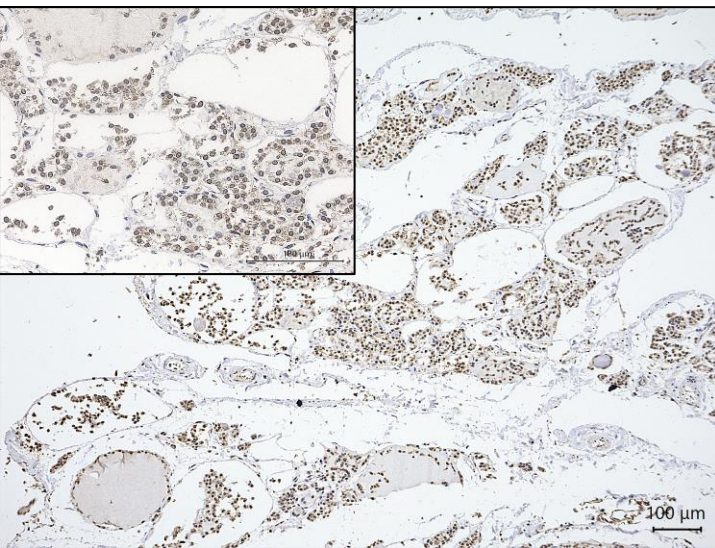
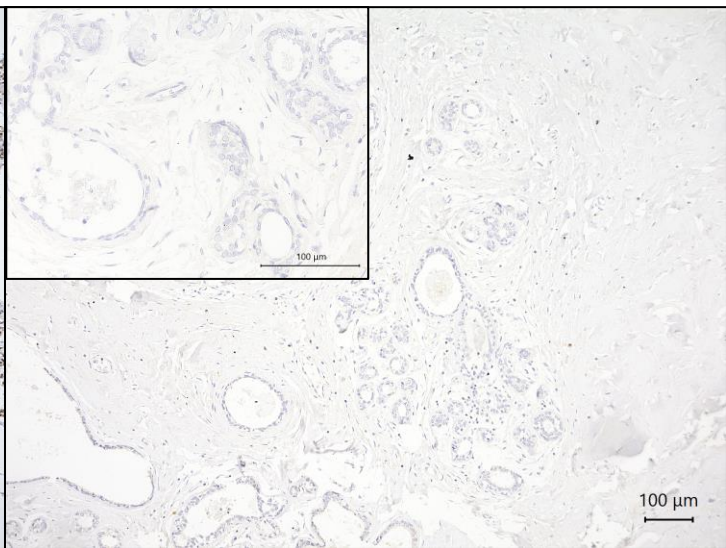


**Suppl. Figure S1: Control stainings for all antibodies used in this study**

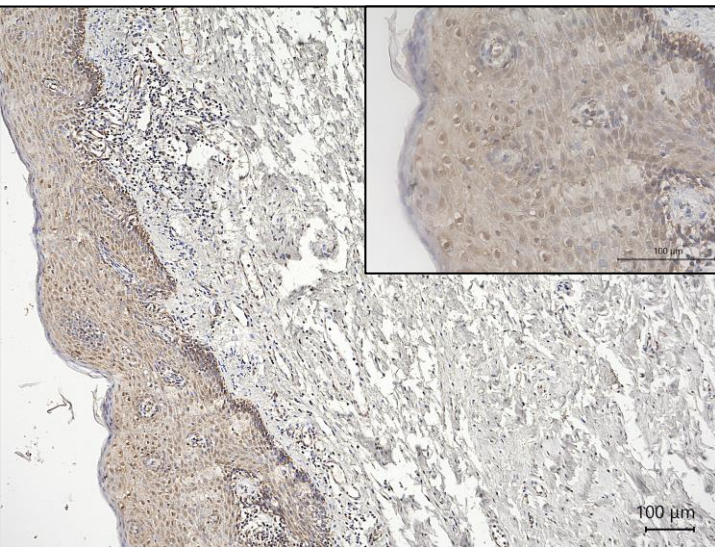
Positive control staining for TR $\alpha$  in thyroid tissue



