Supplemental Tables

Table S1 Sequences of PCR primers and shRNA

PCR primers and shRNA	
CDX2	Forward: 5’- TTCACTACAGTCGCTACATCACC -3’ Reverse : 5’- TTGTTGATTTTCCTCTCCTTTGC -3’
KLF4	Forward: 5’- GTGCCCCGAATAACAGCTCA -3’ Reverse : 5’- TTCTCACCTGTGTGGGTTCG -3’
MUC2	Forward: 5’- AGTCCATCCTGCTGACCATC -3’ Reverse : 5’- GGTGTAGGCATCGCTCTTCTC -3’
VILLIN	Forward: 5’- GGCAAGAGGAACGTGGTAGC -3’ Reverse : 5’- CGGTCCATTCCACTGGATGA -3’
FOXD1	Forward: 5’- ACAACTAAGCCTTTTTGAGG -3’ Reverse : 5’- AAAAGTACACCAGACAAGTG -3’
GAPDH	Forward: 5’-ATGTCGTGGAGTCTACTGGC-3’ Reverse: 5’-TGACCTTGCCCACAGCCTTG-3’
WNT6	Forward: 5’-GCGGAGACGATGTGGACTTC-3’ Reverse: 5’-ATGCACGGATATCTCCACGG-3’
ELF3	Forward: 5’- CTCGGAGCTCCCACTCCTCAGA-3’ Reverse: 5’-GCTCTTCTTGCCCTCGAGACAGT-3’
NFE2	Forward: 5’- ATTTGAGCCCCAAGCCCCAGC-3’ Reverse: 5’-CCAGCCTCTGTCCCCTCCAGC-3’
SLIT3	Forward: 5’- TGATGGCAACGAGGAGAGTA-3’ Reverse: 5’-ACG GCTGTTAGGTGGTTTCC-3’
NEDD4L	Forward: 5’- GCTTTCCTTTAATGCACTAAACCTTTAATATTGT-3′ Reverse: 5’-GGTAAGACTTTGCTTGGTGGGG-3′
GSK3B	Forward: 5’- GCCAAGCCTTGTCAGAAATGA -3’ Reverse: 5’-TTTCTGGGCCATGGTTCTCT-3’
BMP7	Forward: 5’- GGTGGCAGGACTGGATCATC-3’ Reverse: 5’-GCGCATTCTCCTTCACAGTAATAC-3’
SMAD7	Forward: 5’- GGCTGTGTTGCTGTGAATC-3’ Reverse: 5’-GGTATCTGGGAGTAAGGAGGAG-3’
CXCL1	Forward: 5’- TGCTGAACAGTGACAAATCCAAC-3’ Reverse: 5’-TGGGGTTGACATTTCAAAAAGAA-3’
Bcl-xL	Forward: 5’-TATCACACTTCTGTGAGACC-3’ Reverse : 5’-GCAATCTAGTCTCCTTTCTG-3’
CyclinD1	Forward: 5’- CCCGCACGATTTCATTGAAC -3’ Reverse : 5’- AGGGCGGATTGGAAATGAAC -3’
C-MYC	Forward: 5’- ACACATCAGCACAACTACGC -3’ Reverse : 5’- CCTCTTGACATTCTCCTCGGT -3’
COX-2	Forward: 5’- GCTGTTGCTGTTAAGTTTGG -3’ Reverse : 5’- ATGCATTGGAAACATCGACA -3’
TNF-α	Forward: 5’- GGTATGAGCCCATCTATCTG -3’ Reverse : 5’- GCAATGATCCCAAAGTAGAC -3’
IL-6	Forward: 5’- GCACTGGCAGAAAACAACCT -3’ Reverse : 5’- GCTCTGGCTTGTTCCTCACTAC -3’
IL-1β	Forward: 5’- AACAAGCTGGAATTTGAGTC -3’ Reverse : 5’- ATCCTCTTAGCACTACCCTA -3’

