

Supplemental Data S2. Pyrosequencing results for X-linked genes in horse chorionic girdle samples.

NO	Gene name	SNP	Ref/Alter alleles	Sample*	SNP genotype	Informative?	Ref% rep1	Alter% rep1	Ref% rep2	Alter% rep2	Ref% Average	Alter% average
1	<i>PDHAI</i>	CUHSNP00032726	C/T	3654	T	Male control	0.90%	99.10%	NA	NA	0.90%	99.10%
1	<i>PDHAI</i>	CUHSNP00032726	C/T	3879	C/T	YES	49.20%	50.80%	52.50%	47.50%	50.85%	49.15%
1	<i>PDHAI</i>	CUHSNP00032726	C/T	4061	C/T	YES	52.70%	47.30%	NA	NA	52.70%	47.30%
1	<i>PDHAI</i>	CUHSNP00032726	C/T	4102	C/T	YES	49.00%	51.00%	52.60%	47.40%	50.80%	49.20%
1	<i>PDHAI</i>	CUHSNP00032726	C/T	4105	C/C	NO	100.00%	0.00%	NA	NA	100.00%	0.00%
1	<i>PDHAI</i>	CUHSNP00032726	C/T	4119	C/T	YES	33.10%	66.90%	36.80%	63.20%	34.95%	65.05%
2	<i>EIF1AX</i>	CUHSNP00035646	G/A	3654	A	Male control	0.00%	100.00%	0.00%	100.00%	0.00%	100.00%
2	<i>EIF1AX</i>	CUHSNP00035646	G/A	3879	G/A	YES	58.40%	41.60%	57.70%	42.30%	58.05%	41.95%
2	<i>EIF1AX</i>	CUHSNP00035646	G/A	4061	G/A	YES	68.40%	31.60%	68.90%	31.10%	68.65%	31.35%
2	<i>EIF1AX</i>	CUHSNP00035646	G/A	4102	G/A	YES	57.80%	42.20%	58.30%	41.70%	58.05%	41.95%
2	<i>EIF1AX</i>	CUHSNP00035646	G/A	4105	G/A	YES	81.30%	18.70%	80.80%	19.20%	81.05%	18.95%
2	<i>EIF1AX</i>	CUHSNP00035646	G/A	4119	A/A	NO	0.00%	100.00%	0.00%	100.00%	0.00%	100.00%
3	<i>ATP6AP2</i>	CUHSNP00015315	T/C	3654	T	Male control	93.70%	6.30%	NA	NA	93.70%	6.30%
3	<i>ATP6AP2</i>	CUHSNP00015315	T/C	3879	T/C	YES	44.60%	55.40%	44.50%	55.50%	44.55%	55.45%
3	<i>ATP6AP2</i>	CUHSNP00015315	T/C	4061	T/C	YES	50.90%	49.10%	NA	NA	50.90%	49.10%
3	<i>ATP6AP2</i>	CUHSNP00015315	T/C	4102	T/T	NO	100.00%	0.00%	92.00%	8.00%	96.00%	4.00%
3	<i>ATP6AP2</i>	CUHSNP00015315	T/C	4105	T/T	NO	95.20%	4.80%	92.00%	8.00%	93.60%	6.40%
3	<i>ATP6AP2</i>	CUHSNP00015315	T/C	4119	T/C	YES	48.50%	51.50%	46.80%	53.20%	47.65%	52.35%
4	<i>RP2</i>	CUHSNP00028003	G/A	3654	A	Male control	0.00%	100.00%	0.00%	100.00%	0.00%	100.00%
4	<i>RP2</i>	CUHSNP00028003	G/A	3879	G/G	NO	100.00%	0.00%	98.00%	0.20%	99.00%	0.10%
4	<i>RP2</i>	CUHSNP00028003	G/A	4061	G/A	YES	59.80%	40.20%	58.10%	41.90%	58.95%	41.05%
4	<i>RP2</i>	CUHSNP00028003	G/A	4102	G/G	NO	100.00%	0.00%	99.70%	0.30%	99.85%	0.15%
4	<i>RP2</i>	CUHSNP00028003	G/A	4105	G/A	YES	77.90%	22.10%	74.60%	25.40%	76.25%	23.75%
4	<i>RP2</i>	CUHSNP00028003	G/A	4119	G/A	YES	62.70%	37.30%	60.70%	39.30%	61.70%	38.30%
5	<i>CLCN5</i>	CUHSNP00149947	G/A	3654	G	Male control	100.00%	0.00%	100.00%	0.00%	100.00%	0.00%
5	<i>CLCN5</i>	CUHSNP00149947	G/A	3879	G/A	YES	48.60%	51.40%	NA	NA	48.60%	51.40%
5	<i>CLCN5</i>	CUHSNP00149947	G/A	4061	G/A	YES	46.10%	53.90%	46.30%	53.70%	46.20%	53.80%
5	<i>CLCN5</i>	CUHSNP00149947	G/A	4102	G/A	YES	50.10%	49.90%	NA	NA	50.10%	49.90%
5	<i>CLCN5</i>	CUHSNP00149947	G/A	4105	A/A	NO	0.00%	100.00%	0.00%	100.00%	0.00%	100.00%
5	<i>CLCN5</i>	CUHSNP00149947	G/A	4119	G/A	YES	59.60%	40.40%	59.90%	40.10%	59.75%	40.25%

