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27 **Supplementary Figures 1. A-C** Kaplan-Meier analysis of overall survival (OS)  
 28 performed according to the DDX24 protein levels in cohorts 1 (A), 2 (B), and 3 (C),  
 29 respectively. **D-E** Kaplan-Meier analysis of disease-free survival (DFS) performed  
 30 according to the DDX24 protein levels in cohorts 2 and 3, respectively.

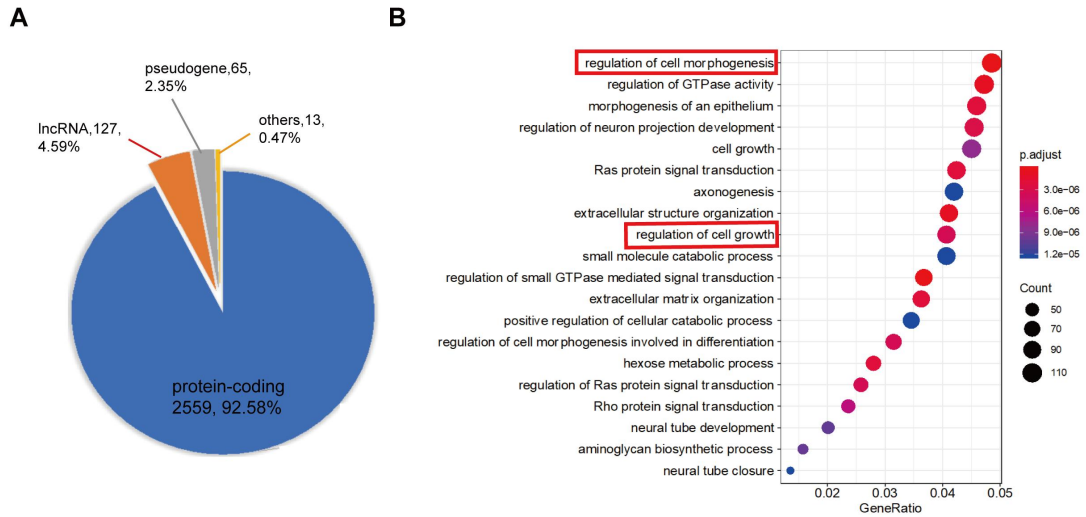
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37 **Supplementary Figure 2. Analysis of RIP-seq using DDX24 antibody. A** Pie chart

38 displayed the RNA distribution from RIP-seq using DDX24 antibody. **B** The top 20 of

39 enriched pathway from RIP-seq.

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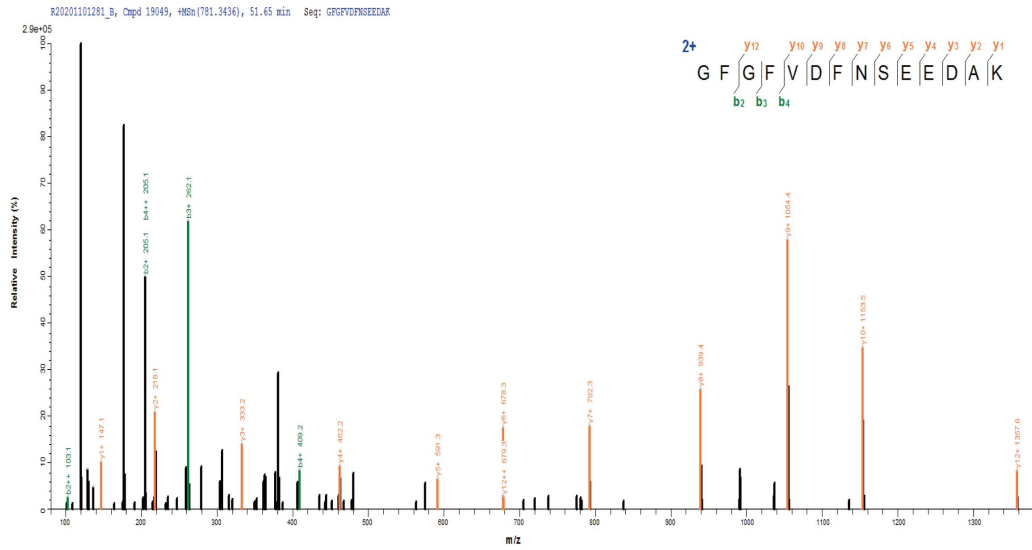
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47 **Supplementary Figure 3. The putative DDX24 targeted protein sequence.**

