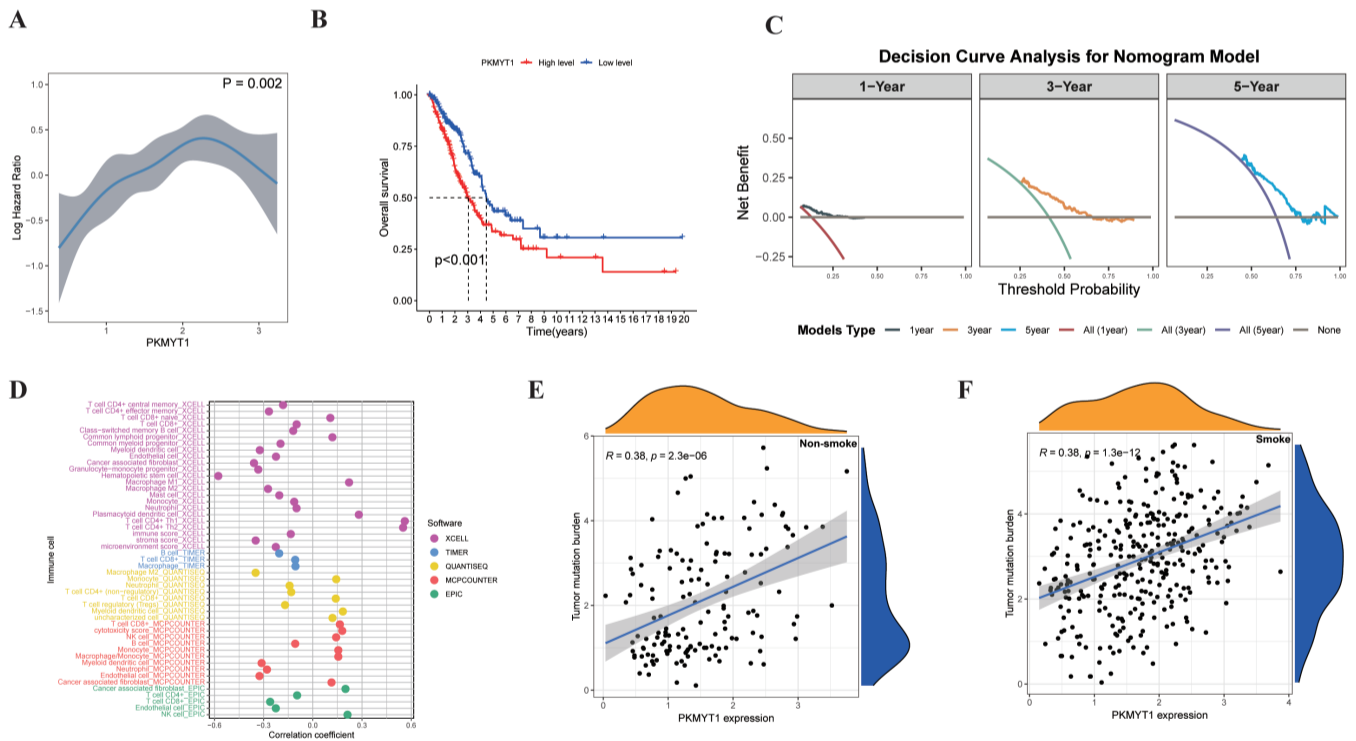
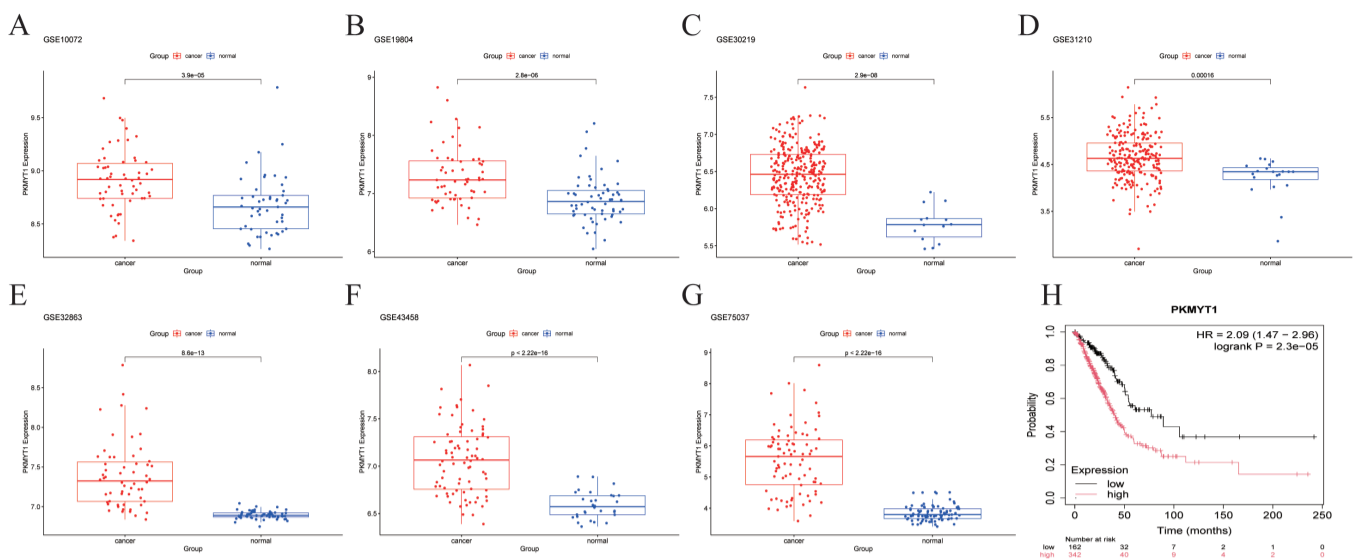


**Figure S1** Association of PKMYT1 expression with clinicopathological parameters in LUAD. Box plots illustrate the correlation between PKMYT1 expression levels and key demographic and tumor characteristics in the TCGA-LUAD cohort. (A) PKMYT1 expression across different age groups. (B) PKMYT1 expression stratified by patient gender. (C) Significantly higher PKMYT1 expression is observed in patients with advanced tumor stages (Stage I vs. Stage II,  $P=0.0081$ ; Stage I vs. Stage III,  $P=0.003$ ). (D-F) PKMYT1 expression is significantly elevated in tumors with advanced T classification (T1 vs. T2,  $P=0.0015$ ; T1 vs. T3,  $P=0.031$ ), positive lymph node involvement (N0 vs. N1,  $P=0.027$ ) and distant metastasis.



**Figure S2** Validation of the prognostic model and supplementary analyses. (A) Restricted cubic spline (RCS) analysis of the association between continuous PKMYT1 expression (log<sub>2</sub>-transformed) and overall survival risk in the TCGA-LUAD cohort, demonstrating a significant linear relationship ( $P=0.002$ ). (B) Kaplan-Meier survival curves based on the optimal cutpoint for PKMYT1 expression (determined by the `surv_cutpoint` function), confirming that patients with high PKMYT1 expression have significantly poorer overall survival ( $P<0.001$ ). (C) Decision-curve analysis (DCA) for the nomogram predicting 1-, 3-, and 5-year overall survival, illustrating significant clinical net benefit across a range of threshold probabilities. (D) Bubble plot comparing immune cell infiltration estimates between CIBERSORT and the xCell algorithm for the TCGA-LUAD cohort, showing consistency in the identified associations between PKMYT1 expression and key immune populations. Specific comparisons include a strong negative correlation for Macrophage M2 ( $R=-0.35, P<0.001$ ) and a positive correlation for Macrophage M1 ( $R=0.22, P<0.001$ ). (E,F) Stratified analysis of the correlation between PKMYT1 expression and tumor mutation burden (TMB) in patients with lung adenocarcinoma. The robust positive correlation is maintained independently of smoking status: (E) in non-smokers ( $R=0.38, P=2.3e-06$ ) and (G) in smokers ( $R=0.38, P=1.3e-12$ ).



**Figure S3** PKMYT1 expression in LUAD tissues and its prognostic value. (A-G) PKMYT1 expression was significantly elevated in LUAD tumor tissues compared to normal tissues across multiple datasets (GSE10072, GSE19804, GSE30219, GSE31210, GSE32863, GSE43458, and GSE75037) ( $P < 0.001$ ). (H) Kaplan-Meier survival analysis demonstrated that higher PKMYT1 expression was associated with poorer overall survival (OS), with a hazard ratio (HR) of 2.09 (95% CI: 1.47–2.96, log-rank  $P = 2.3 \times 10^{-5}$ ).

