ELSEVIER

Contents lists available at ScienceDirect

# **Biochemical and Biophysical Research Communications**

journal homepage: www.elsevier.com/locate/ybbrc



# Essential role of Chk1 in S phase progression through regulation of RNR2 expression

Hiromichi Naruyama <sup>a,b</sup>, Midori Shimada <sup>a</sup>, Hiroyuki Niida <sup>a</sup>, Doaa H. Zineldeen <sup>a</sup>, Yoshihiro Hashimoto <sup>b</sup>, Kenjiro Kohri <sup>b</sup>, Makoto Nakanishi <sup>a,\*</sup>

# ARTICLE INFO

Article history: Received 24 June 2008 Available online 9 July 2008

Keywords: Cell cycle Ribonucleotide reductase Chk1 Transcription DNA replication

#### ABSTRACT

Chk1 is an essential kinase for maintaining genome integrity and cell cycle checkpoints through phosphorylating several downstream targets. Recently, we demonstrated that Chk1 is also required for cell proliferation in somatic cells under unperturbed condition through regulating transcription of several genes. Here, we show that Chk1 is required for S phase progression and RNR2 is a critical downstream target of genes transcriptionally regulated by Chk1. Hence, although RNR2 expression reached maximum at S phase in the presence of Chk1, Chk1 depletion arrested the cell cycle at S phase and reduced RNR2 expression at both mRNA and protein levels. Ectopic expression of RNR2 failed to rescue the S phase arrest observed in Chk1 depleted cells, suggesting the presence of an additional Chk1-target(s) for completion of S phase other than RNR2. Therefore, our results suggest that Chk1 is required for DNA replication at least through regulating RNR2 gene transcription.

© 2008 Elsevier Inc. All rights reserved.

Progression through the cell cycle is regulated carefully to avoid proliferation or mitosis when adverse conditions exist, such as DNA damage and DNA replication fork stalling [1-3]. Abnormal DNA structures are rapidly sensed and transduced to mediators by either the ATR or ATM PI3-kinase related protein kinases (PIKK) [4,5]. One such mediator is Chk1 kinase that is essential for cell cycle arrest upon DNA damage or DNA replication fork stalling through phosphorylating Cdc25 phosphatases [6,7]. In addition to its role as a checkpoint mediator, Chk1 is a constitutively active enzyme and associates with chromatin under unperturbed condition [8,9]. Chk1 phosphorylates histone H3 at threonine 11 (T11) around the promoter regions of cell cycle regulatory genes including cyclin B1 and Cdk1 [10], which accelerate recruitment of GCN5 histone acetyltransferase and subsequent acetylation at lysine 9 (K9) [11]. Increased acetylation of K9 leads to transcriptional activation.

Ribonucleotide reductase (RNR) is essential for de novo synthesis of deoxyribonucleotides (dNTPs), which are required for DNA replication and repair [12,13]. Most eukaryotic RNRs are composed of two essential and non-identical homodimeric subunits, a large subunit (R1) and a small subunit (R2) [12,14]. The former

E-mail address: mkt-naka@med.nagoya-cu.ac.jp (M. Nakanishi).

subunit contains the catalytic site and allosteric regulatory site for both enzyme activity and specificity by binding nucleotide triphosphates [12]. The latter subunit contains a non-heme iron center essential for catalysis. p53-Inducible R2 (53R2) [15], a homologous R2 protein, is also capable of forming an active RNR complex together with the R1 protein [16].

In mammalian cells, the transcription of the R1 and R2 genes is cell cycle dependent, being undetectable in G0/G1 and maximum in S phase [17,18]. The S phase-specific expression of R1 genes is characterized as four different promoter elements, b, a, Inr, and g [19]. Although transcription factor YY1 binds to b and a elements, the cell cycle specific expression is mainly regulated via Inr and g elements. In contrast to R1, the S phase specific expression of R2 is relatively complicated. In mouse cells, S phase-specific transcription of R2 gene requires a repressive E2F-binding site and a promoter-activating region [20]. Interestingly, mutation of the E2F-binding site leads to premature promoter activation in G1 and increase promoter activity. Given that the R1 protein has a long half-life, and its level is apparently constant [21,22] and that the R2 protein is rapidly degraded in mitosis by APC-C [23,24], RNR activity and thus DNA replication are mainly dependent on the level of R2 protein.

