SUPPLEMENTARY FIGURES

miRNA Name	Cancer Abbreviation	T-Test P-value	T-Test FDR	Upregulated in:	Tumor Log2 Mean Expression	Normal Log2 Mean Expression
hsa-miR-214- 3p	BRCA	6.67e- 05	1.78e- 04	Normal	2.32	2.90
hsa-miR-214- 3p	COAD	7.58e- 04	2.79e- 03	Normal	1.24	4.64
hsa-miR-214- 3p	KICH	1.20e- 10	2.73e- 09	Normal	0.13	2.11
hsa-miR-214- 3p	KIRC	8.05e- 17	7.39e- 16	Normal	0.59	2.19
hsa-miR-214- 3p	KIRP	1.89e- 17	1.24e- 14	Normal	0.31	2.61
hsa-miR-214- 3p	LIHC	2.86e- 12	9.62e- 11	Normal	1.09	3.05
hsa-miR-214- 3p	PCPG	2.57e- 02	3.52e- 01	Normal	1.05	2.63
hsa-miR-214- 3p	READ	4.40e- 03	3.70e- 02	Normal	2.21	5.41
hsa-miR-214- 3p	STAD	1.06e- 07	1.00e- 06	Tumor	2.98	1.67
hsa-miR-214- 3p	THCA	6.91e- 17	3.36e- 15	Normal	0.97	3.01

Supplementary Figure 1. The ONCOMIR data indicated that there are 10 cancer types in which tumorigenesis is significantly associated with the expression of miR-214-3p. The data are represented as the means±S.D. from at least three independent experiments. *P<0.05.



Supplementary Figure 2. (A) MiR-214-3p expression was significantly upregulated after transfection with the miR-214-3p mimic but downregulated after transfection with the LV-miR-214-3p inhibitor. (B-E) Colony-formation and EdU assays revealed that miR-214-3p suppresses CRC cell proliferation. (F-G) Western blot analysis revealed that miR-214-3p decreased the expression of cyclin D1, cyclin E and CDK4 and increased the expression of P27. The data are represented as the means±S.D. from at least three independent experiments. *p<0.05.



Supplementary Figure 3. (A–B) Wound-healing assays indicated that miR-214-3p suppressed the migration of CRC cells. (C) qRT-PCR assays showed that miR-214-3p decreased the expression of N-cadherin and vimentin and increased the expression of E-cadherin and Zo1. (D) IF assays showed that miR-214-3p decreased the expression of N-cadherin and increased the expression of E-cadherin. The data are represented as the means±S.D. from at least three independent experiments. *p<0.05.



Supplementary Figure 4. (A–F) The expression levels of the potential targets of miR-214-3p according to the Starbase 3.0 database. (G–H) IF assays showed that miR-214-3p inhibited the expression of PLAGL2. (I) Predicted binding site in the 3'-UTR of PLAGL2. The data are represented as the means \pm S.D. from at least three independent experiments. **P*<0.05.



Supplementary Figure 5. (A–D) WB and qRT-PCR assays revealed that PLAGL2 increased the expression of N-cadherin and vimentin and decreased the expression of E-cadherin and Zo1. (E–F) EdU and colony formation assays revealed that PLAGL2 promoted CRC cell proliferation. (G–H) Transwell and wound-healing assays showed that PLAGL2 promoted the migration and invasion of CRC cells. The data are represented as the means±S.D. from at least three independent experiments. **P*<0.05.



Supplementary Figure 6. (A–B) EdU assays revealed that PLAGL2 downregulation effectively reverses miR-214-3p inhibitor-induced CRC cell proliferation. (C–E) Wound-healing assays indicated that PLAGL2 downregulation effectively reverses miR-214-3p inhibitor-induced CRC cell migration. (F–I) Western blot and qRT-PCR assays indicated that the inhibitory effect of miR-214-3p on EMT was reversed by Sh-PLAGL2 transfection. The data are represented as the means±S.D. from at least three independent experiments. **P*<0.05.



Supplementary Figure 7. (A) IHC analysis indicated that the expression of MYH9 was higher in tumor tissues. (B) IHC analysis indicated that the expression of MYH9 could be regulated by miR-214-3p and PLAGL2, and the inhibition effect of miR-214-3p on MYH9 could be reversed by Sh-PLAGL2 in subcutaneous xenograft tissues. The data are represented as the means±S.D. from at least three independent experiments. **P*<0.05.



Supplementary Figure 8. (A) EdU assays revealed that MYH9 downregulation effectively reversed miR-214-3p inhibitor-induced CRC cell proliferation. (B–E) Transwell and wound-healing assays indicated that MYH9 downregulation effectively reversed miR-214-3p inhibitor-induced CRC cell migration. The data are represented as the means \pm S.D. from at least three independent experiments. **P*<0.05.