

Figure S1. The dynamics of IGF1R-NuMA interaction within 16 h from IR (2 Gy) are represented by the mean *in situ* PLA signal number per cell from  $\geq 50$  cells at each investigated time points. No significant change was observed. IGF1R, insulin-like growth factor 1 receptor; NuMA, nuclear mitotic apparatus protein; IR, ionizing radiation; PLA, proximity ligation assay.

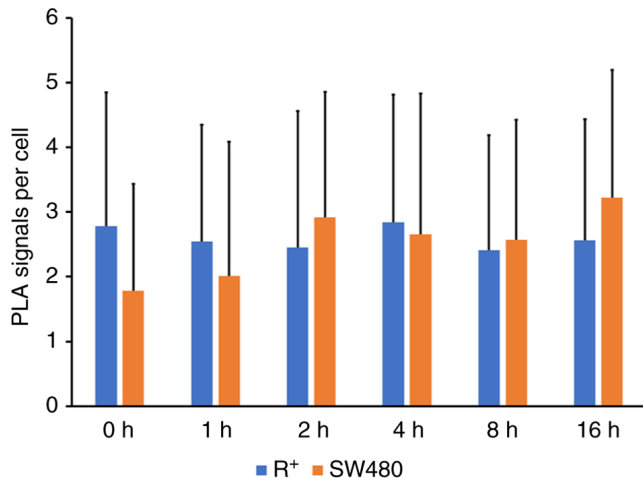


Figure S2. (A) *In situ* PLA showing NuMA-53BP1 colocalization (red dots) after IR (2 Gy) in SW480 and SW480-OE cells. Cell nuclei were stained with DAPI (blue). (B) Dynamic change of NuMA-53BP1 colocalization in response to IR (2 Gy) in SW480 and SW480-OE cells following treatment. The number of NuMA-53BP1 foci represents the mean *in situ* PLA signal number per cell from  $\geq 50$  cells in each condition. PLA, proximity ligation assay; NuMA, nuclear mitotic apparatus protein; 53BP1, NuMA-p53-binding protein 1; IR, ionizing radiation.

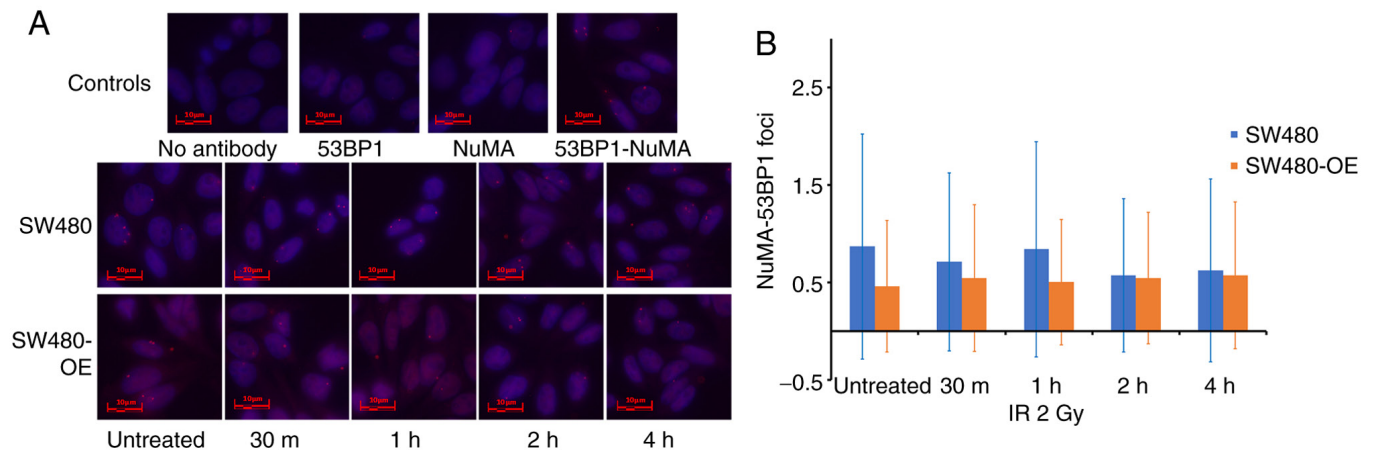


Table S1. nIGF1R interactome revealed by IP-MS in colorectal cancer cell line SW480-OE; all proteins were ranked by *Score* from highest to lowest.

	Accession	Description	Score <sup>a</sup>	Enrichment ratio <sup>b</sup>	Coverage %	Proteins	Unique peptides	Peptides	PSMs
1	Q13813	Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 PE=1 SV=3-[SPTN1_HUMAN]	306.81	-	32.65	12	68	68	101
2	Q01082	Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTBN1 PE=1 SV=2-[SPTB2_HUMAN]	226.16	17.317	27.92	15	50	54	77
3	Q15149	Plectin OS=Homo sapiens GN=PLEC-[PLEC_HUMAN]	225.69	29.657	16.87	4	1	65	82
4	Q14980	Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1-[NUMA1_HUMAN]	182.91	21.368	26.75	26	45	45	65
5	P35579	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4-[MYH9_HUMAN]	122.84	7.454	22.81	24	29	33	41
6	A0A087WV66	Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=1-[A0A087WV66_HUMAN]	110.56	15.187	14.87	4	33	33	42
7	D3DVC4	Nestin, isoform CRA_c OS=Homo sapiens GN=NES PE=3 SV=1-[D3DVC4_HUMAN]	100.63	-	19.93	6	24	24	36
8	B3K RK8	VIMENTIN OS=Homo sapiens PE=2 SV=1-[B3K RK8_HUMAN]	75.12	30.048	47.91	14	17	17	25
9	O75643	U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Homo sapiens GN=SNRNP200 PE=1 SV=2-[U520_HUMAN]	51.41	-	7.35	10	12	12	17
10	Q6P2Q9	Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2-[PRPF8_HUMAN]	47.11	9.255	7.24	7	11	11	16
11	P78527	DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC-[PRKDC_HUMAN]	46.73	-	5.17	3	15	15	18
12	B3KY63	Chromodomain helicase-DNA-binding protein 4 (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1-[B3KY63_HUMAN]	41.31	-	9.38	19	10	10	14
13	P35580	Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV=3-[MYH10_HUMAN]	40.92	-	8.40	11	8	12	14
14	P17844	ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5-[DDX5_HUMAN]	34.04	-	17.57	22	10	10	13
15	Q00610	Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC-[CLH1_HUMAN]	31.76	2.982	6.22	7	5	5	7
16	A0A087WVQ9	Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1-[A0A087WVQ9_HUMAN]	30.11	-	16.10	37	3	3	6
17	Q96BA7	HNRPU protein OS=Homo sapiens PE=2 SV=1-[Q96BA7_HUMAN]	28.27	5.094	19.25	7	9	9	13
18	Q08211	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4-[DHX9_HUMAN]	23.12	-	8.98	4	8	8	9
19	P49792	E3 SUMO-protein ligase RanBP2 OS=Homo sapiens GN=RANBP2 PE=1 SV=2-[RBP2_HUMAN]	22.78	-	4.09	17	8	8	9

