

1 **Supplementary figure legends**

2 **Figure S1. PATZ1 is essential for hESC pluripotency.** (A-B) Immunostaining of
3 endogenous PATZ1 indicated the nucleus distribution of wild-type H1 hESCs (A) and
4 confirmed by western blotting assay (B). DAPI served as nuclear staining. Scale bar =
5 100 μ m. (C) A representative alkaline phosphatase staining of hESCs transfected with
6 scrambled- and *PATZ1*- RNAi. (D) Inducing wild-type H1 hESCs (Left) and *PATZ1*-
7 KD stable cells (Right) into EB cells. Scale bar = 100 μ m. (E) EBs induced from
8 *PATZ1*-depleted hESCs more likely differentiate into mesoderm and endoderm as
9 compared to EBs induced from wild type hESCs, particularly in. The expression of the
10 genes in control cells was arbitrary considered "1". All data were presented as mean \pm
11 SD (n=3).

12

13 **Figure S2. Loss of PATZ1 globally activates human ES cell differentiation.** (A) RT-
14 qPCR validation for RNA-seq results. *β -ACTIN* serves as endogenous controls for
15 quantification. (B-C) RNA-seq heatmap generated from pluripotency (B) and
16 development (C) related gene expression levels. Relatively highly expressed genes
17 were shown in dark blue, while low expressed genes were colored pale green. All data
18 were presented as mean \pm SD (n=3).

19

20 **Figure S3. PATZ1 binds to distal promoters of *OCT4* loci.** (A/B) Top: CR3/CR4
21 region was cloned into the downstream of luciferase gene driven by SV40 promoter.
22 Bottom: Luciferase activity of CR3/CR4 in *PATZ1*-depleted cells.

23

24 **Figure S4. Genome-wide location analysis of PATZ1.** (A) RT-PCR validation for
25 ChIP-Seq. (B) Left: Genomic distribution of PATZ1 binding loci by statistics of ChIP
26 annotation. Right: ngsPlot depicted the distribution of average reads of PATZ1, which
27 were highly enriched in TSS. (C) On average, approximately 500 bp of PATZ1 binding
28 peaks were distributed in a 50-percentile position of summits surrounding the PATZ1
29 motif. (D) Endogenous Co-IP of PATZ1 and OCT4 and NANOG confirmed the
30 interaction of PATZ1/OCT4 and PATZ1/NANOG. The input fraction was total hESC
31 lysate while IgG IP served as negative control. (E) GO analysis of PATZ1-associated
32 genes (biological process). (F) RNA-editing results indicated that the occurrence of
33 differential A \rightarrow G editing events upon *PATZ1* knockdown. High frequency of
34 pluripotency gene, *DPPA4*, *LIN2A* and *NANOG* underwent RNA-editing upon *PATZ1*
35 knockdown. All data were presented as mean \pm SD (n=3).

36

37 **Figure S5. Loss of PATZ1 impairs cell proliferation and triggers cell apoptosis.** (A)
38 Cell viability of hESCs at 24- and 48-hours after transfection of *PATZ1*-RNAi. (B)

39 Wright-Giemsa staining showed the morphology of hESCs upon *PATZ1*-RNAi. The
40 arrows indicated the shrinking chromosome plates. Scale bar=100 μ m. (C) mRNA level
41 of cell cycle genes upon *PATZ1* knockdown. (D) Summary of each cell population
42 labeled with the fluorescence intensity of Annexin V⁺PI⁻. (E) Summary of each cell
43 generation labeled with the fluorescence intensity of CFSE. Right: The summary of each
44 cell cycle labeled with the fluorescence intensity of PI. (F) Statistics of each cell
45 population labeled with the fluorescence intensity of PI. (G) RNA-seq heatmap
46 generated from cell cycle phases gene expression levels. Relatively highly expressed
47 genes were shown in dark purple, while low expressed genes were colored in pale
48 purple. All data were presented as mean \pm SD (n=3). Significance: * $p \leq 0.05$, ** $p \leq$
49 0.01, *** $p \leq 0.001$.

50

51 **Figure S6. Absence of PATZ1 destroys the mitochondrial function.** (A) A
52 representative graph for Seahorse measurements of ECR. (B) Quantification of ECR
53 parameters. (C-D) Knockdown of *PATZ1* did not reduce the transcriptomic (C) and
54 protein level (D) of mitochondria biogenesis genes: MFF, DRP1, and TOM20. GAPDH
55 served as loading control. (E) Loss of *PATZ1* significantly reduced the JC-red
56 fluorescence (polarization, high membrane potential), while increased the JC-green
57 fluorescence. Scale bar=75 μ m. (F) Quantification of mitochondrial DNA copy number,
58 *MT-ND1* and *MT-ND4* relative to nuclear DNA measured qPCR upon *PATZ1* depletion
59 and normalized to *B2M*. (G) Protein sequence alignment of *PATZ1* from different
60 mammals. The reactivity of cysteines is enhanced by positively charged amino acids
61 like arginine (R) and lysine (K), as indicated those amino acids with a '+' sign.

62

63 **Figure S7. PATZ1 regulates homeostasis of hESCs.** (A) knockdown of *PATZ1* caused
64 the misexpression of metabolic genes, including genes involved in glycolysis, fatty acid
65 oxidation, tricarboxylic acid cycle, lipid metabolism, and amino acid biosynthesis. (B)
66 Depletion of *PATZ1* reduced the protein level of representative glycolytic genes:
67 GLUT1, PDH, G6PD, LDHA, HK1, HK2 and PKM2. GAPDH served as loading
68 control. (C) Snapshots of *PATZ1* ChIP-seq signals at metabolic genes loci: *PFKP*,
69 *PHGDH*, *ELOVL5*, *GLUD1*, *PTGER1*, and *PKM*. (D) Heatmap of metabolite levels,
70 as measured by LC/MS/MS metabolomics in hESCs upon *PATZ1* KD.

71

72 **Supplementary figures**

73 Figure S1. *PATZ1* is essential for hESC pluripotency.

74 Figure S2. Loss of *PATZ1* globally activates human ES cell differentiation.

75 Figure S3. *PATZ1* binds to distal promoters of *OCT4* loci.

76 Figure S4. Genome-wide location analysis of *PATZ1*.

77 Figure S5. Loss of PATZ1 impairs cell proliferation and triggers cell apoptosis.

78 Figure S6. Absence of PATZ1 destroys the mitochondrial function.

79 Figure S7. PATZ1 regulates homeostasis of hESCs.

80

81 **Supplementary Tables**

82 Supplementary Table 1. Primers for plasmid construction.

83 Supplementary Table 2. RT-PCR primers being used.

84 Supplementary Table 3. Primary antibodies being used.

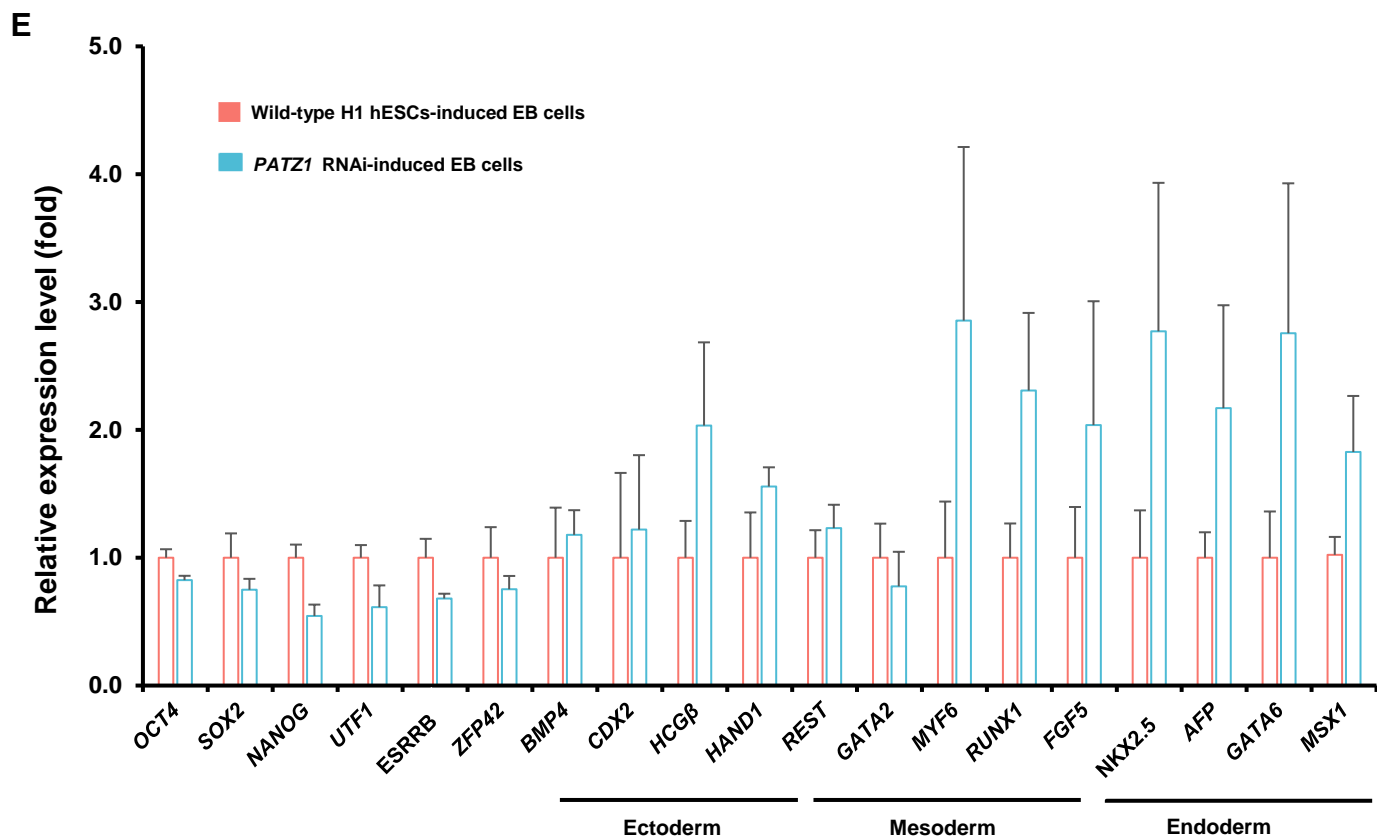
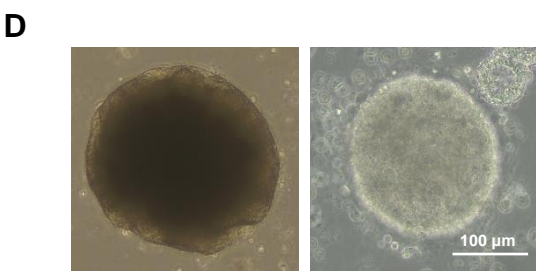
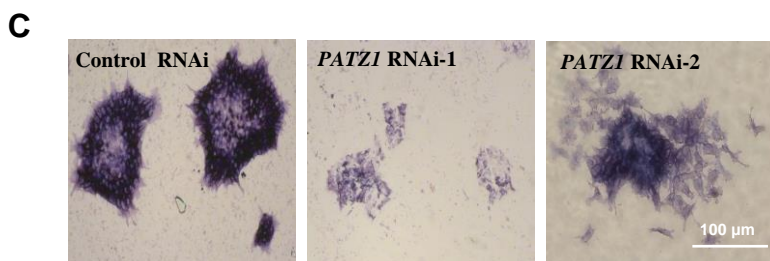
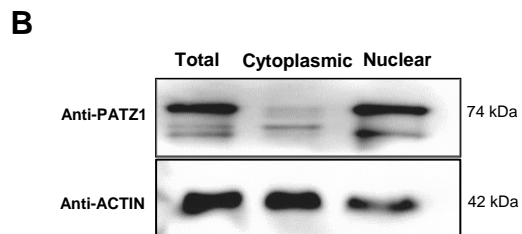
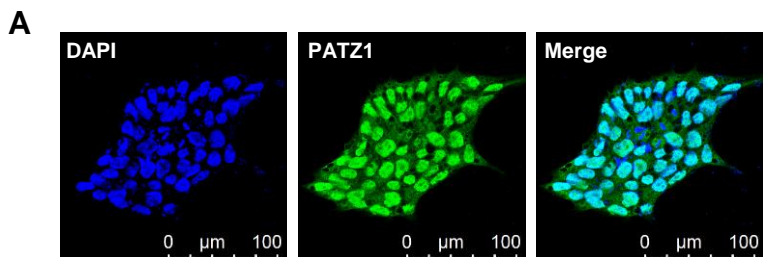
85 Supplementary Table 4. Top 100-ranked peak heights of PATZ1-ChIP peaks.

