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A multimodal treatment of carbon ions irradiation, miRNA-34 and mTOR inhibitor specifically control high-grade chondrosarcoma cancer stem cells

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26 **Running title:** *Efficient multimodal treatment of chondrosarcoma stem cells*

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34 **Declarations of interest**

35 None

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3637 Abbreviations

- 38 ALDH: aldehyde dehydrogenase; CFE: colony forming efficiency; CS: chondrosarcoma; CSC:
- 39 cancer stem cell; LET: linear energy transfer; mTOR: mammalian target of rapamycin; NTCP:
- 40 normal tissue complication probability; OER: oxygen enhancement ratio; PARP: poly ADP ribose
- 41 polymerase; RBE: relative biological effectiveness; TCP: tumor control probability

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42 Abstract

43 Background and purpose

High-grade chondrosarcomas are chemo- and radio-resistant cartilage-forming tumors of bone
that often relapse and metastase. Thus, new therapeutic strategies are urgently needed.

46 *Material and methods*

47 Chondrosarcoma cells (CH-2879) were exposed to carbon-ion irradiation, combined with miR-34
48 mimic and/or rapamycin administration. The effects of treatment on cancer stem cells, stemness49 associated phenotype, radioresistance and tumor-initiating properties were evaluated.

50 *Results*

51 We show that high-grade chondrosarcoma cells contain a population of radioresistant cancer stem 52 cells that can be targeted by a combination of carbon-ion therapy, miR-34 mimic administration and/or 53 rapamycin treatment that triggers FOXO3 and miR-34 over-expression. mTOR inhibition by 54 rapamycin triggered FOXO3 and miR-34, leading to KLF4 repression.

55 *Conclusion*

56 Our results show that particle therapy combined with molecular treatments effectively controls 57 cancer stem cells and may overcome treatment resistance of high-grade chondrosarcoma.

58 Keywords

59 cancer stem cell, chondrosarcoma, particle therapy, mTOR inhibitor, miR-34

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1. Introduction

62 Despite striking improvements in the diagnosis and care of human cancer, treatment resistance remains to this day an issue in some hard-to-treat cancers. Chondrosarcomas (CSs) constitute the 63 64 second most common primary bone tumor in adults [1]. Because these cartilaginous tumors exhibit 65 resistance to chemotherapy and conventional radiation therapy, complete surgical resection still 66 remains the primary treatment, with a 10-year survival rate comprised between 30% and 80% depending on the grade. A significant number of patients experience relapse, metastasis or present 67 68 unresectable disease with poor clinical outcome and high lethality (grade III). For those reasons, the 69 clinical management of CS is considered to be particularly challenging, and new therapeutic 70 approaches are urgently needed. Some subtypes, such as mesenchymal CS, may be more responsive 71 to chemotherapy, while surgery of dedifferentiated CS may be more successful when combined with 72 chemotherapy [2]. Radiation therapy has been used in skull-base and spinal CS [3,4]. Recently published molecular therapy targets for CS have included IDH mutations, Hedgehog, Src and PI3K-73 74 Akt-mTOR pathways, histone deacetylase inhibitors, angiogenesis or immunotherapy with immune checkpoint inhibition [5]. Some of those targets yielded promising results in preclinical studies, but 75 76 early phase clinical results were less conclusive.

77 Cancer stem cells (CSCs) are defined as the subset of dedifferentiated cells within a tumor that possess the ability to self-renew and reconstitute tumor heterogeneity[6]. CSCs are more resistant than 78 their non-CSC counterparts and were suggested to be at least partially responsible for treatment 79 80 resistance, relapse and metastasis[7]. Cancer treatments that do not effectively target CSCs might 81 ultimately fail, thus it is of paramount importance to develop new treatment strategies that include 82 CSCs. Transformed mesenchymal stem and progenitor cells with multipotent differentiation potential 83 are likely to be cells of origin in CS [8]. CSCs have been characterized in osteosarcomas [9], but are 84 not well defined in CS.

85 New high linear energy transfer (LET) radiation therapy modalities (such as heavy-ion particle 86 beams) have emerged, which provide a number of physical and biological advantages over 87 conventional X-ray therapy (including an improved relative biological effectiveness RBE and a lower 88 oxygen enhancement ratio OER) and might finally contribute to overcoming treatment resistance [10]. High LET radiation treatment, in combination with other therapies (for example, the chemotherapeutic 89 90 agent cisplatin or the PARP inhibitor talazoparib), has shown favourable results in bypassing tumor and CSC radioresistance [11–15]. Although we have recently shown that low- and high-LET low-dose 91 92 exposures of CS cells can trigger bystander responses in non-irradiated neighbouring normal 93 chondrocytes [16], the high RBE of carbon ions might allow lower normal tissue complication 94 probability (NTCP) than protons, for the same local tumor control (TCP) [17], indicating that carbon 95 ion therapy might be an appropriate CS treatment modality. In this study, we investigated the ability 96 of high LET radiation combined with targeted treatments to target CS cells and CSCs.

