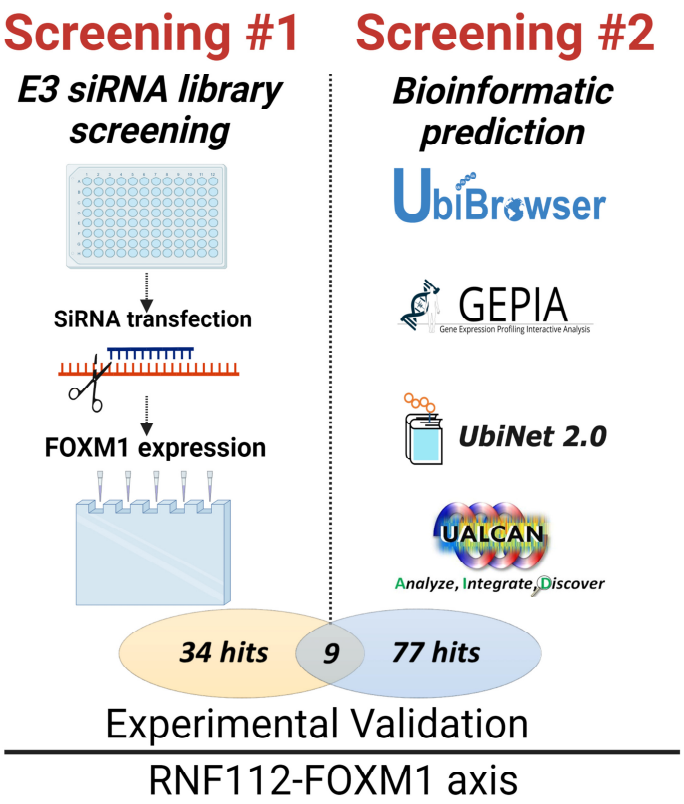
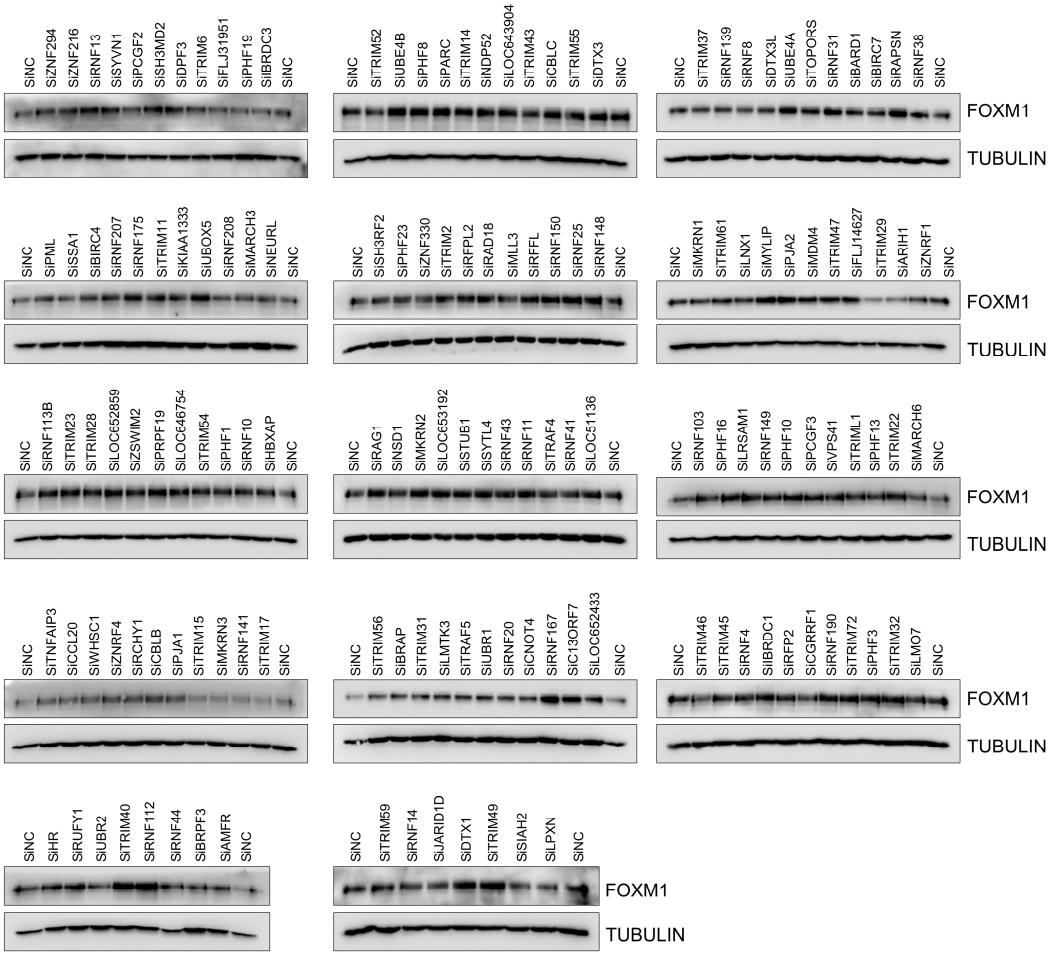


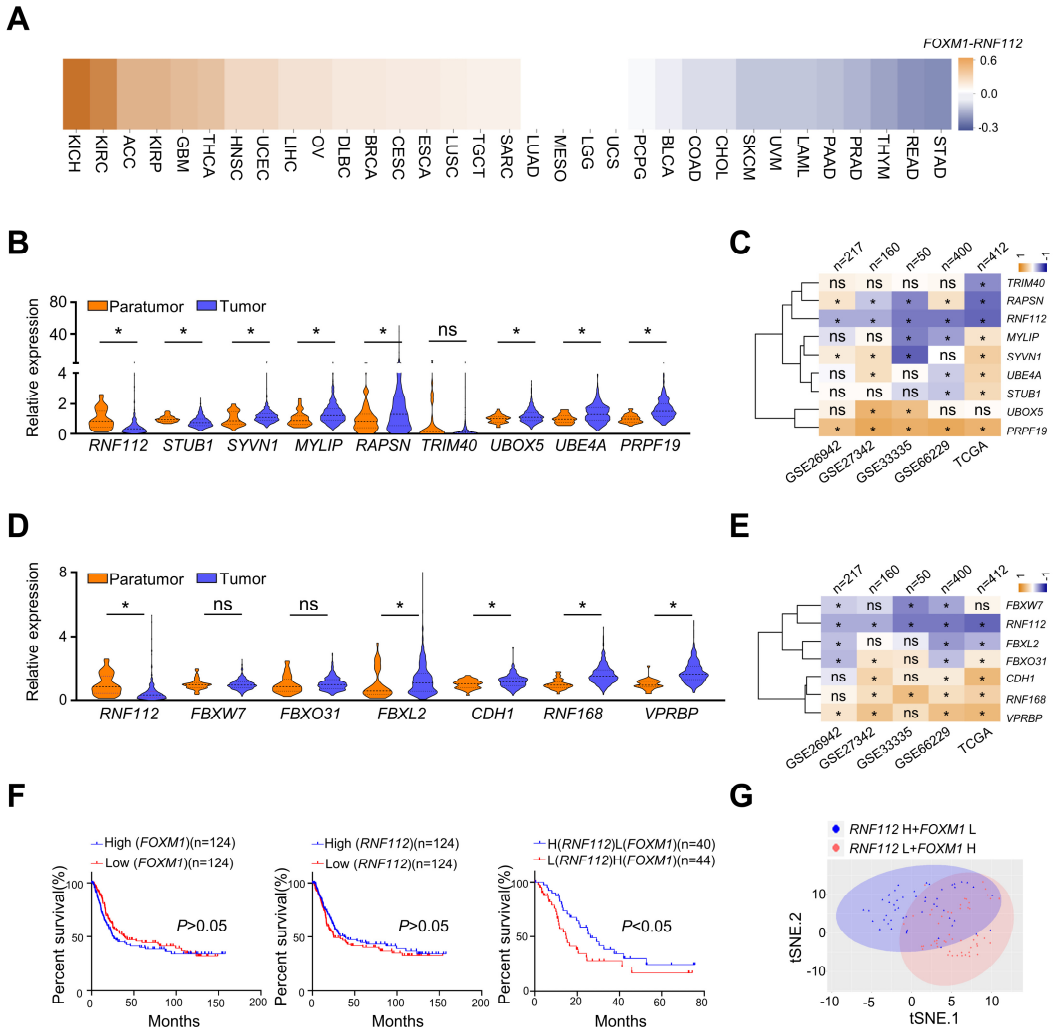
Supplemental Figure 1. Workflow of the identification of novel E3 ubiquitin ligases targeting FOXM1 degradation.

1

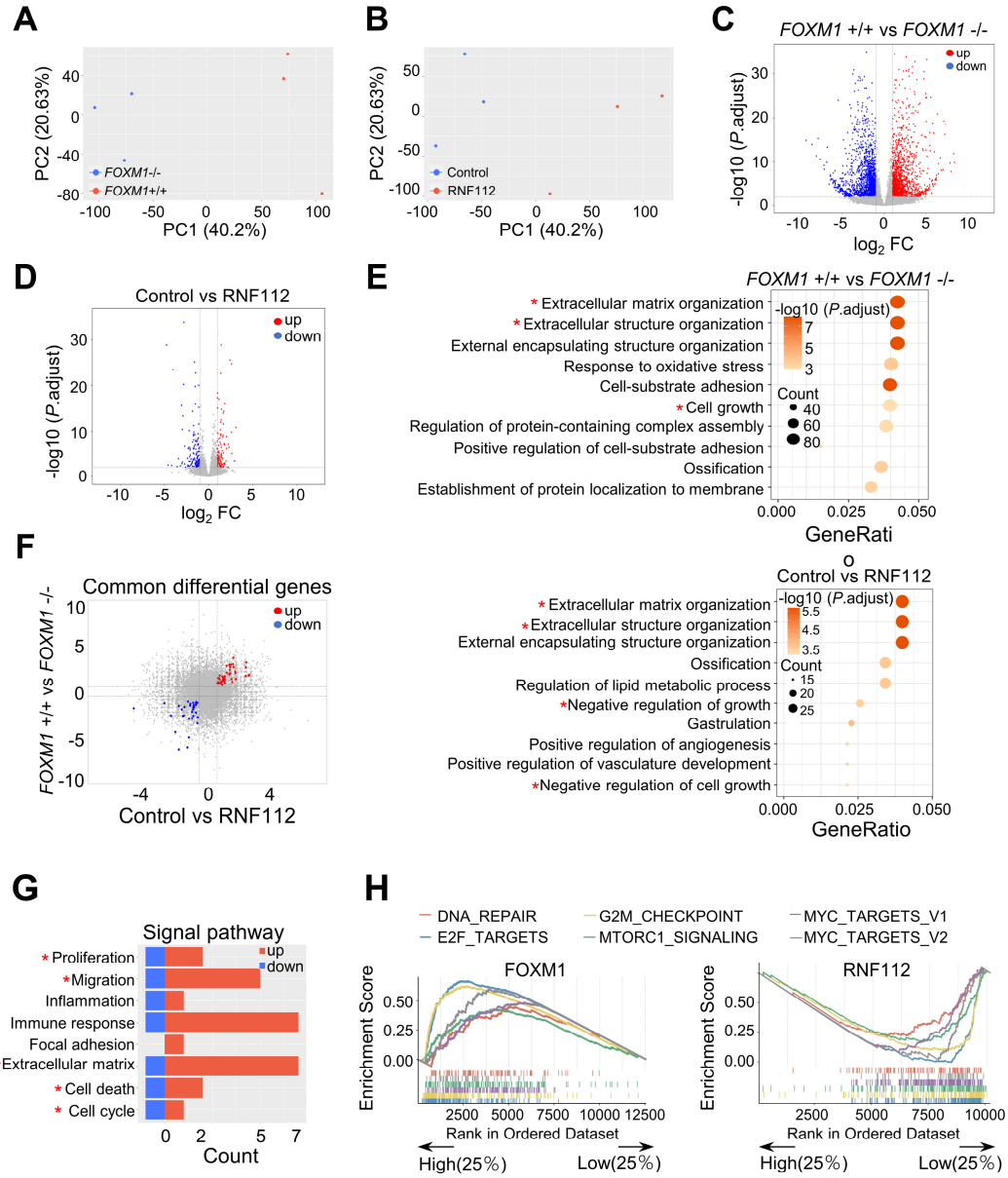


Supplemental Figure 2. Representative immunoblot results of FOXM1 after the transfection of siRNA library targeting E3 ligases in HEK293T cells. Western blot analysis of FOXM1 in HEK293T cells after the knockdown of indicated E3 ligases by siRNA transfection. After HEK293T cells seeded in 96-well plates, The mixture of ON-TARGET plus siRNA library (final siRNA concentration of 50 nM) and Lipofectamine 3000 together with Opti-MEM was added into to each well. The lysates were harvested for immunoblot analysis for endogenous FOXM1 expression 48 h later. Only those with apparent changes were listed.

