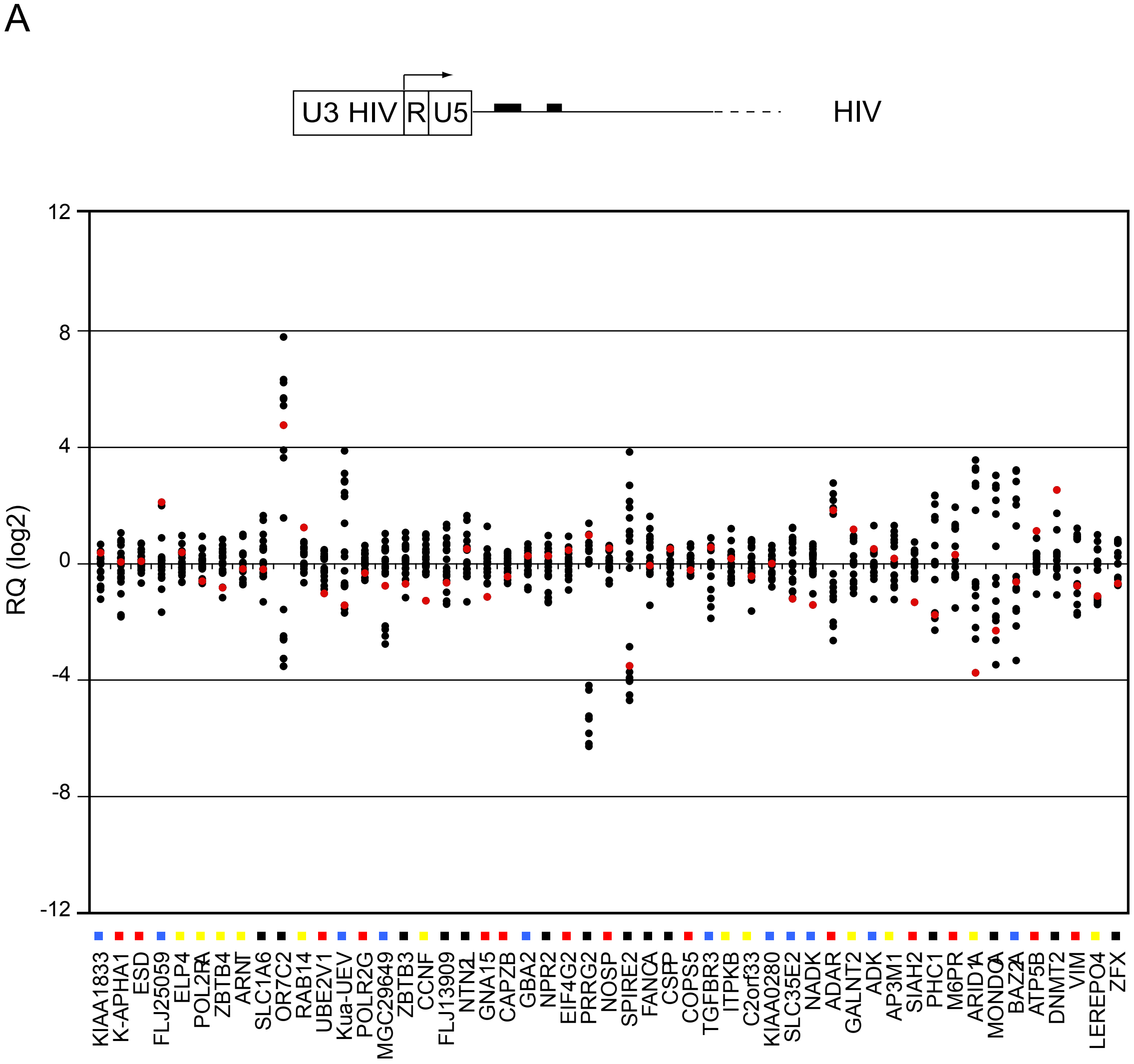
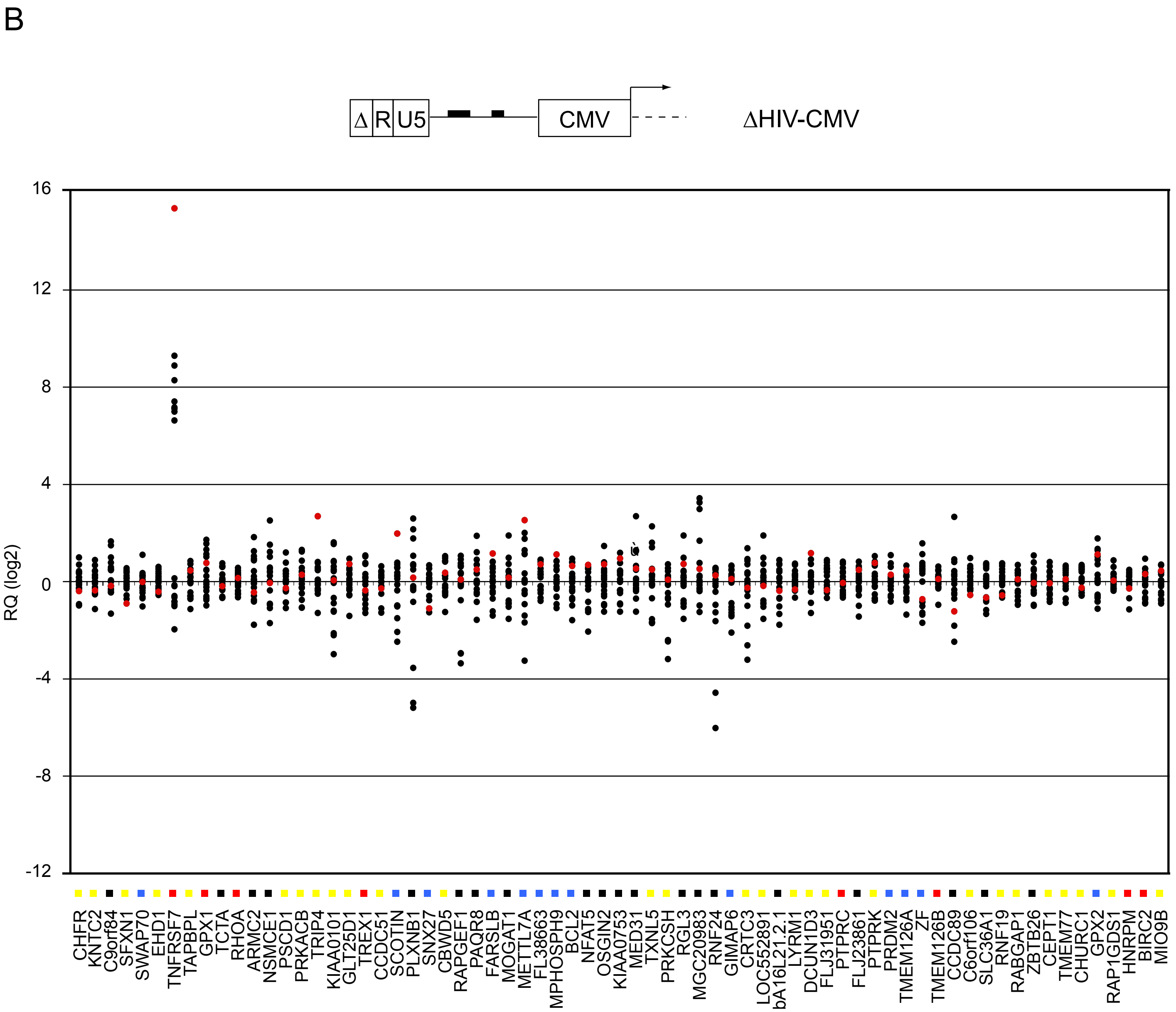
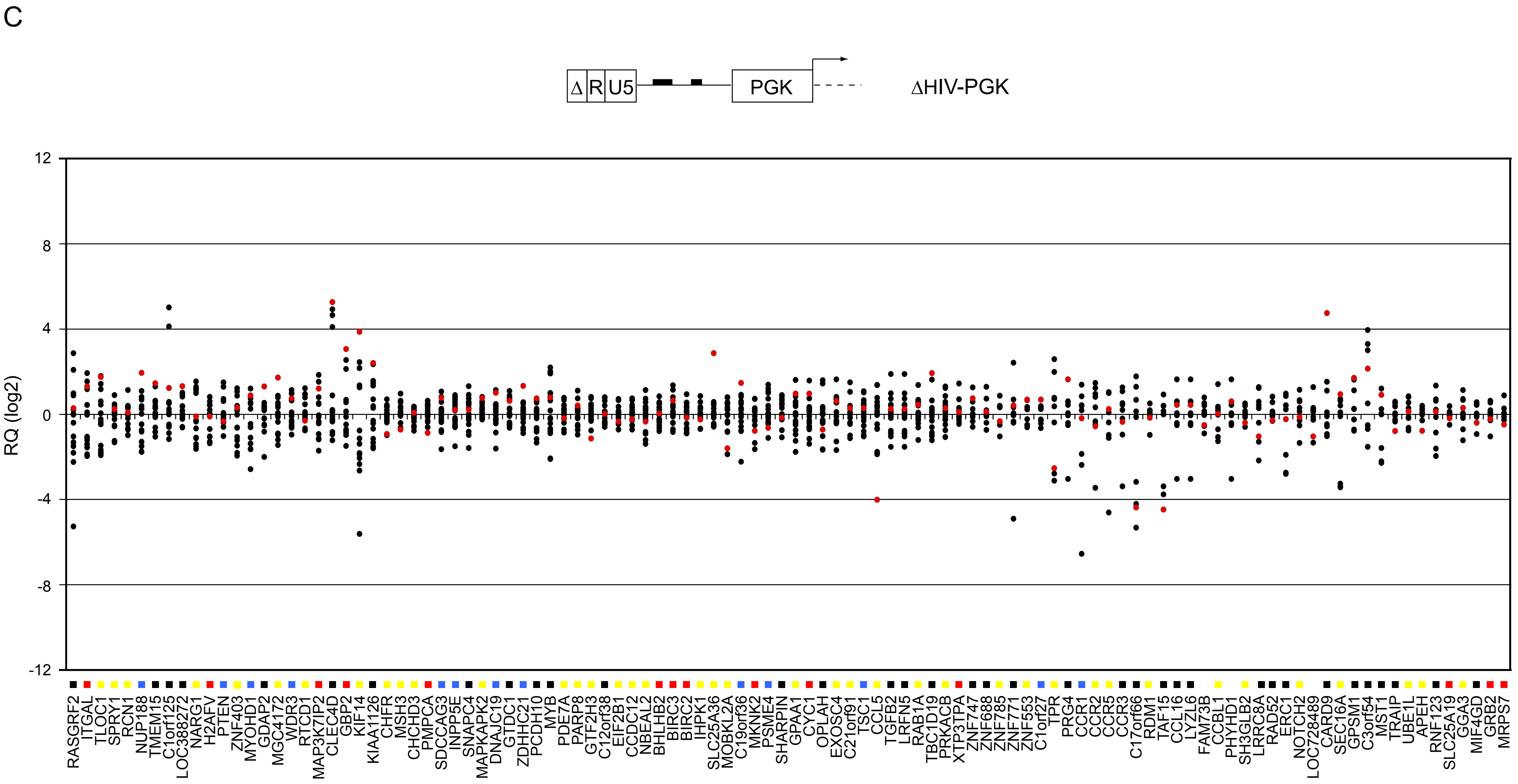
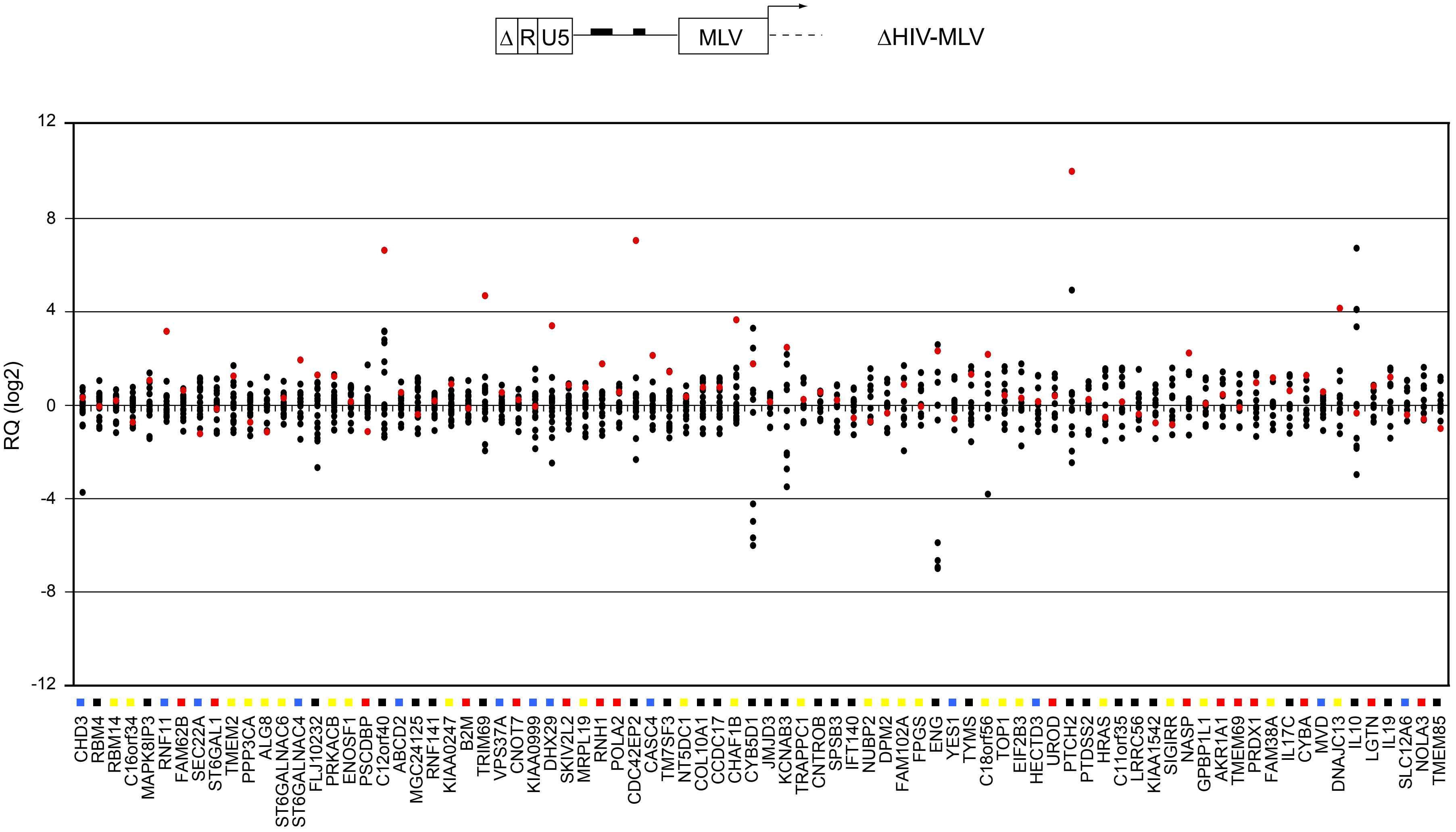
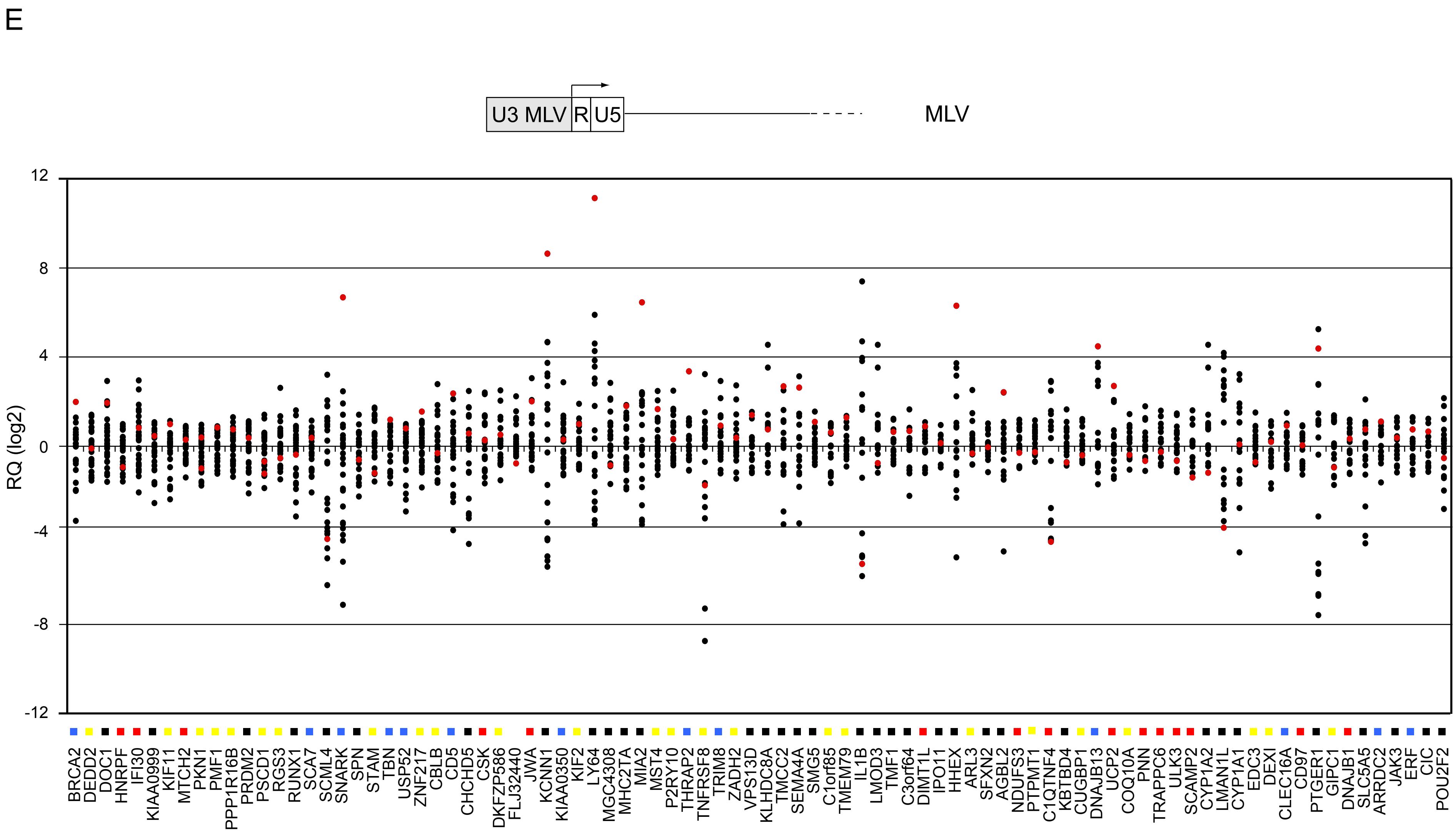

A
U3 HIV
R
U5
HIV
RQ (log2)
12
8
4
0
-4
-8
-12
KIAA1833
K-APHA1
ESD
FLJ25059
ELP4
POL2RA
ZBTB4
ARNT
SLC1A6
OR7C2
RAB14
UBE2V1
Kua-UEV
POLR2G
MGC29649
ZBTB3
CCNF
FLJ13909
NTN2
GNA15
CAPZB
GBA2
NPR2
EIF4G2
PRRG2
NOSP
SPIRE2
FANCA
CSPP
COPS5
TGFBR3
ITPKB
C2orf33
KIAA0280
SLC35E2
NADK
ADAR
GALNT2
ADK
AP3M1
SIAH2
PHC1
M6PR
ARID1A
MONDOA
BAZ2A
ATP5B
DNMT2
VIM
LEREPO4
ZFX


B
Δ
R
U5
