

Figure S1. Histone modification profiles near transcription start sites. The overall histone modification around transcription start sites (TSSs) was calculated. Histone modification levels of genes were separated by their expression levels; 2,000 high, medium, and low genes.

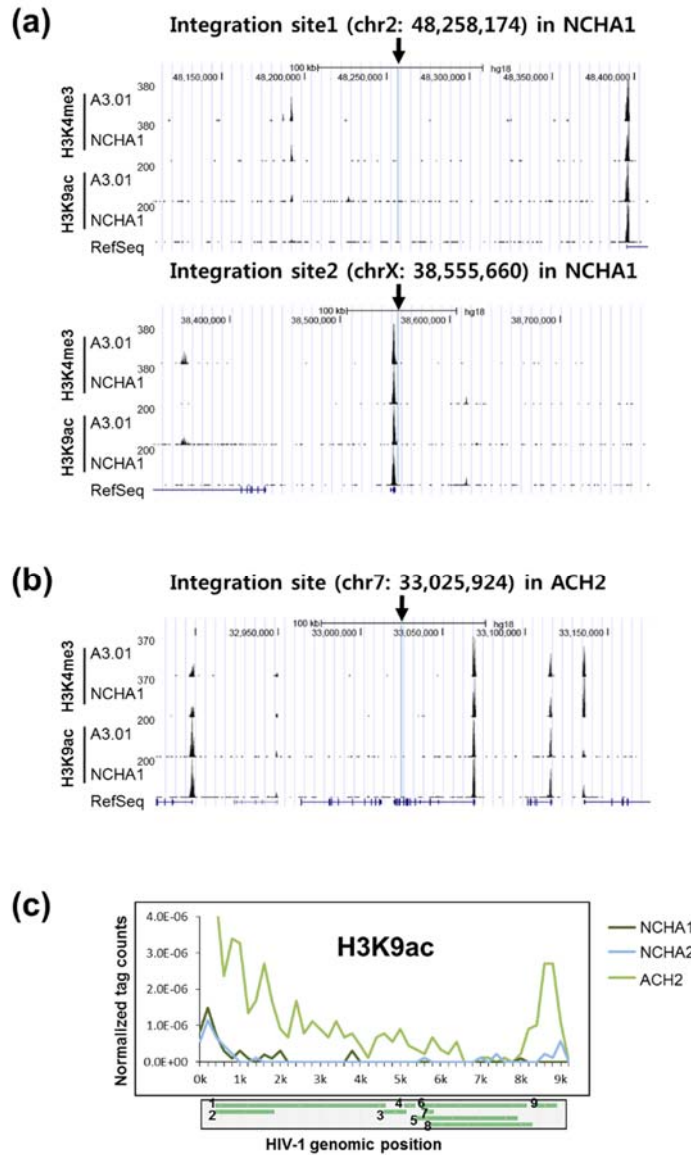


Figure S2. Histone modification enrichment patterns at the integration sites of HIV-1. (a) Two HIV-1 integration sites in NCHA1 cells were marked by arrows in chr2 and chrX. (b) In ACH2 cells, the HIV-1 was integrated in chr7 and marked by arrow. (c) The integrated HIV-1 genome itself was also subjected to enrichment analysis of histone H3K9ac. 1: Gag-Pol (336-4,642), 2: Gag (336-1,838), 3: Vif (4,587-5,165), 4: Vpr (5,105-5,396), 5: Tat (5,377-7,970), 6: Rev (5,516-8,199), 7: Vpu (5,608-5,856), 8: Env (5,771-8,341), 9: Nef (8,343-8,963).

