References cited

- 1. Wagner, A., Regev, A. & Yosef, N. Revealing the vectors of cellular identity with single-cell genomics. *Nat. Biotechnol.* **34,** 1145–1160 (2016).
- 2. Pan, D. An integrative framework for continuous knowledge discovery. *Journal of Convergence Information Technology* (2010).
- 3. Cao, J. *et al.* Comprehensive single-cell transcriptional profiling of a multicellular organism. *Science* **357**, 661–667 (2017).
- 4. Fertig, E. J., Ding, J., Favorov, A. V., Parmigiani, G. & Ochs, M. F. CoGAPS: an R/C++ package to identify patterns and biological process activity in transcriptomic data. *Bioinformatics* **26**, 2792–2793 (2010).
- 5. Fertig, E. J. *et al.* Gene expression signatures modulated by epidermal growth factor receptor activation and their relationship to cetuximab resistance in head and neck squamous cell carcinoma. *BMC Genomics* **13**, 160 (2012).
- 6. Stein-O'Brien, G. et al. PatternMarkers and Genome-Wide CoGAPS Analysis in Parallel Sets (GWCoGAPS) for data-driven detection of novel biomarkers via whole transcriptome Non-negative matrix factorization (NMF). bioRxiv doi:10.1101–083717 (2016). doi:10.1101/083717