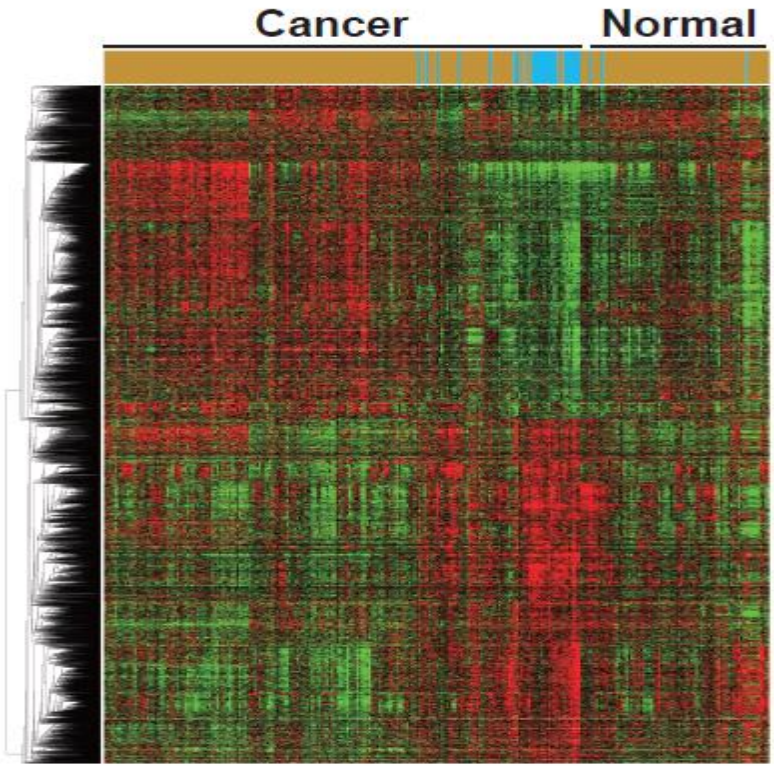
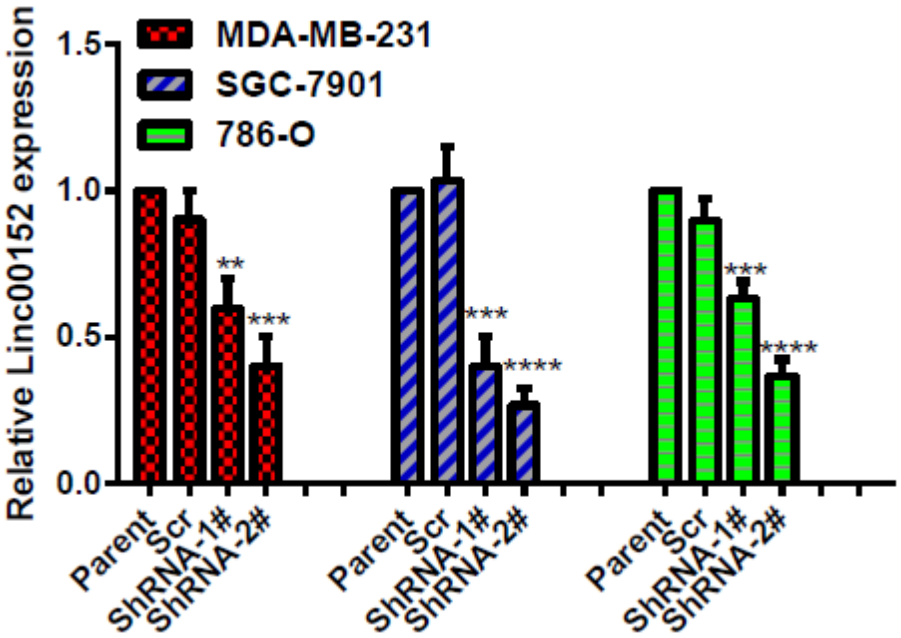
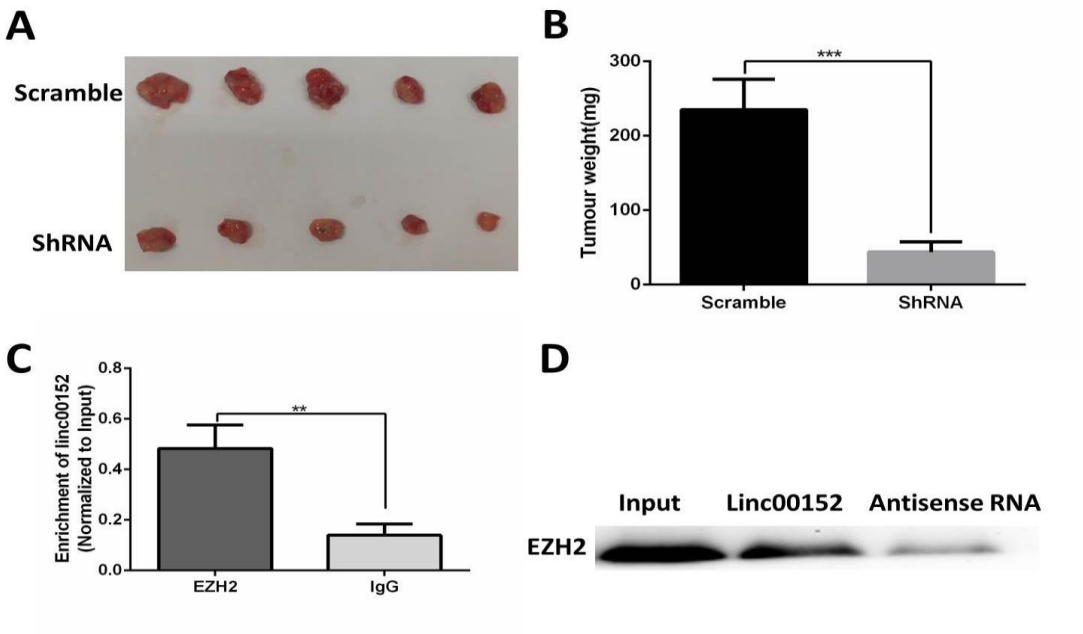
Supplementary Figure 1 The hierarchical clustering for genes including linc00152 in GEO datasets