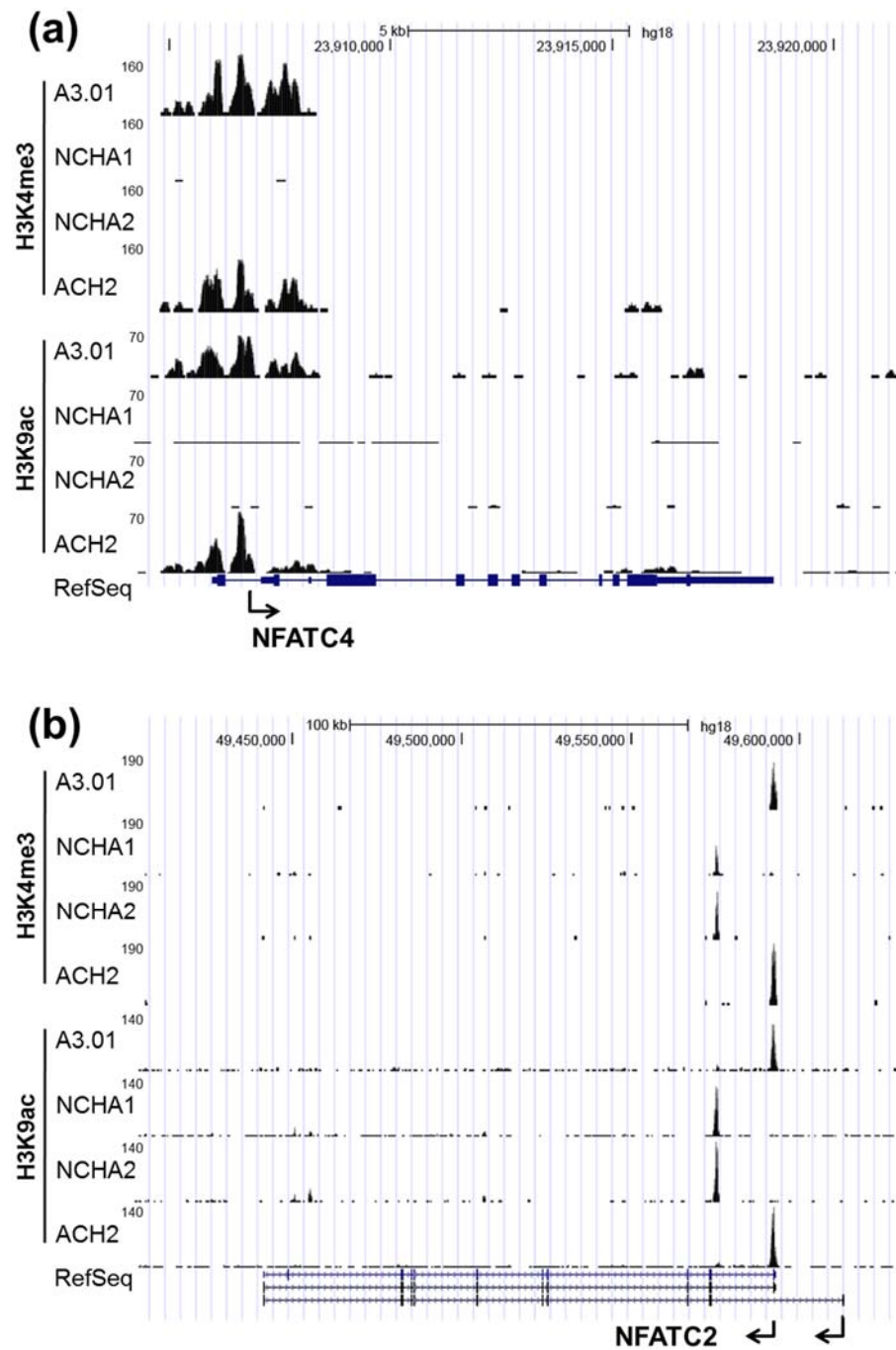


Figure S3. Histone modification enrichment patterns of NFAT family genes. Histone modifications, H3K4me3 and H3K9ac of NFATC4 (a) and NFATC2 (b) loci were displayed on the UCSC genome browser.

Table S1. The top 10 significantly enriched GO terms with down-regulated cluster genes.

