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Deliverable 2.5: Project Outputs

Lead beneficiary: Institute for Research in Biomedicine (IRB Barcelona)
Dissemination level: PUBLIC

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Document history

Version	Contributor(s)	Partner	Date	Comments
0.1	Anna Montras	IRB Barcelona	22/08/2018	First draft
0.2	Mark McDowall	EMBL-EBI	11/10/2018	Additions in sections 6.2 and 7
0.3	Anna Montras	IRB Barcelona	16/10/2018	Second draft
1.0			05/11/2018	Approved by Supervisory Board

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Executive summary

The ultimate objective of MuG is to support the emerging community working in the 3D/4D genomics field in embracing the use of HPC and the adoption of standards by facilitating the way they interact with such elements. It is key in order to enable a wide uptake by the community of the MuG developments that all project outputs are properly characterized and all related documentation is easily accessible to the community of users. It has been a priority of WP2 to coordinate efforts with developers (WP3, 4, 5, 6) and lead users (pilot projects) in order to ensure that (i) the community is made aware of project results and (ii) project results are properly documented, archived and accessible. D2.5 contains a thorough list of the project outputs and provides links to relevant repositories and publications, data, technical documentation and software stored thereby.

1 INTRODUCTION

The main achievement of the MuG project lies in the development of the MuG VRE, a user-friendly platform that makes available to the 3D/4D genomics community tools to integrate navigation and visualization from sequence data to chromatin dynamics data. Beyond the developed software tools and pipelines, which constitute the fundamental outputs generated by the project, a number of side outputs has been generated that must as well be properly characterized and archived in order to ensure the proper uptake of the MuG VRE services by external users (e.g. scientific publications, data sets, training materials, technical documentation, tutorials, etc.) and their long-term sustainability.

In agreement with the EU open access policies, all documents, software and data generated by the project have been deposited in open access repositories, making them traceable and findable beyond the end of the MuG 3-year grant period independently from the maintenance of the MuG website.

The present deliverable compiles a thorough list of project outputs and provides links to their locations in the MuG project website and in external open access repositories.

2 EC REPORTING DOCUMENTS

All reports generated in MuG are tagged as public and are thus accessible to the community. Documentation is available for download from the MuG website, and as the reports become approved, they are incorporated into the MuG community created in Zenodo (see section 8 below).

2.1 Deliverables

http://www.multiscalegenomics.eu/MuG/deliverables/

2.2 Milestones

http://www.multiscalegenomics.eu/MuG/about-mug/milestones/

3 SCIENTIFIC OUTCOME

3.1 Peer-reviewed scientific publications

According to EC rules on open access, publication in either green or gold open access has been adopted by all partners. Regardless of the open access route chosen by partners, a copy of all publications has been deposited in open access repositories to ensure its long-term accessibility. A full list of publications, organized by year, is kept in the MuG website: http://www.multiscalegenomics.eu/MuG/category/publications/

A full table with papers and links to the public repository where each paper is deposited is provided in the table below for easy reference.

In total, consortium members have published **31** MuG-related scientific papers in high-impact journals, including 5 reviews, which have accumulated **326 citations** thus far. It is worthy of note that 3 MuG co-PIs have co-authored a position paper on 4D nucleome data and model standards with leading worldwide researchers in the field.

