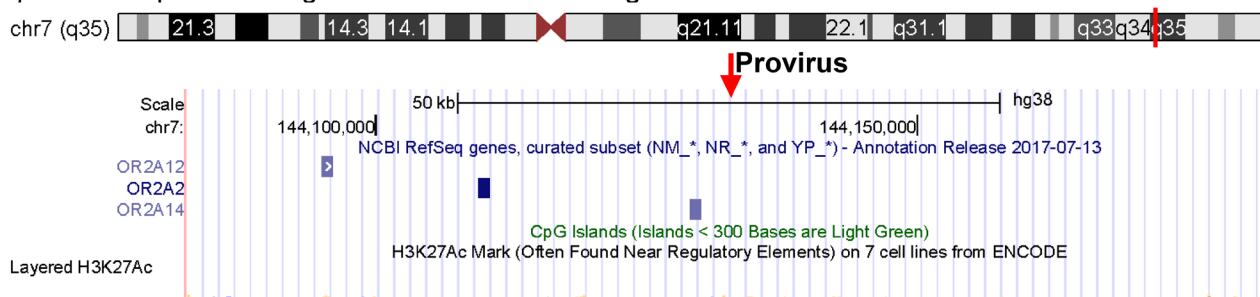


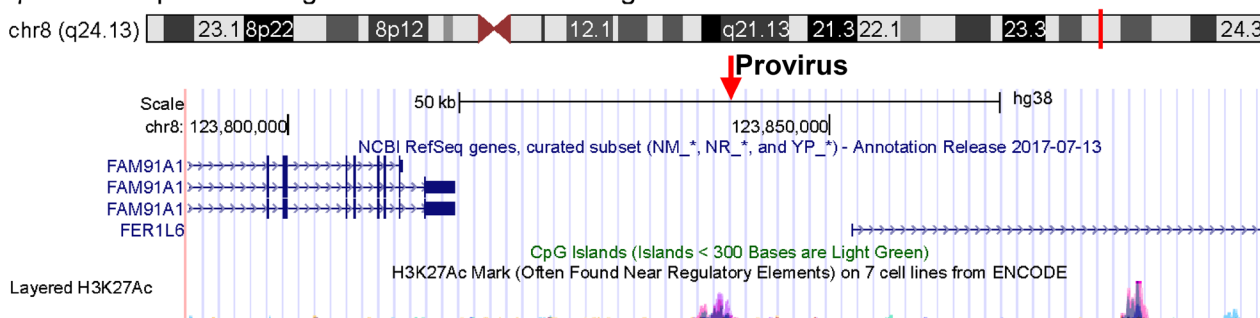
# Replication-incompetent gammaretroviral and lentiviral vector-based insertional mutagenesis screens identify prostate cancer progression genes

## SUPPLEMENTARY MATERIALS

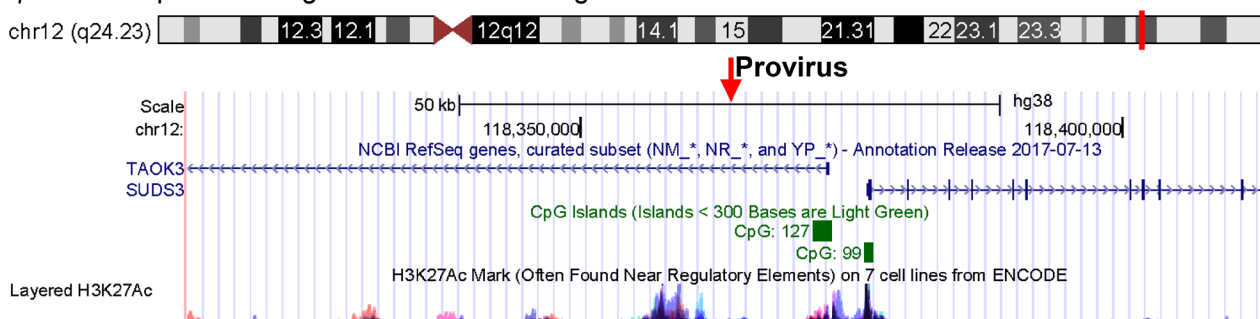
$\gamma$ RV vector proviral integration site near *OR2A14* gene on chromosome 7



