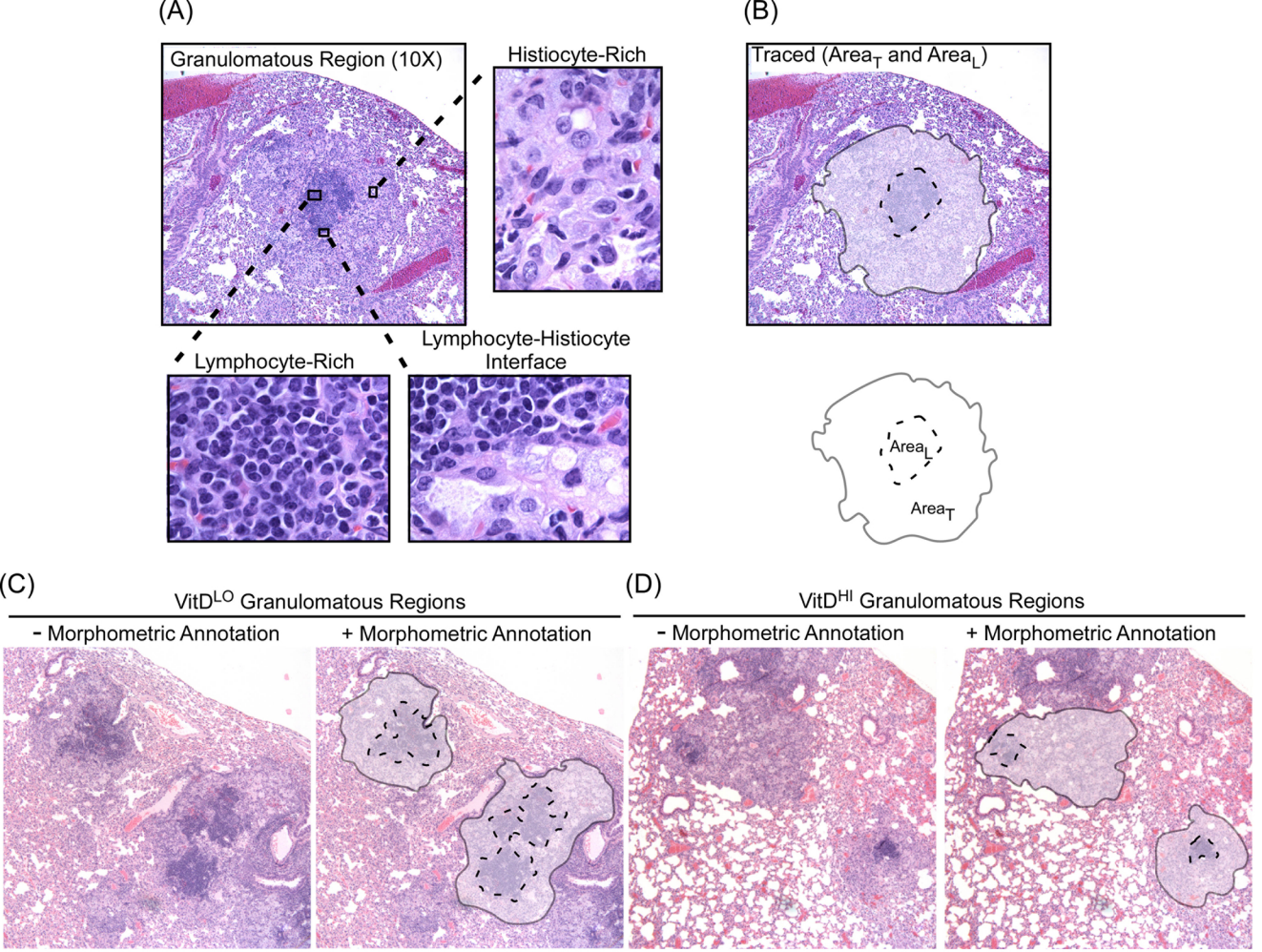
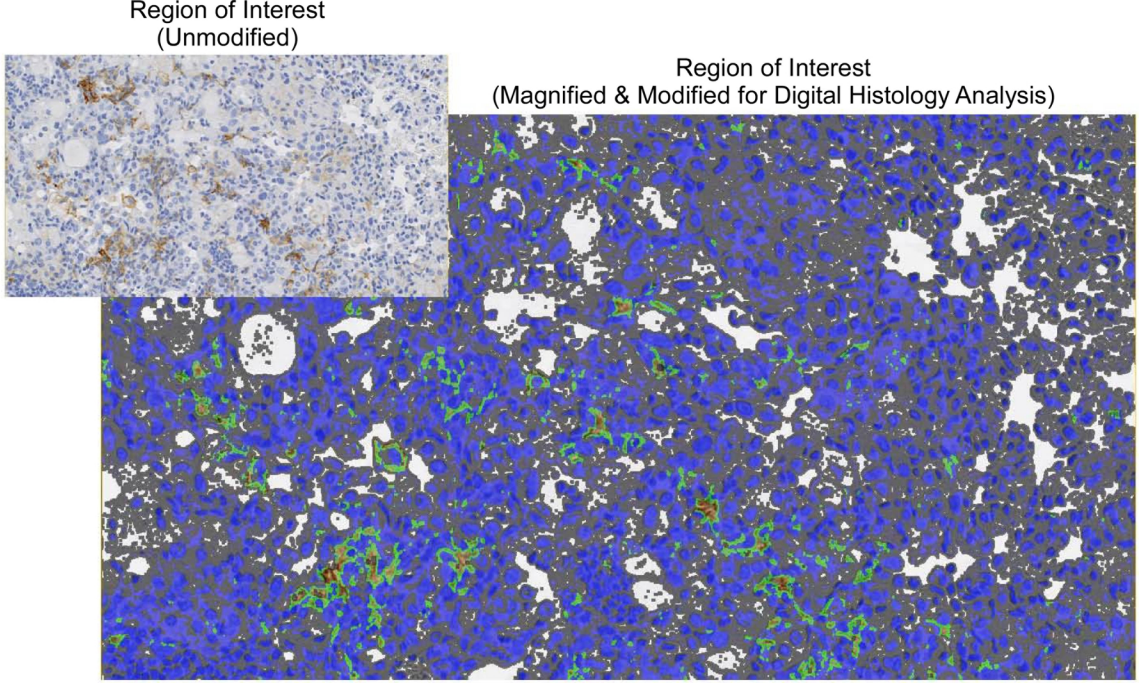
Supplemental Table I. Gene name, primer sequence, corresponding nucleotides, product length and NCBI Accession Number for genes amplified using Real-Time PCR.