**Table S1** Software and R packages used in the bioinformatics analysis

Package	Version
limma	3.62.1
CIBERSORT	0.1.0
estimate	1.0.13
pRRophetic	0.5
clusterProfiler	4.12.6
ggplot2	3.5.2
ggpubr	0.6.1
survival	3.8-3
survminer	0.5.0
timeROC	0.4
ComplexHeatmap	2.20.0
regplot	1.1
rms	8.0-0
org.Hs.eg.db	3.19.1
enrichplot	1.24.4
reshape2	1.4.4
preprocessCore	1.66.0
ggExtra	0.10.1
vioplot	0.5.1
corrplot	0.95
oncoPredict	1.2

**Table S2** Correlation analysis between immune cell infiltration and gene expression with confidence intervals and q-values

Cell	rho	rho_lower	rho_upper	P value	q value
B cells naive	-0.051798011	-0.144478763	0.04178367	0.277744649	0.321599067
B cells memory	-0.052620774	-0.145286458	0.04096007	0.270173085	0.321599067
Plasma cells	-0.15159625	-0.241556358	-0.05905262	0.001408232	0.002581758
T cells CD8	0.207755537	0.116638765	0.295404236	1.09E-05	2.66E-05
T cells CD4 naive	0.032205145	-0.061358958	0.125208185	0.499953085	0.523760375
T cells CD4 memory resting	-0.30181315	-0.384360233	-0.214478252	9.70E-11	3.56E-10
T cells CD4 memory activated	0.355458528	0.271076681	0.434418637	1.40E-14	1.26E-13
T cells follicular helper	0.155518332	0.063054445	0.245335096	0.001050752	0.002101503
T cells regulatory (Tregs)	0.049048626	-0.044534929	0.141778837	0.304083237	0.334491561
T cells gamma delta	-0.065518361	-0.157931701	0.028032724	0.16961043	0.21949585
NK cells resting	0.223816628	0.133221363	0.310702553	2.06E-06	6.48E-06
NK cells activated	-0.100076278	-0.191664734	-0.006759871	0.035648526	0.056019113
Monocytes	-0.219325364	-0.306429118	-0.128579153	3.33E-06	9.15E-06
Macrophages M0	0.354318203	0.269867483	0.433359609	1.72E-14	1.26E-13
Macrophages M1	0.316524887	0.229941686	0.398136753	1.02E-11	5.60E-11
Macrophages M2	-0.07456647	-0.166784729	0.018945022	0.11787785	0.172887514
Dendritic cells resting	-0.312577025	-0.394443465	-0.225787812	1.89E-11	8.31E-11
Dendritic cells activated	-0.157712224	-0.247447616	-0.06529424	0.000889342	0.001956552
Mast cells resting	-0.369896539	-0.447808462	-0.286409778	9.56E-16	2.10E-14
Mast cells activated	0.126081671	0.033091696	0.216907499	0.008030463	0.013590015
Eosinophils	0.02033359	-0.073184948	0.113497665	0.670226259	0.670226259
Neutrophils	-0.066470475	-0.158863986	0.027077171	0.163480827	0.21949585

**Table S3** Significantly correlated immune cell types with gene expression in head and neck acinic cell carcinoma

Cell	rho	rho_lower	rho_upper	P value	q value
Plasma cells	-0.15159625	-0.241556358	-0.05905262	0.001408232	0.002581758
T cells CD8	0.207755537	0.116638765	0.295404236	1.09E-05	2.66E-05
T cells CD4 memory resting	-0.30181315	-0.384360233	-0.214478252	9.70E-11	3.56E-10
T cells CD4 memory activated	0.355458528	0.271076681	0.434418637	1.40E-14	1.26E-13
T cells follicular helper	0.155518332	0.063054445	0.245335096	0.001050752	0.002101503
NK cells resting	0.223816628	0.133221363	0.310702553	2.06E-06	6.48E-06
Monocytes	-0.219325364	-0.306429118	-0.128579153	3.33E-06	9.15E-06
Macrophages M0	0.354318203	0.269867483	0.433359609	1.72E-14	1.26E-13
Macrophages M1	0.316524887	0.229941686	0.398136753	1.02E-11	5.60E-11
Dendritic cells resting	-0.312577025	-0.394443465	-0.225787812	1.89E-11	8.31E-11
Dendritic cells activated	-0.157712224	-0.247447616	-0.06529424	0.000889342	0.001956552
Mast cells resting	-0.369896539	-0.447808462	-0.286409778	9.56E-16	2.10E-14
Mast cells activated	0.126081671	0.033091696	0.216907499	0.008030463	0.013590015

**Table S4** Clinical characteristics of patients with lung adenocarcinoma

Characteristics	Patients (n=39)
Age (mean ± SD)	61±7
Sex (M/F)	18/21
Tumor Stage	I (23), II (16)
Treatment	Surgery (39)

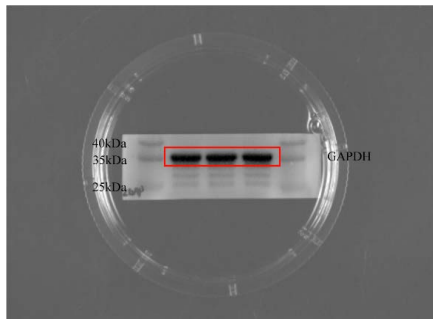
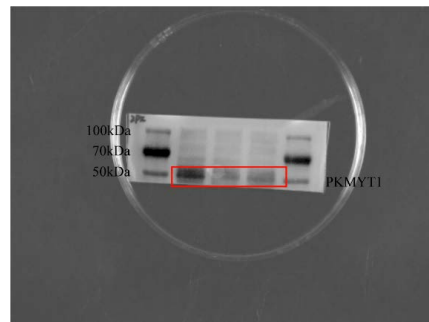
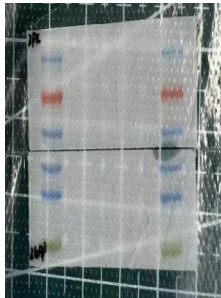
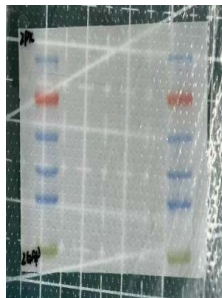
**Table S5** KEGG pathway enrichment analysis based on gene set enrichment analysis (GSEA)

