VirCapSeq-VERT Capture Panel

Detection of viral sequences in complex sample types

The VirCapSeq-VERT Capture Panel enables detection of viral sequences in complex sample backgrounds, including those found in clinical specimens, such as serum, blood, and tissue. The highly multiplexed nature of the system allows both the simultaneous identification and genetic characterization of a comprehensive set of known vertebrate viruses, their genetic variants, and novel related viruses. The VirCapSeq-VERT Capture Panel covers the genomes of 207 viral taxa known to infect vertebrates (including humans) and enables detection of viral sequences in complex sample types. The panel was designed by Professor Ian Lipkin and other researchers using a database of 342,438 representative sequences spanning all virus sequence records, excluding bacteriophages.

Features

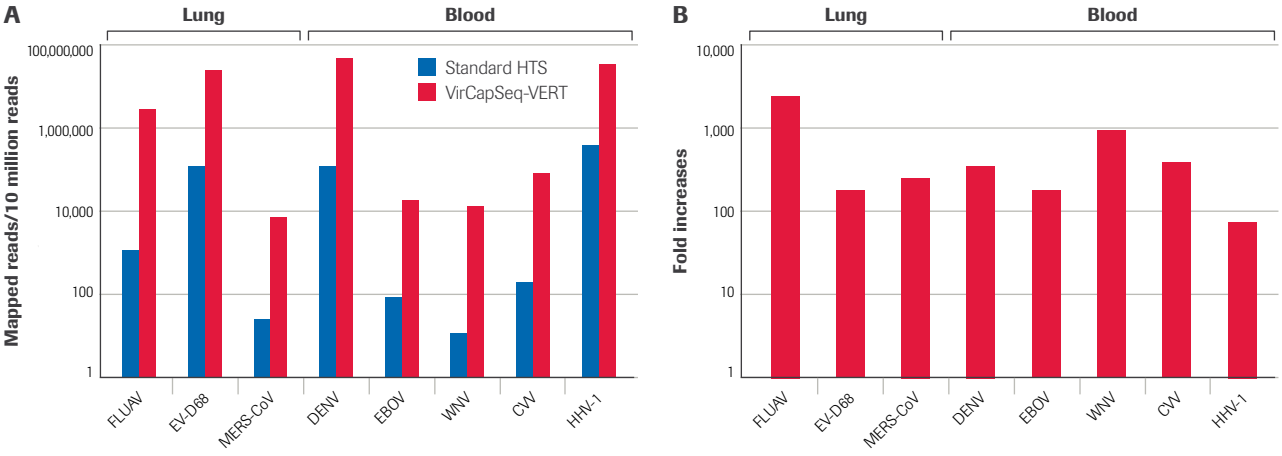
- Targets coding sequence from 271 viral genera with strong emphasis on retroviruses (~55% of panel content)
- Enables sequencing of genomes with as little as 75% sequence identity to input design sequences
- Provides highly multiplexed sample processing and simplified sample handling with reduced risk of cross contamination

Benefits

- Enhanced performance of high-throughput sequencing (HTS): Enables 100- to 1000-fold enrichment of viral sequences from a sample
- Comparable sensitivity with targeted real-time PCR assays, but with the advantage of viral variant detection
- Greater genome coverage and sequencing depth compared to HTS
- Nearly full genome recovery for most viruses even with less than 1,000 copies of target input
- Highly competitive per-sample cost in a 20-plex sample format compared to other target enrichment methods

Enhances performance of high-throughput screening

- VirCapSeq-VERT resulted in a 100- to 1,000-fold increase in on-target (viral) reads[1]
- Reduction of host background reads from 99.7% to 68.2% in lung and from 99.4% to 38.5% in blood[1]



VirCapSeq-VERT enhances the performance of high-throughput sequencing by increasing the number of mapped viral reads recovered from high-background specimens. Eight different viral NAs were quantitated by qPCR and used to spike a background of lung-derived (3 viruses) or blood-derived (5 viruses) NA extracts. Samples were split in two and processed by standard HTS (blue) or with VirCapSeq-VERT (red). FLUAV, influenza A virus; EVD-68, enterovirus D68; MERS-CoV, MERS coronavirus; DENV, dengue virus; EBOV, Ebola virus; WNV, West Nile virus; CVV, Cache Valley virus; HHV-1, human herpesvirus 1.

Enables detection of novel, highly divergent sequences

- VirCapSeq-VERT is comprehensive in its design due to its ability to derive full sequence obtained for sequences differing by up to 25% (from the known sequences)[1]
- Partial sequence in conserved regions obtained for sequences differing by as much as 50% (from known sequences; NSP1 and NSP4)[1]

Capacity of VirCap Seq-VERT to detect divergent sequences

Rotavirus gene	Sequence length (nt)	% mapped	Closest BLASTN hit identity (%)
VP1	3,280	97	78
VP2	2,712	99	93
VP3	2,592	86	78
VP4	2,362	97	75
NSP1	1,614	40	53
VP6	1,194	92	96

Rotavirus gene	Sequence length (nt)	% mapped	Closest BLASTN hit identity (%)
NSP3	1,075	95	76
NSP2	954	88	96
VP7	982	93	82
NSP4	528	19	47
NSP5	630	97	95

Design Share Portfolio

The VirCapSeq-VERT Capture Panel (design name: 150401_VIR_CIlv1_TB_EZ_HX1) is now part of Roche Sequencing Solutions Design Share Portfolio. Design Share makes it easy to access pre-designed NGS panels that are developed by Roche or in collaboration with researchers around the world. Please access the full portfolio at **sequencing.roche.com/designshare**

1. Briese T, Kapoor A, Mishra N et al. Virome Capture Sequencing Enables Sensitive Viral Diagnosis and Comprehensive Virome Analysis. *mBio*. 2015; 6(5)

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