Dysregulated Expression of Long Non-Coding RNA *MINCR* and *EZH2* in Colorectal Cancer

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ABSTRACT

Background: As critical regulators, lncRNAs have attracted attention from researchers for diagnostic, prognostic, and therapeutic purposes in human carcinogenesis via interfering with mRNAs such as *EZH2*. Nevertheless, the potent roles and molecular mechanisms of these RNAs in CRC are not clearly known. **Methods:** In this study, the tissue expressions of lncRNA *MINCR* and *EZH2* mRNA between colorectal tumors and polyps were compared with the adjacent normal tissues collected from 114 Iranian patients, using real-time PCR method. Furthermore, the correlation of the expression levels of *MINCR* and *EZH2* with other clinical parameters was evaluated. **Results:** The significant overexpression of *MINCR* and *EZH2* were observed in the CRC tissues compared to control tissues ($p < 0.0001$). This observation confirmed the association of these expression enhancements with the pathological stage of CRC patients. **Conclusion:** Our findings revealed that the expression of *MINCR* significantly alters during CRC development, and it can be identified as a potential biomarker for the detection of CRC. *DOI: 10.52547/ibj.26.1.64*

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INTRODUCTION

It is widely accepted that CRC is the third commonest cancer, with an increasing incidence in the world, and is affected by genetic, epigenetic and environmental factors[1]. Despite significant progress in CRC therapy and diagnostic techniques so far, a large number of CRC patients are still detected in advanced stages. Moreover, recent therapies are unable to accurately decode key genes and signal cascades involved in human CRC metastasis[2]. The development of molecular mechanisms and investigation of new diagnostic biomarkers for screening patients can be promising approaches to CRC therapy and may result in a 90% five-year survival rate[3,4].

The lncRNAs have been recognized as novel molecules possessing a crucial regulatory role in the biological procedures via interference with mRNAs, direct interaction with proteins to regulate their activities or alter their localization. These molecules also are able to affect the downstream gene expression via inhibiting the RNA polymerase[5]. LncRNAs and the epigenetic mechanism have been suggested to be the key regulators in CRC and can be used for diagnostic, treatment, and prognostic purposes[6]. Deregulation of lncRNAs has been found in several tumors, where it can act as tumor suppressor genes or oncogenes[7].

MINCR, known as an lncRNA, has been related to the *MYC* expression in *MYC*-positive lymphomas[8]. *MINCR* gene is located at the chromosome 8q24.3 and

is intragenic to two coding genes, *ZNF696* and *GLI4*, with 3- and 9.5-kb distances[9]. *MINCR* is upregulated in cancer tissues and has an association with the survival rate, cell migration, and invasion in tumor tissues[9]. The high expression of the *MINCR* has been correlated with the size of the tumor, node, and metastasis stage[10]. According to some studies, *MINCR* dysregulation could be a parameter affecting the development of the human cancers, such as gallbladder cancer and hepatocellular carcinoma[11,12]. Nonetheless, the exact mechanism of *MINCR* function in cancer development is still largely unknown[13].

MINCR could activate the polycomb repressive complexes, i.e. PRC1 and PRC2, to stimulate *EZH2* expression by targeting certain miRNAs[10]. The polycomb group proteins are involved in gene silencing phenomena and are highly conserved between Drosophila and humans[14]. In this regard, the PRC1 and PRC2 members can control the gene silencing via the posttranslational modification of histone proteins[15]. *EZH2* can serve as the catalytic subunit of PRC2. Numerous documents have demonstrated the crucial role of *EZH2* in cancer initiation, progression, metastasis, and drug resistance[16]. Hence, researches have focused on *EZH2* as an encouraging drug target, and several *EZH2* suppressors have been developed and are undergoing clinical trials[17]. Inhibition of *EZH2* has been indicated to enhance the efficacy of many anticancer medicines, which reflect the potential of the combined treatment using the *EZH2* suppressors[18].

To our knowledge, no study has been performed on the expression of lncRNA *MINCR* and its association with *EZH2* in CRC. Hence, the expressions of lncRNA *MINCR* and *EZH2* mRNA in tumors and polyps were compared with adjacent normal tissues to investigate their possible roles in CRC progression. Additionally, the positive expression correlation of lncRNA *MINCR* and *EZH2* mRNA with CRC were reported for the first time in the present study.

