SUPPLEMENTAL MATERIAL

Helmink et al., http://www.jem.org/cgi/content/full/jem.20081326/DC1

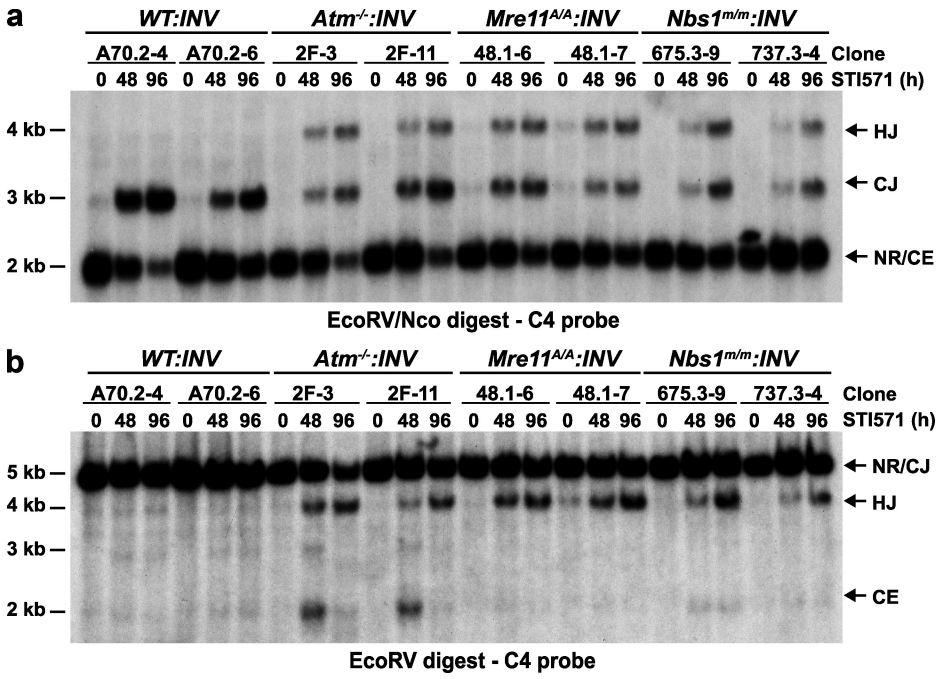


Figure S1. Southern blot analyses of pMX-INV rearrangement on additional abl pre-B cell clones. Analyses were carried out as described in Fig. 1 b (a) and Fig. 1 c (b) on additional abl pre-B cell clones not shown in Fig. 1.

