

Supplemental Table S1. *Summary of mice used for liver gene expression profiling.*

	wt	<i>rsl</i>	Rsl1 Tg	Rsl2 Tg
Male	(1) A: (<i>n</i> = 5) B: (<i>n</i> = 5)	(3) A: (<i>n</i> = 5) B: (<i>n</i> = 5)	(5) A: (<i>n</i> = 3) B: (<i>n</i> = 7)	(7) A: (<i>n</i> = 5) B: (<i>n</i> = 5)
	Female	(2) A: (<i>n</i> = 5) B: (<i>n</i> = 5)	(4) A: (<i>n</i> = 5) B: (<i>n</i> = 5)	(6) A: (<i>n</i> = 10) B: (<i>n</i> = 7)

Eight groups of liver RNA were created to identify gene expression patterns that differ by sex (e.g. (1) x (2)) and Rsl status (e.g. (1) x (3), (1) x (5), (1) x (7), etc.). Duplicate pools (A and B) were analyzed and, for the transgenic mice, each pool was derived from a separate transgenic line.