

Mutations in DNA repair genes *ku70* and *lig4* impair growth, fecundity, and lifespan in the cladoceran *Daphnia magna*

Supplementary Information

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Supplementary Tables

Supplementary Table S1. Guide RNA information used for CRISPR-Cas9 mutagenesis of *ku70* and *lig4*. Target genomic sequences, transcribed guide RNA spacer sequences, protospacer adjacent motifs (PAMs), and GC contents are shown. Sequences are given in the 5'-to-3' direction.

Gene	Target genomic sequence (5'-3')	gRNA spacer (5'-3')	PAM	GC (%)
<i>ku70</i>	GTCCGGTGAAAAAGTTCGTT	GUCCGGUGAAAAAGUUCGUU	TGG	40
<i>lig4</i>	GGAAGCATTCTCTAGACGA	GGAAGCAUCCUCUAGACGA	GGG	50

Supplementary Table S2. Oligonucleotides used to prepare templates for guide RNA synthesis. The gene-specific sense oligonucleotides contain the T7 promoter, 20-nt spacer, and 5' portion of the single-guide RNA scaffold; the universal antisense oligonucleotide completes the scaffold template. Sequences are shown 5'-to-3'.

Oligonucleotide	Sequence (5'-3')
<i>ku70 sense</i>	GAAATTAATACGACTCACTATAGTCCGGTGAAAAAGTTCGTTGTTTATAGAGCTAGAAATAGC
<i>lig4 sense</i>	GAAATTAATACGACTCACTATAGGAAGCATTCTCTAGACGAGTTTATAGAGCTAGAAATAGC
antisense	AAAAGCACCGACTCGGTGCCACTTCTTCAAGTTGATAACGGACTAGCCTTATTTAACTTGCTATTCTAGCTCTAAAC

Supplementary Table S3. Primers used to amplify the *ku70* and *lig4* target loci for genotyping. Amplicons spanned the guide RNA target sites and were analyzed by native PAGE and Sanger sequencing. Primer sequences are shown 5'-to-3'.

Primer	Sequence (5'-3')
<i>ku70 fwd</i>	GGCAGTATTCTCTCTGGCAGC
<i>ku70 rev</i>	GCAATCGCAATCTGGTAACG
<i>lig4 fwd</i>	CCTAAGGATGGACCAGATGC
<i>lig4 rev</i>	ACCTTGAACCATCCTCCTTTG

Supplementary Table S4. Body length by line at Day 0 and Day 28. Values are untransformed group means and standard errors (SE); n is the number of individuals. Day 28 values were calculated from animals that survived to Day 28. WT denotes the wild-type NIES strain, and DR-GFP denotes the parental transgenic line.

Time point	Line	n	Mean (mm)	SE
Body length (Day 0)	WT	8	0.822	0.009
Body length (Day 0)	DR-GFP	8	0.828	0.013
Body length (Day 0)	<i>ku70</i> ^{-/-}	8	0.819	0.014
Body length (Day 0)	<i>lig4</i> ^{-/-}	8	0.807	0.010
Body length (Day 0)	<i>ku70</i> ^{-/-} ; <i>lig4</i> ^{-/-}	8	0.723	0.008
Body length (Day 28)	WT	8	4.265	0.019
Body length (Day 28)	DR-GFP	5	4.159	0.030
Body length (Day 28)	<i>ku70</i> ^{-/-}	6	3.973	0.026
Body length (Day 28)	<i>lig4</i> ^{-/-}	8	3.924	0.053
Body length (Day 28)	<i>ku70</i> ^{-/-} ; <i>lig4</i> ^{-/-}	8	3.755	0.043

Supplementary Table S5. Cumulative fecundity to Day 28 by line. Values are untransformed means and standard errors (SE) of cumulative offspring counts; n is the number of females included in the analysis. Only females that survived to Day 28 were included. For inferential analyses, cumulative counts were square-root transformed before Welch's t-tests.

