

Figure S1: Heatmap of differentially expressed miRNAs of all of the conditions tested. Red and blue indicate z-scores of ≥ 2 or ≤ -2 , respectively, and white indicates a z-score of 0 (row-wise mean), p and $q < 0.25$. Performed in triplicate.

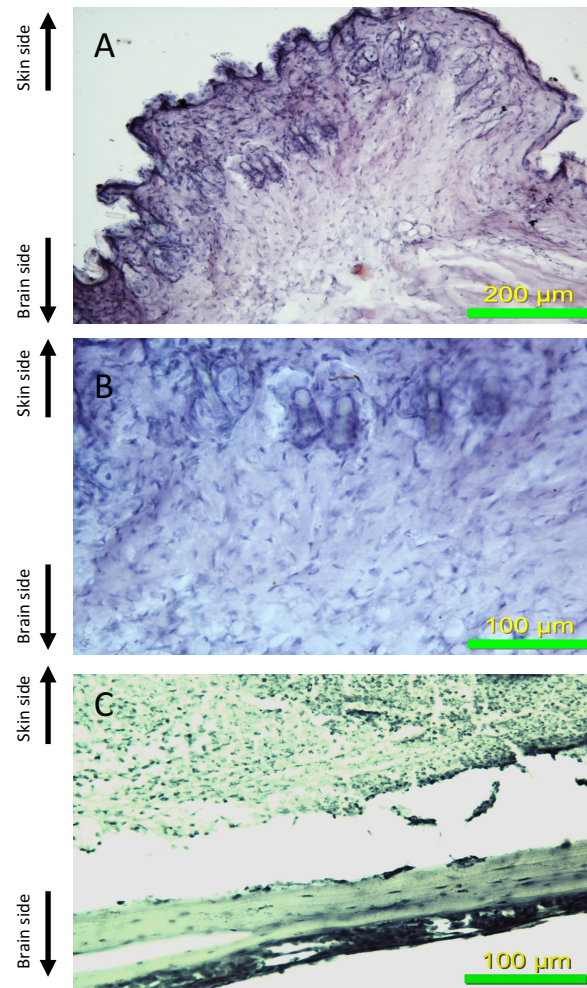


Figure S2: Histological Sections. Representative samples for skin (A-B) & underlying calvarial bone (C) at the middle of the calvaria in an uninfected mouse. TRAP staining for bone (bottom row, 200x) and H&E staining for the skin (Top row, 100x; middle row, 200x).

Pathway	Benjamini corrected <i>p</i> -value
Chemokine signalling pathway	1.3 ^{E-27}
Cytokine-cytokine receptor interaction	2.4 ^{E-8}
TNF signalling pathway	1.9 ^{E-1}

Pathway	Benjamini corrected <i>p</i> -value
Osteoclast differentiation	5.3 ^{E-8}
T cell receptor signalling pathway	6.7 ^{E-7}
Toll-like receptor signalling pathway	4.6 ^{E-6}
MAPK signalling pathway	7.5 ^{E-6}
Chemokine signalling pathway	2.0 ^{E-5}

