## Supplementary Materials

Jwa participates the maintenance of intestinal epithelial homeostasis via ERK/FBXW7mediated NOTCH1/PPARy/STAT5 axis and acts as a novel putative aging related gene Xiong Li ${ }^{1,2,3}$, Jingwen Liu ${ }^{1,2,3}$, Yan Zhou ${ }^{1,2,3}$, Luman Wang ${ }^{1,2,3}$, Yifan Wen ${ }^{1,2,3}$, Kun Ding ${ }^{1,2,3}$, Lu Zou ${ }^{1,2,3}$, Xia Liu ${ }^{1,2,3}$, Aiping Li ${ }^{11,2,3}$, Yun Wang ${ }^{4}$, Heling Fu ${ }^{4}$, Min Huang ${ }^{5}$, Guoxian Ding ${ }^{5}$ and Jianwei Zhou ${ }^{1,2,3, *}$
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## Supplementary Method

## Genotyping of intestinal epithelial Jwa deletion mice

Genomic DNA was isolated from mouse tail and the PCR procedure was performed using the Quick Genotyping Assay Kit for Mouse Tail (Beyotime). The primers used for genotyping were as followed: flox (Forward: 5'-CCACTGTTTCCTCTGTTG-3'; Reverse: 5'-GTGAAAACCACTGAGAACC3'); Vil1-cre (Common Forward: 5'-GCCTTCTCCTCTAGGCTCGT-3', Wild type Reverse : 5'-TATAGGGCAGAGCTGGAGGA-3', Mutant Reverse : 5’-AGGCAAATTTTGGTGTACGG-3'), the products were separated by agarose gel electrophoresis and the images were obtained on the Gel Doc XR Gel Imaging System (Bio-Rad, Hercules, CA, USA). When genotyping for flox, image showed two bands in 341 and 437 bp indicating Jwa ${ }^{\text {fl/ }}$ (Supplementary Fig. S3B, lane 1), one band in 437 bp indicating Jwa ${ }^{\text {f/fl }}$ (Supplementary Fig. S3B, lane 2), one band in 341 bp indicating $\mathrm{Jwa}^{+/+}$ (Supplementary Fig. S3B, lane 3). When genotyping for Vil1-cre, image showed one band in 182 bp indicating wild type, two bands in 150 and 180 bp indicating Vil1-cre. The genotypes of mice were identified combining with the results of genotyping for flox and Vil1-cre. When the results of genotyping for flox and Vil1-cre were Jwa ${ }^{f / / f /}$ and Vil1-cre respectively, the genotype of mouse was Jwa ${ }^{f / / f /}$ Vil1-cre, i.e., the intestinal epithelial Jwa deletion mouse, we abbreviated it as JwalEC ${ }^{+/+}$. When the results of genotyping for flox and Vil1-cre were $J w a^{f / f / f}$ and wild type respectively, the genotype of mouse was Jwa ${ }^{\text {fl/fll}}$, i.e., the littermate wild type mouse, we abbreviated it as Jwa ${ }^{\text {IEC -- }}$ (Supplementary Fig. S3A).

## Supplementary Figures



Supplementary Figure S1. No significant morphological difference is observed in the main organs of $\mathrm{Jwa}^{+/+}$and $\mathrm{Jwa}^{-/-}$mice. (A-G) H\&E staining of the main organs or tissues such as myocardium (A), liver (B), lung (C), kidney (D), stomach (E), spleen (F), and thymus (G) of Jwa ${ }^{+/+}$and Jwa ${ }^{--}$mice at 16-month-old.


## Supplementary Figure S2. The expression profile of JWA in tissues and organs. (A) Jwa mRNA

 levels in multiple tissues or organs, data was from the human protein atlas database (THPA database: https://www.proteinatlas.org); (B) JWA protein levels in multiple tissues or organs, data was from THPA database. (C) Immunochemistry images of JWA in the intestinal sections from THPA database. (D, E) Immunoblotting of JWA (D) and relatively JWA expression (E) in the duodenum, jejunum and ileum crypts of wild-type mice. ${ }^{* *} P<0.01$ and ${ }^{* * *} P<0.001$.

Supplementary Figure S3. Construction and genotyping of intestinal epithelial Jwa deletion mice. (A) Schematic diagram of mouse reproduction. (B) Image of genotyping for flox alleles. (C) Image of genotyping for Vil1-cre alleles. (D) Immunofluorescence of JWA in intestinal sections of 2-month-old JwalEC +/+ and JwalEC -l- mice.


