

Mitotic and meiotic functions for the SUMOylation pathway in the *Caenorhabditis elegans* germline

Reichman Rachel*, Shi Zhuoyue*, Malone Robert* and Smolikove Sarit*[†]

Supplementary tables

Number of nuclei in PMT	N2	<i>ubc-9</i>	<i>smo-1</i>	<i>ubc-9; mre-11(iow1)</i>	<i>mre-11(iow1)</i>	<i>ubc-9;spo-11</i>	<i>spo-11</i>
N2	X						
<i>ubc-9</i>	0.0191	X					
<i>smo-1</i>	0.0006	0.1049	X				
<i>ubc-9; mre-11(iow1)</i>	<0.0001	0.004	0.1376	X			
<i>mre-11(iow1)</i>	0.123	0.4999	0.1375	0.0156	X		
<i>ubc-9;spo-11</i>	<0.0001	0.0142	0.3451	0.5352	0.033	X	
<i>spo-11</i>	0.0965	<0.0001	<0.0001	<0.0001	0.0026	<0.0001	X
Number of nuclei in gonad before diplotene	N2	<i>ubc-9</i>	<i>smo-1</i>	<i>ubc-9; mre-11(iow1)</i>	<i>mre-11(iow1)</i>	<i>ubc-9;spo-11</i>	<i>spo-11</i>
N2	X						
<i>ubc-9</i>	0.0357	X					
<i>smo-1</i>	0.1	>0.9999	X				
<i>ubc-9; mre-11(iow1)</i>	0.1	0.1429	0.4	X			
<i>mre-11(iow1)</i>	>0.9999	0.0357	0.1	0.1	X		
<i>ubc-9;spo-11</i>	0.1	0.1607	0.7	0.1	0.1	X	
<i>spo-11</i>	0.1	0.0357	0.1	0.1	0.4	0.1	X

Table S1: Pairwise comparisons of number of nuclei in the PMT and number of nuclei in the gonad prior to diplotene. The number of nuclei in the PMT and the number of nuclei in the germline from PMT through late pachytene were counted. Significance was determined through Mann-Whitney analysis. Significant p-values < 0.05 are in blue text, non-significant values are in red text.

Gonad Length	N2	<i>ubc-9</i>	<i>smo-1</i>	<i>ubc-9;</i> <i>mre-11(iow1)</i>	<i>mre-11(iow1)</i>	<i>ubc-9;spo-11</i>	<i>spo-11</i>
N2	X						
<i>ubc-9</i>	<0.0001	X					
<i>smo-1</i>	<0.0001	0.4716	X				
<i>ubc-9; mre-11(iow1)</i>	<0.0001	0.0089	<0.0001	X			
<i>mre-11(iow1)</i>	0.123	<0.0001	<0.0001	0.0089	X		
<i>ubc-9;spo-11</i>	<0.0001	0.0089	0.0048	<0.0001	<0.0001	X	
<i>spo-11</i>	0.0005	0.0039	<0.0001	0.9118	0.0355	<0.0001	X
Gonad Width (PMT)	N2	<i>ubc-9</i>	<i>smo-1</i>	<i>ubc-9;</i> <i>mre-11(iow1)</i>	<i>mre-11(iow1)</i>	<i>ubc-9;spo-11</i>	<i>spo-11</i>
N2	X						
<i>ubc-9</i>	0.0021	X					
<i>smo-1</i>	0.3119	0.0059	X				
<i>ubc-9; mre-11(iow1)</i>	0.0853	0.05	0.741	X			
<i>mre-11(iow1)</i>	0.4359	0.0115	0.7088	0.6976	X		
<i>ubc-9;spo-11</i>	0.0065	0.0853	0.0372	0.2398	0.0177	X	
<i>spo-11</i>	0.0784	0.0276	0.5992	0.795	0.7034	0.0452	X
Gonad Width (MLP)	N2	<i>ubc-9</i>	<i>smo-1</i>	<i>ubc-9;</i> <i>mre-11(iow1)</i>	<i>mre-11(iow1)</i>	<i>ubc-9;spo-11</i>	<i>spo-11</i>
N2	X						
<i>ubc-9</i>	0.0002	X					
<i>smo-1</i>	<0.0001	0.0001	X				
<i>ubc-9; mre-11(iow1)</i>	0.0024	0.2475	<0.0001	X			
<i>mre-11(iow1)</i>	0.0045	0.0066	<0.0001	0.3054	X		

<i>abc-9;spo-11</i>	<0.0001	0.1903	0.0031	0.0021	0.0001	X	
<i>spo-11</i>	0.001	0.219	<0.0001	0.8585	0.2419	0.0133	X

Table S2: Pairwise comparisons of gonad length and width measurements. The length of the gonad from PMT to diplotene, width at the midpoint of the PMT, and width at mid-pachytene were measured. Significance of gonad measurements were determined through Mann-Whitney analysis. Significant p-values < 0.05 are in blue text, non-significant values are in red text.