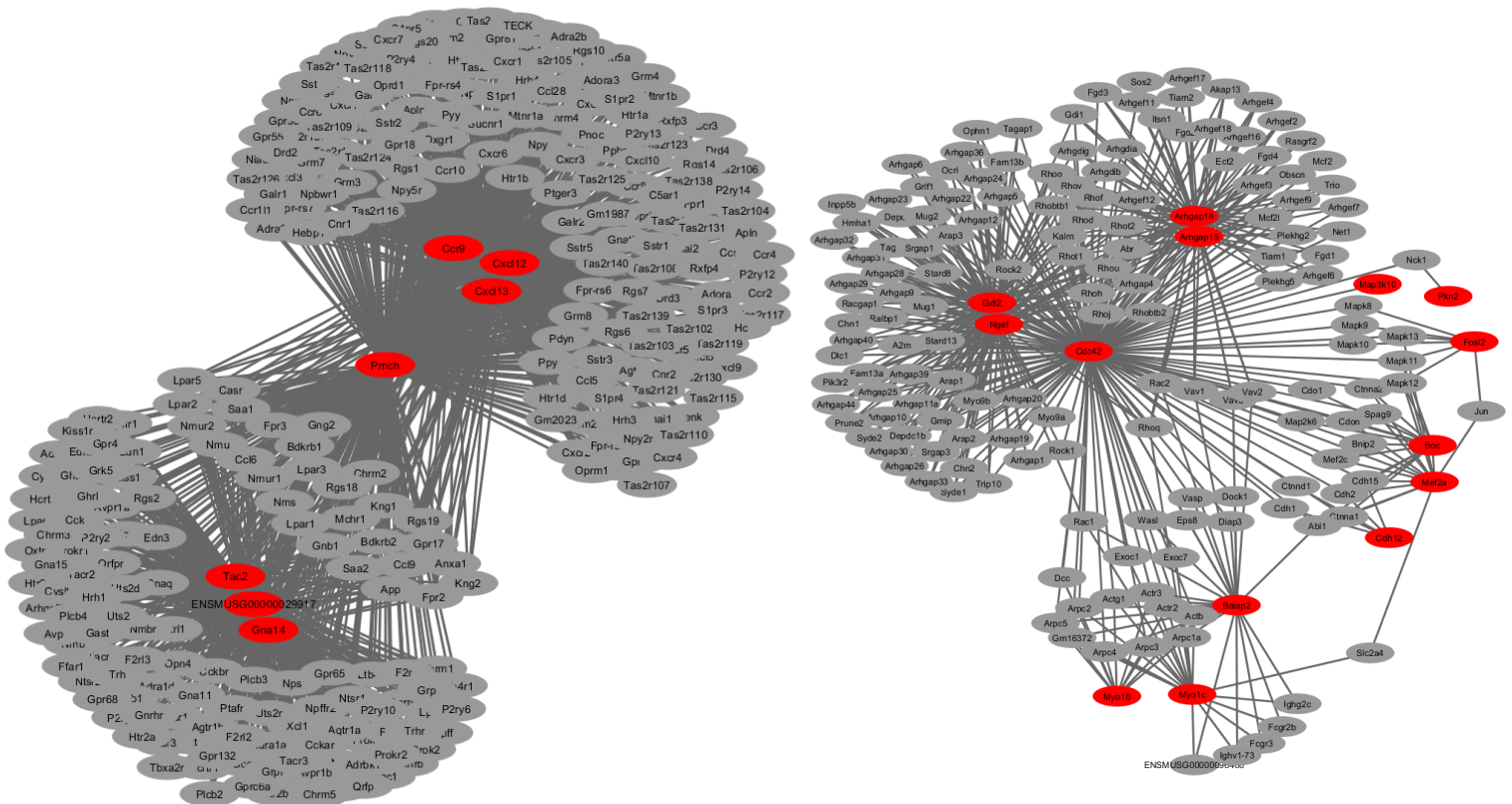


Figure S3: Representative topological modules related to mmu-miR-155 target genes and identified pathways associated to innate immune response. In red, genes identified as directly affected by mmu-miR-155.

Pathway	Benjamini corrected <i>p</i> -value
T-cell receptor signalling pathway	6.6 ^E -12
Osteoclast differentiation	2.2 ^E -11
B-cell receptor signalling pathway	1.9 ^E -11
Bacterial invasion of epithelial cells	7.4 ^E -11
Chemokine signalling pathway	2.6 ^E -10
Jak-STAT signalling pathway	1.1 ^E -8
NF-kappa B signalling pathway	1.4 ^E -5
Apoptosis	3.0 ^E -5
PI3-Akt signalling pathway	1.0 ^E -4
Toll-like receptor signalling pathway	2.5 ^E -4
TNF signalling pathway	3.1 ^E -4

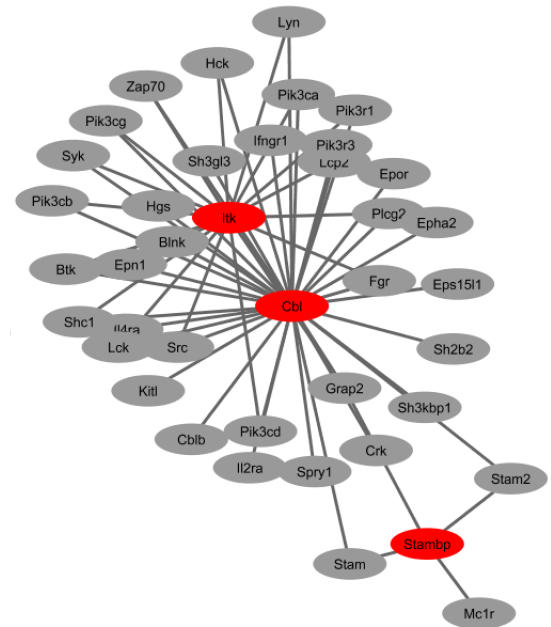


Figure S4: Topological module related to mmu-miR-155 target genes and identified pathways associated to innate immune response. In red, genes identified as directly affected by mmu-miR-155.