CMV
ΔHIV-CMV
RQ (log2)
16
12
8
4
0
-4
-8
-12
CHFR
KNTC2
C9orf84
SFXN1
SWAP70
EHD1
TNFRSF7
TAPBPL
GPX1
TCTA
RHOA
ARMC2
NSMCE1
PSCD1
PRKACB
TRIP4
KIAA0101
GLT25D1
TREX1
CCDC51
SCOTIN
PLXNB1
SNX27
CBWD5
RAPGEF1
PAQR8
FARSLB
MOGAT1
METTL7A
FL38663
MPHOSPH9
BCL2
NFAT5
OSGIN2
KIAA0753
MED31
TXNL5
PRKCSH
RGL3
MGC20983
RNF24
GIMAP6
CRTC3
LOC552891
bA16L21.2.1
LYRM1
DCUN1D3
FLJ31951
PTPRC
FLJ23861
PTPRK
PRDM2
TMEM126A
ZF
TMEM126B
CCDC89
C6orf106
SLC36A1
RNF19
RABGAP1
ZBTB26
CEPT1
TMEM77
CHURC1
GPX2
RAP1GDS1
HNRPM
BIRC2
MIO9B


C
Δ
R
U5
PGK
ΔHIV-PGK
RQ (log2)
12
8
4
0
-4
-8
-12
RASGRF2
ITGAL