	Year		Title	Authors	Reference	DOI	Public repository
1	2016	**ARTICLE**	BIGNASim: a NoSQL database structure and analysis portal for nucleic acids simulation data	Hospital A, Andrio P, Cugnasco C, Codo L, Becerra Y, Dans P, Battistini F, Torres J, Goñi R, **Orozco M, Gelpí J**.	Nucleic Acids Res 44 (D1) D272-278	http://dx.doi.org/10.1093/nar/gkv1301	http://upcommons.upc.edu/handle/2117/84242
2	2016	**REVIEW**	Multiscale simulation of DNA	Dans P, Walther J, Gómez H, **Orozco M**.	Curr Opin Struct Biol 37, 29–45.	https://doi.org/10.1016/j.sbi.2015.11.011	http://diposit.ub.edu/dspace/handle/2445/103226
3	2016	**ARTICLE**	Long-timescale dynamics of the Drew-Dickerson dodecamer	Dans P, Danilāne L, Ivani I, Dršata T, Lankaš F, Hospital A, Walther J, Pujagut R, Battistini F, Gelpí J, Lavery R, **Orozco M.**	Nucleic Acids Res 44 (9): 4052-4066	http://dx.doi.org/10.1093/nar/gkw264	https://upcommons.upc.edu/handle/2117/86576?locale-attribute=en
4	2016	**ARTICLE**	Small details matter: the 2'Hydroxyl as a conformational switch in RNA	Darre L, Ivani I, Dans PD, Gómez H, Hospital A and **Orozco M**	J. Am. Chem. Soc. 138 (50), 16355–16363	http://dx.doi.org/10.1021/jacs.6b09471	http://diposit.ub.edu/dspace/handle/2445/105631
5	2016	**ARTICLE**	Coordinate redeployment of PRC1 proteins suppresses tumor formation during Drosophila development	Vincent Loubiere, Anna Delest, Aubin Thomas, Boyan Bonev, Bernd Schuettengruber, Satish Sati, Anne-Marie Martinez & **Giacomo Cavalli.**	Nature Genetics 48, 1436–1442	https://doi.org/10.1038/ng.3671	https://hal.archives-ouvertes.fr/hal-01393390
6	2016	**REVIEW**	Organization and function of the 3D genome	Boyan Bonev & **Giacomo Cavalli.**	Nature Reviews Genetics 17, 661–678	https://doi.org/10.1038/nrg.2016.112	https://hal.archives-ouvertes.fr/hal-01386805

7	2017	**ARTICLE**	The Role of Unconventional Hydrogen Bonds in Determining BII Propensities in B-DNA	Alexandra Balaceanu, Marco Pasi, Pablo D. Dans, Adam Hospital, Richard Lavery, **Modesto Orozco**	J. Phys. Chem. Lett., 2017, 8 (1), pp 21–28	http://dx.doi.org/10.1021/acs.jpclett.6b02451	http://hdl.handle.net/2445/106380
8	2017	**ARTICLE**	Three-Dimensional Genome Organization and Function in Drosophila	Yuri B. Schwartz, **Giacomo Cavalli.**	Genetics 205 (1) 5-24	https://doi.org/10.1534/genetics.115.185132	https://hal.archives-ouvertes.fr/hal-01427837
9	2017	**REVIEW**	3D modeling of chromatin structure: is there a way to integrate and reconcile single cell and population experimental data?	Le Dily, F., Serra, F. and **Marti-Renom, M.A.**	WIREs Comput Mol Sci 2017, 7:e1308	http://dx.doi.org/10.1002/wcms.1308	http://hdl.handle.net/10230/32133
10	2017	**ARTICLE**	Stable Polycomb-dependent transgenerational inheritance of chromatin states in Drosophila	Filippo Ciabrelli, Federico Comoglio , Simon Fellous, Boyan Bonev, Maria Ninova , Quentin Szabo, Anne Xuéreb, Christophe Klopp , Alexei Aravin, Renato Paro , Frédéric Bantignies & **Giacomo Cavalli.**	Nature Genetics 49, 876–886	http://dx.doi.org/10.1038/ng.3848	http://europepmc.org/abstract/MED/2843698
11	2017	**ARTICLE**	Structural basis of a histidine-DNA nicking/joining mechanism for gene transfer and promiscuous spread of antibiotic resistance	Pluta R, Boer DR, Lorenzo-Diaz F, Russi S, Gómez H, Fernandez-Lopez C, Pérez-Luque R, **Orozco M**, Espinosa M and Coll M	PNAS 114 (32), E6526-E6535	http://dx.doi.org/10.1073/pnas.1702971114	http://diposit.ub.edu/dspace/handle/2445/98742

