PERSONAL INFORMATION

Family name, First name: Bicciato, Silvio
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Date of birth: 08/02/1967

BIBLIOMETRICS INDEXES (Scopus)

Total N. of Publications: 206
H-Index: 62
N. of citations: 22,401

- **CURRENT POSITION**

2023 – present Full Professor of Industrial Bioengineering (SSD: ING-IND/34)
Dept. of Molecular Medicine, University of Padova, Padova, Italy

- **EDUCATION AND TRAINING**

1993 – 1996 PhD, Chemical Engineering (automatic control of biochemical processes)
School of Engineering, University of Padova, Padova, Italy
1986 – 1992 BS, Chemical Engineering (automation of protein synthesis)
School of Engineering, University of Padova, Padova, Italy

- **PROFESSIONAL EXPERIENCES**

2016 – 2023 Full Professor of Industrial Bioengineering (SSD: ING-IND/34)
Dept. of Life Sciences, University of Modena and Reggio Emilia, Modena, Italy
2010 – 2016 Associate Professor of Industrial Bioengineering
Dept. of Life Sciences, University of Modena and Reggio Emilia, Modena, Italy
2007 – 2010 Assistant Professor of Industrial Bioengineering
Dept. of Life Sciences, University of Modena and Reggio Emilia, Modena, Italy
2004 – 2007 Assistant Professor of Industrial Bioengineering
Dept. of Chemical Engineering Processes, University of Padova, Padova, Italy
2000 – 2004 Research Associate
Dept. of Chemical Engineering Processes, University of Padova, Padova, Italy
1998 – 2000 Postdoctoral associate
Dept. of Chemical Engineering Processes, University of Padova, Padova, Italy
1996-1998 Postdoctoral associate
Bioinformatics and Metabolic Engineering Lab (Prof. Gregory N. Stephanopoulos) – MIT Massachusetts Institute of Technology (Cambridge, MA)

- **GRANTS AWARDED**

2019 – present Italian Association for Cancer Research (AIRC) – Special Program Metastatic disease: the key unmet need in oncology 5x1000: Metastasis as mechanodisease (Unit Head)
2015 – 2021 ERC Advanced Grant program H2020: De novo generation of somatic stem cells by YAP/TAZ: regulation and mechanisms of cell plasticity (Unit Head)
2015 – 2018 CARIPLO Foundation: RAN-translation of normal and expanded nucleotide repeats containing transcripts to neurotoxic polypetides (Unit Head)
2012 – 2015 FIRB – Collaborative Research Project RBAP11T3WB: RNA and nanotechnology in the control of neoplastic immunosuppression sustained by amino acid catabolism (Unit Head)
2012 – 2018 Italian Ministry of University and Scientific Research – ITALIAN FLAGSHIP PROJECTS – EPIGEN: Epigenomics flagship project.
1. Sub-project 2 (Unit Head)
2. Sub-project 7.6: Study of mutant p53-dependent epigenetic modifications in HNSCC (Unit Head)
3. Sub-project 9: Organoid Models to Study Cancer Epigenetics and Drug Response (Unit Head)
2010 – 2018 Italian Association for Cancer Research (AIRC) – Special Program Molecular Clinical Oncology 5x1000: Molecular basis for triple negative breast cancer metastasis: new tools for diagnosis and therapy (Unit Head)
2009 – 2010 CARIMO Foundation – Grant for International Projects 2008: Development of a bioinformatics framework for the analysis of complex biological systems: application to the study of myeloid differentiation (PI)
2008 – 2010 PRIN – Collaborative Research Project 2007Y84HTJ: A systems biology approach to reconstruct the networks of molecular interaction and the monocyte/macrophage activation process in response to inflammation under physiological conditions using omic technologies (Unit Head)

2007 – 2010 CARIPARO Foundation – Grant of Excellence 2006: A computational approach to the study of skeletal muscle genomic expression in health and disease (PI)
2006 – 2008 PRIN – Collaborative Research Project 2005069853: Immune response against prostate cancer: molecular basis for novel therapeutic strategies (Unit Head)
2004 – 2007 FIRB – Collaborative Research Project RBAU01935A: Genome-wide analysis of accessory cells that control the immune response (Unit Head)
2003 – 2007 FIRB – Collaborative Research Project RBNE01TZZ8: Biomolecules, fluids, systems and data handling in Bio-chip technology (Unit Head)

