SUPPORTING INFORMATION FIGURE LEGENDS

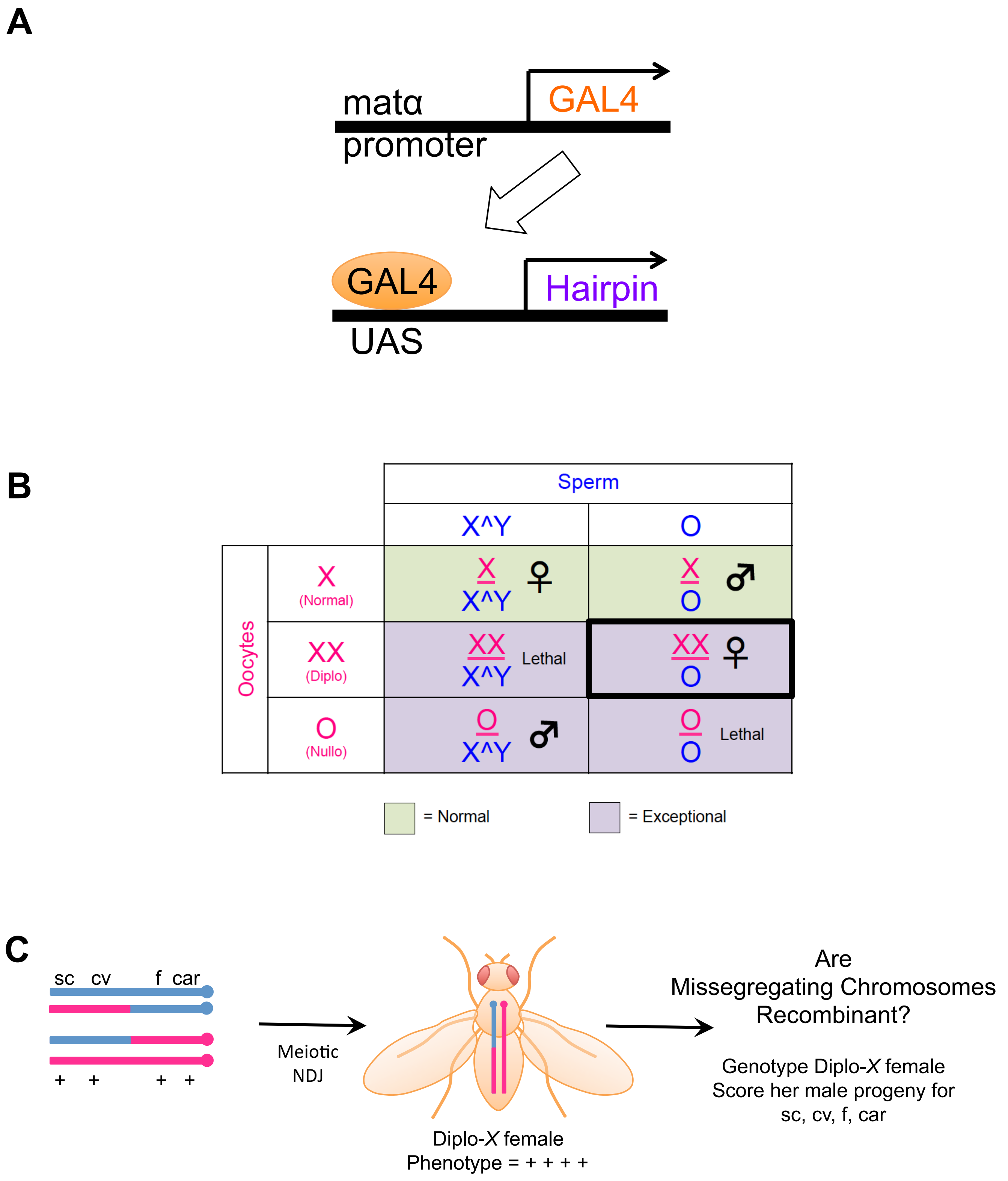
Figure S1. Genetic tools used to induce SOD KD in mid-prophase I, to assay the effect on NDJ, and to assay the frequency of recombinant chromosome missegregation. (A) The matα driver results in GAL4-VP16 expression in the female germline where it activates expression of a transgene encoding an RNAi hairpin. (B) Punnett square for the cross scheme used to assay NDJ. Green boxes represent progeny arising from normal chromosome segregation and purple boxes indicate progeny that arise from NDJ. Sex of viable progeny is indicated. The thick lined black box denotes the Diplo-*X* females collected for recombination history analysis. (C) Schematic illustrating the recombinational history assay. In this example, a bivalent with a single crossover missegregates resulting in a Diplo-*X* female that inherits one recombinant and one non-recombinant homolog. Her genotype is determined by scoring her male progeny for *X* chromosome markers.