Table SI. Continued.

Accession	Description	Score <sup>a</sup>	Enrichment ratio <sup>b</sup>	Coverage %	Proteins	Unique peptides	Peptides	PSMs
20	D6R991 Matrin-3 (Fragment) OS=Homo sapiens GN=MATR3 PE=1 SV=1-[D6R991_HUMAN]	22.35	8.434	13.63	6	5	5	7
21	H0YFX9 Histone H2A (Fragment) OS=Homo sapiens GN=H2AF1 PE=1 SV=1-[H0YFX9_HUMAN]	21.58	9.029	31.52	15	1	1	4
22	P18583 Protein SON OS=Homo sapiens GN=SON-[SON_HUMAN]	21.44	-	7.26	16	7	7	9
23	A4QP80 IQ motif containing GTPase activating protein 1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1-[A4QP80_HUMAN]	20.58	-	4.77	7	4	4	4
24	J3QK86 Bromodomain adjacent to zinc finger domain, 2A, isoform CRA_a OS=Homo sapiens GN=BAZ2A PE=4 SV=1-[J3QK86_HUMAN]	18.19	-	3.68	8	6	6	6
25	O15020 Spectrin beta chain, non-erythrocytic 2 OS=Homo sapiens GN=SPTBN2-[SPTN2_HUMAN]	17.25	-	2.58	3	1	5	7
26	Q5HY54 Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=1-[Q5HY54_HUMAN]	17.01	1.696	4.45	16	7	7	7
27	K7EMV3 Histone H3 OS=Homo sapiens GN=H3F3B PE=1 SV=1-[K7EMV3_HUMAN]	17	-	21.74	15	2	2	7
28	Q59GP7 Interleukin enhancer binding factor 3 isoform c variant (Fragment) OS=Homo sapiens PE=2 SV=1-[Q59GP7_HUMAN]	16.34	-	9.11	15	3	3	5
29	Q9NWX13 RNA-binding protein 28 OS=Homo sapiens GN=RBM28-[RBM28_HUMAN]	15.24	-	12.62	4	6	6	6
30	J3QSA3 Polyubiquitin-B (Fragment) OS=Homo sapiens GN=UBB PE=1 SV=1-[J3QSA3_HUMAN]	15.05	1.657	67.44	40	2	2	5
31	B4DVX2 Isolucyl-tRNA synthetase, cytoplasmic (EC 6.1.1.5) OS=Homo sapiens PE=2 SV=1-[B4DVX2_HUMAN]	14.39	-	3.76	8	2	2	3
32	B7ZZZ1 Scaffold attachment factor B OS=Homo sapiens PE=2 SV=1-[B7ZZZ1_HUMAN]	14.39	-	7.64	13	1	3	5
33	Q15233 Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO-[NONO_HUMAN]	14.21	5.996	20.94	6	5	5	6
34	A0PJ47 SAFB2 protein (Fragment) OS=Homo sapiens GN=SAFB2 PE=2 SV=1-[A0PJ47_HUMAN]	14.06	-	11.79	7	1	3	5
35	Q9NR30 Nucleolar RNA helicase 2 OS=Homo sapiens GN=DDX21 PE=1 SV=5-[DDX21_HUMAN]	13.79	-	9.45	9	5	5	5
36	Q13263 Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28-[TIF1B_HUMAN]	13.69	-	8.23	6	5	5	5
37	Q93077 Histone H2A type 1-C OS=Homo sapiens GN=HIST1H2AC PE=1 SV=3-[H2A1C_HUMAN]	13.63	-	48.46	20	3	5	5
38	P46087 Probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase OS=Homo sapiens GN=NOP2-[NOP2_HUMAN]	12.32	-	6.37	11	4	4	5
39	B4DKU3 rRNA methyltransferase 3 (EC 2.1.1.-) OS=Homo sapiens PE=2 SV=1-[B4DKU3_HUMAN]	12.26	-	8.26	2	4	4	4

Table S1. Continued.

