

# ATPase-dependent quality control of DNA replication origin licensing

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**The regulated loading of the Mcm2–7 DNA helicase (comprising six related subunits, Mcm2 to Mcm7) into pre-replicative complexes at multiple replication origins ensures precise once per cell cycle replication in eukaryotic cells. The origin recognition complex (ORC), Cdc6 and Cdt1 load Mcm2–7 into a double hexamer bound around duplex DNA in an ATP-dependent reaction, but the molecular mechanism of this origin ‘licensing’ is still poorly understood. Here we show that both Mcm2–7 hexamers in *Saccharomyces cerevisiae* are recruited to origins by an essential, conserved carboxy-terminal domain of Mcm3 that interacts with and stimulates the ATPase activity of ORC–Cdc6. ATP hydrolysis can promote Mcm2–7 loading, but can also promote Mcm2–7 release if components are missing or if ORC has been inactivated by cyclin-dependent kinase phosphorylation. Our work provides new insights into how origins are licensed and reveals a novel ATPase-dependent mechanism contributing to precise once per cell cycle replication.**

Stable genome inheritance requires that replication origins initiate efficiently during S phase, and that re-initiation from these origins is subsequently prevented. This is accomplished by first licensing origins during G1 phase with a pre-replicative complex containing an inactive double hexamer of the Mcm2–7 helicase, and then activating the helicase during S phase, when pre-replicative complexes can no longer be assembled<sup>1–9</sup>.

## Mcm3 recruits Cdt1–Mcm2–7 to ORC–Cdc6

We have previously described a system in which pre-replicative complexes can be assembled on DNA with purified proteins<sup>7</sup>. When ATP is present, ORC and Cdc6 load Cdt1–Mcm2–7 heptamers into a salt-resistant Mcm2–7 double hexamer with concomitant release of Cdc6 and Cdt1; in ATP- $\gamma$ S (a slowly hydrolysed analogue of ATP) all pre-replicative complex components are recruited in low salt but are removed by a high-salt wash (HSW) (Supplementary Fig. 1a). To investigate the individual roles of Cdt1 and Mcm2–7, we purified each separately (Supplementary Fig. 1b–d) and showed each protein was functional for loading when re-assembled into a Cdt1–Mcm2–7 complex (Supplementary Fig. 2). Consistent with our previous results<sup>7</sup>, none of the pre-replicative complex components bound to DNA under recruitment conditions (ATP- $\gamma$ S, low salt) in the absence of ORC (Fig. 1A, lanes 1–6). In the absence of Cdc6 (lanes 7–9), ORC bound DNA, but could not recruit Cdt1, Mcm2–7 or Cdt1–Mcm2–7. Cdc6 was recruited to DNA in an ORC-dependent manner (compare lanes 4 and 10) consistent with the formation of an essential ORC–Cdc6 complex<sup>10</sup>. Cdt1 was not recruited in the presence of ORC–Cdc6 (lane 10), but we found significant ORC- and Cdc6-dependent recruitment of Mcm2–7 subunits in the absence of Cdt1 (compare lane 11 to lanes 6 and 9). Cdt1 was only recruited when Mcm2–7 was present along with ORC and Cdc6 (lane 12). From this we conclude that Mcm2–7 can be recruited to ORC–Cdc6 without Cdt1 and that Cdt1 recruitment requires Mcm2–7.

The absence of Cdt1 did not affect Mcm7 recruitment, but did reduce the amount of Mcm2 recruited (Fig. 1A, compare lanes 11 and 12). To explore this further, we tested for the presence of each of the six Mcm2–7 subunits after Mcm2–7 recruitment in ATP- $\gamma$ S in

the presence or absence of Cdt1 using silver staining (Fig. 1B, a) and immunoblotting (Fig. 1B, b). We found that Mcm3, 5 and 7 were recruited to ORC–Cdc6 similarly in the presence and absence of Cdt1 (Fig. 1B); the recruitment of Mcm2, 4 and 6, however, was significantly reduced without Cdt1. This suggests that Mcm3, 5 and 7, which are immediate neighbours in the Mcm2–7 ring, are recruited to ORC–Cdc6 directly without Cdt1, but Cdt1 plays some role in recruiting Mcm2, 4 and 6 (Fig. 1B, c).

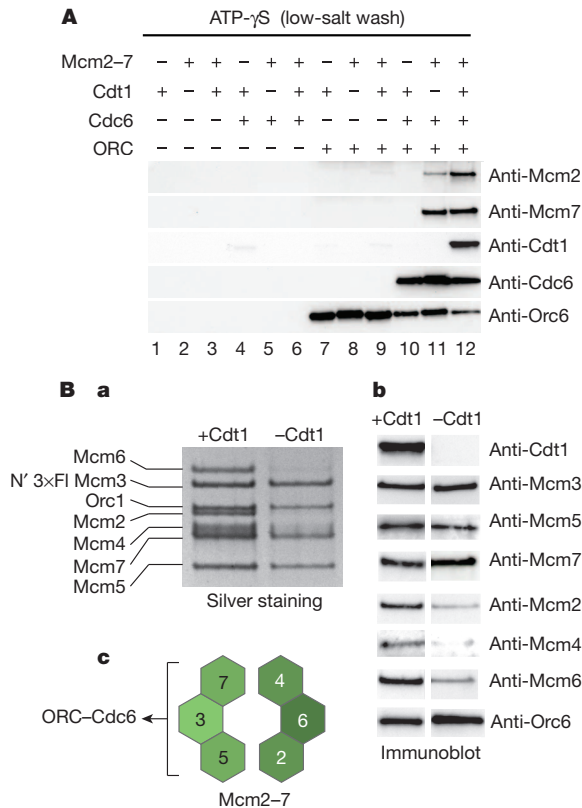
## The extreme C terminus of Mcm3 recruits Cdt1–Mcm2–7

We took several approaches to address which Mcm2–7 subunits were involved in the Cdt1-independent recruitment. We tested each of the six Mcm2–7 subunits individually and found that only Mcm3 could be recruited in a Cdc6-dependent manner without the other subunits (Supplementary Fig. 3a, b, f). We next assembled Mcm2–7 complexes containing all subunit or lacking either Mcm3 or Mcm4 ( $\Delta$ 3 and  $\Delta$ 4, respectively; Supplementary Fig. 3c, d). Mcm5 and 7 were recruited to ORC–Cdc6 in the absence of Cdt1 by the complete complex (Supplementary Fig. 3f, lanes 1 and 5) and by  $\Delta$ 4 (lanes 3 and 7), but not by  $\Delta$ 3 (lanes 2 and 6). Taken together, these results indicate that Mcm3 is critical for recruiting Mcm5 and 7 to ORC–Cdc6 in the absence of Cdt1.

Mcm3 comprises an amino-terminal domain (NTD) and a AAA+ domain, which are both found in all Mcm2–7 subunits<sup>11,12</sup>, and an extended C-terminal tail of unknown function containing a conserved domain at the extreme C terminus (‘C’ in Fig. 2a) that is not found in other Mcm2–7 subunits (Fig. 2a). A version of Mcm3 containing a 3 $\times$ Flag tag at its C terminus could be assembled into a stable heptameric Cdt1–Mcm2–7 complex, but was unable to recruit or load Mcm2–7 (Supplementary Fig. 4). Moreover, a small fragment containing the C-terminal 194 amino acids residues of Mcm3 was recruited in an ORC- and Cdc6-dependent manner (Fig. 2b). These results pointed to the C terminus as being crucial for Mcm3 recruitment.