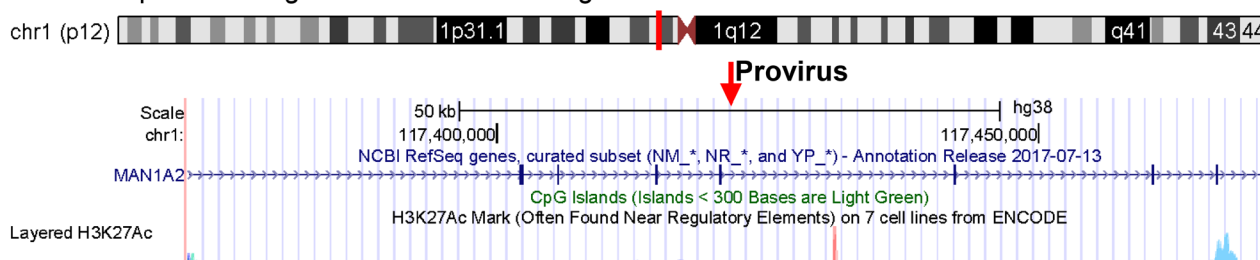
$\gamma$ RV vector proviral integration site near *FER1L6* gene on chromosome 8



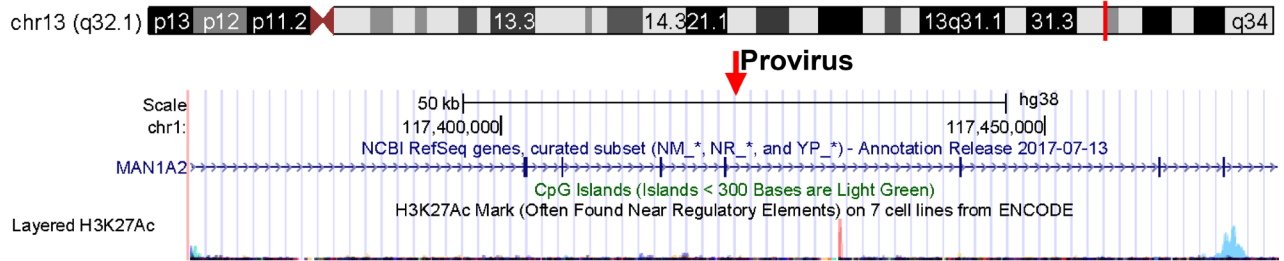
$\gamma$ RV vector proviral integration site in *TAOK3* gene on chromosome 12



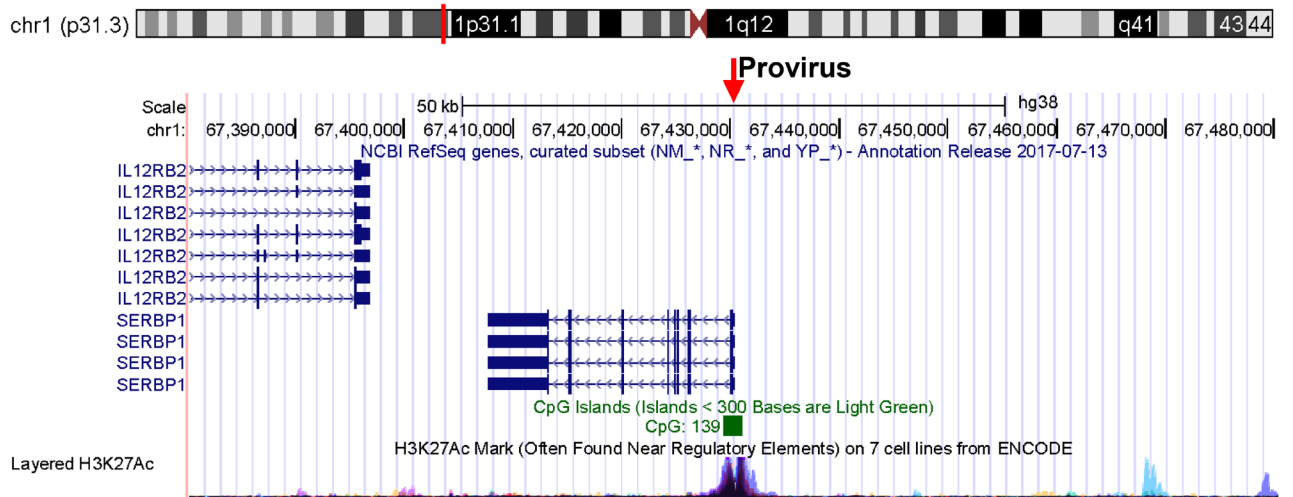
LV vector proviral integration site in *MAN1A2* gene on chromosome 1



