

Expression of genes of your list in reported primary prostate tumors of radical prostatectomy patients ^{1,2,3}

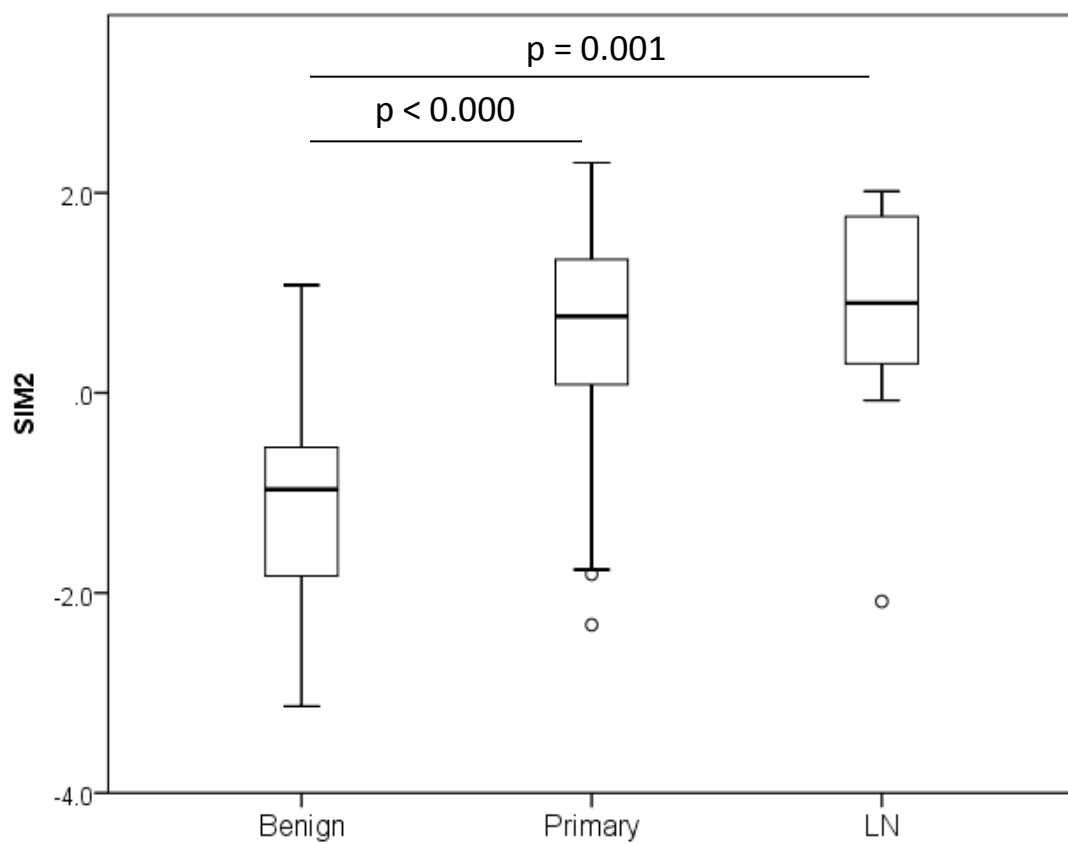
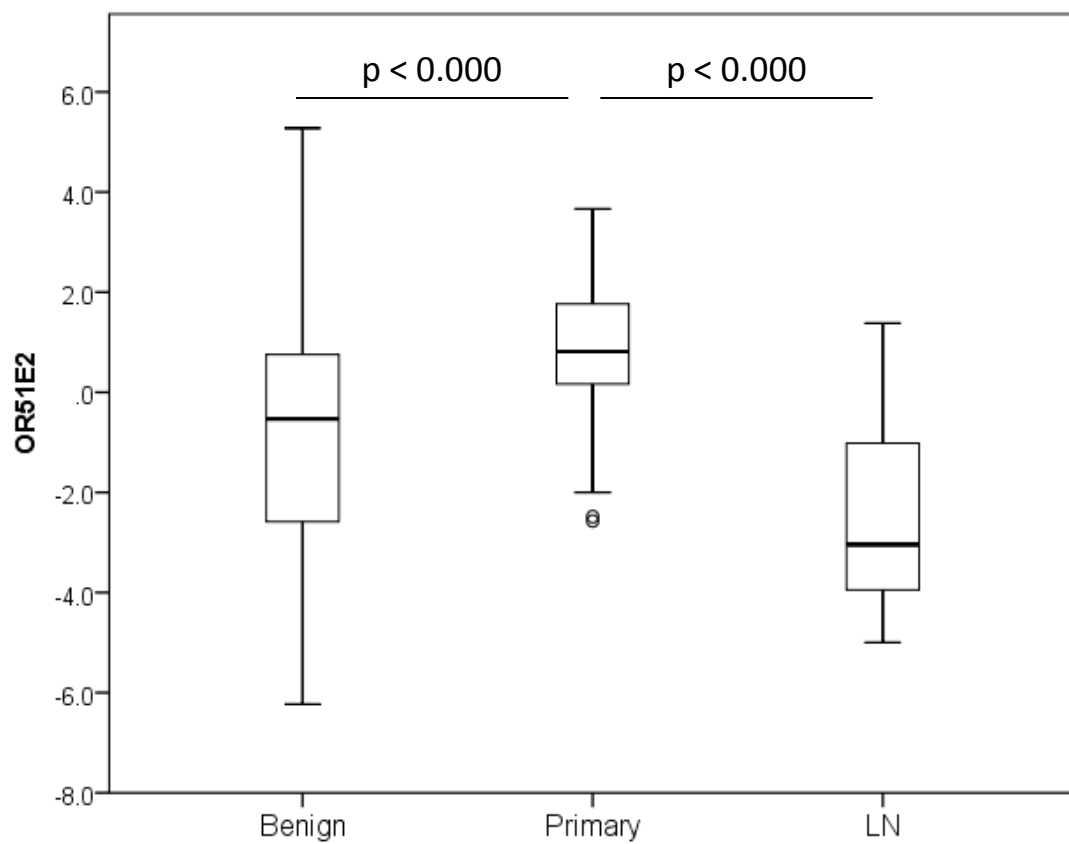
1. **Lapointe J**, Li C, Higgins JP, van de Rijn M et al. Gene expression profiling identifies clinically relevant subtypes of prostate cancer. *Proc Natl Acad Sci U S A* 2004 Jan 20;101(3):811-6.
2. **Ross-Adams H**, Lamb AD, Dunning MJ, et al. Integration of copy number and transcriptomics provides risk stratification in prostate cancer: A discovery and validation cohort study. *EBioMedicine*. 2015;2(9):1133–1144.
3. **Taylor BS**, Schultz N, Hieronymus H, et al. Integrative genomic profiling of human prostate cancer. *Cancer Cell*. 2010;18(1):11–22.

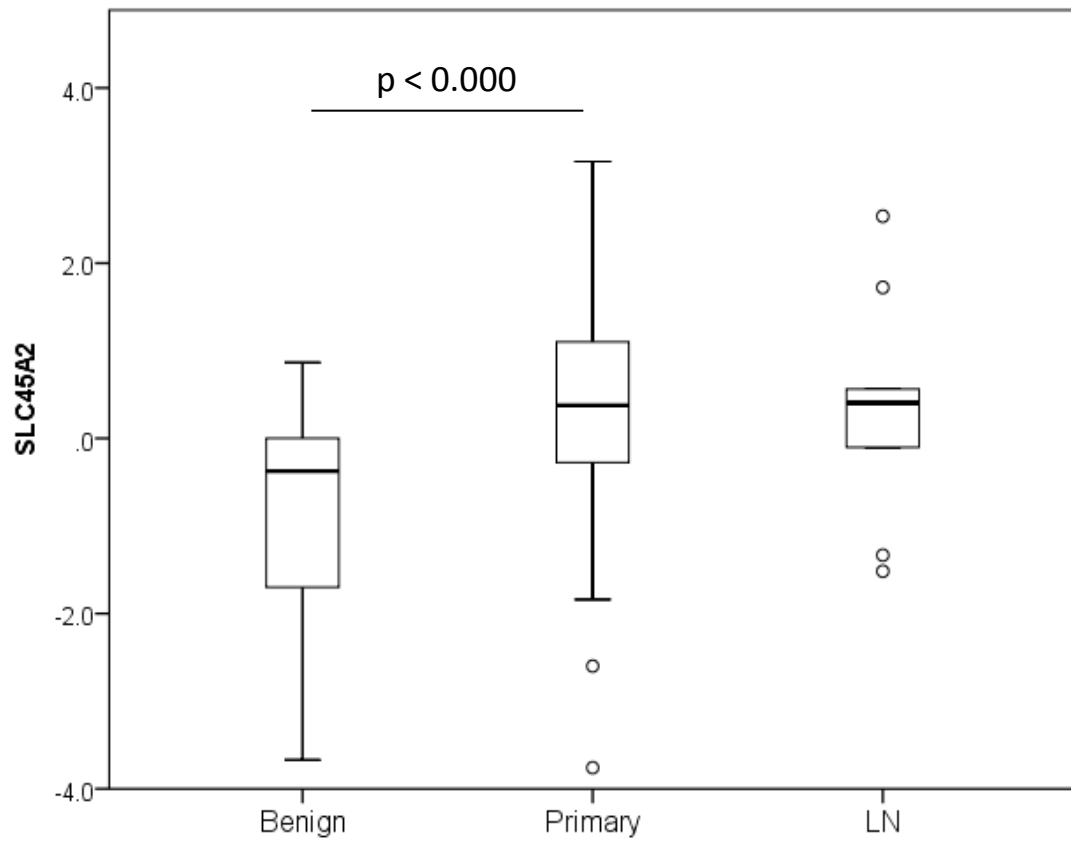
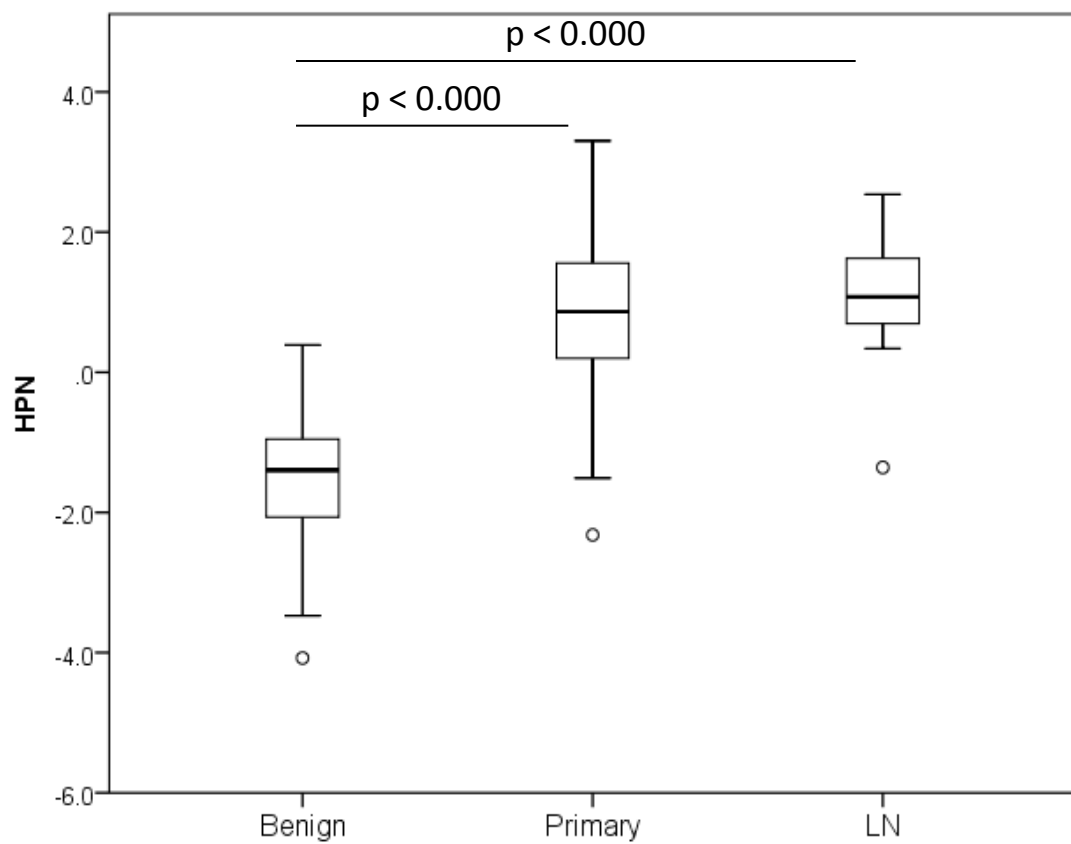
1- Lapointe dataset

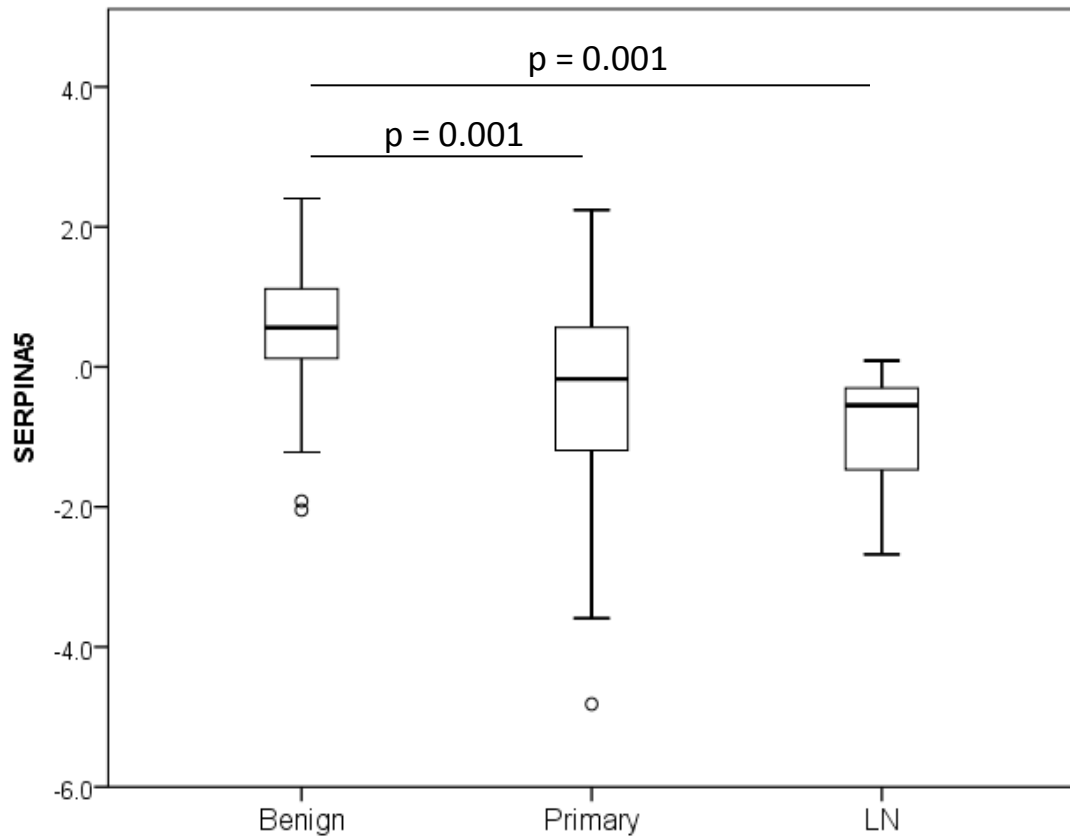
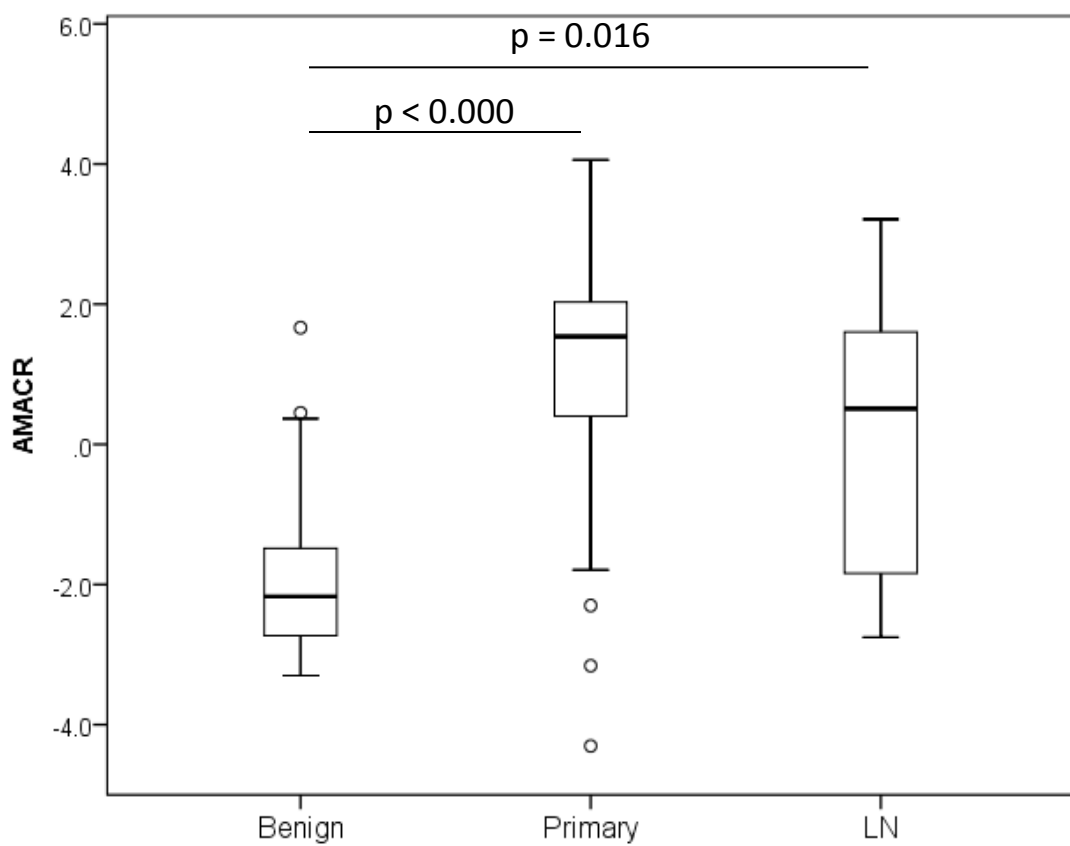
Benign vs. primary tumour vs.
lymph node metastases