Based on the conservation of the Mcm3 C terminus (Fig. 2a), and the fact that a tag at the C terminus interfered with its function, we generated a series of C domain amino acid substitution mutants in full-length Mcm3 (Fig. 2a). We assembled the mutant proteins into

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**Figure 1 | Mcm3 is necessary and sufficient for Mcm2-7 recruitment.** **A**, Protein requirements for Mcm2-7 recruitment. ORC, Cdc6, Cdt1 and Mcm2-7 were purified as described in Methods and in Supplementary Fig. 1. After incubation of the indicated proteins with DNA beads in the presence of ATP- $\gamma$ S, beads were isolated and washed with low salt. DNA was uncoupled with irradiation as described in Methods and bound proteins were analysed by immunoblot with the indicated antibodies. **B**, Recruitment of Mcm2-7 by ORC and Cdc6 was performed as in **A**. Reactions contained Mcm2-7 either with (+) or without (-) Cdt1. **B, a-c**, Bound proteins were visualized by silver staining (**B, a**) or immunoblot (**B, b**). Panel **B, c** summarizes the results in **B, a, b**.

Cdt1-Mcm2-7 complexes (Supplementary Fig. 5) and tested their ability to recruit and load Mcm2-7. The single mutants Mcm3-11 and Mcm3-12, and the Mcm3-13 double mutant were completely defective in recruitment of Cdt1-Mcm2-7 to ORC-Cdc6 (Fig. 2c, lanes 2-4), as was Mcm3 lacking its entire C-terminal domain (3 $\Delta$ C, Fig. 2c, lane 8). In these experiments, Orc1 serves as a useful loading control. These mutant proteins were also not recruited when tested individually in the absence of Cdt1 and the other Mcm2-7 subunits (Supplementary Fig. 6). Consistent with their defect in recruitment, Mcm3-11 and Mcm3 $\Delta$ C were unable to load Mcm2-7 (Fig. 2d, lanes 2 and 6). Mutation of other conserved residues (Mcm3-16, Mcm3-22 and Mcm3-23) generated proteins that were less defective, showing reduced recruitment (Fig. 2c, lanes 5-7 and Supplementary Fig. 6) and a commensurate reduction in loading (Fig. 2d, lanes 3-5). Therefore, the C terminus of Mcm3 is essential for recruitment of all Mcm2-7 subunits. As Mcm2-7 containing Mcm3-11, Mcm3-12 or Mcm3-13 is not recruited even when bound to Cdt1, this indicates that Cdt1 cannot recruit Mcm2-7 to ORC-Cdc6 directly. The reduced association of Mcm2, 4, 6 with ORC-Cdc6 (Fig. 1A, B) therefore probably reflects a role for Cdt1 in retaining or stabilizing these subunits after initial recruitment by Mcm3.

We next expressed the mutant Mcm3 proteins in yeast strains harbouring a temperature-sensitive degron mutant of *MCM3* (*mcm3-td*)<sup>13</sup>. This degron mutant grew well at 25 °C, but not at the restrictive temperature, 37 °C (Fig. 2e, row 1). The growth defect at 37 °C was suppressed by expression of wild-type Mcm3 (Mcm3,

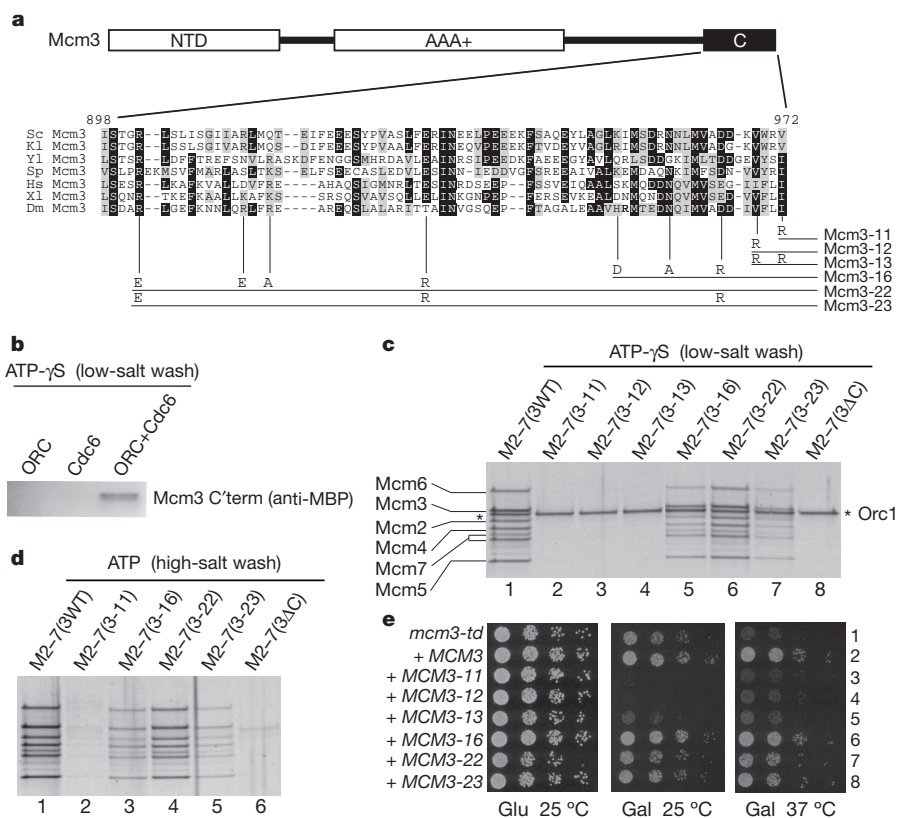
row 2), but not by expression of Mcm3-11, Mcm3-12 or Mcm3-13 (rows 3-5) indicating that these proteins are not functional *in vivo*. Expression of these proteins significantly reduced growth even at 25 °C when the wild-type degron fusion protein was functional (middle panel, GAL 25 °C, compare row 1 with rows 3-5), indicating that these mutants act as dominant-negative inhibitors when over-expressed. Some of the other mutants (Mcm3-16, Mcm3-22, Mcm3-23) showed mild growth defects at 37 °C, consistent with their partial defects in Mcm2-7 loading. Supplementary Fig. 7 shows that *mcm3-11* supported only very slow growth when present as an only copy, whereas *mcm3-12* and *mcm3-13* did not support growth. Taken together, these results indicate that a domain at the extreme C terminus of Mcm3 is necessary for recruiting Cdt1/Mcm2-7 to ORC-Cdc6, and that this function is essential for viability.

### Both Mcm2-7 hexamers require the C terminus of Mcm3

The results in Figs 1 and 2 show that recruitment of the first Mcm2-7 hexamer occurs by interaction of Mcm3 with ORC-Cdc6. If recruitment of the second hexamer occurred by a different mechanism, one that didn't involve Mcm3-ORC-Cdc6 interaction but did require recruitment of the first hexamer, then the Mcm3-11 mutant should be able to be recruited as the second hexamer in the presence of wild-type Cdt1-Mcm2-7. To test this, we first generated two different forms of Mcm3 that could be distinguished after SDS-polyacrylamide gel electrophoresis (SDS-PAGE), one containing an N-terminal fusion to the Flag tag (N' 3 $\times$ Flag-Mcm3), the other containing a larger N-terminal fusion to maltose binding protein (N' MBP-Mcm3). Both proteins supported similar levels of recruitment and loading, and both complemented the *mcm3-td* mutant at 37 °C (Supplementary Fig. 8). We engineered the Mcm3-11 mutation into either the MBP fusion (Fig. 3a) or the Flag fusion (Fig. 3b), generated mutant Cdt1-Mcm2-7 complexes and mixed these complexes in different ratios with Cdt1-Mcm2-7 containing either wild-type Flag-Mcm3 (Fig. 3a) or wild-type MBP-Mcm3WT (Fig. 3b). These experiments show that the Mcm3-11 mutant was not recruited above background levels in ATP or ATP- $\gamma$ S over a wide range of wild type:mutant ratios, showing that the wild-type protein cannot aid recruitment of the Mcm3-11 mutant complex, indicating that recruitment of both hexamers requires the Mcm3 C terminus.

