## Transcriptional orchestration of mitochondrial homeostasis in a cellular model of PGC-1-related coactivator-dependent thyroid tumor

## SUPPLEMENTARY MATERIALS



Supplementary Figure 1: Correlation between the best probes from 48h ChIP-chip analyses issued from two different factors. Each graph showed the correlation of the geometric mean (log base 10) for the best probe of each gene for two transcription factors. The red box corresponded to the correlation between ERR1 (ERRa) and PRC probes (Pearson correlation 0.82, p-value  $\leq 2.2 \ 10^{-16}$ ).



Supplementary Figure 2: Venn diagrams representing the number of positive genes on ChIP-chip analyses after 24h (blue) and 48h (yellow) of serum induction were shown for the six factors studied (CREB, NRF1, GABP, YY1, PRC and ERR1). The percentage of genes commonly positive at 24h and 48h are indicated in brackets.



## Supplementary Figure 3: Motif discovery in positive ChIP-chip promoters for NRF1, GABP, CREB, ERR1 and YY1.

Colored circles represent the motifs discovered in gene promoters tested relative to *consensus* motif indicated in the center of the figure. Motifs discovered for other transcription factors than those explored by ChIP-chip are also shown by the corresponding color code. A high-resolution version of this figure is available on Oncotarget website.

PRC						ERF
GO.ID	Total	Change	Enrichissement	P.Value	Term	GO
785	157	28	2.71	0	chromatin	78
786	55	14	3.87	0	nucleosome	78
1501	289	38	2.00	0	skeletal system development	472
1503	123	21	2.60	0	ossification	592
1568	240	36	2.28	0	blood vessel development	633
1666	79	16	3.08	0	response to hypoxia	635
1944	244	37	2.31	0	vasculature development	813
5694	388	47	1.84	0	chromosome	813
6333	113	21	2.83	0	chromatin assembly or disassembly	965
6334	69	15	3.31	0	nucleosome assembly	979
6793	1106	111	1.53	0	phosphorus metabolic process	998
6796	1106	111	1.53	0	phosphate metabolic process	106
6928	501	57	1.73	0	cell motion	109
8219	979	99	1.54	0	cell death	165
8283	945	100	1.61	0	cell proliferation	170
8285	305	40	1.99	0	negative regulation of cell proliferation	300
9653	1036	106	1.56	0	anatomical structure morphogenesis	329
9888	604	69	1.74	0	tissue development	335
9890	472	57	1.84	0	negative regulation of biosynthetic process	433
9892	631	76	1.83	0	negative regulation of metabolic process	444
9967	246	34	2.10	0	positive regulation of signal transduction	458
10558	454	55	1.84	0	negative regulation of macromolecule biosynthetic process	400
10605	595	69	1.76	0	negative regulation of macromolecule metabolic process	510
10627	217	32	2.24	0	regulation of protein kinase cascade	512
10740	150	24	2.43	0	positive regulation of protein kinase cascade	050
10926	922	109	1.80	0	anatomical structure formation	50
10941	657	70	1.62	0	regulation of cell death	592
16265	983	99	1.53	0	death	660
16477	317	43	2.06	0	cell migration	
22607	668	76	1.73	0	cellular component assembly	686

E	RRα					
G	O.ID	Total	Change	Enrichissement	P.Value	Term
1	785	157	42	2.15	0	chromatin
1	786	55	19	2.77	0	nucleosome
4	725	92	27	2.35	0	protein tyrosine phosphatase activity
15	925	93	26	2.24	0	focal adhesion
6	333	113	33	2.34	0	chromatin assembly or disassembly
6	357	607	116	1.53	0	regulation of transcription from RNA polymerase II promoter
8	134	468	89	1.53	0	transcription factor binding
8	138	40	18	3.61	0	protein tyrosine/serine/threonine phosphatase activity
19	653	1036	198	1.53	0	anatomical structure morphogenesis
19	790	434	83	1.53	0	embryonic development
19	986	253	56	1.78	0	cell surface
1	0628	464	88	1.52	0	positive regulation of gene expression
1	0926	922	177	1.54	0	anatomical structure formation
1	6564	263	57	1.74	0	transcription repressor activity
1	7017	13	8	4.94	0	MAP kinase tyrosine/serine/threonine phosphatase activity
3	0055	100	28	2.25	0	cell-substrate junction
3	2989	359	71	1.59	0	cellular component morphogenesis
