

Table SI. Cancer types from The Cancer Genome Atlas database.

Abbreviation	Full name
ACC	adrenocortical cancer
BLCA	bladder urothelial carcinoma
BRCA	breast invasive carcinoma
CESC	cervical cancer
CHOL	cholangiocarcinoma
COAD	colon carcinoma
DLBC	large B-cell lymphoma
ESCA	esophageal carcinoma
GBM	glioblastoma
HNSC	head and neck squamous carcinoma
KICH	kidney chromophobe
KIRC	kidney renal clear cell carcinoma
KIRP	kidney papillary cell carcinoma
LAML	acute myeloid leukemia
LGG	lower grade glioma
LIHC	liver hepatocellular carcinoma
LUAD	lung adenocarcinoma
LUSC	lung squamous cell carcinoma
MESO	mesothelioma
OV	ovarian cancer
PAAD	pancreatic cancer
PCPG	pheochromocytoma & paraganglioma
PRAD	prostate adenocarcinoma
READ	rectum carcinoma
SARC	sarcoma
SKCM	melanoma
STAD	stomach adenocarcinoma
TGCT	testicular cancer
THCA	thyroid cancer
THYM	thymoma
UCEC	endometrioid cancer
UCS	uterine carcinosarcoma
UVM	ocular melanomas

Table SII. Association between RNF215 expression and clinicopathological parameters in patients with colorectal cancer from The Cancer Genome Atlas.

Characteristics	Low expression of RNF215	High expression of RNF215	P-value
n	322	322	
T stage, n (%)			0.373
T1	7 (1.1%)	13 (2%)	
T2	56 (8.7%)	55 (8.6%)	
T3	225 (35.1%)	211 (32.9%)	
T4	33 (5.1%)	41 (6.4%)	
N stage, n (%)			0.724
N0	189 (29.5%)	179 (28%)	
N1	74 (11.6%)	79 (12.3%)	
N2	57 (8.9%)	62 (9.7%)	
M stage, n (%)			0.618
M0	241 (42.7%)	234 (41.5%)	
M1	42 (7.4%)	47 (8.3%)	
Pathologic stage, n (%)			0.350
Stage I	50 (8%)	61 (9.8%)	
Stage II	129 (20.7%)	109 (17.5%)	
Stage III	88 (14.1%)	96 (15.4%)	
Stage IV	43 (6.9%)	47 (7.5%)	
Sex, n (%)			0.527
Female	146 (22.7%)	155 (24.1%)	
Male	176 (27.3%)	167 (25.9%)	
Race, n (%)			0.155
Asian	6 (1.5%)	6 (1.5%)	
Black or African American	26 (6.6%)	43 (10.9%)	
White	158 (40.1%)	155 (39.3%)	
Age, n (%)			0.001
≤0years	117 (18.2%)	159 (24.7%)	
>65years	205 (31.8%)	163 (25.3%)	
Weight, n (%)			0.727
≤90 kg	113 (32.5%)	131 (37.6%)	
>90 kg	51 (14.7%)	53 (15.2%)	
Height, n (%)			0.807
<170cm	77 (23.4%)	82 (24.9%)	
≥2 (cm	79 (24%)	91 (27.7%)	
BMI, n (%)			0.956
<25 kg/m ²	50 (15.2%)	57 (17.3%)	
≥25 kg/m ²	106 (32.2%)	116 (35.3%)	
Primary therapy outcome, n (%)			0.905
PD	19 (6.1%)	14 (4.5%)	
SD	3 (1%)	2 (0.6%)	
PR	9 (2.9%)	7 (2.2%)	
CR	134 (42.9%)	124 (39.7%)	
Residual tumor, n (%)			0.471

