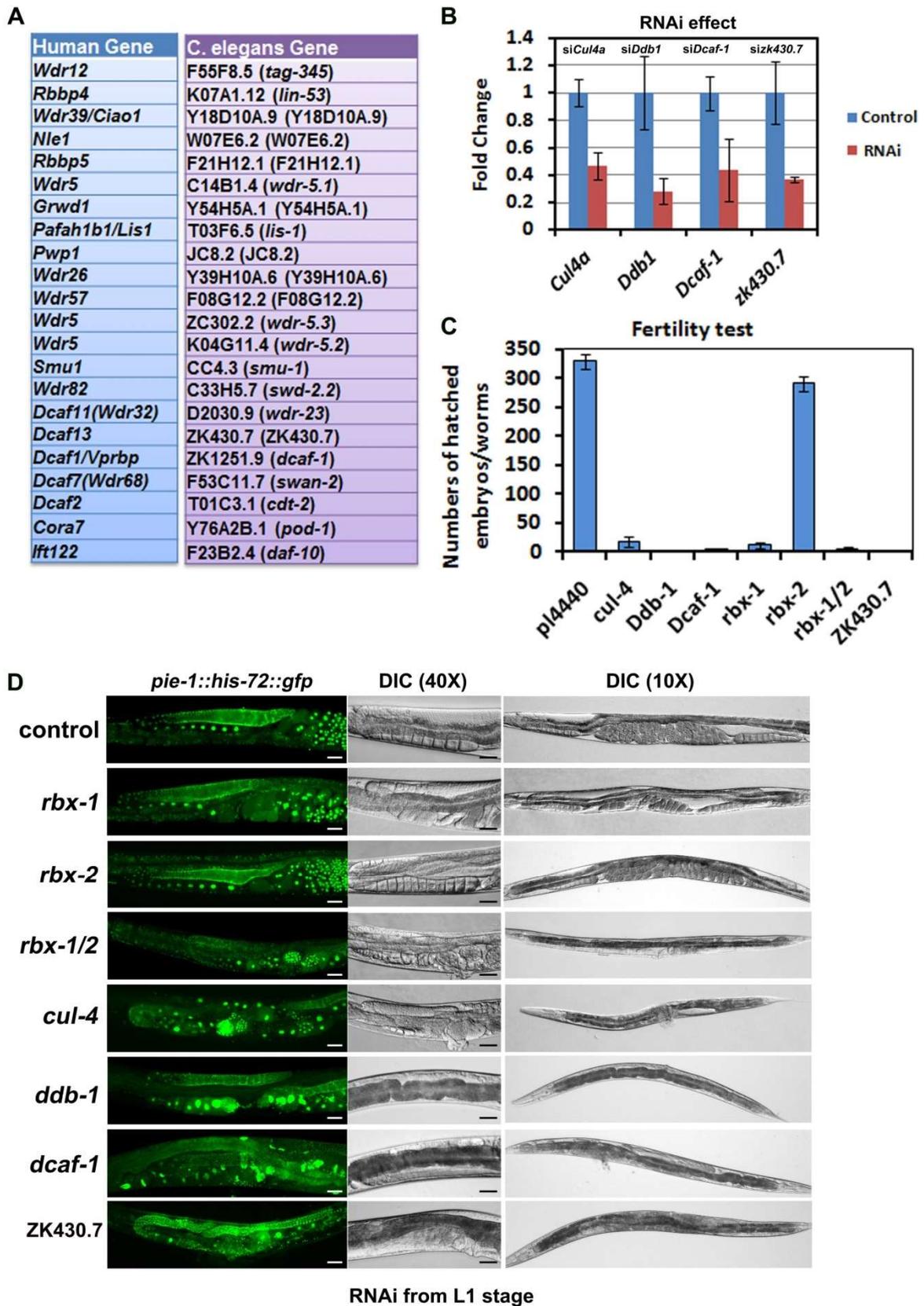


- Supplementary Figures
- Supplementary Figure S1



3

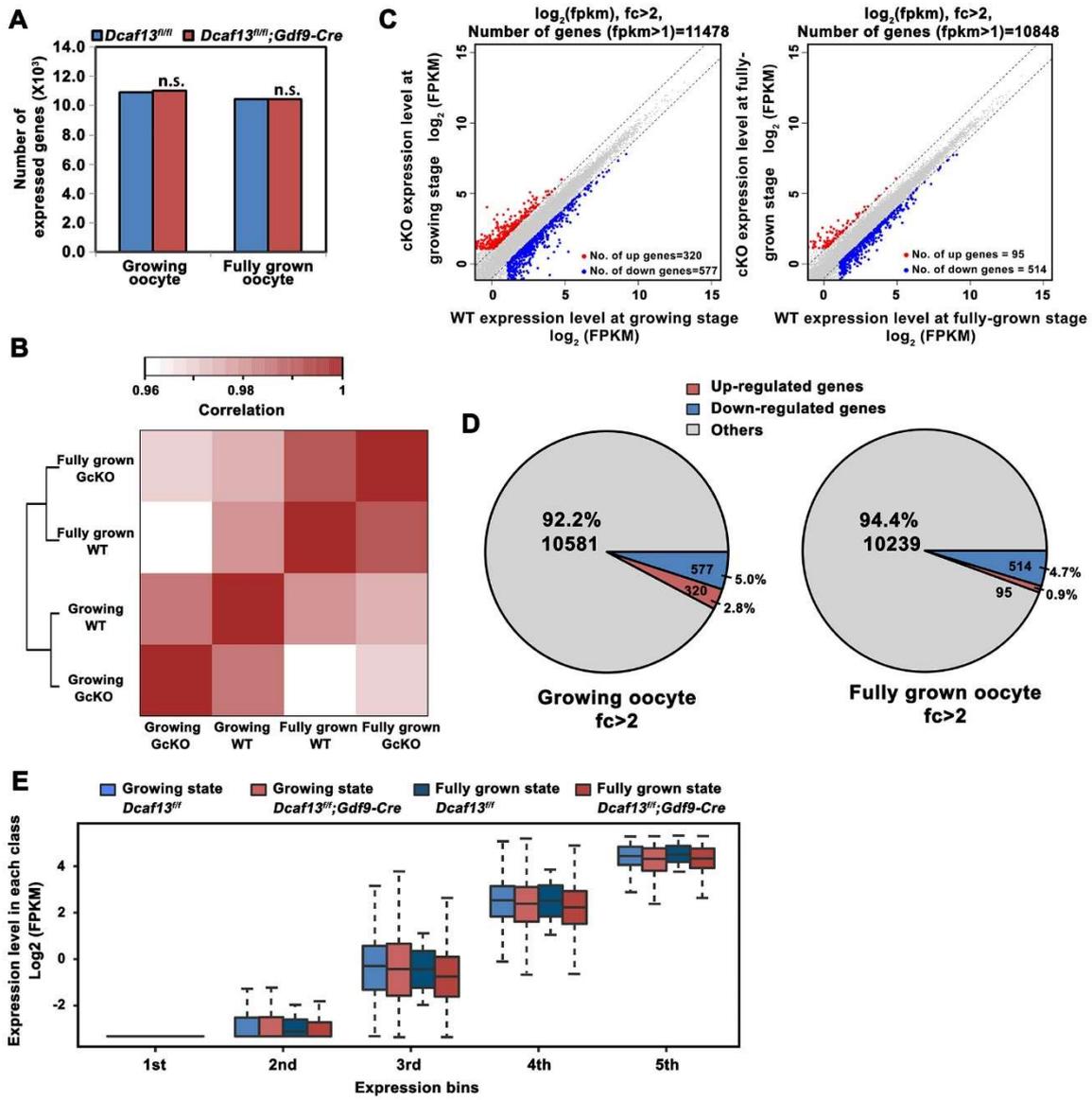
4 **Supplementary Figure S1: ZK430.7, the homologous gene of *Dcaf13*, is required for**
5 **oogenesis in *C.elegans*.**

6 **A:** The gene list showed 19 conserved DCAFs from *C.elegans* to human for RNAi screen. **B:**
7 Quantitative real-time PCR (qRT-PCR) results showing RNAi efficiency of *cul-4*, *ddb-1*, *dcaf-*
8 *1*, ZK430.7 relative to control *C.elegans*. Error bars indicate SEM. **C:** Fertility assessment of
9 control (pl4440) and RNAi-mediated knockdown of several core components of CRL4 E3
10 ligase (*cul-4*, *ddb-1*, *rbx-1*, *rbx-2*), *dcaf-1* and *zk430.7*. The numbers of hatched embryos or
11 larvae were counted in the next 72 h after RNAi. Error bars indicate SEM. **D:** Germlines
12 morphologies in *Pie-1::his-72::GFP* transgene worms after RNAi of *cul-4*, *ddb-1*, *dcaf-1*, and
13 *zk430.7*. GFP-histone H2B epifluorescence (left panels) and DIC images (middle and right
14 panels) of *C. elegans* female gonads showed oogenesis after RNAi depletion of indicated genes.
15 Scale bar, 10 μ m.

