Supplemental Figure Legends

Supplemental Figure 1**.** A. Hybridization and flow chart of the multiple yellow strategy used to detect significant gene expression regulation for 1week CCH and CIH. Color of the block indicates whether Cy3 (green) or Cy5 (red) was used to label the extract. Each of the six arrays used for this timepoint is represented by a two-color rectangle in which the symbols indicate the treatment (C = CCH, N = normoxia, I = CIH), the time point (here 1 week), the gender (M = male, F = female) and the animal number. C1, N1 and I1 indicate the average expression level after the 1w CCH, normoxia or CIH in the red/green/all labeled extracts, and C1/N1 and I1/N1 indicate the expression ratio for 1 week exposure to CCH or CIH for red/green/all labeled extracts. An additional flow chart in which the averages were computed separately for genders was used and the final results averaged between them. B. Representative image of a hybridized slide. Most spots should be yellow because cDNAs from two individual mice of the same gender received the same treatment, either hypoxia or the age matched control. In some spots, the color deviates to red or green indicating gene expression variations between the two individual mice, but not the differential regulations between hypoxia and the control.

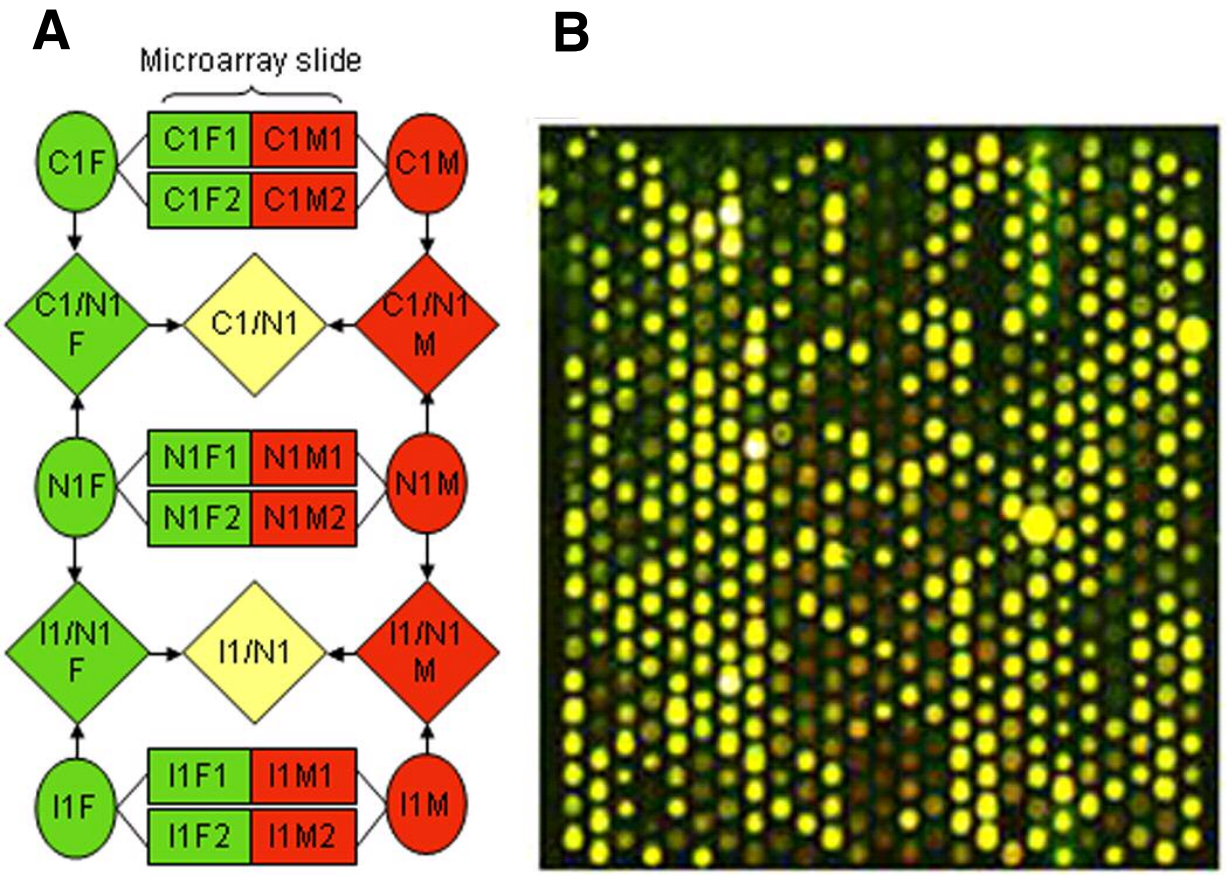
Supplemental Figure 2. Sub-profiling of altered genes in CCH and CIH treated mice hearts. (A and B) Most genes of ribosomal protein subunits were up-regulated in CCH but down-regulated in CIH treated mice hearts, suggesting the differential efficiency of protein synthesis. (C) Most genes of the Rho GTPase family were up-regulated in CCH but all down-regulated in CIH treated mice hearts. (D) Most genes in the MAPK pathway were up-regulated in CCH treated mice hearts. (E) Genes of mitochondrial complex I subunits were mostly up-regulated in CCH but down-regulated in CIH after 1 and 2 weeks of treatment, suggesting differential functional state of mitochondria. (F) Genes related to fibrosis were up-regulated in both CCH and CIH treated mice hearts. (G) Genes related to

cardiac development or growth were mostly up-regulated in CCH but down-regulated in CIH treated animals.

