

## FWO DMP Template - Flemish Standard Data Management Plan

Project supervisors (from application round 2018 onwards) and fellows (from application round 2020 onwards) will, upon being awarded their project or fellowship, be invited to develop their answers to the data management related questions into a DMP. The FWO expects a **completed DMP no later than 6 months after the official start date** of the project or fellowship. The DMP should not be submitted to FWO but to the research co-ordination office of the host institute; FWO may request the DMP in a random check.

At the end of the project, the **final version of the DMP** has to be added to the final report of the project; this should be submitted to FWO by the supervisor-spokesperson through FWO's e-portal. This DMP may of course have been updated since its first version. The DMP is an element in the final evaluation of the project by the relevant expert panel. Both the DMP submitted within the first 6 months after the start date and the final DMP may use this template.

The DMP template used by the Research Foundation Flanders (FWO) corresponds with the Flemish Standard Data Management Plan. This Flemish Standard DMP was developed by the Flemish Research Data Network (FRDN) Task Force DMP which comprises representatives of all Flemish funders and research institutions. This is a standardized DMP template based on the previous FWO template that contains the core requirements for data management planning. To increase understanding and facilitate completion of the DMP, a standardized **glossary** of definitions and abbreviations is available via the following [link](#).

## 1. General Project Information

Name Grant Holder & ORCID	<b>Tine Deconinck</b> <a href="https://orcid.org/0000-0003-2353-3363">https://orcid.org/0000-0003-2353-3363</a>
Contributor name(s) (+ ORCID) & roles	<b>Dirk Daelemans (Promotor)</b> <a href="https://orcid.org/0000-0001-7092-1153">https://orcid.org/0000-0001-7092-1153</a> <b>Frederik De Smet (Co-promotor)</b> <a href="https://orcid.org/0000-0002-6669-3335">https://orcid.org/0000-0002-6669-3335</a>
Project number <sup>1</sup> & title	11M2423N Combinatorial and personalized oncolytic virotherapy in the battle against glioblastoma
Funder(s) GrantID <sup>2</sup>	FWO
Affiliation(s)	<input checked="" type="checkbox"/> <b>KU Leuven</b> <input type="checkbox"/> Universiteit Antwerpen <input type="checkbox"/> Universiteit Gent <input type="checkbox"/> Universiteit Hasselt <input type="checkbox"/> Vrije Universiteit Brussel <input type="checkbox"/> Other: Provide ROR <sup>3</sup> identifier when possible: <b>Rega Institute</b> ( <a href="https://ror.org/03w5j8p12">https://ror.org/03w5j8p12</a> )
Please provide a short project description	<p>Glioblastoma (GBM) is the most aggressive type of brain cancer with poor survival due to tumor recurrence in almost all patients. Current treatment options are limited and can only slow down disease, thus novel intervention strategies are highly needed. Oncolytic virotherapy (OVT) is a strategy with great potential for difficult-to-treat cancers. However, despite promising preclinical results, no oncolytic virus (OV) is associated with encouraging clinical results in GBM patients yet. Reasons for these suboptimal clinical results are the limited understanding of virological aspects of OVT, the lack of patient stratification, the use of cellular models that do not represent human GBM biology, and the use of one single type of OVT. Therefore, in this proposed project, I will identify the cellular host factors important for response of three clinically relevant OVs in patient-derived GBM cell lines through genome wide CRISPR/Cas9 KO screening. These predictive biomarkers will allow patient stratification to the OV that best suits their tumor characteristics. The high inter- and intratumoral heterogeneity of GBM may require combinations of OVs to avoid emergence of resistant subtypes. Therefore, I will match different GBM subtypes with their appropriate OV and combine OVs with different mechanisms of action to reduce the emergence of resistant tumor clones. In conclusion, this project aims at maximizing the efficacy of OVT in GBM treatment by exploring new options for personalized and combinatorial therapy.</p>

<sup>1</sup> "Project number" refers to the institutional project number. This question is optional since not every institution has an internal project number different from the GrantID. Applicants can only provide one project number.

<sup>2</sup> Funder(s) GrantID refers to the number of the DMP at the funder(s), here one can specify multiple GrantIDs if multiple funding sources were used.

<sup>3</sup> Research Organization Registry Community. <https://ror.org/>

## 2. Research Data Summary

List and describe all datasets or research materials that you plan to generate/collect or reuse during your research project. For each dataset or data type (observational, experimental etc.), provide a short name & description (sufficient for yourself to know what data it is about), indicate whether the data are newly generated/collected or reused, digital or physical, also indicate the type of the data (the kind of content), its technical format (file extension), and an estimate of the upper limit of the volume of the data<sup>4</sup>.

