

Table S1. All the primers with their sequences, annealing temperature, and amplicon length for RT-PCR.

Genes	Forward primer	Reverse Primer	Annealing Temp (°C)	Amplicon Length
β -Actin	TCACAATGTGGCCGAGGACTTTT	AGAAGTGGGGTGGCTTTTAGGATG	60	115
CCAR1	AGCTGCATTACAACAGCAATA	GGCTGTGTTAAGAGGGTTTG	60	96
Notch 1	AACAACAGGGAGGAGACA	GGTCCATATGATCCGTGATG	60	112
Notch 2	AAGGGCTTTAAAGGCTATAACT	TGTCATCAAAGCAGGTTCC	60	88
Notch 4	GAGGGTCCACGTTGTGAG	TCTGGGCCTATGAAACCTG	60	137
Ikaros	CGAATACTCTGTCTGCCCTATC	CCCATCTCTTCCCTCTCATA	60	122
CD-11d (ITGAD)	CCAGGCAATGGAGGAAGAA	CTCGGGTCTGCTCATAGTAATG	60	147

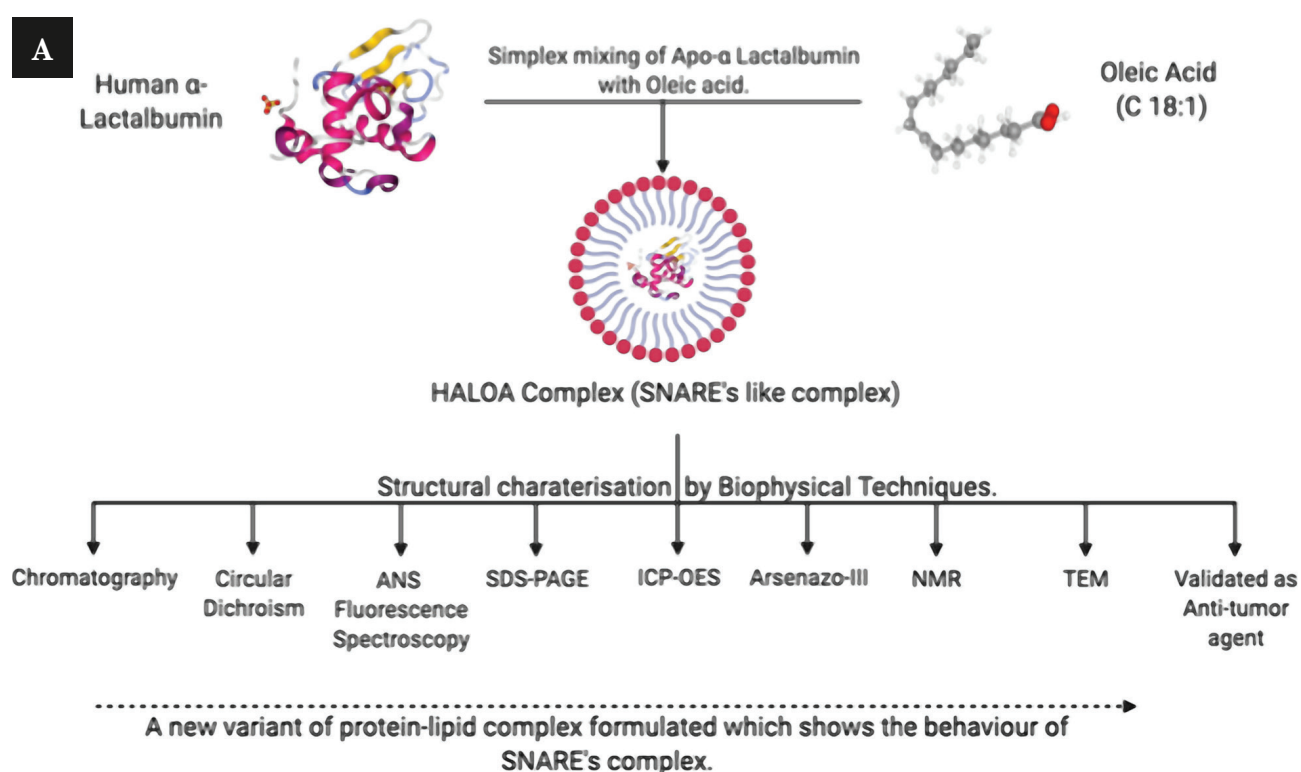


Figure S1. (A) structural characterization of the HALOA complex was previously validated by various biophysical techniques, (B) the HALOA complex led to anoikis in K562 cells but not in NIH-3T3 cells, and (C) cell viability assay after treatment with the HALOA complex at a different concentration was performed, and the IC50 (0.5 mg/mL) value was calculated throughout this study. (D-G) BCRABL1 translocation lane and band analysis by Image Lab software. (H) shows the DNA fragmentation result after the treatment with complex where in the panel of HALOA complex gel image no intact DNA is shown, the result is analysed by image lab software. Error bar indicated the SD. (I) gel electrophoresis image clearly shows that expression of 18 s rRNA found to be high as compared to positive control while after the treatment with complex manages to downregulate the expression of 18s rRNA in k562 cells; (J) result shows the Ct value (Mean \pm SD) of Positive control (PTC)- 15.1269 \pm 0.0733, Control (K562)- 10.575 \pm 0.0050, HLALB- 10.2319 \pm 0.1409, OA- 25.075 \pm 0.1257, HALOA- 26.4197 \pm 0.1339, p-value; 0.001, the result indicate that lower the Ct values greater the amount of nucleic acid. The results are shown as the mean \pm SD. The graph shows the p-value (* $<$ 0.05), and the error bar indicates the SD.

