

# Chromosome Translocation t(10;19)(q26;q13) in a CIC-sarcoma

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**Abstract.** *Background/Aim:* CIC-sarcomas are characterized by rearrangements of the capicua transcriptional repressor (CIC) gene on chromosome subband 19q13.2, generating chimeras in which CIC is the 5'-end partner. Most reported CIC-sarcomas have been detected using PCR amplifications together with Sanger sequencing, high throughput sequencing, and fluorescence in situ hybridization (FISH). Only a few CIC-rearranged tumors have been characterized cytogenetically. Here, we describe the cytogenetic and molecular genetic features of a CIC-sarcoma carrying a t(10;19)(q26;q13), a chromosomal rearrangement not previously detected in such neoplasms. *Materials and Methods:* A round cell sarcoma removed from the right thigh of a 57-year-old man was investigated by G-banding cytogenetics, FISH, PCR and Sanger sequencing. *Results:* The tumor cells had three cytogenetically related clones with the translocations t(9;18)(q22;q21) and t(10;19)(q26;q13) common to all of them. FISH with a BAC probe containing the CIC gene hybridized to the normal chromosome 19, to der(10)t(10;19), and to der(19)t(10;19). PCR using tumor cDNA as template together with Sanger sequencing detected two CIC::DUX4 fusion transcripts which both had a stop TAG codon immediately after the fusion point. Both transcripts are predicted to encode truncated CIC polypeptides lacking the carboxy terminal part of the native protein. This missing part is crucial for CIC's DNA

binding capacity and interaction with other proteins. *Conclusion:* In addition to demonstrating that CIC rearrangement in sarcomas can occur via the microscopically visible translocation t(10;19)(q26;q13), the findings in the present case provide evidence that the missing part in CIC-truncated proteins has important functions whose loss may be important in tumorigenesis.

According to the fifth edition of the World Health Organization classification of soft tissue and bone tumors, published in 2020, CIC-sarcoma is a high-grade, undifferentiated, round cell sarcoma characterized genomically by rearrangements of the capicua transcriptional repressor (CIC) gene on chromosome subband 19q13.2 with generation of fusions in which CIC is the 5'-end partner (1-4). The most common chimera, found in 95 % of the cases, stems from fusion of CIC with the double homeobox 4 gene (DUX4) (5, 6). Rare tumors have also been reported in which CIC fused with forkhead box O4 (FOXO4 on Xq13.1), leucine twenty homeobox (LEUTX on 19q13.2), NUT midline carcinoma family member 1 (NUTM1 on 15q14), and NUT family member 2A (NUTM2A on 10q23.2) (7-15). Recently, a fusion between ataxin 1 (ATXN1 on 6p22.3) and DUX4 was found in two central nervous system sarcomas (16, 17). Because the tumors with ATXN1::DUX4 had the same histology, immunohistochemical staining profile and DNA methylation pattern as CIC-rearranged sarcoma, it was concluded that the term 'CIC-rearranged sarcoma' may include some tumors with non-CIC alterations (16, 17).

The DUX4 gene maps on the q35 band of chromosome 4 and is located within a D4Z4 repeat array associated with the autosomal dominant hereditary disease facioscapulohumeral muscular dystrophy (accession number AF117653) (18). A similar D4Z4 repeat array which also contains DUX4 maps on chromosome band 10q26 (accession number AY028079) (19). DUX4 is expressed and regulates genes during the early stages of embryogenesis (20-22). It is barely expressed in most adult tissues with the exception of testis and thymus (23, 24). In the testes, the DUX4 genes from both 4q35 and 10q26 were in the germ-line lineage (23) shown to be expressed approximately

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**Key Words:** CIC-sarcoma, chromosome translocation, t(10;19)(q26;q13), CIC rearrangement, CIC::DUX4 fusion, truncated CIC protein, proline rich region.



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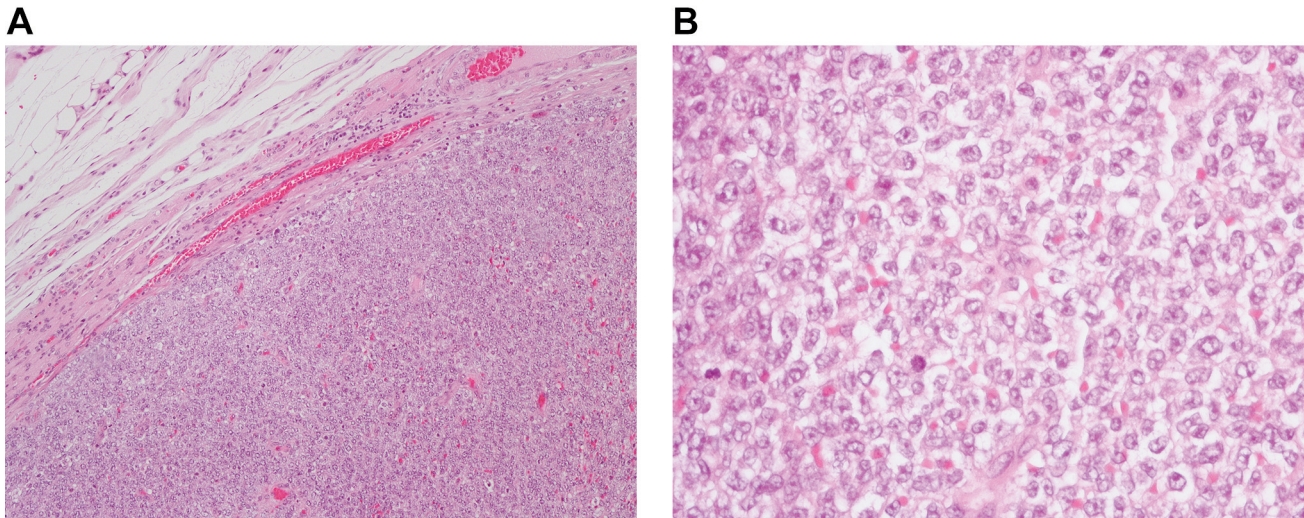


Figure 1. Microscopic examination of the CIC-sarcoma. (A) Hematoxylin and eosin (HE)-stained section showing the small round cell tumor, well-demarcated from the surrounding tissue, magnification  $\times 100$ . (B) HE-stained section showing the round cell morphology. Irregular vesicular nuclei, some with distinct nucleoli, magnification  $\times 400$ .

equally. *In vitro* expression experiments showed that DUX4 protein is localized to the nucleus, induces cell death, is a transcriptional activator of paired-like homeodomain transcription factor 1 (*PITX1*), and also functions as a co-repressor of nuclear receptors of progesterone and glucocorticoids (25-27). In CIC-rearranged tumors, fusion of *CIC* with both 4q35/*DUX4* and 10q26/*DUX4* have been reported (5, 6, 28-38).