Dataset Name	Description	New or Reused	Digital or Physical	ONLY FOR DIGITAL DATA	ONLY FOR DIGITAL DATA	ONLY FOR DIGITAL DATA	ONLY FOR PHYSICAL DATA
				Digital Data Type	Digital Data Format	Digital Data Volume (MB, GB, TB)	Physical Volume
Patient-derived and mouse glioblastoma cell lines	<p>This project uses a total of 14 patient-derived glioblastoma cell lines from the Laboratory of Precision Medicine, headed by Prof. Frederik De Smet. <a href="https://www.lpcm.be/leuven-living-tissue-bank">https://www.lpcm.be/leuven-living-tissue-bank</a></p> <p>Following cell lines will be used: CME014, CME016, CME035, CME036, CME037, CME038, CME027, CME032, LBT007/I, LBT007/B, LBT081, LBT096, LBT024, LBT123.</p> <p>Cells will be stored in liquid nitrogen (A3.A340, Rega Institute).</p> <p>In addition, following mouse glioblastoma cell lines are included: CT2A, mGB2, m005GSC, bRiTs-G3, SB28, KR158. These cells are provided</p>	<input checked="" type="checkbox"/> Generate new data <input checked="" type="checkbox"/> Reuse existing data	<input type="checkbox"/> Digital <input checked="" type="checkbox"/> Physical	<input type="checkbox"/> Observational <input type="checkbox"/> Experimental <input type="checkbox"/> Compiled/aggregated data <input type="checkbox"/> Simulation data <input type="checkbox"/> Software <input type="checkbox"/> Other <input checked="" type="checkbox"/> NA	<input type="checkbox"/> .por <input type="checkbox"/> .xml <input type="checkbox"/> .tab <input type="checkbox"/> .csv <input type="checkbox"/> .pdf <input type="checkbox"/> .txt <input type="checkbox"/> .rtf <input type="checkbox"/> .dwg <input type="checkbox"/> .tab <input type="checkbox"/> .gml <input type="checkbox"/> other: <input checked="" type="checkbox"/> NA	<input type="checkbox"/> < 100 MB <input type="checkbox"/> < 1 GB <input type="checkbox"/> < 100 GB <input type="checkbox"/> < 1 TB <input type="checkbox"/> < 5 TB <input type="checkbox"/> < 10 TB <input type="checkbox"/> < 50 TB <input type="checkbox"/> > 50 TB <input checked="" type="checkbox"/> NA	100*10 <sup>6</sup> cells per cell line

<sup>4</sup> Add rows for each dataset you want to describe.

	by the Laboratory of Tumor Immunology and Immunotherapy (headed by Prof. An Coosemans)						
Virus stocks	This project uses a total of 18 viruses from different resources (ATCC, MTAs, Host laboratory). Following viruses will be included: adenovirus type 5 (WT), adenovirus type 5 (modified, DNX2401), herpes simplex virus type 1 (WT), herpes simplex virus type 1 (modified, G47delta), vesicular stomatitis virus (WT), vesicular stomatitis virus (modified, VSV-GP), Chimera of Polio and rhinovirus (PVSRIPO), Vaccinia virus (Western Reserve and Copenhagen), Measles virus (Edmonston-Zagreb), Zika virus (MR-766), Parvovirus H1, Cocksackievirus A21, Myxoma virus, Reovirus type 3, Newcastle disease virus (La Sota), Sindbis virus (AR-339) and SARS-CoV2.	<input checked="" type="checkbox"/> Generate new data <input type="checkbox"/> Reuse existing data	<input type="checkbox"/> Digital <input checked="" type="checkbox"/> Physical	<input type="checkbox"/> Observational <input type="checkbox"/> Experimental <input type="checkbox"/> Compiled/aggregated data <input type="checkbox"/> Simulation data <input type="checkbox"/> Software <input type="checkbox"/> Other <input checked="" type="checkbox"/> NA	<input type="checkbox"/> .por <input type="checkbox"/> .xml <input type="checkbox"/> .tab <input type="checkbox"/> .csv <input type="checkbox"/> .pdf <input type="checkbox"/> .txt <input type="checkbox"/> .rtf <input type="checkbox"/> .dwg <input type="checkbox"/> .tab <input type="checkbox"/> .gml <input type="checkbox"/> other: <input checked="" type="checkbox"/> NA	<input type="checkbox"/> < 100 MB <input type="checkbox"/> < 1 GB <input type="checkbox"/> < 100 GB <input type="checkbox"/> < 1 TB <input type="checkbox"/> < 5 TB <input type="checkbox"/> < 10 TB <input type="checkbox"/> < 50 TB <input type="checkbox"/> > 50 TB <input checked="" type="checkbox"/> NA	Stock of 60X0.5ml = 30ml per virus
(sc)RNAseq data	<b>REUSE:</b> (sc)RNAseq data of the patient-derived glioblastoma cell lines will be retrieved from the laboratory of precision medicine (Prof. Frederik De Smet). More precisely, RNAseq data will be used for prioritization of hits identified in the CRISPR screen +	<input checked="" type="checkbox"/> Generate new data <input checked="" type="checkbox"/> Reuse existing data	<input checked="" type="checkbox"/> Digital <input type="checkbox"/> Physical	<input type="checkbox"/> Observational <input checked="" type="checkbox"/> Experimental <input type="checkbox"/> Compiled/aggregated data <input type="checkbox"/> Simulation data <input type="checkbox"/> Software	<input type="checkbox"/> .por <input type="checkbox"/> .xml <input type="checkbox"/> .tab <input checked="" type="checkbox"/> .csv <input type="checkbox"/> .pdf <input type="checkbox"/> .txt <input type="checkbox"/> .rtf	<input type="checkbox"/> < 100 MB <input type="checkbox"/> < 1 GB <input type="checkbox"/> < 100 GB <input checked="" type="checkbox"/> < 1 TB <input type="checkbox"/> < 5 TB <input type="checkbox"/> < 10 TB <input type="checkbox"/> < 50 TB	