48 MALDI-TOF/TOF mass spectrometry that was used to identify the putative DDX24

49 targeted protein sequence was GFGFVDFNSEEDAK. The assigned b and y ion peaks

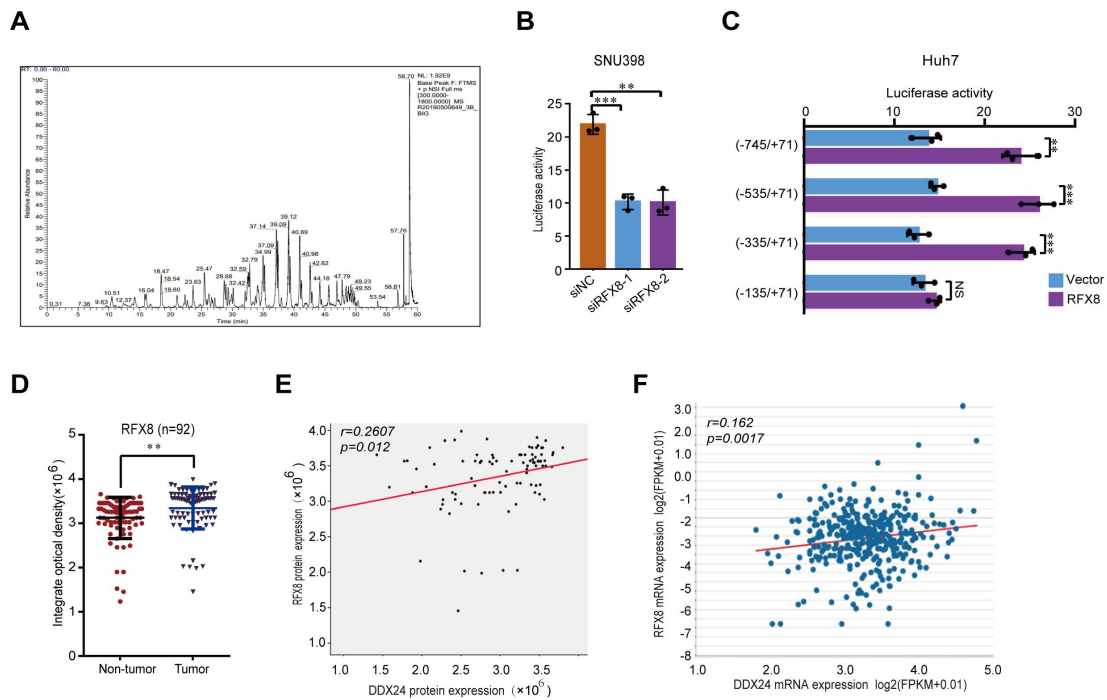
50 on the spectrum are marked with their corresponding m/z values.

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56 **Supplementary Figure 4. MALDI-TOF/TOF mass spectrometry identifying the**

57 **putative DDX24 promoter targeted protein sequence. A** The peak figure of the

58 putative DDX24 promoter-binding protein from MALDI-TOF/TOF mass

59 spectrometry. **B** Relative DDX24 promoter activity in SNU398 cells with RFX8

60 knockdown was determined by dual-luciferase assay. **C** Dual-luciferase reporter

61 assays to determine RFX8 binding region. **D** Expression analysis of RFX8 from the

62 92 HCC tissues and non-tumor tissues (cohort 1). **E** Correlation between RFX8 and

63 DDX24 expression in 92 HCC tissue samples (cohort 1). **F** Correlation between

64 RFX8 and DDX24 expression in 374 HCC patient tissues from the TCGA database.

65 The results are shown as means  $\pm$  SD, \* $p < 0.05$ , \*\*  $p < 0.01$ , \*\*\*  $p < 0.001$ , NS = not

66 significant.

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**Supplementary Table 1. Primer sequences used in the study**

<b>Primer name</b>	<b>Primer sequences</b>
Primers for real-time PCR:	
DDX24	Purchased from GeneCopoeia, Hs-QRP-23370
RFX8	Purchased from GeneCopoeia, Hs-QRP-23954
Flag- sense	5'- AAGTCCGTTCACTCCTAAAGG -3'
Flag- antisense	5'- TCATCGTCATCCTTGTAAGTCGA -3'
LAMB1-sense	5'- ATTCCTGGAGGGAATCCTTG -3'
LAMB1-antisense	5'- TCATTGCTTAAGCCCCAGTG -3'
ITPR1-sense	5'- ACAGCACCACAGACGCAGT -3'
ITPR1-antisense	5'- ATTACGGTCCCCAGCAATTT -3'
CRIM1-sense	5'- GCAATCCCTTTGAGTTTCCA -3'
CRIM1-antisense	5'- CTTCAGGACAACGTGGAGAGA -3'
FBN1-sense	5'-GGCTACCTCCAGCACTACCA -3'
FBN1-antisense	5'- ACATGCACTTGTAGCTCCCC -3'
FBN2-sense	5'- AATCGGAAGCTTCAAATGCC -3'
FBN2-antisense	5'- CAGGAGAAATCCTGCACTCG -3'
TRIO-sense	5'- CTGGAAGACCGGATTCAAGA -3'
TRIO-antisense	5'- AGCTCCTCCAGCCACGTC -3'
DYNC1H1-sense	5'- GTATGCAGAGCCGCTCACTG -3'
DYNC1H1-antisense	5'- CACCTAGTCATTTACGGGG-3'
NC(SEC62)-sense	5'- ACCAATATGATGGGTCACCG -3'
NC(SEC62)-antisense	5'- GCCTTTGCCCACTTTGAATC -3'
Primers for RT-PCR:	
Fragment-1 of DDX24 promoter region-sense	5'- AAGTGAGAGATGTGCGACTC -3'
Fragment-1 of DDX24 promoter region -antisense	5'- ACGTGTGATGAGTGTTTCCTTGT -3'
Fragment-2 of DDX24 promoter region -sense	5'- AGGAACACTCATCACACGTC -3'
Fragment-2 of DDX24 promoter region -antisense	5'- GCTCCCGCACAGTAACGTA -3'
Fragment-3 of DDX24 promoter region -sense	5'- AACTTACGTTACTGTGCGGG -3'
Fragment-3 of DDX24 promoter region -antisense	5'- TCCCGCCCCTATGGCAAA -3'
Fragment-4 of DDX24 promoter region -sense	5'- GGTAGCTGAGTTTGCCATAGG -3'
Fragment-4 of DDX24 promoter region -antisense	5'- CGAGTGAAGAACCTCAGAAAC -3'

