

Supplementary Table S1: RT-qPCR probes and primers.

Clock forward AGGCATGTCACAGTTTCAGC
Clock reverse CTTCTTGCTGCCGATGAATA
Clock probe CATGCGTGTCGCTGCTCTAGC
Arntl forward TAAACTCACCGTGCTCAGGA
Arntl reverse GTGTTTCAGTTCGTCATCGG
Arntl probe TTGAGAGGTGCCACCAACCCA
Npas2 forward CTGGAGAAGGTCATCGGATT
Npas2 reverse TCTAACGCCTCCAACATCAG
Npas2 probe CCAGCAGGACTGGAAGCCTTCA
Per2 forward TCGACGTAACAGGGTGTGTT
Per2 reverse TCCTCTTTGGCTTCTGAGGT
Per2 probe CCCAGGGAAGGACTGTCTTCCTCA
Igfbp2 forward CTACAACGAGCAGCAGGAGA
Igfbp2 reverse AACTGGGAAATCCTCCACAC
Igfbp2 probe AAGCCAGGCACCGACTGGCT
Sds forward TTCAAGATCCGAGGCATTG
Sds reverse GCTGAAGAGCAGACGAAATG
Sds probe TTGCCTTCATCTTGCAGAGATGCC
Got1 forward AAGACATTCGGTCCTATCGC
Got1 reverse CAGGAGCATTCTCCAGATCA
Got1 probe TCAAGTCCTCTCTTCTCTGCATCCCA
Akr1b7 forward GTGACCAATCAGGTCGAGTG
Akr1b7 reverse GGCTTAGCATAAGGCCTGTC
Akr1b7 probe ACTCCAAGGGCATCGCGGTC
Acss2 forward CATTGTGTTTGCAGGCTTCT
Acss2 reverse CAGCTCCTTCAGGTCACAA
Acss2 probe TTCCAGCTGCTGCCTGCTCA
Zfp189 forward TGTGGCTGCTATTCCTGAAG
Zfp189 reverse AAACATCCAGCGAGACCAG
Zfp189 probe ACCCTGTGGTTCGATGTCTTTCTCAA
Apol3 forward CGCCAGAGTCTTGAGGAAAC
Apol3 reverse CACTTTCAGGCTTCGTCTT
Apol3 probe AAGACCTGCAGCTCCTGTTGACCA
Wdm1 forward CAGTGAGACCTCTGCAGCTT
Wdm1 reverse CAGGTAGAAGCTGTTCTTAGCTTG
Wdm1 probe CCCAGTCGCCACTGCAGAGC
Snora5 forward GGAAGTGGCCTAGATGGCT
Snora5 reverse CAGTGTCTGCAGCCAACTT
Snora5 probe CCCAGAGCCCATGAGCAGCA
Rpl13a ABI/Invitrogen Rn00821946_g1
Rn45s ABI/Invitrogen Rn03928990_g1
18s ABI/Invitrogen 4319413E

Supplementary Table S2. 144 significantly differentially expressed liver genes in p21 male offspring: Con vs IPCR.

Probe set	Gene^a	Con mean^{b,c}	IPCR mean^{b,c}	Difference of means^c	p-value
10762324	Sds	7.6	11.1	3.5	0.00201
10924223	Igfbp2	7.8	11.2	3.4	0.001754
10791250	Lpl	7.5	10.7	3.2	0.000416
10815281	Ccrn4lb	6.3	9.5	3.1	0.001567
10775952	Afp	9	11.4	2.4	0.003339
10881861	Per3	7.6	9.8	2.2	0.001294
10706953	Dbp	8.6	10.8	2.2	0.001064
10715364	Got1	10.3	12.4	2.2	0.001804
10745323	Wsb1	10	11.8	1.8	0.001169
10844339	Slc25a25	8.9	10.7	1.8	0.001963
10761493	Glt1d1	6.7	8.5	1.8	0.014526
10923338	Coq10b	7.1	8.7	1.6	0.013637
10910376	Cyp1a1	7.5	9.2	1.6	0.039726
10733310	Zfp354a	7.6	9.2	1.6	0.004918
10726995	Image 7460165	11.2	12.7	1.6	0.01319
10726991	Image 7460165	12.1	13.7	1.5	0.02402
10849522	Hdc	6.5	8	1.5	0.00066
10807815	Tat	11.7	13.2	1.5	0.011687
10769476	Atp1b1	9	10.5	1.5	0.003012
10788198	Slc25a4	8.5	10	1.5	0.001899
10752148	Abcc5	8.6	10	1.4	0.022451
10901910	Amdhd1	8.6	10	1.4	0.036212
10771492	RGD1562220	8.1	9.5	1.4	0.00025
10878938	Plk3	7.4	8.7	1.4	0.023968
10906608	Slc38a2	10.4	11.8	1.4	0.001971
10734882	Per1	7.8	9.1	1.4	0.003983
10839771	Slc20a1	9.1	10.3	1.2	0.010489
10761162	Por	10	11.2	1.2	0.020945
10760131	Cyp3a23	11.7	12.9	1.2	0.001305
10710295	Acsm3	9.4	10.6	1.2	0.020938
10940599	Alas1	10.9	12.1	1.2	0.004876
10757962	Asl	10.8	11.9	1.2	0.018271
10879516	Mfsd2	9.6	10.7	1.1	0.043983
10929842	Per2	7.4	8.5	1.1	0.032426
10865077	Lrtm2	7.1	8.1	1.1	0.006581
10705276	Cyp2a3a	7.4	8.4	1.1	0.002443
10909411	Usp2	8.1	9.2	1	0.007085
10855853	Ppm1k	10.7	11.7	1	0.011481