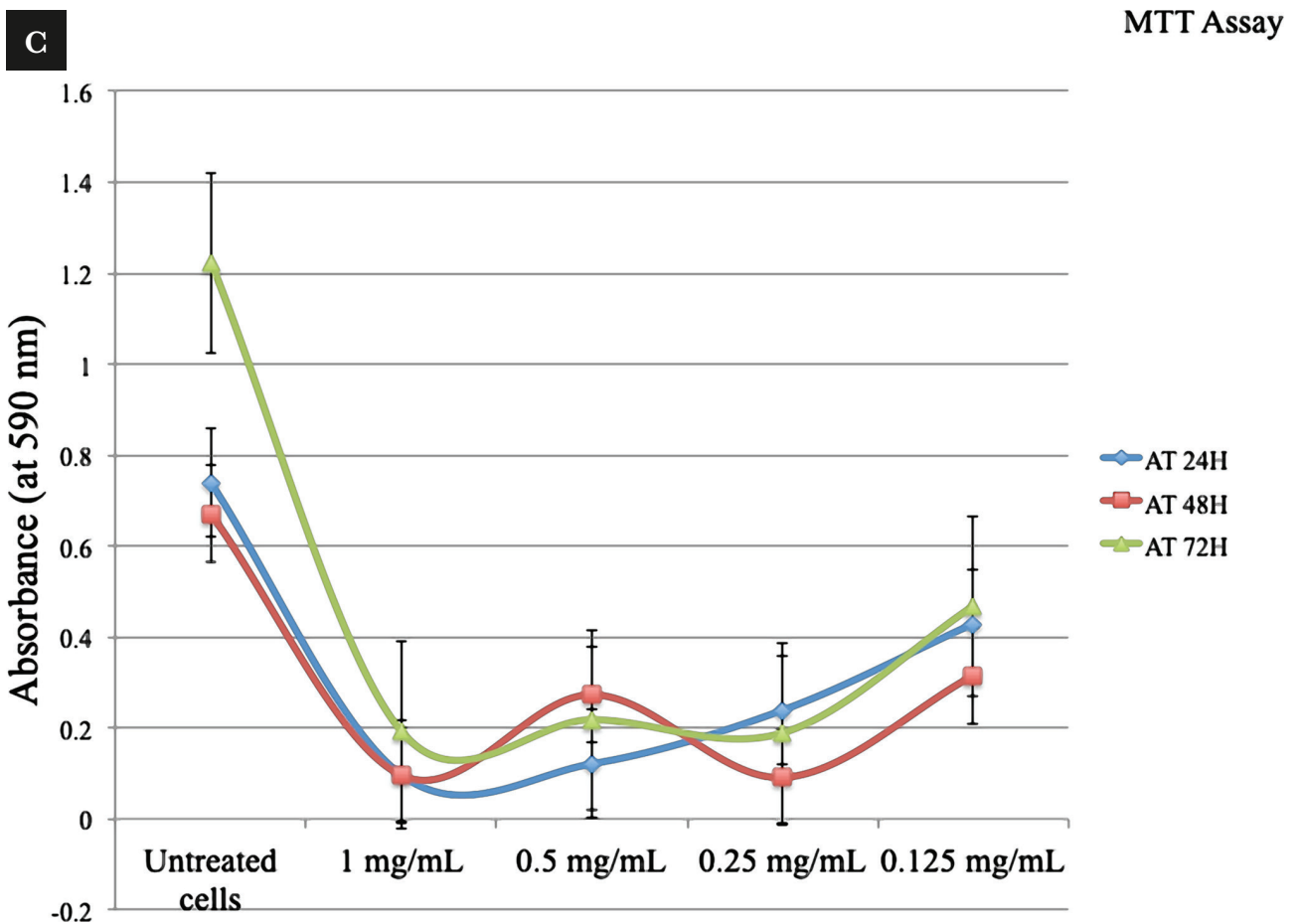
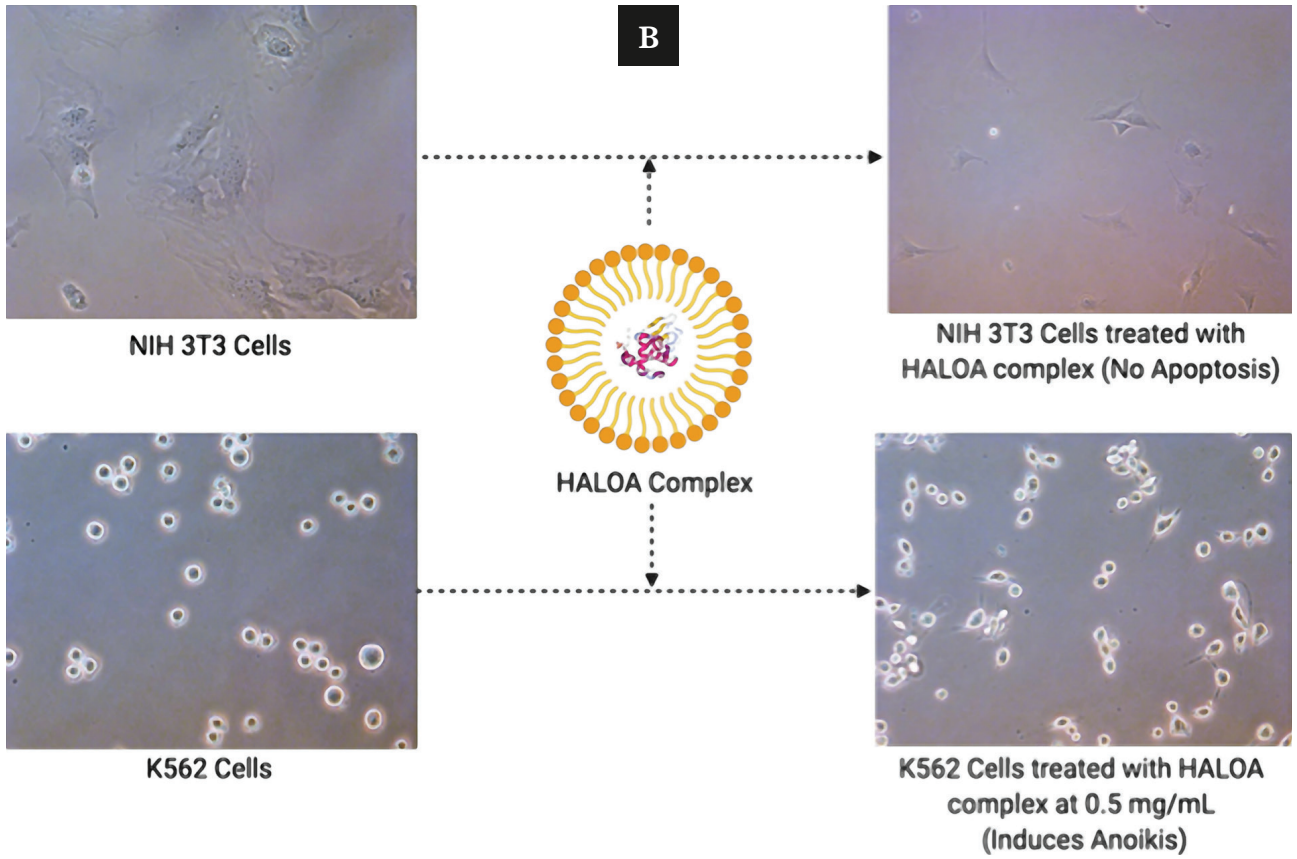
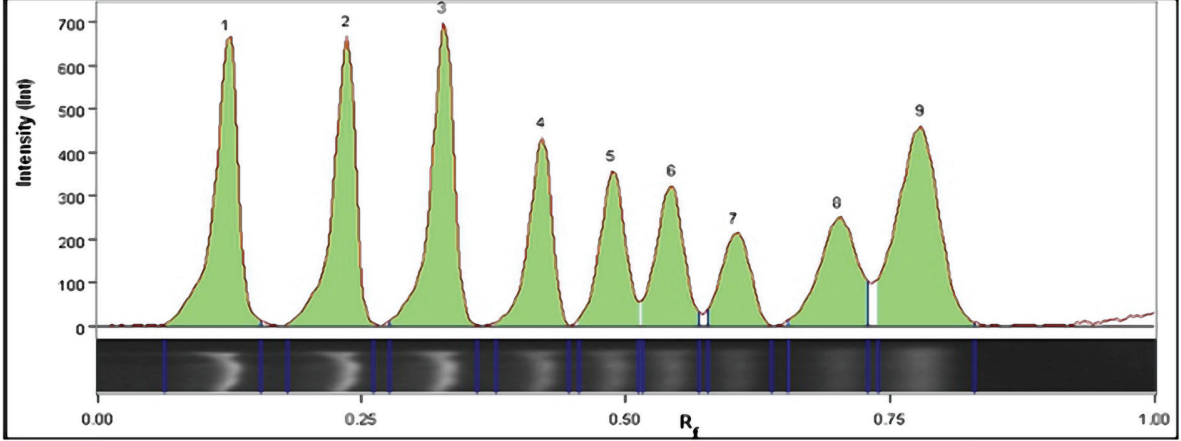