PMT	N2	<i>ubc-9</i>	<i>smo-1</i>	<i>ubc-9;mre-11(iow1)</i>	<i>mre-11(iow1)</i>	<i>ubc-9;spo-11</i>	<i>spo-11</i>	<i>mre-11(ok179)</i>
N2	X							
<i>ubc-9</i>	<0.0001	X						
<i>smo-1</i>	<0.0001	0.0038	X					
<i>ubc-9;mre-11(iow1)</i>	<0.0001	0.1083	<0.0001	X				
<i>mre-11(iow1)</i>	<0.0001	<0.0001	<0.0001	<0.0001	X			
<i>ubc-9;spo-11</i>	<0.0001	0.1083	0.2478	0.005	<0.0001	X		
<i>spo-11</i>	0.7791	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	X	
<i>Mre-11(ok179)</i>	<0.0001	<0.0001	<0.0001	<0.0001	0.5559	<0.0001	<0.0001	X
TZ	N2	<i>ubc-9</i>	<i>smo-1</i>	<i>ubc-9;mre-11(iow1)</i>	<i>mre-11(iow1)</i>	<i>ubc-9;spo-11</i>	<i>spo-11</i>	<i>mre-11(ok179)</i>
N2	X							
<i>ubc-9</i>	<0.0001	X						
<i>smo-1</i>	<0.0001	0.5971	X					
<i>ubc-9;mre-11(iow1)</i>	<0.0001	0.0071	0.062	X				
<i>mre-11(iow1)</i>	0.4544	<0.0001	<0.0001	<0.0001	X			
<i>ubc-9;spo-11</i>	<0.0001	0.0017	0.0235	0.465	<0.0001	X		
<i>spo-11</i>	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	X	
<i>Mre-11(ok179)</i>	0.404	<0.0001	<0.0001	<0.0001	0.9384	<0.0001	<0.0001	X
EP	N2	<i>ubc-9</i>	<i>smo-1</i>	<i>ubc-9;mre-11(iow1)</i>	<i>mre-11(iow1)</i>	<i>ubc-9;spo-11</i>	<i>spo-11</i>	<i>mre-11(ok179)</i>

N2	X							
<i>ubc-9</i>	<0.0001	X						
<i>smo-1</i>	<0.0001	<0.0001	X					
<i>ubc-9;mre-11(iow1)</i>	0.102	<0.0001	<0.0001	X				
<i>mre-11(iow1)</i>	<0.0001	<0.0001	<0.0001	<0.0001	X			
<i>ubc-9;spo-11</i>	0.0003	<0.0001	<0.0001	0.0235	<0.0001	X		
<i>spo-11</i>	<0.0001	<0.0001	<0.0001	<0.0001	0.0008	<0.0001	X	
<i>Mre-11(ok179)</i>	<0.0001	<0.0001	<0.0001	<0.0001	0.0015	0.0004	<0.0001	X
MLP	N2	<i>ubc-9</i>	<i>smo-1</i>	<i>ubc-9;mre-11(iow1)</i>	<i>mre-11(iow1)</i>	<i>ubc-9;spo-11</i>	<i>spo-11</i>	<i>mre-11(ok179)</i>
N2	X							
<i>ubc-9</i>	0.3338	X						
<i>smo-1</i>	0.2895	0.7853	X					
<i>ubc-9;mre-11(iow1)</i>	<0.0001	<0.0001	<0.0001	X				
<i>mre-11(iow1)</i>	<0.0001	<0.0001	<0.0001	<0.0001	X			
<i>ubc-9;spo-11</i>	<0.0001	<0.0001	<0.0001	<0.0001	0.3719	X		
<i>spo-11</i>	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	X	
<i>Mre-11(ok179)</i>	<0.0001	<0.0001	<0.0001	<0.0001	0.0036	0.0006	<0.0001	X

Table S3: Pairwise significance for PMT, TZ, EP, and MLP RAD-51 focus counts (clustered). Mann-Whitney analysis was performed on raw data for each pairwise comparison. n-values were at least 200 nuclei per genotype. Significant p-values are in blue text and non-significant p-values are in red text.