	<p>for finding correlation between response and gene expression. ScRNAseq data will be used for comparison with scRNAseq data after infection.</p> <p><b>NEW:</b> RNAseq data after infection will be retrieved to check immunogenic activations. ScRNAseq data after infection will be obtained to determine resistant populations (comparison with scRNAseq data before infection – REUSE)</p>			<input type="checkbox"/> Other <input type="checkbox"/> NA	<input type="checkbox"/> .dwg <input type="checkbox"/> .tab <input type="checkbox"/> .gml <input checked="" type="checkbox"/> other: .fasta/.fastq, .jpeg, .r, .pzfx <input type="checkbox"/> NA	<input type="checkbox"/> > 50 TB <input type="checkbox"/> NA	
Cell viability (MTS) assays	<p>1) For determination of titers of all viruses, <b>TCID50 assays</b> will be performed using MTS.</p> <p>2) For each virus, <b>oncotoxicity</b> in all patient-derived and mouse glioblastoma cell lines will be tested and evaluated using MTS (absorbance values). For testing combinations of oncolytic viruses, resistant subclones will be established and tested on sensitivity towards the other viruses using MTS (absorbance values).</p>	<input checked="" type="checkbox"/> Generate new data <input type="checkbox"/> Reuse existing data	<input checked="" type="checkbox"/> Digital <input type="checkbox"/> Physical	<input type="checkbox"/> Observational <input checked="" type="checkbox"/> Experimental <input type="checkbox"/> Compiled/aggregated data <input type="checkbox"/> Simulation data <input type="checkbox"/> Software <input type="checkbox"/> Other <input type="checkbox"/> NA	<input type="checkbox"/> .por <input checked="" type="checkbox"/> .xml <input type="checkbox"/> .tab <input checked="" type="checkbox"/> .csv <input type="checkbox"/> .pdf <input type="checkbox"/> .txt <input type="checkbox"/> .rtf <input type="checkbox"/> .dwg <input type="checkbox"/> .tab <input type="checkbox"/> .gml <input checked="" type="checkbox"/> other: .pzip <input type="checkbox"/> NA	<input type="checkbox"/> < 100 MB <input type="checkbox"/> < 1 GB <input checked="" type="checkbox"/> < 100 GB <input type="checkbox"/> < 1 TB <input type="checkbox"/> < 5 TB <input type="checkbox"/> < 10 TB <input type="checkbox"/> < 50 TB <input type="checkbox"/> > 50 TB <input checked="" type="checkbox"/> NA	
Incucyte Live cell imaging system	This system will be used for follow up of the cytopathogenic effect of the viruses on the patient-derived cell lines. Confluence of cells can be	<input checked="" type="checkbox"/> Generate new data <input type="checkbox"/> Reuse existing data	<input checked="" type="checkbox"/> Digital <input type="checkbox"/> Physical	<input checked="" type="checkbox"/> Observational <input checked="" type="checkbox"/> Experimental <input type="checkbox"/> Compiled/aggregated data	<input type="checkbox"/> .por <input checked="" type="checkbox"/> .xml <input type="checkbox"/> .tab <input checked="" type="checkbox"/> .csv	<input type="checkbox"/> < 100 MB <input type="checkbox"/> < 1 GB <input checked="" type="checkbox"/> < 100 GB <input type="checkbox"/> < 1 TB	