Figure S2. SOD1 and SOD2 hairpins used in this study and immunoblots that show the change in SOD protein levels and oxidative damage induced by SOD KD. (A) Hairpins used to knock down SOD1 and SOD2 are diagramed with nucleotides they target in parentheses. Superscripts indicate the vector used for each hairpin. (B) Representative immunoblots using ovary extracts from control and SOD KD genotypes used for the experiments shown in Figure 2. The SOD signal was normalized to tubulin, and mean SOD protein levels relative to the control are indicated below each lane (mean calculated from two repetitions). (C) Representative membrane with total protein (left) and anti-DNP immunoblot (right) on which oxidatively damaged proteins are detected in ovary extracts from $SOD1^{V20}$ KD and control genotypes. The DNP signal was normalized to total protein, and mean DNP levels relative to the control are indicated below each lane ($P < 0.05$, T-test, $n = 3$). Note that the maximum intensity pixel on the anti-DNP blot has a signal level of 47,574 that is well below the saturation value (65,536) of the 16-bit camera used to capture the image.

Figure S3. Percentage of oocytes for which the specified number of FISH arm spots was detected. For each KD genotype and its respective control in the indicated genetic background, the FISH data from Fig. 3C and Table S6 is presented as the distribution of oocytes containing the specified number of arm spots

Figure S4. *X* chromosome crossover frequency and distribution in SOD KD and control *mtrm*$^{+/-}$ oocytes. (A) Diagram shows the relative positions of visible markers along the *X* chromosome that were used to measure recombination. The centromere is represented by a filled in oval and the thicker black line depicts heterochromatin. (B-C) Meiotic crossovers were measured within three intervals: *sc-cv, cv-f,* and *f-car* in control and KD oocytes for SOD1^{V20} (B) and SOD2^{V20} (C). Genotypes correspond to those in Tables S2 and S3 respectively.