NO	Gene name	SNP	Ref/Alter alleles	Sample*	SNP genotype	Informative?	Ref% rep1	Alter% rep1	Ref% rep2	Alter% rep2	Ref% Average	Alter% average
6	<i>HUWE1</i>	CUHSNP00149956	A/G	3654	A	Male control	100.00%	0.00%	NA	NA	100.00%	0.00%
6	<i>HUWE1</i>	CUHSNP00149956	A/G	3879	A/G	YES	47.50%	52.50%	NA	NA	47.50%	52.50%
6	<i>HUWE1</i>	CUHSNP00149956	A/G	4061	A/G	YES	44.80%	55.20%	NA	NA	44.80%	55.20%
6	<i>HUWE1</i>	CUHSNP00149956	A/G	4102	A/G	YES	47.40%	52.60%	NA	NA	47.40%	52.60%
6	<i>HUWE1</i>	CUHSNP00149956	A/G	4105	A/G	YES	24.00%	76.00%	NA	NA	24.00%	76.00%
6	<i>HUWE1</i>	CUHSNP00149956	A/G	4119	A/A	NO	100.00%	0.00%	100.00%	0.00%	100.00%	0.00%
7	<i>RGAG4</i>	CUHSNP00000794	G/A	3654	G	Male control	87.70%	12.30%	91.10%	8.90%	89.40%	10.60%
7	<i>RGAG4</i>	CUHSNP00000794	G/A	3879	G/A	YES	38.00%	62.00%	42.80%	57.20%	40.40%	59.60%
7	<i>RGAG4</i>	CUHSNP00000794	G/A	4061	G/A	YES	42.50%	57.50%	42.50%	57.50%	42.50%	57.50%
7	<i>RGAG4</i>	CUHSNP00000794	G/A	4102	G/A	YES	44.50%	55.50%	51.10%	48.90%	47.80%	52.20%
7	<i>RGAG4</i>	CUHSNP00000794	G/A	4105	G/A	YES	20.20%	79.80%	21.90%	78.10%	21.05%	78.95%
7	<i>RGAG4</i>	CUHSNP00000794	G/A	4119	G/G	NO	96.60%	3.40%	97.40%	2.60%	97.00%	3.00%
8	<i>MAGT1</i>	CUHSNP00082414	C/T	3654	C	Male control	94.70%	5.30%	95.20%	4.80%	94.95%	5.05%
8	<i>MAGT1</i>	CUHSNP00082414	C/T	3879	C/T	YES	46.30%	53.70%	48.00%	52.00%	47.15%	52.85%
8	<i>MAGT1</i>	CUHSNP00082414	C/T	4061	C/T	YES	47.50%	52.50%	49.80%	50.20%	48.65%	51.35%
8	<i>MAGT1</i>	CUHSNP00082414	C/T	4102	C/T	YES	51.10%	48.90%	51.40%	48.60%	51.25%	48.75%
8	<i>MAGT1</i>	CUHSNP00082414	C/T	4105	C/T	YES	23.90%	76.10%	25.50%	74.50%	24.70%	75.30%
8	<i>MAGT1</i>	CUHSNP00082414	C/T	4119	C/T	YES	57.20%	42.80%	57.70%	42.30%	57.45%	42.55%
9	<i>UPF3B</i>	CUHSNP00103214	T/C	3654	T	Male control	98.90%	1.10%	NA	NA	98.90%	1.10%
9	<i>UPF3B</i>	CUHSNP00103214	T/C	3879	T/C	YES	55.40%	44.60%	NA	NA	55.40%	44.60%
9	<i>UPF3B</i>	CUHSNP00103214	T/C	4061	T/C	YES	42.10%	57.90%	NA	NA	42.10%	57.90%
9	<i>UPF3B</i>	CUHSNP00103214	T/C	4102	T/C	YES	52.60%	47.40%	NA	NA	52.60%	47.40%
9	<i>UPF3B</i>	CUHSNP00103214	T/C	4105	T/C	YES	33.20%	66.80%	NA	NA	33.20%	66.80%
9	<i>UPF3B</i>	CUHSNP00103214	T/C	4119	T/C	YES	56.50%	43.50%	NA	NA	56.50%	43.50%
10	<i>GPC3</i>	CUHSNP00010650	G/A	3654	G	Male control	100.00%	0.00%	NA	NA	100.00%	0.00%
10	<i>GPC3</i>	CUHSNP00010650	G/A	3879	G/A	YES	66.40%	33.60%	63.80%	36.20%	65.10%	34.90%
10	<i>GPC3</i>	CUHSNP00010650	G/A	4061	G/A	YES	51.70%	48.30%	49.20%	50.80%	50.45%	49.55%
10	<i>GPC3</i>	CUHSNP00010650	G/A	4102	A/A	NO	0.00%	100.00%	0.00%	100.00%	0.00%	100.00%
10	<i>GPC3</i>	CUHSNP00010650	G/A	4105	G/A	YES	32.30%	67.70%	29.10%	70.90%	30.70%	69.30%
10	<i>GPC3</i>	CUHSNP00010650	G/A	4119	G/G	YES	100.00%	0.00%	100.00%	0.00%	100.00%	0.00%