2

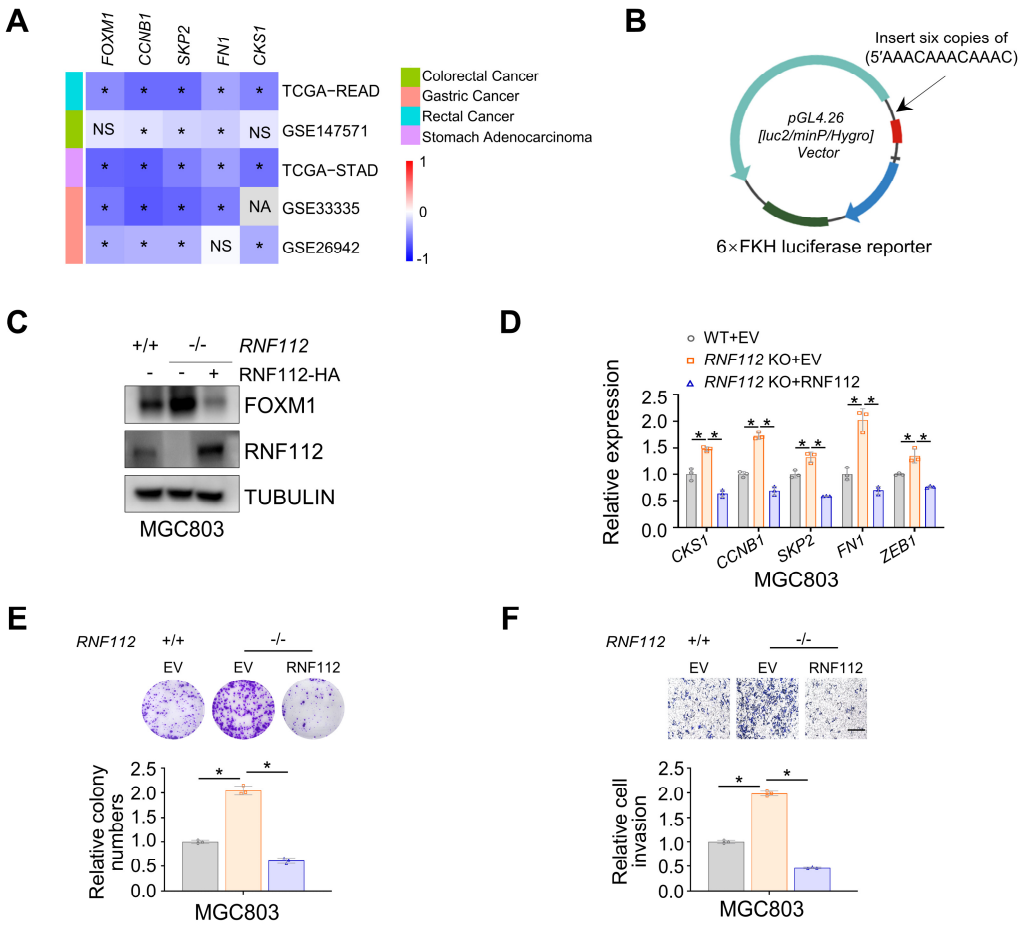


Supplemental Figure 3. The bioinformatic screen for E3 ligases targeting FOXM1. (A) The correlation between *FOXM1* and *RNF112* in 33 types of cancer tissues in TCGA. The color gradient depicts the strength of the correlation. **(B)** Violin plot of the expression of nine potential E3 ligases targeting FOXM1 in gastric cancer and adjacent tissues from TCGA (n=412). **(C)** Heatmap of the correlation between nine potential E3 ligases and *FOXM1* in gastric cancer tissues from five independent cohorts of TCGA and GEO. Orange represents a positive correlation, and blue represents a negative correlation. **(D)** Violin plot of the expression of *RNF112* and six reported E3 ligases targeting FOXM1 in gastric cancer and adjacent normal tissues from TCGA (n=412). **(E)** Heatmap of the correlation between the above E3 ligases and *FOXM1* in five independent gastric cancer cohorts. **(F)** Kaplan–Meier survival curves of gastric patients based on the expression of *FOXM1* and *RNF112* in the GSE15460 cohort. **(G)** tSNE cluster map showing subclusters of gastric cancer patients based on *FOXM1* and *RNF112* expression in GSE15460 cohort. Statistical significance was calculated using Mann–Whitney U test (B, D), Pearson's test (C, E), log-rank test (F). *P< 0.05.



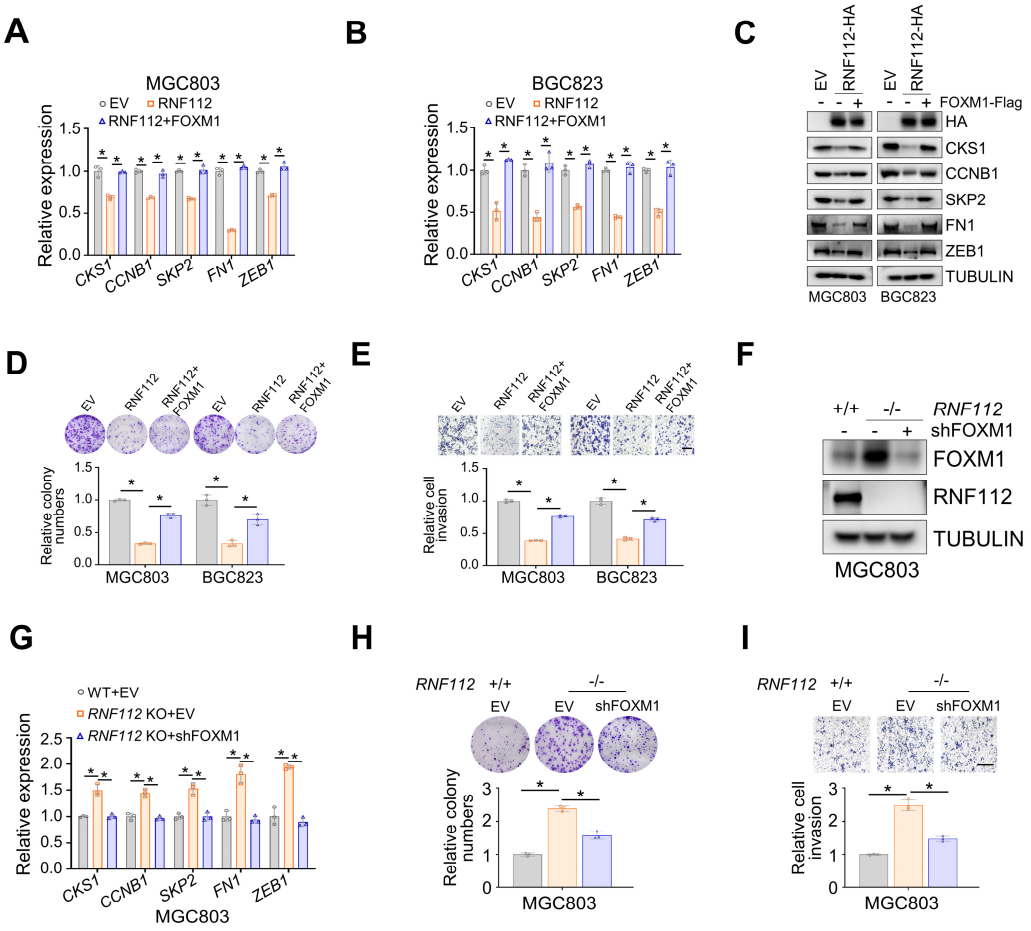
Supplemental Figure 4. FOXM1 and RNF112 are both associated with the proliferation and invasion signaling pathways in gastric cancer. (A-B) PCA analysis of RNA-Seq results of *FOXM1* knockout (A) and RNF112 overexpression MGC803 cells (B). **(C-D)** Volcano plots of differentially expressed mRNA revealed by RNA-seq in MGC803 cells between *FOXM1*+/+ and *FOXM1*-/- group (C) and control and RNF112-overexpressing group (D). **(E)** GO enrichment analysis of biological processes of significantly changed genes from (C-D). **(F)** Scatter plot of common differentially expressed gene between the above two indicated groups. The genes with similar remarkable changes are highlighted. **(G)** GO enrichment analysis of pathways from highlighted genes in (F). **(H)** GSEA analysis based on the expression of *RNF112* and *FOXM1* in TCGA gastric cancer dataset.

4



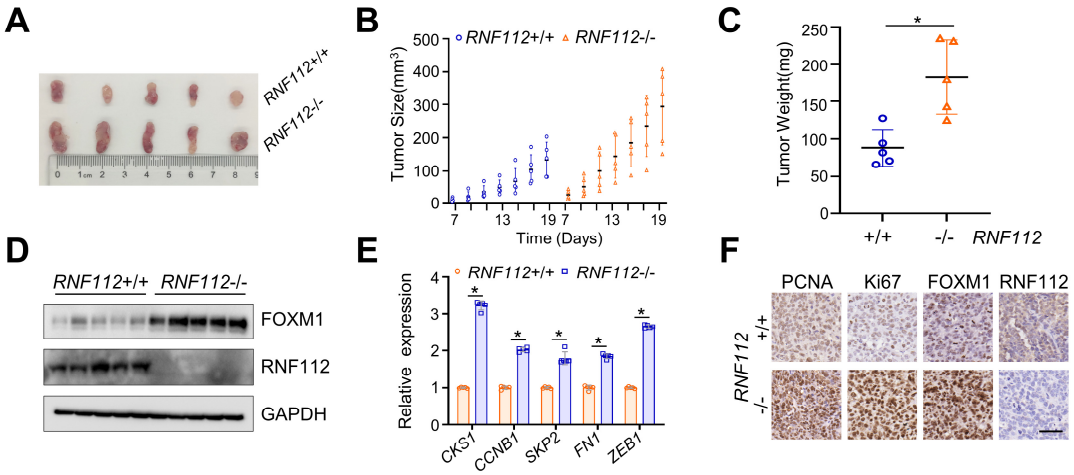
Supplemental Figure 5. RNF112 suppresses FOXM1 downstream genes. (A) The correlation between *RNF112* and *FOXM1*, *CCNB1*, *SKP2*, *FN1*, *CKS1* in several online datasets derived from TCGA and GEO. **(B)** Schematic illustration for the 6×FKH luciferase reporter plasmid containing six copies of the Forkhead consensus sequence (AAACAAACAAAC). **(C-F)** Immunoblot analysis (C), qRT-PCR analysis (D), colony formation assays (E), transwell invasion assays (F) of *RNF112*-depleted MGC803 cells infected with RNF112 lentivirus (n=3). Scale bar, 400 μm. Data are presented as mean±SD. Statistical significance was calculated using Pearson's test (A), one-way ANOVA (D-F)**.** NS, not significant, NA, not available, **P*< 0.05.

5

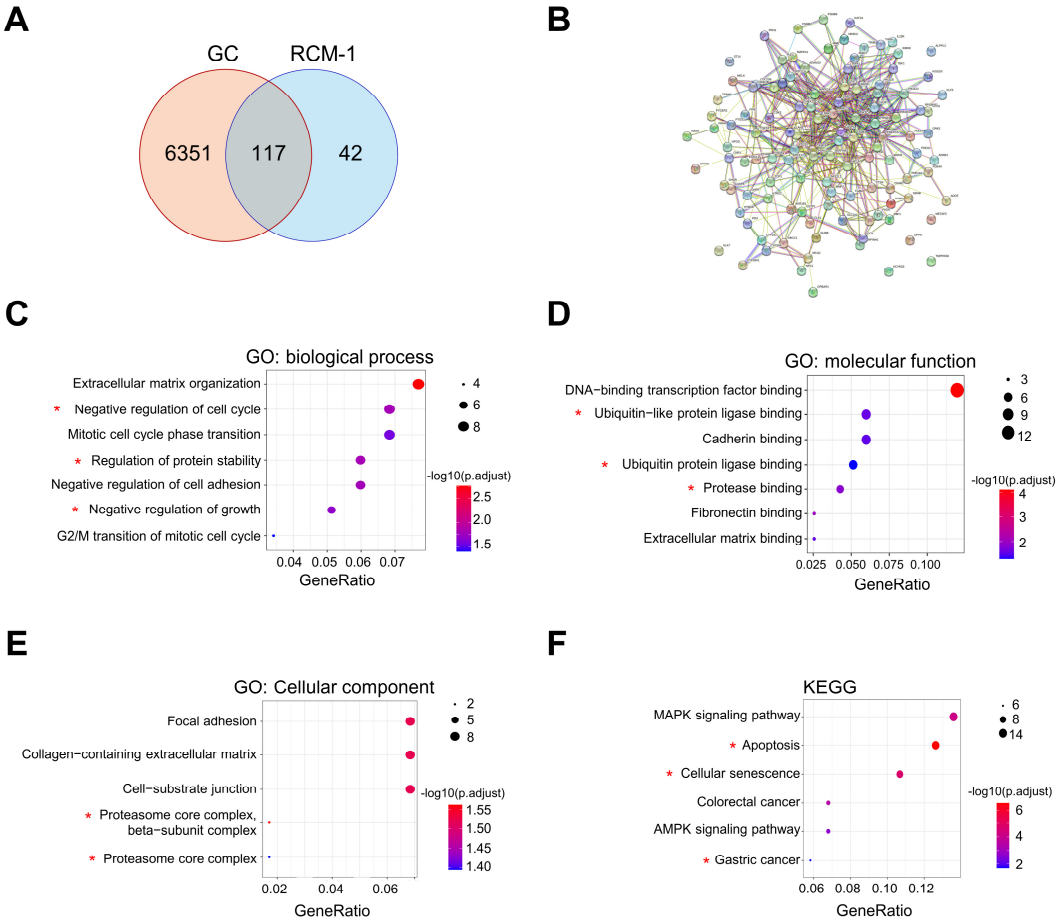


Supplemental Figure 6. Anti-tumor effect of RNF112 is partially owed to FOXM1 degradation. (A-C) qRT-PCR analysis (A-B) and immunoblot analysis (C) of the expression of FOXM1 downstream genes in RNF112 stably overexpressing MGC803 and BGC823 cells after the restoration of FOXM1 (n=3). **(D-E)** Colony formation assays (D) and transwell invasion assays (E) of RNF112 stably overexpressing MGC803 and BGC823 cells after the restoration of FOXM1 (n=3). Scale bar, 400 μm. **(F-I)** Immunoblot analysis (F), qRT-PCR analysis (G), colony formation assays (H), transwell invasion assays (I) of *RNF112* depleted MGC803 cells with FOXM1 knockdown (n=3). Scale bar, 400 μm. Data are presented as mean±SD. Statistical significance was calculated using one-way ANOVA. **P*< 0.05. Complete unedited blots were listed in the supplemental material.