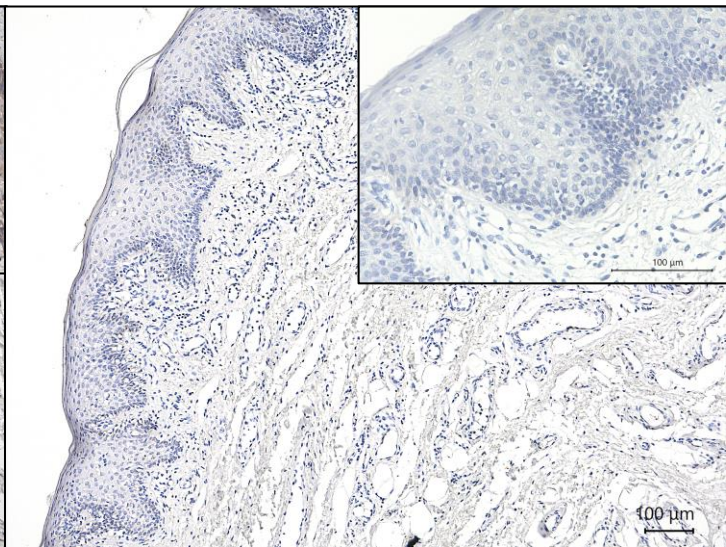
Negative control staining for TR $\alpha$  in thyroid tissue



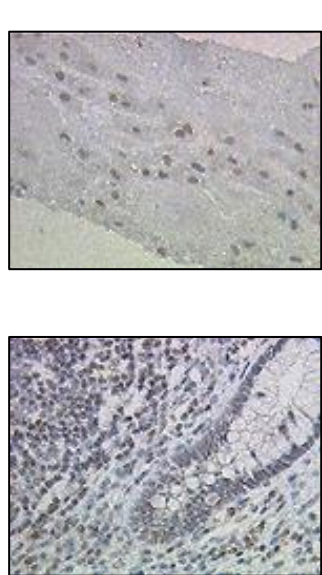
Positive control staining for TR $\alpha$ 2 in human skin



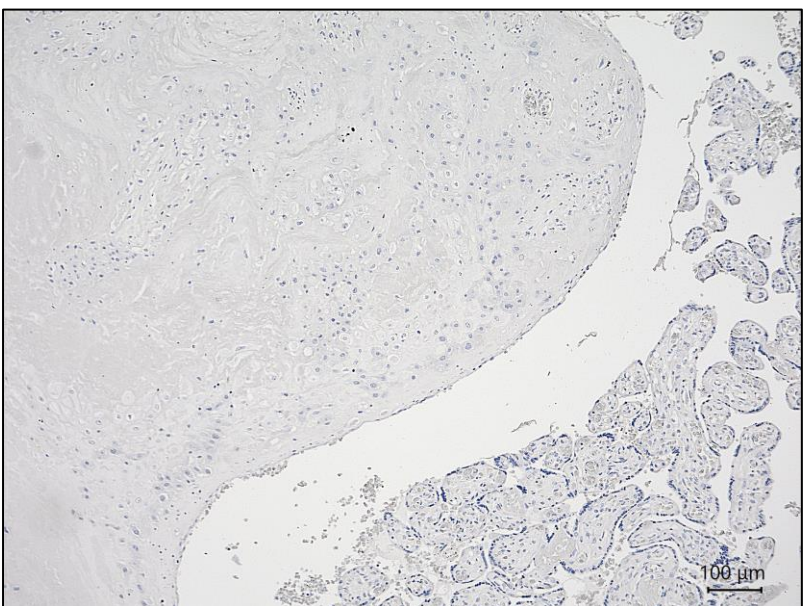
Negative control staining for TR $\alpha$ 2 in human skin



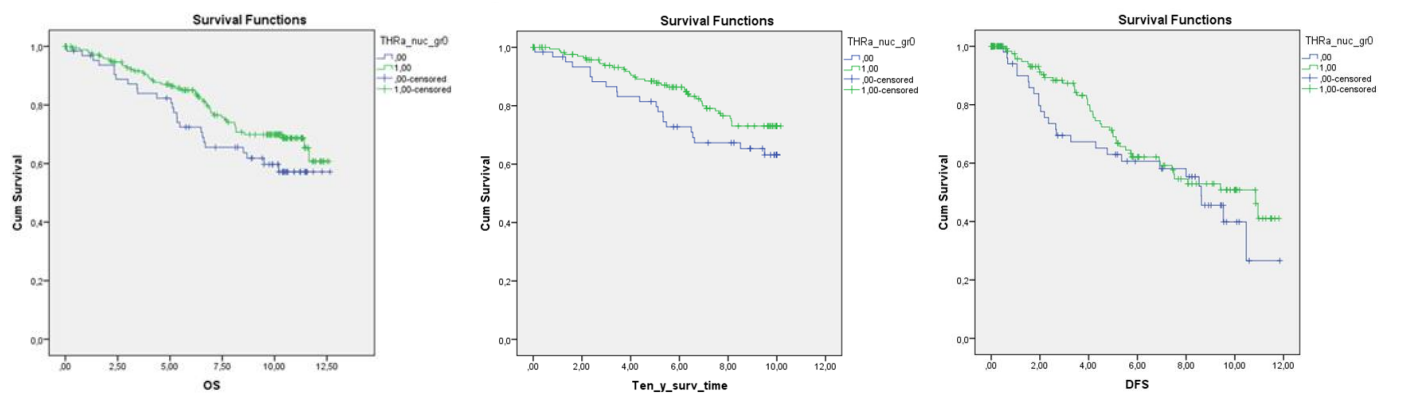
Positive control staining for TR $\alpha$ 1 in human placenta and colon