GO ID	GO terms	p-val	corr p-val	cluster frequency	total frequency
Cluster 1					
7166	cell surface receptor linked signaling pathway	7.47E-13	6.11E-10	17/25 68.0%	1281/14306 8.9%
44419	interspecies interaction between organisms	2.61E-12	1.07E-09	11/25 44.0%	328/14306 2.2%
1775	cell activation	1.54E-11	3.80E-09	10/25 40.0%	276/14306 1.9%
42110	T cell activation	1.86E-11	3.80E-09	8/25 32.0%	120/14306 0.8%
45321	leukocyte activation	1.17E-10	1.91E-08	9/25 36.0%	234/14306 1.6%
23033	signaling pathway	1.61E-10	2.20E-08	18/25 72.0%	2101/14306 14.6%
2684	positive regulation of immune system process	3.66E-10	4.27E-08	9/25 36.0%	266/14306 1.8%
46649	lymphocyte activation	6.56E-10	6.71E-08	8/25 32.0%	187/14306 1.3%
23052	signaling	1.02E-09	8.65E-08	20/25 80.0%	3132/14306 21.8%
2682	regulation of immune system process	1.06E-09	8.65E-08	10/25 40.0%	425/14306 2.9%
Cluster 2					
42221	response to chemical stimulus	7.92E-17	9.71E-14	27/43 62.7%	1465/14306 10.2%
7166	cell surface receptor linked signaling pathway	8.68E-15	5.32E-12	24/43 55.8%	1281/14306 8.9%
23033	signaling pathway	6.62E-13	2.70E-10	27/43 62.7%	2101/14306 14.6%
10033	response to organic substance	1.29E-12	3.97E-10	19/43 44.1%	870/14306 6.0%
65009	regulation of molecular function	4.09E-12	1.00E-09	20/43 46.5%	1063/14306 7.4%
7626	locomotory behavior	1.73E-11	3.54E-09	12/43 27.9%	274/14306 1.9%
23052	signaling	2.48E-11	4.34E-09	30/43 69.7%	3132/14306 21.8%
42325	regulation of phosphorylation	1.71E-10	2.35E-08	14/43 32.5%	519/14306 3.6%
50896	response to stimulus	1.72E-10	2.35E-08	31/43 72.0%	3634/14306 25.4%
51174	regulation of phosphorus metabolic process	3.10E-10	3.40E-08	14/43 32.5%	543/14306 3.7%
19220	regulation of phosphate metabolic process	3.10E-10	3.40E-08	14/43 32.5%	543/14306 3.7%
Cluster 3					
8219	cell death	2.36E-10	9.84E-08	15/40 37.5%	698/14301 4.8%
16265	death	2.60E-10	9.84E-08	15/40 37.5%	703/14301 4.9%
42221	response to chemical stimulus	2.63E-10	9.84E-08	20/40 50.0%	1465/14301 10.2%
60	protein import into nucleus, translocation	2.78E-10	9.84E-08	6/40 15.0%	32/14301 0.2%
44093	positive regulation of molecular function	8.67E-10	2.46E-07	14/40 35.0%	639/14301 4.4%
43085	positive regulation of catalytic activity	1.77E-09	4.15E-07	13/40 32.5%	554/14301 3.8%
7166	cell surface receptor linked signaling pathway	2.05E-09	4.15E-07	18/40 45.0%	1281/14301 8.9%
10033	response to organic substance	4.92E-09	8.11E-07	15/40 37.5%	870/14301 6.0%
32270	positive regulation of cellular protein metabolic process	5.16E-09	8.11E-07	10/40 25.0%	291/14301 2.0%
65009	regulation of molecular function	8.88E-09	1.10E-06	16/40 40.0%	1063/14301 7.4%

Cluster 4					
50850	positive regulation of calcium-mediated signaling	3.16E-09	1.73E-06	4/16 25.0%	18/14304 0.1%
50848	regulation of calcium-mediated signaling	6.18E-09	1.73E-06	4/16 25.0%	21/14304 0.1%
2684	positive regulation of immune system process	6.87E-09	1.73E-06	7/16 43.7%	265/14304 1.8%
2376	immune system process	8.66E-09	1.73E-06	10/16 62.5%	948/14304 6.6%
7165	signal transduction	2.77E-08	4.44E-06	12/16 75.0%	1878/14304 13.1%
23052	signaling	4.31E-08	5.75E-06	14/16 87.5%	3131/14304 21.8%
23060	signal transmission	1.35E-07	1.35E-05	12/16 75.0%	2157/14304 15.0%
23046	signaling process	1.35E-07	1.35E-05	12/16 75.0%	2157/14304 15.0%
2682	regulation of immune system process	1.74E-07	1.54E-05	7/16 43.7%	424/14304 2.9%
42108	positive regulation of cytokine biosynthetic process	2.53E-07	2.02E-05	4/16 25.0%	51/14304 0.3%