10833635	Slc16a10	9.3	10.3	1	0.010252
10726824	Slc25a22	10.5	11.6	1	0.002052
10776954	Rell1	7.8	8.8	1	0.010707
10817547	Hfe2	9.9	8.9	-1	0.001971
10771993	Ugt2b34	10.3	9.3	-1	0.017321
10800696	Lims2	9.4	8.3	-1	0.000105
10813253	C6	10.8	9.8	-1	0.000417
10714782	Mbl2	11.8	10.8	-1	0.010633
10830554	Cd164	12	11	-1	0.007879
10926681	ENSRNOG00000045232	7.6	6.5	-1	0.0113
10901166	Angptl4	9.1	8.1	-1	0.014855
10859527	Slco1b2	12.4	11.4	-1	0.011578
10711210	Hsd3b7	10.2	9.2	-1	0.003088
10781581	Tsc22d1	10.4	9.3	-1	0.042016
10848030	Bbox1	10.5	9.4	-1	0.032203
10755088	Rtp4	6.7	5.6	-1.1	0.01464
10775761	Ccng2	8	7	-1.1	0.008175
10858160	LOC500300	10	8.9	-1.1	0.044179
10877907	Adfp	10.1	9	-1.1	0.005192
10744370	Slc16a13	7.9	6.8	-1.1	0.004198
10787507	Pgpep1	9.3	8.2	-1.1	0.00007
10768249	Cfhl1	10.2	9.2	-1.1	0.018359
10765280	Dpt	10.7	9.7	-1.1	0.043737
10733690	Gm2a	11.8	10.7	-1.1	0.000487
10865329	Apobec1	8.3	7.2	-1.1	0.037658
10806200	NM_001103359	11.1	10	-1.1	0.018416
10906285	Tymp	11.4	10.3	-1.1	0.006857
10793310	Srd5a1	11.7	10.6	-1.1	0.02532
10930675	Es1	9.8	8.7	-1.1	0.000271
10837366	Slc43a3	10.4	9.3	-1.1	0.022214
10831595	Psmb8	8.7	7.6	-1.1	0.00294
10710752	Aqp8	12	10.9	-1.1	0.000239
10933920	RGD1565785	6.1	5	-1.1	0.030331
10783977	Cbln3	8.8	7.6	-1.1	0.005194
10777037	Slc34a2	9.3	8.1	-1.1	0.01605
10933408	RGD1563952	8.6	7.5	-1.1	0.027926
10745994	RGD1311564	9.6	8.5	-1.1	0.004008
10795291	Hist1h1b	9.2	8	-1.2	0.032205
10742348	Irgm	9.1	7.9	-1.2	0.002782
10818262	Slc16a4	9.4	8.2	-1.2	0.000362
10752303	Comt	12.3	11.1	-1.2	0.016557
10932410	Ebp	11	9.8	-1.2	0.038218