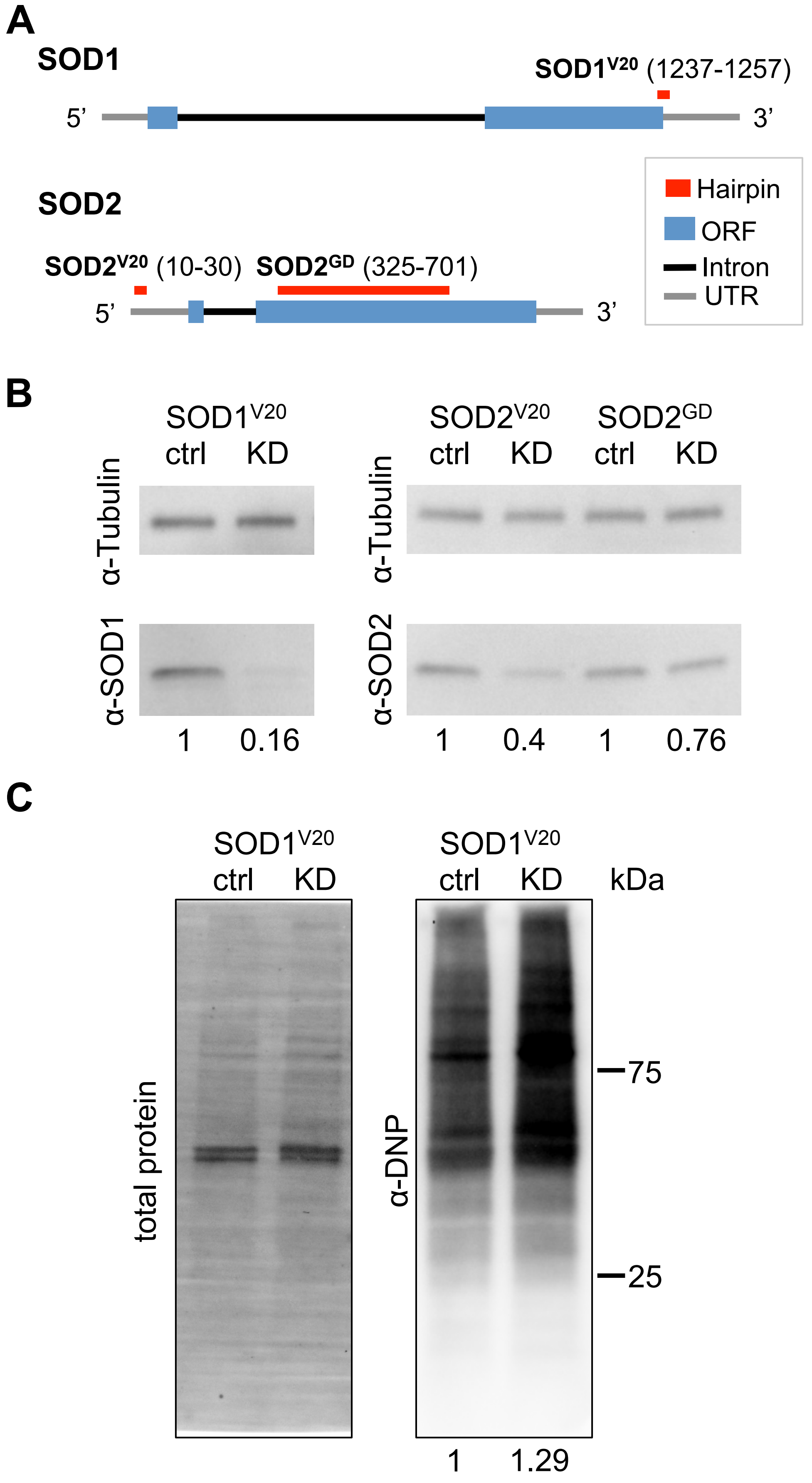
Perkins *et al.* Figure S1

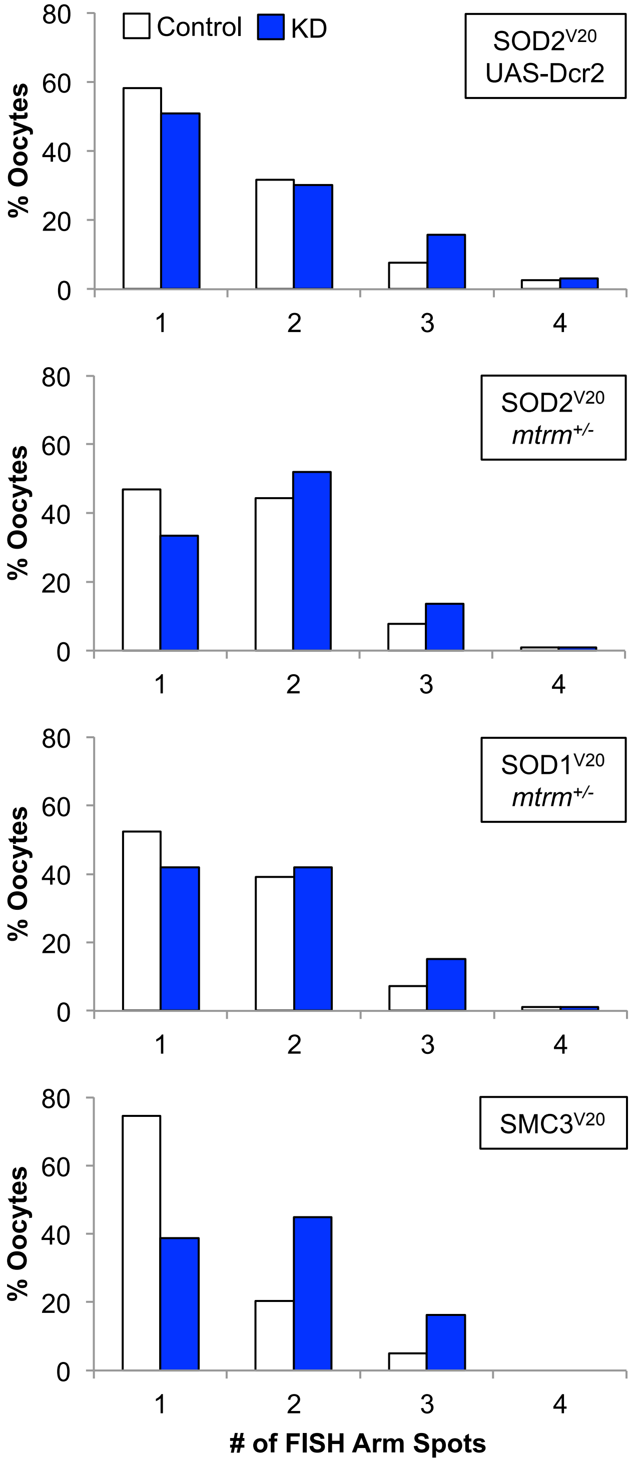


		Sperm	
		X^Y	O
Oocytes	X (Normal)	🟩 X / X^Y ♀	🟩 X / O ♂
	XX (Diplo)	🟪 XX / X^Y Lethal	🟪 **XX / O ♀**
	O (Nullo)	🟪 O / X^Y ♂	🟪 O / O Lethal