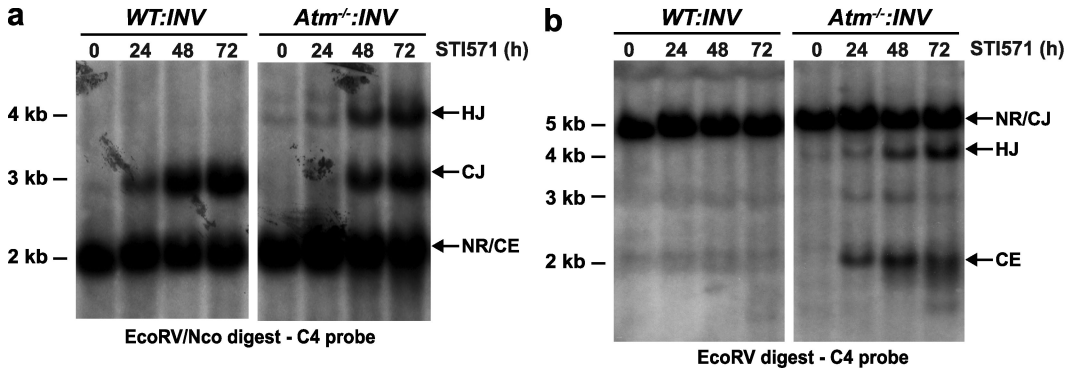
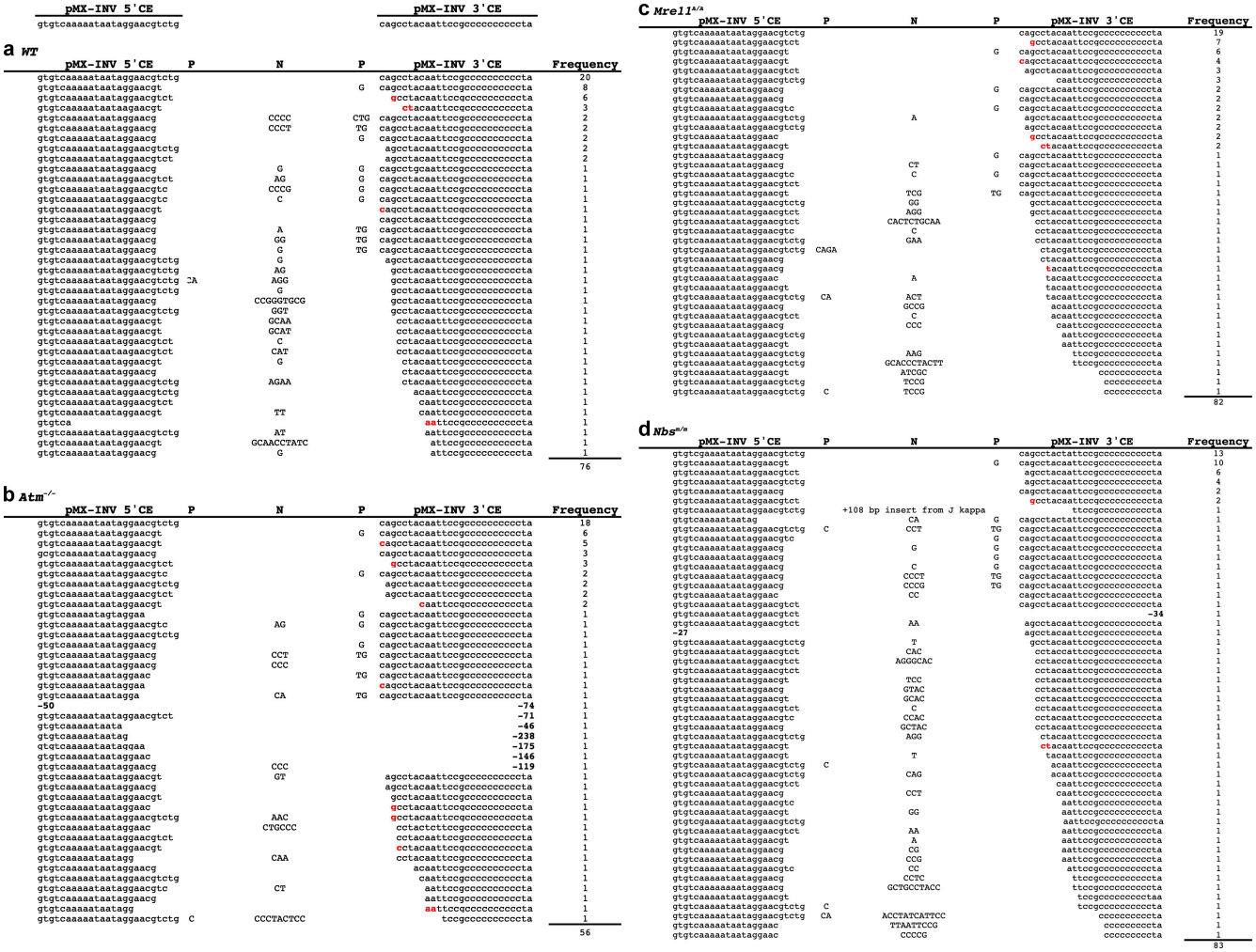


