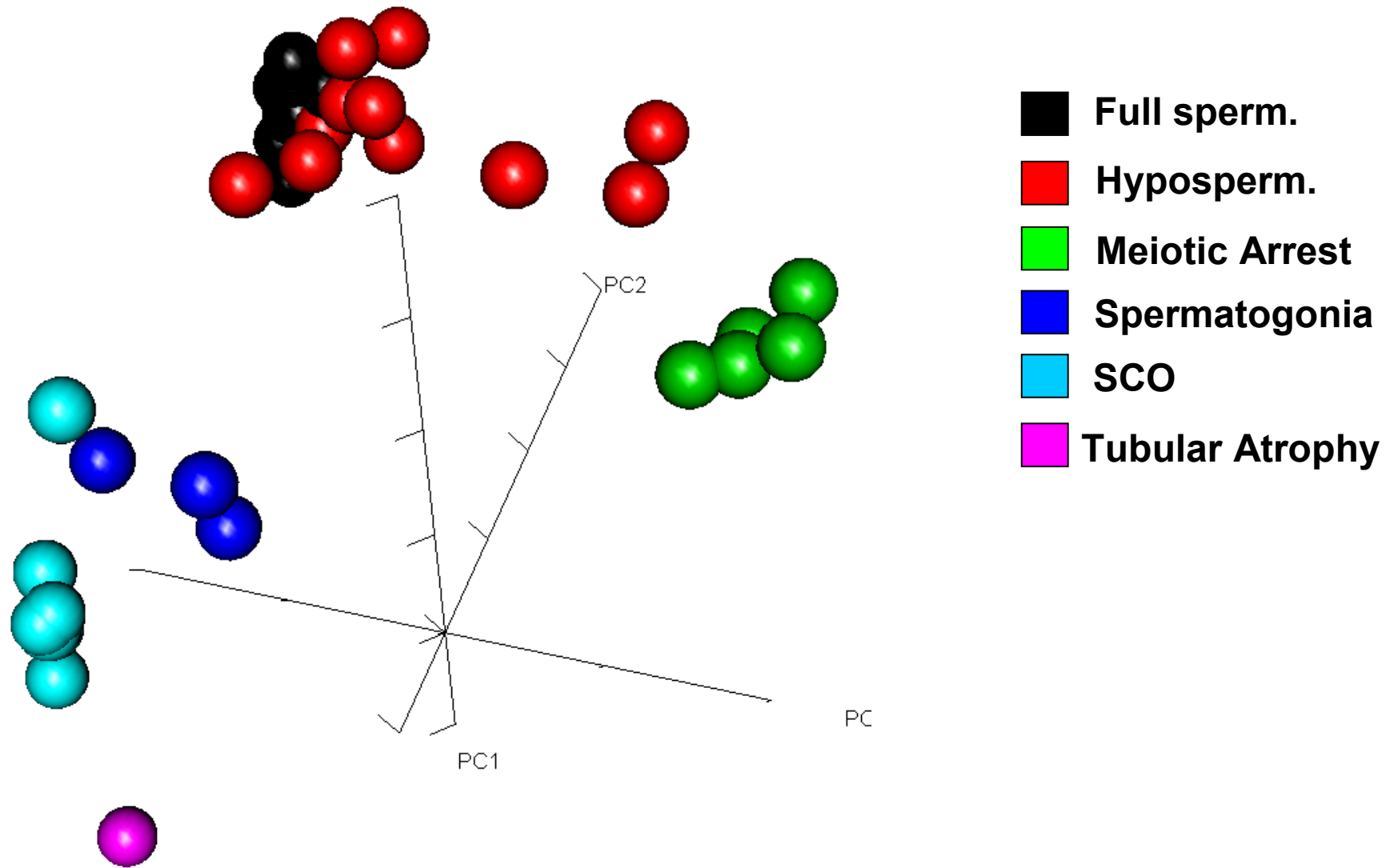