Supplementary Figure S4. Intestinal epithelial Jwa deletion reduces intestinal stem cells and skews the distributions of intestinal epithelial cells lineage. (A) Immunofluorescence staining of KI67 in the intestinal sections of 2-month-old JwalEC +/+ and Jwa ${ }^{\text {IEC -/- }}$ mice. (B) Immunofluorescence staining of OLFM4 in the intestinal sections of 2-month-old Jwa ${ }^{\mathrm{IEC}}+\mathrm{H}^{1+}$ and Jwa ${ }^{\mathrm{IEC}}-1-$ mice. (C, D) Immunoblotting of OLFM4 (C) and relative OLFM4 levels in crypts (D) of 2-month-old Jwal ${ }^{1 E C+/+}$ and $J w a^{\text {IEC }}-1-$ mice, $n=3$ for each genotype. (E, F) Alcian blue staining for the goblet cells (E) and $A B$ positive cell counts in villus (F) of 2-month-old Jwalec +/+ and Jwa ${ }^{\mathrm{IEC}-1-}$ mice, $\mathrm{n}=3$ for each genotype.
(G) Immunofluorescence co-staining of LYZ and MUC2 in the intestinal sections of 2-month-old Jwa ${ }^{\text {IEC }}$
 in villi, Paneth cell marker Mmp7 (I) in crypts, goblet cell marker Spink4 and Tff3 (J), enteroendocrine cell marker Reg4 and $\operatorname{Ngn3}(\mathbf{K})$, and tuft cell marker Hck in villi (L) of 2-month-old Jwa ${ }^{\mathrm{IEC}+/+}$ and Jwa ${ }^{\mathrm{IEC}}$ ${ }^{-/}$mice, $\mathrm{n}=3$ for each genotype. ${ }^{\text {ns }}$ No significance, ${ }^{*} P<0.05$ and ${ }^{* * *} P<0.001$.


Supplementary Figure S5. Intestinal epithelial Jwa deletion disturbs PPARy/STAT5 axis through inhibiting Notch signal pathway. (A, B) Relative STAT5A (A) and STAT5B (B) levels in the jejunum of 2-month-old $\mathrm{Jwa}^{+/+}$and $\mathrm{Jwa}^{-/-}$mice, $\mathrm{n}=3$ for each genotype. (C-E) Relative STAT5A (C), STAT5B (D) levels and relative STAT5 phosphorylation level (E) in crypts of 2-month-old Jwa ${ }^{1 \mathrm{EC}}+1+$ and JwalEC -/- mice, $\mathrm{n}=3$ for each genotype. ( $\mathbf{F}, \mathbf{G}$ ) Immunoblotting of JAK2, p-JAK2 ( $\mathbf{F}$ ) and relative JAK2 phosphorylation level (G) in crypt of 2-month-old Jwal ${ }^{\text {EC }+/+}$ and Jwa ${ }^{1 E C-/-}$ mice, $\mathrm{n}=3$ for each genotype. (H-L) Relative levels of PPARy (H), NOTCH1 (I), NICD (J), HES1 (K) and full length NOTCH1 (L) in crypts of 2-month-old Jwa ${ }^{\mathrm{IEC}+/+}$ and Jwa ${ }^{\mathrm{IEC}-1-}$ mice, $\mathrm{n}=3$ for each genotype. ${ }^{\text {ns }}$ No significance, ${ }^{*} P<0.05,{ }^{* *} P<0.01$ and ${ }^{* * *} P<0.001$.

| A A | Top 5 predicted E3-ubiquitin-protein ligase <br> from the Ubibrowser database |  |  |
| :---: | :---: | :---: | :---: |
| Rank Symbol Score Confidence level <br> 1 MIB1 0.899 HIGH <br> 2 MIB2 0.878 HIGH <br> 3 MDM2 0.87 HIGH <br> 4 STUB1 0.83 HIGH <br> 5 NEDD4L 0.823 HIGH <br> *http://ubibrowser.ncpsb.org.cn/ubibrowser/    |  |  |  |