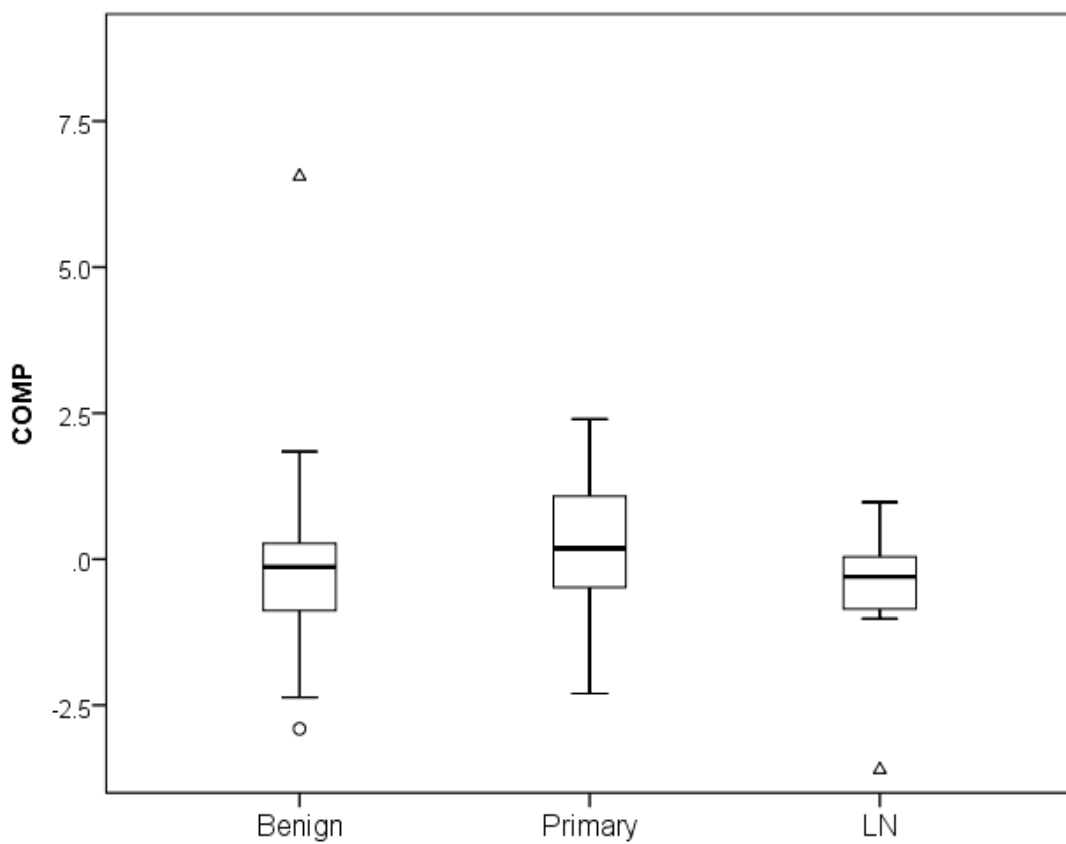
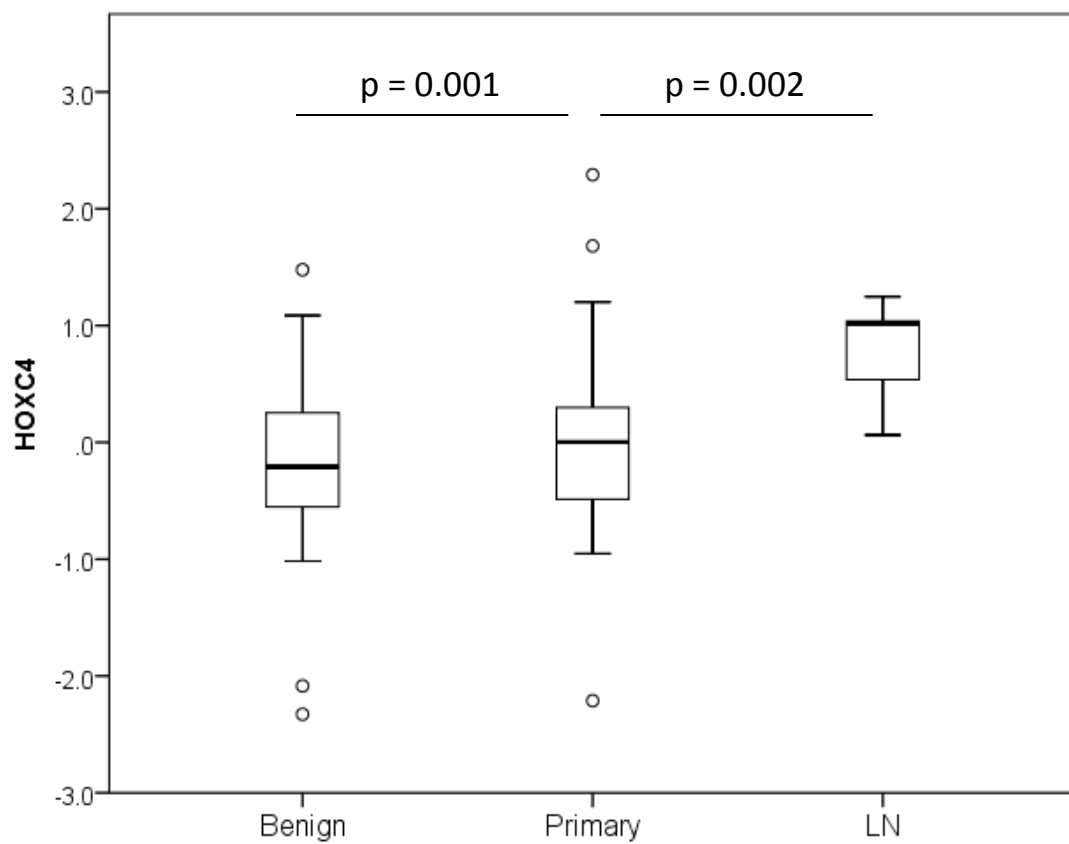
Box plots of z-scores vs. benign,
with genes presented in the
same order for all analyses

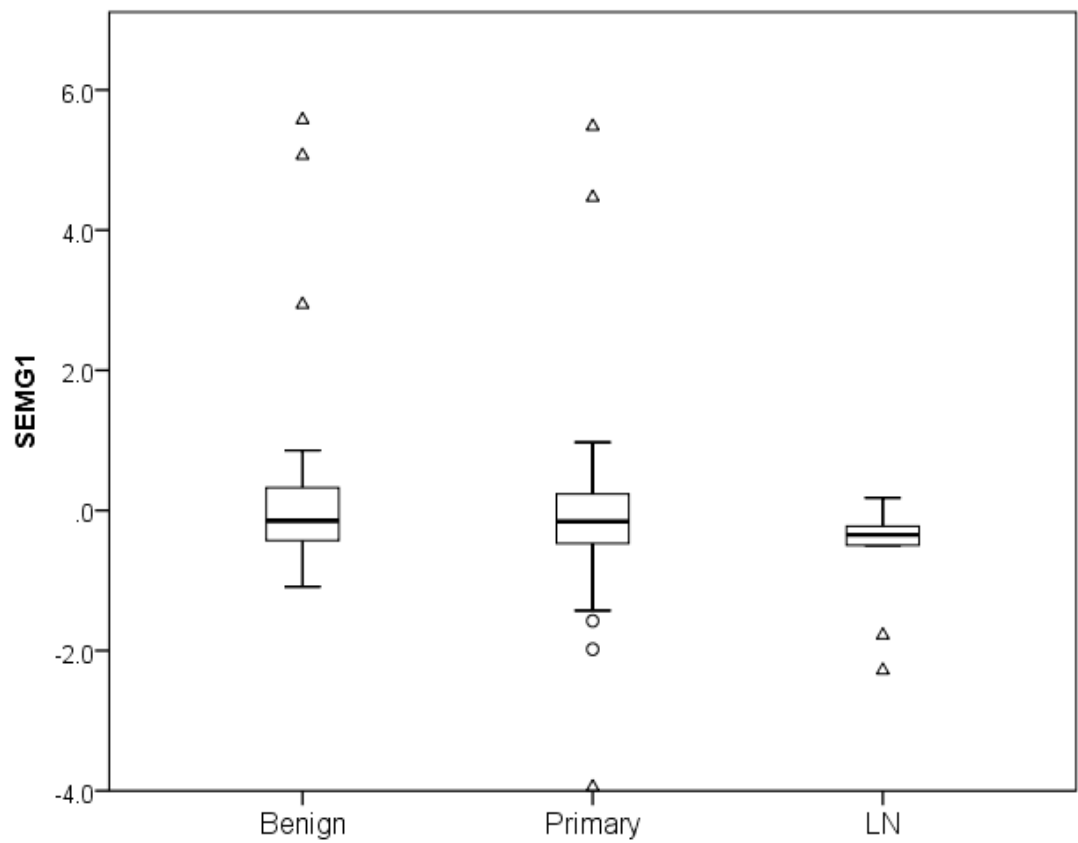
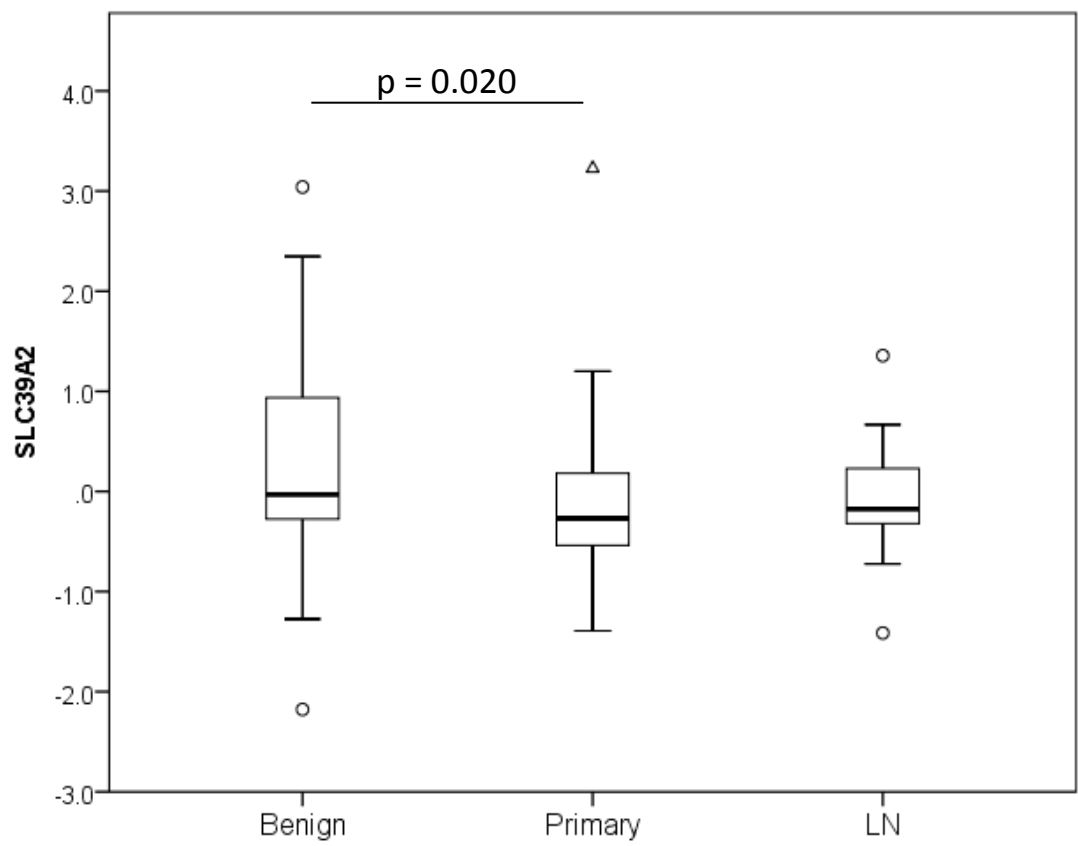
Statistics: Kruskal-Wallis test
with Bonferroni correction for
multiple tests

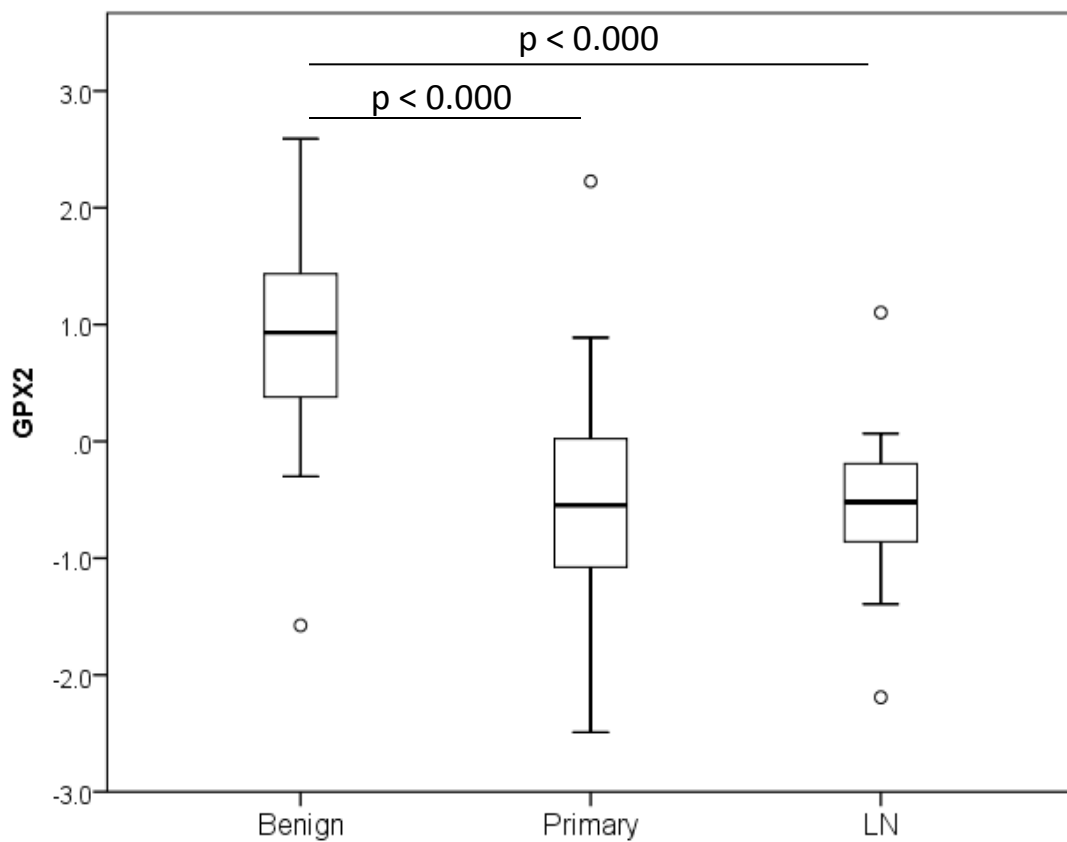
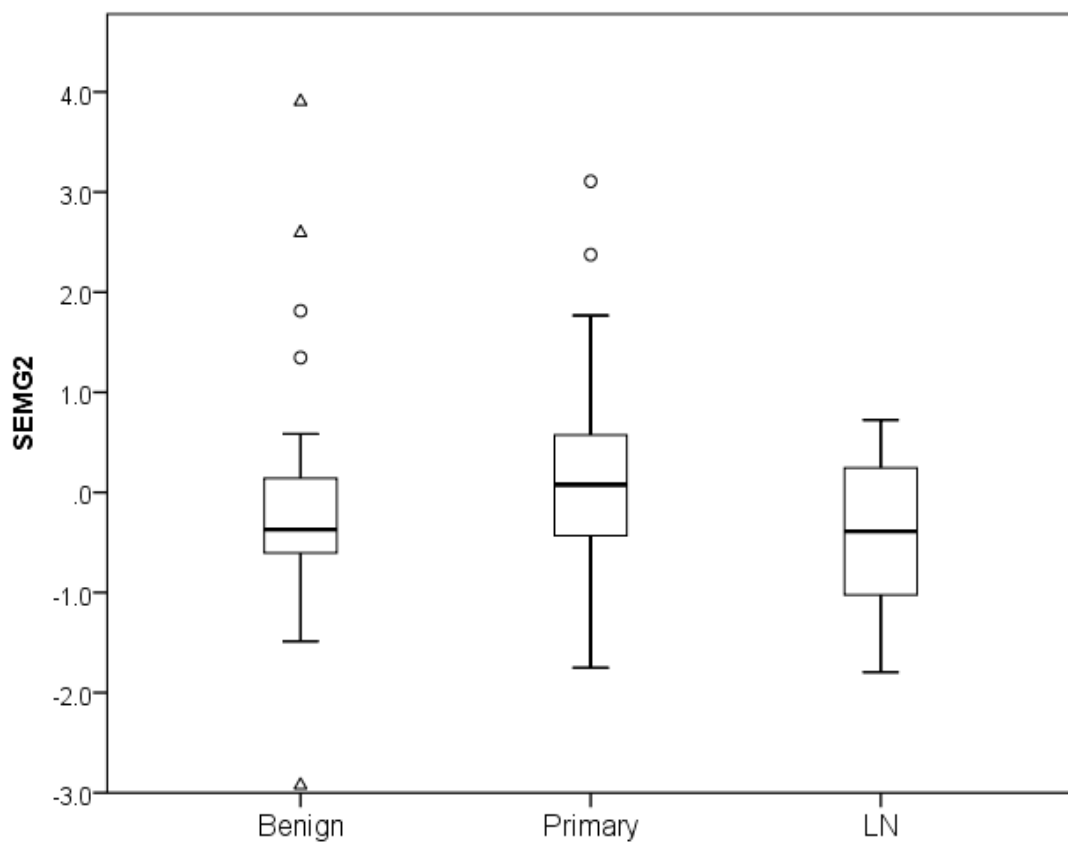


