

Supplementary Table 1. Canine phosphatonin and selected vitamin D-related kidney genes - cytochrome P450 family 24 subfamily A polypeptide 1 (CYP24A1), cytochrome P450 family 27 subfamily B polypeptide 1 (CYP27B1), fibroblast growth factor receptor 1 IIIc (FGFR1IIIc), α -klotho (klotho), sodium-phosphate co-transporter 1 (NPT1), NPT2a, NPT2c, parathyroid hormone 1 receptor (PTH1R), vitamin D receptor (VDR), and reference gene zeta polypeptide (YWHAZ).

Gene	Primer (5'-3')	Amplicon length (bp)	Primer concentration (nM)	PCR efficiency (%)	Regression coefficient (R ²)
<i>CYP24A1</i> ¹	F: GAGGCCGCATTGAAGACTTA R: CATTCTTCCGAAGGAGTCCA	102	450:450	94.7	0.98
<i>CYP27B1</i> ¹	F: GAGCTGCAAATGGCTTTGGCTCAG R: CTGTAGGTTGATGCTCCTCTCGGG	123	300:300	89.2	0.99
<i>FGFR1IIIc</i>	F: GTATACGTGCTTGGCGGGTA R: AACGGTCAACCATGCAGAGT	61	300:300	96.9	0.99
<i>Klotho</i>	F: CCTGTGACTTTGCTTGGGGA R: CAGCCCGTCCACCTTAATCA	131	900:900	95.5	0.99
<i>NPT1</i> (<i>SLC17A1</i>)	F: GGCAATCAAGAGCACACACG R: TTCTTCCTTGGGACGCTGAC	135	900:900	98.2	0.99
<i>NPT2a</i> (<i>SLC34A1</i>)	F: CAGGTGGCTAAGGTCATTCAGA R: GGGGTGATGGCTGAAGTGAA	146	300:300	96.5	0.99
<i>NPT2c</i> (<i>SLC34A3</i>)	F: CATCTGCTCCCTGGACATCC R: TCTGCACGAGAACTGTGACC	143	300:300	90.9	0.98
<i>PTH1R</i>	F: TCATCAACATCGTCCGGGTG R: TTGAGCAGCTTCCGGTACTG	91	900:900	95.0	0.99
<i>VDR</i> ¹	F: AGCATCCAAAAGGTCATTGG	92	900:800	95.2	0.97

	R: GCACTTGATTTCAGCAGCAC				
YWHAZ	F: AGCAGAGAGCAAAGTCTTCTATT	101	900:900	91.4	1.00
	R: GACTGATCCACAATCCCTTTCT				

¹(Azarpeykan et al., 2016 b)

Supplementary Table 2. Ovine phosphatonin and selected vitamin D-related kidney genes - cytochrome P450 family 24 subfamily A polypeptide 1 (CYP24A1), cytochrome P450 family 27 subfamily B polypeptide 1 (CYP27B1), fibroblast growth factor receptor 1 IIIc (FGFR1IIIc), α -klotho (klotho), sodium-phosphate co-transporter 1 (NPT1), NPT2a, NPT2c, parathyroid hormone 1 receptor (PTH1R), vitamin D receptor (VDR), and reference gene zeta polypeptide (YWHAZ).