K


Supplementary Figure S6. Jwa deficiency promotes degradation of Notch1 through

ERK/Fbxw7 axis. (A) The predicted top five E3 ubiquitin ligases target Notch1. (B-G) Immunoblotting of the predicted top five E3 ubiquitin ligases (B), and relative MIB1 (C), MIB2 (D), MDM2 (E), STUB1 (F) and NEDD4L (G) levels in crypts of 2-month-old Jwalec +/+ and JwalEC --- mice, $\mathrm{n}=3$ for each genotype. (H) Immunoblotting of the predicted top five E3 ubiquitin ligases in IEC-6 cells transfected with shJwa plasmid, 3 independent replicates were carried out. (I, J) Relative ERK1/2 phosphorylation level (I) and FBXW7 level ( J ) in crypts of 2-month-old Jwa ${ }^{\mathrm{IEC}+/+}$ and Jwa ${ }^{\mathrm{IEC}-/-}$ mice, $\mathrm{n}=3$ for each
genotype. (K) Immunoblotting of FBXW7, ERK1/2 and p-ERK1/2 in IEC-6 cells transfected with shJwa plasmid, 3 independent replicates were carried out. (L) Immunoblotting of JWA, NICD, HES1, PPARY and STAT5A in IEC-6 cells transfected with shJwa plasmid followed by Pamoic acid ( $10 \mu \mathrm{M}$ ) treatment, 3 independent replicates were carried out. (M) Immunoblotting of JWA, NICD, HES1, PPARy and STAT5A in IEC-6 cells co-transfected with shJwa and siFbxw7, 3 independent replicates were carried out. ${ }^{\text {ns }}$ No significance and ${ }^{* * *} P<0.001$.


Supplementary Figure S7. Restoration of the ERK/FBXW7 and NOTCH1/PPARy/STAT5 axes reverses Jwa deficiency-induced cellular phenotypic changes in vitro. (A-E) Immunoblotting of PCNA in IEC-cells co-tranfected with shJwa and Stat5a OE plasmids (A), co-tranfected with shJwa and Hes1 OE plasmids (B), transfected with shJwa plasmid followed by GW9662 (10 $\mu \mathrm{M})$ treatment (C), transfected with shJwa plasmid followed by Pamoic acid (10 $\mu \mathrm{M})$ treatment (D) or co-tranfected with shJwa and siFbxw7 (E), 3 independent replicates were carried out. (F-J) QRT-PCR detection of ISC marker Olfm4, absorptive enterocyte marker Lct, Paneth cell marker Mmp7, goblet cell marker

Tff3, enteroendocrine cell marker Ngn3 and tuft cell marker Hck in IEC-6 cell co-tranfected with shJwa and Stat5a OE plasmids (F), co-tranfected with shJwa and Hes1 OE plasmids (G), transfected with shJwa plasmid followed by GW9662 $(10 \mu \mathrm{M})$ treatment $(\mathrm{H})$, transfected with shJwa plasmid followed by Pamoic acid ( $10 \mu \mathrm{M}$ ) treatment (I) or co-tranfected with shJwa and siFbxw7 (J), 3 independent replicates were carried out. ${ }^{*} P<0.05,{ }^{* *} P<0.01$ and ${ }^{* * *} P<0.001$.

## Supplementary Tables

Supplementary Table S1. Antibodies used in this study

| Antibodies | Dilution | Manufacture | Catalog No. |
| :---: | :---: | :---: | :---: |
| anti-JWA mouse mAb | IB 1:100 | Our laboratory | - |
|  |  | Sigma Aldrich |  |
| anti-JWA rabbit pAb | IF 1:50 | (St. Louis, MO, USA) | SAB1306837 |
|  |  | Servicebio |  |
| anti-KI67 rabbit pAb | IHC 1:500 |  | GB111499 |
|  |  | (Wuhan, China) |  |
|  |  | Proteintech |  |
| anti-BrdU mAb | IF 1:50 |  | 66241-1-lg |
|  |  | (Wuhan, China) |  |
|  | IB 1:1000 | Cell Signaling Technology |  |
| anti-OLFM4 rabbit mAb |  |  | \#39141 |
|  | IHC/IF 1:200 | (Boston, MA, USA) |  |
|  | IF 1:200 | Abcam |  |
| anti-LYZ rabbit mAb |  |  | ab108508 |
|  | IHC 1:1000 | (Cambridge, UK) |  |
|  |  | Servicebio |  |
| anti-MUC2 rabbit pAb | IF 1:500 |  | GB11344 |
|  |  | (Wuhan, China) |  |
| anti-Cleaved CASPASE-3 |  | Servicebio |  |
|  | IF 1:500 |  | GB11532 |
| rabbit pAb |  | (Wuhan, China) |  |
|  |  | Affinity |  |
| anti-STAT5A rabbit pAb | IB 1:2000 |  | AF6303 |
|  |  | (Changzhou, China) |  |
|  |  | Affinity |  |
| anti-STAT5B rabbit pAb | IB 1:2000 |  | AF6340 |
|  |  | (Changzhou, China) |  |