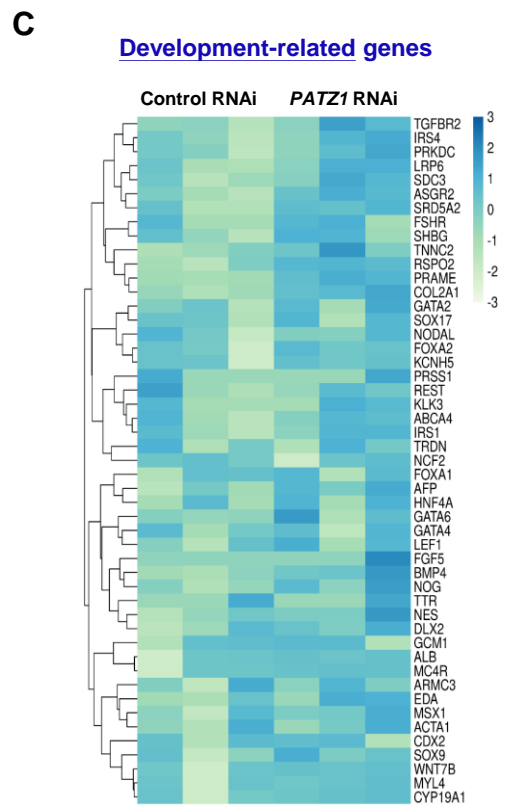
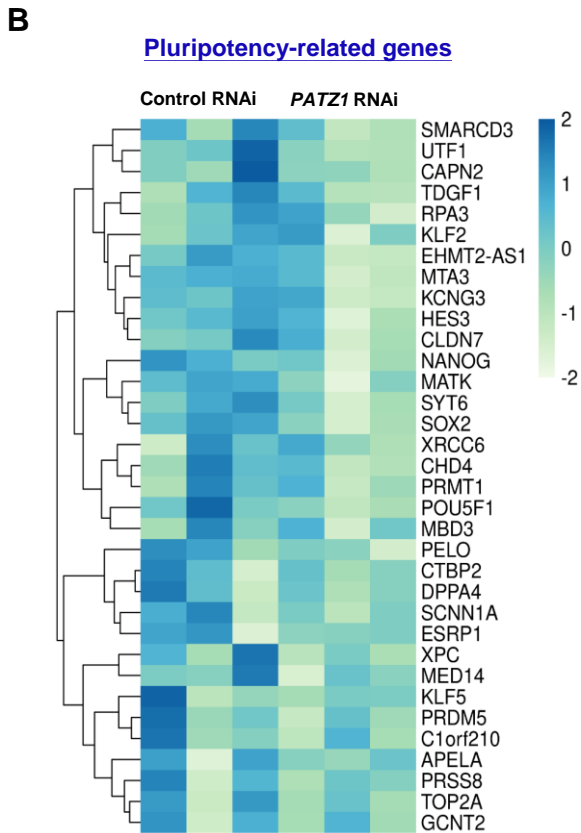
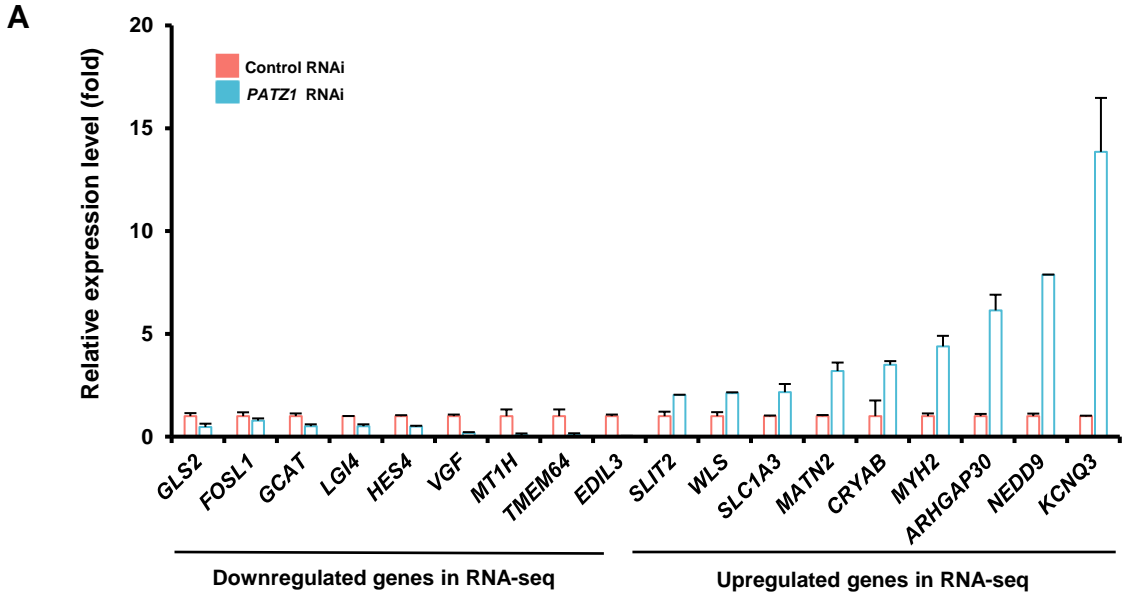
86 Supplementary Table 5. Differential expression analysis of altered gene in RNA-seq
87 analysis upon *PATZ1* RNAi.

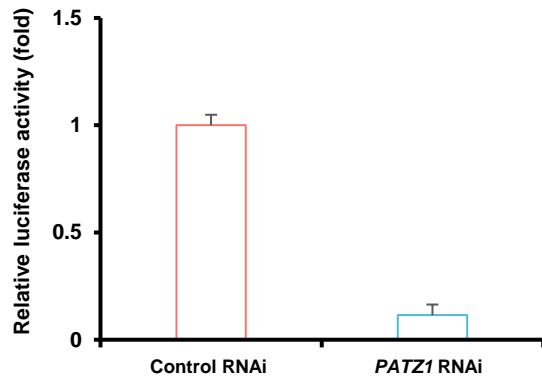
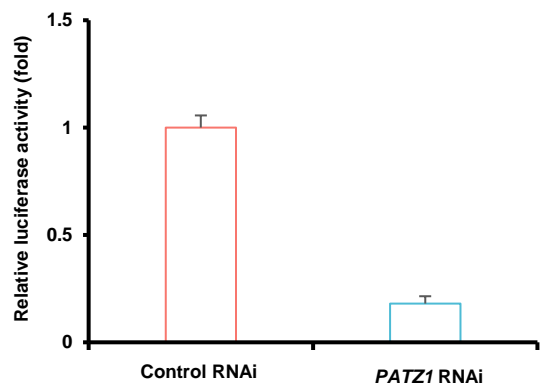
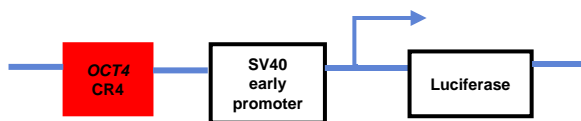
88 Supplementary Table 6. Calculation equations of ATP production from Seahorse assay.

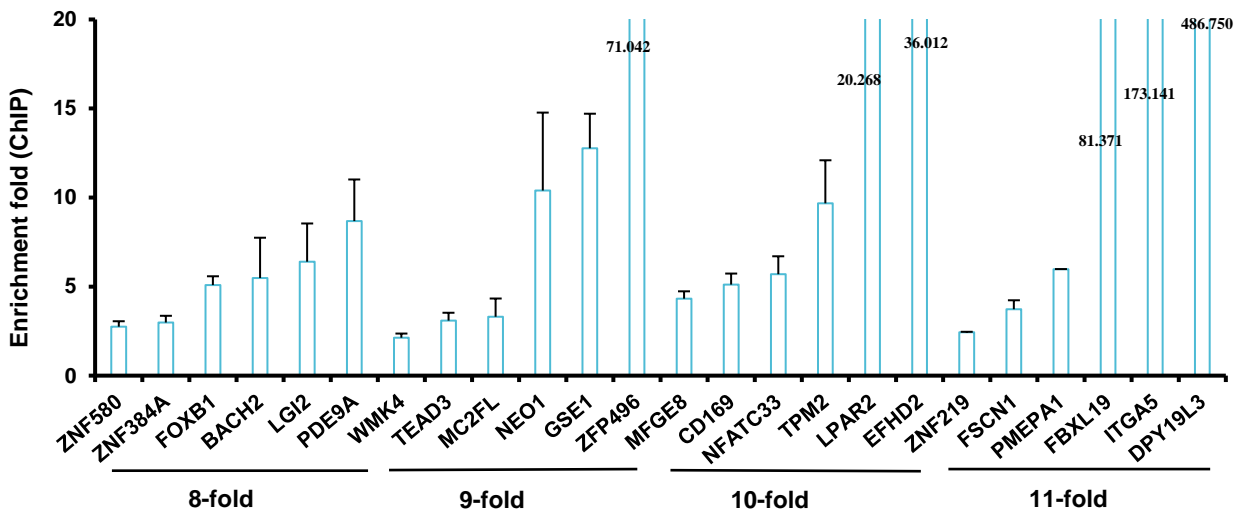
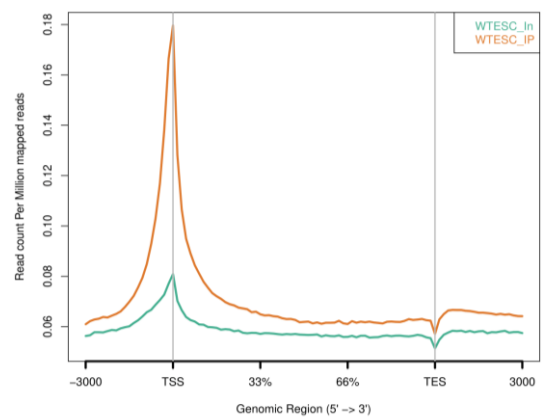
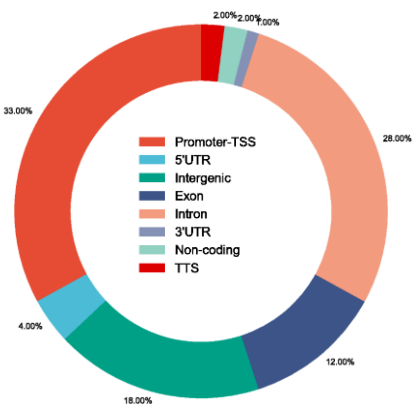
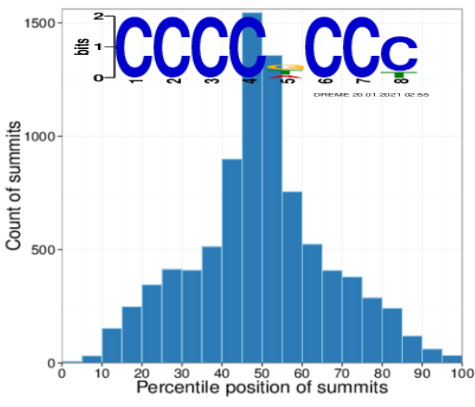
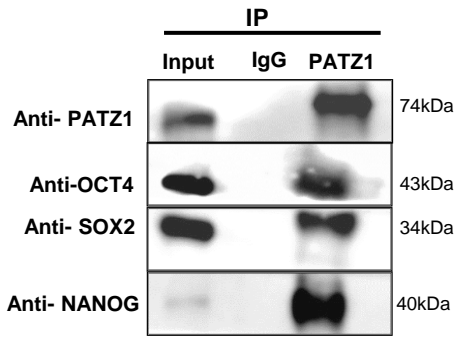
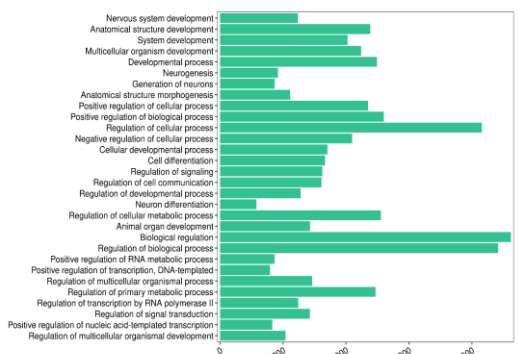
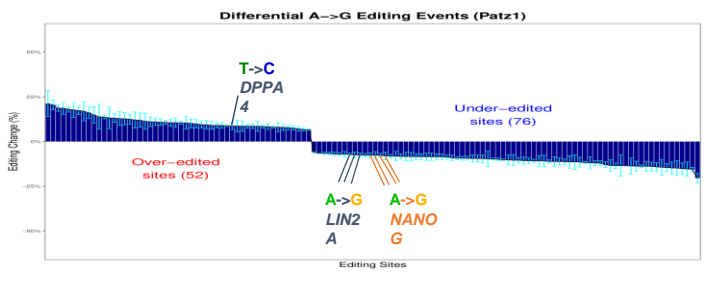
89 Supplementary Table 7. Quantification of metabolites by LC/MS/MS.

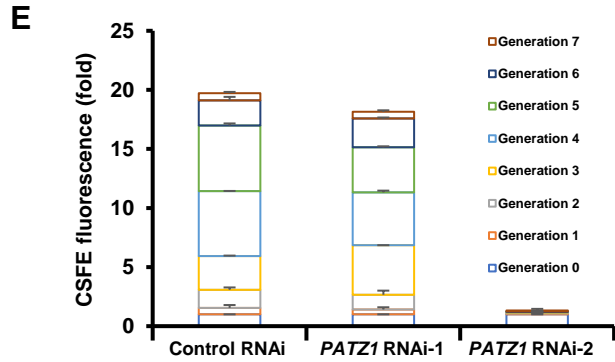
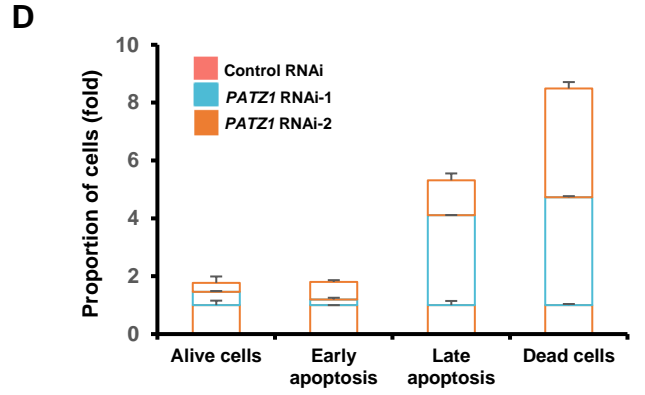
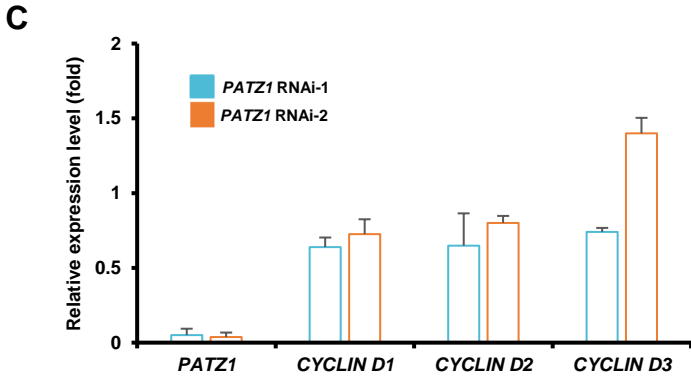
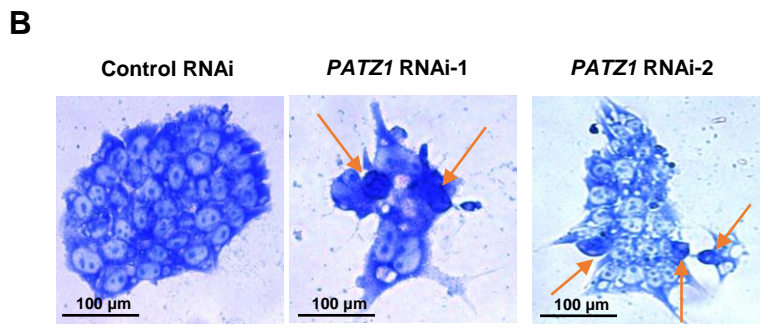
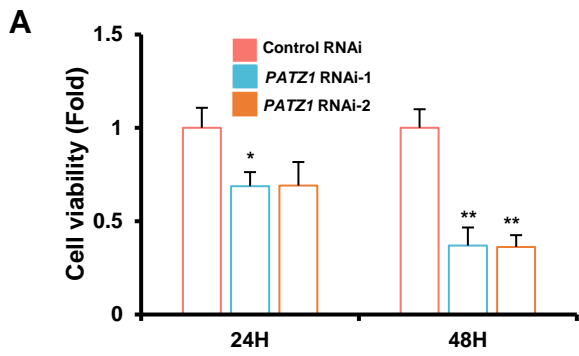
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A**B**

