

Supplementary Table S5. ATF binding site sequences and genomic coordinates (hg19).

Proviral LTR	Strand	Genomic Coordinates (hg19)	Sequence
Consensus sequence			GCCTTAGGGCTGGAG--GTGGGA
1q22 5' LTR	-	chr1:155605040-155605060	GCCTTAGGGCTGGAG--GTGGGA
1q22 3' LTR	-	chr1:155596828-155596848	GCCTTAGGGCTGGAG--GTGGGA
3q12.3 5' LTR	+	chr3:101411318-101411340	GCCTTAGGGCTGGAGGTGTGGGA
3q12.3 3' LTR	+	chr3:101419468-101419488	GCCTTAGGGCTGGAG--GTGGGA
3q21.2 5' LTR	+	chr3:125609870-125609890	GCCTTAGGGCTGGAG--GTGGGA
3q21.2 3' LTR	+	chr3:125618204-125618224	GCCTTAAGGCTGGAA--GTAGGA
5p13.3 5' LTR	-	chr5:30495627-30495647	GCCTTAGGGCTGGAG--GTGGGA
5p13.3 3' LTR	-	chr5:30487131-30487151	GCCTTAGGGCTGGAG--GTGGGA
7p22.1b 5' LTR	-	chr7:4630932-4630952	GCCTTAGGGCTGGAG--GTGGGA
8p23.1c 5' LTR	-	chr8:12082873-12082893	GCCCTGTGATGGGAG--GCAAGA
8p23.1c 3' LTR	-	chr8:12074373-12074393	GCCCTGTGGCGGGAG--GCGAGA
11p15.4 5' LTR	-	chr11:3477585-3477605	GCCCTGTGACGGGAG--GCGAGA
11p15.4 3' LTR	-	chr11:3469059-3469079	GCCCTGTGGCGGGAG--GCGAGA
21q21.1 5' LTR	-	chr21:19941366-19941386	GCCTTAGGGCTGGAG--GTGGGA
22q11.21 5' LTR	+	chr22:18926763-18926783	GCCTTAGGGCTGGAG--GTGGGA
22q11.21 3' LTR	+	chr22:18934970-18934990	GCCTTAGGGCTGGAG--GTGGGA