Gene	Primer (5'-3')	Amplicon length (bp)	Primer concentration (nM)	PCR efficiency (%)	Regression coefficient (R ²)
<i>CYP24A1</i> ¹	F: CTGTGATGAGAGAGGCCGCATTGA R: AGCTTCCTCCCCTGCCTTCTT	128	600:600	103.9	0.99
<i>CYP27B1</i> ¹	F: GCAGAGCTTGAGTTGCACAT R: CTTCTCTCAGGCACCAGGAC	119	250:250	102.2	0.92
<i>FGFR1IIIc</i>	F: ACACCACCGACAAAGAGATGG R: TCAGCCATGCAGAGTGATGG	120	900:900	99.3	0.99
<i>Klotho</i>	F: TGTGGAGAATGGCTGGTTTGT R: TACCCAATGACATCCACCCC	129	300:300	96.0	1.00
<i>NPT1</i> (<i>SLC17A1</i>)	F: TCCCAGTGGCAGCTGAATTT R: CTCAGAGCAGTAAGTCGGCC	148	300:300	98.1	1.00
<i>NPT2a</i> (<i>SLC34A1</i>)	F: CACCATGACCCACTGCCTG R: TCCAGGGAGCAGACGAAGAG	149	300:300	98.8	0.99
<i>NPT2c</i> (<i>SLC34A3</i>)	F: CGACATCCTCAAGGTGCTGA R: AATAAGGCTCCGGTTGGTGG	109	300:300	100	0.99
<i>PTH1R</i>	F: CAGTACCGGAAGCTGCTCAA R: TTGCCAGAGAGTCCCTGAGA	111	900:900	98.6	1.00
<i>VDR</i> ¹	F: TCATGCTGCGCTCCAACCAGT R: TGGAACTTGATGAGGGGCTCGAT	140	400:400	93.5	0.98

<i>YWHAZ</i>	F: AGACGGAAGGTGCTGAGAAA R: CGTTTGGGATCAAGAAGTTT	123	300:300	101.7	0.98
--------------	--	-----	---------	-------	------

¹(Azarpeykan et al., 2016 b)

Supplementary Table 3. Equine phosphatonin and selected vitamin D-related kidney genes - cytochrome P450 family 24 subfamily A polypeptide 1 (CYP24A1), cytochrome P450 family 27 subfamily B polypeptide 1 (CYP27B1), fibroblast growth factor receptor 1 IIIc (FGFR1IIIc), α -klotho (klotho), sodium-phosphate co-transporter 1 (NPT1), NPT2a, NPT2c, parathyroid hormone 1 receptor (PTH1R), vitamin D receptor (VDR), and reference gene zeta polypeptide (YWHAZ).

Gene	Primer (5'-3')	Amplicon length (bp)	Primer concentration (nM)	PCR efficiency (%)	Regression coefficient (R ²)
<i>CYP24A1</i> ¹	F:GTGTGATGAAAGAGGCCACATTGA R: CGTTCTGCTGGAGGAGCCCCG	113	350:350 nM	91.6	0.99
<i>CYP27B1</i> ¹	F: CAGAGACATTCATGTGGGTGA R: GCTGGACGAAAAGAATTTGG	117	300:300 nM	93.9	0.98
<i>FGFR1IIIc</i>	F: ACTGCCGGAGTTAATACCAC R: CTTCCAGAACGGTCAACCA	145	300:300	101.7	0.99
<i>Klotho</i>	F: CCCAAGACAGGCTGAGAGTG R: GCCGTGCGATCGTTAAATGA	121	300:300	102.3	0.98
<i>NPT1</i> (<i>SLC17A1</i>)	F: TTGGTCTCCTAGCAGGTCAG R: AGGCATACACAGAAGAGGGC	124	900:900	104.8	0.99
<i>NPT2a</i> (<i>SLC34A1</i>)	F: ATCATCACGGAGCCCTTCAC R: GGAATAGTGGTGGGAGCCTC	149	300:300	99.0	0.99
<i>NPT2c</i> (<i>SLC34A3</i>)	F: CATCTGCTCCCTGGACATCC R: TCTGCACGAGAACTGTGACC	143	900:900	106.4	0.99
<i>PTH1R</i>	F: CCTGCCATCTTCGTGACTGT R: CACTTCTTGTTCCCGGAGCT	89	300:300	96.1	0.98
<i>VDR</i> ¹	F: ACAGCATCCAAAAGGTGGTC	89	500:500	99.9	0.99

	R: TGACTTCAGCAGCACGATCT				
YWHAZ ²	F: TGTTGTAGGAGCCCGTAGGT	95	300:300	93.4	0.99
	R: ATTCTCGAGCCATCTGCTGT				

¹(Azarpeykan et al., 2016 b) ²(Azarpeykan et al., 2016 a)