6

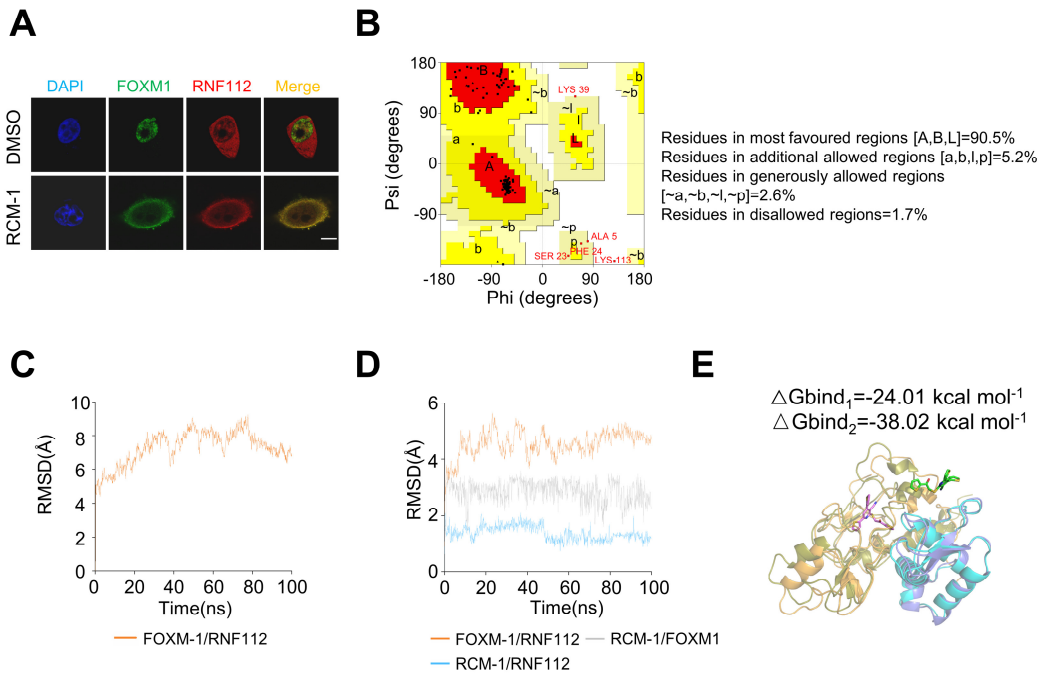


Supplemental Figure 7 *RNF112* depletion promotes gastric cancer cell proliferation in vivo. (A) Tumors were harvested after subcutaneous injection of wild-type or *RNF112*-depleted MGC803 cells in nude mice (n=5). **(B-C)** Tumor volume (B) and tumor weight (C) of the xenograft were calculated (n=5). **(D-F)** Immunoblot analysis (D), qRT–PCR (E) analysis and IHC staining (F) of tumors from the above mice (n=5). Scale bar, 50μm. Data are presented as mean±SD. Statistical significance was calculated using Student's t test (C, E). **P*< 0.05. Complete unedited blots were listed in the supplemental material.



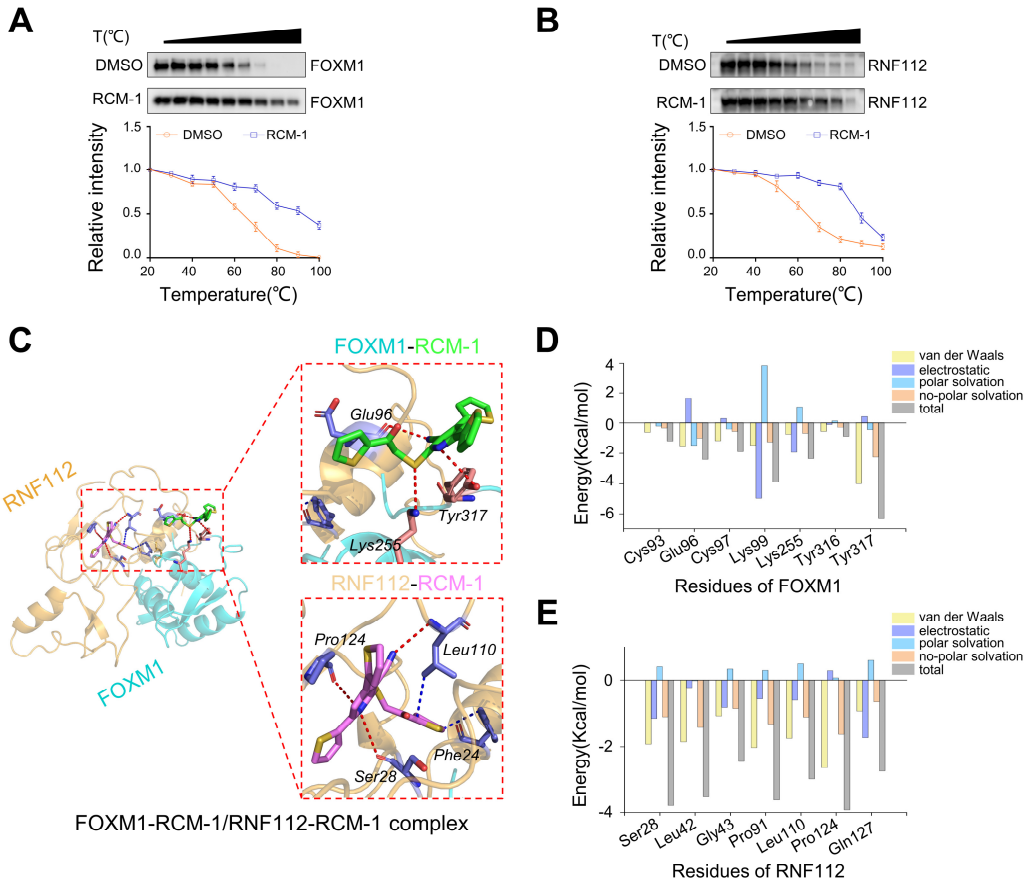
Supplemental Figure 8. Network pharmacology analysis of the role of RCM-1 in gastric cancer. (A) Venn diagram of common RCM-1 targets obtained from SuperPred database, Swiss database and SEA database and key genes of gastric cancer retrieved from GeneCards. **(B)** A component-target-disease model established by Cytoscape software. **(C-F)** GO biological process analysis (C), GO molecular function analysis (D), GO cellular component analysis (E), and KEEG pathway analysis (F) of the common genes in (A).

8



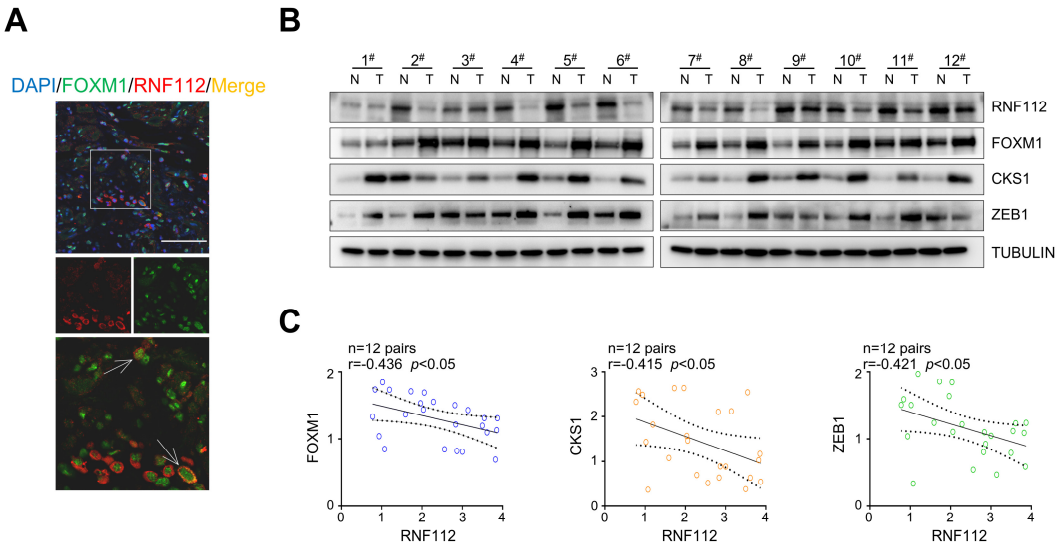
Supplemental Figure 9. Molecular docking and molecular dynamics simulation analysis of FOXM1, RNF112 and RCM-1. (A) Immunofluorescent analysis of cellular distribution of FOXM1 and RNF112 in MGC803 cells after DMSO or RCM-1 treatment (10 μM). Scale bar, 10μm. **(B)** Ramachandran plot analysis of φ and ψ dihedral angles of the model of RNF112. **(C)** RMSDs of FOXM1/RNF112 complex for 100ns MD simulations. **(D)** RMSDs of FOXM1-RCM-1/RNF112-RCM-1 complex for 100ns MD simulations. **(E)** Comparison of binding modes and binding free energies of FOXM1/RNF112 complex (FOXM1, light blue; RNF112, olive; $\triangle G_{bind1}$) with those of FOXM1-RCM-1/RNF112-RCM-1 complex (FOXM1, cyan; RNF112, orange; RCM-1/FOXM1, green; RCM-1/RNF112,violet; $\triangle G_{bind2}$).

9



Supplemental Figure 10. Possible binding modes among FOXM1, RNF112 and RCM-1. (A-B) Thermal shift assays of MGC803 cells in the presence of DMSO or RCM-1 (10 μM). MGC803 cells were lysed using RIPA buffer containing protease inhibitor and the final concentration of the lysates was adjusted to 3mg/ml. The lysates were heated in the presence of 10 μM RCM-1 or DMSO at various temperatures for 4 min and then subjected to immunoblot analysis. **(C)** Docking model of FOXM1-RCM-1/RNF112-RCM-1 complex. Red and blue dashed lines indicate hydrogen bonds and hydrophobic interaction respectively. **(D-E)** Contributions of binding free energies calculated by MM/GBSA method for key residues of FOXM1/RNF112 complex with RCM-1(FOXM1) (D) and RCM-1(RNF112) (E). Data are presented as mean ± SD. Complete unedited blots were listed in the supplemental material.

10



Supplemental Figure 11. RNF112 is negatively correlated with FOXM1 in gastric cancer tissues. (A) Immunofluorescence of the colocalization of FOXM1 and RNF112 in gastric cancer tissues. White arrow indicates the colocalization. Scale bar, 100 μm. **(B)** Immunoblot analysis of the protein expression of FOXM1, RNF112, CKS1, and ZEB1 in 12 pairs of gastric cancer tissues (T) and corresponding non-cancerous tissues (N) (n=12 pairs). **(C)** The correlation between expression of RNF112 and that of FOXM1, CKS1, and ZEB1, respectively (n=12 pairs). Statistical significance was calculated using Pearson's test (C). Complete unedited blots were listed in the supplemental material.