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**Supplementary Table 2. The characteristics of antibodies**

<b>Protein</b>	<b>Application</b>	<b>Origin</b>	<b>City/State/Country</b>	<b>Dilution</b>
DDX24	WB, IF	A300697A, Bethyl Laboratories	Montgomery/TX/USA	1:1000 & 1:200
DDX24	IHC, IP	HPA002554, Sigma-Aldrich	St Louis/MO/USA	1:50
RFX8	WB, IHC, IF	TA330886, OriGene Technologies	Rockville/MD/USA	1:1000 & 1:50 & 1:200
LAMB1	WB, IHC	GTX100787, Genetex	San Antonio/TX/USA	1:1000 & 1:100
p-SRC	WB	44-660G, ThermoFisher	Rockford/IL/USA	1:1000
SRC	WB	#2109S, CST	Danvers/MA/USA	1:1000
Histone H3	WB	#4499S, CST	Danvers/MA/USA	1:1000
$\beta$ -actin	WB	#4970S, CST	Danvers/MA/USA	1:1000
GAPDH	WB	#5174S, CST	Danvers/MA/USA	1:1000
NCL(Nucleolin)	WB	#14574, CST	Danvers/MA/USA	1:1000
NCL(Nucleolin)	IP	#14574, CST	Danvers/MA/USA	1:50
FLAG	IP	#14793, CST	Danvers/MA/USA	1:50
FLAG	WB	#14793, CST	Danvers/MA/USA	1:1000

73 WB, Western blotting; IF, Immunofluorescence staining; IP, immunoprecipitation; IHC,

74 Immunohistochemical (IHC) staining; CST, Signaling Technology

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77 **Supplementary Table 3. Clinical characteristics of 11 HCC patients**

Case	Gender	Age (years)	T stage	N stage	M stage	AJCC stage
1	Male	49	T2	N0	M1	IVB
2	Male	68	T3	N0	M0	IIIA
3	Male	65	T1b	N0	M0	IB
4	Male	60	T3	N0	M0	IIIA
5	Male	49	T1a	N0	M1	IVB
6	Female	43	T1a	N0	M0	IA
7	Male	60	T1b	N0	M0	IB
8	Male	67	T1a	N0	M0	IA
9	Male	77	T1b	N0	M0	IB
10	Male	64	T1b	N0	M0	I
11	Male	55	T2	N0	M0	IVB

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**Supplementary Table 4. Clinical characteristics of 270 HCC patients.**

Patient characteristics	Cohort 1	Cohort 2	Cohort 3
	Tissues	Tissues	Tissues
No. of patients	92	88	90
Gender (male/female)	83/9	72/16	80/10
Age, years (mean, range)	53, 25-73	53,27-84	52, 31-78
Edmondson Grade (I+II/III+IV)	60/32	58/32	44/46
AJCC Grade (1+2/3+4)	51/41	88/0	88/2
Liver Cirrhosis (present/absent)	36/56	76/12	81/9
Tumor Size, cm ( $\leq 3$ / $> 3$ )	22/70	25/63	36/54
T stage (T1+T2/T3+T4)	51/41	88/0	87/3
N stage (N1+N2/N3+N4)	91/1	-	-
M stage (M0/M1)	90/2	-	-
Portal Vein Tumor Thrombus (present/absent)	84/8	-	-
ALT, U/L ( $\leq 45$ / $> 45$ )	-	48/40	59/31
HBcAb (positive/negative)	-	77/11	81/9
AFP ug/L ( $\leq 25$ / $> 25$ )	-	27/61	38/52
HBsAg (positive/negative)	-	75/13	71/19
HCV (present/absent)	-	1/87	2/88
TBIL, umol/L ( $\leq 20$ / $> 20$ )	-	74/14	75/15
Cirrhosis Nodules ( $\leq 3$ / $> 3$ )	-	49/39	56/34
Tumor Capsule (present/absent)	-	45/43	42/48
Tumor Recurrence (present/absent)	-	52/36	49/41
Tumor Number ( $\leq 1$ / $> 1$ )	-	73/15	79/11

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102 **Supplementary Table 5. Correlation between DDX24 expression and HCC**  
 103 **clinicopathologic features in 270 patients.**

	DDX24 expression levels		<i>P</i>
	high expression	low expression	
Gender			
Male	123	112	<i>0.0463<sup>a</sup></i>
Female	12	23	
Age (years)			
≤55	86	76	<i>0.2141</i>
> 55	49	59	
Edmondson Grade			
I+II	77	85	<i>0.3203</i>
III+IV	58	50	
AJCC Grade			
1+2	108	119	<i>0.0673</i>
3+4	27	16	
Tumor Size(cm)			
≤3	33	50	<i>0.0249<sup>a</sup></i>
> 3	102	85	
T			
T1/T2	107	119	<i>0.048<sup>a</sup></i>
T3/T4	28	16	

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 105 <sup>a</sup>*p* values less than .05 were considered statistically significant.