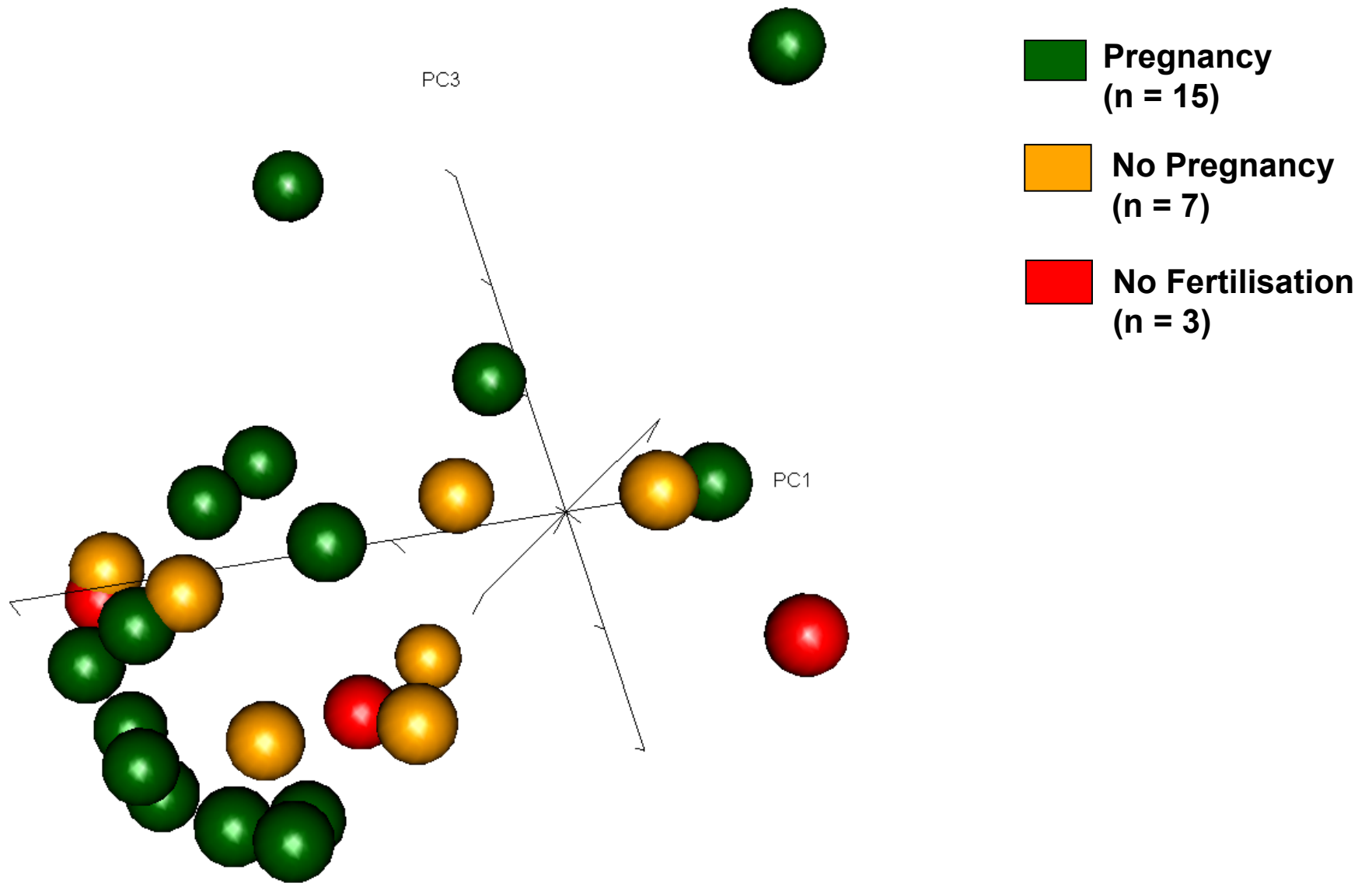


