

Supplementary Table 9. Documenting expression of individual members of independently acquired X-linked multicopy and ampliconic gene families in human and mouse

Mouse _Gene Family #	Gene name	# of mRNA-seq reads <sup>20</sup>	Human _Gene Family #	Gene name	# of mRNA-seq reads <sup>20</sup>
1	<i>Arses2</i>	5	1	<i>CSAG1</i>	25
	<i>Arses1</i>	0		<i>CSAG2</i>	21
2	<i>Gm15107</i>	19	2	<i>CT47A1</i>	0
	<i>Gm15093</i>	0		<i>CT47A2</i>	0
	<i>Gm15114</i>	3		<i>CT47A6</i>	0
	<i>Gm15127</i>	9		<i>CT47A7</i>	6
	<i>Gm15080</i>	1			
	<i>Gm10430</i>	13	3	<i>VCX</i>	83
	<i>Gm15097</i>	4		<i>VCX2</i>	234
	<i>Gm15091</i>	7		<i>VCX3A</i>	34
				<i>VCX3B</i>	2
3	<i>Cyp11</i>	731			
	<i>Cyp17</i>	158	4	<i>PAGE2</i>	77
	<i>Cyp18</i>	20		<i>PAGE2B</i>	214
4	<i>Gm5934</i>	4	5	<i>SPANXN1</i>	3
	<i>Gm4297</i>	19		<i>SPANXN2</i>	35
	<i>Gm5935</i>	10		<i>SPANXN3</i>	148
	<i>Gm10230</i>	0		<i>SPANXN4</i>	66
	<i>Gm10486</i>	0		<i>SPANXN5</i>	24
	<i>Gm14632</i>	0			
	<i>Gm14819</i>	0	6	<i>GAGE1</i>	6
	<i>Gm5169</i>	44		<i>GAGE10</i>	15
	<i>Gm1993</i>	74		<i>GAGE12B</i>	0
	<i>Gm5168</i>	22		<i>GAGE12G</i>	0
	<i>Gm2012</i>	35		<i>GAGE12H</i>	0
	<i>Gm2030</i>	11		<i>GAGE12I</i>	0
	<i>Six</i>	5		<i>GAGE12J</i>	12
	<i>Gm14525</i>	5		<i>GAGE13</i>	0
	<i>Gm6121</i>	37		<i>GAGE2A</i>	0
	<i>Gm10487</i>	22		<i>GAGE2B</i>	0
	<i>Gm10488</i>	10		<i>GAGE2C</i>	0
				<i>GAGE2D</i>	0
5	<i>Gm2933</i>	3		<i>GAGE2E</i>	0
	<i>Gm2799</i>	49		<i>GAGE4</i>	0
				<i>GAGE5</i>	0
6	<i>Gm10922</i>	3		<i>GAGE6</i>	0
	<i>Gm10921</i>	38		<i>GAGE8</i>	0
7	<i>Slx1</i>	1511			
	<i>3830403N16Rik</i>	30			
8	<i>Gm6880</i>	95			
	<i>Gm6890</i>	34			

a. The absence of mRNA-seq reads corresponding to a specific member of a gene family does not necessarily imply that that copy is transcriptionally inactive. For example, the absence of mRNA-seq reads corresponding to a specific copy may be due to insufficient read depth or reflect the absence of that gene variant in the genome of the sampled testis.

b. RNA-seq data from Brawand, D. et al. The evolution of gene expression levels in mammalian organs. *Nature* 478, 343-8 (2011).

c. RNA-seq data from Bradley, R.K. et al. Alternative splicing of RNA triplets is often regulated and accelerates proteome evolution. *PLoS Biol* 10, (2012).