Characteristics	Low expression of RNF215	High expression of RNF215	P-value
R0	234 (45.9%)	234 (45.9%)	
R1	2 (0.4%)	4 (0.8%)	
R2	15 (2.9%)	21 (4.1%)	
CEA level, n (%)			0.737
≤.µg/l	123 (29.6%)	138 (33.3%)	
>5µg/l	76 (18.3%)	78 (18.8%)	
Perineural invasion, n (%)			0.485
No	84 (35.7%)	91 (38.7%)	
Yes	25 (10.6%)	35 (14.9%)	
Lymphatic invasion, n (%)			0.017
No	192 (33%)	158 (27.1%)	
Yes	103 (17.7%)	129 (22.2%)	
History of colon polyps, n (%)			0.956
No	191 (34.4%)	186 (33.5%)	
Yes	89 (16%)	89 (16%)	
Colon polyps present, n (%)			0.423
No	112 (34.7%)	112 (34.7%)	
Yes	44 (13.6%)	55 (17%)	
Neoplasm type, n (%)			0.528
Colon adenocarcinoma	235 (36.5%)	243 (37.7%)	
Rectum adenocarcinoma	87 (13.5%)	79 (12.3%)	
Overall survival event, n (%)			0.018
Alive	270 (41.9%)	245 (38%)	
Dead	52 (8.1%)	77 (12%)	
Disease-specific survival event, n (%)			0.065
Alive	281 (45.2%)	263 (42.3%)	
Dead	31 (5%)	47 (7.6%)	
Progression-free survival event, n (%)			0.367
Alive	245 (38%)	234 (36.3%)	
Dead	77 (12%)	88 (13.7%)	
Age, median (IQR)	69 (60, 75)	66 (56, 76)	0.038
Height, median (IQR)	170 (162.38, 176)	170 (162, 177)	0.979
Weight, median (IQR)	81.35 (65.83, 93.97)	78.5 (65, 93)	0.599
BMI, median (IQR)	27.48 (23.87, 32.38)	26.87 (24.07, 31.17)	0.552
RNF215, ring finger protein 215; IQR, interquartile range.			

Table SIII. Results of GO/KEGG analysis.

Oncology	ID	Description	Gene Ratio	BgRatio	P-value	p.adjust	q-value	Gene ID	Count
BP	GO:0006334	nucleosome assembly	22/122	145/18670	3.62915E-24	3.52391E-21	3.19365E-21	H1-3/H1-4/H1-5/H2BC3/H1-1/H2BC13/H2BC14/H2BC7/H2BC6/H2BC10/H2BC17/H3C1/H3C11/H3C12/H4C4/H4C6/H4C3/H4C2/H4C5/H4C13/H3C7/TSPYL6	22
BP	GO:0031497	chromatin assembly	22/122	165/18670	6.95041E-23	3.37442E-20	3.05818E-20	H1-3/H1-4/H1-5/H2BC3/H1-1/H2BC13/H2BC14/H2BC7/H2BC6/H2BC10/H2BC17/H3C1/H3C11/H3C12/H4C4/H4C6/H4C3/H4C2/H4C5/H4C13/H3C7/TSPYL6	22
BP	GO:0034728	nucleosome organization	22/122	184/18670	8.11226E-22	2.62567E-19	2.3796E-19	H1-3/H1-4/H1-5/H2BC3/H1-1/H2BC13/H2BC14/H2BC7/H2BC6/H2BC10/H2BC17/H3C1/H3C11/H3C12/H4C4/H4C6/H4C3/H4C2/H4C5/H4C13/H3C7/TSPYL6	22
BP	GO:0006333	chromatin assembly or disassembly	22/122	191/18670	1.86981E-21	4.53897E-19	4.11359E-19	H1-3/H1-4/H1-5/H2BC3/H1-1/H2BC13/H2BC14/H2BC7/H2BC6/H2BC10/H2BC17/H3C1/H3C11/H3C12/H4C4/H4C6/H4C3/H4C2/H4C5/H4C13/H3C7/TSPYL6	22
BP	GO:0006323	DNA packaging	22/122	210/18670	1.53592E-20	2.98275E-18	2.70321E-18	H1-3/H1-4/H1-5/H2BC3/H1-1/H2BC13/H2BC14/H2BC7/H2BC6/H2BC10/H2BC17/H3C1/H3C11/H3C12/H4C4/H4C6/H4C3/H4C2/H4C5/H4C13/H3C7/TSPYL6	22
BP	GO:0065004	protein-DNA complex assembly	22/122	248/18670	5.86207E-19	9.48679E-17	8.59771E-17	H1-3/H1-4/H1-5/H2BC3/H1-1/H2BC13/H2BC14/H2BC7/H2BC6/H2BC10/H2BC17/H3C1/H3C11/H3C12/H4C4/H4C6/H4C3/H4C2/H4	22