Supplemental Figure 3. Organ weight of the brain, lung and kidney after CCH and CIH treatment (n=8 to16). The weight of the brain and kidney was lower significantly in both CCH and CIH treated animals, but the wet and dry weight of the lung were higher by 4 weeks of age in both CCH and CIH treated mice when they were compared to the age matched NC. These results suggest that the heart and lung have the similar fashion in responding to hypoxic stress. * indicates $p<0.05$ and ** indicates $p<0.01$ when CCH or CIH compares to normoxic control; whereas + indicates $p<0.05$, ++ indicates $p<0.01$ when CCH compares to CIH.

Supplemental Figure 4. Image of the gene cluster of the individual values and expression ratios of the 7028 adequately quantified genes in all arrays that passed both the ±1.5 fold change and $p<0.05$ criteria in a paired heteroscedastic Student's t-test for at least one comparison between the average expression levels among treatments, namely: 1,2,4I vs 1,2,4N, 1,2,4C vs 1,2,4N, 1,2,4C vs 1,2,4I, where the numbers 1, 2 and 4 indicate the duration of the treatment N = normoxia, I = CIH, C = CCH (data in Supplemental Table 6)**.** The color of the elements in the columns (green for negative, red for positive and black for null values) are associated to the binary logarithms of the normalized and scaled individual measurements of genes for all 36 mice studied (columns labeled **1I1, …, 1I4, …, 4C4**) and to the fold change ratios (negative for down-regulation) when comparing the average expression for the two sets of mice subjected to the indicated treatments for the same period of time (columns labeled **1I/N, …, 4C/N, 1C/I, …, 4C/I**). Individual values were normalized to the average of the corresponding normoxic values and then the results of each group of four mice subjected to the same condition were rescaled with respect to the average of that group so that the standard deviation was reduced by a factor of 4. The genes were clustered through the centered correlation method (i.e. using