Cluster 5					
35467	negative regulation of signaling pathway	8.99E-04	8.77E-02	3/11 27.2%	262/14306 1.8%
7165	signal transduction	1.30E-03	8.77E-02	6/11 54.5%	1878/14306 13.1%
6275	regulation of DNA replication	1.41E-03	8.77E-02	2/11 18.1%	74/14306 0.5%
10648	negative regulation of cell communication	1.72E-03	8.77E-02	3/11 27.2%	328/14306 2.2%
30111	regulation of Wnt receptor signaling pathway	1.94E-03	8.77E-02	2/11 18.1%	87/14306 0.6%
6435	threonyl-tRNA aminoacylation	2.31E-03	8.77E-02	1/11 9.0%	3/14306 0.0%
10633	negative regulation of epithelial cell migration	2.31E-03	8.77E-02	1/11 9.0%	3/14306 0.0%
23060	signal transmission	2.72E-03	8.77E-02	6/11 54.5%	2157/14306 15.0%
23046	signaling process	2.72E-03	8.77E-02	6/11 54.5%	2157/14306 15.0%
90304	nucleic acid metabolic process	3.00E-03	8.77E-02	5/11 45.4%	1460/14306 10.2%

Significant GO terms were identified by BiNGO plugin of Cytoscape with hypergeometric test. Most significantly enriched terms were selected according to their p-value.

Table S2. The top 10 significantly enriched GO terms with up-regulated cluster genes.

GO ID	GO terms	p-val	corr p-val	cluster frequency	total frequency
Cluster 1					
51726	regulation of cell cycle	1.36E-24	1.60E-21	22/36 61.1%	450/14304 3.1%
48522	positive regulation of cellular process	1.76E-20	1.04E-17	30/36 83.3%	2007/14304 14.0%
48523	negative regulation of cellular process	4.62E-20	1.81E-17	29/36 80.5%	1848/14304 12.9%
48518	positive regulation of biological process	2.98E-19	8.76E-17	30/36 83.3%	2211/14304 15.4%
10604	positive regulation of macromolecule metabolic process	5.40E-19	1.17E-16	23/36 63.8%	943/14304 6.5%
48519	negative regulation of biological process	5.99E-19	1.17E-16	29/36 80.5%	2024/14304 14.1%
42127	regulation of cell proliferation	1.44E-18	2.42E-16	22/36 61.1%	851/14304 5.9%
9893	positive regulation of metabolic process	3.12E-18	4.59E-16	23/36 63.8%	1020/14304 7.1%
45786	negative regulation of cell cycle	4.13E-18	5.39E-16	14/36 38.8%	179/14304 1.2%
31324	negative regulation of cellular metabolic process	7.54E-18	8.87E-16	21/36 58.3%	790/14304 5.5%
Cluster 2					
19932	second-messenger-mediated signaling	8.78E-11	3.28E-08	8/17 47.0%	231/14306 1.6%
46834	lipid phosphorylation	6.71E-10	8.35E-08	4/17 23.5%	12/14306 0.0%
46854	phosphoinositide phosphorylation	6.71E-10	8.35E-08	4/17 23.5%	12/14306 0.0%
9755	hormone-mediated signaling pathway	3.12E-09	2.40E-07	5/17 29.4%	52/14306 0.3%
34199	activation of protein kinase A activity	3.22E-09	2.40E-07	4/17 23.5%	17/14306 0.1%
30258	lipid modification	9.82E-09	6.11E-07	5/17 29.4%	65/14306 0.4%
30384	phosphoinositide metabolic process	2.49E-08	1.33E-06	5/17 29.4%	78/14306 0.5%
6644	phospholipid metabolic process	6.89E-08	3.21E-06	6/17 35.2%	197/14306 1.3%
19637	organophosphate metabolic process	9.52E-08	3.58E-06	6/17 35.2%	208/14306 1.4%
7193	inhibition of adenylate cyclase activity by G-protein signaling pathway	1.21E-07	3.58E-06	4/17 23.5%	40/14306 0.2%
Cluster 3					
9893	positive regulation of metabolic process	6.43E-21	1.06E-17	30/54 55.5%	1017/14302 7.1%
31325	positive regulation of cellular metabolic process	2.44E-20	2.02E-17	29/54 53.7%	965/14302 6.7%
44419	interspecies interaction between organisms	1.36E-19	7.27E-17	20/54 37.0%	327/14302 2.2%
48518	positive regulation of biological process	1.76E-19	7.27E-17	38/54 70.3%	2206/14302 15.4%
48522	positive regulation of cellular process	1.02E-18	3.38E-16	36/54 66.6%	2003/14302 14.0%
31323	regulation of cellular metabolic process	1.80E-18	4.96E-16	45/54 83.3%	3734/14302 26.1%
6357	regulation of transcription from RNA polymerase II promoter	2.39E-18	5.66E-16	25/54 46.2%	747/14302 5.2%
10604	positive regulation of macromolecule metabolic process	2.94E-18	6.09E-16	27/54 50.0%	940/14302 6.5%
60255	regulation of macromolecule metabolic process	4.87E-18	8.96E-16	43/54 79.6%	3375/14302 23.5%
10033	response to organic substance	6.05E-18	1.00E-15	26/54 48.1%	869/14302 6.0%
Cluster 4					
51726	regulation of cell cycle	1.03E-26	1.65E-23	30/71 42.2%	451/14301 3.1%