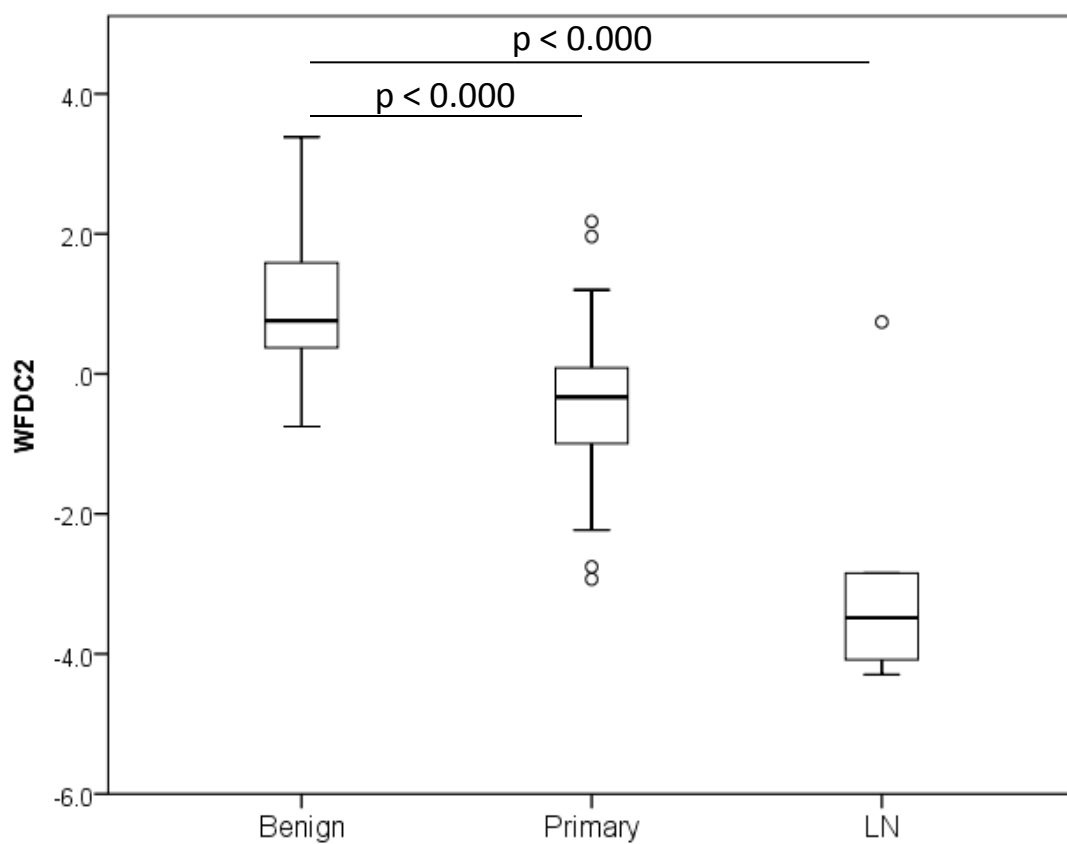
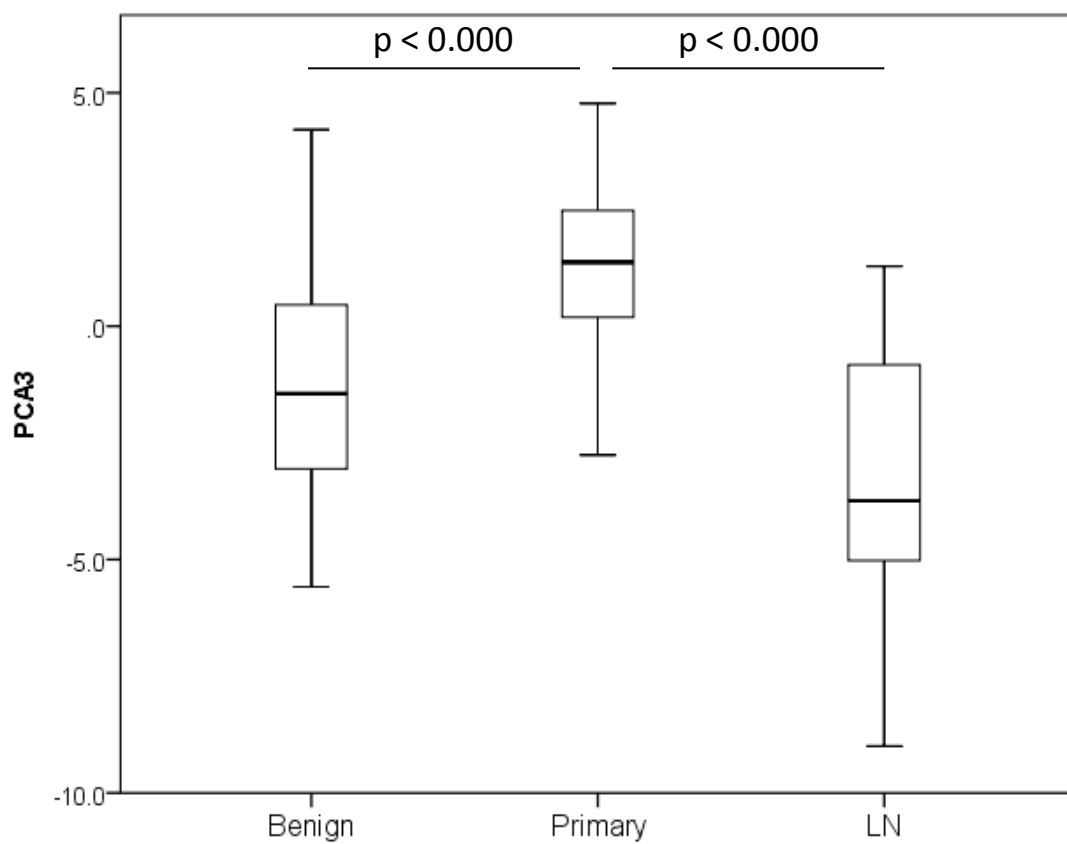












Lapointe Dataset

Summary of Results

P values	Benign vs. Primary	Benign vs. lymph node	Primary vs. Lymph node
OR51E2	<0.000		<0.000
SIM2	<0.000	0.001	
HPN	<0.000	<0.000	
SLC45A2	<0.000		
AMARC	<0.000	0.016	
SERPINA5	0.001	0.001	
HOXC4	0.001		0.002
COMP			
SLC39A2	0.020		
SEMG1			
SEMG2			
GPX2	<0.000	<0.000	
PCA3	<0.000		<0.000
WFDC2	<0.000	<0.000	

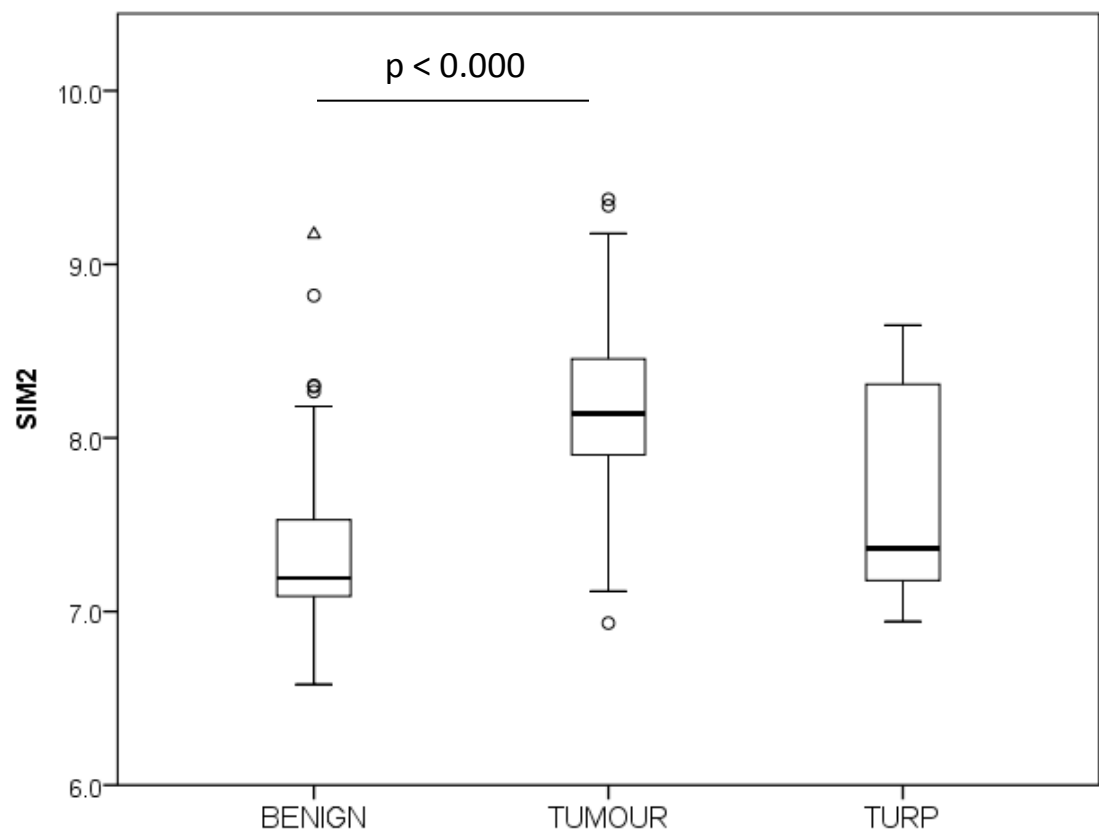
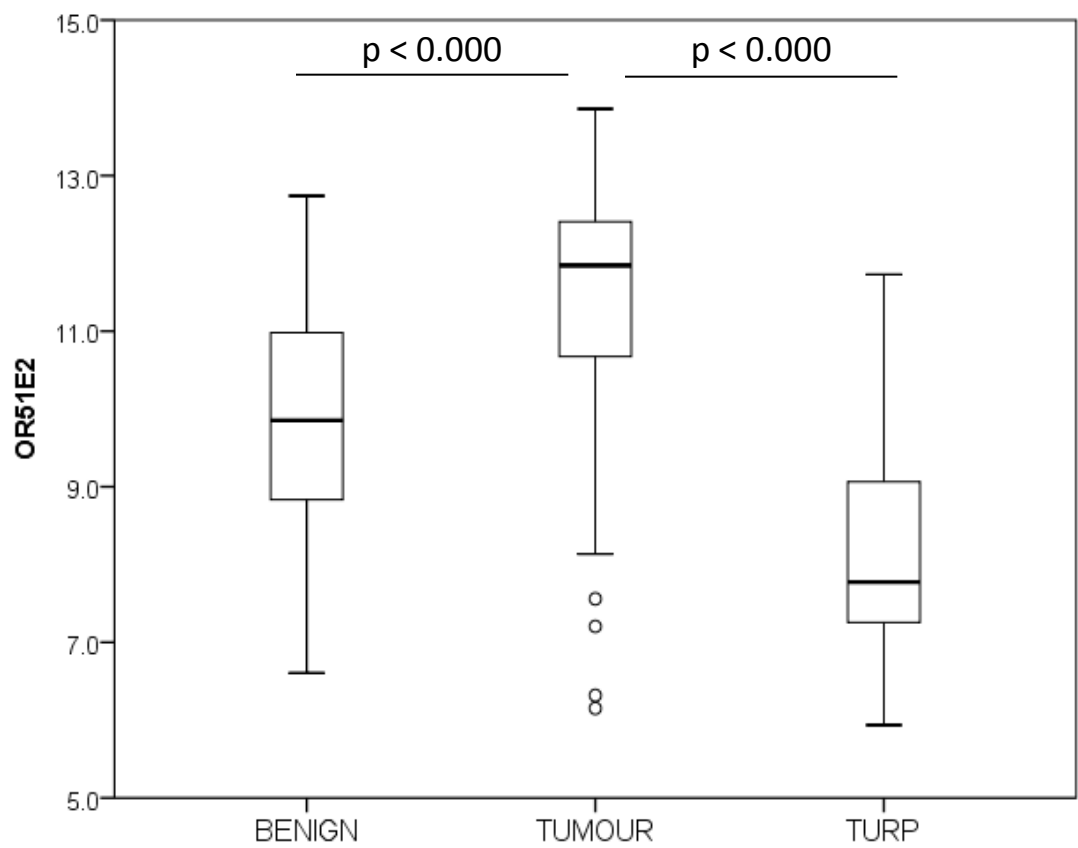
Green: Upregulation (e.g . High in primary vs. Benign)

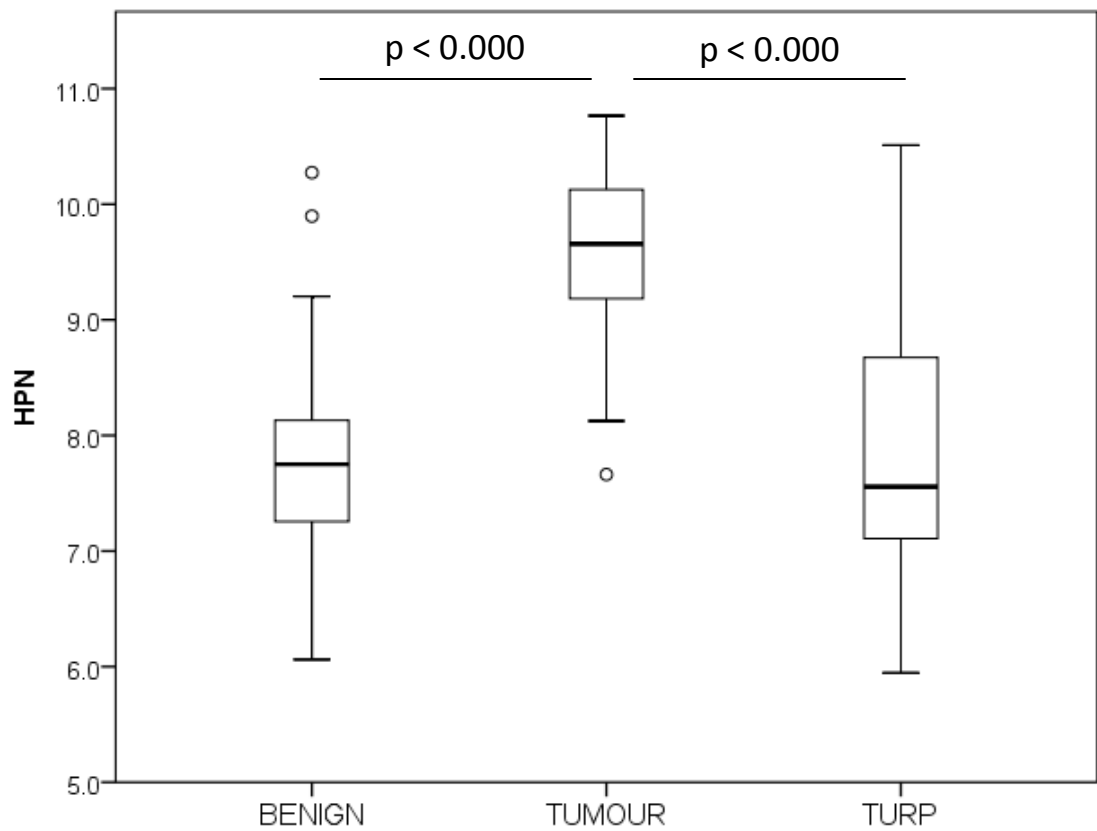
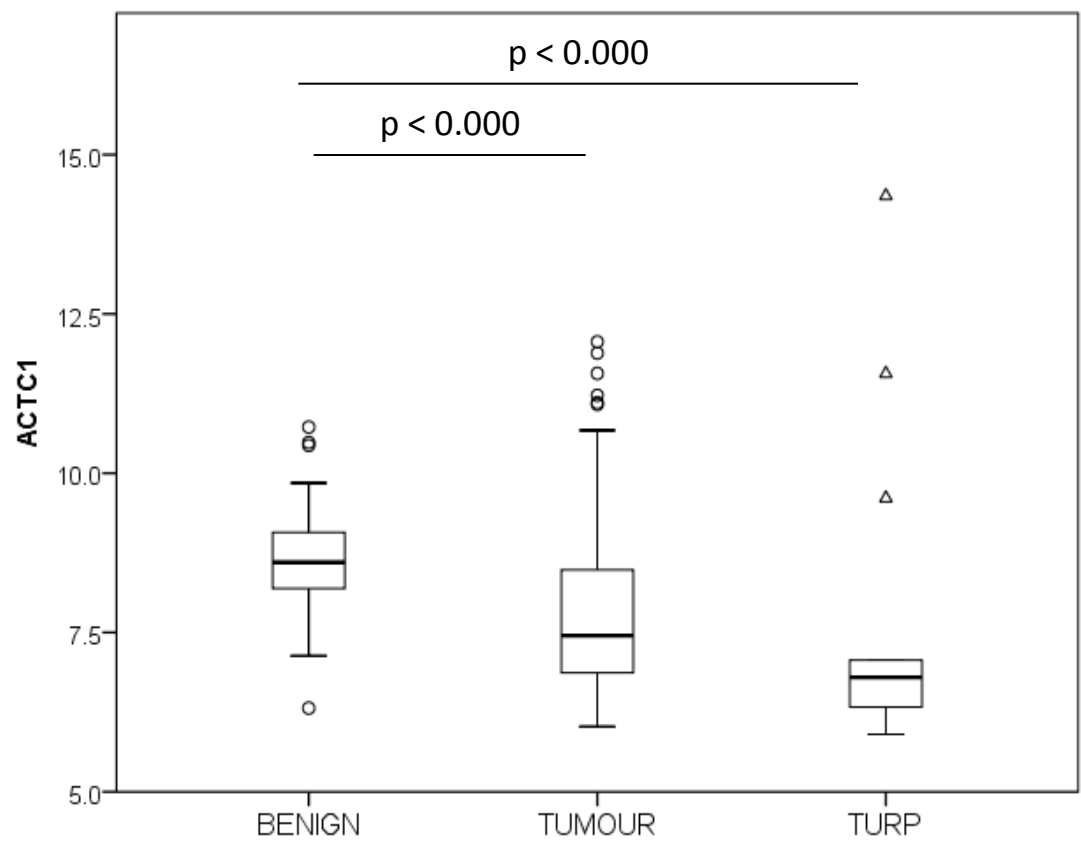
Red: Downregulation (e.g . Low in primary vs. Benign)

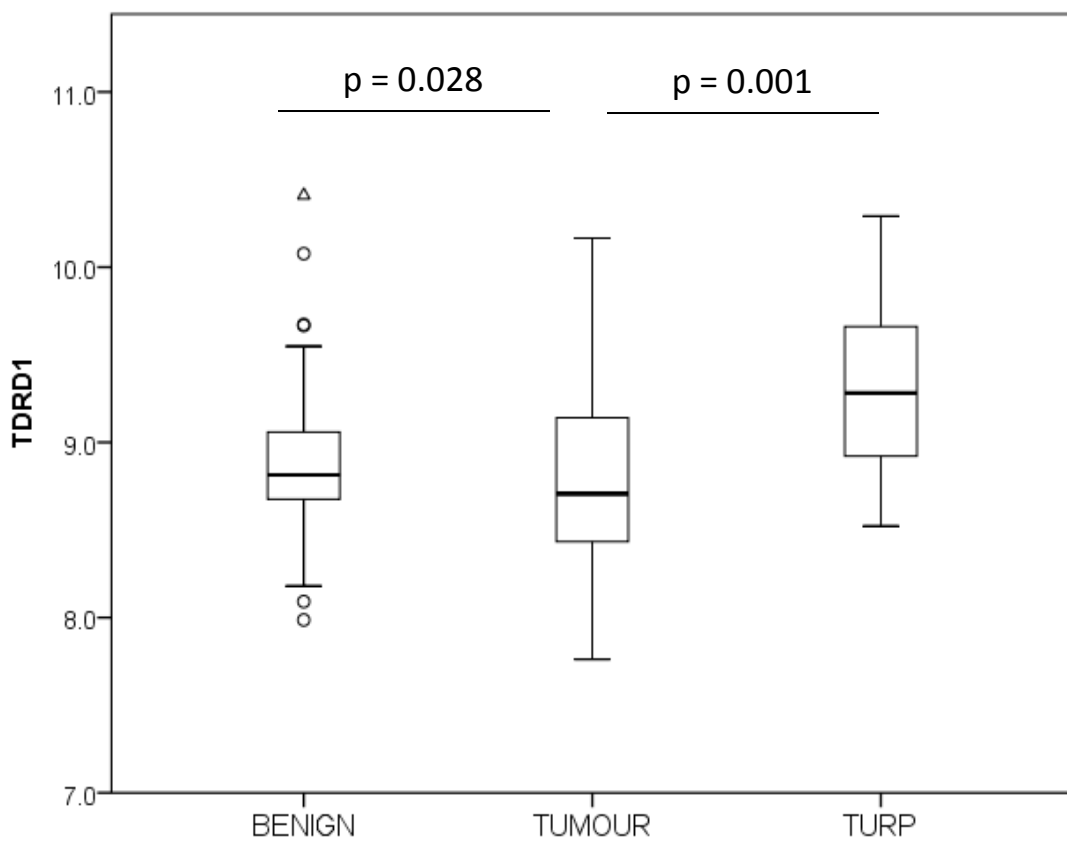
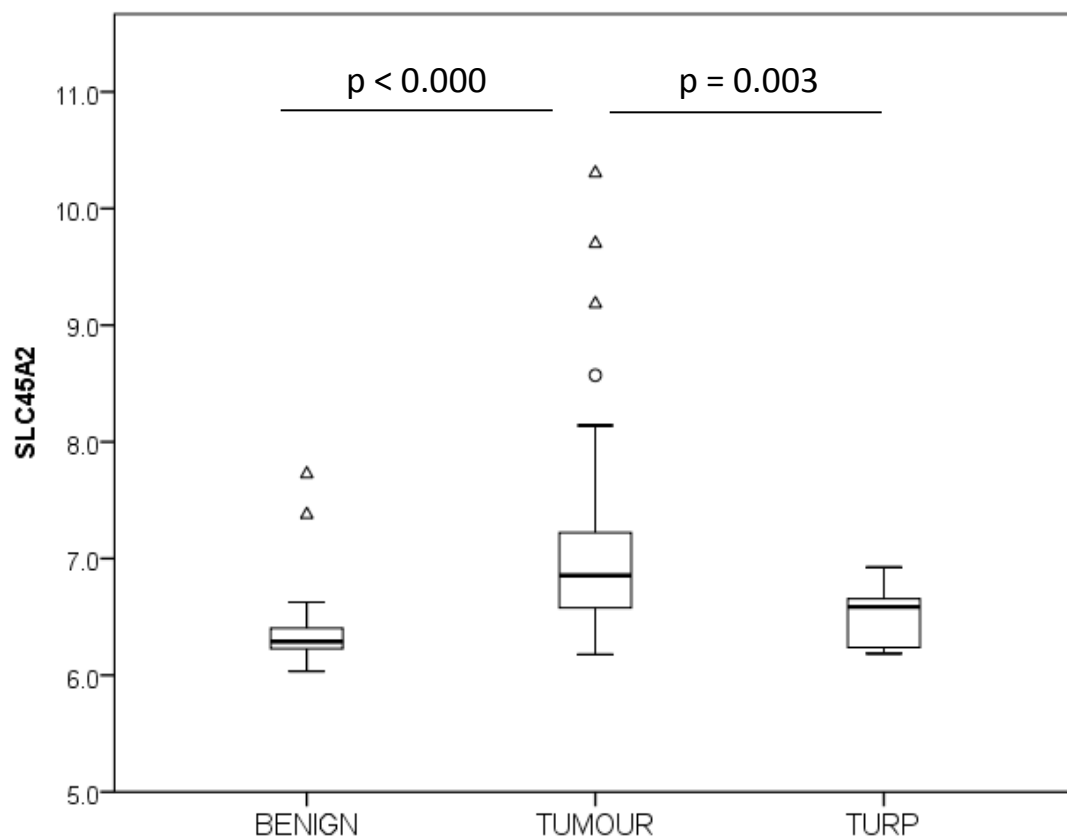
2- Ross-Adams dataset

