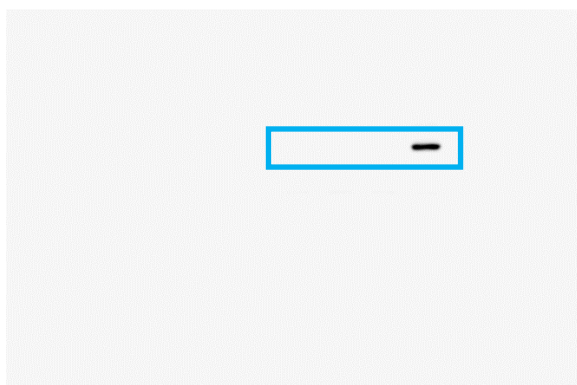


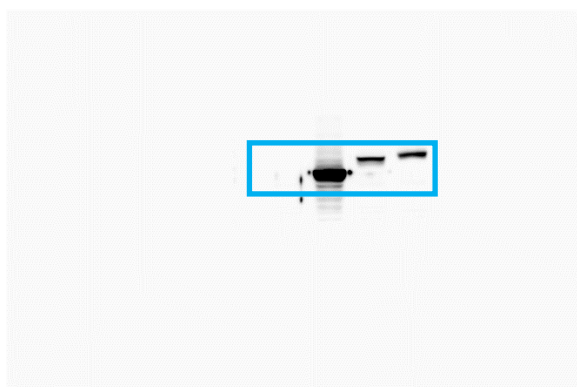
Supplementary information

Figure 1C

GFP



luciferase



GAPDH

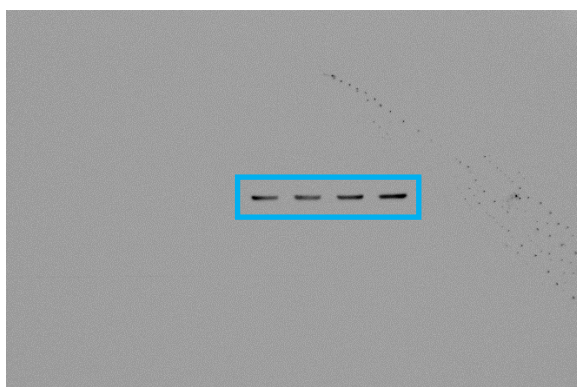
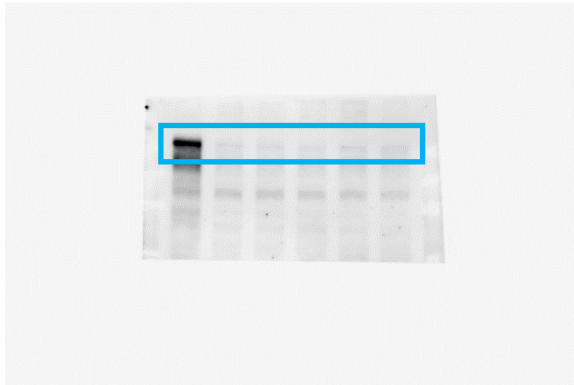
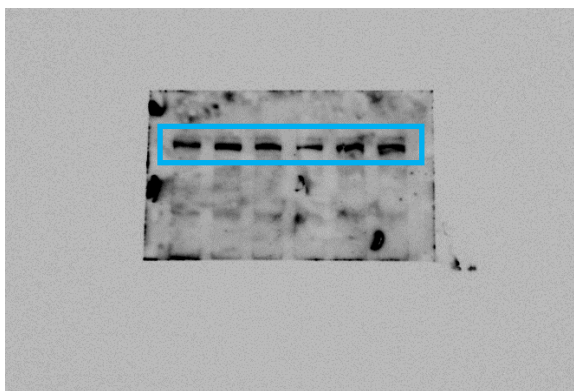