Supplementary Table 1 The List of siRNA Sequences

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RKHD1	399664	42558261	GAGCCGGUCUUCAUCGUGA
RKHD1	399664	42558261	GUAUUGAGUGGUCAGGUUA
RKHD1	399664	42558261	GCGACAAGGAGCCGGUGUU
RKHD1	399664	42558261	GCCGAACACUUCUCCAUCA
TRIM67	440730	52138585	UAACCUGGCUUUAAUAGUG
TRIM67	440730	52138585	GAAGGUGGCGUGUGCAAGG
TRIM67	440730	52138585	GCACAAGGCACAACUAUCU
TRIM67	440730	52138585	GGUAAGGAGACUUUGUGUA
LOC644006	644006	88943821	CCAGAAGCGAACACGGGAA
LOC644006	644006	88943821	GCAGUGACGAUGAGUUGUU
LOC644006	644006	88943821	UUGAAACCCACGUCUGAUA
LOC644006	644006	88943821	GGGCAAUCCCGUUUCCUAA
PHF6	84295	63478059	GCAUGAUAAAGCUCAAAUA
PHF6	84295	63478059	AGAUAGGUCUCCACACAGA
PHF6	84295	63478059	UGUGGACAGUUACUAAUAU
PHF6	84295	63478059	GCACGAAGCUGAUGUGUUC
TRIM63	84676	19924162	GAGGAUUCCCGUCGAGUGA
TRIM63	84676	19924162	GGAAGAAGGACACCAGUAA
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TRIM63	84676	19924162	AGACUGAACUGAAUAACUG
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RFPL4B	442247	61966914	GAUAUUAGGUUUUGUGGAU
RFPL4B	442247	61966914	AAGAAUGGCAAGUGAGCGU
PDZRN3	23024	57529736	GACACGAGCUCUCAGAUAU
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PDZRN3	23024	57529736	GCACUAGAGUAUACAAUUC
C6ORF49	29964	32171176	CCGAAAUACCGGACAACGU
C6ORF49	29964	32171176	GGAUGUCGGACUAAGCGAA
C6ORF49	29964	32171176	AGACUGGACUCGACCGAAC
C6ORF49	29964	32171176	GGGACCAAACCUCGGUGAA
PHF5A	84844	55925655	GGAACUGACUGUGAAGCGA
PHF5A	84844	55925655	UGGCACACCAUAUCGGAGA
PHF5A	84844	55925655	CCUCUUCUAUGAACGCAAA
PHF5A	84844	55925655	UGGUGUUGCCAUCGGAAGA
C20ORF18	10616	14043031	UCACAGUGCGCCCUGAUAU
C20ORF18	10616	14043031	GACAGUGGCGUCUCUCAAG
C20ORF18	10616	14043031	CCUCAUACCAGCCCGACGA
C20ORF18	10616	14043031	GGACAGUGCCUACCUCUAU
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TRIM75	391714	88981293	GAUUGAAAUUGCCAAGCUA
TRIM75	391714	88981293	GAGACCACCUUGUGCGAGA
TRIM75	391714	88981293	GGGCACAACUUCUGUCGUU
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PHF17	79960	40556392	GCUAUGAAGCCCACCCGUA
PHF17	79960	40556392	UGAGGAUUCUGACGACAAU
PHF17	79960	40556392	CAGCGAUGCUACGACAAUA
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TRIM42	287015	29029527	CAGAAUACGUGUUUAAAGU
BAHD1	22893	41281572	GAGCCAGCCAUCCGAAAGA

BAHD1	22893	41281572	CCGCACUAAUGGCUGGGUA
BAHD1	22893	41281572	AAAUCAGGCCCACGAAAGA
BAHD1	22893	41281572	ACACACACUCGGAGAAAGU
WDR24	84219	14149986	GUUCACAGCCCACAACGGA
WDR24	84219	14149986	GAACACAAGCGCACGGUAA
WDR24	84219	14149986	GGGACGUGCAGUUCAGUAU
WDR24	84219	14149986	CGACGUACCUGCCGACUAC
DTX4	23220	51468788	CCACAUCUACUGCUUGGUU
DTX4	23220	51468788	GGAUCGACCUCACUUCCAU
DTX4	23220	51468788	GGCUUUAGCUACGUAAUUG
DTX4	23220	51468788	GGUGAUGAGUGUUAAGGCA
TRIM26	7726	60279912	CAACGAGGCCUGAGGGAAU
TRIM26	7726	60279912	GCAUCGCCCUGGAUUAUGA
TRIM26	7726	60279912	UGAGAGACUUGGAAUAUAA
TRIM26	7726	60279912	CUAAACAGGUAUCCACGGA
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PHF21B	112885	19923936	GUAUUAAACUCGAUCGAUG
PHF21B	112885	19923936	GGACUCAGUUUGCCGUUGA
PHF21B	112885	19923936	UAGCUGAGUGGUAGCGGUA
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OIT3	170392	22749296	CGGUAAAGCAGUACACGUC
OIT3	170392	22749296	CUACAGGGCCAGACGCUAA
OIT3	170392	22749296	UUGAAGAGCCUUACCGGGA
OIT3	170392	22749296	GGAAAUCAUGAGCCGAAAU
MGRN1	23295	44917607	GAGCACUCUUGUCCCUUUA
MGRN1	23295	44917607	GAACUCGGCCUAUCGCUAC
MGRN1	23295	44917607	GAACAUGGAUCUGAACUUC
MGRN1	23295	44917607	CGAAGGAGAUGUGGUGGAA
RNF7	9616	34304332	GCGACAAGAUGUUCUCCCU
RNF7	9616	34304332	CAAGAGGACUGUGUUGUGG
RNF7	9616	34304332	GCAUGUCCCUGUGGGUGAA
RNF7	9616	34304332	UGUCUUAGAUGUCAAGCUG
WDSUB1	151525	22749102	UCCAAUAACUAGAGAACUU
WDSUB1	151525	22749102	CAAUUCGCCUGUACUCGUU
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PCGF1	84759	14249239	ACAAGUAUGUCCGAUGUUC
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PCGF1	84759	14249239	UGUCACCGCUUGAUGCUAA
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TRIM3	10612	32454736	GAAUGAAAUUGUAGUAACG
ZNF645	158506	22749188	AAAGUUCGUCCUCAUAUUG
ZNF645	158506	22749188	GAGAAGACAUAGACGGUAU
ZNF645	158506	22749188	GCCAACACCUCCCGACUAU
ZNF645	158506	22749188	UGACAAAGUCGGAUAUAAA
RNF5	6048	34305290	UCAAUGCCCAUGAGCCUUU
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RNF5	6048	34305290	GGCCAUGUCUUCAUCAGUG
PHF15	23338	40556369	GAAGAGAAGAGGCGAAAAU
PHF15	23338	40556369	GCUAUGACUUGGACGAGAU
PHF15	23338	40556369	GGGAGAGGGUGCAACGAGU
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BRCA1	672	63252875	CCAAAGCGAGCAAGAGAAU
BRCA1	672	63252875	UGAUAAAGCUCCAGCAGGA
BRCA1	672	63252875	CAACAUGCCCACAGAUCAA
BRCA1	672	63252875	GAAGGAGCUUUCAUCAUUC
ZFAND6	54469	21359917	CAAAGACAGAAUAGUAGUA
ZFAND6	54469	21359917	GUGUAUGUAUAUAUCGCUU
ZFAND6	54469	21359917	CAGAUUAUGUUCAUGGGUU
ZFAND6	54469	21359917	UAUGGAAACCCUCGUACAA
SH3RF2	153769	47578102	GCGGCCAGCUCCCUCAUUA
SH3RF2	153769	47578102	GGACAGGUCAGCACUUAUC
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SH3RF2	153769	47578102	GGGCGGAGCAGCAUGAGAA
RNF150	57484	58331203	UCGCAUGGCUCGUCUUUUA
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RNF150	57484	58331203	AAGCAGUGAUUCUGACAUU
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PCGF3	10336	59710102	GCACUUAGAUUCCCAUCGG
PCGF3	10336	59710102	GUACAUCGGUCAUGACAGA
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RNF8	9025	34304335	GAGAUGGUCUGGAGGAUUC
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RNF38	152006	37577182	GUAGUAUGCAUGUGUGAUU
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IRF2BP1	26145	24308114	CCUUCAAUAAACCGAAAGA
IRF2BP1	26145	24308114	CAAGAAGGAUCACGGGCUG
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MLL2	8085	4505196	GAUAUUAGCUACCACACAU
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PARC	23113	63082031	GGAUGACCCUGCCCACUGA
PARC	23113	63082031	GGUGUGGCCUGUACCAGUA
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PARC	23113	63082031	ACGCACAGCUCUAUAGCAA
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PHF23	79142	13236519	GCAAGAAGCGGAAGUUAAA
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RNF25	64320	34878786	UGAGUCAGCUGUAGAUGUC
PHF13	148479	24432092	GGGGAGAGGUGUUCGGUUU
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PHF13	148479	24432092	CAAACAGCCAGGACGCAUU
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DTX3L	151636	31377615	GCACCAUUGUGAUUACUUA

DTX3L	151636	31377615	GGACACCAUUAGUAACAAA
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MKRN3	7681	74272285	GGGGAGAACUGUCGCUAUU
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TRIM14	9830	15208664	AACAGGGUCUGGAGUAUCA
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RUFY1	80230	22095370	GAACUUAACCGGCACUUGA
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RUFY1	80230	22095370	GAAAGAUGACGAAGCGACA
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RNF148	378925	37675276	GAUCACAUCGGAAUUAGGA
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UBE4B	10277	38327033	GCAACUAGACACCGCGAAA
UBE4B	10277	38327033	CAAGAACGCACGCGCAGAA
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CCL20	6364	4759075	CAAUGAAGGCUGUGACAUC
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CCL20	6364	4759075	CCGUAUUCUUCAUCCUAAA
CCL20	6364	4759075	UGAAAUAUAUUGUGCGUCU
RNF141	50862	38045936	UGUCAGAAGUGUAUUGAUA
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TRIM2	23321	15011942	GGUCAACUAUGGCCUCAAA
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TRIM2	23321	15011942	CAACCAAUGUGUGCAGAUA
RNF103	7844	37595534	GUUCAUGUGCCAAUAAAUA
RNF103	7844	37595534	UUACCAAUGUGGCGAUUUA
RNF103	7844	37595534	GCCAUUGUGUGGUAUGAAA
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TOPORS	10210	40805103	ACAAAUGGGAGUAUACUUA
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RC3H2	54542	9256536	GGGAAAGGUUGGCGCUAAU
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PHF16	9767	23110985	AGGAACAGAUCUUCGGUUU
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PHF16	9767	23110985	GGAUGGAACCGAUCACGAA
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TRIM22	10346	15208661	AGUGAAAGCUGGACAUUGA
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RNF31	55072	38045939	GGCGUGGUGUCAAGUUUAA
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RNF166	115992	31343485	GACACAAGUUCUCCUACGA
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LOC649055	649055	89057653	GCAUGAACUCACUGCGAAA
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RAD18	56852	14550404	GCUCUCUGAUCGUGAUUUA
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BARD1	580	4557348	UGGUUUAGCCCUCGAAGUA
BARD1	580	4557348	GAGCACAUCUUCUGUAGUA
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BARD1	580	4557348	CGACAUACCUUCUGUUGAA
RCHY1	25898	58331198	GCACUCUGCUUUAGAUAUG
RCHY1	25898	58331198	GAAAUGUAACUUAUGCCUA
RCHY1	25898	58331198	GCACAUUGUUUGGAGAAUA
RCHY1	25898	58331198	CUAGAUCGCUUUAAAGUGA
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LMO6	4007	7710128	GCACAGAGUUAGCGCCAGC
LMO6	4007	7710128	CACUAGGAGGGCAGCGCUA
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CBLC	23624	20149595	GGCCAACACUCCUCAAGAA
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CBLC	23624	20149595	CAUUUGAGCUCUGCAAGAU
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RNF44	22838	42718018	GCACAUCCCUGGCUGCAGU
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MLL3	58508	10864040	CCAGGUCAAUCAACAGUUA
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RNF149	284996	31543079	UAUACUGGCUCUCAGAUUG
RNF149	284996	31543079	CAUGAUGAUUAUCUCGUUA
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TRIM37	4591	52487175	AUACGAAACUCCACAAAUA
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BIRC7	79444	21536419	GGAGAGAGGUCCAGUCUGA
BIRC7	79444	21536419	GGAAGAACCGGAAGACGCA
BIRC7	79444	21536419	GCUCUGAGGAGUUGCGUCU
BIRC7	79444	21536419	GGAAGAGACUUUGUCCACA
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TRIM55	84675	34878851	UGGUUGAACUCCCUAAAUG
TRIM55	84675	34878851	GCGCAUCUCUGAAUUACAA
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BRPF3	27154	55742814	GUAUAAUGCUAAAGACACA
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RKHD2	51320	39545576	GAAACUAUAUAGAGCUCAA
RKHD2	51320	39545576	GCGCAAGAAUGAUAUCCAA
RKHD2	51320	39545576	CUAAUGGUACCAAUAGUUA
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DTX3	196403	31341899	CGAAUGUCAUCACCUGGAA
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RNF40	9810	37588854	GAACUCCGAGAACGAAUUG
RNF40	9810	37588854	GAGAUGCGCCACCUGAUUA
RNF40	9810	37588854	GCUUAACUCUGGCUACUAU
RNF20	56254	34878776	CAGAAGAAGCUACAUGAUU
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PHF14	9678	55769549	UCGUAAACUUAUGCGGAAA
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RNF34	80196	37595536	CGGCACAGGUACAAAGUGA
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ZNF185	7739	6005971	GGGCAGAAGUGUAGGGUUC
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SMARCA3	6596	21071053	GCAGGAUCUUCUAAGGUUA
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WDR59	79726	58331265	GAGCGGAAAUCAAGACGAU
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VPS11	55823	62865896	UAUUUGAGAUGGCGAUUAA
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BRAP	8315	10800416	GGAGAGAAAGUAGCGAUUA
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IBRDC2	255488	50284695	GAAUAAACUUGGCCACUCA
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PCGF6	84108	37655164	GCAAAGGUUACUUAAUAGA
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PDZRN4	29951	39653318	GCGAACACCUCUUAGUAGA
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AIRE	326	4557294	GAAGAAUGAGGACGAGUGU
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LOC283116	283116	169202725	CCAUCAGGCUUCAUUGUAU
LOC283116	283116	169202725	UGAACGAAAUGUGCCAUAA
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TRAF6	7189	22027628	GAUAUGAUGUAGAGUUUGA
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RNF2	6045	54792140	GUAUCUGGCUGUGAGGUUA
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PXMP3	5828	4506342	AUUUAAACCUGGGCUGUUA
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TRIM25	7706	68160936	GCGGAUGACUGCAAACAGA
TRIM25	7706	68160936	GGGAUGAGUUCGAGUUUCU
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RC3H1	149041	73695472	UGCAAGAUGUGCCUGAAUA
RC3H1	149041	73695472	ACCAACAGAUCGAGAGUUA
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TRIM59	286827	27436876	GCACUGACAAUAUCUUUAC
SIAH2	6478	55925659	AGACAUAUGUGAAUACCGU
SIAH2	6478	55925659	GCAAGCAAGCCGAGAACUU
SIAH2	6478	55925659	GCUAAUAAACCCUGCAGCA
SIAH2	6478	55925659	GACAUCGUCUUUCUAGCUA
RNF43	54894	56711321	GCAGAACAGAAAGCUAUUA
RNF43	54894	56711321	UAUGAUGUGUGGAUCCUAA
RNF43	54894	56711321	GGAGAAAGCUAUUGCACAG
RNF43	54894	56711321	GGUGGAGUCUGAAAGAUCA
IBRDC1	154214	34303935	CAUAGCGGUUGUAAUCGUU
IBRDC1	154214	34303935	GUUGUUAAGUGAUAUGCUA
IBRDC1	154214	34303935	CAUAUGACCUGCUCACAAU
IBRDC1	154214	34303935	GAACUUGGCCGUAUUGAUU
RNF186	54546	9506662	GCACCAAGACCCUGCAACA
RNF186	54546	9506662	GACAACACCUGGUCCAUCA
RNF186	54546	9506662	CAUCUACCCGGGUGUCUUA
RNF186	54546	9506662	AGCCACAUCUCUUCCAUUG
MARCH7	64844	53828927	GGUGACUUAUGUAGAAUUU
MARCH7	64844	53828927	CAUAACAGGACAUUUGAUA
MARCH7	64844	53828927	GGAGUAAUUUGACCGACAA
MARCH7	64844	53828927	GAACAUCAGACCAUACUAA
ZA20D1	56957	9910155	CCGAUUGGCCAGUGUAAUU
ZA20D1	56957	9910155	CCGAGUGGCUGAUUCCUAU
ZA20D1	56957	9910155	GCAUCUAGGUACCAAUGGA
ZA20D1	56957	9910155	UAACGGAGGGAGCAAGUAU
TRIM54	57159	34878869	GACAAUAGCCGGAGGCAGA
TRIM54	57159	34878869	GAACUUCACAGUGGGUUUC
TRIM54	57159	34878869	GGUCUUCGGUGCCCACAAG
TRIM54	57159	34878869	UCUACGGCCUGCAGCGAAA
SYVN1	84447	51317310	UCAUCAAGGUUCUGCUGUA
SYVN1	84447	51317310	GAGAAGAGAUGGUGACUGG
SYVN1	84447	51317310	CAACAUGAACACCCUGUAU
SYVN1	84447	51317310	GGAAAGGCCUCCAGCUCCU
RKHD3	84206	47894110	GAACGUGGAUCGCGCUCGA
RKHD3	84206	47894110	GCGAAGACCAAUACUUACA
RKHD3	84206	47894110	GCGCCAAUCGCAUCUGUGA
RKHD3	84206	47894110	GCGCACAACGGAAACAAUA
RNF14	9604	34577097	UUAAUGGACUUACGAAAUG
RNF14	9604	34577097	GAAUCACUGUCAAAUCUGA

