

**Table S1** Fold change and *p*-value of all differentially expressed transcripts between group PIV and group CON

Gene symbol	Gene description	FC	<i>p</i> -value
<i>Upregulated</i>			
<i>ASPA</i>	aspartoacylase	1.70	0.0281
<i>CXCL9</i>	chemokine (C-X-C motif) ligand 9	1.69	0.0023
<i>ID2</i>	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	1.64	0.0039
<i>LOC102161660</i>	olfactory receptor 7D2-like	1.50	0.0067
<i>HIVEP1</i>	human immunodeficiency virus type I enhancer binding protein 1	1.43	0.0006
<i>LOC100156705</i>	melanoma-associated antigen 8-like	1.42	0.0411
<i>LOC100158167</i>	olfactory receptor 5V1-like	1.41	0.0166
<i>OAS1</i>	2-5-oligoadenylate synthetase 1, 40/46kDa	1.40	0.0114
<i>BCL6</i>	B-cell CLL/lymphoma 6	1.38	0.0197
<i>LOC100621260</i>	phosphatidylcholine transfer protein	1.37	0.0013
<i>SPRY1</i>	sprouty RTK signaling antagonist 1	1.33	0.0124
<i>HTRA4</i>	HtrA serine peptidase 4	1.32	0.0106
<i>LOC100522693</i>	putative olfactory receptor 56B2	1.32	0.0071
<i>LOC102165149</i>	olfactory receptor 51F2-like	1.31	0.0211
<i>LOC100737604</i>	FYVE, RhoGEF and PH domain-containing protein 6	1.31	0.0162
<i>LOC100513557</i>	olfactory receptor 51H1-like	1.30	0.0459
<i>DACT2</i>	dishevelled-binding antagonist of beta-catenin 2	1.30	0.0174
<i>LOC106505929</i>	lysine-specific demethylase 2B-like	1.29	0.0246
<i>LOC100625836</i>	heparan sulfate glucosamine 3-O-sulfotransferase 3A1	1.29	0.0415
<i>AANAT</i>	aralkylamine N-acetyltransferase	1.29	0.0138
<i>GIPC2</i>	GIPC PDZ domain containing family, member 2	1.29	0.0244
<i>PLK3</i>	polo-like kinase 3	1.29	0.0308
<i>LOC100627486</i>	olfactory receptor 4P4-like	1.29	0.0108
<i>ADGRG2</i>	adhesion G protein-coupled receptor G2	1.29	0.0038
<i>MIR221</i>	microRNA mir-221	1.28	0.0362
<i>RND1</i>	Rho family GTPase 1	1.28	0.0292

<i>PQLC2</i>	PQ loop repeat containing 2	1.27	0.0304
<i>LOC106508264</i>	olfactory receptor 52M1-like	1.27	0.0206
<i>SLC13A1</i>	solute carrier family 13 (sodium/sulfate symporter), member 1	1.27	0.0161
<i>LOC100152003</i>	olfactory receptor 2S2-like	1.26	0.0145
<i>LOC100737856</i>	olfactory receptor 51G1	1.26	0.0268
<i>IQSEC2</i>	IQ motif and Sec7 domain 2	1.26	0.0024
<i>JUN</i>	jun proto-oncogene	1.25	0.0128
<i>CHAT</i>	choline O-acetyltransferase	1.25	0.0019
<i>CCDC82</i>	coiled-coil domain containing 82	1.25	0.0238
<i>LOC100513607</i>	tripartite motif-containing protein 60-like	1.25	0.0339
<i>PRKCQ</i>	protein kinase C, theta	1.25	0.0381
<i>LOC100737900</i>	olfactory receptor 51G2	1.25	0.0487
<i>SOX21</i>	SRY (sex determining region Y)-box 21	1.24	0.0125
<i>GPR18</i>	G protein-coupled receptor 18	1.24	0.0088
<i>IL12RB2</i>	interleukin 12 receptor, beta 2	1.24	0.0351
<i>LOC100156296</i>	olfactory receptor 6C6	1.24	0.0240
<i>LOC100514119</i>	olfactory receptor 52R1	1.24	0.0108
<i>BCL9L</i>	B-cell CLL/lymphoma 9-like	1.24	0.0275
<i>SH2D2A</i>	SH2 domain containing 2A	1.23	0.0024
<i>CHRNA9</i>	cholinergic receptor, nicotinic, alpha 9 (neuronal)	1.23	0.0213
<i>TMPRSS4</i>	transmembrane protease, serine 4	1.23	0.0344
<i>C9H11orf71</i>	chromosome 9 open reading frame, human C11orf71	1.23	0.0280
<i>CYLC1</i>	cylicin, basic protein of sperm head cytoskeleton 1	1.23	0.0143
<i>ADGRV1</i>	adhesion G protein-coupled receptor V1	1.23	0.0092
<i>IFIT3</i>	interferon-induced protein with tetratricopeptide repeats 3	1.23	0.0165
<i>NR2E1</i>	nuclear receptor subfamily 2, group E, member 1	1.23	0.0049
<i>TACR2</i>	tachykinin receptor 2	1.23	0.0110
<i>SEPTIN6</i>	septin 6	1.22	0.0136
<i>LOC100512910</i>	olfactory receptor 10G3	1.22	0.0171
<i>DUSP2</i>	dual specificity phosphatase 2	1.22	0.0207
<i>KLHL33</i>	kelch-like family member 33	1.22	0.0368
<i>LRRC18</i>	leucine rich repeat containing 18	1.22	0.0463