Accession	Description	Score <sup>a</sup>	Enrichment ratio <sup>b</sup>	Coverage %	Proteins	Unique peptides	Peptides	PSMs
40	P11388 DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A PE=1 SV=3-[TOP2A_HUMAN]	12.14	-	3.72	5	4	4	4
41	O94906 Pre-mRNA-processing factor 6 OS=Homo sapiens GN=PRPF6-[PRP6_HUMAN]	11.83	-	5.88	2	5	5	5
42	B4DZC0 SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member5 (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1-[B4DZC0_HUMAN]	11.52	-	5.93	4	5	5	5
43	A0A0D9SFE5 Lamin B1, isoform CRA_a OS=Homo sapiens GN=LMBN1 PE=4 SV=1-[A0A0D9SFE5_HUMAN]	11.49	1.812	21.28	6	4	4	4
44	K7EP67 116 kDa U5 small nuclear ribonucleoprotein component (Fragment) OS=Homo sapiens GN=EFTUD2 PE=1 SV=1-[K7EP67_HUMAN]	11.18	-	23.77	11	3	3	4
45	B4DSR0 130 kDa leucine-rich protein (LRP130) (Fragment) OS=Homo sapiens PE=2 SV=1-[B4DSR0_HUMAN]	10.67	4.446	2.67	2	1	1	2
46	Q5C9Z4 Nucleolar MIF4G domain-containing protein 1 OS=Homo sapiens GN=NOM1 PE=1 SV=1-[NOM1_HUMAN]	10.62	-	5.81	1	4	4	4
47	B4E0E1 Poly (ADP-ribose) polymerase 1 (EC 2.4.2.30) OS=Homo sapiens PE=2 SV=1-[B4E0E1_HUMAN]	10.42	-	5.34	3	4	4	4
48	Q9NWH9 SAFB-like transcription modulator OS=Homo sapiens GN=SLTM PE=1 SV=2-[SLTM_HUMAN]	10.31	-	3.29	9	3	3	4
49	Q05CW7 NAT10 protein (Fragment) OS=Homo sapiens GN=NAT10 PE=2 SV=1-[Q05CW7_HUMAN]	10.14	-	4.87	1	1	2	4
50	Q5UIP0 Telomere-associated protein RIF1 OS=Homo sapiens GN=RIF1-[RIF1_HUMAN]	9.79	-	2.78	3	4	4	4
51	B4DYH4 Mediator of DNA damage checkpoint protein 1 OS=Homo sapiens PE=2 SV=1-[B4DYH4_HUMAN]	9.07	-	3.38	8	4	4	4
52	O75691 Small subunit processome component 20 homolog OS=Homo sapiens GN=UTP20 PE=1 SV=3-[UTP20_HUMAN]	9.03	-	2.01	1	3	3	3
53	Q0QET7 Glyceraldehyde-3-phosphate dehydrogenase (Fragment) OS=Homo sapiens GN=GAPDH PE=2 SV=1-[Q0QET7_HUMAN]	8.89	-	22.61	7	2	2	2
54	O75369 Filamin-B OS=Homo sapiens GN=FLNB-[FLNB_HUMAN]	7.97	-	2.52	12	3	3	3
55	Q15631 Translin OS=Homo sapiens GN=TSN-[TSN_HUMAN]	7.86	-	16.22	7	2	2	2
56	P49588 Alanine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=AARS PE=1 SV=2-[SYAC_HUMAN]	7.73	-	2.27	2	1	1	2
57	A0A087X1N2 CCAAT/enhancer-binding protein zeta OS=Homo sapiens GN=CEBPZ PE=1 SV=1-[A0A087X1N2_HUMAN]	7.63	-	4.21	3	3	3	3
58	B9EG90 Topoisomerase (DNA) I OS=Homo sapiens GN=TOP1 PE=2 SV=1-[B9EG90_HUMAN]	7.56	-	5.75	3	3	3	3

Table SI. Continued.

Accession	Description	Score <sup>a</sup>	Enrichment ratio <sup>b</sup>	Coverage %	Proteins	Unique peptides	Peptides	PSMs
59	P53396 ATP-citrate synthase OS=Homo sapiens GN=ACLY-[ACLY_HUMAN]	7.55	-	2.84	3	1	1	2
60	B3GQE6 DEAD box polypeptide 27 OS=Homo sapiens GN=DDX27 PE=2 SV=1-[B3GQE6_HUMAN]	7.49	-	6.27	6	4	4	4
61	A0A087WV29 N-acetyltransferase 10 OS=Homo sapiens GN=NAT10 PE=1 SV=1-[A0A087WV29_HUMAN]	7.41	-	3.00	3	1	2	3
62	A2RUU9 PCM1 protein OS=Homo sapiens GN=PCM1 PE=2 SV=1-[A2RUU9_HUMAN]	7.16	-	1.56	15	3	3	3
63	Q7Z497 SF3B1 protein (Fragment) OS=Homo sapiens GN=SF3B1 PE=2 SV=1-[Q7Z497_HUMAN]	7.11	-	3.17	2	1	1	2
64	Q9Y2W1 Thyroid hormone receptor-associated protein 3 OS=Homo sapiens GN=THRAP3 PE=1 SV=2-[TR150_HUMAN]	7.08	-	3.66	5	3	3	3
65	Q4ZG57 MCM6 (Fragment) OS=Homo sapiens GN=MCM6 PE=3 SV=1-[Q4ZG57_HUMAN]	6.92	-	2.93	2	2	2	2
66	B3KN82 Nucleolar protein NOP5 OS=Homo sapiens PE=2 SV=1-[B3KN82_HUMAN]	6.89	-	7.94	4	3	3	3
67	Q71UI9 Histone H2A.V OS=Homo sapiens GN=H2AFV-[H2AV_HUMAN]	6.88	-	22.81	8	1	3	3
68	B3KSQ7 Drebrin 1, isoform CRA_d OS=Homo sapiens GN=DBN1 PE=2 SV=1-[B3KSQ7_HUMAN]	6.82	-	5.68	7	2	2	2
69	H7C597 Staphylococcal nuclease domain-containing protein 1 (Fragment) OS=Homo sapiens GN=SND1 PE=1 SV=1-[H7C597_HUMAN]	6.41	-	12.55	7	2	2	3
70	B7Z8U9 Tripartite motif-containing protein 29 OS=Homo sapiens PE=2 SV=1-[B7Z8U9_HUMAN]	6.26	-	5.92	12	2	2	3
71	C9J013 DNA replication licensing factor MCM2 (Fragment) OS=Homo sapiens GN=MCM2 PE=1 SV=1-[C9J013_HUMAN]	5.83	-	37.86	6	2	2	2
72	Q15084 Protein disulfide-isomerase A6 OS=Homo sapiens GN=PPIA6-[PPIA6_HUMAN]	5.83	-	8.01	5	1	1	1
73	B7Z854 Homo sapiens estrogen receptor binding protein (ERBP), mRNA OS=Homo sapiens PE=2 SV=1-[B7Z854_HUMAN]	5.81	-	4.83	4	2	2	2
74	P31942 Heterogeneous nuclear ribonucleoprotein H3 OS=Homo sapiens GN=HNRNP3-[HNRH3_HUMAN]	5.78	-	6.51	6	1	1	2
75	Q9H307 Pinin OS=Homo sapiens GN=PNN-[PININ_HUMAN]	5.74	-	4.79	5	2	2	2
76	P52597 Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3-[HNRPF_HUMAN]	5.7	-	7.71	2	2	2	2
77	F8W888 Transketolase OS=Homo sapiens GN=TKT PE=1 SV=1-[F8W888_HUMAN]	5.57	-	17.65	6	1	1	1
78	O60287 Nucleolar pre-ribosomal-associated protein 1 OS=Homo sapiens GN=URB1 PE=1 SV=4-[NPA1P_HUMAN]	5.51	-	0.88	1	2	2	2

