

Supplementary material

The TCGA thyroid cancer dataset of genes VEGFA and NFE2L2.

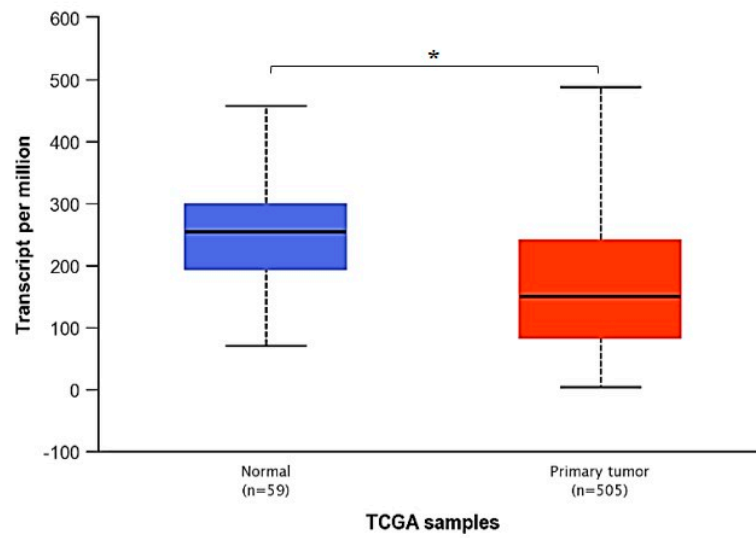


Figure 1. Expression of VEGFA in THCA based on Sample types

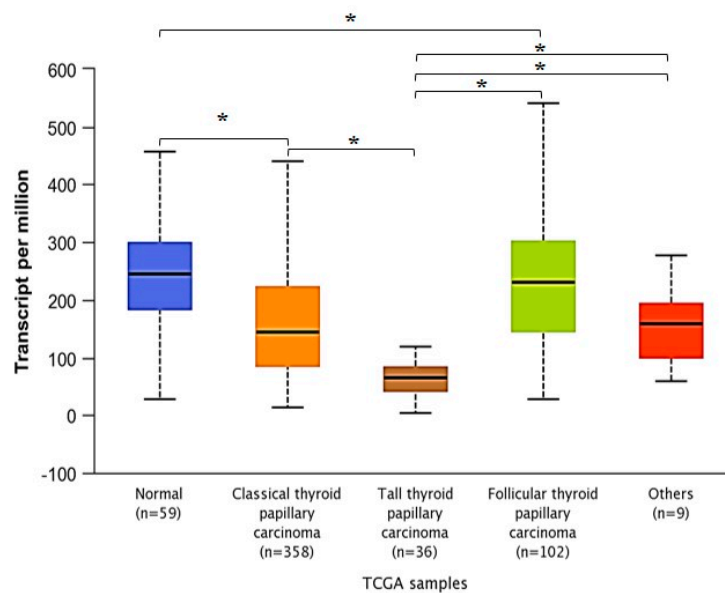


Figure 2. Expression of VEGFA in THCA based on Tumor histology

Tabela 1 – P values for VEGFA gene comparisons.

Comparison	Statistical significance
Normal-vs-Primary	2,82E+07*
Classical-VS-Tall	9,71E+00*
Classical-VS-Follicular	8,74E+07*
Classical-VS-Other	7,64E+05
Classical-VS-Normal	6,28E+07*
Tall-VS-Follicular	1,62E+02*
Tall-VS-Other	2,43E+04*
Tall-VS-Normal	1,62E+02*
Follicular-VS-Other	1,85E+05
Follicular-VS-Normal	9,52E+05
Other-VS-Normal	5,88E+04

Figure 3. Expression of *NFE2L2* in THCA based on Sample types

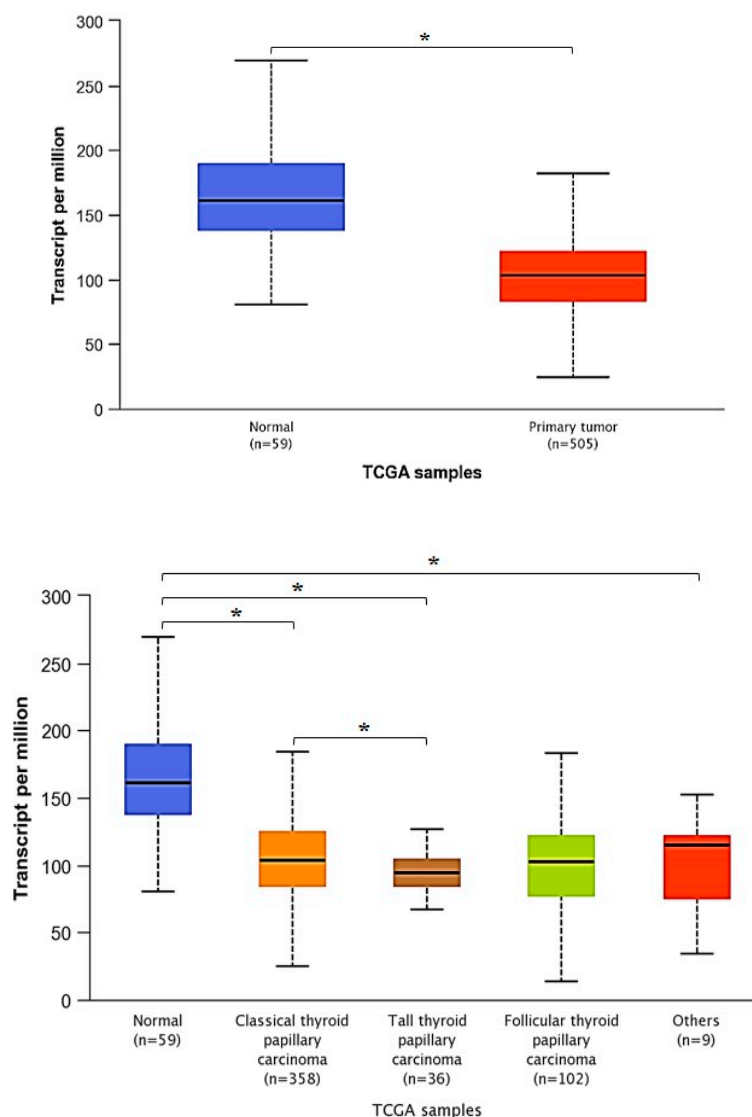


Figure 4. Expression of *NFE2L2* in THCA based on Tumor histology

Tabela 2 – P values for *NFE2L2* gene comparisons.

Comparison	Statistical significance
Normal-vs-Primary	5,44E+06*
Classical-VS-Tall	4,12E+03*
Classical-VS-Follicular	3,90E+05
Classical-VS-Other	6,11E+05
Classical-VS-Normal	4,69E+02*
Tall-VS-Follicular	2,21E+05
Tall-VS-Other	4,89E+05
Tall-VS-Normal	1,64E+02*
Follicular-VS-Other	3,31E+05
Follicular-VS-Normal	4,97E+05
Other-VS-Normal	7,20E+02*