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123 **Supplementary Table 6. Correlation between DDX24 expression and HCC**  
 124 **clinicopathologic features in 92 patients: Cohort 1.**

	DDX24 expression levels		<i>p</i>
	high expression	low expression	
Liver Cirrhosis			0.3928
with	16	20	
without	30	26	
Portal Vein Tumor Thrombus			0.0264 <sup>a</sup>
No	39	45	
Yes	7	1	

125 <sup>a</sup>*p* values less than .05 were considered statistically significant.

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153 **Supplementary Table 7. Correlation between DDX24 expression and HCC**

154 **clinicopathologic features in 88 patients: Cohort2.**

	DDX24 expression levels		<i>p</i>
	high expression	low expression	
Liver Cirrhosis			<i>0.2140</i>
with	40	36	
without	4	8	
ALT			<i>0.3918</i>
≤45	26	22	
> 45	18	22	
HBcAb			<i>0.3336</i>
positive	40	37	
negative	4	7	
AFP			<i>0.8172</i>
≤25	13	14	
> 25	31	30	
HBsAg			<i>0.3674</i>
positive	36	39	
negative	8	5	
HCV			<i>0.3145</i>
with	1	0	
without	43	44	
TBIL			<i>0.0803</i>
≤20	40	34	
> 20	4	10	
Cirrhosis Nodules			<i>0.8301</i>
≤3	25	24	
> 3	19	20	
Tumor Capsule			<i>0.1355</i>
with	26	19	
without	18	25	
Tumor Recurrence			<i>&lt;0.0001<sup>a</sup></i>
with	35	17	
without	9	27	
Tumor Number			<i>0.1564</i>
≤1	39	34	
> 1	5	10	

155 <sup>a</sup>*p* values less than .05 were considered statistically significant.

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157 **Supplementary Table 8. Correlation between DDX24 expression and HCC**

158 **clinicopathologic features in 90 patients: Cohort 3.**

	DDX24 expression levels		<i>P</i>
	high expression	low expression	
Liver Cirrhosis			
with	39	42	<i>0.2918</i>
without	6	3	
ALT			
≤45	31	28	<i>0.5057</i>
> 45	14	17	
HBcAb			
positive	42	39	<i>0.2918</i>
negative	3	6	
AFP			
≤25	21	17	<i>0.3933</i>
> 25	24	28	
HBsAg			
positive	38	33	<i>0.1965</i>
negative	7	12	
HCV			
with	1	1	<i>&gt; 0.9999</i>
without	44	44	
TBIL			
≤20	38	37	<i>0.7773</i>
> 20	7	8	
Cirrhosis Nodules			
≤3	23	33	<i>0.0297<sup>a</sup></i>
> 3	22	12	
Tumor Capsule			
with	18	24	<i>0.2049</i>
without	27	21	
Tumor Recurrence			
with	34	15	<i>&lt; 0.0001<sup>a</sup></i>
without	11	30	
Tumor Number			
≤1	38	41	<i>0.3343</i>
> 1	7	4	

159 <sup>a</sup>*p* values less than .05 were considered statistically significant.

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162 **Supplementary Table 9. The half-time of LAMB1 mRNA in each group**

HCC cell lines	Half-time (hours)	<i>p</i> value
Hep3B NC	> 10	
Hep3B shDDX24-1	2.613±0.1291	< 0.0001
Hep3B shDDX24-2	3.948±0.3587	< 0.0001

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168 **Supplementary Table 10. The five-year survival rate and average survival time**

169 **(months).**

Protein expression level	Five-year survival rate (Ave, OS by months)
DDX24 low	56.52% (60.64)
DDX24 high	19.57% (32.64)
LAMB1 low	67.39% (47.85)
LAMB1 high	6.52% (18.65)
DDX24 low, LAMB1 low	76.67% (52.63)
DDX24 high, LAMB1 high	3.33% (16.77)

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175 **Supplementary Table 11. The b and y values of MALDI-TOF/TOF mass**  
 176 **spectrometry**

Ion Mass	D	I	L	R	N	V	R
b+	116.0342	229.1183	342.2023	498.3034	612.3464	711.4148	
b++	58.207	115.0628	171.6048	249.6554	306.6768	356.2110	
y++		770.4995	657.4155	544.3314	388.2303	274.1874	175.1190
y++		385.7534	329.2114	272.6693	194.6188	137.5973	88.0631

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### Short Tandem Repeat (STR) Profile Report in Hepatoma Cell Lines

178 STR report for L02: Percent match between the sample and the database profile:

179 100%.