Foxj1 promoter Ch-IP NC	Forward: 5’- TATAAATGAACAAACAGCTC -3’ Reverse: 5’- GGAACAGTGAGAACAGGAGAG -3’
Foxj1 promoter Ch-IP 1	Forward: 5’- GAGTTAGGGTCCTGCCCACCTC -3’ Reverse: 5’- CTCACTTTGCAGTTAGCTCTCC -3’
Foxj1 promoter Ch-IP 2	Forward: 5’- GCTCTCCAGCTCCTGGGCAG -3’ Reverse: 5’- CCCAATTAATTTCACCAACC -3’
CDX2 promoter Ch-IP NC	Forward: 5’- CCATAAAGAGCTGCGTGGCTG -3’ Reverse: 5’- AACTTTCTTCATGGTGTGCAC-3’
CDX2 promoter Ch-IP 1	Forward: 5’- AGTTGCTACAGGCTTCTCTG -3’ Reverse: 5’- CTTGGCATTTAGACAGCCCTG -3’
CDX2 promoter Ch-IP 2	Forward: 5’- GACCCATTTTTTGCAATGAG -3’ Reverse: 5’- ATTGTCCCTGTTTTCCAGCTG -3’
FOXJ1	Forward: 5’-CACGTGAAGCCTCCCTACTC-3’ Reverse: 5’- GGATTGAATTCTGCCAGGTG -3’
IκBβ	Forward: 5’- AGGGCGATGAATATGATGACATC3’ Reverse-5´CAAAACCGACAACCG CCT3 -3’
FOXD1 shRNA	#1 5’-CCGGGCCCTTCTCCATCGAGAGCATCTCGAGATGCTCTCGATGGAGAAGGGCTTTTT-3’ #2 5’- CCGGCGAGGAAACAGACATCGACGTCTCGAGACGTCGATGTCTGTTTCCTCGTTTTTG-3’
FOXJ1 shRNA	5’-CCGGCCACCAATCCGCACGTGAATCTCGAGATTCACGTGCGGATTGGTGGTTTTT-3’

Table S2 Upregulated miRNAs in GES-1 cells treated with CDCA.