3	3549	13	8	4.94	0	MAP kinase phosphatase activity
4	3353	7	6	6.87	0	enucleate erythrocyte differentiation
4	4427	319	65	1.63	0	chromosomal part
4	5893	383	77	1.61	0	positive regulation of transcription. DNA-dependent
4	8646	310	67	1.73	0	anatomical structure formation involved in morphogenesis
5	1093	478	92	1.54	0	negative regulation of developmental process
5	1254	385	77	1.60	0	positive regulation of RNA metabolic process
6	5003	501	94	1.50	0	macromolecular complex assembly
	902	328	65	1.59	1.00E-04	cell morphogenesis
5	694	388	75	1.55	1.00E-04	chromosome
16	924	97	26	2.15	1.00E-04	cell-substrate adherens junction
6	605	217	47	1.74	1.00E-04	protein targeting
•						
6	869	138	30	1.74	0.0015	lipid transport

OID Total Change   Encirchissement   P Value   Term     250 II   14   1.80   0   Cell cycle checkpoint   375   181   1.81   0   Cell cycle checkpoint   375   182   48   0   RM splicing, via transeterification reactions     278   422   176   1.50   0   mitotic cell cycle   376   152   48   2.04   0   RM splicing, via transeterification reactions with bulged adenosine as nucl     278   422   176   1.73   0   chromasine.centromeric region   375   148   51   2.24   0   stuctual constituent of rubscome     2842   126   9   1.95   0   nuclear envelope   561   1   0   stuctual constituent of rubscome     2854   388   180   1.65   0   nuclear envelope   561   14   15   0   nuclea/stuctual constituent of rubscome     2854   388   180   1.65   0   nuclear envelope   561   14   15   0   nuclea/stuctual constitu	IRF1						GABP					
75 81 41 1.80 0 cell cycle checkpoint 375 152 42 01 RM splicing, via transetterification reactions   278 422 178 1.50 0 mitotic cell cycle 375 152 48 2.04 0 RM splicing, via transetterification reactions wind splicing, via transetterification reactions   75 175 176 173 0 chromasime. centromeric region 378 182 180 0 nuclear nRM splicing, via transetterification reactions   756 175 60 1.63 0 nuclear nRM splicing, via transetterification reactions 378 183 181 0 nuclear nRM splicing, via transetterification reactions   758 175 60 1.63 0 nuclear nRM splicing, via transetterification reactions 373 18 511 0 neulcaptam   758 160 1.53 0 nuclear nRM splicing, via transetterification reactions 174 174 175 0 nucleaptam 174 174 175 0 nucleaptam 174 174 174 174 0 nucleaptam	GO.ID	Total	Change	Enrichissement	P.Value	Term	GO.ID	Total (	Change	Enrichissement P	Value	Term
226   127   61   1.71   0   microtubule cytoskeleton organization   377   152   44   2.04   0   RMA splicing, via transetterification such bulged adenosine as nuclea     775   102   48   1.68   0   chromosome, centromeric region   378   152   48   1.61   0   RMA splicing, via splicescome     1842   126   69   1.95   0   chromostin   373   1.61   0   nuclear RMA splicing, via splicescome     1842   126   69   1.95   0   ubiquitin-protein ligase activity   556   1.51   0   nuclead armelope   5561   1.51   0   nucleadiasm     6264   38   160   1.65   0   chromosome   5740   48   2.14   0   nucleadiasm     6264   18   1.0   nuclear armetope   574   48   2.14   0   nucleadiasm     6379   18   1.6   1.80   0   peneration of precursor metabolites and energy   570   585   157 <th>75</th> <th>81</th> <th>41</th> <th>1.80</th> <th>0</th> <th>cell cycle checkpoint</th> <th>375</th> <th>152</th> <th>48</th> <th>2.04</th> <th>0</th> <th>RNA splicing. via transesterification reactions</th>	75	81	41	1.80	0	cell cycle checkpoint	375	152	48	2.04	0	RNA splicing. via transesterification reactions
278 422 178 1.50 0 mitotic cell cycle 38 152 48 0 nuclear mRM splicing, via spliceosome   775 102 48 168 0 chromasime. centromeric region 373 148 51 2.0 0 spliceosome   775 102 48 168 0 chromasime. centromeric region 373 148 51 2.0 spliceosome spliceosome   5855 175 80 1.63 0 nuclear mwlope 557 31 16 0 reglection fork   5643 68 35 1.81 0 nuclear onthologo 570 0 spliceosomal complex   5749 208 95 1.63 0 spindle 540 685 174 0 micbohial evelope   5719 11 55 1.63 0 spindle 540 174 15 0 micbohia   5719 14 1.74 0 oxidative phosphorylation 6439 165 174 174 0 micbohia	226	127	61	1.71	0	microtubule cytoskeleton organization	377	152	48	2.04	0	RNA splicing. via transesterification reactions with bulged adenosine as nucleophile