Table S1. Continued.

Accession	Description	Score <sup>a</sup>	Enrichment ratio <sup>b</sup>	Coverage %	Proteins	Unique peptides	Peptides	PSMs
79 B4E187	Zinc finger protein 638 (Fragment) OS=Homo sapiens PE=2 SV=1-[B4E187_HUMAN]	5.23	-	2.27	13	2	2	2
80 P46100	Transcriptional regulator ATRX OS=Homo sapiens GN=ATRX-[ATRX_HUMAN]	5.17	-	1.18	9	2	2	2
81 Q12789	General transcription factor 3C polypeptide 1 OS=Homo sapiens GN=GTTF3C1-[TF3C1_HUMAN]	5.14	-	1.15	5	2	2	2
82 H7C2L4	Transformer-2 protein homolog beta (Fragment) OS=Homo sapiens GN=TRA2B PE=1 SV=1-[H7C2L4_HUMAN]	5.13	2.028	18.69	8	2	2	2
83 A0A0A0MSI0	Peroxiredoxin-1 (Fragment) OS=Homo sapiens GN=PRDX1 PE=1 SV=1-[A0A0A0MSI0_HUMAN]	5	-	14.62	3	1	1	1
84 Q86UA8	SMARCA1 protein (Fragment) OS=Homo sapiens GN=SMARCA1 PE=2 SV=2-[Q86UA8_HUMAN]	4.98	-	2.18	6	2	2	2
85 Q59FS7	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24 variant (Fragment) OS=Homo sapiens PE=2 SV=1-[Q59FS7_HUMAN]	4.86	-	4.73	8	2	2	2
86 B4DM32	GCN1-like protein 1 (Fragment) OS=Homo sapiens PE=2 SV=1-[B4DM32_HUMAN]	4.82	-	3.57	3	1	1	1
87 A1L195	TUBB2B protein (Fragment) OS=Homo sapiens GN=TUBB2B PE=2 SV=2-[A1L195_HUMAN]	4.79	-	9.57	28	1	1	1
88 H3BU13	Pyruvate kinase PKM (Fragment) OS=Homo sapiens GN=PKM PE=1 SV=1-[H3BU13_HUMAN]	4.77	-	15.85	11	1	1	2
89 F8VRN8	LIM domain and actin-binding protein 1 OS=Homo sapiens GN=LIMA1 PE=1 SV=1-[F8VRN8_HUMAN]	4.7	-	4.90	8	2	2	2
90 H0Y2S9	Myosin phosphatase Rho-interacting protein (Fragment) OS=Homo sapiens GN=MPRIP PE=1 SV=3-[H0Y2S9_HUMAN]	4.6	-	1.28	9	2	2	2
91 A0A087WVN4	Farnesyl pyrophosphate synthase (Fragment) OS=Homo sapiens GN=FDPS PE=1 SV=1-[A0A087WVN4_HUMAN]	4.58	-	10.22	4	1	1	1
92 Q8WYP5	Protein ELYS OS=Homo sapiens GN=AHC1 PE=1 SV=3-[ELYS_HUMAN]	4.58	-	1.02	5	2	2	2
93 O00159	Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C-[MYO1C_HUMAN]	4.56	-	2.24	13	2	2	2
94 B4DUK1	Peroxiredoxin-6 (EC 1.11.1.15) OS=Homo sapiens PE=2 SV=1-[B4DUK1_HUMAN]	4.53	-	16.83	2	1	1	1
95 Q14669	E3 ubiquitin-protein ligase TRIP12 OS=Homo sapiens GN=TRIP12-[TRIP12_HUMAN]	4.51	-	1.45	4	2	2	2
96 E9PCY5	DNA topoisomerase 2 (Fragment) OS=Homo sapiens GN=TOP2B PE=1 SV=1-[E9PCY5_HUMAN]	4.4	-	2.00	5	2	2	2
97 Q9Y5B9	FACT complex subunit SPT16 OS=Homo sapiens GN=SPT16H PE=1 SV=1-[SPT16H_HUMAN]	4.35	-	2.01	1	2	2	2

Table SI. Continued.

