

## Expression and Function of ETS Genes in Prostate Cancer

### Stellingen

1. In clinical prostate cancer, full-length ETV1 can be overexpressed by translocation of the complete gene to novel genomic regions (this thesis).
2. Truncated ETV1, lacking the N-terminal transactivation domain, produced by fusion genes in prostate cancer, has not the same molecular and biological properties as full length ETV1 (this thesis).
3. Prostate cancer patients with high expression levels of *TMPRSS2-ERG* fusion transcripts starting at an alternative upstream first exon (exon 0) have a longer PSA-recurrence free survival (this thesis).
4. In ERG-positive prostate cancer a sub-group of patients with rapid progression can be identified (this thesis).
5. Genes involved in cell-cell communication, TGF- $\beta$  signalling and bone remodelling are the major contributors to the gene-classifier of cancer progression in ERG-positive prostate cancers (this thesis).
6. Higher amount of copy-number alterations predicts high-risk prostate cancer disease more robustly than Gleason score (Taylor BS *et al*, Cancer Cell 2010;18:11-22).
7. Mouse studies support the assumption that *ERG* overexpression is not sufficient for prostate cancer development; additional genetic and/or epigenetic alterations are essential. (Zong *et al*, Proc Natl Acad Sci USA 2009;106:12465-70; Klezovitch *et al*, Proc Natl Acad Sci USA 2008;105:2105-10).
8. Paulo *et al*. (Neoplasia 2012;14:600-11) indicate that overexpression of *ERG* and *ETV1* in clinical prostate tumor samples partially affects the same genes but this finding is not sufficiently supported by the experimental data.
9. Although prostate cancer is polyclonal with genetic heterogeneity between the different tumour foci, metastases in a patient (Liu *et al*, Nat Med 2009;15:559-65) seem to have a monoclonal origin.
10. "The last function of reason is to recognize that there are an infinity of things which surpass it" Blaise Pascal
11. "When nothing goes right...go left" Anonymous