🟩 = Normal 🟪 = Exceptional

Perkins *et al.* Figure S2





80
60
40
20
0
% Oocytes
Control
KD
SOD2V20
UAS-Dcr2
SOD2V20
mtrm+/-
SOD1V20
mtrm+/-
SMC3V20
1
2
3
4
# of FISH Arm Spots

A

B

Genotype	n	***X* Chromosome** Crossover Distribution			Map Distance
		sc-cv	*cv-f*	*f-car*	(cM)
SOD1^{V20} Ctrl	597	11.9	37.7	6.7	56.3
SOD1^{V20} KD	810	9.9	42.0	7.4	59.3

C

Genotype	n	***X* Chromosome** Crossover Distribution			Map Distance
		sc-cv	*cv-f*	*f-car*	(cM)
SOD2^{V20} Ctrl	902	13.2	38.9	9.4	61.5
SOD2^{V20} KD	1054	9.7	37.8	6.9	54.4

Table S1: NDJ Results for SOD1 and SOD2 KD

A

Genotype	Stocks (Hairpin)	% NDJ	% Diplo (#)	% Nullo (#)	n	P-value
Control y sc v/y ; cn bw sp/+ ; P{UAS-**SOD1RNAi**^{V20}, y^{+} v^{+}}/+	I-454, H-072 (SH00934.N)	0	0	0	1217	0.001
Knockdown w P{UAS-Dcr2, w^{+}}/y sc v ; + ; P{matalpha-GAL4-VP16, w^{+}}/ P{UAS-**SOD1RNAi**^{V20}, y^{+} v^{+}}	T-712, H-072 (SH00934.N)	1.28	0.81 (7)	0.46 (4)	1714	

B

Control w P{UAS-Dcr2, w^{+}}/y ; cn bw sp/+ ; P{UAS-**SOD2RNAi**^{V20}, y^{+} v^{+}}/+	I-454, V-062, H-028 (SH00930.N)	0	0	0	895	0.008
Knockdown w P{UAS-Dcr2, w^{+}}/w ; + ; P{matalpha-GAL4-VP16, w^{+}}/ P{UAS-**SOD2RNAi**^{V20}, y^{+} v^{+}}	T-273, V-062, H-028 (SH00930.N)	1.44	0.41 (2)	1.03 (5)	962	

C

Control w P{UAS-Dcr2, w^{+}}/y ; P{UAS-**SOD2RNAi**^{GD}, w^{+}}/cn bw sp	I-454, V-061, V-036 (14064)	0.15	0.15 (1)	0	1302	0.008
Knockdown w P{UAS-Dcr2, w^{+}}/w ; P{UAS-**SOD2RNAi**^{GD}, w^{+}}/+ ; P{matalpha-GAL4-VP16, w^{+}}/+	T-273, V-061, V-036 (14064)	1.70	1.13 (6)	0.57 (3)	1049	

Stocks refers to the Bickel Lab stock used to generate the genotype listed, see Table S8 for full descriptions.
Hairpin refers to the TRiP or VDRC collection hairpin ID.
# indicates number of progeny recovered in this category.
n equals total number of progeny scored.
P-value calculated as described in (72).

Table S2: NDJ Results for SOD1^{V20} KD in *mtrm*$^{+/-}$

Experiment #1	**Stocks (Hairpin)**	**% NDJ**	**% Diplo (#)**	**% Nullo (#)**	**n**	**P-value§**
Control y sc cv v f car/y ; + ; mtrm^{KG} ry/ P{UAS-SOD1RNAi^{V20}, y$^+$ v$^+$}	M-835, I-513 (SH00934.N)	1.51	0.93 (8)	0.58 (5)	1714	<0.001
Knockdown y sc cv v f car/y ; + ; P{matalpha-GAL4-VP16, w$^+$} mtrm^{KG} ry/ P{UAS-SOD1RNAi^{V20}, y$^+$ v$^+$}	M-834, I-513 (SH00934.N)	8.18	5.69 (48)	2.49 (21)	1619	

Experiment #2						
Control y sc cv v f car/y ; + ; mtrm^{KG} ry/ P{UAS-SOD1RNAi^{V20}, y$^+$ v$^+$}	M-836, I-513 (SH00934.N)	3.09	2.40 (21)	0.69 (6)	1723	<0.001
Knockdown y sc cv v f car/y ; + ; P{matalpha-GAL4-VP16, w$^+$} mtrm^{KG} ry/ P{UAS-SOD1RNAi^{V20}, y$^+$ v$^+$}	M-834, I-513 (SH00934.N)	7.13	4.40 (37)	2.73 (23)	1622	