PMT	N2	ubc-9	smo-1	ubc-9;iow1	iow1	ubc-9;spo-11	spo-11	ok179
N2	X							
ubc-9	<0.0001	X						
smo-1	<0.0001	0.0001	X					
ubc-9;iow1	<0.0001	0.391	0.0022	X				
iow1	<0.0001	<0.0001	<0.0001	<0.0001	X			
ubc-9;spo-11	<0.0001	0.0236	0.1415	0.1333	<0.0001	X		
spo-11	0.7991	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	X	
ok179	<0.0001	<0.0001	<0.0001	<0.0001	0.8264	<0.0001	<0.0001	X
TZ	N2	ubc-9	smo-1	ubc-9;iow1	iow1	ubc-9;spo-11	spo-11	ok179
N2	X							
ubc-9	<0.0001	X						
smo-1	<0.0001	0.064	X					
ubc-9;iow1	<0.0001	0.0005	0.1875	X				
iow1	0.5765	<0.0001	<0.0001	<0.0001	X			
ubc-9;spo-11	<0.0001	0.0016	0.183	0.8378	<0.0001	X		
spo-11	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	X	
ok179	0.7759	<0.0001	<0.0001	<0.0001	0.7979	<0.0001	<0.0001	X
EP	N2	ubc-9	smo-1	ubc-9;iow1	iow1	ubc-9;spo-11	spo-11	ok179
N2	X							
ubc-9	<0.0001	X						
smo-1	<0.0001	<0.0001	X					

ubc-9;iow1	0.1858	<0.0001	<0.0001	X				
iow1	<0.0001	<0.0001	<0.0001	<0.0001	X			
ubc-9;spo-11	0.0054	<0.0001	<0.0001	0.1178	<0.0001	X		
spo-11	<0.0001	<0.0001	<0.0001	<0.0001	0.0007	<0.0001	X	
ok179	<0.0001	<0.0001	<0.0001	<0.0001	0.0003	0.0012	<0.0001	X
MLP	N2	ubc-9	smo-1	ubc-9;iow1	iow1	ubc-9;spo-11	spo-11	ok179
N2	X							
ubc-9	0.3279	X						
smo-1	0.2694	0.0001	X					
ubc-9;iow1	<0.0001	<0.0001	<0.0001	X				
iow1	<0.0001	<0.0001	<0.0001	<0.0001	X			
ubc-9;spo-11	<0.0001	<0.0001	<0.0001	<0.0001	0.338	X		
spo-11	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	X	
ok179	<0.0001	<0.0001	<0.0001	<0.0001	0.0241	0.004	<0.0001	X

Table S4: Pairwise significance for PMT, TZ, EP, and MLP RAD-51 focus counts (individual). Mann-Whitney analysis was performed on raw data for each pairwise comparison. n-values were at least 200 nuclei per genotype. Significant p-values are in blue text and non-significant p-values are in red text.

singlet	N2	<i>ubc-9</i>	<i>smo-1</i>	<i>ubc-9;mre-11(iow1)</i>	<i>mre-11(iow1)</i>	<i>ubc-9;spo-11</i>	<i>spo-11</i>
N2	X						
<i>ubc-9</i>	<0.0001	X					
<i>smo-1</i>	<0.0001	<0.0001	X				
<i>ubc-9;mre-11(iow1)</i>	<0.0001	<0.0001	<0.0001	X			
<i>mre-11(iow1)</i>	<0.0001	<0.0001	<0.0001	<0.0001	X		
<i>ubc-9;spo-11</i>	<0.0001	<0.0001	<0.0001	0.185	<0.0001	X	
<i>spo-11</i>	<0.0001	<0.0001	<0.0001	<0.0001	0.2918	<0.0001	X
doublet	N2	<i>ubc-9</i>	<i>smo-1</i>	<i>ubc-9;mre-11(iow1)</i>	<i>mre-11(iow1)</i>	<i>ubc-9;spo-11</i>	<i>spo-11</i>
N2	X						
<i>ubc-9</i>	<0.0001	X					
<i>smo-1</i>	<0.0001	0.0003	X				
<i>ubc-9;mre-11(iow1)</i>	<0.0001	<0.0001	0.0306	X			
<i>mre-11(iow1)</i>	<0.0001	0.0087	0.0243	0.008	X		
<i>ubc-9;spo-11</i>	<0.0001	<0.0001	<0.0001	<0.0001	0.0091	X	
<i>spo-11</i>	X	X	X	X	X	X	X
triplet	N2	<i>ubc-9</i>	<i>smo-1</i>	<i>ubc-9;mre-11(iow1)</i>	<i>mre-11(iow1)</i>	<i>ubc-9;spo-11</i>	<i>spo-11</i>
N2	X						
<i>ubc-9</i>	<0.0001	X					
<i>smo-1</i>	<0.0001	0.2313	X				