### Mcm3 binding activates the ORC-Cdc6 ATPase

ATP hydrolysis is required for assembly of the Mcm2-7 double hexamer, but what stage of assembly requires ATP hydrolysis is not known. We therefore tested whether Mcm3 binding affected the ATPase activity of DNA-bound ORC-Cdc6. Neither Mcm3 nor the Mcm3-13 mutant showed appreciable ATPase activity by themselves (Fig. 4a), consistent with the fact that, as a AAA+ ATPase, Mcm3 requires an arginine finger from a binding partner (in this case, Mcm5) to promote ATP hydrolysis. ORC, together with Cdc6 (ORC-Cdc6, Fig. 4a), had some ATPase activity in the presence of DNA, which might reflect a basal level of ATPase from DNA-bound ORC-Cdc6, or might be caused by ORC and/or Cdc6 that is not bound to DNA. Addition of Mcm3, but not Mcm3-13, to ORC-Cdc6 resulted in a three- to fourfold increase in ATPase activity, indicating that the interaction of the C terminus of Mcm3 stimulates the ATPase of ORC-Cdc6. To rule out any contribution from the Mcm3 ATPase, we examined the effect of the Mcm3 C-terminal fragment lacking the AAA+ domain. Figure 4b shows that this domain was as effective as full-length Mcm3 in stimulating the ATPase activity of ORC-Cdc6. Reactions in Fig. 4b contained 2.5 pmol each of ORC and Cdc6, yet addition of Mcm3 resulted in approximately 140 pmol of additional ATP hydrolysis (above the level produced by ORC and Cdc6 alone) over 20 min, indicating that Mcm3 binding can induce multiple rounds of ATP binding and hydrolysis by ORC-Cdc6.



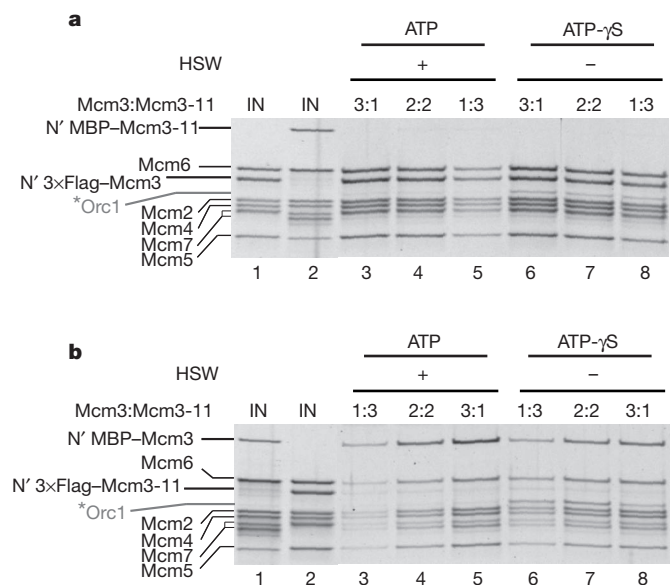
**Figure 2 | The C terminus of Mcm3 is required for Mcm2–7 recruitment.** **a**, The domain architecture of Mcm3 and alignment of the Mcm3 C terminus. The alignment includes Mcm3 from a variety of eukaryotic species (Sc, *Saccharomyces cerevisiae*; Kl, *Kluyveromyces lactis*; Yl, *Yarrowia lipolytica*; Sp, *Schizosaccharomyces pombe*; Hs, *Homo sapiens*; Xl, *Xenopus laevis*; Dm, *Drosophila melanogaster*). Residue numbers above alignment correspond to *S. cerevisiae* Mcm3. The position of various mutants is shown by vertical lines, and the mutant amino acid residue is shown at the bottom of the line. The numbering of alleles begins with 11 to prevent confusion with any existing *mcm3* mutant alleles. **b**, Recruitment assay performed with a C-terminal MBP-tagged Mcm3 fragment (last 194 amino acids) and with the indicated proteins. **c**, **d**, Cdt1–Mcm2–7 complexes (M2–7) containing wild-type (WT) and mutant Mcm3 (digits shown in parentheses) were tested for recruitment (**c**) or for loading (**d**), proteins were analysed by silver staining. **e**, Wild-type and mutant *mcm3* alleles were expressed from a galactose-inducible promoter in strains containing the *mcm3-td* degenon mutant. A dilution series was tested for growth on plates containing either 2% D-glucose (Glu) or 2% D-galactose (Gal) at either 25 °C or 37 °C as indicated.

**ATP hydrolysis by ORC–Cdc6 promotes Mcm2–7 release**

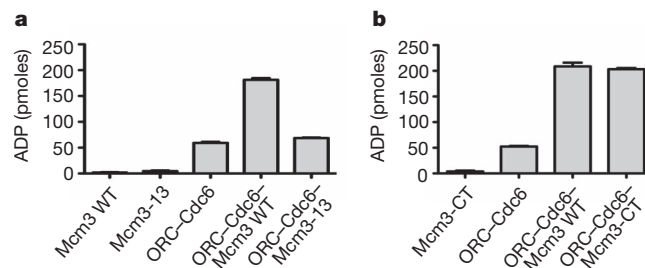
Activation of the ORC–Cdc6 ATPase by the initial recruitment of Mcm3 led us to consider that ATP hydrolysis might play some role early in the Mcm2–7 loading reaction. Supplementary Fig. 9a shows that both ORC and Cdc6 are bound to DNA equally well in ATP and ATP-γS; however, we found that the stable recruitment of Mcm3 we

saw with non-hydrolysable ATP-γS (Supplementary Fig. 3a, f and Fig. 5a, ATP-γS) was lost when hydrolysis was allowed (Fig. 5a, ATP). Similarly, the retention of Mcm3, Mcm5 and Mcm7 seen in ATP-γS in the absence of Cdt1 (for example, Fig. 1) was also lost in the presence of ATP (Fig. 5b, compare lanes 2 and 6). These results indicate that ATP hydrolysis can lead to release of Mcm3 (and associated subunits) when the loading of incomplete Cdt1–Mcm2–7 complexes is attempted.

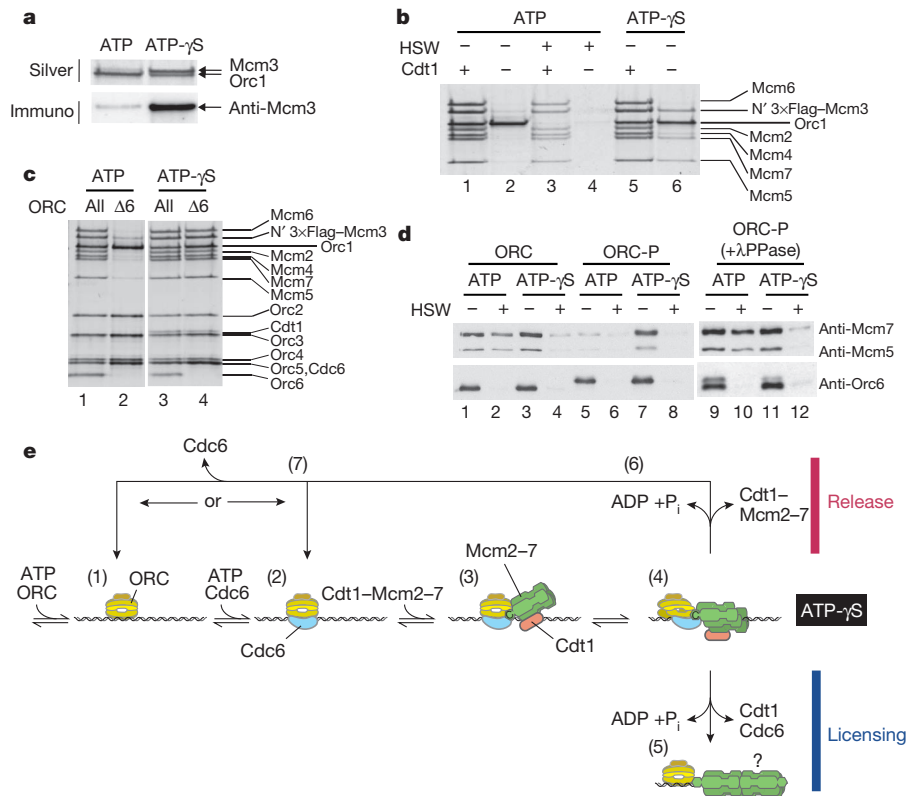
This could be because the remaining Mcm2–7 subunits cannot form stable, topologically closed double hexamers around DNA and are, therefore, released during a futile loading reaction with ATP hydrolysis. ORC is not required for Mcm2–7 to remain bound topologically to the DNA after loading (for example, after a high-salt wash). So, we next looked at the ability of the full, wild-type Cdt1–Mcm2–7 complex to be recruited and loaded by ORC lacking the Orc6 subunit (ORCΔ6), which can still bind DNA<sup>14</sup>. ORCΔ6 was able to recruit all six Mcm2–7 subunits in the presence of ATP-γS as