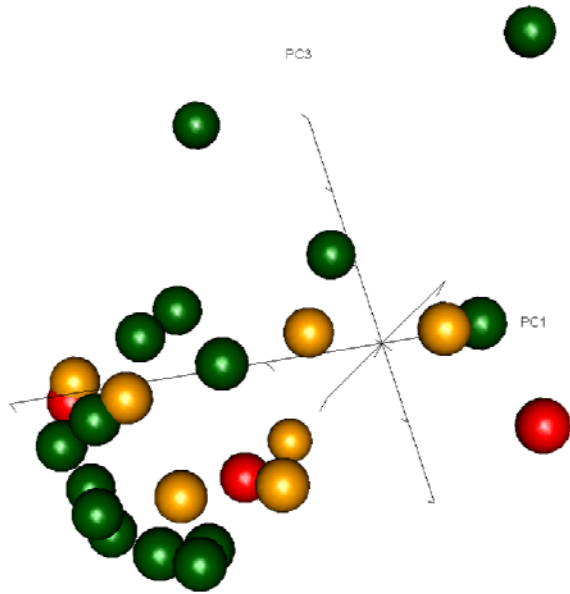
# Human spermatogenesis: ~ 6000 germ cell genes define clustering



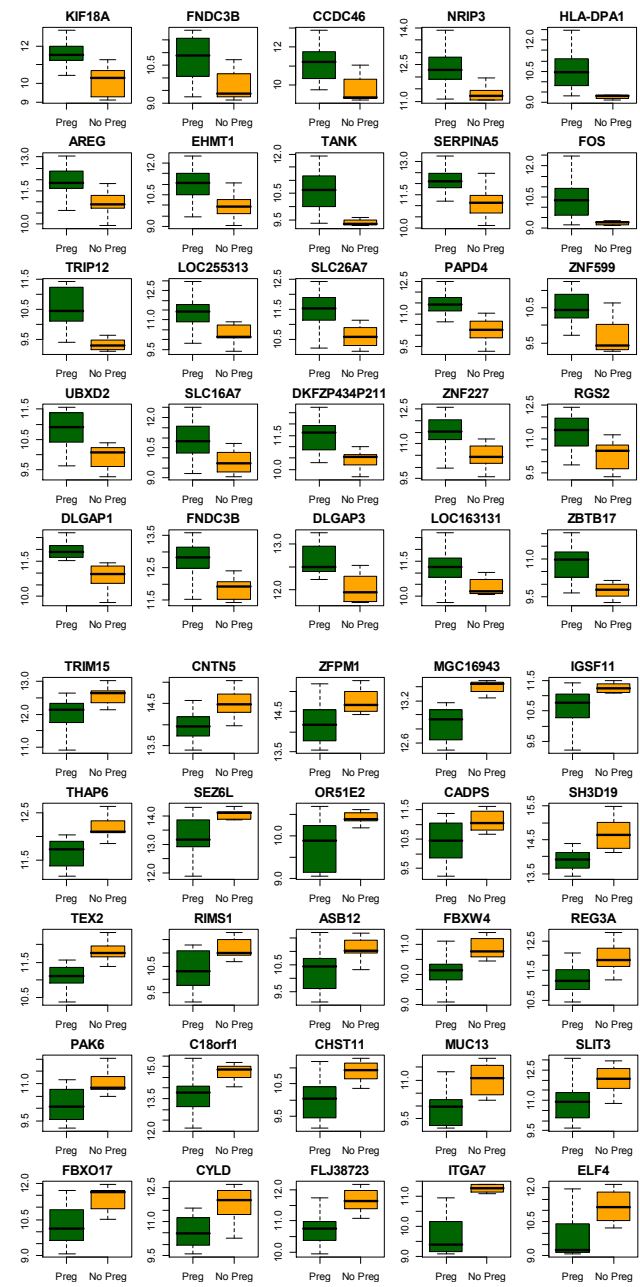
# Overall gene expression in ejaculates is dominated by unknown factors