Line	n	Mean	SE
WT	8	181.6	3.7
DR-GFP	5	158.2	5.5
<i>ku70</i> ^{-/-}	7	146.0	5.0
<i>lig4</i> ^{-/-}	8	130.5	6.6
<i>ku70</i> ^{-/-} ; <i>lig4</i> ^{-/-}	8	133.1	6.0

Supplementary Table S6. Kaplan-Meier survival summary by line. n is the number of animals enrolled at Day 0, and Events is the number of observed deaths. Median survival and Brookmeyer-Crowley 95% confidence intervals (CI) are reported in days. Accidental losses were right-censored; when the exact day was unknown, censoring was assigned to the midpoint between the last day known alive and the first subsequent inspection. NA, upper confidence limit not estimable.

Line	n	Events	Median survival (days)	95% CI lower	95% CI upper
WT	8	8	71	65	NA
DR-GFP	8	5	70	68	NA
<i>ku70</i> ^{-/-}	8	7	44	30	NA
<i>lig4</i> ^{-/-}	8	8	51	48	NA
<i>ku70</i> ^{-/-} ; <i>lig4</i> ^{-/-}	8	8	42	41	NA

Supplementary Table S7. Confirmatory and exploratory pairwise comparisons of life-history endpoints. Body length and fecundity were analyzed using two-sided Welch's t-tests; fecundity counts were square-root transformed before testing. Survival was analyzed using pairwise log-rank (Mantel-Haenszel) tests. Holm's step-down adjustment ($\alpha = 0.05$) was applied within each endpoint to the three pre-specified contrasts versus the DR-GFP parental line. Exploratory comparisons are hypothesis-generating and are reported as nominal P-values.

Analysis	Endpoint	Contrast	P	Holm-adjusted P	Significance
Confirmatory	Body length (Day 0)	DR-GFP vs <i>ku70</i> ^{-/-}	0.665	0.665	n.s.
Confirmatory	Body length (Day 0)	DR-GFP vs <i>lig4</i> ^{-/-}	0.232	0.465	n.s.
Confirmatory	Body length (Day 0)	DR-GFP vs <i>ku70</i> ^{-/-} ; <i>lig4</i> ^{-/-}	<0.001	<0.001	***
Confirmatory	Body length (Day 28)	DR-GFP vs <i>ku70</i> ^{-/-}	0.002	0.003	**
Confirmatory	Body length (Day 28)	DR-GFP vs <i>lig4</i> ^{-/-}	0.003	0.003	**
Confirmatory	Body length (Day 28)	DR-GFP vs <i>ku70</i> ^{-/-} ; <i>lig4</i> ^{-/-}	<0.001	<0.001	***
Confirmatory	Fecundity (to Day 28)	DR-GFP vs <i>ku70</i> ^{-/-}	0.127	0.127	n.s.
Confirmatory	Fecundity (to Day 28)	DR-GFP vs <i>lig4</i> ^{-/-}	0.010	0.030	*
Confirmatory	Fecundity (to Day 28)	DR-GFP vs <i>ku70</i> ^{-/-} ; <i>lig4</i> ^{-/-}	0.011	0.030	*
Confirmatory	Longevity (log-rank)	DR-GFP vs <i>ku70</i> ^{-/-}	0.001	0.003	**
Confirmatory	Longevity (log-rank)	DR-GFP vs <i>lig4</i> ^{-/-}	0.006	0.006	**
Confirmatory	Longevity (log-rank)	DR-GFP vs <i>ku70</i> ^{-/-} ; <i>lig4</i> ^{-/-}	0.002	0.004	**
Exploratory	Body length (Day 0)	WT vs DR-GFP	0.722	—	—
Exploratory	Body length (Day 0)	<i>ku70</i> ^{-/-} vs <i>lig4</i> ^{-/-}	0.490	—	—
Exploratory	Body length (Day 0)	<i>ku70</i> ^{-/-} vs <i>ku70</i> ^{-/-} ; <i>lig4</i> ^{-/-}	<0.001	—	—
Exploratory	Body length (Day 0)	<i>lig4</i> ^{-/-} vs <i>ku70</i> ^{-/-} ; <i>lig4</i> ^{-/-}	<0.001	—	—
Exploratory	Body length (Day 28)	WT vs DR-GFP	0.022	—	—
Exploratory	Body length (Day 28)	<i>ku70</i> ^{-/-} vs <i>lig4</i> ^{-/-}	0.428	—	—
Exploratory	Body length (Day 28)	<i>ku70</i> ^{-/-} vs <i>ku70</i> ^{-/-} ; <i>lig4</i> ^{-/-}	0.001	—	—
Exploratory	Body length (Day 28)	<i>lig4</i> ^{-/-} vs <i>ku70</i> ^{-/-} ; <i>lig4</i> ^{-/-}	0.029	—	—
Exploratory	Fecundity (to Day 28)	WT vs DR-GFP	0.011	—	—
Exploratory	Fecundity (to Day 28)	<i>ku70</i> ^{-/-} vs <i>lig4</i> ^{-/-}	0.084	—	—
Exploratory	Fecundity (to Day 28)	<i>ku70</i> ^{-/-} vs <i>ku70</i> ^{-/-} ; <i>lig4</i> ^{-/-}	0.115	—	—
Exploratory	Fecundity (to Day 28)	<i>lig4</i> ^{-/-} vs <i>ku70</i> ^{-/-} ; <i>lig4</i> ^{-/-}	0.768	—	—
Exploratory	Longevity (log-rank)	WT vs DR-GFP	0.729	—	—
Exploratory	Longevity (log-rank)	<i>ku70</i> ^{-/-} vs <i>lig4</i> ^{-/-}	0.037	—	—
Exploratory	Longevity (log-rank)	<i>ku70</i> ^{-/-} vs <i>ku70</i> ^{-/-} ; <i>lig4</i> ^{-/-}	0.895	—	—
Exploratory	Longevity (log-rank)	<i>lig4</i> ^{-/-} vs <i>ku70</i> ^{-/-} ; <i>lig4</i> ^{-/-}	0.038	—	—

