

Additional Table 1. Primer sequences used for quantitative real-time polymerase chain reaction in the present study

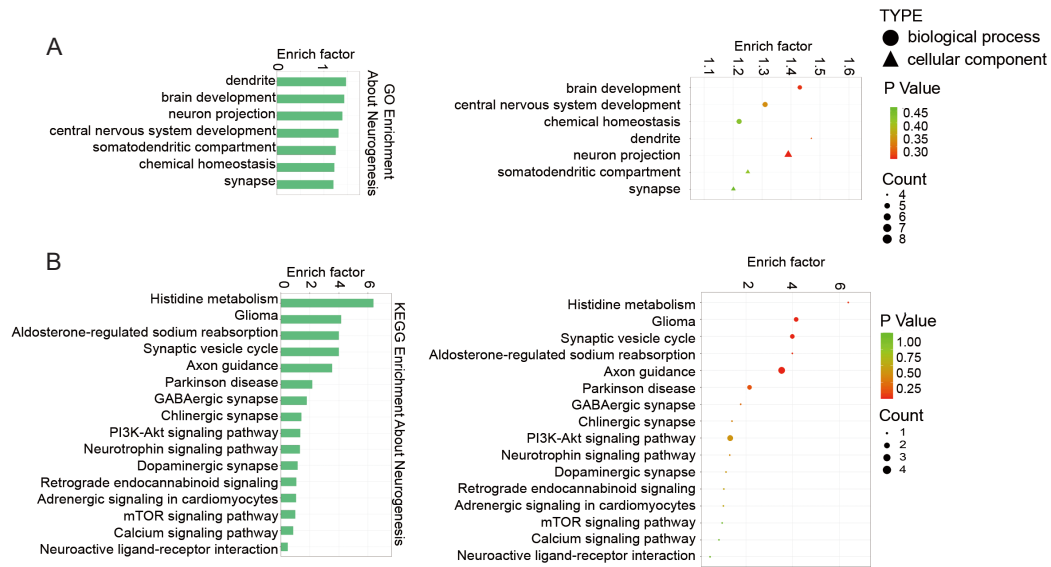
Gene	Sequence (5'-3')
Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit delta	Forward: TCC CCT TCA TTC TCA CCT ACG Reverse: CGG AAC CTT TCA AAC TTC TCA CT
Cathelicidin antimicrobial peptide	Forward: ACC AGC AGT CCC TAG ACA CCA Reverse: CTC CTT CAC TCG GAA CCT CAC
C-X-C motif chemokine receptor 4	Forward: ACC TCT ACA GCA GCG TTC TCA T Reverse: TGG TGG CGT GGA CAA TAG C
MYB proto-oncogene, transcription factor	Forward: CCT ATC CTG TCG CAT TGC AT Reverse: TTC TCA GGG TCT TCG TCG TTA T

Additional Table 2. Representative differentially expressed genes with known or suspected roles in inflammation

