Chen EY, Tan CM, Kou Y, Duan Q, Wang Z, Meirelles GV, Clark NR, Ma'ayan A. Enrichr: interactive and collaborative HTML5 gene list enrichment analysis tool. BMC Bioinformatics. 2013;128(14).

Chen J, Bardes EE, Aronow BJ, Jegga AG 2009. ToppGene Suite for gene list enrichment analysis and candidate gene prioritization. Nucleic Acids Research

doi: 10.1093/nar/gkp427

Dumitriu, Alexandra, Javad Golji, Adam T. Labadorf, Benbo Gao, Thomas G. Beach, Richard H. Myers, Kenneth A. Longo, and Jeanne C. Latourelle. 2016. “Integrative

Analyses of Proteomics and RNA Transcriptomics Implicate Mitochondrial Processes, Protein Folding Pathways and GWAS Loci in Parkinson Disease.” *BMC Medical Genomics* 9 (1). https://doi.org/10.1186/s12920-016-0164-y.

Finotello, F. & Di Camillo, B. Measuring differential gene expression with RNA-seq:

challenges and strategies for data analysis. *Brief. Funct. Genomics* **14**, 130–142 (2015).

Frum, T, M A Halbisen, C Wang, H Amiri, P Robson, and A Ralston. 2013. “Oct4 Cell-Autonomously Promotes Primitive Endoderm Development in the Mouse Blastocyst.” *Dev Cell* 25 (6): 610–22. https://doi.org/10.1016/j.devcel.2013.05.004.

Gao, Yawei, Xiaoyu Liu, She Chen, Lujian Liao, and Shaorong Gao Correspondence. 2017. “Protein Expression Landscape of Mouse Embryos during Pre-Implantation Development.” https://doi.org/10.1016/j.celrep.2017.11.111.

Huntley, R. P., Sawford, T., Martin, M. J. & O’Donovan, C. Understanding how and why the Gene Ontology and its annotations evolve: The GO within UniProt. *GigaScience* **3**, 4 (2014).

Kuleshov MV, Jones MR, Rouillard AD, Fernandez NF, Duan Q, Wang Z, Koplev S, Jenkins SL, Jagodnik KM, Lachmann A, McDermott MG, Monteiro CD, Gundersen GW, Ma'ayan A. Enrichr: a comprehensive gene set enrichment analysis web server 2016 update. Nucleic Acids Research. 2016; gkw377 .

Mi H, Muruganujan A, Thomas PD. 2013, “PANTHER in 2013: modeling the evolution of gene function, and other gene attributes, in the context of phylogenetic trees.” *Nucleic Acids Research* 41(Database issue):D377-86.

Shi, Junchao, Qi Chen, Xin Li, Xiudeng Zheng, Ying Zhang, Jie Qiao, Fuchou Tang, Yi Tao, Qi Zhou, and Enkui Duan. 2015. “Dynamic Transcriptional Symmetry-Breaking in Pre-Implantation Mammalian Embryo Development Revealed by Single-Cell Rna-Seq.” *Development (Cambridge)* 142 (20): 3468–77. <https://doi.org/10.1242/dev.123950>.

Takahashi, Kazutoshi, and Shinya Yamanaka. 2006. “Induction of Pluripotent Stem Cells from Mouse Embryonic and Adult Fibroblast Cultures by Defined Factors.” *Cell* 126 (4): 663–76. https://doi.org/10.1016/j.cell.2006.07.024.

Thomas PD, Campbell MJ, Kejariwal A, Mi H, Karlak B, Daverman R, Diemer K, Muruganujan A, Narechania A. 2003. “PANTHER: a library of protein families and subfamilies indexed by function.” *Genome Research* 13(9):2129-41

Wilhelm, B. T. & Landry, J. R. RNA-Seq-quantitative measurement of expression through massively parallel RNA-sequencing. *Methods* **48**, 249–257 (2009).

Yoon, Sora, Seon-Young Kim, and Dougu Nam. 2016. “Improving Gene-Set Enrichment Analysis of RNA-Seq Data with Small Replicates.” Edited by Dongmei Li. *PLOS ONE* 11 (11): e0165919. https://doi.org/10.1371/journal.pone.0165919.

Young, Matthew D., Matthew J. Wakefield, Gordon K. Smyth, and Alicia Oshlack. 2010. “Gene Ontology Analysis for RNA-Seq: Accounting for Selection Bias.” *Genome Biology* 11 (2): R14. https://doi.org/10.1186/gb-2010-11-2-r14.

Yu, Fangfang, Chen Duan, Xiaodong Zhang, Dandan Yao, Gangquan Si, Ying Gao, Zongqiang Gao, Farooq Umer, and Xiong Guo. 2018. “RNA-Seq Analysis Reveals Different Gene Ontologies and Pathways in Rheumatoid Arthritis and Kashin-Beck Disease.” *International Journal of Rheumatic Diseases* 21 (9): 1686–94. https://doi.org/10.1111/1756-185X.13358.