A**B****C****D****E****F**

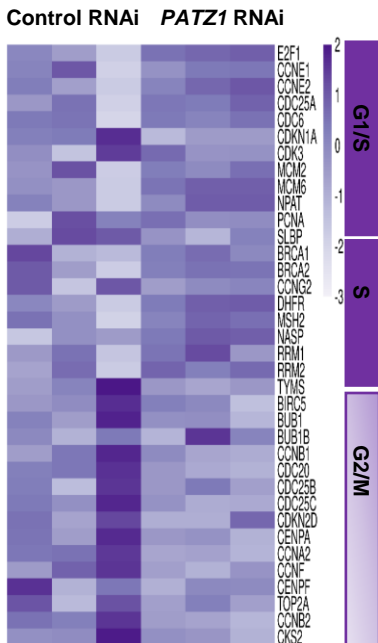


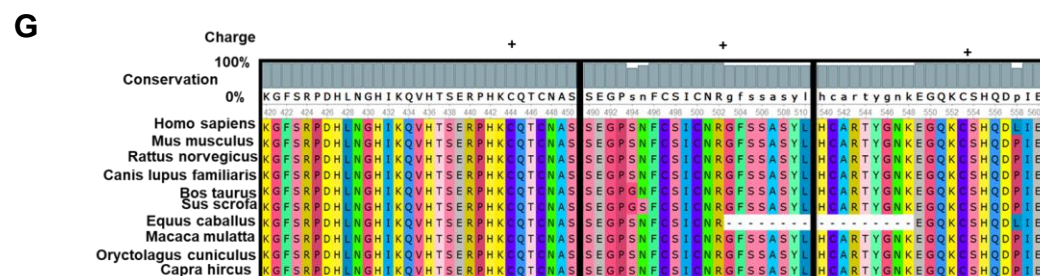
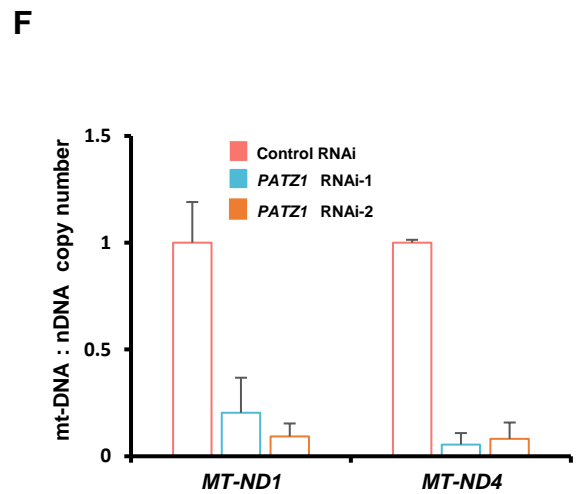
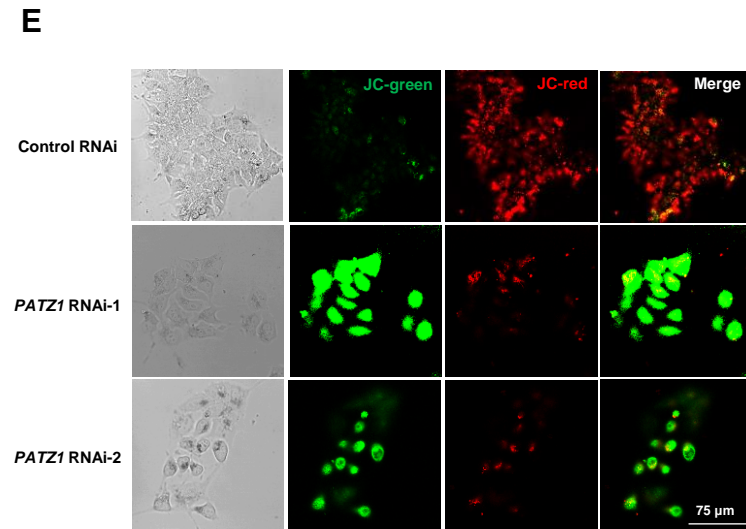
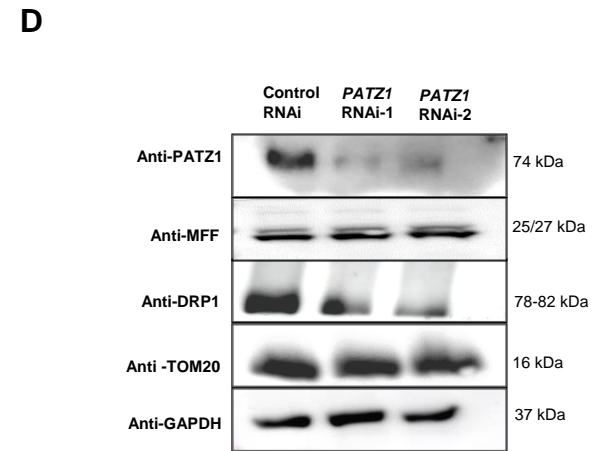
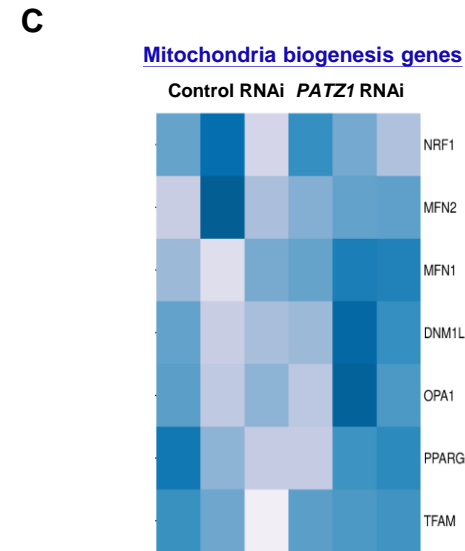
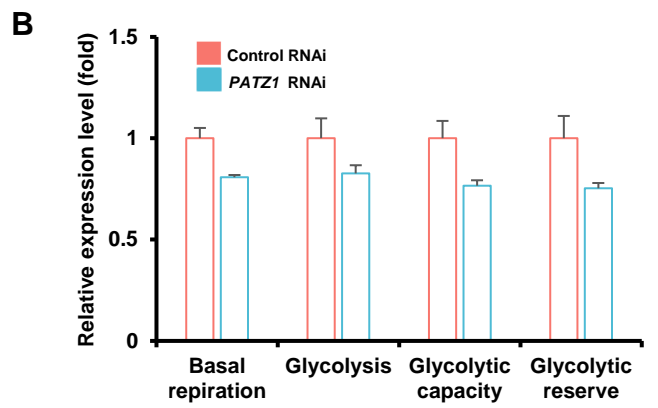
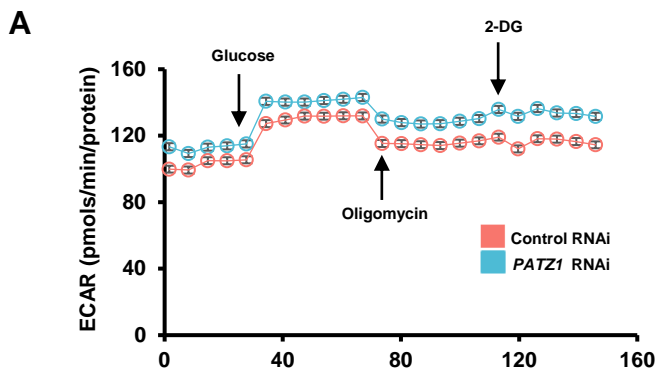
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	Control RNAi	PATZ1 RNAi-1	PATZ1 RNAi-2
Dip G1	40.06 ± 1.92	42.10 ± 1.73	38.77 ± 2.51
Dip S	44.39 ± 1.09	41.68 ± 1.51*	39.27 ± 2.13*
Dip G2	15.55 ± 2.42	16.22 ± 0.86	21.96 ± 3.45*

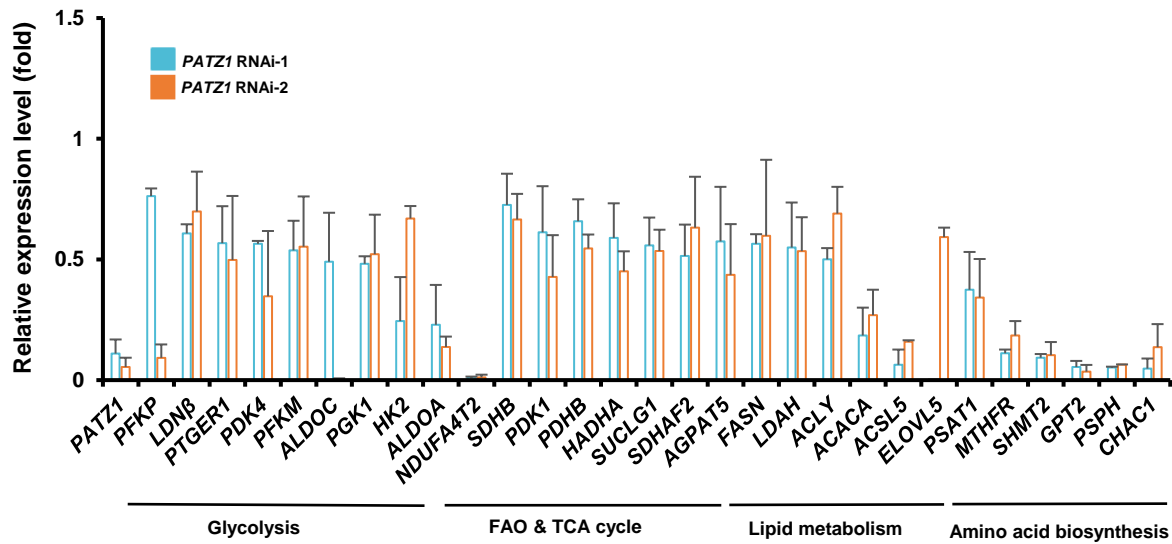
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Cell cycle phase genes

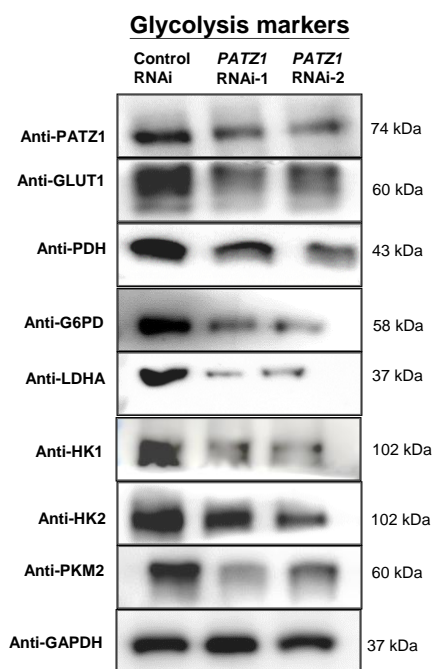




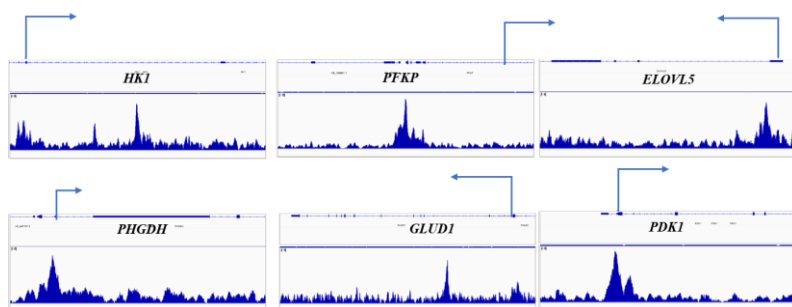
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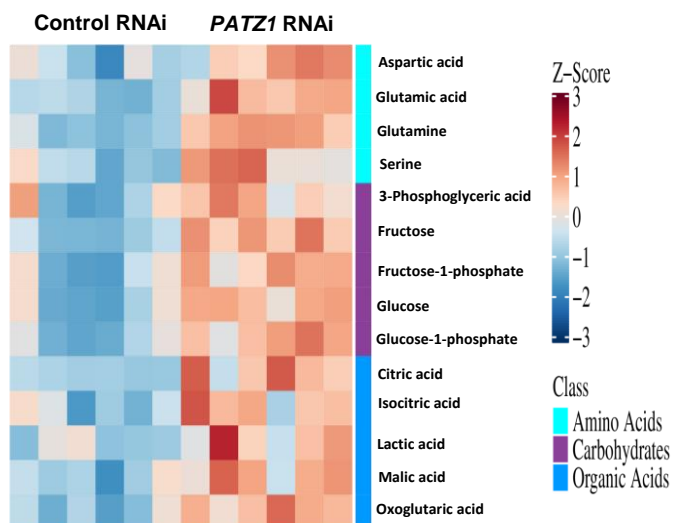
B



C



D



Supplementary Table 1. Primers for plasmid construction.

Description	Sequence
Negative control	GTTCTCCGAACGTGTCACGTT
<i>PATZ1</i> -shRNA-1	GCGCCGATATAATGCTCTTTC
<i>PATZ1</i> -shRNA-2	CGAGTACTTTGAGTCGGTGTT
<i>OCT4</i> CR2-pSV40-Luc	AAAAAATATCTGACTTCAGGTTCAAAGAAG
p <i>NANOG</i> PP-Luc	GCTGGTTTTCAAACCTCCTGACTTCAG

Supplementary Table 2. RT-PCR primers being used.

Description	Forward (5' – 3')	Reverse (3' – 5')
<i>PATZ1</i>	GGCCTGATCACTTGAACGGA	GGCAGAGGAGAAACCTCGG
<i>DPPA4</i>	CTGGTGCCAACAATTGAAGCT	AGGCACACAGGCGCTTATATG
<i>OCT4</i>	GGCTCTCCCATGCATTCAAAC	CCAAAAACCTGGCACAACCT
<i>NANOG</i>	GCATCCGACTGTAAAGAATCTTCA	CATCTCAGCAGAAGACATTTGCA
<i>SOX2</i>	TGCGAGCGCTGCACAT	GCAGCGTGTACTTATCCTTCTTCA
<i>UTF1</i>	CGCCGCTACAAGTTCCTTAAA	GGATCTGCTCGTCAAGGG
<i>ESRRB</i>	CCTCAGAGATGCGCAGGTTA	CCTCCGTGGAATGGTCTGAG
<i>KLF4</i>	GTCTCTTCGTGCACCCACTT	CCAGCCCGAGCTACAAATCC
<i>BMP4</i>	TGGGATTCCCGTCCAAGCTAT	AGGAATCATGGTGTCTTGACAGA
<i>CDX2</i>	CTCGGCAGCCAAGTGAAAA	GGTCCGTGTACACCACTCGAT
<i>HCGβ</i>	ACGACTGAGTCTCTGAGGTCACTT	ACAGATGGTGGTGGTGACGGTGAT
<i>GCM1</i>	CACAGTGCTGTCTGCTTCTCC	CGACTCCCCTCAGAAATGCT
<i>PAX6</i>	CATACCAAGCGTGTCAATAAAC	TGCGCCCATCTGTTGCT
<i>HAND1</i>	GGGTAAACAGGTCTTTGGGCT	CCCTATTAACGCCGCTCCAT
<i>REST</i>	GATCCCCTCCCCGTTTTAG	AACTGCCACCCCAAATGGAA
<i>NESTIN</i>	CCAGAGGTCATGTTGGGGTC	CAAGGTGAAGGGGCATCACT
<i>T</i>	GTGACCAAGAACGGCAGGAGG	TGTTCCGATGAGCATAGGGGC
<i>GATA2</i>	CAGCAAGGCTCGTTCCTGTT	GGCTTGATGAGTGGTCCGGT
<i>MYF6</i>	GGGCTCGTGATAACGGCTAA	AAGGCATCGAAGGCTACTCG
<i>RUNX1</i>	GGAAGTCAACCTCTGCTGCT	CGGACCACAGAGCACTTTCT
<i>NKK2.5</i>	CTTCAAGCCAGAGGCCTACG	CCGCTCTGTCTTCTTCAGC
<i>FGF5</i>	CCGGAAATGTAGCCAGGAGA	ACAATCCCCTGAGACACAGC
<i>FOXA1</i>	GAAGACCGGCCAGCTAGAGG	TGTTGATGGAGAACGGGTGG
<i>FOXA2</i>	TTGCTGGTCTGTTTGTGTGG	GGAGGAGTAGCCCTCGG
<i>GATA4</i>	GGAAGGAGCCAGCCTAGCAG	CTATTGGGGGCAGAAGACGG
<i>GATA6</i>	AGCACCAATCCCGAGAACAG	GCGAGACTGACGCCTATGTA
<i>SOX17</i>	CGCCGAGTTGAGCAAGA	TTCAGCCGCTTACCTG
<i>GLS2</i>	CCTGCGCTACAACAAGCTCT	GGAAAAATTACCTTCCGTGGC