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2. Material and methods

98 Cell culture, treatment and sorting of cancer stem cells. CH-2879 chondrosarcoma cells [18] were authenticated by Short Tandem Repeat (STR) profiling. Cells were grown in RPMI1640 medium 99 100 (Nacalai, Kyoto, Japan) supplemented with 10% fetal bovine serum (FBS) (Cosmo Bio, Tokyo, Japan) 101 and antibiotic-antimycotic solution (Penicillin, Streptomycin, Amphotericin B. Gibco ThermoFisher, Carlsbad, CA, USA). Cultures were grown in 5% CO2 at 95% humidity. Cells were treated for 48h 102 103 with rapamycin at a final concentration of 1 nM. Cells were transfected with miRCURY LNA miR-104 34a Mimic (Qiagen, Hilden, Germany) using Lipofectamine RNAiMax reagent (Invitrogen), 105 according to the manufacturer's instructions, at a final concentration of 5 nM. Cells not transfected 106 with the mimic were treated with lipofectamine alone. ALDH activity in the cells was measured by 107 flow cytometry using the ALDEFLUOR kit (Stemcell technologies, Vancouver, BC, Canada) as 108 previously [19]. Cells with low and high levels of ALDH enzymatic activity (respectively ALDH⁻ and 109 ALDH⁺ cells) were sorted using a FACSAria cell sorter (BD Biosciences, Franklin Lakes, NJ, USA).

As a negative control, cells were treated with diethylaminobenzaldehyde (DEAB), a specific ALDHinhibitor.

Radiation exposure. X-ray irradiations were conducted using an M-150WE X-ray generator (Softex, Tokyo, Japan) at 140 kVp, 8 mA, 80V. Irradiation dose-rate was 1.3 Gy/min. Particle therapy experiments were performed at the Heavy Ion Medical Accelerator in Chiba (HIMAC). Cells were irradiated with a 290 MeV/n carbon-ion beam at the center of a 6 cm Spread-Out Bragg Peak (SOBP) as previously [11].

Sphere formation assay. Cells were seeded in triplicate in ultra-low attachment plates (Corning,
Corning, NY, USA) with serum-free culture medium at defined densities and grown for 10 days.
Spheres larger than 60 µm in size were counted.

120 Colony Forming Efficiency (CFE) assay. After irradiation, cells were seeded at defined densities 121 and incubated for 10–14 days then stained. Colonies with more than 50 cells were scored and surviving 122 fractions were determined after correcting for the plating efficiency as previously described [20]. 123 Survival curve data were fitted to the linear (carbon-ion) or linear-quadratic model (X-rays) and are 124 presented as the mean of at least three independent experiments.

Invasion scratch assay. Cells were seeded in triplicate in 24-well plates. 16 hours before assays,
culture medium was replaced with serum-free medium, then a wound was introduced into the confluent
monolayer with a pipette tip. Percentage of wound closure 24 hours later was measured with ImageJ
software.

Oxidative stress quantification. Intracellular levels of reactive oxygen species (ROS) were measured using 5-(and-6)-chloromethyl-29,79-dichloro- dihydrofluorescein diacetate, acetyl ester (CM-H2DCFDA, Molecular Probes, Eugene, OR, USA). Cells were plated in 6-well plates, then 24 hours later 10 mM CM-H2DCFDA was added and cells were incubated for 40 minutes. Fluorescence intensities were measured using a SpectraMax M5 microplate reader (Molecular Devices, Sunnyvale,
CA, USA) (excitation at 493 nm, emission at 520 nm). Unstained cells were used as negative control.
Results are presented as the mean of three independent experiments.

136 Real-time PCR gene expression profiling. RNA was extracted using TRIzol reagent and 137 PureLink RNA Mini Kit (ThermoFisher). cDNA was synthesized using the PrimeScript RT kit (Takara 138 Bio, Kusatsu, Japan) for mRNAs or the Mir-X First-Strand Synthesis Kit (Takara Bio) for microRNAs. 139 Then quantitative real-time polymerase chain reaction (qRT-PCR) was run in triplicate in 384-well 140 plates, using SYBR Premix Ex Taq II (for mRNAs, Takara Bio) or TB Green Advantage qPCR Premix 141 (for microRNAs, Takara Bio), on a ViiA 7 real-time PCR system (ThermoFisher). Relative mRNA 142 levels were calculated using the $\Delta\Delta$ Ct method and normalized to GAPDH (for mRNAs) or U6 (for 143 microRNAs).

Western blotting. CH-8279 cells were lysed with radioimmunoprecipitation assay (RIPA) buffer
(Santa Cruz Biotechnology, Dallas, TX, USA). Protein concentrations were determined using the
Protein Assay CBB solution (Nacalai) using bovine serum albumin (BSA) as a standard. Protein
expression levels were measured using a Wes Simple Western instrument (ProteinSimple, San Jose,
CA, USA), with KLF4 (Cell Signaling Technologies, Danvers, MA, USA, #4038S) and GAPDH (Cell
Signaling #2118L) antibodies, according to the manufacturer's instructions [21]. Raw
electropherograms were used to generate blot-like images.