								C5/H4C13/H3C7/TSPYL6	
BP	GO:0071824	protein-DNA complex subunit organization	22/122	288/18670	1.46523E-17	2.03248E-15	1.842E-15	H1-3/H1-4/H1-5/H2BC3/H1-1/H2BC13/H2BC14/H2BC7/H2BC6/H2BC10/H2BC17/H3C1/H3C11/H3C12/H4C4/H4C6/H4C3/H4C2/H4C5/H4C13/H3C7/TSPYL6	22
BP	GO:0071103	DNA conformation change	22/122	327/18670	2.16166E-16	2.62372E-14	2.37783E-14	H1-3/H1-4/H1-5/H2BC3/H1-1/H2BC13/H2BC14/H2BC7/H2BC6/H2BC10/H2BC17/H3C1/H3C11/H3C12/H4C4/H4C6/H4C3/H4C2/H4C5/H4C13/H3C7/TSPYL6	22
BP	GO:0006335	DNA replication-dependent nucleosome assembly	10/122	32/18670	5.57247E-15	5.41087E-13	4.90378E-13	H3C1/H3C11/H3C12/H4C4/H4C6/H4C3/H4C2/H4C5/H4C13/H3C7	10
BP	GO:0034723	DNA replication-dependent nucleosome organization	10/122	32/18670	5.57247E-15	5.41087E-13	4.90378E-13	H3C1/H3C11/H3C12/H4C4/H4C6/H4C3/H4C2/H4C5/H4C13/H3C7	10
BP	GO:0006342	chromatin silencing	14/122	120/18670	4.51328E-14	3.98399E-12	3.61062E-12	H1-3/H1-4/H1-5/H1-1/H3C1/H3C11/H3C12/H4C4/H4C6/H4C3/H4C2/H4C5/H4C13/H3C7	14
BP	GO:0000183	chromatin silencing at rDNA	10/122	40/18670	7.00836E-14	5.67093E-12	5.13947E-12	H3C1/H3C11/H3C12/H4C4/H4C6/H4C3/H4C2/H4C5/H4C13/H3C7	10
BP	GO:0045814	negative regulation of gene expression, epigenetic	14/122	136/18670	2.62702E-13	1.96218E-11	1.77829E-11	H1-3/H1-4/H1-5/H1-1/H3C1/H3C11/H3C12/H4C4/H4C6/H4C3/H4C2/H4C5/H4C13/H3C7	14
BP	GO:0060968	regulation of gene silencing	14/122	155/18670	1.61329E-12	1.11893E-10	1.01407E-10	H1-3/H1-4/H1-5/H1-1/H3C1/H3C11/H3C12/H4C4/H4C6/H4C3/H4	14

									C2/H4C5/H4C13/H3C7	
BP	GO:0051290	protein heterotetramerization detection of chemical stimulus involved in sensory perception of bitter taste		10/122	54/18670	1.83265E-12	1.18634E-10	1.07516E-10	H3C1/H3C11/H3C12/H4C4/H4C6/H4C3/H4C2/H4C5/H4C13/H3C7	10
BP	GO:0001580	sensory perception of bitter taste		9/122	41/18670	4.73257E-12	2.87208E-10	2.60291E-10	TAS2R3/TAS2R13/TAS2R39/TAS2R43/TAS2R31/TAS2R46/TAS2R30/TAS2R19/TAS2R50	9
BP	GO:0050913	sensory perception of bitter taste		9/122	45/18670	1.17119E-11	6.68954E-10	6.06261E-10	TAS2R3/TAS2R13/TAS2R39/TAS2R43/TAS2R31/TAS2R46/TAS2R30/TAS2R19/TAS2R50	9
BP	GO:0050912	detection of chemical stimulus involved in sensory perception of taste		9/122	47/18670	1.78136E-11	9.60943E-10	8.70885E-10	TAS2R3/TAS2R13/TAS2R39/TAS2R43/TAS2R31/TAS2R46/TAS2R30/TAS2R19/TAS2R50	9
BP	GO:0050907	detection of chemical stimulus involved in sensory perception regulation of megakaryocyte differentiation		20/122	477/18670	3.60038E-11	1.83998E-09	1.66754E-09	OR6A2/TAS2R3/TAS2R13/OR2D3/OR2D2/OR1N2/OR10A5/TAS2R39/TAS2R43/TAS2R31/TAS2R46/TAS2R30/TAS2R19/TAS2R50/OR10A4/OR13D1/OR52B6/OR10A2/OR13H1/OR52H1	20
BP	GO:0045652	sensory perception of taste		10/122	79/18670	9.62232E-11	4.67163E-09	4.23382E-09	H3C1/H3C11/H3C12/H4C4/H4C6/H4C3/H4C2/H4C5/H4C13/H3C7	10
BP	GO:0050909	sensory perception of taste		9/122	67/18670	5.0111E-10	2.31704E-08	2.09989E-08	TAS2R3/TAS2R13/TAS2R39/TAS2R43/TAS2R31/TAS2R46/TAS2R30/TAS2R19/TAS2R50	9