RNF14	9604	34577097	CUAGCAUACUUGAAUAUUG
RNF14	9604	34577097	UUAGACGGAUGUAACAAGA
LPXN	9404	4758669	CAACGACUACCACCAACUU
LPXN	9404	4758669	UCCAGGAGCUCAAUGUCUA
LPXN	9404	4758669	GCGCAGCUCGUGUAUACUA
LPXN	9404	4758669	CUUCGGAGAUCCUUUCUAU
RNF11	26994	34452682	GAUGACUGGUUGAUGAGAU
RNF11	26994	34452682	UAGGAUAGCUCAAAGAAUA
RNF11	26994	34452682	GGGAGUGUGUGAUCUGUAU
RNF11	26994	34452682	GCACUGCUUUCAUCCUAUG
RFP2	10206	47132520	GAAGGGAGUGUGCGGAAUU
RFP2	10206	47132520	GACACUGGCACAUUCAUUA
RFP2	10206	47132520	UAAAACAGCCGAUUUCAUA
RFP2	10206	47132520	GAGACCAGCUCCAUUCAAG
TRIM58	25893	40353772	CUAUGAAGCCGGUGAAAUU
TRIM58	25893	40353772	GAAAGUCCUCGCUGCAUUG
TRIM58	25893	40353772	UCACAAGGCUGGAAGCAGA
TRIM58	25893	40353772	GAUUGGAGUUUGAGAAGCA
BFAR	51283	7706090	GGACAUCACGGUUUCUCAU
BFAR	51283	7706090	GCUACGACAUCCUGGUUAA
BFAR	51283	7706090	UAACACAGGCCGAGCGAAU
BFAR	51283	7706090	AGAAAUAUGGGAAUGAUCA
RNF19	25897	35493781	ACAAAUACCUCUUCUGACA
RNF19	25897	35493781	GCAAGUAGAUAUUGAGUCA
RNF19	25897	35493781	GGUGUAACGUUGUCUGUAA
RNF19	25897	35493781	ACGAUGUGCUGCUUAUAUA
BRPF1	7862	51173721	GAACUGGGCCCUUAAAGAA
BRPF1	7862	51173721	GAUCAAGGUUCAGCAGAUU
BRPF1	7862	51173721	GACUACAUCUGGCUGGAUA
BRPF1	7862	51173721	CGAAAGGUCUACAAGAGUU
RNF126	55658	37622891	CAUCACACAGCUCCUCAAU
RNF126	55658	37622891	GAACAAAACUGCUCCAACA
RNF126	55658	37622891	CGGAUUAUAUCUGUCCAAG
RNF126	55658	37622891	UGUCUAACCUCACCCUCUA
TRIM38	10475	24497622	GGCCCUAUUUCCAGGUUUA
TRIM38	10475	24497622	CAGCAAUGCGAAUAACUAA
TRIM38	10475	24497622	GUGUAUAACAGACUUCUUU
TRIM38	10475	24497622	CGGAUGGGAUUUAGGAGUU
RNF169	254225	51468839	GAUGAACCAUUAGUACUGA
RNF169	254225	51468839	GAACAGGACAGUGAUAAUA
RNF169	254225	51468839	UUACUAGGCUCUGAAGGUA
RNF169	254225	51468839	CCGAAGAACUAAACCAUUU
CBLL1	79872	13376203	GACAAGAUAUAGACCGUAU
CBLL1	79872	13376203	GGGGUGAGCUGUUUGCAAA
CBLL1	79872	13376203	UAUCAACCAUCGCCAUAUG
CBLL1	79872	13376203	GGGAAUGAGUCCUGGUAUA
LNX1	84708	14249127	GGAAGAAUUACUCUAACUA
LNX1	84708	14249127	GCACGGCCCUUUGAGAGAU
LNX1	84708	14249127	CGAUAGUACUCAAAGCUUU
LNX1	84708	14249127	GGAGAAUGACCGUGUGUUA
ARIH1	25820	9966762	CGAGAUAUUUCCCAAGAUU
ARIH1	25820	9966762	GAGAGUCGACGAAGGGUUU
ARIH1	25820	9966762	CCAAAUGCCAUGUCACAAU
ARIH1	25820	9966762	GGAUAUGCCUUGUCAGAUC
RNF175	285533	27734858	GGGAUGUUCUCCGUUAUUA
RNF175	285533	27734858	CACGAUUGGUCUACAAAUG
RNF175	285533	27734858	GACAAUAUCUGUGCAGUCU
RNF175	285533	27734858	CAUUUGGUGUUGUGGGUUA
NEURL	9148	21314780	CCGCAGAACUCACUCAACU
NEURL	9148	21314780	CCACAAGGCUGUCAAGAGG
NEURL	9148	21314780	CUGACUCGCUGCCCAAGUA
NEURL	9148	21314780	GGUAACAACUUCUCCAGUA

LNX2	222484	34222215	GGACAUACAUUCUGCUACA
LNX2	222484	34222215	CAACGAAACACCUUUGAUU
LNX2	222484	34222215	CUUCAUAGCUGCCACGAUA
LNX2	222484	34222215	CCAAGUGGCUCUUCAUAAA
RNF17	56163	14277695	GAACUUUCUUGUUACGAUA
RNF17	56163	14277695	UGAUGUACAUUUAGAAGCA
RNF17	56163	14277695	GCCCUGAUGUGAUAAUUGA
RNF17	56163	14277695	GCAAGAGCAUUACAAUUAU
RNF24	11237	10518498	GGGCAGAGAACAUUGUAUA
RNF24	11237	10518498	GAAUUUACAUGAGCUCUGU
RNF24	11237	10518498	ACAGAAAGUGCCUUAUUAA
RNF24	11237	10518498	GCUCGGAUUUCCCACAUUA
RNF146	81847	33636757	GGACGUCGCAGGAAGAUUA
RNF146	81847	33636757	GAUGGACAGUGCACAGUAA
RNF146	81847	33636757	CCGUAAACCUAGCAAGAGA
RNF146	81847	33636757	GGAUGUAUCUGCAGUUGUU
PHF2	5253	24797090	AGGAGUUUGUGGACUAUUA
PHF2	5253	24797090	GCUCAAGAUCGACGAGUUU
PHF2	5253	24797090	ACGGGAAACUACUCCUUUA
PHF2	5253	24797090	CUUCACAGCUAAUCAAAGA
PEX10	5192	24797087	UCUCAGAUGUGGCCUACUU
PEX10	5192	24797087	GAGAGAGCCGUUUCCAGAA
PEX10	5192	24797087	CGCAGAAGGACGAGUACUA
PEX10	5192	24797087	UCACCACACUUGCAGGCUA
MYLIP	29116	38788242	GGUGAAAGUUUAUGGCUAA
MYLIP	29116	38788242	CCAGAACACUGCCAAGUAU
MYLIP	29116	38788242	GACUUUAGCCCAAUUAAUA
MYLIP	29116	38788242	UAACAGAGACGCACGCAUU
ZNRF1	84937	30089958	ACGAUGAUGUGCUGACUAA
ZNRF1	84937	30089958	GAACAGAUCUUGUCCGGAA
ZNRF1	84937	30089958	GGAAAUGCACUUUAUAAUG
ZNRF1	84937	30089958	GCAUAGUGGUUUCAAGUGC
TRIM11	81559	24497621	CCGAAGACCUCAAGGCGAA
TRIM11	81559	24497621	CCGAUGGGUCACUGCUAUU
TRIM11	81559	24497621	UGGGUGAGUUCGAGCGUCU
TRIM11	81559	24497621	AGGCGAAGCUGGAGAAGUC
TRIM5	85363	15011943	GCAGAAAGUUGAUCAUUGU
TRIM5	85363	15011943	GGAAUCCUGGUUAAUGUAA
TRIM5	85363	15011943	GAGAACAUACGGCCUAAUC
TRIM5	85363	15011943	GGGUGUGGAUGGCGUCAUA
TRAF7	84231	45594313	GCAAGAGUGCCCGCUACAA
TRAF7	84231	45594313	GGGCACACGUUCUGUAGGA
TRAF7	84231	45594313	CGGUGAAGCUGUGCUGUCA
TRAF7	84231	45594313	GACCUUCGGACCCGCCUUU
PHF8	23133	32698699	GGUGAUGGAAGACGAAUUU
PHF8	23133	32698699	CUCAUGAGUGUGCGAGAUA
PHF8	23133	32698699	UGGGAGUGUUAGUAAUCAA
PHF8	23133	32698699	UCAAGAAGGCAGAGCGAAA
RNF170	81790	21361953	GGCCAAAUAUCAAGGUGAA
RNF170	81790	21361953	GAUCUACCCACUUUACUGA
RNF170	81790	21361953	GGGCAACCCAGAUCUAUUA
RNF170	81790	21361953	UAGACAAACGGUAACCUUA
RNF182	221687	22749454	GAGCCUCGUUAUUCUUAUG
RNF182	221687	22749454	UACAAUCGAUACAAUCUGA
RNF182	221687	22749454	GUUAGUAGCCUGCCCGAUG
RNF182	221687	22749454	UAUGGCACCUCCUUCUUAA
UHRF1	29128	16507203	GCCAUACCCUCUUCGACUA
UHRF1	29128	16507203	GUAAAGUGGAGGAGACGUU
UHRF1	29128	16507203	GCGGAACAGUCUUGUGAUC
UHRF1	29128	16507203	GCAAGGGCAUGGCCUGUGU
DKFZP547C195	257160	46409321	GAAUGUUCGUGACCAAUUU
DKFZP547C195	257160	46409321	GAACAUUGCUGUACAGACU
DKFZP547C195	257160	46409321	UGUAAGCUAUGUCUAAUGU