- **PRICES AND AFFILIATIONS**

1998 – 2000 Postdoctoral fellowship, Dept. of Chemical Engineering Processes, University of Padova, Padova, Italy
1996 – 1998 NATO-CNR Postdoctoral fellowship, Bioinformatics and Metabolic Engineering Lab (Prof. Gregory N. Stephanopoulos) – MIT Massachusetts Institute of Technology (Cambridge, MA)
1994 – 1996 PhD scholarship, School of Engineering, Dept. of Chemical Engineering Processes, University of Padova, Padova, Italy

- **RESEARCH ACTIVITY**

I started my first independent, bioinformatics lab at the University of Padova in 2004. In 2007, I moved to Modena where I created the Bioinformatics Core at the Center for Genome Research, an interdisciplinary group that includes computer scientists, molecular biologists, statisticians, biotechnologists, and engineers who cooperate in the generation and application of bioinformatics tools for the analysis of high-throughput molecular data. In 2023, I moved my research group at the Dept. of Molecular Medicine of the University of Padova. Currently, the team consists of 1 associate professor, 3 postdocs, 2 PhD students, and 3 MS students. In the last 16 years, I raised more than 2.7M € in research funds from national and international competitive grants. Within my group, I trained more than 25 undergraduate students, 15 PhD students, and 12 postdocs. The principal research interest of my group is the design and application of computational biology and bioinformatics methods to organize, analyze, compare, interpret, and visualize -omics data. From a methodological standpoint, our current research lines comprise the development of methods, resources and tools for i) integrative analysis of multi -omics and phenotypic data; ii) epigenomics and 3D genome; iii) computational systems biology; and iv) single cell genomics. From an applicative perspective, my group support wet biologists in national and international research institutions in investigating the genomic bases of complex biological systems, with particular emphasis on onco-genomics, immunogenomics, and neurosciences. With some of these groups, we are operating like one extended laboratory, where we provide key support to bioinformatics analyses of -omics data.
Following is a summary of my contributions in computational biology and basic life-science research.

1. **Integrative analysis of multi-omics and phenotype data.** We developed pioneering methods to merge different type of genomics data and -omics data with phenotype characteristics, clinical information, outcomes, and drug responses. Specifically:
   a. we designed tools for the batch retrieval from public repositories of raw data files and of any related meta-information, their local organization, the re-annotation of samples to create user-defined batches of data, the integrative analysis of data obtained from different platforms, and the sharing of data, meta-information, analysis flows and results (Ferrari et al., Bioinformatics 2007; Bisognin et al., BMC Bioinformatics 2009; Fallarino et al., Nat Med 2010; Bessede et al., Nature 2014);
   b. we constructed and analyzed in-silico databases of high throughput experimental data and clinical information (more than 6800 breast cancer samples and more than 1500 lung cancers), obtained from whole transcriptome sequencing and microarray assays. Gene expression profiling allowed stratifying cancers into molecularly and clinically different subtypes with distinct gene expression patterns and the identification, testing, and validation of prognostic and predictive signatures in cancer tissues (Adorno et al., Cell 2009; Cordenonsi et al., Cell 2011; Montagner et al., Nature 2012; Rustighi et al., EMBO Mol Med. 2014; Di Minin et al., Mol Cell. 2014; Enzo et al., EMBO J 2015; Sorrentino et al., Nat Commun. 2017; Santinon et al., EMBO J 2018; Ingallina et al., Nat Cell Biol. 2018; Poli et al., Nat Commun. 2018; Romani et al., Nat Cell Biol. 2019; Panciera et al., Nature Materials, 2020; Marigo et al., Cancer Discovery 2020; de la Fuente et al., Science Translational Medicine 2020; Caronni et al., Nat Commun. 2021; Consonni et al., Nat Commun. 2021; Simoncello et al., Oncoimmunology 2022);
   c. we implemented novel integrative approaches to complement gene expression data with other types of gene information, as copy number and chromosomal localization (Callegaro et al., Bioinformatics. 2006; Bicciato et al., Nucleic Acids Res. 2009; Ferrari et al., Bioinformatics 2011; Lahti et al., Brief Bioinform. 2013) and the transcriptional landscape of non-coding RNAs (Tenedini et al., Cell Death Dis. 2010; Lionetti et al., Blood 2009; Martello et al., Cell 2010; Sales et al., Nucleic Acids Res. 2010; Ganci et al., Mod Pathol. 2017; Pruszko et al., EMBO Rep. 2017; Lo Sardo et al., Carcinogenesis. 2017; Dori e Bicciato, Genes 2019);
   d. we defined new procedures for the integrative analysis of gene expression, genome-wide binding sites, and genomic interactions data to elucidate the mechanisms of action of transcriptional regulators (see

Bioinformatics for epigenomics and 3D genome);
e. we deployed web-based tools for the integrative analysis of genomic traits (mutational status and transcriptional activation) and drug responses in cancer (Taccioli et al., Oncotarget 2015; Caroli et al., Nucleic Acids Res. 2018; Caroli et al., Fronte Oncol. 2020).