TLOC1
SPRY1
RCN1
NUP188
TMEM15
C1orf125
LOC388272
NARG1
H2AFV
PTEN
ZNF403
MYOHD1
GDAP2
MGC4172
WDR3
RTCD1
MAP3K7IP2
CLEC4D
GBP2
KIF14
KIAA1126
CHFR
MSH3
CHCHD3
PMPCA
SDCCAG3
INPP5E
SNAPC4
MAPKAPK2
DNAJC19
GTDC1
ZDHHC21
PCDH10
MYB
PDE7A
PARP8
GTF2H3
C12orf38
EIF2B1
CCDC12
NBEAL2
BHLHB2
BIRC3
BIRC2
IHPK1
SLC25A36
MOBKL2A
C19orf36
MKNK2
PSME4
SHARPIN
GPAA1
CYC1
OPLAH
EXOSC4
C21orf91
TSC1
CCL5
TGFB2
LRFN5
RAB1A
TBC1D19
PRKACB
XTP3TPA
ZNF747
ZNF688
ZNF785
ZNF771
ZNF553
C1orf27
TPR
PRG4
CCR1
CCR2
CCR5
CCR3
C17orf66
RDM1
TAF15
CCL16
LYZL6
FAM73B
CCBL1
PHYHD1
SH3GLB2
LRRC8A
RAD52
ERC1