the Pearson correlation coefficient $r = \frac{1}{45}\sum_{i=1}^{45}\left(\frac{X_i - \bar{X}}{\sigma_X}\right)\left(\frac{Y_i - \bar{Y}}{\sigma_Y}\right)$ between any two series *X* and *Y*, each composed of 45 numbers: the 36 normalized and scaled individual measurements + the 9 fold changes when comparing the averages of any two treatments for all three durations) without any additional filtering and normalization. We used the GeneCluster and the TreeView programs of Michael Eisen (**http://rana.lbl.gov/EisenSoftware.htm**). Note both the variability and the reproducibility of the gene expression patterns among the mice subjected to the same condition. The columns of the individual normoxic mice are mostly black (i.e. values close to $0 = \log_2 1$) since the averages of their individual values were used to normalize the individual values of all mice exposed for the same duration to normoxia, CCH and CIH. Green/red colors in the last three columns indicate the differences between the two hypoxic treatments at each duration, with green indicating smaller fold change in CCH than in CIH.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C1M1
C1M
C1F2
C1M2
C1/N1 F
C1/N1
C1/N1 M
N1F
N1F1
N1M1
N1M
N1F2
N1M2
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I1M2
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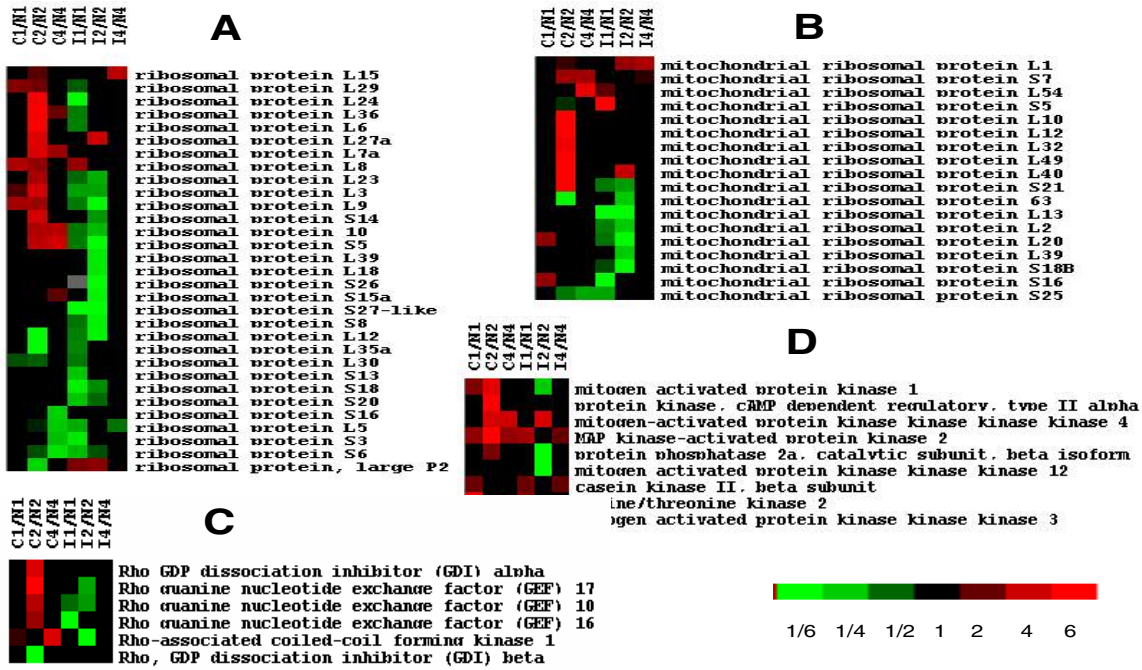
C1/N1
C2/N2
C4/N4
I1/N1
I2/N2
I4/N4
A
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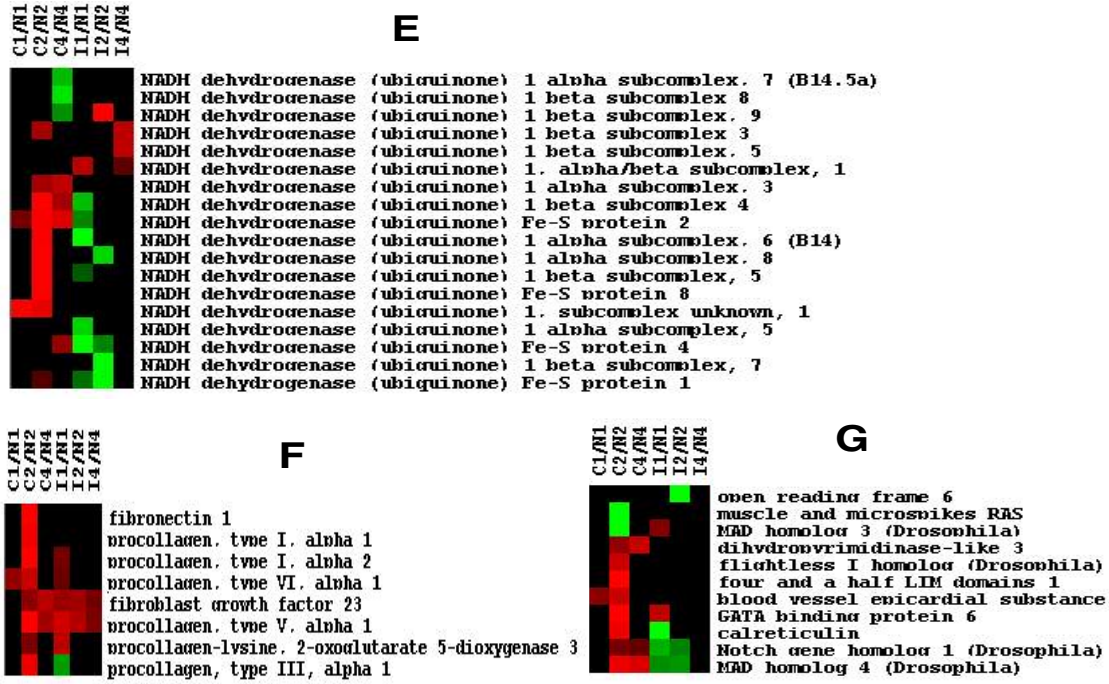
ribosomal protein L36
ribosomal protein L6
ribosomal protein L27a
ribosomal protein L7a
ribosomal protein L8
ribosomal protein L23
ribosomal protein L3
ribosomal protein L9
ribosomal protein S14
ribosomal protein 10
ribosomal protein S5
ribosomal protein L39
ribosomal protein L18
ribosomal protein S26
ribosomal protein S15a
ribosomal protein S27-like
ribosomal protein S8
ribosomal protein L12
ribosomal protein L35a
ribosomal protein L30
ribosomal protein S13
ribosomal protein S18
ribosomal protein S20
ribosomal protein S16
ribosomal protein L5
ribosomal protein S3
ribosomal protein S6
ribosomal protein, large P2
B
mitochondrial ribosomal protein L1
mitochondrial ribosomal protein S7
mitochondrial ribosomal protein L54
mitochondrial ribosomal protein S5
mitochondrial ribosomal protein L10
mitochondrial ribosomal protein L12
mitochondrial ribosomal protein L32
mitochondrial ribosomal protein L49
mitochondrial ribosomal protein L40
mitochondrial ribosomal protein S21
mitochondrial ribosomal protein 63
mitochondrial ribosomal protein L13
mitochondrial ribosomal protein L2
mitochondrial ribosomal protein L20
mitochondrial ribosomal protein L39
mitochondrial ribosomal protein S18B
mitochondrial ribosomal protein S16
mitochondrial ribosomal protein S25
D
mitogen activated protein kinase 1
protein kinase, cAMP dependent regulatory, type II alpha
mitogen-activated protein kinase kinase kinase kinase 4
MAP kinase-activated protein kinase 2
protein phosphatase 2a, catalytic subunit, beta isoform
mitogen activated protein kinase kinase kinase 12
casein kinase II, beta subunit
ine/threonine kinase 2
gen activated protein kinase kinase kinase 3
C
Rho GDP dissociation inhibitor (GDI) alpha
Rho guanine nucleotide exchange factor (GEF) 17
Rho guanine nucleotide exchange factor (GEF) 10
Rho guanine nucleotide exchange factor (GEF) 16
Rho-associated coiled-coil forming kinase 1
Rho, GDP dissociation inhibitor (GDI) beta
1/6 1/4 1/2 1 2 4 6