In this study, we found that Chk1 depletion results in incomplete S phase, suggesting that Chk1 may be required for transcription of some essential genes for DNA replication. To address this question, we examined changes in the transcription of known genes involved in S phase progression after Chk1 depletion in MEFs. Only

<sup>&</sup>lt;sup>a</sup> Department of Cell Biology, Graduate School of Medical Sciences, Nagoya City University, 1 Kawasumi, Mizuho-cho, Mizuho-ku, Nagoya 467-8601, Japan

<sup>&</sup>lt;sup>b</sup> Department of Urology, Graduate School of Medical Sciences, Nagoya City University, 1 Kawasumi, Mizuho-cho, Mizuho-ku, Nagoya 467-8601, Japan

<sup>\*</sup> Corresponding author. Address: Department of Cell Biology, Graduate School of Medical Sciences, Nagoya City University, Kawasumi, Mizuho-cho, Mizuho-ku, Nagoya 467-8601, Japan. Fax: +81 52 842 3955.

RNR2 among genes tested was drastically reduced following loss of Chk1. Therefore, our results suggest an essential function of Chk1 in DNA replication at least through activating RNR2 gene transcription.

### **Materials and methods**

*Cells and culture condition.* Chk1<sup>flox/-</sup> MEFs were generated as described previously [10] and were cultured in DMEM supplemented with 10% FBS.

Immunoblotting. Cells were lysed as described previously [10], and extracts were subjected to immunoblotting using anti-Chk1 (sc8408; Santa Cruz), anti-RNR2 (sc10844; Santa Cruz), anti-RNR1 (sc11733; Santa Cruz) antibodies.

Northern blotting. Total RNA was extracted using ISOGEN (Wako) and northern blotting was performed as described previously [25]. <sup>32</sup>P-labeled fragment of RNR2 and RNR1 was used as a probe.

Cell cycle analysis. Cells were incubated with  $10\,\mu M$  BrdU for  $30\,min$ , harvested, washed once in PBS and fixed with in 70% ethanol. Cells were prepared for FACS analysis as described previously [26].

Real time PCR. Real-time PCR was carried out with single-stranded cDNAs prepared with the SuperScript First-Strand Synthesis System (Invitrogen, Carlsbad, CA, USA). Briefly, total RNA from each sample after transfection was reverse-transcribed with Oligo-DT primer. PCR reactions were performed with Power SYBR Green PCR Master Mix and 7500 Fast Real-Time PCR System (Applied Biosystems, Foster City, CA, USA). Seuence-Specific primers were designed by Primer3 software (http://frodo.wi.mit.edu/cgi-bin/primer3/primer3\_www.cgi) as follows; GAPDH, AAC TTTGGCATTGTGGAAGG and GGATGCAGGGATGATGTTCT, Asf1, CAG GCCATTTTACCTTCAGC and GGCTGAGCTTGTTTCTGGAC, MCM4,

GACCCTCAGGATGAGGCATA and GGGGCATGATGGTACTATGG, Cdc25C. AAAGACAGGGCTCTGAACCA and TGGTGAAGCATGGGAC AGTA. RNR1. GGTCGTGTCCGAAAAGTTGT and GTTCTGCTGGTTG CTCTTCC RNR2, CGTTGTCTTTCCCATCGAGT and CTCTCATCGGG TTTCAGAGC, Cdc7, GCCCTGCAGAGAAACTCATC and GTTTCCCTC ATCACGCTGTT, Cdc6, TTTCGGAAGTTGATGGGAAC and GGGTCAA AAGCAGCAAAGAG Orc1, ACTGCCATACCCAACCATGT and CAGCA CGTCATTCTGGCTAA, Orc2, TTTGTGCCTTCCTTTTCTGC and CCCA AG CCATAAAGCACAAT, Wee1, GAGAGCTGGAGGACGACTTG and CAGAA AGTAGGCGGTCGAAG, Cdc45, GTTCCTGCCTACGACGACAT and CTC TTCCTGTTTCGCTCCAC. GAPDH primer was used as an internal control. Real-Time PCR was carried out, in duplicate, by 40 cycles of 95°C for 10 sec and 60°C for 1 min. Productions of the expected amplification fragments without unanticipated products and primers were confirmed by melting-curve analysis. To determine the relative amounts of the products, we used the comparative Ct (threshold cycle) method according to the instructions supplied by Applied Biosystems. Conventional PCR was performed with the Ex-Taq system (Takara Bio Inc., Shiga, Japan).