**Figure 3 | Both Mcm2–7 hexamers must interact with ORC–Cdc6 through Mcm3.** **a**, Complexes containing wild-type 3×Flag–Mcm3 and MBP–Mcm3-11 were assembled (IN) and mixed in the indicated ratios, with a fixed amount of total Mcm2–7 complex (4 pmol) and tested for loading and recruitment as above. **b**, Loading and recruitment of mixed complexes containing 3×Flag–Mcm3-11 and MBP–Mcm3WT in the indicated ratios.



**Figure 4 | Mcm3 binding activates the ORC–Cdc6 ATPase.** **a**, **b**, The conversion of [<sup>32</sup>P]ATP to [<sup>32</sup>P]ADP was monitored as described in Methods in reactions containing the indicated proteins (Mcm3 wild type; Mcm3-13 mutant; Mcm3-CT, a polypeptide containing the C-terminal 194 amino acid residues of Mcm3; ORC and Cdc6). Error bars depict standard error of the mean from five reactions.



**Figure 5 | ATP hydrolysis by ORC-Cdc6 can promote Mcm2-7 release.**

**a**, Mcm3 was tested for recruitment (low-salt wash) in reactions containing ORC, Cdc6 and either ATP or ATP- $\gamma$ S. Bound proteins were analysed by silver staining (silver) or immunoblotting with anti-Mcm3 antibody (immuno). **b**, Recruitment and loading assays were performed as above with ORC, Cdc6 and Mcm2-7 either with (+) or without (-) Cdt1 in ATP or ATP- $\gamma$ S. Proteins were visualized by silver staining. **c**, Complexes containing either the complete six-subunit ORC complex (All) or a complex lacking Orc6 ( $\Delta$ 6), purified as described in Methods, were tested for recruitment (low-salt wash) in either

efficiently as the complete ORC complex (Fig. 5c, lanes 3 and 4). Although the recruited complex was slightly more salt-sensitive than the complex recruited with the complete ORC complex (Supplementary Fig. 9b), the only significant difference between Fig. 5c lanes 3 and 4 was the absence of Orc6 in lane 4. Recruitment of Mcm2-7 subunits in the absence of Orc6 still required the C terminus of Mcm3, because it was completely defective in the Mcm3-11 mutant (Supplementary Fig. 9d, lane 4). Notably, although ORC $\Delta$ 6 recruited all six Mcm2-7 subunits in ATP- $\gamma$ S, it was unable to stably recruit any of these subunits in the presence of ATP (compare Fig. 5c, lanes 2 and 4). ORC $\Delta$ 6 and Cdc6 are bound equally well in ATP and ATP- $\gamma$ S (Supplementary Fig. 9a). Thus, although the entire Mcm2-7 ring is efficiently recruited, ATP hydrolysis promotes release of Cdt1-Mcm2-7 in the absence of Orc6.

To rule out the possibility that the non-physiological absence of Orc6 somehow alters the function of ORC-Cdc6, and to examine the role of ATP-dependent Mcm2-7 release *in vivo*, we examined a physiologically relevant situation where ORC has been functionally inactivated. Phosphorylation of Orc6, along with Orc2, by cyclin-dependent kinase (CDK) plays a role in preventing re-replication<sup>15,16</sup> by blocking the ability of ORC to load Mcm2-7<sup>17</sup>. We phosphorylated purified ORC (ORC-P) with the yeast mitotic CDK, Clb2-Cdc28, and examined its ability to recruit and load Mcm2-7. ORC-P cannot load Mcm2-7 (Fig. 5d, compare lanes 2 and 6), but it can recruit Mcm2-7 subunits as well as the unphosphorylated ORC in the presence of ATP- $\gamma$ S (compare lanes 3 and 7). However, ORC-P was unable to accumulate Mcm2-7 subunits in the presence of ATP (compare lanes 1 and 5). Lambda phosphatase treatment of ORC-P restored its ability

to recruit and load Mcm2-7 in ATP (Fig. 5d, lanes 9-12). These

results show that, as in the cases of Mcm3 alone, Mcm2-7 without Cdt1, and ORC $\Delta$ 6, the CDK-phosphorylated ORC is competent to recruit Mcm2-7 to ORC-Cdc6, but ATP hydrolysis then promotes Mcm2-7 release.

To provide additional evidence that ATP hydrolysis can promote Mcm2-7 release from ORC $\Delta$ 6, we have looked at Mcm2-7 recruitment in ATP at reduced temperatures, to slow ATP hydrolysis. In contrast to 30 °C (Fig. 5c), the recruitment of Mcm2-7 by ORC $\Delta$ 6 occurred equally well in ATP and ATP- $\gamma$ S at 8 °C (Supplementary Fig. 10). However, when these reactions were shifted to 30 °C after 9 min, recruitment of Mcm2-7 continued in ATP- $\gamma$ S but Mcm2-7 was significantly reduced in the presence of ATP, consistent with the idea that elevated temperature promotes ATP hydrolysis and subsequent Mcm2-7 dissociation.

Our results support a model for origin licensing wherein Cdt1-Mcm2-7 is first recruited to origins by interaction between the C terminus of Mcm3 and ORC-Cdc6 (Fig. 5e step 3). Cdt1 is not required for this initial recruitment, in contrast to previous experiments in crude extracts<sup>17-19</sup>. We suggest, by analogy to other AAA+ proteins<sup>20</sup>, that domain movements in ORC-Cdc6 triggered by Mcm3 binding activate the ATPase of ORC and/or Cdc6 by bringing arginine fingers in contact with ATP binding sites in adjacent subunits (Fig. 5e step 4). We further suggest that these domain movements are transmitted to Mcm2-7, leading to destabilization of Mcm2, Mcm4 and Mcm6 when Cdt1 is missing (Fig. 1A, B). Cdt1 stabilizes Mcm2-7

## Discussion

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in this new conformation by a mechanism that does not require its interaction with Orc6 (Fig. 5c). Because both hexamers must interact with ORC–Cdc6 (Fig. 3), our results indicate they are either loaded sequentially or there is more than one Mcm3 binding site in ORC–Cdc6, allowing concerted loading.