NOTCH2
LOC728489
CARD9
SEC16A
GPSM1
C3orf54
MST1
TRAIP
UBE1L
APEH
RNF123
SLC25A19
GGA3
MIF4GD
GRB2
MRPS7

D


Δ
R
U5
MLV
ΔHIV-MLV
RQ (log2)
12
8
4
0
-4
-8
-12
CHD3
RBM4
RBM14
C16orf34
MAPK8IP3
RNF11
FAM62B
SEC22A
ST6GAL1
TMEM2
PPP3CA
ALG8
ST6GALNAC6
ST6GALNAC4
FLJ10232
PRKACB
ENOSF1
PSCDBP
C12orf40
ABCD2
MGC24125
RNF141
KIAA0247
B2M
TRIM69
VPS37A
CNOT7
KIAA0999
DHX29
SKIV2L2
MRPL19
RNH1
POLA2
CDC42EP2
CASC4
TM7SF3
NT5DC1
COL10A1
CCDC17
CHAF1B
CYB5D1
JMJD3
KCNAB3
TRAPPC1
CNTROB
SPSB3
IFT140
NUBP2
DPM2
FAM102A
FPGS
ENG
YES1
TYMS
C18orf56
TOP1
EIF2B3
HECTD3
UROD
PTCH2
PTDSS2
HRAS