51716	cellular response to stimulus	2.95E-22	2.36E-19	35/71 49.2%	991/14301 6.9%
48522	positive regulation of cellular process	1.20E-20	6.41E-18	44/71 61.9%	2008/14301 14.0%
48523	negative regulation of cellular process	4.79E-20	1.91E-17	42/71 59.1%	1849/14301 12.9%
48518	positive regulation of biological process	6.12E-20	1.96E-17	45/71 63.3%	2212/14301 15.4%
10604	positive regulation of macromolecule metabolic process	1.34E-19	3.58E-17	32/71 45.0%	944/14301 6.6%
42127	regulation of cell proliferation	1.00E-18	2.29E-16	30/71 42.2%	852/14301 5.9%
9893	positive regulation of metabolic process	1.38E-18	2.52E-16	32/71 45.0%	1021/14301 7.1%
48519	negative regulation of biological process	1.52E-18	2.52E-16	42/71 59.1%	2025/14301 14.1%
31324	negative regulation of cellular metabolic process	1.57E-18	2.52E-16	29/71 40.8%	791/14301 5.5%

Cluster 5

6414	translational elongation	2.46E-05	5.69E-03	3/9 33.3%	97/14306 0.6%
46606	negative regulation of centrosome cycle	6.29E-04	3.69E-02	1/9 11.1%	1/14306 0.0%
46600	negative regulation of centriole replication	6.29E-04	3.69E-02	1/9 11.1%	1/14306 0.0%
6412	translation	6.39E-04	3.69E-02	3/9 33.3%	291/14306 2.0%
46599	regulation of centriole replication	1.89E-03	8.22E-02	1/9 11.1%	3/14306 0.0%
71680	response to indole-3-methanol	3.14E-03	8.22E-02	1/9 11.1%	5/14306 0.0%
71681	cellular response to indole-3-methanol	3.14E-03	8.22E-02	1/9 11.1%	5/14306 0.0%
6729	tetrahydrobiopterin biosynthetic process	3.77E-03	8.22E-02	1/9 11.1%	6/14306 0.0%
85020	protein K6-linked ubiquitination	4.40E-03	8.22E-02	1/9 11.1%	7/14306 0.0%
46146	tetrahydrobiopterin metabolic process	4.40E-03	8.22E-02	1/9 11.1%	7/14306 0.0%

Cluster 6

44260	cellular macromolecule metabolic process	2.80E-08	2.55E-05	20/26 76.9%	3508/14306 24.5%
44237	cellular metabolic process	2.49E-07	9.82E-05	22/26 84.6%	4990/14306 34.8%
43170	macromolecule metabolic process	3.23E-07	9.82E-05	20/26 76.9%	4017/14306 28.0%
44419	interspecies interaction between organisms	1.38E-06	3.16E-04	7/26 26.9%	327/14306 2.2%
44267	cellular protein metabolic process	4.72E-06	8.61E-04	14/26 53.8%	2153/14306 15.0%
44238	primary metabolic process	6.18E-06	9.40E-04	21/26 80.7%	5288/14306 36.9%
8152	metabolic process	8.30E-06	1.08E-03	22/26 84.6%	5959/14306 41.6%
23034	intracellular signaling pathway	1.85E-05	2.11E-03	10/26 38.4%	1158/14306 8.0%
6461	protein complex assembly	2.46E-05	2.25E-03	7/26 26.9%	507/14306 3.5%
70271	protein complex biogenesis	2.46E-05	2.25E-03	7/26 26.9%	507/14306 3.5%

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test. Most significantly enriched terms were selected according to their p-value.