

Reviewer Report

Title: Genomic data imputation with variational autoencoders

Version: Revision 2 **Date: 6/16/2020**

Reviewer name: Natalie Davidson

Reviewer Comments to Author:

Thank you for adding further details to your manuscript; it is now clear to me that your method is intended to be used downstream of a normalization/pre-processing method that can identify untrustworthy genes (batch effect, contamination, lowly expressed). These genes are then replaced with a NA. I only suggest a little more clarification in your sentence "VAE thus can be an important tool to analyze the large amounts of publicly available data from 1000s of studies that are publicly available in the Gene Expression omnibus (Barrett, et al., 2012)." Is this joining RNA-Seq + array?

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