Table S1. List of computer programs and scripts used in this study (available upon request)

A. Perl Scripts		
Script Name	**Function/Description**	**Author**
CombineIntegrationsFiles.pl	Combines serial number Integration files from multiple experiments into 1 file with all the data.	Esnault
location_t_SN-1.0.pl	Analyzes intergenic regions, or regions between motif locations, and tabulates how many Tf1 insertion events occur in ORFs or motifs, as well as in the regions between. It will also assign intergenic/inter motif insertions to an ORF, or a motif, based on proximity	Guo
ORF_map_v5.3.pl	Takes the output from location_t_SN-1.0.pl, aligns all the ORF/Motifs, and tabulates the total integration at position flanking them (1000 positions upstream and 1000 positions downstream).	Guo, Hickey
Map_binding_profile_around_Tf1.pl	Used to align the Tf1 serial number data with Sap1-CHIPseq data.	Esnault
Sap1_Integration_Counter.pl	Counts the number of TF1 integration events that occur in regions of Sap1 enrichment, and groups insertions based on size of the peaks they are found in.	Hickey
GR_converter.pl	Converts an Integration serial number text file and generates 3 .gr files from it; one for each chromosome	Hickey
group_orientations_inGr-141027.pl	Takes an integration .gr file that has 2 sets of insertions values for the same positions, one for each orientation/strand (indicated by +/- values), and generates a new .gr file where those positions have singe positive values (the absolute values of both numbers combined).	Esnault
Master_GR_maker.pl	Takes 3 integration .gr files, one for each chromosome, and combines the data into a single master gr-like file, in the following format, chromosome # (as chr #), location, and # of insertions.	Hickey
gr_peakfinderv2.pl	Identifies Sap1 peak locations from Sap1 .gr files. Will assign peaks positions to any values above a selected threshold. This program not only gives coordinates of Sap1-peaks but also calculates the peak area by summing up all the Y-axis values of all coordinates within the peak.	Hickey
Sap1peakintcountV5.pl	Counts the number of Tf1 integration events that occurs in each Sap1 peak, and list as an output peak position, # of insertions, peak length, the percentage of peak total peak length each peak is, and peak area.	Hickey
Int_Peak_sorter.pl	Sorts the output of Sap1peakintcountV4.p, and groups peaks based on the number of Tf1 insertion evens in each peak.	Hickey
gr_fillerV2.pl	Scans a .gr file for nucleotide positions with no reported values and assigns them a value of "-1", indicating that Sap1 binding in not enriched for these positions. Such a manipulation was necessary for some future analyses.	Hickey
Master_Sap1_Gr_maker.pl	Takes 3 Sap1 .gr files, one for each chromosome, and combines the data into a single master .gr-like file, in the following format, chromosome # (as chr-#), location, and # of insertions. If the Sap1 .gr file is a "filled" .gr file (see gr_filler.pl) it replaces all values of "-1" with "0." This is necessary when tabulating Sap1 binding values around insertion sites.	Hickey
Master_Sap1_Gr_maker_chrm.pl	Similar to "Master_Sap1_Gr_maker.pl" except that for the output each chromosome is represented only as its number and does not have the "chr" prefix before it. Output format is: chromosome # (as #),	Hickey

	location, # of insertions	
Gr_to_Csv.pl	Converts the output from any of the above master .gr maker files and converts them to .csv format	Hickey
Combine_integration_into_mastermatrix.pl	Creates a comparative matrix of insertion positions and numbers between each position from 2 or more Integration serial number files.	Esnault
matrix_converter.pl	Takes a matrix output integration file that has 2 sets of insertions values for the same positions, one for each orientation/strand (indicated by +/- values), and generates a new .gr file where those positions have single positive values (the absolute values of both numbers combined).	Hickey
matrix_eliminator.pl	Allows the user to designate the minimum cutoff value required and will remove any values lower from the matrix file for further analysis. i.e. it was used to remove positions from the output file generated from matrixconverter.pl that were less than 3 insertions.	Hickey
matrix_eliminated_sorter.pl	Used to identify integration positions (based on the output from matrix-eliminator.pl) in which there is a greater than two fold difference in the number of Tf1 integrations in the *Sap1*$^{+}$ and *Sap1-1* strains. This program was also used to sort identified positions based on whether Tf1 integration is increased or decreased in the *Sap1-1* strain, as well as how many insertions were in these positions in the Sap1+ reference strain.	Hickey
LTR_PEAK_indentifier.pl	Identifies peaks that are associated with LTRs and lists them.	Hickey
duplicate_trimmer.pl	Some peaks are large and are associated with multiple LTRs, and as a result, are listed multiple times. This programs eliminated duplicate peaks from the list	Hickey
B. Python Scripts		
Script Name	**Function/Description**	**Author**
wigConverter.py	Used to calculate the Log 2 ratio of Sap1 signal to that of WCE, and generate the output as a WIG file.	Yang
aligner.py	Used to sort intergenic regions into bins of 500 TSSs and sorted them based on TF1 insertion number. It also aligned integration events in the region with Sap1 binding and nucleosome occupancy	Yang
C. R-Scripts		
Script **Name**	**Function/Description**	**Author**
Density_scatterplot-3datasets.R	Used to generate density plots comparing numbers of integration events as specific nucleotide positions in s*ap1*$^{+}$ and *sap1-1* cells.	Esnault