NO	Gene name	SNP	Ref/Alter alleles	Sample*	SNP genotype	Informative?	Ref% rep1	Alter% rep1	Ref% rep2	Alter% rep2	Ref% Average	Alter% average
11	<i>RBMX</i>	CUHSNP00018344	T/G	3654	T	Male control	100.00%	0.00%	100.00%	0.00%	100.00%	0.00%
11	<i>RBMX</i>	CUHSNP00018344	T/G	3879	T/G	YES	57.70%	42.30%	61.10%	38.90%	59.40%	40.60%
11	<i>RBMX</i>	CUHSNP00018344	T/G	4061	T/G	YES	59.90%	40.10%	62.50%	37.50%	61.20%	38.80%
11	<i>RBMX</i>	CUHSNP00018344	T/G	4102	T/T	NO	100.00%	0.00%	100.00%	0.00%	100.00%	0.00%
11	<i>RBMX</i>	CUHSNP00018344	T/G	4105	T/T	NO	100.00%	0.00%	100.00%	0.00%	100.00%	0.00%
11	<i>RBMX</i>	CUHSNP00018344	T/G	4119	T/G	YES	60.80%	39.20%	60.90%	39.10%	60.85%	39.15%
12	<i>CXorf40A</i>	CUHSNP00070042	T/C	3654	T	Male control	97.70%	2.30%	100.00%	0.00%	98.85%	1.15%
12	<i>CXorf40A</i>	CUHSNP00070042	T/C	3879	T/C	YES	44.40%	55.60%	45.20%	54.80%	44.80%	55.20%
12	<i>CXorf40A</i>	CUHSNP00070042	T/C	4061	T/C	YES	41.40%	58.60%	40.90%	59.10%	41.15%	58.85%
12	<i>CXorf40A</i>	CUHSNP00070042	T/C	4102	C/C	NO	0.00%	100.00%	0.00%	100.00%	0.00%	100.00%
12	<i>CXorf40A</i>	CUHSNP00070042	T/C	4105	T/C	YES	23.30%	76.70%	23.00%	77.00%	23.15%	76.85%
12	<i>CXorf40A</i>	CUHSNP00070042	T/C	4119	T/C	YES	44.70%	55.30%	45.50%	54.50%	45.10%	54.90%
13	<i>NAA10</i>	CUHSNP00040545	A/G	3654	G	Male control	0.00%	100.00%	NA	NA	0.00%	100.00%
13	<i>NAA10</i>	CUHSNP00040545	A/G	3879	A/G	YES	52.70%	47.30%	52.00%	48.00%	52.35%	47.65%
13	<i>NAA10</i>	CUHSNP00040545	A/G	4061	A/G	YES	56.10%	43.90%	51.50%	48.50%	53.80%	46.20%
13	<i>NAA10</i>	CUHSNP00040545	A/G	4102	A/A	NO	93.20%	6.80%	91.50%	8.50%	92.35%	7.65%
13	<i>NAA10</i>	CUHSNP00040545	A/G	4105	A/G	YES	69.90%	30.10%	68.70%	31.30%	69.30%	30.70%
13	<i>NAA10</i>	CUHSNP00040545	A/G	4119	A/G	YES	53.90%	46.10%	53.20%	46.80%	53.55%	46.45%
14	<i>FLNA</i>	CUHSNP00105456	C/T	3654	C	Male control	NA	NA	NA	NA	NA	NA
14	<i>FLNA</i>	CUHSNP00105456	C/T	3879	C/T	YES	57.60%	42.40%	61.30%	38.70%	59.45%	40.55%
14	<i>FLNA</i>	CUHSNP00105456	C/T	4061	C/T	YES	63.50%	36.50%	62.20%	37.80%	62.85%	37.15%
14	<i>FLNA</i>	CUHSNP00105456	C/T	4102	T/T	NO	99.30%	0.70%	100.00%	0.00%	99.65%	0.35%
14	<i>FLNA</i>	CUHSNP00105456	C/T	4105	C/T	YES	80.70%	19.30%	81.80%	18.20%	81.25%	18.75%
14	<i>FLNA</i>	CUHSNP00105456	C/T	4119	C/T	YES	62.90%	37.10%	67.20%	32.80%	65.05%	34.95%

*: Horse 3645 is the male control. 100% monoallelic/maternal expression is expected for X-linked genes outside PAR.

The raw pyrosequencing allele quantification ratios were listed here without background subtraction.