Reporter assays. CH-2879 cells were transfected using Lipofectamine 3000 reagent with pGL3FOXO3-Luciferase reporter, pRL-TK control reporter and/or pCMV-FOXO3 expression vector.
Firefly and Renilla luciferase activities were measured using the Dual Luciferase Assay System
(Promega, Madison, WI, USA). Normalized luciferase activities were obtained as previously.

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155 Mouse experiments. 4-week old BALB/c nu/nu male mice (Japan SLC, Hamamatsu, Japan) were 156 distributed 3 animals to a cage and maintained on a 12-hr light/12-hr dark cycle in a temperature-157 controlled (22°C) barrier facility with free access to water and a normal diet (CLEA Japan, Tokyo, 158 Japan). Mice were allowed to acclimatize for 5 days before the experiment. Variable numbers of ALDH- and ALDH+ chondrosarcoma cells mixed 1:1 with Matrigel Growth Factor Reduced (Corning, 159 160 Corning, NY, USA) were injected subcutaneously into mouse flank on both sides under isoflurane anesthesia. 4 to 9 mice were used per experimental group (for a total of 31 mice). Five days later, 161 162 miRCURY LNA miR-34 Mimic (Qiagen) was injected on one side with MaxSuppressor in vivo 163 RNALancer II delivery system (Bioo Scientific, Austin, TX, SA), according to manufacturer 164 instructions; 25 µL of mimic/phospholipid-oil emulsion diluted in PBS were injected (1 nmol total 165 miRNA mimic). On the other side, phospholipid-oil emulsion without mimic was injected. Tumor 166 volumes were measured using calipers [22]. After experiments, mice were euthanized by carbon 167 dioxide inhalation. Mouse experiment protocols were approved by the Animal Care and Use 168 Committee at Okinawa Institute of Science and Technology Graduate University.

169 Statistical analysis. Clonogenic survival curve data were fitted to the linear-quadratic model (for 170 X-ray irradiations) or linear model (for carbon-ion irradiation), using the CS-Cal software 171 (www.oncoexpress.de), as previously [23]. Statistical significance of the difference between dose-172 response curves was performed using one-sided 2-class t-test, Welsh and Sattlewaith approximation 173 for each dose, with SigmaPlot software (systatsoftware.com/products/sigmaplot/) (* P<0.05). Other 174 significant differences were assessed using Student's t-test (* P<0.05). Errors bars represent standard 175 deviation.

176 **3. Results**

Subpopulations of cancer stem cells (CSCs) have been identified in sarcomas [24]. Among a panel
of four chondrosarcoma cell lines (CH-2879, OUMS27, L835, SW-1353) (Table A1), CH-2879 cells

and, to a lesser extent, OUMS27 cells, could grow as spheres, indicating that they may contain CSCs
[25,26]. The CH-2879 cell line was established from a recurrent Grade III chondrosarcoma of the chest
wall [18], with tumorigenic and invasive abilities. Because CSCs have been associated with
tumorigenicity and metastasis, CH-2879 may be a good model to study treatment responses of grade
III chondrosarcomas.

184 We and others have previously shown that aldehyde dehydrogenase (ALDH) activity is a useful marker for CSC-like populations in various cancer models [19]. Here, CH-2879 cells contained an 185 186 ALDH⁺ subpopulation (around 1%) that exhibited increased sphere formation and invasion abilities 187 associated with a low level of reactive oxygen species (ROS) (Figure 1abcd). Exposure of CH-2879 188 cells to carbon-ion beam resulted in significant cell death and the induction of stress response pathways 189 (Figure A1). We then compared clonogenic survival of ALDH⁻ and ALDH⁺ cells after exposure to X-190 rays and carbon-ion beam (Figure 1e). As expected, particle therapy had a higher relative biological 191 efficiency (RBE) and ALDH⁺ cells were markedly more radioresistant to X-rays and carbon-ion beam 192 (Table 1). However, relative biological efficiencies (RBEs) for ALDH⁻ and ALDH⁺ cells were similar, 193 suggesting that particle therapy alone was not sufficient to target CSCs in CS.

miR-34 is a tumor-suppressive micro-RNA associated with the regulation of stem-like cells in
prostate cancer, pancreatic cancer or glioblastoma [28–30]. Administration of a synthetic miR-34
mimic decreased sphere formation and invasion capabilities of CH-2879 ALDH+ cells (Figure 1bc),
and increased ROS levels (Figure 1d), indicating that the maintenance of chondrosarcoma stem-like
phenotype may rely also on miR-34 repression. Indeed, miR-34 expression levels were lower in
ALDH+ cells than in ALDH- cells (Figure 2a)

The effect of miR-34 mimic did not rely on the selective elimination of CSCs via apoptosis (Figure A2), but rather on the disturbance of the dynamic equilibrium between CSCs and non-CSCs. Expression of miR-34 target genes [31] *NOTCH1*, *C-MYC*, *LMTK3* and *KLF4* were repressed in

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response to miR-34 mimic treatment (Figure 2b), resulting in lower proportion of ALDH+ cells (Figure
1a). KLF4 protein expression was detected in ALDH+ cells, but not in ALDH- cells or ALDH+ cells
treated with miR-34 mimic (Figures 2c, A3). As observed in breast cancer [19], KLF4 seems to play
a role in CSC maintenance in CS, since treatment with *KLF4* siRNA partially recapitulated the effects
of miR-34 mimic (Figure 2d).