Figure 1F

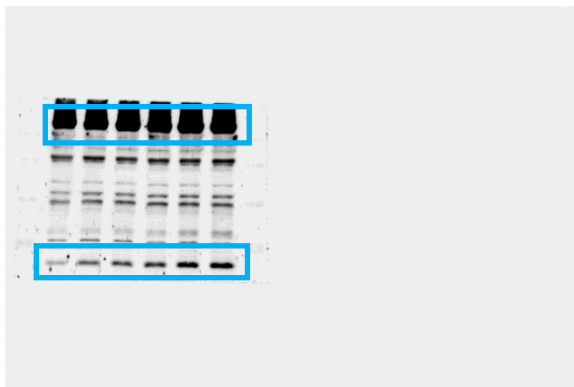
p-ABL



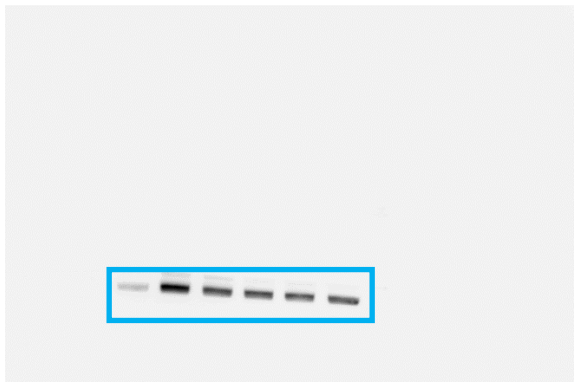
T-ABL



NIADS



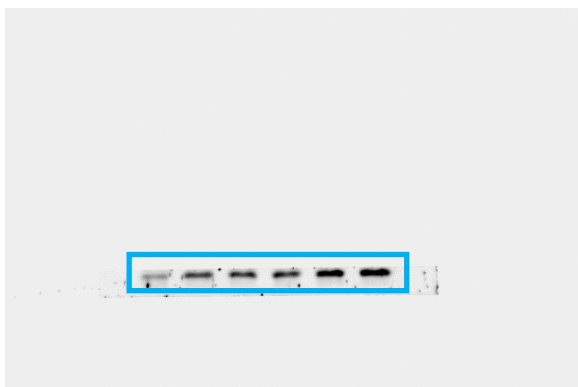
c-PARP



c-caspase 3



P21



P27



GAPDH

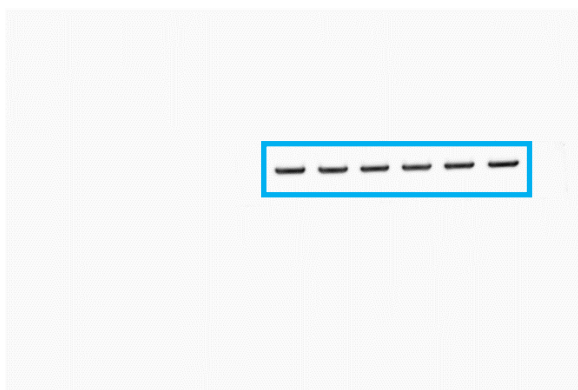
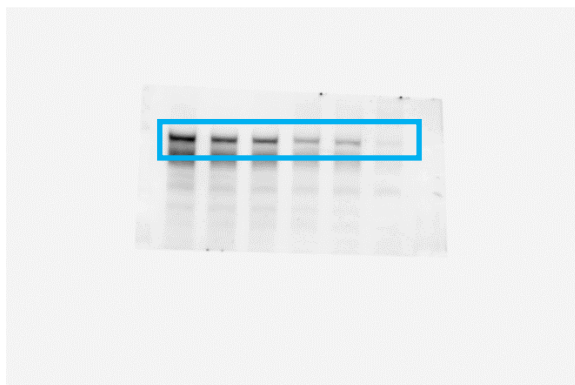
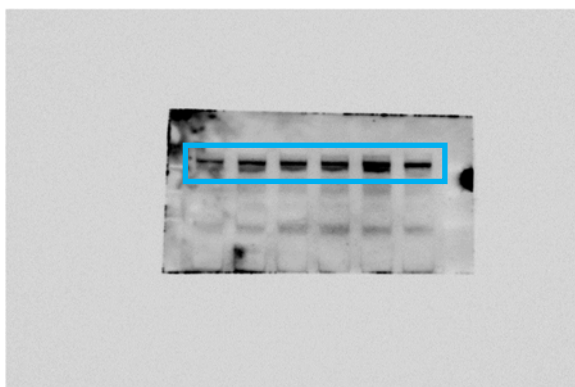


Figure 1G

p-ABL



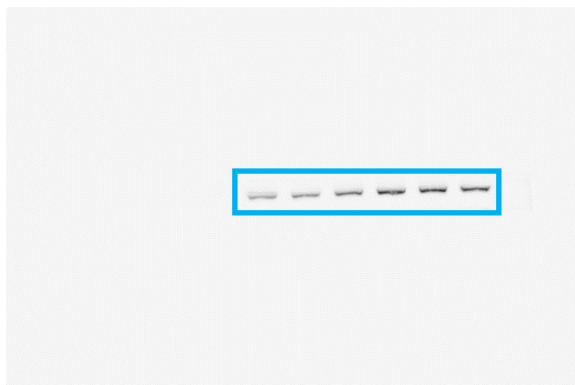
T-ABL



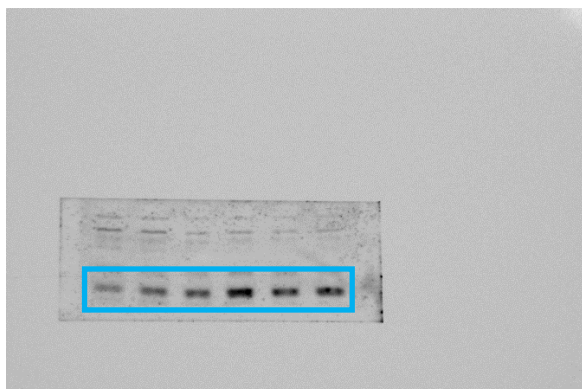
NIADS



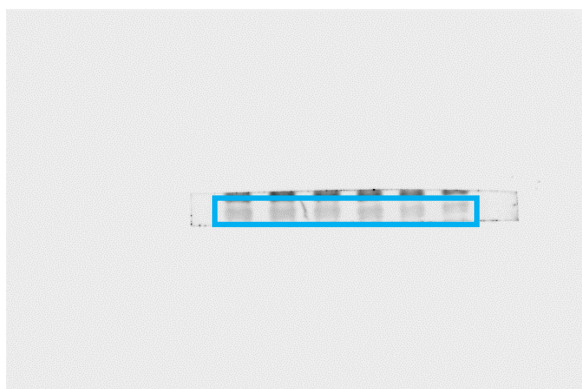
c-PARP



c-caspase 3



P21



P27



GAPDH

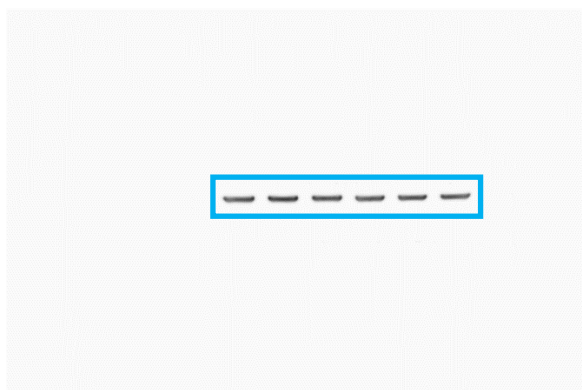
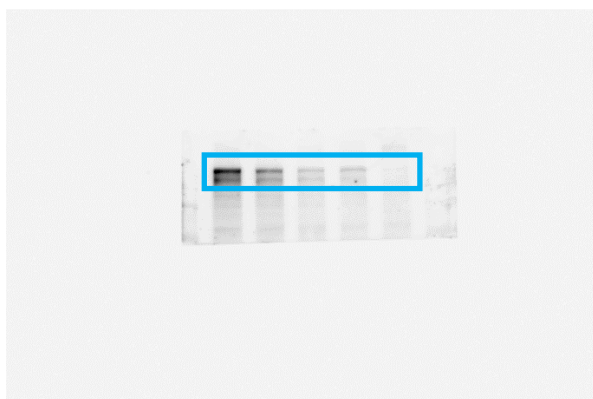
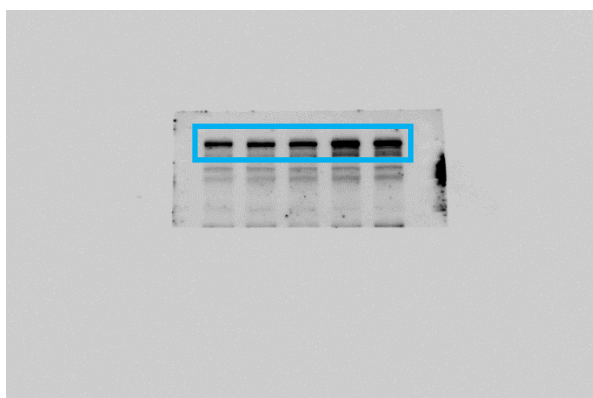