| Antibodies | Dilution | Manufacture | Catalog No. |
| :---: | :---: | :---: | :---: |
| anti-pY-STAT5 rabbit pAb | IB 1:1000 | Bioworlde (Nanjing, China) | BS4185 |
|  |  | Proteintech |  |
| anti-NOTCH1 rabbit pAb | IB 1:1000 | (Wuhan, China) | 20687-1-AP |
|  | IB 1:2000 | Abclonal |  |
| anti-NOTCH1 rabbit mAb |  |  | A19090 |
|  | IP 1:200 | (Wuhan, China) |  |
| anti-Cleaved NOTCH1 |  |  |  |
|  |  | Cell Signaling Technology |  |
| (Val1744) [NICD] rabbit | IB 1:1000 |  | \#4147 |
|  |  | (Boston, MA, USA) |  |
| pAb |  |  |  |
|  |  | Affinity |  |
| anti-HES1 rabbit pAb | IB 1:2000 |  | AF7575 |
|  |  | (Changzhou, China) |  |
|  |  | Proteintech |  |
| anti-PPARy rabbit pAb | IB 1:5000 |  | 16643-1-AP |
|  |  | (Wuhan, China) |  |
|  |  | Wanleibio |  |
| anti-JAK2 rabbit pAb | IB 1:500 |  | WL02188 |
|  |  | (Shenyang, China) |  |
|  |  | Wanleibio |  |
| anti-p-JAK2 rabbit pAb | IB 1:500 |  | WL02997 |
|  |  | (Shenyang, China) |  |
|  |  | Affinity |  |
| anti-ERK1/2 mouse mAb | IB 1:2000 |  | BF8004 |
|  |  | (Changzhou, China) |  |
|  |  | Affinity |  |
| anti-p-ERK1/2 rabbit pAb | IB 1:2000 |  | AF1015 |
|  |  | (Changzhou, China) |  |



Antibodies
Alexa Fluor 555-

|  | Abcam | ab150078 |
| :---: | :---: | :---: |
| conjugated Goat Anti- 1:500 | (Cambridge, UK) |  |
| Rabbit IgG H\&L |  |  |

Supplementary Table S2. Target sequence of shRNAs and siRNA used in this study

| Name | Specie | Target sequence |
| :---: | :---: | :---: |
| shJwa \#1 | Rat | 5'-GACTTCGAAACCTCAAGAACA-3' |
| shJwa \#2 | Rat | 5'-CCAGCTACTTCCTCATATCC-3' |
| shJwa \#3 | Rat | 5'-TTGTTGATGTTCATCCATGC-3' |
| siFbxw7 | Rat | 5'-ACAGGACAGTGTTTACAGA-3' |