Significance codes: *** $P < 0.001$, ** $P < 0.01$, * $P < 0.05$; n.s., not significant. Day 28 endpoints were calculated from animals that survived to Day 28. Exploratory comparisons were not used to support primary conclusions. —, not applicable because exploratory comparisons were not adjusted for multiple testing.

Supplementary Figure S1. Multiple-sequence alignment of Ku70 orthologs showing conserved domain organization. Amino-acid alignment of Ku70 from seven species (top to bottom): *Daphnia magna* (ATP-dependent DNA helicase 2 subunit; Ku70/XRCC6), *Daphnia pulex* (ATP-dependent DNA helicase 2 subunit), *Drosophila melanogaster* (IRBP; the Ku70 homolog), *Danio rerio* (XRCC6), *Gallus gallus* (Ku70/XRCC6), *Mus musculus* (XRCC6), and *Homo sapiens* (XRCC6). Residues are color-shaded according to the *D. magna* Ku70 domain boundaries and projected onto all sequences in the alignment: N-terminal domain (blue), β -barrel domain (green), C-terminal domain (yellow), and SAP domain (purple). The alignment was generated with Clustal Omega (default settings). Consensus symbols beneath each block follow the Clustal convention: an asterisk (*) indicates a fully conserved residue, a colon (:) indicates conservation of residues with strongly similar physicochemical properties, and a period (.) indicates conservation of residues with weakly similar properties.

[illegible]

Supplementary Figure S2. Multiple-sequence alignment of Ku70 from the WT line and edited alleles. Amino-acid sequences of *Daphnia magna* Ku70 were aligned with Clustal Omega (default settings). From top to bottom the alignment shows: WT, DR-GFP (ku70^{-/-}) allele 1, DR-GFP (ku70^{-/-}) allele 2, DR-GFP (ku70^{-/-}; lig4^{-/-}) allele 1, and DR-GFP (ku70^{-/-}; lig4^{-/-}) allele 2. Residues are color-shaded according to the Ku70 domain boundaries in *D. magna*: N-terminal domain (blue), β -barrel domain (green), and C-terminal domain (yellow). Asterisks (*) beneath the alignment mark positions with identical residues across all sequences; hyphens (-) denote alignment gaps (including truncations caused by frameshift mutations). Numbers at the right indicate residue positions in each sequence.

