV           SKLMEGTPNF           KKLLTGKMEI           680           ED           PFLXXLTGKMEI           680           ED           QA-NNGKLV           KKLLTGKMEI           680           ED           QA-NNGKLV           KKLTGKMEI           680           ED           QA-NNGKS           QA-NNGKS           YG-NFMPDSI           820           PFLKPSFSHL           PFLKPSYSMF           HFLQPSYSMF           HFLQPSYSMF	K N C 1069 550 D F M ET EN 1194 EF H ET ES 1204 D FY ET ES 1204 D FY ET ES 1172 D FQ DT ES 1145 EF A VT KN 1256 E F A VT KN 1256 E I R FV AT 1112 KMQ FT I S 1195 690 - S S P G I S 1300 1261 - Q A E G 1277 - I CQ K S G 125 A C S VD 1071 - V L D E E 1371 LWKAANK 1249 LKKMAA I 1312 1364 1364 1183

HsB1m/1-651 DrB1m/1-662 OIBLM/1-630 XIBLM/1-630 GgBLM/1-659 DmBLM/1-704 KIBLM/1-621 ScSgs1/1-674	1 MAAVPQNNL 1 MSSLPQNNL 1 MSSLPQNNL 1 MAALPQNNL 1 MEEARAATNGG 1 MSKKPVAQR 1 MVKPSHNL 1 MVKPSHNL	Q EQLERHSART KEHLERHNNAA EEQLARHNNAA Q KQLELFPAK S GESQKLSN G KQLTLSSFIG RREHKWLKDTI RREHKWLKETJ	T L N N K L S L <mark>S K P K F</mark> S AQ N – K L S L L K P K P C NQ S – K L S L A K P K T C G T S N K L S L Q C T K S E K S S Q L E P G D V G N E K S S Q L E P G D V G N L D G N S Q S Q P K S R A A E A Y L P D K S V L G I L C A T L Q E D K D F V F Q A	G F T F K K K T S S D M G F C F K K K S S S G I JAF L F K K K S S S G I V F T F K K K C S P N L L A D I E L E E D D Y S V R S K P P A V Y N F Q K H V T A K R S A T L M Q K H V T A K R S A T L M	INVSVTNVSVAK SKVEVPQKVTG TNVEYPAKVTA (S-ASTGFIPFQ LDVVPPSPEEE IFLDASSSDDE SGVENDLARRT SPPTTPSKDEC	T <mark>P</mark> VLRNKDVN S S VLANRS VN S S VLANRNVN QHVLKDKNVN L PS F S PS VR N T E I S S Q S NN G S T L D Q V <mark>P</mark> R N G P G T T N F I T S	VT EDFS IPSNFEVTKNF VPKNSLLTKSS VKQD VSNIFKE GTIATKKSSRC LTSSMPVSS-C IPASGPTNTAT	- FSEPLPNTT VTFSQKPERV VTFSNKLERT GTHTALPKAT SPTDGRSAVH PRTAKLKKHT AVTTAQTAVA KQHEVMQTLS	NQQRVKDFFKN AP-KVN-FFTA QKSKINSFFTV ERNKINCFFTP GTESEPELMAP Y LDLSVSPLAE GTWDEGSYTNT NDTEWLSYTAT	A P A G Q E T Q R G Q P S K - P K T N T V N N S K - C Q S D S V I V Y T - K S G Q P P Q K Q P A A E Q D S A L S A K K Y A R D S P T I A V A T V L D S D S N Q Y A D V P M V D	SKSLLPDFLQT 114 PLANPFALNKT 116 PACR NP 113 VVAL K 105 EHADKG L 114 PKPTSLDLSVS 120 GDSDLELIADR 118 IPASTSVVSNP 120
HsBIm/1-651 DrBIm/1-662 OIBLM/1-630 XIBLM/1-603 GgBLM/1-659 DmBLM/1-704 KIBLM/1-621 ScSgs1/1-674	1,30 115 PKEVVCTTQ 117 PLVQSTIKA 114 PAVSGNNGA 106 DHVHGNDSA 115 HLEQQLYSV 121 PLAELPAKK 119 PSANNSNVT 121 RTPNGSKTHNF	140 NT PT VK L PKSAA ITQTKT NKPPST MED ICK SDR DPPF SS ITAQ NTFR PHMASS	150 KSRDTALKKLEFS PKDSTNDQTVELF - DNHSINATNAPS - EDAASKKTGIN VDAIPLHELTSI FKPVQNENSYTYRC ITQKTEINTNGKS LVENDSSRNLGSR	160 SPDSLSTINDWD GDSLSTINDWD FDPSQFPLDDWD SFGSVTSLEEWD CAKELLQQRELR SLSESPVENKSIG