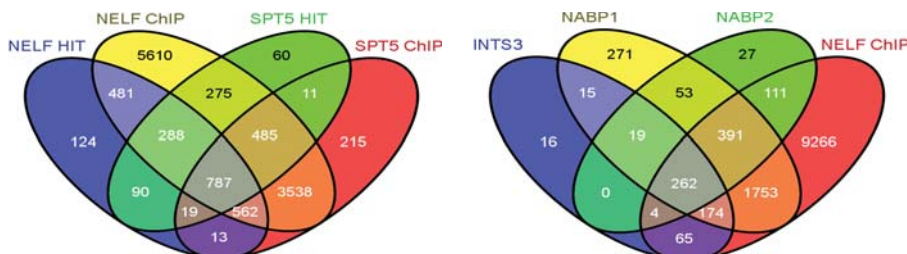


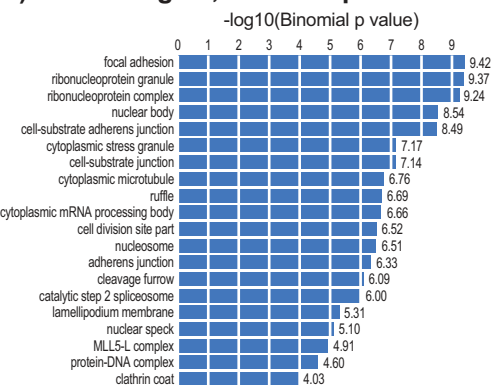
A)

Targets	INTS3	NABP1	NABP2	INTS9	NELF HIT-Seq	SPT5 HIT-Seq	NELFA ChIP-Seq	SPT5 ChIP-Seq	
INTS3	554	X	84.8	51.4	50	72.4	68.8	91.2	69.1
NABP1	2337	X	24.7	21.8	44.5	41.1	87.8	56	
NABP2	867	32.9	83.6	X	35.4	57	55	88.6	62.9
INTS9	1092	20.8	58.7	28.1	X	48.4	40.2	87.5	48.7
NELF HIT-Seq	2364	17	55.2	20.9	22.4	X	50.1	89.6	58.4
SPT5 HIT-Seq	2015	18.9	60	23.7	21.8	58.8	X	91.1	64.6
NELF ChIP-Seq	12026	4.2	21.4	6.4	7.9	17.6	15.3	X	44.7
SPT5 ChIP-Seq	5630	6.8	29.2	9.7	9.4	24.5	23.1	95.4	X

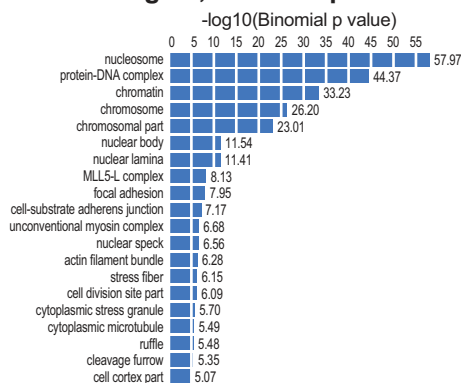
B)



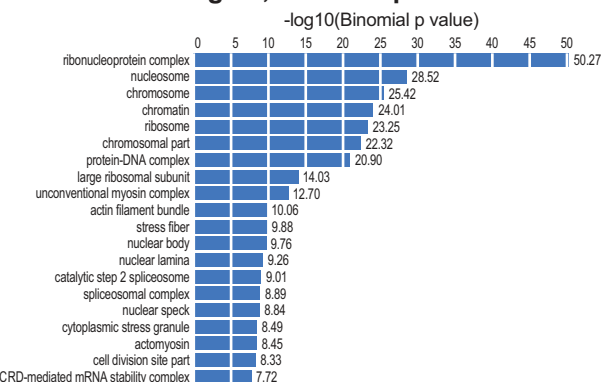
C) INTS9 Targets, Cell Compartment



NELF Targets, Cell Compartment



SPT5 Targets, Cell Compartment



Supplementary information, Figure S2 Extended Intersection and Gene

Ontology analysis of HIT-Seq data.

A) The percent intersection of target genes for each pair-wise combination is shown. The analysis includes the INTS3, NABP1, NABP2, INTS9, SPT5, and NELF composite HIT-Seq analyses and the existing NELF A and SPT5 ChIP-Seq analyses. HIT-Seq targets were defined as genes intersecting with a 2kb window containing six virus integration events, and ChIP-Seq targets were defined by intersection of peaks with genes.

B) The left Venn diagram shows the validation of the NELF composite and SPT5 HIT-Seq analyses by comparison with existing NELF A and SPT5 ChIP-Seq datasets. Gene targets were defined as in (A). The right Venn diagram shows the intersection of the INTS3, NABP1, and NABP2 HIT-Seq datasets with the NELF A ChIP-Seq dataset.

C) The gene ontology analysis for the cell compartment of INTS9, NELF, and SPT5 was performed using HIT-Seq data and GREAT.