<i>TMEM178A</i>	transmembrane protein 178A	1.22	0.0389
<i>FGF14</i>	fibroblast growth factor 14	1.22	0.0317
<i>TMEM163</i>	transmembrane protein 163	1.22	0.0175
<i>GPX2</i>	glutathione peroxidase 2	1.21	0.0181
<i>KLF1</i>	Kruppel-like factor 1 (erythroid)	1.21	0.0376
<i>MIR551A</i>	microRNA mir-551a	1.21	0.0190
<i>KEL</i>	Kell blood group, metallo-endoropeptidase	1.21	0.0444
<i>ZAP70</i>	zeta-chain (TCR) associated protein kinase 70kDa	1.21	0.0492
<i>LOC106504774</i>	centromere protein J-like	1.21	0.0333
<i>KLF3</i>	Kruppel-like factor 3 (basic)	1.21	0.0307
<i>PPP1R16B</i>	protein phosphatase 1, regulatory subunit 16B	1.21	0.0442
<i>LOC100514488</i>	olfactory receptor 3A2	1.21	0.0388
<i>LOC106506271</i>	sodium channel protein type 1 subunit alpha-like	1.21	0.0208
<i>DNAJC5B</i>	DnaJ (Hsp40) homolog, subfamily C, member 5 beta	1.21	0.0044
<i>ZDHHC15</i>	zinc finger, DHHC-type containing 15	1.21	0.0394
<i>GNAT3</i>	guanine nucleotide binding protein, alpha transducing 3	1.21	0.0116
<i>TOX</i>	thymocyte selection-associated high mobility group box	1.21	0.0284
<i>GPR52</i>	G protein-coupled receptor 52	1.21	0.0113
<i>Downregulated</i>			
<i>TRAPPC2</i>	trafficking protein particle complex 2	-1.21	0.0476
<i>LOC102165624</i>	olfactory receptor 2AE1-like	-1.21	0.0150
<i>BASPI</i>	brain abundant, membrane attached signal protein 1	-1.21	0.0368
<i>SLC25A47</i>	solute carrier family 25, member 47	-1.21	0.0397
<i>CRELD2</i>	cysteine-rich with EGF-like domains 2	-1.21	0.0396
<i>OTUB2</i>	OTU deubiquitinase, ubiquitin aldehyde binding 2	-1.21	0.0469
<i>C13H3orf17</i>	chromosome 13 open reading frame, human C3orf17	-1.21	0.0031
<i>UNC119B</i>	unc-119 lipid binding chaperone B	-1.21	0.0293
<i>SLA-7</i>	MHC class I antigen 7	-1.21	0.0321
<i>AEN</i>	apoptosis enhancing nuclease	-1.21	0.0355
<i>NDFIP2</i>	Nedd4 family interacting protein 2	-1.22	0.0091
<i>LOC100522040</i>	glutamate formimidoyltransferase-like	-1.22	0.0249