DKFZP547C195	257160	46409321	GGAAAGAGUUACUGGUACU
PJA2	9867	41281511	GCAGGAGGGUAUCAGACAA
PJA2	9867	41281511	GAAGCACCCUAAACCUUGA
PJA2	9867	41281511	GUUAGAUUCUGUACCAUUA
PJA2	9867	41281511	AGACUGCUCUGGCCCAUUU
PML	5371	67089153	GGACAUGCACGGUUUCCUG
PML	5371	67089153	GGAAAGAUGCAGCUGUAUC
PML	5371	67089153	GCAACCAGUCGGUGCGUGA
PML	5371	67089153	GAGCUCAAGUGCGACAUCA
UBOX5	22888	40806195	GGAGAAGUGUAACCGCAGU
UBOX5	22888	40806195	GGCGGUAUCCCUUGUAUCA
UBOX5	22888	40806195	GCAACAAGAUAUCAGCUGA
UBOX5	22888	40806195	GACAGUAACUUUGGUGUAA
TRIM65	201292	38679904	AGCCAAGCCUGUGGACUUA
TRIM65	201292	38679904	GCGCCAACCGUCACUUCUA
TRIM65	201292	38679904	GCAGCCAGAUCCAGAACUC
TRIM65	201292	38679904	GUAGGACCCUGACCCUGUG
DPF2	5977	21536317	GAAGAUACUCCCAAGCGUC
DPF2	5977	21536317	GACCAACAGUCGAGCGCGA
DPF2	5977	21536317	GGAGUAGCCCAGAGCAAUU
DPF2	5977	21536317	CCGGACAGCUGUACUCCUA
JARID1C	8242	11321604	GACAAGACUCUGCGGAAGA
JARID1C	8242	11321604	CUACGAACGCAUUGUUUAU
JARID1C	8242	11321604	GAGCAGGCUACCCGGGAAU
JARID1C	8242	11321604	UCGCAGAGAAAUCGGGCAU
BAZ1B	9031	14670391	CCAAUAAGCUGCACACUAA
BAZ1B	9031	14670391	AUAAGGAGAUAGUUCGAUA
BAZ1B	9031	14670391	GCAUUCAGAUUGGUGGAUA
BAZ1B	9031	14670391	GCACGUAGAUCGCCACGAA
AOF1	221656	60685218	GUAAUUGAGUAGCAGUAAA
AOF1	221656	60685218	CCUAAGGACUACCACAAUA
AOF1	221656	60685218	CCGGUAGGCAGGCGAAGAA
AOF1	221656	60685218	AAGGCAGGCUGUACGGCAA
RNF113A	7737	5902157	GCGAAAGAAUUGAUUGCUA
RNF113A	7737	5902157	UUACUUAGGUUUCCCAUAA
RNF113A	7737	5902157	GACAAGAUCUAUCGGGGAA
RNF113A	7737	5902157	GGGUGGUGCUUCCGACUUG
PCGF5	84333	83816965	GAGGUUGGACAAUACAUUA
PCGF5	84333	83816965	CAACAACAGUGACGGAAUG
PCGF5	84333	83816965	GAAGAAAUUCAUUCGAUGU
PCGF5	84333	83816965	ACAAAUUGCUAUCUGUCUA
MDM4	4194	4505138	CCACGAGACGGGAACAUUA
MDM4	4194	4505138	CGUCAGAGCUUCUCCGUAA
MDM4	4194	4505138	CCUAAAGAUGCGUAUAUAA
MDM4	4194	4505138	AAGCAUGGGAGAACAGUUA
SSA1	6737	56549143	UCUCAGAGCUAGAUCGAAG
SSA1	6737	56549143	GAAUGUGCCUUUACAGGAC
SSA1	6737	56549143	GCAGCACGCUUGACAAUGA
SSA1	6737	56549143	AAUAUUGGAUCACAAGGAU
KIAA1333	55632	33620748	GAGCCUAUUCCAAGUUAUA
KIAA1333	55632	33620748	CCAUCGACCUGUUCAAAUA
KIAA1333	55632	33620748	UAAACCCACUCCUUCAAUU
KIAA1333	55632	33620748	UCGAAGAUGUCGUUGCAAA
LOC399940	399940	51470744	GCAAGAAGACAAUACAGCA
LOC399940	399940	51470744	GAACACAGAAACCACCAGA
LOC399940	399940	51470744	CAUCAAAUGGGACAAAUAA
LOC399940	399940	51470744	GAAAGAACCAAUAGUCAUA
TRIM50A	135892	31342404	GUACGAAGCCUUUGCCUGC
TRIM50A	135892	31342404	GGCUCUACCUGCACUAUGA
TRIM50A	135892	31342404	CGUAAGGGCAAGCUGAACA
TRIM50A	135892	31342404	GAACUCACCUUCUUCGAUG
MEFV	4210	4557742	GCAUAUGACACCCGCGUAU
MEFV	4210	4557742	GCAGGCCCUUCGAAGUGUA

MEFV	4210	4557742	GCCCGCAAAUCCAGAAAUU
MEFV	4210	4557742	GCUACUGGGUGGUGAUAAU
RBBP6	5930	38683864	AGACAUAUGUUAUAAGUCG
RBBP6	5930	38683864	UAUUGGAGGUGUUAAAUCU
RBBP6	5930	38683864	CGAAAGAAGAAUAUACUGA
RBBP6	5930	38683864	CCUCUAAACUCAACUAUGA
UNK	85451	89041820	CCACCAAGUGCAACGACAU
UNK	85451	89041820	CCUGAAAGAAUUCCGCACA
UNK	85451	89041820	GGAGAAGACUUUCGAUAAC
UNK	85451	89041820	AAGCACAAAUACAGGUCGU
RNF111	54778	37595552	GAGUUGAGAUGAUUAAUAG
RNF111	54778	37595552	GCAAAUAGUAGUUCUGGUA
RNF111	54778	37595552	UGAGACGUCUUCCAUGUAU
RNF111	54778	37595552	GCGCUUCCAUUAACAAUUC
TRIM68	55128	37622898	GAGAGAUCCUGAAGACUUA
TRIM68	55128	37622898	GAGGAUGUCUUGAUAAUGU
TRIM68	55128	37622898	GAAGGGAAAUGAGUACCGA
TRIM68	55128	37622898	GAACUGGGGUUACACCUGU
TRIM47	91107	54792145	CCAAAGGUGUCAAGAGGGU
TRIM47	91107	54792145	GUACGGGACGGCAAGAUGA
TRIM47	91107	54792145	CCCAAGACCUCGAGAGUAC
TRIM47	91107	54792145	CAUCAAGAGUGCAGCCGUA
BIRC4	331	32528298	GAAAGAGAUUAGUACUGAA
BIRC4	331	32528298	GGACUCUACUACACAGGUA
BIRC4	331	32528298	GUAGAUAGAUGGCAAUAUG
BIRC4	331	32528298	GAACUGGGCAGGUUGUAGA
RNF208	727800	119220602	GGACAUGCCUGCCUUGGAA
RNF208	727800	119220602	AUUGUGAAUCAGUACGUGA
RNF208	727800	119220602	CAGAGAUCAUUGUCAACCA
RNF208	727800	119220602	UGAAAAGUUCCCUGAGCUA
NHLRC1	378884	40255282	GGCGAUCGCUCCAUCAAAG
NHLRC1	378884	40255282	GUGUUUAGCUCAAGUAUGC
NHLRC1	378884	40255282	CAGAAUGGGAUUGUGGUAA
NHLRC1	378884	40255282	GAUCAAGCUUGUCAUUGGA
BIRC8	112401	44680138	GCAGCGCGGUUAUUGAUUU
BIRC8	112401	44680138	CUAUAGGUCAAGAGGAUAA
BIRC8	112401	44680138	GUGAUACCAUCUUCCCUAA
BIRC8	112401	44680138	GAUGUACUCCGUUAACAAA
TRIM48	79097	34147361	UGGGAGAAGCUGUUAAAGA
TRIM48	79097	34147361	GAGCUUCGUUGAUGUUAGU
TRIM48	79097	34147361	GAUAUUACUCUGCAUCACA
TRIM48	79097	34147361	GCAUAAAGACAAUACAGCA
MARCH1	55016	53759068	CAAGAUAUCAACCAUGUAU
MARCH1	55016	53759068	CAUGUAAUGUAAACACAGA
MARCH1	55016	53759068	GGUUUGGUCUUUGUAUGUA
MARCH1	55016	53759068	GCAGCCACGUUUGUUGUAA
MLLT10	8028	57546898	UAGCAAGACUUAGUGAUAA
MLLT10	8028	57546898	CAGCAAUGAUGUAGCAGUA
MLLT10	8028	57546898	GGCAAUAGAUCAAAUUCAU
MLLT10	8028	57546898	GUAACCAACUGGCAAUUAA
ZNF364	27246	33859667	CAAACUACCGGAAUAUAUA
ZNF364	27246	33859667	GCAAGCAACAGAUUUAGCA
ZNF364	27246	33859667	ACAAGUUGAUAUGGGUUUA
ZNF364	27246	33859667	CCUGACAGAUCUCCAGCUA
MKRN1	23608	21359891	UCAAGUCUCUCAUCGAUAG
MKRN1	23608	21359891	GAGUGGGACUUGUUUCAUG
MKRN1	23608	21359891	GCAAGUGGAGGAGUGCUAA
MKRN1	23608	21359891	UGACUUGGAUCUAUAGCAA
FLJ14627	84900	14249505	GGACGUGUGGGCGGAGUUA
FLJ14627	84900	14249505	GUAGGUUACUAGUGAAUAC
FLJ14627	84900	14249505	GACGGAACCCAGUGUAUUA
FLJ14627	84900	14249505	UGAAGGGGCACAAGAAAUU
RNF207	388591	124487386	CCGAGGAGGAGGACGCUAU

RNF207	388591	124487386	CCAGGAAGUGUCCCGGAAA
RNF207	388591	124487386	GUGCAGAGCCAAUACGAAG
RNF207	388591	124487386	GGAGGGAACACCCGACUUA
MARCH3	115123	31341961	UCCAAAGUCUGUCAAUGUA
MARCH3	115123	31341961	GCGCAAACCCAGGCCGUUA
MARCH3	115123	31341961	GGAGGAUUGUGGCAGCCUA
MARCH3	115123	31341961	UGAAUGGGCAGCCGCAGUA
TRIM74	378108	38524611	GAAAUGAGGACCACCAUGA
TRIM74	378108	38524611	GGAAGAUAGAGGAAAGUCA
TRIM74	378108	38524611	CUACAGAAAUACUAGAGGA
TRIM74	378108	38524611	CAAGGAGUCCCUAAUGCUA
RNF165	494470	57165360	CCACACAGAUGGUCGUCCA
RNF165	494470	57165360	UGUUUGGCUCUGUGCGAAA
RNF165	494470	57165360	GGAUACAUUCCAUACGAAA
RNF165	494470	57165360	UGACAAACAACUACGAAUA
TRIM10	10107	16519562	CCAGAGGAUUCGGGACUUU
TRIM10	10107	16519562	UGAGGGAGCCGGUCACUAU
TRIM10	10107	16519562	UCGCACACCUGAGGAAGUU
TRIM10	10107	16519562	CAUCAGAAGCACUCUAAUA
EEA1	8411	55770887	GCAGUCAGCUGGAAAGUCA
EEA1	8411	55770887	GAACCUUGAAGCUUUAUUA
EEA1	8411	55770887	GUUCAAACACUAAUGGAUA
EEA1	8411	55770887	GAAGCAACGGUUCAGAAUA
RFP	5987	18641280	GAACCAGCUCGACCAUUUA
RFP	5987	18641280	GAGAUGGGCGUGUGCGAGA
RFP	5987	18641280	UAAGAGAGGCUCAGUUAUA
RFP	5987	18641280	CGGAGAGUCUAAAGCAGUU
C17ORF27	57674	66571326	CAACAUCGCUCGUGGACAA
C17ORF27	57674	66571326	GUCCAUUGCUCUAAGAUUU
C17ORF27	57674	66571326	CAACACAACGGAAGCUAUA
C17ORF27	57674	66571326	ACACAGAAUUGUCAACUAA
TRIM61	391712	60099473	GGAGAGAGUGGAACUAAUU
TRIM61	391712	60099473	UCAGAAAGACCUAGAGCUU
TRIM61	391712	60099473	CUGGGUAGUUUGACUGAAA
TRIM61	391712	60099473	GGAUCUACAUGAUAGUUUC
TRIM29	23650	17402906	GGAAUUUGGUGCAUUGAUG
TRIM29	23650	17402906	AGCCGUAACUUCAUUGAGA
TRIM29	23650	17402906	GAAGCCACCCGUUACCUUU
TRIM29	23650	17402906	GAAGAGAUACUCCAUGUAC

Supplementary Table 2 The List of Primers

Gene	sense (5'-3')	antisense (5'-3')
hCKS1	AATCTTGGCGTTCAGCA	TTGGTTTCTTGGGTAGTGG
hCCNB1	CTTTCGCCTGAGCCTATTT	CCATCTTCTGCATCCACAT
hFN1	ATTCTGTAGGCCGTTGGA	TACTGCTGGATGCTGATGA
hSKP2	TACAGGTGGCTGTTGCG	TGGAGGTAGTTGAGCTGGA
hZEB1	GCCTGAGTCCTCTGTTTCA	GCTCTTCTGCACTTGGTTG