2. **Development of methods, resources, and tools.** The translation of ideas, formalisms, and models first into algorithms and codes and then their implementations into user-friendly and professional software solutions with increasing levels of sophistication are among our methodological aims. We coded:
   a. SIMCA, a computational procedure for marker identification and for classification of multiclass gene expression data through the application of disjoint principal component models (Bicciato et al., Bioinformatics 2003; Bicciato et al., Methods Inf Med. 2004);
   b. BCGA, an algorithm for automatic genotype calling based on the full course of real-time PCR data (Callegaro et al., Nucleic Acids Res. 2006);
   c. SODEGIR, a procedure to identify significant overlap of differentially expressed and genomic imbalanced regions in cancer datasets (Bicciato et al., Nucleic Acids Res. 2009);
   d. PREDA, an R package that builds on our previous LAP locally adaptive statistical procedure (Callegaro et al., Bioinformatics. 2006) to detect regional variations in genomics data (Ferrari et al., Bioinformatics. 2011).

   From a *developer* perspective, I perceive the gap between algorithms and codes designed by bioinformaticians and the need of wet biologists (the end *users*) to have friendly, flexible, and usable tools to explore molecular data. Thus, we developed, made available to the scientific community, and maintained user-friendly bioinformatics tools to handle and analyze large volumes of -omics data. Specifically, we designed:
   a. A-MADMAN (Bisognin et al., BMC Bioinformatics 2009), an open source web application which allows the retrieval, annotation, organization and meta-analysis of gene expression datasets obtained from Gene Expression Omnibus;
   b. UCbase 2.0, a platform-independent Web resource dedicated to the analysis of ultraconserved sequences (Lomonaco et al., Database 2015);
   c. APTANI, a computational tool to identify target-specific aptamers from HT-SELEX data and secondary structure information (Caroli et al., Bioinformatics 2015; Caroli et al., Bioinformatics 2020; Speransky et al., Breast Cancer Res Treat. 2019; De La Fuente et al., Sci Transl Med. 2020; Van Simaeys et al., Nat Comm 2022);
   d. WoPPER, a web tool integrating gene expression and genomic annotations to identify differentially expressed chromosomal regions in bacteria (Puccio et al., Nucleic Acids Res. 2017);
   e. MDP (Taccioli et al., Oncotarget 2015) and GDA (Caroli et al., Nucleic Acids Res. 2018), two web-based tools for Genomics and Drugs integrated Analysis that combine drug response data for >50,800 compounds with mutations and gene expression profiles across 73 cancer cell lines;
   f. popsicleR, a R package to interactively guide skilled and unskilled command line-users in the pre-processing and QC analysis of scRNA-seq data (Grandi et al., J Mol Biol 2022).

3. **Bioinformatics for epigenomics and 3D genome.** We developed and applied computational methods for the analysis of linear epigenomic marks and regulatory elements and their integration with transcriptional profiles in different physiological and pathological cellular systems (Coppe et al., Nucleic Acids Res. 2009; Poletti et al., PLoS One. 2015; Cavazza et al., Stem Cell Reports. 2016; Romano et al., Sci Rep. 2016; Hirsch et al., Nature 2017). We also introduced algorithmic approaches to superimpose chromosome conformation data to genome-wide maps of expression levels, epigenomic marks, regulatory elements, and transcription factor binding sites (Zanconato et al., Nat Cell Biol. 2015; Zanconato et al., Nat Med. 2018; Della Chiara et al., Nat Commun. 2021). We quantitatively compared the performances of Hi-C data analysis methods for the identification of multi-scale chromatin structures (Forcato et al., Nat Methods. 2017; Nicoletti et al., Curr Opin Biotechnol. 2018) and evidenced some crucial limitations of existing methods (e.g., their inefficacy in capturing subtle interaction patterns and changes in the chromatin architecture). Currently, in line with projects to study the 3D genome organization in the nucleus, we are working on novel algorithms to analyze Hi-C data and study the dynamics of epigenetic landscapes.

