

**Supplemental Table S3. *Paxx*<sup>-/-</sup> *Xlf*<sup>-/-</sup> embryos start dying after E14.5.**

Embryos were genotyped by PCR analysis of DNA extracted from the yolk sacks. Day of vaginal plug was considered E0.5. Expected values represent the combined Mendelian percentages and numbers from several crosses involving different parental genotypes of the *Paxx/Xlf* mice at E10.5 (A) and E18.5 (B). The significant values of observed and expected genotype frequencies were calculated using the  $\chi^2$  and the representative data was graphed in Figure 3.

**A E14.5**

Genotype		% Expected	% Observed	# Expected	# Observed
<i>Paxx</i> <sup>+/+</sup>	<i>Xlf</i> <sup>+/+</sup>	0	0	0	0
	<i>Xlf</i> <sup>+/-</sup>	12	3	4	1
	<i>Xlf</i> <sup>-/-</sup>	16	13	5	4
<i>Paxx</i> <sup>+/-</sup>	<i>Xlf</i> <sup>+/+</sup>	0	0	0	0
	<i>Xlf</i> <sup>+/-</sup>	12	17	4	5
	<i>Xlf</i> <sup>-/-</sup>	38	43	11	13
<i>Paxx</i> <sup>-/-</sup>	<i>Xlf</i> <sup>+/+</sup>	0	0	0	0
	<i>Xlf</i> <sup>+/-</sup>	6	7	2	2
	<i>Xlf</i> <sup>-/-</sup>	16	17	5	5
<b>TOTAL</b>		<b>100</b>	<b>100</b>	<b>30</b>	<b>30</b>

**B E18.5**

Genotype		% Expected	% Observed	# Expected	# Observed
<i>Paxx</i> <sup>-/-</sup>	<i>Xlf</i> <sup>+/+</sup>	25	38	6	9
	<i>Xlf</i> <sup>+/-</sup>	50	50	12	12
	<i>Xlf</i> <sup>-/-</sup>	25	13	6	3(2)
<b>TOTAL</b>		<b>100</b>	<b>100</b>	<b>24</b>	<b>24</b>