208 CH-2978 cells were able to generate tumor xenografts in nude mice (Figure 2e). Tumors were 209 observed when as few as 10,000 ALDH⁺ cells were injected (with 100% of the mice developing 210 tumors), whereas ALDH⁻ cells had very low tumor initiation potential. Administration of miR-34 211 mimic together with tumor cells resulted in a significant decrease in tumor formation, with less than 212 half of mice developing tumors after injection of 100,000 ALDH+ cells (Table 2). However, when 213 miR-34 mimic was delivered one month after xenograft, it couldn't shrink tumors and could only slow 214 down tumor growth (Figure 2f). This suggested that miR-34 treatment alone may not be sufficient in 215 established tumors (or that mimic delivery efficiency needs to be improved) and that combination 216 therapies might be necessary.

The PI3K-Akt-mTOR pathway has recently emerged as a promising target for intervention in chondrosarcoma [32–35]. Compelling evidence also indicates an important role of mTOR pathway in CSC maintenance. Rapamycin, an mTORC1 inhibitor, inhibited the proliferation of CH-2879 cells (Figure A4). Although rapamycin had a slight radio-sensitizing effect (Figure A5), it decreased the proportion of ALDH+ CSCs (Figure 1a). Interestingly, rapamycin administration led to slightly increased levels of miR-34 (Figure 3a) and lower miR-34 target gene levels (*NOTCH1, C-MYC*, *LMTK3, KLF4* and *Rictor*), with a significant repression of *KLF4* expression (Figure 3b).

Forkhead box O (FOXO) transcription factors are crucial regulators of cell signaling, and coordinate Akt and mTOR activities [36]. Over-expression of FOXO3 enhanced FOXO3 promoter activity (Figure 3c) and was associated with ALDH⁺ cells losing sphere forming abilities (Figure 3d). Finally, FOXO3 over-expression resulted in higher miR-34 expression levels (Figure 3e) and lower levels of miR-34 target genes, including KLF4 transcript (Figure 3f) and protein (Figure 2c). The effect of Rapamycin on CSCs was counteracted when using an siRNA for FOXO3 (Figures 1 and 3d). Altogether, these results suggest that rapamycin effects in chondrosarcoma rely on FOXO3 activity.

231 Combined action of rapamycin and miR-34 mimic led to sustained inhibition of sphere-forming 232 abilities of CH-2879 cells, compared to individual treatments (Figure 4a). Using combined treatment, 233 it was possible to effectively control CSC subpopulations after exposure to carbon-ion doses as low as 234 1 Gy, as the resulting cell populations contained at least 10 times less CSCs than non-treated population 235 (Figure 4b). Such control was not observed when cells were exposed with a roughly equivalent X-ray 236 dose of 2 Gy, based on an RBE of ~1.9 (Table 1). By altering CSC-like phenotype, rapamycin and 237 miR-34 mimic treatments (alone or combined) prompted the radio-sensitization of ALDH+ cells. 238 Although the overall effect of those treatments on the global radio-sensitivity is limited (Figure A5), 239 the near-complete elimination of CSC-like phenotype after combination treatments may effectively 240 address CSC-associated treatment resistance.

241 **4. Discussion**

Surgical resection constitutes the cornerstone of treatment for chondrosarcoma (CS), as chemotherapy is most often ineffective. Histologic grade is considered to be the most important indicator of prognosis, and the outcome for grade III CS with surgical resection alone is usually relatively poor [37]. CH-2879, a cell line isolated from recurrent grade III CS, was selected as a suitable model for the development of new therapeutic strategies in hard-to-treat CSs.

Cancer stem cells (CSCs) have long been presented as an important culprit for treatment resistance [38]. Indeed, different tumors harbor various CSC contents, and the proportion of CSCs may be correlated with radio-resistance [39]. Stem-like properties of CSCs confer them a survival advantage during cancer therapy. Those include higher reactive-oxygen species (ROS) scavenging abilities

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251 (resulting in lower radiation-induced ROS) and improved DNA damage repair activation [40]. It is 252 therefore of outmost importance to properly identify and target the stem-like population when 253 establishing new treatment regimen. In CS, a subpopulation of CD133+ cells have been identified that 254 display stem-like characteristics and were capable of inducing and sustain tumor growth in vivo [24]. Significant evidence indicates that enhanced aldehyde dehydrogenase (ALDH) activity is a hallmark 255 256 of CSCs and is directly involved in CSC-associated resistance [41]. ALDH+ breast cancer cells exhibit increased DNA repair abilities and higher survival in response to radiation exposure, associated with 257 258 the stimulation of Nanog, BM1, Notch1 and Akt [42]. For these reasons, identification of ALDH+ 259 cells is generally considered to be a reliable marker for stem-like subpopulations [43]. Moreover, the 260 identification of ALDH as a key player in resistance to radiation therapy and tumor recurrence suggest 261 that ALDH may be considered as a potential therapeutic target [44]. Here, sorted ALDH+ CH-2879 262 cells exhibited a number of CSC distinctive features, such as lower ROS levels, increased self-263 renewing abilities (as indicated by sphere formation assay), enhanced invasiveness, radioresistance 264 and in vivo tumorigenicity. This suggested that in addition to CD133, ALDH expression should also 265 be an appropriate marker for the identification of stem-like radioresistant subpopulations in CS.