C11orf35
LRRC56
KIAA1542
SIGIRR
NASP
GPBP1L1
AKR1A1
TMEM69
PRDX1
FAM38A
IL17C
CYBA
MVD
DNAJC13
IL10
LGTN
IL19
SLC12A6
NOLA3
TMEM85


E
U3 MLV
R
U5
MLV
RQ (log2)
12
8
4
0
-4
-8
-12
BRCA2
DEDD2
DOC1
HNRPF
IFI30
KIAA0999
KIF11
MTCH2
PKN1
PMF1
PPP1R16B
PRDM2
PSCD1
RGS3
RUNX1
SCA7
SCML4
SNARK
SPN
STAM
TBN
USP52
ZNF217
CBLB
CD5
CHCHD5
CSK
DKFZP586
FLJ32440
JWA
KCNN1
KIAA0350
KIF2
LY64
MGC4308
MHC2TA
MIA2
MST4
P2RY10
THRAP2
TNFRSF8
TRIM8
ZADH2
VPS13D
KLHDC8A
TMCC2
SEMA4A
SMG5
C1orf85
TMEM79
IL1B
LMOD3
TMF1
C3orf64
DIMT1L
IPO11
HHEX
ARL3
SFXN2
AGBL2
NDUFS3
PTPMT1
C1QTNF4
KBTBD4
CUGBP1
DNAJB13