SDQDLHRLVSLI INNKSVIDNSSIG	170         16           D MD D F DT S ET S         5           D L D D F ET P V KS         5           D F D F ET P V KT         6           D L D D F ET P V KT         7           D L D D F ET P V KT         7           D L D D F ET P V KT         7           D L D D F ET P V KT         7           D L D F F ET P V KT         7           D L D F F ET P V KT         7           D L D F F ET P V KT         7           D L L R K P P K ER         7           WQ S EL L Q E         8           KQ L EN D I K L EV         7	10 14 15 16 17 17 17 17 17 17 17 17 17 17	00 200 QSHFVRVSTAC GTSTKKPSVSC GKVTKPSSPDE GGKTPQKCKNT RNWKACVQQDF SDSPEKKVTQM TSLSQDNKRSK LKEQSKLLLQK	) 240 24 S K K G K R N 2 Q N T S S 2 E F P E F T G K Q S 2 S R P G T P L C S 3 S R P G T P L C S 1 G S F I N P T L N C S I I E S T S L S	220 F F K A Q L Y L T N T S C S S K C E E T K V S D T S H V T P E L I F K I Q S I S P E G P G P G R G V S V G S R F S F E D F P N K E R I K Q Q I S A M D N E D A K R L Q L S R D	230 VKT D L PPPS S N E E S Q AT ET I T I E D Q P C M E I K T T E K H D C A K L L P K S T N L P S V L N G N R H H L L T L S L L P S L P Q A R A V I R P Q L S N M S I R	240 S E Q I D L T E E Q K 225 A P K D V L S A A N G 224 E P E I I V S N N S T 224 Y D N N E V A S E P R 211 S R T V N S S S F S T 227 D S P P P Q P V K K 233 P D L Q S F P A V S R 229 I D S L E K E I I K A 242
HsBlm/1-651 DrBlm/1-662 OlBLM/1-630 KlBLM/1-633 GgBLM/1-659 DmBLM/1-704 KlBLM/1-621 ScSgs1/1-674	250 225 D D S E WL S S 225 V S T E T 225 V S P G P G I L Q E T 212 K N N Q 228 I R N Q 234 P E K T - MWQ N E T 230 N A S A S K	260 DVICIDDGPIA AEREPEDSPI VQFEVEDSPVF LHAKTAESPDC LDKLDTSYSS KTIQDKDSPAT ASISRRNSPT DQSKGRSQVSS	270 A E V H I N E D A Q E S D S K K S K R P K K S V Q H T A R G T R R R P F E H K S Q - S L V C L A S V E P T H K E T D Q E V I C L E P A A N L V S N N L A S I S T I P H A T E S V N P I P S E S Q D D N I I S S I L P S F	280 290 LKT H L E D E LLS D T E D E E I I H V LS D S E D L P S P K V N G K D D S R A P N D I D I D I P S L E Y N T S S R N	) RDNSEKK ICVSPDTNQKNF DTNTVVE GSTSLSR SQTQL SQTQL SNLTST	310 KNLEEAELHS KSVAVAEKDK KIETKSDGKK GTDDLEHDQE PSEASFNGSW FEDSPEKSGS TQQHNSSSPK ATTVTKALAI	320 TEKVPCIEFD WGEPNVIDSDC WIDPKVIELQC TLSQVLIEEEC CEKPTGRDSGN GEQGNKLGSAK IQPSRRLRHR TGAKQNITNNT	330 DDYD CEENNHYEGF NSEPEVD DCEP WRVPERPTAS SENEIPTKPAT PNON GKNSNNDSNN	340 T D F V P P S P E I E D F I P P S P I P E F D C I P P S P S D E T A L KAQHTAPA A S L E R N S V T S S - Y Y I P T L S Q MD D D L I Q V L D D E D	350 I S A S S S S K C L E I S L S V S D K E K E T S Y T S S A L Q T S L S S P P V L V I G N P A S G C W D V N P S P A A P L K P R V E N P H L L Q E S L L D I D C D P P V I L K	360 STLKDLDTSDR 330 SSEPVTPANK 340 RSKTGKTQSRF 332 SAQRKHKVSSL 305 DTDFDLDHFDI 336 SVAFDNSLADY 348 SKRRTTSTN - 323 EGAPHSPAFPH 353