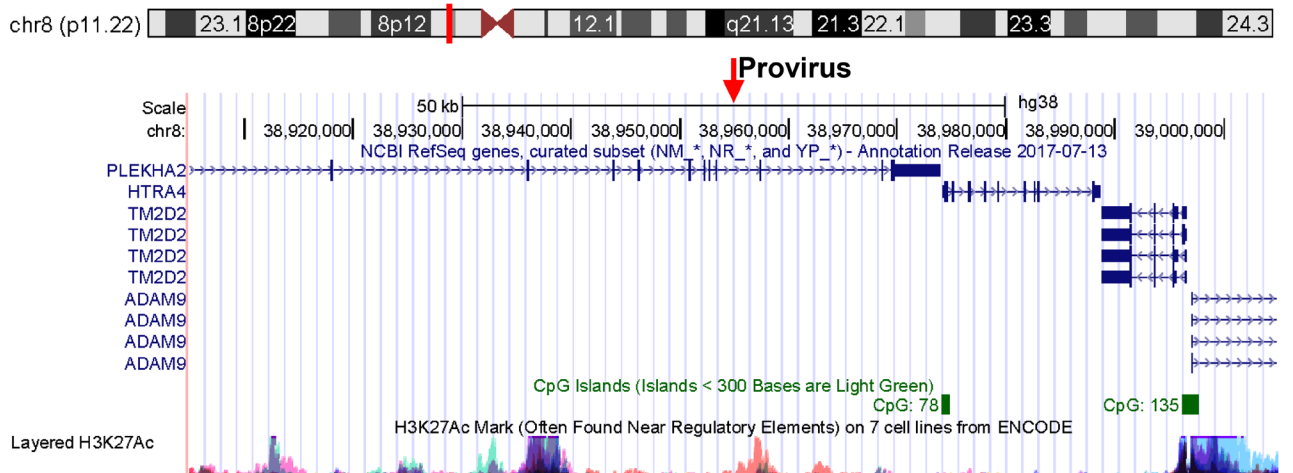
$\gamma$ RV vector proviral integration site in *MBNL2* gene on chromosome 13



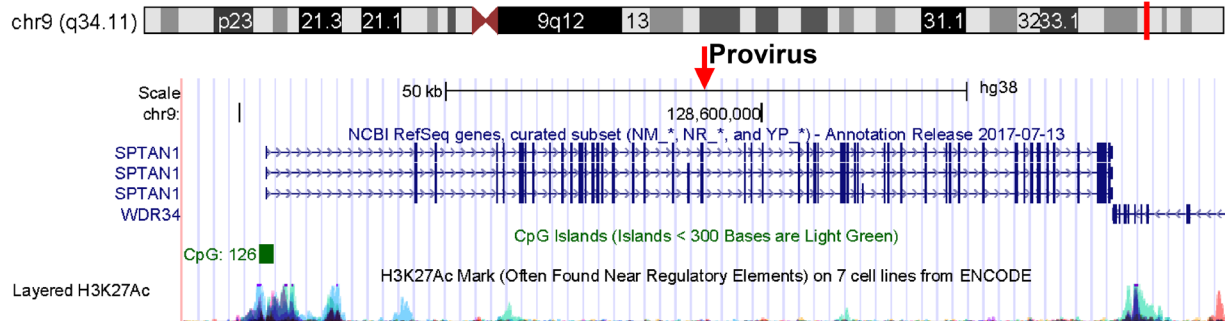
$\gamma$ RV vector proviral integration site in *SERBP1* gene on chromosome 1