Figure S2. Longer exposure of the *WT:INV* and *Atm*$^{-/-}$*:INV* Southern blot analyses. The lighter exposure is shown in Fig. 1 d (a) and Fig. 1 e (b).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pMX-INV 3'CE
cagcctacaattccgcccccccccta
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gtgtcaaaaataatagggaacgt ctacaattccgcccccccccta 3
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gtgtcaaaaataatag -238 1
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gtgtcaaaaataatagggaac -146 1
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56
c Mre11A/A
pMX-INV 5'CE P N P pMX-INV 3'CE Frequency
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82
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gtgtcaaaaataatagggaac TTAATTCCG ccccccccta 1
gtgtcaaaaataatagggaac CCCCG ccccccccta 1
83

Figure S3. Sequences of pMX-INV coding joints from *WT:INV*, *Atm*$^{-/-}$*:INV*, *Mre11*$^{A/A}$*:INV*, and *Nbs1*$^{m/m}$*:INV* abl pre-B cells. N and P nucleotides are indicated, as are potential microhomologies (red). Complete coding end sequence is noted at the top of the figure.

pMX-DEL^{SJ} 5'SE		pMX-DEL^{SJ} 3'SE
ttttgttccagtctgtagcactgtg		cacagtggtagtactccactgtctggc

a ***WT***

pMX-DEL^{SJ} 5'SE	N	pMX-DEL^{SJ} 3'SE	Frequency
ttttgttccagtctgtagcactgtg	0	cacagtggtagtactccactgtctggc	56
ttttgttccagtctgtagcactgtg	GAG	cacagtggtagtactccactgtctggc	1
ttttgttccagtctgtagcactgtg	AG	cagtggtagtactccactgtctggc	1
ttttgttccagtctgtagcactgtg	GGCACAGTG	ggtagtactccactgtctggc	1
ttttgttccagtctgtagcactgtg	TGTG	ggtagtactccactgtctggc	1
			60

b ***Atm$^{-/-}$***

pMX-DEL^{SJ} 5'SE	N	pMX-DEL^{SJ} 3'SE	Frequency
ttttgttccagtctgtagcactgtg	0	cacagtggtagtactccactgtctggc	69
ttttgttccagtctgtagcactgtg	GGG	acagtggtagtactccactgtctggc	1
ttttgttccagtctgtagcactgtg	G	cacagtggtagtactccactgtctggc	1
			71

c ***Mre11$^{A/A}$***

pMX-DEL^{SJ} 5'SE	N	pMX-DEL^{SJ} 3'SE	Frequency
ttttgttccagtctgtagcactgtg	0	cacagtggtagtactccactgtctggc	84
ttttgttccagtctgtagcactgtg	AG	cacagtggtagtactccactgtctggc	1
ttttgttccagtctgtagcac	CGTG	cacagtggtagtactccactgtctggc	1
ttttgttccagtctgtagcactgtg	0	agtggtagtactccactgtctggc	1
ttttgttccagtctgtagcactgtg	0	cagtggtagtactccactgtctggc	1
ttttgttccagtctgtagcactg	CG	cacagtggtagtactccactgtctggc	1
ttttgttccagtctgtagcactgtg	GA	cacagtggtagtactccactgtctggc	1
			90