MATERIALS AND METHODS

Patients and tissue samples

Samples, including control (tumor adjacent normal tissue), polyp (hyperplastic), and tumor (adeno-carcinoma) tissues, were obtained from 114 patients. All the patients referred to the Taleghani Hospital's Research Center for gastroenterology and liver diseases were pathologically diagnosed with CRC, from 2015 to 2017. The clinical data were gathered from all the medical records of the patients. No preoperative treatment was administered to the patients, and cases who underwent any treatment and those with other

diseases were excluded. Demographic and clinic-pathological characteristics of patients are given in Table 1. All tissues were directly stored in the liquid nitrogen and maintained at 80 °C till the RNA extraction.

RNA extraction

Total RNA was extracted from the miRNeasy Mini Kit (Qiagen, Germany) based on Company's guidelines. The quality and quantity of the separated RNAs were estimated by agarose gel electrophoresis (2% agarose; Gibco/BRL USA) and spectro-photometery (Nanodrop Technologies, Wilmington, Delaware, USA). Finally, cDNA was synthesized using RevertAid RT kit (Thermo Scientific, USA) and kept at -20 °C.

Table 1. Demographic and clinicopathological data

Data	Number (%)
Gender	
Female	61 (53.5)
Male	53 (46.5)
Age	
≤50	15 (13.2)
>50	99 (86.8)
BMI (kg/m^2)	
18.5-24.9	59 (51.6)
25-29.9	48 (42.1)
30-35	7 (6.1)
Smoking status	
Yes	7 (6.1)
No	107 (93.9)
Family history	
Yes	11 (9.6)
No	103 (90.4)
Sample location	
Colon	105 (92.1)
Rectum	9 (7.9)
Clinical stage	
II	14 (32.6)
III	29 (67.4)
Type of samples	
Tumor tissues	43 (37.8)
Polyp tissues	36 (31.6)
Control tissues	35 (30.6)
Underlying disease	
Hypertension	
Yes	11 (8.4)
No	103 (91.6)
IBD	
Yes	10 (8.8)
No	104 (91.2)

BMI, body mass index; IBD, inflammatory bowel disease

Table 2. The sequences of the primers utilized in our study

Gene	Forward primer sequence	Reverse primer sequence	Fragment (bp)
MINCR	5'-TAAAACTGGTGCGCGGGTTC-3'	5'-TCAGTCACTGCTTCATCCCA-3'	114
EZH2	5'-ACAGTGATAGGGAAGCAGGG-3'	5'-ACTCCACTCCACATTCTCAGG-3'	174
Beta-globin	5'-CCCTTCATTGACCTCAACTACATG-3'	5'-TGGGATTTCCATTGATGACAAGC-3'	117

Real-time PCR

The SYBR Premix Ex Taq (Takara, Japan) was used for qPCRs. The normalization of the outputs was then carried out using beta-globin expression level. The software Primer3 was used to design the primers. Table 2 shows the primers sequences utilized in our study. In the next stage, a 7900 Fast Real-Time PCR System (Applied Biosystems, Thermo Fisher Scientific, Inc. USA) was used to analyze RT-qPCR and collect the required data. Thermal cycling conditions included the initial denaturation phase (95 °C for 30 s), PCR reaction phase (40 cycles of 95 °C for 5 s and 60 °C for 34 s), and dissociation phase (95 °C for 15 s, 60 °C for 1 min, and 95 °C for 15 s). The tumor adjacent normal tissue was considered as a reference sample. In the end, the PCR products were visualized on 2% agarose gel stained with green viewer, and fold changes in the relative expressions of all the target mRNAs were computed based on the comparative $2^{-\Delta\Delta CT}$ technique[19].

Statistical analyses

The statistical analyses were performed using GraphPad Prism version 8.01 and the SPSS/PC V 26.0., Chicago, IL, USA. Student's t-test and one-way ANOVA were conducted to estimate the significant differences between two groups and multi groups, respectively. Analysis of the relationship between the expression levels and clinicopathological data was performed using $\chi2$ or Fisher's exact test. The descriptive analysis for quantitative data was performed using mean ± SD., and a *p value* less than 0.05 was considered statistically significant. All experiments were carried out in triplicate.

Ethical statement

The above-mentioned sampling protocols were approved by the Medical Ethics Committee of the Shahid Beheshti University of Medical Sciences (SBUMS), Tehran, Iran (ethical code: IRC89001357). Written informed consents were collected from each participant before inclusion in the research.

RESULTS

Demographic and clinicopathological data

This study included 114 patients (53 males [46.5%] and 61 females [53.5%]) with the age range of 30 to 75 years (the average of 60.33 years). The associated demographic and clinicopathological data, including gender, age, body mass index, smoking status, family history, sample location, clinical stages, type of samples (tumor or polyp tissues), hypertension, inflammatory bowel disease of the patients are shown in Table 1.