# Overall gene expression in ejaculates is dominated by unknown factors



**T-test  $p < 0.01$   
132 genes**



**Gene Ontology:**  
Organic Anion Transport  
(SLC16A7, SLC26A7)

**TFBS:**  
BACH1, FOXD1, SRY, SOX9

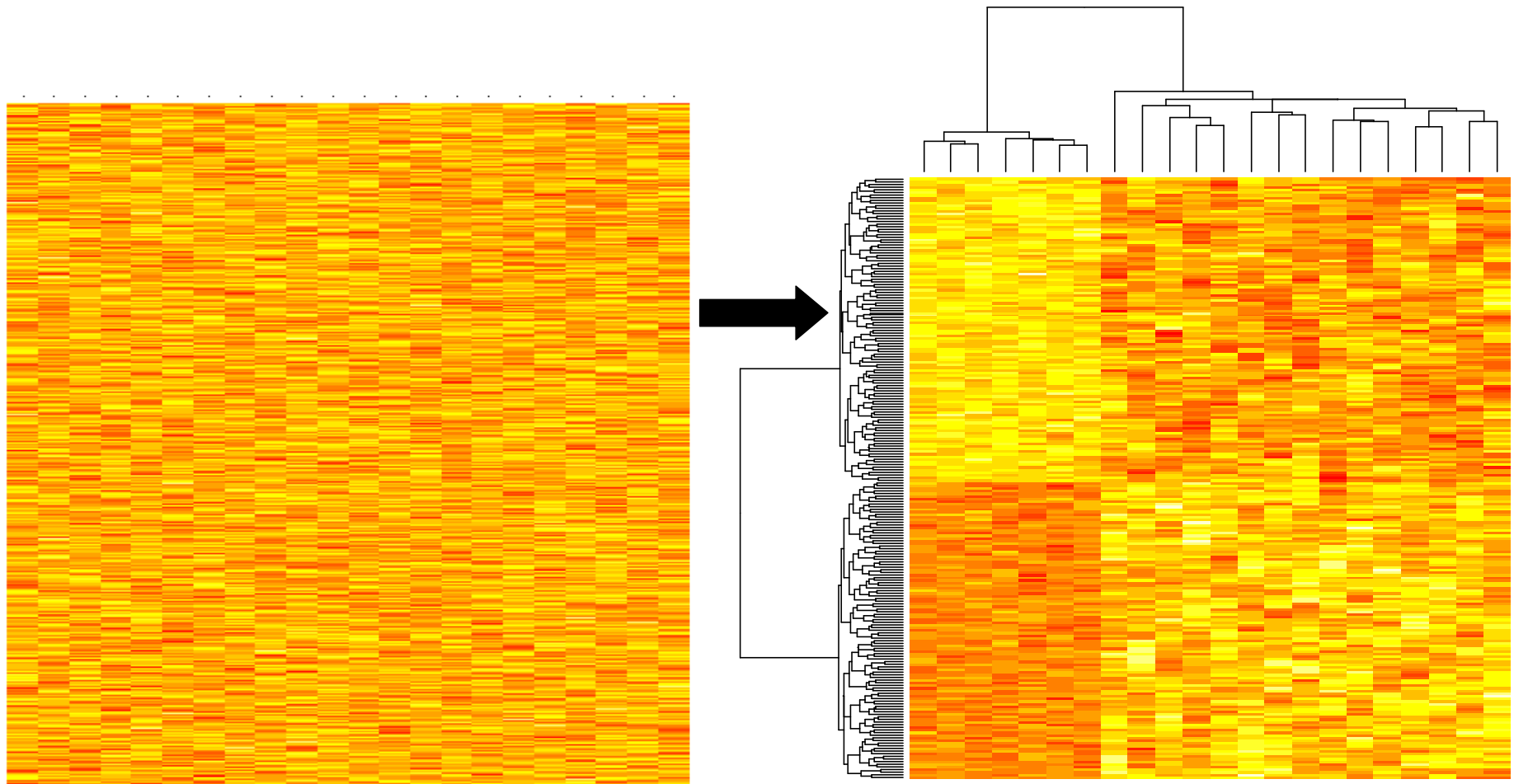
=> Oxidative stress, tumor formation, male sex differentiation