SystematicName	foldchange	active_sequence	chr	mirbase.accession.No
hsa-miR-92a-1*	118.9592	AGCATTGCAACCGATCCC	chr13	MIMAT0004507
hsa-miR-3613-3p	82.96875	GAAGGGTTGGGCTTT	chr13	MIMAT0017991
hsa-miR-20a*	80.67127	CTTTAAGTGCTCATAATGCAG	chr13	MIMAT0004493
hsa-miR-532-3p	68.75526	TGCAAGCCTTGGGTG	chrX	MIMAT0004780
hsa-miR-4323	66.93926	TCTGAGGCTGTGGGG	chr19	MIMAT0016875
hsa-miR-486-5p	65.52789	CTCGGGGCAGCTCA	chr8	MIMAT0002177
hsa-miR-129-3p	62.36737	ATGCTTTTTGGGGTAAGGG	chr11	MIMAT0004605
hsa-miR-505*	59.45964	ACATCAATACTTCCTGGCTC	chrX	MIMAT0004776
hsa-miR-29c*	57.40266	GAACACCAGGAGAAATCGGT	chr1	MIMAT0004673
hsa-miR-634	57.02373	GTCCAAAGTTGGGGTGCT	chr17	MIMAT0003304
hsa-miR-129*	56.31835	ATACTTTTTGGGGTAAGGG	chr7	MIMAT0004548
hsa-miR-502-3p	51.99796	TGAATCCTTGCCCAGG	chrX	MIMAT0004775
hsa-miR-500a*	49.69044	CAGAATCCTTGCCCAGGT	chrX	MIMAT0002871
hsa-miR-371-5p	47.99462	AGTGCCCCCACAG	chr19	MIMAT0004687
hsa-miR-132*	45.07946	AGTAACAATCGAAAGCCACG	chr17	MIMAT0004594
hsa-miR-378*	44.3644	ACACAGGACCTGGAGTCA	chr5	MIMAT0000731
hsa-miR-296-5p	42.06981	ACAGGATTGAGGGGGG	chr20	MIMAT0000690
hsa-miR-188-5p	40.78087	CCCTCCACCATGC	chrX	MIMAT0000457
hsa-miR-1237	39.09473	CTGGGGGACGG	chr11	MIMAT0005592
hsa-miR-106b*	36.15195	GCAGCAAGTACCCAC	chr7	MIMAT0004672
hsa-miR-182	22.59231	AGTGTGAGTTCTACCAT	chr7	MIMAT0000259
hsa-miR-892b	20.10454	TCTACCCAGAAAGGAGCCA	chrX	MIMAT0004918
hsa-miR-501-5p	19.32261	TCTCACCCAGGGACAAAG	chrX	MIMAT0002872
hsa-miR-630	11.46209	ACCTTCCCTGGTACAGA	chr15	MIMAT0003299
hsa-miR-29b-1*	5.203511	TCTAAACCACCATATGAAACCAG	chr7	MIMAT0004514
hsa-miR-550a	4.88794	GGGCTCTTACTCCCT	chr7	MIMAT0004800
hsa-miR-629*	4.313794	GCTGGGCTTACGTTGG	chr15	MIMAT0003298
hsa-miR-132	4.049532	CGACCATGGCTGTAGA	chr17	MIMAT0000426
hsa-miR-2116*	3.616291	GGGAGTTCTTGGCATG	chr15	MIMAT0011161
hsa-miR-3138	3.306166	ACTCCCTCTACCTCACT	chr4	MIMAT0015006
hsa-miR-1268	3.071671	CCCCCACCACCAC	chr15	MIMAT0005922
hsa-miR-19b-1*	2.977145	GCTGGATGCAAACCTGC	chr13	MIMAT0004491
hsa-miR-92b	2.955225	GGAGGCCGGGACG	chr1	MIMAT0003218
hsa-miR-3676	2.844162	AAAGCGTGGGGGAA	chr17	MIMAT0018100
hsa-miR-1539	2.738363	GGGCATCTGGGACG	chr18	MIMAT0007401
hsa-miR-4310	2.607495	GGGACATGAATGCTGC	chr15	MIMAT0016862
hsa-miR-221*	2.412646	AAATCTACATTGTATGCCAGG	chrX	MIMAT0004568
hsa-miR-3180-5p	2.30178	CGACGTGGGGCG	chr16	MIMAT0015057
hsa-miR-1288	2.236374	TCTCCAGATCAGGGCA	chr17	MIMAT0005942
hsa-miR-33b*	2.232399	GGGCTGCACTGCCG	chr17	MIMAT0004811
hsa-miR-29a	2.230837	TAACCGATTTCAGATGGTGC	chr7	MIMAT0000086
hsa-miR-100	2.196514	CACAAGTTCGGATCTACGG	chr11	MIMAT0000098
hsa-miR-223	2.177022	TGGGGTATTTGACAAACTGAC	chrX	MIMAT0000280
hsa-miR-575	2.17027	GCTCCTGTCCAACTGGCT	chr4	MIMAT0003240
hsa-miR-21*	2.1668	ACAGCCCATCGACTG	chr17	MIMAT0004494
hsa-miR-25*	2.111165	CAATTGCCCAAGTCTCC	chr7	MIMAT0004498
hsa-miR-362-5p	2.084048	ACTCACACCTAGGTTCC	chrX	MIMAT0000705

Table S3. miR-92a-1-5p expression in gastric IM tissue array.

