

3. Singh, D., et al., *Gene expression correlates of clinical prostate cancer behavior*. *Cancer Cell*, 2002. **1**: p. 203-209.
4. van't Veer, L., et al., *Gene expression profiling predicts clinical outcome of breast cancer*. *Nature*, 2002. **415**: p. 530-536.
5. Braga-Neto, U. and E. Dougherty, *Is cross-validation valid for small-sample microarray classification?* *Bioinformatics*, 2004. **20**: p. 374-380.
6. Chuaqui, R., et al., *Post-analysis follow-up and validation of microarray experiments*. *Nature Genetics*, 2002. **32**: p. 509-514.
7. Morey, J., J. Ryna, and F. Van Dolah, *Microarray validation: factors influencing correlation between oligonucleotide microarrays and real-time PCR*. *Biol. Proced. Online*, 2006. **8**(1): p. 175-193.
8. Shi, L., et al., *The MicroArray Quality Control (MAQC) project shows inter- and intraplatform reproducibility of gene expression measurements*. *Nat Biotechnol*, 2006. **24**(9): p. 1151-61.
9. Stokes, T., et al., *chip artifact CORRECTION (caCORRECT): A Bioinformatics System for Quality Assurance of Genomics and Proteomics Array Data*. *Annals of Biomedical Engineering*, 2007. **35**: p. 1068-1080.
10. Aerts, S., et al., *Gene prioritization through genomic data fusion*. *Nature Biotechnology*, 2006. **24**(5): p. 537-544.
11. Kuffner, R., K. Fundel, and R. Zimmer, *Expert knowledge without the expert: integrated analysis of gene expression and literature to derive active functional contexts*. *Bioinformatics*, 2005. **21**: p. ii259-ii267.
12. Kong, S., W. Pu, and P. Park, *A multivariate approach for integrating genome-wide expression data and biological knowledge*. *Bioinformatics*, 2006. **22**(19): p. 2373-2380.
13. Mukherjee, S. and S. Roberts, *A theoretical analysis of the selection of differentially expressed genes*. *J Bioinformatics Comput Biol*, 2005. **3**: p. 627-643.
14. Bellazzi, R. and B. Zupan, *Towards knowledge-based gene expression data mining*. *Journal of Biomedical Informatics*, 2007. **40**: p. 787-802.
15. Efron, B. and R. Tibshirani, *Improvements on Cross-Validation: The .632+ Bootstrap Method*. *Journal of the American Statistical Association*, 1997. **92**(438): p. 548-560.
16. Jones, J., et al., *Gene signatures of progression and metastasis in renal cell cancer*. *Clin Cancer Res*, 2005. **11**(16): p. 5730-9.
17. Schrader, A., et al., *CXCR4/CXCL12 expression and signalling in kidney cancer*. *British Journal of Cancer*, 2002. **86**: p. 1250-1256.
18. Rosendahl, A. and G. Forseberg, *IGF-I and IGFBP-3 augment transforming growth factor-beta actions in human renal carcinoma cells*. *Kidney International*, 2006. **70**: p. 1584-1590.
19. Ivanov, S., et al., *Two novel VHL targets, TGFBI (BIGH3) and its transactivator KLF10, are up-regulated in renal clear cell carcinoma and other tumors*. *Biochem Biophys Res Commun*, 2008.