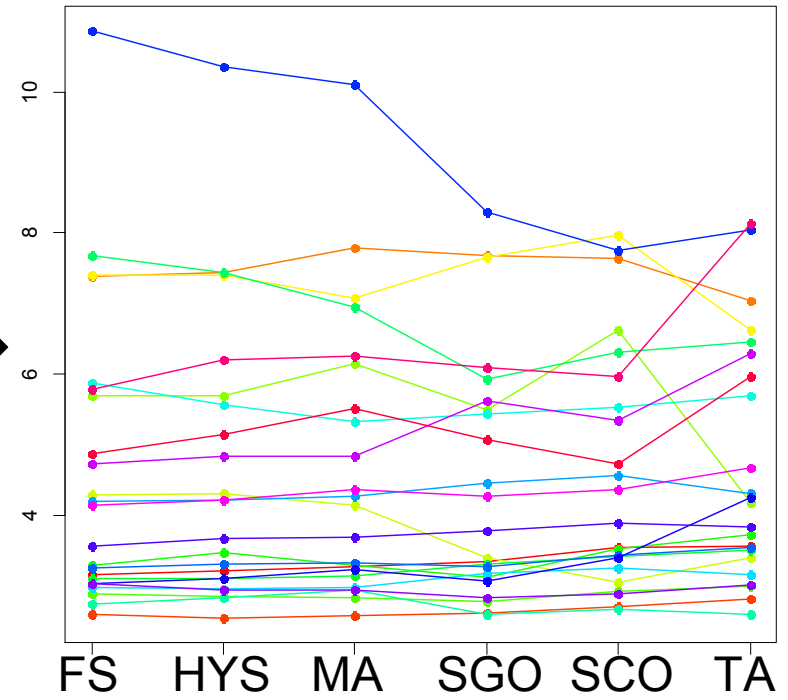
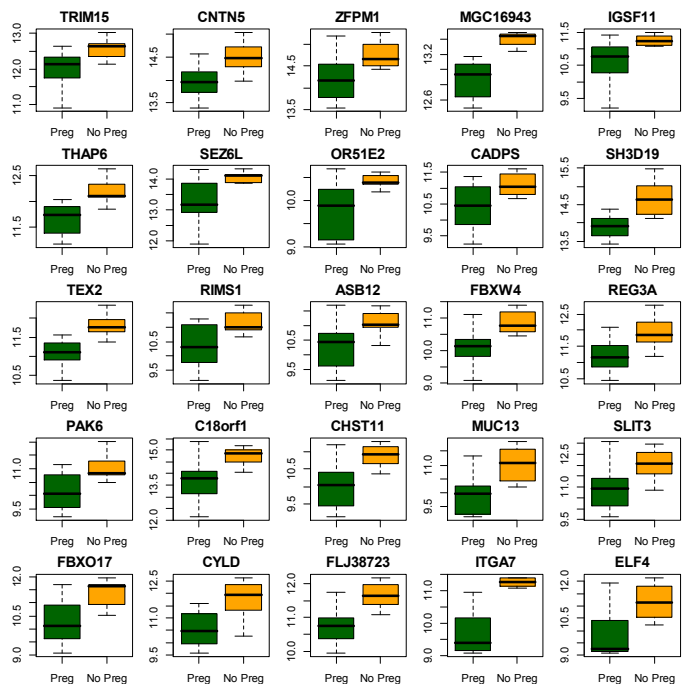
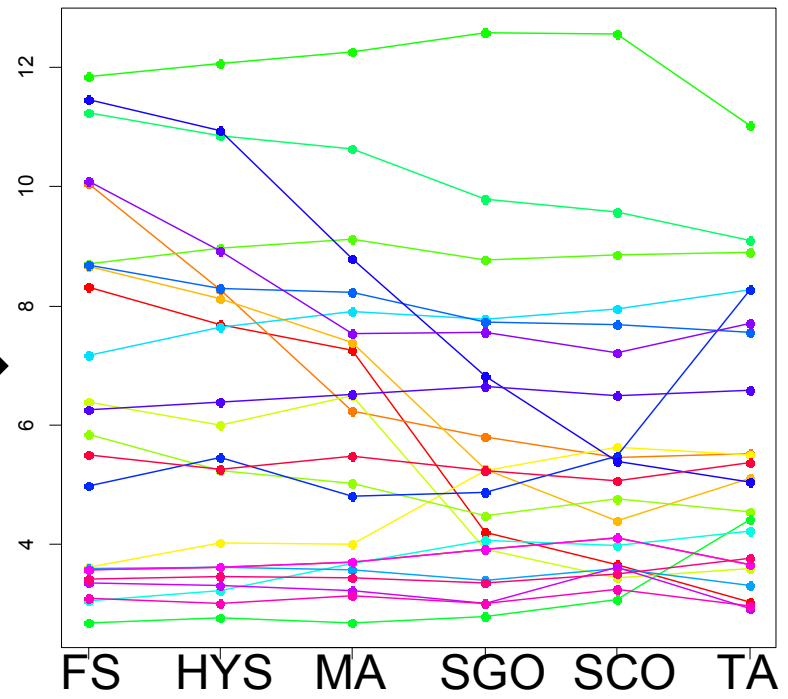