	Cases	miR-92a-1-5p ISH levels				P value
		Negative	Weak	Moderate	Strong	
Normal	72	33	22	16	1	
IM	72	15	16	28	13	＜0.0001

Table S4 Overlapped targets between mRNA profile and bioinformational results

FOXD1	ALDH3B1	MEIS1	NICN1	MTHFR	GPR124	GLT8D2
PRRT2	ABAT	ATP1B2	LLGL2	CORO2A	ZNF395	SYNGR1
KRT80	BDKRB2	FLJ40125	SPON2	SAP30L	SEMA6B	SMC1A
FXYD6	CACNB3	STAC2	GPR124	HOXC13	SMARCC2	TP53I11
ATP8B3	SULT1A1	ACCN2	DACT3	CLMN	TBXA2R	YPEL2
RASSF4	RASSF4	CXCL12	EPB41L1	TIMP3	C20orf108	KCNH3
MXD4	GDPD5	COL1A1	TSPAN15	MTL5	KIAA1549	ALPP
RASSF2	EFNA1	OLFML2A	ACOT11	PRICKLE2	GAS2L1	MTHFR
SALL2	ELFN2	PALM	VWA1	KIAA1549	MTL5	MTHFR
GATS	PBX1	MRC2	C15orf52	TMEM44	BMP7	CBFA2T3
PPL	C1orf21	PBX1	NRM	PLEKHG2	FOXA1	MBOAT2
PDE4B	ATCAY	COL8A2	CCDC85A	ATP7B	EMP2	MBOAT2
SPINT1	GPX3	PLEKHA6	PLAT	SOX12	GPR124	THY1
MXD4	EFNA1	KRT80	JAK3	C15orf52	ZNF395	DOC2A
ATP2B4	EPB41L1	MAPT	FOXA1	FARP1	SEMA6B	AKAP12
GDPD5	GATS	EME1	DNAJC18	ENSA	SMARCC2	ZNF618
MKI67	PDLIM2	ADAM19	CMBL	HDAC1	RPS6KA2	

Table S5 Potential Foxd1 binding site on Foxj1 promoter.

Score	Relative score	Start	End	Strand	Predicted site sequence
8.114	0.852144958799813	-1669	-1662	1	GTCAACAG
11.362	0.96141588557064	-1188	-1181	-1	GTAAACAG
8.245	0.856552129799499	-947	-940	1	GTAATCAA
8.188	0.854634505776735	-589	-582	-1	GTAAGCAG
8.265	0.857224980333802	-32	-25	-1	ATAAACAG

Predicted in Jaspar using symbol FOXD1: http://jaspar.genereg.net/

Table S6 p-p65 expression in gastric IM tissue array.

	Cases	p-p65 IHC levels				P value
		Negative	Weak	Moderate	Strong	
Normal	72	33	21	13	5	
IM	72	10	14	17	31	＜0.0001

Table S7 CDX2 expression in gastric IM tissue array.

	Cases	CDX2 IHC levels				P value
		Negative	Weak	Moderate	Strong	
Normal	72	56	11	3	2	
IM	72	12	27	21	12	＜0.0001

Table S8 Potential NF-kB binding site on CDX2 promoter.

Score	Relative score	Start	End	Strand	Predicted site sequence
9.412	0.886280953038696	-1029	-1019	1	GGGGCTTCTCA
6.148	0.838663983672203	-965	-955	-1	AGGGCTTTCTT
3.976	0.806977691556999	-509	-499	-1	TGGAGTGCTCC
9.723	0.890817986578211	-489	-479	1	CGGGCTTCCCT
3.938	0.806423327330306	-53	-43	1	CGGACCTCCCC

Predicted in Jaspar using symbol NFKB1: http://jaspar.genereg.net/

Table S9 FOXD1 expression in gastric IM tissue array.

	Cases	FOXD1 IHC levels				P value
		Negative	Weak	Moderate	Strong	
Normal	72	0	2	13	57	
IM	72	0	13	42	17	＜0.0001