The majority of reported CIC-rearranged tumors were detected using various types of PCR amplifications together with Sanger sequencing, high throughput sequencing, and fluorescence *in situ* hybridization techniques (5, 6, 29-31, 33-35, 37-41). The detection of *CIC::DUX4* chimera has become crucial in establishing a correct diagnosis for tumors that are otherwise difficult to classify (42, 43).

Only very few CIC-rearranged tumors have been cytogenetically examined in spite of the fact that a chromosomal corollary to the gene fusion should be readily visible in suitably stained preparations intended for karyotyping. The translocation t(4;19)(q35;q13) was first described in 1992, as part of a complex karyotype, in an embryonal rhabdomyosarcoma (RMS) cell line (44) and as part of a three-way translocation, t(4;19;12)(q35;q13.1;q13), in a tumor diagnosed as undifferentiated/embryonal RMS (45). In 1996, t(4;19)(q35;q13) was found as a sole cytogenetic abnormality in a poorly differentiated extraskeletal mesenchymal sarcoma (46). That finding, together with the other two above-mentioned cases, led the authors to suggest that that t(4;19)(q35;q13) represents a recurrent chromosomal aberration typical of mesenchymal stem cells (46). It was subsequently found also in an

intrabdominal teratoma (47), a subcutaneous primitive neuroectodermal tumor/Ewing sarcoma without *EWSR1* rearrangements (48), and in two cases of Ewing-like sarcoma (5). Molecular investigation of the latter two tumors led to cloning and identification of the *CIC::DUX4* chimera (5). Later, a t(4;19)(q35;q13) was, in some cases together with a *CIC::DUX4* chimera, reported in seven more tumors diagnosed as undifferentiated round cell sarcomas (28, 31, 33, 36). A chromosome translocation t(4;22)(q35;q12), shown by FISH to fuse *EWSR1* with *DUX4*, was found in an embryonal rhabdomyosarcoma (49). Finally, a t(X;19) generating a *CIC::FOXO4* chimera was reported in both a desmoplastic small round cell tumor and an undifferentiated round cell sarcoma (8, 50).

Here, we update information about the genetics of CIC sarcomas and describe the genomic and pathological features of a diagnostically challenging tumor found to carry a t(10;19)(q26;q13) chromosome translocation leading to a *CIC::DUX4* chimera.

## Materials and Methods

**Ethics statement.** The study was approved by the regional ethics committee (Regional komité for medisinsk forskningsetikk Sør-Øst, Norge, <http://helseforskning.etikkom.no>). Written informed consent was obtained from the patient to publication of the case details. The ethics committee's approval included a review of the consent procedure. All patient information has been de-identified.

**Case report.** The patient was a 57-year-old, previously healthy man who had experienced pain in his left inguinal region for one month. Radiological imaging showed a well demarcated tumour measuring

11.0×11.5×8.0 cm in the left adductor magnus muscle. The surgical specimen had a heterogeneous cut surface, brown and fleshy with areas of necrosis (<50% of tumour volume). Representative areas were selected for pathology analyses.

On microscopic examination (Figure 1), the tumour showed a small round cell neoplasm growing in sheets and lobules. The background was partly fibrotic, partly oedematous. The tumour cells had irregular vesicular chromatin, often with small nucleoli and a thin brim of light eosinophilic or clear cytoplasm. The mitotic rate was 23/10 HPF (1,734 mm<sup>2</sup>). Immunohistochemical staining was positive for CD99, TLE1, cyclinD1, and BCOR (weak). MDM2, AE1/AE3, Cam5.2, and CD117 were focally positive. Myogenin, desmin, S100, CD34, TdT, CD3, CD20, MUM1, SOX10, Chromogranin A, and Synapthophysin were negative. Molecular analysis with the Oncomine childhood cancer panel (ThermoFisher Scientific, Waltham, MA, USA) showed no fusion transcripts.

**Chromosome banding analysis.** A representative tumor area was investigated cytogenetically as previously described (51). The material was mechanically and enzymatically disaggregated, and the resulting cells were short-term cultured, harvested and processed for cytogenetic examination. To obtain G-banding of chromosomes, Wright's stain was used (Sigma Aldrich; St Louis, MO, USA). The cytogenetic analysis and karyotype description followed the recommendations of the International System for Human Cytogenomic Nomenclature (ISCN) 2020 guidelines (52).

**Fluorescence in situ hybridization (FISH).** The BAC clone RP11-556K23, which maps to 19q13.2 and contains the *CIC* gene, was used (33). The FISH probe was prepared from bacteriophage Phi29 DNA polymerase amplified BAC DNAs using previously described methodology and labelled with fluorescein-12-dCTP (PerkinElmer, Boston, MA, USA) to obtain a green signal (53, 54). Fluorescent signals were captured and analyzed using the CytoVision system (Leica Biosystems, Newcastle, UK). BAC DNA was also sequenced with T7 (5'-TAATACGACTCACTATAGGG-3') and SP6 (5'-ATTTAGGTGACACTATAG-3') primers using the BigDye terminator v1.1 cycle sequencing kit (ThermoFisher Scientific) in order to obtain BAC-end sequences and verify the map position of BAC clone RP11-556K23.

