PI	Matteo Della Porta
PROJECT TITLE	Genomics and Personalized Medicine for all though Artificial Intelligence in Haematological Diseases – GENOMED4ALL H2020 project https://cordis.europa.eu/project/id/101017549 https://genomed4all.eu/
ABSTRACT	GENOMED4ALL will support the pooling of genomic, clinical and other "omics" health data through a secure and privacy respectful data sharing platform based on the novel Federated Learning scheme, to advance research in personalised medicine for haematological diseases, thanks to innovative AI models and standardized sharing of cross-border data. GENOMED4ALL will make use of the existing infrastructures and initiatives, including High Performance Computing facilities, hospital registries and pre-existing repositories, starting from 10 clinical partners' repositories to be enlarged by the resources provided by ERN-EuroBloodNet (the EU reference network of hematological diseases). GENOMED4ALL will demonstrate the potential and benefits of trustable and explainable AI technologies, with a novel approach to AI models using advanced deep learning, variational autoencoders, generative models, besides combining with advanced statistical and machine learning approaches to exploit the powerful set of "-omics" data which will be at researchers' disposal. This will allow for identifying new knowledge, to support clinical research and decision making in hematology by linking Europe's relevant genomic repositories, while ensuring full compliance with data protection and ethical principles, and increasing the AI trust for personalized medicine.
FUNDING REFERENCE (AMOUNT, STARTING DATE AND DURATION)	European Union, H2020 program Call: DT-TDS-04-2020 - AI for Genomics and Personalised Medicine Project coordinator: UNIVERSIDAD POLITECNICA DE MADRID Scientific coordinator: HUMANITAS RESEARCH HOSPITAL Funding to Humanitas: Euro 702.500 Starting date of the project: January 2021 Project duration: 4 years
MAIN TECHNICAL APPROACHES TO CARRY OUT THE PRESENT PROJECT	- Multi-Omics Factor Analysis (MOFA) - Advanced deep learning (machine learning and statistical learning) - Deep generative models (Variational Autoencoders) - Convolutional neural networks (CNN)
SCIENTIFIC REFERENCES RELATED TO THE PRESENT PROJECT	1: Bernard E, Nannya Y, Hasserjian RP, …, Della Porta MG, et al. Implications of TP53 allelic state for genome stability, clinical presentation and outcomes in myelodysplastic syndromes. Nat Med. 2021 Feb 9. doi: 10.1038/s41591-021-01253-5. 2: Bersanelli M, Travaglino E, Meggendorfer M, … and Della Porta MG. Classification and Personalized Prognostic Assessment on the Basis of Clinical and Genomic Features in Myelodysplastic Syndromes. J Clin Oncol. 2021 Feb

	4:JCO2001659. doi: 10.1200/JCO.20.01659. Epub ahead of print. PMID: 33539200 3. Haibe-Kains B et al. Transparency and reproducibility in artificial intelligence. Nature 2020;586:E14 4. Sutskever I et al. Sequence to sequence learning with neural networks. Advances in neural information processing systems 2014;27:3104 5.Argelaguet R et al.Multi-Omics Factor Analysis—a framework for unsupervised integration of multi-omics data sets. Molecular systems biology, 2018;14:e8124