12	2017	**ARTICLE**	Prevalent sequences in the human genome can form mini i-motif structures at physiological pH	Bartomeu Mir, Israel Serrano, Diana Buitrago, **Modesto Orozco**, Nuria Escaja, and Carlos González	J. Am. Chem. Soc 139 (40), 13985-13988	https://dx.doi.org/10.1021/jacs.7b07383	http://hdl.handle.net/2445/117632
13	2017	**REVIEW**	Genome Regulation by Polycomb and Trithorax: 70 Years and Counting	Bernd Schuettengruber, Henri-Marc Bourbon, Luciano Di Croce and **Giacomo Cavalli**	Cell 171, 1, 34-57	http://dx.doi.org/10.1016/j.cell.2017.08.002	https://europepmc.org/abstract/MED/28938122
14	2017	**ARTICLE**	Multi-scale 3D genome rewiring during mouse neural development	Bonev, B., Mendelson Cohen, N., Szabo, Q., Fritsch, L., Papadopoulos, G., Lubling, Y., Xu, X., Lv, X., Hugnot, J.-P., Tanay, A, and **Cavalli, G.**	Cell 171, 3, 557-572	https://doi.org/10.1016/j.cell.2017.09.043	http://europepmc.org/articles/PMC5651218
15	2017	**REVIEW**	Challenges for visualizing three-dimensional data in genomic browsers	Mike Goodstadt and **Marc A Marti-Renom**	FEBS Letters 591 , 2505–2519	http://dx.doi.org/10.1002/1873-3468.12778	http://europepmc.org/articles/PMC5638070
16	2017	**ARTICLE**	Pmut. A web-based tool for the annotation of pathological variants on proteins, 2017 update	López Ferrando, Gazzo, de la Cruz, **Orozco** and **Gelpi**	Nucleic Acids Res. 45, W222-W228	https://doi.org/10.1093/nar/gkx313	http://hdl.handle.net/2445/120776
17	2017	**ARTICLE**	Spatial RNA proximities reveal a bipartite nuclear transcriptome and territories of differential density and transcription elongation rates	Morf J, Wingett SW, Farabella I, Cairns J, Furlan-Magaril M, Liu X, Craig FF, Andrews S, **Marti-Renom MA** and Fraser P	BioRxiv 2017 (preprint)	https://doi.org/10.1101/196147	https://www.biorxiv.org/content/early/2017/09/29/196147

18	2017	ARTICLE	The spatial position of budding yeast chromosomes affects gene expression	Di Giovanni F, Di Stefano M, Bàu D, Carey LB, **Marti-Renom MA** and Mendoza M	BioRxiv 2017 (preprint)	https://doi.org/10.1101/237263	https://www.biorxiv.org/content/early/2017/12/20/237263
19	2017	ARTICLE	Single-cell absolute contact probability detection reveals chromosomes are organized by multiple low-frequency yet specific interactions	Cattoni DI, Cardozo Gizzi AM, Georgieva M, DiStefano M, Valeri A, Chamousset D, Houbron Ch, Déjardin S, Fiche JB, González I, Chang JM, Sexton T, **Marti-Renom MA**, Bantignies F, **Cavalli G** and Nollmann M	Nature Communications 8, 1753	doi: 10.1038/s41467-017-01962-x	https://www.biorxiv.org/content/early/2017/10/24/159814
20	2017	ARTICLE	DNA structure directs positioning of the mitochondrial genome packaging protein Abf2p	Chakraborty A, Lyonnais S, **Battistini F, Hospital A**, Medici G, Prohens R, **Orozco M**, Vilardell J and Solà M	Nucleic Acids Res. 45(2), 951–967.	10.1093/nar/gkw1147	http://europepmc.org/articles/PMC5314765
21	2017	ARTICLE	Expanding the repertoire of DNA shape features for genome-scale studies of transcription factor binding	Jinsen Li, Jared M. Sagendorf, Tsu-Pei Chiu, **Marco Pasi**, Alberto Perez, Remo Rohs	Nucleic Acids Res. 45(2), 12877-12887	10.1093/nar/gkx1145	http://europepmc.org/articles/PMC5728407
22	2017	PROCEEDINGS PAPER	Transparent Execution of Task-Based Parallel Applications in Docker with COMP Superscalar	Victor Anton, Cristian Ramon-Cortes, Jorge Ejarque, **Rosa M. Badia**	2017 25th Euromicro International Conference on Parallel, Distributed and Network-based Processing (PDP)	10.1109/PDP.2017.26	http://hdl.handle.net/2117/104660

