

## Role of miRNA clusters in epithelial to mesenchymal transition in cancer

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### 1. ABSTRACT

Epithelial to mesenchymal transition (EMT) is a multistep biological process in which epithelial cells acquire characteristics of mesenchymal cells. Inappropriate activation of EMT contributes to the acquisition of pro-metastatic characteristics and cancer progression. EMT process involves the downregulation of epithelial markers (*EpCAM*, *CDH1*) and upregulation of mesenchymal markers (*VIM*, *CDH2*) and EMT-transcription factors (*ZEB1/2*, *TWIST1/2*, *SNAI1*, *SLUG*). MicroRNAs, a class of non-coding RNA post-transcriptionally govern gene expression by binding to the target mRNAs. A large proportion of miRNAs occur as miRNA clusters consisting of two or more miRNA coding genes.

MiRNA clusters are reported to regulate diverse biological functions, including EMT. This comprehensive review discusses the role of miRNA clusters in EMT.

### 2. INTRODUCTION

An epithelial to mesenchymal transition (EMT) is a biological process in which epithelial cells lose their polarity and cell-cell adhesion properties, and gain migratory and invasive properties to become mesenchymal cells (1). Early changes in EMT include loss of cell to cell adhesion and the advanced stages are characterized by degraded

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basement membrane and cellular delamination (2). EMT engages new transcriptional programs that lead to epithelial to mesenchymal transition. Thus, the completion of EMT is marked by the degradation of the underlined basement membrane, formation of mesenchymal cells and migration of these cells away from its origin (epithelial layers) (3). During EMT, polarized epithelial cells undergo several biochemical changes and acquire mesenchymal characters such as enhanced migration, invasiveness and increased extracellular matrix (ECM) production (4).

EMT process was first observed by Elizabeth Hay in 1960 when working with chicken embryogenesis (1). Epithelial cells are characterized by the presence of adherent and tight junctions, desmosomes and apicobasal polarity (5). EMT is classified as type 1 (organ development and embryogenesis), type 2 (wound healing, tissue regeneration, and organ fibrosis) and type 3 (cancer invasion and metastasis) (6). From a clinical perspective, EMT is associated with self-renewal, resistance to chemotherapy and radiotherapy, enhanced migration and invasion, anoikis resistance, evasion of the immune system and metastasis of cancer cells.

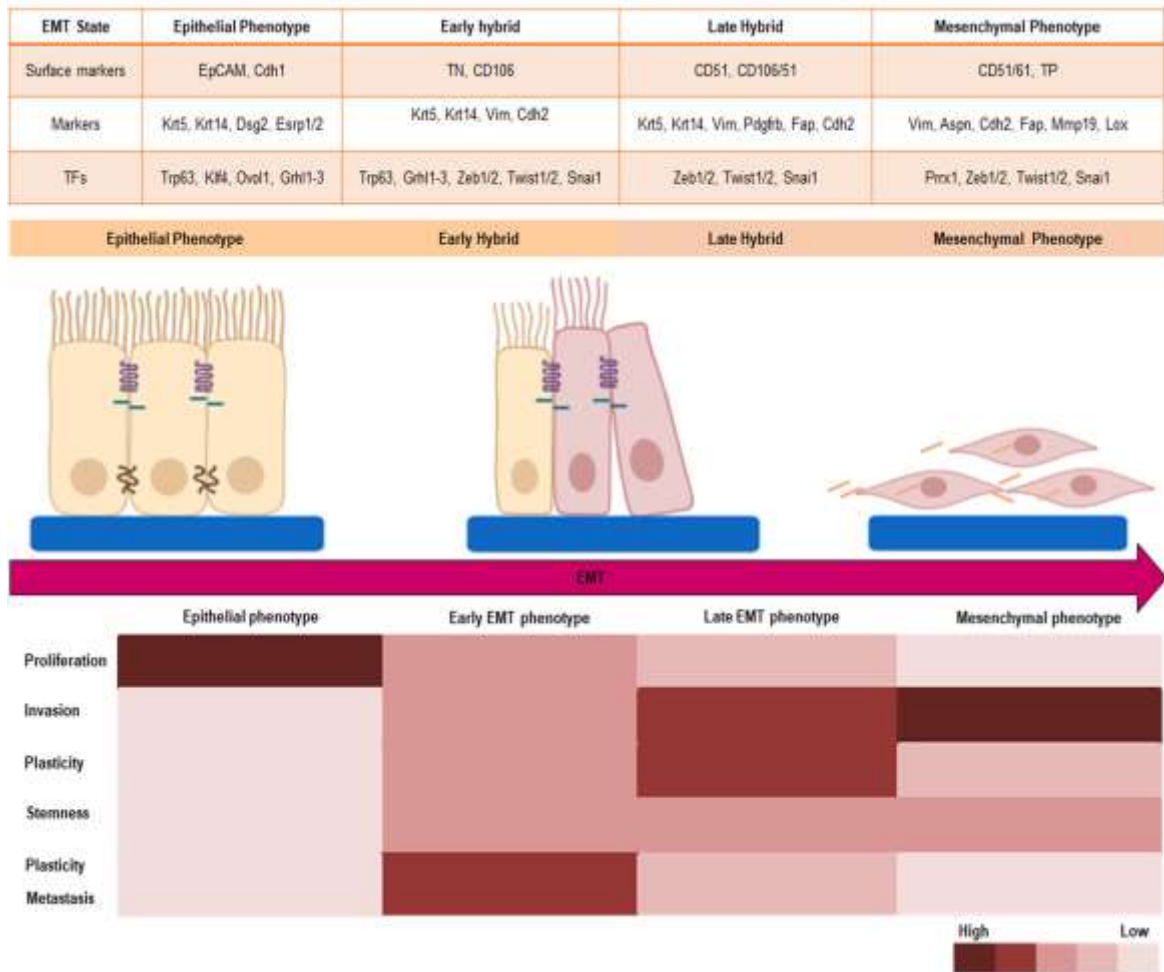
### 3. MOLECULAR PATHOGENESIS OF EMT

EMT involves (i) dissolution of cell junctions including tight junctions, (ii) destabilization of adherence junction, and (iii) loss of apicobasal polarity. Cytoskeletal changes include the reorganization of cortical actin and the formation of actin-rich membrane projections (7). Formation of actin stress fiber is characterized by activation of Rho GTPases namely Ras homolog gene family, member A (*RhoA*) and the Rac family small GTPase1 (*RAC1*) and Cell division cycle 42 (*CDC42*) (8). Directional cell polarity is important for cell migration and is achieved by the relocalization of proteins namely protein associated with tight junctions (PATJ) to the leading edge of the cells. *RAC1* and *CDC42* promote actin polymerization leading to the formation of membrane protrusions facilitating migration. Localization of *RhoA* to the rear end of the cells results in disassembly of adhesion complexes and cell retractions resulting in enhanced migration (8).