266 The relative biological efficiency (RBE) of the spread-out Bragg peak (SOBP) carbon-ion beam 267 at the Heavy Ion Medical Accelerator in Chiba (HIMAC), relative to conventional X-rays, was within 268 the previously observed range (1.5-2.5) in other experimental models [11–13]. It was lower than the 269 RBE of the monoenergetic carbon-ion beam at the Grand Accélérateur National d'Ions Lourds 270 (GANIL) [16]. Although ALDH+ cells were more radioresistant than ALDH- cells, their respective 271 RBEs (whether at D10 or at D37) were not significantly different. While carbon-ion beam alone may 272 be more efficient against CSCs in some models [45,46], these results demonstrated that the treatment 273 of CS should not rely solely on particle therapy and therefore combination treatments may be needed. 274 The relationship between CSCs and non-stem cancer cells (NSCCs) has been a matter of 275 enormous attention. CSCs and NSCCs coexist in a highly dynamic, bidirectional equilibrium state, 276 whose maintenance is under the control of a not fully understood molecular crosstalk between CSCs, 277 NSCCs and the tumor microenvironment [47]. microRNAs closely regulate pluripotency and 278 differentiation mechanisms, and a number of CSC-associated microRNA regulations have been 279 described [48]. miR-34 is a well-known tumor-suppressor transcriptionally activated by p53, which has been associated with cancer stem cell homeostasis in several experimental models [29,30,49]. mir-280 281 34 expression is downregulated in chondrosarcoma cell lines, compared to primary non-tumorous 282 articular chondrocytes [50]. Here, we show that in CH-2879 CS cell line, administration of a miR-34 283 mimic was capable of decreasing stem-like radioresistant subpopulations.

284 Hundreds of direct miR-34 targets have been identified, with an over-representation of mRNAs 285 involved in cell cycle control, DNA damage response and apoptosis [51]. Notch homolog 1 (NOTCH1), 286 C-MYC, Lemur Tyrosine Kinase 3 (LMTK3) and Krüppel-like factor 4 (KLF4) have all been 287 identified as having a role in maintenance of self-renewal, chemoresistance, invasion and/or stem-like 288 properties in cancer [52-55]. KLF4, one of the so-called Yamanaka pluripotency factors, was 289 described either as a tumor-suppressor or as an oncogene, depending on the cancer type [56]. In 290 osteosarcoma, KLF4 enhances proliferation and metastasis via alpha-crystallin B chain (CRYAB) [57]. 291 In breast cancer, expression of KLF4 is determinant for the maintenance of CSCs [19,58] and KLF4 292 seems to play a similar role in CS. Because KLF4 siRNA only partially recapitulated the effect of miR-293 34 on CSC-like phenotype, we can hypothesize that while KLF4 is a probably a major effector of miR-294 34 in CSCs, other pathways regulated by miR-34 are expected to be involved. As a matter of fact, miR-295 34 is able to suppress stem-like characteristics in breast cancer by downregulating Notch pathway [59]. 296 Furthermore, ALDH mRNA levels are reduced in tumor tissues of miR-34-treated mice [60]. Because 297 ALDHs are involved in ROS scavenging [41,61], miR-34 effects might rely on ROS accumulation, 298 leading to increased radiosensitivity. Although miR-34 expression levels may not be directly correlated

with survival in TCGA data of sarcoma patients, low expression of several miR-34 target genes (CMYC, Cyclin-dependent kinase 4 – CDK4, Cyclin-dependent kinase 6 – CDK6, E2F Transcription
Factor 3 – E2F3) is associated with better sarcoma survival (Table A3, Figure A6). miR-34 therapy
may be effective mainly as a combination with other treatment modalities.

303 Mammalian target of rapamycin (mTOR) is a Ser/Thr kinase that is regulated in an extensive list 304 of functions, including proliferation, survival, cytoskeleton organization or metabolism. mTOR is the 305 catalytic subunit of two functionally distinct protein complexes: mTOR complex 1 (mTORC1) and 306 mTORC2. The aberrant activation of mTOR activity is observed in multiple cancer types, resulting 307 from phosphoinositide 3-kinase (PI3K) amplification/mutation, phosphatase and tensin homolog 308 (PTEN) loss of function, or from the overexpression of Akt, Ribosomal protein S6 kinase beta-1 309 (S6K1), eukaryotic translation initiation factor 4E-binding protein 1 (eIF4EBP1) or eIF4E. For this 310 reason, mTOR pathway inhibition is regarded as an important target for the development of new cancer 311 therapies. Phosphorylation of S6K1 was detected in 69% of conventional CS and 44% of 312 dedifferentiated CS [32], suggesting that mTOR inhibition may be a good strategy for CS therapy.