Negative control staining for TR $\alpha$ 1 in human placenta



**Suppl. Figure S2:** Survival Function of nuclear TRα, TRα is not a significant prognosticator for overall Survival, ten year survival or disease free survival



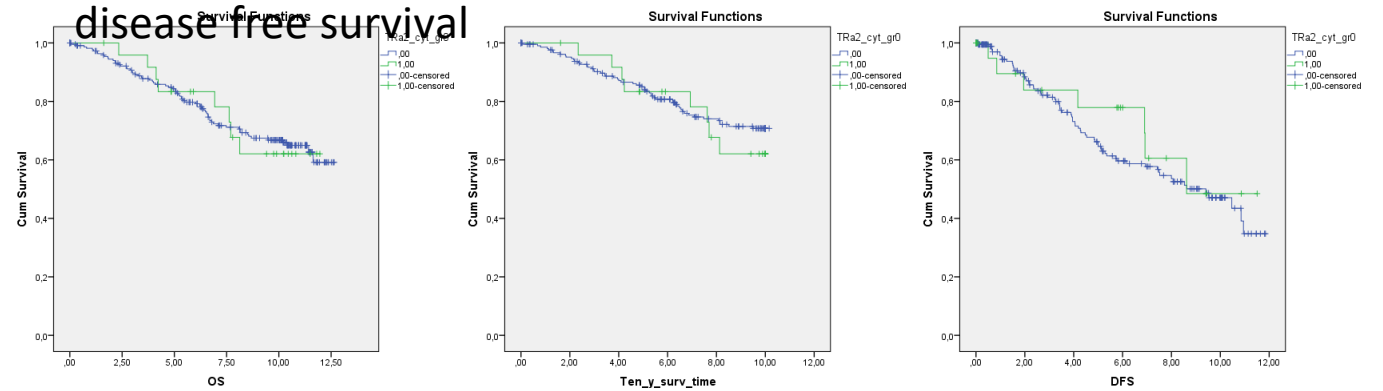
Means for Survival Time				
THRa_nuc_gr0	Mean			
	Estimate	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
0	9.39	0.537	8.337	10.442
1	10.246	0.299	9.66	10.833
Overall	10.026	0.265	9.506	10.546
a. Estimation is limited to the largest survival time if it is censored.				
Overall Comparisons				
	Chi-Square	df	Sig.	
Log Rank (Mantel-Cox)	2.34	1	0.126	
Test of equality of survival distributions for the different levels of THRa_nuc_gr0.				

Means for Survival Time				
THRa_nuc_gr0	Mean			
	Estimate	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
0	7.93	0.405	7.136	8.725
1	8.82	0.205	8.417	9.222
Overall	8.605	0.189	8.236	8.975
a. Estimation is limited to the largest survival time if it is censored.				
Overall Comparisons				
	Chi-Square	df	Sig.	
Log Rank (Mantel-Cox)	2.582	1	0.108	
Test of equality of survival distributions for the different levels of THRa_nuc_gr0.				

Means for Survival Time				
THRa_nuc_gr0	Mean			
	Estimate	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
0	7.213	0.637	5.965	8.462
1	8.129	0.406	7.333	8.926
Overall	7.872	0.345	7.197	8.548
a. Estimation is limited to the largest survival time if it is censored.				
Overall Comparisons				
	Chi-Square	df	Sig.	
Log Rank (Mantel-Cox)				
	1.395	1	0.238	
Test of equality of survival distributions for the different levels of THRa_nuc_gr0.				