WT	MDDRNDPDGITDDTDFDGRDATIFLVDASAPMFEKTSPSVDNIEAEPTIDDCPFTLAIRCA	60
DR-GFP ku70- allele1	MDDRNDPDGITDDTDFDGRDATIFLVDASAPMFEKTSPSVDNIEAEPTIDDCPFTLAIRCA	60
DR-GFP ku70- allele2	MDDRNDPDGITDDTDFDGRDATIFLVDASAPMFEKTSPSVDNIEAEPTIDDCPFTLAIRCA	60
DR-GFP ku70-/lig4- allele1	MDDRNDPDGITDDTDFDGRDATIFLVDASAPMFEKTSPSVDNIEAEPTIDDCPFTLAIRCA	60
DR-GFP ku70-/lig4- allele2	MDDRNDPDGITDDTDFDGRDATIFLVDASAPMFEKTSPSVDNIEAEPTIDDCPFTLAIRCA	60

WT	FNTLNKIFTAPYDSVAIVLFGTKKKKPNKEYGVYSNTYLLQDLQKPDCEPILQLEMLN	120
DR-GFP ku70- allele1	FNTLNKIFTAPYDSVAIVLFGTKKKKPNKEYGVYSNTYLLQDLQKPDCEPILQLEMLN	120
DR-GFP ku70- allele2	FNTLNKIFTAPYDSVAIVLFGTKKKKPNKEYGVYSNTYLLQDLQKPDCEPILQLEMLN	120
DR-GFP ku70-/lig4- allele1	FNTLNKIFTAPYDSVAIVLFGTKKKKPNKEYGVYSNTYLLQDLQKPDCEPILQLEMLN	120
DR-GFP ku70-/lig4- allele2	FNTLNKIFTAPYDSVAIVLFGTKKKKPNKEYGVYSNTYLLQDLQKPDCEPILQLEMLN	120

WT	KDGGIDEYVYAVDQQSISLADALWLCSSIFSCHKSKKDNKKIFLFTNNDEPHSKFSNKQK	180
DR-GFP ku70- allele1	KDGGIDEYVYAVDQQSISLADALWLCSSIFSCHKSKKDNKKIFLFTNNDEPHSKFSNKQK	180
DR-GFP ku70- allele2	KDGGIDEYVYAVDQQSISLADALWLCSSIFSCHKSKKDNKKIFLFTNNDEPHSKFSNKQK	180
DR-GFP ku70-/lig4- allele1	KDGGIDEYVYAVDQQSISLADALWLCSSIFSCHKSKKDNKKIFLFTNNDEPHSKFSNKQK	180
DR-GFP ku70-/lig4- allele2	KDGGIDEYVYAVDQQSISLADALWLCSSIFSCHKSKKDNKKIFLFTNNDEPHSKFSNKQK	180

WT	QAEKRIGDLQDGNVSIFLFPIGEAFDTSKVYQELLSMNEYGSILSGSMTADELLSKICRK	240
DR-GFP ku70- allele1	QAEKRIGDLQDGNVSIFLFPIGEAFDTSKVYQELLSMNEYGSILSGSMTADELLSKICRK	240
DR-GFP ku70- allele2	QAEKRIGDLQDGNVSIFLFPIGEAFDTSKVYQELLSMNEYGSILSGSMTADELLSKICRK	240
DR-GFP ku70-/lig4- allele1	QAEKRIGDLQDGNVSIFLFPIGEAFDTSKVYQELLSMNEYGSILSGSMTADELLSKICRK	240
DR-GFP ku70-/lig4- allele2	QAEKRIGDLQDGNVSIFLFPIGEAFDTSKVYQELLSMNEYGSILSGSMTADELLSKICRK	240

WT	GQKKRPVANLVFNVDSENTKFGVKLYNLIRPAPTPKRMQLDKRTNEIVKSVTTKFNAAETAE	300
DR-GFP ku70- allele1	GQKKRPVANLVFNVDSENTKFGVKLYNLIRPAPTPKRMQLDKRTNEIVKSVTTKFNAAETAE	300
DR-GFP ku70- allele2	GQKKRPVANLVFNVDSENTKFGVKLYNLIRPAPTPKRMQLDKRTNEIVKSVTTKFNAAETAE	300
DR-GFP ku70-/lig4- allele1	GQKKRPVANLVFNVDSENTKFGVKLYNLIRPAPTPKRMQLDKRTNEIVKSVTTKFNAAETAE	300
DR-GFP ku70-/lig4- allele2	GQKKRPVANLVFNVDSENTKFGVKLYNLIRPAPTPKRMQLDKRTNEIVKSVTTKFNAAETAE	300