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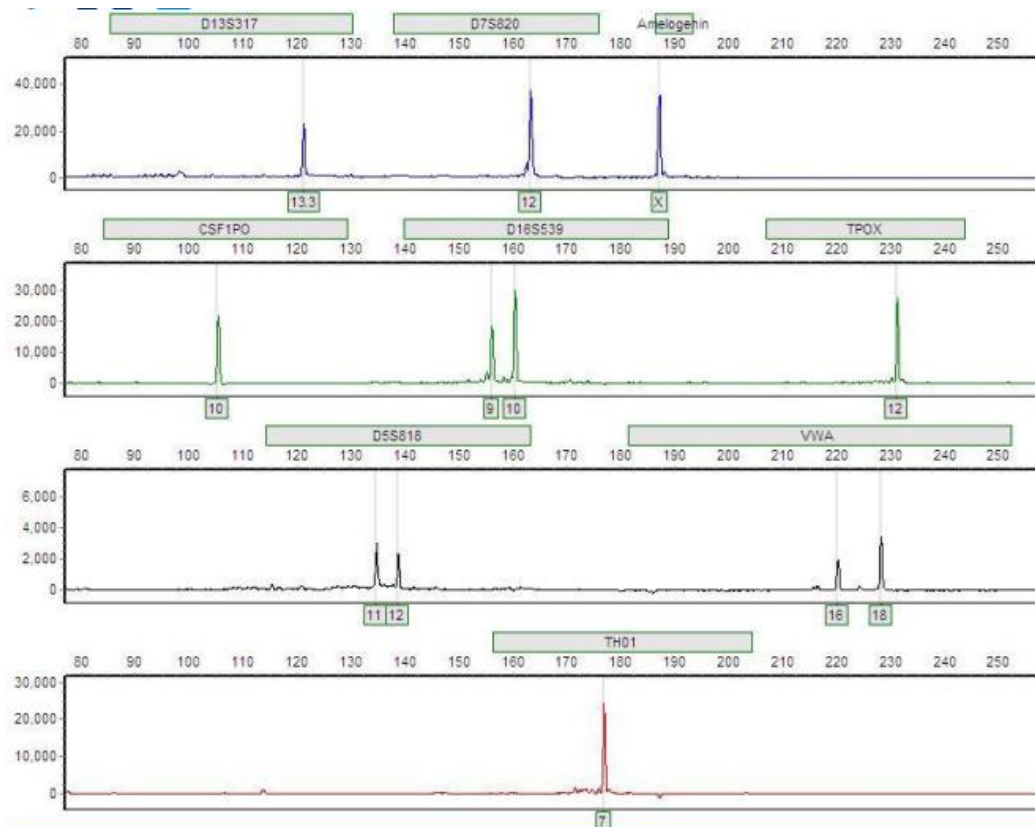
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STR Profile:

Genetic Site	Customer sample		ExPASy	
	L-02		L-02	
Amelogenin	X	X	X	X
CSF1PO	10	10	10	10
D13S317	13.3	13.3	13.3	13.3
D16S539	9	10	9	10
D5S818	11	12	11	12
D7S820	12	12	12	12
TH01	7	7	7	7
TPOX	12	12	12	12
vWA	16	18	16	18

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185 STR report for SNU449: Percent match between the sample and the database

186 profile: 94.4%.

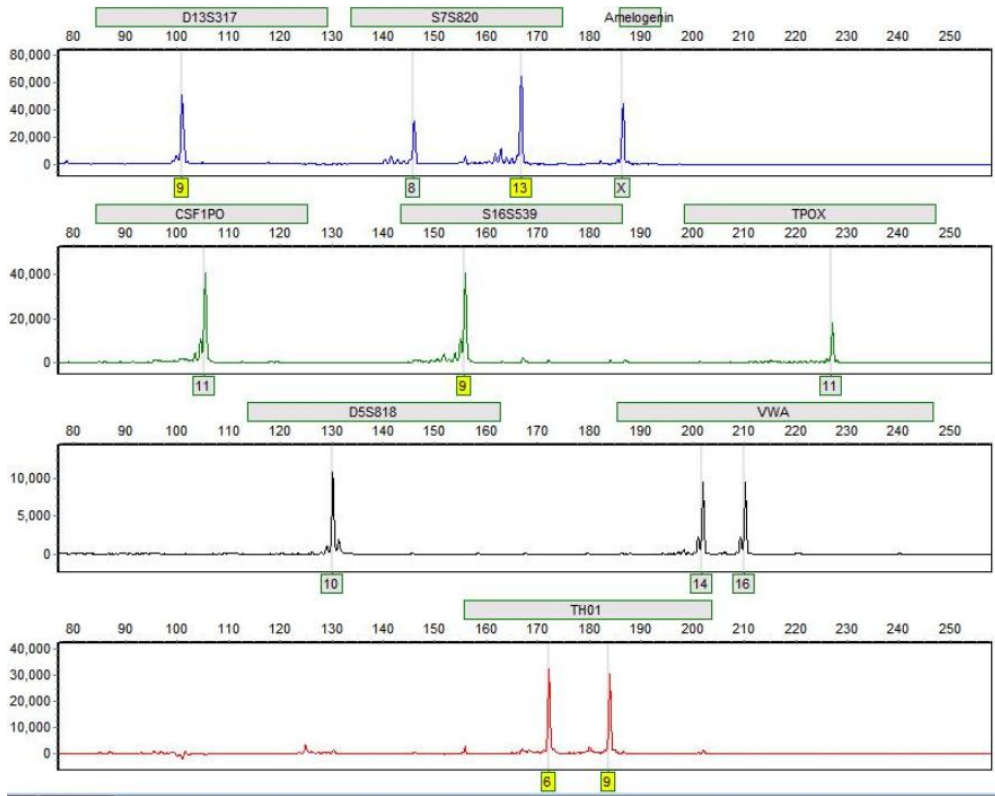
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188 STR Profile:

Genetic Site	Customer sample		ATCC	
	SNU-449		SNU-449	
Amelogenin	X	X	X	Y
CSF1PO	11	11	11	11
D13S317	9	9	9	9
D16S539	9	9	9	9
D5S818	10	10	10	10
D7S820	8	13	8	13
TH01	6	9	6	9
TPOX	11	11	11	11
vWA	14	16	14	16