Figure 2D

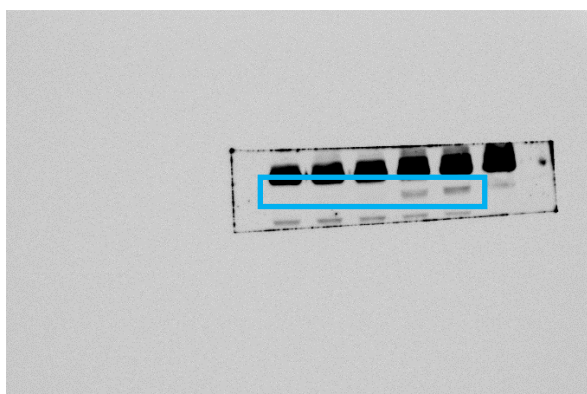
p-ABL



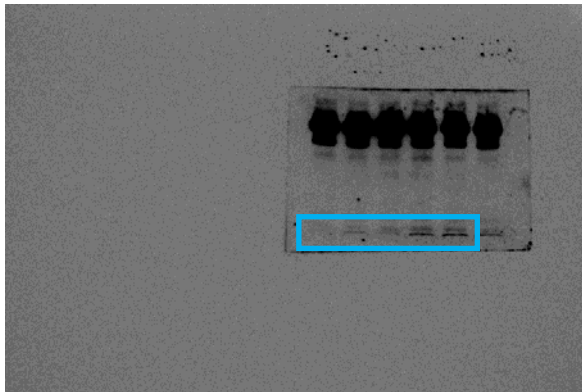
T-ABL



c.PARP



c.Caspase-3



GAPDH

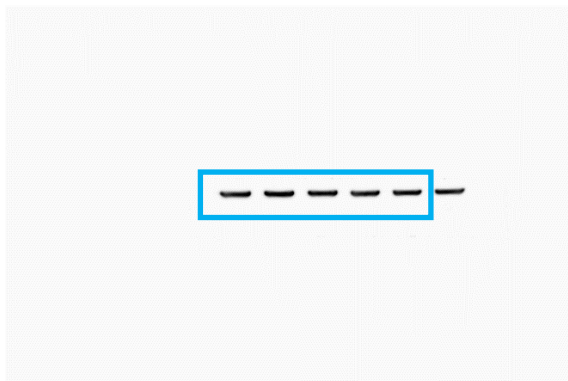
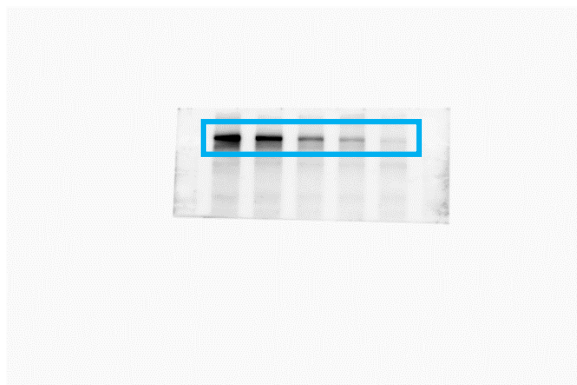
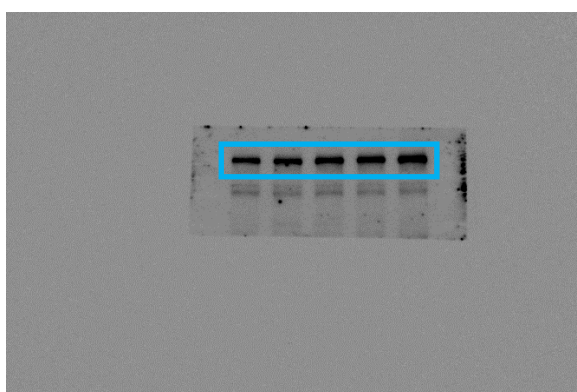


