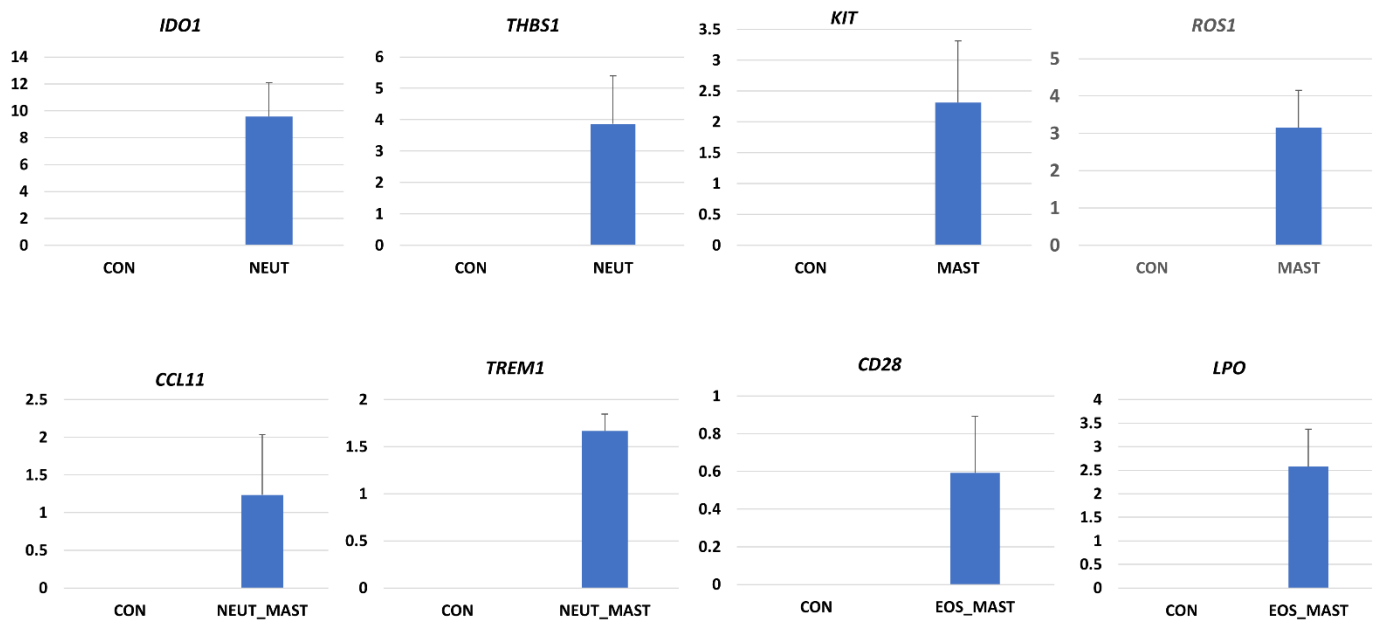


Expression profile of RNA-seq and qPCR data. Expression profile of RNA-seq and qPCR data for selected genes across all comparisons were compared using the same samples. **A)** The data are consistent with the results of RNA-seq analysis for these genes in the same samples; IDO1, THBS1 (Group_B_NEUT), 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 log2 values of the fold change and are representative of a minimum of 3 biological replicates. **B)** RNA-seq and qPCR log2 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 log2 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	CAGACTCCGCATCGCAAAAG	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	ACGGTCGAGATAGAACTGGCT	
<i>CD28</i>	F	TCTTTGTACTTGCTGGATGAGG	110
	R	CGTAGGGCTGGTAGTGCTTTC	
<i>LPO</i>	F	CGCTTTTTGGAAGGACCATGT	124
	R	AGACAGACGTGCGAGGAAAC	
<i>SDHA</i>	F	GGACAGAGCCTCAAGTTTGG	116
	R	GTATCATATCGTAGAGACCTTCATA	