

Table S1 Enrichment analysis results of hub genes of *EGFR*

Enrichment	Name	FDR
GO biological process		
GO:0070268	Keratinization	1.48E-06
GO:0060429	Epithelial development	3.40E-05
GO:0030855	Epithelial cell differentiation	3.77E-05
GO:0045109	Intermediate filament organization	3.77E-05
GO:0048513	Animal organ development	3.77E-05
GO:0048869	Cell development	1.10E-04
GO:0007010	Cytoskeleton organization	1.50E-04
GO:0012501	Programmed cell death	2.20E-04
GO:0045110	Intermediate tow components	3.10E-04
GO molecular function		
GO:0005200	Structural components of the cytoskeleton	2.51E-05
GO:0005198	Structural molecular activity	7.30E-04
GO:0019215	Intermediate filament bondage	1.20E-03
GO:0046934	Phosphatidylinositol-4,5-bisphosphate 3-kinase activity	1.81E-02
GO cellular components		
GO:0005882	Intermediate wire	2.92E-06
GO:0045095	Keratin filaments	4.00E-04
GO:0044444	Cytoplasmic part	8.30E-03
GO:0005911	Cell connection	1.11E-02
KEGG		
hsa04915	Estrogen signaling pathway	2.20E-03
hsa05224	Breast cancer	2.20E-03
hsa04917	Prolactin signaling pathway	1.00E-02
hsa05221	Acute myeloid leukemia	1.00E-02
hsa01522	Endocrine resistance	1.19E-02
hsa04640	Hematopoietic cell lineage	1.19E-02
hsa04919	Thyroid hormone signaling pathway	1.26E-02
hsa05200	Cancer-related pathways	1.37E-02
hsa05205	Proteoglycans in cancer	2.72E-02

EGFR, epidermal growth factor receptor; GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; FDR, false discovery rate.

Table S2 Enrichment analysis results of hub genes of *EZH2*

Enrichment	Name	FDR
GO biological process		
GO:0051301	Cell division	6.89E-14
GO:1903047	Mitotic cell cycle process	1.60E-13
GO:0007059	Chromosome segregation	7.24E-12
GO:0051303	Establishment of chromosome location	8.34E-11
GO:0098813	Nuclear chromosome segregation	1.20E-10
GO:0051983	Regulation of chromosome segregation	2.77E-10
GO:0000280	Nuclear division	7.73E-10
GO:0000819	Sister chromatid separation	9.15E-10
GO:0140014	Mitotic nuclear division	1.41E-09
GO:0030071	Regulation of metaphase/late mitotic transition	1.61E-09
GO molecular function		
GO:0004693	Cyclin-dependent protein serine/threonine kinase activity	7.20E-05
GO:0035173	Histone kinase activity	1.30E-03
GO:0004674	Protein serine/threonine kinase activity	1.40E-03
GO:0140096	Catalytic activity acting on protein	3.13E-02
GO:0016740	Transferase activity	3.27E-02
GO:0008022	Protein C-terminal binding	4.10E-02
GO cellular components		
GO:0000775	Chromosome centromeric region	1.14E-10
GO:0000777	Condensed chromosome kinetochore	3.05E-10
GO:0000940	Condensed extrachromosomal kinetochore	8.41E-10
GO:0015630	Microtubule cytoskeleton	9.86E-10
GO:0044430	Cytoskeleton	1.38E-08
GO:0000942	Condensed nuclear extrachromosomal kinetochore	3.62E-08
GO:0005819	Spindle	4.12E-08
GO:0005815	Microtubule Organization Center	6.46E-08
GO:0005813	Centrosome	2.72E-07
GO:0043232	Intracellular non-membrane organelles	7.83E-07
KEGG		
hsa04110	Cell cycle	2.45E-08
hsa04114	Oocyte meiosis	2.45E-08
hsa04914	Progesterone-mediated oocyte maturation	4.85E-07
hsa04115	p53 signaling pathway	1.62E-05
hsa04218	Cell senescence	1.50E-04
hsa04068	FOXO signaling pathway	3.90E-03
hsa05203	Viruses cause cancer	6.50E-03
hsa05166	HTLV-I infection	1.04E-02

EZH2, zeste gene enhancer homolog 2; GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; FDR, false discovery rate.