Epigenomics

Research Article Reporting Checklist for Bioinformatic and Data Re-analysis Studies

This is a submission requirement for Research Articles reporting the results of a bioinformatic study and/or re-analysis of available online data. The checklist is intended as an aid to authors to inform reviewers and readers of their methods and findings clearly, completely and transparently. This checklist will also be used as a tool to evaluate the suitability and novelty of manuscripts for publication in *Epigenomics*.

Please read the checklist below and indicate if the following information is available in your manuscript (or supplementary material). In cases where you have confirmed that the stipulated information is present in your article, please detail where it can be found by providing the page/paragraph/line number.

Criteria	Information is located on page/paragraph/line of the manuscript	N/A
Explain if and how you generated and analysed your own data (e.g. cell samples, tissue samples, mouse models, human models)	For promoter methylation analysis of *BRCA2* by quantitative PCR, detailed experimental and analyzing procedure can be found in page 6, paragraph entitled "Quantifying BRCA2 promoter methylation by qPCR". For *BRCA2* mRNA and protein expression, detailed experimental and analyzing procedure can be found in page 7, paragraph entitled "BRCA2 mRNA and protein quantification". For mutational signature 3 quantification, detailed experimental and analyzing procedure can be found in page 8, paragraph entitled "Mutational Signature 3 quantification". For *ex vivo* Olaparib treatment response assay, detailed experimental and analysis procedure can be found in page 9, paragraph entitled "*Ex vivo* drug response assay".	
Explain how you have adjusted for differences between data types (e.g. data derived from different cell, tissue and population types) and data sets (both own and previously published) **AND** Detail how you have processed the different datasets to make them comparable	We obtained and cleaned Infinium HumanMethylation 27K data and generated normalized beta-value for each probe from GSE42042 (including 71 MPNs and 13 MPNs-LT) according to the description in page 4, paragraph "Obtaining and cleaning of Infinium HumanMethylation 27K data".	
Describe how you have identified a suitable tool for the data analysis **OR** description of the novel bioinformatic tool/technology developed in your study	R package minfi was used to normalize the beta-value of HM 27K array data. (page 4, paragraph "Obtaining and cleaning of Infinium HumanMethylation 27K data"). FastQC and Trimmonmatic were used for quality control and trimming of whole-exome sequencing reads. Picard was used to mark duplicates. Genetic variants were characterized using Genome Analysis Tool Kit (GATK) according to the best practice pipeline. R package "deconstructSigs" was used to generate mutational signature 3 activity (page 8, paragraph entitled "Mutational Signature 3 quantification").	
Detailed comparison of your own new findings against the findings of the original study in which the data was first generated	Comparing to the previous general analysis identifying significant hypermethylation of immune-related pathways during leukemic transformation of MPNs (PMID: 23716560). Our study focused on the epigenetic silencing of DNA damage repair genes and experimentally confirmed *BRCA2* promoter hypermethylation as an actionable marker for the malignant transformation of MPNs.	
Explain in detail the impact of your findings within the field of epigenomics	Leukemic transformation is a critical complication of MPNs. BRCA2 promoter hypermethylation is a powerful risk factor for this malignant transformation, and an actionable biomarker enlightening the potential targeted MPNs therapy using PARPi.	

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Clearly show that your study has implemented the FAIR principles on data management*	**F**indable: **A**ccessible: **I**nteroperable: **R**eusable:	N/A
*In 2016, the 'FAIR Guiding Principles for scientific data management and stewardship' were published in *Scientific Data*. The authors intended to provide guidelines to improve the Findability, Accessibility, Interoperability, and Reuse of digital assets. Visit the GO FAIR website for more guidance on the FAIR Principles.		

For more information on the journal, please visit our website. If you have any questions regarding the criteria listed above, please contact Storm Johnson, Commissioning Editor of *Epigenomics*: s.johnson@futuremedicine.com

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