	measured, as well as red/green fluorescence objects. Output of this system consists of images and data that can be exported in excel files.			<input type="checkbox"/> Simulation data <input type="checkbox"/> Software <input type="checkbox"/> Other <input type="checkbox"/> NA	<input type="checkbox"/> .pdf <input type="checkbox"/> .txt <input type="checkbox"/> .rtf <input type="checkbox"/> .dwg <input type="checkbox"/> .tab <input type="checkbox"/> .gml <input checked="" type="checkbox"/> other: .jpg, .xls <input type="checkbox"/> NA	<input type="checkbox"/> < 5 TB <input type="checkbox"/> < 10 TB <input type="checkbox"/> < 50 TB <input type="checkbox"/> > 50 TB <input type="checkbox"/> NA	
Preparation of samples for sequencing	To enable sequencing of the samples from the CRISPR screens following techniques have to be used: gDNA extraction, Nested PCR, gel extraction.	<input checked="" type="checkbox"/> Generate new data <input type="checkbox"/> Reuse existing data	<input checked="" type="checkbox"/> Digital <input type="checkbox"/> Physical	<input type="checkbox"/> Observational <input checked="" type="checkbox"/> Experimental <input type="checkbox"/> Compiled/aggregated data <input type="checkbox"/> Simulation data <input type="checkbox"/> Software <input type="checkbox"/> Other <input type="checkbox"/> NA	<input type="checkbox"/> .por <input checked="" type="checkbox"/> .xml <input type="checkbox"/> .tab <input checked="" type="checkbox"/> .csv <input type="checkbox"/> .pdf <input type="checkbox"/> .txt <input type="checkbox"/> .rtf <input type="checkbox"/> .dwg <input type="checkbox"/> .tab <input type="checkbox"/> .gml <input checked="" type="checkbox"/> other: .jpg, .xls <input type="checkbox"/> NA	<input type="checkbox"/> < 100 MB <input type="checkbox"/> < 1 GB <input checked="" type="checkbox"/> < 100 GB <input type="checkbox"/> < 1 TB <input type="checkbox"/> < 5 TB <input type="checkbox"/> < 10 TB <input type="checkbox"/> < 50 TB <input type="checkbox"/> > 50 TB <input type="checkbox"/> NA	
Genomic data and R script from CRISPR screens	After the genome-wide CRISPR/Cas9 KO screens, illumina sequencing of the sgRNA sequences will results in genomic data and the subsequent analysis of the reads will be performed in Rstudio.	<input checked="" type="checkbox"/> Generate new data <input type="checkbox"/> Reuse existing data	<input checked="" type="checkbox"/> Digital <input type="checkbox"/> Physical	<input type="checkbox"/> Observational <input checked="" type="checkbox"/> Experimental <input type="checkbox"/> Compiled/aggregated data <input type="checkbox"/> Simulation data	<input type="checkbox"/> .por <input checked="" type="checkbox"/> .xml <input type="checkbox"/> .tab <input checked="" type="checkbox"/> .csv <input type="checkbox"/> .pdf <input type="checkbox"/> .txt	<input type="checkbox"/> < 100 MB <input type="checkbox"/> < 1 GB <input type="checkbox"/> < 100 GB <input checked="" type="checkbox"/> < 1 TB <input type="checkbox"/> < 5 TB <input type="checkbox"/> < 10 TB	

				<input type="checkbox"/> Software <input type="checkbox"/> Other <input type="checkbox"/> NA	<input type="checkbox"/> .rtf <input type="checkbox"/> .dwg <input type="checkbox"/> .tab <input type="checkbox"/> .gml <input checked="" type="checkbox"/> other: .fasta, .fastq, .r, .pzfx <input type="checkbox"/> NA	<input type="checkbox"/> < 50 TB <input type="checkbox"/> > 50 TB <input type="checkbox"/> NA	
Validation of hits from CRISPR screens	Hits identified in the genome-wide CRISPR/Cas9 KO screens will be validated and further investigated through establishment of KO cell lines (cloning, transformation, miniprep, lentiviral production, transduction), TCID50 assays using MTS, Immunofluorescence, Western Blot (Protein Simple- WES), RT-qPCR (Quantstudio), ...	<input checked="" type="checkbox"/> Generate new data <input type="checkbox"/> Reuse existing data	<input checked="" type="checkbox"/> Digital <input type="checkbox"/> Physical	<input type="checkbox"/> Observational <input checked="" type="checkbox"/> Experimental <input type="checkbox"/> Compiled/aggregated data <input type="checkbox"/> Simulation data <input type="checkbox"/> Software <input type="checkbox"/> Other <input type="checkbox"/> NA	<input type="checkbox"/> .por <input checked="" type="checkbox"/> .xml <input type="checkbox"/> .tab <input checked="" type="checkbox"/> .csv <input type="checkbox"/> .pdf <input type="checkbox"/> .txt <input type="checkbox"/> .rtf <input type="checkbox"/> .dwg <input type="checkbox"/> .tab <input type="checkbox"/> .gml <input checked="" type="checkbox"/> other: .jpg, .xls, . <input type="checkbox"/> NA	<input type="checkbox"/> < 100 MB <input type="checkbox"/> < 1 GB <input checked="" type="checkbox"/> < 100 GB <input type="checkbox"/> < 1 TB <input type="checkbox"/> < 5 TB <input type="checkbox"/> < 10 TB <input type="checkbox"/> < 50 TB <input type="checkbox"/> > 50 TB <input type="checkbox"/> NA	
Immunogenic cell death assays	Occurrence of immunogenic cell death will be determined through 3 main assays: 1) FACS 2) ATP Bioluminescence 3) ELISA	<input checked="" type="checkbox"/> Generate new data <input type="checkbox"/> Reuse existing data	<input checked="" type="checkbox"/> Digital <input type="checkbox"/> Physical	<input type="checkbox"/> Observational <input checked="" type="checkbox"/> Experimental <input type="checkbox"/> Compiled/aggregated data <input type="checkbox"/> Simulation data <input type="checkbox"/> Software	<input type="checkbox"/> .por <input checked="" type="checkbox"/> .xml <input type="checkbox"/> .tab <input checked="" type="checkbox"/> .csv <input type="checkbox"/> .pdf <input type="checkbox"/> .txt <input type="checkbox"/> .rtf	<input type="checkbox"/> < 100 MB <input type="checkbox"/> < 1 GB <input checked="" type="checkbox"/> < 100 GB <input type="checkbox"/> < 1 TB <input type="checkbox"/> < 5 TB <input type="checkbox"/> < 10 TB <input type="checkbox"/> < 50 TB	

