

1 Supplemental Figure Legends

2 **Figure S1.** Schematic diagram of the construction of Rpb1 conditional knock-out cell line.

3 **Figure S2.** Amino-acid sequence comparison between human (denoted as query) and chicken
4 (subject) Rpb1 using blastp.

5 **Figure S3.** Ser 2, Ser 5 and Ser 7 phosphorylation patterns in mutant cells. Cells were treated
6 with tet for 24 hours. Cell lysates were analyzed by western blotting using indicated antibodies.
7 (A) Ser 7 levels. (B) CTD phosphorylation status in various mutant cells. Thr4P was not detected
8 in S5A and S7A samples. This negative result is difficult to interpret because the antibody could
9 simply not recognize Thr4P on the CTD with S5A or S7A mutations. Samples were prepared as in
10 Figure 4B.

11 **Figure S4.** Coomassie blue staining of purified GST-CTD, Fcp1, Fcp1 (M271E), and CDK9/cyclin T
12 complex. Arrow indicates the purified protein resolved by SDS-PAGE.

13 **Figure S5.** *In vitro* phosphorylation of Thr 4. GST-CTD was incubated with HeLa nuclear extract
14 (left lane) or the indicated amount of CDK9/cyclinT plus or minus indicated inhibitors. Samples
15 were analyzed by western blotting with antibodies that detect P-Thr 4, P-Ser 2, P-Ser 5, and P-
16 Ser 7.

17 **Figure S6.** Fcp1 mRNA levels in shRNA-treated HEK293 cells. Cells were transfected with
18 plasmids expressing shRNAs targeting Fcp1 or GFP (control). RNA was extracted 22 h or 41 h
19 after transfection, and RT-qPCR was performed to determine Fcp1 mRNA levels. Levels of Fcp1
20 mRNA in Fcp1 shRNA expressing cells relative to control were plotted.

Construction of targeting vectors



Disrupt one allele of *Rpb1* with the targeting vector carrying hygromycin-resistance gene



Introduce tetracycline repressive expression vector of HA-tagged human *Rpb1* and the tTA expression vector (tet-off)



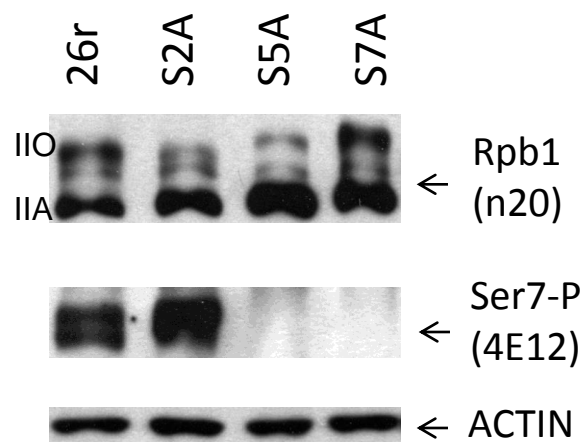
Disrupt second allele of *Rpb1* with the targeting vector carrying zeocin-resistance gene