The downregulation of *CDH1*, cytokeratins, claudins,  $\gamma$ -catenin, and *ZO-1* are often observed during EMT. The most common upregulated proteins during EMT include N-cadherin (*CDH2*), vimentin (*VIM*), fibronectin,  $\alpha$  smooth muscle actin (*ACTA2*), matrix metalloproteinases (MMPs) and integrins (5). Additionally, there is also the upregulation of EMT-transcription factors (EMT-TFs) such as Zinc finger E-box binding homeobox 1 (ZEBs), Snail Family Transcriptional Repressor 1 (SNAIL), Snail Family Transcriptional Repressor 2 (SLUG), and Twist Family BHLH Transcription Factor (TWIST) (9). EMT can be induced by cytokines, hypoxia, growth factors from tumor microenvironment, metabolic changes, and immune responses (innate and adaptive) via activation of signaling pathways (10, 11). EMT can also be induced by epigenetic modifications, alternative splicing and non-coding RNAs (microRNAs and long-non-coding RNAs) (1, 6, 10, 12–14).

Many signaling pathways activate EMT by inducing the expression of zinc finger proteins (SNAIL family), basic helix loop helix (TWIST family) and zinc finger E box binding proteins (ZEB family) (1). Transforming Growth Factor Beta (TGF- $\beta$ ), receptor tyrosine kinases (RTKs), integrin, WNT, NOTCH, Hedgehog, hypoxia-inducible factor 1 $\alpha$  (HIF1 $\alpha$ ), and Janus kinase2/Signal Transducer and Activator of Transcription (JAK/STAT) pathways are reported to regulate EMT cascade (15). The EMT-TFs recruit co-activators and co-repressors to target genes and alters the rate of transcription. Among the genes, the most commonly targeted include genes belonging to the cell to cell adhesion such as cadherins. The loss of *CDH1* is an important and critical step in the induction of EMT. Downregulation of claudin and occluding (tight junctions), desmoplakin and plakophilin (desmosomes), cytokeratins and intermediate filaments were also reported to have occurred during EMT (15). Tumor necrosis factor (TNF $\alpha$ ) bound to TNF receptor superfamily member 1A (TNFR) can activate nuclear factor kappa B subunit 11 (NF $\kappa$ B) via I $\kappa$ B and induces the expression of *SNAIL1/2*, *ZEB1/2*, and *TWIST1* (16). Interleukin 6 (IL6), via binding to IL6R, induces the expression of *TWIST1* (17). Epidermal growth factor (EGF) can induce EMT by upregulation of MMP3 via the

## miRNA clusters in EMT



**Figure 1.** Schematic representation of characteristics of epithelial to mesenchymal. An EMT occurs through distinct cellular states from transition of polarized epithelial cells to mobile mesenchymal cells. Different epithelial and mesenchymal markers and transcriptional factors (TFs) are shown (14, 196).

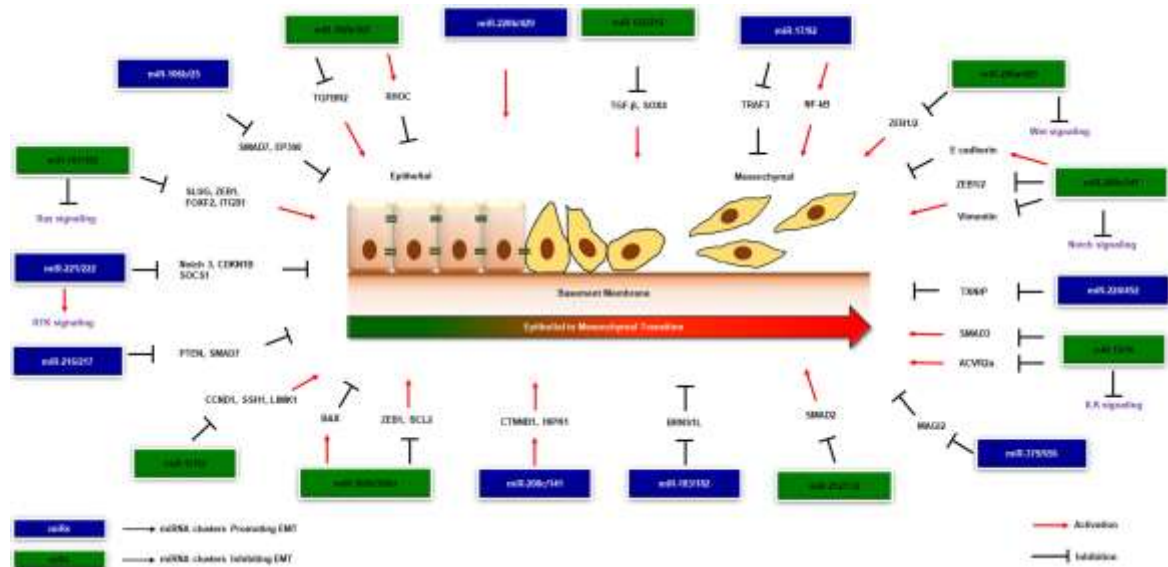
JAK/STAT pathway (18). Induction of HIF1 $\alpha$  via Phosphoinositide-3-Kinase- AKT Serine/Threonine Kinase 1-Mammalian Target of Rapamycin (PI3K-AKT-mTOR) can induce EMT (19). Pro-EMT nature of Rat sarcoma-mitogen-activated protein kinase 1 (RAS-MAPK) and MAPK1-mitogen-activated protein kinase 1(MKK)-p38-SMAD is also reported (20, 21). TGF- $\beta$  by binding to TGF $\beta$ R can induce the expression of *SNAIL*, *SLUG*, *ZEB1/2*, and *TWISTs* promoting EMT. WNT1-Beta-catenin axis is reported to promote EMT via activating *SNAIL* expression. Notch signaling induces EMT through activation of *SNAIL*, *SLUG*, *ZEB1/2* and *TWIST* (15). The induction of *SNAIL1* and *TWIST1* by HIF $\alpha$

also induces EMT (22). Similarly, extracellular matrix protein can also induce EMT. For example, collagen 1 via activation of SRC Proto-Oncogene (SRC) and MAPK1 can induce *SNAIL1* expression (23). The induction of *TWIST1* via Lysyl oxidase (LOX) by CD44 has also been reported (24) (Figure 1).