Supplementary Table 3 The Clinicopathologic Features of Microarrays

Patient	Survival state	Survival time	Sex	Age	Tumor location	T	N	M	TNM stage
1	1	3	male	73	gastric cardia	T4a	N3b	M0	IIIC
2	0	88	male	56	gastric angle	T3	N3a	M0	IIIB
3	1	17	female	79	gastric body	T3	N0	M0	IIA
4	0	88	female	69	gastric angle	T3	N1	M0	IIB
5	1	8	male	68	lesser curvature of gastric body	T4a	N3a	M0	IIIC
6	1	10	male	71	gastric antrum	T4a	N2	M0	IIIB
7	1	5	female	68	lesser curvature	T4a	N1	M0	IIIA
8	1	11	female	68	gastric angle	T3	N1	M0	IIB
9	1	44	male	71	gastric antrum	T3	N2	M0	IIIA
10	0	88	male	50	gastric antrum	T4a	N2	M0	IIIB
11	1	16	female	52	lesser curvature	T3	N3b	M0	IIIB
12	1	8	male	78	lesser curvature of gastric body	T3	N3b	M0	IIIB
13	0	88	male	67	gastric fundus	T3	N0	M0	IIA
14	1	0	male	75	lesser curvature of gastric antrum	T4b	N3a	M0	IIIC
15	1	7	male	75	gastric antrum	T4a	N3b	M0	IIIC
16	0	87	male	78	gastric body	T3	N0	M0	IIA
17	1	10	male	51	remnant stomach	T3	N2	M0	IIIA
18	1	67	male	74	gastric antrum	T4a	N2	M0	IIIB
19	1	4	female	67	gastric antrum	T3	N3a	M0	IIIB
20	1	12	male	62	remnant stomach	T3	N0	M0	IIA
21	1	2	male	66	lesser curvature	T4a	N3a	M0	IIIC
22	0	87	male	67	lesser curvature	T3	N0	M0	IIA
23	1	26	male	73	gastric antrum	T3	N2	M0	IIIA
24	1	14	female	76	gastric antrum	T3	N1	M0	IIB
25	1	54	male	59	gastric antrum	T4a	N2	M0	IIIB
26	1	14	male	59	gastric antrum	T3	N2	M0	IIIA
27	0	86	male	58	gastric angle	T2	N0	M0	IB
28	0	86	female	31	greater curvature	T2	N0	M0	IB
29	0	86	male	64	gastric body	T2	N1	M0	IIA
30	1	22	male	52	stomach	T3	N1	M0	IIB
31	1	19	male	54	gastric antrum	T3	N3a	M0	IIIB
32	1	15	male	63	stomach	T3	N3b	M0	IIIB
33	0	85	male	67	lesser curvature	T3	N0	M0	IIA
34	1	28	female	65	lesser curvature of gastric antrum	T3	N3b	M0	IIIB
35	1	15	male	54	gastric cardia	T3	N2	M0	IIIA
36	1	22	male	72	lesser curvature of gastric body	T3	N1	M0	IIB
37	0	84	female	46	gastric antrum	T1b	N0	M0	IA
38	1	17	female	60	gastric body	T4a	N2	M0	IIIB
39	1	54	female	68	stomach	T3	N0	M0	IIA
40	1	50	male	61	gastric cardia	T3	N2	M0	IIIA
41	1	38	male	59	gastric antrum	T3	N3a	M0	IIIB
42	0	84	female	78	gastric cardia	T4a	N2	M0	IIIB
43	1	0	male	76	gastric antrum	T4a	N3b	M0	IIIC
44	1	22	male	77	gastric fundus	T2	N2	M0	IIB
45	1	13	male	68	gastric antrum	T3	N2	M0	IIIA
46	1	27	female	52	lesser curvature of gastric cardia	T4b	N3b	M0	IIIC
47	0	83	female	52	gastric fundus	T3	N1	M0	IIB
48	1	7	female	82	gastric antrum	T3	N2	M0	IIIA
49	1	26	male	59	gastric cardia	T3	N2	M0	IIIA
50	1	28	female	62	lesser curvature of gastric body	T3	N3b	M0	IIIB
51	1	37	female	83	gastric cardia of fundus	T3	N0	M0	IIA
52	1	23	female	72	gastric cardia	T3	N3a	M0	IIIB
53	1	9	male	65	gastric cardia	T4b	N2	M0	IIIB
54	1	39	male	53	gastric antrum	T3	N1	M0	IIB
55	1	44	male	75	gastric body	T3	N1	M1	IV
56	1	10	male	50	stomach	T4a	N3a	M0	IIIC

57	1	12	female	61	stomach	T3	N3a	M0	IIIB
58	1	9	female	77	lesser curvature	T3	N1	M0	IIB
59	1	6	male	80	gastric cardia	T3	N2	M0	IIIA
60	1	16	male	81	lesser curvature of gastric antrum	T4a	N2	M0	IIIB
61	1	35	male	67	gastric cardia	T4a	N1	M0	IIIA
62	1	5	male	71	gastric antrum	T3	N3b	M0	IIIB
63	0	97	male	70	gastric fundus	T3	N0	M0	IIA
64	1	14	female	53	remnant stomach	T4a	N0	M0	IIB
65	1	35	female	52	lesser curvature of gastric antrum	T3	N3a	M0	IIIB
66	1	11	male	69	lesser curvature	T3	N3a	M0	IIIB
67	1	28	male	61	gastric body	T3	N0	M0	IIA
68	1	32	male	55	lesser curvature of gastric antrum	T3	N2	M0	IIIA
69	0	97	female	65	gastric body,gastric antrum	T2	N1	M0	IIA
70	0	97	female	53	lesser curvature of gastric body	T3	N0	M0	IIA
71	1	67	male	62	lesser curvature of gastric angle	T2	N3a	M0	IIIA
72	1	27	male	58	lesser curvature of gastric cardia	T3	N2	M0	IIIA
73	1	10	male	49	lesser curvature of gastric antrum	T3	N3a	M0	IIIB
74	0	96	male	71	gastric cardia	T3	N0	M0	IIA
75	1	8	male	64	lesser curvature of gastric body	T3	N3a	M0	IIIB
76	1	35	male	79	gastric antrum	T3	N2	M0	IIIA
77	1	18	female	67	lesser curvature	T3	N3a	M0	IIIB
78	1	2	male	73	pylorus	T3	N0	M0	IIA
79	1	24	male	57	lesser curvature	T3	N2	M0	IIIA
80	1	46	male	54	gastric body	T3	N1	M0	IIB
81	1	42	male	63	lesser curvature	T3	N2	M0	IIIA
82	1	6	female	52	gastric body	T3	N3a	M0	IIIB
83	1	58	male	81	gastric antrum	T3	N2	M0	IIIA
84	1	23	female	77	lesser curvature of gastric antrum	T2	N1	M0	IIA
85	1	25	female	72	lesser curvature	T4a	N2	M0	IIIB
86	1	5	female	62	lesser curvature of gastric antrum	T4a	N3a	M0	IIIC
87	1	15	male	68	gastric antrum	T3	N3a	M1	IV
88	1	15	female	79	gastric antrum	T3	N1	M0	IIB
89	0	94	male	72	gastric antrum	T1a	N0	M0	IA
90	1	3	male	81	lesser curvature of gastric antrum	T2	N3a	M0	IIIA
91	1	22	female	72	gastric antrum	T3	N3a	M0	IIIB
92	1	22	male	55	gastric body	T3	N3a	M0	IIIB
93	1	18	male	80	gastric cardia	T3	N3a	M0	IIIB
94	1	24	male	57	stomach	T4a	N3b	M1	IV
95	1	27	female	65	gastric antrum	T3	N1	M0	IIB
96	1	31	male	59	gastric antrum	T3	N3a	M0	IIIB
97	1	11	male	83	gastric antrum	T3	N2	M0	IIIA
98	1	39	male	75	gastric antrum	T4a	N2	M0	IIIB
99	1	9	male	59	gastroenteric stoma	T4a	N3a	M0	IIIC
100	1	42	female	73	lesser curvature	T3	N3a	M0	IIIB
101	1	19	male	59	gastric antrum	T3	N3a	M0	IIIB
102	1	2	male	78	gastric antrum	T3	N3a	M0	IIIB
103	1	63	male	82	gastric fundus	T3	N2	M0	IIIA
104	1	24	male	62	gastric cardia of fundus	T3	N3a	M0	IIIB
105	1	21	male	73	gastric cardia	T3	N1	M0	IIB
106	1	44	male	58	gastric cardia of fundus	T3	N3a	M0	IIIB
107	1	43	male	67	gastric cardia of fundus	T4a	N1	M0	IIIA
108	1	27	male	67	lesser curvature of gastric antrum	T3	N2	M0	IIIA
109	1	30	male	71	gastric antrum	T3	N1	M0	IIB
110	1	13	male	80	gastric cardia	T4a	N2	M0	IIIB

Unedited blot and gel

Full unedited gels for Figure. 1

Figure.1B

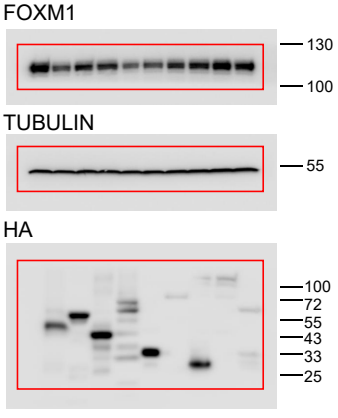


Figure.1C

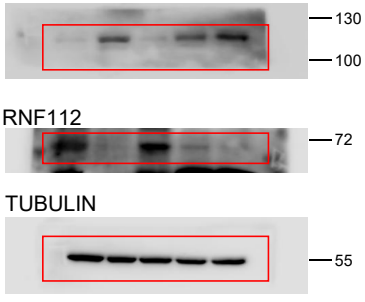


Figure.1D

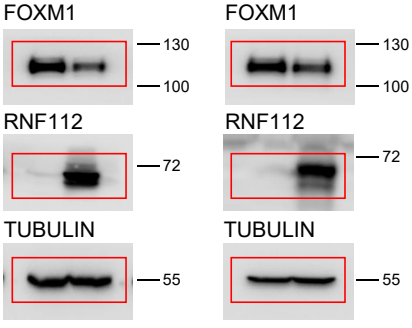


Figure.1E

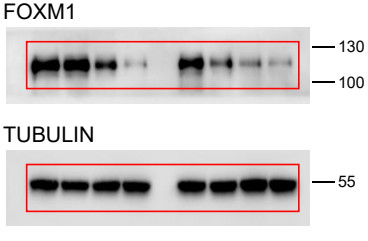


Figure.1F

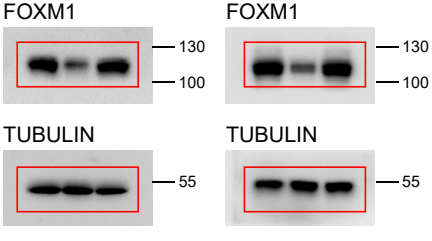


Figure.1G

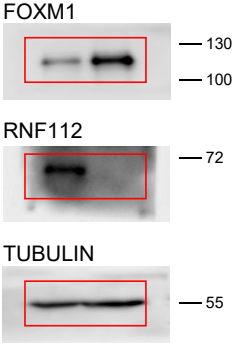
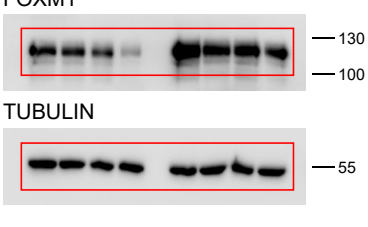


Figure.1H



Unedited blot and gel

Full unedited gels for Figure. 2

Figure.2D

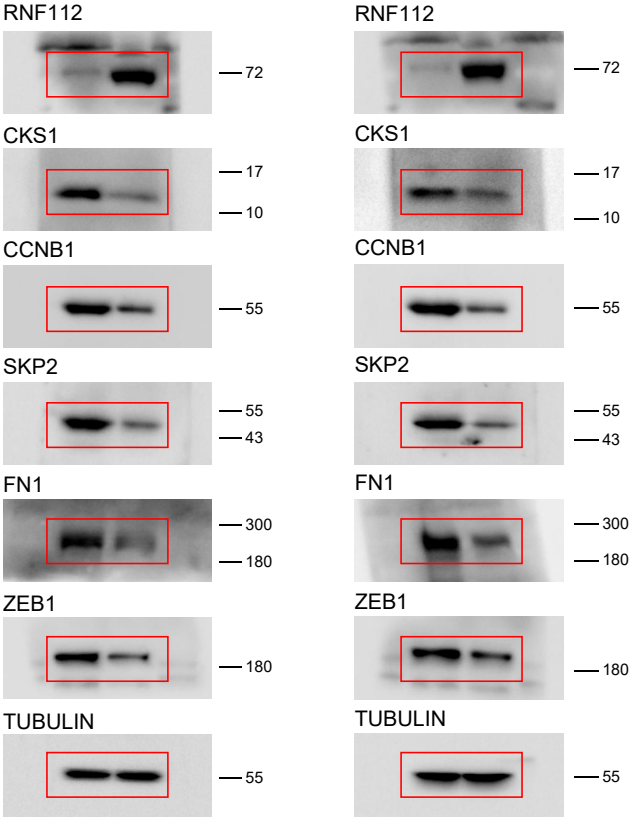
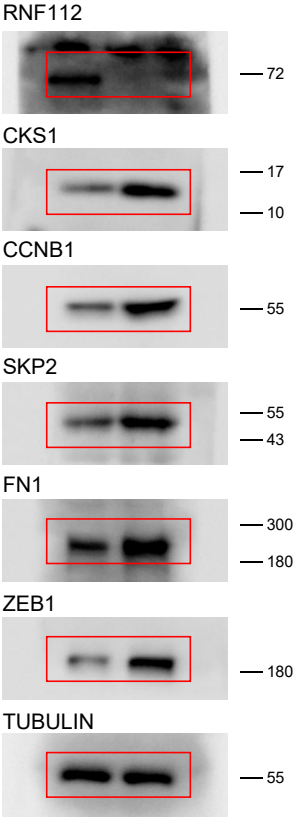