# Suppl. Figure S3: Survival Function of cytoplasmic TRα2, cytoplasmic TRα2 is not a significant prognosticator for overall Survival, ten year survival or disease free survival

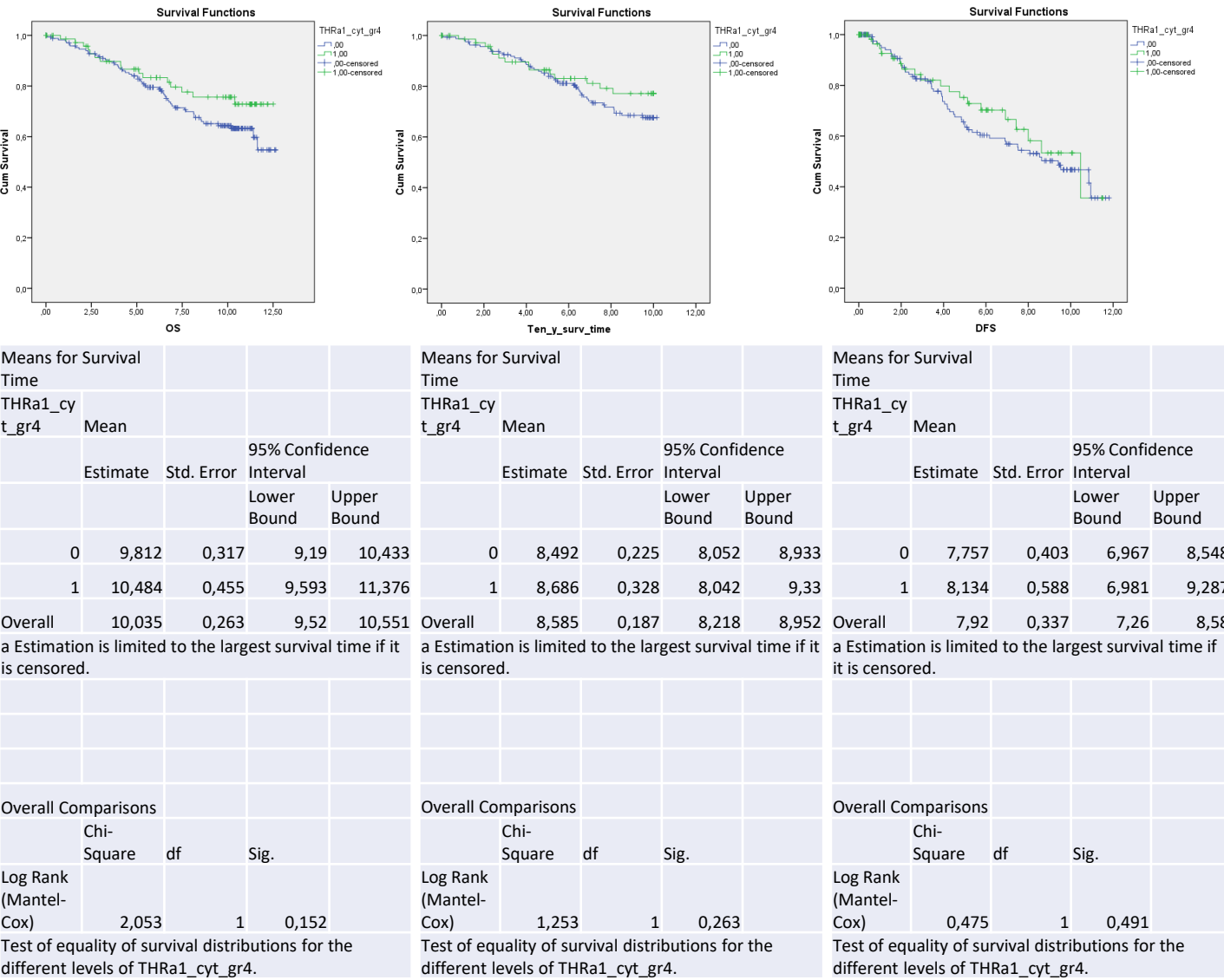


Means for Survival Time				
TRa2_cyt_gr0	Mean			
	Estimate	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
0	9.921	0.281	9.371	10,471
1	9.642	0.685	8.299	10,984
Overall	9.932	0.264	9,414	10,449
a Estimation is limited to the largest survival time if it is censored.				
Overall Comparisons				
	Chi-Square	df	Sig.	
Log Rank (Mantel-Cox)				
	0,002	1	0,969	
Test of equality of survival distributions for the different levels of TRa2_cyt_gr0.				