## 4. miRNA CLUSTER

MicroRNAs (miRNAs) are a class of non-coding RNAs used by cells for fine-tuning the expression of genes in a variety of cell and tissue types (25). miRNAs bind to the target mRNA via

## miRNA clusters in EMT



**Figure 2.** miRNA Cluster regulates EMT pathway via targeting different genes and associated signaling pathways.

complementary base-pairing and affect its expression by mRNA degradation or translational repression (25). Furthermore, it is clear that miRNAs often show deregulated expression leading to the acquisition of multiple cancer hallmarks (26). miRNA clusters consist of two or more miRNAs encoding genes transcribed together in the same orientation without having any miRNAs in the opposite direction (27). More than thirty percent of miRNAs occur in clusters. Chromosome 19 is the largest miRNA cluster in the human genome consisting of 46 miRNAs located in chr19q13.42 (28). Since the miRNA cluster consists of many miRNA encoding genes, its dysregulation can affect multiple cellular functions as opposed to single miRNA alteration. Similar to individual miRNAs, aberrant expression of the miRNA cluster is also reported in multiple cancer. In this review, we discuss the role of miRNA cluster in the multi-step EMT program during carcinogenesis.

### 4.1. miRNA Cluster and EMT

There are several miRNA clusters whose expression is altered contributing to the induction of EMT in different cancer conditions. For example, the miR-200c/141 cluster promotes EMT in breast cancer by targeting Homeodomain Interacting

Protein Kinase 1 (HIPK1) and by activating *CTNNB1* (29). MiR-221/222 promotes EMT in breast cancer by targeting Phosphatase and Tensin Homolog (*PTEN*), Suppressor of Cytokine Signaling 1 (*SOCS1*), Cyclin-Dependent Kinase Inhibitor 1B (*CDKN1B*) and Notch Receptor 3 (*NOTCH3*) (30–32). Similarly, miR-183/182 activates EMT in breast cancer by targeting Growth Hormone Receptor (*GHR*) (33). MiR-216/217 induces EMT by targeting *PTEN* and SMAD Family Member 7 (*SMAD7*), resulting in the activation of PI3K/AKT signaling and sorafenib resistance in liver cancer (34). MiR-17/92 cluster modulates NF- $\kappa$ B signaling via targeting of TNF Receptor Associated Factor 3 (*TRAF3*) in gastric cancer to induce EMT (35) (Figure 2).

Several studies have shown the inhibition of EMT by miRNA clusters. For instance, miR-15a/16 inhibits EMT in prostate cancer by suppressing TGF- $\beta$  (36). MiR-200c/141 inhibits EMT in colon and lung cancer by targeting Achaete-Scute Family BHLH Transcription Factor 2 (*ASCL2*) and Forkhead Box F2 (*FOXF2*) respectively (37, 38). *FOXF2* is also inhibited by the miR-183/182 cluster in colon cancer (37). MiR-17/92 inhibited EMT by downregulation of CyclinD1 (*CCND1*), Slingshot Protein Phosphatase 1 (*SSH1*), LIM Domain Kinase 1

**Table 1.** miRNA cluster promoting EMT

miRNA Cluster	Cancer	Signaling/Gene	Reference
miR-200c/141	Breast Cancer	Targets <i>HIPK1</i> and activated $\beta$ -catenin	(29)
miR-17/92	Gastric Cancer	Targets <i>TRAF3</i> and modulates NF-kB	(35)
miR-221/222	Breast Cancer	Targets <i>PTEN</i> and activating Akt/NF-kB/Cox-2 pathway	(30)
miR-183/182	Breast cancer	Targets <i>BRMS1L</i>	(33)
miR-224/452	Melanoma	Targets <i>TXNIP</i>	(40)
miR-221/222	Breast Cancer	Targets <i>SOCS1</i> and <i>CDKN1B</i>	(31)
miR-106b/25	Breast Cancer	Targets <i>EP300</i>	(41)
miR-379/656	Lung Adenocarcinoma	Targets <i>MAGI2</i>	(42)
miR-200b/429	Breast Cancer	-	(43)
miR-216/217	Liver Cancer	Targets <i>PTEN</i> and <i>SMAD7</i>	(34)
miR-106b/25	Breast Cancer	Targets <i>SMAD7</i> and activates TGF-1 alpha	(44)
miR-221/222	Breast Cancer	<i>Notch3</i>	(32)

Abbreviations: HIPK1, homeodomain interacting protein kinase; TRAF3, TNF receptor associated factor 3; PTEN, phosphatase and tensin homolog; BRMS1L, BRMS1 Like Transcriptional Repressor; TXNIP, Thioredoxin Interacting protein; SOCS1, Suppressor of Cytokine Signaling 1; CDKN1B, Cyclin Dependent Kinase Inhibitor 1B; EP300, E1A binding protein 300; MAGI2, Membrane Associated Guanylate Kinase; SMAD7, SMAD Family Member 7.

(*LIMK1*), Fibroblast Growth Factor 4 (*FGFD4*) and RhoGTPase (39) (Tables 1 - 2).

#### 4.2. *SLUG* and miRNA cluster

Snail Family Transcriptional Repressor 2 (*SNAIL2*), commonly known as the SLUG is located at 8q11.21. SLUG is overexpressed and amplified in numerous cancers is reported to promote cell migration, invasion, metastasis, cell cycle progression and resistance to apoptosis (52–57). SLUG is a transcription factor belonging to the zinc finger family induces transcriptional repression of *CDH1* and is anti-apoptotic in nature. Highly aggressive tumors show overexpression and enhanced activity of SLUG. Both SNAIL and SLUG promote invasion and metastasis by altering the expression of *CDH1* and *VIM* (58). They inhibit *CDH1* by binding to the E-box sequences present in its promoter region (59). Further, SLUG is also capable of downregulating Claudin-1 (*CLDN1*) in Madin-Darby canine kidney (MDCK) cells (60). SLUG induces cell migration and invasion via TGF- $\beta$  signaling (61). SLUG utilizes the SNAG domain to suppress target gene expression by recruiting histone deacetylases. Elevated SLUG expression is connected to *CDH1* downregulation, induction of EMT, advanced tumor grade, lymph node

metastasis and poor survival (62).

SLUG participates in TWIST1 induced EMT pathways by repressing the transcription of *CDH1* (52, 63). Many of the miRNA clusters downregulate SLUG expression and inhibit EMT. For instance, miR-17/92 cluster expression is correlated with inhibition of SLUG and induction of *CDH1* with inhibitory effect on EMT (39). MiR-34, a member of the miR-34b/c cluster acts as a tumor suppressor and inhibitor of EMT by targeting SLUG (64). MiR-96/183 promotes the expression of key EMT inducers such as ZEB1, ZEB2, SNAIL2, MMP2, and MMP9 by suppressing the breast cancer metastasis suppressor 1-like (*BRMS1L*) (33). MiR-183/182 is another miRNA cluster that promotes EMT by promoting the expression of mesenchymal genes and EMT-TFs such as SNAIL, and SLUG (49, 65). In colorectal cancer, miR-182 targets *FOXF2* and induces growth and migration of cancer cells (66). MiR-182, along with miR-203, acts as an inducer of EMT by targeting SLUG expression in prostate cancer (67). MiR-183 and miR-96 are a suppressor of EMT by targeting ZEB1, SLUG, Integrin beta 1 (*ITGB1*), and Kruppel-like factor 4 (*KLF4*) (49). Taken together, SLUG is an important inducer of EMT whose expression is upregulated in cancer via altered expression of miRNA clusters.