<i>FOSL1</i>	CATGTTCCGAGACTTCGGGG	GTGTTGATGCTTGGCACCAG
<i>GCAT</i>	TCCGGGTACAGATCTCAGCA	TGGCTCCTGCCTGATTCTTC
<i>LGI4</i>	GCTGTCACTCTCACTCGTCA	GTGTAAGCGAGCGAAGTCCT
<i>HES4</i>	ATCCGCCCTAGGGGCTC	GAGGGTTTTGAGCTGAGCGA
<i>VGF</i>	GCACAAGGTGGTTTTTCGTCC	ACCCGTTGATCAGCAGAAGG
<i>MT1H</i>	GCAAAGGGGCGTCAGAGAAGT	GGAATGTAGCAAATGAGTCGGAGT
		T
<i>TMEM64</i>	TGGGCATGGGTCTGATGATG	GCAGGGTGGTACCCAAGTAA
<i>EDIL3</i>	GGATCATGAAGCGCTCGGTA	CAGGGACCAACCTCCACAAC
<i>SLIT2</i>	TGTCTGCAGTGATGAGGAAGA	AGCTCCAGGAGGGATGACTT
<i>WLS</i>	CACAACGGCAGTGTCTACA	GGGGAGGGGAATGTGAACAG
<i>SLC1A3</i>	ACCCCAAGCATTCTGTGCAT	CCAGTCCACACTGAGTGCAT
<i>MATN2</i>	GGATGGGAAGAGGTGTGTGG	ATCCTTCATGGCACTGGCAA
<i>CRYAB</i>	CAAACGGCCTGGGTGGATA	TTGTGATCCGGGATTTGGCA
<i>MYH2</i>	GCCTTTCAAGAGGGACTG	TCAAAGGGCTATTCTGGGC
<i>ARHGAP30</i>	CTGGTAGGGCACAGGTCTTG	TTGGAGGAGACCCTGAGAG
<i>NEDD9</i>	CCTCTAGAAGCAAGTCCGCTC	GAGGTGACAGCTAGTCTGC
<i>KCNQ3</i>	GCTGCCCTAAACTTCCACAA	TGAAAAGCCACCACTAGCCA
p2	GGACTCGGAAGAGGTTACCTTCGG	GTCGCCTCCGCTTGCTGAACTCAA
		TGC
<i>OCT4</i>	GGCCAGAAATACACCACCTACAGTA	CAGTGTTTCTCAGCTTGCCATCCTC
amplicon 1	CAAAT	
<i>OCT4</i>	CCACCCCCACCAGGCCCCATAATCTA	GTTGCCTCTGTTCGTGTGCCATCT
amplicon 2	CC	CCTGT
<i>OCT4</i>	AGAAGTGAACACAGCTGCAACCCCA	TCTTCATCTTGGTGGCATCCGTGA
amplicon 3	CTG	GTCTTT
<i>OCT4</i>	GGCAGTCTACTCTTGAAGATGGGGT	CTATCCCTCAATGCATCAACAGCC
amplicon 4	GAAAT	ATAA
<i>NANOG</i>	GTGCTGATTAAGAGAGACAGGAGGG	GTGAAACAAGGAAATGAAATTGG
amplicon 1	CAAGT	GCGTAA
<i>NANOG</i>	CAATACTTTTCGAGTCTTTGCATTGT	CCCAAACCCAACATTCAAGAAACC
amplicon 2	GAAC	TA
<i>NANOG</i>	GATTTAAAAGTTGGAAACGTGGTGA	CCTTGTGAATTCTCAGTTAATCCCG
amplicon 3	ACCTA	TCT
<i>NANOG</i>	TTAGCCAGAAGACCTAACGTCATAGC	CCCAGTAACATCCACAAACCCAGA
amplicon 4	TCAG	GA
<i>ZNF580</i>	GGGTTCCCATAAACAAGGGGA	TCCCTCTCCCTGTTACACACA
<i>ZNF385A</i>	AGGAACAAAGGCAAACCGAGG	ACAGGAAGGGATCCTGGAGAC

<i>FOXB1</i>	GGCCGGATCTCTTTACGTCT	CTTTCCTAACTCCCAGCGCC
<i>BACH2</i>	AGTTCGTGGGTCACCGAAAG	TAGCGATTGAGAGTGTGGGC
<i>LGI2</i>	ATCCGATGCCTGCAATACCT	ATCAAGCCGGTTCTCCACAC
<i>PDE9A</i>	CTGGACATCGATGGACGCAT	TGTGCCAGCCCTTGAATGTA
<i>WNK4</i>	GTAAGTGTGGCCAAGGGGAG	GGCCAGAGTGGCTGTTTTTG
<i>TEAD3</i>	TCAGGGCTGGAAGCTCTGAATC	CTGGGTGTGGAGGGGTGTC
<i>MCF2L</i>	GGTTTCCAAGCACACGGGTA	AGAAAGGAACACGAGGGCG
<i>NEO1</i>	GCCGAAGAGAAAGGGGATCG	GAACCTGCCTCCAGGTACAA
<i>GSE1</i>	CGGCCAGTGCGGGTATAAAT	GCAGACCACAAACGAAAAGGG
<i>ZNF496</i>	CTTCCTGCTCCGCTCTAGGA	CCAGAGAAGGAGAACAGCGG
<i>MFGE8</i>	TTCTCCTCTGGGACCGGAAT	AAGAGGCAGATATCGCGGAC
<i>CD169</i>	GGAGAAAGCTAAGGCTCGCA	CCCGTAGGATTCCCGTTGG
<i>NFATC3</i>	ACTCAACTTCCAGCAAGGGAC	CTCAGAGTTACCTGGACGCC
<i>LPAR2</i>	CGAAAATTCCCGCCGTGACC	GAGCCAAGTCGGATCAGGGA
<i>EFHD2</i>	ACCCTCATTGAGAACGCCAG	CTCTTCGTGCCCACTGTAGC
<i>ZNF219</i>	TGGGAAAATCCCCCTCCCAG	GCGGCTGTAAGTCAAGCTTTT
<i>FSCN1</i>	GAGACAACCTAGTTGGGCGT	CAAGGACGAGCGAGGTTTGA
<i>PMEPA1</i>	CAAGGAGATCGGGTTTCGCT	CCTAGCTCTGGCCCTTTAAGA
<i>FBXL19</i>	GGACACGTGTGAGGTGGGTT	GGCTGGAGATGAGTTTGGAGTA
<i>ITGA5</i>	GGCCGGTAAAGTCCACTGA	GCGTTGAGTCATTTCGCTCT
<i>DPY19L3</i>	ACAGACCGGACTCAATGCG	CGCGGAGCTTTGTGGAAATG
<i>BNIP3</i>	CCACCCTCAGCATGAGGAAC	TGGCCACCCCAGGATCTAAC
<i>HK1</i>	CGCAGCTCCTGGCCTATTA	CTTCCACTCCGCTCGCTTTA
<i>PKM</i>	CCCGATCAGTGGAGCTGAAG	AGGAAGTCGGCACCTTTCTG
<i>PFKP</i>	GTCACACCGCTTCCCTTGTC	TTCTGCACGGCCTCCTTATC
<i>LDNβ</i>	CCTGGTAGGTTTCGGCTCAG	CAAGGACAAGTAGGGCCTGG
<i>PTGER1</i>	GTACATCTACTGCGCCAGG	GGGCCTCTGGTTGTGCTTAG
<i>PDK4</i>	TTCCCGGAATGCTCCTTTGG	GCACTGGTGTAGACCCACTT
<i>PFKM</i>	GGCGGAGGAGAGCTAAGACTA	TACCAACTCGAACCACAGCC
<i>ALDOC</i>	CAGCCTCATCTGTTTTCGGGA	ATGGTGACAGCTCCCTGTGC
<i>PGK1</i>	ACCGAATCACCGACCTCTCT	TGGGACAGCAGCCTTAATCC
<i>HK2</i>	GTGAATCGGAGAGGTCCCAC	CAAGCAGATGCGAGGCAATC
<i>ALDOA</i>	TCCCCATCAATAGGGCCGAC	CCACATGTGTCCCCGATCTT
<i>NDUFA4L2</i>	GTGTGTTGCCATCGCGTCT	GGCTCCTGCCATATCGTTGT
<i>IDH3B</i>	TACGCAGTCTTTGAGACGGG	GGCGTGAAGGTGAAGCTGAT
<i>ECH1</i>	TACTGACCCGGCGACTGA	CGAAGCCATGTCCATCAGGT
<i>MLYCD</i>	CTTCGTGACAGACGGTGTGA	ACTCTGGAGGCAGCAGGATA
<i>PDHA2</i>	CGAGTTGCCAGAAATCAGC	GGTGACAGAAACCGCGAATG

<i>SDHB</i>	CACTCTAGCTTGCACCCGAA	CCAGCGATAGGCCTGCATAA
<i>PDK1</i>	AAGCAGTTCCTGGACTTCGG	TCTTGCAGGCCATACAGCAT
<i>PDHB</i>	AGAGGCGCTTTCCTGGAC	ATTCACAAATGGGCCGCAAC
<i>HADHA</i>	GGTTTGGAGGTGAAACCCA	CAGGCGGAACTGGATGTCTT
<i>SUCLG1</i>	TCTTTGTGCGTTGGCATTGG	CCGGCATGACCCATTCTTCT
<i>SDHAF2</i>	GATGCTTGCTCTGTCAAGGC	TAGGCTCGTTAATCAGGCGG
<i>CPTIC</i>	GATGCTTGCTCTGTCAAGGC	AAGGACGTCAATTCGGGACC
<i>DGAT2</i>	GCTTCAGCCATGAAGACCCT	CCACTCCCCATCTCCCAGA
<i>G2E3</i>	TTTGAATCCTGTGGGCGTT	AACACAAGCAAGGAGAGCTGG
<i>AGPAT5</i>	GCGCTACGTGCTGAAAGAAG	AGCAAATGCCTGACTAGCTGA
<i>FASN</i>	CCTGGCTGCCTACTACATCG	CACATTTCAAAGGCCACGCA
<i>LDAH</i>	GGTGAGCGTAAAAGTCTGGATTC	TGGGTGACTCAGACATTCGT
<i>ACLY</i>	GGACTTCGGCAGAGGTAGAG	AGGAGTTCTTTGCCCGTCTG
<i>ACACA</i>	CGAGGACTGGGAGGATGGG	GTTATCCCCAAACCCAGGCA
<i>ACSL5</i>	GTACACGGGGAGAGCTTACG	GGCTTTGACTTGGTTTTGGCA
<i>ELOVL5</i>	TCCAAAAGGGAGCAACCCC	ATCTGATTCTCCTGCGGTGC
<i>ASNS</i>	CGCCAGATTTTCTTCAATCACA	TTCCAAACAGCGGGTCAACT
<i>PHGDH</i>	AACCGCAGCTTCTTGGCTTA	ACTGATGAGCACTTTCGGCA
<i>MTHFD2</i>	AGAGCTTTGGAGAAACCAGCC	CCTAGCTTGGCACAACCTGT
<i>PSAT1</i>	AAAAACAATGGAGGTGCCGC	ATGCCTCCCACAGACACGTA
<i>GLUD1</i>	TTCTTGGGCTTTTGTATCCGTT	ATAGTGCCCTATGGTGCTGG
<i>MTHFR</i>	CGCTAGGAATATGGGCCTCG	CTTTGGAGCTCTCACTGCCA
<i>SHMT2</i>	TACACAGCCCTTCTGCAACC	TCAGTGCCAGGTTGAGCTTAT
<i>GPT2</i>	CAAGCCTGGCTAAAACGAGA	TAGGGCAGACACACAACGTG
<i>PSPH</i>	AGAAAGCTGCAGGACTGGTG	AAAGGGAGTCCGCTCAAAGG
<i>CHAC1</i>	AGTGCAAGGGGAGCAGAAC	TCTTGTGCACTGGAGTGGGT

Supplementary Table 3. Primary antibodies being used.

Primary antibodies		
Protein specificity	Source	Identifier
Anti- β -ACTIN	Santa Cruz Biotechnology	sc-47778
Anti-GAPDH	Santa Cruz Biotechnology	sc-47724
Anti-PATZ1	Santa Cruz Biotechnology	sc-292109
Anti-OCT-3/4	Santa Cruz Biotechnology	sc-5279
Anti-NANOG	Santa Cruz Biotechnology	sc-134218
Anti-SOX2	Santa Cruz Biotechnology	sc-365823
Anti-SMAD2/3	Cell Signaling Technology	8685S
Anti-LIN28	Santa Cruz Biotechnology	sc-67266

Anti-GATA4	Santa Cruz Biotechnology	sc-25310
Anti-GATA6	Santa Cruz Biotechnology	sc-518050
Anti-SOX17	Santa Cruz Biotechnology	sc-130295
Anti-Rabbit IgG	Cell Signaling Technology	2729
Anti-Mouse IgG1	Cell Signaling Technology	5415S
Anti-Ki-67	Cell Signaling Technology	9449S
Anti-BAX	Cell Signaling Technology	5023S
PARP	Cell Signaling Technology	9532S
Anti-Cleaved PARP	Cell Signaling Technology	5625S
Anti-CYCLIN A1	Santa Cruz Biotechnology	sc-53233
Anti-CYCLIN B1	Cell Signaling Technology	12231S
Anti-GLUT1	Cell Signaling Technology	12939S
Anti-PDH	Cell Signaling Technology	2784S
Anti-G6PD	Cell Signaling Technology	12263S
Anti-LDHA	Cell Signaling Technology	3582S
Anti-HK1	Cell Signaling Technology	2024S
Anti-HK2	Cell Signaling Technology	2867S
Anti-PKM2	Cell Signaling Technology	4053S
Anti-MFF	Cell Signaling Technology	84580S
Anti-DRP1	Cell Signaling Technology	8570S
Anti-TOM20	Cell Signaling Technology	42406S

Secondary antibodies

Protein specificity	Source	Identifier
Anti-Mouse HRP-linked	Cell Signaling Technology	7076P2
Anti-rabbit IgG, HRP-linked	Cell Signaling Technology	7074P2
Anti-Mouse IgG Alexa Fluor 488	Invitrogen	A-11001
Anti-Rabbit IgG Alexa Fluor 488	Invitrogen	A-11008
Anti-Rabbit IgG Alexa Fluor 555	Invitrogen	A-21429
Anti-Mouse IgG Alexa Fluor 555	Invitrogen	A-21422
Anti-Mouse IgG Alexa Fluor 647	Invitrogen	A-21235

Anti-Rabbit IgG Alexa Invitrogen

A-21245

Fluor 647

Supplementary Table 4. Top 100-ranked peak heights of PATZ1-ChIP peaks.