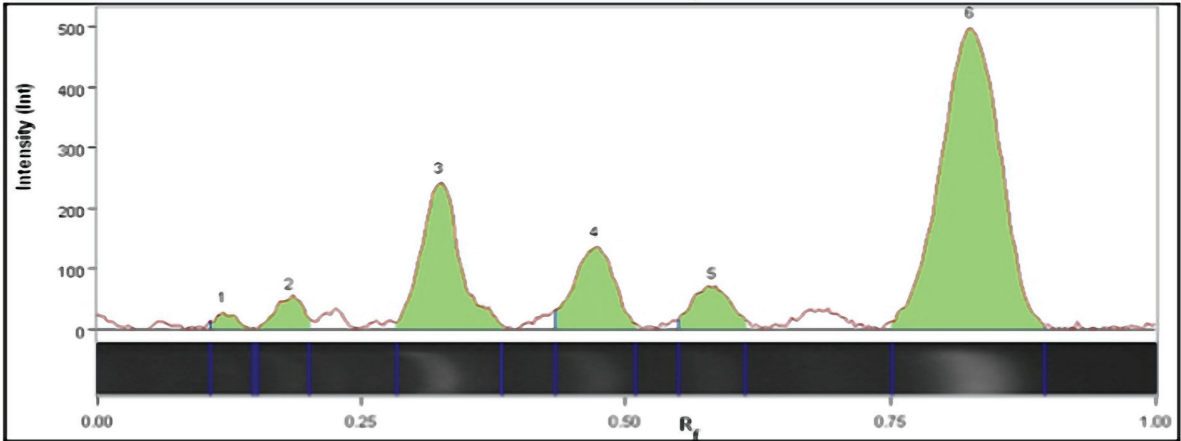
Figure S1. Continued.

D

Lane 1

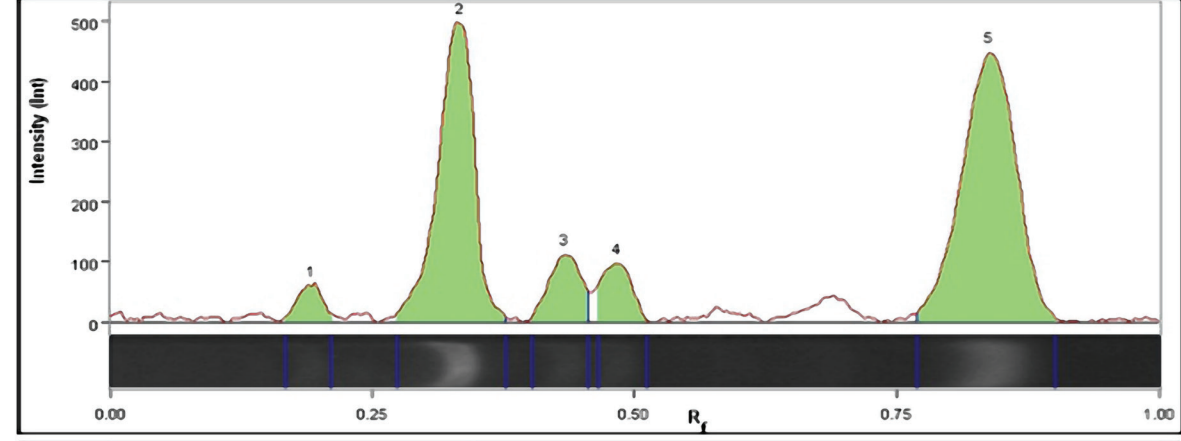


Lane 2



E

Lane 3



Lane 4

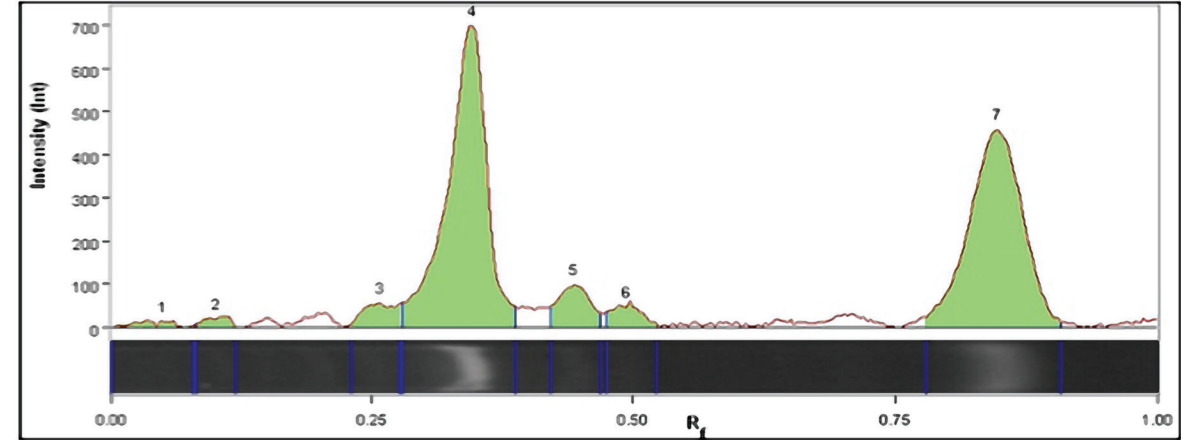
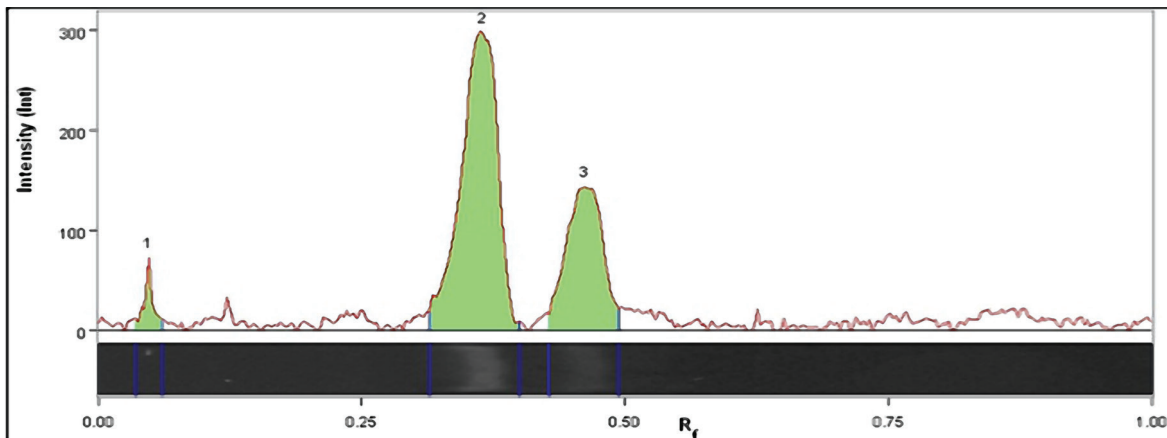


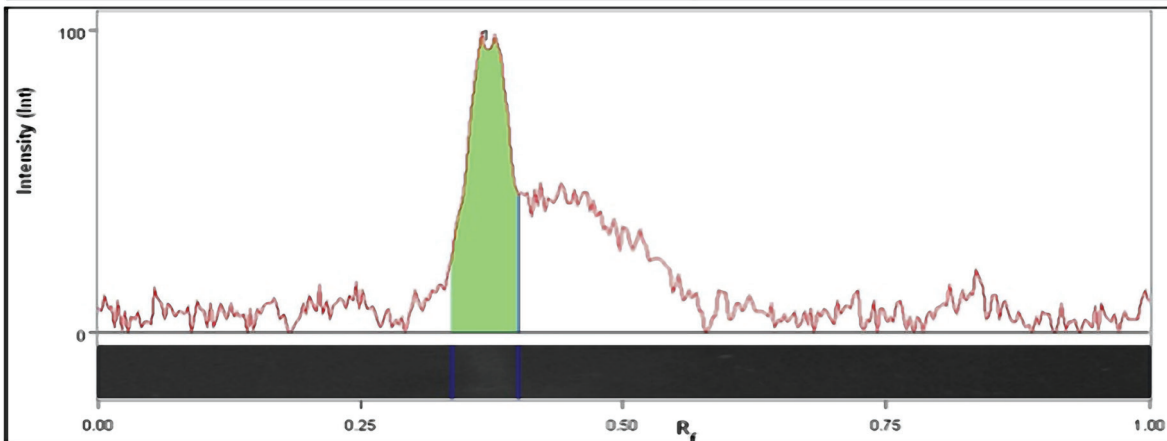
Figure S1. Continued.