**Table 2.** miRNA cluster inhibiting EMT

miRNA Cluster	Cancer	Signaling/Gene	References
miR-15/16	Prostate Cancer	Target <i>SMAD3</i> and <i>ACVR2A</i>	(36)
miR-302b/302d	Endometrial carcinoma	Target <i>ZEB1</i> , <i>Bcl-2</i> and promoted expression of <i>BAX</i>	(45)
miR-302b/367	Colon cancer	Inhibiting <i>TGFBR2</i> and activating <i>RHOC</i>	(46)
miR-302b/367	Melanoma	Inhibiting <i>TGFBR2</i> and activating <i>RHOC</i>	(46)
miR-132/212	Prostate Cancer	Target <i>SOX4</i> and inhibits TGF-beta	(47)
miR-17/92	Prostate Cancer	Decreased expression of cyclin D1, <i>SSH1</i> , <i>LIMK1</i> and <i>FGD4</i>	(39)
miR-212/132	Cervical Cancer	Downregulate <i>SMAD2</i> and suppresses G1/S transition	(48)
miR-200c/141	Lung cancer	Target <i>FOXF2</i>	(37)
miR-183/182	Lung cancer	Target <i>FOXF2</i>	(37)
miR-200c/141	Colon cancer	Target <i>ASCL2</i>	(38)
miR-183/182	Overexpressed p21 colon and breast cancer cell lines	Target <i>SLUG</i> , <i>ZEB1</i> , <i>ITGB1</i> , <i>KLF4</i>	(49)
miR-200a/429	Mammary carcinoma	Target <i>ZEB1</i> and <i>ZEB2</i>	(50)
miR-200c/141	Biliary tract cancer	Positively correlated with <i>CDH1</i> and negatively correlated with <i>VIM</i>	(51)

Abbreviations: *SMAD3*, SMAD family member 3; *ACVR2A*, Activin A Receptor Type 2A; *ZEB1*, Zinc finger E-box binding homeobox1; *TGFBR2*, transforming growth factor beta receptor 2; *RHOC*, Ras homolog family member C; *SOX4*, SRY-Box 4; TGF- $\beta$ 1, transforming growth factor beta 1; *SSH1*, Slingshot protein phosphatase 1; *LIMK1*, LIM domain kinase 1; *FGD4*, FYVE, RhoGEF And PH Domain Containing 4; *FOXF2*, forkhead box F2; *SLUG*, Snail Family Transcriptional Repressor 2; *ZEB*, Zinc Finger E-Box Binding Homeobox; *ITGB1*, Integrin Subunit Beta 1; *KLF4*, Kruppel Like Factor 4; *ASCL2*, Achaete-Scute Family BHLH Transcription Factor 2; *CDH1*, E-cadherin, *VIM*, Vimentin.

### 4.3. SNAIL and miRNA cluster

Snail Family Transcriptional Repressor 1 (*SNAIL1*) is a pro-EMT gene overexpressed in many metastatic cancers promoting cell survival and migration. *SNAIL*, via its N-terminal SNAG domain, interacts with and recruits co-repressors and repressors to the promoter region of *CDH1* thereby promoting EMT. Pro-EMT signaling pathways [RTKs, TGF- $\beta$ , Notch, Wnt, TNF- $\alpha$ , and bone morphogenetic protein 2 (BMP)] along with tumor microenvironment are reported to promote EMT by inducing *SNAIL* expression. From the clinical perspective, *SNAIL* expression levels are correlated with tumor grade, metastasis to lymph node and clinical outcome in metastatic cancer. Moreover, *SNAIL* overexpression is reported to induce metabolic reprogramming and to promote drug resistance, recurrence, and metastasis (68–70).

Emerging evidence suggests crosstalk between miRNA cluster and *SNAIL* during EMT

program. miR-23a/24/27a located at 19p13.12 is regulated through MAPK and TGF- $\beta$  signaling. miR-23a-3p inhibits EMT via TGF- $\beta$ /Akt/MAPK/Snail axis (71). In bladder cancer, miR-323a-3p/MET proto-oncogene (MET)/SMAD3/SNAIL axis is reported to regulate EMT (72). miR-106b/25 cluster enhances non-small cell lung cancer (H1299) cell migration and invasion via targeting of F-box and WD repeat domain containing 11 ( $\beta$ -TRCP2) by enhancing the expression of *SNAIL* (73). miR-206 of miR-206/133b cluster targets MET and PI3k/Akt/mTOR pathways and suppresses EMT (74). miR-183 cluster consists of miRs-183, -96 and -182, and is overexpressed in numerous cancers. miR-182 directly targets metastasis suppressor 1 (*MTSS1*) and induces the proliferation of breast cancer cells (75). As a member of the miR-181 family, miR-181a is associated with cell proliferation and invasion in multiple cancer. miR-181a is reported as an inducer of EMT in prostate cancer by targeting TGF- $\beta$  induced factor homeobox (*TGIF2*) (76). In breast cancer, miR-181b-3p acts as a

**Table 3.** miRNA cluster and signaling pathway

miRNA	Cancer	Target gene/Signaling Pathway	Reference
miR-221/222	Breast Cancer	Tyrosine kinase	(110)
miR-143/145	Breast Cancer	<i>ERBB3</i> /tyrosine kinase	(111)
miR-17/92	large B-cell lymphoma	ITIM/tyrosine kinase	(112)
miR-15/16a	Ovarian Cancer	Integrin-linked Kinase pathway	(113)
miR-143/145	Breast Cancer	<i>PTEN</i> /RAS Pathway	(114)
miR-221/222	Breast Cancer	<i>TRPS1</i> / RAS Pathway	(115, 116)
miR-106b/25	Breast Cancer	<i>NEDD4L</i> /NOTCH signaling	(117)
miR-200c/429	Pancreatic Cancer	Notch	(118)
miR-17/92	Lung Cancer	p38 $\alpha$ kinase/wnt signalling	(119)
miR-200a/429	Hepatocellular carcinoma	Wnt signaling	(120)
miR-17/92	Medulloblastoma	Hedgehog signaling	(121)