Top 100-ranked peak heights of PATZ1-ChIP peaks in human ESCs									
Chr	Start	End	Fold Change	P-vale (-log₁₀)	Annotation	Detailed Annotation	Distance to TSS	Nearest Refseq	Gene Name
chr10	1.25E+08	1.25E+08	50.1487	391.253	intron (NM_001290214, intron 1 of 10)	CpG	6666	NM_001329	CTBP2
chr5	1.4E+08	1.4E+08	40.0777	302.103	Intergenic	CpG	-7660	NM_032289	PSD2
chr22	31345384	31347350	36.1356	262.354	promoter-TSS (NM_032052)	promoter-TSS (NM_032052)	-21	NM_014323	PATZ1
chr22	38397923	38399514	36.024	254.13	5' UTR (NM_001289912, exon 1 of 15)	5' UTR (NM_001289912, exon 1 of 15)	197	NM_001289912	TPTEP2-CSNK1E
chr19	55283443	55284885	33.5169	228.832	5' UTR (NM_032430, exon 1 of 19)	5' UTR (NM_032430, exon 1 of 19)	167	NM_032430	BRSK1
chr11	1.18E+08	1.18E+08	33.496	337.369	promoter-TSS (NM_001197104)	promoter-TSS (NM_001197104)	-9	NM_005933	KMT2A
chr1	27234192	27235387	31.1218	283.319	5' UTR (NM_015023, exon 1 of 16)	5' UTR (NM_015023, exon 1 of 16)	157	NM_015023	WDTC1

chr21	825785 4	8260823	27.8883	3056.2	non-coding (NR_003287, exon 2 of 3)	non-coding (NR_003287, exon 2 of 3)	2557	NR_146120	RNA5-8SN4
chr4	769490 93	7695017 1	27.0524	141.569	promoter-TSS (NM_018243)	promoter-TSS (NM_018243)	-120	NM_01824 3	SEPTIN11
chr21	844089 8	8447105	25.7497	7292.23	non-coding (NR_046235, exon 1 of 1)	non-coding (NR_046235, exon 1 of 1)	2855	NR_003287	RNA28SN5
chr7	1.43E+ 08	1.43E+0 8	25.4178	153.869	promoter-TSS (NM_001362783)	promoter-TSS (NM_001362783)	78	NR_161353	LOC1005075 07
chr9	1.21E+ 08	1.21E+0 8	25.4178	153.869	intron (NM_001286840, intron 1 of 14)	CpG	346	NM_01565 1	PHF19
chr15	896551 33	8965576 4	24.4737	152.016	promoter-TSS (NM_198525)	promoter-TSS (NM_198525)	19	NM_19852 5	KIF7
chr8	182314 7	1824494	24.342	126.73	promoter-TSS (NM_014629).2	promoter-TSS (NM_014629).2	-106	NM_01462 9	ARHGEF10
chr13	1.01E+ 08	1.01E+0 8	23.5287	137.757	promoter-TSS (NM_001286453)	promoter-TSS (NM_001286453)	-131	NM_03281 3	TMTC4
chr15	328991 23	3289975 1	23.1999	214.139	intron (NM_001277313, intron 14 of 20)	intron (NM_001277313, intron 14 of 20)	168737	NM_19850 0	FMN1
chr18	301226 7	3013109	22.9201	113.616	promoter-TSS (NM_014646)	promoter-TSS (NM_014646)	-741	NM_01464 6	LPIN2

chr5	904096 52	9041024 2	22.5739	105.362	promoter-TSS (NM_004365)	promoter-TSS (NM_004365)	-53	NR_105024	LOC731157
chr11	697020 79	6970339 2	21.9353	119.247	intron (NM_005117, intron 2 of 2)	CpG	1287	NM_005117	FGF19
chr19	458018 6	4582214	21.8248	134.448	Intergenic	CpG	-21516	NM_02024 1	SEMA6B
chr17	773727 58	7737372 6	21.5241	120.799	promoter-TSS (NM_001113493)	promoter-TSS (NM_001113493)	-95	NM_00664 0	SEPTIN9
chr11	473995 95	4740079 1	21.3519	119.393	promoter-TSS (NR_039707)	promoter-TSS (NR_039707)	-777	NR_039707	MIR4487
chr15	830668 23	8306759 2	21.3421	142.89	promoter-TSS (NM_025238)	promoter-TSS (NM_025238)	45	NM_02523 8	BTBD1
chr1	544877 69	5448979 1	20.817	136.604	Intergenic	Intergenic	-59448	NM_01554 7	ACOT11
chr17	762741 8	7628237	20.808	109.776	promoter-TSS (NM_001289115)	promoter-TSS (NM_001289115)	-6	NM_13349 1	SAT2
chr11	1.17E+ 08	1.17E+0 8	20.773	137.351	promoter-TSS (NM_025164)	promoter-TSS (NM_025164)	39	NM_02516 4	SIK3
chr1	1.55E+ 08	1.55E+0 8	20.6154	173.498	promoter-TSS (NM_017582)	promoter-TSS (NM_017582)	65	NM_01758 2	UBE2Q1
chr12	571277 85	5712983 6	20.324	128.727	5' UTR (NM_002332, exon 1 of 89)	5' UTR (NM_002332, exon 1 of 89)	327	NM_00233 2	LRP1

chr2	858885 52	8588947 1	20.2485	102.053	promoter-TSS (NM_001354227)	promoter-TSS (NM_001354227)	-21	NM_00389 6	ST3GAL5
chr19	402846 93	4028559 8	20.2415	107.299	intron (NM_001626, intron 1 of 13)	CpG	200	NM_00162 6	AKT2
chr17	449843 4	4499370	20.2363	102.897	promoter-TSS (NM_001124758)	promoter-TSS (NM_001124758)	21	NM_001124 758	SPNS2
chr16	387959 5	3881267	20.1726	117.651	promoter-TSS (NM_001079846)	promoter-TSS (NM_001079846)	282	NM_00438 0	CREBBP
chr14	687928 86	6879645 3	20.0616	130.498	promoter-TSS (NM_004926)	promoter-TSS (NM_004926)	-755	NM_00492 6	ZFP36L1
chr19	475150 89	4751568 6	20.0339	119.856	promoter-TSS (NR_038456)	promoter-TSS (NR_038456)	-324	NM_00382 7	NAPA
chr8	946401 41	9464153 0	19.7233	117.13	promoter-TSS (NM_001034915)	promoter-TSS (NM_001034915)	-339	NM_01769 7	ESRP1
chr1	1.56E+ 08	1.56E+0 8	19.6166	177.954	promoter-TSS (NM_001282625)	promoter-TSS (NM_001282625)	705	NM_00109 3725	MEX3A
chr17	441230 15	4412406 2	19.6093	115.901	5' UTR (NM_005474, exon 1 of 27)	5' UTR (NM_005474, exon 1 of 27)	103	NM_00547 4	HDAC5
chr11	461196 96	4612259 8	19.5641	85.5172	promoter-TSS (NM_001352032)	promoter-TSS (NM_001352032)	-162	NM_01662 1	PHF21A
chr1	1.51E+ 08	1.51E+0 8	19.5637	136.634	intron (NM_001194938, intron 1 of 17)	CpG	533	NM_01510 0	POGZ

chr16	900188 69	9002014 6	19.4068	104.041	promoter-TSS (NM_001286209)	promoter-TSS (NM_001286209)	-51	NM_02404 3	DBNDD1
chr17	672444 64	6724643 6	19.3206	92.6227	promoter-TSS (NM_014877)	promoter-TSS (NM_014877)	-254	NM_01487 7	HELZ
chr17	678250 86	6782634 6	19.2691	88.2085	5' UTR (NM_004459, exon 1 of 30)	5' UTR (NM_004459, exon 1 of 30)	213	NM_00445 9	BPTF
chr2	2.2E+0 8	2.2E+08	19.2574	113.065	TTS (NM_013335)	TTS (NM_013335)	-7128	NM_01867 4	ASIC4
chr16	704387 37	7043961 2	19.1954	118.033	promoter-TSS (NM_006927)	promoter-TSS (NM_006927)	-74	NM_00692 7	ST3GAL2
chr2	2.36E+ 08	2.36E+0 8	19.0634	101.332	Intergenic	CpG	8868	NM_00148 5	GBX2
chr19	154489 82	1545027 2	18.8227	97.2317	promoter-TSS (NR_031716)	promoter-TSS (NR_031716)	79	NR_031716	MIR1470
chr3	191467 95	1914867 8	18.8067	89.557	promoter-TSS (NM_144633)	promoter-TSS (NM_144633)	-774	NM_14463 3	KCNH8
chr16	730327 31	7303384 1	18.6142	101.71	intron (NM_006885, intron 1 of 9)	intron (NM_006885, intron 1 of 9)	14842	NM_00688 5	ZFHX3
chr2	432261 80	4322698 0	18.5954	110.111	promoter-TSS (NR_027251)	promoter-TSS (NR_027251)	26	NM_00688 7	ZFP36L2
chr7	188280	189099	18.5449	98.1261	Intergenic	Intergenic	-3882	NM_02022 3	FAM20C

chr2	1.67E+08	1.67E+08	18.5191	92.9954	Intergenic	CpG	105432	NM_152381	XIRP2
chr18	3447545	3448721	18.4201	122.216	intron (NM_173207, intron 1 of 2)	CpG	591	NM_003244	TGIF1
chr17	43024690	43025646	18.3542	114.387	promoter-TSS (NM_005440)	promoter-TSS (NM_005440)	-63	NM_005440	RND2
chr11	1968980	1970196	18.3394	91.6548	Intergenic	Intergenic	20257	NR_132974	SNORD131
chr19	15199591	15201097	18.2749	90.6377	intron (NM_000435, intron 1 of 32)	CpG	651	NM_000435	NOTCH3
chr20	50931194	50932007	18.2741	77.301	promoter-TSS (NM_181442)	promoter-TSS (NM_181442)	-163	NM_015339	ADNP
chr9	1.37E+08	1.37E+08	18.2386	99.7428	Intergenic	Intergenic	29077	NR_135288	LINC01451
chr1	2.24E+08	2.24E+08	18.129	122.014	exon (NM_015176, exon 1 of 5)	exon (NM_015176, exon 1 of 5)	186	NM_015176	FBXO28
chr19	56120163	56121862	18.115	148.873	intron (NM_001002836, intron 1 of 2)	CpG	283	NM_001002836	ZNF787
chr3	1.77E+08	1.77E+08	18.0591	75.951	promoter-TSS (NM_001321193)	promoter-TSS (NM_001321193)	263	NM_024665	TBL1XR1
chr1	2314279	2315694	18.0329	93.288	Intergenic	CpG	37675	NM_001127577	LOC100129534

chr1	2.11E+08	2.11E+08	17.9031	146.274	promoter-TSS (NM_001136225)	promoter-TSS (NM_001136225)	-17	NM_018254	RCOR3
chr3	1.97E+08	1.97E+08	17.8974	101.198	promoter-TSS (NM_002577)	promoter-TSS (NM_002577)	45	NM_002577	PAK2
chr13	74133886	74135654	17.786	78.562	promoter-TSS (NM_007249)	promoter-TSS (NM_007249)	-841	NM_007249	KLF12
chr12	1.22E+08	1.22E+08	17.6905	117.093	intron (NR_152740, intron 2 of 3)	CpG	2777	NR_002809	LINC01089
chr10	68074796	68075721	17.6747	79.0973	promoter-TSS (NM_001278187)	promoter-TSS (NM_001278187)	25	NM_015601	HERC4
chr11	1.1E+08	1.1E+08	17.6517	74.137	promoter-TSS (NM_001260492)	promoter-TSS (NM_001260492)	-3	NM_002906	RDX
chr7	1.02E+08	1.02E+08	17.6202	86.3332	promoter-TSS (NM_181500)	promoter-TSS (NM_181500)	-191	NM_001913	CUX1
chr1	2.26E+08	2.26E+08	17.5551	129.004	5' UTR (NM_018212, exon 1 of 14)	5' UTR (NM_018212, exon 1 of 14)	253	NM_018212	ENAH
chr20	43390184	43390708	17.5524	78.7818	Intergenic	Intergenic	-67450	NM_006275	SRSF6
chr2	43100444	43101595	17.5177	89.3252	intron (NR_151714, intron 1 of 1)	CpG	1426	NR_151714	LINC02580
chr17	29567892	29568993	17.3855	84.8628	promoter-TSS (NM_001346079)	promoter-TSS (NM_001346079)	166	NM_138349	TP53I13

chr19	306107 2	3063011	17.3391	87.9932	intron (NR_031672, intron 1 of 2).3	CpG-13254	454	NM_001130	TLE5
chr6	329682 52	3296971 7	17.0737	102.64	5' UTR (NM_005104, exon 1 of 13).3	5' UTR (NM_005104, exon 1 of 13).3	390	NM_005104 4	BRD2
chr17	433002 01	4330091 7	17.0674	220.495	promoter-TSS (NR_002716).10	promoter-TSS (NR_002716).10	-328	NR_002716	RNU2-1
chr16	702893 46	7029004 4	17.0613	79.1089	promoter-TSS (NM_001257174)	promoter-TSS (NM_001257174)	-72	NM_00724 2	DDX19B
chr19	160759 41	1607722 2	16.963	86.0938	promoter-TSS (NM_001367837)	promoter-TSS (NM_001367837)	86	NM_00329 0	TPM4
chr17	384507 08	3845136 6	16.9552	110.343	intron (NM_001199417, intron 1 of 23).2	intron (NM_001199417, intron 1 of 23).2	22573	NM_02087 6	ARHGAP23
chr21	821400 3	8216191	16.8092	2547.43	non-coding (NR_146144, exon 1 of 1)	non-coding (NR_146144, exon 1 of 1)	1209	NR_003287	RNA28SN5
chr14	1.05E+ 08	1.05E+0 8	16.8065	79.2225	promoter-TSS (NM_002226)	promoter-TSS (NM_002226)	-287	NM_00222 6	JAG2
chr14	996639 44	9966462 7	16.7891	100.07	intron (NM_001329411, intron 7 of 8)	intron (NM_001329411, intron 7 of 8)	19175	NM_03242 5	HHIPL1

chr16	115198 5	1154387	16.7741	79.9328	promoter-TSS (NM_021098)	promoter-TSS (NM_021098)	-55	NM_02109 8	CACNA1H
chr5	1.42E+ 08	1.42E+0 8	16.7726	91.9639	intron (NR_120664, intron 3 of 3)	CpG	31754	NR_120664	SPRY4-AS1
chr2	1.71E+ 08	1.71E+0 8	16.7692	67.9643	5' UTR (NM_012290, exon 1 of 21)	5' UTR (NM_012290, exon 1 of 21)	281	NM_01229 0	TLK1
chr19	336568 2	3367871	16.6421	95.5616	intron (NM_001245002, intron 1 of 10)	CpG	193	NM_00559 7	NFIC
chr1	275270 80	2752837 7	16.6349	122.859	Intergenic	Intergenic	-37561	NM_00699 0	WASF2
chr20	411373 68	4113845 3	16.6238	83.5039	promoter-TSS (NR_109889)	promoter-TSS (NR_109889)	90	NR_109889	PLCG1-AS1
chr7	758786 59	7587923 0	16.5101	96.728	promoter-TSS (NM_001346189)	promoter-TSS (NM_001346189)	-48	NM_02068 4	RHBDD2
chr14	1E+08	1E+08	16.4967	89.5039	Intergenic	CpG	8164	NR_106822	MIR6764
chr12	532209 78	5322379 1	16.3845	97.9042	intron (NM_001243730, intron 2 of 8)	intron (NM_001243730, intron 2 of 8)	-2022	NM_00096 6	RARG
chr19	128380 96	1283912 2	16.3568	81.9324	promoter-TSS (NM_014975)	promoter-TSS (NM_014975)	94	NM_01497 5	MAST1
chr12	533799 76	5338087 0	16.3476	93.0083	promoter-TSS (NM_003109)	promoter-TSS (NM_003109)	-221	NM_00310 9	SP1