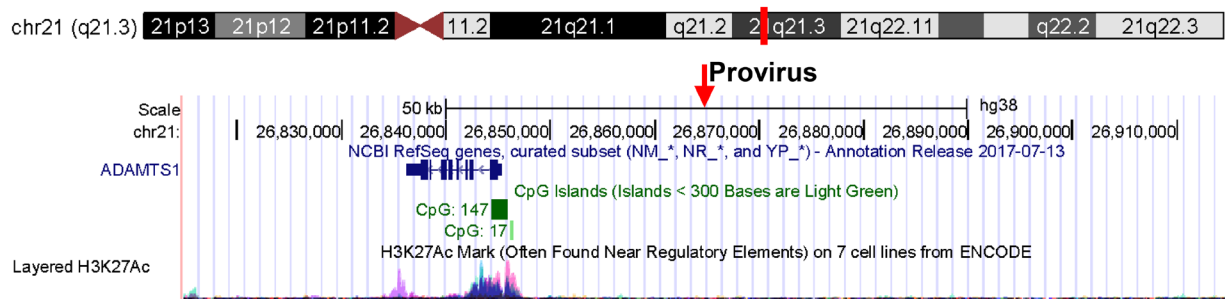
LV vector proviral integration site in *PLEKHA2* gene on chromosome 8



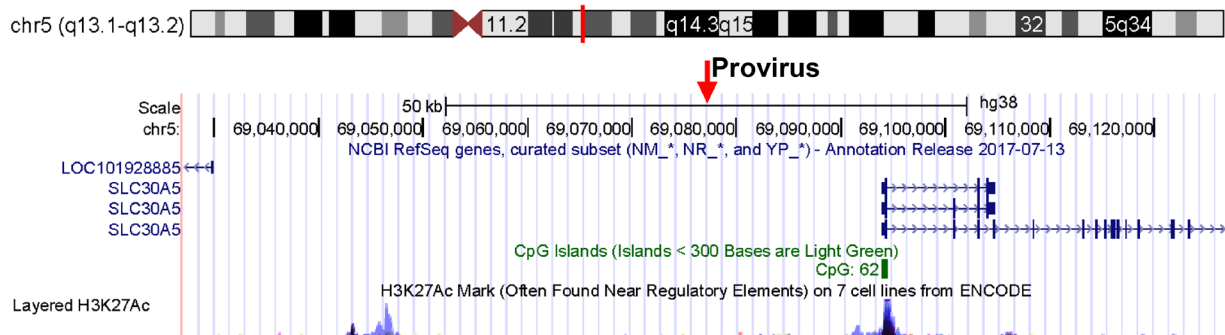
LV vector proviral integration site in *SPTAN1* gene on chromosome 9



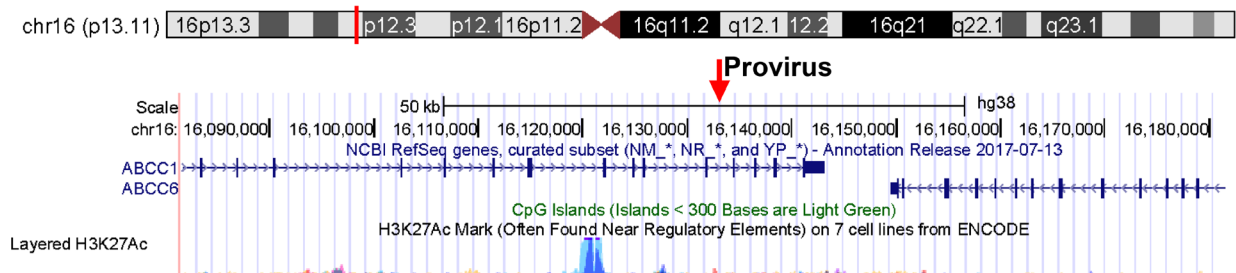
LV vector proviral integration site near *ADAMTS1* gene on chromosome 21