Abbreviations: ERBB3, Erb-B2 Receptor Tyrosine Kinase 3; ITIM, immunoreceptor tyrosine inhibitory motifs; PTEN, phosphatase and tensin homolog; TRPS1, Transcriptional Repressor GATA Binding 1; NEDD4L, Neural Precursor Cell Expressed, Developmentally Down-Regulated 4-Like, E3 Ubiquitin Protein Ligase

promoter of EMT via SNAIL stabilization by targeting Tyrosine 3-Monooxygenase/Tryptophan 5-Monooxygenase Activation Protein Gamma (77). The role of Smad2/3/4-dependent pathway in EMT is reported in gastric cancer. Smad2/3/4 pathway induces the expression of miRNA-181b and targets TIMP metalloproteinase inhibitor 3 (*TIMP3*) to promote EMT and metastasis (78). MiR-200 family consists of anti-EMT miRNAs their expression is important to determine the epithelial phenotypes in cancer. MiR-200 family activates *CDH1* expression by targeting *ZEB1* and *ZEB2* (65). The down-regulation of miR-200 is reported to enhance the expression of SNAIL and SLUG (79). Studies have shown that miR-34/SNAIL/miR-200/ZEB1 can regulate EMT dynamics (80). Inhibition of miR-200c/141 results in the upregulation of *VIM* and *SNAIL* in breast cancer stem cells (29). MiR-424/503 is another miRNA cluster with tumor suppressive function, the downregulation of which is correlated with resistance to chemotherapy in breast cancer (81). Thus, taken together, miRNA clusters are important regulators of SNAIL expression.

#### 4.4. TWIST and miRNA cluster

*TWIST1* and *TWIST2* belong to the basic helix-loop-helix (bHLH) transcription factor family. They promote EMT and enhance the motility and dissemination of cancer cells (82). In benign tumors activation of TWISTs favors malignant transformation

via inhibition of apoptosis and senescence pathways. TWIST proteins with their bHLH motif recognize E-box and can act as an activator or repressor of target gene expression (83). TWIST overexpression is correlated with aggressive cancer, poor prognosis, metastasis, and poor survival. Pathways such as Wnt, IGF, EGF, TNF- $\alpha$ , IL-17 either induce TWIST expression or stabilize via their target genes (NF- $\kappa$ B, STAT3, and c-MYC) (16, 84–87). Cytokines, chemokines (IL6, EGF) and hypoxia are reported to induce the expression of TWISTs to promote EMT (17, 86, 88).

Many miRNA clusters participate in the TWIST induced EMT program. MiR-15a-3p and miR-16-1-3p belonging to the miR-15 cluster, are reported to inhibit invasion and metastasis of gastric cancer cells by *TWIST1* repression (89). *TWIST1* is also reported to regulate the expression of miRNA clusters. An example includes the regulation of miR-199a/214 cluster expression by *TWIST1* during development (90). In breast cancer, it induces EMT via the miR-373-TXNIP-HIF1 $\alpha$ -TWIST signaling axis (91). Both up and down-regulation of the members of the miR-199a/214 cluster are reported to contribute to EMT in cancer (92). Transcription of miR-214 is regulated by *TWIST1* and *ZEB1* (93). MiR-424(322)/503 is another miRNA cluster linked with TWIST. The upregulation of miR-424 in TWIST1 or SNAIL-induced EMT is reported (94). MiR-106b/25 is

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an oncogenic cluster in many cancers and has two paralogs in humans namely miR-106b/25 and miR-17/92. MiR-106b is a pro-metastatic miRNA cluster in hepatocellular carcinoma cells (95). Hypoxia is reported to induce EMT via controlling miRNA cluster expression. For instance, Twist/miR-214/CDH1 interaction is promoted by hypoxia in the induction of renal tubular EMT (96). MiR-524-5p is a member of the chromosome19 miRNA cluster (C19MC) which directly targets *TWIST1* to inhibit EMT (97). Taken together, miRNA clusters and the TWIST axis could be a potential target in cancer therapy.

### 4.5. ZEB and miRNA cluster

*ZEB1* and *ZEB2* are located in short arm of chromosome 10 and 2 belonging to zinc finger E-box binding homeobox (ZEB) family. ZEB family induces EMT most often through activating genes such as *CDH2*, Vitronectin (*VTN*) and MMPs. ZEB induced EMT also shows the downregulation of *CDH1*, Claudins, *ZO-1*, and plakophilins. ZEBs are commonly known as Smad interacting protein 1 (SIP1) consisting of two zinc finger clusters and a central homeodomain (98). ZEB induced EMT also involves miRNA clusters. MiR-200c/miR-141 targets *ZEB1* and *ZEB2* thereby inhibiting migration and EMT in head and neck cancer cells (99). Loss of miR-200c/miR-141 cluster is important for lymph endothelial invasiveness in 5-fluorouracil resistant cells (100). By targeting members of C terminal binding protein (CtBP)/ZEB complex, miR-141-200c cluster regulates EMT (101). MiR-143/145 is downregulated in multiple cancers and is an EMT and metastatic suppressor. In response to stress, serum starvation or anti-cancer agents, p53 can activate this cluster. This miRNA cluster is suppressed by activated Ras via binding to Ras-responsive element-binding protein (RREB1) (102). MiR-132 suppresses lung cancer cell migration by targeting *ZEB2* (103). MiRNA-23b/27b/24 is an oncogenic miRNA cluster that promotes metastasis of breast cancer by suppressing Prosaposin (PSAP) (104). MiR-23b targets Protein Tyrosine Kinase 2 Beta (*PTK2β*) and suppresses EMT and metastasis in hepatocellular carcinoma (105). MiR23b targets *ZEB1*, and acts as a tumor suppressor preventing migration and invasion of bladder cancer cells (106). MicroRNA-200/ZEB/CDH1 and miR-

200/ZEB/TGF- $\beta$  axis are also reported in cancer (107, 108). MiR-544 is a member of the miR-379/miR-544 cluster and highly expressed in neonatal muscle. MiR-544's role as an oncogene is established in gastric cancer. It promotes invasion of lung cancer cells by targeting *CDH1* and upregulation of *VIM*. MiR-544a induces EMT by activation of WNT signaling in gastric cancer and immune escape in hepatoma cells. Reduction of *CDH1* and upregulation of *VIM*, *SNAI1*, and *ZEB1* by miR-544a induces EMT (109). MiR-544a directly targets *CDH1* and *AXIN2* leading to nuclear translocation and stabilization of *CTNBN1*. These data collectively suggest that the expression of ZEB is regulated by miRNA cluster and that ZEB along with other EMT-TFs induces EMT and metastasis in multiple cancer. Thus, targeting the ZEB-miRNA cluster axis could be used for the management of cancer.

Taken together, a wide array of transcription factors is associated and required to drive the multistep EMT program and are being regulated by a variety of EMT-TFs and signaling pathways. The EMT-TFs acting exclusively or synergistically, and target common pathways to induce EMT. MiRNA clusters reported to regulate multiple signaling pathways associated with EMT are discussed below.