BP	GO:0030219	megakaryocyte differentiation	10/122	96/18670	6.86463E-10	3.0298E-08	2.74585E-08	H3C1/H3C11/H3C12/H4C4/H4C6/H4C3/H4C2/H4C5/H4C13/H3C7	10
BP	GO:0051291	protein heterooligomerization	11/122	128/18670	7.50253E-10	3.16737E-08	2.87053E-08	GLRA1/H3C1/H3C11/H3C12/H4C4/H4C6/H4C3/H4C2/H4C5/H4C13/H3C7	11
BP	GO:0045653	negative regulation of megakaryocyte differentiation	6/122	18/18670	1.19748E-09	4.84481E-08	4.39076E-08	H4C4/H4C6/H4C3/H4C2/H4C5/H4C13	6
BP	GO:0060964	regulation of gene silencing by miRNA	10/122	113/18670	3.44288E-09	1.33721E-07	1.21189E-07	H3C1/H3C11/H3C12/H4C4/H4C6/H4C3/H4C2/H4C5/H4C13/H3C7	10
BP	GO:0060147	regulation of posttranscriptional gene silencing	10/122	117/18670	4.83894E-09	1.74023E-07	1.57714E-07	H3C1/H3C11/H3C12/H4C4/H4C6/H4C3/H4C2/H4C5/H4C13/H3C7	10
BP	GO:0060966	regulation of gene silencing by RNA	10/122	117/18670	4.83894E-09	1.74023E-07	1.57714E-07	H3C1/H3C11/H3C12/H4C4/H4C6/H4C3/H4C2/H4C5/H4C13/H3C7	10
BP	GO:0051262	protein tetramerization	10/122	172/18670	1.92067E-07	6.66061E-06	6.03639E-06	H3C1/H3C11/H3C12/H4C4/H4C6/H4C3/H4C2/H4C5/H4C13/H3C7	10
BP	GO:0032200	telomere organization	10/122	175/18670	2.25654E-07	7.5555E-06	6.84742E-06	H3C1/H3C11/H3C12/H4C4/H4C6/H4C3/H4C2/H4C5/H4C13/H3C7	10
BP	GO:0034080	CENP-A containing nucleosome assembly	6/122	44/18670	3.96394E-07	1.24161E-05	1.12525E-05	H4C4/H4C6/H4C3/H4C2/H4C5/H4C13	6
BP	GO:0061641	CENP-A containing chromatin organization	6/122	44/18670	3.96394E-07	1.24161E-05	1.12525E-05	H4C4/H4C6/H4C3/H4C2/H4C5/H4C13	6

BP	GO:0031055	chromatin remodeling at centromere	6/122	48/18670	6.74566E-07	2.04688E-05	1.85506E-05	H4C4/H4C6/H4C3/H4C2/H4C5/H4C13	6
BP	GO:0006336	DNA replication-independent nucleosome assembly	6/122	54/18670	1.37507E-06	4.04605E-05	3.66686E-05	H4C4/H4C6/H4C3/H4C2/H4C5/H4C13	6
BP	GO:0016233	telomere capping	6/122	55/18670	1.53525E-06	4.25924E-05	3.86007E-05	H4C4/H4C6/H4C3/H4C2/H4C5/H4C13	6
BP	GO:0034724	DNA replication-independent nucleosome organization	6/122	55/18670	1.53525E-06	4.25924E-05	3.86007E-05	H4C4/H4C6/H4C3/H4C2/H4C5/H4C13	6
BP	GO:0034508	centromere complex assembly	6/122	56/18670	1.71036E-06	4.61321E-05	4.18087E-05	H4C4/H4C6/H4C3/H4C2/H4C5/H4C13	6
BP	GO:0043486	histone exchange	6/122	60/18670	2.58168E-06	6.77517E-05	6.14022E-05	H4C4/H4C6/H4C3/H4C2/H4C5/H4C13	6
BP	GO:0016584	nucleosome positioning	4/122	17/18670	3.86738E-06	9.88216E-05	8.95603E-05	H1-3/H1-4/H1-5/H1-1	4
BP	GO:0045637	regulation of myeloid cell differentiation	10/122	251/18670	5.94491E-06	0.000148013	0.000134142	H3C1/H3C11/H3C12/H4C4/H4C6/H4C3/H4C2/H4C5/H4C13/H3C7	10
BP	GO:0031936	negative regulation of chromatin silencing	4/122	20/18670	7.75431E-06	0.000188236	0.000170595	H1-3/H1-4/H1-5/H1-1	4
BP	GO:0006303	double-strand break repair via nonhomologous end joining	6/122	86/18670	2.11146E-05	0.000500056	0.000453192	H4C4/H4C6/H4C3/H4C2/H4C5/H4C13	6

