***eLife’s* transparent reporting form**

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**Sample-size estimation**

* You should state whether an appropriate sample size was computed when the study was being designed
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* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

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In the Method section, sample -size is addressed in **Gene selection based on Z score and batch standardization** as well as in the **Quantification and statistical analysis** section.

**Replicates**

* You should report how often each experiment was performed
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(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

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* Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
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* Include model definition files including the full list of parameters used
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Please indicate the figures or tables for which source data files have been provided:

This study did not generate new unique reagents. This study generated new python3 **code** available on **GitHub**: <https://github.com/extavourlab/hpo_ova_eggL_screen>. All **raw data** generated during the course of this study can also be found on **Github** at the aforementioned address.