775   102   48   1.68   0   chromasome.centromeric region   775   102   48   1.68   0   chromasim     1842   126   69   1.95   0   ubiquitin-protein ligase activity   555   175   80   1.63   0   nuclear envelope   556   175   80   1.61   0   nuclear envelope   556   1.75   103   161   0   nuclear envelope     5636   1.63   0   nuclear envelope   556   1.75   0   nucleato fork     5647   3.8   1.00   1.65   0   chromosome   570   641   1.74   1.75   0   nucleato fork     579   2.08   5   1.63   0   chromosome   570   641   1.74   1.75   0   nucleato fork     5819   11   56   1.80   0   chromatim amitrix   570   65   157   2.01   0   RNA pocessing     5825   3.4   1.49 <t< th=""><th>278</th><th>422</th><th>178</th><th>1.50</th><th>0</th><th>mitotic cell cycle</th><th>398</th><th>152</th><th>48</th><th>2.04</th><th>0</th><th>nuclear mRNA splicing, via spliceosome</th></t<>	278	422	178	1.50	0	mitotic cell cycle	398	152	48	2.04	0	nuclear mRNA splicing, via spliceosome
785 177 6 1.73 0 chromatin 775 188 51 2.23 0 statuctal constituent of hiosome   824 126 69 1.95 0 unclear envelope 555 175 180 163 0 nuclear envelope 5561 12 24 0 splicotion fork   8544 88 180 1.65 0 chromosome 5571 248 163 14 175 18 1.13 0 mitochondrial matrix 550 163 163 163 163 163 163 163 163 163 163 164 175 18 164 175 18 164 175 18 164 175 18 164 175 18 163 163 163 164 156 18 164 175 18 164 175 18 164 175 18 164 174 175 18 164 174 175 18 164 174 175 18 175 18 164 174	775	102	48	1.68	0	chromosome. centromeric region	3723	647	155	1.55	0	RNA binding
1482   126   69   1.95   0   ubiquito.protein ligase activity   654   75   178   161   0   nucleogiam     564   76   183   0   nuclear pre   657   75   88   184   0   nuclear pre   551   175   88   180   0   nucleogiam     5643   38   180   1.65   0   nuclear pre   551   12   48   2.41   0   splicessomal complex     5749   208   95   1.53   0   mitochondrial matrix   574   858   85   1.55   0   nucleogiam     5719   208   95   1.53   0   generation of precursor metabolites and energy   535   15   0   nitAlprocessing     5719   84   1   1.74   0   oxidative phosphorylation   639   56   157   0   nitAlprocessing     572   218   1.58   0   chromatin assembly or disassembly   639   64   12	785	157	76	1.73	0	chromatin	3735	148	51	2.23	0	structural constituent of ribosome
655   175   80   1.63   0   nuclear envelope   657   34   16   3.04   0   replication fork     6543   68   35   1.84   0   nuclear envelope   6581   38   180   1.65   0   chromsome   6581   358   180   1.65   0   chromsome   570   203   55   65   155   0   nucleave   5819   111   56   1.80   0   spindle   570   203   55   15   0   nucleave   5819   111   56   1.80   0   spindle   530   16   41   2.14   0   nicobandia envelope     5011   11   56   1.80   0   spindle   530   16   41   2.14   0   nicobandia envelope     5200   207   8   1.52   0   DNA repsing   533   16   41   101   1.59   1   1.53   0   nitracellular protein transport   533	4842	126	69	1.95	0	ubiquitin-protein ligase activity	5654	753	188	1.61	0	nucleoplasm
643   65   1.84   0   nuclea pore   650   128   48   2.41   0   splicesoomal complex     644   88   35   1.85   0   niconomas   570   203   95   1.63   0   mitochondrial matrix   5740   355   55   1.55   0   micochondrial envelope     519   11   56   1.80   0   spindle   5769   203   55   1.55   0   micochondrial envelope     519   129   1.53   0   generation of precursor metabolites and energy   536   517   201   0   RNA pocessing     5255   344   149   1.54   0   chormatin organization   639   612   70   18   1.89   0   translation     5335   54   1.83   0   chormatin assembly or disasembly   683   612   70   18   1.89   0   translation     5345   154   71   1.64   0   protein folding	5635	175	80	1.63	0	nuclear envelope	5657	34	16	3.04	0	replication fork