4. **Computational systems biology.** We have been active in developing bioinformatics and computational biology approaches for reverse engineering and reconstruction of the cell regulatory landscape (Bicciato et al., Biotechnol Bioeng. 2003; Bicciato, Curr Opin Mol Ther. 2004; Biasiolo et al., Pac Symp Biocomput. 2010; Agnelli et al., Clin Cancer Res. 2011). Methodologically, we introduced the concept of the critical analysis of network components to inspect the transcriptional and post-transcriptional regulatory networks reconstructed from mRNA and microRNA expression data in pathological samples (Lionetti et al., Blood. 2009; Agnelli et al., Clin Cancer Res. 2011). Recently, we developed a multistep computational procedure that first reconstructs a coarse gene regulatory network (GRN) from single cell gene expression profiles and transcription factors active in a specific cancer tissue, then "prunes" the GRN by anchoring inferred regulatory interactions to putative direct target genes of transcriptional regulators (TRs), and finally prioritizes master TRs from the differential enrichment of their regulons in different cell states (Castellan et al., Nat Cancer, 2020).

5. **Methods for single cell genomics.** Recent advances in single-cell techniques are providing exciting

opportunities for dissecting cell heterogeneity and investigating cell identity, fate, and function. However, the analysis and modeling of single cell data -omics poses incredible computational challenges and needs entirely new bioinformatics techniques and methods. We are currently working on the development of i) new multi-dimensional approaches to extract, from the background noise, the higher-order information embedded into the 3D spatial, architectural and mutual organization of cells; ii) novel multi-scale algorithms to identify and model the molecular connections among cell regulatory circuits, dynamics and functional output (Castellan Nat Cancer. 2021); and iii) visualization tools to display and navigate cell atlases. Specifically, we are using machine-learning, deconvolution, and projection methods to associate variations in single cell gene expression profiles with specific regulatory mechanisms, define transcriptional fingerprints associated with tissues and phenotypes, and assess the spatial distribution of gene expression signatures within cellular subpopulations (Malecova et al., Nat Commun. 2018; Enzo et al., Nat Commun. 2021; Grandi et al., J Mol Biol 2022; Sladitschek-Martens et al., Nature 2022).

6. **Onco-genomics, immunogenomics, and neurosciences.** We applied tools and computational expertise to analyze genomics data from three main areas of research: onco-genomics, immunogenomics, and neurosciences. This inspired new interdisciplinary ideas and posed new bioinformatics challenges. Specifically, we supported the discovery that the transcription co-factor YAP and TAZ are important determinants of cancer and cancer metastasis (Cordenonsi et al., Cell 2011; Azzolin et al., Cell 2012; Azzolin et al., Cell 2014; Zanconato et al. al., Nat Cell Biol 2015; Zanconato et al., Nat Med 2018; Castellan et al., Nat Cancer 2021; Sladitschek-Martens et al., Nature 2022), that these factors translate cell mechanics into coordinated changes of gene expression (Dupont et al., Nature 2011; Bertolio et al., Nat Commun. 2019; Romani et al., Nat Cell Biol. 2019; Panciera et al., Nat Mater. 2020), and that their activation turns differentiated cells of different types into their corresponding somatic stem cells (Panciera et al., Cell Stem Cell 2016). We participated in the identification of novel metastasis inducing and suppressing mechanisms (Adorno et al., Cell 2009; Martello et al., Cell 2010; Montagner et al., Nature 2012) e alla decodifica della regolazione da parte di diversi oncogeni in svariati contesti tumorali (Rustighi et al., EMBO Mol Med. 2014; Di Minin et al., Mol Cell. 2014; Enzo et al., EMBO J. 2015; Sorrentino et al., Nat Commun. 2017; Santinon et al., EMBO J. 2018; Ingallina et al., Nat Cell Biol. 2018; Poli et al., Nat Commun. 2018; Marigo et al., Cancer Discov. 2020; Capaci et al., Nat Commun. 2020; Canu et al., Cell Death and Differentiation 2021; Caronni et al., Nat Comm 2021). In the area of immunogenomics, we contributed to deciphering the role of the enzyme indoleamine 2,3-dioxygenase (IDO) in the immunosuppressive pathway of tryptophan catabolism (Orabona et al., Blood 2006) and its involvement in intracellular signaling events (Pallotta et al., Nat Immunol. 2011; Bessede et al., Nature 2014) and disease (Mondanelli et al., Immunity 2017; Mondanelli et al., Front Immunol. 2017; Orabona et al., JCI Insight. 2018; Iacono et al., EMBO Rep 2020). We contributed in the characterization of circulating inflammatory-type monocytes (Gallina et al., J Clin Invest. 2006) and of myeloid-derived suppressor cells (MDSCs MDSCs; Marigo et al., Immunity. 2010; Zoso et al., Eur J Immunol. 2014). We supported the discovery that a network of pro-tumor factors can be targeted to boost cancer immunotherapies (Marigo et al., Cancer Cell. 2016) and that mechanisms of iNKT cells might be harnessed for therapeutically reprogramming the tumor microenvironment in prostate cancer (Cortesi et al., Cell Rep. 2018). In the area of neurosciences, we contributed to the identification of signaling molecules involved in dampening the immune response during neuroinflammation, highlighting pathways that could be exploited therapeutically in chronic autoimmune diseases such as multiple sclerosis (Fallarino et al., Nat Med. 2010; Volpi et al., Neuropharmacology. 2016). Finally, we analyzed the transcriptional landscape of astrocytes differentiation and supported the characterization of a cellular system to study human disorders derived from developmental and functional impairment of astrocytes (Magistri et al., Eur J Neurosci. 2016; Velmeshev et al., Mol Neurobiol. 2020).