10795218	Slc17a3	11.4	10.2	-1.2	0.006964
10722718	cdna	9.4	8.2	-1.2	0.002818
10705223	Cyp2b3	12.8	11.6	-1.2	0.007661
10806229	Es1	12.4	11.2	-1.2	0.049603
10721871	Fgf21	8.5	7.3	-1.2	0.034715
10903053	Inhbc	10.4	9.2	-1.2	0.031163
10886611	LOC299282	11.6	10.4	-1.2	0.001617
10854482	Tmem140	9.6	8.4	-1.2	0.009438
10711566	Htra1	9.8	8.5	-1.2	0.01501
10924274	Pnkd	10	8.8	-1.2	0.001461
10828827	Cdkn1a	9.3	8	-1.3	0.032107
10702955	RGD1562948	9.2	7.9	-1.3	0.023445
10875863	Pnrc1	11.2	9.9	-1.3	0.023175
10824439	Efna1	10.4	9.1	-1.3	0.023337
10922745	Npas2	8.7	7.4	-1.3	0.000719
10800434	Rnf125	10.1	8.8	-1.3	0.04706
10794779	RGD1310224	11.1	9.8	-1.3	0.002057
10878170	Cyp2j3	10.9	9.6	-1.3	0.01384
10828357	Psmb9	8.4	7.1	-1.3	0.005072
10771965	Ugt2b5	9.4	8.1	-1.3	0.034168
10778254	Gck	8	6.7	-1.3	0.021114
10808302	Osgin1	9.3	7.9	-1.3	0.001511
10727438	RGD1307603	12.5	11.2	-1.4	0.001151
10814528	Tnfsf10	9.2	7.8	-1.4	0.012033
10923432	Aox3	9.6	8.2	-1.4	0.008707
10730898	Gpam	11.5	10.1	-1.4	0.001714
10710258	Acsm2	10.4	9	-1.4	0.045482
10894582	Aldh1l2	9.8	8.3	-1.4	0.00182
10799337	LOC364773	7	5.6	-1.4	0.01669
10749874	Gbe1	10.7	9.3	-1.4	0.006925
10719937	cdna	10.8	9.4	-1.4	0.003379
10705235	Cyp2b3	10.8	9.4	-1.4	0.003379
10754179	Popdc2	8.3	6.8	-1.4	0.049985
10895747	Avpr1a	11.7	10.3	-1.4	0.00236
10819500	cdna	8.5	7.1	-1.5	0.003618
10907542	Csad	11.3	9.8	-1.5	0.002004
10832378	Lss	9.9	8.4	-1.5	0.038736
10824409	ncrna	9.2	7.6	-1.6	0.039699
10751931	Bcl6	9.2	7.6	-1.6	0.012796
10863688	RGD1561619	8.8	7.2	-1.6	0.014223
10702945	Acat2	9.5	7.8	-1.6	0.04169
10822242	Car3	12.3	10.6	-1.6	0.004845
10804288	Spink3	9	7.4	-1.6	0.022506

10712706	Chka	9.4	7.8	-1.7	0.001343
10800919	Egr1	9.7	8	-1.7	0.021821
10891991	Serpina3k	13.6	11.8	-1.8	0.013974
10733056	Ifi47	9.9	8.1	-1.8	0.009077
10728123	Tm7sf2	10.2	8.4	-1.8	0.021315
10903048	Inhbe	9.5	7.6	-1.9	0.00452
10801975	MGC108823	6.8	4.8	-2	0.001644
10912305	Paqr9	11.2	9.2	-2	0.003411
10894606	Slc41a2	10.3	8.2	-2	0.011889
10710028	Arntl	9	6.9	-2.1	0.011631
10930766	Cyp2c12	13	10.9	-2.1	0.026897
10841348	Acss2	10.4	8.1	-2.3	0.033097
10775731	Cxcl13	9	6.7	-2.3	0.004889
10702695	Esr1	8.2	5.9	-2.3	0.001544
10732239	Igfals	10.7	8.4	-2.3	0.000743
10803692	Nrep	11	8.5	-2.5	0.000089
10834022	Arrdc3	11.8	9.1	-2.7	0.000599
10854427	Akr1b7	9.7	6.9	-2.9	0.002169
10763758	Pigr	11.8	8.9	-2.9	0.00606
10719187	Sult2a1	10.4	7.3	-3.1	0.030156
10730013	Cyp2c7	11	7.7	-3.4	0.009484

Probesets have been screened for the following criteria: a minimum of 1 or greater log base 2 difference (absolute value) between p21 Con versus p21 IPCR with a p-value less than 0.05 using an Welch modified two sample t-test (corresponds to a minimum of 100% increase or maximum 50% decrease as compared to Con samples); and mean expression greater than 6 (log base 2) in p21 Con samples. Genes are listed from most up-regulated (top of list) to most down-regulated (bottom of list).