WT	TLLPSELMKSTIVSGEKVRLDKNLTLKSKFAVGFTLLGFKPIEKLKFLHLYSPASFIY	360
DR-GFP ku70- allele1	TLLPSELMKSTIVF---GQKRLNKLKIEV---CGWIHVAVVQ-----AY-----	338
DR-GFP ku70- allele2	TLLPSELMKSTIVSGEKVGGKRLNKLKIEV---CGWIHVAVVQ-----AY-----	342
DR-GFP ku70-/lig4- allele1	TLLPSELMKSTIVSGEKVWTKTT-----CGWIHVAVVQ-----AY-----	323
DR-GFP ku70-/lig4- allele2	TLLPSELMKSTIVF---GQKRLNKLKIEV---CGWIHVAVVQ-----AY-----	338

WT	PDDELVKGSRVLFGLMDRCQVRGFAPLCILKCTAATKPRIVALLPNAEQDPEQPSVFGF	420
DR-GFP ku70- allele1	-----	338
DR-GFP ku70- allele2	-----	342
DR-GFP ku70-/lig4- allele1	-----	323
DR-GFP ku70-/lig4- allele2	-----	338

WT	HVIYLPFLNDVRKFNYSGLVSTLVLKDERKYVPEVWRADRGQIDAAVAIVKKLSKTSY	480
DR-GFP ku70- allele1	-----	338
DR-GFP ku70- allele2	-----	342
DR-GFP ku70-/lig4- allele1	-----	323
DR-GFP ku70-/lig4- allele2	-----	338

WT	TPAQFEDPALHTKWKTELEGLALGREDVESVDDLALPDCCDCIDRLGQRSTIFNDLVFPLG	540
DR-GFP ku70- allele1	-----	338
DR-GFP ku70- allele2	-----	342
DR-GFP ku70-/lig4- allele1	-----	323
DR-GFP ku70-/lig4- allele2	-----	338

WT	YQSRNFQASILTFRDPQHEATVEDAARNGWLDKMKVDILKGYLSNQGVHGVSKMKKAECI	600
DR-GFP ku70- allele1	-----	338
DR-GFP ku70- allele2	-----	342
DR-GFP ku70-/lig4- allele1	-----	323
DR-GFP ku70-/lig4- allele2	-----	338

WT	QNIKLHLNLK	610
DR-GFP ku70- allele1	-----	338
DR-GFP ku70- allele2	-----	342
DR-GFP ku70-/lig4- allele1	-----	323
DR-GFP ku70-/lig4- allele2	-----	338

Supplementary Figure S3. Multiple-sequence alignment of Lig4 from the WT line and edited alleles. Amino-acid sequences of *Daphnia magna* DNA ligase IV (Lig4) were aligned with Clustal Omega (default settings). From top to bottom the alignment shows: WT, DR-GFP (lig4^{-/-}) allele 1, DR-GFP (lig4^{-/-}) allele 2, DR-GFP (ku70^{-/-}; lig4^{-/-}) allele 1, and DR-GFP (ku70^{-/-}; lig4^{-/-}) allele 2. Residues are color-shaded according to the *D. magna* Lig4 domain boundaries and projected onto all sequences: N-terminal domain (blue), adenylation domain (green), C-terminal OB-fold domain (yellow), and BRCT domains (orange). Asterisks (*) beneath the alignment mark positions with identical residues across all sequences; hyphens (-) denote alignment gaps (including truncations arising from indels). Numbers at the right indicate residue positions in each sequence.