C1/N1
C2/N2
C4/N4
I1/N1
I2/N2
I4/N4
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NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9
NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3
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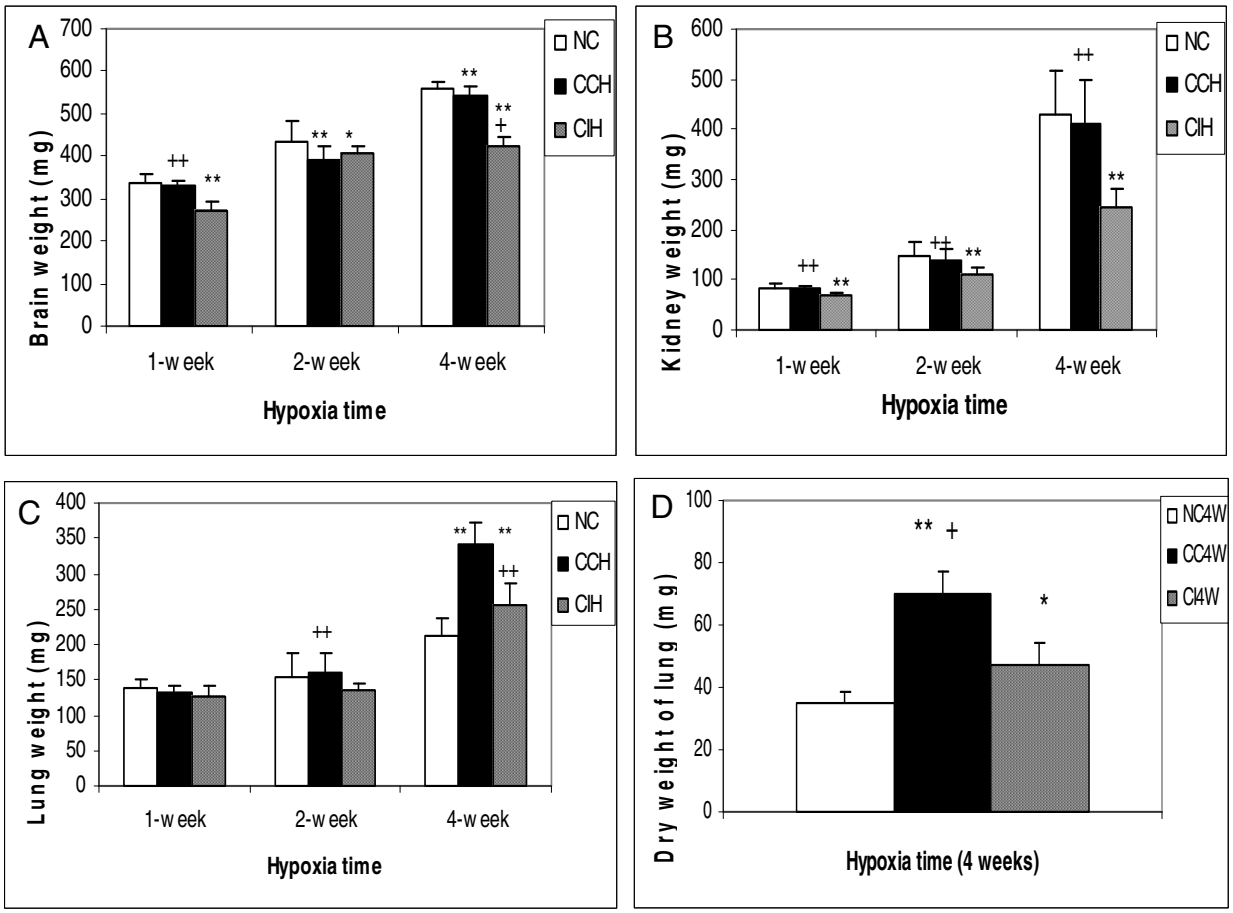
NADH dehydrogenase (ubiquinone) Fe-S protein 4
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7
NADH dehydrogenase (ubiquinone) Fe-S protein 1