23	2017	**ARTICLE**	How accurate are accurate force-fields for B-DNA?	Dans, P. D., Ivani, I., Hospital, A., Portella, G., González, C., & **Orozco, M.**	Nucleic acids research, 45 (7), 4217-4230.	https://doi.org/10.1093/nar/gkw1355	https://www.repository.cam.ac.uk/handle/1810/268997
24	2018	**ARTICLE**	Promoter bivalency favors an open chromatin architecture in embryonic stem cells	Mas G, Blanco E, Ballaré C, Sansó M, Spill YG, Hu D, Aoi Y, Le Dily F, Shilatifard A, **Marti-Renom MA** and Di Croce L	Nature Genetics 2018 (17 September)	https://doi-org.sire.ub.edu/10.1038/s41588-018-0218-5	https://repositori.upf.edu/handle/10230/20545
25	2018	**ARTICLE**	TADs are 3D structural units of higher-order chromosome organization in Drosophila	Quentin Szabo, Daniel Jost, Jia-Ming Chang, Diego I. Cattoni, Giorgio L. Papadopoulos, Boyan Bonev, Tom Sexton, Julian Gurgo, Caroline Jacquier, Marcelo Nollmann, Frédéric Bantignies, **Giacomo Cavalli**	Sci Adv. 2018 Feb; 4(2): eaar8082.	https://doi.org/10.1126/sciadv.aar8082	http://europepmc.org/articles/PMC5829972
26	2018	**ARTICLE**	Distinct roles of cohesin-SA1 and cohesin-SA2 in 3D chromosome organization	Kojic A, DeKoninck M, Giménez-Llorente D, Rodríguez-Corsino M, Gómez-López G, LeDily F, **Marti-Renom MA** and Losada A	Nature Structural & Molecular Biology 25, 496–504	https://doi.org/10.1038/s41594-018-0070-4	https://www.biorxiv.org/content/early/2017/07/20/166264
27	2018	**ARTICLE**	Allosterism and signal transfer in DNA	Balaceanu A, Pérez A, Dans PD and **Orozco M.**	Nucleic Acids Research 46 (15), 7554–7565	https://doi.org/10.1093/nar/gky549	http://diposit.ub.edu/dspace/handle/2445/98742
28	2018	**ARTICLE**	Challenges and guidelines towards 4D nucleome data and model standards	**Marti-Renom MA,** Almouzni G, Bickmore WA, Bystricky K, **Cavalli G**, Fraser P, Gasser SM, Heard E, Nicodemi M, **Orozco**	Nature Genetics 50, 1352–1358	https://doi.org/10.1038/s41588-018-0236-3	https://edoc.mdc-berlin.de/17780/

				M, Pombo A and Torres-Padilla ME			
29	2018	**ARTICLE**	Polycomb-Dependent Chromatin Looping Contributes to Gene Silencing during Drosophila Development	Ogiyama Y, Schuettengruber B, Papadopoulos GL, Chang JM and **Cavalli G**	Molecular Cell 71 (1), 73-88.E5	https://doi.org/10.1016/j.molcel.2018.05.032	http://europepmc.org/abstract/med/30008320
30	2018	**ARTICLE**	Loss of PRC1 induces higher-order opening of Hox loci independently of transcription during Drosophilaembryogenesis	Cheutin T and **Cavalli G**	Nature communications 9, 3898	https://doi.org/10.1038/s41467-018-05945-4	https://europepmc.org/articles/PMC6156336
31	2018	**ARTICLE**	SKEMPI 2.0: An updated benchmark of changes in protein-protein binding energy, kinetics and thermodynamics upon mutation.	Jankauskaité, J., Jiménez-García, B., Dapkūnas, J., Fernández-Recio, J., Moal, I.H.	Bioinformatics (in press)	https://doi.org/10.1093/bioinformatics/bty635	Will be deposited in UPCommons when published. https://upcommons.upc.edu/handle/2117/23714?locale-attribute=ca

3.2 Data sets

Data generated by the pilot projects throughout the MuG project have been deposited in public repositories according to the MuG data management policies defined in D4.2 (Data Management Plan).