Figure 2E

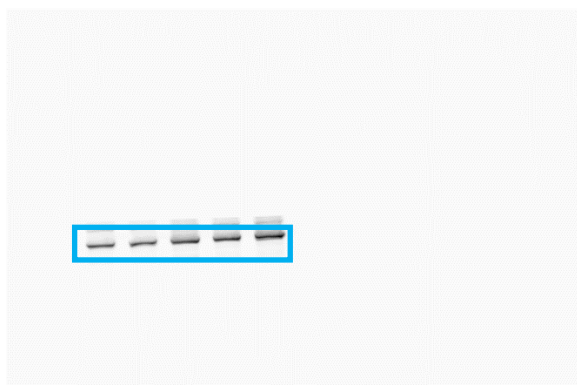
p-ABL



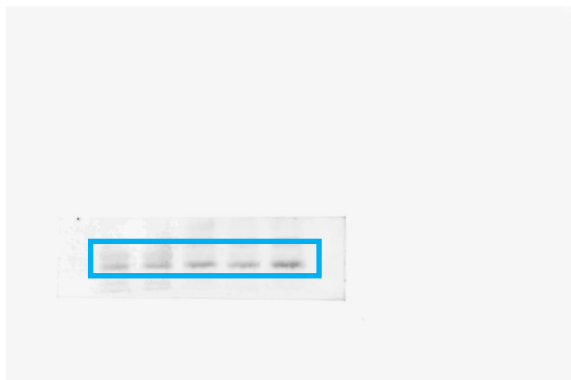
T-ABL



c.PARP



c.Caspase-3

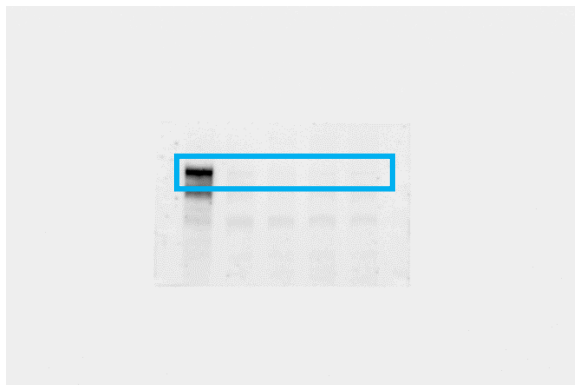


GAPDH

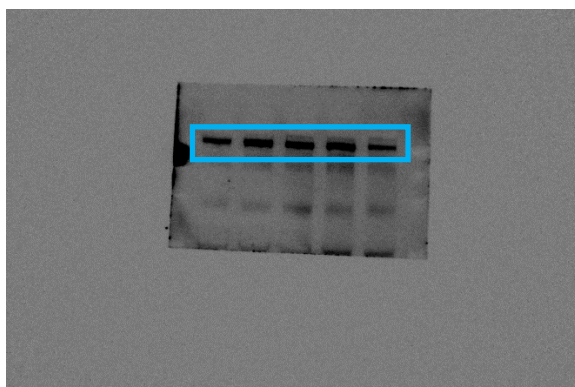


Figure 2F

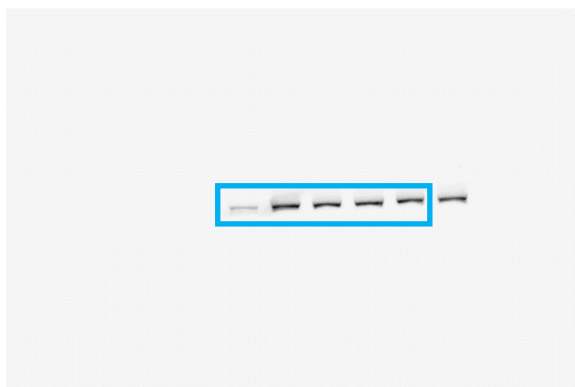
p-ABL



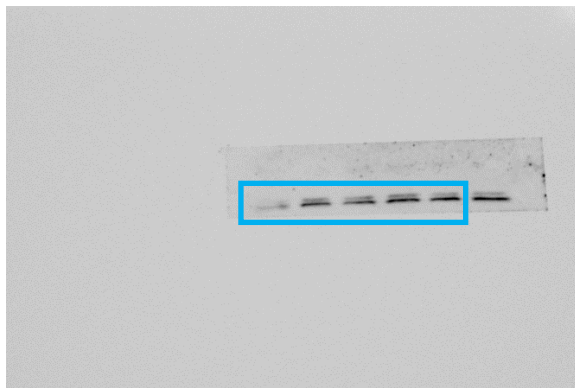
T-ABL



c.PARP



c.Caspase-3



GAPDH

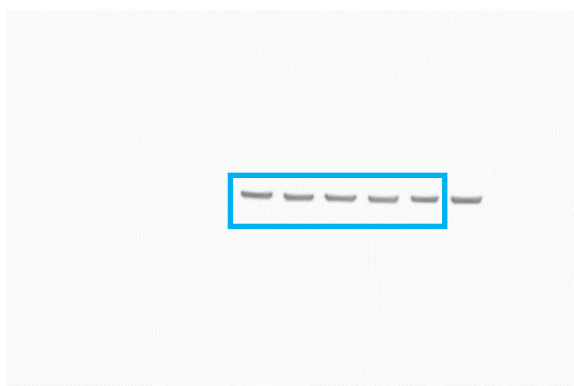
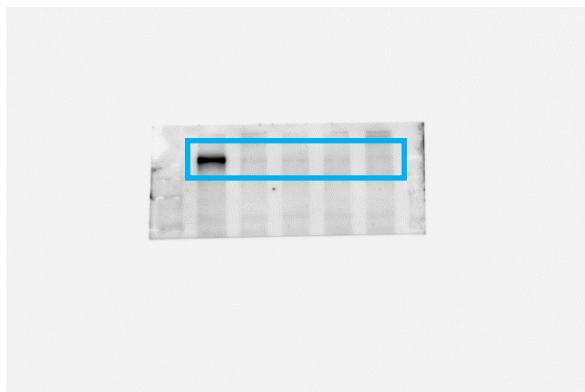
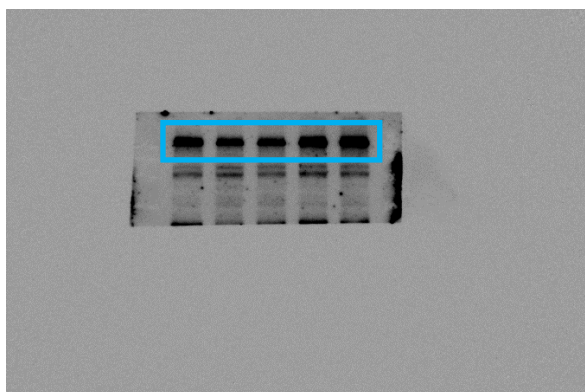


Figure 2G

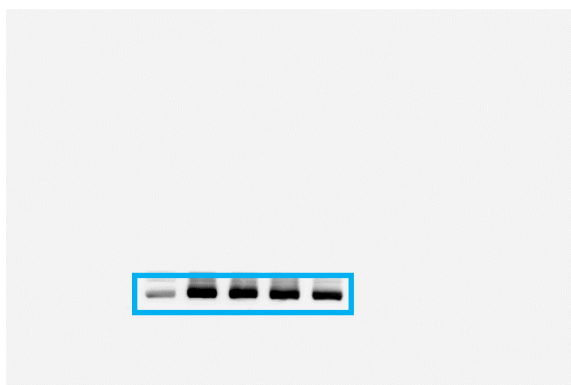
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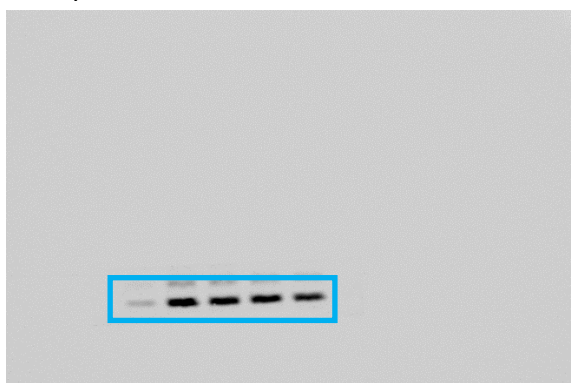
T-ABL