ID	Description	setSize	enrichmentScore	NES	pvalue	p.adjust	qvalue	rank	leading_edge	core_enrichment
KEGG_CELL_CYCLE	KEGG_CELL_CYCLE	124	0.6175118	2.1476824	3.06E-09	5.70E-07	5.52E-07	13327	tags=49%, list=24%, signal=37%	PKMYT1/ESPL1/CDC20/CDKN2A/PLK1/CDC45/CCNE1/CDC6/SMC1B/BUB1B/TTK/CDC25A/ORC1/CCNA2/E2F2/BUB1/E2F1/CDC25C/MCM2/CHEK1/CCNB2/CCNB1/CDK1/MAD2L1/MCM4/ORC6/MCM7/SKP2/CDC7/PTTG1/MCM6/DBF4/MCM5/CCNE2/TFDP1/PCNA/CDK2/MCM3/CDK6/CCNA1/RBL1/CHEK2/MYC/CDKN2C/PRKDC/YWHAG/CDK4/CDKN2D/E2F3/HDAC2/MAD2L2/SMC1A/ANAPC7/CCNB3/CDC25B/BUB3/GADD45A/SMC3/YWHAZ/MAD1L1/SFN
KEGG_SPLICEOSOME	KEGG_SPLICEOSOME	127	0.5349625	1.8579695	8.04E-06	0.0007477	0.0007235	23107	tags=83%, list=42%, signal=48%	HSPA6/ALYREF/HSPA2/HSPA1A/SNRPF/HSPA1B/SNRPD1/SNRPB/SNRPA1/EIF4A3/SNRPA/SF3A2/SART1/SF3B4/WBP11/EFTUD2/LSM5/PRPF19/PRPF4/U2AF2/PRPF40B/SRSF9/CHERP/MAGOHB/THOC3/PPIH/HNRNPM/MAGOH/RBM17/U2SURP/LSM4/LSM8/ISY1/SF3B2/SNRPC/CTNBL1/LSM7/DDX23/PRPF31/NCBP2/SNRNP200/PUF60/SNRPD3/NCBP1/SF3B6/THOC1/PPI1/PRPF40A/BUD31/TCERG1/HNRNPA3/SNRPG/ACIN1/DHX16/SRSF2/SNRPD2/SRSF1/SNW1/TRA2B/SF3B3/PRPF3/LSM2/RBM8A/USP39/PQBP1/TXNL4A/PLRG1/PCBP1/DHX38/SNRPE/HNRNPC/CDC5L/DHX8/PHF5A/SNRNP70/SF3A3/SNRNP40/XAB2/HNRNPU/SNRPB2/LSM6/HNRNPA1P60/SMNDC1/SF3B5/SRSF7/LSM3/HNRNPA1/SNRNP27/DHX15/SRSF4/HNRNPK/PRPF38A/SRSF3/THOC2/CWC15/PRPF6/DDX42/HNRNPA1L2/BCAS2/PPIE/RBMX/CRNKL1/SNU13/HSPA1L/DDX46/RBM25
KEGG_OLFACTORY_TRANSDUCTION	KEGG_OLFACTORY_TRANSDUCTION	374	0.3926687	1.5399899	3.67E-05	0.0022728	0.0021995	6664	tags=28%, list=12%, signal=25%	OR14A16/GUCA1C/OR6C4/OR8K1/OR511/OR51G1/OR5M9/OR4C46/OR10A7/OR6Q1/OR4D5/OR8H3/OR4M2/OR4C11/OR4A15/OR5M3/OR10G3/OR52A5/OR6C75/OR4P4/OR56A1/OR5M8/OR4N4/OR51G2/OR6M1/OR4C6/OR52E2/CLCA4/OR10Z1/OR56A3/OR8G1/OR51V1/CALML3/OR51S1/OR8D4/OR51B5/OR10G4/OR4S1/OR51F2/OR5T1/OR2Z1/OR56A4/OR2T33/OR1F1/OR10G9/OR8J1/OR10H5/OR4C15/OR51A7/OR11L1/OR9Q2/CLCA1/OR2M2/OR8J3/OR2T8/OR5J2/OR1N2/OR2W3/OR2V2/OR52B4/OR51B2/CAMK2B/OR51B4/OR4K2/OR10H2/OR2M7/OR6C1/OR6C6/OR10H1/OR8A1/OR9K2/OR3A2/OR51T1/OR10G8/CALML5/OR6C68/OR2B6/OR5T3/OR2C3/OR6C2/OR10S1/OR7A5/OR3A1/OR6C70/OR4F5/OR1A2/OR4F4/OR2H2/OR8G5/OR51E1/OR5AC2/OR51E2/OR1S2/CLCA2/OR4C13/OR4M1/OR7A17/OR13G1/OR8G2P/OR4L1/OR6B3/OR10C1/OR2M3/OR7C1/OR7D4
KEGG_DNA_REPLICATION	KEGG_DNA_REPLICATION	36	0.6817859	1.9003135	0.0001457	0.0067733	0.0065548	14128	tags=75%, list=26%, signal=56%	MCM2/MCM4/MCM7/RFC4/FEN1/POLE2/MCM6/RNASEH2A/DNA2/RFC3/MCM5/POLE/POLA2/PRIM1/PCNA/MCM3/LIG1/RFC5/POLD1/RFC2/POLD2/PRIM2/POLD3/RNASEH1/RPA3/POLA1/SSBP1
KEGG_PROTEASOME	KEGG_PROTEASOME	46	0.5827736	1.6859918	0.0028557	0.1062325	0.1028057	20631	tags=83%, list=38%, signal=52%	IFNG/PSMD2/PSMB9/PSMD11/PSMD3/SEM1/PSMC1P4/PSME2/PSMB5/PSMB3/PSMC4/PSMB2/PSMD1/PSME3/PSMC5/PSMD14/PSMD4/PSMD12/PSME4/PSMB4/PSMC1/PSMB7/PSMC2/PSMD7/PSMA7/PSMB8/PSMC3/PSMB6/PSMA6/PSMA5/PSMB11/PSMA2/PSMA4/PSMB1/PSMA3/PSMD8/POMP/PSMB10
KEGG_HOMOLOGOUS_RECOMBINATION	KEGG_HOMOLOGOUS_RECOMBINATION	28	0.66205	1.7485556	0.0034469	0.1068526	0.1034057	17256	tags=82%, list=32%, signal=56%	RAD54L/EME1/XRCC2/RAD51/BLM/POLD1/RAD54B/BRCA2/XRCC3/POLD2/SEM1/POLD3/RPA3/TOP3A/RAD51C/MUS81/SSBP1/TOP3B/NBN/RAD51D/POLD4/MRE11/RAD52
KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION	KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION	56	0.5183809	1.5507626	0.0061024	0.1621494	0.1569188	14873	tags=43%, list=27%, signal=31%	TUBA3E/TUBA3C/TUBB2B/TUBB4A/TUBB3/TUBB/TUBA1B/TUBA1C/TUBB8/TUBB6/ARPC1A/TUBA4A/KRT18/ARPC1B/TUBB4B/TUBAL3/ACTG1/NCL/YWHAZ/CLDN1/TUBA8/ACTB/TUBB2A/ITGB1
KEGG_BASE_EXCISION_REPAIR	KEGG_BASE_EXCISION_REPAIR	35	0.5693799	1.5777148	0.0128541	0.2468373	0.2388748	18263	tags=71%, list=33%, signal=48%	NEIL3/FEN1/POLE2/POLE/PCNA/LIG1/POLD1/UNG/POLD2/HMGB1P1/PARP2/TDG/POLD3/LIG3/APEX2/MUTYH/PARP1/SMUG1/APEX1/POLE3/POLD4/MBD4/XRCC1/HMGB1P40/POLE4
KEGG_OOCYTE_MEIOSIS	KEGG_OOCYTE_MEIOSIS	112	0.4352808	1.4823093	0.0132708	0.2468373	0.2388748	10372	tags=29%, list=19%, signal=23%	CALML3/PKMYT1/SPDYC/ESPL1/CDC20/PLK1/CCNE1/SMC1B/CAMK2B/SGO1/BUB1/CDC25C/CALML5/AURKA/CCNB2/CCNB1/CDK1/FBXO43/MAD2L1/MOS/ADCY8/PTTG1/FBXO5/CCNE2/CDK2/MAPK12/STAG3/REC8/YWHAG/CALML6/ADCY3/ADCY1
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	271	0.3416872	1.30244	0.0119053	0.2468373	0.2388748	8308	tags=26%, list=15%, signal=22%	NTSR2/CSH1/GALR1/F2/GRIA2/GLRA2/CHRN2/PRL/TAAR1/HTR2C/DRD2/GABRA1/TAAR2/PTH2R/CGA/GCGR/GABRA3/P2RY4/GRM4/MTNR1B/HTR1E/HRH3/GABRQ/MCHR2/FSHB/NPBWR1/CCKBR/GH2/GRIN2B/GALR3/LEP/NPY5R/NPBWR2/HTR1D/GPR50/PRSS3/PRLHR/GRIN2D/TAAR8/TRHR/GRIK5/S1PR5/GALR2/GABRR1/GPR83/NPY1R/GPR156/CHRM4/PLG/GRIN1/CHRNA9/GRIK1/OXTR/DRD4/AVPR1A/HCRTR2/GRM8/BDKRB1/CHRM3/GABRA5/GABRG2/HTR6/KISS1R/NTSR1/F2RL2/GRIN2C/NPFFR2/UTS2R/GPR35/SSTR2
KEGG_MISMATCH_REPAIR	KEGG_MISMATCH_REPAIR	23	0.6442725	1.6356	0.0156572	0.2647496	0.2562093	14128	tags=61%, list=26%, signal=45%	EXO1/RFC4/RFC3/PCNA/LIG1/RFC5/POLD1/RFC2/POLD2/MSH2/MSH6/POLD3/RPA3/SSBP1
KEGG_P53_SIGNALING_PATHWAY	KEGG_P53_SIGNALING_PATHWAY	68	0.4660013	1.4454598	0.0231448	0.3587445	0.3471721	13469	tags=38%, list=25%, signal=29%	CDKN2A/GTSE1/CCNE1/RRM2/SERPIN5/CHEK1/CCNB2/CCNB1/CDK1/PMAIP1/CCNE2/RPRM/ADGRB1/CDK2/CDK6/CHEK2/CDK4/IGFBP3/PERP/CYCS/PIDD1/CCNB3/GADD45A/SFN/BID/SERPINE1
KEGG_SMALL_CELL_LUNG_CANCER	KEGG_SMALL_CELL_LUNG_CANCER	84	0.4233156	1.3682107	0.0297321	0.425398	0.4116755	17710	tags=48%, list=32%, signal=32%	LAMA1/CCNE1/E2F2/E2F1/LAMC2/COL4A6/SKP2/CCNE2/CKS1B/CDK2/CDK6/ITGA6/LAMB3/MYC/ITGA2B/CDK4/NOS2/BIRC3/LAMA5/E2F3/FN1/LAMA3/CYCS/TRAF2/LAMB1/TRAF4/ITGA3/AKT2/PTGS2/PIAS4/ITGB1/IKBK/PIK3R2/PIK3R3/COL4A2/LAMC1/RELA/LAMB4/COL4A1/TRAF3
KEGG_NUCLEOTIDE_EXCISION_REPAIR	KEGG_NUCLEOTIDE_EXCISION_REPAIR	44	0.513488	1.4844839	0.0372571	0.494987	0.4790197	19646	tags=59%, list=36%, signal=38%	RFC4/POLE2/RFC3/POLE/PCNA/LIG1/RFC5/POLD1/RFC2/POLD2/CUL4A/POLD3/RPA3/ERCC2/GTF2H4/RAD23A/RAD23B/GTF2H3/POLE3/POLD4/MNAT1/POLE4/ERCC3/RPA1/CUL4B/DDB1
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	132	0.3806985	1.3287804	0.0464132	0.5755238	0.5569585	14922	tags=33%, list=27%, signal=24%	IFNA2/KIR2DL1/IFNA13/IFNA8/KLRC2/IFNA1/HLA-G/IFNA14/KIR2DL4/GZMB/IFNA10/IFNA4/IFNG/KLRC3/KIR2DL3/RAET1G/RAC3/RAET1E/IFNB1/KIR3DL2/PRKCG/CSF2/NAV3/IFNA6/MICB/KIR3DL1/NCR1/ULBP2/KLRC1/KIR2DS4/FASLG/RAET1L/NFATC4/SH3BP2/NAV2/BID/ULBP1/PAK1/SHC4/HRAS/KLRK1/KLRD1/MAP2K2/PTPN11

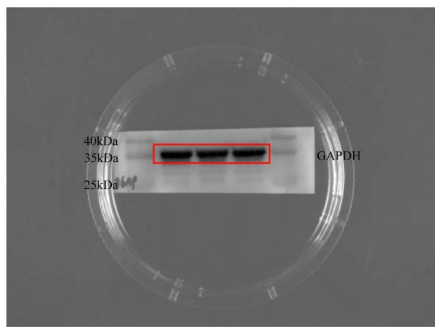
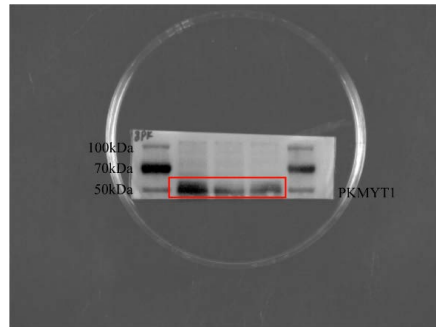
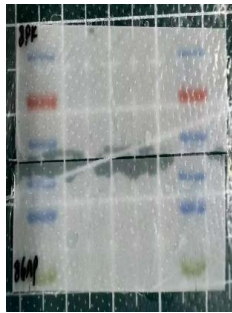
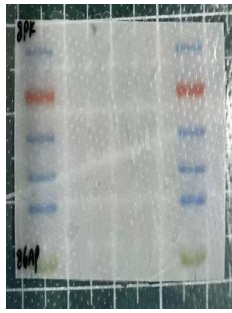
# Appendix 1 The molecular weight marker for Western Bolts is on the image