d ***Nbs$^{m/m}$***

pMX-DEL^{SJ} 5'SE	N	pMX-DEL^{SJ} 3'SE	Frequency
ttttgttccagtctgtagcactgtg		cacagtggtagtactccactgtctggc	61
ttttgttccagtctgtagcactgtg	A	agtactccactgtctggc	1
ttttgttccagtctgtagcactgtg	GCC	cacagtggtagtactccactgtctggc	1
ttttgttccagtctgtagcactg	AGCA	cacagtggtagtactccactgtctggc	1
ttttgttccagtctgtagcactgtg	GCCCTG	cacagtggtagtactccactgtctggc	1
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ttttgttccagtctgtagcactgtg	CC	cacagtggtagtactccactgtctggc	1
ttttgttccagtctgtagcactgtg	AT	cacagtggtagtactccactgtctggc	1
-67	CTCTGTTCCACTGTG	cacagtggtagtactccactgtctggc	1
ttttgttccagtctgtagcactgtg	A	gtctggc	1
ttttgttccagtctgtagcactgt	CC	cacagtggtagtactccactgtctggc	1
-67	TCCGCCCCCCCCCCTGTG	cacagtggtagtactccactgtctggc	1
ttttgttccagtctgtagcactgtg	AAGGG	cacagtggtagtactccactgtctggc	1
ttttgttccagtctgtagcactgtg	CTC	cacagtggtagtactccactgtctggc	1
ttttgttccagtctgtagcactgtg	CGCAC	tggtagtactccactgtctggc	1
			76

Figure S4. Sequences of pMX-DEL^{SJ} signal joints from *WT:DEL^{SJ}*, *Atm$^{-/-}$:DEL^{SJ}*, *Mre11$^{A/A}$:DEL^{SJ}*, *and Nbs1$^{m/m}$:DEL^{SJ}* abl pre-B cells. The complete signal end sequences are noted at the top of the figure.

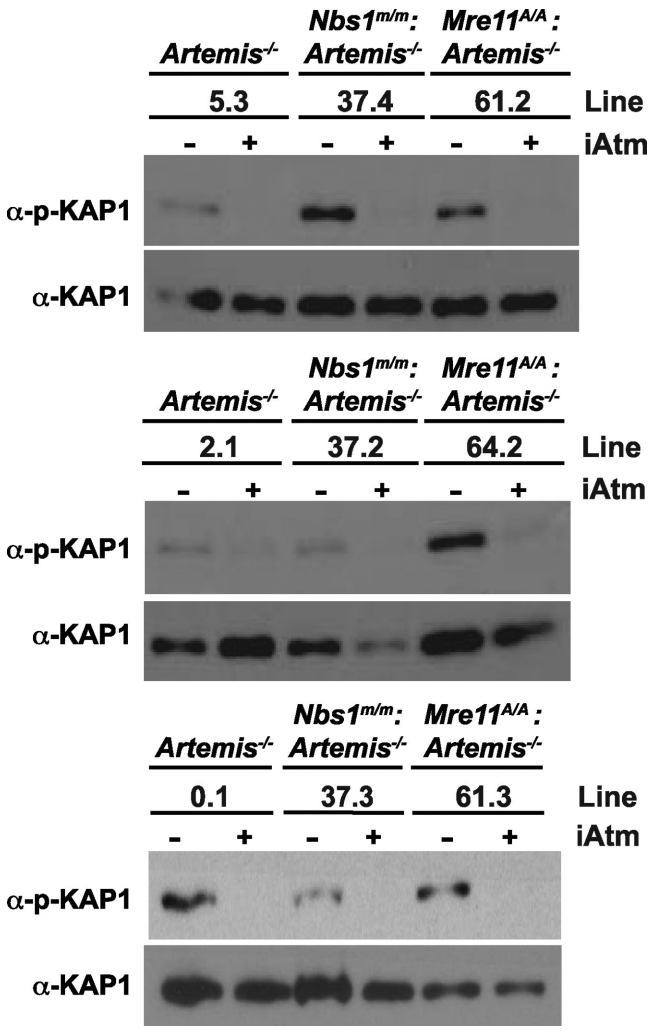

Figure S5. Analysis of KAP-1 phosphorylation carried out as described in Fig. 4 a on additional *Artemis*$^{-/-}$, *Artemis*$^{-/-}$:*Nbs1*$^{m/m}$, and *Artemis*$^{-/-}$:*Mre11*$^{A/A}$ abl pre-B cell lines.