chr15	857944 95	8579537 3	16.3376	74.7716	promoter-TSS (NM_022480)	promoter-TSS (NM_022480)	-9	NM_02248 0	KLHL25
chr1	2.06E+ 08	2.06E+0 8	16.2081	125.879	intron (NM_022731, intron 1 of 6)	CpG	582	NM_02273 1	NUCKS1
chr15	788724 96	7887303 0	16.1577	76.6371	promoter-TSS (NM_001265605)	promoter-TSS (NM_001265605)	-18	NM_00679 1	MORF4L1
chr10	980300 29	9803151 4	16.1075	76.4959	promoter-TSS (NM_018058)	promoter-TSS (NM_018058)	57	NM_01805 8	CRTAC1
chr13	279613 01	2796216 6	16.1075	76.4959	3' UTR (NM_001354700, exon 3 of 3)	3' UTR (NM_001354700, exon 3 of 3)	7582	NM_00126 5	CDX2
chr19	495907 98	4959360 1	16.1075	86.7087	intron (NM_020719, intron 1 of 13)	CpG	1017	NM_02071 9	PRR12
chr12	488519 46	4885248 5	16.1041	85.126	promoter-TSS (NM_004818)	promoter-TSS (NM_004818)	-52	NM_00481 8	DDX23
chr20	435903 87	4359099 9	16.0794	92.9202	promoter-TSS (NM_001303459)	promoter-TSS (NM_001303459)	-244	NM_01600 4	IFT52

Supplementary Table 5. Differential expression analysis of altered gene in RNA-seq analysis upon *PATZ1* RNAi.

Differential expression analysis of pluripotency genes upon <i>PATZ1</i> RNAi									
Gene_ name	log2 fold change	pvalue	P adjust	Control RNAi fpkm	Control RNAi fpkm	Control RNAi fpkm	<i>PATZ1</i> RNAi fpkm	<i>PATZ1</i> RNAi fpkm	<i>PATZ1</i> RNAi fpkm
<i>SMARCD3</i>	-0.35969	0.250188	0.63102	2.939595	2.062871	3.522572	2.684312	1.80114	1.971093
<i>UTF1</i>	-0.80098	0.004318	0.089069	8.371304	9.381131	18.36595	8.074416	6.037973	6.198554
<i>CAPN2</i>	-0.23862	0.20836	0.590405	27.62578	25.42786	40.31131	26.78734	26.61334	24.21318
<i>TDGF1</i>	-0.04762	0.751399	0.920855	778.6861	840.0527	875.1391	832.8368	772.9164	772.3121
<i>RPA3</i>	-0.04595	0.783226	0.933135	69.89669	74.78333	81.45395	79.86254	71.03998	64.78331
<i>KLF2</i>	-0.09749	0.87472	0.965732	0.348949	0.516961	0.710488	0.767489	0.217694	0.452867
<i>EHMT2-AS1</i>	-0.52348	0.054936	0.341143	5.381228	7.349757	6.620706	6.178256	3.491222	3.601115
<i>MTA3</i>	-0.19728	0.229264	0.610356	76.30681	78.56499	79.42889	76.83918	60.84271	63.31992
<i>KCNG3</i>	-0.31523	0.240022	0.620856	1.836903	1.72813	2.105075	2.06265	1.170119	1.219327
<i>HES3</i>	-0.75418	0.231063	0.612289	31.34707	38.90582	52.09101	42.34224	10.25327	18.28609
<i>CLDN7</i>	-0.06293	0.685853	0.894616	98.69314	100.0887	109.0502	104.5929	90.13777	95.10179
<i>NANOG</i>	-0.29202	0.090015	0.426778	94.12503	87.0886	77.62782	79.02595	58.44372	70.05766
<i>MATK</i>	-0.29502	0.114716	0.473438	21.77245	23.43893	23.11367	19.51475	15.35111	19.9541
<i>SYT6</i>	-0.46904	0.023278	0.221885	14.68286	18.35614	20.4592	15.14181	10.24927	12.68945
<i>SOX2</i>	-0.19082	0.211998	0.594187	177.2632	191.5512	187.5786	169.1889	149.844	161.4132
<i>XRCC6</i>	-0.00635	0.969516	0.992003	386.6647	474.3803	437.1251	456.883	417.3649	403.5784
<i>CHD4</i>	-0.16385	0.39067	0.740412	12.57552	16.33665	14.17453	14.35984	11.61096	12.06791

<i>PRMT1</i>	-0.06876	0.684159	0.893922	553.0841	673.4699	610.8004	630.1578	533.6376	567.1663
<i>POU5F1</i>	-0.10908	0.477186	0.790893	2181.782	2431.669	2169.23	2131.052	2011.549	2065.9
<i>MBD3</i>	-0.08776	0.682236	0.893426	35.4579	50.96569	38.44159	44.83285	30.72153	40.88919
<i>PELO</i>	-0.14626	0.414475	0.755778	8.990931	8.707734	7.445133	7.839691	7.729228	6.803814
<i>CTBP2</i>	-0.06138	0.736697	0.915933	181.8853	155.8653	115.5049	152.563	132.3009	141.6068
<i>DPPA4</i>	-0.03595	0.814513	0.945914	758.0605	686.3243	594.6124	677.2144	622.9404	654.5651
<i>SCNN1A</i>	-0.16451	0.406332	0.750262	85.66466	95.82127	62.08351	76.07676	63.50068	75.17198
<i>ESRP1</i>	-0.00871	0.954628	0.988175	73.90409	74.83772	63.86782	69.15961	69.3621	69.83203
<i>XPC</i>	-0.27012	0.119979	0.481207	38.51684	30.58518	46.24368	28.89998	34.60178	30.23233
<i>MED14</i>	-0.15126	0.349008	0.712003	68.5876	67.32108	83.46328	56.75323	71.11884	66.68889
<i>KLF5</i>	-0.15237	0.658241	0.882567	2.146482	1.046043	1.229179	1.159184	1.363011	1.346428
<i>PRDM5</i>	-0.17632	0.296639	0.671648	25.33572	18.40743	20.09679	16.50247	20.62947	18.22352
<i>C1orf210</i>	-0.12921	0.541606	0.82551	11.01633	7.872519	8.347788	7.258819	9.417678	7.736131
<i>APELA</i>	-0.03224	0.849548	0.956202	86.32988	57.19952	86.10282	72.35694	69.55783	77.04358
<i>PRSS8</i>	-0.02351	0.866437	0.962947	121.4816	99.66324	114.4369	103.8034	111.3172	108.6974
<i>TOP2A</i>	-0.11914	0.443627	0.77055	454.7559	322.4182	457.8502	354.5155	402.8876	354.3603
<i>GCNT2</i>	-0.04296	0.778091	0.930828	62.21859	46.26366	59.04406	50.20665	58.32479	50.68604

DEA of developmental genes upon *PATZ1* RNAi

Gene_	log2	pvalue	P	Control	Control	Control	<i>PATZ1</i>	<i>PATZ1</i>	<i>PATZ1</i>
name	fold		adjust	RNAi	RNAi	RNAi	RNAi	RNAi	RNAi
	change			fpkm	fpkm	fpkm	fpkm	fpkm	fpkm
<i>BMP4</i>	0.804634	0.00765	0.119927	2.102038	1.936085	2.474329	3.034034	3.196468	4.94456

<i>CDX2</i>	0.327828	0.85761	1	0.016202	0	0.065979	0.030545	0.069312	0
<i>GCM1</i>	1.035888	0.656036	1	0	0.012704	0.013822	0.025596	0.029041	0
<i>REST</i>	0.052577	0.751318	0.920855	35.385	26.80231	25.26986	26.94994	31.91384	30.07908
<i>FOXA1</i>	2.234314	0.173625	1	0	0.055273	0.03007	0.278417	0	0.122665
<i>FOXA2</i>	1.242109	0.325449	0.692601	1.074382	0.626472	0.015852	2.113518	0.782665	1.034639
<i>GATA2</i>	0.630956	0.380896	0.735372	0.212336	0.278148	0.108084	0.340257	0.136252	0.440914
<i>GATA4</i>	0.336035	0.748349	1	0.194011	0.045383	0.123444	0.182877	0.025936	0.226609
<i>GATA6</i>	1.585369	0.086368	1	0.064437	0.048234	0.05248	0.315845	0.027565	0.133803
<i>MSX1</i>	0.683585	0.434641	1	0.153354	0.057396	0.37469	0.202375	0.229611	0.477657
<i>AFP</i>	1.095602	0.002635	0.065373	1.738013	4.481109	2.437796	6.407476	4.089255	8.060012
<i>SOX17</i>	4.582916	0.02746	0.241575	0.032059	0.014998	0	0.634604	0	0.449348
<i>FGF5</i>	2.542085	0.491889	1	0	0	0	0	0	0.042137
<i>NES</i>	0.264487	0.129477	0.495771	82.15404	92.66266	104.987	100.9394	100.5604	130.0021
<i>NOG</i>	0.665894	0.222141	0.603663	0.337314	0.241353	0.303	0.44888	0.318306	0.597424
<i>NODAL</i>	0.143419	0.846593	0.956202	36.38597	21.9506	5.851747	17.96558	17.20673	33.9512
<i>MYL4</i>	1.098721	0.506129	1	0.102571	0	0.104422	0.048343	0.109697	0.266235
<i>TRDN</i>	0.033277	0.860742	0.96057	56.62428	36.25596	46.71376	35.87455	56.26863	47.59599
<i>ACTA1</i>	0.153731	0.545014	0.826817	15.43611	11.83422	24.81559	14.22514	17.95333	24.50224
<i>TNNC2</i>	0.485981	0.096401	0.440144	3.376178	3.724782	4.257883	4.749898	6.628635	4.342379
<i>PRSS1</i>	0.993088	0.775964	1	0.041805	0	0	0	0	0.086808
<i>HNF4A</i>	3.278841	0.11317	1	0	0.013753	0	0.055422	0	0.091566
<i>ALB</i>	1.366455	0.511016	1	0	0.032524	0.035387	0.065531	0.037175	0.072179
<i>AFP</i>	1.095602	0.002635	0.065373	1.738013	4.481109	2.437796	6.407476	4.089255	8.060012

<i>ASGR2</i>	1.406329	0.141562	1	0.16451	0.092356	0.066991	0.217097	0.351876	0.273281
<i>DLX2</i>	0.887135	0.44097	1	0.017445	0.032645	0.106557	0.082218	0.05597	0.144895
<i>ABCA4</i>	0.705455	0.485729	1	0.22731	0.032721	0.017801	0.065928	0.205701	0.163387
<i>TTR</i>	0.992998	0.774354	1	0	0	0.045175	0	0	0.092144
<i>KCNH5</i>	0.923375	0.300711	1	0.090066	0.084272	0	0.162077	0.043783	0.119013
<i>PRAME</i>	1.831087	0.002871	0.068919	0.188108	0.176008	0.191502	0.531941	0.775966	0.641708
<i>ARMC3</i>	0.126596	0.870325	1	0.212396	0.124208	0.351371	0.200208	0.312333	0.220519
<i>LRP6</i>	0.525737	0.007134	0.11603	25.40734	17.28396	16.71239	21.25815	31.44477	31.0686
<i>RSPO2</i>	1.891199	0.024144	1	0.079536	0.049613	0.161942	0.349869	0.3686	0.330312
<i>WNT7B</i>	1.655497	0.110978	1	0.058415	0	0.118937	0.165187	0.124945	0.242594
<i>SOX9</i>	0.379437	0.10298	0.45128	2.504013	1.421856	1.984863	2.864813	2.177125	2.421164
<i>TGFBR2</i>	0.334027	0.096355	0.440144	2.457708	2.505201	2.12094	2.500776	3.350831	2.974165
<i>LEF1</i>	0.810954	0.220365	0.601483	0.411496	0.177704	0.644492	1.01446	0.236967	0.821601
<i>EDA</i>	0.257326	0.19596	0.577507	6.250274	6.051137	7.647685	6.430574	8.624454	8.43405
<i>MC4R</i>	1.865384	0.325205	1	0	0.020494	0.022298	0.041291	0.070273	0.04548
<i>SRD5A2</i>	3.556637	0.059257	1	0.008077	0	0	0.02284	0.008638	0.067086
<i>IRS4</i>	1.194032	0.06149	0.356606	1.424038	0.938962	0.428108	0.945929	2.361107	2.966918
<i>SDC3</i>	0.433718	0.013014	0.162794	29.15371	20.12384	23.50711	26.17889	36.60066	33.4861
<i>CYP19A1</i>	1.810069	0.214671	1	0.096507	0	0.032749	0.060646	0.137615	0.233794
<i>PRKDC</i>	0.373686	0.055412	0.342272	152.2854	138.8067	101.1004	132.4172	170.6403	197.9086
<i>FSHR</i>	2.304097	0.359918	1	0.025731	0	0	0.024254	0.110073	0
<i>SHBG</i>	0.737382	0.295434	0.670665	0.659387	0.370182	0.223761	0.870166	0.846233	0.319482
<i>IRS1</i>	0.338125	0.089183	0.424596	9.721706	6.922011	5.86938	7.569505	10.12967	10.20039

<i>KLK3</i>	2.14458	0.31294	1	0.064228	0	0	0	0.240413	0.033342
<i>COL2A1</i>	1.940539	5.11E-16	4.67E-12	4.101126	2.601251	3.512716	9.552933	11.4079	17.31846
<i>NCF2</i>	0.532856	0.683179	1	0.049625	0.18573	0.02526	0	0.079608	0.309135