c.PARP



c.Caspase-3



GAPDH

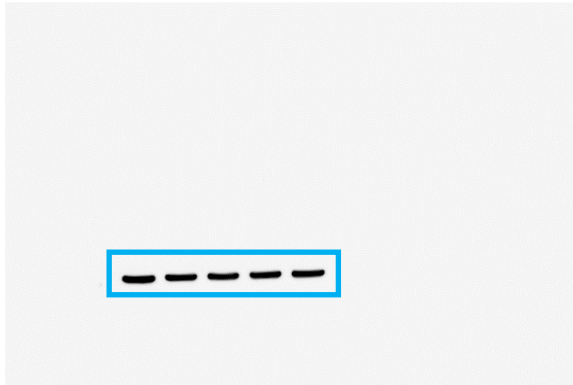
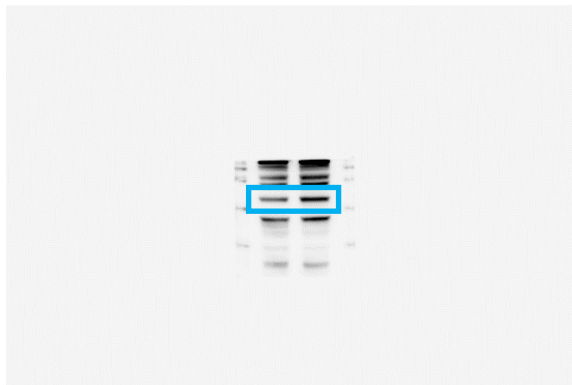
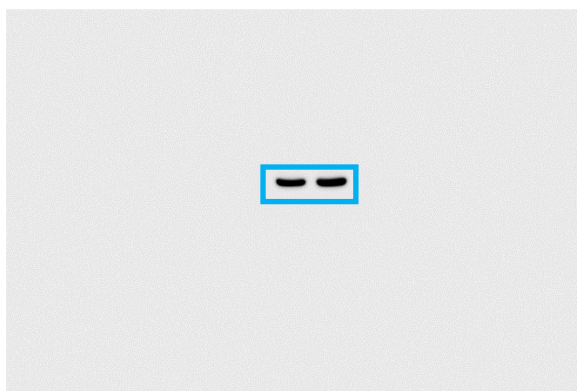


Figure 2J

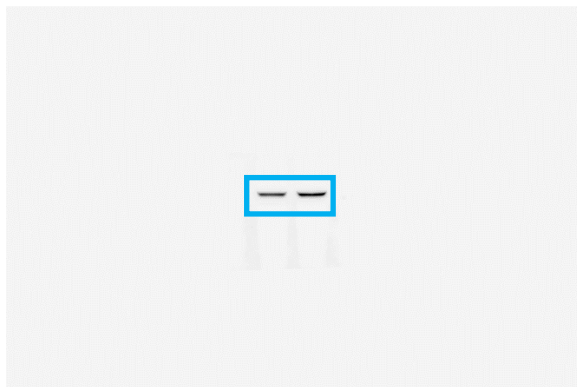
IL6R



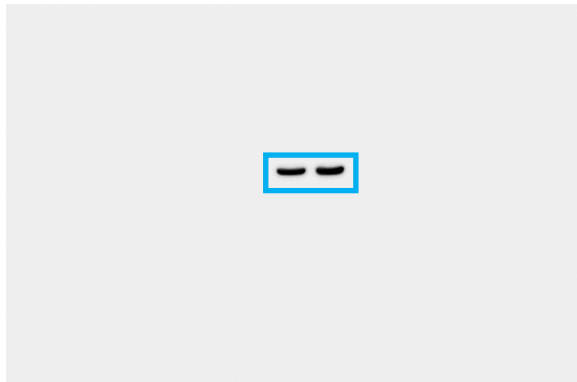
GAPDH



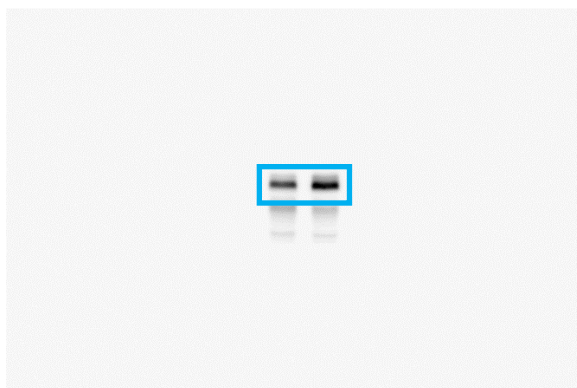
IL7R



GAPDH



MYC



GAPDH

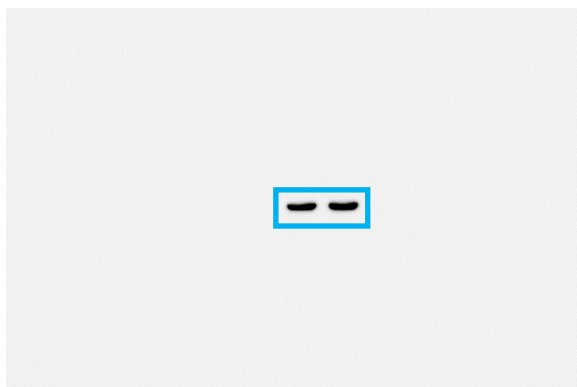
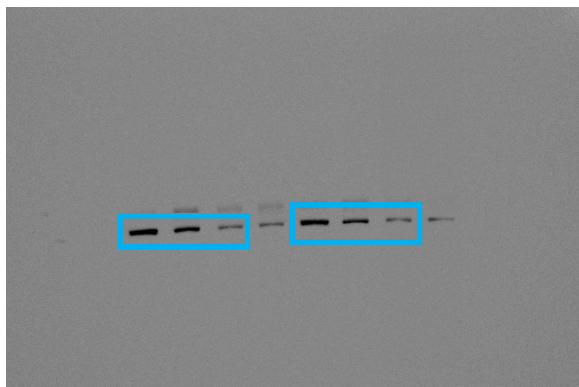
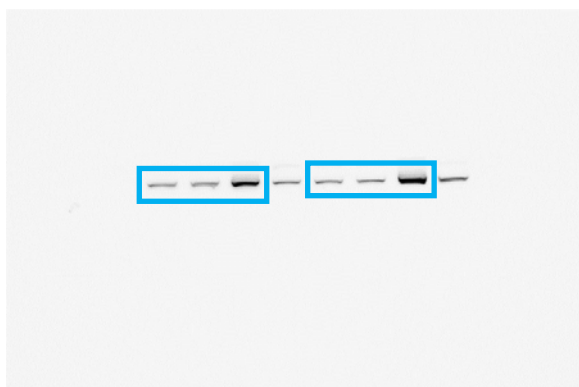