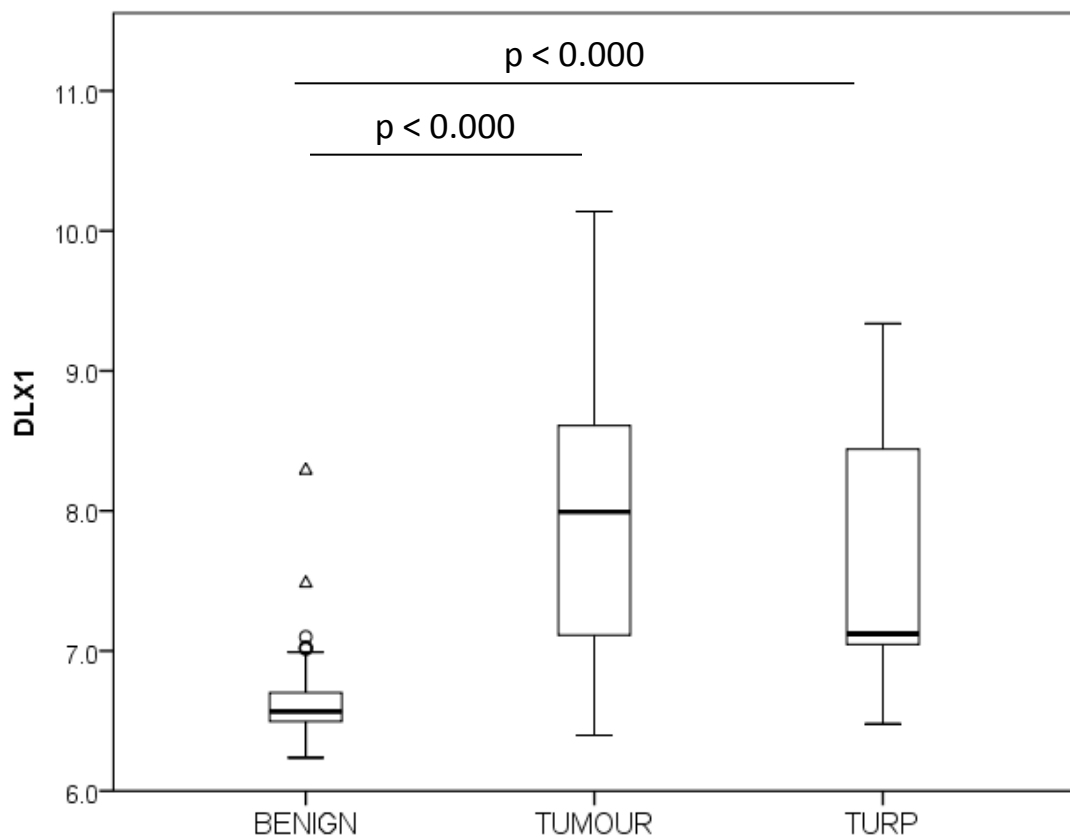
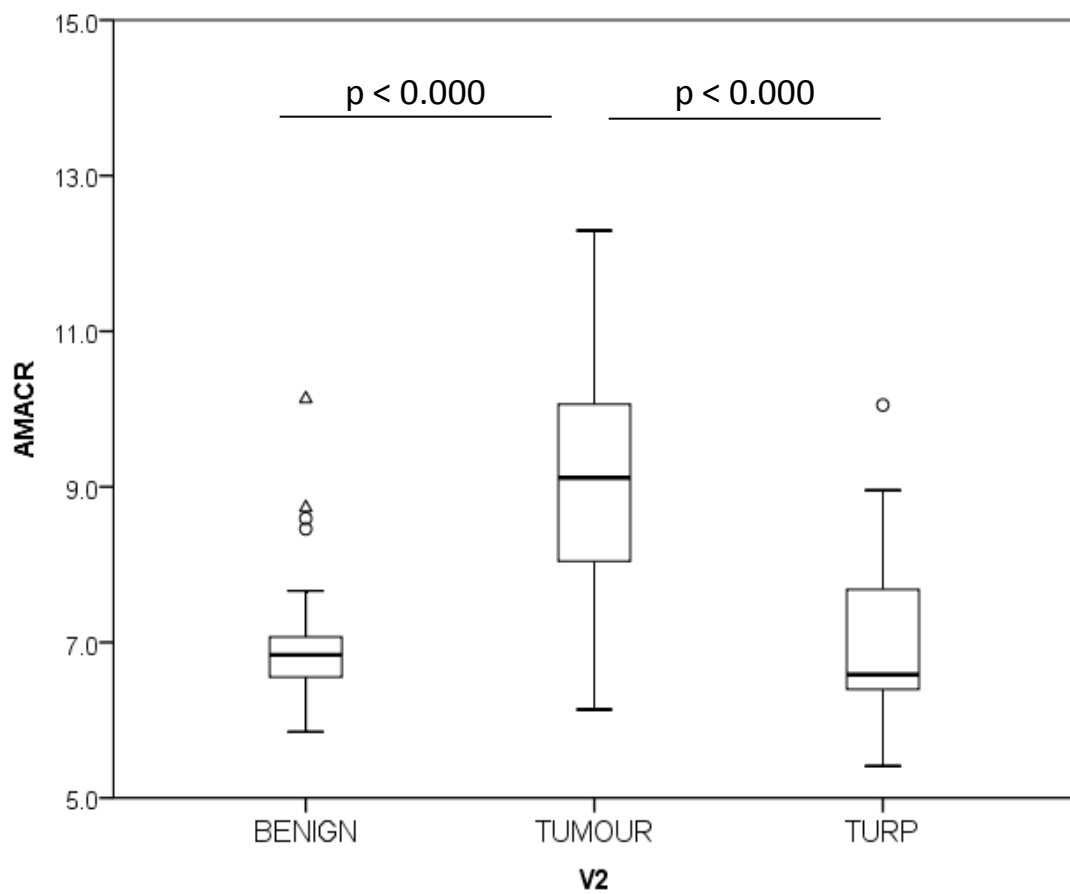
Benign vs. radical
prostatectomy vs. TURP cases

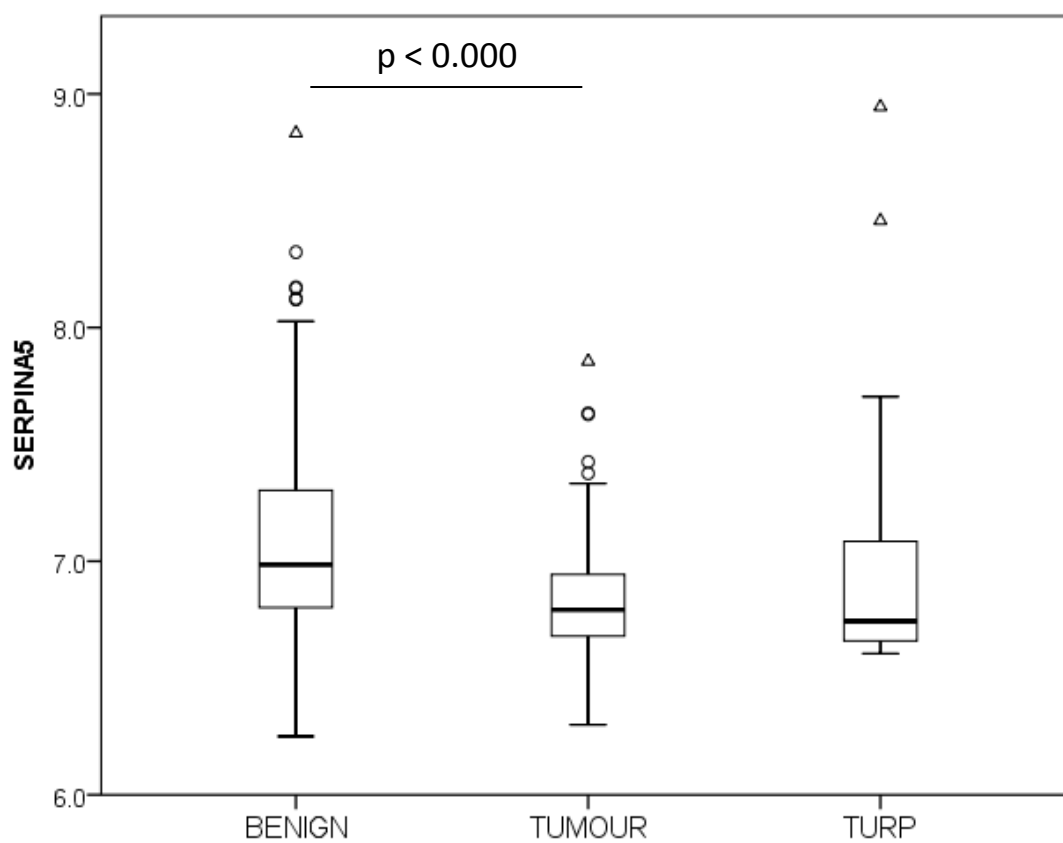
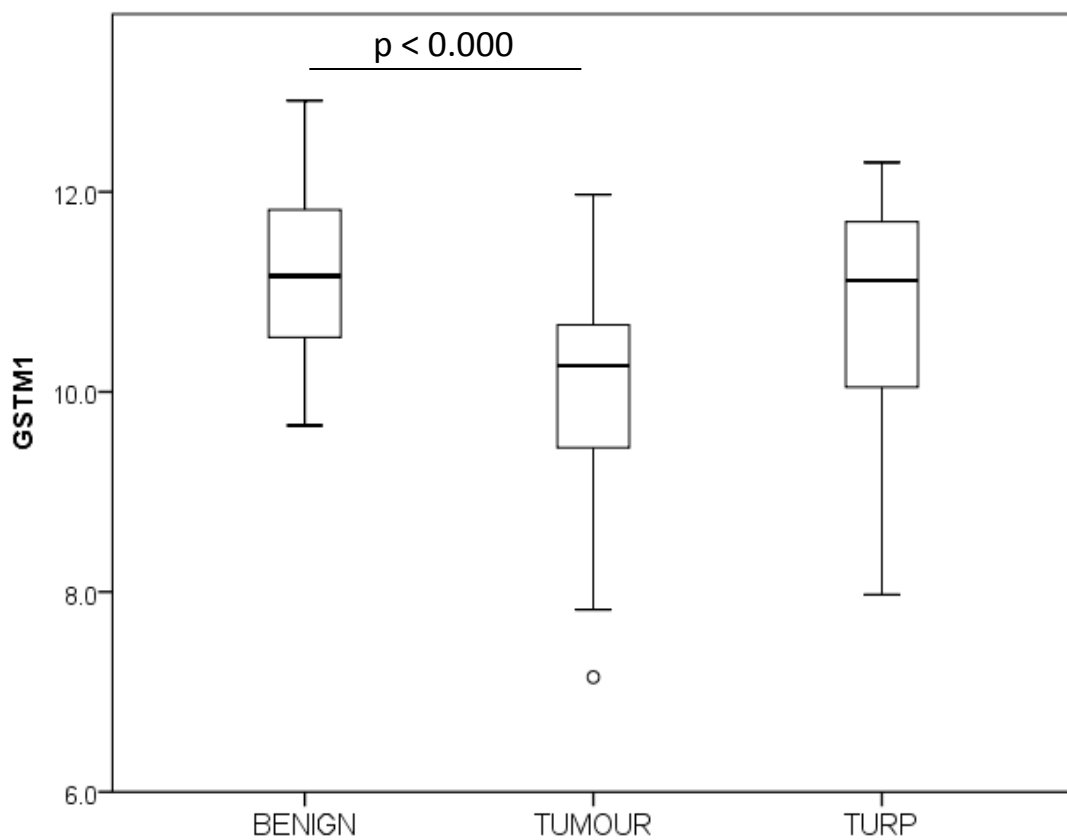
Statistics: Kruskal-Wallis test
with Bonferroni correction for
multiple tests

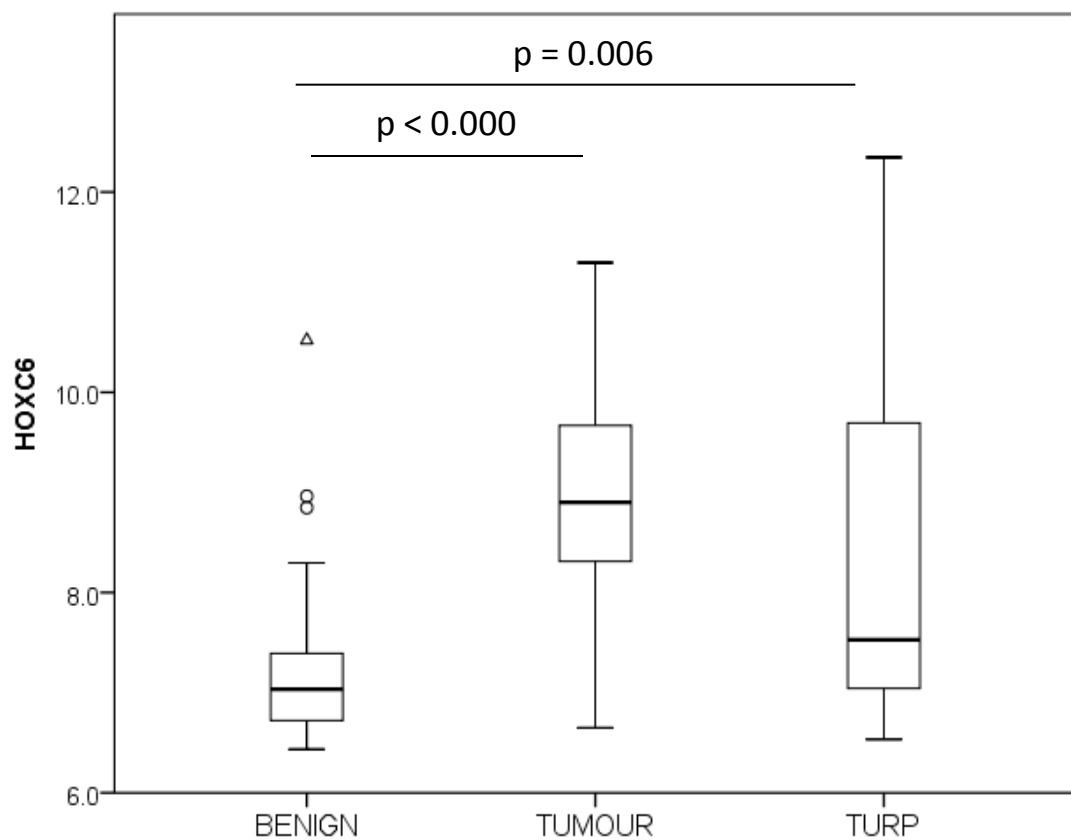
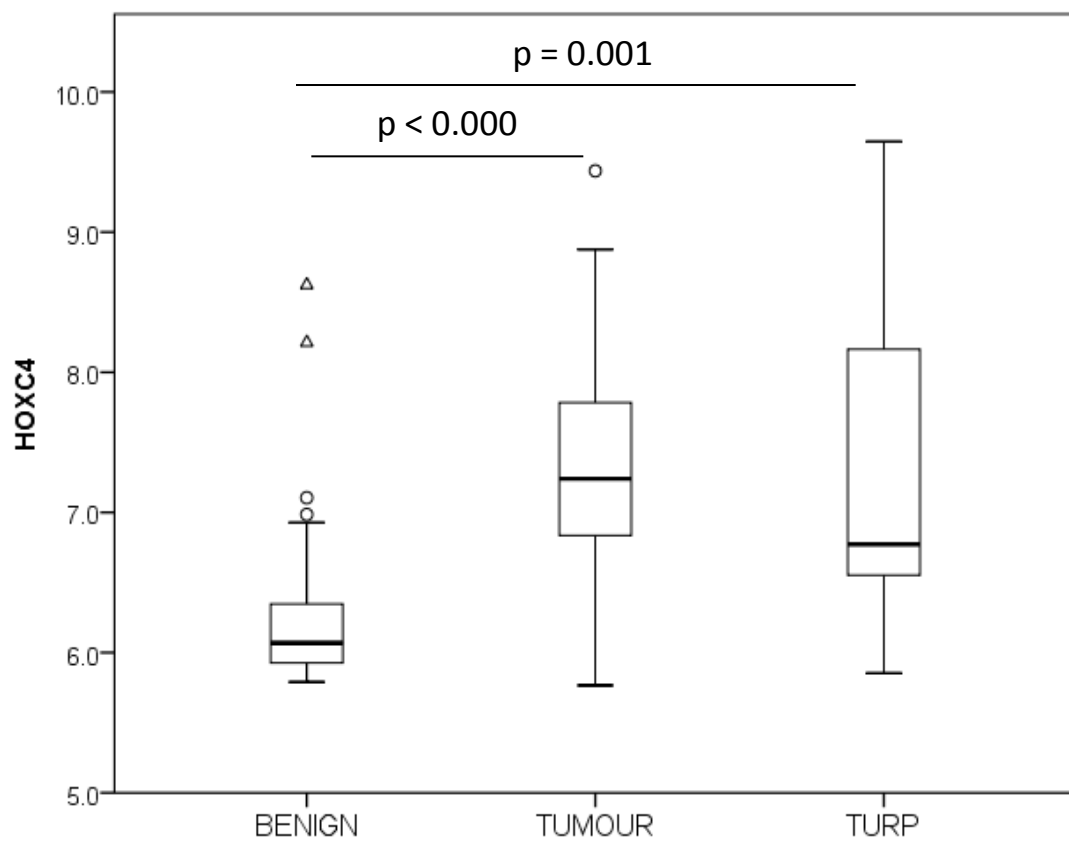