F

Lane 5

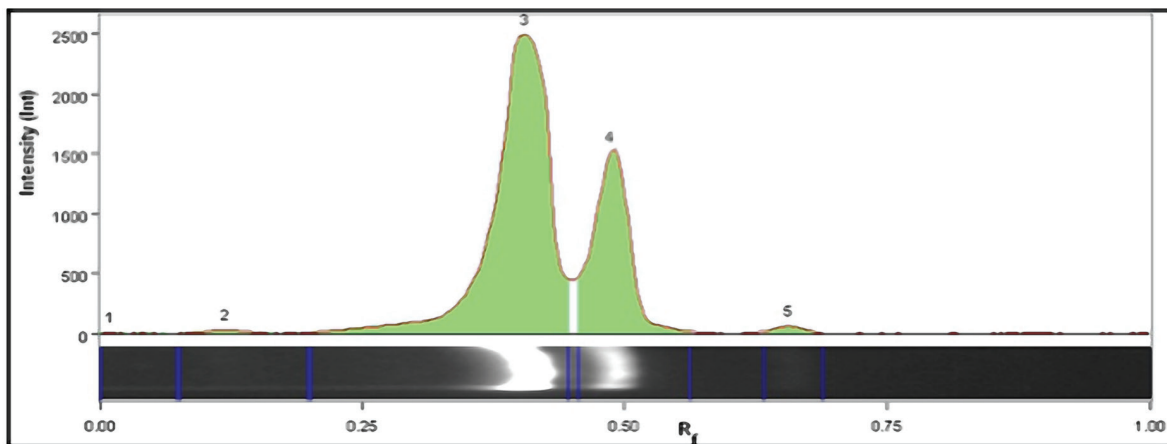


Lane 6



G

Lane 7



Lane 8

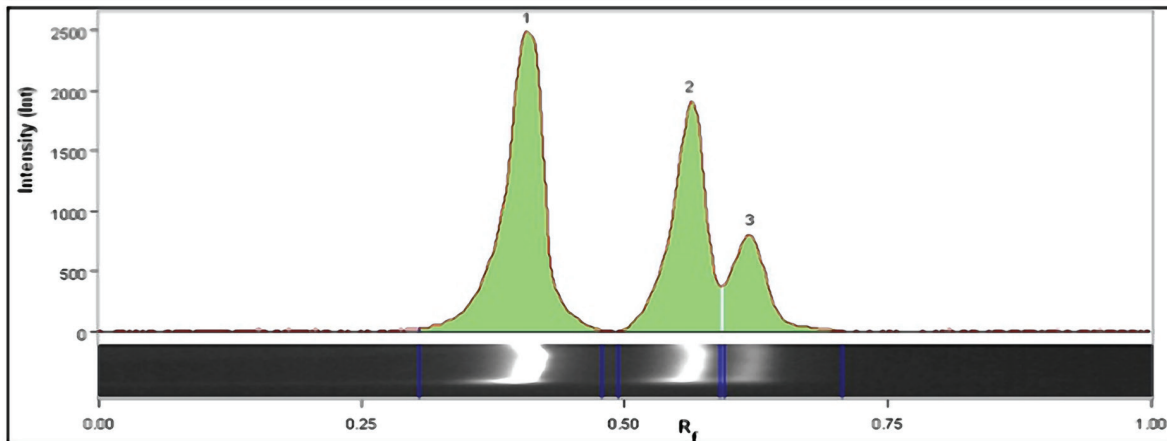


Figure S1. Continued.

H

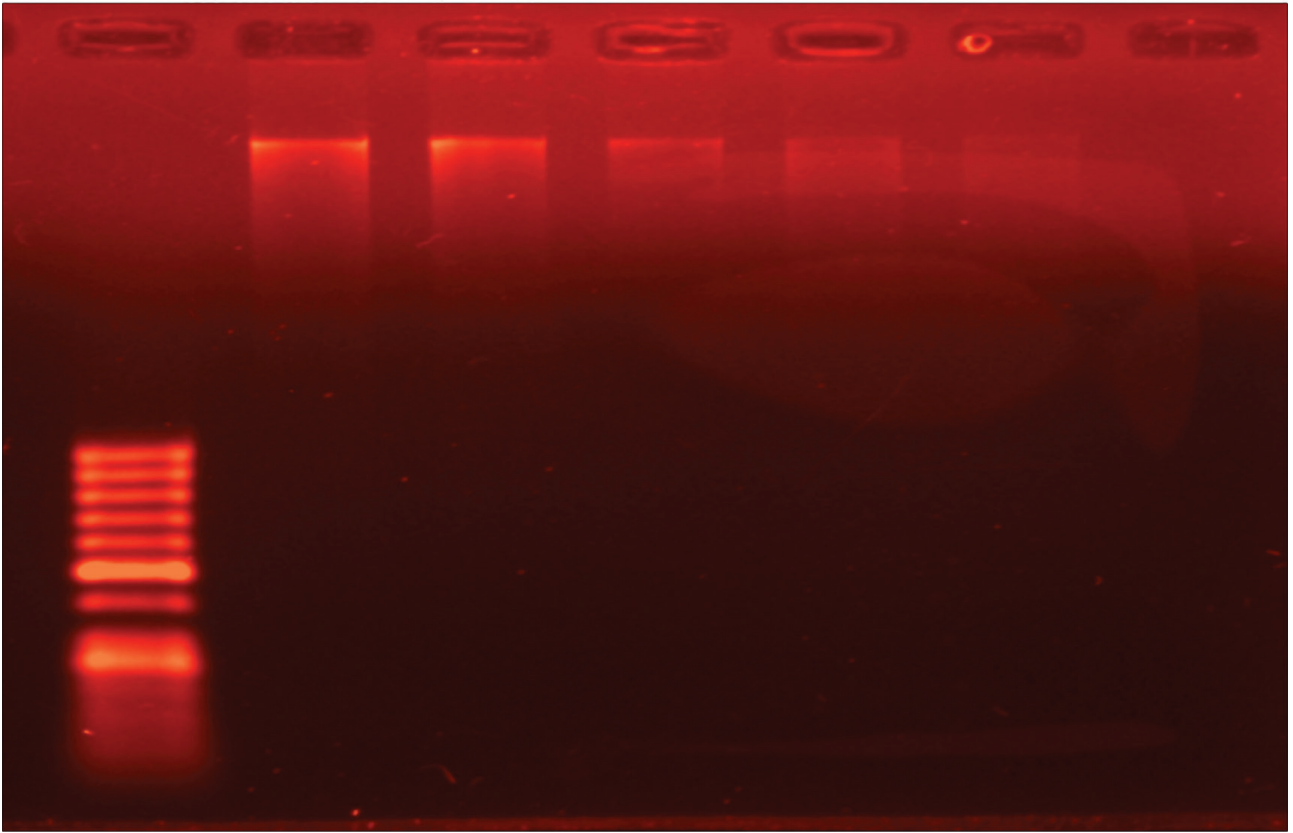
NIH cells
Treated
with HALOA

Control
(K562)

HLALB

OA

HALOA



I

PTC

Control
(K562)