## WB,A549 knock-down

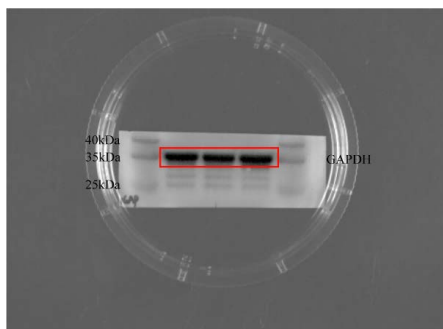
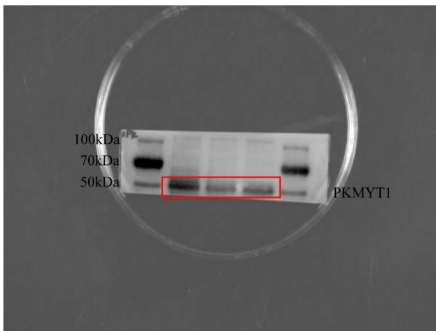
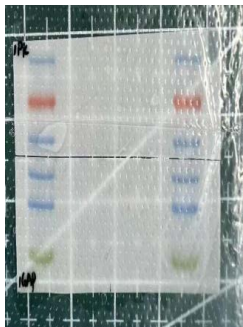
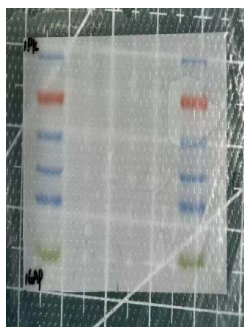
WB,A549 knock-down,count 1 2



WB,A549 knock-down,count 2 8



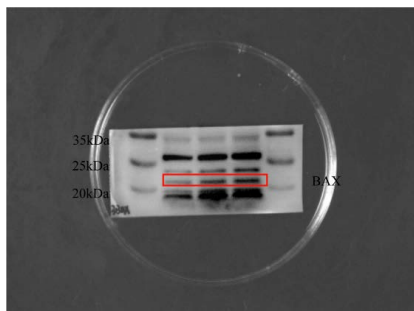
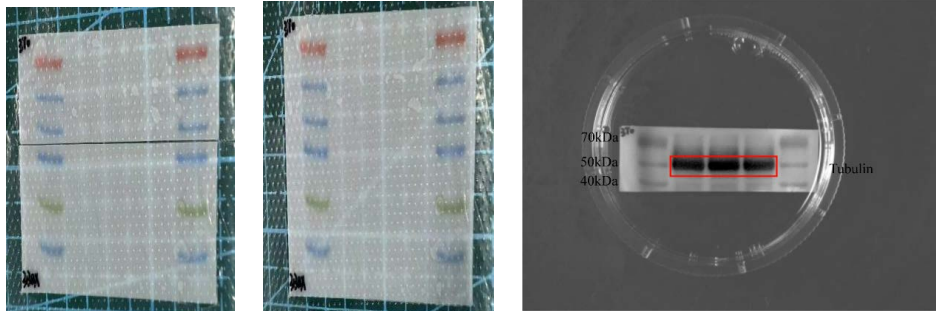
WB,A549 knock-down,picture



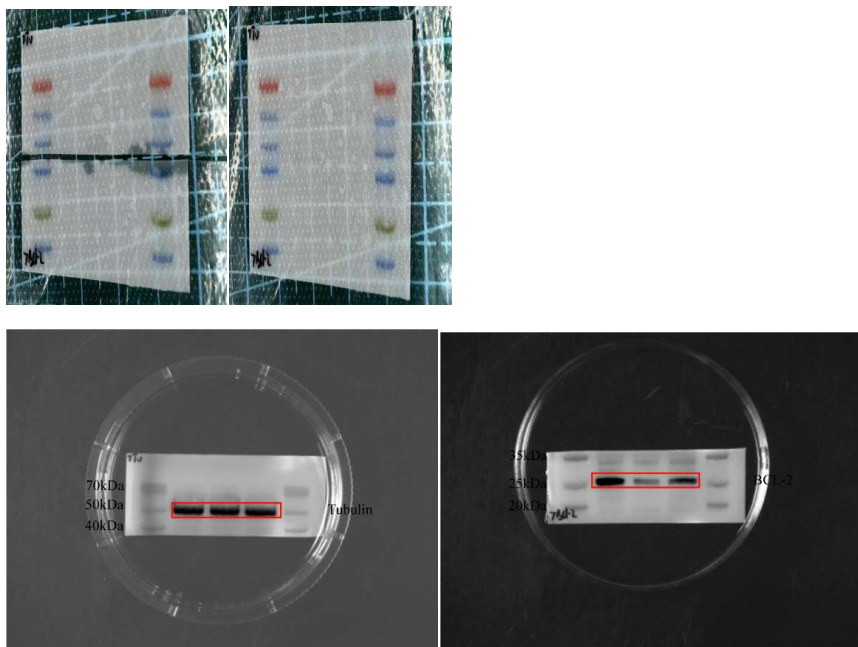
## WB, apoptin

WB, apoptin,A549,count 1

BAX:

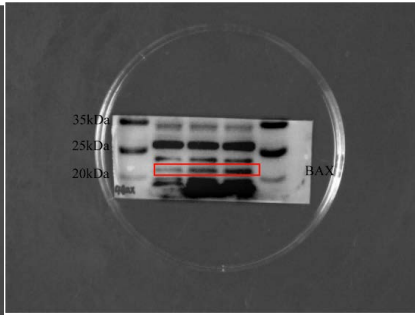
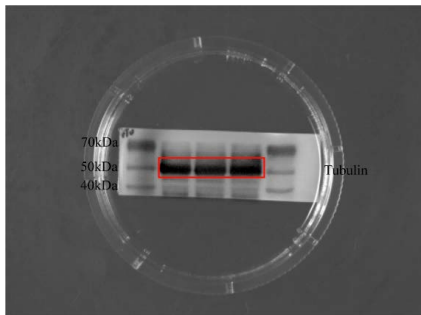
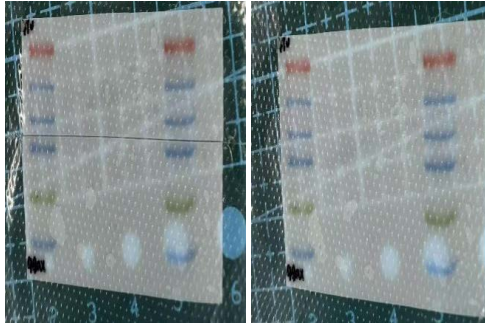


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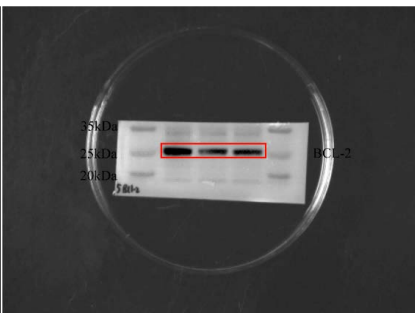
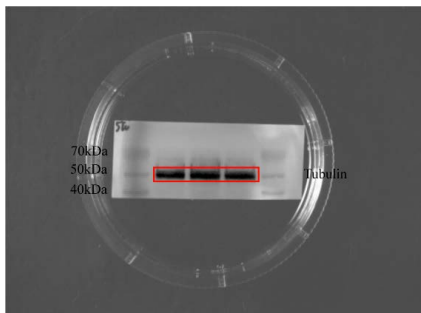
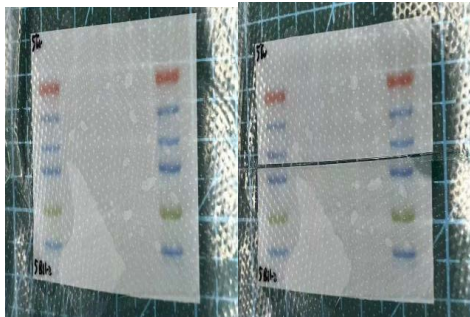


WB, apoptin,A549,count 2

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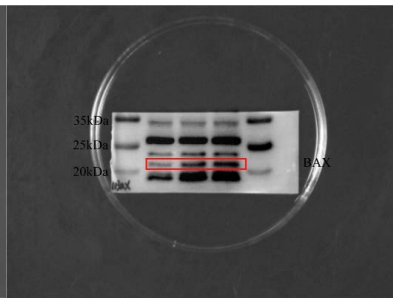
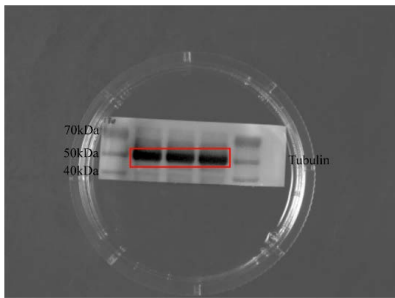
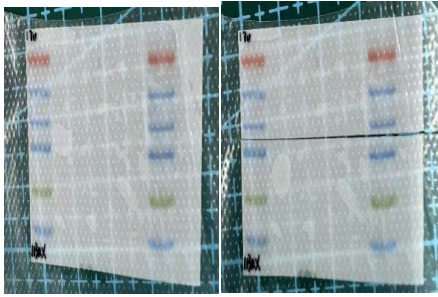


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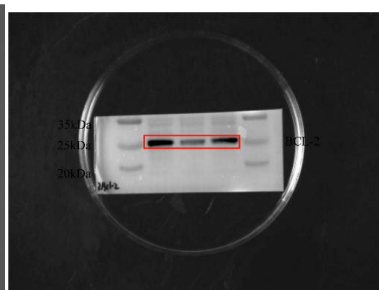
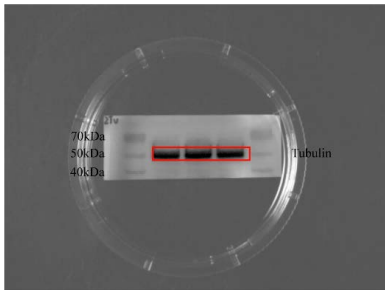
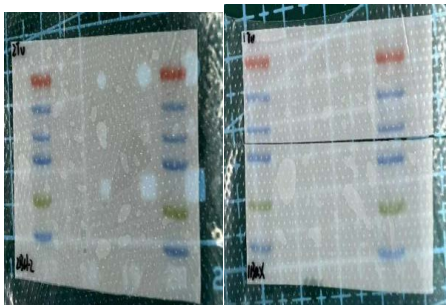