BP	GO:0043044	ATP-dependent chromatin remodeling	6/122	88/18670	2.40809E-05	0.000556728	0.000504553	H4C4/H4C6/H4C3/H4C2/H4C5/H4C13	6
BP	GO:0045638	negative regulation of myeloid cell differentiation	6/122	91/18670	2.91509E-05	0.000658269	0.000596577	H4C4/H4C6/H4C3/H4C2/H4C5/H4C13	6
BP	GO:0000726	non-recombinational repair	6/122	94/18670	3.50456E-05	0.000773393	0.000700912	H4C4/H4C6/H4C3/H4C2/H4C5/H4C13	6
BP	GO:0038111	interleukin-7-mediated signaling pathway	4/122	30/18670	4.17001E-05	0.000899794	0.000815468	H3C1/H3C11/H3C12/H3C7	4
BP	GO:0031935	regulation of chromatin silencing	4/122	37/18670	9.70085E-05	0.002047723	0.001855815	H1-3/H1-4/H1-5/H1-1	4
BP	GO:0050911	detection of chemical stimulus involved in sensory perception of smell	11/122	427/18670	0.000113508	0.002345021	0.002125251	OR6A2/OR2D3/OR2D2/OR1N2/OR10A5/OR10A4/OR13D1/OR52B6/OR10A2/OR13H1/OR52H1	11
BP	GO:0060969	negative regulation of gene silencing	4/122	39/18670	0.0001196	0.002419416	0.002192674	H1-3/H1-4/H1-5/H1-1	4
BP	GO:0098760	response to interleukin-7	4/122	40/18670	0.000132221	0.002567738	0.002327095	H3C1/H3C11/H3C12/H3C7	4
BP	GO:0098761	cellular response to interleukin-7	4/122	40/18670	0.000132221	0.002567738	0.002327095	H3C1/H3C11/H3C12/H3C7	4
BP	GO:0045910	negative regulation of DNA	4/122	44/18670	0.000192484	0.003616914	0.003277945	H1-3/H1-4/H1-5/H1-1	4

		recombination							
BP	GO:0007608	sensory perception of smell	11/122	454/18670	0.000193697	0.003616914	0.003277945	OR6A2/OR2D3/OR2D2/OR1N2/OR10A5/OR10A4/OR13D1/OR52B6/OR10A2/OR13H1/OR52H1	11
BP	GO:0030261	chromosome condensation	4/122	47/18670	0.000249117	0.004564005	0.004136277	H1-3/H1-4/H1-5/H1-1	4
BP	GO:0030099	myeloid cell differentiation	10/122	416/18670	0.000405861	0.007297978	0.006614027	H3C1/H3C11/H3C12/H4C4/H4C6/H4C3/H4C2/H4C5/H4C13/H3C7	10
BP	GO:0002227	innate immune response in mucosa defense	3/122	24/18670	0.00049841	0.008799203	0.007974561	H2BC7/H2BC6/H2BC10	3
BP	GO:0050830	response to Gram-positive bacterium	5/122	101/18670	0.000527021	0.009138171	0.008281762	CRP/KRT6A/H2BC7/H2BC6/H2BC10	5
BP	GO:1903707	negative regulation of hemopoiesis	6/122	155/18670	0.000544169	0.009269969	0.008401208	H4C4/H4C6/H4C3/H4C2/H4C5/H4C13	6
BP	GO:0000723	telomere maintenance	6/122	162/18670	0.000686501	0.011492975	0.010415879	H4C4/H4C6/H4C3/H4C2/H4C5/H4C13	6
BP	GO:1905268	negative regulation of chromatin organization	4/122	62/18670	0.000722546	0.011891401	0.010776965	H1-3/H1-4/H1-5/H1-1	4
BP	GO:0045815	positive regulation of gene expression, epigenetic	4/122	63/18670	0.00076767	0.012423467	0.011259167	H1-3/H1-4/H1-5/H1-1	4
BP	GO:0070268	cornification	5/122	112/18670	0.000843192	0.013421951	0.012164075	IVL/KRT5/KRT6A/KRT14/KRT16	5
BP	GO:1903706	regulation of hemopoiesis	10/122	475/18670	0.001123498	0.017595434	0.015946429	H3C1/H3C11/H3C12/H4C4/H4C6/H4C3/H4C2/H4C5/H4C13/H3C7	10