## 5. miRNA CLUSTERS AND SIGNALING PATHWAYS

Major signaling pathways responsible for the induction of EMT include tyrosine kinases, integrin-linked kinase, RAS, Wnt, Notch, and Hedgehog. miRNA clusters and target signaling pathways are listed in Table 3.

### 5.1. Tyrosine kinases pathway

Receptor tyrosine kinases (RTKs) are high-affinity transmembrane receptors which bind to growth factors, cytokines, and hormones. RTKs play an important role in growth, proliferation differentiation and movement of cells (122). RTKs, inappropriately regulated, and expressed in many cancer types, are strongly implicated in EMT (15). Binding of growth factors (EGF, FGF, IGF, HGF,



CFC) to RTKs leads to activation of EMT-TFs such as SNAIL, SLUG, ZEB and TWIST via multiple signaling axis notably PI3K-AKT-glycogen synthase kinase 3 beta (GSK3 $\beta$ )- $\beta$ -catenin axis or RAS-MAPK signaling (15).

The miRNA cluster can either activate or inhibit the expression of tyrosine kinase pathway genes (123). For example, miRNA cluster 23a/24-2 regulates EGFR and c-MET expression in lung cancer. Cancer cell invasion and metastasis are driven by c-MYC induced miR-23a/27a cluster (124). The treatment of NSCLC cells by TGF- $\beta$ 1 activates miR-134/miR-487b/miR-655 cluster. MiR-134/miR-487b/miR-655 by targeting membrane-associated guanylate kinase (*MAGI2*) induces gefitinib resistance (42). In chronic myelogenous leukemia (CML) both miR-17/92 cluster and tyrosine kinase activity were reported (125). Overexpression of receptor tyrosine kinases and miR-221/222 is reported in breast cancer. MET, EGF, and miR-3a/24-2 interaction are reported in non-small cell lung cancer (124). MiR-143/145 cluster is downregulated in KRAS mutant pancreatic cancer cells. Further, forced expression of this miRNA cluster inhibited tumorigenesis (126). Interestingly, the miR-143/145 cluster also targets *KRAS* and *RREB1* and is an inhibitor of Ras signaling (127). MiRNA clusters can promote EMT by targeting and inhibiting negative regulators of PI3K-AKT signaling. For example, miR-106b/25 (128), miR-23a/24-2 (129) and miR-17/106 (130) activate PI3K- AKT signaling by downregulation of *PTEN*. MiR-27a belonging to miR-23a/24-2 synergizes with AKT by targeting *FOXO1* (131). MiR-15/16 is a tumor suppressive cluster that inhibits prostate cancer cell invasion by suppressing the TGF- $\beta$  signaling pathway (132). TGF- $\beta$  and FGF-2 are reported to promote EMT in lung adenocarcinoma (PC-9 and HCC-827) cells through Smad3, MEK/extracellular-signal-regulated kinase (ERK), and mTOR pathways. Overexpression of miR-16 reduces the expression of fibroblast growth factor receptor 1 (*FGFR1*) and vascular endothelial growth factor receptor 2 (*VEGFR2*) in endothelial cells (133). MiR-143/145 is repressed by the activation of EGFR and Ras signaling (114). The miR-143 expression has been negatively correlated with EGFR in NSCLC cells.

Transfection studies have shown that EGFR is a target of miR-143. MiR-99a/let-7/miR-125b is downregulated in malignant pleural mesothelioma (134, 135). MiRNA-99a targets (insulin-like growth factor 1 receptor) IGF1R/PI3K/AKT/mTOR and inhibits proliferation, migration, and invasion of cancer cells (136). Thus, altered expression of miRNAs can lead to inappropriate activation of tyrosine kinase pathways contributing to aggressiveness, progression and tumor resistant phenotypes in cancer cells via activation of EMT.

### 5.2. Integrin-linked kinase (ILK) pathway-integrin signaling

ILKs belong to Raf-like kinases (RAF) subfamily and are an intracellular serine/threonine kinase. It consisting of 5 ankyrin repeats, a phosphoinositide binding motif, and a kinase catalytic domain. ILKs act as a regulator of development and tissue homeostasis (137, 138). Being a downstream mediator of the Smad-TGF- $\beta$ 1 signaling pathway, the ILK pathway is implicated in EMT and the acquisition of invasive and metastatic phenotypes (138). ILKs interact with integrins and can be stimulated by growth factors and chemokines in a PI3K dependent manner. Overexpression of ILKs is reported in multiple cancers and inhibition of their activities could be used as a potential mechanism to control invasion and metastasis in cancer (139). ILKs are required for integrin-dependent focal adhesion. ILKs promote EMT via AKT1/GSK3 $\beta$ /CTNNB1 axis. Forced expression of ILK increased invasion and migration of cancer cells through nuclear translocation of CTNNB1 and downregulation of CDH1 (140). MiR-424/503 cluster expression is downregulated in SRC-transformed cells with its forced expression inhibiting cancer cell invasion (141). MiR-23b and miR-27b belonging to miR-23b/24-1 have also been downregulated during cSrc-induced transformed cells (142). MiRNAs have been reported to regulate the expression of specific integrins. The miR-17/92 cluster consists of 6 miRNA encoding genes namely miR-17, miR-18a, miR-19a, miR-19b, miR-20a and miR-92a (143). MiR-92a is reported to suppress integrin  $\alpha$ 5 expression (144). In renal cell cancers, integrin  $\alpha$ 5 promotes metastasis (145). In ovarian cancer, the silencing of ILK upregulates miR-15a-miR-16-1 cluster (113). Integrin- $\alpha$ 6 $\beta$ 4 is a receptor for

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laminin binding which promotes motility of cells in various types of cancer. In breast cancer, Integrin- $\alpha 6\beta 4$  downregulates the expression of miR-25/32/92abc/363/363-3p/ 367 and miR-99ab/100 (146).