Supplementary Figure 2 Knockdown efficiency of linc00152



Supplementary Figure 3 Linc00152 promotes tumor growth *in vivo* and can binding EZH2 directly



Supplementary Table 1 GEO dataset list

GSE1378
GSE1456
GSE16391
GSE17907
GSE19615
GSE20685
GSE20711
GSE21653
GSE33926
GSE4922
GSE6532
GSE9195

Supplementary Table 2 Gene ontology term enrichment and KEGG pathway analysis for linc00152

Gene ontology term enrichment analysis

Term	Bonferroni	Benjamini	FDR
GO:0050900~leukocyte migration	7.07E-20	7.07E-20	4.40E-20
GO:0030198~extracellular matrix organization	2.65E-19	1.33E-19	1.65E-19
GO:0007155~cell adhesion	1.17E-16	3.90E-17	7.28E-17
GO:0006954~inflammatory response	2.24E-11	5.59E-12	1.39E-11
GO:0001525~angiogenesis	3.36E-11	6.71E-12	2.09E-11
GO:0030574~collagen catabolic process	4.38E-10	7.30E-11	2.73E-10
GO:0007165~signal transduction	4.39E-09	6.27E-10	2.73E-09
GO:0050776~regulation of immune response	6.76E-09	8.45E-10	4.21E-09
GO:0006955~immune response	4.10E-08	4.56E-09	2.55E-08
GO:0030199~collagen fibril organization	2.42E-07	2.42E-08	1.51E-07

GO:0045087~innate immune response	4.05E-06	3.68E-07	2.52E-06
GO:0035987~endodermal cell differentiation	5.39E-06	4.49E-07	3.36E-06
GO:0042102~positive regulation of T cell proliferation	1.65E-04	1.27E-05	1.03E-04
GO:0006928~movement of cell or subcellular component	0.002956	2.11E-04	0.001843
GO:0007229~integrin-mediated signaling pathway	0.003198	2.14E-04	0.001994
GO:0001666~response to hypoxia	0.005262	3.30E-04	0.003285
GO:0042060~wound healing	0.005335	3.15E-04	0.00333
GO:0045766~positive regulation of angiogenesis	0.006069	3.38E-04	0.00379
GO:0007159~leukocyte cell-cell adhesion	0.015258	8.09E-04	0.009572
GO:0001501~skeletal system development	0.016717	8.43E-04	0.010495
GO:0070374~positive regulation of ERK1 and ERK2 cascade	0.020598	9.91E-04	0.012957
GO:0031295~T cell costimulation	0.022557	0.001037	0.014204
GO:0071222~cellular response to lipopolysaccharide	0.023567	0.001036	0.014847
GO:0048661~positive regulation of smooth muscle cell proliferation	0.027315	0.001153	0.017241
GO:0006909~phagocytosis	0.032742	0.001331	0.020723
GO:0002250~adaptive immune response	0.033328	0.001303	0.021101
GO:0060333~interferon-gamma-mediated signaling pathway	0.042876	0.001622	0.027279