UCP2
COQ10A
PNN
TRAPPC6
ULK3
SCAMP2
CYP1A2
LMAN1L
CYP1A1
EDC3
DEXI
CLEC16A
CD97
PTGER1
GIPC1
DNAJB1
SLC5A5
ARRDC2
JAK3
ERF
CIC
POU2F2

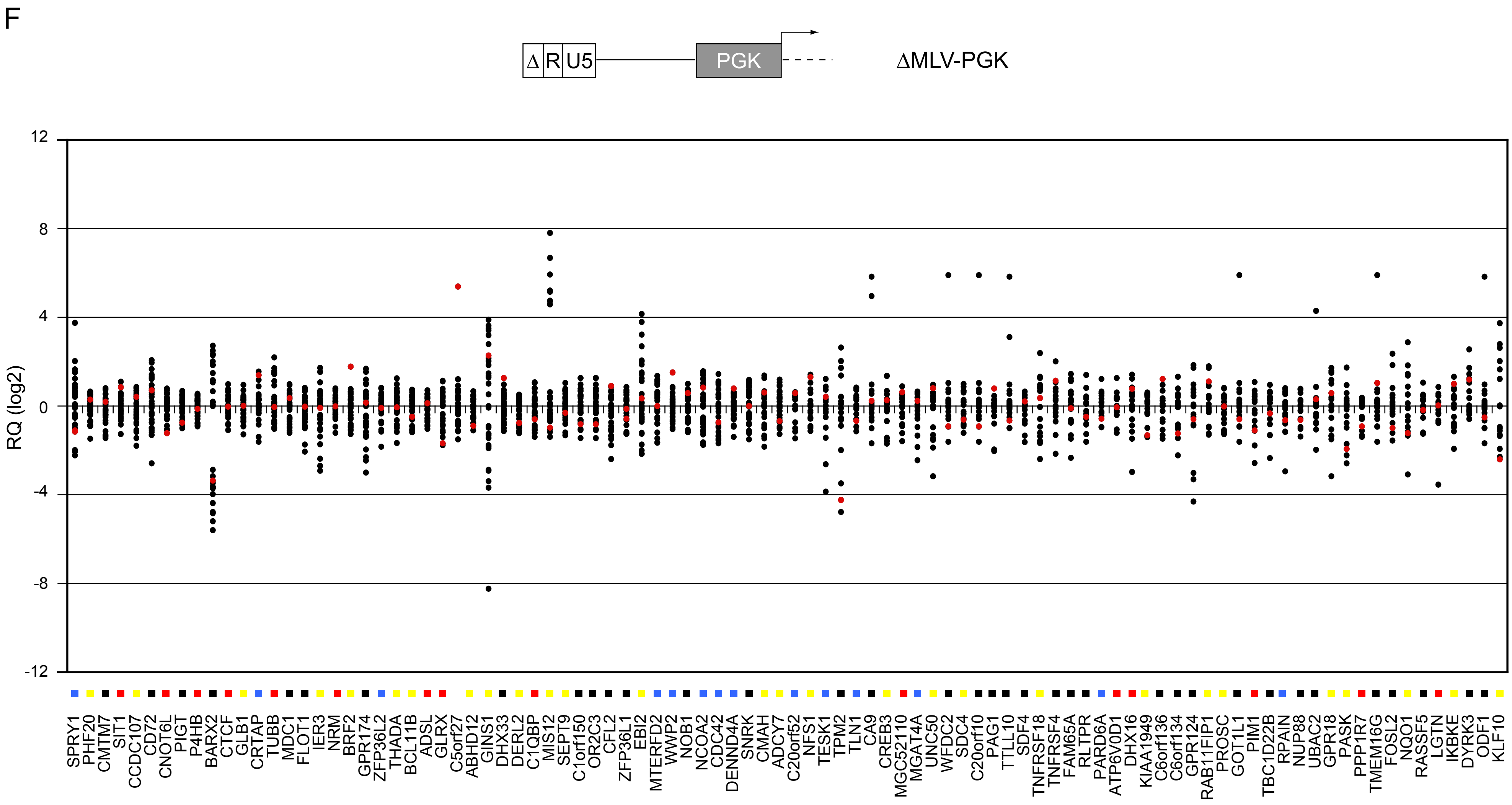

F
Δ
R
U5
PGK
ΔMLV-PGK
RQ (log2)
12
8
4
0
-4
-8
-12
SPRY1
PHF20
CMTM7
SIT1
CCDC107
CD72
CNOT6L
PIGT
P4HB
BARX2
CTCF
GLB1
CRTAP
TUBB
MDC1
FLOT1
IER3
NRM
BRF2
GPR174
ZFP36L2
THADA
BCL11B
ADSL
GLRX
C5orf27
ABHD12
GINS1
DHX33
DERL2
C1QBP
MIS12
SEPT9
C1orf150
OR2C3
CFL2
ZFP36L1
EBI2
MTERFD2
WWP2
NOB1
NCOA2
CDC42
DENND4A
SNRK
CMAH
ADCY7
C20orf52
NFS1
TESK1
TPM2
TLN1
CA9
CREB3
MGC52110
MGAT4A
UNC50
WFDC2
SDC4