C1/N1
C2/N2
C4/N4
I1/N1
I2/N2
I4/N4
F
fibronectin 1
procollagen, type I, alpha 1
procollagen, type I, alpha 2
procollagen, type VI, alpha 1
fibroblast growth factor 23
procollagen, type V, alpha 1
procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3
procollagen, type III, alpha 1
G
open reading frame 6
muscle and microspikes RAS
MAD homolog 3 (Drosophila)
dihydropyrimidinase-like 3
flightless I homolog (Drosophila)
four and a half LIM domains 1
blood vessel epicardial substance
GATA binding protein 6
calreticulin
Notch gene homolog 1 (Drosophila)
MAD homolog 4 (Drosophila)


A
Brain weight (mg)
700
600
500
400
300
200
100
0
1-week
2-week
4-week
Hypoxia time
NC
CCH
ClH
B
Kidney weight (mg)
600
500
400
300
200
100
0
1-week
2-week
4-week
Hypoxia time
NC
CCH
ClH
C
Lung weight (mg)
400
350
300
250
200
150
100
50
0
1-week
2-week
4-week
Hypoxia time
NC
CCH
ClH
D
Dry weight of lung (mg)
100
80
60
40
20
0
Hypoxia time (4 weeks)
NC4W
CC4W
Cl4W

Supplemental Table Legends

Supplemental Table 1. Significantly regulated genes in all three time points in CCH heart. CHR = chromosomal location of the gene, C1,2,4 = expression ratio after 1,2,4 weeks CCH treatment, P-C1,2,4 = p-value of the expression regulation after 1,2,4 weeks CCH.

Supplemental Table 2. Significantly regulated genes in all three time points in CIH heart. CHR = chromosomal location of the gene, I1,2,4 = expression ratio after 1,2,4 weeks CIH treatment, P-I1,2,4 = p-value of the expression regulation after 1,2,4 weeks CIH.

Supplemental Table 3. Significantly regulated genes over 5-fold in CCH heart. Missing values indicate either not-quantified or not-significant regulation at that time-point.

Supplemental Table 4. Significantly regulated genes over 5-fold in CIH heart. Missing values indicate either not-quantified or not-significant regulation at that time-point.

Supplemental Table 5. Primers used in QRT-PCR, a description of their genebank numbers, gene symbols, gene names and functions.

Supplemental Table 6. Individual values and expression ratios before Bonferroni correction and data averaging to reduce the redundancy. The table was restricted to the 7028 adequately quantified spots in all arrays that passed both the ±1.5 fold change and $p<0.05$ criteria in a paired heteroscedastic Student's t-test for at least one comparison between the average expression levels among treatments, namely: 1,2,4I vs 1,2,4N, 1,2,4C vs 1,2,4N, 1,2,4C vs 1,2,4I, where the numbers 1, 2 and 4 indicate the duration of the treatment N = normoxia, I = CIH, C = CCH. **1I1, …, 1I4, …, 4C4 =** binary logarithms of individual measurements of genes for all 36 studied mice (4 mice for each combination duration-treatment). Each value was normalized to the average of the corresponding normoxic values and then

the results of each group of four mice subjected to the same condition were rescaled with respect to the average of that group so that the standard deviation was reduced by a factor of 4. **1I/N, …, 4C/N, 1C/I, …, 4C/I =** fold change (negative for down-regulation) when comparing the two sets of four mice subjected to the indicated treatments for 1, 2 or 4 weeks. P(1I/N), …, P(4C/I) = p-values. The genes were clustered through the centered correlation method (i.e. using the Pearson correlation coefficient $r = \frac{1}{45}\sum_{i=1}^{45}\left(\frac{X_i - \bar{X}}{\sigma_X}\right)\left(\frac{Y_i - \bar{Y}}{\sigma_Y}\right)$ between any two series *X* and *Y*, each composed of 45 numbers: the 36 normalized and scaled individual measurements + the 9 fold changes when comparing the averages of any two treatments for all three durations) using the GeneCluster program of Michael Eisen (**http://rana.lbl.gov/EisenSoftware.htm**) without any additional filtering and normalization.