**Reverse transcription (RT) PCR and Sanger sequencing analyses.** Total RNA was extracted using the miRNeasy Mini Kit (Qiagen, Hilden, Germany) from a frozen (-80°C) part of the tumor specimen adjacent to where material had been taken for cytogenetic analysis and histologic examination. cDNA was synthesized from one µg of total RNA in a 20 µl reaction volume using iScript Advanced cDNA Synthesis Kit for RT-qPCR according to the manufacturer's instructions (Bio-Rad, Hercules, CA, USA). cDNA corresponding to 20 ng total RNA was used as template in a 25 µl reaction volume PCR assay containing 12.5 µl Premix Ex Taq™ DNA Polymerase Hot Start Version (Takara Bio Europe/SAS, Saint-Germain-en-Laye, France) and 0.4 µM of each of the forward (CIC-4377F) and reverse (DUXL4-1553R1) primers. The sequence of the CIC-4377F primer was 5'-CCG AGG ACG TGC TTG GGG AGC TA-3' corresponding to position 4573-4595 of the NCBI Reference Sequence NM\_015125.5 [Homo sapiens capicua transcriptional repressor (*CIC*), mRNA, reported 12-JUN-2022]. The sequence of the DUXL4-1553R1 primer was 5'-CCA GGA AAG AAT GGC AGT TCT CCG C-3' corresponding to position 1577-1553 of the reference sequence XM\_047445716.1

(reported 05-April-2022) which represents a predicted *Homo sapiens* double homeobox protein 4-like protein 4 and maps on chromosome 10 ([https://www.ncbi.nlm.nih.gov/nucore/XM\\_047445716.1](https://www.ncbi.nlm.nih.gov/nucore/XM_047445716.1)). The DUXL4-1553R1 primer corresponds also to position 1472-1448 (with a nucleotide substitution) of the reference sequence NM\_001306068.3 (reported 24-July-2022) which represents the *Homo sapiens* double homeobox 4 (*DUX4*), transcript variant 1, mRNA and maps on 4q35.2.

PCR amplification was conducted on a C-1000 Thermal cycler (Bio-Rad) using the following thermal cycling profile: An initial denaturation step of 30 sec at 94°C followed by 35 cycles of 7 s at 98°C, 30 s at 60°C, 30 s at 72°C and a final extension step for 5 min at 72°C. Three µl of the PCR products were stained with GelRed (Biotium, Fremont, CA, USA), analyzed by electrophoresis through 1.0 % agarose gel, and photographed. DNA gel electrophoresis was performed using lithium borate buffer (55). The remaining PCR products were purified with the MinElute PCR Purification Kit (Qiagen) and cloned to pCR4-TOPO TA vector using the TOPO TA cloning kit for sequencing (ThermoFischer Scientific). Twelve colonies were sequenced with the dideoxy procedure using the BigDye terminator v1.1 cycle sequencing kit following the company's recommendations (ThermoFisher Scientific).

**Bioinformatics.** The sequences obtained by Sanger sequencing were compared to the NCBI Reference Sequences NM\_015125.3 (*CIC*) and NM\_001306068.3 (*DUX4*) using the Basic Local Alignment Search Tool (BLAST) (56). They were aligned to the sequences on the Human GRCh37/hg19 assembly and the recently described T2T-CHM13 v2.0 human genome (57) using the BLAST-like alignment tool (BLAT) and the human genome browser at UCSC (58, 59). They were also compared with the sequences reported in the articles by Italiano *et al.* (6), Machado *et al.* (32), Gambarotti *et al.* (34), Kao *et al.* (60), Tsukamoto *et al.* (37), Yoshida *et al.* (41), and Cocchi *et al.* (38). For multiple sequence alignment, the MultAlin software (61) was used (<http://multalin.toulouse.inra.fr/multalin/>).

## Results

G-banding analysis of tumor cells detected three related clones which had the translocations t(9;18)(q22;q21) and t(10;19)(q26;q13) in common. The karyotype describing clonal evolution was: 46,XY,del(1)(p34p35),t(9;18)(q22;q21), t(10;19)(q26;q13)[5]/46,idem,-del(1),add(6)(p21), +r[3]/47,idem,-del(1),add(6),+8,+r[5]. A karyogram of the third clone is shown in Figure 2.

Sequencing of the BAC-probe RP11-556K23-end with the primer SP6 showed that this part of the clone corresponds to chr19:42,725,294-42,725,782 (GRCh37/hg19) (Figure 3A). Sequencing of the other end of the probe with the T7 primer showed it to correspond to chr19:42,941,280-42,941,801 (Figure 3B). The sequencing data verified that the BAC probe RP11-556K23 maps to subband 19q13.2 (Figure 3C) and contains many genes, among them *CIC* (Figure 3D). FISH with the BAC probe RP11-556K23 on metaphase spreads showed the probe hybridizing to three chromosomes resulting in green signals on the normal chromosome 19, on der(10)t(10;19), and on der(19)t(10;19) (Figures 3E and 3F).