Overexpression of *MINCR* and *EZH2* expression in the CRC patients

We determined the expression level of *MINCR* in CRC tissues. qRT-PCR analysis was performed in 43 tumor tissue samples, 36 polyp tissue samples, and 35 tumor adjacent normal tissue samples (control tissues). Results showed a higher expression level of *MINCR* in the tumor and polyp tissues in comparison to the neighboring normal tissues. According to the relative *MINCR* expression ratio (2.42) in the tumor tissue, *MINCR* demonstrated a significant upregulation in the CRC tissue as compared to the neighboring normal CRC tissues (Fig. 1A). We also investigated the association of the *MINCR* expression in the tumor tissue samples with clinicopathological characteristics. The results implied that the overexpression of *MINCR* had a significant association with the clinical stage ($p = 0.0178$) and type of samples ($p = 0.0358$), as represented in Table 3. Using real-time PCR, we evaluated the *EZH2* expression in CRC specimens. *EZH2* expression was significantly greater in the tumor and polyp tissues in comparison to adjacent normal tissues (Fig. 1B). The Fisher's exact test results indicated a significant association of the high *EZH2* with the clinical stage ($p = 0.0185$) and type of samples (tumor and polyp tissues; $p = 0.0478$), as illustrated in Table 3.
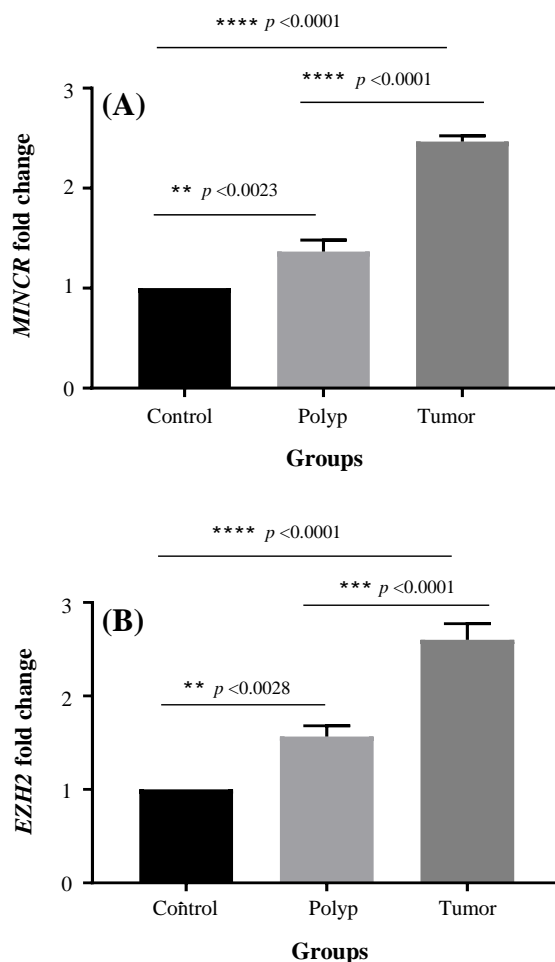
DISCUSSION

LncRNAs are unique molecules to function in tumorigenesis so that the aberrant and the dysregulation of their expression have been shown to

be necessary in malignancy and tumor CRC expansion[20,21]. LncRNAs such as *MINCR* may essentially contribute to both *MYC*-positive lymphomas and numerous types of *MYC*-dependent cancers[6]. In this regard, the amplification of *MYC*-containing genomic region has been a common event in cancer and *MINCR* can mediate the effects of *MYC*

Fig. 1. Expressions of *MINCR* (A) and *EZH2* (B) mRNA in polyp and tumor tissues compared to the control group (tumor-adjacent normal tissue). . (B) $^{*}p < 0.05$, $^{**}p < 0.01$, $^{***}p < 0.001$, and $^{****}p < 0.0001$.

overexpression on cancer progression[22]. In the present research, the expression level of *MINCR* in tumor and polyp tissue samples was evaluated. We first found that the *MINCR* was considerably overexpressed in both CRC and polyp tissues compared to the control group. In line with our data, Wang *et al.*'s[13] study showed a positive correlation between the expression level of *MINCR* and TNM stage, larger tumor sizes, lymphatic metastasis, as well as shorter overall survival in gallbladder cancer.