<i>ubc-9;mre-11(iow1)</i>	<0.0001	0.3629	0.4088	X			
<i>mre-11(iow1)</i>	<0.0001	0.386077	0.34426957	0.5790305	X		
<i>ubc-9;spo-11</i>	<0.0001	0.0302	0.0037	0.0078	0.3618	X	
<i>spo-11</i>	X	X	X	X	X	x	X
quadruplet	N2	<i>ubc-9</i>	<i>smo-1</i>	<i>ubc-9;mre-11(iow1)</i>	<i>mre-11(iow1)</i>	<i>ubc-9;spo-11</i>	<i>spo-11</i>
N2	X						
<i>ubc-9</i>	0.061156	X					
<i>smo-1</i>	0.128205	0.478107	X				
<i>ubc-9;mre-11(iow1)</i>	0.15151	1	0.678571	X			
<i>mre-11(iow1)</i>	0.2222222	0.999999	0.999999	1	X		
<i>ubc-9;spo-11</i>	0.02424	0.493292	0.249999	1	1	X	
<i>spo-11</i>	X	X	X	X	X	X	X
strings	N2	<i>ubc-9</i>	<i>smo-1</i>	<i>ubc-9;mre-11(iow1)</i>	<i>mre-11(iow1)</i>	<i>ubc-9;spo-11</i>	<i>spo-11</i>
N2	X						
<i>ubc-9</i>	0.24615	X					
<i>smo-1</i>	0.382352	0.2145856	X				
<i>ubc-9;mre-11(iow1)</i>	1	0.834458	0.3763996	X			
<i>mre-11(iow1)</i>	0.666666	0.869988	0.637981	0.8951	X		
<i>ubc-9;spo-</i>	0.0047619	0.0184907	0.01165	0.01612358	0.0496685	X	

<i>11</i>							
<i>spo-11</i>	1	1	1	1	1	1	X

Table S5: Pairwise comparison of typical and atypical RAD-51 foci in different germline stages. Pairwise comparison of genotypes for typical and atypical RAD-51 foci. Chi-squared analysis was used for singlets, doublets, and triplets. Fisher's exact test with the Freeman-Halton extension was used for *mre-11(iow1)* comparisons for triplets, as well as all quadruplet and string comparisons due to low sample size of these atypical RAD-51 structures.

Germline stage	P-value
PMT	0.52
TZ	0.32
EP	0.93
LP	0.25

Table S6: Statistical analysis of RAD-51 strings upon IR exposure. There were no significant differences in number of strings observed in any stage of the germline (wild type or *ubc-9* mutant) upon exposure to IR.

LARVAL	<i>+/nT1</i>	<i>ubc-9/nT1</i>	<i>mre-11(ok179)/nT1</i>	<i>ubc-9; mre-11(ok179)/nT1</i>	<i>rad-50/nT1</i>	<i>ubc-9;rad-50/nT1</i>
<i>+/nT1</i>	X					
<i>ubc-9/nT1</i>	0.0012	X				
<i>mre-11(ok179)/nT1</i>	0.0006	0.9397	X			
<i>ubc-9; mre-11(ok179)/nT1</i>	>0.0001	0.2391	0.2764	X		
<i>rad-50/nT1</i>	1	0.0272	0.021	0.0024	X	
<i>ubc-9;rad-50/nT1</i>	0.13266	0.4201	0.3653	0.0805	0.254446	X
ADULT	<i>+/nT1</i>	<i>ubc-9/nT1</i>	<i>mre-11(ok179)/nT1</i>	<i>ubc-9; mre-11(ok179)/nT1</i>	<i>rad-50/nT1</i>	<i>ubc-9;rad-50/nT1</i>
<i>+/nT1</i>	X					
<i>ubc-9/nT1</i>	>0.0001	X				
<i>mre-11(ok179)/nT1</i>	0.0053	0.0131	X			
<i>ubc-9; mre-11(ok179)/nT1</i>	>0.0001	0.02	>0.0001	X		
<i>rad-50/nT1</i>	0.791147	0.0004	0.1119	>0.0001	X	
<i>ubc-9;rad-50/nT1</i>	0.012927	0.2707	0.5156	0.0045	0.064139	X