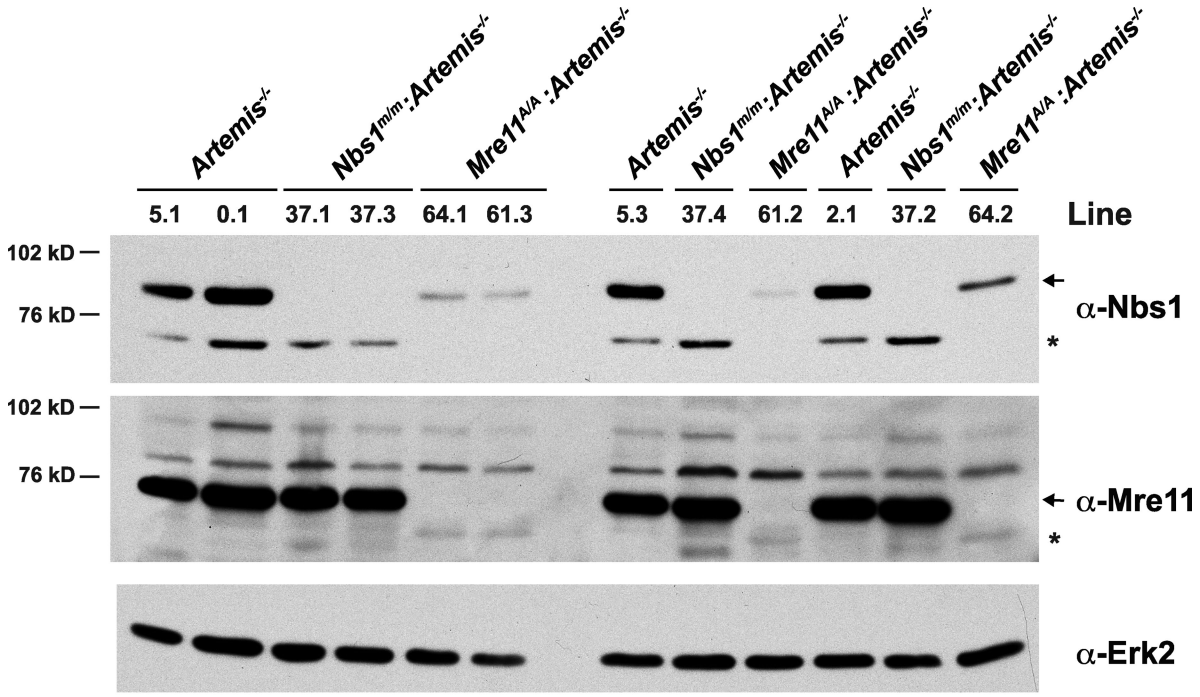

Figure S6. Nbs1 and Mre11 western blot analyses in the different *Artemis*$^{-/-}$, *Artemis*$^{-/-}$*:Nbs1*$^{m/m}$, and *Artemis*$^{-/-}$*:Mre11*$^{A/A}$ abl pre-B cells analyzed. Erk2 is shown as a protein loading control. The arrows indicate the native WT Nbs1 and Mre11 proteins. The asterisks indicate bands of expected size for the hypomorphic Nbs1 and Mre11 proteins. The identity of the band in the *Artemis*$^{-/-}$ abl pre-B cells that is of similar size to that expected for the Nbs1^{m} hypomorphic protein is not known.