EZH2 has been considered as one of the histone-lysine N-methyltransferase enzymes engaged in DNA methylation[23]. Moreover, its overexpression has been observed in the tumor tissues, but not normal ones[24,25]. Chen *et al.*[26] have emphasized that the high expression of *EZH2* is related to tumor growth, metastasis, apoptosis suppression, and poor prognosis in cancer patients. The oncogenic contribution of *EZH2* has shown in multiple kinds of the human cancers such as the breast and ovarian cancers[27,28] so that it induces the expression of the tumor inhibitor genes [29]. Some researchers have recently suggested *EZH2* a dual-faced molecule that could function both as a transcriptional repressor and an activator of post-translational alterations[30,31]. Our results showed that *EZH2* significantly increased in tumor and polyp tissues compared to the control group. This finding is in agreement with that of Boostani *et al.*[32] who documented a significant association between *EZH2* and lymph node status.

The upregulation of *MINCR* may participate in cancer initiation via triggering the *EZH2* expression. Systematically, findings have signified that *MINCR/EZH2* axis contributes to the rapid growth of the cells, cell invasion, and also apoptosis in the cancer cells. In addition, functional assays have revealed the suppression of the cell growth and G1/S arrest and the increase of the cell apoptosis through the *MINCR* knockdown. *MINCR* could stimulate the expression of *EZH2* via targeting miR-26a[8]. Therefore, MiR-26a has been considered as one of the essential regulators in tumorigenesis and cancer development

Table 3. Correlation between the expression of *MINCR* and *EZH2* with clinicopathological characteristics

lncRNA/mRNA Characteristics	*MINCR*		*EZH2*	
	Number (%)	*p* value	Number (%)	*p* value
Clinical stage				
II	14 (32.6)	0.0178	14 (32.6)	0.0185
III	29 (67.4)		29 (67.4)	
Type of samples				
Tumor	43 (37.8)	0.0358	43 (37.8)	0.0478
Polyp	36 (31.6)		36 (31.6)	

and suppressors of tumor growth and metastasis[7,10]. Some studies have indicated that miR-26a may function as an oncogene in some cancer cells via the *AKT* pathway by targeting *PTEN* to promote cancer progression[11,13]. Yamamoto *et al.*[33] have exhibited that *EZH2* expression is a prognostic biomarker in CRC patients treated with anti-epidermal growth factor receptor therapeutics. In our study, there had been an association between the high expression of *MINCR* and *EZH2* with the type of samples (tumor and polyp) and clinical stage.

According to the obtained information, our research is the first that evaluated the expression of lncRNA *MINCR* in CRC. We herein explored that *MINCR* may exert oncogenic effects in CRC and can be used as a potential biomarker for the detection of this cancer.

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CONFLICT OF INTEREST. None declared.

REFERENCES

1. Rawla P, Sunkara T, Barsouk A. Epidemiology of colorectal cancer: incidence, mortality, survival, and risk factors. *Przeglad GastroenterologicZNY* 2019; **14**(2): 89-103.

2. Guler I, Askan G, Klostergaard J, Sahin IH. Precision medicine for metastatic colorectal cancer: an evolving era. *Expert review of gastroenterology and hepatology* 2019; **13**(10): 919-931.

3. Pellino G, Gallo G, Pallante P, Capasso R, De Stefano S, Maretto I, Malapelle U, Qiu Sh, Nikolaou S, Barina A, Clerico G, Reginelli A, Giuliani A, Sciaudone G, Kontovounisios C, Brunese L, Trompetto M, Selvaggi F. Noninvasive biomarkers of colorectal cancer: Role in diagnosis and personalised treatment perspectives. *Gastroenterology research and practice* 2018; **2018**: 2397863.

4. Gonzalez-Pons M, Cruz-Correa M. Colorectal cancer biomarkers: Where are we now? *BioMed research international* 2015; **2015**: 149014.

5. Guttman M, Rinn JL. Modular regulatory principles of large non-coding RNAs. *Nature* 2012; **482**(7385): 339.

6. Wilusz JE, Sunwoo H, Spector DL. Long noncoding RNAs: functional surprises from the RNA world. *Genes and development* 2009; **23**(13): 1494-1504.

7. Aukema SM, Kreuz M, Kohler CW, Rosolowski M, Hasenclever D, Hummel M, Küppers R, Lenze D, Ott G, Pott Ch, Richter J, Rosenwald A, Szczepanowski M, Schwaenen C, Stein H, Trautmann H, Wessendorf S, Trümper L, Loeffler M, Spang R, Kluin PM, Klapper W, Siebert R. Biological characterization of adult MYC-translocation-positive mature B-cell lymphomas other than molecular Burkitt lymphoma. *Haematologica* 2014; **99**(4): 726-735.