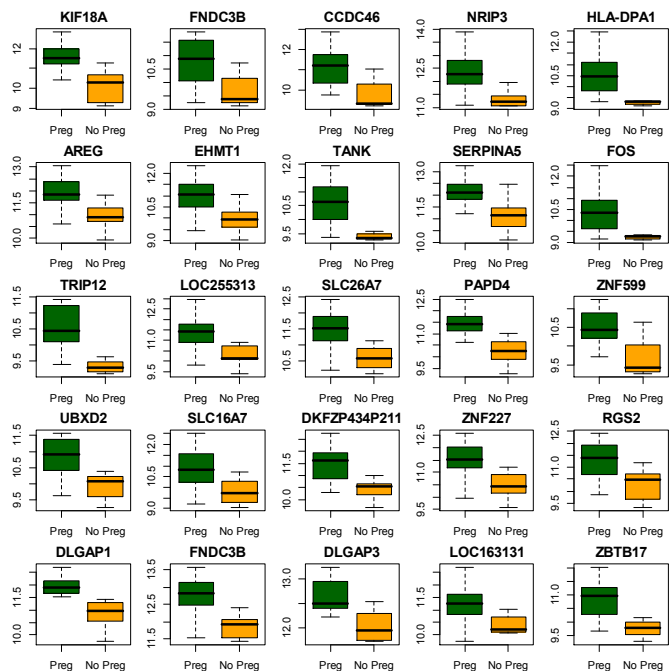
**Gene Ontology:**  
Proteolysis  
(FBXW4, FBXO17, ASB12, CYLD)  
Cell adhesion  
(CNTN5, IGSF11, ITGA7, REG3A)