## Supplementary Table S3. Primers used in QRT-PCR

| Primer Name | Specie | Sequence |
| :---: | :---: | :---: |
| Jwa | Mouse | Forward: 5'-GGCAGCGCACAATAAAGACAT-3' |
|  |  |  |
|  |  | Reverse: 5'-ACACCCCCGAACATGGATATG-3' |
| Lgr5 | Mouse | Forward: 5'-TAAAGACGACGGCAACAGTG-3' |
|  |  |  |
|  |  | Reverse: 5'-GCCTTCAGGTCTTCCTCAAA-3' |
| Lgr5 | Rat | Forward: 5'-CGTAGGCAACCCTTCTCTTATC-3' |
|  |  |  |
|  |  | Reverse: 5'-GTAATTTGCGAGGCACCATTC-3' |
| Olfm4 | Mouse | Forward: 5'-TGAAGGAGATGCAAAAACTGG-3' |
|  |  |  |
|  |  | Reverse: 5'-CTCCAGCTTCTCTACCAAGAGG-3' |
| Olfm4 | Rat | Forward: 5'-TGAGCTCTACACATTCCCTGG-3' |
|  |  |  |
|  |  | Reverse: 5'-GTACCACCTTCTGTCCACGAC-3' |
| Smoc2 | Mouse | Forward: 5'-GGAGCAGGGAAAGCAGATGAT-3' |
|  |  |  |
|  |  | Reverse: 5'-AACTTGCTCGGTCCAGAGTG-3' |
| Ascl2 | Mouse | Forward: 5'-CCTCTCTCGGACCCTCTCTCAG-3' |
|  |  |  |
|  |  | Reverse: 5'-CAGTCAAGGTGTGCTTCCATGC-3' |
| Msi1 | Mouse | Forward: 5'-CTCTCACCCCTGGACGATGG -3' |
|  |  |  |
|  |  | Reverse: $5^{\prime \prime}$-TGGTACCCATTGGTGAAGGC -3' |
| Sis | Mouse | Forward: 5'-CGTTTCCGGTTCAAGCTCACA-3' |
|  |  |  |
|  |  | Reverse: 5'-CCTGATGACTTTGATGCTGAACG-3' |
| Sis | Rat | Forward: 5'-GACCCTGCCATCTCCATAAAT-3' |
|  |  |  |
|  |  | Reverse: 5'-CTGGCCATACCTCTCCAATAAG-3' |


| Primer Name | Specie | Sequence |
| :---: | :---: | :---: |
| Lct |  | Forward: 5'-CTGTCATGGGCACAACTTCTC-3' |
|  | Mouse |  |
|  |  | Reverse: 5'-TGTGGCATAATCAGCAAAGAGG-3' |
| Lct |  | Forward: 5'-CCAGGGAATGGTGTGAAAGA-3' |
|  | Rat |  |
|  |  | Reverse: 5'-TCAGGGTTCGAAGGATGTTTAG-3' |
| Dpp4 |  | Forward: 5'-CACCTCTGATGGAAGCAGCTTC-3' |
|  | Mouse |  |
|  |  | Reverse: 5'-GATAATCGCTGGTCAGAGCTTCG-3' |
| Lyz1 |  | Forward: 5'-GGAATGGATGGCTACCGTGG-3' |
|  | Mouse |  |
|  |  | Reverse: 5'-CATGCCACCCATGCTCGAAT-3' |
| Lyz |  | Forward: 5'-AGCTCAGCATGAGAGCAATTA-3' |
|  | Rat |  |
|  |  | Reverse: 5'-TGCCGTCATTACACCAGTATC-3' |
| Mmp7 |  | Forward: 5'-AGGAAGCTGGAGATGTGAGC-3' |
|  | Mouse |  |
|  |  | Reverse: 5'-TCTGCATTTCCTTGAGGTTG-3' |
| Mmp7 |  | Forward: 5'-CAGTGGACAAACTGAGGGAAA-3' |
|  | Rat |  |
|  |  | Reverse: 5'-CACCTGGGCTTCTGCATTAT-3' |
| Muc2 |  | Forward: 5'-GAAGCCAGATCCCGAAACCA-3' |
|  | Mouse |  |
|  |  | Reverse: 5'-GAATCGGTAGACATCGCCGT-3' |
| Muc2 |  | Forward: 5'-CGTCATCCCCTGGAACAACA-3' |
|  | Rat |  |
|  |  | Reverse: 5'-TTGGCCCTGTTGTGGTCTTT-3' |
| Spink4 |  | Forward: 5'-TGCAGTCACATAGCTCACAAG-3' |
|  | Mouse |  |
|  |  | Reverse: 5'-CCATGCCAAGGAGGGGAA-3' |