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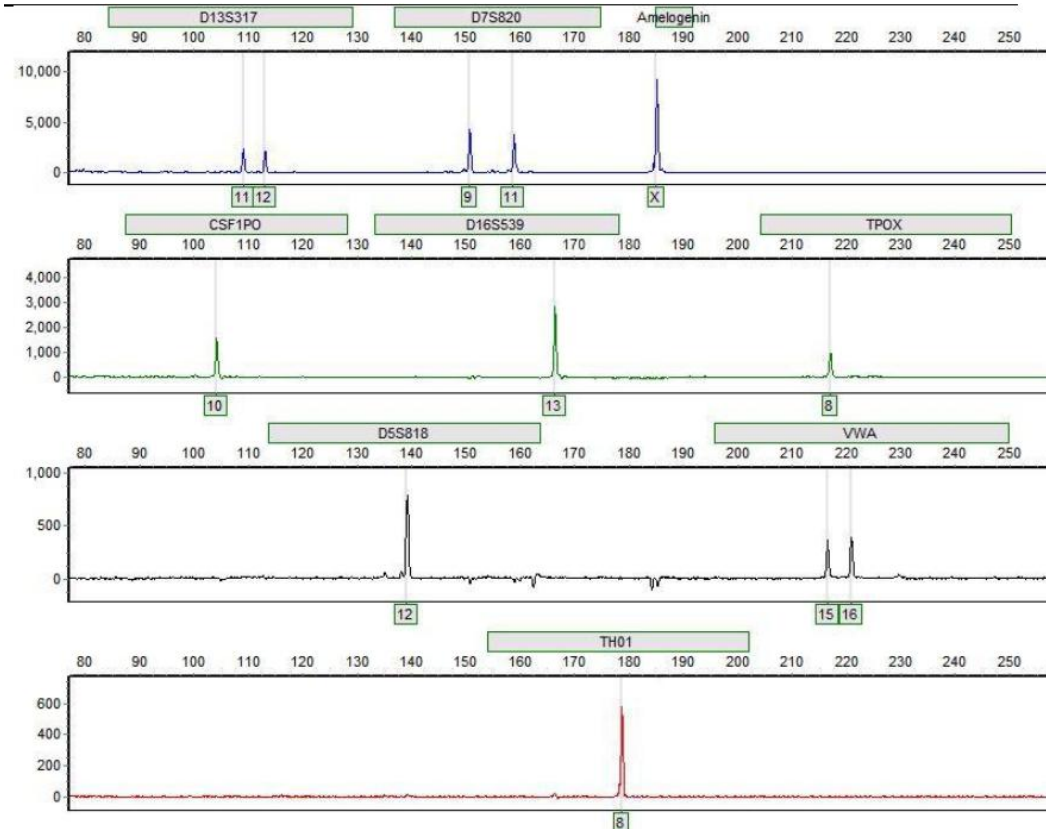
193 STR report for Huh7: Percent match between the sample and the database

194 profile: 94.4%.

195 STR Profile:  
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Genetic Site	Customer sample		JCRB	
	HUH-7		HUH-7	
Amelogenin	X	X	X	X
CSF1PO	11	11	11	11
D13S317	10	11	10	11
D16S539	10	10	10	10
D5S818	11	12	12	12
D7S820	11	11	11	11
THO1	7	7	7	7
TPOX	8	11	8	11
vWA	16	18	16	18

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201 STR report for PLC/PRF/5: Percent match between the sample and the database

202 profile: 100%.

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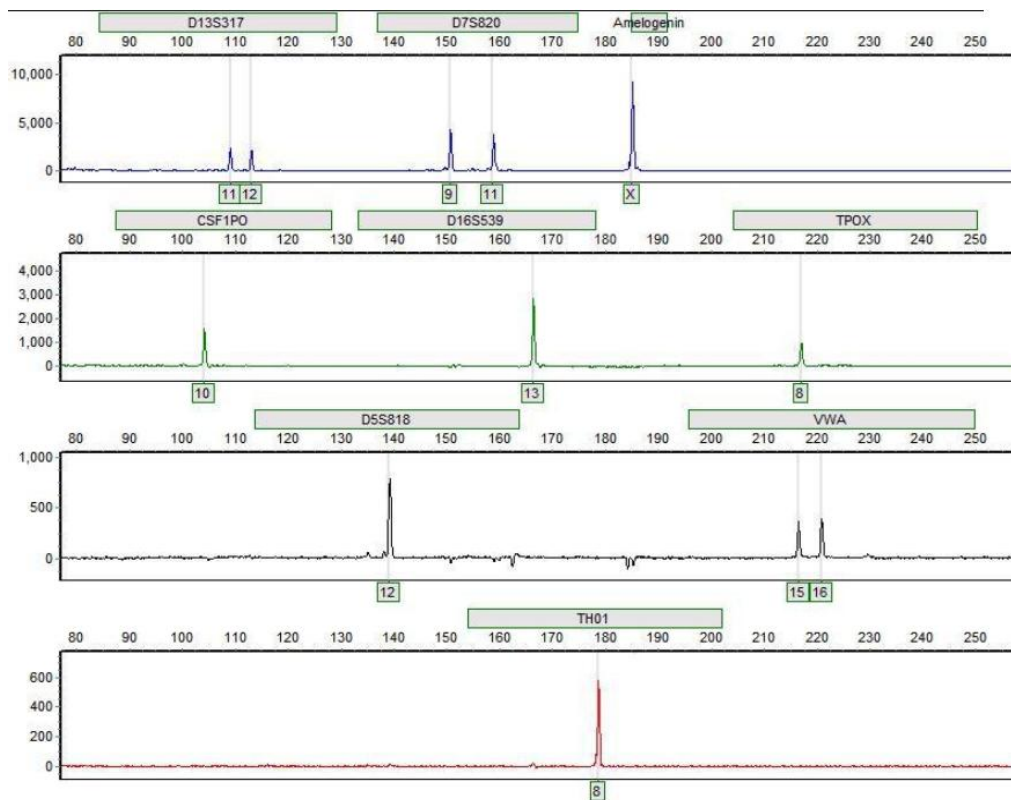
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STR Profile:

Genetic Site	Customer sample		ATCC	
	PLC/PRF/5		PLC/PRF/5	
Amelogenin	X	X	X	X
CSF1PO	10	10	10	10
D13S317	11	12	11	12
D16S539	13	13	13	13
D5S818	12	12	12	12
D7S820	9	11	9	11
TH01	8	8	8	8
TPOX	8	8	8	8
vWA	15	16	15	16

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211 STR report for SNU398: Percent match between the sample and the database

212 profile: 100%.

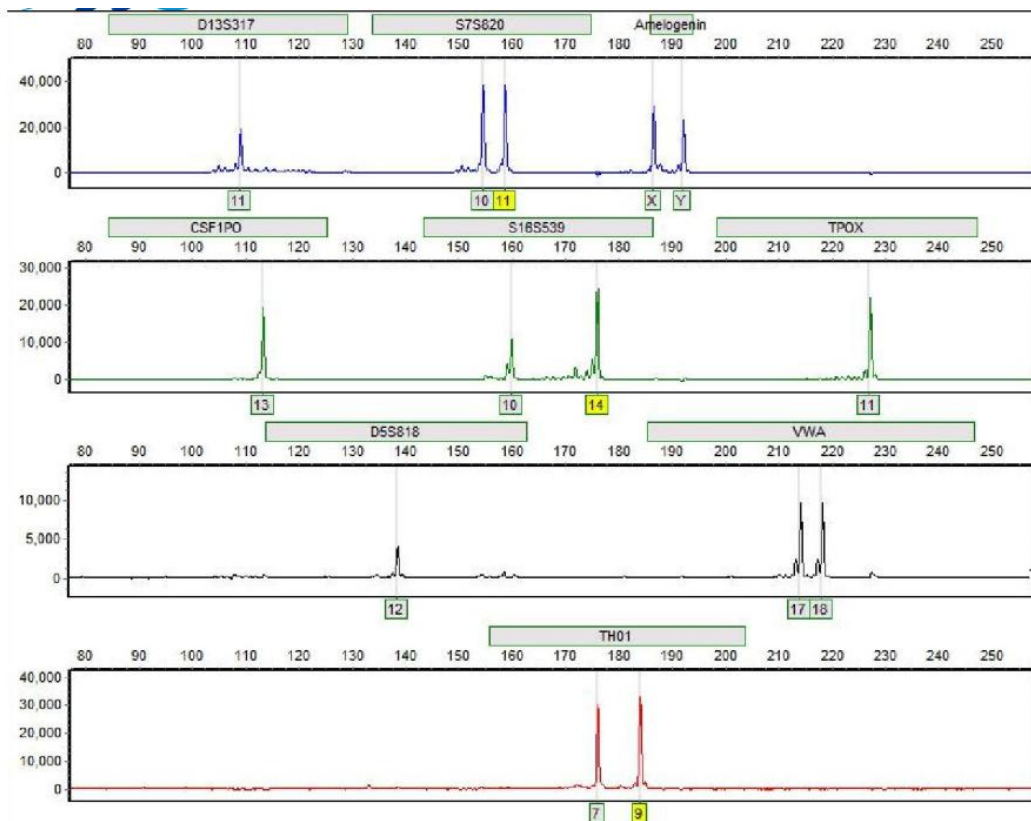
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214 STR Profile:

Genetic Site	Customer sample		ATCC	
	SNU-398		SNU-398	
Amelogenin	X	Y	X	Y
CSF1PO	13	13	13	13
D13S317	11	11	11	11
D16S539	10	14	10	14
D5S818	12	12	12	12
D7S820	10	11	10	11
THO1	7	9	7	9
TPOX	11	11	11	11
vWA	17	18	17	18

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221 **STR report for Hep3B: Percent match between the sample and the database**