When all pre-replicative complex components are present and in the correct post-translational modification state, ATP hydrolysis promotes loading of the ring around DNA (Fig. 5e step 5). However, when criteria for correct licensing are not met, ATP hydrolysis instead is coupled to irreversible dissociation of inappropriate protein assemblies, preventing the accumulation of non-productive complexes (Fig. 5e step 6). Cdc6 is bound to ORCΔ6 in both ATP and ATP-γS (Supplementary Fig. 9e), indicating either that Cdc6 remains bound to ORC after Cdt1–Mcm2–7 release, or that Cdc6 is released, but rebinds quickly (Fig. 5e step 7). This ATPase-dependent quality control mechanism contributes to preventing licensing by CDK-phosphorylated ORC outside of G1 phase, and therefore has a role in ensuring once per cell cycle replication. We note that the block to re-replication in metazoans works largely through inhibition and degradation of Cdt1<sup>21,22</sup>, and our results (Fig. 5b) indicate that this will also prevent licensing via this ATPase-dependent mechanism. Although a great deal is known about the multiple pathways contributing to a robust block to re-assembly of pre-replicative complexes after replication in eukaryotes<sup>23,24</sup>, few quality control mechanisms contributing to efficient pre-replicative complex assembly during G1 phase have been described (see ref. 25). The mechanism we have described here may also have a role during G1 phase to ensure assembly of complete, functional pre-replicative complexes.

## METHODS SUMMARY

All strains are listed in Supplementary Table 1 and strain constructions are described in Methods. Mcm2–7 loading reactions were performed as described (ref. 7 and Methods). After isolation and washing of the beads, DNA was cleaved from beads using irradiation with a 330 nm light source, which does not induce significant levels of DNA crosslinking (see Methods and Supplementary Fig. 11). Proteins were analysed after SDS–PAGE by either silver staining or immunoblotting with a variety of antibodies (Methods). All proteins were expressed in either *S. cerevisiae* or *Escherichia coli* and were purified as described in Methods. Cdt1 and Mcm2–7 expressed in both bacteria and yeast were proficient for loading (Supplementary Fig. 12). ATPase assays were based on the method described in ref. 26 with the modifications described in Methods.

**Full Methods** and any associated references are available in the online version of the paper.

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**Supplementary Information** is available in the online version of the paper.

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## METHODS

**Cdt1–Mcm2–7 overexpressed in yeast (yJF38).** To obtain a yeast strain overexpressing the Cdt1–Mcm2–7 complex, four new vectors were generated using the pRS30<sub>series</sub><sup>27</sup>. Making use of the bidirectional inducible *GALI-10* promoter, the six *MCM* subunits, *CDT1* and *GAL4* genes were cloned and overexpressed in the strain yJF38. *GAL4* is a positive regulator of *GAL* genes in response to galactose, it was therefore overexpressed together with the *MCM2–7* and *CDT1* genes to increase protein yield.

*GAL4* and *MCM2* were amplified using the primer pairs JF1-2 and JF3-4, respectively. *GAL4* was cloned into pRS303 (pJF2.1) and *MCM2* into pRS306 (pJF5.1) between *Sma*I and *Bam*HI sites. *MCM7* and *MCM5* were amplified with JF5-6 and JF7-8 primer pairs and cloned into a *Sma*I site in pRS304 (pJF4.1) and pRS306 (pJF3.1), respectively. The forward primers inserted a unique *Asc*I site at the 5' end of the start codon of these genes. *MCM3*, *MCM6*, *MCM4* and *CDT1* were amplified using the following primer pairs: JF9-10, JF11-12, JF13-14 and JF15-16. The PCR products were cloned between *Spe*I and *Not*I sites into pJF5.1, 4.1, 3.1 and 2.1, respectively, to yield pJF5.2, 4.2, 3.2 and 2.2. In this case, a unique *Sgr*AI site was inserted at the 5' end of their start sites. In addition a 3×Flag tag<sup>28</sup> was inserted using a *Sgr*AI site present upstream of *MCM3* in pJF5.2 (pJF6.2). Finally, the *GALI-10* promoter was cloned between the *Asc*I and *Sgr*AI sites previously inserted, yielding pJF2, 3, 4 and 6. These vectors were integrated into the strain yJF1 (yJF38).

**Cdt1–Mcm2–7 overexpressed in yeast (yJF35, yJF59 and yJF73).** yJF35 and yJF59 are analogous to yJF38 except that the 3×Flag tag on *MCM3* was inserted at its C terminus in yJF35 and on the C terminus of *CDT1* in yJF59. The vectors integrated into yJF1 were pJF2, 3, 4 and 5. The C-terminal 3×Flag on *MCM3* and *CDT1* was inserted afterwards by PCR-based tagging using pBP83. pJF2, 3, 4 and 39 vectors were integrated into the strain yJF1, yielding yJF73.

**Mcm2–7 overexpressed in yeast (yJF39).** To obtain a Mcm2–7 complex without Cdt1, a strategy similar to the design of yJF38 was followed, except that pJF2 was not integrated into the final strain and the endogenous *CDT1* locus was tandem affinity purification (TAP)-tagged<sup>29</sup> using pJF21, thus producing yJF39.

**ORC overexpressed in yeast (ySD-ORC).** To overexpress ORC in yeast, we modified pJF2, 3 and 5 as follows. In pJF5, *MCM2* and *MCM3* were replaced with calmodulin binding peptide-tobacco etch virus (CBP-TEV)-*ORC1* and -*ORC2*, respectively (pJF19). In pJF2 *GAL4* and *CDT1* were substituted with *ORC3* and *ORC4*, respectively (pJF17). In pJF3, *MCM5* and *MCM4* were replaced with *ORC5* and *ORC6*, respectively (pJF18). All ORC genes were codon optimized. Finally, pJF19, 17 and 18 were integrated into yJF1, producing the strain ySD-ORC.

**ORC(Δ6) overexpressed in yeast (ySD-ORC(Δ6)).** In pJF3, *MCM5* was replaced with *ORC5* and *MCM4* was deleted, producing the vector pJF20. To obtain ORC without Orc6, yJF1 was transformed with pJF17, 19 and pJF20, instead of pJF18. Furthermore, a C-terminal 3×Flag tag was added to the endogenous copy of *ORC6*, using pBP83.

***MCM3* mutants.** *MCM3* mutants were cloned into two different vectors: pMAL-C2P to purify recombinant proteins, and pRS306 for complementation studies in yeast.

pMAL-C2P was a gift from S. Mochida and was derived from pMAL-C2 (NEB) by introducing a PreScission protease site before the *Eco*RI site in the polylinker region<sup>30</sup>. *MCM3* was amplified from *S. cerevisiae* genomic DNA using AM51 and AM52 and cloned into pMAL-C2P using *Xba*I and *Sal*I sites (pAM5). *MCM3* contains a *Kpn*I site at position 2690. Mutant fragments of 231 base pairs in length, between this site and the stop codon were synthesized by GeneArt. The mutated sequences incorporated a *Not*I, followed by a *Sal*I restriction site at the 3' end of the stop codon. Using *Kpn*I and *Sal*I sites, the mutant sequences were cloned into pAM5, to yield pJF27 (Mcm3-11), pJF28 (Mcm3-12), pJF29 (Mcm3-13), pJF32 (Mcm3-16), pJF35 (Mcm3-22) and pJF36 (Mcm3-23).

*MCM2* in pJF5 was removed, to yield pGC003. *MCM3* mutant sequences were excised from pJF27, 28, 29, 32, 35 and 36 vectors using *Avr*II and *Not*I sites, and cloned into pGC003 (pJF8, 9, 10, 13, 15 and 16). Mcm2 in pJF6 was removed, to yield pJF37. MBP tag was amplified from pMAL-C2P using the primers JF19 and 20 and cloned into pGC003 using *Sgr*AI unique site, originating pJF38. Finally, these vectors were integrated into a *MCM3* degtron strain (yKL43<sup>13</sup>), producing the strains yJF63, 64, 65, 66, 69, 71, 72, 78 and 79.

***MCM3* mutants in a diploid background.** Wild-type C-terminal Mcm3 was amplified from pGC003, C-terminal Mcm3 mutants were amplified from pJF27 (Mcm3-11), pJF28 (Mcm3-12) and pJF29 (Mcm3-13) using primers JF17 and JF18. The PCR products contained the *URA3* gene and were used to transform the diploid strain W303 (all amplified products were sequenced before transformation). Transformants were selected for on media lacking uracil. These were shown by PCR to be heterozygous for replacement of the C terminus of

Mcm3 with either wild-type or mutant Mcm3 cassettes as above. Sporulation and tetrad dissection of these transformants was performed to examine their viability.