6644   38   100   1.65   0   chromsome mitochondrial matrix   570   200   673   643   74   1.75   0   nucleolus     5819   100   1.65   0   spindle   570   208   570   208   570   208   570   208   570   208   570   208   570   208   570   208   570   208   208   100   100   spindle   570   580   158   0   mitochondrial matrix     5819   101   1.52   0   protein toppication   587   30   9   650   177   201   0   mitAprocessing     5323   14   1.91   1.52   0   Intracellular protein transport   537   10   184   164   164   164   10   184   164   1830   1   11   154   174   174   174   174   174   174   174   174   174   174   174 <t< th=""><th>5643</th><th>68</th><th>35</th><th>1.84</th><th>0</th><th>nuclear pore</th><th>5681</th><th>129</th><th>48</th><th>2.41</th><th>0</th><th>spliceosomal complex</th></t<>	5643	68	35	1.84	0	nuclear pore	5681	129	48	2.41	0	spliceosomal complex
S759   208   95   1.63   0   mitochondrial matrix   570   270   280   1.63   0   mitochondrial matrix     S819   111   56   1.80   0   spindle   540   1.53   0   generation of precursor metabolites and energy   536   556   1.51   0   mitochondrial envelope     S119   84   41   1.74   0   oxidative phosphorylation   539   10   54   2.01   0   RNA processing     S252   344   1.49   1.54   0   chromatin assembly or disasembly of disasembly   688   11   10   tansilation     S336   505   219   1.55   0   RNA processing   830   670   180   0   transilation     S412   370   158   1.52   0   RNA processing   830   1607   36   12   19   0   transilation     S412   370   158   152   14   11   1.64   0   pro	5694	388	180	1.65	0	chromosome	5730	643	174	1.75	0	nucleolus
S819   111   56   1.80   0   spindle	5759	208	95	1.63	0	mitochondrial matrix	5740	355	85	1.55	0	mitochondrial envelope
Story   1.53   0   generation of precursor metabolites and energy   635   656   17   2.01   0   RNA processing     5260   207   88   1.52   0   DNA replication   639   105   41   2.33   0   replication   639   105   41   101   1.53   0   replication   639   105   50   replication   639   105   50   replication   639   105   0   replication   639   105   0   replication   639   105   105   150   replication   105   101   140   replication replication   105   101   140   replication replication   replication replication   105   101   140   repl	5819	111	56	1.80	0	spindle	5840	186	62	2.16	0	ribosome
1119 84 1 1,74 0 oxidative phosphorylation 6397 301 95 2,04 0 mRIA processing   2020 207 84 1,52 0 DNA replication 6397 505 0 mRIA processing   2020 207 84 1,54 0 chromatin organization 6412 370 1,85 0 trinstation   2030 505 219 1,55 0 RNA processing 603 6412 370 1,89 0 intracellular protein transport   2039 105 53 1,80 0 translation 1601 141 101 1,814 matcellular protein transport   2142 370 1,56 1,82 0 translation 1601 146 12.2 0 trinsportein complex biogenesis   2142 370 1,56 0 ortopini transport transport 1601 156 2.19 0 trinsportein complex biogenesis   2142 370 1,56 0 ortopini transport transport transport t	6091	301	129	1.53	0	generation of precursor metabolites and energy	6396	505	157	2.01	0	RNA processing
S260   207   88   1.52   0   DNA reglication   619   165   41   2.53   0   HNA metabolic process     S253   344   449   1.54   0   chromatin organization   617   70   108   1.52   0   HNA metabolic process     S333   13   58   1.83   0   chromatin assembly or disassembly   685   411   101   1.59   0   IntraceIlular protein transport     S339   105   53   1.80   0   translation   6805   411   101   1.59   0   RNA splicing     S471   154   0   protein folding   2261   105   5   2.19   0   ribourcleoprotein complex biogenesis     S511   122   9   1.56   0   anti-apoltosis   3165   2   2.04   0   ribourcleoprotein complex biogenesis     S516   13   1.54   0   intraceIlular protein transport   3156   2   2.04   0   ribourcleoprotein complex	6119	84	41	1.74	0	oxidative phosphorylation	6397	301	95	2.04	0	mRNA processing