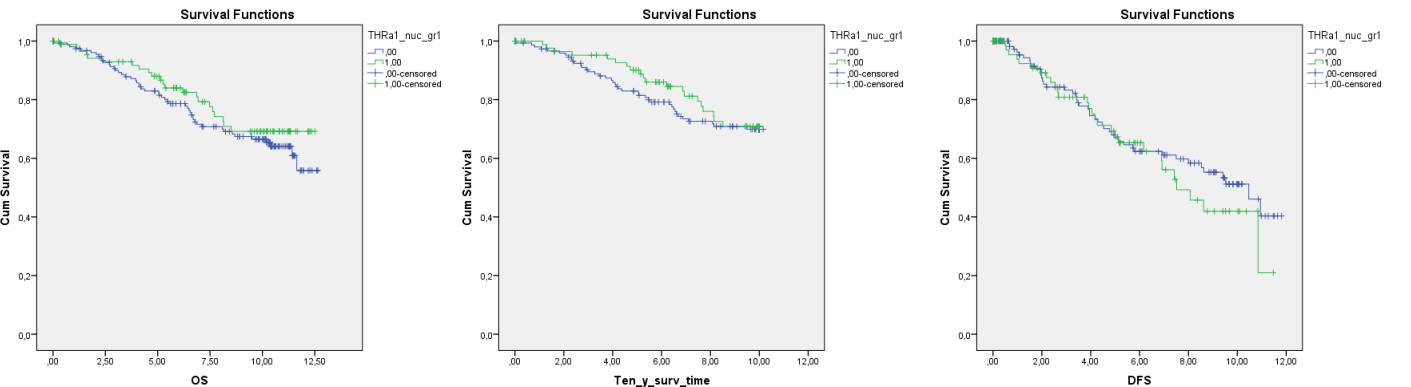
Means for Survival Time					
TRa2_cyt_gr0	Mean		95% Confidence		
	Estimate	Std. Error	Interval		
			Lower Bound	Upper Bound	
0	8,53	0,203	8,131	8,928	
1	8,425	0,498	7,45	9,4	
Overall	8,526	0,19	8,154	8,899	
a Estimation is limited to the largest survival time if it is censored.					
Overall Comparisons					
	Chi-Square	df	Sig.		
Log Rank (Mantel-Cox)					
	0,278	1	0,598		
Test of equality of survival distributions for the different levels of TRa2_cyt_gr0.					

Means for Survival Time				
TRa2_cyt_gr0	Mean			
	Estimate	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
0	7,725	0,358	7,024	8,426
1	8,249	0,964	6,359	10,138
Overall	7,814	0,337	7,153	8,475
a Estimation is limited to the largest survival time if it is censored.				
Overall Comparisons				
	Chi-Square	df	Sig.	
Log Rank (Mantel-Cox)	0,428	1	0,513	
Test of equality of survival distributions for the different levels of TRa2_cyt_gr0.				

**Suppl. Figure S4:** Survival Function of cytoplasmic TRα1, cytoplasmic TRα1 is not a significant prognosticator for overall Survival, ten year survival or disease free survival



**Suppl. Figure S5:** Survival Function of nuclear TRα1, nuclear TRα1 is not a significant prognosticator for overall Survival, ten year survival or disease free survival



Means for Survival Time				
THRa1_nuc_gr1	Mean			
	Estimate	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
0	9,846	0,335	9,19	10,502
1	10,291	0,414	9,48	11,102
Overall	10,035	0,263	9,52	10,551
a Estimation is limited to the largest survival time if it is censored.				
Overall Comparisons				
	Chi-Square	df	Sig.	
Log Rank (Mantel-Cox)				
	0,852	1	0,356	
Test of equality of survival distributions for the different levels of THRa1_nuc_gr1.				

Means for Survival Time				
THRa1_nuc_gr1	Mean			
	Estimate	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
0	8,429	0,248	7,942	8,916
1	8,736	0,266	8,214	9,258
Overall	8,585	0,187	8,218	8,952
a Estimation is limited to the largest survival time if it is censored.				
Overall Comparisons				
	Chi-Square	df	Sig.	
Log Rank (Mantel-Cox)				
	0,321	1	0,571	
Test of equality of survival distributions for the different levels of THRa1_nuc_gr1.				

Means for Survival Time					
THRa1_nuc_gr1	Mean				
	Estimate	Std. Error	95% Confidence Interval		
			Lower Bound		Upper Bound
0	8,062	0,425	7,229	8,895	
1	7,422	0,53	6,383	8,46	
Overall	7,92	0,337	7,26	8,58	
a Estimation is limited to the largest survival time if it is censored.					
Overall Comparisons					
	Chi-Square	df	Sig.		
Log Rank (Mantel-Cox)	0,594	1	0,441		
Test of equality of survival distributions for the different levels of THRa1_nuc_gr1.					