				<input type="checkbox"/> Other <input type="checkbox"/> NA	<input type="checkbox"/> .dwg <input type="checkbox"/> .tab <input type="checkbox"/> .gml <input checked="" type="checkbox"/> other: .jpg, .xls, .fcs <input type="checkbox"/> NA	<input type="checkbox"/> > 50 TB <input type="checkbox"/> NA	
Electronic lab notes	All experiments performed will be logged in an electronic lab notebook (ELN) that tracks every change that is made.	<input checked="" type="checkbox"/> Generate new data <input type="checkbox"/> Reuse existing data	<input checked="" type="checkbox"/> Digital <input type="checkbox"/> Physical	<input checked="" type="checkbox"/> Observational <input checked="" type="checkbox"/> Experimental <input checked="" type="checkbox"/> Compiled/aggregated data <input type="checkbox"/> Simulation data <input type="checkbox"/> Software <input type="checkbox"/> Other <input type="checkbox"/> NA	<input type="checkbox"/> .por <input checked="" type="checkbox"/> .xml <input type="checkbox"/> .tab <input checked="" type="checkbox"/> .csv <input checked="" type="checkbox"/> .pdf <input checked="" type="checkbox"/> .txt <input type="checkbox"/> .rtf <input type="checkbox"/> .dwg <input type="checkbox"/> .tab <input checked="" type="checkbox"/> .gml <input checked="" type="checkbox"/> other: .jpg, .xls, .fcs <input type="checkbox"/> NA	<input type="checkbox"/> < 100 MB <input type="checkbox"/> < 1 GB <input type="checkbox"/> < 100 GB <input checked="" type="checkbox"/> < 1 TB <input type="checkbox"/> < 5 TB <input type="checkbox"/> < 10 TB <input type="checkbox"/> < 50 TB <input type="checkbox"/> > 50 TB <input type="checkbox"/> NA	



<p><i>GUIDANCE:</i></p> <p><i>DATA CAN BE DIGITAL OR PHYSICAL (FOR EXAMPLE BIOBANK, BIOLOGICAL SAMPLES, ...). DATA TYPE: DATA ARE OFTEN GROUPED BY TYPE (OBSERVATIONAL, EXPERIMENTAL ETC.), FORMAT AND/OR COLLECTION/GENERATION METHOD.</i></p> <p><i>EXAMPLES OF DATA TYPES: OBSERVATIONAL (E.G. SURVEY RESULTS, SENSOR READINGS, SENSORY OBSERVATIONS); EXPERIMENTAL (E.G. MICROSCOPY, SPECTROSCOPY, CHROMATOGRAMS, GENE SEQUENCES); COMPILED/AGGREGATED DATA<sup>5</sup> (E.G. TEXT &amp; DATA MINING, DERIVED VARIABLES, 3D MODELLING); SIMULATION DATA (E.G. CLIMATE MODELS); SOFTWARE, ETC.</i></p> <p><i>EXAMPLES OF DATA FORMATS: TABULAR DATA (.POR, .SPSS, STRUCTURED TEXT OR MARK-UP FILE XML, .TAB, .CSV), TEXTUAL DATA (.RTF, .XML, .TXT), GEOSPATIAL DATA (.DWG, .GML, ..), IMAGE DATA, AUDIO DATA, VIDEO DATA, DOCUMENTATION &amp; COMPUTATIONAL SCRIPT.</i></p> <p><i>DIGITAL DATA VOLUME: PLEASE ESTIMATE THE UPPER LIMIT OF THE VOLUME OF THE DATA PER DATASET OR DATA TYPE.</i></p> <p><i>PHYSICAL VOLUME: PLEASE ESTIMATE THE PHYSICAL VOLUME OF THE RESEARCH MATERIALS (FOR EXAMPLE THE NUMBER OF RELEVANT BIOLOGICAL SAMPLES THAT NEED TO BE STORED AND PRESERVED DURING THE PROJECT AND/OR AFTER).</i></p>	
<p>If you reuse existing data, please specify the source, preferably by using a persistent identifier (e.g. DOI, Handle, URL etc.) per dataset or data type.</p>	<p>Patient-derived glioblastoma cell lines from the Laboratory of Precision Medicine, headed by Prof. Frederik De Smet, will be used. <a href="https://www.lpcm.be/leuven-living-tissue-bank">https://www.lpcm.be/leuven-living-tissue-bank</a></p> <p>Following cell lines will be used: CME014, CME016, CME035, CME036, CME037, CME038, CME027, CME032, LBT007/I, LBT007/B, LBT081, LBT096, LBT024, LBT123. Data is pseudonymized.</p> <p>RNAseq data (raw data) of all cell lines mentioned above will be reused and is provided by the Laboratory of Precision Medicine.</p> <p>Mouse GBM cell lines will be provided by the Laboratory of Tumor Immunology and Immunotherapy, headed by Prof. An Coosemans.</p> <p><b><u>Overview data set:</u></b></p> <p>Oncotoxicity screen data: all cell lines</p> <p>Genome-wide CRISPR/Cas9 KO screen: eligible patient derived cell lines (based on oncotoxicity screens)</p> <p>Validation of CRISPR/Cas9 KO screen: all patient derived cell lines</p>

<sup>5</sup> These data are generated by combining multiple existing datasets.