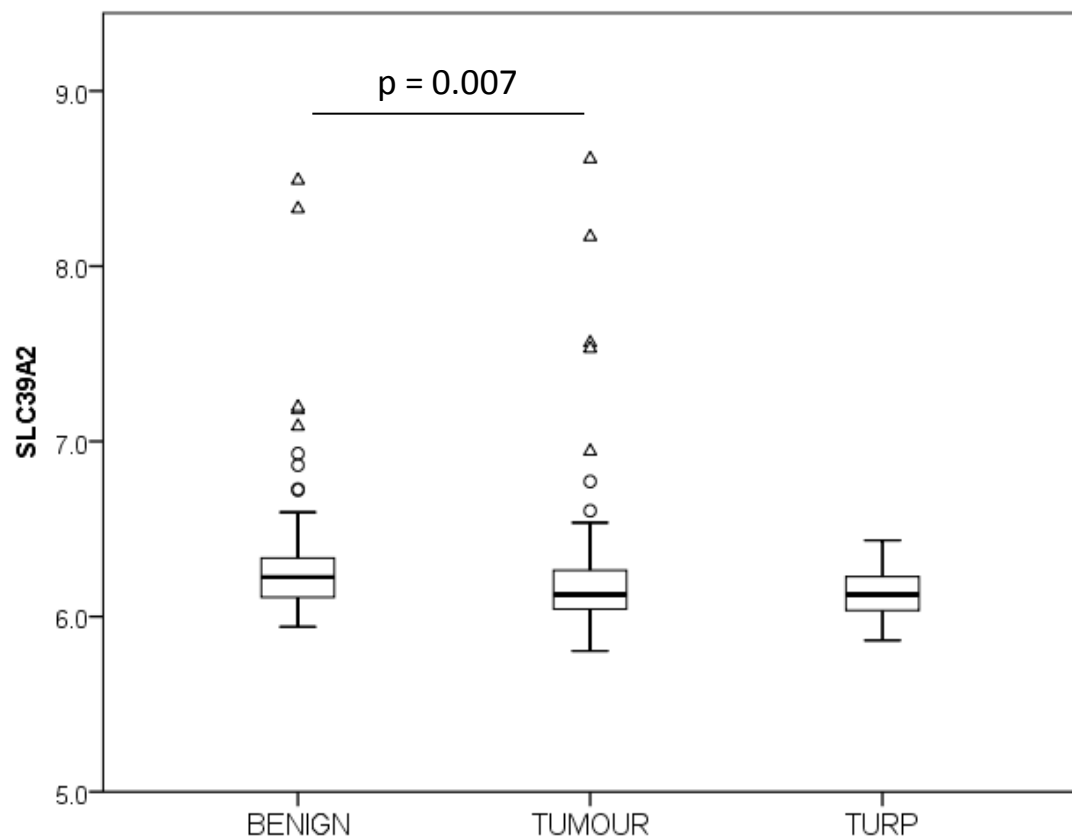
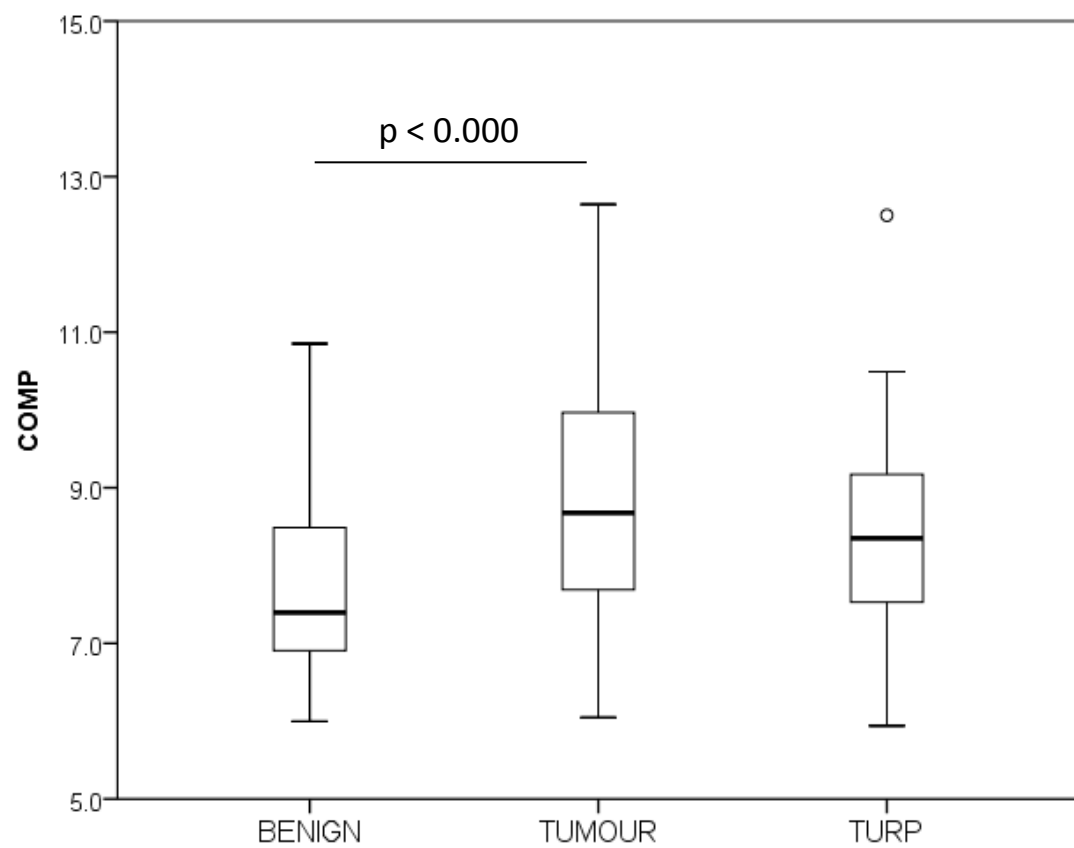


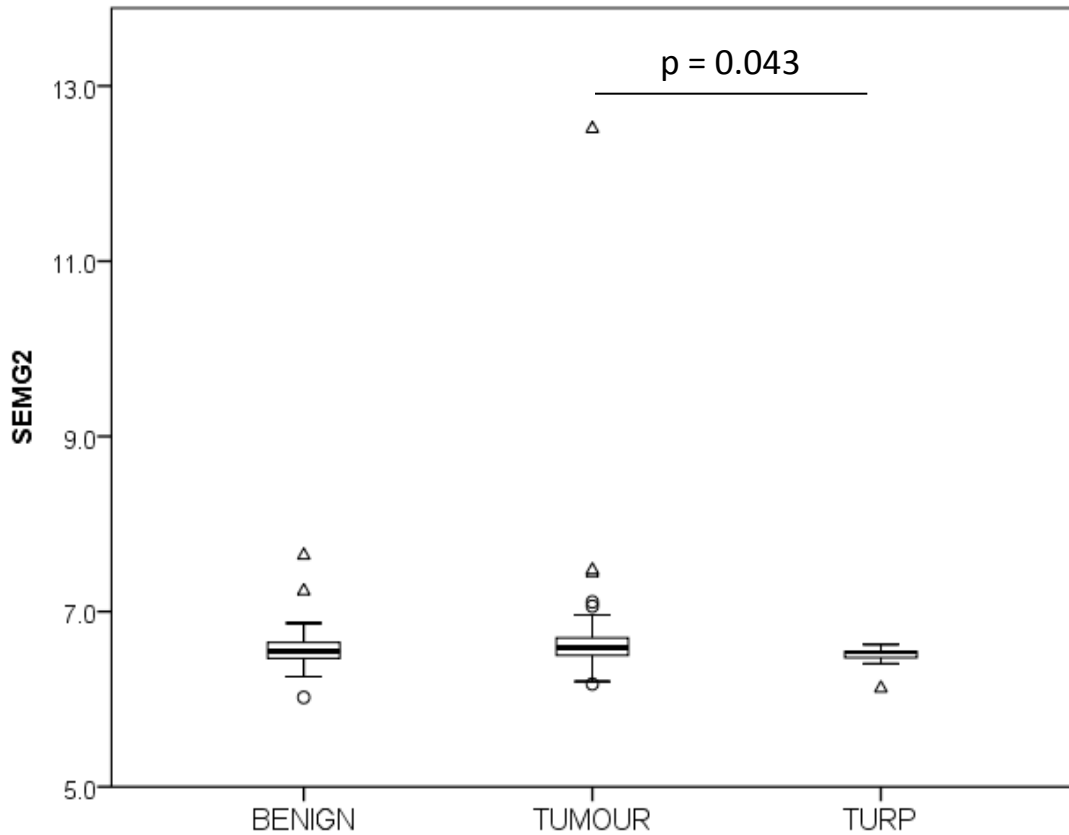
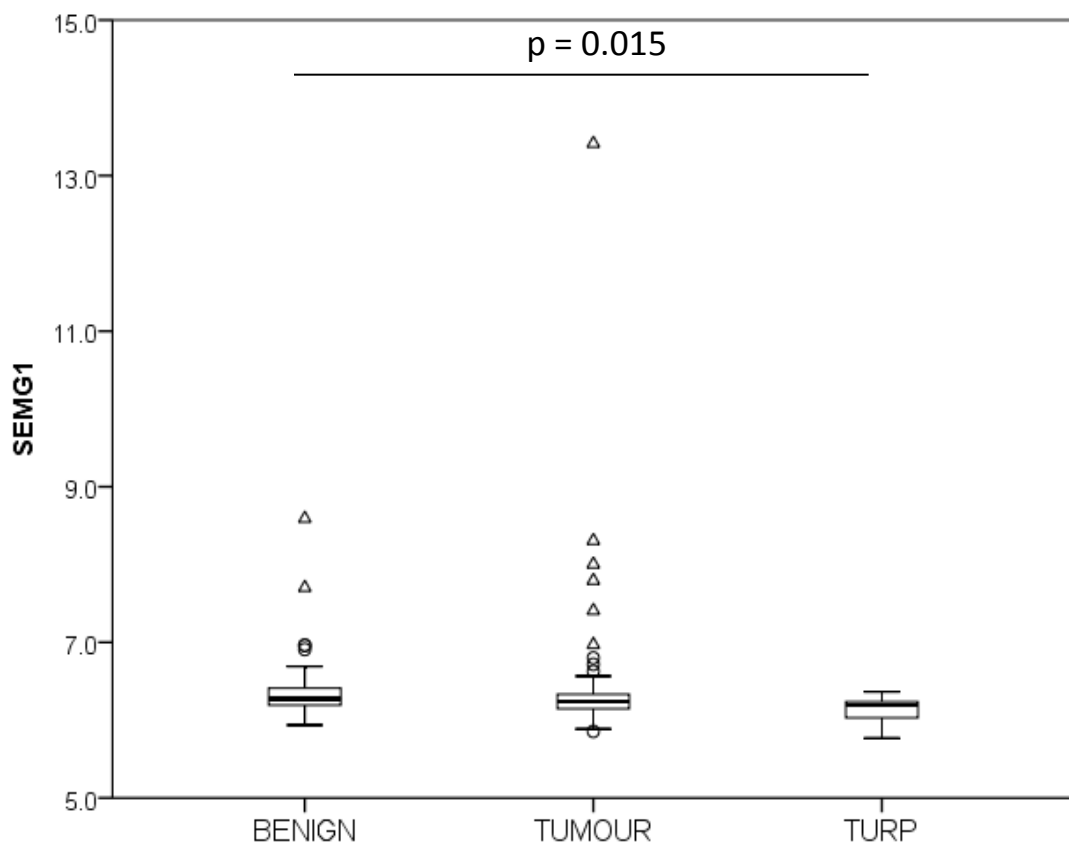


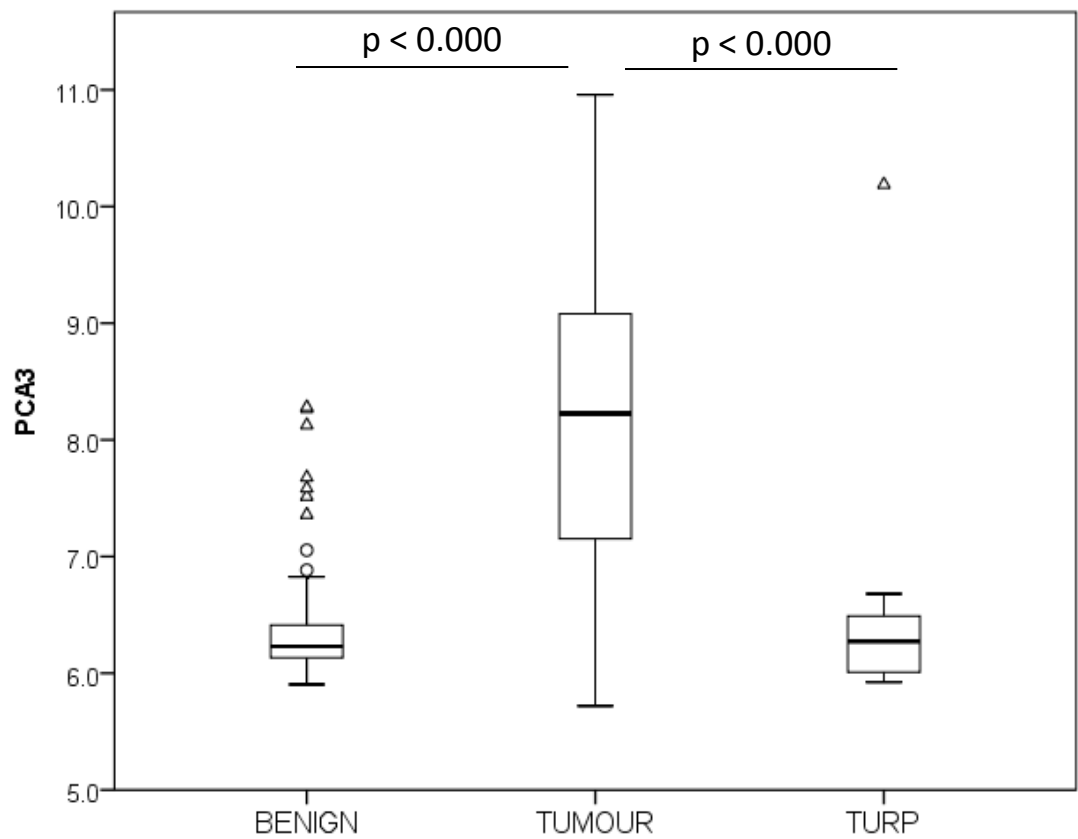
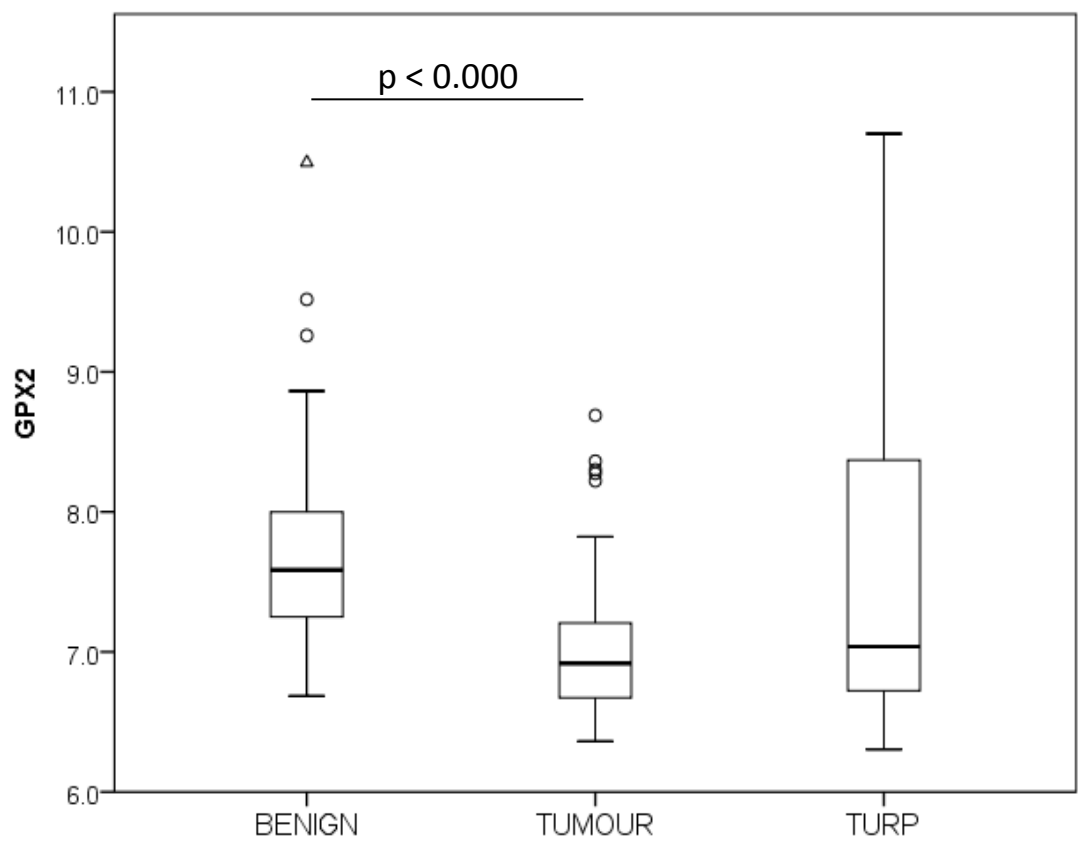