313 Surprisingly, inhibition of mTORC1 by rapamycin lowered the proportion of CSCs. The role of 314 S6K1 and eIF4eBP1 in mTORC1-mediated regulation of translation is well known. Moreover, 315 forkhead box O (FOXO) transcription factors are crucial regulators of cellular homeostasis and are 316 known tumor suppressors in human cancers [62]. The complex interplay between FOXO, mTOR and 317 Akt has been described [36]. FOXOs decrease ROS levels and inhibit mTORC1 via Sestrin3 [63]. On 318 the other hand, it was also reported that the mTOR pathway is capable of regulating FOXO3 activity 319 by downregulating glucocorticoid-inducible kinase 1 (SGK1), which is responsible for FOXO3 320 phosphorylation. The inactivation of mTORC1 induced by p18 depletion led to FOXO3 321 hypophosphorylation at Ser314 [64]. Here, we show that inhibition of mTORC1 led to increased 322 FOXO3 promoter activity and that it directly led to the reversal of CSC-like phenotype. FOXO3 is a transcriptional regulator of miR-34 [65,66] and its activation led to the inhibition of miR-34 targets
like KLF4.

Therefore, inactivation of mTORC1 by rapamycin has direct effects on miR-34-associated 325 326 pathways. Rapamycin treatment together with miR-34 mimic administration had a sustain inhibitory 327 effect on CSC-like phenotype. However, the fact that the combination of miR-34 mimic and rapamycin 328 administration is more potent than rapamycin alone suggests that alternative molecular mechanisms 329 are also likely to be involved. In non-treated cells, only higher irradiation doses led to significant effects (such as the induction of cell death pathways). However, high dose exposures can lead to a 330 331 relative CSC enrichment [67,68]. By delivering a combination treatment, it was then possible to further 332 decrease irradiation doses while efficiently suppressing CSC-like attributes.

Altogether, these results suggest that mTOR inhibition by rapamycin supplemented with miR-34 mimic treatment may be able to overcome CSC-associated radioresistance in chondrosarcoma during carbon-ion therapy. Combination treatments might also improve the effectiveness of carbon-ion therapies at lower doses, decrease risks of relapse and metastasis, and better preserve surrounding normal tissues against non-targeted effects.

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- 531

532 Figure legends

533 Figure 1. CH-2879 chondrosarcoma cells contain a radioresistant cancer stem cell subpopulation suppressed by miR-34. a Sorting of ALDH+ cancer stem cells. DEAB-treated cells served as negative 534 535 control. The proportion of ALDH+ cells was measured after carbon-ion irradiation and/or treatment 536 with miR-34 mimic (34m), rapamycin (rap) or rapamycin + FOXO3 siRNA (rap+Fsi). **b,c,d** Invasion scratch assay (b), sphere-formation assay (c) and reactive oxygen species (ROS) level measurements 537 538 (d) were performed in ALDH- and ALDH+ cells after treatment with miR-34 mimic (34m). e Dose-539 response curves for clonogenic survival of CH-2879 chondrosarcoma cells. ALDH- and ALDH+ cells 540 were exposed to X-rays or carbon-ion beam (the differences of clonogenic survival between ALDH-541 and ALDH+ cells were significant for every dose after X-ray irradiation and after 2-5 Gy carbon-ion). 542 Results are expressed as the mean \pm SD of three or more independent experiments.

543 Figure 2. miR34 exerts its effects via KLF4 and protects against tumor formation. a,b Expression 544 of miR-34 (a) and miR-34 target genes (b) in ALDH+ cells, relative to ALDH- cells. c KLF4 protein 545 expression levels in ALDH- and ALDH+ cells after treatment with miR-34 mimic (34m) or 546 transfection with FOXO3 expression vector (fox). d Sphere formation assay in ALDH+ cells after 547 treatment with KLF4 siRNA. Results are expressed as the mean \pm SD of three or more independent 548 experiments. e,f Growth of chondrosarcoma subcutenous xenografts (e) was measured by external 549 caliper in nude mice, after injection of ALDH- or ALDH+ cells and/or miR-34 administration (f). 550 Results are expressed as the mean \pm SD for five or more animals.

Figure 3. mTOR inhibition by Rapamycin targets chondrosarcoma stem cells via FOXO3 and miR-34. **a,b** Expression of miR-34 (**a**) and miR-34 target genes (**b**) after rapamycin treatment, relative to non-treated cells. **c** FOXO3 promoter activity after transfection with FOXO expression vector or rapamycin treatment. **d** Sphere formation assay in ALDH+ cells after treatment with FOXO expression vector (FOXO3), rapamycin (rap) or rapamycin + FOXO3 siRNA (Fsi). **e,f** Expression of miR-34 (**e**) and miR-34 target genes (f) in cells transfected with FOXO expression vector, relative to cells treated with control vector. Results are expressed as the mean \pm SD of three or more independent experiments.

Figure 4. a Sphere formation assay after treatment with miR-34 mimic and/or rapamycin, when cells where plated at various times following treatment. b Proportion of remaining ALDH+ CSCs after exposure to 1 Gy carbon-ion, equivalent dose 2 Gy X-rays in cells treated with rapamycin alone or in combination with miR-34 mimic, relative to the proportion of ALDH+ cells in non-irradiated, untreated cells. Results are expressed as the mean \pm SD of three or more independent experiments.