Accession	Description	Score <sup>a</sup>	Enrichment ratio <sup>b</sup>	Coverage %	Proteins	Unique peptides	Peptides	PSMs
98	Q16777 Histone H2A type 2-C OS=Homo sapiens GN=HIST2H2AC PE=1 SV=4-[H2A2C_HUMAN]	4.24	1.797	22.48	2	1	1	1
99	H3BQZ7 HCG2044799 OS=Homo sapiens GN=HNRNPUL2-BSCL2 PE=4 SV=1-[H3BQZ7_HUMAN]	3.91	-	4.69	2	2	2	3
100	Q6PIX2 SFPQ protein (Fragment) OS=Homo sapiens GN=SFPQ PE=2 SV=1-[Q6PIX2_HUMAN]	3.81	-	4.38	5	1	1	1
101	Q86V81 THO complex subunit 4 OS=Homo sapiens GN=ALYREF PE=1 SV=3-[THOC4_HUMAN]	3.79	-	7.00	2	1	1	1
102	Q59G78 Lactate dehydrogenase B variant (Fragment) OS=Homo sapiens PE=2 SV=1-[Q59G78_HUMAN]	3.77	-	15.50	2	1	1	1
103	Q53T09 XRCC5 (Fragment) OS=Homo sapiens GN=XRCC5 PE=4 SV=1- [Q53T09_HUMAN]	3.74	-	4.58	2	1	1	1
104	Q9UKM9 RNA-binding protein Raly OS=Homo sapiens GN=RALY- [RALY_HUMAN]	3.67	-	11.03	4	1	1	1
105	B4DUP0 Elongation factor 1-gamma OS=Homo sapiens PE=2 SV=1-[B4DUP0_HUMAN]	3.65	-	15.05	3	1	1	1
106	Q8NCW5 NAD(P)H-hydrate epimerase OS=Homo sapiens GN=APOA1BP- [NNRE_HUMAN]	3.61	-	17.84	4	1	1	1
107	A0A087WZJ0 Exophilin-5 (Fragment) OS=Homo sapiens GN=EXPH5 PE=1 SV=1-[A0A087WZJ0_HUMAN]	3.41	-	2.39	9	1	1	1
108	S4R3B5 Protein transport protein Sec61 subunit beta OS=Homo sapiens GN=SEC61B PE=1 SV=1-[S4R3B5_HUMAN]	3.4	-	66.67	3	1	1	1
109	B4DFU8 Liprin-beta-1 (Fragment) OS=Homo sapiens PE=2 SV=1- [B4DFU8_HUMAN]	3.35	-	2.02	6	1	1	1
110	Q8TDD1 ATP-dependent RNA helicase DDX54 OS=Homo sapiens GN=DDX54 PE=1 SV=2-[DDX54_HUMAN]	3.29	-	1.25	2	1	1	1
111	Q96ES5 HEATR1 protein OS=Homo sapiens GN=HEATR1 PE=1 SV=1-[Q96ES5_HUMAN]	3.25	-	6.30	10	1	1	1
112	J3QSB4 60S ribosomal protein L13 (Fragment) OS=Homo sapiens GN=RPL13 PE=1 SV=1-[J3QSB4_HUMAN]	3.2	-	8.73	3	1	1	1
113	Q59GY3 Arginine/serine-rich splicing factor 6 variant (Fragment) OS=Homo sapiens PE=2 SV=1-[Q59GY3_HUMAN]	3.19	-	5.02	5	1	1	2
114	Q9H0D6 5'-3' exoribonuclease 2 OS=Homo sapiens GN=XRN2- [XRN2_HUMAN]	3.17	-	1.37	4	1	1	1
115	X6RJY0 U3 small nucleolar RNA-associated protein 14 homolog A (Fragment) OS=Homo sapiens GN=UTP14A PE=1 SV=1- [X6RJY0_HUMAN]	3.17	-	3.75	5	1	1	1
116	O75934 Pre-mRNA-splicing factor SPF27 OS=Homo sapiens GN=BCAS2 PE=1 SV=1-[SPF27_HUMAN]	3.12	-	5.78	2	1	1	1



Table SI. Continued.

Accession	Description	Score <sup>a</sup>	Enrichment ratio <sup>b</sup>	Coverage %	Proteins	Unique peptides	Peptides	PSMs
117	P16401 Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3-[H15_HUMAN]	3.1	-	5.75	1	1	1	1
118	U6A3P2 Mutant hemoglobin alpha 2 globin chain (Fragment) OS=Homo sapiens GN=HBA2 PE=3 SV=1-[U6A3P2_HUMAN]	3.1	-	29.27	14	1	1	1
119	B5BU08 U2 small nuclear RNA auxiliary factor 1 isoform a OS=Homo sapiens GN=U2AF1 PE=2 SV=1-[B5BU08_HUMAN]	3.07	-	5.42	2	1	1	1
120	B7Z752 Importin beta-1 subunit OS=Homo sapiens PE=2 SV=1-[B7Z752_HUMAN]	3.06	-	3.56	4	1	1	1
121	F4ZCG4 FAM83H variant 2 (Fragment) OS=Homo sapiens GN=FAM83H PE=2 SV=1-[F4ZCG4_HUMAN]	3	-	13.79	2	1	1	2
122	F5GXX5 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1 OS=Homo sapiens GN=DAD1 PE=1 SV=1-[F5GXX5_HUMAN]	2.99	-	24.71	3	1	1	1
123	D3DV75 Adenosine deaminase, RNA-specific, isoform CRA_b OS=Homo sapiens GN=ADAR PE=4 SV=1-[D3DV75_HUMAN]	2.96	-	1.24	10	1	1	1
124	P09417 Dihydropteridine reductase OS=Homo sapiens GN=QDPR-[DHPR_HUMAN]	2.94	-	12.68	2	1	1	1
125	F8VUA6 60S ribosomal protein L18 (Fragment) OS=Homo sapiens GN=RPL18 PE=1 SV=1-[F8VUA6_HUMAN]	2.92	-	10.00	10	1	1	1
126	Q3SYB5 SERPINB12 protein OS=Homo sapiens GN=SERPINB12 PE=2 SV=1-[Q3SYB5_HUMAN]	2.89	-	14.21	3	1	1	1
127	B7WP74 Pre-mRNA-splicing factor CWC22 homolog (Fragment) OS=Homo sapiens GN=CWC22 PE=1 SV=1-[B7WP74_HUMAN]	2.88	-	2.82	2	1	1	1
128	M0R2U2 rRNA 2'-O-methyltransferase fibrillar (Fragment) OS=Homo sapiens GN=FBL PE=1 SV=1-[M0R2U2_HUMAN]	2.85	-	8.28	10	1	1	1
129	Q9H6R4 Nucleolar protein 6 OS=Homo sapiens GN=NOL6-[NOL6_HUMAN]	2.83	-	2.00	6	1	1	1
130	Q01780 Exosome component 10 OS=Homo sapiens GN=EXOSC10-[EXOSC_HUMAN]	2.82	-	1.16	2	1	1	1
131	P46783 40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1-[RS10_HUMAN]	2.81	-	5.45	4	1	1	1
132	P19105 Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=2-[ML12A_HUMAN]	2.81	-	6.43	4	1	1	1
133	E9PC74 Translation initiation factor eIF-2B subunit epsilon OS=Homo sapiens GN=EIF2B5 PE=1 SV=1-[E9PC74_HUMAN]	2.74	-	3.26	2	1	1	1
134	E9PQI8 U4/U6,U5 tri-snRNP-associated protein 1 OS=Homo sapiens GN=SART1 PE=1 SV=1-[E9PQI8_HUMAN]	2.74	-	12.20	3	1	1	1
135	H0YLE2 Annexin A2 (Fragment) OS=Homo sapiens GN=ANXA2 PE=1 SV=1-[H0YLE2_HUMAN]	2.65	-	22.22	18	1	1	1