**Fragments of *MCM3*.** A C-terminal fragment of *MCM3* (588 base pairs) was amplified from *S. cerevisiae* genomic DNA using AM54 and AM52. This PCR product was cloned in pMAL-C2P using *Xba*I and *Sal*I sites (pAM6). An N-terminal fragment of *MCM3* (2,331 bp) was amplified from *S. cerevisiae* genomic DNA using AM51 and AM53. This PCR product was cloned in pMAL-C2P using *Xba*I and *Sal*I sites (pAM7).

**Individual MCM subunits expressed in bacteria.** *MCM4* and 5 were amplified by PCR using NC1-2 and NC3-4 primer pairs. These PCR products were cloned between *Nde*I and *Xho*I restriction sites into pET22b, to yield pET22b-*MCM4* and pET22b-*MCM5*. *MCM6* was excised from pET16b-*MCM6* using *Nde*I and *Bam*HI<sup>31</sup> and cloned into pET11a (pET11a-*MCM6*).

**Cdt1 expression in bacteria.** *CDT1* was amplified from *S. cerevisiae* genomic DNA using NC5 and NC6 and cloned into pGEX-6p-1 (GE Healthcare), using *Bam*HI and *Not*I sites (pGEX-6p-1-*CDT1*).

**Cdc6 expression in bacteria.** *S. cerevisiae CDC6* was amplified from pET15b-*CDC6* using the primers AM1 and AM2. The PCR product was cloned between *Bam*HI and *Xho*I restriction sites in pGEX-6p-1 (GE Healthcare), generating pAM3.

**Purification of Cdt1–Mcm2–7 from yJF38, yJF35, yJF59 and yJF73.** 2 l of cells were grown in YP-raffinose at 30 °C to a cell density of  $4 \times 10^7$  cells per ml and arrested for 3 h with 100 ng ml<sup>-1</sup> of alpha-factor. Protein expression was induced by adding galactose (2%) and incubating at 30 °C for 3–4 h. Cells were collected, washed with ice-cold 25 mM HEPES-KOH pH 7.6, 1 M sorbitol, then washed with buffer A (45 mM HEPES-KOH pH 7.6, 0.02% NP-40, 10% glycerol, 5 mM magnesium acetate (Mg(OAc)<sub>2</sub>) and 0.1 M K-glutamate). The pellet was resuspended in 0.5 volumes of buffer A/1 mM DTT/protease inhibitors (Roche) and frozen drop-wise in liquid nitrogen. Frozen drops of cells were crushed using a freezer mill (SPEX CertiPrep 6850 Freezer/Mill) with 6 cycles of 2 min crushing at rate 15. Frozen cell powder was thawed at room temperature, resuspended in 1 volume of buffer A/1 mM DTT/protease inhibitors, and the concentration of K-glutamate was adjusted to 0.5 M. The suspension was centrifuged for 1 h at 50,000 r.p.m. using a Ti70.1 rotor (257,000g). The clear phase was recovered, dialysed twice for 1 h against buffer B (25 mM HEPES-KOH pH 7.6, 0.02% NP-40 and 10% glycerol)/0.1 M K glutamate/5 mM Mg(OAc)<sub>2</sub>, and then centrifuged for 30 min at 50,000 r.p.m. Anti-Flag immunoprecipitation was performed by adding 1 ml packed bead volume of washed anti-Flag M2 agarose (Sigma) to the supernatant and incubating for 1 h at 4 °C. Beads were recovered, and washed with ten bed resin volumes (BVs) of buffer B/0.1 M K glutamate/1 mM ATP/5 mM Mg(OAc)<sub>2</sub>. Elution was performed by adding 0.5 mg ml<sup>-1</sup> 3×Flag peptide. After 20 min at 4 °C, the flow-through was collected, concentrated using a Microcon YM-10, 10000 MWCO (Millipore) and fractionated on a 24 ml Superdex 200 10/300 GL column (GE Healthcare) pre-equilibrated in buffer B/0.1 M K acetate. Peak fractions were pooled and aliquoted.

**Purification of Mcm2–7 from yJF39.** yJF39 was purified as described for yJF38. The only difference was a pre-incubation step with IgG Sepharose 6 Fast Flow beads (GE Healthcare), to remove endogenous Cdt1, before the sample was loaded onto the gel filtration column. 100 μl of IgG packed resin was added to the 3×Flag peptide-eluted sample and incubated for 30 min at 4 °C. The unbound fraction was recovered, concentrated and loaded onto a Superdex 200 10/300 GL column (GE Healthcare), as described for yJF39.

**Purification of ORC from ySD-ORC.** 2 l of cells were grown in YP-raffinose at 30 °C to a cell density of  $4 \times 10^7$  cells per ml and arrested for 3 h with 100 ng ml<sup>-1</sup> of alpha-factor. After arrest, protein expression was induced by adding galactose (2%) for 3–4 h at 30 °C. Cells were collected, washed with ice-cold 25 mM HEPES-KOH pH 7.6/1 M sorbitol, then washed with buffer C (25 mM HEPES-KOH pH 7.6, 0.05% NP-40 and 10% glycerol)/0.1 M KCl. The pellet was resuspended in 0.5 volumes of buffer C/0.1 M KCl/1 mM DTT/Protease inhibitors (Roche) and frozen drop-wise in liquid nitrogen. Frozen drops of cells were crushed using a freezer mill (SPEX CertiPrep 6850 Freezer/Mill) with 6 cycles of 2 min crushing at rate 15. Frozen cell powder was thawed at room temperature, resuspended in 1 volume of buffer C/0.1 M KCl/1 mM DTT/protease inhibitors, and the concentration of KCl was adjusted to 0.5 M. The suspension was centrifuged for one hour at 50,000 r.p.m. using a Ti70.1 rotor. The clear phase was recovered, and subjected to calmodulin affinity purification by adding 2 mM CaCl<sub>2</sub> and 1.5 ml of packed beads of Calmodulin affinity resin (Stratagene). After 3 h at 4 °C, beads were collected, washed with 10 BVs of buffer C/0.3 M KCl/2 mM CaCl<sub>2</sub>/2 mM β-mercaptoethanol. Elution was performed with buffer C/0.3 M KCl/2 mM EGTA/1 mM EDTA/2 mM β-mercaptoethanol, peak fractions were pooled and subjected to fractionation over a Superdex 200 10/300 GL column (GE Healthcare), pre-equilibrated in buffer C/0.15 mM KCl/2 mM β-mercaptoethanol. Fractions containing ORC were pooled and concentrated

over a 1 ml MonoQ 5/50 GL column (GE Healthcare) using an elution gradient of 0.15–0.5 M KCl over 10 column volumes. Peak fractions containing ORC were pooled, dialysed against buffer C/0.3 M K-acetate and stored in aliquots.

**Purification of ORC( $\Delta 6$ ) from ySD-ORC( $\Delta 6$ ).** To purify ORC without Orc6, a similar protocol to the purification of ORC was followed, except that Flag immunoprecipitation of endogenous Orc6 was included, to remove complexes containing Orc6 (Supplementary Fig. 9c). This was performed as follows: pooled fractions from the gel filtration were incubated for 30 min at 4 °C with 1 ml packed bead volume of anti-Flag M2 agarose (Sigma). Flow-through was collected and concentrated over a MonoQ 5/50 GL column (GE Healthcare), as described for the purification of ORC.

**Proteins expressed in bacteria.** All expression plasmids were transformed into BL21 DE3 Codon+ RIL cells (Stratagene) (unless indicated). 31 of cells (unless indicated) were grown at 37 °C to a density of  $D_{600\text{ nm}} = 0.5\text{--}0.8$ . Cells were chilled on ice, and then IPTG was added to 1 mM. Induction was carried out overnight at 18 °C.