16

17

18 **Supplementary Figure S2**



19

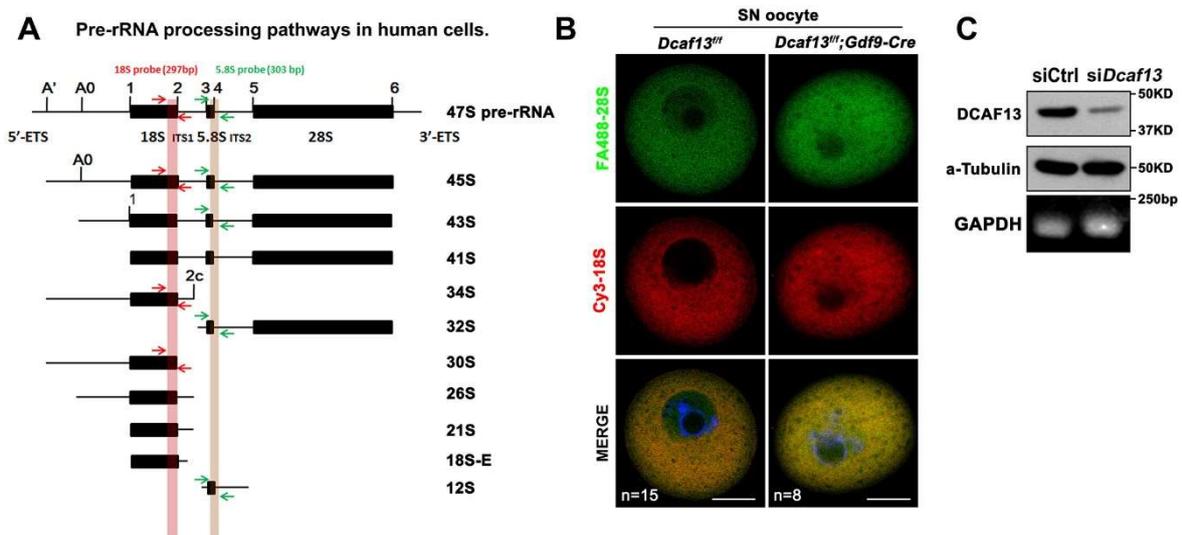
20

21 **Supplementary Figure S2. The level of mRNA transcripts is not altered in DCAF13-**
22 **deleted oocytes**

23 **A:** Bar graph showed the number of transcripts in *Dcaf13^{fl/fl}* and *Dcaf13^{fl/fl};Gdf9-Cre* oocytes
24 at growing and fully-grown stages. **B:** Heatmap and Cluster tree showed the correlation among
25 4 samples including growing and fully-grown oocytes (*Dcaf13^{fl/fl}* and *Dcaf13^{fl/fl};Gdf9-Cre*).
26 Correlation method: pearson correlation; Cluster method: complete; Correlation test: $p < 0.01$.
27 **C:** Scatter plots of RNA-seq data illustrated transcriptional change in *Dcaf13* knocked out
28 oocytes. The left graph for growing oocyte and the right graph for fully-grown oocyte. Genes
29 up-regulated were shown in red dots, while down-regulated genes were shown in blue dots.
30 Genes showing an expression difference larger than two-fold were considered differentially
31 expressed. **D:** Pie chart presentation of the overall genomic distribution of up-regulated genes,
32 down-regulated genes and the others. **E:** Box-plots of the whole genes expression levels in four
33 samples. The expression value (FPKM) was divided into five groups according to their
34 expression levels in *Dcaf13^{fl/fl}* fully grown oocytes. The outliers were filtered.

35

36 **Supplementary Figure S3.**



37

38 **Supplementary Figure S3. Schematic diagram of pre-rRNA processing pathways and**
 39 **probes used in human and mouse.**

40 Pol I-transcribed premature rRNA (47S in human) precursor embedded in noncoding spacers:
 41 5' and 3' external transcribed spacers (5' and 3' ETSs) and internal transcribed spacers 1 and 2
 42 (ITS1 and ITS2). Then, the various rRNA intermediates were processed step by step from pre-
 43 rRNA following a pathway involving both endo- and exonucleolytic digestions at sites A0, 1,
 44 and 2 in nucleolus. **A:** Pre-rRNA processing pathways in human cells. The pink area represented
 45 the location of 18S probe and the brown area represents the location of 5.8S probe used for
 46 Northern blotting. The probes information was listed in Supplementary Table-1. **B:** Fluorescent
 47 *in situ* hybridization (FISH) of antisense oligonucleotide probes recognizing the mouse 28S
 48 rRNA (Green) and 18S rRNA (Red) in *Dcaf13^{fl/fl}* and *Dcaf13^{fl/fl};Gdf9-Cre* SN oocytes. Scale
 49 bars, 25 μ m. **C:** Western blot showing DCAF13 knockdown efficiency in HeLa cells
 50 transfected with non-targeting (*siCtrl*) or *Dcaf13*-targeted siRNA (*siDcaf13*). α -Tubulin was
 51 blotted as a loading control.