Figure S2

Query	13	CPLRTIKRVQFGVLSPELKRMSVTEGGIKYPETTEGGRPKLGGMLDPRQGVIERTGRCQTCAGNMTECPGHFGHIELAKPVFHVGFVLK	102
Sbjct	1	CPLRTIKRVQFG+LSPDE+KRMSVTEGGI+YPETTEGGRPKLGGMLDPRQGVIERTGRCQTCAGNMTECPGHFGHIELAKPVFHVGF L K CPLRTIKRVQFGILSPDEMCRMSVTEGGIRYPETTEGGRPKLGGMLDPRQGVIERTGRCQTCAGNMTECPGHFGHIELAKPVFHVGF LK	90
Query	103	TMKVLRCVCFSCSKLLVDSNNPKIKDILAKSKGQPKKRLTHVYDLCKGKNICEGGEEMDNKFGVEQPEGEDDLTKEKGHGGCGRYQPRIR	192
Sbjct	91	TMK+LRCVCFSCSKLLVD+NNPKIKDILAKSKGQPKKRLTHVYDLCKGKNICEGGEEMD+KFGVEQ EGDE +EKHGGCGRYQPRIR TMKILRCVCFSCSKLLVDANNPKIKDILAKSKGQPKKRLTHVYDLCKGKNICEGGEEMDHKFGVEQHEGDEP-GREKGGCGRYQPRIR	179
Query	193	RSGLELYAEWKHVNEDSQEKKILLSPERVHEIFKRISDEECFVLGMEPRYARPEWMIVTVLPVPPLSVRPAVVMQGSARNQDDLTHKLAD	282
Sbjct	180	R GLELYAEWKHVNEDSQEKKILLSPERVHE+ KR+ D+EC VLG M+P+YARPEWM+ TVLPVPP L+VRPAVVMQGSARNQDDLTHKLAD RVGLELYAEWKHVNEDSQEKKILLSPERVHEVLKRVDPDDECLVLGMDPKYARPEWMVCTVLPVPP LAVRPAVVMQGSARNQDDLTHKLAD	269
Query	283	IVKINNQLRRNEQNGAAAHVIAEDVKLLQFHVATMVDNELPGLPRAMQKSGRPLKSLKQRLKKGEGRVRGNLMGKRVDFSARTVITPDPN	372
Sbjct	270	IVKINNQLRRNEQNGAAAHVIAEDVKLLQFHVATMVDNELPGLPRAMQKSGRPLKSLKQRLKKGEGRVRGNLMGKRVDFSARTVITPDPN IVKINNQLRRNEQNGAAAHVIAEDVKLLQFHVATMVDNELPGLPRAMQKSGRPLKSLKQRLKKGEGRVRGNLMGKRVDFSARTVITPDPN	359
Query	373	LSIDQVGVPRISIAANMTFAEIVTPFNIDRLQELVRRGNSQYPGAKYIIRDNGRIDLRFHFKPSDLHLQTGYKVERHMCDDGDIVIFNRQP	462
Sbjct	360	L+IDQVGVPRISIAANMTFAEIVTPFNIDRLQELVRRGNSQYPGAKYIIRDNGRIDLRFHFKPSDLHLQTGYKVERHMCDDGDIVIFNRQP LAIDQVGVPRISIAANMTFAEIVTPFNIDRLQELVRRGNSQYPGAKYIIRDNGRIDLRFHFKPSDLHLQTGYKVERHMCDDGDIVIFNRQP	449
Query	463	TLHKMSMMGHRVRIIPWSTFRLNLSVTTTPYNADFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQSNRPFVMGIVQDTLTAVRKFTKRD	552
Sbjct	450	TLHKMSMMGHRVRIIPWSTFRLNLSVTTTPYNADFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQSNRPFVMGIVQDTLTAVRKFTKRD TLHKMSMMGHRVRIIPWSTFRLNLSVTTTPYNADFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQSNRPFVMGIVQDTLTAVRKFTKRD	539
Query	553	VFLERGEVMNLLMFLSTWDGKVPQPAILKPRPLWTGKQIFSLIIPGHINCIRTHSTHPDDEDSGPYKHISPGDTKVVVENGELIMGILCK	642
