

Figure S1 Volcano plot of differentially expressed genes (DEGs). Red, green and black denote up-regulated, down-regulated and non-significantly expressed genes, respectively.

Figure S2 Gene and functional network constructed by GO enrichment analysis.

Figure S1

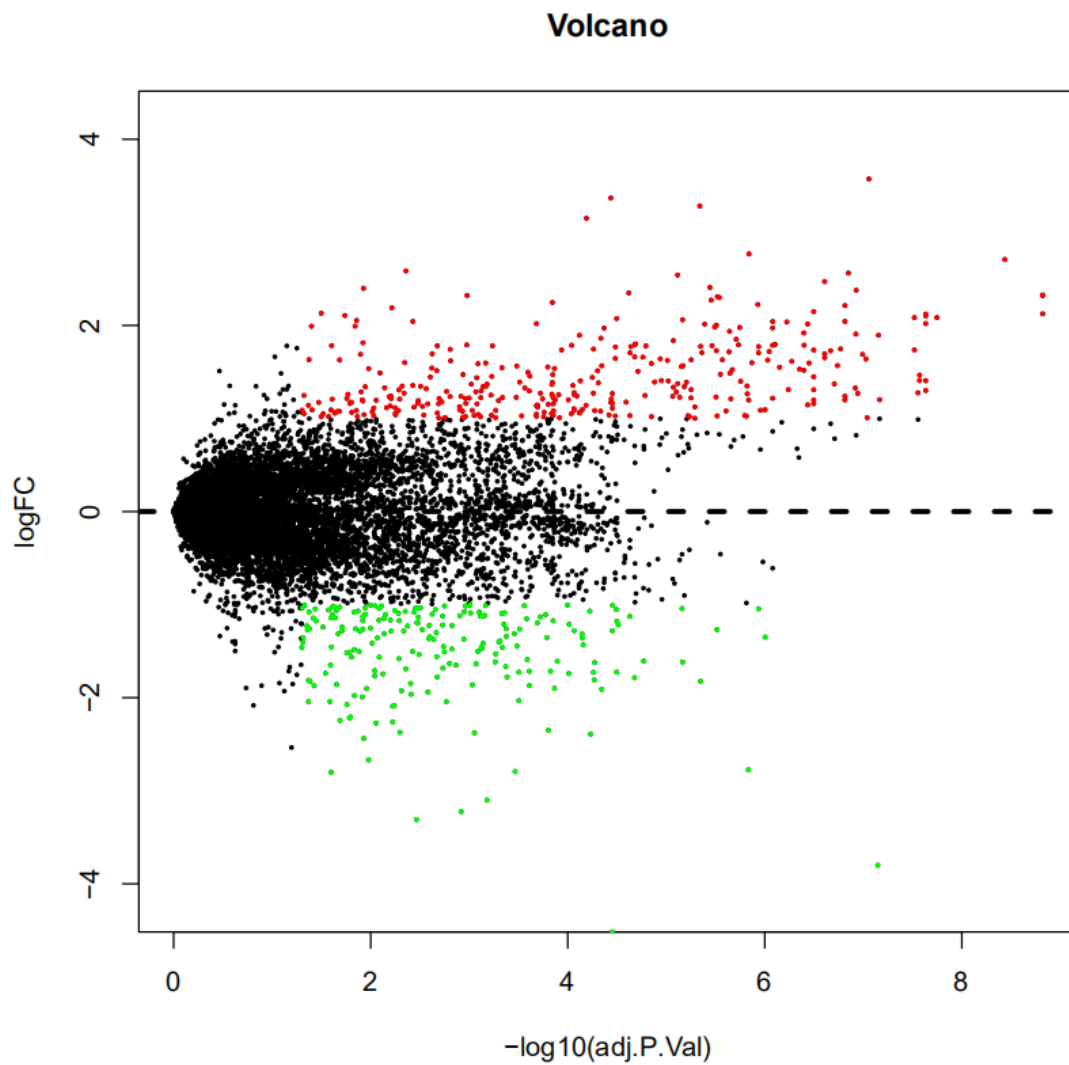


Figure S2

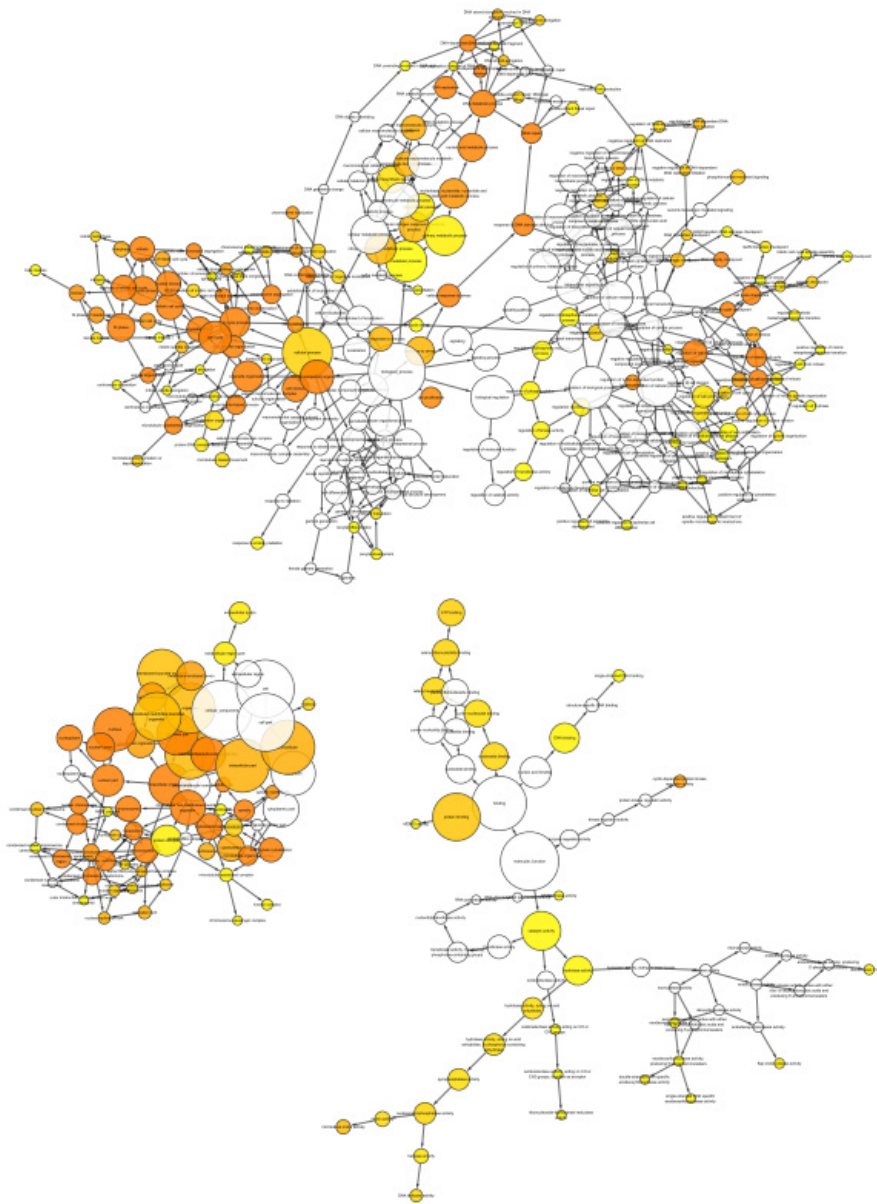


Table S1 Clinical evaluation of cervical specimens

	Normal (n=24)	CIN1 (n=14)	CIN2 (n=22)	CIN3 (n=40)
Median age	28.5	27	24	30.5
HPV genotype				
HPV 16	16 (16.2)	12 (12.1)	20 (20.2)	32 (32.3)
HPV 18	1 (25.0)	0	0	2 (50.0)
other high-risk HPV	5 (25.0)	2 (10.0)	2 (10.0)	6 (25.0)
other HPV	2 (40.0)	0	0	1 (20.0)
Study cytology				
HSIL+	16 (14.3)	13 (11.6)	22 (19.6)	37 (32.1)
LSIL	3 (50.0)	1 (16.7)	0	2 (33.3)
ASC-US	2 (40.0)	0	0	2 (40.0)
Normal	3 (100.0)	0	0	0
Missing	0	0	0	0
Colposcopy impression				
Cancer	0	0	1 (3.2)	8 (25.8)
High grade	7 (29.2)	0	7 (29.2)	9 (37.5)
Low grade	13 (23.6)	11 (20.0)	14 (25.5)	15 (25.5)
Metaplasia & Equivocal	3 (25.0)	2 (16.7)	0	6 (50.0)
Normal	1 (100.0)	0	0	0
Missing	0	1 (20.0)	0	3 (60.0)

HSIL = high grade squamous intraepithelial lesion; LSIL = low grade squamous intraepithelial lesion; ASC-US = atypical squamous cells of undetermined significance

Roemeling C A V , Radisky D C , Marlow L A , et al. Neuronal pentraxin 2 supports clear cell renal cell carcinoma by activating the AMPA-selective glutamate receptor-4[J]. Cancer Research, 2014, 74(17):4796-810.