3.2.1 Senescence

"Differential 4D genome rewiring in different types of cell senescence"

- Public repository link:

https://www.ebi.ac.uk/arrayexpress/experiments/E-MTAB-5829/

- Status: under embargo (publication pending)

3.2.2 Whole Yeast Data

"Chromatin structure changes upon oxidative stress or UV irradiation in the yeast Saccharomyces cerevisiae":

- Public repository link:

https://www.ebi.ac.uk/arrayexpress/experiments/E-MTAB-5825

- Status: under embargo (publication pending)

3.2.3 Transcription factor binding and DNA bending

Atomic resolution structural data generated by this pilot project have been deposited in a MuG-specific section of the BIGNASim nucleic acids simulation database.

A more detailed description of the datasets is provided in the description for milestones MS29-MS33.

4 TECHNICAL DOCUMENTATION

4.1 Infrastructure

A detailed description of the infrastructure and all the elements that compose the MuG VRE is accessible from the main menu in the MuG VRE homepage: http://www.multiscalegenomics.eu/MuGVRE/ (*"What's MuG VRE"*)

- Clouds: http://www.multiscalegenomics.eu/MuGVRE/clouds/
- Components: http://www.multiscalegenomics.eu/MuGVRE/components/
- Tool catalog: http://www.multiscalegenomics.eu/MuGVRE/tools-catalog/
- Visualizers: http://www.multiscalegenomics.eu/MuGVRE/visualizers-catalog/

4.2 Code

4.2.1 Source code

All the code been developed by MuG is stored in a GitHub repository (https://github.com/Multiscale-Genomics).

Links to the repository are available from the http://www.multiscalegenomics.eu/MuGVRE/source-code/

4.2.2 MuG coding standards

http://multiscale-genomics.readthedocs.io/en/latest/coding_standards.html#

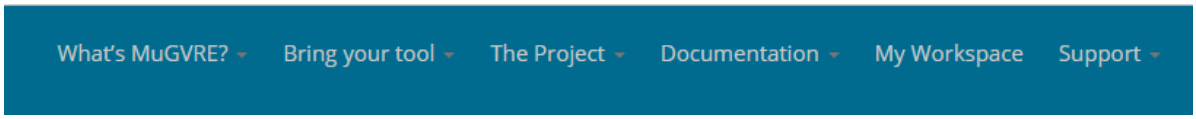
4.3 Data

- Supported File types: http://www.multiscalegenomics.eu/MuGVRE/file-types/
- Supported data types: http://www.multiscalegenomics.eu/MuGVRE/data-types/
- Available assemblies http://www.multiscalegenomics.eu/MuGVRE/available-assemblies/

4.4 External tool integration

The MuGVRE tool integration API has been conceived to facilitate collaborative work in further development of the VRE, allowing external tool developers to integrate their tools, subject to terms of use (http://www.multiscalegenomics.eu/MuGVRE/terms-of-use/).

A "Bring your tool" section is visible on top of the MuG VRE home page:



From there, a drop-down menu provides external tool developers all necessary information to integrate their tool into the MuG VRE:

- Why bring your tool to the VRE? http://www.multiscalegenomics.eu/MuGVRE/policy/
- Instructions: http://www.multiscalegenomics.eu/MuGVRE/instructions/
- Tool integration: http://www.multiscalegenomics.eu/MuGVRE/integration-of-tools/

4.5 VRE help

Help is fully integrated into the MuG VRE. The user can access the help from the menu bar accessible from the VRE user interface.

The help information is divided into the following categories:

- General: https://vre.multiscalegenomics.eu/help/general.php
- Getting started: https://vre.multiscalegenomics.eu/help/starting.php

- Data upload: https://vre.multiscalegenomics.eu/help/upload.php
- Workspace: https://vre.multiscalegenomics.eu/help/ws.php
- Job launching: https://vre.multiscalegenomics.eu/help/launch.php

4.6 Tools help

Help for each tool integrated in the VRE is likewise available from the same drop-down menu:

4.6.1 External analysis tools integrated in the MuG VRE

Individual help for each tool integrated in the MuG VRE
https://vre.multiscalegenomics.eu/help/tools.php

- Chromatin dynamics
- MC-DNA
- MD Energy Refinement
- NAFlex Analyses
- Nucleosome dynamics
- 3D consensus
- Process Genomes
- TADbit

4.6.2 Other Tools

- MuG information network: http://www.multiscalegenomics.eu/MuGVRE/modules/ConnectivityBrowser/
- BiGNASim: http://www.multiscalegenomics.eu/MuGVRE/modules/BigNASimMuG/
- Flexibility browser: http://www.multiscalegenomics.eu/MuGVRE/flexibility-browser/