Mean	**Hairpin**	**% NDJ**	**P-value¶**
Control y sc cv v f car/y ; + ; mtrm^{KG} ry/ P{UAS-SOD1RNAi^{V20}, y$^+$ v$^+$}	SH00934.N	2.30	0.030
Knockdown y sc cv v f car/y ; + ; P{matalpha-GAL4-VP16, w$^+$} mtrm^{KG} ry/ P{UAS-SOD1RNAi^{V20}, y$^+$ v$^+$}	SH00934.N	7.66	

Stocks refers to the Bickel Lab stock used to generate the genotype listed, see Table S8 for full descriptions.
Hairpin refers to the TRiP collection hairpin ID.
# indicates number of progeny recovered in this category.
n equals total number of progeny scored.
§ P-value calculated as described in (72).
¶ P-value calculated using a T-test, n = 2.

Table S3: NDJ Results for SOD2^{V20} KD in *mtrm*$^{+/-}$

Experiment #1	Stocks (Hairpin)	% NDJ	% Diplo (#)	% Nullo (#)	n	P-value§
Control y sc cv v f car/y ; + ; mtrm^{KG} ry/ P{UAS-SOD2RNAi^{V20}, y$^+$ v$^+$}	M-836, I-515 (SH00930.N)	1.68	0.91 (7)	0.78 (6)	1533	<0.001
Knockdown y sc cv v f car/y ; + ; P{matalpha-GAL4-VP16, w$^+$} mtrm^{KG} ry/ P{UAS-SOD2RNAi^{V20}, y$^+$ v$^+$}	M-834, I-515 (SH00930.N)	7.12	5.69 (24)	1.42 (6)	813	

Experiment #2						
Control y sc cv v f car/y ; + ; mtrm^{KG} ry/ P{UAS-SOD2RNAi^{V20}, y$^+$ v$^+$}	M-835, I-515 (SH00930.N)	3.56	2.16 (20)	1.4 (13)	1823	<0.001
Knockdown y sc cv v f car/y ; + ; P{matalpha-GAL4-VP16, w$^+$} mtrm^{KG} ry/ P{UAS-SOD2RNAi^{V20}, y$^+$ v$^+$}	M-834, I-515 (SH00930.N)	7.99	5.11 (46)	2.89 (26)	1730	

Mean	Hairpin	% NDJ	P-value¶
Control y sc cv v f car/y ; + ; mtrm^{KG} ry/ P{UAS-SOD2RNAi^{V20}, y$^+$ v$^+$}	SH00930.N	2.62	0.041
Knockdown y sc cv v f car/y ; + ; P{matalpha-GAL4-VP16, w$^+$} mtrm^{KG} ry/ P{UAS-SOD2RNAi^{V20}, y$^+$ v$^+$}	SH00930.N	7.56	

Stocks refers to the Bickel Lab stock used to generate the genotype listed, see Table S8 for full descriptions.
Hairpin refers to the TRiP collection hairpin ID.
# indicates number of progeny recovered in this category.
n equals total number of progeny scored.
§ P-value calculated as described in (72).
¶ P-value calculated using a T-test, n = 2.

Table S4: NDJ Results for SOD2^{GD} KD in *mtrm*$^{+/-}$

Experiment #1	**Stocks (Hairpin)**	**% NDJ**	**% Diplo (#)**	**% Nullo (#)**	**n**	**P-value**§
Control y sc cv v f car/y ; P{UAS-SOD2RNAi^{GD}, w+}/+ ; mtrm^{KG} ry/+	M-836, I-514 (14064)	2.85	1.43 (13)	1.43 (13)	1798	<0.001
Knockdown y sc cv v f car/y ; ; P{UAS-SOD2RNAi^{GD}, w^{+}}/+ ; P{matalpha-GAL4-VP16, w^{+}} mtrm^{KG} ry/+	M-834, I-514 (14064)	6.87	5.05 (47)	1.83 (17)	1799	

Experiment #2						
Control y sc cv v f car/y ; P{UAS-SOD2RNAi^{GD}, w+}/+ ; mtrm^{KG} ry/+	M-835, I-514 (14064)	1.95	1.58 (17)	0.37 (4)	2128	<0.001
Knockdown y sc cv v f car/y ; ; P{UAS-SOD2RNAi^{GD}, w^{+}}/+ ; P{matalpha-GAL4-VP16, w^{+}} mtrm^{KG} ry/+	M-834, I-514 (14064)	7.03	4.16 (45)	2.87 (31)	2085	

Mean	**Hairpin**	**% NDJ**	**P-value**¶
Control y sc cv v f car/y ; P{UAS-SOD2RNAi^{GD}, w+}/+ ; mtrm^{KG} ry/+	14064	2.40	0.010
Knockdown y sc cv v f car/y ; P{UAS-SOD2RNAi^{GD}, w^{+}}/+ ; P{matalpha-GAL4-VP16, w^{+}} mtrm^{KG} ry/+	14064	6.95	

Stocks refers to the Bickel Lab stock used to generate the genotype listed, see Table S8 for full descriptions.
Hairpin refers to the VDRC collection hairpin ID.
# indicates number of progeny recovered in this category.
n equals total number of progeny scored.
§ P-value calculated as described in (72).
¶ P-value calculated using a T-test, n = 2.