WT	MLFREPCSACEEICLSKRSEKLDRLKLLRECRQRLDDPNLTTYSVMRLLLPHLDRSRA	60
DR-GFP lig4 ⁻ allele1	MLFREPCSACEEICLSKRSEKLDRLKLLRECRQRLDDPNLTTYSVMRLLLPHLDRSRA	60
DR-GFP lig4 ⁻ allele2	MLFREPCSACEEICLSKRSEKLDRLKLLRECRQRLDDPNLTTYSVMRLLLPHLDRSRA	60
DR-GFP ku70 ⁻ /lig4 ⁻ allele1	MLFREPCSACEEICLSKRSEKLDRLKLLRECRQRLDDPNLTTYSVMRLLLPHLDRSRA	60
DR-GFP ku70 ⁻ /lig4 ⁻ allele2	MLFREPCSACEEICLSKRSEKLDRLKLLRECRQRLDDPNLTTYSVMRLLLPHLDRSRA	60
WT	SYGIKEASLAKLYIKIFCLPKDGPDAIRLLTYKVPKTTQTAKDFADICYNILTRCSSD	120
DR-GFP lig4 ⁻ allele1	SYGIKEASLAKLYIKIFCLPKDGPDAIRLLTYKVPKTTQTAKDFADICYNILTRCSSD	120
DR-GFP lig4 ⁻ allele2	SYGIKEASLAKLYIKIFCLPKDGPDAIRLLTYKVPKTTQTAKDFADICYNILTRCSSD	120
DR-GFP ku70 ⁻ /lig4 ⁻ allele1	SYGIKEASLAKLYIKIFCLPKDGPDAIRLLTYKVPKTTQTAKDFADICYNILTRCSSD	120
DR-GFP ku70 ⁻ /lig4 ⁻ allele2	SYGIKEASLAKLYIKIFCLPKDGPDAIRLLTYKVPKTTQTAKDFADICYNILTRCSSD	120
WT	VSSLVSEINQYLENLSKTYMSKKLENTEKLLQPLMKLPALQKWLIRIILRDVKLTGL	180
DR-GFP lig4 ⁻ allele1	VSSLVSEINQYLENLSKTYMSKKLENTEKLLQPLMKLPALQKWLIRIILRDVKLTGL	180
DR-GFP lig4 ⁻ allele2	VSSLVSEINQYLENLSKTYMSKKLENTEKLLQPLMKLPALQKWLIRIILRDVKLTGL	180
DR-GFP ku70 ⁻ /lig4 ⁻ allele1	VSSLVSEINQYLENLSKTYMSKKLENTEKLLQPLMKLPALQKWLIRIILRDVKLTGL	180
DR-GFP ku70 ⁻ /lig4 ⁻ allele2	VSSLVSEINQYLENLSKTYMSKKLENTEKLLQPLMKLPALQKWLIRIILRDVKLTGL	180
WT	SDKIVLSAYHPDAKELYDVSNDLEKVCITLLNPLSRSEIEISLFNPFPRMLADRLMSK	240
DR-GFP lig4 ⁻ allele1	SDKIVLSAYHPDAKELYDVSNDLEKVCITLLNPLSRSEIEISLFNPFPRMLADRLMSK	240
DR-GFP lig4 ⁻ allele2	SDKIVLSAYHPDAKELYDVSNDLEKVCITLLNPLSRSEIEISLFNPFPRMLADRLMSK	240
DR-GFP ku70 ⁻ /lig4 ⁻ allele1	SDKIVLSAYHPDAKELYDVSNDLEKVCITLLNPLSRSEIEISLFNPFPRMLADRLMSK	240
DR-GFP ku70 ⁻ /lig4 ⁻ allele2	SDKIVLSAYHPDAKELYDVSNDLEKVCITLLNPLSRSEIEISLFNPFPRMLADRLMSK	240
WT	IFAKMGNKPFYVETKIDGERMQIHSGKRYGYSSRRGFDYTSNFGTSSSSGNLSPRLEEC	300
DR-GFP lig4 ⁻ allele1	IFAKMGNKPFYVETKIDGERMQIHSGKRYGYSSRRGFDYTSNFGTSSSSGNLSPR---	297
DR-GFP lig4 ⁻ allele2	IFAKMGNKPFYVETKIDGERMQIHSGKRYGYSSRRGFDYTSNFGTSSSSGNLSPRGS--	298
DR-GFP ku70 ⁻ /lig4 ⁻ allele1	IFAKMGNKPFYVETKIDGERMQIHSGKRYGYSSRRGFDYTSNFGTSSSSGNLSPRGNAS	300
DR-GFP ku70 ⁻ /lig4 ⁻ allele2	IFAKMGNKPFYVETKIDGERMQIHSGKRYGYSSRRGFDYTSNFGTSSSSGNLSPRGNLS	300
