VirMAP for Cancer: Characterization of the Intratumoral Virome in Virally-Associated Cancers and a Resource for Investigators

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Leading Edge of Cancer Symposium Abstract

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Current landscape of viral associations in cancer

- **HCV**
  - 50 nm
  - 10 kb ssRNA (+)

- **HBV**
  - 42 nm
  - 3.2 kb dsDNA

- **HPV**
  - 60 nm
  - 8 kb dsDNA

- **EBV**
  - 150–200 nm
  - 172 kb dsDNA

**Known association of common viruses in oncogenesis**

**Effects of oncoviruses on cancer progression and metastasis**

**True associations between intratumoral viral signatures and clinical outcomes?**

**Microenvironment tuning**
- Phenotypic modification
  - Genetic instability

**CellPress REVIEWS**
VirMAP – A powerful tool for cancer virome interrogation

Hallmarks of the VirMAP algorithm

- Viral genomic reconstruction
- Accurate taxonomic classifications
- Quantitative viral signals

17,625 samples
591.6 TB

RNA Sequencing
Whole genome sequencing
Whole exome sequencing

TCGA
NATIONAL CANCER INSTITUTE

ACC
BLCA
LGG
BRCA
CESC
COAD
ESCA
GBM
HNSC
KIRC
KICH
LGG
LUAD
LUSC
DLBC
MESO
OV
PAAD
PCPG
PRAD
READ
SARC
SKCM
STAD
THYM
THCA
UCEC
UCS
UVM

Primary Tumor
Blood Derived Normal
Solid Tissue Normal
Metastatic
Recurrent Tumor
Additional
Serotype-level virome resolution allows for nuanced exploration