Table S5: NDJ Results for SOD2^{GD} KD in *smc1Δ/+*

Genotype	**Stocks (Hairpin)**	**% NDJ**	**% Diplo (#)**	**% Nullo (#)**	**n**	**P-value**
smc1Δ w, P{UAS-Dcr2, w$^+$}/y ; P{UAS-SOD2RNAi^{GD}, w$^+$}/+ ; smc1Δ/+	T-733, I-540 (14064)	0.09	0.09 (1)	0	2311	0.582 <0.001
Control w, P{UAS-Dcr2, w$^+$}/y ; P{UAS-SOD2RNAi^{GD}, w$^+$}/+ ; +	T-733, I-514 (14064)	0.17	0.08 (1)	0.08 (1)	2393	0.024
SOD2^{GD} KD w, P{UAS-Dcr2, w$^+$}/y ; P{UAS-SOD2RNAi^{GD}, w$^+$}/+ ; P{matα-GAL4-VP16, w$^+$}/+	T-712 I-514 (14064)	0.89	0.30 (3)	0.59 (6)	2024	0.009
SOD2^{GD} KD, smc1Δ w, P{UAS-Dcr2, w$^+$}/y ; P{UAS-SOD2RNAi^{GD}, w$^+$}/+ ; P{matα-GAL4-VP16, w$^+$}/smc1Δ	T-712, I-540 (14064)	2.23	1.19 (15)	1.03 (13)	2485	

Stocks refers to the Bickel Lab stock used to generate the genotype listed, see Table S8 for full descriptions.
Hairpin refers to the TRiP or VDRC collection hairpin ID.
# indicates number of progeny recovered in this category.
n equals total number of progeny scored.
P-value calculated as described in (72).

Table S6: Summary of FISH Data

SOD2^{V20} with UAS-Dcr2	**Experiment 1**		**Experiment 2**		**Sum of Experiments**			
	Control	**KD**	**Control**	**KD**	**Control**	**KD**	**Fold Increase**	**P-value**[§]
N (oocytes scored)	49	40	30	23	79	63		
	% Oocytes with Cohesion Defects (#)							
Arm Defects Only	14.3 (7)	20.0 (8)	3.3 (1)	17.4 (4)	10.1 (8)	19.0 (12)	-	-
Centromere Defects Only	0	0	0	0	0	0	-	-
Both Arm and Centromere Defects	0	0	0	0	0	0	-	-
Total Arm Defects*	14.3 (7)	20.0 (8)	3.3 (1)	17.4 (4)	10.1 (8)	19.0 (12)	1.88	0.150

SOD2^{V20} with *mtrm*$^{+/-}$	**Experiment 1**		**Experiment 2**		**Sum of Experiments**			
	Control	**KD**	**Control**	**KD**	**Control**	**KD**	**Fold Increase**	**P-value**[§]
N (oocytes scored)	44	40	73	56	117	96		
	% Oocytes with Cohesion Defects (#)							
Arm Defects Only	6.8 (3)	10.0 (4)	9.6 (7)	16.1 (9)	8.5 (10)	13.5 (13)	-	-
Centromere Defects Only	0	0	0	1.8 (1)	0	1.0 (1)	-	-
Both Arm and Centromere Defects	0	2.5 (1)	0	0	0	1.0 (1)	-	-
Total Arm Defects*	6.8 (3)	12.5 (5)	9.6 (7)	16.1 (9)	8.5 (10)	14.6 (14)	1.71	0.194

SOD1^{V20} with *mtrm*$^{+/-}$	**Experiment 1**		**Experiment 2**		**Sum of Experiments**			
	Control	**KD**	**Control**	**KD**	**Control**	**KD**	**Fold Increase**	**P-value**[§]
N (oocytes scored)	47	35	35	51	82	86		
	% Oocytes with Cohesion Defects (#)							
Arm Defects Only	4.3 (2)	11.4 (4)	14.3 (5)	17.6 (9)	8.5 (7)	15.1 (13)	-	-
Centromere Defects Only	0	0	2.9 (1)	0	1.2 (1)	0	-	-
Both Arm and Centromere Defects	0	0	0	2.0 (1)	0	1.2 (1)	-	-
Total Arm Defects*	4.3 (2)	11.4 (4)	14.3 (5)	19.6 (10)	8.5 (7)	16.3 (14)	1.91	0.163