Figure.2I

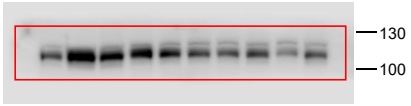


Unedited blot and gel

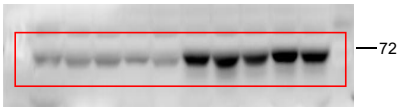
Full unedited gels for Figure. 3

Figure.3D

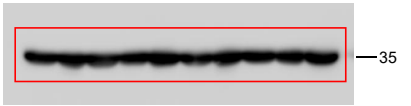
FOXM1



RNF112



GAPDH



Unedited blot and gel

Full unedited gels for Figure. 4

Figure.4A

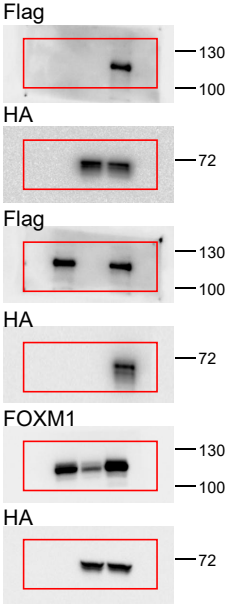


Figure.4B

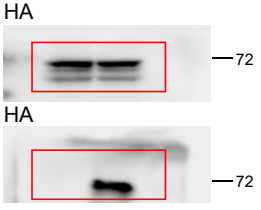


Figure.4F

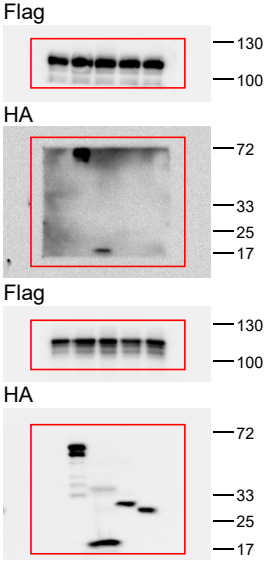


Figure.4G

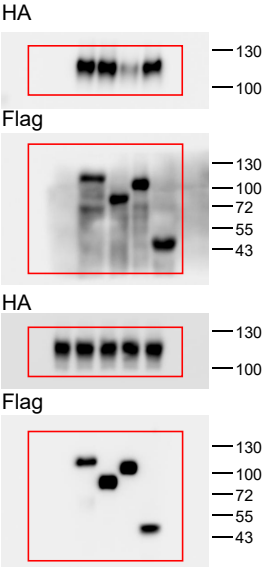
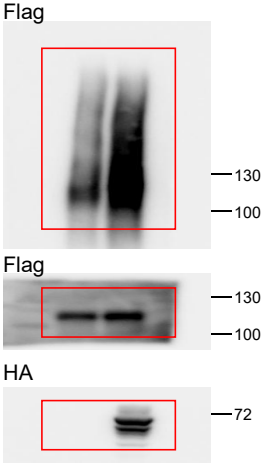


Figure.4H



Unedited blot and gel

Full unedited gels for Figure. 5

Figure.5B

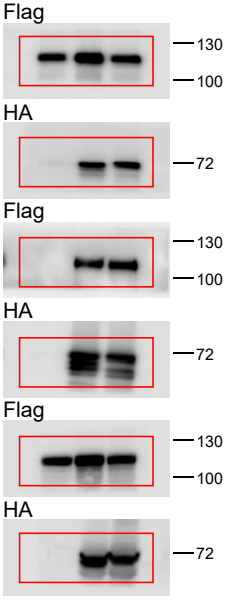


Figure.5C

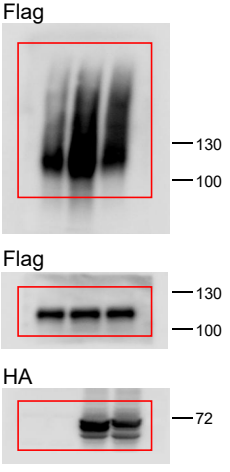
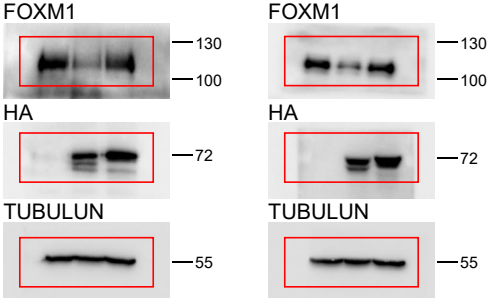


Figure.5D

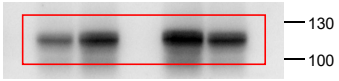


Unedited blot and gel

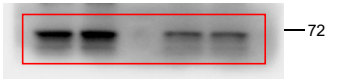
Full unedited gels for Figure. 6

Figure.6A

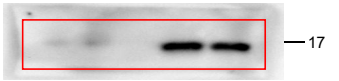
FOXM1



RNF112



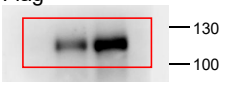
H3



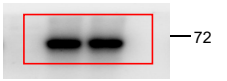
TUBULIN

Figure.6B

Flag



HA



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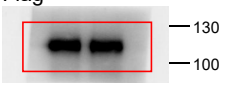

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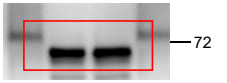
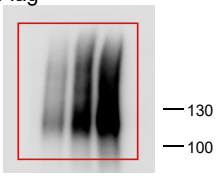


Figure.6C

Flag



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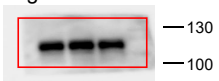

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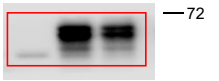
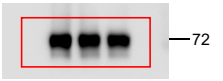


Figure.6E

Flag

HA



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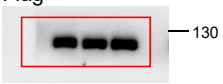

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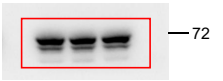
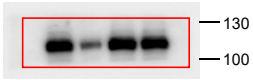
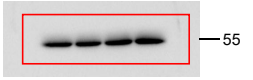


Figure.6F

FOXM1



TUBULIN



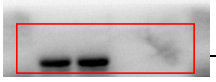
Unedited blot and gel

Full unedited gels for Figure. 7

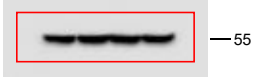
Figure.7A

FOXM1

RNF112



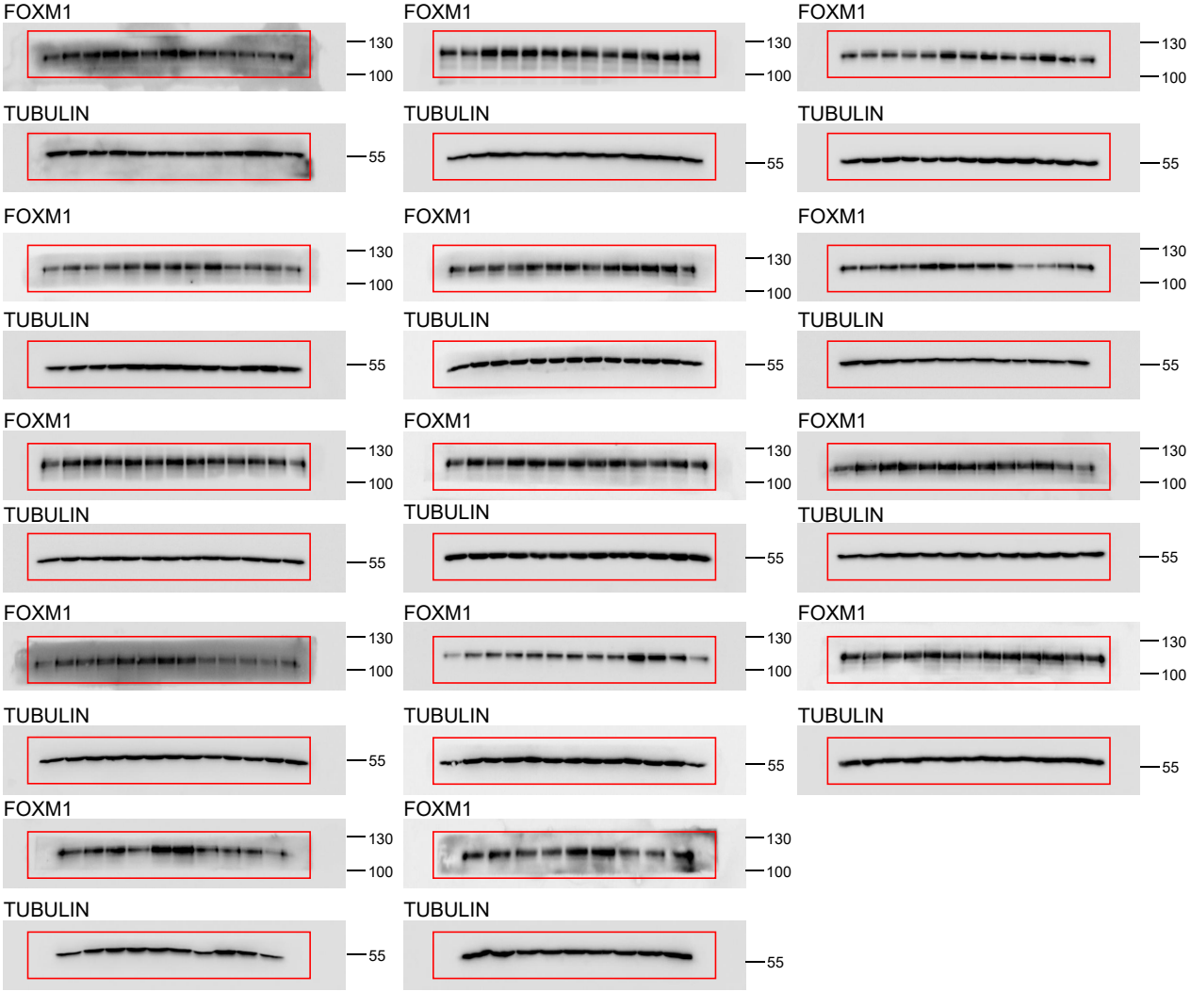
TUBULIN



Unedited blot and gel

Full unedited gels for Supplemental Figure. 2

Supplemental Figure. 2



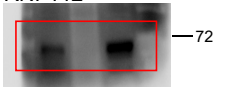
Unedited blot and gel

Full unedited gels for Supplemental Figure. 5

Supplemental Figure. 5C

FOXM1

RNF112

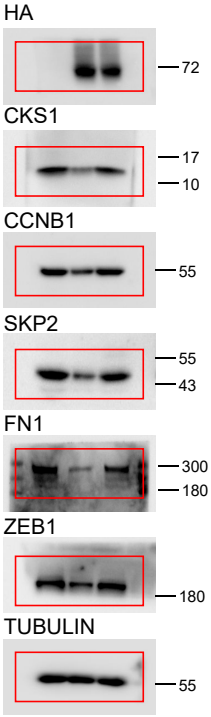


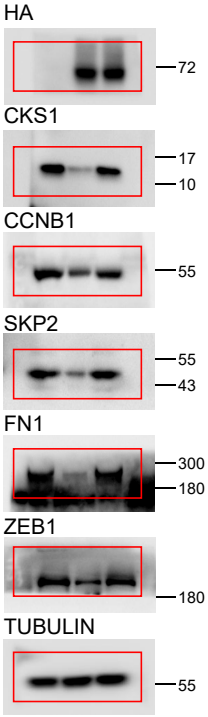
TUBULIN

Unedited blot and gel

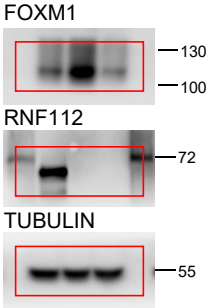
Full unedited gels for Supplemental Figure. 6

Supplemental Figure. 6C





Supplemental Figure. 6F

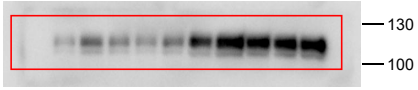


Unedited blot and gel

Full unedited gels for Supplemental Figure. 7

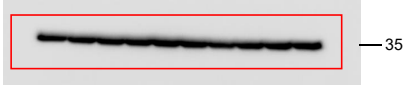
Supplemental Figure. 7D

FOXM1



RNF112

GAPDH

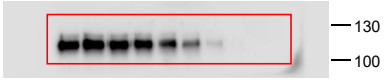


Unedited blot and gel

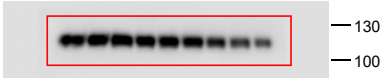
Full unedited gels for Supplemental Figure. 10

Supplemental Figure. 10A

FOXM1



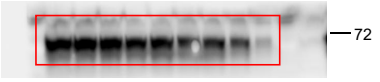
FOXM1



Supplemental Figure. 10B

RNF112

RNF112



Unedited blot and gel

Full unedited gels for Supplemental Figure. 11

Supplemental Figure. 11B