Sbjct	540	VFLERGEVMNLLMFLSTWDGKVPQPAILKPRPLWTGKQIFSLIIPGHINCIRTHSTHPDDEDSGPYKHISPGDTKVVVENGELIMGILCK VFLERGEVMNLLMFLSTWDGKVPQPAILKPRPLWTGKQIFSLIIPGHINCIRTHSTHPDDEDSGPYKHISPGDTKVVVENGELIMGILCK	629
Query	643	KSLGTSAGSLVHISYLEMGHDITRFLYSNIQTVINNWLLIEGHTIGIGDSIADSKTYQDIQNTIKKAKQDVIEIEKAHNELEPTPGNT	732
Sbjct	630	KSLGTSAGSLVHISYLEMGHD TRFLYSNIQTVINNWLLIEGHTIGIGDSIAD+KTYQDIQNTIKKAKQDVIEIEKAHNELEPTPGNT KSLGTSAGSLVHISYLEMGHDTTRFLYSNIQTVINNWLLIEGHTIGIGDSIADAKTYQDIQNTIKKAKQDVIEIEKAHNELEPTPGNT	719
Query	733	LRQTFENQVNRILNDARDKTGSSAQKSLSEYNNFKSMVSVGAKGSKINISQVIAVVGQQNVEGKRIPFGFKHRTLPHFIKDDYGPESRGF	822
Sbjct	720	LRQTFENQVNRILNDARDKTGSSAQKSLSEYNNFKSMVSVGAKGSKINISQVIAVVGQQNVEGKRIPFGFKHRTLPHFIKDDYGPESRGF LRQTFENQVNRILNDARDKTGSSAQKSLSEYNNFKSMVSVGAKGSKINISQVIAVVGQQNVEGKRIPFGFKHRTLPHFIKDDYGPESRGF	809
Query	823	VENSYLAGLTPTEFFFHAMGGREGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVRNSINQVVQLRYGEDGLAGESVEFQNLATLKPS	912
Sbjct	810	VENSYLAGLTPTEFFFHAMGGREGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVRNSINQVVQLRYGEDGLAGESVEFQNLATLKPS VENSYLAGLTPTEFFFHAMGGREGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVRNSINQVVQLRYGEDGLAGESVEFQNLATLKPS	899
Query	913	NKAFEEKKFRDYTNERALRRTLQEDLVKDVLSNAHIQNELEREFERMREDREVLRFVIFPTGDSKVVLPCNLLRMIWNAQKIFHINRPLPS	1002
Sbjct	900	NKAFEEKK+FDYTNERALRRTLQE+LVKD+LSNAHIQNELEREFERMREDREVLRFVIFPTGDSKVVLPCNLLRMIWNAQKIFHIN RLPS NKAFEEKKFRDYTNERALRRTLQEEVLKDVLSNAHIQNELEREFERMREDREVLRFVIFPTGDSKVVLPCNLLRMIWNAQKIFHINSRLPS	989
Query	1003	DLHPKVVVEGVKELSKKLVIVNGDDPLSRQAQENATLLFNIHLRSTLCSRRMAEEFRLSGEAFDWLLGEIESKFNQAIHAPGEMVGALAA	1092
Sbjct	990	DLHP+KVVVEGVKELS+KLVIVNG+DPLSRQAQENATLLFNIHLRSTLCSRRM EEFRLSGEAFDWLLGEIESKFNQAIHAPGEMVGALAA DLHPKVVVEGVKELSRKLVIVNGEDPLSRQAQENATLLFNIHLRSTLCSRRMVEEFRLSGEAFDWLLGEIESKFNQAIHAPGEMVGALAA	1079
Query	1093	QSLGEPATQMTLNTFHYAGVSAKNVTLGVPRKELINISKKPKTPSLTVFLGQSARDAERAKDILCRLEHTTLRKVTANTAIYYDPNPQ	1182
Sbjct	1080	QSLGEPATQMTLNTFHYAGVSAKNVTLGVPRKELINISKKPKTPSLTVFLGQSARDAERAKDILCRLEHTTLRKVTANTAIYYDPNPQ QSLGEPATQMTLNTFHYAGVSAKNVTLGVPRKELINISKKPKTPSLTVFLGQSARDAERAKDILCRLEHTTLRKVTANTAIYYDPNPQ	1169