BP	GO:0006338	chromatin remodeling DNA-template	6/122	182/18670	0.001255129	0.019096472	0.017306792	H4C4/H4C6/H4C3/H4C2/H4C5/H4C13	6
BP	GO:0006352	d transcription, initiation antimicrobial humoral immune response mediated by antimicrobial peptide mucosal immune response positive regulation of glutamate secretion alanine transport organ or tissue specific immune response glycine transport hemidesmosome assembly spinal cord motor neuron cell fate specification	7/122	249/18670	0.001258676	0.019096472	0.017306792	H4C4/H4C6/H4C3/H4C2/H4C5/H4C13/MORC1	7
BP	GO:0061844	response mediated by antimicrobial peptide mucosal immune response positive regulation of glutamate secretion alanine transport organ or tissue specific immune response glycine transport hemidesmosome assembly spinal cord motor neuron cell fate specification	4/122	73/18670	0.001334137	0.019929958	0.018062166	KRT6A/H2BC7/H2BC6/H2BC10	4
BP	GO:0002385	immune response positive regulation of glutamate secretion alanine transport organ or tissue specific immune response glycine transport hemidesmosome assembly spinal cord motor neuron cell fate specification	3/122	36/18670	0.001660677	0.024432081	0.02214236	H2BC7/H2BC6/H2BC10	3
BP	GO:0014049	regulation of glutamate secretion alanine transport organ or tissue specific immune response glycine transport hemidesmosome assembly spinal cord motor neuron cell fate specification	2/122	10/18670	0.001841609	0.026297093	0.023832587	CCK/NTSR1	2
BP	GO:0032328	alanine transport organ or tissue specific immune response glycine transport hemidesmosome assembly spinal cord motor neuron cell fate specification	2/122	10/18670	0.001841609	0.026297093	0.023832587	SLC36A2/SLC36A3	2
BP	GO:0002251	specific immune response glycine transport hemidesmosome assembly spinal cord motor neuron cell fate specification	3/122	39/18670	0.002095569	0.029489813	0.026726092	H2BC7/H2BC6/H2BC10	3
BP	GO:0015816	glycine transport hemidesmosome assembly spinal cord motor neuron cell fate specification	2/122	12/18670	0.002678024	0.036624809	0.033192411	SLC36A2/SLC36A3	2
BP	GO:0031581	hemidesmosome assembly spinal cord motor neuron cell fate specification	2/122	12/18670	0.002678024	0.036624809	0.033192411	KRT5/KRT14	2
BP	GO:0021520	motor neuron cell fate specification	2/122	13/18670	0.003151442	0.042500702	0.038517629	HOXC10/NKX6-2	2

BP	GO:0019731	antibacterial humoral response positive regulation of	3/122	46/18670	0.003367189	0.044788233	0.040590778	H2BC7/H2BC6/H2BC10	3
BP	GO:0060732	inositol phosphate biosynthetic process	2/122	14/18670	0.003661013	0.048038434	0.043536377	LHCGR/NTSR1	2
CC	GO:0000786	nucleosome	27/126	107/19717	3.01991E-36	3.44269E-34	3.08348E-34	H1-3/H1-4/H1-5/H2BC3/H1-1/H2 AC13/H2AC16/H2AC4/H2AC17/ H2BC13/H2BC14/H2BC7/H2BC6 /H2BC10/H2BC17/H3C1/H3C11/ H3C12/H4C4/H4C6/H4C3/H4C2/ H4C5/H4C13/H3C7/H2AC12/H2 AC21	27
CC	GO:0044815	DNA packaging complex	27/126	115/19717	2.67262E-35	1.52339E-33	1.36444E-33	H1-3/H1-4/H1-5/H2BC3/H1-1/H2 AC13/H2AC16/H2AC4/H2AC17/ H2BC13/H2BC14/H2BC7/H2BC6 /H2BC10/H2BC17/H3C1/H3C11/ H3C12/H4C4/H4C6/H4C3/H4C2/ H4C5/H4C13/H3C7/H2AC12/H2 AC21	27
CC	GO:0032993	protein-DNA complex	27/126	202/19717	3.15448E-28	1.1987E-26	1.07363E-26	H1-3/H1-4/H1-5/H2BC3/H1-1/H2 AC13/H2AC16/H2AC4/H2AC17/ H2BC13/H2BC14/H2BC7/H2BC6 /H2BC10/H2BC17/H3C1/H3C11/ H3C12/H4C4/H4C6/H4C3/H4C2/ H4C5/H4C13/H3C7/H2AC12/H2 AC21	27
CC	GO:0000788	nuclear nucleosome	11/126	38/19717	4.83557E-16	1.37814E-14	1.23434E-14	H1-4/H3C1/H3C11/H3C12/H4C4/ H4C6/H4C3/H4C2/H4C5/H4C13/ H3C7	11
CC	GO:0000790	nuclear	20/126	377/19717	3.46212E-13	7.89363E-12	7.07001E-12	H1-3/H1-4/H1-5/H1-1/H2AC13/H	20