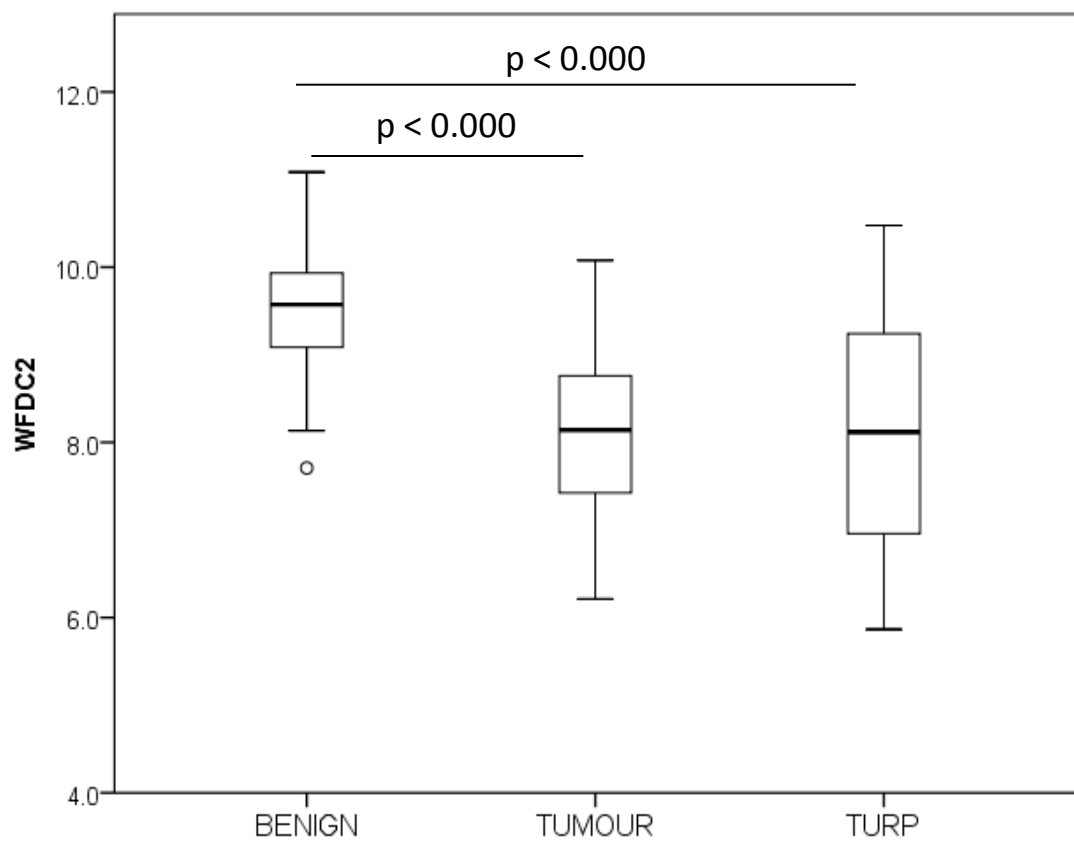












Ross-Adams Dataset

Summary of Results

Gene	Benign vs. RP	Benign vs. TURP	RP vs. TURP
	P	P	P
OR51E2	<0.000		<0.000
SIM2	<0.000		
ACTC1	<0.000	<0.000	
HPN	<0.000		<0.000
SLC45A2	<0.000		0.003
TDRD1	0.028		0.001
AMARC	<0.000		<0.000
DLX1	<0.000		<0.000
GSTM1	<0.000		
SERPINA5	<0.000		
HOXC4	<0.000	0.001	
HOXC6	<0.000	0.006	
COMP	<0.000		
SLC39A2	0.007		
SEMG1		0.015	
SEMG2			0.043
GPX2	<0.000		
PCA3	<0.000		<0.000
WFDC2	<0.000	<0.000	

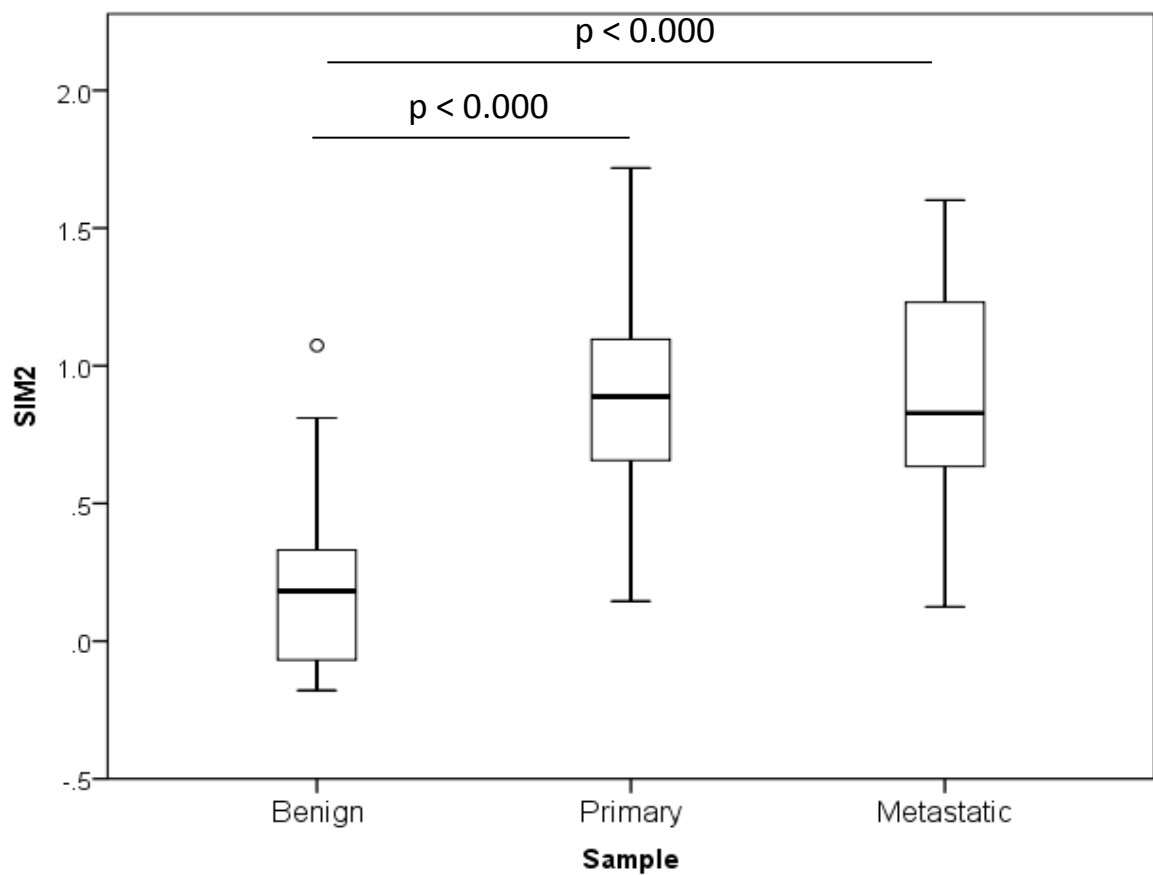
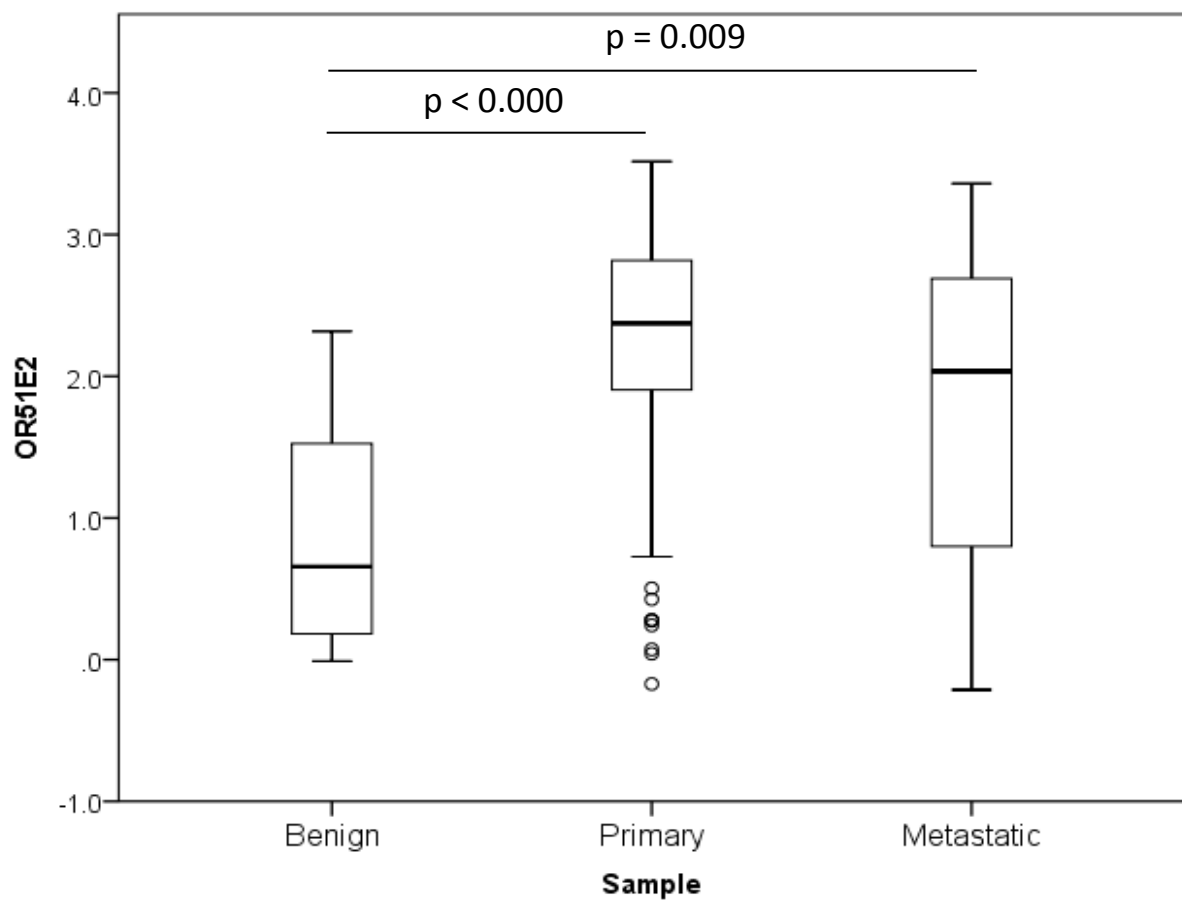
Green: Upregulation (e.g . High in primary vs. Benign)

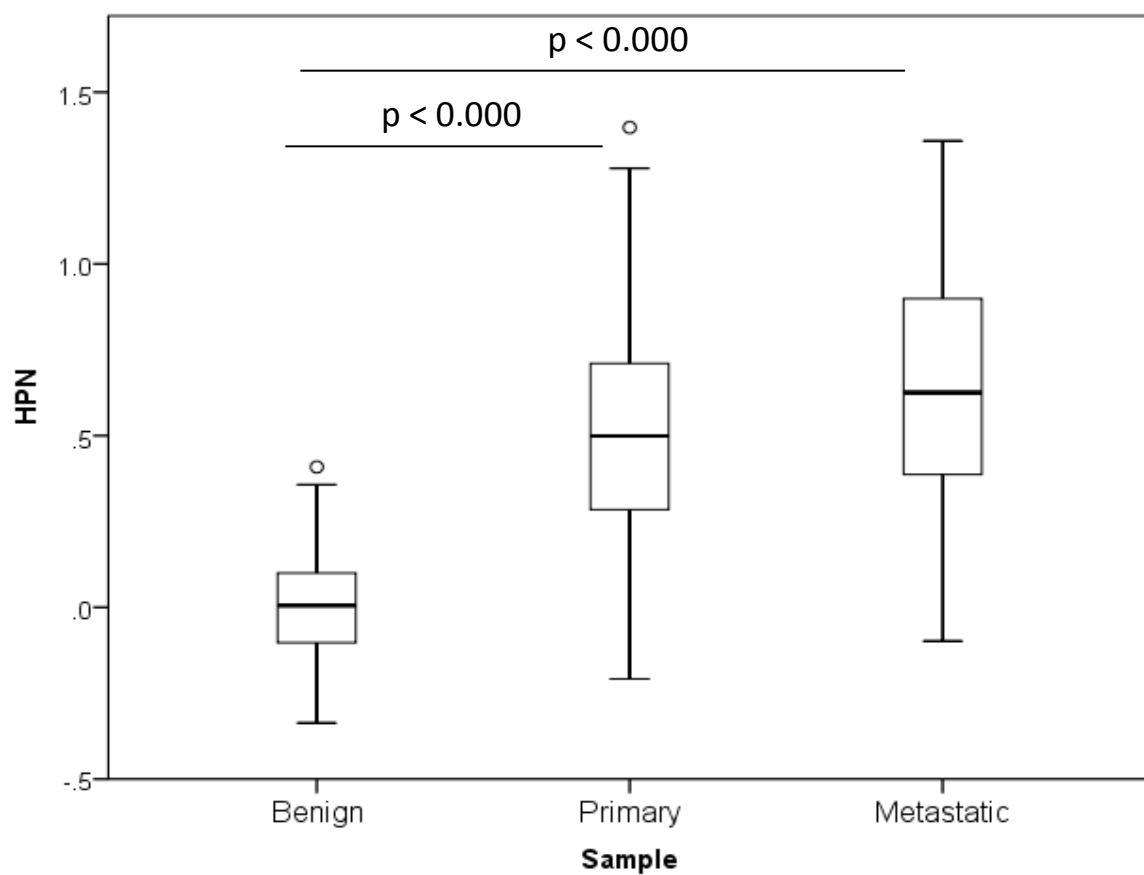
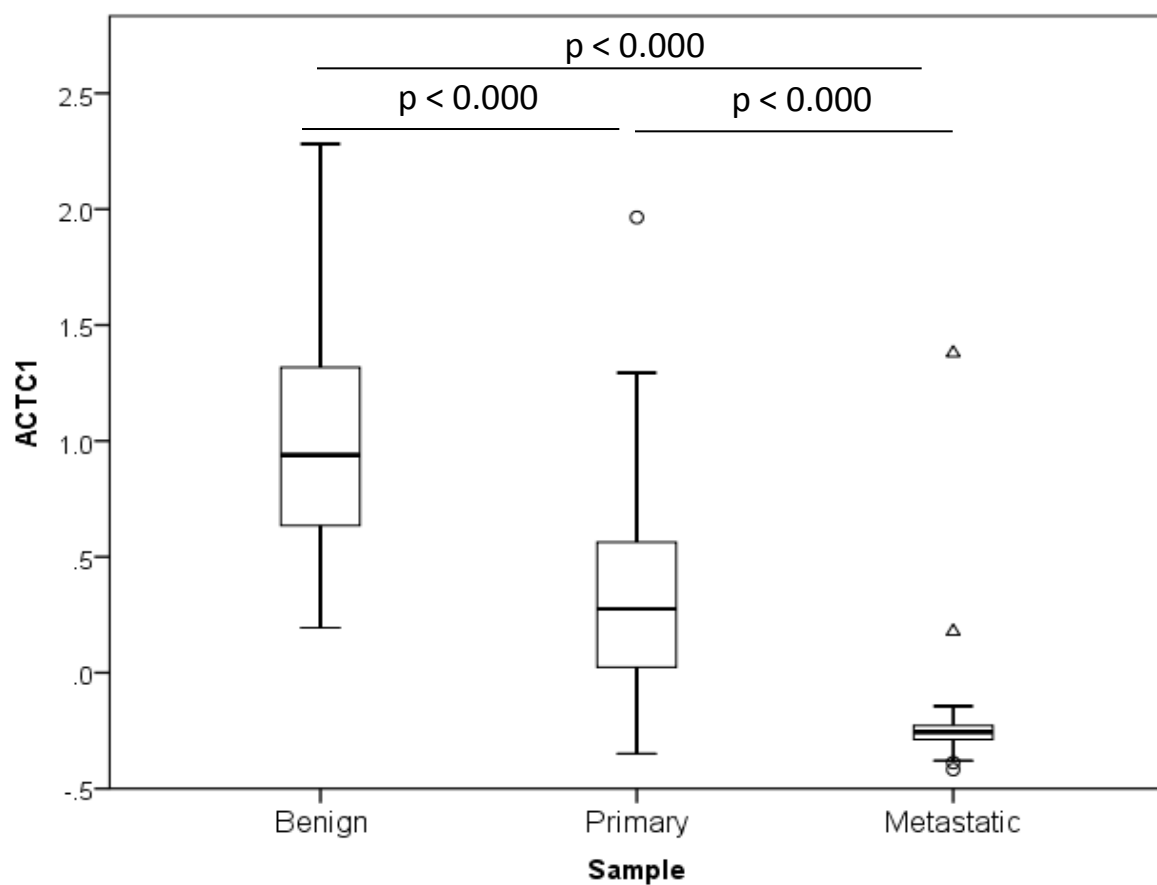
Red: Downregulation (e.g . Low in primary vs. Benign)