HsBIm/1-651 DrBIm/1-662 OIBLM/1-630 XIBLM/1-633 GBLM/1-659 DmBLM/1-704 XIBLM/1-621 ScSgs1/1-674	370 331 KEDVLSTSKDL 341 KE 333 FS 306 TD 37 DDFDEGwEE 349 LKDLAQ 324 354 LHMTSE	380 L S K P E K M S M Q S S R S A S G A Q S K S S A V N D C E N T A V A P E A A P E A N D N F S I N E Q D E L T R F	390 400 ELNPETSTDCDARC LPAPLDQSAKGI PTRPEFSLCLSH TDHLQGQSVSTSLC PPAPQWQPLREGSZ DPNKQNTETLKSTI I HHNDNDSDASAEA RRNMRSREPVNYR	D 410 LISLQQQLIHVME KGADDALFSVME (NSTREQLYSIME SKVPSQLITLME SKRCRLAAAAA GFFRNTYVELME GFFRNTYVELME PDRDDPFDYVMC	420 H - I C K L I D T I P S - I C C L V D T I P S - I C A L V D S I P E - I C D L V D K I P K - Y C S L I D Q I P K - Y C S L I D Q I P K - Y C S L I D Q I P K S L R D D Y P D M E	430 DD - KLKLLDC EH - ELIALTC EH - ELIS LSC IS - ELHVLSC KSGCGISAKS AMHFNEIAGF ESDKDFVVDG REEDELTMEA	440 GNELLQQRNIR GTELLLQRAHR GNELLLRRAHR GLDLKKKRDMR SSEPLVHNPAF QPNTFLKLKVV NYLDYDEGPEA EDDAHSSYMT	450 KRILAKGGSS KRILAKGGSS KRILATGGDF KRLSNDSVF ERFRGMKFSH ROKFKARTQL DAEYHEEDDS RDEEKEENEL	460 KSDAS RTSHSDSVSTP SFRMQQPDST- RSSPADSSTVS SEEMLKIFHRK VQNSLDKKESQ NVPFEKERSSN LNQSDFDFVVN	470 LLGSLWRYR GFLNRPTFGVT -VISDASFKET -LTSCTSSTQ FGLHSFRTNQL LKAEQEALEKE QIIIDSSPGSS DDLDPTQDTDY	480 P D S L D G P M E G D 442 P S N L T S L T P V T 446 S S - C C V L T P S S 435 N R D E N V N A P K G 411 E A I N A A L L G E D 455 E I E M Q A E Q A R Q 460 P R H L N P P S Q P P 425 H D N M D V S A N I Q 467
HsBIm/1-651 DrBIm/1-662 OIBLM/1-630 KIBLM/1-603 GgBLM/1-659 DmBLM/1-704 KIBLM/1-621 ScSgs1/1-674	490 443 S C P T G N S M K E L 447 S G K R E G V K T G F 436 S A V L D S R K S Q Q 412 A E S L S G S S V S K 456 C F I L M P T G G G K 461 T V L S S S S P E K C 426 L Q Q Q T Q N T S Q E 468 E S S Q E G D T R S T	500 5 N F S H L PS N S V S S F R K S I A S V M S P R R P S V I S V F K F N K L A V H G S L C Y Q L P A C V S S L C Y Q L P A C V S F Q PT P Q L R L L G I T L S Q N K N V Q S	510 5 PGDCLLTTTLG 5 VGDESVFEDSDC 5 LDYDSDHSDR 0 IGTKESENSAN 5 AGVTVVISPLR EIKDEKIPNRNQLI 0 DDVEFLEDPIS- VILSSPTAQSVP	530 INGVET PGGTWN TAFNPLS PDLCGEPDNFSF	540 FSATRKNLFER NSSTKISAGR SKSSRAICVED APNFMEKIGNK - SLIIDQVQKL PSSPRDTQLIP ESLPQDHTVAV	550 P L F N T D T F N G S I Q T L E S I C D S L T S F S F R K T L D I A S T Y L K R Q Q L I N D L C H S E E F E P L S D E H I D L L E D D L	560 H L Q K S E V S S NV S K P E S K T D K C Y S T P R L L K Q P C F A G C D S I M E N S F T G D I T D A D A S K G E P D D F S P P S K T D L E E F D A E R E E K D A I L D D S MS	570 /A ET P R S R LS F N E S ES T S R N F H S T Y MQLS K Q N D P H L R K C I D Q T Q F S F G R Q H MP M	580 LGKKNESSYFP SSNQTDLFYSP LDEDDAHFFSP SVLSNSRFNTP KDPIIKLLYVT ELVHDLCEEP FDEIKELDDDL SHSDLELIDSE	590 GNVLT STAVKD KRVDSGSRNAD KKPVSVEQNKS QNEKPISSSTC PEKVCASNRLL DOYLAQSMMLD KIISEAKLDAE KENEDFEEDNN	600 QNKHTA <mark>SINDL 543</mark> SSVEINIAGSS 565 KTPTCTTADNT 539 TRPYSQPIDDM 510 SALENLYNRKL 559 GDLEEEQLNGP 582 DVPLSFAIKKE 528 NNGIEYLSDSD 573