DEA of cell cycle-regulatory genes upon *PATZ1* RNAi

Gene_ name	log2 fold change	pvalue	P adjust	Control RNAi fpkm	Control RNAi fpkm	Control RNAi fpkm	<i>PATZ1</i> RNAi fpkm	<i>PATZ1</i> RNAi fpkm	<i>PATZ1</i> RNAi fpkm
<i>E2F1</i>	0.539141	0.003424	0.07649	19.72294	16.89646	12.59694	22.32348	23.43498	24.55708
<i>CCNE1</i>	0.063459	0.712033	0.905624	42.34353	46.0585	35.5055	40.9349	43.43739	43.59805
<i>CCNE2</i>	0.547712	0.017612	0.190098	8.792892	6.811527	4.911712	8.476672	10.04489	10.93721
<i>CDC25A</i>	0.341169	0.099495	0.446434	47.11946	58.07373	33.97187	56.77533	55.72126	62.39492
<i>CDC6</i>	0.212673	0.319162	0.688397	87.01065	88.56911	49.60306	86.30194	81.53266	89.86381
<i>CDKN1A</i>	-1.98521	0.000884	0.031902	41.5576	44.52147	132.6466	11.71145	21.30591	21.29544
<i>CDK3</i>	-0.02907	0.954521	0.988175	0.829821	0.465864	1.621999	1.188944	0.780972	0.792631
<i>MCM2</i>	0.136806	0.518004	0.81339	101.1939	134.4376	76.57096	114.1367	106.6959	120.2164
<i>MCM6</i>	0.688812	0.000309	0.016687	107.4235	99.94689	66.1919	132.5049	151.8713	150.462
<i>NPAT</i>	0.408711	0.036398	0.278013	11.64572	10.1791	7.611144	11.05271	13.68485	13.74968
<i>PCNA</i>	0.038931	0.831637	0.952242	147.6079	206.6747	184.7833	193.5401	177.4166	178.0641
<i>SLBP</i>	-0.01985	0.898408	0.972809	45.53407	48.92276	48.55875	46.5386	45.27183	47.27544
<i>BRCA1</i>	0.192658	0.323196	0.69091	25.02739	15.45151	14.7756	20.45457	21.9012	19.2403
<i>BRCA2</i>	0.307462	0.180342	0.558724	6.730202	4.360727	3.091303	5.418372	5.9133	5.819068
<i>CCNG2</i>	-0.06973	0.704459	0.902478	14.635	9.654985	14.73552	11.33511	12.32383	12.63098

<i>DHFR</i>	0.525578	0.003375	0.075813	115.0111	100.4261	74.35662	124.0972	142.2198	144.2524
<i>MSH2</i>	0.308082	0.106223	0.457034	124.9456	105.5784	72.66757	113.4158	130.7612	125.0855
<i>NASP</i>	0.299057	0.059062	0.349918	626.1305	750.3659	721.2724	813.5725	873.4663	865.7558
<i>RRM1-ASI</i>	-0.8431	0.07761	0.396919	2.929506	4.365384	4.418306	2.556845	2.55283	1.351796
<i>RRM2</i>	0.511541	0.043132	0.300807	54.00779	86.13083	38.52594	91.04194	74.85872	88.35781
<i>TYMS</i>	-0.19558	0.258446	0.638769	90.07616	99.01085	126.6078	91.92094	87.89602	91.65753
<i>BIRC5</i>	-0.05656	0.710203	0.904935	136.7891	139.6883	158.3332	143.2523	141.0054	127.3286
<i>BUB1</i>	-0.25844	0.147807	0.522025	160.9528	140.6336	217.8586	149.5263	150.6081	125.552
<i>BUB1B</i>	0.094034	0.538212	0.824333	174.9506	157.2063	183.2272	156.0177	206.6867	178.6037
<i>CCNB1</i>	-0.37104	0.064016	0.364438	241.9	302.1704	404.274	270.9214	230.5174	221.4057
<i>CDC20</i>	-0.30656	0.047823	0.31771	208.6012	214.9159	253.8861	189.1677	177.2527	172.5489
<i>CDC25B</i>	-0.10907	0.57447	0.843649	18.3221	13.47843	23.32978	15.9249	18.61616	15.45008
<i>CDC25C</i>	-0.3981	0.033435	0.265683	26.41002	23.04076	35.3052	22.86528	19.90607	20.19706
<i>CDKN2D</i>	-0.17108	0.608743	0.860202	1.886035	1.512608	2.163878	1.439174	1.440755	1.958163
<i>CENPA</i>	-0.4845	0.027366	0.241196	28.02262	20.43761	39.84543	21.56013	22.41054	17.66308
<i>CCNA2</i>	-0.33358	0.023908	0.225783	83.64534	84.3303	97.02843	69.68544	70.80989	66.51274
<i>CCNF</i>	-0.16738	0.312828	0.684361	25.06378	28.71965	30.91447	24.8898	23.81921	25.69844
<i>CENPF</i>	-0.07588	0.589299	0.851949	231.878	177.794	205.7547	178.3716	197.3279	196.2842
<i>TOP2A</i>	-0.11914	0.443627	0.77055	454.7559	322.4182	457.8502	354.5155	402.8876	354.3603
<i>CCNB2</i>	-0.65583	0.000176	0.011753	96.89538	88.35166	129.2301	69.66505	66.93604	59.18243
<i>CKS2</i>	-0.35693	0.073711	0.389492	238.4747	243.1896	387.1712	239.6254	231.2664	195.5197

DEA of positive impact to flux in TCA cycle genes upon *PATZ1* RNAi

Gene_ name	log2 fold change	pvalue	P adjust	Control RNAi fpkm	Control RNAi fpkm	Control RNAi fpkm	<i>PATZI</i> RNAi fpkm	<i>PATZI</i> RNAi fpkm	<i>PATZI</i> RNAi fpkm
<i>ACSS2</i>	0.254632	0.186746	0.567668	17.39254	19.02664	16.22763	18.74655	24.81434	18.59904
<i>MPC2</i>	0.295947	0.059338	0.350603	29.5099	30.02904	28.3944	35.62148	36.08754	34.67834
<i>DLAT</i>	0.2458	0.161048	0.537798	37.29966	48.03016	38.78671	46.15353	49.50855	50.27189
<i>MPC1</i>	0.043913	0.861738	0.961002	10.98455	16.18479	8.783365	12.57578	11.79266	12.54073
<i>PDPR</i>	0.172254	0.397964	0.744922	34.53427	31.47695	24.64213	24.2513	35.73588	40.77932
<i>PDP2</i>	0.069587	0.721294	0.90936	31.57535	24.26392	36.16654	24.08933	37.84989	32.8108
<i>ACACB</i>	0.120355	0.53406	0.822037	5.44645	3.770831	5.009562	4.610874	5.606188	4.911892
<i>LDHB</i>	-0.0184	0.928781	0.980652	148.1059	163.983	161.7544	203.1735	137.3244	119.7798
<i>PDHX</i>	-0.0951	0.53832	0.824333	50.79288	50.33043	50.77284	48.71296	48.45575	42.83201
<i>DLD</i>	-0.02141	0.886681	0.969181	84.29735	85.64521	88.65146	88.05877	84.63049	78.17829
<i>PDHA2</i>	-0.88997	0.703023	1	0.051567	0.024125	0.026249	0	0.05515	0
<i>PDHB</i>	-0.04143	0.794533	0.938516	82.05861	94.71953	90.04531	83.99465	91.67235	80.63811
<i>PDP1</i>	-0.75247	0.000168	0.011426	29.25932	17.25637	27.00645	11.55527	14.83972	16.15335
<i>PDHA1</i>	-0.19874	0.21669	0.600727	83.09941	86.5174	101.6997	83.96854	75.15357	73.46131
<i>ACSS1</i>	-0.43322	0.205029	0.587805	0.654458	0.728495	1.114271	0.606265	0.506841	0.702917

DEA of negative impact to flux in TCA cycle genes upon *PATZI* RNAi

Gene_ name	log2 fold change	pvalue	P adjust	Control RNAi fpkm	Control RNAi fpkm	Control RNAi fpkm	<i>PATZI</i> RNAi fpkm	<i>PATZI</i> RNAi fpkm	<i>PATZI</i> RNAi fpkm
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<i>LDHA</i>	0.127211	0.485601	0.795027	355.5421	405.3888	292.3308	423.4305	350.1026	362.9646
<i>LDHB</i>	-0.0184	0.928781	0.980652	148.1059	163.983	161.7544	203.1735	137.3244	119.7798
<i>LDHC</i>	-0.27931	0.553094	0.831316	1.43373	1.023776	1.037081	1.173631	1.089472	0.548417
<i>PDK2</i>	0.011363	0.95191	0.98687	12.10655	12.00002	14.48274	12.25837	13.94651	12.08466
<i>PDK1</i>	0.084023	0.654309	0.880367	18.76309	15.06201	11.8248	14.16312	16.92917	16.45033
<i>PDK3</i>	0.170015	0.411391	0.753652	8.183989	5.989391	5.410377	5.857778	8.008019	7.756572
<i>PDK4</i>	-1.50482	0.17226	1	0.228445	0.07125	0.232566	0.047852	0.054292	0.07906
<i>PCK2</i>	-0.22751	0.247555	0.628104	101.1687	54.21313	60.77968	56.52818	62.30812	60.65518

DEA of TCA cycle regulatory genes upon *PATZ1* RNAi

Gene_ name	log2 fold change	pvalue	P adjust	Control RNAi fpkm	Control RNAi fpkm	Control RNAi fpkm	<i>PATZ1</i> RNAi fpkm	<i>PATZ1</i> RNAi fpkm	<i>PATZ1</i> RNAi fpkm
<i>MFN1</i>	0.34806	0.027004	0.239642	22.33029	18.75896	23.98056	24.71297	28.51328	28.05363
<i>DNM1L</i>	0.209228	0.159321	0.535717	73.26809	62.61406	66.40759	67.5673	84.87886	77.45653
<i>OPA1</i>	0.115679	0.427105	0.762335	45.02476	40.13277	42.76266	40.27933	50.46386	45.61987
<i>MLYCD</i>	0.051042	0.79629	0.938932	1.315202	1.046207	1.299677	1.292224	1.351588	1.071939
<i>SUCLG2</i>	0.05109	0.730627	0.9136	53.3841	46.80796	53.47063	49.28578	58.49698	48.69862
<i>SDHAF3</i>	0.01772	0.918348	0.978243	25.98409	24.31257	30.73831	26.11621	29.99924	24.55418
<i>EME2</i>	0.398454	0.056799	0.344926	18.08051	16.16553	19.74052	22.93799	16.73967	30.03515
<i>CPTIC</i>	0.169621	0.269639	0.646928	48.73174	42.68261	45.00898	51.0016	45.48457	54.0581
<i>DLST</i>	0.023184	0.870431	0.964078	135.1803	129.743	129.0024	132.2708	131.4914	130.1328
<i>SUCLA2</i>	0.009346	0.948408	0.98618	75.38271	63.34971	65.78341	64.10306	72.70075	65.35843

<i>TFAM</i>	0.188346	0.286961	0.662716	64.91555	59.51829	43.44015	61.34626	63.03518	63.96237
<i>PDK1</i>	0.084023	0.654309	0.880367	18.76309	15.06201	11.8248	14.16312	16.92917	16.45033
<i>PPARGC1B</i>	0.103793	0.707749	0.903977	5.388421	3.269822	2.503153	2.485356	4.498305	4.758034
<i>GLUD1</i>	-0.02266	0.875509	0.96607	144.1149	145.4532	145.835	138.9402	149.0986	134.373
<i>PDHA2</i>	-0.88997	0.703023	1	0.051567	0.024125	0.026249	0	0.05515	0
<i>IDH3A</i>	-0.17123	0.275602	0.652063	30.63859	25.86679	27.2476	23.86779	25.19673	23.94914
<i>ACO1</i>	-0.33165	0.024356	0.227643	18.95077	18.89419	20.69022	14.81255	16.01861	14.97759
<i>OGDHL</i>	-0.68759	0.000218	0.013517	15.13728	11.43809	18.35995	9.098613	9.660295	8.525667
<i>MDH1</i>	-0.36954	0.015226	0.175661	418.4014	399.3369	476.4085	351.7067	336.7339	295.963
<i>SUCLG1</i>	-0.23818	0.165594	0.541964	51.94688	50.57677	54.72272	50.58723	39.27524	41.03053
<i>ME1</i>	-0.12076	0.58769	0.851202	2.728438	2.750903	3.208482	3.201708	2.370116	2.266226
<i>DLD</i>	-0.02141	0.886681	0.969181	84.29735	85.64521	88.65146	88.05877	84.63049	78.17829
<i>SDHAF1</i>	-0.1829	0.348606	0.711178	11.89753	13.4278	12.45432	11.75334	11.21442	9.875047
<i>OGDH</i>	-0.11628	0.493878	0.799335	35.06814	43.11312	44.22409	37.80203	35.75177	38.03329
<i>HADHA</i>	-0.10976	0.495213	0.800006	76.47963	87.71127	93.20169	81.98527	79.99239	73.43594
<i>IDH3G</i>	-0.03579	0.824379	0.949569	28.39153	29.53861	30.71689	28.67149	28.2724	28.24456
<i>ECH1</i>	-0.28029	0.132297	0.498824	84.42074	111.6696	117.9508	90.02199	84.69252	81.05618
<i>ACO2</i>	-0.18018	0.256558	0.637919	78.16982	90.10362	91.09537	74.51964	76.6036	74.96998
<i>IDH3B</i>	-0.23833	0.157181	0.532652	100.8566	119.8482	119.4466	102.9913	90.32537	91.33363
<i>SDHA</i>	-0.36064	0.037155	0.280441	64.64509	67.70356	90.41166	58.72369	56.32981	55.6091
<i>SDHB</i>	-0.32993	0.07873	0.399401	83.91851	98.06248	130.1387	77.89121	85.85367	81.23405
<i>SDHC</i>	-0.09869	0.52593	0.81724	87.31638	90.15275	107.6002	87.17654	93.12603	81.91518
<i>MDH2</i>	-0.1442	0.40464	0.749207	201.4408	245.9469	282.6275	209.5115	232.7253	210.7093

<i>PDHB</i>	-0.04143	0.794533	0.938516	82.05861	94.71953	90.04531	83.99465	91.67235	80.63811
<i>PRPS1</i>	0.061836	0.682474	0.893426	95.15554	102.6393	100.1144	98.12467	108.8187	100.0304
<i>NRF1</i>	-0.01032	0.959073	0.988589	8.796497	10.20073	7.256247	9.364916	8.623622	7.788878
<i>SDHAF2</i>	-0.13194	0.591159	0.852882	11.38836	17.68941	13.88508	15.02027	10.39831	13.45961
<i>MFN2</i>	0.020413	0.909186	0.976217	47.817	63.12295	50.12621	52.52689	54.64059	54.88392

DEA of glycolysis genes upon *PATZI* RNAi

Gene_ name	log2 fold change	pvalue	P adjust	Control RNAi fpkm	Control RNAi fpkm	Control RNAi fpkm	<i>PATZI</i> RNAi fpkm	<i>PATZI</i> RNAi fpkm	<i>PATZI</i> RNAi fpkm
<i>PGAM2</i>	0.178708	0.684696	0.894264	0.876105	1.844428	2.631135	2.518776	1.873935	1.591817
<i>ENO3</i>	-0.19634	0.262905	0.641724	316.4177	403.8881	354.3883	340.5817	295.0742	292.3028
<i>ENO1</i>	-0.06624	0.699765	0.900304	1506.315	1917.775	1704.853	1753.272	1551.808	1541.786
<i>TPI1</i>	-0.04494	0.790259	0.93675	617.3205	744.5859	710.8136	736.2428	638.4199	609.8123
<i>BPGM</i>	-0.0457	0.80947	0.944058	12.25977	13.72079	15.0256	14.58553	13.23875	11.31982
<i>LDHB</i>	-0.0184	0.928781	0.980652	148.1059	163.983	161.7544	203.1735	137.3244	119.7798
<i>GAPDHS</i>	-0.34888	0.34769	0.711151	1.897237	2.039581	2.260225	1.560061	2.029038	1.215405
<i>PGK1</i>	-0.08814	0.551826	0.830594	245.3528	266.8444	254.121	237.237	242.1724	232.0602
<i>ENO2</i>	-0.42664	0.04815	0.319533	94.48153	70.45816	138.8856	83.3989	75.89313	61.30518
<i>PFKL</i>	-0.13669	0.374857	0.730362	42.77763	38.1305	50.48427	38.9933	38.56042	39.70895
<i>GCK</i>	-0.14351	0.579483	0.846445	3.170924	3.67237	4.988928	3.469698	4.268652	2.831744
<i>PFKM</i>	-0.01437	0.92795	0.980652	76.15842	79.07571	95.8198	80.38708	87.14947	77.31502
<i>PFKP</i>	-0.28466	0.112663	0.469423	108.5718	115.9509	152.2301	86.50482	108.2832	110.1769