Immunohistochemical analysis. Chk1flox/— MEFs were infected with adenoviruses expressing either Cre or LacZ (negative control). Immunohistochemical analyses using anti-RNR1 and anti-RNR2 antibodies were performed as described previously [9].

#### Results and discussion

Loss of Chk1 resulted in incomplete DNA replication

Recent findings that Chk1 is a histone H3-T11 kinase unravel a mechanism underlying DNA damage-induced transcriptional repression. In this concept, Chk1 is an essential for transcription of some genes under unperturbed condition. Actually, Chk1 depletion in

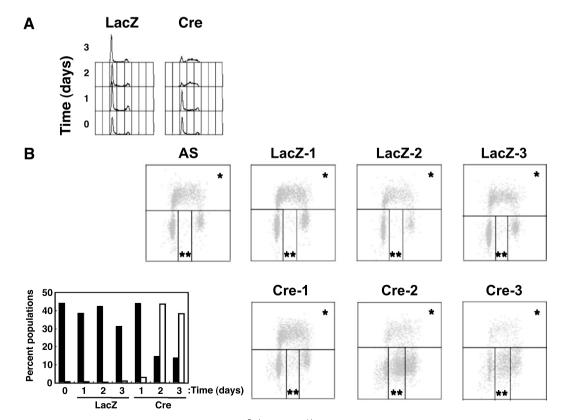


Fig. 1. Chk1 depleted MEFs show S phase arrest. (A) Cell cycle profile of Chk1<sup>flox/-</sup> and Chk1<sup>Δ/-</sup> MEFs at the indicated days after adenoviral infection. (B) Chk1<sup>flox/-</sup> MEFs were treated with 10 μM BrdU for 30 min before cells were harvested at the time indicated after infection and analysed by FACS. The percentages of BrdU positive (\*) and negative (\*\*) cells are shown as a graph (black: BrdU positive; white: BrdU negative).

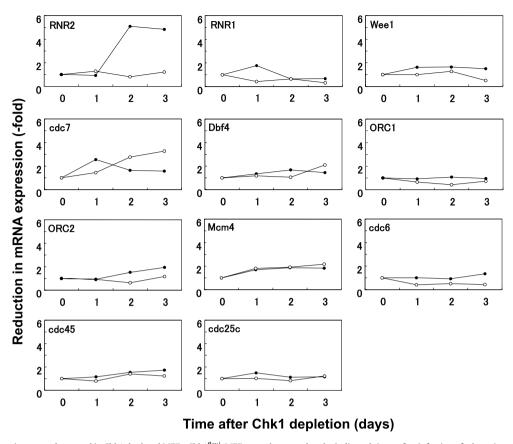
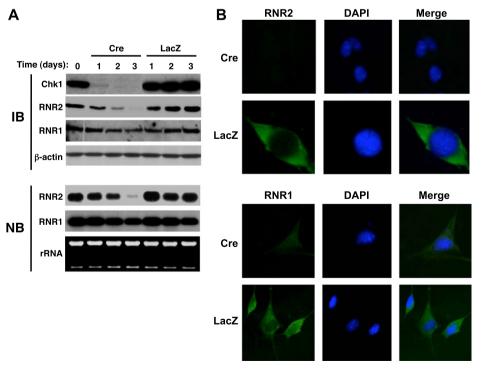


Fig. 2. RNR2 mRNA transcripts were decreased in Chk1 depleted MEFs. Chk1<sup>flox/-</sup> MEFs were harvested at the indicated times after infection of adenoviruses expressing LacZ (open circles) or Cre (closed circles) and their total RNA was extracted. After treatment with reverse transcriptase using random primers, real time PCR was performed using their specific primers to measure the transcripts involved in DNA replication or cell cycle control. The results are presented as a fold-reduction of controls (before infection of adenoviruses).



**Fig. 3.** Specific reduction in RNR2 protein in Chk1 depleted MEFs. Chk1<sup>flox/-</sup> MEFs were harvested at the indicated times after infection of adenoviruses expressing LacZ or Cre. The resultant whole cell extracts and total RNA were prepared and subjected to immunoblotting (IB) using the indicated antibodies or northern blotting (NB) analysis using RNR2 or RNR1 probes. (B) Immunohistochemical analysis of RNR2 and RNR1 in Chk1 depleted cells. Chk1<sup>flox/-</sup> MEFs were infected with adenoviruses expressing either LacZ or Cre. Three days after infection the resultant cells were fixed and stained with anti-RNR2 or anti-RNR1 antibodies. Cells were also counterstained with DAPI.