4.7 Tutorials

From the drop-down menu "support" on the MuG VRE homepage, tutorials for different integrated tools are available.

http://www.multiscalegenomics.eu/MuGVRE/nucleosome-dynamics/

5 TRAINING MATERIALS

5.1 Webinars

MuG has collaborated with the BioExcel CoE in delivering different webinars. Such collaboration allows MuG to take advantage of established training infrastructure by the BioExcel CoE and provides BioExcel with the specialized expertise in different topics of relevance to the 3D/4D genomics community and the wider computational biomolecular research community. Recordings of webinars delivered by MuG in collaboration with BioExcel are available through the BioExcel YouTube channel (https://www.youtube.com/channel/UCd2hq8Q_ZyTU4YafEhweE5g)

- BioExcel MDWeb (https://www.youtube.com/watch?v=-dZpGKifp2I)
- BioExcel NA Flex (https://www.youtube.com/watch?v=ZTUFsFPU_kw&t=100s)

5.2 Workshop documentation

Training documentation related to the different courses delivered by the MuG team, including supporting materials, presentations, programme, etc. is available for download from the *"Training"* area of the MuG website: http://www.multiscalegenomics.eu/MuGVRE/training/

Documentation on the MuG website is available for the following courses.

- EBI April 2017
- IEC (BioMed) Nov 2017
- BSC Dec 2017
- Barcelona (ISQBP) BioExcel joint workshop
- API workshop EBI Sept 2018

In addition, documentation related to the 3DAROC course, in which the use of 3C analysis tools in their MuGVRE-integrated version has now been fully incorporated, is available in the following Github: https://github.com/Pfern/3DAROC . The course is held every two years as part of the Gulbenkian Training Programme in Bioinformatics of the Instituto Gulbenkian de Ciencia. MuG was incorporated in the 2016 and 2018 editions.

6 LEGAL AND IP

6.1 VRE terms of use

A "Terms of Use" document has been produced which is available from download from the MuG VRE homepage (under "Documentation").

The terms of use are also visible (as a pop-up window) that appears after clicking on the link provided at the bottom of each page of the VRE) and have to be accepted by users when logging in to the personal workspace.

http://www.multiscalegenomics.eu/MuGVRE/terms-of-use/

6.2 Licensing info

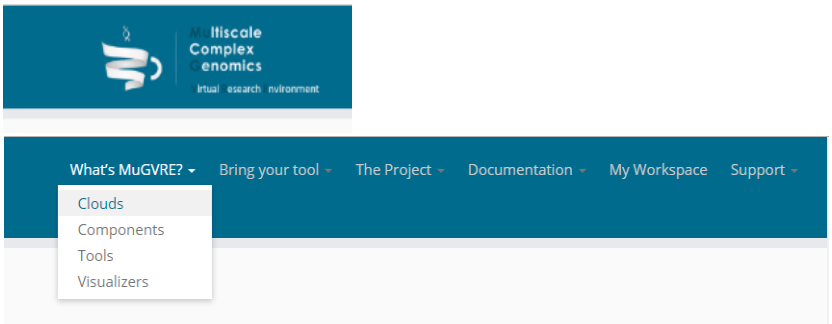
Licensing information on MuGVRE components is available in the documentation section (https://www.multiscalegenomics.eu/MuGVRE/documentation/) from which links to the relevant section in the MuG GitHub repository are provided (https://github.com/Multiscale-Genomics). All software assets fully developed within MuG have been released under an Apache 2.0 open source license.