222 **profile: 98%.**

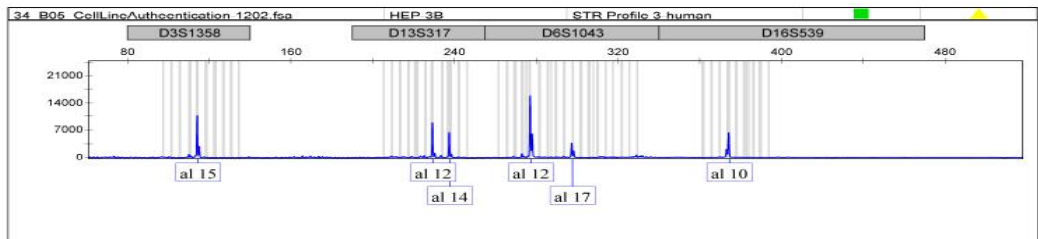
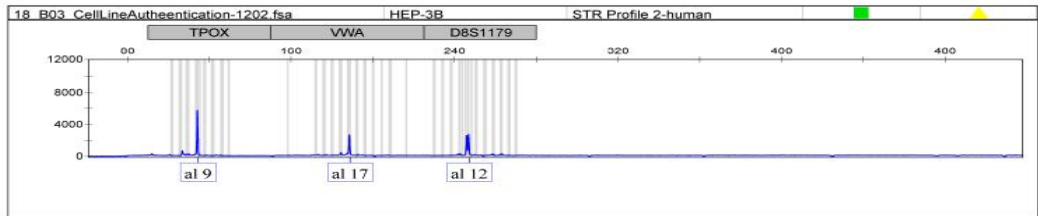
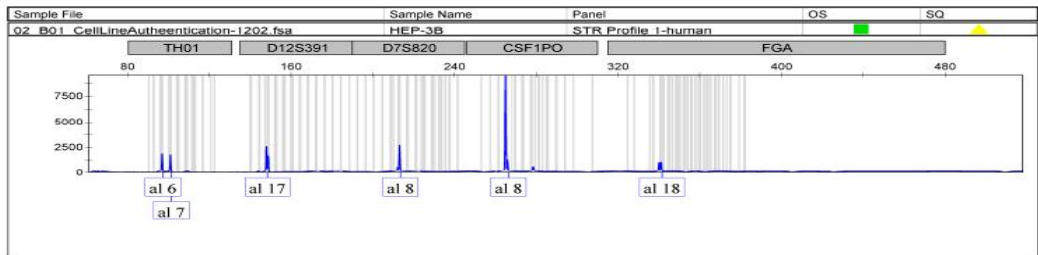
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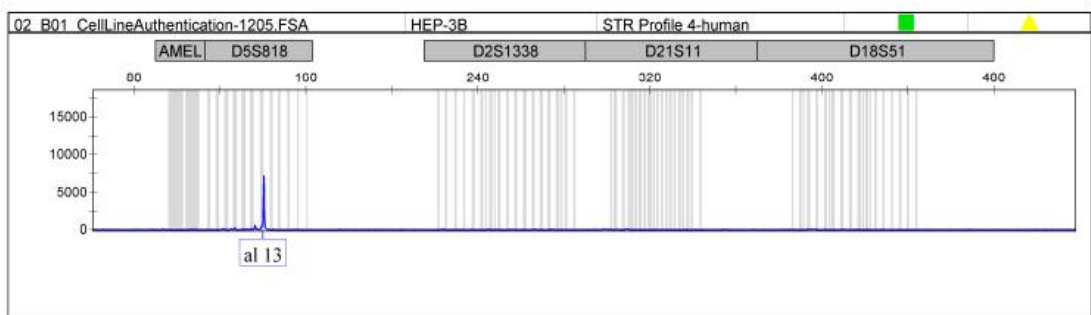
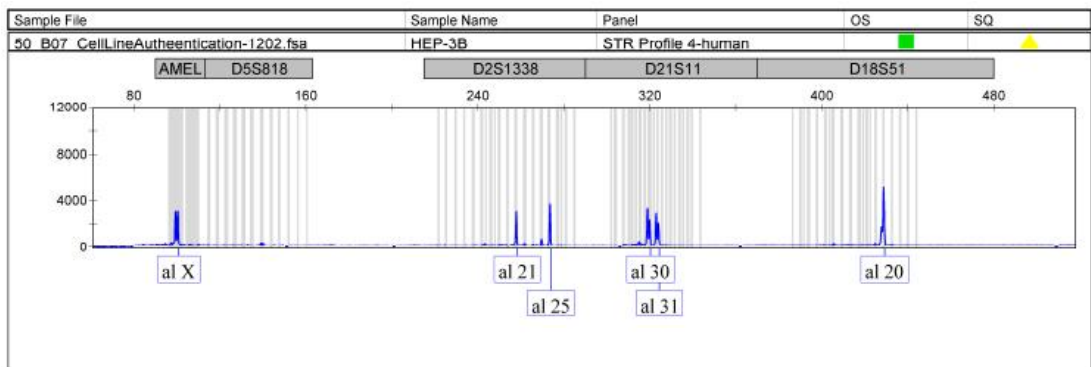
STR Profile:

Marker	Hep3B				ATCC		
	Allele1	Allele2	Allele3	Allele4	Allele1	Allele2	Allele3
D5S818	13	13			13	13	
D13S317	12	14			12	14	
D7S820	8	8			8	10	
D16S539	10	10			10	10	
VWA	17	17			17	17	
TH01	6	7			6	7	
AMEL	X	X			X	X	
TPOX	9	9			9	9	
CSF1PO	8	8			8	8	
D12S391	17	17					
FGA	18	18					
D2S1338	21	25					
D21S11	30	31					
D18S51	20	20					
D8S1179	12	12					
D3S1358	15	15					
D6S1043	12	17					
PENTAE	5	16					
D19S433	12.2	14					
PENTAD	12	14					

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