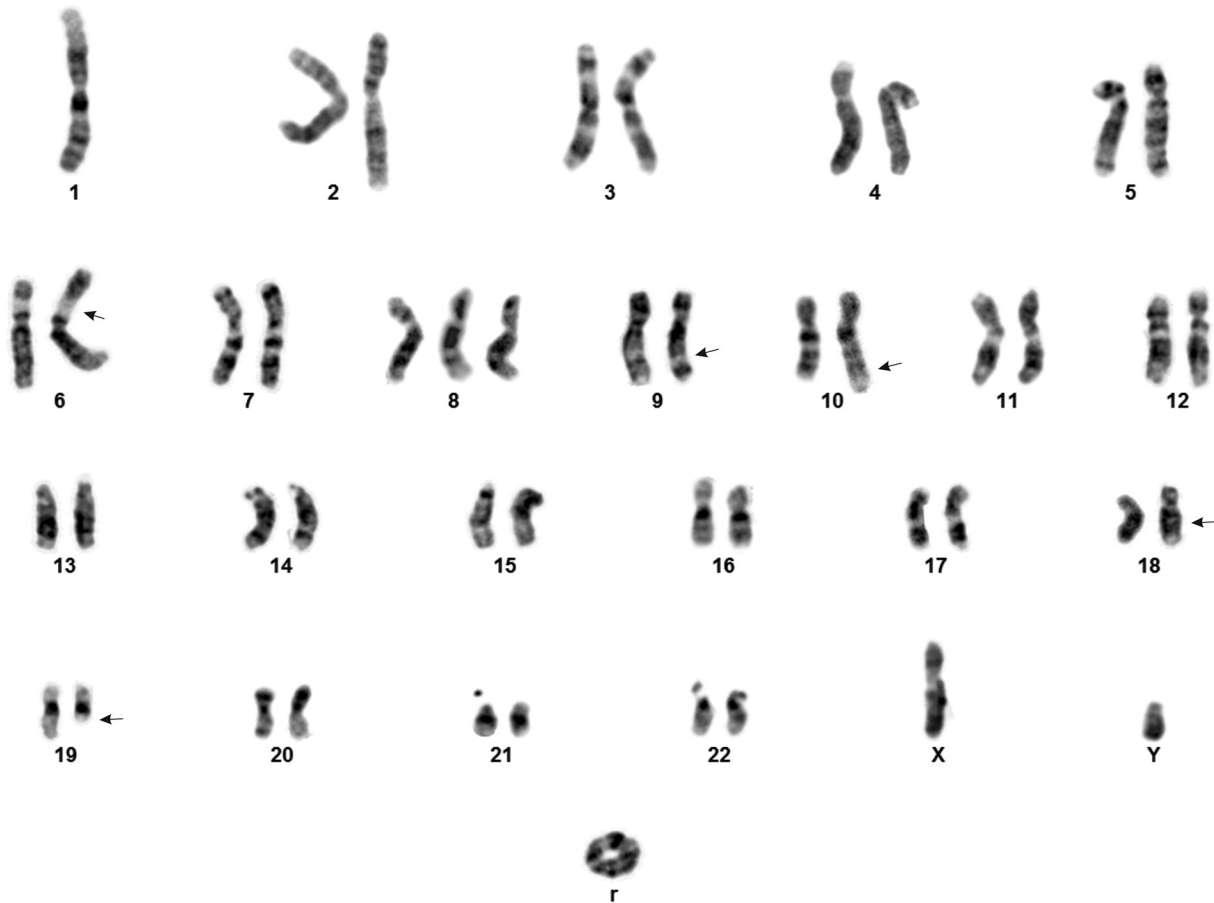


Figure 2. G-Banding analysis of the *CIC*-sarcoma represented by a karyogram of the clone 47,XY,-1,add(6)(p21),+8,t(9;18)(q22;q21),t(10;19)(q26;q13),+r. Arrows indicate breakpoints.

RT-PCR with primers CIC-4377F and DUXL4-1553R1 amplified an approximately 300 bp cDNA fragment (Figure 4A). Cloning to pCR4-TOPO TA vector and sequencing of the cloned amplified PCR product showed that it actually consisted of two chimeric *CIC::DUX4* cDNA fragments. In the first fragment, named type 1 fusion, nucleotide 4750 of the *CIC* sequence with accession number NM\_015125.5 fused to nucleotide 1418 of *DUX4* sequence with accession number NM\_001306068.3 (Figure 4B). In the second fragment, the type 2 *CIC::DUX4* fusion transcript, nucleotide 4777 of the *CIC*/NM\_015125.3 sequence had fused to nucleotide 1418 of *DUX4*/NM\_001306068 (Figure 4C). At the junction, both transcripts had four nucleotides, AGGT, which were thus common to both *CIC* and *DUX4* sequences (Figure 4B and C). Comparison of the type 1 and 2 *CIC::DUX4* fusion transcripts with other published sequences showed that they are recurrent (Figure 5).

Because both *CIC::DUX4* cDNA fragments had a stop TAG codon immediately after the fusion point (Figure 4B

and C), they would code for a truncated *CIC* protein. Thus, *CIC::DUX4* fusion transcript type 1 would code for a truncated protein lacking the last 103 amino acids corresponding to amino acids 1506 to 1608 of the *CIC* protein with reference number NP\_055940.3 (isoform CIC-S), whereas the type 2 *CIC::DUX4* transcript would code for a truncated protein that lacks the last 94 aa of *CIC* corresponding to amino acids 1515 to 1608 of the *CIC* protein/NP\_055940.3 (isoform CIC-S) (Figure 6).

## Discussion

In the present study, we used chromosome banding, FISH and RT-PCR/Sanger sequencing methodologies to reach the diagnosis *CIC* sarcoma for a tumor whose morphologic features alone were insufficient to arrive at this conclusion. Cytogenetic analysis showed, among several aberrations, a t(10;19)(q26;q13) chromosome translocation, while FISH showed splitting of a probe