SUPPLEMENTAL TABLE 1: SIGNIFICANTLY REGULATED GENES IN ALL THREE TIMEPOINTS IN CCH HEART								
GENE NAME	**SYMBOL**	**CHR**	**C1**	**P-C1**	**C2**	**P-C2**	**C4**	**P-C4**
a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 4	Adamts4	1	-1.68	0.006	-2.93	0.000	-2.77	0.002
alkaline phosphatase 5	Akp5	1	2.04	0.040	-2.93	0.004	-2.52	0.001
annexin A7	Anxa7	14	1.51	0.002	-1.54	0.029	1.90	0.036
ATPase, H+ transporting, V0 subunit C	Atp6v0c	17	1.82	0.010	1.68	0.007	1.84	0.022
BCL2/adenovirus E1B 19kDa-interacting protein 1, NIP3	Bnip3	7	1.57	0.029	3.02	0.003	-1.72	0.040
Bernardinelli-Seip congenital lipodystrophy 2 homolog (human)	Bscl2	19	1.68	0.013	1.64	0.026	-1.57	0.008
ceroid-lipofuscinosis, neuronal 2	Cln2	7	1.91	0.020	-1.97	0.016	1.63	0.038
chemokine (C-X-C motif) ligand 12	Cxcl12	6	2.01	0.022	2.79	0.001	1.86	0.019
citrate synthase	Cs	10	1.67	0.022	2.22	0.049	-2.03	0.012
deformed epidermal autoregulatory factor 1 (Drosophila)	Deaf1	7	-1.96	0.005	-2.51	0.001	-2.35	0.024
dynamin 1-like	Dnm1l	16	2.09	0.025	-1.62	0.025	1.92	0.028
filamin, alpha	Flna	X	1.77	0.018	1.92	0.000	-1.96	0.019
follistatin-like	Fstl	16	2.21	0.005	1.65	0.005	-2.95	0.015
glypican 3	Gpc3	X	1.54	0.006	1.72	0.000	2.61	0.040
golgi apparatus protein 1	Glg1	8	1.66	0.021	1.52	0.038	-2.34	0.005
Harvey rat sarcoma oncogene, subgroup R	Rras	7	1.51	0.008	1.67	0.005	2.31	0.029
heat shock protein 1 (chaperonin)	Hspd1	11	1.75	0.038	2.25	0.008	2.16	0.031
integral membrane protein 2B	Itm2b	11	1.55	0.003	2.08	0.008	1.69	0.017
kinesin family member 5B	Kif5b	18	1.65	0.022	1.91	0.008	1.98	0.012
LIM domain only 2	Lmo2	2	1.62	0.012	-1.69	0.004	-2.46	0.008
makorin, ring finger protein, 2	Mkrn2	6	1.73	0.004	1.87	0.002	-1.78	0.030
MAP kinase-activated protein kinase 2	Mapkapk2	1	1.64	0.015	2.36	0.008	1.64	0.016
MAP kinase-activated protein kinase 5	Mapkapk5	5	-1.77	0.001	1.83	0.048	-2.58	0.006
mitochondrial ribosomal protein L28	Mrpl28	17	-2.64	0.000	1.80	0.018	1.87	0.007
NADH dehydrogenase (ubiquinone) Fe-S protein 2	Ndufs2	1	1.54	0.009	2.56	0.001	2.32	0.019
pleckstrin homology domain containing, family C (with FERM domain) member 1	Plekhc1	14	2.09	0.006	1.84	0.044	2.26	0.019
protein phosphatase 1, regulatory subunit 9B	Ppp1r9b	11	1.82	0.001	-2.93	0.001	-2.54	0.004
serine/threonine kinase 23	Stk23	X	-1.54	0.000	-1.66	0.031	-2.48	0.002
Sloan-Kettering viral oncogene homolog	Ski	4	1.87	0.018	1.99	0.004	-2.59	0.011
sno, strawberry notch homolog 1 (Drosophila)	Sbno1	5	-1.76	0.002	-1.54	0.002	-1.81	0.015
solute carrier family 12, member 2	Slc12a2	18	2.08	0.004	2.07	0.002	1.64	0.003
solute carrier family 31, member 1	Slc31a1	4	1.53	0.020	2.05	0.016	-1.61	0.041
solute carrier family 43, member 1	Slc43a1	2	2.11	0.020	-1.79	0.006	-1.75	0.004
spectrin beta 2	Spnb2	11	1.79	0.003	1.88	0.001	1.93	0.025
synaptopodin	Synpo	18	1.86	0.042	-2.30	0.000	-1.79	0.002
syndecan binding protein	Sdcbp	4	1.52	0.014	-4.15	0.000	-2.08	0.022
von Hippel-Lindau binding protein 1	Vbp1	X	1.71	0.030	-1.56	0.010	2.90	0.044
zinc finger protein 91	Zfp91	19	1.64	0.030	2.29	0.003	1.65	0.028