### 5.3. Ras pathway

Ras is a small GTP-binding protein that controls proliferation, differentiation, adhesion, apoptosis, and migration of cells in normal and pathological conditions (147). Overexpression of Ras signaling promotes growth, proliferation, migration, and invasion of cancer cells. Ras overexpression induces actin cytoskeleton remodeling, inhibits apoptosis and confers resistance to anticancer agents (147). Ras signaling induced EMT involves activation of MAPK, Hypoxia-Inducible Factor 1-Alpha (HIF1 $\alpha$ ) and PI3K/AKT/mTOR pathways, induction of *SANIL2*, *TWIST1/2*, *ZEB1*, and inhibition of *CDH1* (148). Activation of the RAS pathway is reported to regulate the expression of many miRNA clusters and vice versa (149). Ras initiates tumor-promoting pathways by repression of the miR-143/145 cluster (126). MiR-379/miR-656 is a downregulated miRNA cluster in glioblastoma (GBM) (127). Lassad *et al* 2015, showed an inverse correlation between expression of CYLD lysine 63 deubiquitinase (*CYLD*) and *KRAS* with the miR-183-96-182 cluster (150). The upregulation of AKT signaling is reported to induce EMT. MiR-154 and miR-37, belonging to DLK1-DIO3 microRNA mega-cluster, is elevated in prostate cancer, and it results in activation of E2F signaling, Ras pathway, hypoxia-inducible factor signaling, and the WNT and TGF- $\beta$  pathways (151). MiR-144/451 inhibits esophageal cancer cell migration by downregulation of ERK/c-Myc signaling (152). Many previous studies have established the role of the Ras–MEK–ERK signaling pathway in EMT. The miR182 activates Ras–MEK–ERK signaling by suppressing RAS p21 protein activator 1 (*RASA1*) and sprouty-related EVH1 domain containing 1 (*SPRED1*) expression in squamous cell carcinoma of the oral cavity (153). *KRAS* overexpression induces NF- $\kappa$ B and inhibits *CDH1* expression via *SNAIL* and *MMP9* (154, 155). Ras-Raf-MEK1/2-ERK activates *SLUG* and represses *CDH1* expression (156). Ras-Ral-RAC family small GTPase (Rac), P21 activated kinases

(PAK), Myosin light chain phosphatase (MLCP), Megalencephalic Leukoencephalopathy with Subcortical Cysts 1 (MLC) axis are implicated in focal adhesion formation contributing to EMT (157). MiR-23/24/27 cluster is downregulated in keratinocytes having HRas protooncogene (HrasG12 V) (158). MiR-17-92 regulation of Ras signaling is also reported (159). MiR-411 is a member of 4q32.31 miRNA cluster which promotes growth, proliferation, and metastasis in non-small-cell lung carcinoma (NSCLC) cell (160). miR-411-5p targets growth factor receptor bound protein 2 (GRB2)-son of sevenless homolog (SOS)-Ras signaling to prevent migration and invasion of breast cancer cells (161). Activation of the miR-221/222 cluster by Ras signaling is reported in basal-like breast cancer cells resulting in induction of EMT by downregulation Transcriptional Repressor GATA Binding 1 (TRPS1), a repressor of *ZEB2* (115, 116).

### 5.4. Notch signaling pathway

Notch signaling is one of the highly conserved signaling pathways important for a cell to cell communication, cell differentiation, proliferation, invasion, migration, and apoptosis. Activation of Notch is reported to drive aberrant expression of EMT-TFs such as *TWIST*, *SNAIL*, *SLUG*, and *ZEB1/2*, with concomitant downregulation of *CDH1* (162). Notch signaling activates genes associated with differentiation, survival, migration, invasion such as *CCND1*, c-Myc, and others. Notch crosstalk with EMT-TFs (*SNAIL*, *SLUG*) and growth factors (TGF- $\beta$ , FGF, and PDGF) is implicated in EMT, chemoresistance, and metastasis (162). Overexpression of miR-200b inhibits Notch-1 expression (163, 164). Direct repression of the Delta/Notch pathway by miR-449 cluster controls vertebrate multiciliogenesis (165). Notch signaling can also activate oncogenic miRNA clusters. For instance, the activation of miR-17/92 in cancer by the Notch pathway leads to cellular proliferation. MiR-17/92 cluster promoter is predicted to poses a binding site for Hes family transcription factor 1 (*HES1*), an effector of Notch signaling. Moreover, B-Raf proto-oncogene (BRAFV600E) induces the expression of miR-17-92 via activation of Notch signaling (166). MiRNA-134 is a member of the delta-like non-canonical notch ligand -

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iodothyronine deiodinase (DLK1-DIO3) cluster. MiR-134 is reported to regulate the expression of protein O-glucosyltransferase 1 (POGLUT1) and Notch pathway proteins in human endometrial cancers (167). Members of miR-206/miR-133b are reported to target NOTCH 3 in HeLa cells (168, 169).

### 5.5. Wnt signaling pathway

Activation of the canonical Wnt pathway, non-canonical planar cell polarity pathway, and non-canonical Wnt/calcium pathway is reported in various cancers. Many members of WNT signaling (WNTs, CTNNB1) either directly or indirectly activates SNAIL, SLUG, ZEB1/2, TWISTs, inhibit CDH1, and participate in the induction of EMT program (15, 170). MiRNA clusters are important for precise regulation of WNT signaling. Aberrant expression of miRNA clusters is reported to activate WNT signaling and to contribute to EMT. For example, transactivation of miR-371-373 by CTNNB1/ lymphoid enhancer binding factor 1 (LEF1) modulates Wnt/ $\beta$ -catenin-signaling pathways (171). MiR-30a/b/c/d/e-5p interaction with members of the canonical WNT pathway is reported to affect the treatment outcome in multiple myeloma (172). Crosstalk between PTEN/PI3K and Wnt pathway plays an important role in the subcellular localization of CTNNB1. Activation of the Wnt/ $\beta$ -catenin pathway and loss of *PTEN* activity is important for the initiation and progression of endometrial cancer (173). MiR-17/92 cluster by targeting PTEN/PI3K pathway promotes chemotherapeutic resistance and metastasis (174, 175). Metastasis suppressor protein 1 (*MTSS1*) is regulated by *PTEN* and is reported to inhibit EMT via inactivation of PI3K/AKT signaling (176). MiR-200a is an inhibitor of *CTNNB1*. MiR-145 is a tumor-suppressive miRNA belonging to the miR-143/miR-145 cluster. It targets catenin  $\delta$ -1, disturbs the nuclear translocation of CTNNB1, and inhibits the transcription of c-Myc and *CCND1* (177).

### 5.6. Hedgehog signaling pathway

This pathway plays an important role in embryonic development, adult tissue

maintenance, renewal, regeneration, differentiation, polarity, and proliferation. The defect in the hedgehog signaling pathway is reported in some cancers, especially during metastasis (178). It is a crucial regulator of EMT and is responsible for chemoresistance properties of human pancreatic Panc-1 cancer stem cells (179). Hedgehog (Hh) signaling participates in metastatic cascade by induction of EMT and angiogenesis (180). Hh signaling contributes to tumor development by inducing the expression of pro-tumorigenic genes such as *CCND1*, *ABCG2*, *BCL2*, *SNAIL*, *WNT2*, *VEGF* and *TGF- $\beta$*  (181). In liver cancer, hedgehog enhances the expression of FAK/AKT, leading to increased secretion of MMP2 and MMP9 inducing EMT (182). Hedgehog via patched (*PTCH*) and glioma-associated oncogene (*GLI*) is reported to induce SNAIL expression and EMT (183). Human medulloblastoma shows constitutive activation of Sonic Hedgehog signaling and overexpression miR-17/92 cluster (184, 185). MiR-193b/365a cluster is downregulated in cutaneous squamous cell carcinomas (186). Hedgehog signaling activates its downstream target genes such as *BCL2*, *FOXC2*, Jagged 2 (*JAG2*), and *MYCN* via Smoothened (*SMO*) and *GLI* (187). MiR-193b is a transcriptional repressor of *SMO*. In colorectal cancer, hedgehog promotes EMT by activation of MMP2 and MMP9 via the induction of FAK and AKT. MiR-125b belonging to miR-99a/let-7c/miR-125b cluster expression is significantly low in ovarian, oral, cholangiocarcinoma and prostate cancer (188–191). MiR-125b has been reported to inhibit EMT by targeting hedgehog (192).

