Table S1 List of all primers

Primer	Sequence (5’ to 3’)
OligodT Adapter:	GCGAGCACAGAATTAATACGACTCACTATAGGTTTTTTTTTTTTVN
Let-7d-F(forward primer)	AGAGGTAGTAGGTTGCATAGTT
Let-7d-R (reverse primer)	GCGAGCACAGAATTAATACGAC
U6-F	CTCGCTTCGGCAGCACA
U6-R	AACGCTTCACGAATTTGCGT
IL-10-F	TCCCTGTGAAAACAAGAGCA
IL-10-R	ATAGAGTCGCCACCCTGATG
IL-13-F	GCTTAGACCTCAGCCTGTGC
IL-13-R	GTTGCCTGTGTGTGAAGTGG
TNF-α-F	TGTAGCAAACCCTCAAGCTG
TNF-α-R	TTGATGGCAGAGAGGAGGTT
TGF-β-F	CAACAATTCCTGGCGATACC
TGF-β-R	GAACCCGTTGATGTCCACTT
PIGF-F	ACCAAACCTCAAAGCATGGC
PIGF-R	TAGCCAAAGGTCGCTCCAAG
CD204-F	GGGAA CATTCTCAGACCTTG
CD204-R	AA TCCTCGTGGACCACTTTC
CD68-F	TCAGCTTTGGATTCATGCAGG
CD68-R	AAAGAATGATGCTCGAGTTGC
VEGF-F	AGGCCAGCACATAGGAGAGA
VEGF-R	ACGCGAGTCTGTGTTTTTGC
PDGFA-F	TGCGGTCTTTGTTCTCCTCC
PDGFA-R	TCTGGAGTCGTTCCCAAAGC
MMP-9-F	GGACAAGCTCTTCGGCTTCT
MMP-9-R	TTCAGGGCGAGGACCATAGA
PDGFB-F	TGTGCGGAAGAAGCCAATCT
PDGFB-R	CTAGGCTCCAAGGGTCTCCT
b-FGF-F	CTTCTCGAACCGCTGTGTCT
b-FGF-R	GGAACTGCAGCCATGCAAAA
IL-1β-F	ACGATGCACCTGTACGATCA
IL-1β-R	TCTTTCAACACGCAGGACAG
IL-6-F	TACCCCCAGGAGAAGATTCC
IL-6-R	TTTTCTGCCAGTGCCTCTTT
CD163-F	TGGACCGATATGGCTCAATG
CD163-R	AGCGACCTGTTGTGGCTTTT
CD206-F	GGGTTGCTATCACTCTCTATGC
CD206-R	TTTCTTGTCTGTTGCCGTAGTT
CD80-F	AAAGTGTACGCCCTGTATAACA
CD80-R	TGTGCCCACCATATTCC

CD86-F	GAGGGAAGAGAGTGAACAGAC
CD86-R	GAGCAGAGCTGGAGTTACAG
HLA-DR-F	GCCCAACCTGGAAATCATGACA
HLA-DR-R	AGGGCTGTTGTGAGCACA
CCL22-F	CGAGGAAGAGGT TCGGTTCACC
CCL22-R	CAT CTTCACCCAGGGCACTCT
GAPDH-F	AATCCCATCACCATCTTCCA
GAPDH-R	TGGACTCCACGACGTACTCA

Figure S1. Downregulation of let-7d was associated with lymphatic metastasis and poor prognosis in RCC. (A) Relative let-7d expression in normal kidney tissues and RCC tissues from TCGA RCC (KIRC, KIRP, KICH) dataset. (B) Relative let-7d expression between N1 and N0 stage from TCGA RCC dataset. Horizontal lines in (A-B) represent the median value of let-7d expression. RPM, reads per million. (C) Kaplan-Meier curves of overall survival (OS) time between high and low let-7d group using Log-rank (Mantel-Cox) test in 71 ccRCC patients from TCGA KIRC dataset. Cutoff value as indicated. The TCGA RCC RNA-Seq gene expression data and the clinical data were downloaded from the UCSC Xena database (http://xena.ucsc.edu/). (D) A linear regression and correlation in data from qRT-PCR vs. MVD in RCC tissue from 80 patients in our institute was shown with r (spearman) and P-values indicated. Expression status was shown in a log scale.

Figure S2. Quantitative RT–PCR analyses of the expression of angiogenic factors in the M0 macrophages cocultured with let-7d-overexpressing or control RCC cells. (A) Expression of VEGF, PDGFA, PDGFB, bFGF and MMP-9 in M0 macrophages cocultured with let-7d-overexpressing or control 786O cells. (B) Expression of VEGF, PDGFA, PDGFB, bFGF and MMP-9 in M0 macrophages cocultured with let-7d-overexpressing or control 769P cells. The mRNA expression was normalized to GAPDH mRNA. The data represented the mean ± SD of three independent RT–PCRs (RNAs were from the same set). Different numbers between two groups were analyzed by two-tailed Student's t test. $^{*}p<0.05$.

Figure S3. Upregulation of CD68 and CD204 was associated with high stage of the disease and poor prognosis in RCC. (A) Relative CD68 mRNA expression level in normal kidney tissues and RCC tissues from TCGA RCC (KIRC, KIRP, KICH) dataset. (B) Relative CD68 mRNA expression level in different stage of the disease from TCGA RCC dataset. (C) Kaplan-Meier curves of overall survival (OS) time between high and low CD68 expression group using Log-rank (Mantel-Cox) test in 174 RCC patients from TCGA RCC dataset. Cutoff value for high group: 90th percentile, low group: 10th percentile (total n=864). (D) Relative CD204 mRNA expression level in normal kidney tissues and RCC tissues from TCGA RCC (KIRC, KIRP, KICH) dataset. (E) Relative CD204 mRNA expression level in different stage of the disease from TCGA RCC dataset. (F) Kaplan-Meier curve of overall survival (OS) time between high and low CD204 (MSR1) expression group using Log-rank (Mantel-Cox) test in 88 RCC patients from TCGA RCC dataset. Cutoff value for high group: 95th percentile, low group: 5th percentile (total n=864). (G)

The linear regression and correlation between CD 68 mRNA expression and CD 31 mRNA expression in TCGA RCC dataset. (H) The linear regression and correlation between CD 204 mRNA expression and CD 31 mRNA expression in TCGA RCC dataset. Horizontal lines in (A, B, D, E) represent the median value of mRNA expression. The TCGA RCC RNA-Seq gene expression data and the clinical data were downloaded from the UCSC Xena database (http://xena.ucsc.edu/). Survival plots in C and F were obtained using the GEPIA web server (http://gepia.cancer-pku.cn/detail.php). FPKM, fragments per kilobase million. TMP, transcripts per million.