		chromatin						2AC16/H2AC4/H2AC17/H3C1/H3C11/H3C12/H4C4/H4C6/H4C3/H4C2/H4C5/H4C13/H3C7/H2AC12/H2AC21	
CC	GO:0000784	nuclear chromosome, telomeric region	7/126	125/19717	1.57191E-05	0.000298663	0.0002675	H2BC3/H4C4/H4C6/H4C3/H4C2/H4C5/H4C13	7
CC	GO:0005719	nuclear euchromatin	4/126	30/19717	3.83071E-05	0.000623858	0.000558765	H1-3/H1-4/H1-5/H1-1	4
CC	GO:0000781	chromosome, telomeric region	7/126	161/19717	7.95015E-05	0.001132897	0.001014691	H2BC3/H4C4/H4C6/H4C3/H4C2/H4C5/H4C13	7
CC	GO:0000791	euchromatin	4/126	38/19717	9.91826E-05	0.001256313	0.00112523	H1-3/H1-4/H1-5/H1-1	4
MF	GO:0033038	bitter taste receptor activity	9/116	23/17697	1.23265E-14	2.2311E-12	2.102E-12	TAS2R3/TAS2R13/TAS2R39/TAS2R43/TAS2R31/TAS2R46/TAS2R30/TAS2R19/TAS2R50	9
MF	GO:0008527	taste receptor activity	9/116	29/17697	1.46199E-13	1.3231E-11	1.24654E-11	TAS2R3/TAS2R13/TAS2R39/TAS2R43/TAS2R31/TAS2R46/TAS2R30/TAS2R19/TAS2R50	9
MF	GO:0031492	nucleosomal DNA binding	8/116	55/17697	2.51449E-09	1.51708E-07	1.42929E-07	H1-3/H1-4/H1-5/H1-1/H3C1/H3C11/H3C12/H3C7	8
MF	GO:0031491	nucleosome binding	8/116	85/17697	8.44323E-08	3.82056E-06	3.59948E-06	H1-3/H1-4/H1-5/H1-1/H3C1/H3C11/H3C12/H3C7	8
MF	GO:0031490	chromatin DNA binding	8/116	119/17697	1.14392E-06	4.141E-05	3.90138E-05	H1-3/H1-4/H1-5/H1-1/H3C1/H3C11/H3C12/H3C7	8
MF	GO:0004984	olfactory receptor activity	11/116	427/17697	0.000114954	0.003467771	0.003267106	OR6A2/OR2D3/OR2D2/OR1N2/OR10A5/OR10A4/OR13D1/OR52B6/OR10A2/OR13H1/OR52H1	11
MF	GO:0016500	protein-hormone receptor activity	3/116	19/17697	0.000246301	0.00636864	0.006000114	FSHR/GNRHR/LHCGR	3
KEGG	hsa05322	Systemic lupus	24/68	136/8076	2.69017E-26	1.26438E-24	1.1327E-24	H2BC3/H2AC13/H2AC14/H2AC16/H2AC4/H2AC17/H2BC13/H2B	24