In summary, as suggested by the over 22,000 citations of my work (according to Scopus), I believe I made important contributions in supporting molecular biologists and oncologists to understand the genomic bases of complex biological systems in physiological and pathological states. The complete list of my publications is available in PubMed MyBibliography: https://www.ncbi.nlm.nih.gov/myncbi/1T7KaQCI9gr/bibliography/public/

- **SELECTED PUBLICATIONS (20 IN THE LAST 5 YEARS)**

1. Tombari C, Zannini A, Bertolio R, Pedretti S, Audano M, Triboli L, Cancila V, Vacca D, Caputo M, Donzelli S, Segatto I, Vodret S, Piazza S, Rustighi A, Mantovani F, Belletti B, Baldassarre G, Blandino G, Tripodo C, Bicciato S, Mitro N, Del Sal G. Mutant p53 sustains serine-glycine synthesis and essential amino acids intake promoting breast cancer growth. Nat Commun. 2023 Oct 25;14(1):6777.
2. Andreoletti G, Romano O, Chou HJ, Sefid-Dashti MJ, Grilli A, Chen C, Lakshman N, Purushothaman P, Varfaj F, Mavilio F, Bicciato S, Urbinati F. High-throughput transcriptome analyses from ASPIRO, a phase 1/2/3 study of gene replacement therapy for X-linked myotubular myopathy. Am J Hum Genet. 2023 Oct 5;110(10):1648-1660.
3. Weed DT, Zilio S, McGee C, Marnissi B, Sargi Z, Franzmann E, Thomas G, Leibowitz J, Nicolli E, Arnold D, Bicciato S, Serafini P. The Tumor Immune Microenvironment Architecture Correlates with Risk of Recurrence in Head and Neck Squamous Cell Carcinoma. Cancer Res. 2023 Dec 1;83(23):3886-3900.
4. Sladitschek-Martens HL, Guarnieri A, Brumana G, Zanconato F, Battilana G, Xiccato RL, Panciera T, Forcato M, Bicciato S, Guzzardo V, Fassan M, Ulliana L, Gandin A, Tripodo C, Foiani M, Brusatin G,