HsBlm/1-651 DrBlm/1-662 OlBLM/1-630 KlBLM/1-633 GgBLM/1-659 DmBLM/1-704 KlBLM/1-621 ScSgs1/1-674	620 544 ER ET Q 566 S L RT G A E P V 540 E T 511 D P V D 560 L A R F V D 583 T Q G T T T S G M D 529 P K S L D 574 L E R F D E E	630 PSYDDDFDI DDFLLDDFDI DDFYFDDFDI LDFDIDNFDI EAHCVSQWGHI GEDDLEGLLA TQLQTELVPVF RENRTQVADI	640 D F D D D D D D W E D D F D E N D E D L D D I H F R K D Y K R L NM E I E D E HQ K MQ AR R S P E V I E D D Q E L D N D L K I I T E R -	650 IPDYYEE IPEYFEE LRKKFHS EFNGY <u>SY</u> KELEA DFSMADL KLT <u>G</u> DNE	660 SKSSTAAYQPI PPSVLESRNNS APTSSVBRQNS APSVSSKNVPQ VPMMALTATAN VKVKEKHKETP EPYMEETEKCT HPPPSWSPKIK	670 K E G R P I K S V S 	680 ERLSSAKTDCL VKTPSVQEGGS TAT-AVKEGGF PTIREAQLDSR RVQKDIQNQLE PEYDEAMFEQM - RENSVQPQYA - REKSSVQPQYA	690 SKS - FERK - T SKS SWDKK P NKEKNTRNNT MLKPQVFTMS IHSQAAANKSR WTSEMYHKLR EEDDFDDDFS	700 71 F S ES I Q N Y T D K FT PP AP KS I KT S VST PK P KL G D T T N P S L L S D F N R HN L KY D VL V S S A GP S T S KS H V F G L D S F R P N L S D I V S K S N L S	0 720 SAQNLASRNLK PNPEPLYRNPA CSPEPTFRNPA SLLKPQIENPA PKKPKKVAMDC VVPTKQTSALH QLEAVNATLQG SKTNGPTYPWS	730 HERFQSLSFPH 651 HDRFRGFNFPH 662 HDRFRGFNFPH 663 LEWIKKY – HPH 663 SCKLSGNFHAN 704 KDAFVLMPTGG 621 DEVLYRLHEVF 674











## Supplementary Table S1

## Oligonucleotides used in this study

Oligo Name	Original name	Size	DNA sequence (5'-3')
1	1253	50	TGGGTCAACGTGGGCAAAGATGTCCTAGCAATGTAATCGTCTAT GACGTT
2	1254	50	TGCCGAATTCTACCAGTGCCAGTGATGGACATCTTTGCCCACGT TGACCC
3	2558	25	TGGGTCAACGTGGGCAAAGATGTCC
4	2559	25	GGACATCTTTGCCCACGTTGACCCA
5	2600	25	TCACTGGCACTGGTAGAATTCGGCA
6	2625	32	TCCTTTTGATAAGAGGTCATTTTTGCGGATGG
7	2640	32	TCCTTTTGATAAGAGCTCATTTTTGCGGATGG
8	2651	94	CTTTAGCTGCATATTTACAACATGTTGACCTACAGCACCAGATT CAGCAATTAAGCTCTAAGCCATCCGCAAAAATGAGCTCTTATCA AAAGGA
9	2655	57	CCAGATTCAGCAATTAAGCTCTATCCCATCCGCAAAAATGACCT CTTATCAAAAGGA
10	2624	57	CCATCCGCAAAAATGACCTCTTATCAAAAGGATGGACATCTTTG CCCACGTTGACCC
11	2626	94	CTTTAGCTGCATATTTACAACATGTTGACCTACAGCACCAGATT CAGCAATTAAGCTCTAAGCCATCCGCAAAAATGACCTCTTATCA AAAGGA
12	2653	34	TCTCCTTTTGATAAGAGGTCATTTTTGCGGATGG
13	2654	34	TCCTTTTGATAAGAGGTCATTTTTGCGGATGGCT
14	2639	32	CCATCCGCAAAAATGACCTCTTATCAAAAGGA
15	2641	32	CCATCCGCAAAAATGAGCTCTTATCAAAAGGA
16	2129 (Phi- X174)	50	AAAGGTCGCAAAGTAAGAGCTTCTCGAGCTGCGCAAGGATAGG TCGAATT
17	2044 (D-loop)	50	CGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGA GATCCAG
18	1317 (DNA binding)	90	GATCCGAATTCTGGCTTGCTAGGACATCTTTGCCCACGTTGACC CGGGTTGGCGTTAGGAGATAGTCAGTTATAGCTGCGGCTGCTA AGG