SUPPLEMENTAL TABLE 2: SIGNIFICANTLY REGULATED GENES IN ALL THREE TIMEPOINTS IN CIH HEART								
GENE NAME	**SYMBOL**	**CHR**	**I1**	**P-I1**	**I2**	**P-I2**	**I4**	**P-I4**
acetyl-Coenzyme A dehydrogenase, long-chain	Acadl	1	1.51	0.048	-2.15	0.028	1.63	0.029
aldolase 2, B isoform	Aldo2	4	-2.19	0.034	-3.86	0.009	-2.48	0.017
ATPase, H+ transporting, V0 subunit	Atp6v0e	17	-1.68	0.042	-2.10	0.003	1.53	0.037
BCL2/adenovirus E1B 19kDa-interacting protein 1, NIP3	Bnip3	7	1.56	0.037	2.13	0.018	-1.59	0.021
ceroid-lipofuscinosis, neuronal 2	Cln2	7	1.99	0.015	-1.68	0.029	1.63	0.001
complement component 1, q subcomponent, gamma polypeptide	C1qg	4	1.77	0.002	-1.76	0.008	-1.61	0.024
DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	Ddx24	12	2.04	0.000	-1.84	0.025	1.87	0.016
DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	Ddx5	11	1.61	0.045	-2.29	0.012	1.82	0.002
fibroblast growth factor 23	Fgf23	6	1.78	0.014	1.84	0.002	1.54	0.024
hyaluronidase 2	Hyal2	9	-1.64	0.016	1.90	0.031	-1.67	0.020
isocitrate dehydrogenase 2 (NADP+), mitochondrial	Idh2	7	-1.62	0.010	1.71	0.044	1.53	0.034
karyopherin (importin) alpha 1	Kpna1	11	2.51	0.000	-1.63	0.000	-2.03	0.000
large tumor suppressor 2	Lats2	14	1.93	0.023	-1.83	0.003	1.60	0.001
NMDA receptor-regulated gene 1	Narg1	3	1.64	0.042	-1.81	0.012	1.66	0.040
polyadenylate binding protein-interacting protein 1	Paip1	13	-1.66	0.000	-2.33	0.001	1.58	0.002
polymerase (RNA) II (DNA directed) polypeptide B	Polr2b	5	-1.56	0.039	-1.50	0.035	-1.64	0.036
proteasome (prosome, macropain) 28 subunit, alpha	Psme1	14	-1.66	0.004	2.49	0.014	-1.62	0.046
proteasome (prosome, macropain) inhibitor subunit 1	Psmf1	2	2.19	0.011	-1.77	0.012	-1.77	0.000
replication factor C 1	Recc1	5	-1.68	0.016	1.60	0.014	-1.74	0.028
ribosomal protein 10	Rpl10	X	-1.63	0.027	-2.14	0.006	1.69	0.046
ribosomal protein S5	Rps5	12	-1.64	0.019	-2.17	0.037	2.18	0.009
secreted frizzled-related sequence protein 1	Sfrp1	8	5.63	0.000	1.80	0.001	1.57	0.005
thymopoietin	Tmpo	10	-1.72	0.027	1.86	0.015	1.63	0.023
tripartite motif protein 6	Trim6	7	4.07	0.035	-1.69	0.025	-1.97	0.001
tubulin, alpha 8	Tuba8	6	-3.16	0.000	-2.26	0.034	2.43	0.028
ubiquitin-like 5	Ubl5	9	-1.51	0.011	-2.64	0.019	1.79	0.019
unc-5 homolog B (C. elegans)	Unc5b	10	-1.79	0.023	-1.88	0.023	-1.51	0.018
vacuolar protein sorting 28 (yeast)	Vps28	15	-1.56	0.008	-1.83	0.042	1.59	0.007

SUPPLEMENTAL TABLE 3. SIGNIFICANTLY REGULATED GENES OVER 5-FOLD IN CCH								
GENE NAME	**SYMBOL**	**CHR**	**C1**	**P-C1**	**C2**	**P-C2**	**C4**	**P-C4**
afamin	Afm	5	-1.67	0.005	-5.52	0.001		
aldo-keto reductase family 1, member A4 (aldehyde reductase)	Akr1a4	4	1.83	0.000	-5.03	0.010		
ankyrin repeat and SOCS box-containing protein 3	Asb3	11	-1.90	0.003	-5.45	0.000		
catenin src	Catns	2			-7.30	0.000		
epidermodysplasia verruciformis 2	Ever2	11			-10.16	0.002		
glucose phosphate isomerase 1	Gpi1	7			5.18	0.000		
golgi associated PDZ and coiled-coil motif containing	Gopc	10			-6.33	0.002		
heat shock protein 4	Hsp70-4	2			-5.58	0.001	-1.50	0.019
integrin beta 1 binding protein 1	Itgb1bp1	12			-7.59	0.000		
interferon consensus sequence binding protein 1	Icsbp1	8			-6.06	0.000		
isocitrate dehydrogenase 2 (NADP+), mitochondrial	Idh2	7			5.25	0.000		
myosin light chain, phosphorylatable, fast skeletal muscle	Mylpf	7			-39.43	0.043		
natriuretic peptide precursor type B	Nppb	4	2.66	0.037	5.64	0.000		
Ngg1 interacting factor 3-like 1 (S. pombe)	Nif3l1	1			-6.17	0.000	-1.58	0.028
ornithine decarboxylase antizyme inhibitor	Oazin	15			-9.50	0.000		
peptidyl arginine deiminase, type II	Padi2	4			-5.24	0.001		
prostaglandin D2 synthase (brain)	Ptgds	2			5.21	0.001		
protein kinase C and casein kinase substrate in neurons 2	Pacsin2	15	2.17	0.032	-5.76	0.008		
regulating synaptic membrane exocytosis 3	Rims3	4			-6.15	0.000	-1.54	0.008
retinol binding protein 1, cellular	Rbp1	9			-10.13	0.001		
ribosomal protein L35a	Rpl35a	11			-8.03	0.000		
ribosomal protein L36	Rpl36	11			6.59	0.000	1.52	0.033
ribosomal protein S27a	Rps27a	9	1.52	0.044	-17.50	0.000		
small optic lobes homolog (Drosophila)	Solh	17			-6.04	0.000	-1.69	0.021
TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor	Taf10	7			-5.32	0.002		
thioredoxin-like	Txnl	18			-6.34	0.000		
Zinc finger protein 212	Znf212	6	-3.01	0.032	5.93	0.000		