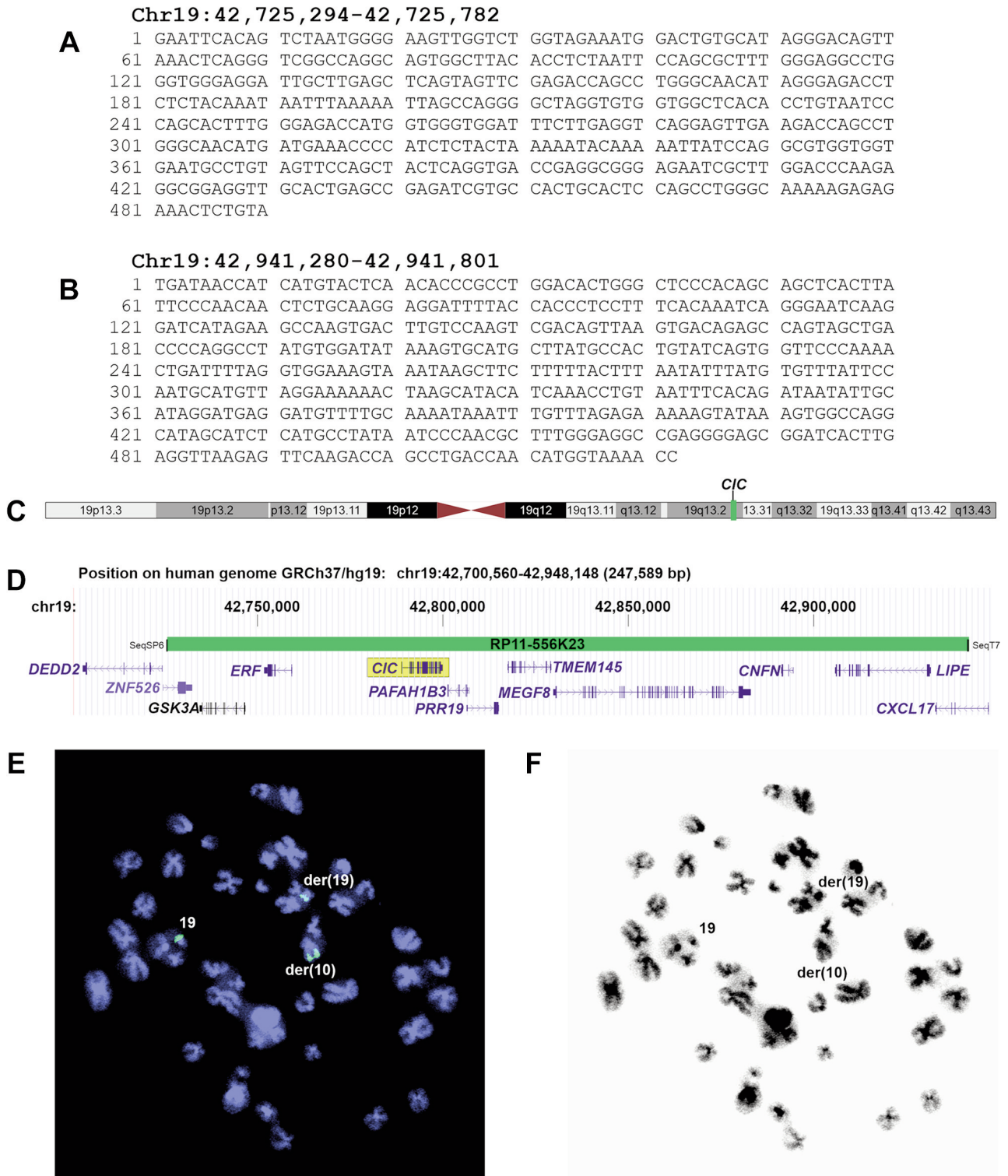


Figure 3. Fluorescence in situ hybridization (FISH) examination of the CIC-sarcoma. (A) Partial sequence of the BAC clone RP11-556K23 using the SP6 primer. (B) Partial sequence of the BAC clone RP11-556K23 using the T7 primer. (C) Ideogram of the chromosome 19 showing the mapping positions of the CIC gene (vertical line) and the BAC clone RP11-556K23 probe (green box). (D) Diagram showing the mapping pattern of the FISH probe RP11-556K23 for the CIC gene. Some neighboring genes in the region are also shown. (E) FISH results on a metaphase spread. Green signals are seen on chromosomes 19, der(10)t(10;19) and der(19)t(10;19). (F) Inverted DAPI staining of the metaphase spread used for FISH experiments.