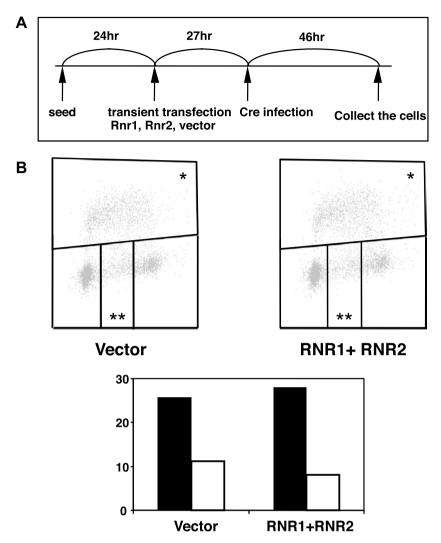


Fig. 4. Ectopic expression of RNR2 and RNR1 is insufficient for complement S phase arrest in Chk1 depleted MEFs. (A) Time course strategy for transient transfection of RNR2 and RNR1, and Chk1 depletion by Ade-Cre infection. (B) BrdU staining and FACS analysis were performed as indicated in Fig. 1. The percentages of each cell cycle distribution were also shown (black: BrdU positive; white: BrdU negative).

somatic cells by infection of adenoviruses expressing Cre reduced expression of more than 200 transcripts [10]. Therefore, increased S phase population in Chk1 depleted MEFs (Fig. 1A) are likely due to S phase arrest but not enhanced initiation of DNA replication. To address this question, we first examined BrdU incorporation in Chk1 depleted MEFs. After infection of adenoviruses expressing Cre, Chk1 del/- MEFs were incubated with culture medium containing  $10\,\mu\text{M}$  BrdU for  $30\,\text{min}$ . Cells were then fixed, immunostained with anti-BrdU antibodies, and analyzed by FACScan. As shown in Fig. 1B, majority of S phase cells in control MEFs were BrdU positive and infection of adenoviruses expressing LacZ did not affect cell cycle progression. In contrast, although most of S phase cells in Chk1 del/- MEFs were BrdU positive at 1 day after adenoviral infection, they became negative at two days or thereafter, indicating that increased S phase population is due to S phase arrest.

Transcriptional changes in genes involved in DNA replication after Chk1 depletion

We next examined the changes in the expression of genes involved in DNA replication after Chk1 depletion. Quantitative real time PCR revealed that the expression of RNR2, but not RNR1, was significantly reduced at two days after Chk1 depletion, whereas those of the other genes tested were almost constant during this experi-

mental period (Fig. 2). Given that expression of many genes involved in RNR2, ASK, ORC1, cdc6, and cdc25c were dependent on the functional E2Fs [20,27–30], reduction in RNR2 expression was not likely due to the impairment of E2F functions. In addition, because RNR2 expression is cell cycle dependent, reaching at a maximum at S phase [20], decreased expression of RNR2 did not solely reflect the changes in cell cycle profile following Chk1 depletion (Fig. 1A).

The reduction in RNR2 protein as well as its mRNA was also confirmed by northern blotting, immunoblotting, and immunohistochemistry using specific antibodies to RNR2, respectively (Fig. 3A and B). The reduction in RNR2 protein was obvious at two days after Chk1 depletion, supporting the observation that S phase arrest in Chk1 depleted cells was detected at two days after infection. RNR2 was predominantly localized at cytoplasm and RNR1 was localized at both cytoplasm and nucleus, consistent with the previous reports [12], but signal of RNR2, but not RNR1, was almost disappeared after Chk1 depletion. Thus, S phase arrest following Cre infection appeared to be correlated well with the reduction in RNR2 protein.