<i>LOC100518088</i>	uncharacterized LOC100518088	-1.22	0.0079
<i>PIGH</i>	phosphatidylinositol glycan anchor biosynthesis, class H	-1.22	0.0207
<i>GMPPB</i>	GDP-mannose pyrophosphorylase B	-1.22	0.0083
<i>POGK</i>	pogo transposable element with KRAB domain	-1.22	0.0345
<i>TORIA</i>	torsin family 1, member A (torsin A)	-1.22	0.0131
<i>NDUFB5</i>	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa	-1.22	0.0177
<i>LOC100518801</i>	pro-opiomelanocortin-like	-1.23	0.0239
<i>LOC102165772</i>	uncharacterized LOC102165772	-1.23	0.0150
<i>LOC100154839</i>	tumor necrosis factor receptor superfamily member 10A-like	-1.24	0.0181
<i>FREM1</i>	FRAS1 related extracellular matrix 1	-1.24	0.0406
<i>CBX4</i>	chromobox homolog 4	-1.24	0.0235
<i>PRDM13</i>	PR domain containing 13	-1.24	0.0408
<i>LOC102158532</i>	putative ATP-dependent RNA helicase DHX57	-1.24	0.0305
<i>SLC22A5</i>	solute carrier family 22 (organic cation/carnitine transporter), member 5	-1.24	0.0218
<i>LOC102162630</i>	putative protein ZNF720	-1.25	0.0159
<i>CRISP3</i>	cysteine-rich secretory protein 3	-1.25	0.0487
<i>S100A4</i>	S100 calcium binding protein A4	-1.26	0.0445
<i>PHPT1</i>	phosphohistidine phosphatase 1	-1.26	0.0031
<i>LOC102159828</i>	40S ribosomal protein S20 pseudogene	-1.26	0.0064
<i>LOC100623627</i>	zinc finger protein 583	-1.26	0.0059
<i>ORC1</i>	origin recognition complex, subunit 1	-1.27	0.0158
<i>LOC100523301</i>	olfactory receptor 1L1-like	-1.27	0.0326
<i>LOC100522543</i>	olfactory receptor 140-like	-1.27	0.0381
<i>RPL27A</i>	ribosomal protein L27a	-1.28	0.0322
<i>RPS26</i>	ribosomal protein S26	-1.28	0.0217
<i>LOC100154493</i>	olfactory receptor 2G3-like	-1.28	0.0360
<i>FAM184A</i>	family with sequence similarity 184, member A	-1.29	0.0496
<i>DPH5</i>	diphthamide biosynthesis 5	-1.29	0.0480
<i>ABHD5</i>	abhydrolase domain containing 5	-1.29	0.0373
<i>ZNF641</i>	zinc finger protein 641	-1.29	0.0150

<i>HACL1</i>	2-hydroxyacyl-CoA lyase 1	-1.29	0.0337
<i>SLC44A5</i>	solute carrier family 44, member 5	-1.29	0.0152
<i>SH2D1B</i>	SH2 domain containing 1B	-1.30	0.0482
<i>CLDN2</i>	claudin 2	-1.30	0.0061
<i>TP53TG5</i>	TP53 target 5	-1.31	0.0381
<i>LOC100511607</i>	protein LEG1 homolog	-1.31	0.0078
<i>SFRP1</i>	secreted frizzled-related protein 1	-1.32	0.0167
<i>MIR138</i>	microRNA mir-138	-1.32	0.0324
<i>KIAA1551</i>	KIAA1551 ortholog	-1.34	0.0053
<i>MDM1</i>	Mdm1 nuclear protein	-1.34	0.0186
<i>ZFAND2A</i>	zinc finger, AN1-type domain 2A	-1.34	0.0020
<i>LOC102158467</i>	uncharacterized LOC102158467	-1.34	0.0448
<i>LONRF1</i>	LON peptidase N-terminal domain and ring finger 1	-1.35	0.0373
<i>MOCS1</i>	molybdenum cofactor synthesis 1	-1.37	0.0333
<i>JCHAIN</i>	joining chain of multimeric IgA and IgM	-1.39	0.0064
<i>LOC100524260</i>	zinc finger protein 45	-1.40	0.0381
<i>TRIM25</i>	tripartite motif containing 25	-1.43	0.0028
<i>LOC100525902</i>	calcium/calmodulin-dependent 3,5-cyclic nucleotide phosphodiesterase 1C	-1.45	0.0306
<i>TNFRSF11B</i>	tumor necrosis factor receptor superfamily, member 11b	-1.54	0.0183
<i>CYP2J34</i>	cytochrome P450, family 2, subfamily J, polypeptide 34	-1.61	0.0334
<i>LOC102166306</i>	alpha-fetoprotein-like	-1.71	0.0076
<i>CISH</i>	cytokine inducible SH2-containing protein	-2.50	0.0188