<i>PKM</i>	-0.12078	0.483637	0.793876	467.8639	563.2172	653.6536	463.554	551.0072	517.2096
<i>FBP2</i>	0.012253	0.987812	1	0.316438	0.161499	0.205003	0.244046	0.215359	0.209071
<i>HK2</i>	0.151865	0.435317	0.766644	31.65653	25.3663	17.93207	25.34117	27.68864	28.74984
<i>LDHA</i>	0.127211	0.485601	0.795027	355.5421	405.3888	292.3308	423.4305	350.1026	362.9646
<i>PGAMI</i>	0.114742	0.472295	0.788496	329.1176	369.6191	301.0144	349.5763	359.7986	360.7099
<i>GAPDH</i>	0.138462	0.451429	0.775888	2437.129	3282.436	2389.33	3064.143	2889.552	2903.816
<i>ALDOC</i>	0.037486	0.831022	0.952011	42.10786	52.0499	45.50327	43.75889	52.10916	46.18225
<i>HK1</i>	0.116085	0.457168	0.777905	141.4741	138.5944	152.3588	129.8736	175.0673	157.1787

DEA of energy genes upon *PATZ1* RNAi

Gene_ name	log2 fold change	pvalue	P adjust	Control RNAi fpkm	Control RNAi fpkm	Control RNAi fpkm	<i>PATZ1</i> RNAi fpkm	<i>PATZ1</i> RNAi fpkm	<i>PATZ1</i> RNAi fpkm
<i>ALDOA</i>	0.103171	0.610865	0.861218	11.50619	13.62623	11.64383	12.10855	12.01165	14.94169
<i>PPA1</i>	0.185524	0.221636	0.602956	116.4844	123.7459	112.4419	133.5031	136.5831	125.6555
<i>PDK3</i>	0.170015	0.411391	0.753652	8.183989	5.989391	5.410377	5.857778	8.008019	7.756572
<i>PDK1</i>	0.084023	0.654309	0.880367	18.76309	15.06201	11.8248	14.16312	16.92917	16.45033
<i>IDH3A</i>	-0.17123	0.275602	0.652063	30.63859	25.86679	27.2476	23.86779	25.19673	23.94914
<i>NDUFB8</i>	-0.12993	0.480945	0.792274	37.06285	33.11251	39.07035	38.14781	31.58221	28.11541
<i>COX8A</i>	-0.46617	0.006507	0.110451	335.056	352.5082	379.6959	298.4491	236.9348	224.5585
<i>COX5B</i>	-0.28083	0.074372	0.390194	247.5576	251.8774	279.8865	233.0863	200.5649	197.2178
<i>NDUFS7</i>	-0.45835	0.004903	0.094953	39.82961	40.51183	49.96155	32.14005	31.02651	30.1206
<i>COX7A2</i>	-0.39319	0.027796	0.243109	224.8568	233.3638	311.1027	215.3204	185.5331	174.856

<i>NDUFB5</i>	-0.26685	0.096965	0.440953	89.94874	86.92975	102.2501	83.44877	77.00857	67.51334
<i>NDUFS4</i>	-0.03437	0.820488	0.948148	81.43896	78.89347	90.29543	79.1962	82.47871	79.07429
<i>SDHB</i>	-0.32993	0.07873	0.399401	83.91851	98.06248	130.1387	77.89121	85.85367	81.23405
<i>MDH2</i>	-0.1442	0.40464	0.749207	201.4408	245.9469	282.6275	209.5115	232.7253	210.7093
<i>UQCRH</i>	-0.21978	0.178362	0.556989	458.3365	535.6312	563.1568	470.1301	429.7293	419.6686
<i>CYCI</i>	-0.24549	0.144732	0.517555	119.6178	145.8477	146.819	121.5762	111.2682	110.7207
<i>PGK1</i>	-0.08814	0.551826	0.830594	245.3528	266.8444	254.121	237.237	242.1724	232.0602
<i>NDUFB10P1</i>	1.956355	0.627805	1	0	0	0	0	0	0.149623
<i>UQCRC1</i>	-0.24423	0.162554	0.5397	212.7725	276.8086	259.8443	221.9816	197.9412	206.1026
<i>PDHB</i>	-0.04143	0.794533	0.938516	82.05861	94.71953	90.04531	83.99465	91.67235	80.63811
<i>TPII</i>	-0.04494	0.790259	0.93675	617.3205	744.5859	710.8136	736.2428	638.4199	609.8123
<i>BPGM</i>	-0.0457	0.80947	0.944058	12.25977	13.72079	15.0256	14.58553	13.23875	11.31982

DEA of cell ETC genes upon *PATZ1* RNAi

Gene_ name	log2 fold change	pvalue	P adjust	Control RNAi fpkm	Control RNAi fpkm	Control RNAi fpkm	<i>PATZ1</i> RNAi fpkm	<i>PATZ1</i> RNAi fpkm	<i>PATZ1</i> RNAi fpkm
<i>MT-ND1</i>	0.510751	0.003367	0.075719	1480.595	1649.311	1287.791	2269.934	1828.168	2113.552
<i>NDUFS7</i>	-0.45835	0.004903	0.094953	39.82961	40.51183	49.96155	32.14005	31.02651	30.1206
<i>NDUFB1</i>	0.399209	0.014036	0.168867	61.45423	67.1847	71.13587	89.67873	85.59172	84.42743
<i>NDUFB7</i>	-0.43118	0.017845	0.191599	155.1226	198.2306	204.2879	150.6941	130.295	127.6673
<i>MT-ND2</i>	0.416704	0.024496	0.22807	1609.655	1955.567	1766.957	2803.024	1988.38	2232.486
<i>NDUFS8</i>	-0.3581	0.029133	0.249045	100.0773	112.2223	128.1178	87.80478	87.2918	86.80505

<i>SDHA</i>	-0.36064	0.037155	0.280441	64.64509	67.70356	90.41166	58.72369	56.32981	55.6091
<i>SDHB</i>	-0.32993	0.07873	0.399401	83.91851	98.06248	130.1387	77.89121	85.85367	81.23405
<i>SDHC</i>	-0.09869	0.52593	0.81724	87.31638	90.15275	107.6002	87.17654	93.12603	81.91518
<i>SDHD</i>	-0.0828	0.652596	0.87991	73.53314	88.49734	86.2232	89.41164	76.01033	65.98616
<i>UQCR11</i>	-0.48226	0.005753	0.10322	54.33858	62.51849	62.53912	46.14351	40.94747	39.58579
<i>UQCRC2</i>	-0.27828	0.073748	0.389492	174.0158	174.3389	218.2233	153.5474	154.8137	151.2092
<i>UQCRFS1</i>	-0.28209	0.082052	0.407268	43.0399	48.41844	53.75865	41.47632	38.95902	37.31676
<i>CYCI</i>	-0.24549	0.144732	0.517555	119.6178	145.8477	146.819	121.5762	111.2682	110.7207
<i>UQCRC1</i>	-0.24423	0.162554	0.5397	212.7725	276.8086	259.8443	221.9816	197.9412	206.1026
<i>UQCRH</i>	-0.21978	0.178362	0.556989	458.3365	535.6312	563.1568	470.1301	429.7293	419.6686
<i>COX17</i>	-0.51945	0.002409	0.06154	78.87693	83.12334	102.7894	62.34198	61.52805	57.97267
<i>COX8A</i>	-0.46617	0.006507	0.110451	335.056	352.5082	379.6959	298.4491	236.9348	224.5585
<i>COX7A2</i>	-0.39319	0.027796	0.243109	224.8568	233.3638	311.1027	215.3204	185.5331	174.856
<i>COX6C</i>	-0.33474	0.049247	0.323062	227.8519	218.0146	284.8895	215.2228	181.5573	171.8298
<i>COX14</i>	-0.33976	0.065534	0.369194	28.82222	27.5397	28.94644	24.13208	23.51926	18.62352
<i>ATPIA2</i>	0.999501	9.10E-07	0.000302	39.65378	27.93362	36.51424	46.21723	84.55633	73.38095
<i>ATP6V0C</i>	-0.68497	0.001141	0.03808	24.15879	25.41477	21.40228	17.52684	11.76131	14.12335
<i>ATP6V1E1</i>	-0.51266	0.001294	0.041454	117.6403	114.6455	138.6516	92.70674	83.25839	79.48029
<i>ATP8B3</i>	-1.13961	0.001382	0.043273	2.116722	1.661111	5.018852	1.634819	1.343657	0.907426
<i>ATP6V1C2</i>	-0.76965	0.00346	0.077057	7.677211	8.945299	10.19975	7.373186	3.847079	4.210996
<i>ATP6V0E2-AS1</i>	-1.06388	0.00553	0.101203	1.044775	0.811877	1.099679	0.433988	0.435579	0.514788
<i>ATPIA3</i>	0.705181	0.007126	0.11603	1.861722	2.274795	2.363562	2.807816	4.169504	3.524737
<i>ATP2A1</i>	-0.62047	0.017403	0.189266	5.877121	3.924435	8.17082	3.441056	4.264106	3.709514

<i>ATP8A2</i>	0.492267	0.020063	0.203733	2.354157	1.724258	1.650137	2.582841	2.847889	2.464222
<i>ATP6V0A2</i>	0.33623	0.040452	0.291433	25.02739	20.9985	18.97193	23.86026	27.9873	28.80033
<i>DNM1L</i>	0.209228	0.159321	0.535717	73.26809	62.61406	66.40759	67.5673	84.87886	77.45653
<i>MFN1</i>	0.34806	0.027004	0.239642	22.33029	18.75896	23.98056	24.71297	28.51328	28.05363
<i>MFN2</i>	0.020413	0.909186	0.976217	47.817	63.12295	50.12621	52.52689	54.64059	54.88392
<i>OPA1</i>	0.115679	0.427105	0.762335	45.02476	40.13277	42.76266	40.27933	50.46386	45.61987

DEA of cell mitochondria biogenesis genes upon *PATZ1* RNAi

Gene_ name	log2 fold change	pvalue	P adjust	Control RNAi fpkm	Control RNAi fpkm	Control RNAi fpkm	<i>PATZ1</i> RNAi fpkm	<i>PATZ1</i> RNAi fpkm	<i>PATZ1</i> RNAi fpkm
<i>NRF1</i>	-0.01032	0.959073	0.988589	8.796497	10.20073	7.256247	9.364916	8.623622	7.788878
<i>MFN2</i>	0.020413	0.909186	0.976217	47.817	63.12295	50.12621	52.52689	54.64059	54.88392
<i>MFN1</i>	0.34806	0.027004	0.239642	22.33029	18.75896	23.98056	24.71297	28.51328	28.05363
<i>DNM1L</i>	0.209228	0.159321	0.535717	73.26809	62.61406	66.40759	67.5673	84.87886	77.45653
<i>OPA1</i>	0.115679	0.427105	0.762335	45.02476	40.13277	42.76266	40.27933	50.46386	45.61987
<i>PPARGC1B</i>	0.103793	0.707749	0.903977	5.388421	3.269822	2.503153	2.485356	4.498305	4.758034
<i>TFAM</i>	0.188346	0.286961	0.662716	64.91555	59.51829	43.44015	61.34626	63.03518	63.96237

Supplementary Table 6. Calculation equations of ATP production from Seahorse assay.

Calculated values	Equations
OCR_{mito}	$= (OCR_{total} - OCR_{rot/myc})$
OCR_{couple}	$= (OCR_{total} - OCR_{oligo}) \times$ <i>hyperpolarization correction factor</i>
PPP_{total}	$= \left(\frac{ECR_{total}}{\text{buffering power}} \right)$
PPP_{resp}	$= (OCR_{mito} \times K_{PPR_{resp}})$
PPP_{glyc}	$= (PPR_{total} - PPP_{resp})$
<i>Glycolytic ATP J</i> (ATP_{glyc})	$= \left(PPR_{glyc} \times \frac{ATP}{lactate} \right) + (OCR_{mito} \times 2 \times \frac{ATP}{[O]_{glyc}})$
<i>Oxidative ATP J</i> (ATP_{ox})	$= \left(OCR_{couple} \times 2 \times \frac{ATP}{[O]_{oxphos}} \right) + (OCR_{mito} \times 2 \times \frac{ATP}{[O]_{TCA}})$

Parameters	Values
hyperpolarization correction factor	0.908
buffering powder (mH/pmol H ⁺)	0.045
$\frac{ATP}{lactate}$	1.000
$\frac{ATP}{[O]_{glyc}}$	0.167
$\frac{ATP}{[O]_{oxphos}}$	2.486
$\frac{ATP}{[O]_{TCA}}$	0.121

Supplementary Table 7. Quantification of metabolites by LC/MS/MS

Quantification of metabolites by LC/MS/MS							
Metabolites	Class	HMDB	KEGG	Uni FDR	FC	Log2FC	OPLSDA VIP
Glutamic acid	Amino acids	HMDB0000148	C00025	1.0E-4	1.546	0.6286	1.3633
Malic acid	Organic acids	HMDB0000156	C00149	0.0046	1.4843	0.5698	1.2566
Aspartic acid	Amino acids	HMDB0000191	C00049	0.0114	1.1999	0.2629	1.0457
Lactic acid	Organic acids	HMDB0000190	C00186	0.026	1.2872	0.3643	1.0922
Serine	Amino acids	HMDB0000187	C00065	0.0052	1.9245	0.9445	1.1881
Glutamine	Amino acids	HMDB0000641	C00064	<0.0001	3.4987	1.8068	1.3752
Glucose	Carbohydrates	HMDB0000122	C00221	0.0087	4.957	2.3095	1.2481
Fructose	Carbohydrates	HMDB0000660	C02336	<0.0001	5.0138	2.3259	1.3179
3-Phosphoglyceric acid	Carbohydrates	HMDB0000807	C00597	0.039	1.9587	0.9699	1.0235
Citric acid	Organic acids	HMDB0000094	C00158	0.0022	2.6074	1.3826	1.0625
Isocitric acid	Organic acids	HMDB0000193	C00311	0.0131	1.4121	0.4978	1.2048
Oxoglutaric acid	Organic acids	HMDB0000208	C00026	3.0E-4	2.1531	1.1064	1.0366
Glucose-1-phosphate	Carbohydrates	HMDB0001586	C00103	9.0E-4	3.1027	1.6335	1.1634
Fructose-1-phosphate	Carbohydrates	HMDB0001076	C01094	0.0035s	2.5133	1.3296	1.0644