Ectopic expression of RNR2 is not sufficient for complement S phase arrest in  $Chk1^{del/-}$  MEFs

We finally asked whether ectopic expression could reverse the S phase arrest in Chk1<sup>del/-</sup> MEFs. Experimental protocols were summarized in Fig. 4A. In brief, MEFs were transfected with both expression vectors for RNR1 and RNR2 and then infected with Cre. Forty six hours after infection, cells were incubated with the medium containing 10 µM BrdU and analyzed by FACScan. As shown in Fig. 4B, coexpression of RNR1 and RNR2 was not capable of reducing BrdU negative S phase population. These results suggests that ectopic expression of RNR1 and RNR2 is not sufficient for rescue the S phase arrest in Chk1 deficient MEFs and thus existence of unidentified transcriptional targets of Chk1 which is essential for completion of DNA replication. Clearly, additional work is necessary to clarify those Chk1 targets and their role in S phase progression.

## Acknowledgments

We thank Dr. Yamada-Namikawa for discussion and technical assistance. This work was supported in part by the Ministry of Education, Science, Sports, and Culture of Japan through a Grant-in-Aid for Scientific Research (B) awarded to M.N.

#### References

- M. Nakanishi, M. Shimada, H. Niida, Genetic instability in cancer cells by impaired cell cycle checkpoints, Cancer Sci. 97 (2006) 984–989.
- [2] M. Shimada, M. Nakanishi, DNA damage checkpoints and cancer, J. Mol. Histol. 37 (2006) 253–260.
- [3] J.W. Harper, S.J. Elledge, The DNA damage response: ten years after, Mol. Cell. 28 (2007) 739–745.
- [4] R.T. Abraham, Cell cycle checkpoint signaling through the ATM and ATR kinases, Genes Dev. 15 (2001) 2177–2196.
- [5] Y. Shiloh, ATM and related protein kinases: safeguarding genome integrity, Nat. Rev. Cancer 3 (2003) 155–168.
- [6] Y. Sanchez, C. Wong, R.S. Thoma, R. Richman, Z. Wu, H. Piwnica-Worms, S.J. Elledge, Conservation of the Chk1 checkpoint pathway in mammals: linkage of DNA damage to Cdk regulation through Cdc25, Science 277 (1997) 1497– 1501
- [7] C.Y. Peng, P.R. Graves, R.S. Thoma, Z. Wu, A.S. Shaw, H. Piwnica-Worms, Mitotic and G2 checkpoint control: regulation of 14-3-3 protein binding by phosphorylation of Cdc25C on serine-216, Science 277 (1997) 1501–1505.
- [8] V.A. Smits, P.M. Reaper, S.P. Jackson, Rapid PIKK-dependent release of Chk1 from chromatin promotes the DNA-damage checkpoint response, Curr. Biol. 16 (2006) 150–159.
- [9] H. Niida, Y. Katsuno, B. Banerjee, M.P. Hande, M. Nakanishi, Specific role of Chk1 phosphorylations in cell survival and checkpoint activation, Mol. Cell. Biol. 27 (2007) 2572–2581.
- [10] M. Shimada, H. Niida, D.H. Zineldeen, H. Tagami, M. Tanaka, H. Saito, M. Nakanishi, Chk1 is a Histone H3 Threonine 11 kinase that regulates DNA damageinduced transcriptional repression, Cell 132 (2008) 221–232.
- [11] J.E. Brownell, J. Zhou, T. Ranalli, R. Kobayashi, D.G. Edmondson, S.Y. Roth, C.D. Allis, Tetrahymena histone acetyltransferase A: a homolog to yeast Gcn5p linking histone acetylation to gene activation. Cell 84 (1996) 843–851.
- [12] P. Nordlund, P. Reichard, Ribonucleotide reductases, Annu. Rev. Biochem. 75 (2006) 681–706.