Figure 4B

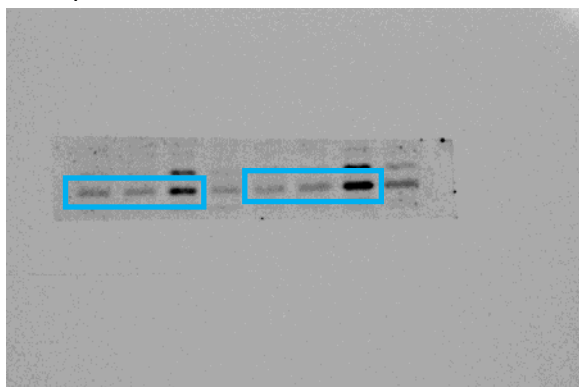
IL6R



c.PARP



c.Caspase-3



GAPDH

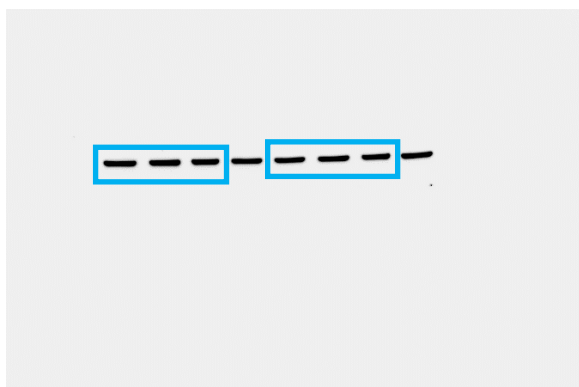
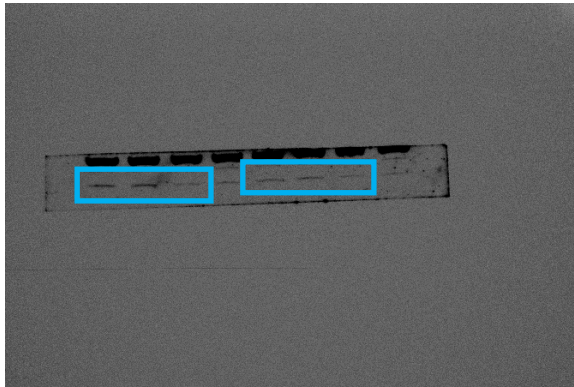
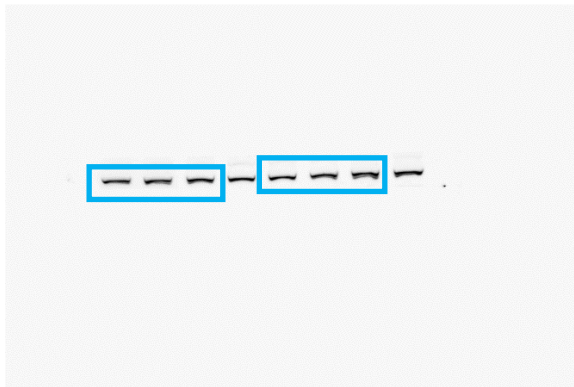


Figure 4C

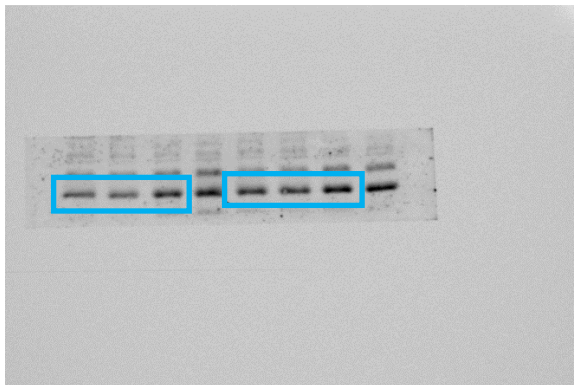
IL7R



c.PARP



c.Caspase-3



GAPDH

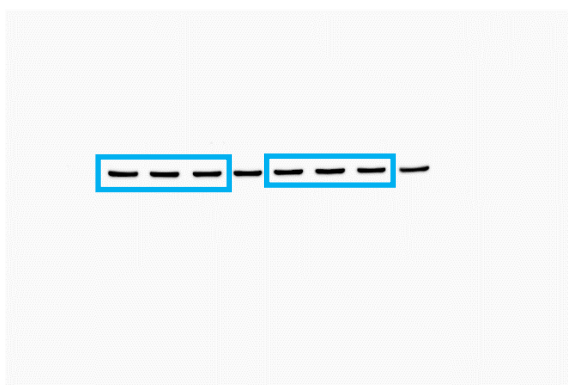
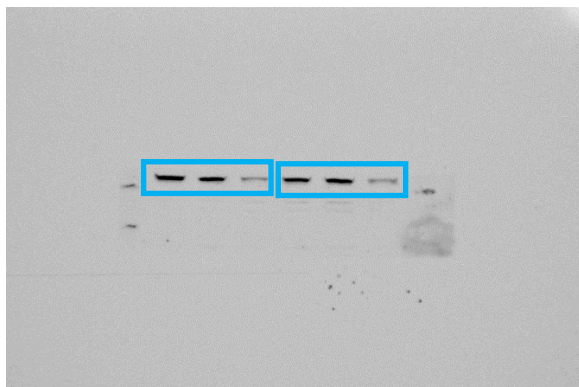


Figure 4D

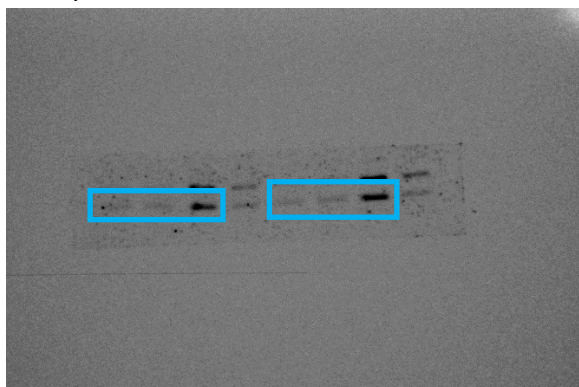
MYC



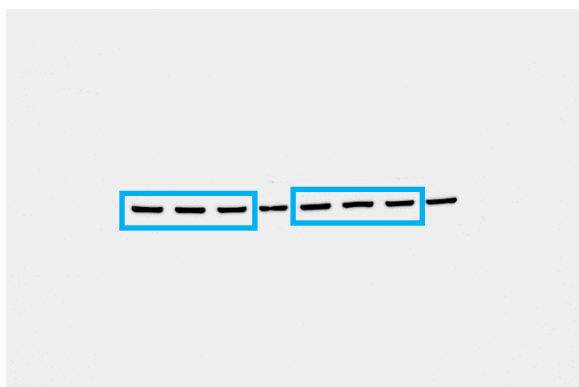
c.PARP



c.Caspase-3



GAPDH



DNA alignment

K562 and K562-IR BCR12-ABL10

Forward sequence

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Matrix: EDNAFULL
Gap penalty: 2.0
Extend penalty: 2.0
Score: 5222.0
K562 length:1050
K562-IR length:1050
Alignment length: 1054
Identity: 1046/1054 (99.24%)
Similarity: 1046/1054 (99.24%)
Gaps: 8/1054 (0.76%)