KEGG pathway analysis

Term	Bonferroni	Benjamini	FDR
hsa05150:Staphylococcus aureus infection	5.91E-17	5.91E-17	3.26E-16
hsa04145:Phagosome	6.10E-12	3.05E-12	3.37E-11
hsa04510:Focal adhesion	4.60E-10	1.53E-10	2.54E-09
hsa04380:Osteoclast differentiation	2.04E-08	5.11E-09	1.13E-07
hsa04512:ECM-receptor interaction	1.27E-07	2.53E-08	6.98E-07
hsa05140:Leishmaniasis	1.29E-07	2.15E-08	7.10E-07
hsa05152:Tuberculosis	2.80E-07	3.99E-08	1.54E-06
hsa04151:PI3K-Akt signaling pathway	1.37E-05	1.72E-06	7.57E-05
hsa05146:Amoebiasis	2.91E-05	3.23E-06	1.61E-04
hsa04670:Leukocyte transendothelial migration	4.00E-05	4.00E-06	2.20E-04
hsa04672:Intestinal immune network for IgA production	3.63E-04	3.30E-05	0.002002
hsa05323:Rheumatoid arthritis	9.04E-04	7.54E-05	0.004988
hsa04514:Cell adhesion molecules (CAMs)	9.38E-04	7.22E-05	0.005172
hsa05416:Viral myocarditis	0.003164	2.26E-04	0.017472

hsa04640:Hematopoietic cell lineage	0.011581	7.76E-04	0.064209
hsa05133:Pertussis	0.012398	7.79E-04	0.068763
hsa05322:Systemic lupus erythematosus	0.017051	0.001011	0.094779
hsa04974:Protein digestion and absorption	0.017131	9.60E-04	0.095228
hsa05144:Malaria	0.02186	0.001163	0.121792
hsa04610:Complement and coagulation cascades	0.023089	0.001167	0.128718
hsa05332:Graft-versus-host disease	0.030782	0.001488	0.172244
hsa05130:Pathogenic Escherichia coli infection	0.031028	0.001432	0.173641

Supplementary Table 3 The proteins that were expressed positively or negatively with linc00152 in TCGA

Cancer type	Protein Symbol	Correlation	P-value
BLCA	Fibronectin	0.54	2.29E-11
BLCA	Annexin-1	0.503	2.98E-09
BLCA	p21	0.498	4.56E-09
BLCA	PAI-1	0.491	8.11E-09
BLCA	LKB1	0.488	1.06E-08
BLCA	ACVRL1	0.467	5.36E-08
BLCA	PEA-15	0.436	3.45E-07
BLCA	Transglutaminase	0.431	6.28E-07
BLCA	Chk1	0.426	6.71E-07
BLCA	Lck	0.425	8.99E-07
BLCA	TIGAR	0.413	1.89E-06
BLCA	Caspase-7_cleavedD198	0.403	3.57E-06
BLCA	AR	-0.41	1.9E-06
BLCA	HER3	-0.414	1.8E-06
BLCA	Chk1_pS345	-0.421	1.15E-06
BLCA	SF2	-0.444	2.62E-07
BLCA	FASN	-0.449	1.82E-07
BLCA	Rb_pS807_S811	-0.463	7.14E-08
BLCA	HER2	-0.486	1.24E-08
BLCA	GATA3	-0.547	0
LGG	ASNS	0.466	0
LGG	eIF4G	0.466	0
LGG	IGFBP2	0.582	0
LGG	p21	0.404	2.15E-11
LGG	PAI-1	0.499	0
GBM	Bax	0.43	0.000236
GBM	Fibronectin	0.468	0.000055
GBM	IGFBP2	0.497	1.57E-05
GBM	Myosin-IIa_pS1943	0.518	5.97E-06
GBM	PAI-1	0.516	6.63E-06