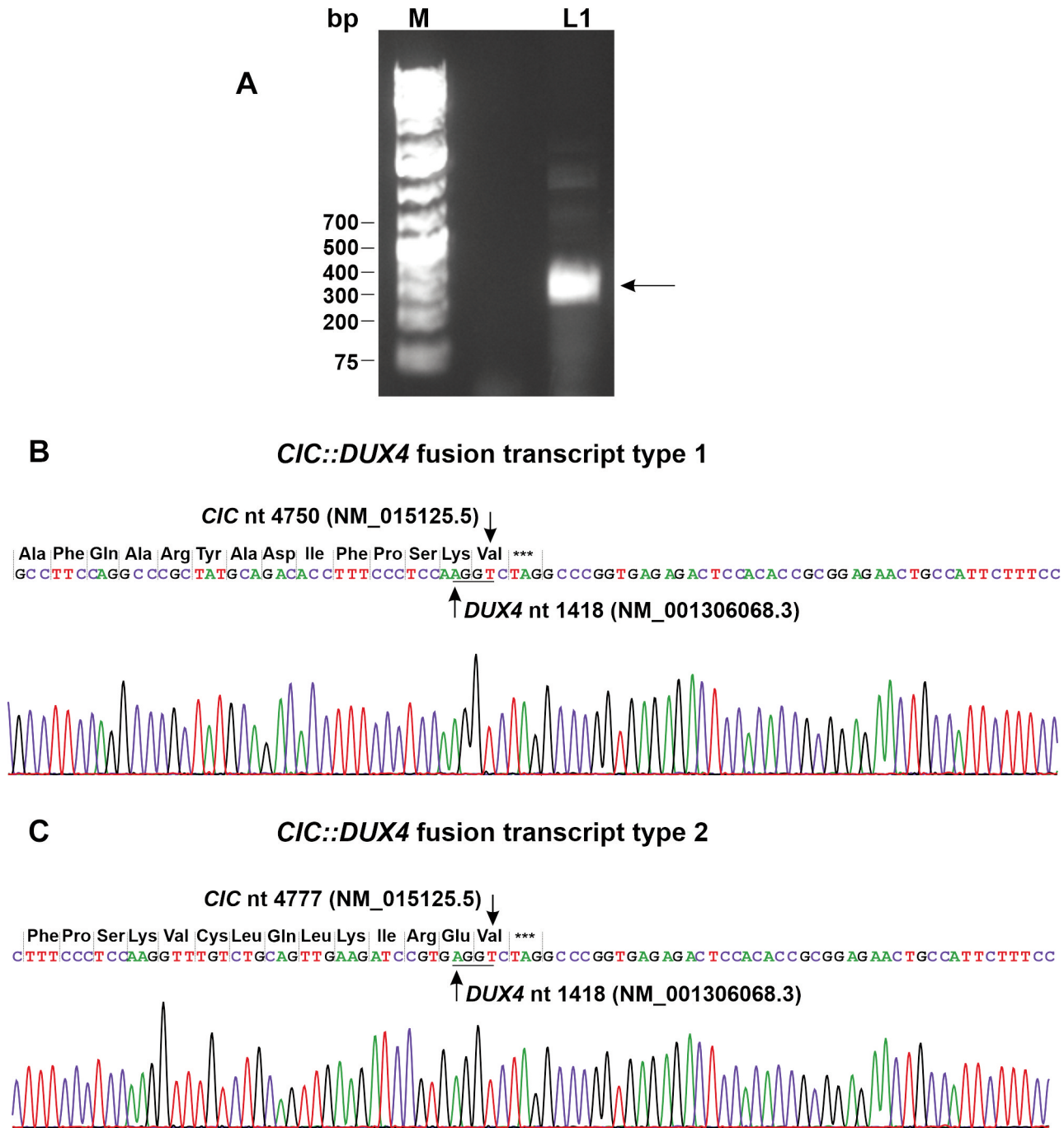


Figure 4. Molecular genetic analysis of the *CIC*-sarcoma. (A) Gel electrophoresis of reverse transcription (RT) PCR amplification products: lane 1, amplification of a 300 bp cDNA fragment using the forward primer *CIC*-4377F and the reverse primer *DUX4*-1553R1. M, GeneRuler 1 kb Plus DNA ladder (ThermoFisher Scientific). (B) Partial sequence chromatogram showing the junction in the *CIC::DUX4* fusion transcript type 1. (C) Partial sequence chromatogram showing the junction in the *CIC::DUX4* fusion transcript type 2. The triplets and the corresponding coding amino acids are shown. Stop codon is noted with \*\*\*. The common four nucleotides AGGT at the junctions are underlined.

which contained the *CIC* gene and RT-PCR/Sanger sequencing confirmed the presence of a *CIC::DUX4* chimeric gene (Figure 2 and Figure 3).

To the best of our knowledge, this is the second solid tumor (of altogether four malignant neoplasms) in which a t(10;19)(q24;q13) translocation was detected. The

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Present study, type 1      AGACATCTTT CCCTCCAAGG T----- -----CT AGGCCCGGTG AGAGACT
Cocchi et al., case 18   AGACATCTTT CCCTCCAAGG T----- -----CT AGGCCCGGTG AGAGACT
Gambarotti et al., case 1 AGACATCTTT CCCTCCAAGG T----- -----CT AGGCCCGGTG AGAGACT
Gambarotti et al., case 2 AGACATCTTT CCCTCCAAGG T----- -----CT AGGCCCGGTG AGAGACT
Gambarotti et al., case 3 AGACATCTTT CCCTCCAAGG T----- -----CT AGGCCCGGTG AGAGACT
Gambarotti et al., case 6 AGACATCTTT CCCTCCAAGG T----- -----CT AGGCCCGGTG AGAGACT
Gambarotti et al., case 7 AGACATCTTT CCCTCCAAGG T----- -----CT AGGCCCGGTG AGAGACT
Kao et al., case 6       AGACATCTTT CCCTCCAAGG T----- -----CT AGGCCCGGTG AGAGACT
Machado et al.          AGACATCTTT CCCTCCAAGG T----- -----CT AGGCCCGGTG AGAGACT
Tsukamoto et al.       AGACATCTTT CCCTCCAAGG T----- -----CC AGGCCCGGTG AGAGACT
Yoshida et al., case 6a AGACATCTTT CCCTCCAAGG T----- -----CT AGGCCCGGTG AGAGACT
Yoshida et al., case 10 AGACATCTTT CCCTCCAAGG T----- -----CT AGGCCCGGTG AGAGACT
Yoshida et al., case 13 AGACATCTTT CCCTCCAAGG T----- -----CT AGGCCCGGTG AGAGACT
Cocchi et al., case 5    AGACATCTTT CCCTCCAAGG ----- --AGGTCT AGGCCCGGTG AGAGACT
Cocchi et al., case 6    AGACATCTTT CCCTCCAAGG ----- --AGGTCT AGGCCCGGTG AGAGACT
Cocchi et al., case 7    AGACATCTTT CCCTCCAAGG TTTGTCTGCA GTTGAAGATC C-----CT AGGCCCGGTG AGAGACT
Cocchi et al., case 8    AGACATCTTT CCCTCCAAGG TTTGTCTGCA GTTGAAGA-- --AGGTCT AGGCCCGGTG ATAG