<p>Are there any ethical issues concerning the creation and/or use of the data (e.g. experiments on humans or animals, dual use)? If so, please describe these issues further and refer to specific datasets or data types when appropriate.</p>	<p> <input checked="" type="checkbox"/> Yes, human subject data  <input type="checkbox"/> Yes, animal data  <input type="checkbox"/> Yes, dual use  <input type="checkbox"/> No         </p> <p>If yes, please describe: Cell lines used in all data sets are derived from GBM patients. All cell lines are registered in the Biobank and are approved by the EC research UZ/KU Leuven (S67312).</p>
<p>Will you process personal data<sup>6</sup>? If so, briefly describe the kind of personal data you will use. Please refer to specific datasets or data types when appropriate. If available, add the reference to your file in your host institution's privacy register.</p>	<p> <input type="checkbox"/> Yes  <input checked="" type="checkbox"/> No         </p> <p>If yes:</p> <ul style="list-style-type: none"> <li>- Short description of the kind of personal data that will be used:</li> <li>- Privacy Registry Reference:</li> </ul>
<p>Does your work have potential for commercial valorization (e.g. tech transfer, for example spin-offs, commercial exploitation, ...)? If so, please comment per dataset or data type where appropriate.</p>	<p> <input type="checkbox"/> Yes  <input checked="" type="checkbox"/> No         </p> <p>If yes, please comment:</p>

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<sup>6</sup> See Glossary Flemish Standard Data Management Plan

<p>Do existing 3rd party agreements restrict exploitation or dissemination of the data you (re)use (e.g. Material/Data transfer agreements, research collaboration agreements)?</p> <p>If so, please explain to what data they relate and what restrictions are in place.</p>	<p><input checked="" type="checkbox"/> Yes  <input type="checkbox"/> No</p> <p>If yes, please explain:  All data obtained with the modified VSV-GP, Myxoma, NDV La Sota and Parvo-H1 virus is subject to regulations mentioned in the MTA set up by the respective organizations.</p> <p><b><u>Restrictions:</u></b></p> <ul style="list-style-type: none"> <li>- Use for research purposes only</li> <li>- Use only in affiliated facility (Laboratory of Virology and Chemotherapy, Rega Institute)</li> <li>- Restricted time frame: period of 2-4 years, but can be extended</li> <li>- Acknowledgement section in case of publication</li> </ul>
<p>Are there any other legal issues, such as intellectual property rights and ownership, to be managed related to the data you (re)use?</p> <p>If so, please explain to what data they relate and which restrictions will be asserted.</p>	<p><input type="checkbox"/> Yes  <input checked="" type="checkbox"/> No</p> <p>If yes, please explain:</p>

### 3. Documentation and Metadata

<p>Clearly describe what approach will be followed to capture the accompanying information necessary to keep <b>data understandable and usable</b>, for yourself and others, now and in the future (e.g. in terms of documentation levels and types required, procedures used, Electronic Lab Notebooks, README.txt files, Codebook.tsv etc. where this information is recorded).</p>	<p>A daily overview of research tasks, raw data and analysis files will be saved in an Electronic Lab Notebook (ELN, <a href="https://www.elabjournal.com/">https://www.elabjournal.com/</a>). Extra data that cannot be uploaded in the ELN will be stored in a personal folder on a shared drive (provided by the KU Leuven) and linked to the appropriate experiment in the ELN. All adaptations are registered in the ELN and a back-up of the shared drive is performed automatically.</p> <p>Following sections will be included for experiments in the ELN:</p> <ul style="list-style-type: none"> <li>- Background/aim</li> <li>- Protocol/Methodology and origin of products/cells used during experiment</li> <li>- Raw data</li> <li>- (statistical) analysis of raw data</li> <li>- Graphs (Graphpad or Excel)</li> <li>- Images (if any)</li> <li>- Conclusion</li> </ul>
<p>Will a metadata standard be used to make it easier to <b>find and reuse the data</b>?</p> <p>If so, please specify which metadata standard will be used. If not, please specify which metadata will be created to make the data easier to find and reuse.</p> <p><i>REPOSITORIES COULD ASK TO DELIVER METADATA IN A CERTAIN FORMAT, WITH SPECIFIED ONTOLOGIES AND VOCABULARIES, I.E. STANDARD LISTS WITH UNIQUE IDENTIFIERS.</i></p>	<p><input type="checkbox"/> Yes  <input checked="" type="checkbox"/> No</p> <p>If yes, please specify (where appropriate per dataset or data type) which metadata standard will be used:</p> <p>If no, please specify (where appropriate per dataset or data type) which metadata will be created:  Metadata will be generated by instruments (Simple WES, SpectraMax Microplate Reader, Quantstudio II, etc.) and will be present in raw data files stored in the ELN per experiment. These metadata consist of the date/time of read-out and conditions/settings of measurements such as wavelengths, duration, temperature, exposure time, ...</p> <p>In the ELN, a search function is present which makes it easier to find and reuse data. Furthermore, each experiment is categorized in its unique project, study and study group which are defined according to predefined rules in the lab.</p>