563 Annex A. Supplementary data

564 Supplementary data available.

565 **Table A1.** Chondrosarcoma cell lines.

566 **Table A2.** Primers for quantitative real-time PCR.

Table A3. TCGA survival Cox regression results for miR-34 and for 18 miR-34 target genes in
 sarcoma patients.

Figure A1. Transcriptional response of CH-2879 cells to carbon-ion irradiation (a) Number of
deregulated genes 24h after exposure to various irradiation doses (b) Multi-dimensional scaling (MDS)
plot showing sample relations. (c) Top Regulator Effect Networks in Ingenuity Pathway Analysis
(IPA). p53-associated networks are highlighted in pink.

- 573 Figure A2. Apoptosis of CH-2879 cells after miR-34 mimic administration.
- 574 **Figure A3.** Electropherograms for KLF4 and GAPDH expression.
- 575 Figure A4. CH-2879 cell proliferation after rapamycin treatment.

20

- Figure A5. Dose-response curves for clonogenic survival of CH-2879 cells after rapamycin
 treatment and carbon-ion irradiation.
- 578 Figure A6. Kaplan-Meier survival curves of sarcoma patients with high (top third) or low (bottom
 579 third) expression.

580

		D10	D37	SF2	RBE _(D10)	RBE _(D37)
X-rays	ALDH-	2.97	1.29	0.21		
	ALDH+	3.64	1.62	0.29		
Carbon-ion	ALDH-	1.57	0.68	0.05	1.89	1.90
	ALDH+	1.96	0.84	0.09	1.86	1.93

Table 1: Clonogenic survival characteristics of CH-2879 cells exposed to X-rays or Carbon-ion beam.

Injection	Control	miR-34 mimic
1,000 ALDH-	0/4 (0 %)	0/4 (0 %)
1,000 ALDH+	0/4 (0 %)	0/4 (0 %)
10,000 ALDH-	0/4 (0 %)	0/4 (0 %)
10,000 ALDH+	5/5 (100 %)	1/5 (20 %)
100,000 ALDH-	1/5 (20%)	0/5 (0 %)
100,000 ALDH+	9/9 (100%)	4/9 (45 %)

Table 2. Induction of xenograft tumors in nude mice after administration of increasingnumbers of CH-2879 cells and miR-34 mimic.





Figure 2







Figure 4

Appendix A. Supplementary Information

A multimodal treatment of carbon ions irradiation, miRNA-34 and mTOR inhibitor specifically control high-grade chondrosarcoma cancer stem cells

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Table A1
Chondrosarcoma cell lines
Primers for quantitative real time DCD
Finners for quantitative real-time FCK
Figure A1
Transcriptional response of CH-2879 cells to carbon-ion irradiation
Figure A2
Apoptosis of CH-2879 cells after miR-34 mimic administration
Figure A3
Flectronherograms for KI F4 and GAPDH expression
Electrophotograms for REF F and Orit Eff expression
Figure A4
CH-2879 cell proliferation after rapamycin treatment
Figure A5
and carbon-ion irradiation
Table A3
regression results for mik-34 and for 18 mik-34 larget genes in sarcoma
patients.
Figure A6
Kaplan-Meier survival curves of sarcoma patients with high (top third) or low (bottom third) expression.
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Name	Diagnosis	Grade	Reference
CH-2879	Chondrosarcoma		1
OUMS27	Chondrosarcoma	III	2
L835	Chondrosarcoma		3
SW-1353	Chondrosarcoma	II	4

 Table A1:
 Chondrosarcoma cell lines.

Gene	Forward	Reverse
NOTCH1	CTGAAGAACGGGGCTAACAA	AGTGGTCCAGCAGCACCTT
C-MYC	CCACACATCAGCACAACTACGC	CGGTTGTTGCTGATCTGTCTCA
LMTK3	TCGGCTTCAAGGAATTTGAGA	GGGTGGTCATGTCTGAGTGTGA
KLF4	GCCCCTCGGGCGGCTTCGTGGCCGAGCTC	CGTACTCGCTGCCAGGGGCG
RICTOR	CCGTGTCGGAGGTTCATACA	GCCTCTGCTTCTTCATGCATT
GAPDH	GAAGGTGAAGGTCGGAGTCA	TTGATGGCAACAATATCCACTT

 Table A2: Primers for quantitative real-time PCR.



Figure A1: Transcriptional response of CH-2879 cells to carbon-ion irradiation (a) Number of deregulated genes 24h after exposure to various irradiation doses (b) Multi-dimensional scaling (MDS) plot showing sample relations. (c) Top Regulator Effect Networks in Ingenuity Pathway Analysis (IPA). p53-associated networks are highlighted in pink.

Using RNA-Seq, we measured gene regulations in CH-2879 cells one day after carbon-

ion exposure. A number of genes were up- or down-regulated (Figure A1a), and multi-

dimensional scaling (MDS) analysis supported the partition of irradiation doses into two

groups ("low doses" and "high doses"). The investigation of individual gene deregulations as

well as the determination of regulator effect networks suggested that only high doses (in

particular the highest dose of 5 Gy) predominantly activated stress response pathways and

cell death-associated mechanisms.