Query	1183	STVVAEDQEWNVVYEMPFDVARI SPWLLRVELDRKHMTDRKLTMEQIAEKINAGFGDDLNCIFNDDNAEKLVLIRIRIMNSDENKMQUEE	1272
Sbjct	1170	STVVAEDQEWNVVYEMPFDV+RISPWLLR+ELDRKHMTDRKLTMEQIAEKINAGFGDDLNCIFNDDNAEKLVLIRIRIMNSDENKMQUEE STVVAEDQEWNVVYEMPFDVSRISPWLLRIELDRKHMTDRKLTMEQIAEKINAGFGDDLNCIFNDDNAEKLVLIRIRIMNSDENKMQUEE	1259
Query	1273	EEVVDKMDDDVFLRCIESNMLTDMTLQGIEQISKVYMHLPTDNKKKIIITEDGEFKALQEWILETDGVS LMRVLSEKDVDPVRTSNDI	1362
Sbjct	1260	EEVVDKMDDDVFLRCIESNMLTDMTLQGIEQISKVYMHLPTDNKKKIIITEDGEFKALQEWILETDGVS LMRVLSEKDVDPVRTSNDI EEVVDKMDDDVFLRCIESNMLTDMTLQGIEQISKVYMHLPTDNKKKIIITEDGEFKALQEWILETDGVS LMRVLSEKDVDPVRTSNDI	1349
Query	1363	VEIFTVLGIEAVRKALERELYHVISFDGSYVNYRHALLCOTMTCRGHLMAITRHGVNRQDTGPLMKCSFEETVDVLMEEAAHGESDPMK	1452
Sbjct	1350	VEIFTVLGIEAVRKALERELYHVISFDGSYVNYRHALLCOTMT RGHLMAITRHGVNRQDTGPLMKCSFEETVDVLMEEAAHGESDPMK VEIFTVLGIEAVRKALERELYHVISFDGSYVNYRHALLCOTMTSRGHLMAITRHGVNRQDTGPLMKCSFEETVDVLMEEAAHGESDPMK	1439
Query	1453	GVSENI MLGQLAPAGTGCFDLLLD A EKCKY GMEIPTNI PGLGAAGPTGMFFGSAPS PMGGISPAMTPWNQATPAYGAWSPSVGSGMTPG	1542
Sbjct	1440	GVSENI MLGQLAPAGTGCFDLLLD A EKCK+GMEIP+ IPGLG G TGMFFGSAPS PMG +SPAMTPWNQATPAYGAWSPSVGSGMTPG GVSENI MLGQLAPAGTGCFDLLLD A EKCKHGMEIPSAIPGLGVGGSTGMFFGSAPS PMGNMSPAMTPWNQATPAYGAWSPSVGSGMTPG	1529
Query	1543	AAGFSPSAASDASGSPGYS PAWSPTPGSPGSPGSSPYIPSPGGAMSPYSPTS PAYEPRSPGGYTPQSPSYSPTS SPYSPTS SPYSPTS	1632
Sbjct	1530	AAGFSPSAASDASGSPGYS PAWSPTPGSPGSPGSSPYIPSPGGAMSPYSPTS PAYEPRSPGGYTPQSPSYSPTS SPYSPTS SPYSPTS GAGFSPSAASDASGSPGYS PAWSPTPGSPGSPGSSPYIPSPGGAMSPYSPTS PAYEPRSPGGYTPQSPSYSPTS SPYSPTS SPYSPTS	1619
Query	1633	SPNYSPTS SPYSPTS SPYSPTS SPYSPTS SPYSPTS SPYSPTS SPYSPTS SPYSPTS SPYSPTS SPYSPTS SPYSPTS SPYSPTS SPYSPTS	1722
Sbjct	1620	SPNYSPTS SPYSPTS SPYSPTS SPYSPTS SPYSPTS SPYSPTS SPYSPTS SPYSPTS SPYSPTS SPYSPTS SPYSPTS SPYSPTS SPNYSPTS SPYSPTS SPYSPTS SPYSPTS SPYSPTS SPYSPTS SPYSPTS SPYSPTS SPYSPTS SPYSPTS SPYSPTS SPYSPTS	1709
Query	1723	TSPSYSPTS SPYSPTS SPYSPTS SPNYSPTS 1752	
Sbjct	1710	TSPSYSPTS SPYSPTS SPYSPTS SPNYSPTS 1739	