#### 4. Data Storage & Back-up during the Research Project

Where will the data be stored?	<ul style="list-style-type: none"> <li>- Central storage facility of the research unit: J drive provided by KU Leuven, only accessible to members of the laboratory</li> <li>- Electronic Labjournal (DD group) – <a href="http://www.elabjournal.com">www.elabjournal.com</a></li> </ul>
<p>How will the data be backed up?</p> <p><i>WHAT STORAGE AND BACKUP PROCEDURES WILL BE IN PLACE TO PREVENT DATA LOSS? DESCRIBE THE LOCATIONS, STORAGE MEDIA AND PROCEDURES THAT WILL BE USED FOR STORING AND BACKING UP DIGITAL AND NON-DIGITAL DATA DURING RESEARCH.<sup>7</sup></i></p> <p><i>REFER TO INSTITUTION-SPECIFIC POLICIES REGARDING BACKUP PROCEDURES WHEN APPROPRIATE.</i></p>	<p>The data will be stored on the research unit servers (provided by KU Leuven) with automatic daily backup procedures.</p>
<p>Is there currently sufficient storage &amp; backup capacity during the project? If yes, specify concisely. If no or insufficient storage or backup capacities are available, then explain how this will be taken care of.</p>	<p><input checked="" type="checkbox"/> Yes  <input type="checkbox"/> No</p> <p>If yes, please specify concisely: the J drive provided by KU Leuven has enough capacity for storage of all data that will be gathered during the project. Next to this, for large data files (e.g. sequencing data) a large volume storage drive (L drive) is provided. Automatic backups of the research unit servers are made daily and sufficient capacity is provided for these backups.</p> <p>If no, please specify:</p>

<sup>7</sup> Source: Ghent University Generic DMP Evaluation Rubric: <https://osf.io/2z5g3/>

<p>How will you ensure that the data are securely stored and not accessed or modified by unauthorized persons?</p> <p><i>CLEARLY DESCRIBE THE MEASURES (IN TERMS OF PHYSICAL SECURITY, NETWORK SECURITY, AND SECURITY OF COMPUTER SYSTEMS AND FILES) THAT WILL BE TAKEN TO ENSURE THAT STORED AND TRANSFERRED DATA ARE SAFE. <sup>7</sup></i></p>	<p>The research unit servers are only accessible to members of the research unit (password protection). The registered documents in the ELN are only accessible to members of the research unit and can only be adapted by me (password protection). Every modification is registered in elabjournal.</p>
<p>What are the expected costs for data storage and backup during the research project? How will these costs be covered?</p>	<p>The internal storage drive is provided by the KU Leuven. Seats in the ELN are paid for yearly and are covered by the research unit.</p> <p>Although FWO has no earmarked budget at its disposal to support correct research data management, FWO allows for part of <b>the allocated project budget</b> to be used to cover the cost incurred.</p>

#### 5. Data Preservation after the end of the Research Project

<p>Which data will be retained for at least five years (or longer, in agreement with other retention policies that are applicable) after the end of the project? In case some data cannot be preserved, clearly state the reasons for this (e.g. legal or contractual restrictions, storage/budget issues, institutional policies...).</p>	<p>All data will be retained for at least 10 years, conform the KU Leuven RDM policy.</p>
<p>Where will these data be archived (stored and curated for the long-term)?</p>	<p>Data will be stored on the research unit shared drives with automatic back up procedures and in the ELN for at least 10 years after the end of the project.</p>

<p>What are the expected costs for data preservation during the expected retention period? How will these costs be covered?</p>	<p>The internal storage drive is provided by the KU Leuven, costs are covered by the KU Leuven, also after the end of the project. My personal seat in the ELN will not be paid for after the end of my research, but experiments in the ELN will be accessible to all members of the research unit. So no extra costs are applicable.</p> <p>Although FWO has no earmarked budget at its disposal to support correct research data management, FWO allows for part of <b>the allocated project budget</b> to be used to cover the cost incurred.</p>
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## 6. Data Sharing and Reuse

Will the data (or part of the data) be made available for reuse after/during the project? Please explain per dataset or data type which data will be made available.

*NOTE THAT 'AVAILABLE' DOES NOT NECESSARILY MEAN THAT THE DATA SET BECOMES OPENLY AVAILABLE, CONDITIONS FOR ACCESS AND USE MAY APPLY. AVAILABILITY IN THIS QUESTION THUS ENTAILS BOTH OPEN & RESTRICTED ACCESS. FOR MORE INFORMATION: [HTTPS://WIKI.SURFNET.NL/DISPLAY/STANDARDS/INFO-EU-REPO/#INFOEU-REPO-ACCESSRIGHTS](https://wiki.surfnet.nl/display/STANDARDS/INFO-EU-REPO/#INFOEU-REPO-ACCESSRIGHTS)*

- ☒ Yes, in an Open Access repository
- ☒ Yes, in a restricted access repository (after approval, institutional access only, ...)
- ☐ No (closed access)
- ☐ Other, please specify:

Articles will be published in Open Access.