Gene Name	Symbol	Primer Sequence 5'-3'	Nucleotides	Product Size (bp)	NCBI Accession #
Interferon gamma	*ifnγ*	F –TCA AGT GGC ATA GAT GTG GAA GAA R –TGG CTC TGC AGG ATT TTC ATG	224-247 315-295	71	NM_008337.4
1 alpha hydroxylase	*cyp27b1*	F –GGG CCA ATA TGG TCT GGC AG R –GGA CAG TGA CTT TCT TGT CGC	217-236 314-294	98	NM_010009.2
Cathelicidin-Related Antimicrobial Peptide	*cramp*	F –GCC GCT GAT TCT TTT GAC AT R –ATT CTT CTC CCC ACC TTT GC	362-381 469-450	107	NM_009921.2
Vitamin D Receptor	*vdr*	F –GAA TGT GCC TCG GAT CTG TGG R –ATG CGG CAA TCT CCA TTG AAG	54-74 203-183	150	D31969.1



SUPPLEMENTAL FIGURE 1. For morphometric analysis of granulomatous regions in Mtb-infected VitD^{LO} and VitD^{HI} mice, H&E stained lung sections were first visually assessed at 10× to determine where granulomatous regions were present. Shown is (**A**) a representative granulomatous region at 10× magnification, alongside 100× magnifications of the lymphocyte-rich region, histiocyte-rich region, and the lymphocyte-histiocyte interface. (**B**) NIS-Elements software (Nikon) was used to annotate and determine the area of both the total granulomatous region (solid line around the outer edge of the histiocyte-rich region, Area$_T$) and its cognate lymphocyte-rich region (hatched-line drawn on the lymphocyte-histiocyte interface, Area$_L$); dividing Area$_L$/Area$_T$ was used to determine lymphocytes' contribution to each granulomatous region (% granuloma area). (**C-D**) The representative (**C**) VitD^{LO} and (**D**) VitD^{HI} granulomatous regions of Figure 4 are reproduced here, respectively, and shown with or without morphometric annotation of their associated Area$_T$ and Area$_L$. The results of our morphometric analyses are shown in **Figure 3** and **Figure 7**.



SUPPLEMENTAL FIGURE 2. Immunohistochemistry stained slides were digitally scanned in high resolution using a NanoZoomer HT 2.0. Images were viewed at 20× resolution and analyzed for detectable antibody (DAB) positive areas within the region of interest (ROI). Four ROI's were used per tissue section and each ROI was analyzed using an unbiased, software assisted analysis. Using Visiopharm software, pixels staining positive with hematoxylin are colored blue, unstained tissue/background are grey, DAB positive areas are brown and empty background is white. DAB positive areas were outlined in green and the area measured in microns. This area was then divided by the total tissue area (green outlined DAB, plus blue/grey background tissue) to give percent DAB positive area within the ROI.