- [13] A. Chabes, B. Georgieva, V. Domkin, X. Zhao, R. Rothstein, L. Thelander, Survival of DNA damage in yeast directly depends on increased dNTP levels allowed by relaxed feedback inhibition of ribonucleotide reductase, Cell 112 (2003) 391–401.
- [14] J. Stubbe, J. Ge, C.S. Yee, The evolution of ribonucleotide reduction revisited, Trends Biochem. Sci. 26 (2001) 93–99.
- [15] H. Tanaka, H. Arakawa, T. Yamaguchi, K. Shiraishi, S. Fukuda, K. Matsui, Y. Takei, Y. Nakamura, A ribonucleotide reductase gene involved in a p53-dependent cell-cycle checkpoint for DNA damage, Nature 404 (2000) 42–49.
- [16] O. Guittet, P. Hakansson, N. Voevodskaya, S. Fridd, A. Graslund, H. Arakawa, Y. Nakamura, L. Thelander, Mammalian p53R2 protein forms an active ribonucle-otide reductase in vitro with the R1 protein, which is expressed both in resting cells in response to DNA damage and in proliferating cells, J. Biol. Chem. 276 (2001) 40647–40651.
- [17] S. Bjorklund, S. Skog, B. Tribukait, L. Thelander, S-phase-specific expression of mammalian ribonucleotide reductase R1 and R2 subunit mRNAs, Biochemistry 29 (1990) 5452–5458.
- [18] M. Hengstschlager, I. Mudrak, E. Wintersberger, E. Wawra, A common regulation of genes encoding enzymes of the deoxynucleotide metabolism is lost after neoplastic transformation, Cell Growth Differ. 5 (1994) 1389–1394.
- [19] E. Johansson, K. Hjortsberg, L. Thelander, Two YY-1-binding proximal elements regulate the promoter strength of the TATA-less mouse ribonucleotide reductase R1 gene, J. Biol. Chem. 273 (1998) 29816–29821.
- [20] A.L. Chabes, S. Bjorklund, L. Thelander, S Phase-specific transcription of the mouse ribonucleotide reductase R2 gene requires both a proximal repressive E2F-binding site and an upstream promoter activating region, J. Biol. Chem. 279 (2004) 10796–10807.
- [21] S. Eriksson, A. Graslund, S. Skog, L. Thelander, B. Tribukait, Cell cycle-dependent regulation of mammalian ribonucleotide reductase. The S phase-correlated increase in subunit M2 is regulated by de novo protein synthesis, J. Biol. Chem. 259 (1984) 11695–11700.
- [22] Y. Engstrom, S. Ériksson, I. Jildevik, S. Skog, L. Thelander, B. Tribukait, Cell cycle-dependent expression of mammalian ribonucleotide reductase. Differential regulation of the two subunits, J. Biol. Chem. 260 (1985) 9114–9116.
- [23] A. Chabes, L. Thelander, Controlled protein degradation regulates ribonucleotide reductase activity in proliferating mammalian cells during the normal cell cycle and in response to DNA damage and replication blocks, J. Biol. Chem. 275 (2000) 17747–17753.
- [24] A.L. Chabes, C.M. Pfleger, M.W. Kirschner, L. Thelander, Mouse ribonucleotide reductase R2 protein: a new target for anaphase-promoting complex-Cdh1mediated proteolysis, Proc. Natl. Acad. Sci. USA 100 (2003) 3925–3929.
- [25] M. Shimada, C. Namikawa-Yamada, M. Nakanishi, H. Murakami, Regulation of Cdc2p and Cdc13p is required for cell cycle arrest induced by defective RNA splicing in fission yeast, J. Biol. Chem. 280 (2005) 32640–32648.
- [26] M. Zhu, R.S. Weiss, Increased common fragile site expression, cell proliferation defects, and apoptosis following conditional inactivation of mouse Hus1 in primary cultured cells, Mol. Biol. Cell 18 (2007) 1044–1055.
- [27] Z. Kherrouche, A. Blais, E. Ferreira, Y. De Launoit, D. Monte, ASK-1 (apoptosis signal-regulating kinase 1) is a direct E2F target gene, Biochem. J. 396 (2006) 547–556.
- [28] K. Ohtani, J. DeGregori, G. Leone, D.R. Herendeen, T.J. Kelly, J.R. Nevins, Expression of the HsOrc1 gene, a human ORC1 homolog, is regulated by cell proliferation via the E2F transcription factor, Mol. Cell. Biol. 16 (1996) 6977–6984.
- [29] K. Ohtani, A. Tsujimoto, M. Ikeda, M. Nakamura, Regulation of cell growthdependent expression of mammalian CDC6 gene by the cell cycle transcription factor E2F, Oncogene 17 (1998) 1777–1785.
- [30] U. Haugwitz, M. Wasner, M. Wiedmann, K. Spiesbach, K. Rother, J. Mossner, K. Engeland, A single cell cycle genes homology region (CHR) controls cell cycle-dependent transcription of the cdc25C phosphatase gene and is able to cooperate with E2F or Sp1/3 sites, Nucleic Acids Res. 30 (2002) 1967–1976.