HALOA

HLALB

OA

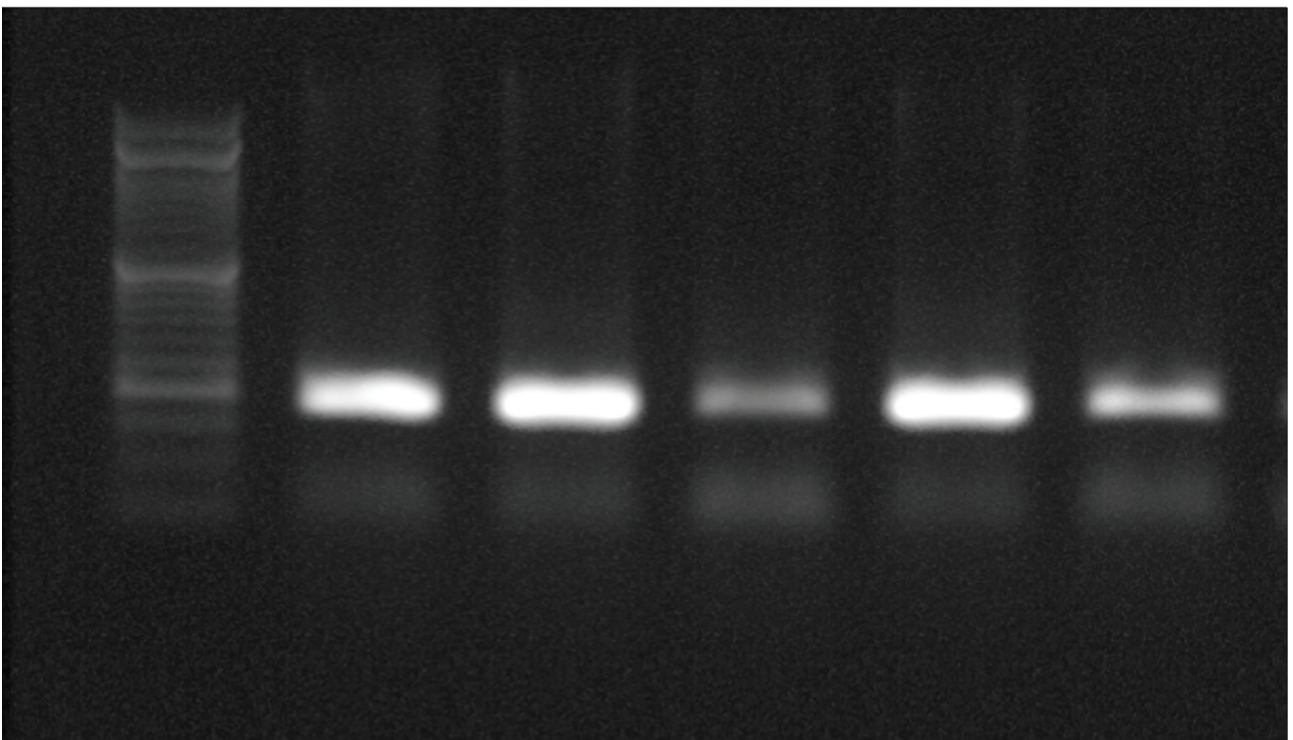


Figure S1. Continued.

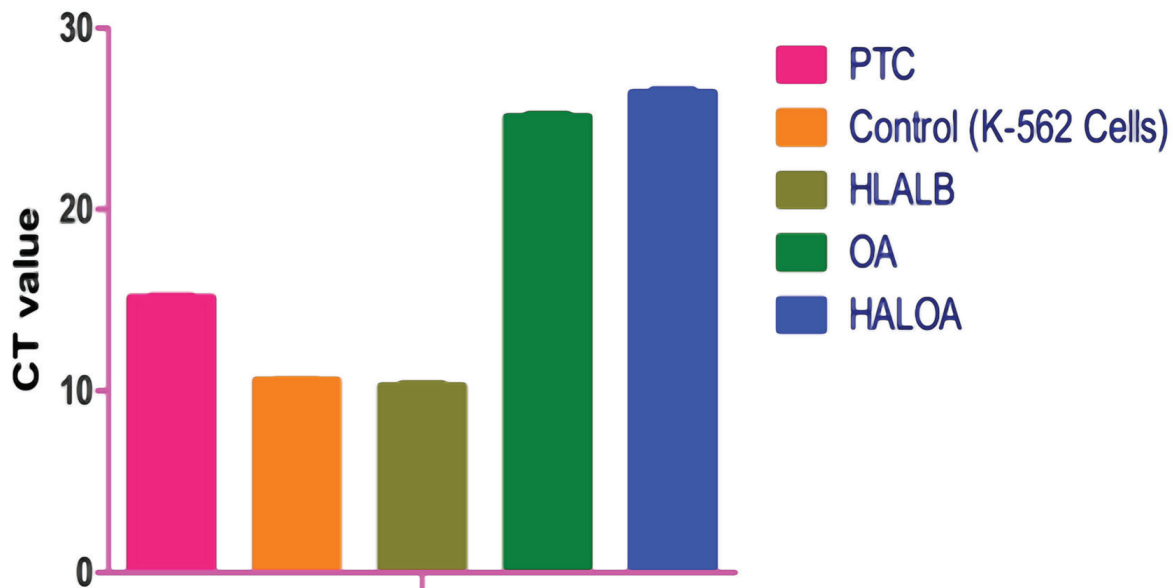


Figure S1. Continued.

Table S2. BCR-ABL translocation in all the samples (PTC-Positive control; HALOA-Human alpha-lactalbumin oleic acid complex; HLALB; Human alpha-lactalbumin; OA1, OA2, and OA3 (at different concentration)).

S.No.	Name of Sample	BCR-ABL Translocation
1.	PTC	b2a2, e1a2
2.	K562 Cell line	b3a2 (major)
3.	HALOA	No BCR-ABL translocation
4.	HLALB	b3a2 (down-regulated)
5.	OA1	e1a3 and mixed
6.	OA2	e1a3 and mixed
7.	OA3	e1a3 and mixed

Table S3. Ct (Ct±SD) value of 18s rRNA of RT-PCR (TaqMan assay).

S.No.	Samples	Ct±SD
1.	Positive control (PTC)	15.1269±0.0733
2.	Control (K562)	10.575±0.0050
3.	HLALB	10.2319±0.1409
4.	OA	25.075±0.1257
5.	HALOA	26.4197±0.1339