52

53 **Supplementary Table-1.**

54

Primer and probe information

Genotyping primers				
Name	Species	Sequence		Length
<i>Dcaf13</i> GP1	mouse	5'- TACTTGACTGGGTTCCAGATAC-3'		WT: 212 bp (GP1+GP2) Flox:246 bp (GP1+GP2) KO: 464 bp (GP1+GP3)
<i>Dcaf13</i> GP2	mouse	5'- AGTCACTTACAAACCTTATCAAAAC-3'		
<i>Dcaf13</i> GP3	mouse	5'- AACCTTCATGTGCTTGTATTGT-3'		
<i>Gdf9- Cre</i>	mouse	FP	5'- GGTTTCTGTTGGGCTCTCAC-3'	470 bp
	mouse	RP	5'- ATCAGAGGTGGCATCCACAG-3'	
<i>Zp3- Cre</i>	mouse	FP	5'- AAGAACCTGATGGACATGTTTCAG-3'	470 bp
	mouse	RP	5'- CTGATCCTGGCAATTTTCGG-3'	
Real time-PCR primers information				
Name	Species	Sequence		Length
<i>Dcaf13</i>	Human	FP	5'- TTTCCTGTAGACAAAAGTCGAAGCA - 3'	143bp
	Human	RP	5'- GCATTAGCTTCCACAGGCG -3'	
<i>Fbl</i>	Mouse	FP	5'- CAAAATTGAGTACAGAGCCTGGA - 3'	160bp
	Human	RP	5'- CGGGCCGACAATATCAGAGA -3'	
siRNA sense sequence information				
Name	Species	Sequence		
NC	Mouse & Human	5'- UUCUCCGAACGUGUCACGUTT -3'		

<i>Dcaf13</i>	Mouse & Human	5'- GUGCUUACAUCACGAGAAATT -3'	
<i>Fbl</i>	Mouse	5'- CCTCCCAAGGTGAAGAACT -3'	
	Mouse	5'- CGTCATGAAGGTGTCTTTA -3'	
	Mouse	5'- CCCTGGAGAGTCTGTGTAT -3'	
Oligonucleotide probes used for detection of rRNAs			
Antisense probes	Species	Sequence	Length
5.8 S	Human	FP	5'- GCTACGCCTGTCTGAGCGTCG -3'
	Human	RP	5'- CGGCTCTCTCTTTCCCTCTCCG -3'
18S	Human	FP	5'- CGTCGCTACTACCGATTGGATGG -3'
	Human	RP	5'- AACGAGCGAGCGAACGAACG -3'
18S	Mouse	FP	5'- TGATTAAGTCCCTGCCCTTTG -3'
	Mouse	RP	5'- CTTCTCTCACCTCACTCCAGACAC -3'
28S	Mouse	FP	5'- CGTGTGAGTAAGATCCTCCACC -3'
	Mouse	RP	5'- GAGTTTACCACCCGCTTTGG -3'
Cy3-18S	Mouse	5'-Cy3-CCATTATTCCTAGCTGCGGTATCCAGGCGG-3'	
AF488-28S	Mouse	5'-Alexa Fluor 488-GAGGGAACCAGCTACTAGATGGTTCGATTA -3'	

56 **Supplementary Table-2.**57 **Antibody information**

Antibody Name	Company	Cat#NO.	Application
anti-FLAG	Santa Cruz	sc-807	WB (1:20,00)
anti-HA tag	CST	#3724	WB (1:20,00)
anti-DCAF13	Abcam	Ab195588	IHC(1:100) WB (1:20,00); IF(1:200)
anti-pS II	Abcam	ab5095	IF(1:200)
anti-B23	Abcam	ab10530	IF(1:200)
anti- Fibrillarin	Abcam	ab166630	IF(1:200)
anti-ERK1/2	Santa Cruz	sc-93	WB (1:10,000)
anti-FOXO1	CST	#2880S	IHC (1:100)
anti-MVH	Abcam	Ab13840	IHC (1:200)

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