

A

Gene Symbol	Fold change FC55 vs FRT	p-value
<i>ABLIM3</i>	3.68	2.43e-03
<i>IFI204</i>	4.09	3.72e-18
<i>SOX6</i>	3.16	9.72e-04
<i>CELSR2</i>	4.24	4.10e-246
<i>RHOQ</i>	3.04	3.93e-103
<i>CLSTN3</i>	3.66	8.10e-03
<i>CFH</i>	1197.50	8.53e-64
<i>LCP1</i>	337.86	0.00e+00
<i>UNC13D</i>	-4.78	1.26e-11
<i>DPP4</i>	-3.64	7.08e-108
<i>CAV1</i>	20.73	1.19e-03
<i>TAC4</i>	-3.35	4.73e-02
<i>SLC1A2</i>	14.36	3.85e-21
<i>HEPH</i>	1673.75	1.44e-180
<i>ADM</i>	5.61	2.03e-06

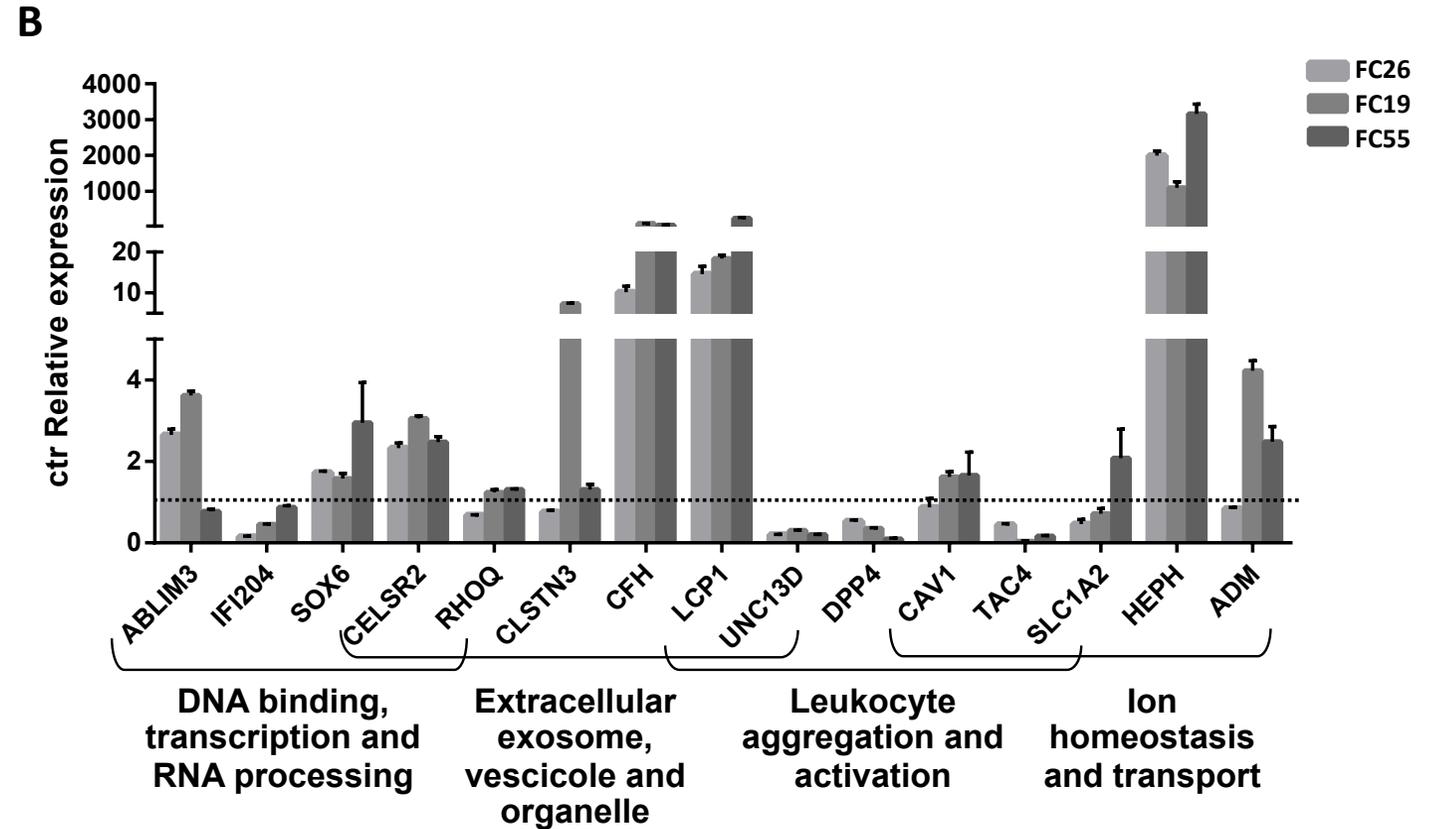


Figure S1: Validation of DEG in FRT-overexpressing clones. A. Selected genes from the results of RNA-seq performed on *FOXE1* overexpressing CF55. **B.** A qrt-PCR analysis, for the genes in A, was performed on *FOXE1*-clones compared to control FRT cells (ctr). The data are shown as ctr-relative expression ($2^{-\Delta\Delta Ct}$) and reported referring to the functional category they belong to. The dotted line represents the ctr value set to 1. *TUBULIN* was used to normalize.