WT	FRETVTSCIIDGEMVAVNVKGSFIVSKGENIDVKSISSTGELIPCFVAFDILLNGEVL	360
DR-GFP lig4 ⁻ allele1	-RGMLF-----	302
DR-GFP lig4 ⁻ allele2	-RGMLF-----	303
DR-GFP ku70 ⁻ /lig4 ⁻ allele1	VKL-----	303
DR-GFP ku70 ⁻ /lig4 ⁻ allele2	SRGMLF-----	306
WT	NLPYKERLKLLESVAVKIKESVIQFPNRKLVTTKMEVTNLLNDAIDQREGIVLKNPDSIY	420
DR-GFP lig4 ⁻ allele1	-----	302
DR-GFP lig4 ⁻ allele2	-----	303
DR-GFP ku70 ⁻ /lig4 ⁻ allele1	-----	303
DR-GFP ku70 ⁻ /lig4 ⁻ allele2	-----	306
WT	KPNERKGGWFKVPEYVNMMDHLDLIILGGYHGQGRRNLIAMFLVGAVFSLKEKEEQ	480
DR-GFP lig4 ⁻ allele1	-----	302
DR-GFP lig4 ⁻ allele2	-----	303
DR-GFP ku70 ⁻ /lig4 ⁻ allele1	-----	303
DR-GFP ku70 ⁻ /lig4 ⁻ allele2	-----	306
WT	LEFYSFARVSGSGFSDKQLASLLEKLNPHWQKWDKNAPPPKIHCSREKPDVWINPSSSAIL	540
DR-GFP lig4 ⁻ allele1	-----	302
DR-GFP lig4 ⁻ allele2	-----	303
DR-GFP ku70 ⁻ /lig4 ⁻ allele1	-----	303
DR-GFP ku70 ⁻ /lig4 ⁻ allele2	-----	306
WT	EIKASEIISNSYKAGSTLRFPRVERVEDPAWYSCMTFSEINEMRKMASGKLVTRHCSF	600
DR-GFP lig4 ⁻ allele1	-----	302
DR-GFP lig4 ⁻ allele2	-----	303
DR-GFP ku70 ⁻ /lig4 ⁻ allele1	-----	303
DR-GFP ku70 ⁻ /lig4 ⁻ allele2	-----	306
WT	QDDIPSGKRIKTASVIAGVATPFQAADISDVKRSSNCFSDEKICVLNGSSSFTKQELERS	660
DR-GFP lig4 ⁻ allele1	-----	302
DR-GFP lig4 ⁻ allele2	-----	303
DR-GFP ku70 ⁻ /lig4 ⁻ allele1	-----	303
DR-GFP ku70 ⁻ /lig4 ⁻ allele2	-----	306
WT	VVSGGQVVVQHPTSTFCIIAAKDDIRVKSLEKAPKWDIVCPAWLLRCLNMLRILPFRPQ	720
DR-GFP lig4 ⁻ allele1	-----	302
DR-GFP lig4 ⁻ allele2	-----	303
DR-GFP ku70 ⁻ /lig4 ⁻ allele1	-----	303
DR-GFP ku70 ⁻ /lig4 ⁻ allele2	-----	306
WT	DLVVVTQATKEILAQNFDAPGNSLREATSVEDVGPIQQVKDLENPVPLSVYEIADLEYE	780
DR-GFP lig4 ⁻ allele1	-----	302
DR-GFP lig4 ⁻ allele2	-----	303
DR-GFP ku70 ⁻ /lig4 ⁻ allele1	-----	303
DR-GFP ku70 ⁻ /lig4 ⁻ allele2	-----	306
WT	IFGKLHKYGFIRTCIVYVDVWETISDFNSLIISRELRIISLDLRIYGAQVLNMDHVSHT	840
DR-GFP lig4 ⁻ allele1	-----	302
DR-GFP lig4 ⁻ allele2	-----	303
DR-GFP ku70 ⁻ /lig4 ⁻ allele1	-----	303
DR-GFP ku70 ⁻ /lig4 ⁻ allele2	-----	306
WT	VVCDPVAYPHRAMWKSINRQQEVFKLVPEWIAHSITQGNLLDEIYCP	891
DR-GFP lig4 ⁻ allele1	-----	302
DR-GFP lig4 ⁻ allele2	-----	303
DR-GFP ku70 ⁻ /lig4 ⁻ allele1	-----	303
DR-GFP ku70 ⁻ /lig4 ⁻ allele2	-----	306