C20orf10
PAG1
TTLL10
SDF4
TNFRSF18
TNFRSF4
FAM65A
RLTPR
PARD6A
ATP6V0D1
DHX16
KIAA1949
C6orf136
C6orf134
GPR124
RAB11FIP1
PROSC
GOT1L1
PIM1
TBC1D22B
RPAIN
NUP88
UBAC2
GPR18
PASK
PPP1R7
TMEM16G
FOSL2
NQO1
RASSF5
LGTN
IKBKE
DYRK3
ODF1
KLF10

Figure S1. (A-F) Quantitative PCR analysis of the expression in individual T-cell clones of all the analyzed genes in a window of ±100-kb around the integration sites of the RV and LV vectors indicated in Figure 1A. Expression levels (*y* axis) were measured as relative mRNA quantity (RQ) after normalization for the level of GAPDH, and plotted as log2 variations from the median level (0) in all analyzed clones. For each gene (*x* axis), the expression value in the test clone is indicated by red dots, the expression values in the control clones (10 to 31) are indicated by black dots. Color-coded symbols on the *x*-axis indicate the average expression level of each gene in proliferating T cells as determined by Affymetrix microarray analysis (black: no expression; blue: low expression; yellow: intermediate expression; red: high expression). The name and schematic structure of the analyzed vector is indicated above each panel.