WB, apoptin,A549,picture

BAX:

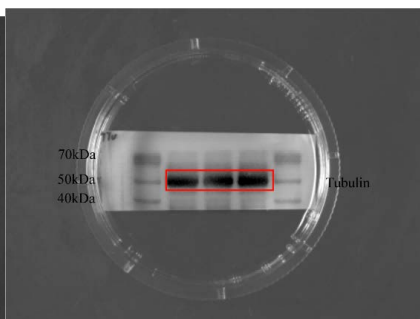
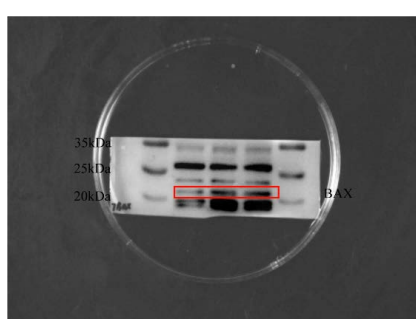
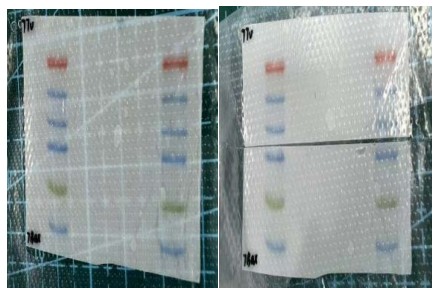


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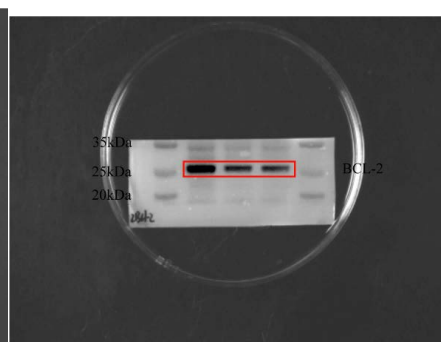
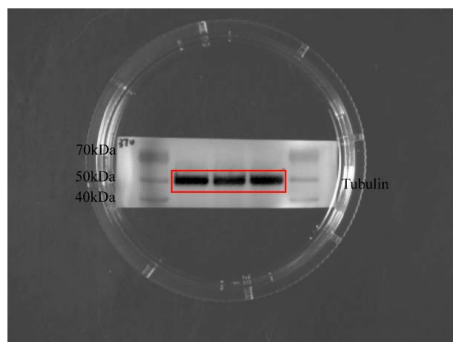
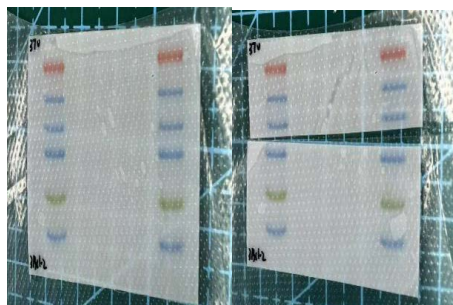


WB, apoptin,H1299,count 1

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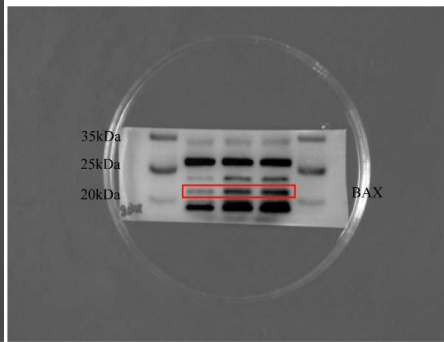
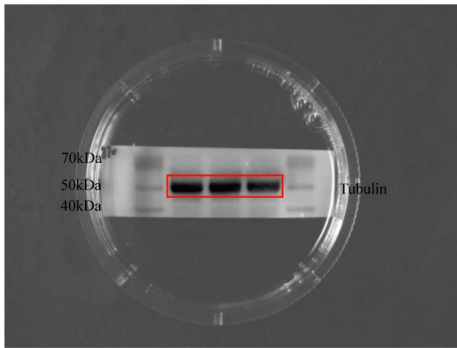
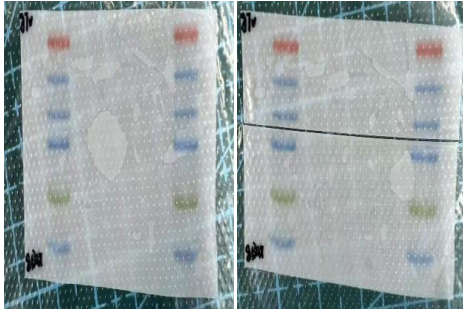


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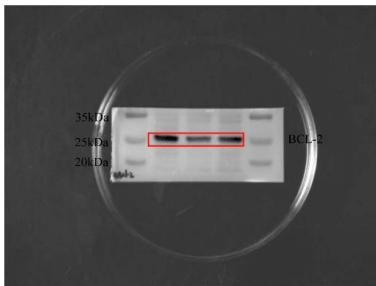
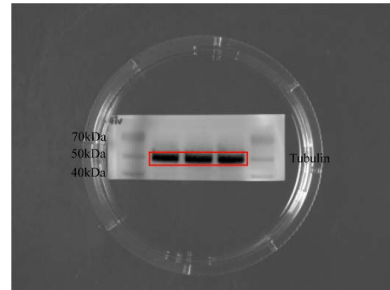
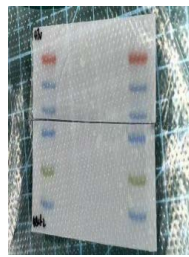
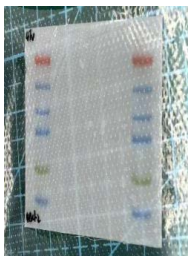


WB, apoptin,H1299,count 2

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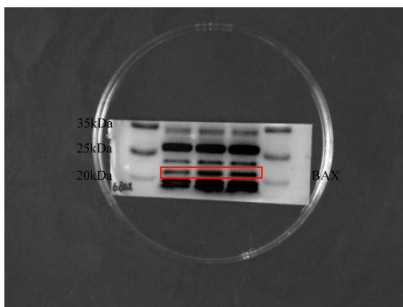
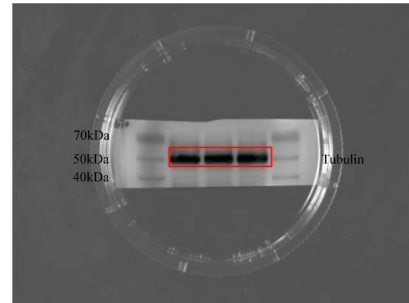
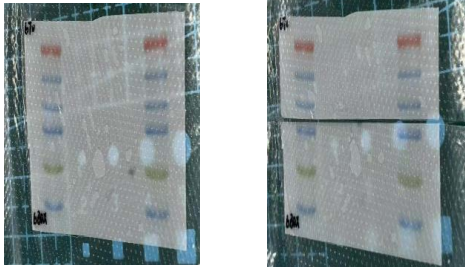


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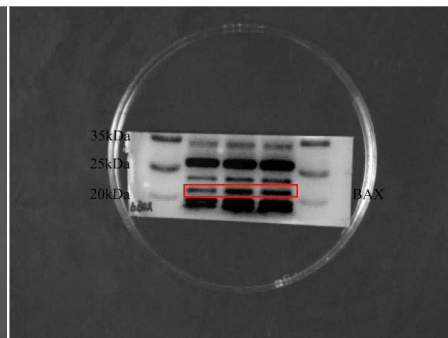
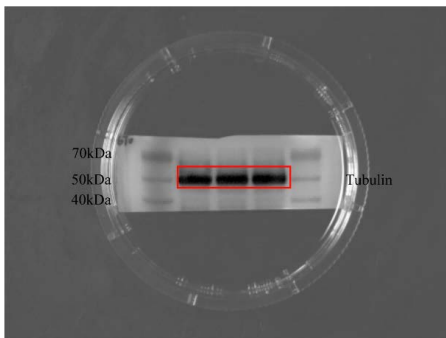
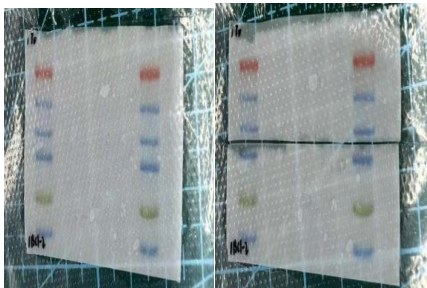


WB, apoptin, H1299, picture

BAX:



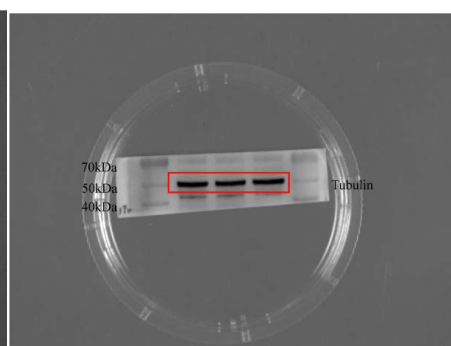
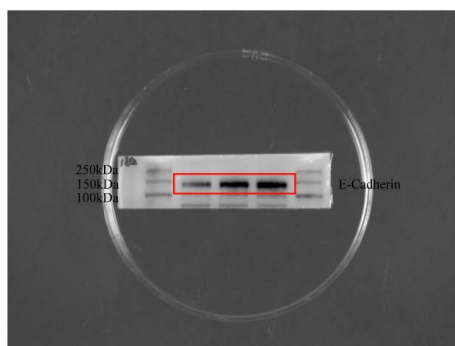
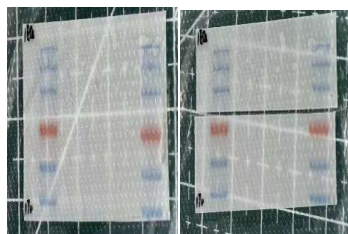
BCL-2:



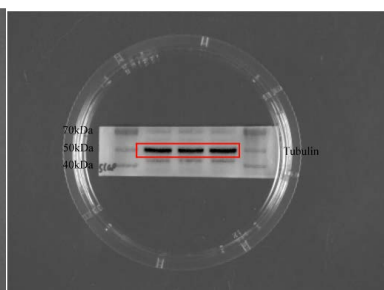
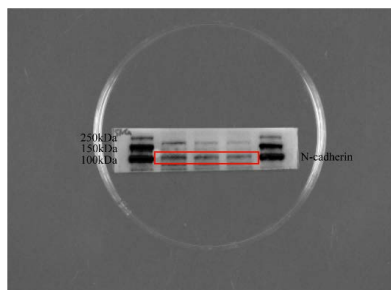
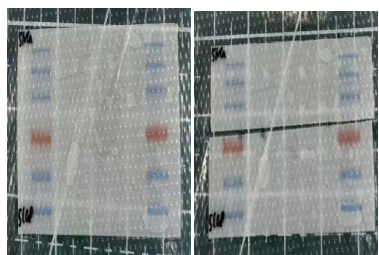
## WB, EMT

WB, EMT,A549,count 1

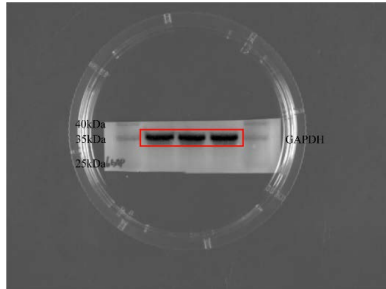
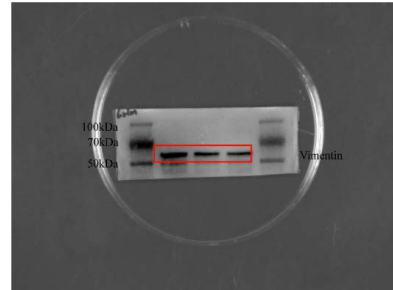
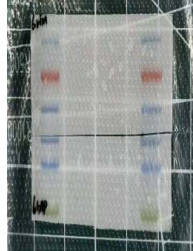
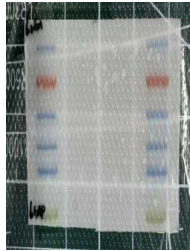
E-Ca:



N-Ca:

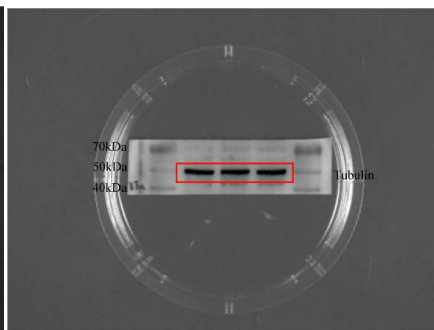
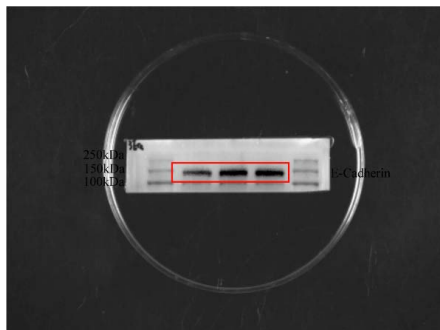
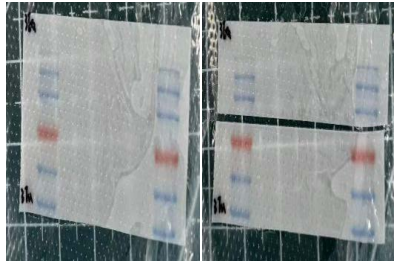


Vimentin:

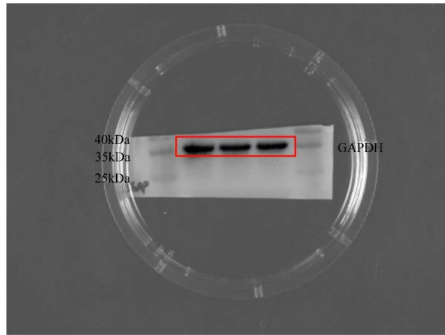
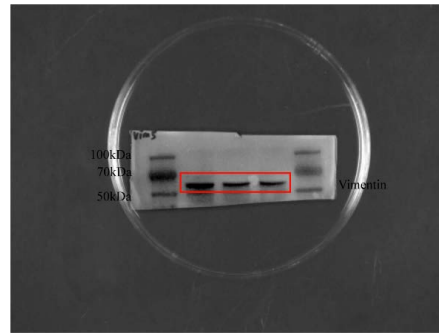
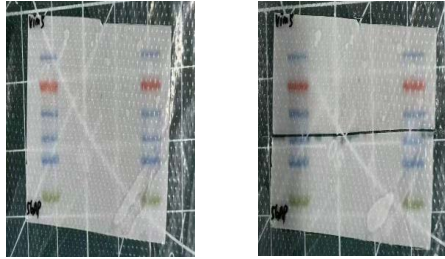


WB, EMT,A549,count 2

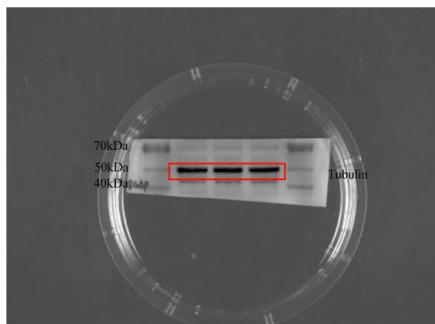
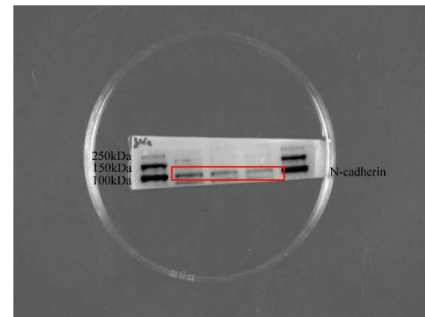
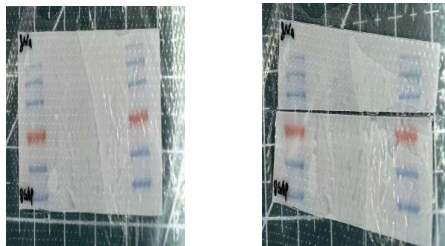
E-Ca:



Vimentin:

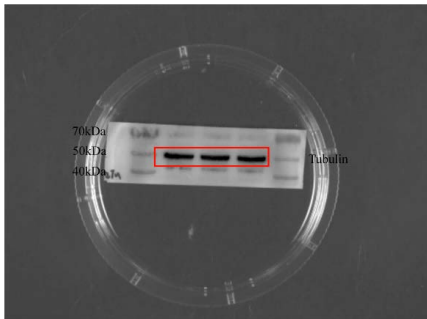
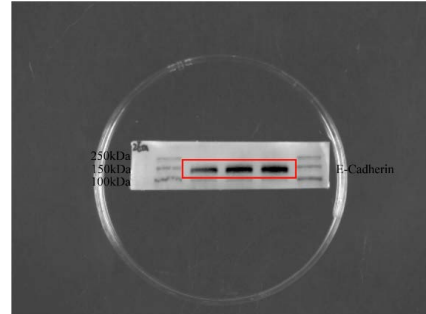
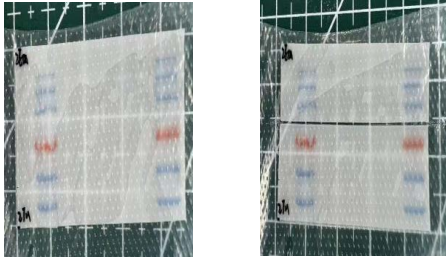


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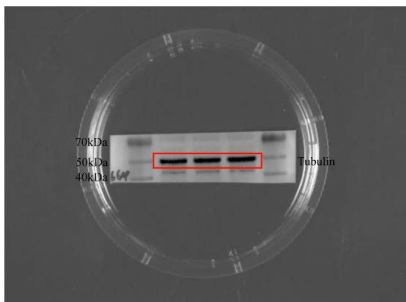
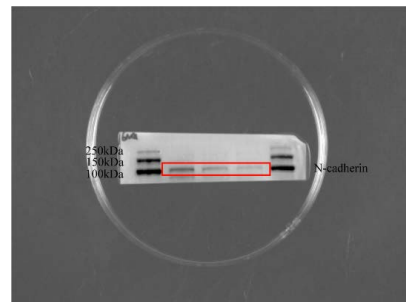
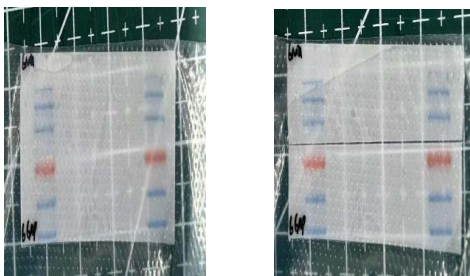


