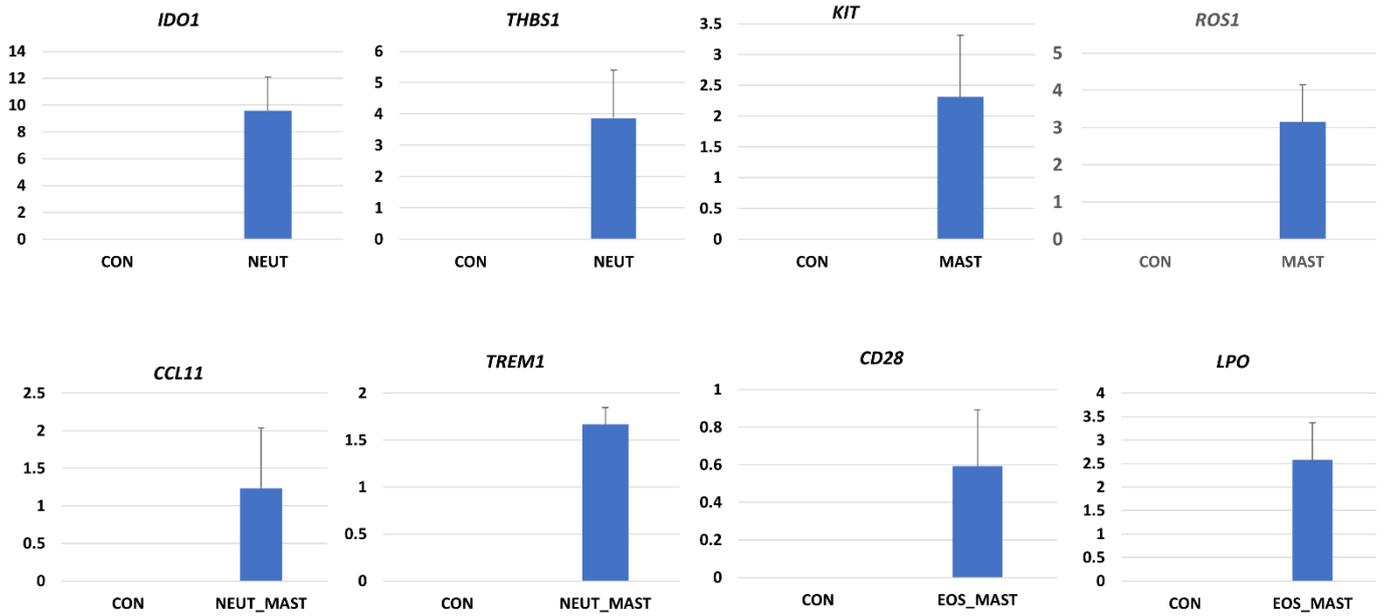


**Expression profile of RNA-seq and qPCR data.** Expression profile of RNA-seq and qPCR data for selected genes across all comparisons were compared using the same samples. **A)** The data are consistent with the results of RNA-seq analysis for these genes in the same samples; *IDO1*, *THBS1* (Group\_B\_NEUT), *KIT*, *ROS1* (Group\_C\_MAST), *CCL11*, *TREM1* (Group\_D\_NEUT\_MAST), *CD28*, *LPO* (Group\_E\_EOS\_MAST). Expression was normalized using *SDHA* as a reference gene in qPCR. Results represent mean values and are expressed as log<sub>2</sub> values of the fold change and are representative of a minimum of 3 biological replicates. **B)** RNA-seq and qPCR log<sub>2</sub> values of the fold change were significantly correlated with a correlation coefficient  $r = 0.93$  (Spearman's rank correlation test) and  $P$  value = 0.002, after testing for normality using *shapiro.test*. Statistical analysis and graphs were generated in R.



**Expression profile of qPCR data.** The relative gene expression of selected genes, obtained from qPCR data, is presented across all comparisons. qPCR was performed on the same samples used for the RNA-seq analysis. *IDO1*, *THBS1* were tested in Group\_B\_NEUT versus control, *KIT*, *ROS1* in Group\_C\_MAST versus Control, *CCL11*, *TREM1* in Group\_D\_NEUT\_MAST versus Control, and *CD28*, *LPO* in Group\_E\_EOS\_MAST versus Control. Expression was normalized using *SDHA* as a reference gene in qPCR. Results represent mean values and are expressed as log<sub>2</sub> values of the fold change and are representative of a minimum of 3 biological replicates.

### *Primers used in this study*

Target	Primer orientation	Primer Sequence (5'-3')	Size (bp)
<i>IDO1</i>	F	ATCAAAGAAATTCCGTTATATTCAA	94
	R	TGCGTAGACAAGAAGAAGTTATATCAAT	
<i>THBS1</i>	F	CAGACTCCGCATCGCAAAG	134
	R	GGAGGACATTGGTAGAGCTGG	
<i>KIT</i>	F	AGAGCTGTGCCAGTTGTGTC	137
	R	CTGTTCTTTAGTCCGGCTGT	
<i>ROS1</i>	F	ATCTGAGTGAACCGTGCATCC	71
	R	TTCCTCTTCGTACGCACCTT	
<i>CCL11</i>	F	ACCAGCCCAGAAACCAACAG	102
	R	ACGGTCGAGATAGAAACTGGCT	
<i>CD28</i>	F	TCTTTGTA CTGCTGGATGAGG	110
	R	CGTAGGGCTGGTAGTGCTTTC	
<i>LPO</i>	F	CGCTTTTTGGAAGGACCATGT	124
	R	AGACAGACGTGCGAGGAAAC	
<i>SDHA</i>	F	GGACAGAGCCTCAAGTTTGG	116
	R	GTATCATATCGTAGAGACCTCCATA	