## 6. CONCLUSION

Taken together, miRNA clusters are a key regulator of the EMT process. Aberrant expression of miRNA contributes to the acquisition of various hallmarks of cancer including EMT. During metastasis, cancer cells adapt to permanently changing microenvironment and undergo transitions from differentiated to undifferentiated or partial EMTs (193). The partial or incomplete EMTs are activated by EMT-TFs. They increase the motility of cancer cells and favors metastasis and invasion. Apart from activation of EMT, EMT-TFs has several other

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functions such as double-strand repair, senescence, pro-survival and anti-apoptotic phenotype under various types of stress conditions (194). Also, these EMT-TFs are tissue-specific, for example, SNAIL triggers metastasis in breast cancer with no effect being reported in pancreatic cancer (195). Therefore, further detailed studies are required to elucidate the role of miRNAs in partial EMT during cancer metastasis. With the involvement of miRNA clusters in various health and disease conditions, it is quite relevant to explore and understand the possibility of miRNA clusters in therapy as reviewed by Kabekkodu *et al.*, 2018 (197). Unraveling miRNA regulation in EMT will make the mechanism more transparent and is likely to uncover novel biomarkers for different cancer types. Taken together, miRNA cluster and EMT-TF cross-talk coordinately regulate multiple members of pro-EMT signaling pathways and promotes EMT. Thus, inhibition of pro-EMT miRNA clusters or reactivation of anti-EMT miRNA clusters may be beneficial in controlling EMT and cancer metastasis.

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**Abbreviations:** EMT, epithelial to mesenchymal transition; miRNA, microRNA; ZEB1, Zinc finger E-box binding homeobox 1; Wnt, -wingless; ECM, extra cellular matrix; Hh, Hedgehog; FOXO1, forkhead box protein O1; PTEN, phosphatase and tensin homolog; ECM, extra cellular matrix; CDH1, Cadherin 1; CTNBB1, Catenin Beta 1; RAC1, Rac family small GTPase1; RHO, Rhodopsin; CDC42, Cell division cycle 42; PAR, partition-defective; PATJ, Protein associated to tight junctions; MMP, matrix metalloproteinases; EMT-TFs, EMT-transcription factors ; TGF- $\beta$ , transforming growth factor beta; RTKs, receptor tyrosine kinases; HIF1 $\alpha$ , hypoxia-inducible factor 1 $\alpha$ ; JAK/STAT, Janus kinase2/signal transducer and activator of transcription; TNF $\alpha$ , tumor necrosis factor alpha; TNFR, TNF receptor superfamily member 1A; NF $\kappa$ B, nuclear factor kappa B subunit 11; IKB, IKappaB; IL6, interleukin 6; EGF, Epidermal growth factor; PI3K-AKT-mTOR, Phosphoinositide-3-Kinase- AKT Serine/Threonine Kinase 1-Mammalian Target Of Rapamycin; Ras-MAPK, Rat sarcoma-mitogen-activated protein kinase 1; MKK, mitogen-activated protein kinase kinase1; LOX, Lysyl oxidase; HIPK1, Homeodomain Interacting Protein Kinase 1; PTEN, phosphatase and tensin homolog; SOCS1, suppressor of Cytokine Signaling 1; *CDKN1B*, Cyclin-Dependent Kinase Inhibitor 1B; GHR, Growth Hormone Receptor; TRAF3, TNF Receptor Associated Factor 3; ASCL2, Achaete-Scute Family BHLH Transcription Factor 2; FOXF2, Forkhead Box F2; CCND1, cyclinD1; SSH1, Slingshot Protein Phosphatase 1; LIMK1, LIM Domain Kinase 1; *FGFD4*, fibroblast growth factor 4; SNAIL2,

Snail Family Transcriptional Repressor 2; VIM, vimentin VIM; MDCK, madin-darby canine kidney; BRMS1L, breast cancer metastasis suppressor 1-like; ITGB1, integrin beta 1; KLF4, Kruppel-like factor 4; SNAIL1, Snail Family Transcriptional Repressor 1; MET, MET proto-oncogene;  $\beta$ -TRCP2, F-box and WD repeat domain containing 11; MTSS1, metastasis suppressor 1; TGIF2, TGFB induced factor homeobox; YWHAG, Tyrosine 3-Monooxygenase/Tryptophan 5-Monooxygenase Activation Protein Gamma; TIMP3, TIMP metalloproteinase inhibitor 3; bHLH, basic helix-loop-helix; C19MC, chromosome19 miRNA cluster; SIP1, smad interacting protein 1; RREB1, Ras-responsive element-binding protein; PSAP, Prosaposin; GSK3 $\beta$ , glycogen synthase kinase 3 beta; MAGI2, membrane-associated guanylate kinase; CML, chronic myelogenous leukemia; ERK, extracellular-signal-regulated kinase; VEGF, vascular endothelial growth factor; IGF1R, insulin like growth factor 1 receptor; RAF, RAf-like-kinases; GBM, Glioblastoma; CYLD, CYLD lysine 63 deubiquitinase; RAL, RAL GTPase; RAC, RAC family small GTPase; PAK, P21 activated kinases; MLCP, myosin light chain phosphatase; MLC, Megalencephalic Leukoencephalopathy With Subcortical Cysts 1; HRAS, HRas proto-oncogene; NSCLC, non-small-cell lung carcinoma, GRB2, growth factor receptor bound protein 2; SOS, son of sevenless homolog; TRPS1, Transcriptional Repressor GATA Binding 1; HES1, Hes family transcription factor 1; BRAF, B-Raf proto-oncogene; DLK1, delta like non-canonical notch ligand; DIO3, iodothyronine deiodinase; POGLUT1, protein O-glucosyltransferase 1; LEF1, lymphoid enhancer binding factor 1; MTSS1, Metastasis suppressor protein 1; PTCH, Patched1; GLI, glioma-associated oncogene; JAG2, Jagged 2

**Key Words:** MicroRNA cluster, EMT, Signaling

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