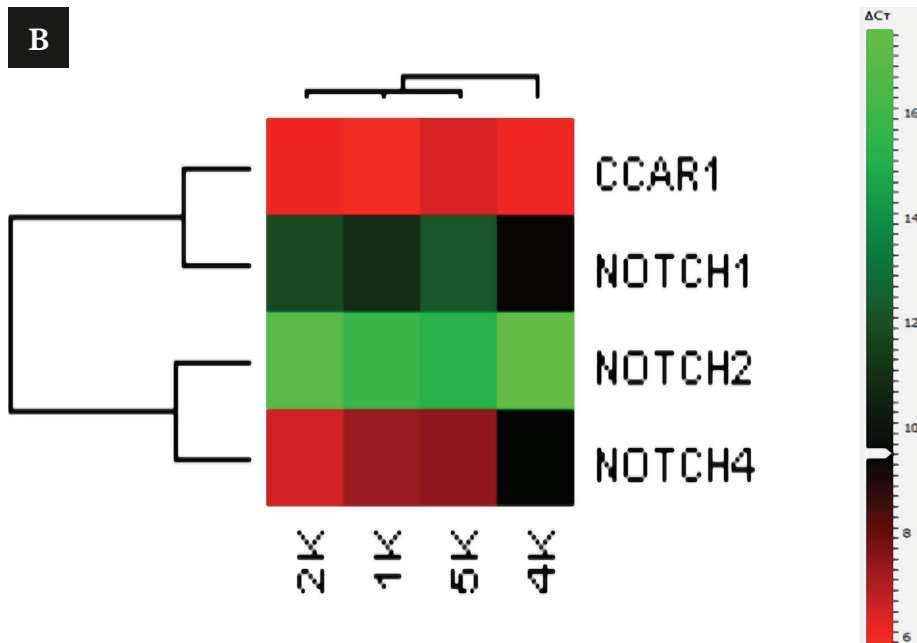
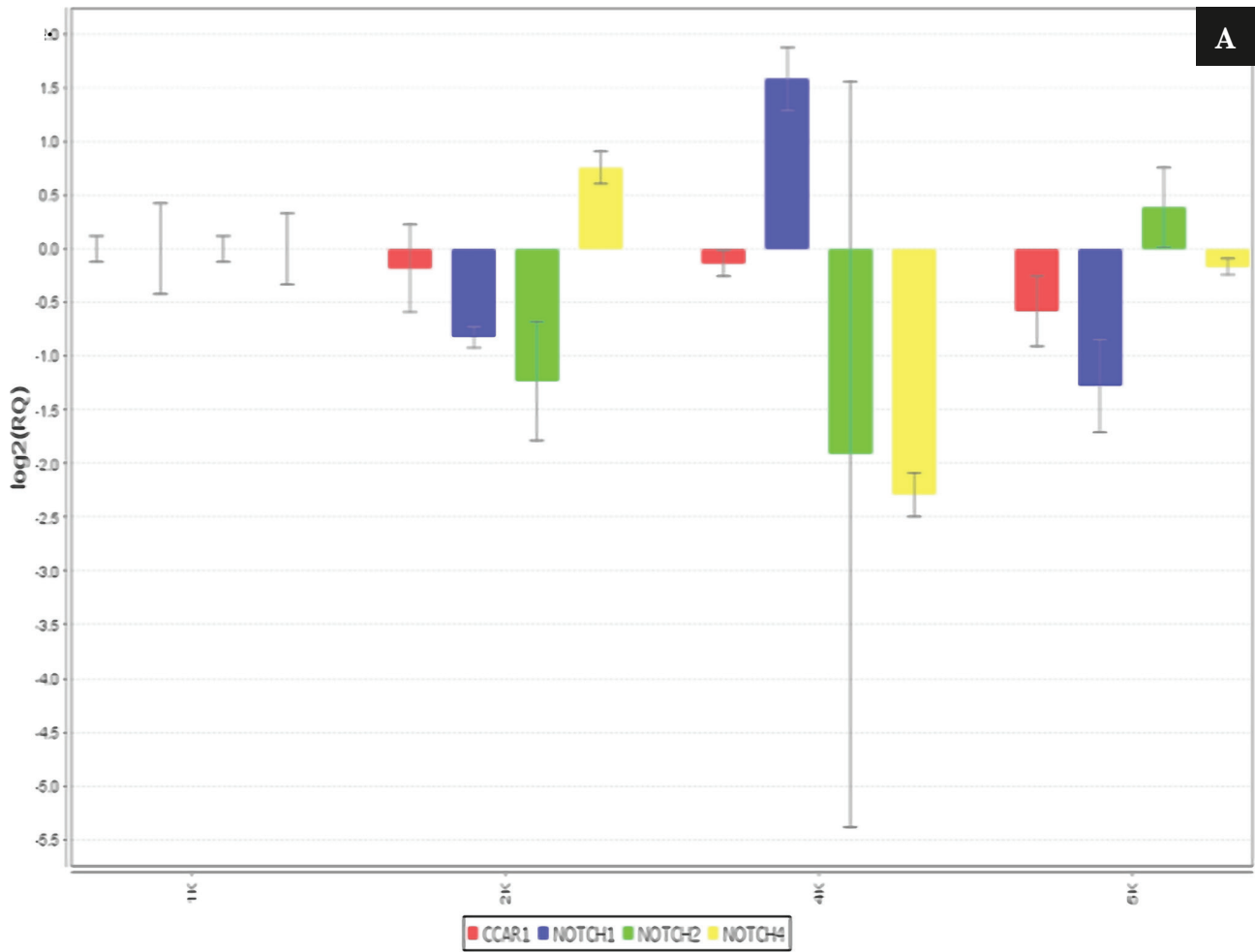
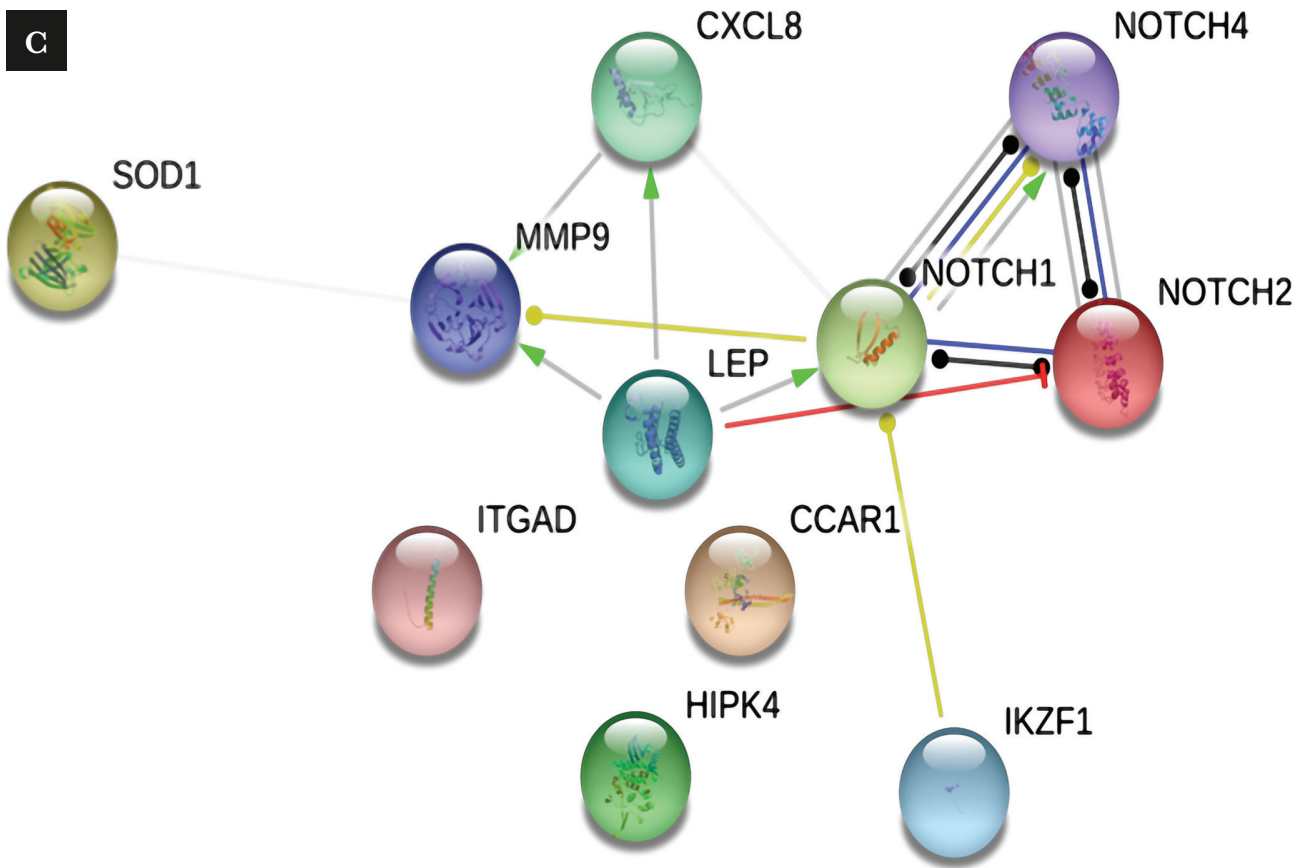