| Primer Name | Specie | Sequence |
| :---: | :---: | :---: |
| Tff3 |  | Forward: 5'-TTGCTGGGTCCTCTGGGATAG-3' |
|  | Mouse |  |
|  |  | Reverse: 5'-TACACTGCTCCGATGTGACAG-3' |
| Tff3 |  | Forward: 5'-CCAGGAATTTGTTGGCCTATCT-3' |
|  | Rat |  |
|  |  | Reverse: 5'-GGTTGTTACACTGCTCTGATGT-3' |
| Gcg |  | Forward: 5'-CTTCCCAGAAGAAGTCGCCA-3' |
|  | Mouse |  |
|  |  | Reverse: 5'-GTGACTGGCACGAGATGTTG-3' |
| Gcg |  | Forward: 5'-AGAACCACTTGAAGACCCTAATC-3' |
|  | Rat |  |
|  |  | Reverse: 5'-GGAGTCCAGGTATTTGCTGTAG-3' |
| Ngn3 |  | Forward: 5'-TCTCAAGCATCTCGCCTCTTC-3' |
|  | Mouse |  |
|  |  | Reverse: 5'-ACAGCAAGGGTACCGATGAGA-3' |
| Ngn3 |  | Forward: 5'-CGGATGACGCCAAACTTACA-3' |
|  | Rat |  |
|  |  | Reverse: 5'-TAGAAGCTGTGGTCCGCTAT-3' |
| Reg4 |  | Forward: 5'-CTGAGCTGGAGTGTCAGTCAT-3' |
|  | Mouse |  |
|  |  | Reverse: 5'-GTCCACTGCCATAATTGCTTCT-3' |
| Dclk1 |  | Forward: 5'-GGGTGAGAACCATCTACACCATC-3' |
|  | Mouse |  |
|  |  | Reverse: 5'-CCAGCTTCTTAAAGGGCTCGAT-3' |
| Dclk1 |  | Forward: 5'-CTCCTCCACTTCACTTTCATCC-3' |
|  | Rat |  |
|  |  | Reverse: 5'-TCTCCCGACTTTGTATCTCTCT-3' |
| Hck |  | Forward: 5'-TCCTCCGAGATGGAAGCG-3' |
|  | Mouse |  |
|  |  | Reverse: 5'-ACAGTGCGACCACAATGGTAT-3' |


| Primer Name | Specie | Sequence |
| :---: | :---: | :---: |
| Hck | Rat | Forward: 5'-CGTATGCCTCGACCAGATAAC-3' |
|  |  |  |
|  |  | Reverse: 5'-AGCACGCTCTGGATGTATTC-3' |
| Cpt1a | Mouse | Forward: 5'-GGCATAAACGCAGAGCATTCCTG-3' |
|  |  |  |
|  |  | Reverse: 5'-CAGTGTCCATCCTCTGAGTAGC-3' |
| Cpt2 | Mouse | Forward: 5'-GATGGCTGAGTGCTCCAAATACC-3' |
|  |  |  |
|  |  | Reverse: 5'-GCTGCCAGATACCGTAGAGCAA-3' |
| Cd36 | Mouse | Forward: 5'-GGACATTGAGATTCTTTTCCTCTG-3' |
|  |  |  |
|  |  | Reverse: 5'-GCAAAGGCATTGGCTGGAAGAAC-3' |
| Stat5a | Mouse | Forward: 5'-CCGAAACCTCTGGAATCTGA-3' |
|  |  |  |
|  |  | Reverse: 5'-ACGAACTCAGGGACCACTTG-3' |
| Stat5b | Mouse | Forward: 5'-GTGAAGCCACAGATCAAGCA-3' |
|  |  |  |
|  |  | Reverse: 5'-TCGGTATCAAGGACGGAGTC-3' |
| PPARY | Mouse | Forward: 5'-ATTGAGTGCCGAGTCTGTGG-3' |
|  |  |  |
|  |  | Reverse: 5'-GGCATTGTGAGACATCCCCA-3' |
| Notch1 | Mouse | Forward: 5'-GCTGCCTCTTTGATGGCTTCGA-3' |
|  |  |  |
|  |  | Reverse: 5'-CACATTCGGCACTGTTACAGCC-3' |
| Hes1 | Mouse | Forward: 5'-CCAGCCAGTGTCAACACGA-3' |
|  |  |  |
|  |  | Reverse: 5'-AATGCCGGGAGCTATCTTTCT-3' |
| Hes2 | Mouse | Forward: 5'-CTGAAGGGTCTCGTATTGCCG-3' |
|  |  |  |
|  |  | Reverse: 5'-CGCAGGTGCTCTAGTAGGC-3' |