5325   3.4   14   9   1.54   0   chromatin arganization   6412   70   108   1.89   0   translation     333   113   5   18   0   chromatin arganization   6805   11   101   1.99   0   translation     333   16   5   18   0   chromatin arganembly of disasembly   6805   11   101   1.99   0   translation     339   105   53   180   0   translation   cprotein folding   2307   105   12   0   tRNA metabolic process     2457   154   71   1.64   0   protein folding   2201   155   5   19   0   translation     2457   154   71   1.64   0   protein folding   2201   155   5   19   0   translation     2105   163   84   1.55   0   approtein transport   anti-approtein transport   31145   2   2	6260	207	88	1.52	0	DNA replication	6399	105	41	2.53	0	tRNA metabolic process
5333   113   58   1.83   0   chromatin assembly or disassembly   688   411   110   1.59   0   intracellular protein transport     3369   505   53   1.80   0   chromatin assembly or disassembly   688   411   110   1.59   0   intracellular protein transport     3396   505   53   1.80   0   tRNA processing   830   274   91   2.56   0   RNA splicing     3471   154   71   1.64   0   protein folding   22613   165   2.91   0   ribroucleoprotein complex togenesis     5816   411   178   1.55   0   anti-appotais   3116   5   2.19   0   ribroucleoprotein complex togenesis     5816   411   178   1.55   0   anti-appotais   3116   5   2.19   0   ribroucleoprotein complex dependent proteasomal ubiquitin-dependent protein stransport     5816   411   178   1.57   0   mitochondrian emitonemitogo angliza-dependent prot	6325	344	149	1.54	0	chromatin organization	6412	370	108	1.89	0	translation
S396   505   219   1.55   0   RNA processing   8033   65   25   2.40   101   MA processing     399   105   3   1.80   0   tRNA metabolic process   830   427   91   0   mBA processing     3412   370   158   1.52   0   translation   16011   345   122   191   0   mBA processing     5457   154   71   1.64   0   protein folding   2291   5   5   2.19   0   mBA processing     5866   411   178   1.54   0   intracellular protein transport   3115   2   2   2   2   0   respiratory electron transport chain     7005   16   1.72   0   mitochondrion organization   3195   35   8   1.54   0   mitochondrial membrane     7005   16   1.72   0   mitochondrian regulation of gene expression   3194   10   mitochondrian membrane   mitochondrian membra	6333	113	58	1.83	0	chromatin assembly or disassembly	6886	411	101	1.59	0	intracellular protein transport
S399   105   5.3   1.80   0   tRNA metabolic process   S380   274   91   2.16   0   RMA splicing     242   370   156   1.52   0   translation   1607   156   1.2   0   RMA splicing     2447   370   156   1.52   0   protein folding   22613   156   52   2.9   0   ribonucleoprotein complex biogenesis     5816   111   778   1.54   0   intra-eoptosis   3106   2   2.2   2.0   0   ribonucleoprotein complex biogenesis     5705   106   51   1.72   0   mitochondrion organization   3196   32   0   ribonucleoprotein complex     7005   16   51   1.72   0   mitochondrion organization   3196   325   0   ribonucleoprotein complex   mitochondrion organization   3197   453   0   mitochondriol membrase     0503   457   1.51   0   pottramitoripoint orgenization   3197	6396	505	219	1.55	0	RNA processing	8033	66	25	2.45	0	tRNA processing