Figure S3

A



B

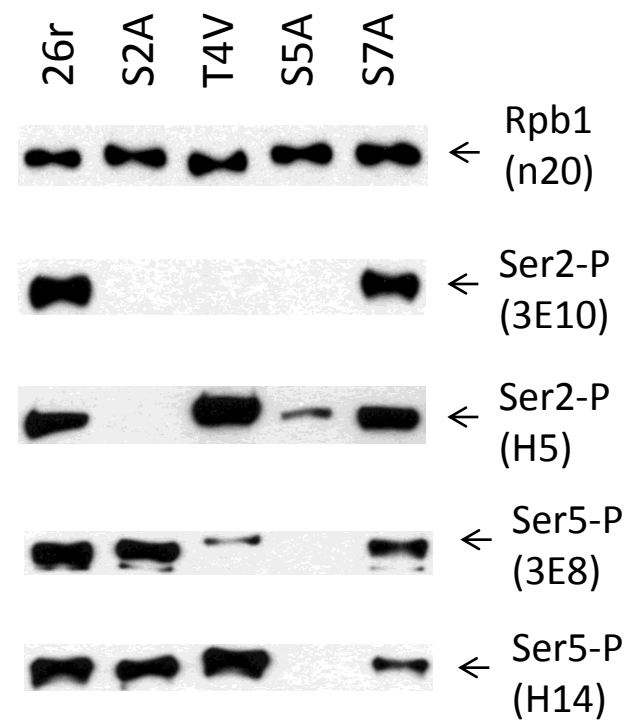


Figure S4

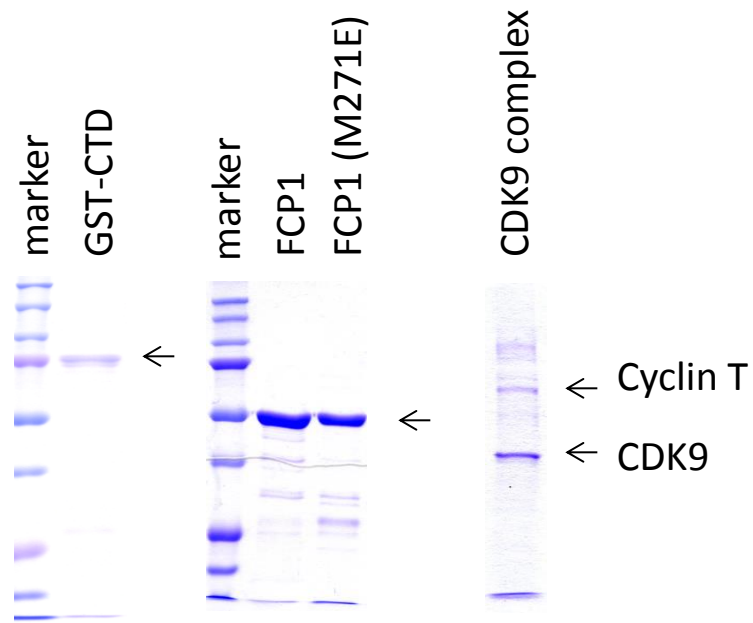


Figure S5

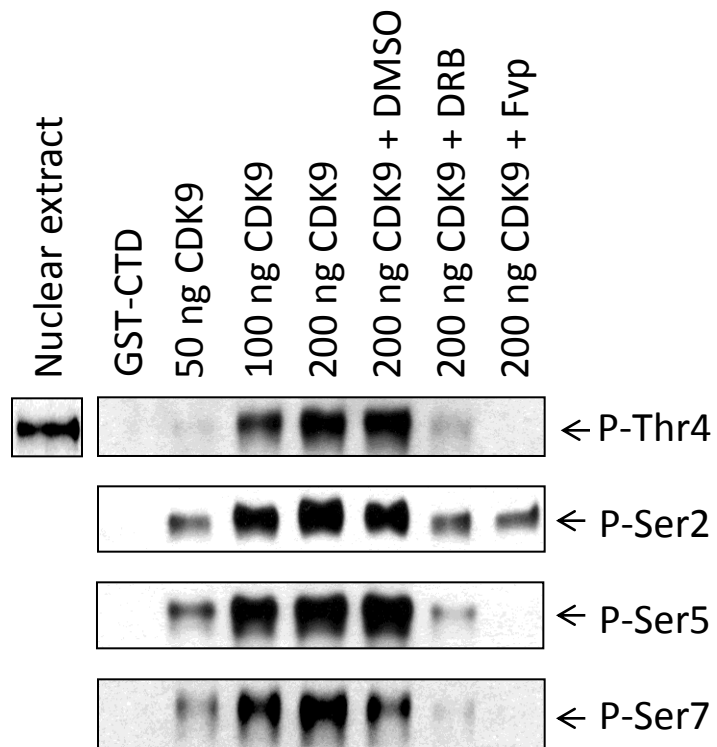


Figure S6

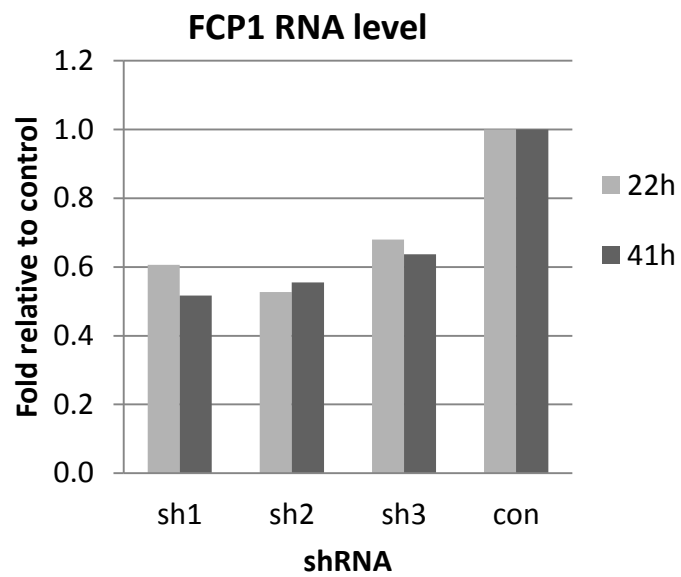


Table S1. Primer sequence list.

Amplicon	Primer	Sequence
Unspliced egr1	egr1_F2	CGTTGCTGCTGGAGACCT
	egr1_2R1	GGCATGGTTTTCTCGTTGTC
Spliced egr1	egr1_1F1	GCCACTATCCCAAAGTGGAG
	egr1_2R1	GGCATGGTTTTCTCGTTGTC
Uncut egr1	egr1_2F2	CATGCGGTTTCATTATTTTGTG
	egr1_3'R3	GCACCCCTTACTTCCTAGCAG
Total egr1	egr1_2F5	AAGACTCAAAATGTGGCAGAA
	egr1_2R7	TTAAGGCAAGATGCAAAGCA
Rplp1_A	rplp1_p_F1	TATGACAGCCATGAGGCAAG
	rplp1_p_R1	ACGACCTAACATTTGAAGAAGC
Rplp1_B	rplp1_p_F2	TGGCTGATGGAGCCCTTAT
	rplp1_p_R2	GGAACGGCCTTAGCTTCAG
Rplp1_C	rplp1_F3	AGCTGAGAACAGAGGGACGA