^a Gene symbol, gene locus, or RGD/IMAGE/Ensembl/Genbank accession number

^b The group mean microarray signal intensity incorporating the three replicates is reported here

^c Note data is log transformed and displayed as a power with a base of 2

Supplementary Table S3. Probesets differentially expressed between d450 Con versus d450 IUCR.

Probe set	Gene or locus^a	d450 Con mean^{b,c}	d450 IUCR mean^{b,c}	d450 Con mean^{b,d}	d450 Iucr mean^{b,d}	Percent difference^e	p-value
10939699	Line 1 element	7.7	8.6	213.8	382.7	79	0.024617
10771998	RGD1559459	8.6	9.4	382.7	670.9	75	0.017552
10715250	Line 1 element	8.9	9.7	487.8	849.2	74	0.036162
10930593	tRNA-His	9.5	10.2	709.2	1201	69	0.028747
10930604	tRNA-Gln	8.9	9.6	484.4	786.9	62	0.037453
10855946	ncrna:ENSRNOG000000352	6.5	7.1	90.5	141	56	0.028046
10770313	Cabc1	10.8	11.5	1807.8	2797.7	55	0.027134
10924274	Pnkd	9.5	10.1	734.2	1128.4	54	0.019633
10855185	Y3 small cytoplasmic RNA	9	9.6	494.6	749.6	52	0.034174
10930569	tRNA-Met	9.6	10.2	765.4	1144.1	49	0.025844
10924260	Pnkd	9.4	10	666.3	989.1	48	0.014247
10880562	RGD1562033	9.1	9.7	560.3	831.7	48	0.046231
10705411	ENSRNOG00000037675	11.9	12.5	3875.1	5712.9	47	0.043911
10821067	chr2:32877353-32915109	11.9	12.5	3875.1	5712.9	47	0.043911
10772272	ENSRNOG000000039	6.8	7.3	109.9	160.9	46	0.002622
10824788	chr2:187300619-187301692	9.6	10.2	781.4	1136.2	45	0.016082
10838130	Slc1a2	7.7	8.3	212.3	308.7	45	0.03305
10938837	ENSRNOG00000037905	7.1	7.6	136.2	195.4	43	0.018543
10763863	Slc45a3	7.5	8	179.8	257.8	43	0.024793
10882534	RGD1311939	8.5	9	367.1	526.4	43	0.007475
10721698	ncrna:ENSRNOG00000035279	7.8	8.4	229.1	326.3	42	0.003869
10839771	Slc20a1	10.1	9.5	1097.5	714.1	-35	0.0446
10760568	LOC679750	6.4	5.8	86.2	54.6	-37	0.012841
10922931	RGD1562818	6.5	5.9	93.1	58.1	-38	0.013312
10855862	Abcg2	7.9	6.9	230.7	119.4	-48	0.038721
10752266	IMAGE:6921248	7.5	6.6	182.3	94.4	-48	0.005557

Probesets have been screened for the following criteria: a minimum of 0.5 or greater log base 2 difference (absolute value) between d450 Con versus d450 IUCR with a p-value less than 0.05 using an Welch modified two sample t-test (corresponds to either a maximum 79% increase in expression or 48% decrease in expression as compared to control samples); mean expression greater than 6 (log base 2) in d450 Con samples; and accessioned genes through either RGD, Image, Ensembl, or PubMed. Genes are listed from most up-regulated (top of list) to most down-regulated (bottom of list).

^a Gene symbol, gene locus, or RGD/IMAGE/Ensembl/Genbank accession number

^b The group mean microarray signal intensity incorporating the three replicates is reported here.

^c Note data is log transformed and displayed as a power with a base of 2.

^d Data expressed linear (not log transformed)

^e Percent difference is calculated from the linear data

Supplementary Table S4. Probesets differentially expressed between d450 Con versus d450 IPCR.