Cordenonsi M, Piccolo S. YAP/TAZ activity in stromal cells prevents ageing by controlling cGAS-STING. Nature. 2022 Jul;607(7920):790-798.
5. Van Simaeys D, De La Fuente A, Zilio S, Zoso A, Kuznetsova V, Alcazar O, Buchwald P, Grilli A, Caroli J, Bicciato S, Serafini P. RNA aptamers specific for transmembrane p24 trafficking protein 6 and Clusterin for the targeted delivery of imaging reagents and RNA therapeutics to human β cells. Nat Commun. 2022 Apr 5;13(1):1815.
6. Musiu C, Caligola S, Fiore A, Lamolinara A, Frusteri C, Del Pizzo FD, De Sanctis F, Canè S, Adamo A, Hofer F, Barouni RM, Grilli A, Zilio S, Serafini P, Tacconelli E, Donadello K, Gottin L, Polati E, Girelli D, Polidoro I, Iezzi PA, Angelucci D, Capece A, Chen Y, Shi ZL, Murray PJ, Chilosi M, Amit I, Bicciato S, Iezzi M, Bronte V, Ugel S. Fatal cytokine release syndrome by an aberrant FLIP/STAT3 axis. Cell Death Differ. 2022 Feb;29(2):420-438.
7. Enzo E, Secone Seconetti A, Forcato M, Tenedini E, Polito MP, Sala I, Carulli S, Contin R, Peano C, Tagliafico E, Bicciato S, Bondanza S, De Luca M. Single- keratinocyte transcriptomic analyses identify different clonal types and proliferative potential mediated by FOXM1 in human epidermal stem cells. Nat Commun. 2021 May 4;12(1):2505.
8. Castellan M, Guarnieri A, Fujimura A, Zanconato F, Battilana G, Panciera T, Sladitschek HL, Contessotto P, Citron A, Grilli A, Romano O, Bicciato S, Fassan M, Porcù E, Rosato A, Cordenonsi M, Piccolo S. Single-cell analyses reveal YAP/TAZ as regulators of stemness and cell plasticity in Glioblastoma. Nat Cancer. 2021 Feb;2(2):174-188.
9. Forcato M, Bicciato S. Computational Analysis of Hi-C Data. Methods Mol Biol. 2021;2157:103-125.
10. Forcato M, Romano O, Bicciato S. Computational methods for the integrative analysis of single-cell data. Brief Bioinform. 2021 Jan 18;22(1):20-29.
11. Caroli J, Dori M, Bicciato S. Computational Methods for the Integrative Analysis of Genomics and Pharmacological Data. Front Oncol. 2020 Feb 27;10:185.
12. Caroli J, Forcato M, Bicciato S. APTANI2: update of aptamer selection through sequence-structure analysis. Bioinformatics. 2020 Apr 1;36(7):2266-2268.
13. Dori M, Bicciato S. Integration of Bioinformatic Predictions and Experimental Data to Identify circRNA-miRNA Associations. Genes (Basel). 2019 Aug 24;10(9):642.
14. Zanconato F, Battilana G, Forcato M, Filippi L, Azzolin L, Manfrin A, Quaranta E, Di Biagio D, Sigismondo G, Guzzardo V, Lejeune P, Haendler B, Krijgsveld J, Fassan M, Bicciato S, Cordenonsi M, Piccolo S. Transcriptional addiction in cancer cells is mediated by YAP/TAZ through BRD4. Nat Med. 2018 Oct;24(10):1599-1610.
15. Caroli J, Sorrentino G, Forcato M, Del Sal G, Bicciato S. GDA, a web-based tool for Genomics and Drugs integrated analysis. Nucleic Acids Res. 2018 Jul 2;46(W1):W148-W156.
16. Santinon G, Brian I, Pocaterra A, Romani P, Franzolin E, Rampazzo C, Bicciato S, Dupont S. dNTP metabolism links mechanical cues and YAP/TAZ to cell growth and oncogene-induced senescence. EMBO J. 2018 Jun 1;37(11):e97780.
17. Nicoletti C, Forcato M, Bicciato S. Computational methods for analyzing genome-wide chromosome conformation capture data. Curr Opin Biotechnol. 2018 Dec;54:98-105.
18. Ingallina E, Sorrentino G, Bertolio R, Lisek K, Zannini A, Azzolin L, Severino LU, Scaini D, Mano M, Mantovani F, Rosato A, Bicciato S, Piccolo S, Del Sal G. Mechanical cues control mutant p53 stability through a mevalonate-RhoA axis. Nat Cell Biol. 2018 Jan;20(1):28-35.
19. Hirsch T, Rothoeft T, Teig N, Bauer JW, Pellegrini G, De Rosa L, Scaglione D, Reichelt J, Klausegger A, Kneisz D, Romano O, Secone Seconetti A, Contin R, Enzo E, Jurman I, Carulli S, Jacobsen F, Luecke T, Lehnhardt M, Fischer M, Kueckelhaus M, Quaglino D, Morgante M, Bicciato S, Bondanza S, De Luca M. Regeneration of the entire human epidermis using transgenic stem cells. Nature. 2017 Nov 16;551(7680):327-332.
20. Forcato M, Nicoletti C, Pal K, Livi CM, Ferrari F, Bicciato S. Comparison of computational methods for Hi-C data analysis. Nat Methods. 2017 Jul;14(7):679-685.