8. Li CH, Chen Y. Targeting long non-coding RNAs in cancers: progress and prospects. *The international journal of biochemistry and cell biology* 2013; **45**(8): 1895-1910.

9. Doose G, Haake A, Bernhart SH, López C, Duggimpudi S, Wojciech F, Bergmann AK, Borkhardt A, Burkhardt B, Claviez A, Dimitrova L, Haas S, Hoell JI, Hummel M, Karsch D, Klapper W, Kleo K, Kretzmer H, Kreuz M, Küppers R, Lawerenz C, Lenze D, Loeffler L, Mantovani-Löffler L, Möller P, Ott G, Richter J, Rohde M, Rosenstiel P, Rosenwald A, Schilhabel M, Schneider M, Scholz I, Stilgenbauer S, Stunnenberg HG, Szczepanowski M, Trümper L, Weniger MA. MINCR is a MYC-induced lncRNA able to modulate MYC's transcriptional network in burkitt lymphoma cells. *Proceedings of the national academy of sciences of the United States of America* 2015; **112**(38): E5261-E5270.

10. Sabò A, Kress TR, Pelizzola M, de Pretis S, Gorski MM, Tesi A, Morelli MJ, Bora P, Doni M, Verrecchia A, Tonelli C, Fagà G, Bianchi V, Ronchi A, Low D, Müller H, Guccione E, Campaner S, Amati B. Selective transcriptional regulation by Myc in cellular growth control and lymphomagenesis. *Nature* 2014; **511**(7510): 488-492.

11. Kim T, Jun Jeon Y, Cui R, Hoon Lee J, Peng Y, Hak Kim S, Tili E, Alder H, Croce CM. Role of MYC-regulated long noncoding RNAs in cell cycle regulation and tumorigenesis. *Journal of the national cancer institute* 2015; **107**(4): dju505.

12. Cao J, Zhang D, Zeng L, Liu F. Long noncoding RNA MINCR regulates cellular proliferation, migration, and invasion in hepatocellular carcinoma. *Biomedicine pharmacother* 2018; **102**: 102-106.

13. Wang SH, Yang Y, Cai Wu X, Di Zhang M, Zhe Weng M, Zhou D, Dong Wang J, Wei Quan Z. Long non-coding RNA MINCR promotes gallbladder cancer progression through stimulating EZH2 expression. *Cancer letters* 2016; **380**(1): 122-133.

14. Golbabapour S, Golbabapour SH, Abdul Majid N, Hassandarvish P, Hajrezaie M, Abdulla MA, Hadi HA. Gene silencing and polycomb group proteins: an overview of their structure, mechanisms and phylogenetics. *Omics* 2013; **17**(6): 283-296.

15. Laugesen A, Højfeldt JW, Helin K. Role of the polycomb repressive complex 2 (PRC2) in transcriptional regulation and cancer. *Cold spring harbor perspectives in medicine* 2016; **6**(9): a026575.

16. Gan L, Yang Y, Li Q, Feng Y, Liu T, Guo W. Epigenetic regulation of cancer progression by EZH2: from biological insights to therapeutic potential. *Biomarker research* 2018; **6**(1): 10.

17. Sauvageau M, Sauvageau G. Polycomb group proteins: multi-faceted regulators of somatic stem cells and

cancer. *Cell stem cell* 2010; **7**(3): 299-313.

18. Duan R, Du W, Guo W. EZH2: a novel target for cancer treatment. *Journal of hematology and oncology* 2020; **13**(1): 104.

19. Waliullah S, Hudson O, Oliver JE, Brannen PM, Ji P, Emran Ali Md. Comparative analysis of different molecular and serological methods for detection of Xylella fastidiosa in blueberry. *PLoS one* 2019; **14**(9): e0221903.

20. Akhoond MR, Kazemnejad A, Hajizadeh E, Ganbary Motlagh A, Zali MR. Comparison of influential factors affecting survival of patients with colon and rectum cancer using competing risks model. *Koomesh* 2011; **12**(2): 119-128.

21. Sun M, Nie F, Wang Zh, De D. Involvement of lncRNA dysregulation in gastric cancer. *Histology and histopathology* 2016; **31**(1): 33-39.