WB, EMT,A549,picture

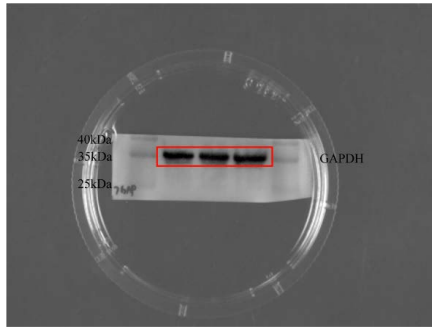
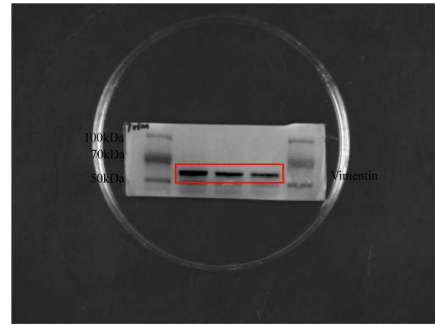
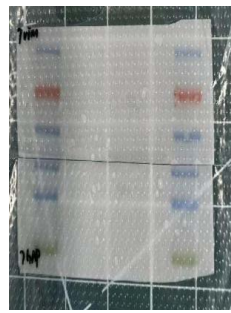
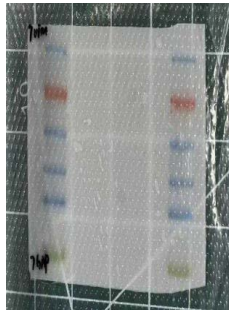
E-Ca:



N-Ca:

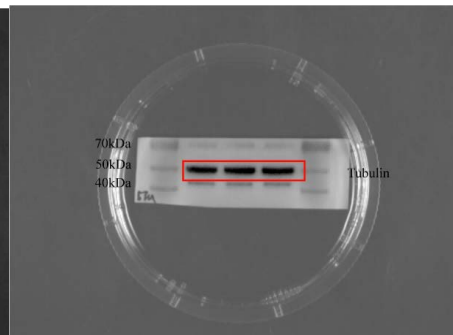
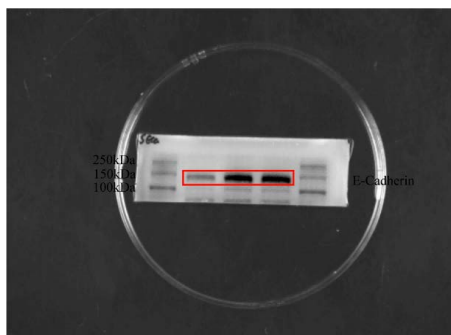
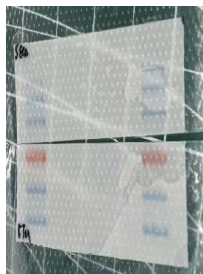


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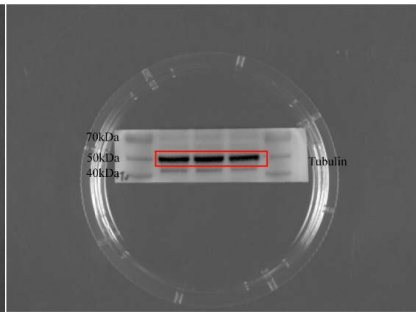
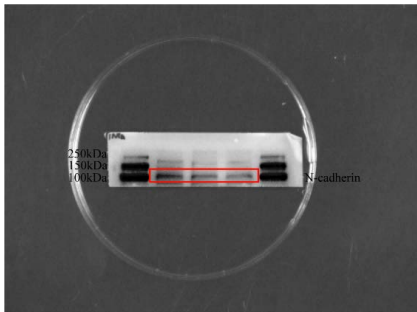
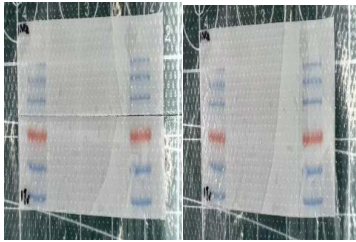


WB, EMT,H1299,count 1

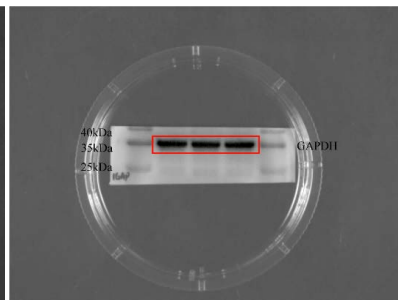
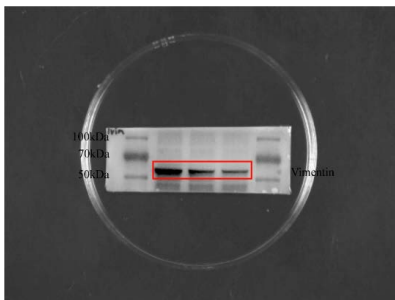
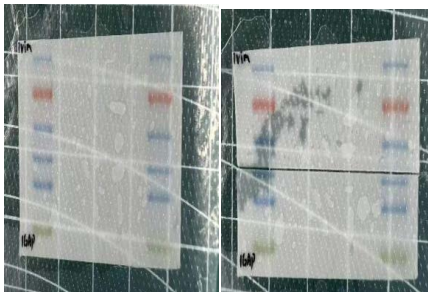
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N-Ca:

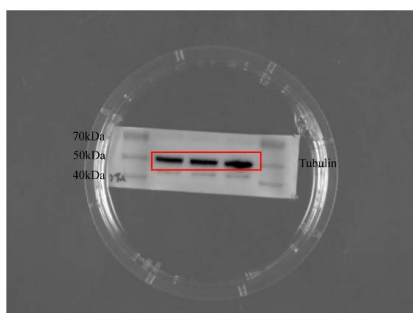
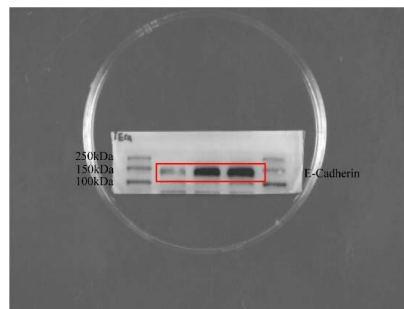
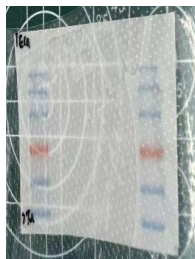


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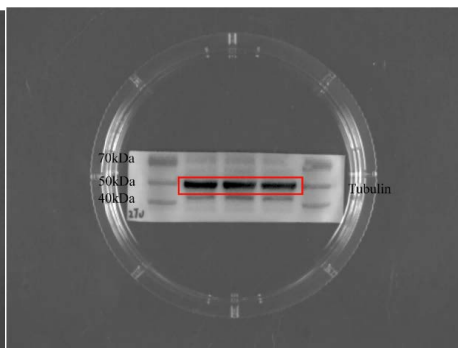
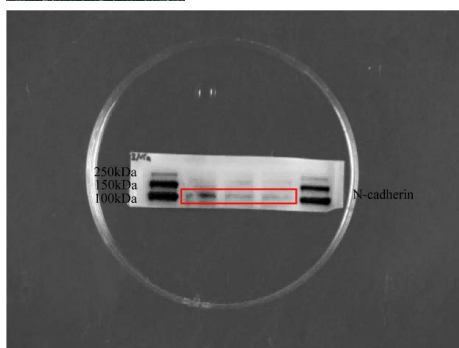
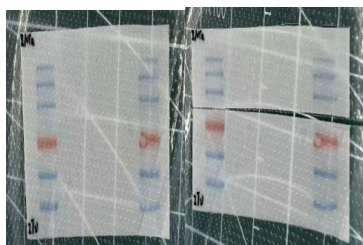


WB, EMT,H1299,count 2

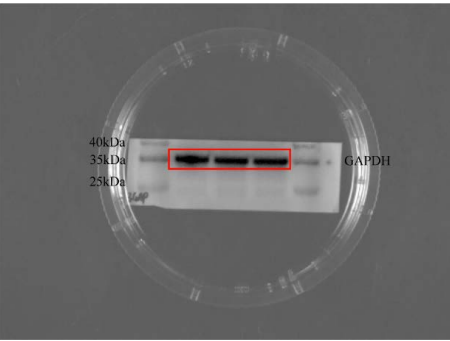
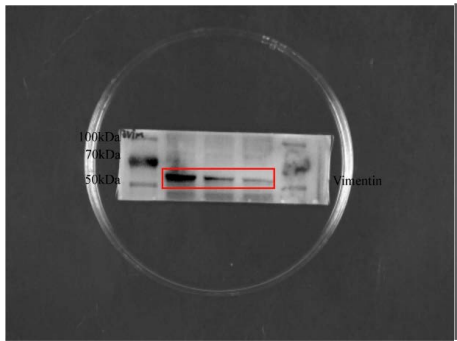
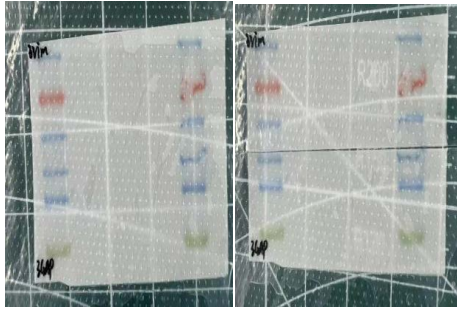
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N-Ca:

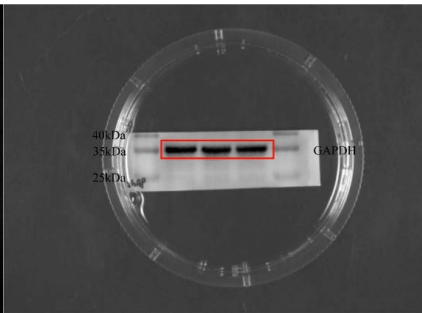
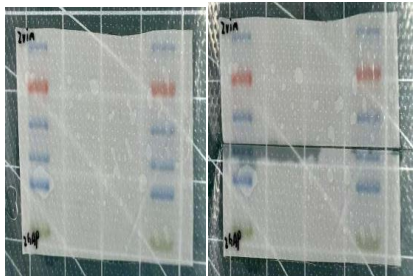