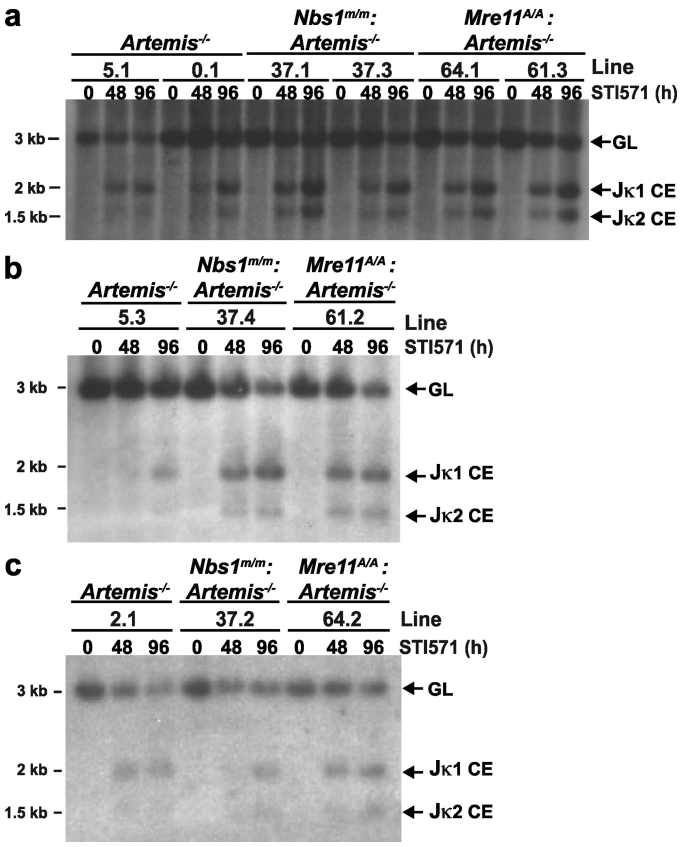

Figure S7. Southern blot analyses of IgL-κ locus Jκ coding ends after Rag induction in the different *Artemis*$^{-/-}$, *Artemis*$^{-/-}$*:Nbs1*$^{m/m}$, and *Artemis*$^{-/-}$*:Mre11*$^{A/A}$ abl pre-B cell lines. Analyses were carried out as described in Fig. 3 a.

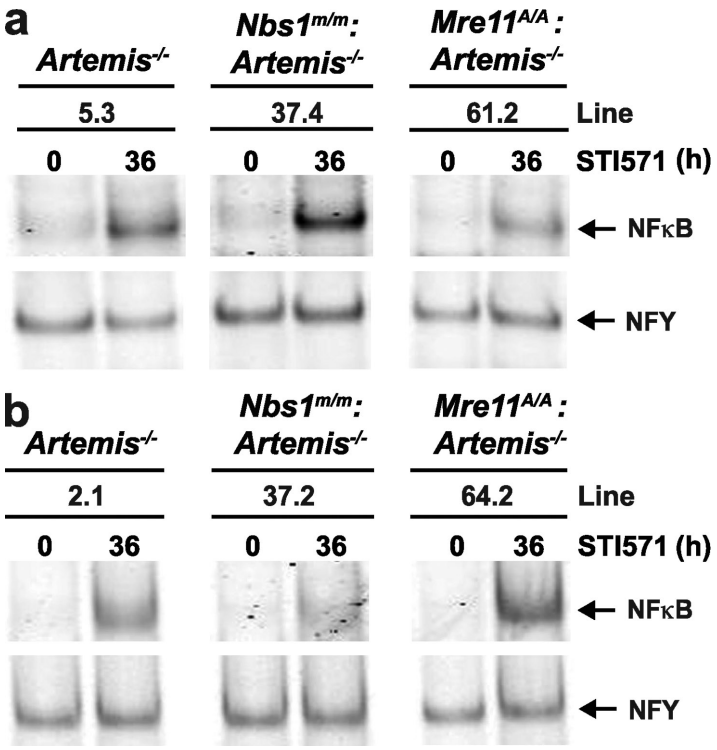

Figure S8. EMSA analyses of NF-κB translocation to the nucleus in the additional *Artemis*$^{-/-}$, *Artemis*$^{-/-}$*:Nbs1*$^{m/m}$, and *Artemis*$^{-/-}$*:Mre11*$^{A/A}$ abl pre-B cells not analyzed in Fig. 4 c. Analyses were carried out as described in Fig. 4 c.