

TABLE S1
Statistical analysis of gene targeting parameters

Males		----- p values -----		
Genotypes		%Yielders	%ry	%HR
M1 : M2	wt vs. <i>spnA</i> ^{+/-}	0.81	0.623	0.14
M1 : M3	“	0.19	0.126	0.40
M1 : M4	wt vs. <i>spnA</i> ^{-/-}	0.69	0.024	9 x 10 ⁻⁶
M1 : M5	“	0.028	0.51	0.00064
M1 : M6	“	0.00042	0.222	0.00059
M1 : M7	wt L vs. C	0.76	0.118	0.30
M1 : M12	wt L2 vs. L3	1.0	0.017	0.67
M7 : M8	wt vs. <i>spnA</i> ^{+/-} C	0.094	0.00025	0.013
M7 : M9	“	0.50	0.381	0.22
M7 : M10	wt vs. <i>spnA</i> ^{-/-} C	0.010	0.011	3 x 10 ⁻⁵
M7 : M11	“	0.53	0.261	3 x 10 ⁻⁵
M12 : M13	wt vs. <i>okr</i> ^{+/-}	0.21	0.614	0.010
M12 : M14	wt vs. <i>okr</i> ^{-/-}	0.47	0.194	0.071
M1 : M15	wt vs. <i>lig4</i>	1.6 x 10 ⁻⁵	0.000425	7 x 10 ⁻¹¹
M1 : M16	wt vs. <i>lig4 spnA</i> ^{-/-}	0.0019	0.219	0.028
M7 : M17	wt vs. <i>lig4</i> C	0.0056	7.7 x 10 ⁻⁸	0.019
M7 : M18	wt vs. <i>lig4 spnA</i> ^{-/-} C	0.00087	0.38	0.0025
M15 : M16	<i>lig4</i> vs. <i>lig4 spnA</i> ^{-/-}	0.83	0.0016	9.5 x 10 ⁻¹⁴
M17 : M18	<i>lig4</i> vs. <i>lig4 spnA</i> ^{-/-} C	1.0	0.00048	4.4 x 10 ⁻⁷
M5 : M10	<i>spnA</i> ^{-/-} L vs. C	0.84	0.061	0.060
M6 : M11	“	0.011	0.439	0.0031
M15 : M17	<i>lig4</i> L vs. C	0.83	0.278	0.0043
M16 : M18	<i>lig4 spnA</i> ^{-/-} L vs. C	1.0	0.487	0.014

Females		----- p values -----		
Genotypes		%Yielders	%ry	%HR
F1 : F2	wt vs. <i>spnA</i> ^{+/-}	0.68	0.8	0.19
F1 : F3	“	0.026	0.223	1.0
F1 : F6	wt vs. <i>spnA</i> ^{-/-}	8 x 10 ⁻⁹	0.485	5 x 10 ⁻⁸
F1 : F7	wt L vs. C	0.62	0.731	0.32
F1 : F12	wt L2 vs. L3	0.84	0.588	0.0040
F7 : F8	wt vs. <i>spnA</i> ^{+/-} C	0.14	0.0623	0.033
F7 : F9	“	1.0	0.587	0.14

F7 : F11	wt vs. <i>spnA</i> ^{-/-} C	0.00026	0.95	4 x 10 ⁻⁷
F1 : F19	wt vs. <i>lig4</i> ^{+/-}	0.69	0.0923	0.025
F1 : F20	wt vs. <i>lig4</i> ^{-/-}	0.012	0.00046	8 x 10 ⁻²⁵
F7 : F21	wt vs. <i>lig4</i> ^{-/-} C	0.0053	0.00395	4 x 10 ⁻⁵
F20 : F21	<i>lig4</i> ^{-/-} L vs. C	0.86	0.803	6.5 x 10 ⁻⁸
F19 : F20	<i>lig4</i> ^{-/-} L vs. <i>lig4</i> ^{+/-}	0.0042	6.7 x 10 ⁻⁶	9.4 x 10 ⁻¹¹

Males vs. Females		----- p values -----		
Genotypes		%Yielders	%ry	%HR
M1 : F1	wt L	0.54	0.191	0.035
M2 : F2	<i>spnA</i> ^{+/-}	1.0	0.158	0.15
M3 : F3	“	0.0035	9.6 x 10 ⁻⁹	0.046
M6 : F6	<i>spnA</i> ^{-/-}	0.00042	0.49	0.11
M7 : F7	wt C	0.72	0.524	0.22
M8 : F8	<i>spnA</i> ^{+/-} C	1.2 x 10 ⁻⁵	1.2 x 10 ⁻¹⁰	0.024
M11 : F11	<i>spnA</i> ^{-/-} C	0.0027	0.825	1.0
M12 : F12	wt AB3	0.46	0.0274	4.6 x 10 ⁻⁶
M13 : F13	<i>okr</i> ^{+/-}	0.30	2.52 x 10 ⁻⁵	1.0
M15 : F20	<i>lig4</i>	0.63	0.394	1.9 x 10 ⁻¹²
M17 : F21	<i>lig4</i> C	0.63	0.089	0.0030

Genotypes are as in Table 2, with M indicating males and F indicating females of specified class. %Yielders, %ry and %HR have the same meanings as in Table 2 of the main text. L denotes linear donor, C denotes circular donor. As stated in the main text, p values were calculated with Fisher's exact test for %Yielders and %HR, and with the glm function of the R software package for %ry.