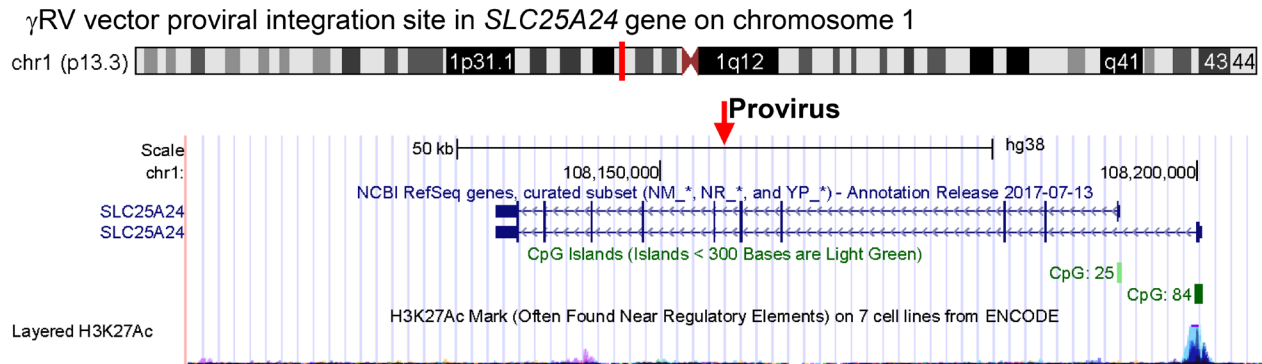
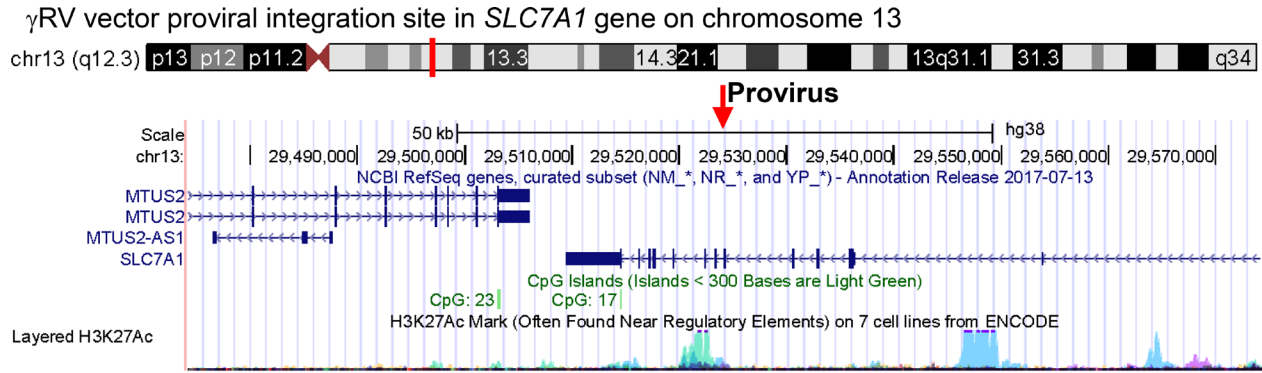