Present study, type 2      AGACATCTTT CCCTCCAAGG TTTGTCTGCA GTTGAAGATC CGTGAGGCT AGGCCCGGTG AGAGACT
Cocchi et al., case 1    AGACATCTTT CCCTCCAAGG TTTGTCTGCA GTTGAAGATC CGTGAGG-CT AGGCCCGGTG AGAGACT
Cocchi et al., case 2    AGACATCTTT CCCTCCAAGG TTTGTCTGCA GTTGAAGATC CGTGAGG-CT AGGCCCGGTG AGAGACT
Cocchi et al., case 3    AGACATCTTT CCCTCCAAGG TTTGTCTGCA GTTGAAGATC CGTGAGG-CT AGGCCCGGTG AGAGACT
Cocchi et al., case 4    AGACATCTTT CCCTCCAAGG TTTGTCTGCA GTTGAAGATC CGTGAGGCT AGGCCCGGTG AGAGACT
Cocchi et al., case 13   AGACATCTTT CCCTCCAAGG TTTGTCTGCA GTTGAAGATC CGTGAGGCCG AGGCCCGGTG AGAGACT
Cocchi et al., case 14   AGACATCTTT CCCTCCAAGG TTTGTCTGCA GTTGAAGATC CGTGAGGCT AGGCCCGGTG AGAGACT
Cocchi et al., case 16   AGACATCTTT CCCTCCAAGG TTTGTCTGCA GTTGAAGATC CGTGAGGCC T AGGCCCGGTG AGAGACT
Cocchi et al., case 17   AGACATCTTT CCCTCCAAGG TTTGTCTGCA GTTGAAGATC CGTGAGGCT AGGCCCGGTG AGAGACT
Cocchi et al., case 19   AGACATCTTT CCCTCCAAGG TTTGTCTGCA GTTGAAGATC CGTGAGG-CT AGGCCCGGTG AGAGACT
Gambarotti et al., case 4 AGACATCTTT CCCTCCAAGG TTTGTCTGCA GTTGAAGATC CGTGAGGCT AGGCCCGGTG AGAGACT
Gambarotti et al., case 5 AGACATCTTT CCCTCCAAGG TTTGTCTGCA GTTGAAGATC CGTGAGGCT AGGCCCGGTG AGAGACT
Italiano et al., SBRCT9  AGACATCTTT CCCTCCAAGG TTTGTCTGCA GTTGAAGATC CGTGAGGCC T AGGCCCGGTG AGAGACT
Kao et al., case 7      AGACATCTTT CCCTCCAAGG TTTGTCTGCA GTTGAAGATC CGTGAGGCC T AGGCCCGGTG AGAGACT
Tsukamoto et al.       AGACATCTTT CCCTCCAAGG TTTGTCTGCA GTTGAAGATC CGTGAGGTC AGGCCCGGTG AGAGACT
Yoshida et al., case 6b AGACATCTTT CCCTCCAAGG TTTGTCTGCA GTTGAAGATC CGTGAGGCT AGGCCCGGTG AGAGACT
Yoshida et al., case 10b AGACATCTTT CCCTCCAAGG TTTGTCTGCA GTTGAAGATC CGTGAGGCT AGGCCCGGTG AGAGACT
Yoshida et al., case 13b AGACATCTTT CCCTCCAAGG TTTGTCTGCA GTTGAAGATC CGTGAGGCT AGGCCCGGTG AGAGACT
CIC-NM_015125.5:4730-4789 AGACATCTTT CCCTCCAAGG TTTGTCTGCA GTTGAAGATC CGTGAGGTGC GCCAGAAGAT
DUX4-NM_001306068.3:1414-1440                                     TTCTAGGCT AGGCCCGGTG AGAGACT

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Figure 5. Multiple sequence alignment of the *CIC::DUX4* fusion transcripts type 1 and type 2 with previously reported *CIC::DUX4* fusion transcripts by Cocchi *et al.* (38), Gambarotti *et al.* (34), Kao *et al.* (60), Machado *et al.* (32), Tsukamoto *et al.* (37), Yoshida *et al.* (41) and Italiano *et al.* (6). *CIC* sequence is written in red and *DUX4* sequence in black letters. The tetranucleotide AGGT which was found at the junction and was common to both *CIC* and *DUX4* is written in blue letters. The stop codon TAG or TGA is underlined.

translocation was previously reported in two acute lymphoblastic leukemias as the sole cytogenetic abnormality (62, 63), and in a primary malignant neuroepithelial tumor of the kidney which had the karyotype 45,XX,der dic(1)t(1;13)(p1?3;p13),del(9)(p13),t(10;19)(q26;q13),-13 (64). At the DNA level, t(10;19)(q24;q13) has been shown to target different genes. It resulted in truncation of the *FAM53B* gene on subband 10q26.1 (63) in acute lymphoblastic leukemia, whereas in sarcomas it generates *CIC::DUX4* chimeric genes as shown by the present case and the tumors of references (6) and (37).

We detected two types, 1 and 2, of *CIC::DUX4* fusion transcript (Figure 4 and Figure 5), both of which were also reported in previous articles (Figure 5) (6, 32, 34, 37, 38, 41, 60). The common features of both transcripts are: 1) that the *CIC* gene breakpoint occurs in the coding region of the last exon (exon 20 in reference sequence NM\_015125.5); 2) that the breakpoint in the *DUX4* gene occurs within the 3'-end untranslated region; 3) that at the junction there is a four

nucleotide sequence, AGGT, common to both *CIC* and *DUX4*, and 4) that a stop TGA codon is introduced after the fusion point resulting in a truncated *CIC* protein instead of the chimeric *CIC::DUX4* protein.

The truncated protein encoded by *CIC::DUX4* fusion transcript 1 lacks the last 103 amino acids of the normal *CIC* protein (amino acid 1506-1608 in CIC/NP\_055940.3), whereas the truncated protein coded for by *CIC::DUX4* fusion transcript 2 lacks the last 94 amino acids of the *CIC* protein (Figure 6A) (amino acids 1515-1608 in CIC/NP\_055940.3). The N-terminal of the missing part contains the phylogenetically conserved peptide CLQLKIREVRQKIMQ (or RQKIMQ for the protein coded by *CIC::DUX4* fusion transcript 2) (Figure 6A and B) that is part of the C1 region of the *CIC* protein important for the repressor activity of *CIC* (65-67). Electrophoretic mobility shift assays with *CIC* protein from *Drosophila melanogaster* showed that deletion of the LKIREV or RQKL was enough for the *CIC* protein to lose its ability to bind at optimal *CIC* binding sites T(C/G)AATGAA (66, 67).

**A CIC protein : NP\_0055940.3**

1506 **CLQLKIREVR QKIMQAATPT** EQPPGAEAPL **PVPPPTGTAA APAPT** **PS**PAG 1555  
 1556 **GDDPTSPSSD** SGTAQAAPPL **PPPPESGPGQ** **PGWEGAPQPS** **PPPPGP**STAA 1605  
 1606 TGR

**B**

*Homo sapiens* (NP\_055940.3: 1506-1525)  
*Canis lupus familiaris* (XP\_038512754.1: 1510-1529)  
*Mus musculus* (NP\_001289740.1: 2408-2427 )  
*Xenopus tropicalis* (XP\_004916315.1: 2444-2463)  
*Crocodylus porosus* (XP\_019397247.1: 2158-2177)  
*Danio rerio* (XP\_005173570.1: 1324-1343)  
*Ciona intestinalis* (XP\_026689955.1: 2565-2584)  
*Drosophila melanogaster* (NP\_524992.1: 1344-1363)  
 Consensus

1 10 20  
 |-----+-----|  
 CLQLKIREVRQKIMQAATPT  
 CLQLKIREVRQKIMQAATPT  
 CLQLKIREVRQKIMQAATPT  
 CLQLKIREVRQKIMQAATPT  
 CLQLKIREVRQKIMQAATPA  
 CLQLKIREVRQKIMQAAPS  
 CLQLKIREVRQKIMQAQGED  
 DLQLKIREVRQKLLGQASCT  
 cLQLKIREVRQK.\*q.a...