---

**Table S2** qPCR validation of microarray data for selected differentially expressed transcripts

	Fold change		<i>p</i> -value
	Microarray	qPCR	qPCR
<i>ASPA</i>	1.70	1.35	0.115
<i>CXCL9</i>	1.69	1.37	0.342
<i>ID2</i>	1.64	1.80	0.279
<i>PQLC2</i>	1.27	1.30	0.138
<i>JUN</i>	1.25	1.23	0.290
<i>GPR18</i>	1.24	2.35	0.416
<i>GMPPB</i>	-1.22	-2.07	0.105
<i>S100A</i>	-1.26	-1.20	0.615
<i>ABHD5</i>	-1.29	-2.17	0.012
<i>DPH5</i>	-1.29	-1.45	0.222
<i>HACL1</i>	-1.29	-1.80	0.024
<i>MOCS</i>	-1.37	-2.03	0.036
<i>JCHAIN</i>	-1.39	-1.67	0.192
<i>TRIM25</i>	-1.43	-1.41	0.378

Microarray and qPCR fold changes were calculated from *n* = 6 animals/group.

**Table S3** Characteristics of gene-specific primers used for qPCR analysis

Gene symbol	Primer sequence (forward, reverse)	NCBI GenBank accession no.	Product size (bp)
Reference genes			
<i>ACTB</i>	GACATCCGCAAGGACCTCTA ACATCTGCTGGAAGGTGGAC	XM_003124280	205
<i>ATP5G1</i>	CAGTCACCTTGAGCCGGGCGA TAGCGCCCCGGTGGTTTGC	NM_001025218	94
<i>RPS9</i>	GTCGCAAGACTTATGTGACC AGCTTAAAGACCTGGGTCTG	XM_003356050	325
Target genes			
<i>ASPA</i>	CAGCCTCAAGGAGTTCTGCG CCCCAGGGTGCAATGGTTTC	NM_001123077	232
<i>CXCL9</i>	GCAGTGTTGCCTTGCTTTTGG TTGGCTGGTGTGATGCAGG	NM_001114289	104
<i>ID2</i>	GCACCCCACTATTGTCAGCC AGAGCCTGTGGATTTGTTGCTG	NM_001037965	240
<i>PQLC2</i>	CTGCAATCTCATCGGCTCCTTC CGTCATGCCCACGATGAACAAG	NM_001243851	181
<i>JUN</i>	ATGACCCTGAACCTGGCTGAC GGGCATAGGAACTGGGTAGGG	NM_213880	188
<i>GPR18</i>	TGACACAAGCGACTCAAAGACG GGCCAGGGTGAGTTTGGTTG	XM_003131059	153
<i>GMPPB</i>	CGGTTCCGGAGCCTCGAATC TGAGGGAGTGGGCTTTGTGG	NM_001244541	232

<i>S100A</i>	AAGTACTCAGGCAAGGAGGGTG CTCGTTGTCCCTGTTGCTGTC	NM_001252605	156
<i>ABHD5</i>	ACACAACCTGGGTGGGTTCC TCAGCAAGGTCTGGTCGCTC	NM_001012407	114
<i>DPH5</i>	TGAACCAAGCAGCACAGCAG TCCTCAGCTCCA ACTCTGGC	NM_001243679	118
<i>HACL1</i>	GGAGTCGGTTTGGGATTTGCC CTGGAGGGGGCCATATCCTTCC	NM_001206454	223
<i>MOCS</i>	TCAAGGTCTGCCTCTTCGGG GATGCTCGGAATGGCTGGTG	XM_001928708	236
<i>JCHAIN</i>	AGCACCGTCATTTGCACAGTC ACTAGGGTCTTCAGCAGAGCG	XM_003356961	245
<i>TRIM25</i>	TCGAGACTTCTTCTGCCCTG CGATGCACCGTTGATCTGAC	XM_005656971	163

---