Figure A2: Apoptosis of CH-2879 cells after miR-34 mimic administration.

	KLF4	GAPDH
ALDH+ control		
ALDH- Control	2000 100 1000 1	
ALDH+ m34		
ALDH+ fox	1500 1500	170,000 00,000 0 12 0 0 0 0 0 0 0 0 0 0 0 0 0
Ladder		

Figure A3: Electropherograms for KLF4 and GAPDH expression after in ALDH- and ALDH+ cells after treatment with miR-34 mimic (34m) or transfection with FOXO3 expression vector (fox).



Figure A4: CH-2879 cell proliferation after rapamycin treatment.



Figure A5: Dose-response curves for clonogenic survival of CH-2879 cells after rapamycin treatment and carbon-ion irradiation.

Transcript	Сох	P-Value	FDR	Rank
	Coefficient		Corrected	
hsa-MIR-34A-5P	0.069	0.51	0.622	373
NOTCH1	-0.117	0.27	0.565	7716
C-MYC	0.265	0.012	0.113	1703
LMTK3	0.027	0.8	0.915	14126
KLF4	-0.103	0.31	0.605	8240
RICTOR	-0.114	0.29	0.586	8008
BCL2	0.097	0.37	0.654	9054
CCND1	-0.04	0.69	0.863	12876
CCNE2	0.121	0.24	0.532	7204
CDK4	0.213	0.033	0.191	2764
CDK6	0.144	0.18	0.460	6195
E2F3	0.395	1.80 x 10 ⁻⁴	0.0146	197
HDAC1	0.237	0.034	0.193	2825
JAG1	-0.152	0.11	0.352	4947
MDM4	0.004	0.97	0.987	15907
MET	0.101	0.35	0.639	8819
NOTCH2	-0.02	0.86	0.944	14748
SIRT1	0.083	0.43	0.701	9934
WNT1	-0.053	0.62	0.826	12179

Table A3: TCGA survival Cox regression results for miR-34 and for 18 miR-34 targetgenes in sarcoma patients.

Transcript	Logrank p-Value	
hsa-MIR-34A-5P	0.742	and a star idea star star star star star star star sta
NOTCH1	0.0373	
C-MYC	0.0078	10 10 10 10 10 10 10 10 10 10
LMTK3	0.341	
KLF4	0.416	
RICTOR	0.454	and
BCL2	0.721	and a star star star star star star star st
CCND1	0.627	100
CCNE2	0.0558	and a star star star star star star star st
CDK4	0.00961	10 10 10 10 10 10 10 10 10 10
CDK6	0.0115	10 10 10 10 10 10 10 10 10 10

E2F3	3.79e-05	$\begin{array}{c} 100 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0$
HDAC1	0.147	100 m
JAG1	0.379	100 100 100 100 100 100 100 100
MDM4	0.384	and a star star star star star star star st
C-MET	0.16	under ander
NOTCH2	0.277	and the star star star star star star star star
SIRT1	0.272	biology of the star star star star star star star star
WNT1	0.994	100

Figure A6: Kaplan-Meier survival curves of sarcoma patients with high (top third) or low (bottom third) expression.

Supplementary material and methods

RNA-Seq. RNA was extracted using Trizol and a column-based PureLink RNA Mini Kit (Invitrogen, Carlsbad, CA, USA). RNA-sequence libraries were prepared with the TruSeq Stranded mRNA NeoPrep kit (Illumina, San Diego, CA, USA). Sequencing was performed on a HiSeq 4000 machine (Illumina) to generate 150 nucleotide paired-end reads at a depth of at least 40 million reads. After quality control with FastQC, reads were mapped to the hg19 reference human genome using tophat2 software (v2.1.1), assembled and quantified using the cufflinks software suite (v2.2.1)⁵. Differentially expressed genes were counted and analyzed with Ingenuity Pathway Analysis (Qiagen, Hilden, Germany)⁶. Mapped reads were also sorted with samtools (v1.3.1), read counts were then quantified with HTSeq-count (v0.9.1) and analyzed with the edgeR package (v3.22.5, using Bioconductor v3.7 on R v3.5.0) for multi-dimensional scaling (MDS)⁷. The sequencing data have been deposited in the Gene Expression Omnibus (GEO) database (Accession Number GSE135371).

Apoptosis. Cells were washed with PBS, then stained with Annexin V-FITC and PI at room temperature in the dark using Annexin V-FITC Apoptosis Detection Kit (Nacalai, Kyoto, Japan). The stained cells were analyzed with a FACSAria flow cytometer (Becton Dickinson, San Jose, CA, USA). Apoptosis was shown as the percentage of apoptotic cells to the total number of counted cells.

TCGA analysis. Data from 259 sarcoma patients downloaded from the Cancer Genome Atlas (TCGA) were used to correlate gene expression and survival, using OncoLnc tool (<u>http://www.oncolnc.org/</u>). For each gene, Cox regression analysis was performed then sarcoma patients were divided in high (top third) or low (bottom third) expression groups and survival of the two groups was compared using Kaplan-Meier plots and log rank analysis⁸.

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