SMC3^{V20}	**Experiment 1**			
	Control	**KD**	**Fold Increase**	**P-value**[§]
N (oocytes scored)	59	49		
	% Oocytes with Cohesion Defects (#)			
Arm Defects Only	5.1 (3)	16.3 (8)	-	-
Centromere Defects Only	0	0	-	-
Both Arm and Centromere Defects	0	0	-	-
Total Arm Defects*	5.1 (3)	16.3 (8)	3.21	0.064

Sum of SOD Genotypes	Ctrl	KD	Fold Increase	P-value[§]
N	278	249		
% Oocytes with Cohesion Defects (#)				
Total Arm Defects	9.0 (25)	16.1 (40)	1.79	0.017

* % total arm defects for each genotype graphed in Fig. 3C.

[§] P-value calculated using Fisher's exact test.

Table S7: Recombinational History Data for SOD KD and control in *mtrm*$^{+/-}$

SOD1^{V20}	Experiment 1		Experiment 2		Sum of Experiments		
	Control	KD	Control	KD	Control	KD	**P-value** (χ^2 test)
N (flies scored)	1714	1619	1723	1622	3437	3241	
	Frequency = X/N x 10^3 (X = # of Diplos genotyped)						
Non-recombinant Diplos§	1.2 (2)	5.6 (9)	2.9 (5)§	4.3 (7)	2.0 (7)	4.9 (16)	0.070
All Recombinant Diplos	2.9 (5)	19.1 (31)	5.2 (9)	12.9 (21)	4.1 (14)	16.0 (52)	< 0.001
Recombinant Reductional Diplos	2.9 (5)	17.3 (28)	2.9 (5)	9.9 (16)	2.9 (10)	13.6 (44)	< 0.001
Recombinant Equational Diplos	0	1.9 (3)	2.3 (4)	3.1 (5)	1.2 (4)	2.5 (8)	0.333

SOD2^{V20}	Experiment 1		Experiment 2		Sum of Experiments		
	Control	KD	Control	KD	Control	KD	**P-value** (χ^2 test)
N (flies scored)	1533	813	1823	1730	3356	2543	
	Frequency = X/N x 10^3 (X = # of Diplos genotyped)						
Non-recombinant Diplos*	2.0 (3)	4.9 (4)	1.1 (2)	4.0 (7)	1.5 (5)	4.3 (11)	0.069
All Recombinant Diplos	2.0 (3)	17.2 (14)	6.0 (11)	16.2 (28)	4.2 (14)	16.5 (42)	< 0.001
Recombinant Reductional Diplos	1.3 (2)	11.1 (9)	5.5 (10)	13.9 (24)	3.6 (12)	13.0 (33)	< 0.001
Recombinant Equational Diplos	0.7 (1)	6.2 (5)	0.5 (1)	2.3 (4)	0.6 (2)	3.5 (9)	0.022

SOD2^{GD}	Experiment 1		Experiment 2		Sum of Experiments		
	Control	KD	Control	KD	Control	KD	**P-value** (χ^2 test)
N (flies scored)	1798	1799	2128	2085	3926	3884	
	Frequency = X/N x 10^3 (X = # of Diplos genotyped)						
Non-recombinant Diplos*	2.2 (4)	3.9 (7)	1.4 (3)	2.4 (5)	2.0 (8)	3.1 (12)	0.489
All Recombinant Diplos	4.4 (8)	15.0 (27)	6.6 (14)	12.0 (25)	5.6 (22)	13.4 (52)	< 0.001
Recombinant Reductional Diplos	4.4 (8)	14.5 (26)	6.1 (13)	11.5 (24)	5.3 (21)	12.9 (50)	< 0.001
Recombinant Equational Diplos	0	0.6 (1)	0.5 (1)	0.5 (1)	0.3 (1)	0.5 (2)	0.993

§ One non-recombinant Diplo arose from an equational error.

*All non-recombinant Diplos arose from reductional errors.