All other data will be stored in the J drive of the institution and in the ELN which are both available to members of the research team.

If access is restricted, please specify who will be able to access the data and under what conditions.

Data used for publication in journals will have Open Access due to the Open Access policy. Data can be requested via email to Prof. Daelemans, following the signing of a data-sharing agreement.

All data will remain available to the members of the research unit only (on the J drive or in the ELN – password protection).



<p>Are there any factors that restrict or prevent the sharing of (some of) the data (e.g. as defined in an agreement with a 3rd party, legal restrictions)? Please explain per dataset or data type where appropriate.</p>	<div data-bbox="770 197 1218 424"> <input type="checkbox"/> Yes, privacy aspects  <input checked="" type="checkbox"/> Yes, intellectual property rights  <input type="checkbox"/> Yes, ethical aspects  <input type="checkbox"/> Yes, aspects of dual use  <input type="checkbox"/> Yes, other  <input type="checkbox"/> No </div> <div data-bbox="770 472 2130 703"> <p>If yes, please specify:  MTAs are in charge for following viruses: DNX2401; Parvo-H1, Myxoma, Newcastle disease virus, VSV-GP (dataset: virus stocks) These materials cannot be shared outside of the research facility without permission of the owner.  Upon publication of data using these materials, the origin and contribution of the owner has to be acknowledged.</p> </div>
<p>Where will the data be made available?  If already known, please provide a repository per dataset or data type.</p>	<div data-bbox="815 753 2136 1134"> <ul style="list-style-type: none"> <li>- <b>Publication</b>  Generated data will be published in multiple manuscripts (articles). Datasets described in articles (e.g. host factors determined through CRISPR/Cas9 screenings) will be accessible through the manuscripts. Specific data and protocols can be requested via email to Prof. Daelemans, following signing of a data-sharing agreement.</li>   <li>- <b>On request</b>  Articles will be published in journals with Open Access policy. Specific data and protocols can be requested via email to Prof. Daelemans, following signing of a data-sharing agreement.</li> </ul> </div>
<p>When will the data be made available?</p> <p><i>THIS COULD BE A SPECIFIC DATE (DD/MM/YYYY) OR AN INDICATION SUCH AS 'UPON PUBLICATION OF RESEARCH RESULTS'.</i></p>	<p>Data will be made available upon publication of research results.</p>

<p>Which data usage licenses are you going to provide? If none, please explain why.</p> <p><i>A DATA USAGE LICENSE INDICATES WHETHER THE DATA CAN BE REUSED OR NOT AND UNDER WHAT CONDITIONS. IF NO LICENCE IS GRANTED, THE DATA ARE IN A GREY ZONE AND CANNOT BE LEGALLY REUSED. DO NOTE THAT YOU MAY ONLY RELEASE DATA UNDER A LICENCE CHOSEN BY YOURSELF IF IT DOES NOT ALREADY FALL UNDER ANOTHER LICENCE THAT MIGHT PROHIBIT THAT.</i></p> <p><i>EXAMPLE ANSWER: E.G. "DATA FROM THE PROJECT THAT CAN BE SHARED WILL BE MADE AVAILABLE UNDER A CREATIVE COMMONS ATTRIBUTION LICENSE (CC-BY 4.0), SO THAT USERS HAVE TO GIVE CREDIT TO THE ORIGINAL DATA CREATORS." <sup>8</sup></i></p>	<p>The KU Leuven Research Data Repository (RDR) will be used to describe, upload and share research data at the end of the project. In the RDR, data will be made available under a Creative Commons Attribution License. Users have to give credit to the original data creator.</p>
<p>Do you intend to add a PID/DOI/accession number to your dataset(s)? If already available, please provide it here.</p> <p><i>INDICATE WHETHER YOU INTEND TO ADD A PERSISTENT AND UNIQUE IDENTIFIER IN ORDER TO IDENTIFY AND RETRIEVE THE DATA.</i></p>	<p><input checked="" type="checkbox"/> Yes  <input type="checkbox"/> No  If yes:</p>
<p>What are the expected costs for data sharing? How will these costs be covered?</p>	<p>Although FWO has no earmarked budget at its disposal to support correct research data management, FWO allows for part of <b>the allocated project budget</b> to be used to cover the cost incurred.</p>

## 7. Responsibilities

Who will manage data documentation and metadata during the research project?	During the research project, I, Tine Deconinck, will be responsible for the correct storage and preservation of the generated data. The head of the research group, Prof. Daelemans, bears the overall responsibility.
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<sup>8</sup> Source: Ghent University Generic DMP Evaluation Rubric: <https://osf.io/2z5g3/>

Who will manage data storage and backup during the research project?	I, Tine Deconinck , will manage data storage and backup during the project. After the end of the research project, Prof. Daelemans will have the responsibility.
Who will manage data preservation and sharing?	I, Tine Deconinck, will manage data preservation and sharing during the project. After the end of the research project, Prof. Daelemans will have the responsibility.
Who will update and implement this DMP?	I, Tine Deconinck, will update and implement this DMP. Prof. Daelemans has the final responsibility.