Table S2 31 genes with the high connectivity in grey module were taken as candidate hub genes for CIN high grade risk

Gene	colorNE W	kMEblue	kMEbrown	kMEgreen	kMEgrey	kMETurquoise	kMEyellow
SYCP2	grey	-0.31933	0.813579	0.748354	0.902993	0.792075	0.674302
TCAM1P	grey	-0.56294	0.687622	0.70513	0.890289	0.765379	0.66542
DCLRE1B	grey	-0.57014	0.753084	0.756259	0.87688	0.789789	0.769592
CDC7	grey	-0.26862	0.860968	0.809275	0.872573	0.84401	0.704296
TOPBP1	grey	-0.30903	0.832814	0.742776	0.863863	0.871869	0.642696
ACTL6A	grey	-0.60488	0.653026	0.693032	0.86191	0.78691	0.641038
CKLF	grey	-0.48131	0.737526	0.716072	0.86049	0.822085	0.667799
C18orf54	grey	-0.5212	0.699997	0.663395	0.859988	0.783101	0.671595
CENPQ	grey	-0.62882	0.688158	0.671624	0.858939	0.817186	0.651964
ATAD2	grey	-0.23736	0.772421	0.788452	0.8506	0.79	0.547155
PRIM2	grey	-0.34016	0.786596	0.746414	0.848956	0.796391	0.641971
RAD54L	grey	-0.30243	0.886984	0.84222	0.842679	0.750092	0.825727
EXO1	grey	-0.63054	0.740341	0.723948	0.840726	0.760152	0.790412
KIAA0101	grey	-0.51815	0.739371	0.812399	0.83823	0.820286	0.697761
HENMT1	grey	-0.14286	0.777	0.733399	0.837402	0.73288	0.58583
TOP2A	grey	-0.47398	0.750826	0.848469	0.834757	0.841481	0.689668
NCAPH	grey	-0.40566	0.811809	0.873767	0.826243	0.818959	0.701439
ZWILCH	grey	-0.31397	0.783499	0.825587	0.825152	0.823406	0.622159
LINC00925	grey	-0.42662	0.649481	0.661172	0.823625	0.630425	0.627539
CENPO	grey	-0.39311	0.832394	0.781135	0.820124	0.715549	0.843433
ZFR2	grey	-0.38531	0.633341	0.665261	0.818176	0.741588	0.468172
RIBC2	grey	-0.71674	0.551642	0.599487	0.816547	0.654397	0.6715
SYNGR3	grey	-0.53921	0.535436	0.609433	0.814336	0.677193	0.509219
ASPM	grey	-0.46706	0.67391	0.728141	0.814137	0.717365	0.671502

LOC375196	grey	-0.2865	0.664535	0.677685	0.814128	0.662071	0.560577
RFC4	grey	-0.09753	0.868167	0.855795	0.813682	0.8086	0.610759
DHFR	grey	-0.18802	0.815199	0.854834	0.810412	0.830256	0.555871
CDKN2A	grey	-0.32164	0.646347	0.717055	0.806906	0.749467	0.439761
MLF1	grey	-0.25365	0.691977	0.622876	0.804038	0.674678	0.53789
CDC45	grey	-0.21746	0.869529	0.888799	0.803326	0.789017	0.706893

Table S3 Protein to Protein Interaction with high interaction score

node 1	node 2	neighborhood_on_chromosome	gene_fusion	phylogenetic_cooccurrence	homology	coexpression	experimentally_determined_interaction	database_annotated	automated_textmining	combined_score
CENPO	CENPQ	0	0	0	0	0.107	0.917	0.9	0.903	0.999
CD C45	CDC7	0	0	0	0	0.431	0.264	0.9	0.919	0.996
PRI M2	CDC45	0	0	0	0	0.863	0	0.9	0.593	0.993
PRI M2	RFC4	0	0	0	0	0.874	0.157	0.9	0.442	0.993
RFC4	EXO1	0	0	0	0	0.74	0.186	0.9	0.503	0.988
RFC4	TOPBP1	0	0	0	0	0.589	0.18	0.9	0.606	0.984
CD C45	TOPBP1	0	0	0	0	0.26	0.829	0	0.86	0.98
EXO1	TOPBP1	0	0	0	0	0.271	0	0.9	0.694	0.975
RFC4	KIAA0101	0	0	0	0	0.757	0	0.9	0.09	0.975
TOP2A	ASP M	0	0	0	0	0.967	0	0	0.234	0.973
TOP2A	KIAA0101	0	0	0	0	0.949	0	0	0.263	0.961
TOP2A	NCA PH	0	0	0	0	0.775	0.572	0	0.569	0.954
CENPO	ZWILCH	0	0	0	0	0.098	0	0.9	0.512	0.952
CENPQ	ZWILCH	0	0	0	0	0.194	0	0.9	0.441	0.951
CD C45	EXO1	0	0	0	0	0.902	0	0	0.527	0.951
CD C45	RFC4	0	0	0	0	0.852	0.064	0	0.658	0.948
PRI M2	CDC7	0	0	0	0	0.213	0	0.9	0.273	0.937
RAD54L	EXO1	0	0	0	0	0.75	0.147	0	0.699	0.93
ASP M	EXO1	0	0	0	0	0.918	0.104	0	0.089	0.927

ASP M	NCA PH	0	0	0	0	0.903	0	0	0.15	0.914
ASP M	KIA A010 1	0	0	0	0	0.903	0	0	0.068	0.906
