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**Series GSE55945**
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Status Public on Mar 18, 2014  
 Title Gene Expression Profiling of Prostate Benign and Malignant Tissue  
 Organism [Homo sapiens](#)  
 Experiment type Expression profiling by array  
 Summary We profiled genome-wide gene expression of human prostate benign and malignant tissue to identify potential biomarkers and immunotherapy targets. We stratified malignant specimens according to their TMPRSS2:ERG gene fusion status.

Overall design Radical prostatectomy tissue samples were obtained from the Hershey Foundation Prostate Cancer Serum and Tumor Bank at our institution. Morphologic diagnosis was done by a pathologist. OCT blocks containing >30% of PCa tissue (with Gleason score of 6 or 7) were selected for RNA purification. A biopsy punch was used to select the PCa tissues from the OCT sample blocks. Benign or PCa tissues were homogenized using a TissueLyser (Qiagen) at 28 Hz for 5 min. Total RNA was isolated using Trizol reagent. RNA was quantified by NanoDrop ND-1000 spectrophotometer, and quality was evaluated with Agilent RNA 6000 NanoChip and the 2100 Bioanalyzer, with 28S/18S ratios and RIN determined by 2100 Expert software.

Contributor(s) [Arredouani MS, Lu B, Sanda M](#)

Citation(s) Arredouani MS, Lu B, Bhasin M, Eljanne M et al. Identification of the transcription factor single-minded homologue 2 as a potential biomarker and immunotherapy target in prostate cancer. *Clin Cancer Res* 2009 Sep 15;15(18):5794-802. PMID: [19737960](#)

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Platforms (1) [GPL570](#) [HG-U133\_Plus\_2] Affymetrix Human Genome U133 Plus 2.0 Array

Samples (21) [GSM1348933](#) Prostate Cancer\_MS 36D6

[More...](#)

[GSM1348934](#) Prostate Cancer\_MS 36C1

[GSM1348935](#) Prostate Cancer\_MS 36D7

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Supplementary file	Size	Download	File type/resource
GSE55945_RAW.tar	96.9 Mb	<a href="#">(http)</a> <a href="#">(custom)</a>	TAR (of CEL)
<i>Raw data provided as supplementary file</i>			
<i>Processed data included within Sample table</i>			