Supplementary Materials

The Role of MicroRNAs in the Regulation of Gastric Cancer Stem Cells: A Meta-Analysis of the Current Status

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Table S1. Significant KEGG pathway by predicted up regulated miRNAs.

KEGG pathway	*p-value*	N. of Genes	N. of miRNAs
Metabolism of xenobiotics by cytochrome P450	0	3	1
TGF-beta signaling pathway	3.96E-05	19	3
Estrogen signaling pathway	0.0002	16	3
Prolactin signaling pathway	0.0005	20	2
Axon guidance	0.0017	27	2
Lysine degradation	0.0023	7	1
Hippo signaling pathway	0.0080	19	1
Regulation of actin cytoskeleton	0.0177	32	1
Biotin metabolism	0.0261	1	1

P-value < 0.05 was considered as statistically significant.

Table S2. Significant KEGG pathway by predicted down regulated miRNAs.

KEGG pathway	*p-value*	N. of Genes	N. of miRNAs
Lysine degradation	0	14	10
Signaling pathways regulating pluripotency of stem cells	0	60	11
Estrogen signaling pathway	0	29	13
Proteoglycans in cancer	0	67	13
TGF-beta signaling pathway	0	36	16
Axon guidance	1.05E-08	39	11
Prion diseases	0.0001	3	1
Thyroid hormone signaling pathway	0.0004	21	2
Glioma	0.0012	26	8
MAPK signaling pathway	0.0019	65	6
Neurotrophin signaling pathway	0.0045	25	8
FoxO signaling pathway	0.0103	48	4
Prolactin signaling pathway	0.0193	20	7
Morphine addiction	0.0245	19	6
Hippo signaling pathway	0.0271	46	5
Regulation of actin cytoskeleton	0.0316	35	6
Pancreatic cancer	0.0387	10	2
Chronic myeloid leukemia	0.0475	22	3

P-value < 0.05 was considered as statistically significant.

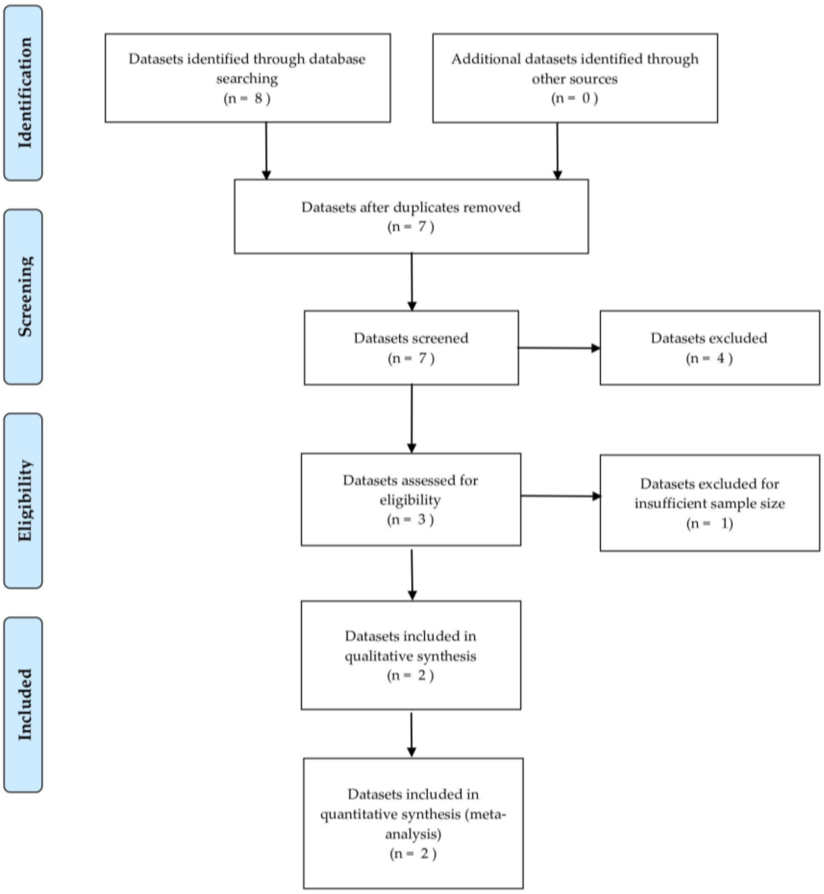

Figure S1. PRISMA (Preferred Reporting Items for Systemic Reviews and Meta-Analyses) flow diagram.