**C**

1 10 20 30 40 50 60 70 \* 80 88  
 |-----+-----+-----+-----+-----+-----+-----+-----+-----|  
 1: AATPTEQPPGAEAPLVPPPTGTAAAPAPTSPAGGPDPTSPSSDSTGAQAAPPLPPPPESGPGQPGWEGAPQPSPPPPGPSTAAATGR  
 2: AATPTEQPPGAEAPLVPPPTGMAATPVPTSPAGGPDPTSPGSDSGTAQVAPPLPPPPESGPGQPGWEGAPQPSPPPSGPSTAAATGR  
 3: AATPTEQPPGADAPLVGPPPAAGTAAAPVPTSPAGGPDPTSPGSDSGTAPAAPPLPPPPESGPGQPGWEGAPQPSPPPPGPSTAAATGR  
 C: AATPTEQPPGA#APLVgPPPtGtAAaPvPTSPAGGPDPTSPgSDSGTAqaAPPLPPPPEpGPGQPGWEGaQPSPPPpGPSTAAATGR

- 1: *Homo sapiens* (NP\_055940.3: 1506-1525)
- 2: *Canis lupus familiaris* (XP\_038512754.1: 1510-1529)
- 3: *Mus musculus* (NP\_001289740.1: 2408-2427 )
- C: Consensus

Figure 6. The C-terminal part of the CIC protein is absent from the truncated protein encoded by CIC::DUX4 fusion transcript 1. (A) The amino acid sequence of the missing part corresponds to amino acids 1506-1608 in CIC/NP\_055940.3. The intrinsically disordered region containing 30 P (in bold) and 15 A amino acid residues is in gray background. The serine in the PSPP motif, which can be phosphorylated, is in red and underlined. (B) The phylogenetically conserved peptide CLQLKIREVRQKIMQ in various species. (C) Conservation of the intrinsically disordered region in mammals. \*above serine in the PSPP motif.

The carboxyl-terminal part of the missing sequence (amino acids 1521-1608 in CIC/NP\_055940.3) is conserved in placental mammals and is 34% rich in the hydrophobic amino acid proline (P) and 17% rich in alanine (A) (Figure 6A and C). Proline rich regions are found in intrinsically disordered regions of proteins and are involved in protein-protein interactions by binding SRC homology 3 (SH3), WW, GYF and EVH1 domains (68-76). Intrinsically disordered regions play important roles in a plethora of cellular functions (76-83). According to the database of protein disorder and mobility annotations (MobiDB), the missing part of the CIC protein (amino acids 1521-1608 in CIC/NP\_055940.3) is an intrinsically disordered region (<https://mobidb.org/Q96RK0>) (84-86). It contains short motifs which may interact with the above-mentioned domains (Figure 6C). For example, LPVPP, APPLP and LPPPP may bind to the SH3 domain of a number of proteins (87, 88). The PPLP short motif may bind to Group

II WW domains, such as the WW domains of the amyloid beta precursor protein binding family B member 1 (APBB1, also known as FE65) and pre-mRNA processing factor 40 homolog A (PRPF40A, also known as FBP11) (89, 90). The motifs PPPP, LPPP and PSPP may bind to EVH1 domains from various proteins (69, 74). In addition, the serine (S) in PSPP (position 1595 in reference sequence NP\_055940.3) can be phosphorylated (pS). Motif pSP was shown to bind to group IV WW domains, such as those from Pin1 (49), PDX-1 C-terminus-interacting factor, and NEDD4 proteins (91-93).

Proline rich regions are also found in repression domains of various transcription factors. The TP53 transcription factor has a 41.4% proline-rich and a 34.5% alanine-rich region between amino acids 64-92 in sequence with accession number NP\_000537.3. This transcription repression domain is essential for the induction of apoptosis, for the activation of TP53 DNA binding capacity to tumor protein p53



inducible protein 3 (TP53I3, also known as PIG3), and for activation of TP53 following ionizing radiation (94-96). The HHEX (officially full name is haematopoietically expressed homeobox, also known as PRH) transcription factor has an N-terminal transcription repression domain between amino acids 1-143 in sequence with accession number NP\_002720.1. It is 20% rich in proline and 11.4% rich in alanine (97-100). Finally, the transcription repression domain of the WT1 protein, found between amino acids 71-180 in sequence with accession number NP\_000369.4, is 20%, 14%, and 13.6% rich in amino acids proline, glycine, and alanine, respectively (101-103).

## Conclusion

Although functional studies are still lacking, current knowledge suggests that the missing part of CIC in the truncated proteins translated from *CIC::DUX4* fusion transcripts 1 and 2 influences the CIC protein's DNA binding capacity, the transcription repression function, and interaction with other proteins, possibly in particular interactions with proteins carrying an SH3, WW, GYF and EVH1 domain. Absence of this part of CIC seems to be crucial in CIC-mediated tumorigenesis.

## Conflicts of Interest

The Authors declare that they have no potential conflicts of interest.

## Authors' Contributions

IP designed and supervised the research, performed molecular genetic experiments and bioinformatics analysis, and wrote the manuscript. KA performed molecular genetic experiments and interpreted the data. LG performed cytogenetic analysis. HRH, TDP, and IL performed the pathological examination. FM evaluated the data. SH assisted with experimental design and writing of the manuscript. All Authors read and approved of the final manuscript.

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