Figure S2. (A) shows that the complex reduces Notch 1 and 2, which are oncogenic in nature, while it manages to upregulate the expression of Notch 4, CD-11d, and Ikaros (tumor suppressive); (B) indicates the heat map of correlation between all these factors. The representation shows 1K-Control (K562 cells), 2K-HALO complex, 3K-HLAB, and 4K-OA treated cells. (C) Protein-protein interactions were predicted by STRING software, which shows a strong interaction between all the factors. Error bar indicated the SD. (D) Crystal structure of activated Notch, CSL, and MAML on HES-1 promoter DNA sequence (PDB; 2F8X); (E) sequence alignment of the notch (PDB; 4J2X_1) with RBP-Jk (PDB; 2F8X_3); (F) shows the root mean square deviation (RMSD) of 1; RBP-Jk with Notch, 2; Notch with HALOA complex, 3; RBP-Jk with complex where 1-10 shows the rank of favorable docking; (G) average interaction energy score between ligand and receptors.

C



D

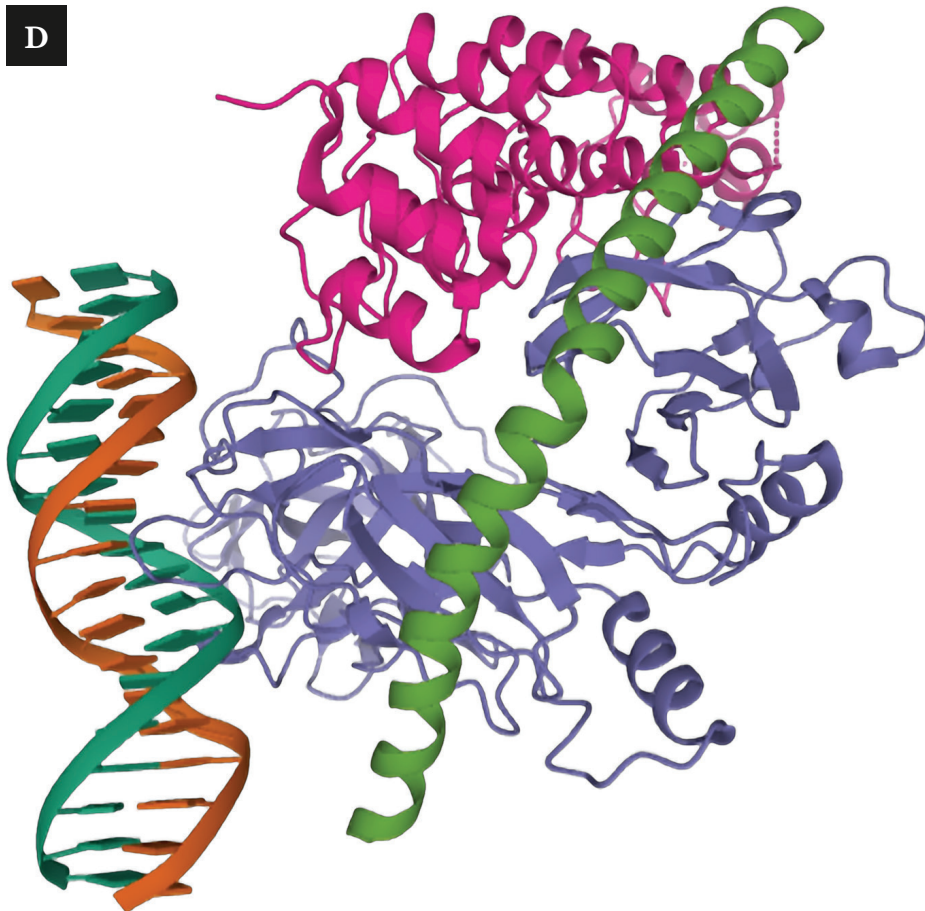


Figure S2. Continued.

E

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4J2X_1|Chains  GPLGSPPKRLTREAMRNYLKERGDQTVLILHAKVAQKSYGNEKRFFCPPPCVYLMGSGWK 60
2F8X_3|Chain    MGERPPPKRLTREAMRNYLKERGDQTVLILHAKVAQKSYGNEKRFFCPPPCVYLMGSGWK 60
                *****

4J2X_1|Chains  KKKEQMETDGCSEQESQPCAFIGIGNSDQEMQQLNLEGKNYCTAKTLYISDSDKRKHFML 120
2F8X_3|Chain    KKKEQMERDGCSEQESQPCAFIGIGNSDQEMQQLNLEGKNYCTAKTLYISDSDKRKHFML 120
                *****

4J2X_1|Chains  SVKMPFYGNSDDIGVFLSKRIKVISKPSKKKQSLKNADLCIASGTKVALFNRLRSQTVSTR 180
2F8X_3|Chain    SVKMPFYGNSDDIGVFLSKRIKVISKPSKKKQSLKNADLCIASGTKVALFNRLRSQTVSTR 180
                *****

4J2X_1|Chains  YLHVEGGNFHASSQQWGAFFIHLDDDESEGEFTVRDGYIHYGQTVKLVCSVTGMALPR 240
2F8X_3|Chain    YLHVEGGNFHASSQQWGAFFIHLDDDESEGEFTVRDGYIHYGQTVKLVCSVTGMALPR 240
                *****

4J2X_1|Chains  LIIRKVDKQTALLDADDPVSQLHKCAFYLKDERMYLCLSQERIIQFQATPCPKENKEM 300
2F8X_3|Chain    LIIRKVDKQTALLDADDPVSQLHKCAFYLKDERMYLCLSQERIIQFQATPCPKENKEM 300
                *****

4J2X_1|Chains  INDGASWTIISTDKAEYTFYEGMGPVLAPVTPVPVVESSLQNGGGDVAMLELTGQNFTPN 360
2F8X_3|Chain    INDGASWTIISTDKAEYTFYEGMGPVLAPVTPVPVVESSLQNGGGDVAMLELTGQNFTPN 360
                *****

4J2X_1|Chains  LRVWFGDVEAETMYRCGESMLCVVVDISAFREGWRWVRQPVPVTLVRNDGVIYSTSLT 420
2F8X_3|Chain    LRVWFGDVEAETMYRCGESMLCVVVDISAFREGWRWVRQPVPVTLVRNDGVIYSTSLT 420
                *****

4J2X_1|Chains  FTYTPEP----- 427
2F8X_3|Chain    FTYTPEPGHHHHHH 434
                *****