Probe set	Gene ^a	d450 Con ^{b,c}	d450 IPCR ^{b,c}	Difference of means ^c	p value
10930602	tRNA-thr	5.8	7.3	1.5	0.030776
10776209	ENSRNOG00000039301	10.2	11.5	1.3	0.01185
10875324	Cyp7a1	10	11.3	1.3	0.038971
10930555	tRNA-phe	6.7	7.9	1.2	0.010012
10832563	Gstt3	8.8	9.9	1.1	0.004823
10897360	Gpt	9.1	10.2	1.1	0.035002
10923432	Aox3	9.8	10.8	1.1	0.024205
10935693	chrX:152771705-152771745	12	11	-1	0.014593
10752266	RGD1564318	7.5	6.5	-1	0.00544
10939615	ENSRNOG00000037531	12.2	11.1	-1	0.015005
10924441	ENSRNOG00000037792	10.8	9.8	-1.1	0.000569
10868796	chr5:62428918-62429008	10.5	9.4	-1.1	0.010987
10791650	ENSRNOG00000030037	13	11.9	-1.1	0.026372
10918480	ENSRNOG00000006879	9.9	8.8	-1.1	0.000226
10939888	ENSRNOG00000037431	9.3	8.1	-1.2	0.003482
10821115	chr2:34010638-34010676	11.1	9.8	-1.3	0.012014
10851484	Jph2	10.6	9.3	-1.4	0.001033
10923393	Aox1	10.9	9.6	-1.4	0.006587
10802970	ENSRNOG00000034905	11.4	10	-1.4	0.01462
10780173	TCR alpha joining region	10.7	9.3	-1.4	0.000576
10742402	Ltc4s	9.1	7.7	-1.4	0.002053
10912908	Cish	9.3	7.8	-1.4	0.031377

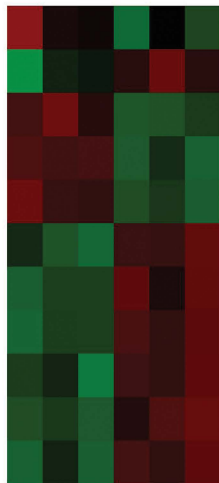
Probesets have been screened for the following criteria: a minimum of 1 or greater log base 2 difference (absolute value) between d450 Con versus d450 IPCR with a p-value less than 0.05 using an Welch modified two sample t-test (corresponds to either a minimum 100% increase in expression or a maximum 50% decrease in expression as compared to control samples); mean expression greater than 6 (log base 2) in d450 Con samples; and accessioned genes through either RGD, Image, Ensembl, or PubMed. Genes are listed from most up-regulated (top of list) to most down-regulated (bottom of list).

^a Gene symbol, gene locus, or RGD/IMAGE/Ensembl/Genbank accession number

^b The group mean microarray signal intensity incorporating the three replicates is reported here

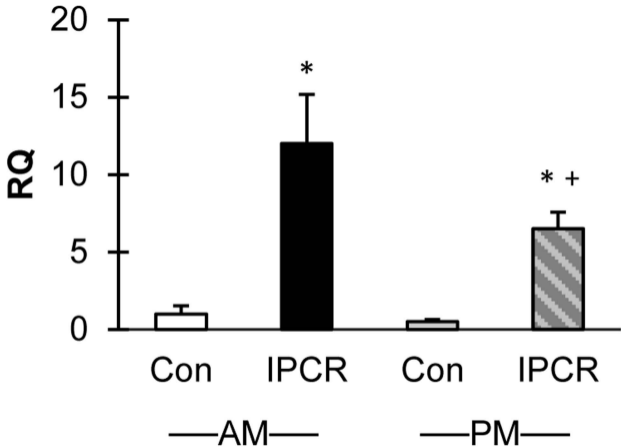
^c Note data is log transformed and displayed as a power with a base of 2

p21 Con A
p21 Con B
p21 Con C
p21 IPCR A
p21 IPCR B
p21 IPCR C

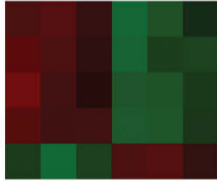


-3.0 -1.5 0 1.5 3.0

Nr1f1
Nr1d1
Clock
Arntl
Npas2
Per1
Per2
Per3
Cry1
Cry2
Ccrn4lb



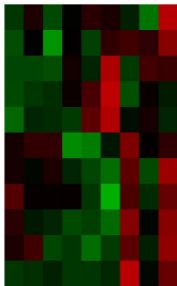
p21 Con A
p21 Con B
p21 Con C
p21 IPCR A
p21 IPCR B
p21 IPCR C



-3.0 -1.8 -0.6 0.6 1.8 3.0

Ghr
Stat5b
Igf1
Igfals
Igfbp2

d450 Con A
d450 Con B
d450 Con C
d450 IUCR A
d450 IUCR B
d450 IUCR C
d450 IPCR A
d450 IPCR B
d450 IPCR C



Nr1f1
Nr1d1
Clock
Arntl
Npas2
Per1
Per2
Per3
Cry1
Cry2
Ccrn4lb

-3.0 -2.3 -1.7 -1.0 -0.3 0.3 1.0 1.7 2.3 3.0