5412 370 158 1.52 0 translation f6071 346 102 1.91 0 mRVA metabolic process   5471 15.4 0 protein folding 22613 55 56 0 mbiting 22613 55 0 0 reports holes   5511 212 93 1.56 0 ubiquitin-dependent protein catabolic process 2294 52 20 2.49 0 reports holes   5866 411 176 1.54 0 intra-eplotisis 2294 52 20 2.49 0 reports holes   5916 133 84 1.55 0 anglass-gronting complex-dependent protein catabolic process 3115 5 2.23 0 maphass-gronting complex-dependent protein catabolic process   7005 106 51 1.72 0 mitotic cell cycle checkpoint 3194 3.5 0 maphass-gronting complex-dependent protein sci anglass   3080 274 16 1.51 0 RNA splicing 3191 18 39 2.14 0 micchondrial membrane-dosed luma<	6399	105	53	1.80	0	tRNA metabolic process	8380	274	91	2.15	0	RNA splicing
9457   154   71   1.64   0   protein fidding   22613   155   52   2.0   0   nbouncleoprotein complex biogenesis     511   212   3   1.56   0   ubiquitin dependent protein catabolic process   22043   155   2.0   0   nbouncleoprotein complex biogenesis     5886   411   178   1.54   0   intracellular protein transport   30529   447   1.7   2.13   0   nbouncleoprotein complex     7005   105   51   1.72   0   mitochondrion organization   3195   32   0   nbouncleoprotein complex     3030   274   165   1.51   0   mitochondrion organization   3196   35   80   1.54   0   michochondrion mechane   1264   0   michochondrion mechane   1264   0   michochondrion mechane   1264   0   michochondrion   1264   18   0   michochondrion   1147   0   michochondrion   1264   0   michochondrion   1264   0	6412	370	158	1.52	0	translation	16071	346	102	1.91	0	mRNA metabolic process
5511   212   93   1.56   0   ubiquitin-dependent protein catabolic process   2234   52   2.48   0   repiratory electron transport chain     886   111   178   1.54   0   intracellular protein transport   3029   42   2.0   2.48   0   repiratory electron transport chain     5916   193   84   1.55   0   anti-apoptosis   3114   63   23   2.36   0   mitochoodial membrane     903   49   2.8   2.04   0   mitocic cell cycle checkpoint   3194   747   40   1.58   0   mitochoodial membrane     9309   2.74   1.61   1.51   0   RNA splicing   3194   128   2.7   1.64   0   nuclear lumen     9300   7.5   1.51   0   posttranscriptional regulation of gene expression   3191   18   12   2.14   0   nclear lumen     6530   15   12   2.85   0   cyclin-dependent protein kinase regulator activity   <	6457	154	71	1.64	0	protein folding	22613	165	56	2.19	0	ribonucleoprotein complex biogenesis
8886   411   178   1.54   0   intracellular protein transport   3629   447   1/7   2.13   0   inbonucleoprotein complex     9716   193   44   1.55   0   anti-apoptosis   3116   2   2.0   0   mitochondrian membrane     9705   106   51   1.72   0   mitochondrian organization   3195   335   80   1.54   0   mitochondrian membrane     9708   49   28   2.04   0   mitocic oell cycle checkpoint   3196   335   80   1.54   0   mitochondrian membrane   mitochondrian membrane     9708   49   28   2.04   0   mitotic cell cycle checkpoint   3197   168   0   mitochondrian membrane	6511	212	93	1.56	0	ubiquitin-dependent protein catabolic process	22904	52	20	2.49	0	respiratory electron transport chain
9916   193   84   1.55   0   anti-apoptosis   31145   63   23   2.36   0   anaphase-pronoting complex-dependent proteasomal ubiquitin dependent protein ca     7093   49   28   2.04   0   mitochcondroil a membrase-anologica   31965   58   1.51   0   mitochcondroil a membrase-anologica   3196   1.58   0   membrase-anologica   31974   1637   400   1.58   0   membrase-anologica   3196   326   2.7   1.64   0   membrase-anologica   31974   1637   400   1.58   0   membrase-anologica   3196   327   1.64   0   membrase-anologica   3196   327   1.64   0   nuclear lumen     0500   177   75   1.51   0   microtubule cytoskeleton   3197   3297   1.64   0   nuclear lumen     0503   15   12   2.85   0   cyclin-dependent protein kinase regulator activity   3197   18   3271   18   3213   0   ncRNA spice	6886	411	178	1.54	0	intracellular protein transport	30529	447	147	2.13	0	ribonucleoprotein complex