SUPPLEMENTAL TABLE 4. SIGNIFICANTLY REGULATED GENES OVER 5-FOLD IN CIH								
GENE NAME	**SYMBOL**	**CHR**	**I1**	**P-I1**	**I2**	**P-I2**	**I4**	**P-I4**
actinin alpha 3	Actn3	19			-5.45	0.000		
aminolevulinic acid synthase 2, erythroid	Alas2	X	2.50	0.007	6.68	0.040		
brachyury 2	T2	17	5.49	0.036				
carboxypeptidase B2 (plasma)	Cpb2	14	5.63	0.001				
CDC23 (cell division cycle 23, yeast, homolog)	Cdc23	18	5.14	0.001				
creatine kinase, mitochondrial 1, ubiquitous	Ckmt1	2	-2.04	0.001	-6.54	0.005		
cyclin L1	Ccnl1	3	-1.69	0.004	-5.52	0.003		
dopachrome tautomerase	Dct	14	1.55	0.011	-8.02	0.037		
ferrochelatase	Fech	11	2.29	0.048	5.12	0.039		
growth factor independent 1B	Gfi1b	2	6.80	0.000	1.99	0.008		
hemoglobin Y, beta-like embryonic chain	Hbb-y	7			-5.96	0.049		
interferon activated gene 203	Ifi203	1	6.05	0.006	1.81	0.002		
interferon-stimulated protein	Isg20	7			5.68	0.044		
membrane-spanning 4-domains, subfamily A, member 4C	Ms4a4c	19	5.51	0.000				
myosin light chain, phosphorylatable, fast skeletal muscle	Mylpf	7			-19.72	0.048		
nuclear receptor-binding SET-domain protein 1	Nsd1	8	5.99	0.000				
peptidylprolyl isomerase A	Ppia	11			6.21	0.000		
resistin like beta	Retnlb	16	6.45	0.000	1.54	0.041		
secreted frizzled-related sequence protein 1	Sfrp1	8	5.63	0.000	1.80	0.001	1.57	0.005
small optic lobes homolog (Drosophila)	Solh	17	7.07	0.000	2.53	0.000		
synaptonemal complex protein 1	Sycp1	3	5.16	0.001	-2.13	0.009		
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4	Galnt4	10	6.36	0.000	1.97	0.002		
uncoupling protein 2, mitochondrial	Ucp2	7			5.39	0.002		
uridine phosphorylase 1	Upp1	11	5.80	0.000	2.48	0.001		
vacuolar protein sorting 4b (yeast)	Vps4b	1	6.34	0.000				
zinc finger protein 60	Zfp60	7	5.02	0.021	1.99	0.001		

Supplemental Table 5. Primers in QRT-PCR

Gene Symbols	Gene Name	GenBank	Function	Primer Sequence
Bnip3l	BCL2/adenovirus E1B 19kDa-interacting protein 3-like	AA028342	Apoptosis	F: cacgttccttcctcgtcttc R: atctgcccatcttcttgtgg
Egln1	EGL nine homolog 1 (C. elegans)	C78486	HIF degradation	F: cgccaaggtaagtggaggta R: ggcgtatgctggctgtactt
Madh4	MAD homolog 4 (Drosophila)	AW551817	Development	F: atggctatgtggatccttcg R: ccaaacgtcaccttcacctt
Solh	small optic lobes homolog (Drosophila)	AA245131	Proteolysis	F: cgactctgtggacatctgc R: gaagagggcaaactccagtg
Capn5	calpain 5	AA268162	Proteolysis	F: gggacctcgacaccagagta R: gcccagaaattcatccttca
Slc19a1	solute carrier family 19 (folate transporter), member 1	AA475033	Transport	F: cctgtggagaagcactgaca R: accagcttggaccacagagt
Slc6a8	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	AA473227	Transport	F: gctggctttgtggtcttctc R: acaggcatcagtgtgacagc
Slc12a2	solute carrier family 12, member 2	AW553645	Transport	F: agactgtggtggagctgctt R: caatctgagcctttgcttcc
Notch1	Notch gene homolog 1 (Drosophila)	AA265694	Development	F: cctgccactatggttcctgt R: tggcactcattgatgttggt
Rpl36	ribosomal protein L36	AI464570	Translation	F: caccaaacacaccaagttcg R: cgcttgtccttggacacttt
Eif2s1	eukaryotic translation initiation factor 2, subunit 1 alpha	AW546615	Translation	F: tggaagcaatgtgctttgac R: tctccacaggccttcagact
Eif4e	eukaryotic translation initiation factor 4E	AU016482	Translation	F: taccactaatcccccacctg R: agagtgcccacctgttctgt
Ndufb4	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4	AA434897	Metabolism	F: tgccgagtatgacgtgtctc R: tttggggtcgttgtactgaa