1      GGAGTCTCCGGGGGCTCTATGGGTTTCTGAATGTCATCGTCCACTCAGCCACTGGA 60
1      GGAGTCTCCGGGGGCTCTATGGGTTTCTGAATGTCATCGTCCACTCAGCCACTGGA 59
61     TTTAAGCAGAGTTTCAAAAGCCCTTCAGCGGCCAGTAGCATCTGACTTTGAGCCTCAGGGT 120
60     TTTAAGCAGAGTTTCAAAAGCCCTTCAGCGGCCAGTAGCATCTGACTTTGAGCCTCAGGGT 119
121    CTGAGTGAAAGCCGCTCGTTGGAACTCCAAGGAAAAACCTTCTCGCTGGACCCAGTGAAAAAT 180
120    CTGAGTGAAAGCCGCTCGTTGGAACTCCAAGGAAAAACCTTCTCGCTGGACCCAGTGAAAAAT 179
181    GACCCCAACCTTTTCTGTTGCACTGTATGATTTTGTGGCCAGTGGAGATAACACTCTAAGC 240
180    GACCCCAACCTTTTCTGTTGCACTGTATGATTTTGTGGCCAGTGGAGATAACACTCTAAGC 239
241    ATAACCTAAAGGTGAAAAAGCTCCGGGTCTTAGGCTATTAATCACAATGGGGAATGGTGTGAA 300
240    ATAACCTAAAGGTGAAAAAGCTCCGGGTCTTAGGCTATTAATCACAATGGGGAATGGTGTGAA 299
301    GCCCCAAACCAAAAAATGGCCAAAGGCTGGGTCCCAAGCAACTACATCACGCCAGTCAACAGT 360
300    GCCCCAAACCAAAAAATGGCCAAAGGCTGGGTCCCAAGCAACTACATCACGCCAGTCAACAGT 359
361    CTGGAGAAAACTCTCTGGTACCATGGGCTGTGTCCCGCAATGCCGCTGAGTATCTGCTG 420
360    CTGGAGAAAACTCTCTGGTACCATGGGCTGTGTCCCGCAATGCCGCTGAGTATCTGCTG 419
421    AGCAGCGGGATCAATGGCAGCTTCTTGGTGCGTGAGAGTGAGAGCAGTCTTGCCAGAGG 480
420    AGCAGCGGGATCAATGGCAGCTTCTTGGTGCGTGAGAGTGAGAGCAGTCTTGCCAGAGG 479
481    TCCATCTCGCTGAGATACGAAGGGAGGGTGTACCATTAACAGGATCAACACTGCTTCTGAT 540
480    TCCATCTCGCTGAGATACGAAGGGAGGGTGTACCATTAACAGGATCAACACTGCTTCTGAT 539
541    GGCAAGCTCTACGTCTCCTCCGAGAGCGCTTCAACACCCCTGGCCGAGTTGGTTTCATCAT 600
540    GGCAAGCTCTACGTCTCCTCCGAGAGCGCTTCAACACCCCTGGCCGAGTTGGTTTCATCAT 599
601    CATTCAACGGTGGCCGACGGGCTCATCACACGCTCCATTATCCAGCCCCAAAGCGCAAC 660
600    CATTCAACGGTGGCCGACGGGCTCATCACACGCTCCATTATCCAGCCCCAAAGCGCAAC 659
661    AAGCCCCACTGTCTATGGTGTGTCCCCCAACTACGACAAGTGAGGAGATGGAACGCACGGAC 720
660    AAGCCCCACTGTCTATGGTGTGTCCCCCAACTACGACAAGTGAGGAGATGGAACGCACGGAC 719
721    ATCACCATGAAGCACAAAGCTGGGCGGGGGCCAGTACGGGGAGGTGTACGAGGGCGTGTGG 780
720    ATCACCATGAAGCACAAAGCTGGGCGGGGGCCAGTACGGGGAGGTGTACGAGGGCGTGTGG 779
781    AAGAAATACAGCCTGACGGTGGCCGTGAAGAGCTTGAAGGAGGACACCATGGAGGTGGAA 840
780    AAGAAATACAGCCTGACGGTGGCCGTGAAGAGCTTGAAGGAGGACACCATGGAGGTGGAA 839
841    GAGTTCTTGAAAGAAAGCTGCAAGTATGAAAGAGATCAAAACACCTTAACCTGGTGCAGCTC 900
840    GAGTTCTTGAAAGAAAGCTGCAAGTATGAAAGAGATCAAAACACCTTAACCTGGTGCAGCTC 899
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DNA alignment

K562 and K562-IR BCR12-ABL10

Reverse sequence

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Matrix: EDNAFULL
Gap penalty: 2.0
Extend penalty: 2.0
Score: 5190.0
Sequence 1 length:1050
Sequence 2 length:1050
Alignment length: 1057
Identity: 1042/1057 (98.58%)
Similarity: 1042/1057 (98.58%)
Gaps: 14/1057 (1.32%)