V105   0.5   5.1   1.7.2   0   mitochondrion organization   31956   335   80   1.5.4   0   mitochondrial membrane     038.0   2.74   1.6   1.5.1   0   RNLA splicing   3194   1.67   400   1.68   0   mutochondrial membrane     0608   17.7   7.5   1.5.1   0   Posttranscriptional regulation of gene expression   3191   126   2.7   1.6.4   0   mutochondrial membrane     0508   15.7   1.5.1   0   posttranscriptional regulation of gene expression   3191   118   39   2.14   0   mutochondrial membrane     0530   455   153   1.2   2.85   0   cyclin-dependent protein kinase regulator activity   3401   164   54   2.13   0   ncRNA processing     0531   15   12   2.85   0   cyclin-dependent protein kinase regulator activity   34513   441   117   1.7   0   cellular protein kinazianin     05657   117   64	6916	193	84	1.55	0	anti-apoptosis	31145	63	23	2.36	0	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process
V093   49   28   2.04   0   mitotic cell cycle checkpoint   319/24 f637   400   1.58   0   membrane-molosed lumen     3380   274   116   1.51   0   RNA splicing   319/24 f637   400   1.58   0   nuclear lumen     0508   177   5   1.51   0   posttranscriptional regulation of gene expression   322/9   116   39   2.14   0   nicosmal subunit     6530   456   193   1.51   0   microtubule cytoskeleton   34/10   164   44   1.95   o   ncRNA splicing     6531   12   2.85   0   cyclin-dependent protein kinase regulator activity   34613   411   107   1.57   0   cellular potein localization     6567   17   64   1.95   0   protein ubiquitination   34600   V1   72.25   0   ncRNA metabolic process	7005	106	51	1.72	0	mitochondrion organization	31966	335	80	1.54	0	mitochondrial membrane
3380   274   116   1.51   0   RNA splicing   31981 128   327   1.64   0   nuclear luman     0508   177   75   1.51   0   posttranscriptional regulation of gene expression   3379   11983   227   1.64   0   nuclear luman     5630   456   193   1.51   0   microtubule cytoskeleton   3470   16   54   2.13   0   ncRNA spicessing     6538   15   12   2.85   0   cyclin-dependent protein kinase regulator activity   34613   441   107   1.57   0   cellular protein luciazion     6567   117   64   1.95   0   protein ubiquitination   3460   24   71   2.6   0   cellular protein ubiquitoscess	7093	49	28	2.04	0	mitotic cell cycle checkpoint	31974	1637	400	1.58	0	membrane-enclosed lumen
0608   177   75   1.51   0   posttranscriptional regulation of gene expression   32279   118   39   2.14   0   infotomal submit     15630   456   193   1.51   0   microtubule cytoskeleton   34470   144   54   2.13   0   ncRNA processing     6538   15   2   2.85   0   cyclin-dependent protein kinase regulator activity   34613   4441   107   157   0   ellular prein localization     6576   117   64   1.95   0   protein ubiquitination   3460   204   71   2.25   0   ncRNA metabolic process	8380	274	116	1.51	0	RNA splicing	31981	1286	327	1.64	0	nuclear lumen
6503   6503   6503   6503   15   12   2.85   0   cyclin-dependent protein kinase regulator activity   34/10   164   54   2.13   0   ncRNA protein ubication     6538   15   12   2.85   0   cyclin-dependent protein kinase regulator activity   34613   4411   107   1.57   0   cellular protein ubicatization     6567   117   64   1.95   0   protein ubiquitination   34600   22.25   0   ncRNA metabolic process	0608	177	75	1.51	0	posttranscriptional regulation of gene expression	33279	118	39	2.14	0	ribosomal subunit
6538   15   12   2.85   0   cyclin-dependent protein kinase regulator activity   34613   441   107   1.57   0   cellular protein localization     6567   117   6.4   1.95   0   protein ubiquitination   3469   246   7.1   2.25   0   ncMM netabolic process	5630	456	193	1.51	0	microtubule cytoskeleton	34470	164	54	2.13	0	ncRNA processing
16567 117 64 1.95 0 protein ubiquitination 34660 204 71 2.25 0 ncRNA metabolic process	6538	15	12	2.85	0	cyclin-dependent protein kinase regulator activity	34613	441	107	1.57	0	cellular protein localization