| Primer Name | Specie | Sequence |
| :---: | :--- | :--- |
| Hes5 | Mouse | Forward: 5'-AGTCCCAAGGAGAAAAACCGA-3' |
| Hes6 | Reverse: 5'-GCTGTGTTTCAGGTAGCTGAC-3' |  |
|  | Mouse | Forward: 5'-ACCACCTGCTAGAATCCATGC-3' |
| Hes7 | Reverse: 5'-GCACCCGGTTTAGTTCAGC-3' |  |
|  |  | Forward: 5'-CGGGAGCGAGCTGAGAATAG-3' |
| Actb | Rouse | Forward: 5'-AGATGTGGATCAGCAAGCA-3' |
|  |  | Reverse: 5'-GCGCAAGTTAGGTTTTGTCA-3' |
|  |  | Forward: 5'-CCGCGAGTACAACCTTCTTGC-3' |
| Actb |  | Reverse: 5'-TCGTCATCCATGGCGAACTGG-3' |

Supplementary Table S4. Down-regulated proteins in jejunum tissues induced by Jwa

| deletion (Fold Change: Jwa ${ }^{-1}$ vs $\mathrm{Jwa}^{+/+}$) |  |  |  |
| :---: | :---: | :---: | :---: |
| Protein Name | Fold Chage | Regulation | Rank |
| FLNA | 0.0013 | Down | 1 |
| STAT5A | 0.0013 | Down | 2 |
| RHBDL2 | 0.0018 | Down | 3 |
| PLEKHH2 | 0.0018 | Down | 4 |
| MARCKS | 0.0020 | Down | 5 |
| MRE11A | 0.0020 | Down | 6 |
| PLA2G12B | 0.0022 | Down | 7 |
| MGST1 | 0.0022 | Down | 8 |
| ENO2 | 0.0024 | Down | 9 |
| SRP19 | 0.0027 | Down | 10 |
| TBC1D2 | 0.0031 | Down | 11 |
| HAUS3 | 0.0032 | Down | 12 |
| MRPS34 | 0.0033 | Down | 13 |
| NAA10 | 0.0036 | Down | 14 |
| JTB | 0.0042 | Down | 15 |
| NUPR1 | 0.0042 | Down | 16 |
| PKIG | 0.0049 | Down | 17 |
| GNG12 | 0.0189 | Down | 18 |
| METTL7B | 0.0287 | Down | 19 |


| Protein Name | Fold Chage | Regulation | Rank |
| :---: | :---: | :---: | :---: |
| MYADM | 0.0288 | Down | 20 |
| TRMT61A | 0.0329 | Down | 21 |
| ELF1 | 0.0373 | Down | 22 |
| GNAO1 | 0.0470 | Down | 23 |
| STAT5B | 0.0596 | Down | 24 |
| CHIA1 | 0.0619 | Down | 25 |
| NT5C | 0.0648 | Down | 26 |
| KLHL9 | 0.0663 | Down | 27 |
| BMI1 | 0.0690 | Down | 28 |
| CYP1A2 | 0.0698 | Down | 29 |
| CD93 | 0.0728 | Down | 30 |
| ANKIB1 | 0.0871 | 0.5104 | Down |

Supplementary Table S5. Predicted transcript factors bind to the Pparg promotor

|  |  |  | Relative | Score | Start | End | Strand |
| :--- | :--- | :--- | :---: | :--- | :---: | :---: | :---: |
| Matrix ID | Name | Score | Predicted sequence |  |  |  |  |
| MA1099.2 | HES1 | 14.4264 | 0.999430951 | 704 | 713 | + | GGCACGTGCC |
| MA1099.2 | HES1 | 14.4264 | 0.999430951 | 704 | 713 | - | GGCACGTGCC |
| MA0616.2 | HES2 | 16.1882 | 1.000000009 | 704 | 713 | + | GGCACGTGCC |
| MA0616.2 | HES2 | 16.1882 | 1.000000009 | 704 | 713 | - | GGCACGTGCC |
| MA0821.1 | HES5 | 18.7952 | 0.978104532 | 703 | 714 | - | TGGCACGTGCCT |
| MA0821.1 | HES5 | 18.719 | 0.977138462 | 703 | 714 | + | AGGCACGTGCCA |
| MA1493.1 | HES6 | 12.8217 | 0.920264948 | 704 | 713 | + | GGCACGTGCC |
| MA1493.1 | HES6 | 12.8217 | 0.920264948 | 704 | 713 | - | GGCACGTGCC |
| MA0822.1 | HES7 | 19.0547 | 0.97173189 | 703 | 714 | + | AGGCACGTGCCA |


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