Table SI. Continued.

Accession	Description	Score <sup>a</sup>	Enrichment ratio <sup>b</sup>	Coverage %	Proteins	Unique peptides	Peptides	PSMs
136 Q9UIG0	Tyrosine-protein kinase BAZ1B OS=Homo sapiens GN=BAZ1B PE=1 SV=2-[BAZ1B_HUMAN]	2.63	-	1.62	1	1	1	1
137 B4DMT4	Alpha-centractin OS=Homo sapiens PE=2 SV=1-[B4DMT4_HUMAN]	2.62	-	9.60	6	1	1	1
138 Q9H6F5	Coiled-coil domain-containing protein 86 OS=Homo sapiens GN=CCDC86 PE=1 SV=1-[CCD86_HUMAN]	2.62	-	6.11	1	1	1	1
139 S4R3A2	Fatty acid-binding protein, heart OS=Homo sapiens GN=FABP3 PE=1 SV=1-[S4R3A2_HUMAN]	2.59	-	14.61	4	1	1	1
140 Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens GN=KHDRBS1-[KHDR1_HUMAN]	2.59	-	3.47	5	1	1	1
141 D6R939	Ras GTPase-activating-like protein IQGAP2 (Fragment) OS=Homo sapiens GN=IQGAP2 PE=1 SV=5-[D6R939_HUMAN]	2.58	-	3.52	6	1	1	1
142 E7EMB7	Importin-11 OS=Homo sapiens GN=IPO11 PE=1 SV=1-[E7EMB7_HUMAN]	2.55	-	35.11	3	1	1	1
143 Q5HY57	Emerin OS=Homo sapiens GN=EMD PE=1 SV=1-[Q5HY57_2.53_HUMAN]	-	5.48%	2	1	1	1	1
144 Q9BSN3	NOP56 protein OS=Homo sapiens GN=NOP56 PE=2 SV=1-[Q9BSN3_HUMAN]	2.53	-	8.62	6	1	1	1
145 Q59FH1	Transformation/transcription domain-associated protein variant (Fragment) OS=Homo sapiens PE=2 SV=1-[Q59FH1_HUMAN]	2.52	-	0.28	5	1	1	1
146 Q8N9K4	ALPHA-ADAPTIN A OS=Homo sapiens PE=2 SV=1-[Q8N9K4_HUMAN]	2.51	-	1.87	8	1	1	1
147 B4DUL5	Ubiquinol-cytochrome-c reductase complex coreprotein I, mitochondrial (EC 1.10.2.2) OS=Homo sapiens PE=2 SV=1-[B4DUL5_HUMAN]	2.48	-	2.74	2	1	1	1
148 A0A087X1B7	Chromatin target of PRMT1 protein OS=Homo sapiens GN=CHTOP PE=1 SV=1-[A0A087X1B7_HUMAN]	2.46	-	17.11	5	1	1	1
149 B3KM65	Probable ATP-dependent RNA helicase DDX52 (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1-[B3KM65_HUMAN]	2.46	-	6.54	3	1	1	1
150 Q03188	Centromere protein C OS=Homo sapiens GN=CENPC-[CENPC_HUMAN]	2.43	-	1.85	3	1	1	1
151 Q6LCG8	Catenin-4 (Fragment) OS=Homo sapiens PE=2 SV=1-[Q6LCG8_HUMAN]	2.42	-	2.11	5	1	1	1
152 O76021	Ribosomal L1 domain-containing protein 1 OS=Homo sapiens GN=RSL1D1-[RL1D1_HUMAN]	2.41	-	4.07	5	1	1	1
153 V9GYG0	ADP/ATP translocase 1 OS=Homo sapiens GN=SLC25A4 PE=1 SV=1-[V9GYG0_HUMAN]	2.37	-	3.85	8	1	1	1

Table SI. Continued.