	rplp1_R1	GCACACAGAAAGAGGATCTGC
Rplp1_D	rplp1_3'_F1	GATGACATGGGCTTTGGTCT
	rplp1_3'_R1	CAGCCATCCTTGAGAAACACT
Rplp1_E	rplp1_3'_F2	TGATAACAGTGCCTGCCTTG
	rplp1_3'_R2	GAACAGCAGTGAGCATCCAA
Actb_A	actb_p_F1	CTGACTGACCGCGTACTCC
	actb_p_R1	CAGAAAAGAAACGAGCCGTCA
Actb_B	actb_2F	ATGATATTGCTGCGCTCGTT
	actb_2R	CCCACGATAGATGGGAACAC
Actb_C	actb_3'_F	GGCTTGACTGGTGTGGTTT
	actb_3'_R	GCAGATAGCTGACCCACACA
H2A_TSS	H2A_F3	TCTTCGGTTGTACAGCAAGC
	H2A_R2	CGACTTGGCCTTAGCTCTGA
H2A_3'	H2A_F2	TTCAGAGCCACCCACTTTCT
	H2A_R1	GCGTTAAAAACAAAGGCACA
U1	U1_F1	CATGATCAGGCAGGTGGTTT
	U1_R1	AGTCGAGTTTCCCGCATT
U2	U2_F1	CTCGGCCTTTTGGCTAAGAT
	U2_R1	CGCCAAAAATCCGTTTAAT
U1_uncleaved	U1_F4	AGACACCATGATCAGGCAGG
	U1_3'_R4	TTGAACCGCGCAAATCAGG
U2_uncleaved	U2_F1	CTCGGCCTTTTGGCTAAGAT
	U2_3'_R	CGCCTTCCTTCTCTCCTTC