		erythematosus						C14/H2BC7/H2BC6/H2BC10/H2BC17/H3C1/H3C11/H3C12/H4C4/H4C6/H4C3/H4C2/H4C5/H4C13/H3C7/H2AC12/H2AC21 H2BC3/H2AC13/H2AC14/H2AC16/H2AC4/H2AC17/H2BC13/H2BC14/H2BC7/H2BC6/H2BC10/H2BC17/H3C1/H3C11/H3C12/H4C4/H4C6/H4C3/H4C2/H4C5/H4C13/H3C7/H2AC12/H2AC21 H2BC3/H2BC13/H2BC14/H2BC7/H2BC6/H2BC10/H2BC17/H4C4/H4C6/H4C3/H4C2/H4C5/H4C13 TAS2R3/TAS2R13/TAS2R39/TAS2R43/TAS2R31/TAS2R46/TAS2R30/TAS2R19/TAS2R50 H2AC13/H2AC14/H2AC16/H2AC4/H2AC17/H2AC12/H2AC21 OR6A2/OR2D3/OR2D2/OR1N2/OR10A5/OR10A4/OR13D1/OR52B6/OR10A2/OR13H1/OR52H1	
KEGG	hsa05034	Alcoholism	24/68	187/8076	7.90875E-23	1.85856E-21	1.665E-21	24	
KEGG	hsa05203	Viral carcinogenesis	13/68	204/8076	1.07546E-08	1.68489E-07	1.50942E-07	13	
KEGG	hsa04742	Taste transduction	9/68	86/8076	3.39635E-08	3.99072E-07	3.57511E-07	9	
KEGG	hsa04217	Necroptosis	7/68	159/8076	0.000355571	0.003342363	0.002994278	7	
KEGG	hsa04740	Olfactory transduction	11/68	447/8076	0.001152803	0.009030287	0.008089843	11	
GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; BP, biological process; CC, cellular component; MF, molecular function.									

Table SIV. Results of ring finger protein 215gene set enrichment analysis.

Description	Set Size	Enrichment Score	NES	P-value	p.adjust	q-values	rank
KEGG_MAPK_SIGNALING_PATHWAY	267	0.353441973	1.608712582	0.001655629	0.023940789	0.019535692	4520
WP_RAS_SIGNALING	184	0.375016562	1.624218799	0.001642036	0.023940789	0.019535692	4857
WP_PI3KAKT_SIGNALING_PATHWAY	339	0.376447338	1.754277231	0.001644737	0.023940789	0.019535692	4242
KEGG_PATHWAYS_IN_CANCER	325	0.368609446	1.707378957	0.001669449	0.023940789	0.019535692	4857
KEGG_MELANOGENESIS	101	0.398533909	1.573324883	0.003558719	0.03130095	0.025541586	2706
WP_WNT_SIGNALING	113	0.444985641	1.797408382	0.001757469	0.023940789	0.019535692	3383
REACTOME_SIGNALING_BY_ME T	79	0.41415556	1.575160669	0.005405405	0.041928486	0.03421366	3642
REACTOME_DNA_METHYLATIO N	63	-0.88839195	-3.338197277	0.002173913	0.023940789	0.019535692	659
KEGG_PROPANOATE_METABOL ISM	32	-0.52831687	-1.681346085	0.004347826	0.036170862	0.029515436	8218
Gene sets with FDR<0.25 and p.adjust<0.05 are considered as significant. NES,normalized enrichment score; FDR, false discovery rate.							

Table SV. Summary of 36 recognized angiogenesis-associated genes.

Gene	Type
APOH	Angiogenesis
APP	Angiogenesis
CCND2	Angiogenesis
COL3A1	Angiogenesis
COL5A2	Angiogenesis
CXCL6	Angiogenesis
FGFR1	Angiogenesis
FSTL1	Angiogenesis
ITGAV	Angiogenesis
JAG1	Angiogenesis
JAG2	Angiogenesis
KCNJ8	Angiogenesis
LPL	Angiogenesis
LRPAP1	Angiogenesis
LUM	Angiogenesis
MSX1	Angiogenesis
NRP1	Angiogenesis

OLR1	Angiogenesis
PDGFA	Angiogenesis
PF4	Angiogenesis
PGLYRP1	Angiogenesis
POSTN	Angiogenesis
PRG2	Angiogenesis
PTK2	Angiogenesis
S100A4	Angiogenesis
SERPINA5	Angiogenesis
SLCO2A1	Angiogenesis
SPP1	Angiogenesis
STC1	Angiogenesis
THBD	Angiogenesis
TIMP1	Angiogenesis
TNFRSF21	Angiogenesis
VAV2	Angiogenesis
VCAN	Angiogenesis
VEGFA	Angiogenesis
VTN	Angiogenesis