22. Beroukhim R, Mermel CH, Porter D, Wei G, Raychaudhuri S, Donovan J, Barretina J, Boehm JS, Dobson J, Urashima M, Henry K, Pinchback RM, Ligon AH, Cho Y, Haery L, Greulich H, Reich M, Winckler W, Lawrence MS, Weir BA, Tanaka KE, Chiang DY, Bass AJ, Loo A, Hoffman C, Prensner J, Liefeld T, Gao Q, Yecies D, Signoretti S, Maher E, Kaye FJ, Sasaki H, Tepper JE, Fletcher JA, Tabernero J, Baselga J, Tsao M, Demichelis F, Rubin M, Janne PA, Daly MJ, Nucera C, Levine R, Ebert BL, Gabriel S, Rustgi AK, Antonescu CR, Ladanyi M, Letai A, Garraway A, Loda M, Beer D, True LD, Okamoto A, Pomeroy SL, Singer S, Golub TR, Lander ES, Getz G, WR, Meyerson M. The landscape of somatic copy-number alteration across human cancers. *Nature* 2010; **463**(7283): 899-905.

23. Viré E, Brenner C, Deplus R, Blanchon L, Fraga M, Didelot C, Morey L, Eynde AV, Bernard D, Vanderwinden JM, Bollen M, Esteller M, Croce LD, Launoit Y, Fuks F. The Polycomb group protein EZH2 directly controls DNA methylation. *Nature* 2006; **439**(7078): 871.

24. Sato T, Kaneda A, Tsuji S, Isagawa T, Yamamoto S, Fujita T, Yamanaka R, Tanaka Y, Nukiwa T, Marquez VE, Ishikawa Y, Ichinose M, Aburatani H. PRC2 overexpression and PRC2-target gene repression relating to poorer prognosis in small cell lung cancer. *Scientific reports* 2013; **3**: 1911.

25. Crea F, Hurt EM, Farrar WL. Clinical significance of polycomb gene expression in brain tumors. *Molecular cance* 2010; **9**(1): 265.

26. Chen JF, Luo X, Xiang LS, Li HT, Zha L, Li N, He JM, Xie GF, Xie X, Liang HJ. EZH2 promotes colorectal cancer stem-like cell expansion by activating p21^{cip1}-Wnt/β-catenin signaling. *Oncotarget* 2016; **7**(27): 41540-41558.

27. Kleer CG, Cao Q, Varambally S, Shen R, Ota I, Tomlins SA, Ghosh D, Sewalt R, Otte AP, Hayes DF, Sabel MS, Livant D, Weiss SJ, Rubin MA, Chinnaiyan AM. EZH2 is a marker of aggressive breast cancer and promotes neoplastic transformation of breast epithelial cells. *Proceedings of the national academy of sciences* 2003; **100**(20): 11606-11611.

28. Kuang Y, Lu F, Guo J, Xu H, Wang Q, Xu CH, Zeng L, Yi S. Histone demethylase KDM2B upregulates histone methyltransferase EZH2 expression and contributes to the progression of ovarian cancer in vitro and in vivo. *Oncotargets and therapy* 2017; **10**: 3131.

29. Trošelj KG, Kujundzic RN, Ugarkovic D. Polycomb repressive complex's evolutionary conserved function: The role of EZH2 status and cellular background. *Clinical epigenetics* 2016; **8**(1): 55.

30. Lu H, Li G, Zhou C, Jin W, Qian X, Wang ZH, Pan H, Jin H, Wang X. Regulation and role of post-translational modifications of enhancer of zeste homologue 2 in cancer development. *American journal of cancer research* 2016; **6**(12): 2737.

31. Wen Y, Cai J, Hou Y, Huang Z, Wang Z. Role of EZH2 in cancer stem cells: from biological insight to a therapeutic target. *Oncotarget* 2017; **8**(23): 37974.

32. Boostani F, Dolatkhah R, Fakhrjou A, Farassati F, Sanaat Z. Association of clinicopathologic characteristics and outcomes with EZH2 expression in patients with breast cancer in East Azerbaijan, Iran. *Oncotargets and therapy* 2018; **11**: 449-457.

33. Yamamoto I, Nosho K, Kanno SH, Igarashi H, Kurihara H, Ishigami K, Ishiguro K, Mitsuhashi K, Maruyama R, Koide H, Okuda H, Hasegawa T, Sukawa K, Okita K, Takemasa I, Yamamoto H, Shinomura Y, Nakase H. EZH2 expression is a prognostic biomarker in patients with colorectal cancer treated with anti-EGFR therapeutics. *Oncotarget* 2017; **8**(11): 17810-17818.