BMC Medical Genomics

CORRECTION Open Access

Correction to: Systematic characterization of germline variants from the DiscovEHR study endometrial carcinoma population

Jason E. Miller[1], Raghu P. Metpally[2], Thomas N. Person[2], Sarathbabu Krishnamurthy[3], Venkata Ramesh Dasari[3], Manu Shivakumar[2], Daniel R. Lavage[2], Adam M. Cook[3], David J. Carey[3], Marylyn D. Ritchie[1], Dokyoon Kim[2,4,5,6], Radhika Gogoi[3*] and on behalf of the DiscovEHR collaboration

Miller et al. BMC Medical Genomics (2019) 12:59. https://doi.org/10.1186/s12920-019-0504-9

Following publication of the original article [1], the authors reported that Fig. 1 was not correctly processed during the production process. The correct Fig. 1 is given below.

The publishers apologise for the inconvenience caused. The original article [1] has been corrected.

Author details
[1]Department of Genetics, Institute for Biomedical Informatics, Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA 19104, USA. [2]Biomedical & Translational Informatics Institute, Geisinger Health System, Danville, PA 17822, USA. [3]Weis Center for Research, Geisinger Medical Center, Danville, PA 17822, USA. [4]Huck Institute of the Life Sciences, Pennsylvania State University, University Park, Pennsylvania, PA 16802, USA. [5]Department of Biostatistics, Epidemiology and Informatics, Perelman School of Medicine, University of Pennsylvania, Philadelphia, USA. [6]Institute for Biomedical Informatics, University of Pennsylvania, Philadelphia, USA.

Received: 8 May 2019 Accepted: 8 May 2019
Published online: 22 May 2019

Reference

1. Miller, et al. Systematic characterization of germline variants from the DiscovEHR study endometrial carcinoma population. BMC Med Genet. 2019; 12:59. https://doi.org/10.1186/s12920-019-0504-9.

* Correspondence: radhika.gogoi@gmail.com; rpgogoi@geisinger.edu
[3]Weis Center for Research, Geisinger Medical Center, Danville, PA 17822, USA
Full list of author information is available at the end of the article

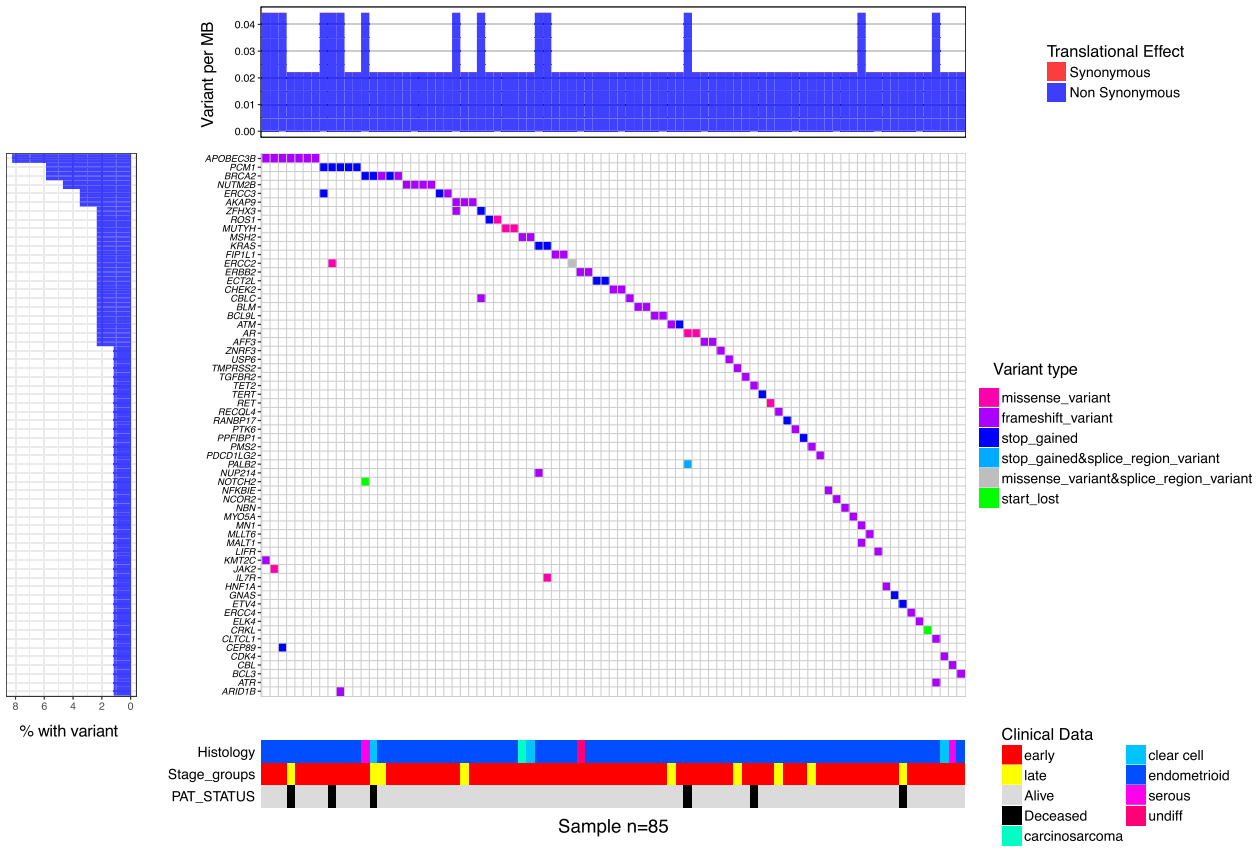

Fig. 1 Waterfall plot of all genes with pathogenic variants. Waterfall plot of all EMCA samples that contained rare variants that passed the filter from Additional file 1: Figure S1. The main heatmap contains columns which represent an individual participant ($N = 86$), and rows that represent genes, while the color that fills in the cell represents the type of variant present for a specific participant in a specific gene. The heatmap below illustrates that histology, cancer stage and patient survival status, each column represents a different participant. "Undiff" refers to undifferentiated histology. The graph to the left shows the percentage of participants who have a rare variant in a gene, relative to all participants with variants, while the bar plot above the main graph represents the variant burden for each participant