Table S7: Pairwise comparison of GFP negative offspring from balanced hermaphrodites. Fisher's exact test was performed on each pair of genotypes. Significant p-values < 0.05 are in blue text, non-significant values are in red text.

	N2	<i>ubc-9</i>	<i>smo-1</i>	<i>ubc-9; mre-11(iow1)</i>	<i>mre-11(iow1)</i>	<i>ubc-9;spo-11</i>	<i>spo-11</i>	<i>mre-11(ok179)</i>
N2	X							
<i>ubc-9</i>	0.0174	X						
<i>smo-1</i>	0.1744	0.4269	X					
<i>ubc-9;mre-11(iow1)</i>	>0.0001	0.0121	0.0009	X				
<i>mre-11(iow1)</i>	0.0017	>0.0001	0.0001	>0.0001	X			
<i>ubc-9;spo-11</i>	0.7486	0.0941	0.4171	> 0.0001	0.0061	X		
<i>spo-11</i>	0.4485	0.0033	0.05	>0.0001	0.0199	0.3574	X	
<i>mre-11(ok179)</i>	>0.0001	0.0032	0.0001	1	>0.0001	>0.0001	>0.0001	X

Table S8: Pairwise comparison of S-phase PMT nuclei. Cells positive for PCN-1 were counted; significance was determined through Fisher's exact test. Significant p-values < 0.05 are in blue text, non-significant values are in red text.

	N2	<i>ubc-9</i>	<i>smo-1</i>	<i>ubc-9; mre-11(iow1)</i>	<i>mre-11(iow1)</i>	<i>ubc-9;spo-11</i>	<i>spo-11</i>	<i>mre-11(ok179)</i>
N2	X							
<i>ubc-9</i>	0.0003	X						
<i>smo-1</i>	>0.0001	0.0001	X					
<i>ubc-9;mre-11(iow1)</i>	>0.0001	0.3779	0.0033	X				
<i>mre-11(iow1)</i>	0.3893	0.0534	>0.0001	0.0011	X			
<i>ubc-9;spo-11</i>	>0.0001	0.4188	0.0128	0.0002	1	X		
<i>spo-11</i>	0.0409	0.0388	>0.0001	0.001	0.3777	0.0053	X	
<i>mre-11(ok179)</i>	0.0096	0.2433	>0.0001	0.0252	0.0798	0.0638	0.3015	X

Table S9: Pairwise comparison of M-phase PMT nuclei. Cells positive for PH3 were counted; significance was determined through Fisher's exact test. Significant p-values < 0.05 are in blue text, non-significant values are in red text.

	<i>ubc-9(tm2610)</i>	N2	p-Value
Average:	5.77	5.82	0.84

Table S10: GFP::*COSA-1* statistics in wild type and *ubc-9* mutants. GFP::*COSA-1* foci were counted. Averages are displayed and Mann-Whitney p-value is not significant.

Chromosome	non-recombinant chromosomes	recombinant chromosomes	Double recombinant chromosomes	map distance (cM)	Chi-square p-value:
II					
Wild Type	36	42	1	33.4	0.001
<i>abc-9(tm2610)/+</i>	31	29	13	50.3	
I					
Wild Type	54	21	4	20.44	0.0139
<i>abc-9(tm2610)/+</i>	43	43	7	37.78	

Table S11: Chi-squared analysis of recombination frequencies from wild type and *abc-9* heterozygotes.

Recombination frequencies were used to determine map distance (equation can be found in materials and methods). Chi-squared analysis was used to determine significance.