Accession	Description	Score <sup>a</sup>	Enrichment ratio <sup>b</sup>	Coverage %	Proteins	Unique peptides	Peptides	PSMs
154	Myosin-18A OS=Homo sapiens PE=2 SV=1-[B4E0T8_HUMAN]	2.37	-	1.95	9	1	1	1
155	Gem-associated protein 4 OS=Homo sapiens GN=GEMIN4 PE=1 SV=1-[I3L2C7_HUMAN]	2.36	-	1.05	5	1	1	1
156	Nesprin-3 OS=Homo sapiens GN=SYNE3-[SYNE3_HUMAN]	2.35	-	1.85	4	1	1	1
157	Neurabin-2 OS=Homo sapiens GN=PPP1R9B PE=1 SV=2-[NEB2_HUMAN]	2.34	-	2.09	2	1	1	1
158	Methionine-tRNA ligase, cytoplasmic (Fragment) OS=Homo sapiens GN=MARS PE=1 SV=1-[H0YHL6_HUMAN]	2.29	-	12.35	7	1	1	1
159	Rho GTPase-activating protein 32 OS=Homo sapiens GN=ARHGAP32-[RHG32_HUMAN]	2.28	-	4.04	8	1	1	1
160	Homo sapiens activity-dependent neuroprotector (ADNP), mRNA OS=Homo sapiens PE=2 SV=1-[B2RBM8_HUMAN]	2.27	-	1.00	3	1	1	1
161	Chromodomain-helicase-DNA-binding protein 1 OS=Homo sapiens GN=CHD1-[CHD1_HUMAN]	2.24	-	0.59	2	1	1	1
162	SUN domain-containing protein 1 (Fragment) OS=Homo sapiens GN=SUN1 PE=1 SV=1-[H7C2K3_HUMAN]	2.24	-	3.75	11	1	1	1
163	Ribosome biogenesis protein BOP1 OS=Homo sapiens GN=BOP1 PE=2 SV=1-[A8K3R2_HUMAN]	2.22	-	1.88	3	1	1	1
164	Retinoblastoma-like protein 2 (Fragment) OS=Homo sapiens GN=RBL2 PE=1 SV=2-[F5H837_HUMAN]	2.21	-	0.94	4	1	1	1
165	Eukaryotic initiation factor 4A-III (Fragment) OS=Homo sapiens GN=EIF4A3 PE=1 SV=1-[I3L3H2_HUMAN]	2.19	-	11.20	2	1	1	1
166	Coronin-1C (Fragment) OS=Homo sapiens GN=CORO1C PE=1 SV=1-[H0YHL7_HUMAN]	2.18	-	7.27	10	1	1	1
167	Guanine nucleotide binding protein-like 3 (Nucleolar), isoform CRA_b OS=Homo sapiens GN=GNL3 PE=4 SV=1-[A0A024R2Z6_HUMAN]	2.18	-	2.79	3	1	1	1
168	RNA-binding protein 12B OS=Homo sapiens GN=RBM12B PE=1 SV=2-[B9ZVT1_HUMAN]	2.18	-	1.14	2	1	1	1
169	RNA-binding protein 14 OS=Homo sapiens PE=2 SV=1-[B4DNG4_HUMAN]	2.17	-	4.69	2	1	1	1
170	WD repeat-containing protein 36 OS=Homo sapiens GN=WDR36 PE=1 SV=1-[A0A0A0MTB8_HUMAN]	2.17	-	1.34	2	1	1	1
171	Small ubiquitin-related modifier 2 OS=Homo sapiens GN=SUMO2-[SUMO2_HUMAN]	2.16	-	14.08	2	1	1	1
172	Double-strand-break repair protein rad21 homolog OS=Homo sapiens GN=RAD21 PE=1 SV=2-[RAD21_HUMAN]	2.15	-	1.58	1	1	1	1
173	NUCLEAR PORE COMPLEX PROTEIN NUP107 OS=Homo sapiens PE=2 SV=1-[B3KMK0_HUMAN]	2.14	-	2.19	4	1	1	1

Table SI. Continued.

Accession	Description	Score <sup>a</sup>	Enrichment ratio <sup>b</sup>	Coverage %	Proteins	Unique peptides	Peptides	PSMs
174	Q96I17 NOLC1 protein OS=Homo sapiens GN=NOLC1 PE=2 SV=1-[Q96I17_HUMAN]	2.13	-	2.39	6	1	1	1
175	Q8IY37 Probable ATP-dependent RNA helicase DHX37 OS=Homo sapiens GN=DHX37 PE=1 SV=1-[DHX37_HUMAN]	2.13	-	1.04	1	1	1	1
176	B4E310 Caldesmon OS=Homo sapiens PE=2 SV=1-[B4E310_HUMAN]	2.12	-	1.92	17	1	1	1
177	B4DS83 Nucleolar protein 10 OS=Homo sapiens PE=2 SV=1-[B4DS83_HUMAN]	2.12	-	1.88	4	1	1	1
178	P05089 Arginase-1 OS=Homo sapiens GN=ARG1-[ARGI1_HUMAN]	2.11	-	4.66	3	1	1	1
179	B4DW05 Prohibitin-2 OS=Homo sapiens PE=2 SV=1-[B4DW05_HUMAN]	2.11	-	3.76	7	1	1	1
180	H7C5W9 Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 (Fragment) OS=Homo sapiens GN=ATP2A2 PE=1 SV=1-[H7C5W9_HUMAN]	2.11	-	1.07	6	1	1	1
181	F8WD73 MICOS complex subunit MIC19 OS=Homo sapiens GN=CHCHD3 PE=1 SV=1-[F8WD73_HUMAN]	2.1	-	12.70	5	1	1	1
182	P07305 Histone H1.0 OS=Homo sapiens GN=H1F0-[H10_HUMAN]	2.09	-	7.34	2	1	1	1
183	H0YB22 40S ribosomal protein S14 (Fragment) OS=Homo sapiens GN=RPS14 PE=1 SV=1-[H0YB22_HUMAN]	2.08	-	9.17	3	1	1	1
184	O60424 CBP (Fragment) OS=Homo sapiens GN=CBP PE=1 SV=1-[O60424_HUMAN]	2.08	-	1.08	3	1	1	1
185	H7C267 Pescadillo homolog (Fragment) OS=Homo sapiens GN=PES1 PE=1 SV=1-[H7C267_HUMAN]	2.05	-	4.12	6	1	1	1
186	H7C151 Tumor suppressor p53-binding protein 1 (Fragment) OS=Homo sapiens GN=TP53BP1 PE=1 SV=1-[H7C151_HUMAN]	2.05	-	20.83	8	1	1	1
187	H0Y390 Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 (Fragment) OS=Homo sapiens GN=MACF1 PE=1 SV=1-[H0Y390_HUMAN]	2.04	-	0.54	8	1	1	1
188	A8K6V7 Homo sapiens Ras-GTPase activating protein SH3 domain-binding protein 2 (G3BP2), transcript variant 3, mRNA OS=Homo sapiens PE=2 SV=1-[A8K6V7_HUMAN]	2.02	-	2.90	3	1	1	1
189	Q99848 Probable rRNA-processing protein EBP2 OS=Homo sapiens GN=EBNA1BP2 PE=1 SV=2-[EBP2_HUMAN]	2.02	-	3.27	2	1	1	1
190	M0R088 Serine/arginine repetitive matrix protein 1 (Fragment) OS=Homo sapiens GN=SRRM1 PE=1 SV=1-[M0R088_HUMAN]	2.02	-	1.47	6	1	1	1
191	Q5VU81 Ubiquitin-associated protein 2-like (Fragment) OS=Homo sapiens GN=UBAP2L PE=1 SV=1-[Q5VU81_HUMAN]	2	-	6.04	12	1	1	1
192	H7C0W8 Adipocyte enhancer-binding protein 1 (Fragment) OS=Homo sapiens GN=AEBP1 PE=1 SV=1-[H7C0W8_HUMAN]	0	-	23.08	1	1	1	1
193	F8WBL2 Bystin OS=Homo sapiens GN=BYSL PE=1 SV=1-[F8WBL2_HUMAN]	0	-	10.31	2	1	1	1

