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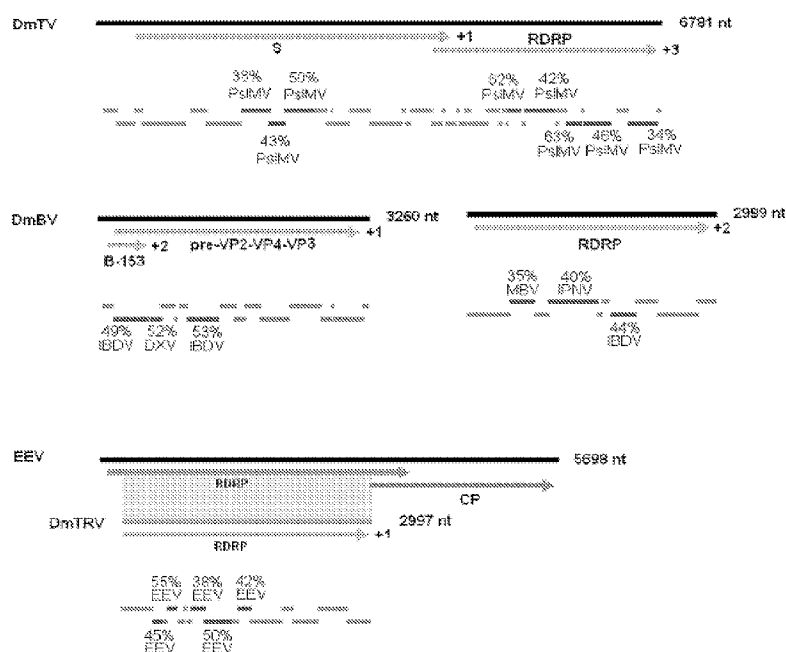
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[Continued on next page]

(54) Title: VIRUS DISCOVERY BY SEQUENCING AND ASSEMBLY OF VIRUS-DERIVED SIRNAS, MIRNAS, PIRNAS

FIGURE 2



(57) Abstract: In one embodiment, the disclosure provides methods and systems for identifying viral nucleic acids in a sample. In another embodiment the invention provides methods for viral genome assembly and viral discovery using small inhibitory RNAs, or "small silencing," RNAs (siRNAs), microRNAs (miRNAs) and/or PIWI-interacting RNAs (piRNAs), including siRNAs, miRNAs and/or piRNAs isolated or sequenced from invertebrate organisms such as insects (*Anthropoda*), nematodes (*Nemapoda*), *Mollusca*, *Porifera*, and other invertebrates, and/or plants, fungi or algae, *Cyanobacteria* and the like.

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A. CLASSIFICATION OF SUBJECT MATTER*C12Q 1/68(2006.01)i, C12Q 1/70(2006.01)i, C40B 40/06(2006.01)i*

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

C12Q 1/68

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Korean utility models and applications for utility models

Japanese utility models and applications for utility models

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

eKOMPASS(KIPO internal), Google & PubMed

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	KREUZE J.F. et al. "Complete viral genome sequence and discovery of novel viruses by deep sequencing of small RNAs: a generic method for diagnosis, discovery and sequencing of viruses" Virology, 25 May 2009, Vol. 388, No. 1, pp 1-7	1-11, 13, 14
Y	See Abstract ; Figures 1-3; Pages 3; Column 1; Table 1	12, 15-17
Y	LI Z. et al. "Improved rapid amplification of cDNA ends (RACE) for mapping both the 5' and 3' terminal sequences of paramyxovirus genomes" J. Virol Methods, December 2005, Vol. 130, No. 1-2, pp. 154-156 See Abstract; Figures 1, 2	12, 15-17
A	ZERBINO D.R. et al. "Velvet: algorithms for de novo short read assembly using de Bruijn graphs" Genome Res., May 2008, Vol. 18, No. 5, pp. 821-829 See Abstract; Figure 1; Pages 821; Column 1	1-17
PX	WU Q. et al. "Virus discovery by deep sequencing and assembly of virus-derived small silencing RNAs" Proc Natl Acad Sci U S A., 26 January 2010, Vol. 107, No. 4, pp. 1606-1611 See Abstract; Figures 1-4	1-17



Further documents are listed in the continuation of Box C.



See patent family annex.

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"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US2010/036849

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.b of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of :

a. a sequence listing filed or furnished

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furnished subsequently to this Authority for the purposes of search

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3. Additional comments:

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No.

PCT/US2010/036849Patent document
cited in search reportPublication
datePatent family
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None