**Purification of MBP–Mcm3.** 0.5 l of cells expressing MBP–Mcm3 were grown as described above. Cells were collected, washed once with ice-cold 25 mM HEPES-KOH pH 7.6/1 M sorbitol, once with buffer D (50 mM Tris-HCl pH 7.5, 0.05% NP-40, 10% glycerol)/1 M NaCl and then the pellet was resuspended in 20 ml of buffer D/1 M NaCl/2 mM  $\beta$ -mercaptoethanol/protease inhibitors (Roche). 50  $\mu$ l of lysozyme (50 mg ml<sup>-1</sup>) was added and the suspension incubated for 20 min at 4 °C. Cells were kept on ice and sonicated 3  $\times$  30 s at 15 microns using a sonicator Soniprep 150 (Sanyo). Lysate was centrifuged for 1 h at 45,000 r.p.m. using a Ti45 rotor (235,400g). The soluble phase was collected and incubated with 2 ml packed amylose bead volume (NEB) at 4 °C for 1 h. Beads were washed with ten BVs of buffer D/0.3 M NaCl/2 mM  $\beta$ -mercaptoethanol. Elution was performed with buffer D/0.3 M NaCl/2 mM  $\beta$ -mercaptoethanol/10 mM maltose. Peak fractions were pooled and 0.5 ml were subjected to fractionation over a Superdex 200 10/300 GL column (GE Healthcare) pre-equilibrated in buffer D/0.3 M NaCl/2 mM  $\beta$ -mercaptoethanol. The peak fraction, of correct molecular weight, was collected and subjected to PreScission protease cleavage with 100 units of PreScission protease (GE healthcare). After 30 min at room temperature, 1 volume of buffer D/2 mM  $\beta$ -mercaptoethanol was added, and the sample was fractionated over a 0.15 ml MonoQ PC1.6/5 column (GE Healthcare), using an elution gradient of 0.15–0.7 M NaCl over 50 column volumes. Peak fractions containing untagged Mcm3 proteins were kept. The same protocol was used to purify Mcm3 fragments and mutants.

**Purification of Mcm2, Mcm7 and Mcm3.** To purify these proteins, we followed the protocol described in ref. 31. The starting cultures were 3 l in volume.

**Purification of Mcm5.** Cells were grown and expressed as described above. Cells were collected, washed once with ice-cold 25 mM HEPES-KOH pH 7.6/1 M sorbitol, once with buffer E (50 mM Tris-HCl pH 7.5, 0.05% NP-40, 10% glycerol, 1 mM EDTA and 1 mM DTT)/1 M NaCl, and the pellet was resuspended in 40 ml of buffer E/1 M NaCl/protease inhibitors (Roche). Cells were sonicated and the lysate centrifuged as described for the purification of MBP–Mcm3. The soluble fraction from centrifugation was treated with 0.3 g ml<sup>-1</sup> ammonium sulphate, and stirred for 20 min at 4 °C. The mixture was centrifuged at 17,000 r.p.m. (34,600g) for 20 min. The pellet was resuspended in 40 ml of buffer E containing 0.25 g ml<sup>-1</sup> of ammonium sulphate and centrifuged as before. This was repeated with 0.20 mg ml<sup>-1</sup> ammonium sulphate. The pellet was resuspended in 30 ml of buffer E and dialysed against buffer E for one hour at 4 °C. After checking that the conductivity of the sample was below that of buffer E/0.1 M NaCl, the sample was applied to a 5 ml FF Q column (GE Healthcare), pre-equilibrated in buffer E/0.1 M NaCl. Elution was done using a gradient of 0.1 M to 0.5 M NaCl over 10 column volumes. Peak fractions were pooled and diluted down to a conductivity below that of buffer E/0.1 M NaCl. The sample was then applied to a 5 ml Heparin column (GE healthcare) pre-equilibrated in buffer E/0.1 M NaCl. Flow through was collected and subjected to fractionation over an 8 ml MonoQ column (GE Healthcare). Elution was performed using a gradient of 0.1 M to 0.5 M NaCl over 20 column volumes. Peak fractions were collected and subjected to fractionation over a Superdex 200 10/300 GL column (GE Healthcare) pre-equilibrated with buffer E/0.3 M NaCl. Peak fractions were pooled, concentrated using a Microcon YM-10, 10000 MWCO (Millipore) and aliquoted.

**Purification of Mcm4.** 3 l of expressing cells were grown and we followed the purification process described in ref. 31. At the end of the described protocol, we introduced an extra gel filtration step using a Superdex 200 10/300 GL column (GE Healthcare), pre-equilibrated in buffer E/0.3 M NaCl.

**Purification of Mcm6.** To purify Mcm6, the same protocol as that described for Mcm5 was followed, the difference being that Mcm6 was bound to a 5 ml heparin column (GE Healthcare). Bound protein was eluted using a gradient of 0.1 to 0.5 M NaCl over 20 column volumes. Peak fractions were pooled and the conductivity was reduced to below that of buffer E/0.1 M NaCl. The sample

was then applied to an 8 ml MonoQ column (GE Healthcare), as described in the purification of Mcm5.

**Purification of Cdt1.** Expressing cells were grown and induced as described before. Cells were collected, washed with PBS pH 7.5, and then washed with buffer F (PBS pH 7.5, 10% glycerol, 1 mM DTT and 0.3 M NaCl). The pellet was resuspended in 40 ml of buffer F/protease inhibitors (Roche) and sonicated 3  $\times$  30 s using a sonicator Soniprep 150 (Sanyo) at 15 microns. Lysate was centrifuged at 45,000 r.p.m. (235,400g) for 60 min using a Ti45 rotor. 2 ml of packed bead volume glutathione Sepharose 4Fast Flow (GE Healthcare) were added to the soluble phase and incubated for 2.5 h at 4 °C. The solution was centrifuged at 3,000 r.p.m. (1,400g) for 3 min, beads were collected, 10 column volumes of buffer F were added, and the mixture was incubated for 10 min at 4 °C. This wash step was repeated with 20 column volumes of buffer F, and 10 column volumes of buffer E/0.3 M NaCl. The pellet was then resuspended in 2 ml of buffer E/0.3 M NaCl. 125 units of PreScission Protease (GE Healthcare) were added and the mixture was incubated overnight at 4 °C. The flow through was collected and concentrated using a Microcon YM-10, 10000 MWCO (Millipore), then the sample was loaded onto a gel filtration column (Superdex 200 10/300 GL column (GE Healthcare)) pre-equilibrated in buffer B/1 mM EDTA/1 mM DTT/0.3 M NaCl. Peak fractions were pooled, concentrated and aliquoted.

**Formation of MCM complexes from individually purified subunits.** MCM complexes were formed by combining 10  $\mu$ g of individually purified subunits and fractionated over a Superdex 200 PC 3.2/30 column (GE Healthcare), pre-equilibrated in buffer B/0.1 M K acetate. High molecular weight fractions containing Cdt1–Mcm2–7 complex were pooled, concentrated and aliquoted. Supplementary Fig. 12 shows that this complex can be loaded as efficiently as the complex purified from yeast.