Table SI. Continued.

	Accession	Description	Score <sup>a</sup>	Enrichment ratio <sup>b</sup>	Coverage %	Proteins	Unique peptides	Peptides	PSMs
194	Q86VR6	DDX10 protein (Fragment) OS=Homo sapiens GN=DDX10 PE=2 SV=1-[Q86VR6_HUMAN]	0	-	2.55	5	1	1	1
195	B4DRA9	General transcription factor II-1 OS=Homo sapiens PE=2 SV=1-[B4DRA9_HUMAN]	0	-	4.15	8	1	1	1
196	B4DES7	RRP5 protein homolog OS=Homo sapiens PE=2 SV=1-[B4DES7_HUMAN]	0	-	3.76	3	1	1	1
197	F6VJE8	U3 small nucleolar RNA-associated protein 18 homolog (Fragment) OS=Homo sapiens GN=UTP18 PE=1 SV=1- [F6VJE8_HUMAN]	0	-	32.56	3	1	1	1

<sup>a</sup>Score, the sum of the ion scores of all peptides that were identified. PSMs, the number of peptide spectrum matches. Coverage, the percentage of the protein sequence covered by identified peptides. Proteins, the number of identified proteins in the Protein Group Members view. Unique peptides, the number of peptide sequences that are unique to a protein group. Peptides: The total number of distinct peptide sequences identified in the protein group. <sup>b</sup>Enrichment ratio is defined by Score (IP)/Score (IgG). Enrichment cutoff is set at 1.5 to filter potential binding partners. '-' indicated peptides of protein were only discovered in IP group instead of IgG group. nIGF1R, nuclear insulin-like growth factor 1 receptor; IP-MS, immunoprecipitation coupled-mass spectrometry. The newly established IGF1R-overexpressing colorectal cancer cell line is defined as SW480-OE.

Table SII. nIGF1R interactors related with the DSB pathway as revealed by IP-MS.

Accession	Description	Score <sup>a</sup>	Enrichment ratio <sup>b</sup>	Coverage %	Proteins	Unique peptides	Peptides	PSMs
1	Q14980 Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1-[NUMA1_HUMAN]	182.91	21.368	26.75	26	45	45	65
2	P78527 DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC-[PRKDC_HUMAN]	46.73	-	5.17	3	15	15	18
3	P11388 DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A PE=1 SV=3-[TOP2A_HUMAN]	12.14	-	3.72	5	4	4	4
4	B4E0E1 Poly (ADP-ribose) polymerase 1 (EC 2.4.2.30) OS=Homo sapiens PE=2 SV=1-[B4E0E1_HUMAN]	10.42	-	5.34	3	4	4	4
5	Q5UIP0 Telomere-associated protein RIF1 OS=Homo sapiens GN=RIF1-[RIF1_HUMAN]	9.79	-	2.78	3	4	4	4
6	B4DYH4 Mediator of DNA damage checkpoint protein 1 OS=Homo sapiens PE=2 SV=1-[B4DYH4_HUMAN]	9.07	-	3.38	8	4	4	4
7	B9EG90 Topoisomerase (DNA) I OS=Homo sapiens GN=TOP1 PE=2 SV=1-[B9EG90_HUMAN]	7.56	-	5.75	3	3	3	3
8	E9PCY5 DNA topoisomerase 2 (Fragment) OS=Homo sapiens GN=TOP2B PE=1 SV=1-[E9PCY5_HUMAN]	4.4	-	2.00	5	2	2	2
9	Q53T09 XRCC5 (Fragment) OS=Homo sapiens GN=XRCC5 PE=4 SV=1-[Q53T09_HUMAN]	3.74	-	4.58	2	1	1	1
10	O60216 Double-strand-break repair protein rad21 homolog OS=Homo sapiens GN=RAD21 PE=1 SV=2-[RAD21_HUMAN]	2.15	-	1.58	1	1	1	1
11	H7C151 Tumor suppressor p53-binding protein 1 (Fragment) OS=Homo sapiens GN=TP53BP1 PE=1 SV=1-[H7C151_HUMAN]	2.05	-	20.83	8	1	1	1

<sup>a</sup>Score, the sum of the ion scores of all peptides that were identified. PSMs, the number of peptide spectrum matches. Coverage, the percentage of the protein sequence covered by identified peptides. Proteins, the number of identified proteins in the Protein Group Members view. Unique Peptides, the number of peptide sequences that are unique to a protein group. Peptides, the total number of distinct peptide sequences identified in the protein group. <sup>b</sup>Enrichment ratio is defined by Score (IP)/Score (IgG). Enrichment cutoff is set at 1.5 to filter potential binding partners. '-' indicated peptides of protein were only discovered in IP group instead of IgG group. nIGF1R, nuclear insulin-like growth factor 1 receptor; IP-MS, immunoprecipitation coupled-mass spectrometry DSB, DNA double-strand break.