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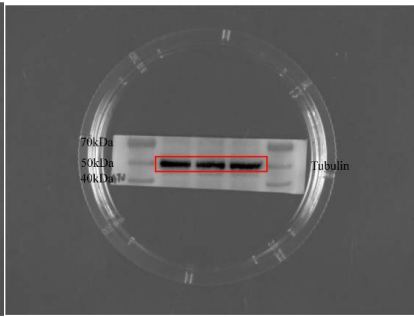
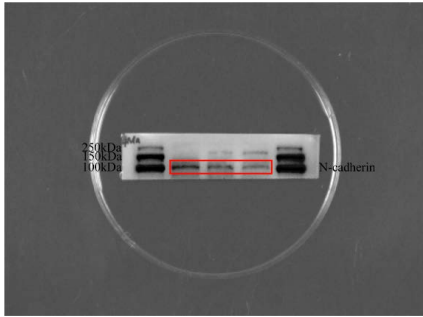
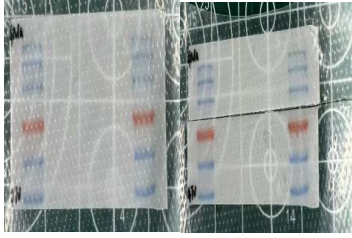


WB, EMT,H1299,picture

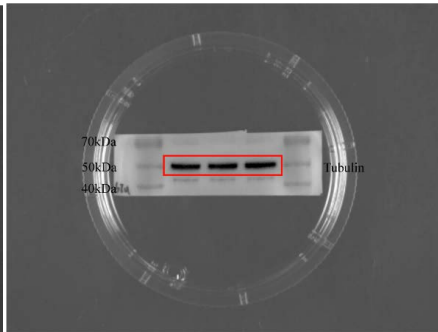
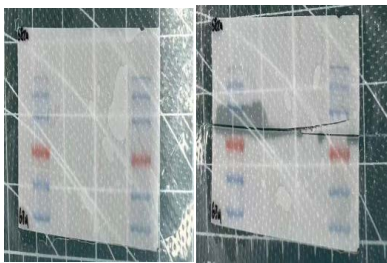
Vimentin:



N-Ca:

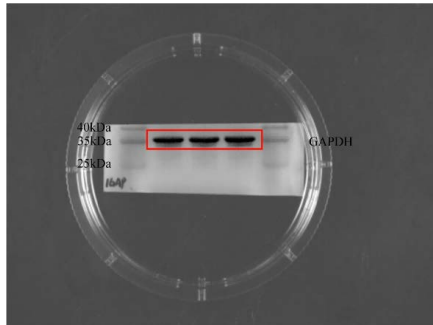
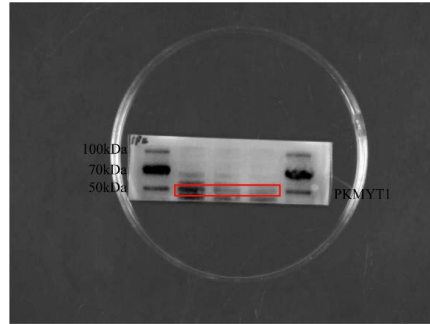
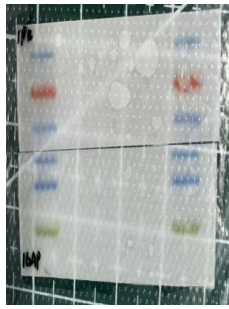
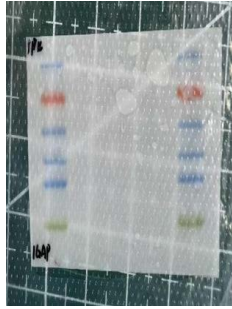


E-Ca:

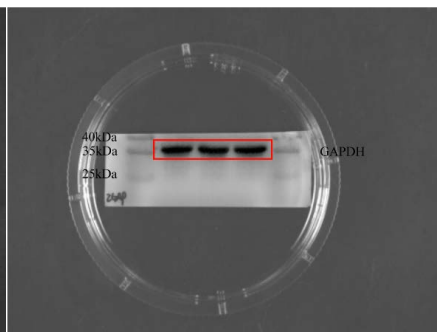
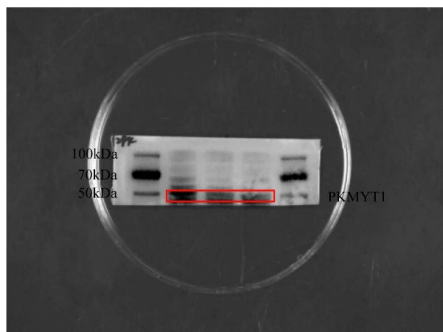
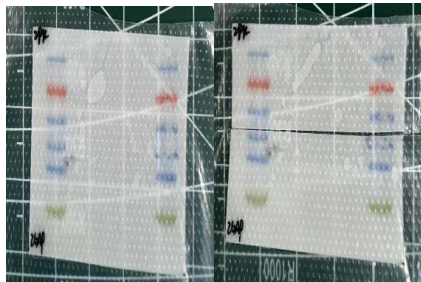


## WB,H1299 knock-down

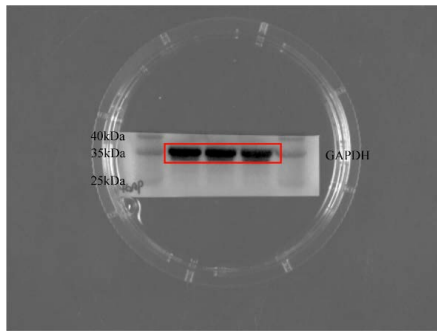
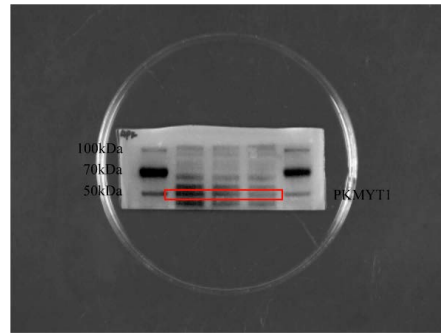
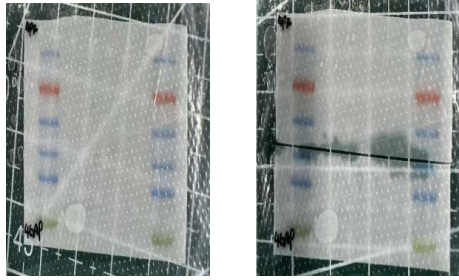
WB,H1299 knock-down,count1



WB,H1299 knock-down,count2

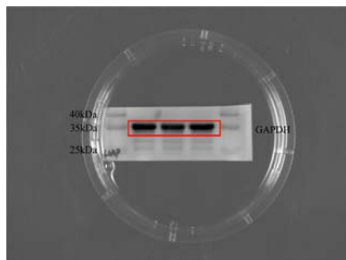
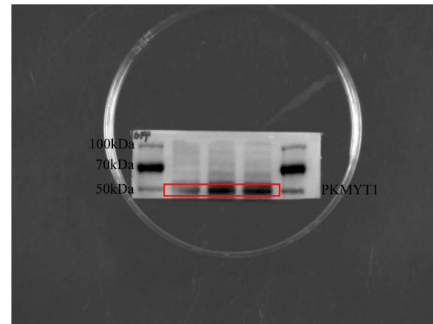
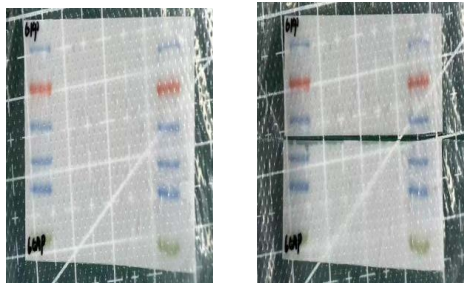


WB,H1299 knock-down,picture

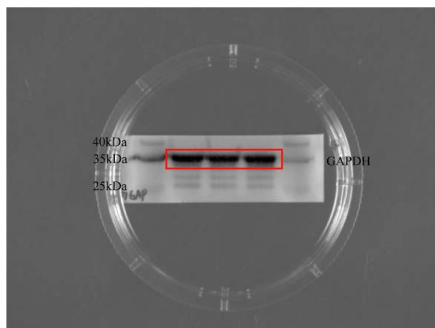
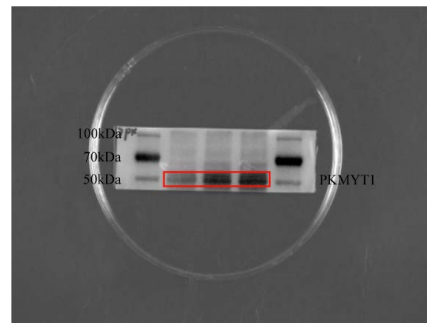
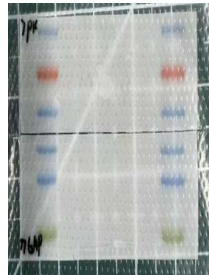
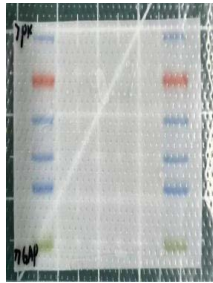


**WB,normal and cancer**

WB,normal and cancer,count 1 6



WB,normal and cancer,count 2 7



WB,normal and cancer,picture 5