**Purification of GST–Cdc6.** This protocol is modified from that described in ref. 10. 1 l of expressing cells were grown at 37 °C to  $D_{600\text{ nm}} = 0.6$ , then induced with 0.5 mM IPTG for 5 h at 18 °C. Cells were collected at 6,000 r.p.m. (6,100g) in an SLA-3000 rotor (Sorvall) for 10 min. Pellets were resuspended in 50 ml buffer G (50 mM K<sub>2</sub>HPO<sub>4</sub>/KH<sub>2</sub>PO<sub>4</sub>, pH 7.5, 5 mM MgCl<sub>2</sub>, 1% Triton X-100 and 1 mM DTT)/2 mM ATP/0.15 M KOAc/protease inhibitors (Roche) and 100  $\mu$ g ml<sup>-1</sup> lysozyme added. The mixture was incubated at 4 °C for 30 min and sonicated for 2 min (5 s off, 5 s on) at 15 microns. The suspension was centrifuged at 15,000 r.p.m. (27,000g) for 15 min in a SS34 rotor (Sorvall) and the supernatant transferred to 2 ml bed resin glutathione Sepharose (GE Healthcare). This was rotated at 4 °C for 3 h. Glutathione beads and bound proteins were recovered and washed with 20 column volumes of buffer G/0.15 M KOAc/2 mM ATP. A 50% slurry with buffer G/0.15 M KOAc/2 mM ATP was made and 100 units preScission protease (GE Healthcare) added. The mixture was incubated for 2 h at 4 °C. The flow-through was recovered and the concentration of KOAc diluted to 75 mM with buffer G/2 mM ATP. This was incubated with 2 ml bed resin hydroxyapatite prewashed in buffer G/0.075 M KOAc/2 mM ATP. The protein–hydroxyapatite was washed with 5 BVs of buffer G/2 mM ATP and then washed with 5 BVs of buffer G/0.15 M KOAc/15% glycerol. Cdc6 was eluted with buffer G/0.4 M KOAc/15% glycerol. Peak fractions were pooled and concentrated using a Centricon Plus-20 Centrifugal Filter (Millipore), then aliquoted.

**Purification of ORC-P.** To purify CDK-phosphorylated ORC (ORC-P), ORC was isolated from 50 l of alpha-factor-arrested G1 yeast (YDR11) cells via calmodulin pull-down as described<sup>8</sup>, incubated with TEV protease overnight at 4 °C to remove the tag, dialysed against 25 mM HEPES-KOH pH 7.6/0.1 M KCl/5 mM Mg(OAc)<sub>2</sub>/0.02% NP40/10% glycerol/1 mM DTT, and concentrated to a final volume of 2 ml.

In a parallel preparation, 50 l of YDR12 (*MATa ade2-1 ura3-1 his3-11,15 trp1-1 leu2-3,112 can1-100 cdc15-2 bar1::kanMX pep4::HIS3 ura3::Pgall,10-CDC6-TAPtcp (URA3)*) were grown at 25 °C in YP-rafinosse to 2  $\times$  10<sup>7</sup> cells per ml. Cdc6–TAP<sup>TCP</sup> expression was induced by addition of 2% galactose for 8 h at 25 °C, upon which the cells arrest with a long-budded phenotype and with replicated DNA in G2/M phase. The cells were collected by centrifugation, washed twice with cold buffer containing 25 mM HEPES-KOH pH 7.6/1 M sorbitol, once with cold buffer containing 45 mM HEPES-KOH pH 7.6/0.1 M KCl/0.02% NP-40/10% glycerol, resuspended in 0.5 volume of packed cell volume of buffer containing 45 mM HEPES-KOH pH 7.6/0.1 M KCl/0.02% NP-40/10% glycerol/2 mM DTT/2 $\times$  complete protease inhibitor cocktail (Roche), and the resulting cell suspension frozen drop-wise directly in liquid nitrogen. The frozen cell suspension was crushed using a SPEX 6870 Freezer/Mill, the resulting frozen powder thawed on ice, diluted with 1 volume of 45 mM HEPES-KOH pH 7.6/0.1 M KCl/0.02% NP-40/10% glycerol/1 mM DTT, the salt concentration adjusted to 0.3 M KCl, and the resulting lysate clarified by centrifugation in a Beckman 45 Ti rotor at 42,000 r.p.m. (205,000g) for 1 h. The clarified extract was supplemented with 2 mM CaCl<sub>2</sub>, and a complex containing Cdc6–TAP<sup>TCP</sup>–Cib2–Cdc28–Cks1 was isolated from this extract using calmodulin affinity

purification in buffer containing 45 mM HEPES-KOH pH 7.6/0.3 M KCl/0.02% NP-40/10% glycerol/1 mM DTT. This partially purified complex was incubated with TEV protease overnight at 4 °C to remove the tag from Cdc6, dialysed against 25 mM HEPES-KOH pH 7.6/0.1 M KCl/5 mM Mg(OAc)<sub>2</sub>/0.02% NP40/10% glycerol/1 mM DTT, and concentrated to a final volume of 2 ml.

The concentrated calmodulin-purified and TEV-protease-digested ORC and Cdc6-Clb2-Cdc28-Cks1 fractions were combined, supplemented with 3 mM ATP, and incubated for 45 min at 30 °C. The phosphorylated ORC (ORC-P) resulting from this reaction was re-isolated from the reaction by gel-filtration on a 120 ml Superdex 200 column in a buffer containing 25 mM HEPES-KOH pH 7.6/0.1 M KCl/0.02% NP40/10% glycerol/1 mM DTT, followed by fractionation on a 1 ml MonoQ ion-exchange column as described<sup>8</sup>.

**Loading reaction.** In this study, four main differences to the conditions described in ref. 7 were introduced in the loading reactions. K-glutamate was substituted with K-acetate in the binding and washing buffers. For silver staining purposes we increased the amount of protein used in the assays by four fold compared to ref. 7. In addition, ARS305 was amplified using an oligonucleotide primer with a photocleavable biotin (Integrated DNA technologies) at one end, as described in ref. 32. We have optimised the photocleavage to minimise DNA damage by irradiating for 10 min at 330 nm (See Supplementary Fig. 11). And finally, 2.5 pmol of DNA molecules have been used, instead of the 1 pmol used before.

**Loading assays with ORC and ORC-P.** Mcm2-7 loading onto immobilized linear 1 kb ARS305-containing DNA using 50 nM purified ORC or ORC-P was performed as described<sup>8</sup>. To test the effect of ORC-P dephosphorylation by lambda-phosphatase, 20 pmol of purified ORC-P at a concentration of 0.67 mM was supplemented with 20 mM MnCl<sub>2</sub>, and incubated for 20 min at 30 °C with either 400 units of l-phosphatase (NEB) or a buffer control before addition of the treated ORC-P to the loading reaction.

**ATPase assays.** Based on the method described in ref. 26 with the following modifications. Reactions were carried out at 30 °C for 20 min, buffer contained 25 mM HEPES-KOH, pH 7.6/0.1% NP-40/5 mM Mg(OAc)<sub>2</sub>/1 mM EDTA/1 mM EGTA/100 mM K-acetate/5% glycerol/1 mM DTT/100 μM ATP (including 2.5 μCi of [ $\alpha$ -<sup>32</sup>P]ATP). Each reaction contained 2.5 pmol of 1 kb linear

ARS305 DNA. Where indicated, 2.5 pmol of each protein were also included in these reactions. Reactions were stopped by spotting 1 μl of each reaction on PEI-cellulose TLC plates (CamLab). The cellulose membrane was developed in 0.6 M Na<sub>2</sub>HPO<sub>4</sub>/NaH<sub>2</sub>PO<sub>4</sub> pH 3.5, and quantified on a Phosphorimager (GE Healthcare).

**Antibodies for western blot analysis.** Anti-Mcm2 (yN-19, sc-6680, Santa Cruz), anti-Mcm7 (yN-19, sc-6688, Santa Cruz), anti-Mcm4 (yC-19, sc-6685, Santa Cruz), anti-Mcm5 (yC-19, sc-6687, Santa Cruz), anti-Orc6 (SB49), anti-Cdc6 (98H/5), anti-Cdt1<sup>33</sup>, anti-Flag M2-peroxidase (Sigma), anti-PAP (peroxidase-anti-peroxidase)-HRP (horseradish peroxidase) (Sigma), anti-MBP (maltose binding protein)-HRP (NEB). Antibodies against Mcm6 and Mcm3 were gifts from the Labib laboratory<sup>34</sup>.

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