	6567	117	64	1.95	0	protein ubiquitination	34660	204	71	2.25	0	ncRNA metabolic process

CREB						YY1					
GO.ID	Total	Change	Enrichissement	P.Value	Term	GO.ID	Total	Change E	nrichissement	P.Value	Term
75	81	45	1.74	0	cell cycle checkpoint	313	49	14	5.40	0	organellar ribosome
87	238	129	1.70	0	M phase of mitotic cell cycle	314	19	7	6.96	0	organellar small ribosomal subunit
151	77	45	1.84	0	ubiguitin ligase complex	375	152	27	3.35	0	RNA splicing. via transesterification reactions
226	127	65	1.61	0	microtubule cytoskeleton organization	377	152	27	3.35	0	RNA splicing. via transesterification reactions with bulged adenosine as nucleophile
278	422	221	1.64	0	mitotic cell cycle	398	152	27	3.35	0	nuclear mRNA splicing. via spliceosome
279	334	169	1.59	0	M phase	3723	647	83	2.42	0	RNA binding
280	236	128	1.70	0	nuclear division	3735	148	29	3.70	0	structural constituent of ribosome
502	46	28	1.91	0	proteasome complex	5739	966	94	1.84	0	mitochondrion
775	102	65	2.00	0	chromosome. centromeric region	5759	208	31	2.81	0	mitochondrial matrix
776	61	42	2.16	0	kinetochore	5761	49	14	5.40	0	mitochondrial ribosome
777	42	29	2.17	0	condensed chromosome kinetochore	5763	19	7	6.96	0	mitochondrial small ribosomal subunit
779	46	30	2.05	0	condensed chromosome. centromeric region	5840	186	34	3.45	0	ribosome
785	157	85	1.70	0	chromatin	6396	505	72	2.69	0	RNA processing
793	98	55	1.76	0	condensed chromosome	6397	301	45	2.82	0	mRNA processing
910	35	23	2.06	0	cytokinesis	6412	370	61	3.11	0	translation
3697	55	35	2.00	0	single-stranded DNA binding	8380	274	42	2.89	0	RNA splicing
3713	201	100	1.56	0	transcription coactivator activity	10467	3247	280	1.63	0	gene expression
3723	647	312	1.51	0	RNA binding	16070	2157	180	1.58	0	RNA metabolic process
3735	148	79	1.68	0	structural constituent of ribosome	16071	346	48	2.62	0	mRNA metabolic process
4298	19	15	2.48	0	threonine-type endopeptidase activity	16607	93	19	3.86	0	nuclear speck
4386	125	69	1.73	0	helicase activity	30529	447	61	2.58	0	ribonucleoprotein complex
4842	126	67	1.67	0	ubiquitin-protein ligase activity	319/4	1637	136	1.57	U	membrane-enclosed lumen
5635	175	100	1.79	0	nuclear envelope	31980	208	31	2.81	0	mitochondrial lumen
5643	68	45	2.08	Ō	nuclear pore	32991	2342	194	1.56	0	macromolecular complex
5654	753	360	1.50	0	nucleoplasm	33279	118	20	3.20	U	ribosomai subunit
5657	34	24	2.22	0	replication fork	34660	204	28	2.59	U	nckNA metabolic process
5681	129	70	1.70	0	spliceosomal complex	43233	1007	135	1.59	0	organelle lumen
5694	388	214	1.73	Ő	chromosome	44267	2354	193	1.55	0	cellular protein metabolic process
5759	208	100	1.51	0	mitochondrial matrix	44429	010	20	2.11	1 005 04	ATD such as a such a last a transmit
6281	263	133	1.59	ō	DNA repair	42/13	40	10	4.20	1.00E-04	ATP synthesis coupled electron transport
				-							

Supplementary Figure 4: For each transcription factor and PRC coactivator most representative gene ontologies (n=30) for positive genes on ChIP-chip were determined using GOMiner software.

## Supplementary Table 1: Primers used for quantitative RT-PCR analysis

CYCS	For: 5'-CCAGTGCCACACCGTTGAA-3' Rev: 5'-TCCCCAGATGATGCCTTTGTT-3';
CITED2	For: 5'-GCGAAGGAGGATGCCAACC-3' Rev: 5'-CAGCTGCATACTAGCCAGCA-3'
COX18	For: 5'-CATCAGCACCACTTCACGAA-3' Rev: 5'-CCACCAACTGTCAGAAGCAT-3'
CAMK2A	For: 5'-TACGGCGACGAGAAGCTGAG-3' Rev: 5'-AGACACCAGGAGGTGCCTTG-3'
COX4I2	For: 5'-GGTGGAAGACGAGGGATGCA-3' Rev: 5'-CAGCTGGGTCCAGCTTCCCT-3'
HIF1	For: 5'-AGGAGCTGAGTTGGAATAGTG-3' Rev: 5'-CCAGCTATCTTACTAGTGGGTG-3'
NDUFC1	For: 5'-GCCGTCTGGTTACTGTAATC-3' Rev: 5'-GGTTACTCAGTGTCATCTTG-3'
POLG2	For: 5'-CAACGGAGGTGAGCGTGC-3' Rev: 5'-GAGGTGTATATAGAAGGTGAT-3'
UCP2	For: 5'-CATTCTGACCATGGTGCGTACTGA-3' Rev: 5'-GTTCATGTATCTCGTCTTGACCAC-3'
UQCR	For: 5'-CTTCCTGGGCCCACGCTACC-3' Rev: 5'-GTCCAGGATCAGCCGCCAAT-3'
β-globin	For: 5'-CAACTTCATCCACGTTCACC-3' Rev: 5'-ACACAACTGTGTTCACTAG-3'