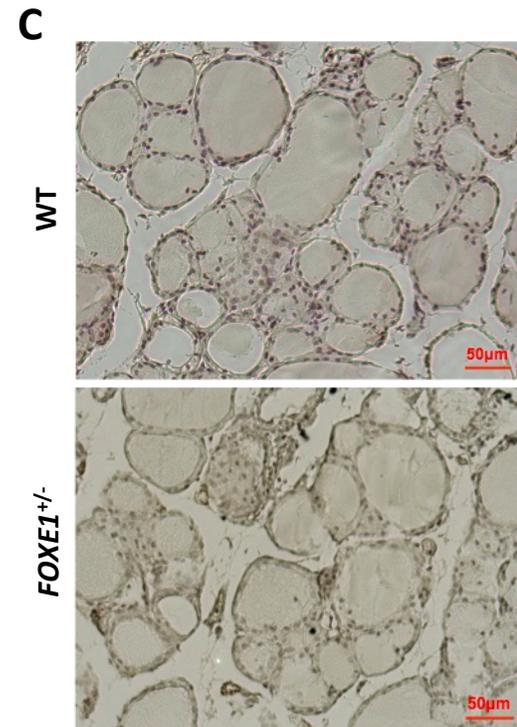
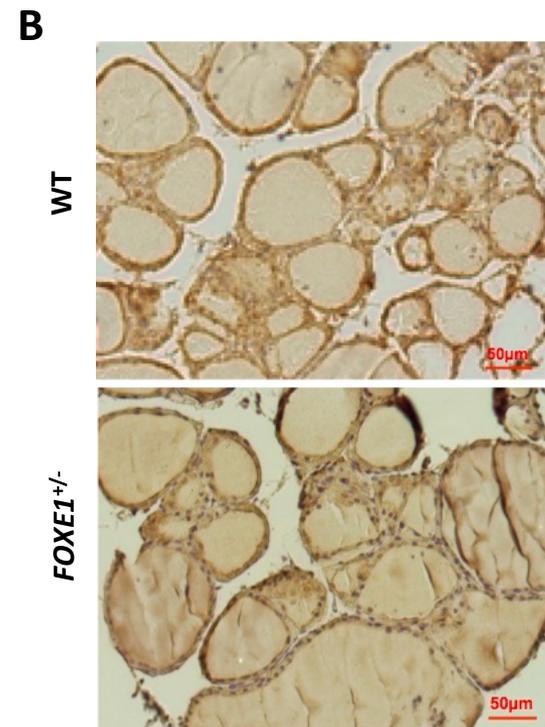
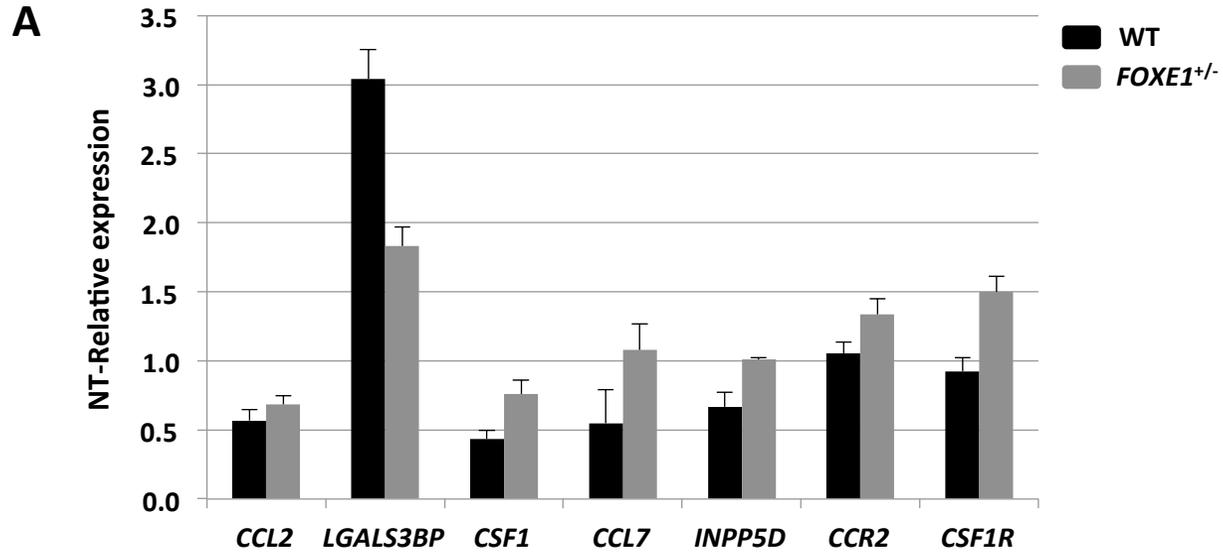


Figure S2: A. Total RNA was extracted from thyroids of doxycycline treated and untreated (NT) WT and *Foxe1*^{+/-} mice and macrophages related markers were analyzed by quantitative RT-PCR. Results are reported as the fold change ($2^{-\Delta\Delta C_t}$) of WT and *Foxe1*^{+/-} treated mice respect to the corresponding untreated mice. Means \pm SD are shown. T-Test was performed on data founding no significance. **B, C.** IHC staining for IBA1 (B) and GALECTIN-3 (C) was performed on 7 μ m section of thyroids from WT and *Foxe1*^{+/-} mice after doxycycline treatment. Hematoxylin was used to stain the nuclei. 20X magnifications are shown. Each image is representative of six different images.