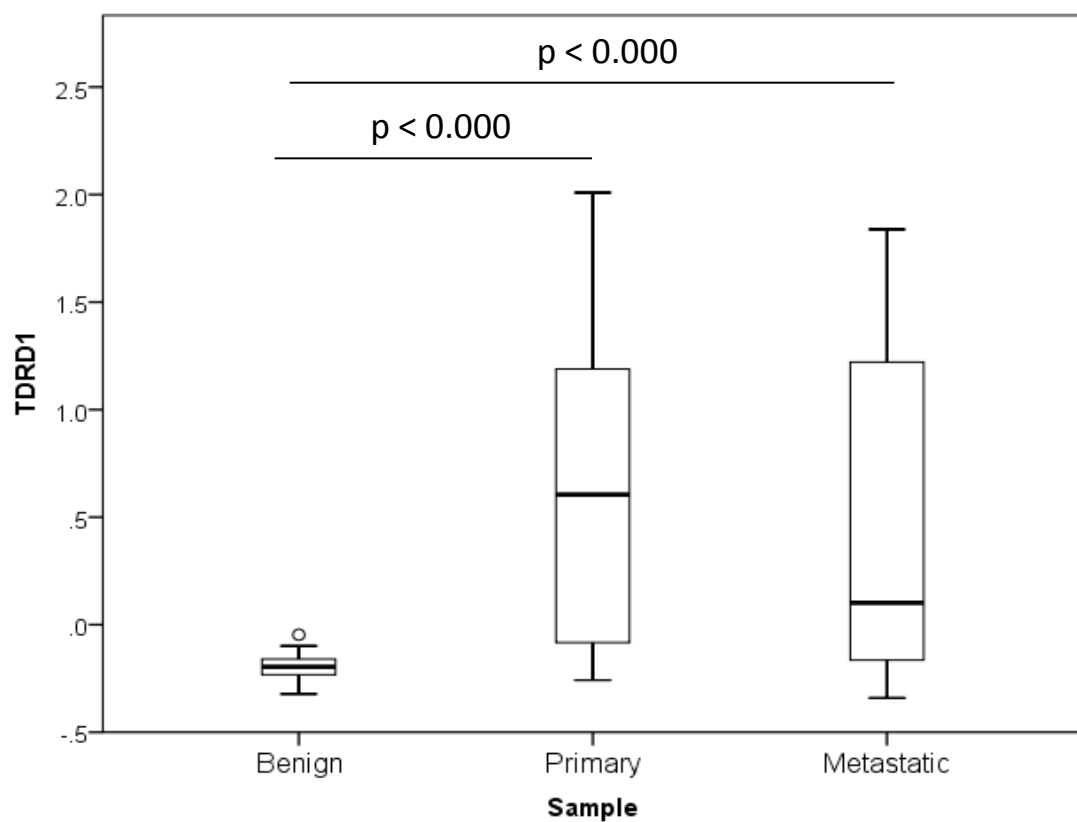
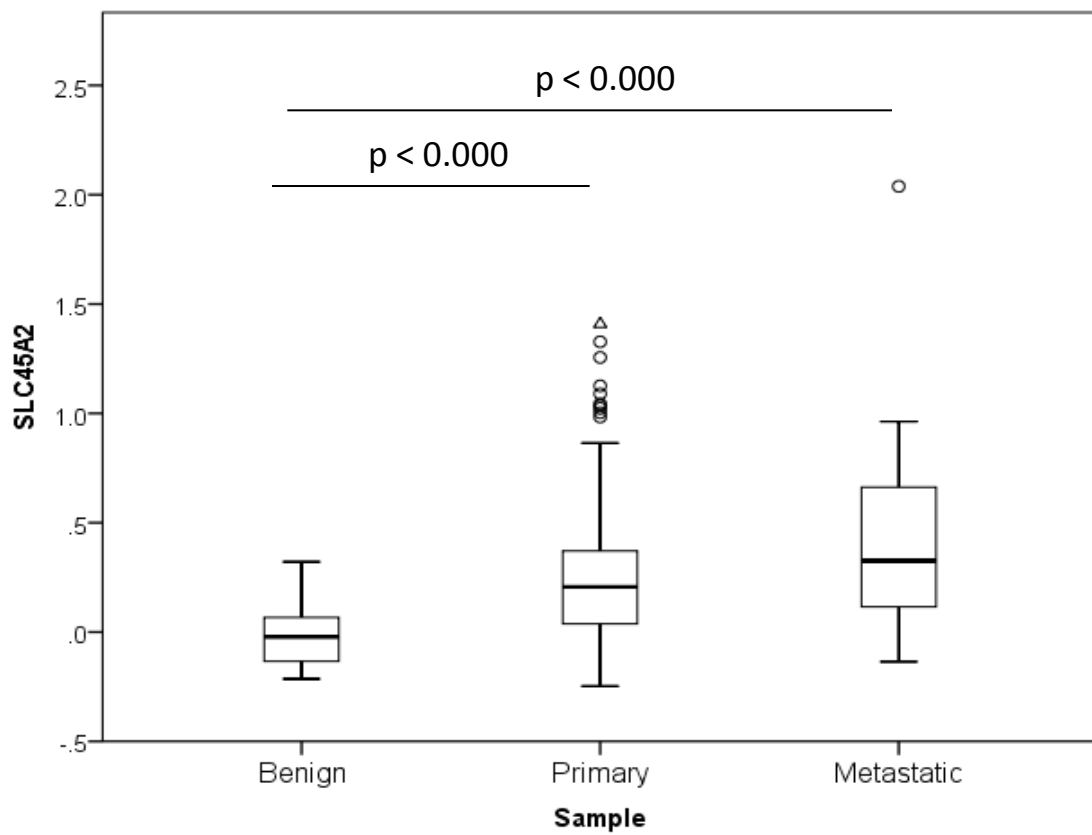
3- Taylor dataset

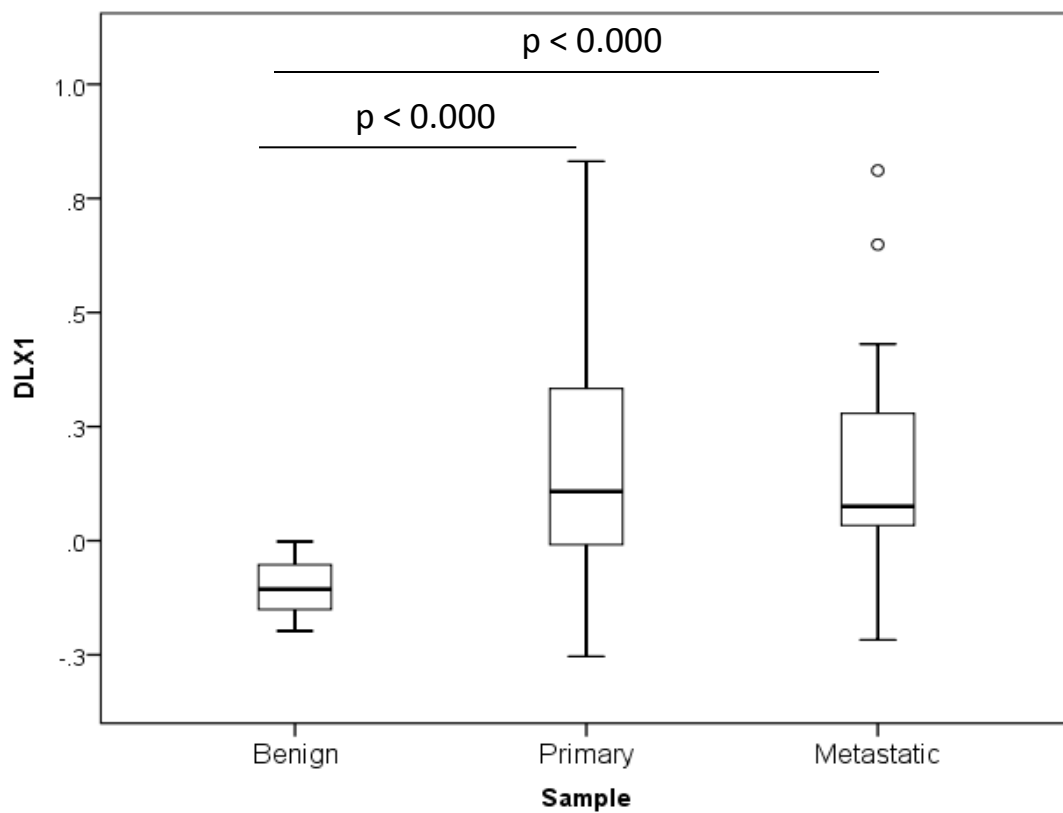
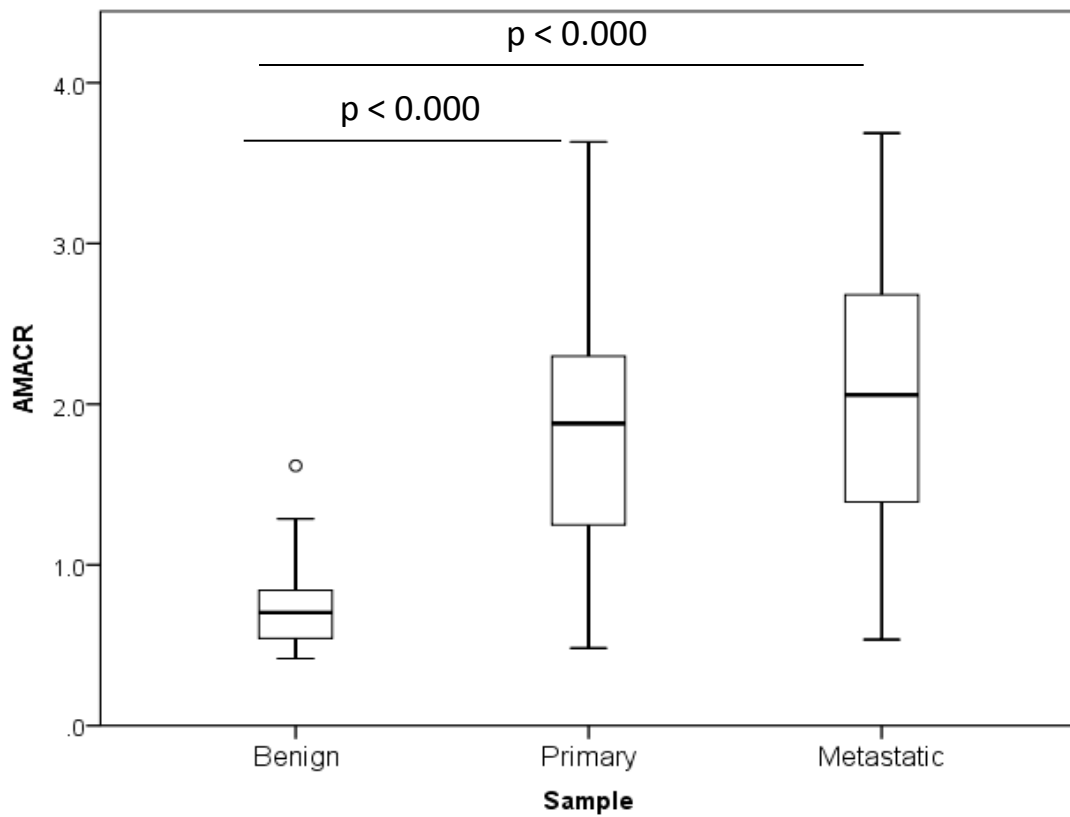
Benign vs. primary tumours vs.
diverse metastases

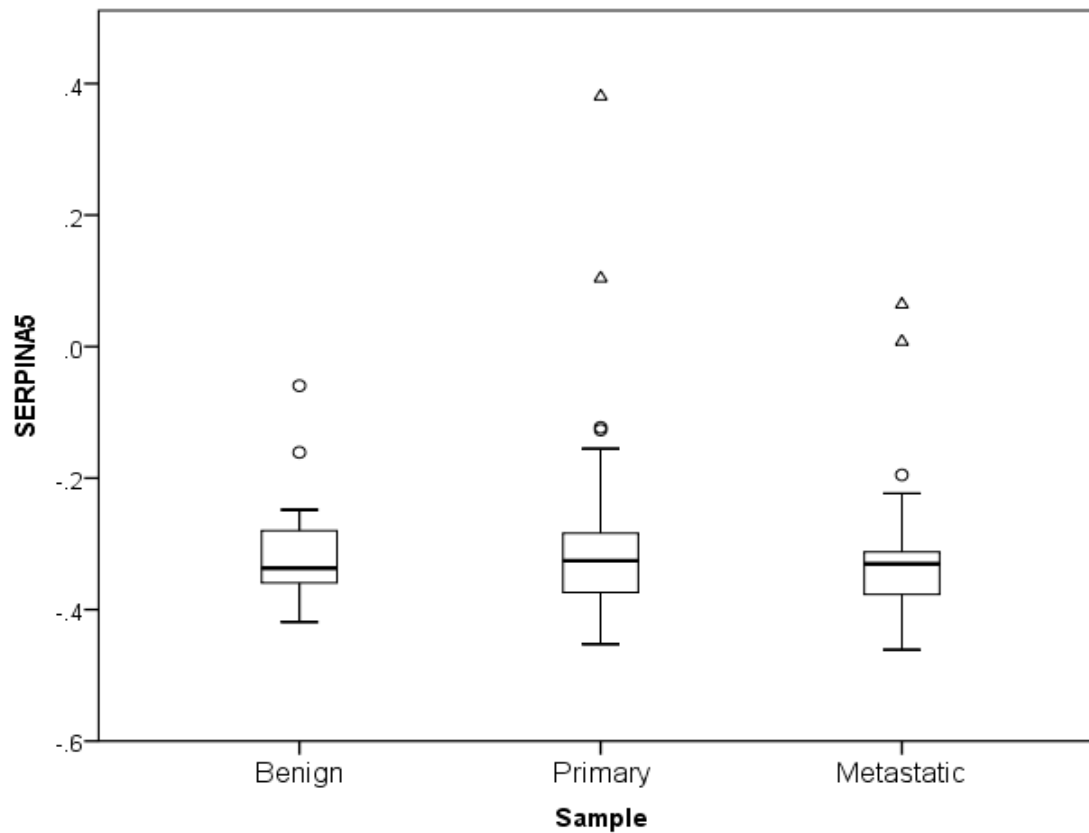
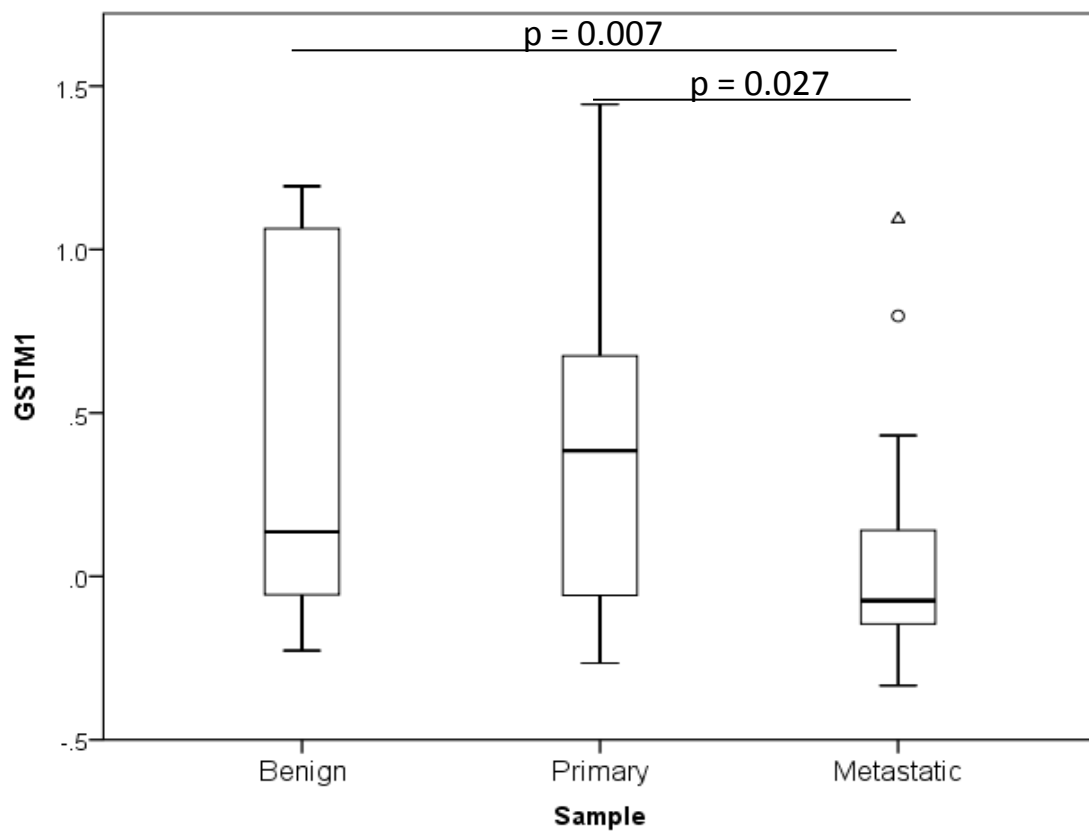
Statistics: Kruskal-Wallis test
with Bonferroni correction for
multiple tests

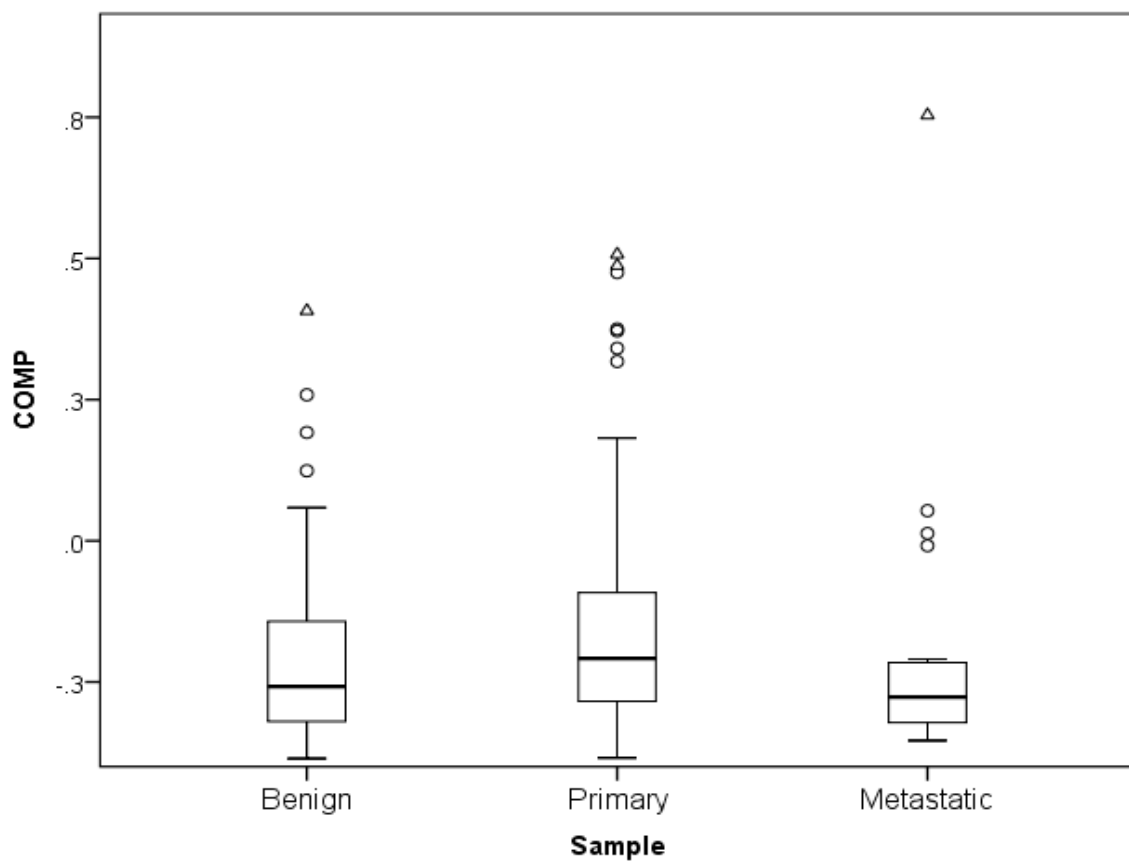
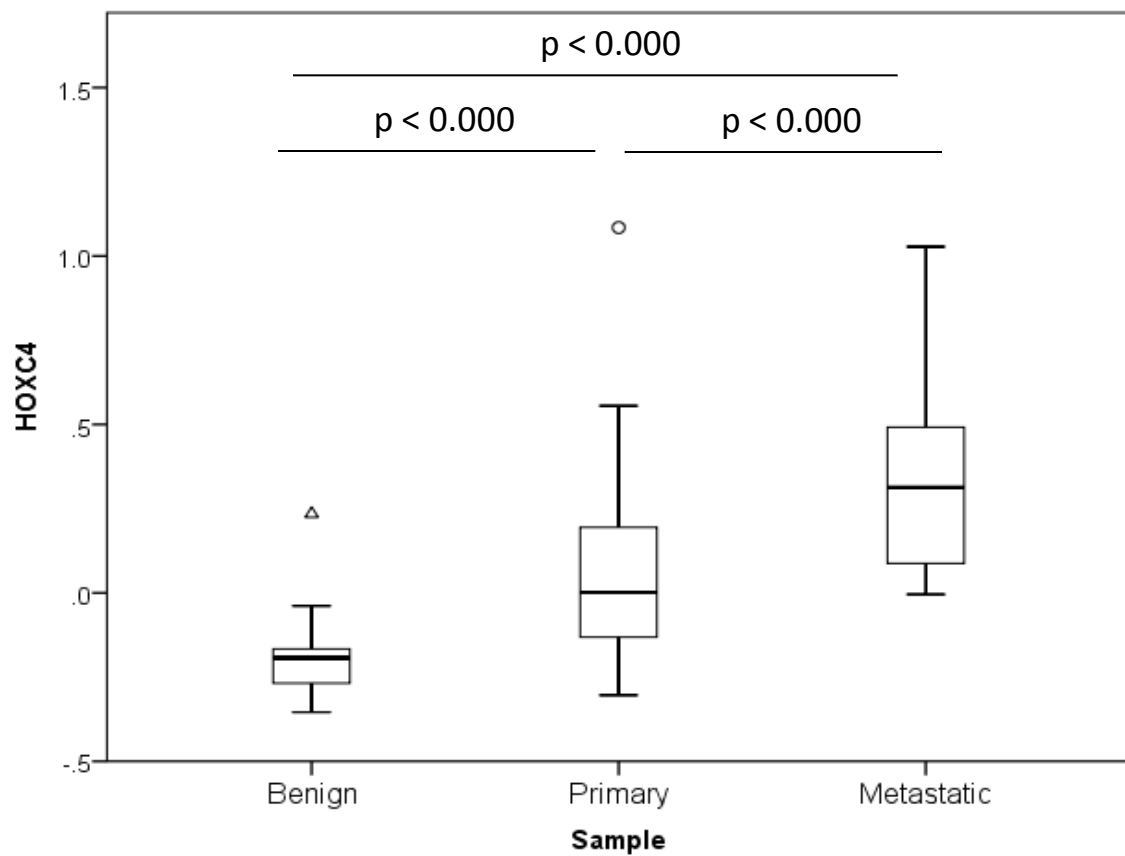