1          GCATCTCAGGCACGTCAGTGGTGTCTCTGTGCTCTGCAGCTCT 57
1          GCATCTCAGGCACGTCAGTGGTGTCTCTGTGCTCTGCAGCTCT 59
58  CCTGGAGGCTCTCTGCTCTTGGTGGGCAGCTCTGGGGCCTGCAGCAAGGTACTCACAGCCCC 117
60  CCTGGAGGCTCTCTGCTCTTGGTGGGCAGCTCTGGGGCCTGCAGCAAGGTACTCACAGCCCC 119
118 ACAGGACGCCCTTGTCTTCCAGCTCTCTTTTCACTTCGTCTGAGATACTGGATTCTGGAA 177
120 ACAGGACGCCCTTGTCTTCCAGCTCTCTTTTCACTTCGTCTGAGATACTGGATTCTGGAA 179
178 CATTGTTTCAAAGGCTTGGTGGGATTTAGCAAAAGGAGGGCCGGTCAAGAGGATTTCCACTG 237
180 CATTGTTTCAAAGGCTTGGTGGGATTTAGCAAAAGGAGGGCCGGTCAAGAGGATTTCCACTG 239
238 CCAACATGCTCGCATGAGTTTATAGACCTTCTCTGGGGCAGCCTTCTGGGCGCTCCATGCG 297
240 CCAACATGCTCGCATGAGTTTATAGACCTTCTCTGGGGCAGCCTTCTGGGCGCTCCATGCG 299
298 GTAGTCTCTTCTCTAGCAGCTCATACACCTGGGACAGGTCAAATTCCTGGGTAAGGGGACAT 357
300 GTAGTCTCTTCTCTAGCAGCTCATACACCTGGGACAGGTCAAATTCCTGGGTAAGGGGACAT 359
358 GCCATAGGTAAGCAATTTCCAAAGCAATACTCCAAATGCCAGACGTCGGACTTGATGGA 417
360 GCCATAGGTAAGCAATTTCCAAAGCAATACTCCAAATGCCAGACGTCGGACTTGATGGA 419
418 GAACTTGTGTAGGCGCAGGCTCTCTGGGTGCAGTCCATTTGATGGGGAACCTTGCTCCAGC 477
420 GAACTTGTGTAGGCGCAGGCTCTCTGGGTGCAGTCCATTTGATGGGGAACCTTGCTCCAGC 479
478 ATGGGCTGTGTAGGCTGTCCCTGTATCAACCTGCTCAGGCCAAAAATCAGCTACCTTCAC 537
480 ATGGGCTGTGTAGGCTGTCCCTGTATCAACCTGCTCAGGCCAAAAATCAGCTACCTTCAC 539
538 CAAGTGGTTCTCCCTTACCAGGCAGTTTCTGGGCAGCAAGATCTCTGTGGATGAAGTTTTT 597
540 CAAGTGGTTCTCCCTTACCAGGCAGTTTCTGGGCAGCAAGATCTCTGTGGATGAAGTTTTT 599
598 CTTCTCCAGGTACTCCATGGCTGACGAGATCTGAGTGGCCATGTACAGCAGCACCCAGGC 657
600 CTTCTCCAGGTACTCCATGGCTGACGAGATCTGAGTGGCCATGTACAGCAGCACCCAGGC 659
658 GTTCACCTCCTGCCGGTTGCACTCCCTCAGGTAGTCCAGGAGGTTCCCGTAGGTCATGAA 717
660 GTTCACCTCCTGCCGGTTGCACTCCCTCAGGTAGTCCAGGAGGTTCCCGTAGGTCATGAA 719
718 CTCAGTGATGATATAGAAACGGGGGCTCCCGGGTGCAGACCCCAAGGAGCTGCACCAGGTT 777
720 CTCAGTGATGATATAGAAACGGGGGCTCCCGGGTGCAGACCCCAAGGAGCTGCACCAGGTT 779
778 AGGGTGTTTGTATCTCTTTCATGACTGCAGCTTCTTTCAAGAACTCTTCCACCTCCATGGT 837
780 AGGGTGTTTGTATCTCTTTCATGACTGCAGCTTCTTTCAAGAACTCTTCCACCTCCATGGT 839
838 GTCTCTCTTCAAAGGCTTTCACGGCCACCGTCAAGGCTGTATTTCTTCCACACGCCCTCGTA 897
840 GTCTCTCTTCAAAGGCTTTCACGGCCACCGTCAAGGCTGTATTTCTTCCACACGCCCTCGTA 899
```



Human Cell Line Identification Report

Requester	臺北醫學大學	Receive Date	2024.03.28
Trustee	李嘉華/謝筱巧	Report Date	2024.03.29
Sample Type	☐ Human Cell Line ☒ Human gDNA		
Analysis Type	☐ Comparison between samples ☒ Comparison with DSMZ database		
Sample Name	K562		
Note			

✧ Workflow :



- DNA Extraction : Use DNeasy Blood & Tissue Kit (QIAGEN, 69504) to perform DNA extraction and purification. The detail operation procedure refer kit's User Manual.
- Multiplex PCR : Use AmpFLSTR™ Identifiler™ Plus PCR Amplification Kit (ThermoFisher, 4427368) . The Kit can amplified 16 human STR gene loci. The detail operation procedure refer kit's User Manual.
- Fluorescent Capillary Electrophoresis : The STR PCR product were analyzed with DNA Analyzer 3730XL.
- Data Analysis with GeneMapper v4.0
- STR profiling analysis with **DSMZ** database .

✧ Result :

■ STR loci genotype :

Locus Name	D5S818	D13S317	D7S820	D16S539	vWA	TH01	AMEL	TPOX	CSF1PO
Allele genotype	11.12	8.8	9.11	11.12	16.16	9.3.9.3	XX	8.9	9.10

■ STR loci genotype comparison result :

◆ Matching Algorithm description :

- The human STR profile database includes data sets of 2455 cell lines from ATCC, DSMZ, JCRB and RIKEN.
- The similarity score is calculated.

$$\frac{2 \cdot A_{shared}}{A_{query} + A_{ref}}$$



- Results highlighted in green are usually authentic as long as the cells do not carry a deficiency in DNA mismatch repair (MMR). Results highlighted in yellow indicate a distant relationship when there is a drift of STR alleles in MMR-negative cell lines. Clearly incorrect cell lines are present when the background is red.

◆ **Conclusion :**

Base on comparison with DSMZ database, this human cell line was highly identical with

- K562/Vin (Source : RCB2111) (Similarity 100%)

Similarity	Cell line	Source	Shared	D5S818	D7S820	D13S317	D16S539	vWA	TH01	TPOX	CSF1PO	Amelogenin
		Your query		11, 12	9, 11	8, 8	11, 12	16, 16	9, 3, 9, 3	8, 9	9, 10	X, X
100 %	K562/Vin	RCB2111	9	11, 12	9, 11	8, 8	11, 12	16, 16	9, 3, 9, 3	8, 9	9, 10	X, X

✧ Ref1: STR loci genotype result

技術人員 : 陳柏翰

實驗室主管: 陳素蓮