Direct links to the main MuG IP assets are compiled in the table below:

Element ID	Brief Description	Repository	License
mg-dm-api	Data Management API	https://github.com/Multiscale-Genomics/mg-dm-api	Apache 2.0
mg-tool-api	Tool API for wrapping workflows and tools	https://github.com/Multiscale-Genomics/mg-tool-api	Apache 2.0
mg-process-test	Template repository for developers wishing to wrap a tool or create a workflow	https://github.com/Multiscale-Genomics/mg-process-test	Apache 2.0
mg-process-fastq	Workflows for processing FASTQ data, including ChIP-seq, Hi-C, RNA-seq and WGBS	https://github.com/Multiscale-Genomics/mg-process-fastq	Apache 2.0
mg-process-files	Tools for converting un-indexed genomics file formates into their indexed equivalents	https://github.com/Multiscale-Genomics/mg-process-files	Apache 2.0

mg-rest-util	Common library for the RESTful interfaces. Currently only covers authorisation	https://github.com/Multiscale-Genomics/mg-rest-util	Apache 2.0
mg-rest-dm	RESTful interface to the DM API	https://github.com/Multiscale-Genomics/mg-rest-dm	Apache 2.0
mg-rest-files	RESTful interface to the Dparts for the DM API that allow file access	https://github.com/Multiscale-Genomics/mg-rest-file	Apache 2.0
mg-rest-service	RESTful meta server for linking between the distinct RESTful servers	https://github.com/Multiscale-Genomics/mg-rest-service	Apache 2.0
mg-rest-adjacency	RESTful interface to retrieve values from calculated adjacency matrices	https://github.com/Multiscale-Genomics/mg-rest-adjacency	Apache 2.0
mg-rest-3d	RESTful interface to models generated by TADbit	https://github.com/Multiscale-Genomics/mg-rest-3d	Apache 2.0
mg-docs	Documentation for developers about creating pipelines and tools to run within the VRE. Includes descriptions about coding standards, testing, license and how this is enforced	https://github.com/Multiscale-Genomics/mg-docs	Apache 2.0
VRE	VRE core release 1.0. Web interface and backend	https://github.com/Multiscale-Genomics/VRE	Apache 2.0

In addition, a full inventory of external tools, components, visualizers and other external infrastructure elements integrated, used, or partially developed within the MuG framework is accessible from the main menu on the MuG website (http://www.multiscalegenomics.eu/MuGVRE). Licensing information for external tools will be available from the Tools' Help section within the VRE.



7 OTHER DISSEMINATION AND COMMUNICATION TOOLS

In addition to peer-reviewed scientific publications, other contributions to scientific gatherings have been key to make the community aware of the MuG advances. Contributions to conferences or relevant workshops have been widely announced in the MuG website, with links to download related dissemination materials when available.

Materials and information devoted to disseminating the project are available from the MuG website:

- Press releases and news items:

http://www.multiscalegenomics.eu/MuG/category/news-events/

- Project brochure:
http://www.multiscalegenomics.eu/MuG/wp-content/uploads/2016/05/MuG_Factsheet.pdf
- Newsletter archive:
http://www.multiscalegenomics.eu/MuG/about-mug/newsletters/
- MuG visual identity and acknowledgement kit:
https://vre.multiscalegenomics.eu/help/ackn.php

Finally, social media have been a key tool to enhance both dissemination and communication. MuG has active accounts in the following social media networks:

- YouTube channel:
https://www.youtube.com/channel/UCzDZ3b80ecK24S_m2oKq6-g/videos?view_as=public
- Twitter: https://twitter.com/MuG_genomics
- LinkedIn: https://www.linkedin.com/groups/8572323/

8 OPEN ACCESS REPOSITORIES

To ensure long-term public availability and findability of all outputs generated by the MuG project, all publications (peer-reviewed or not – including project deliverables, milestones, etc), data and technical documentation generated by the project have been deposited in public repositories.

- **Peer-reviewed publications:** all partner institutions have agreements with open access repositories in which MuG published papers have been deposited, e.g. HAL archives-ouvertes (CNRS), UPCommons (BSC), Diposit Digital UB (IRB Barcelona). The publication of pre-prints (e.g. biorxiv.org) has also been favoured by partners.
- **Data repositories:** data sets generated within the project have been deposited in open access repositories according to the policies defined in the MuG data management plan (D4.2).
- **Other publications and outputs:** All publications and materials generated by MuG are accessible for download from the MuG website. IRB Barcelona as coordinator has agreed to maintain the MuG domain beyond the end of the MuG 3-year grant period. However, in order to guarantee long-term availability of the generated publications and to facilitate its findability, all publications are also being deposited in the Zenodo MuG community: (https://zenodo.org/communities/mug/?page=1&size=20).
- **Software:** Software and documentation is stored in the MuG Github repository: https://github.com/Multiscale-Genomics