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Percent Identity Matrix

1: 4J2X_1|Chains 100.00 97.89
 2: 2F8X_3|Chain 97.89 100.00

F

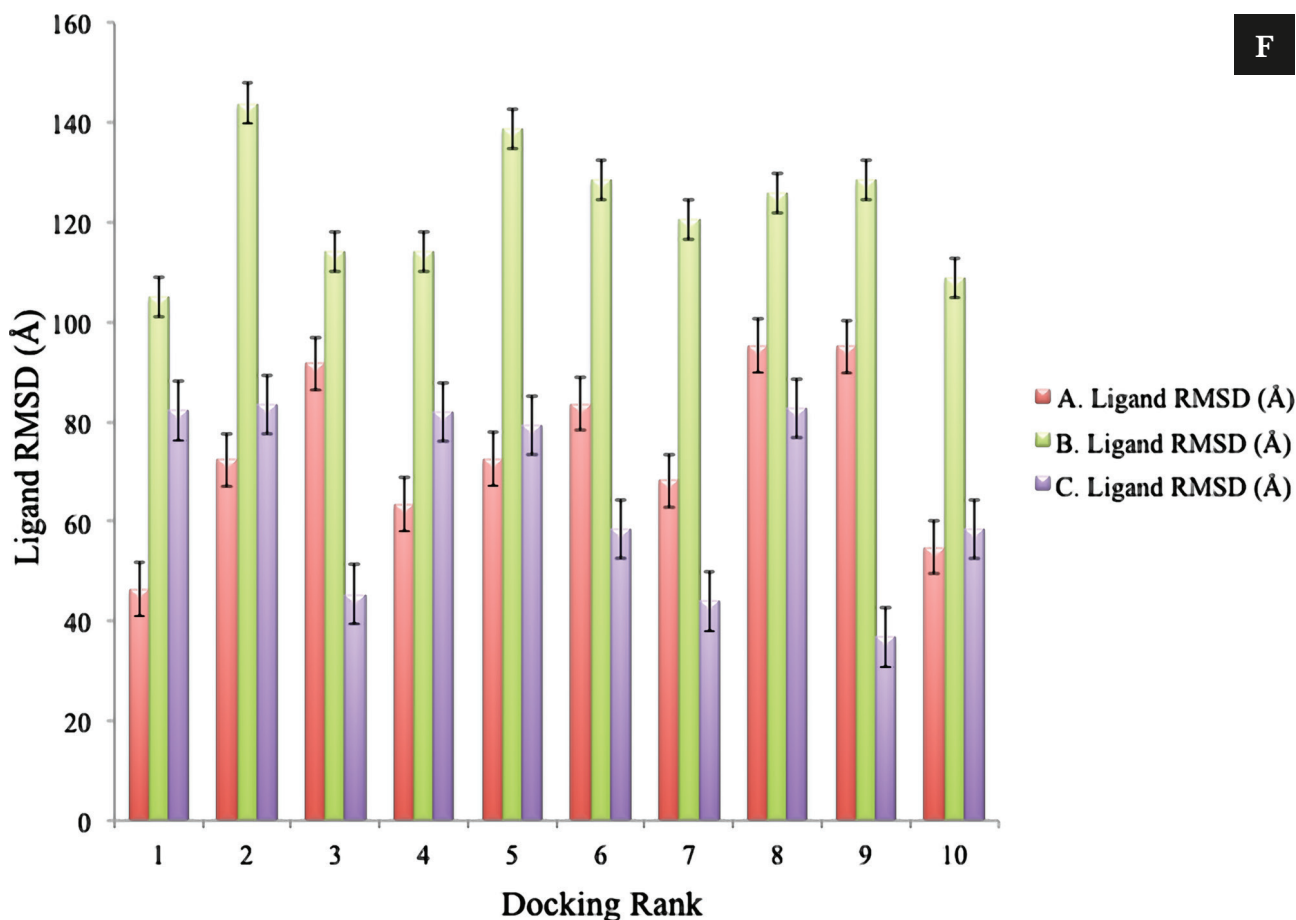


Figure S2. Continued.

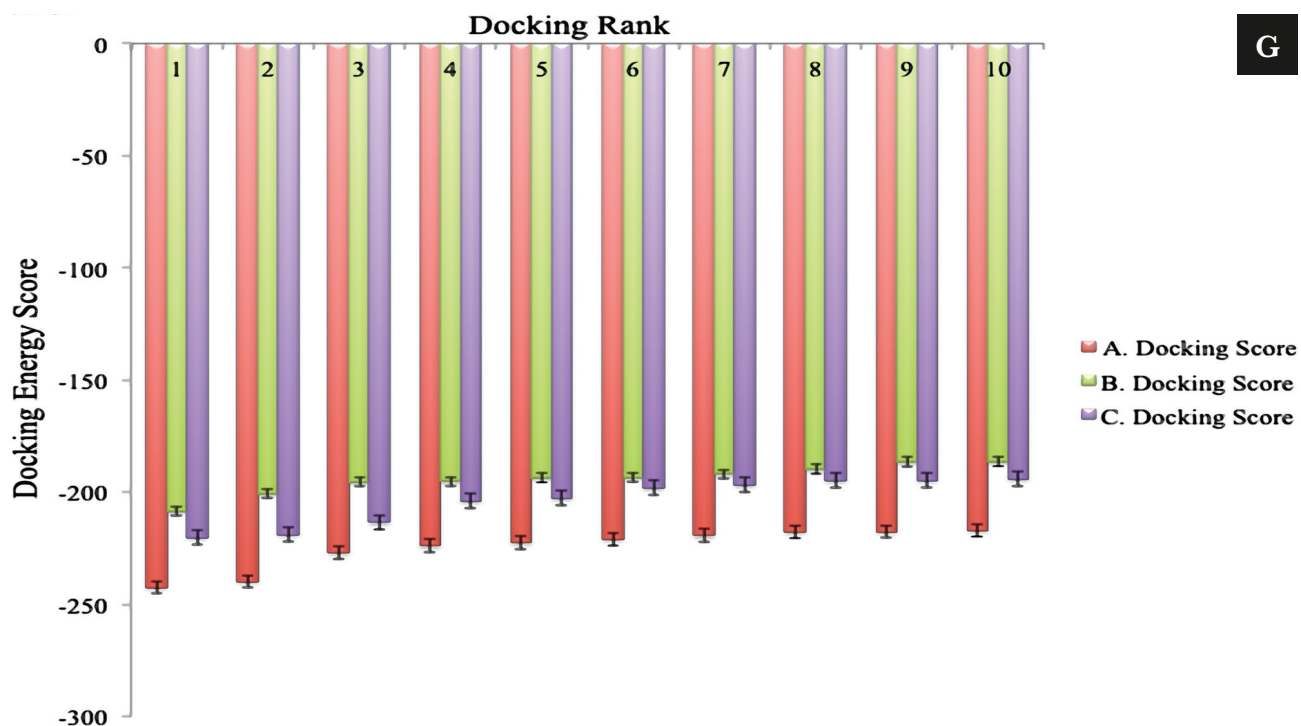


Figure S2. Continued.

Table S4. Relative fold change (RQ) results from RT-PCR analysis.

S.No.	Assay	RQ-Control (K562)	RQ-HLALB	RQ-OA	RQ-HALOA
1.	β-Actin	1	1	1	1
2.	CCAR1	1	0.9096	0.6695	0.882
3.	Notch 1	1	3.0061	0.4121	0.5655
4.	Notch 2	1	0.2662	1.3109	0.4257
5.	Notch 4	1	0.205	0.8899	1.6911
6.	Ikaros	1	0.5005	2.6418	5.4932
7.	CD-11d/ITGAD	1	0.3086	18.6956	32.2181

Table S5. Edge score of protein-protein interaction (PPI).

S.No.	Node 1	Node 2	Edge score
1.	MMP-9	CXCL8/IL-8	0.933
2.	NOTCH4	NOTCH1	0.923
3.	NOTCH4	NOTCH2	0.922
4.	NOTCH1	NOTCH2	0.913
5.	LEP	CXCL8	0.828
6.	MMP9	NOTCH1	0.764
7.	IKZF1	NOTCH1	0.746
8.	MMP9	LEP	0.707
9.	LEP	NOTCH1	0.656
10.	CXCL8	NOTCH1	0.510
11.	LEP	NOTCH2	0.450
12.	MMP9	SOD1	0.420