Table S8: Fly stocks used in this study

Genotype	Hairpin ID	Vector	Abbrevi-ation	Source	Bickel Stock #
y^{1} sc^{1} v^{1}; P{y$^{+t7.7}$ v$^{+t1.8}$=TRiP. **SOD2**.HMS00499}attP2	SH00930.N	Valium 20	SOD2 RNAi^{V20}	TRiP #32496	H-028
y; P{y$^{+t7.7}$ v$^{+t1.8}$=TRiP. **SOD2**.HMS00499}attP2	SH00930.N	Valium 20	SOD2 RNAi^{V20}	Bickel lab derivative of H-028	I-515
y^{1} sc^{1} v^{1}; P{y$^{+t7.7}$ v$^{+t1.8}$=TRiP. **SOD1**.HMS00698}attP2 / TM3 Sb^{1}	SH00934.N	Valium 20	SOD1 RNAi^{V20}	TRiP #32909	H-072
y; P{y$^{+t7.7}$ v$^{+t1.8}$=TRiP. **SOD1**.HMS00698}attP2 / TM3 Sb^{1}	SH00934.N	Valium 20	SOD1 RNAi^{V20}	Bickel lab derivative of H-072	I-513
w ; P{VDRC.**SOD2**.42162, w^{+}}	14064	GD	SOD2 RNAi^{GD}	VDRC #42162	V-036
y ; P{VDRC.**SOD2**.42162, w^{+}}	14064	GD	SOD2 RNAi^{GD}	Bickel lab derivative of V-036	I-514
y^{1} sc^{1} v^{1} ; P{y$^{+t7.7}$ v$^{+t1.8}$=TRiP. **SMC3**.HMS00318}attP2	SH00137.N	Valium 20		TRiP #33431	H-010
y ; P{y$^{+t7.7}$ v$^{+t1.8}$=TRiP. **SMC3**.HMS00318}attP2	SH00137.N	Valium 20	SMC3 RNAi^{V20}	Bickel lab derivative of H-010	I-520
y w ; smc1^{exc46} / TM3, Sb^{1} Ser^{1}			smc1Δ	Hawley Lab	M-720
y ; P{VDRC.**SOD2**.42162, w^{+}} ; smc1^{exc46} / TM3, Ser^{1}	14064	GD		Bickel Lab derivative of I-514, M-720	I-540
y/y^{+}Y ; cn bw sp					I-454
y^{1} Df(1)w^{67c23}			y w		A-062
y^{1} ; + ; P{SUPor-P, y$^{+mDint2}$ w$^{BR.E.BR}$}mtrm^{KG08051} ry^{506}/TM3, Sb^{1} Ser^{1}			mtrm^{KG}	Bloomington #14932	M-755
y w / B^{S} Y ; + ; mtrm^{KG}/TM3, Sb^{1} Ser^{1}				Bickel lab derivative of M-755	W-086

y sc cv v f car/B^S Y ; + ; $mtrm^{KG}$/TM3, Sb^1 Ser^1 Maintained as FM7a balanced stock				Bickel lab derivative of W-086	M-835
y sc cv v f car/B^S Y ; + ; $mtrm^{KG}$/TM3, Sb^1 Ser^1 Maintained with C(1)DX, y w f/B^SY females				Bickel lab derivative of W-086	M-836
w^* ; P{w^{+mC}=matalpha4-GAL4-VP16}V37			matα driver	Bloomington #7063	T-273
y w ; + ; P{w^{+mC}=matalpha4-GAL4-VP16}V37				Bickel lab derivative of T-273	W-063
y w / B^S Y ; + ; $mtrm^{KG}$ P{w^{+mC}=matalpha4-GAL4-VP16}V37/TM3, Sb				Bickel lab derivative of W-086, & T-273	W-076
y sc cv v f car/B^SY ; + ; $mtrm^{KG}$ P{w^{+mC}=matalpha4-GAL4-VP16}V37 /TM3, Sb^1 Ser^1 Maintained as FM7a balanced stock				Bickel lab derivative of W-076	M-834
y sc cv v f car/B^S Y Maintained with C(1)DX, y w f/B^SY females					A-192
y sc cv v f car/B^S Y ; P{w^{+mC}=matalpha4-GAL4-VP16}V37 Maintained as FM7a balanced stock				Bickel lab derivative of T-712	A-199
C(1)RM, y^2, su(w^a) w^a/ X^Y,v f B			*X^Y, v f B*		C-200
w^{1118}, P{UAS-Dicer-2, w^+}				VDRC #60007	V-058
w^{1118}, P{UAS-Dicer-2, w^+} / B^SY				Bickel lab derivative of V-058	T-733
w^{1118}, P{UAS-Dicer-2, w^+} ; Pin/CyO				VDRC #60010	V-061
w^{1118}, P{UAS-Dicer-2, w^+} ; + ; Ly/ TM3				VDRC #60011	V-062
w^{1118}, P{UAS-Dicer-2, w^+}/B^S Y; P{w^{+mC}=matalpha4-GAL4-VP16}V37				Bickel lab derivative of T-273 & V-062	T-712