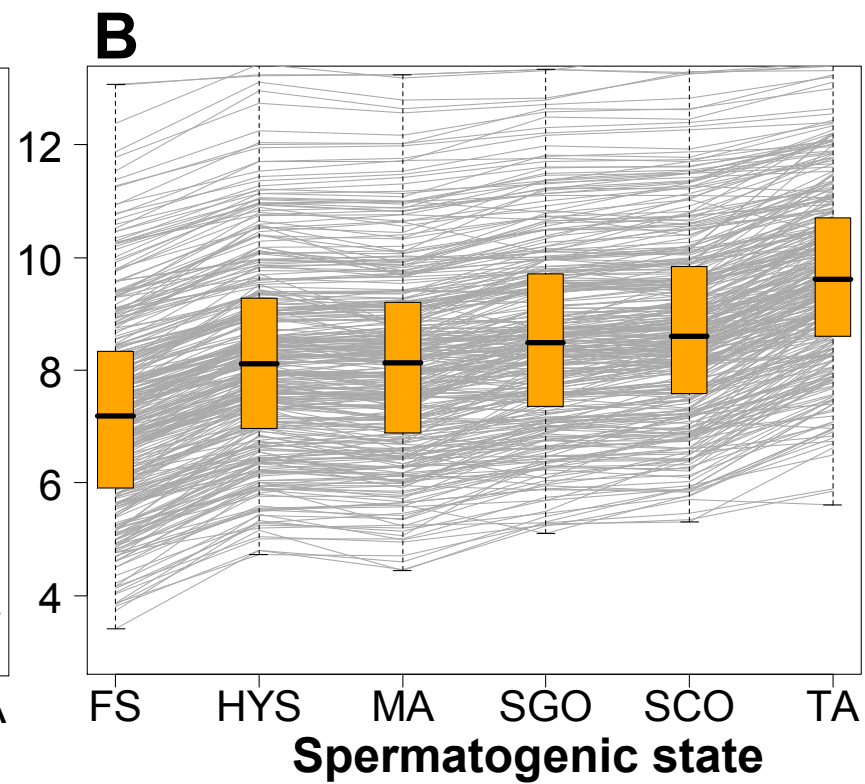
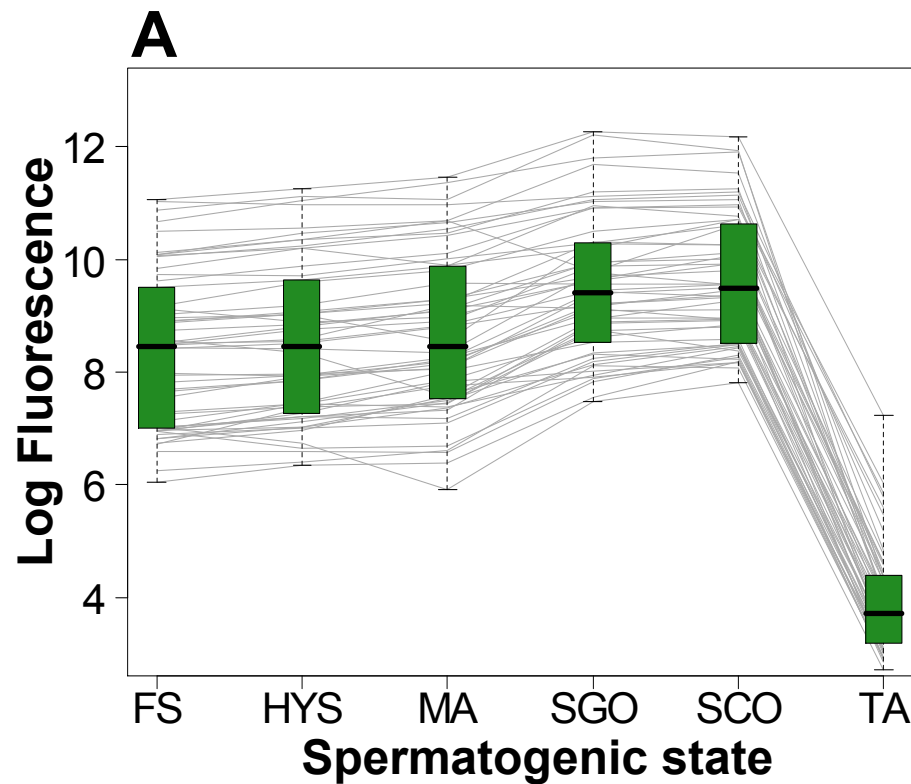
**TFBS:**  
ZNF238, CDP, CABLES1, NCX

=> Chromatin assembly, differentiation, cell cycle

**229 differential genes  $p < 0.01$  from pure noise !**







**C**

	FS	HYS	MA	SGO	SCO	TA
FS (n = 8)		1.15 ± 0.38	1.31 ± 0.41	2.27 ± 0.85	2.40 ± 0.87	0.06 ± 0.03
HYS (n = 10)	1.72 ± 0.68		1.12 ± 0.33	1.97 ± 0.79	2.09 ± 0.83	0.05 ± 0.03
MA (n = 5)	1.82 ± 0.58	1.05 ± 0.40		1.72 ± 0.66	1.86 ± 0.68	0.04 ± 0.02
SGO (n = 2)	2.36 ± 0.95	1.35 ± 0.58	1.30 ± 0.47		1.06 ± 0.28	0.02 ± 0.01
SCO (n = 5)	2.69 ± 1.13	1.53 ± 0.63	1.46 ± 0.53	1.11 ± 0.33		0.02 ± 0.01
TA (n = 1)	4.99 ± 2.87	2.77 ± 1.56	2.69 ± 1.39	2.01 ± 0.85	1.82 ± 0.67	

Sertoli cell markers

Leydig cell markers