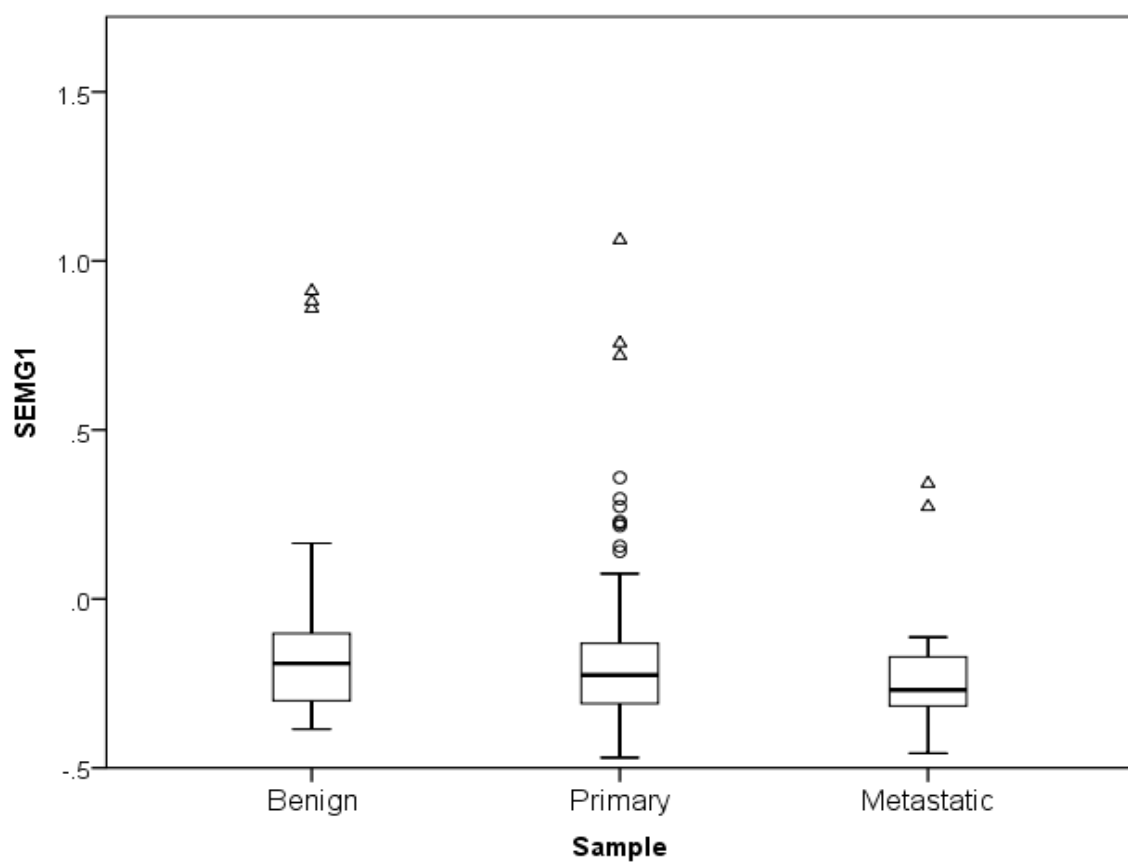
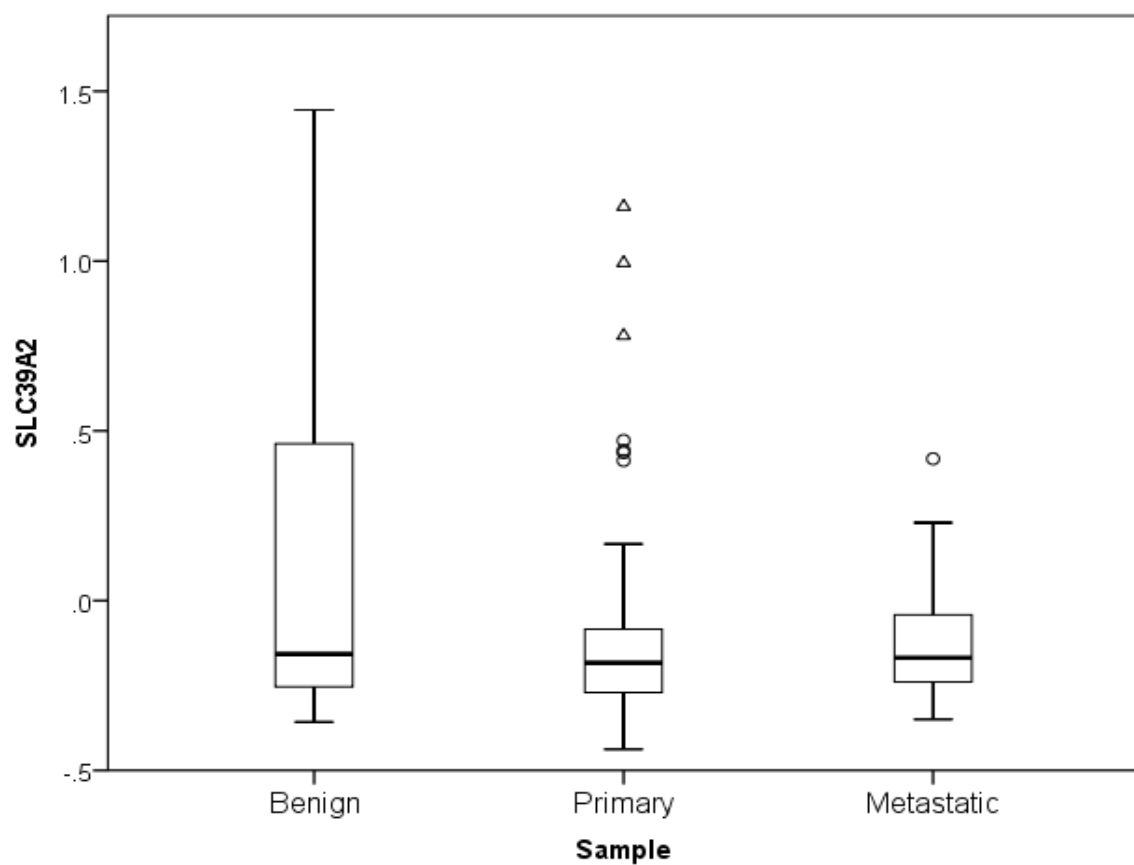


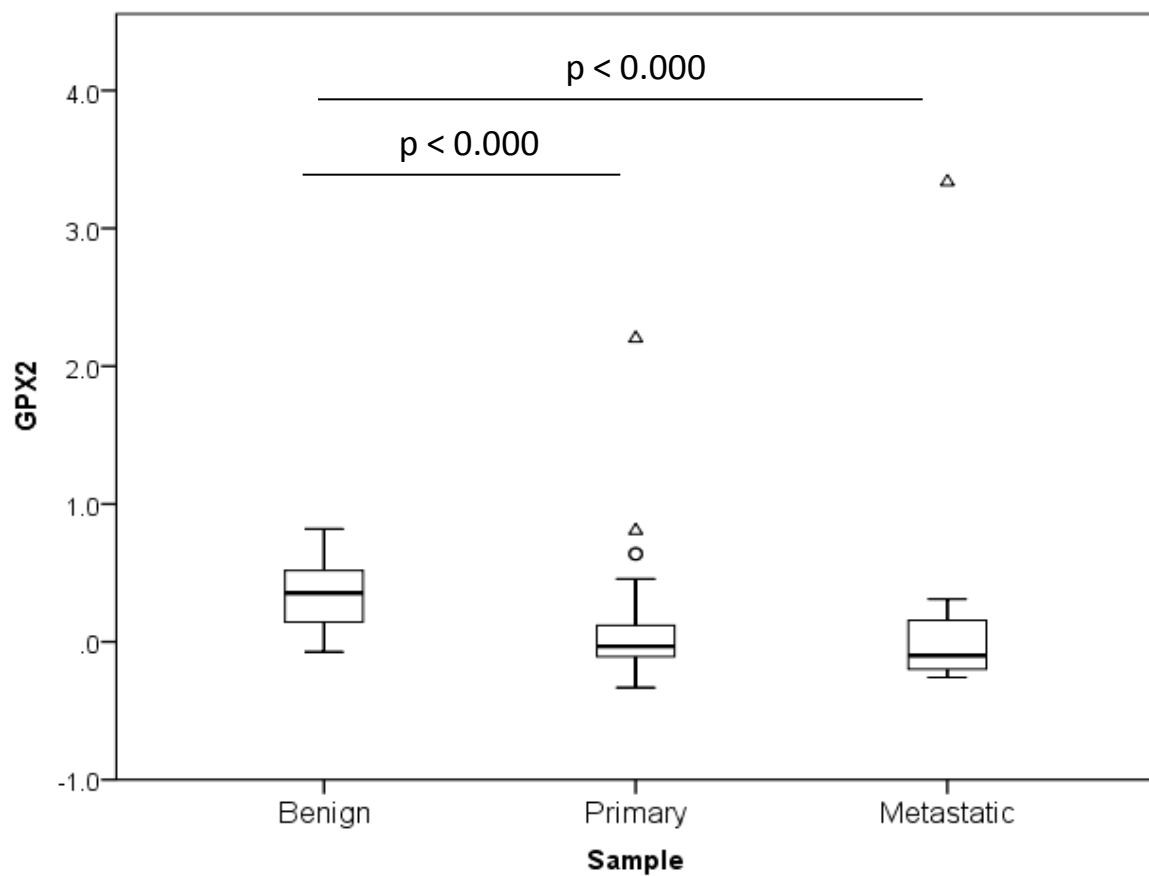
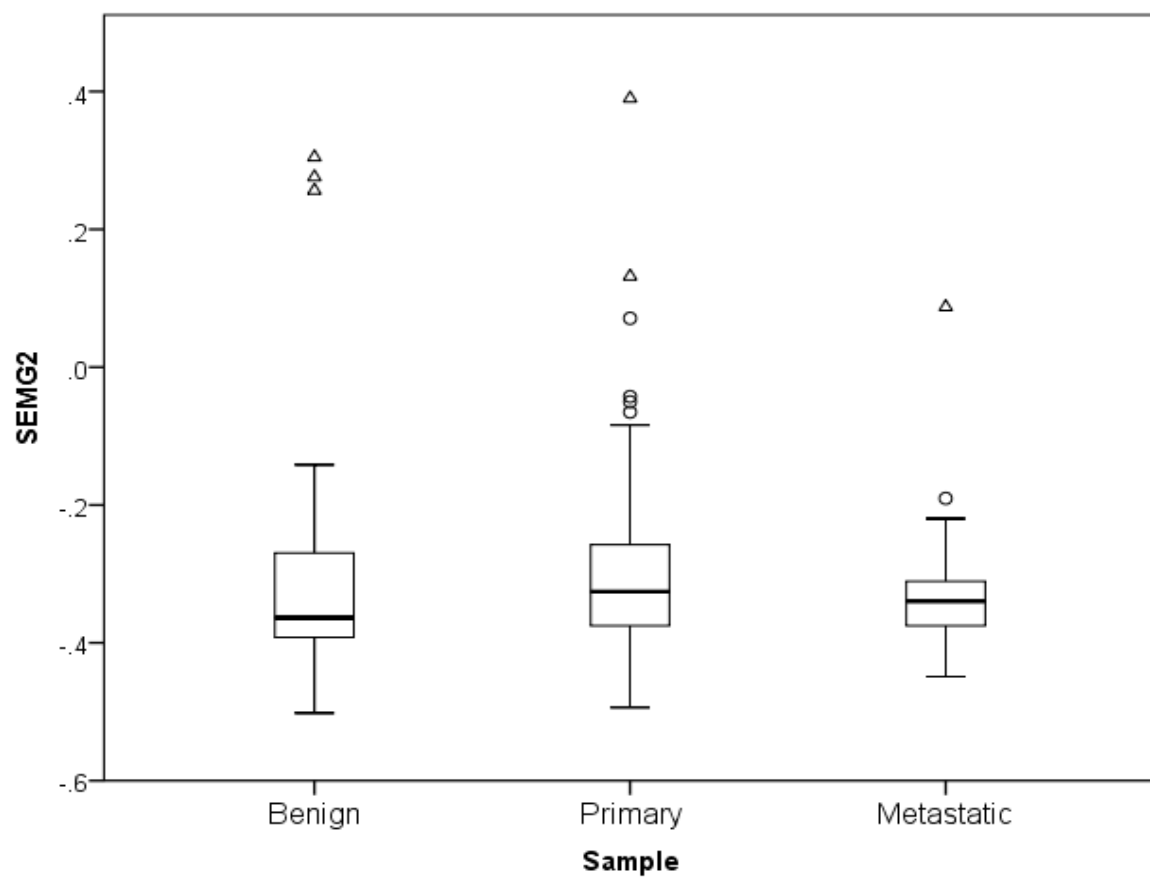


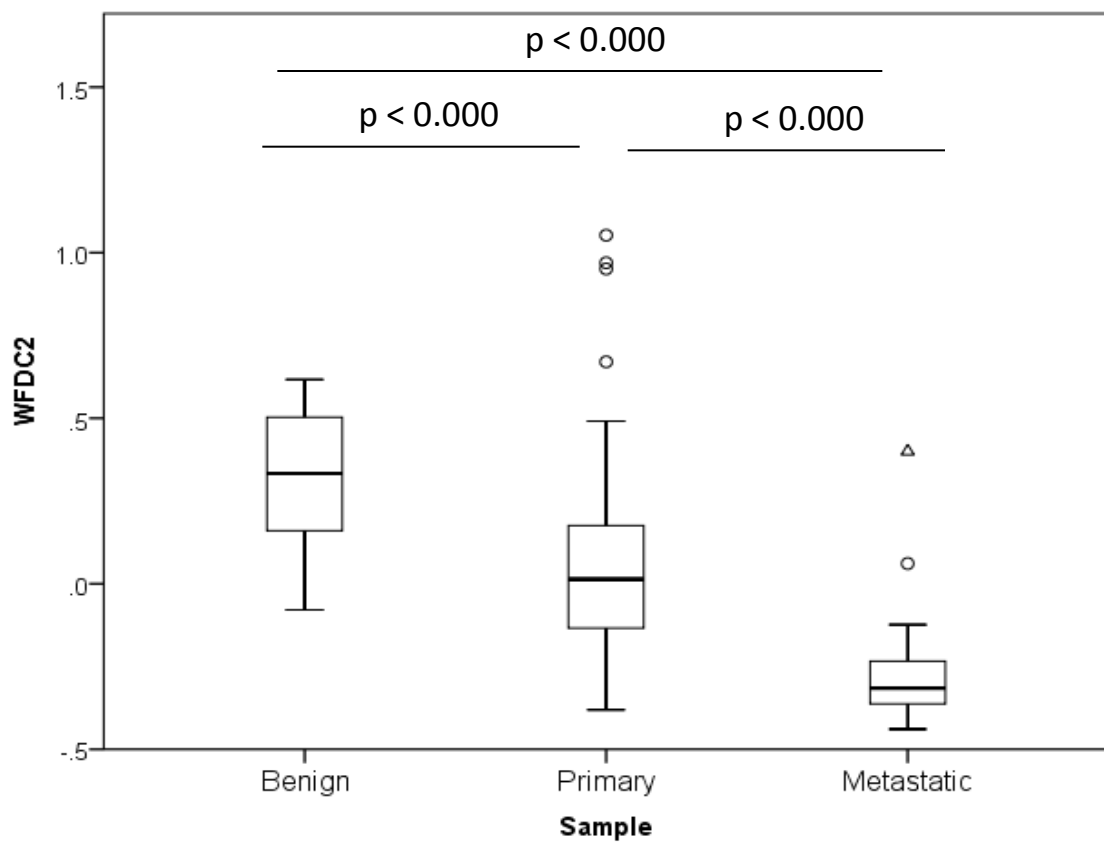












Taylor Dataset

Summary of Results

P values	Benign vs. Primary	Benign vs. Metastases	Primary vs. Metastases
ORE51E2	0.009	< 0.000	
SIM2	< 0.000	< 0.000	
ACTC1	< 0.000	< 0.000	< 0.000
HPN	< 0.000	< 0.000	
SLC45A2	< 0.000	< 0.000	
TDRD1	< 0.000	< 0.000	
AMARC	< 0.000	< 0.000	
DLX1	< 0.000	< 0.000	
GSTM1		0.07	0.027
SERPINA5			
HOXC4	< 0.000	< 0.000	< 0.000
COMP			
SLC39A2			
SEMG1			
SEMG2			
GPX2	< 0.000	< 0.000	
WFDC2	< 0.000	< 0.000	< 0.000

Green: Upregulation (e.g . High in primary vs. Benign)

Red: Downregulation (e.g . Low in primary vs. Benign)

Summary for genes listed

Gene name	Lapointe	Ross-Adams	Taylor	Up vs. down*
ORE51E2	✓	✓	✓	Up
SIM2	✓	✓	✓	Up
ACTC1		✓	✓	Down
HPN	✓	✓	✓	Up
SLC45A2	✓	✓	✓	Up
TDRD1		✓	✓	Up
AMARC	✓	✓	✓	Up
DLX1		✓	✓	Up
GSTM1		✓	X	Down
SERPINA5	✓	✓	X	Down
HOXC4	✓	✓	✓	Up
HOXC6		✓		Up
COMP	X	✓	X	Up
SLC39A2	✓	✓	X	Down
SEMG1	X	X	X	---
SEMG2	X	X	X	---
GPX2	✓	✓	✓	Down
PCA3	✓	✓		Up
WFDC2	✓	✓	✓	Down

Green: significant difference in expression between benign and primary tumours at p lower than 0.05; **Red:** no significant difference; **Black:** not available.* Consistant up vs. down-regulation in primary tumours vs. benign