LV vector proviral integration site near *SLC30A5* gene on chromosome 5

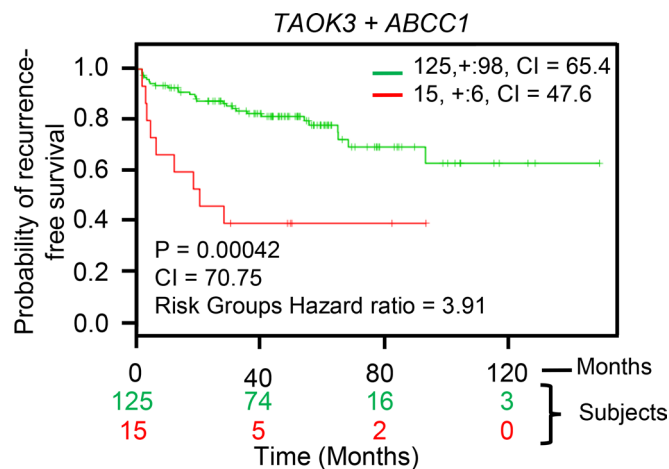


LV vector proviral integration site in *ABCC1* gene on chromosome 16





**Supplementary Figure 1: Proviral integration sites mapped to the human genome (hg38) using the UCSC genome browser. Redarrows indicate the provirus integration site.**



**Supplementary Figure 2: Combination of *TAOK3* and *ABCC1* expression predicts clinical outcomes in AIPC patients after treatment.** The Kaplan-Meier survival curves generated using SurvExpress biomarker tool showing the ability of a  $\gamma$ RV and LV-tagged gene expression to predict recurrence-free survival outcome in PC patients after androgendepression therapy using cohorts from Taylore et al. 2010 data. The insets in the right present the number of individuals, number censored, and concordance index (CI) of each risk group and '+' represent censoring samples. High and low risk groups are shown in red and green respectively. Box-plots show expression levels and *p*-values resulting from *t*-test of the difference in expression between high risk (red) and low risk (green) groups in BC patients.

1. Prostate Carcinoma vs. Normal. *Arredouani Prostate, Clin Cancer Res, 2009*
2. Prostate Carcinoma vs. Normal. *Grasso Prostate, Nature, 2012*
3. Prostate Carcinoma vs. Normal. *Holzbeierlein Prostate, Am J Pathol, 2004*
4. Prostate Carcinoma vs. Normal. *Lapointe Prostate, Proc Natl Acad Sci U S A, 2004*
5. Prostate Carcinoma vs. Normal. *LaTulippe Prostate, Cancer Res, 2002*
6. Prostate Carcinoma vs. Normal. *Liu Prostate, Cancer Res, 2006*
7. Prostate Carcinoma vs. Normal. *Luo Prostate 2, Mol Carcinog, 2002*
8. Prostate Carcinoma vs. Normal. *Magee Prostate, Cancer Res, 2001*
9. Prostate Carcinoma vs. Normal. *Singh Prostate, Cancer Cell, 2002*
10. Prostate Carcinoma vs. Normal. *Taylor Prostate 3, Cancer Cell, 2010*
11. Acinar Prostate Adenocarcinoma vs. Normal. *TCGA Prostate, No Associated Paper, 2012*
12. Prostate Adenocarcinoma vs. Normal. *TCGA Prostate, No Associated Paper, 2012*
13. Benign Prostatic Hyperplasia Epithelia vs. Normal. *Tomlins Prostate, Nat Genet, 2007*
14. Benign Prostatic Hyperplasia Stroma vs. Normal. *Tomlins Prostate, Nat Genet, 2007*
15. Prostate Carcinoma Epithelia vs. Normal. *Tomlins Prostate, Nat Genet, 2007*
16. Prostatic Intraepithelial Neoplasia Epithelia vs. Normal. *Tomlins Prostate, Nat Genet, 2007*
17. Prostate Adenocarcinoma vs. Normal. *Vanaja Prostate, Cancer Res, 2003*
18. Prostate Carcinoma vs. Normal. *Varambally Prostate, Cancer Cell, 2005*
19. Prostate Adenocarcinoma vs. Normal. *Wallace Prostate, Cancer Res, 2008*
20. Prostate Carcinoma vs. Normal. *Welsh Prostate, Cancer Res, 2001*
21. Prostate Carcinoma vs. Normal. *Yu Prostate, J Clin Oncol, 2004*

**Supplementary Figure 3: Datasets used for OncoPrint analysis.**

**Supplementary Table 1: Provirus tagged candidate PC AQ2 metastasis genes.** See Supplementary\_Table\_1

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