# nuclei in gonad	N2	<i>ubc-9</i>	<i>smo-1</i>	<i>ubc-9;</i> <i>mre-11(iow1)</i>	<i>mre-11(iow1)</i>	<i>ubc-9;spo-11</i>	<i>spo-11</i>
N2	X						
<i>ubc-9</i>	>0.0001	X					
<i>smo-1</i>	0.0527	>0.0001	X				
<i>ubc-9; mre-11(iow1)</i>	>0.0001	0.384	>0.0001	X			
<i>mre-11(iow1)</i>	1	>0.0001	0.0483	>0.0001	X		
<i>ubc-9;spo-11</i>	>0.0001	0.5701	>0.0001	0.093	>0.0001	X	
<i>spo-11</i>	1	>0.0001	0.073	>0.0001	1	>0.0001	X

Table S12: Pairwise comparison of diakinesis EMO nuclei. EMO nuclei and total nuclei were counted in all genotypes listed. Significance was determined through Fisher's exact test. Significant p-values < 0.05 are in blue text, non-significant values are in red text.

0hr	N2	ok	ubc-9
N2	X		
ok	0.0653	X	
ubc-9	<0.0001	<0.0001	X
2hr	N2	ok	ubc-9
N2	X		
ok	<0.0001	X	
ubc-9	0.4328	0.0024	X
4hr	N2	ok	ubc-9
N2	X		
ok	0.7526	X	
ubc-9	0.0011	<0.0001	X
6hr	N2	ok	ubc-9
N2	X		
ok	0.1775	X	
ubc-9	<0.0001	<0.0001	X
8hr	N2	ok	ubc-9
N2	X		
ok	<0.0001	X	
ubc-9	<0.0001	<0.0001	X

Table S13: CPT pair-wise comparisons between genotypes at each time point. N2 is wild type, ok is *mre-11(ok179)*, and ubc-9 is the *ubc-9(tm2610)* strain. All comparisons were performed using the Mann-Whitney test.

N2	0	2	4	6	8
0	x				
2	<0.0001	x			
4	<0.0001	0.0702	x		
6	<0.0001	<0.0001	<0.0001	x	
8	<0.0001	<0.0001	<0.0001	<0.0001	x
ok179	0	2	4	6	8
0	x				
2	<0.0001	x			
4	<0.0001	<0.0001	x		
6	<0.0001	<0.0001	<0.0001	x	
8	<0.0001	<0.0001	<0.0001	<0.0001	x
ubc-9	0	2	4	6	8
0	x				
2	<0.0001	x			
4	<0.0001	<0.0001	x		
6	<0.0001	<0.0001	0.4397	x	
8	<0.0001	<0.0001	0.0003	0.0026	x

Table S14: CPT pair-wise comparisons within a genotype at each time point. N2 is wild type, ok is *mre-11(ok179)*, and ubc-9 is the *ubc-9(tm2610)* strain. All comparisons were performed using the Mann-Whitney test.

0hr	N2	ok	ubc-9
N2	X		
ok	<0.0001	X	
ubc-9	<0.0001	0.4438	X
2hr	N2	ok	ubc-9
N2	X		
ok	<0.0001	X	
ubc-9	<0.0001	<0.0001	X
4hr	N2	ok	ubc-9
N2	X		
ok	<0.0001	X	
ubc-9	<0.0001	<0.0001	X
6hr	N2	ok	ubc-9
N2	X		
ok	<0.0001	X	
ubc-9	<0.0001	0.02	X
8hr	N2	ok	ubc-9
N2	X		
ok	<0.0001	X	
ubc-9	<0.0001	0.0275	X

Table S15: HU pair-wise comparisons between genotypes at each time point. N2 is wild type, ok is *mre-11(ok179)*, and ubc-9 is the *ubc-9(tm2610)* strain. All comparisons were performed using the Mann-Whitney test.

N2	0	2	4	6	8
0	X				
2	<0.0001	X			
4	<0.0001	<0.0001	X		
6	<0.0001	0.6458	<0.0001	X	
8	<0.0001	<0.0001	<0.0001	<0.0001	X
ok	0	2	4	6	8
0	X				
2	0.0022	X			
4	0.485	<0.0001	X		
6	0.0034	<0.0001	0.0188	X	
8	<0.0001	<0.0001	<0.0001	0.0002	X
ubc-9	0	2	4	6	8
0	X				
2	<0.0001	X			
4	<0.0001	<0.0001	X		
6	<0.0001	0.0112	<0.0001	X	
8	<0.0001	0.0002	0.2321	<0.0001	X

Table S16: HU pair-wise comparisons within a genotype at each time point. N2 is wild type, ok is *mre-11(ok179)*, and ubc-9 is the *ubc-9(tm2610)* strain. All comparisons were performed using the Mann-Whitney test.