Gene symbol	Description	P-value	Fold change	Up/down-regulation
<i>BCL11A</i>	B cell CLL/lymphoma 11A	0.0243	4.1625	Up
<i>BTK</i>	Bruton agammaglobulinemia tyrosine kinase	0.0285	4.3301	Up
<i>CAMP</i>	Cathelicidin antimicrobial peptide	0.0413	7.9126	Up
<i>CD19</i>	CD19 antigen	0.0014	3.5259	Up
<i>CD22</i>	CD22 antigen	0.0385	2.9035	Up
<i>CD37</i>	CD37 antigen	0.022	3.8764	Up
<i>CD79A</i>	CD79A antigen (immunoglobulin-associated alpha)	0.0044	2.7651	Up
<i>CD79B</i>	CD79B antigen	0.0218	4.5229	Up
<i>CXCR4</i>	Chemokine (C-X-C motif) receptor 4	0.0082	3.5457	Up
<i>DOCK8</i>	Adult male thymus cDNA	0.0393	2.5315	Up
<i>E2F2</i>	E2F transcription factor 2	0.0421	4.3995	Up
<i>ELANE</i>	Elastase	0.0465	14.2298	Up
<i>FFAR2</i>	Free fatty acid receptor 2	0.0254	5.8122	Up
<i>IGHM</i>	Immunoglobulin heavy chain 6	0.0175	4.3101	Up
<i>IKZF3</i>	IKAROS family zinc finger 3	0.0015	5.3701	Up
<i>IRF4</i>	Interferon regulatory factor 4	0.0448	4.1317	Up
<i>IRF8</i>	Interferon regulatory factor 8	0.046	2.9861	Up
<i>KLRA7</i>	Killer cell lectin-like receptor, subfamily A, member 7	0.0346	4.8636	Up
<i>LY6D</i>	Lymphocyte antigen 6 complex, locus D	0.0117	4.7527	Up
<i>MPO</i>	Myeloperoxidase	0.0449	11.1979	Up
<i>MS4A1</i>	Membrane-spanning 4-domains, subfamily A, member 1	0.0128	5.4576	Up
<i>MYB</i>	Myeloblastosis oncogene	0.0263	3.804	Up
<i>MZB1</i>	Marginal zone B and B1 cell-specific protein 1	0.0362	3.9208	Up
<i>NCKAP1L</i>	NCK associated protein 1 like	0.0469	2.1408	Up
<i>PIK3CD</i>	Phosphatidylinositol 3-kinase catalytic delta polypeptide	0.0398	2.1535	Up
<i>RASGRP1</i>	RAS guanyl releasing protein 1	0.0309	2.2987	Up
<i>RHOH</i>	Ras homolog gene family, member H	0.0358	3.1159	Up
<i>SIGLECG</i>	Sialic acid binding Ig-like lectin G	0.0162	3.7754	Up
<i>SPIB</i>	Spi-B transcription factor (Spi-1/PU.1 related)	0.0273	5.4265	Up
<i>STAP1</i>	Signal transducing adaptor family member 1	0.0499	6.0973	Up
<i>TNFRSF13B</i>	Tumor necrosis factor receptor superfamily, member 13b	0.0486	3.1712	Up
<i>TNFRSF13C</i>	Tumor necrosis factor receptor superfamily, member 13c	0.0087	4.5224	Up
<i>TNFRSF17</i>	Tumor necrosis factor receptor superfamily, member 17	0.016	2.4257	Up
<i>TRIM12C</i>	Tripartite motif-containing 12C	0.0265	2.3185	Up
<i>VPREB3</i>	Pre-B lymphocyte gene 3	0.0445	4.3671	Up
<i>WDFY4</i>	WD repeat and FYVE domain containing 4	0.0484	3.2119	Up

Additional Table 3. Representative differentially expressed genes with known or suspected roles in angiogenesis

Gene symbol	Description	P-value	Fold change	Up/down-regulation
<i>BTK</i>	Bruton agammaglobulinemia tyrosine kinase	0.0285	4.3301	Up
<i>CFL1</i>	Cofilin 1	0.0477	2.1187	Up
<i>CXCR4</i>	Chemokine (C-X-C motif) receptor 4	0.0082	3.5457	Up
<i>FFAR2</i>	Free fatty acid receptor 2	0.0254	5.8122	Up
<i>H2AFX</i>	H2A histone family, member X	0.0499	2.5043	Up
<i>LY6D</i>	Lymphocyte antigen 6 complex, locus D	0.0117	4.7527	Up
<i>MYB</i>	Myeloblastosis oncogene	0.0263	3.804	Up
<i>PIK3CD</i>	Phosphatidylinositol 3-kinase catalytic delta polypeptide	0.0398	2.1535	Up
<i>RASGRP1</i>	RAS guanyl releasing protein 1	0.0309	2.2987	Up
<i>CD19</i>	CD19 antigen	0.0014	3.5259	Up
<i>RTKN2</i>	Rhotekin 2	0.0365	3.8247	Up
<i>IKZF3</i>	IKAROS family zinc finger 3	0.0015	5.3701	Up
<i>IRF4</i>	Interferon regulatory factor 4	0.0448	4.1317	Up
<i>UBD</i>	Ubiquitin D	0.0288	4.791	Up
<i>CAMP</i>	Cathelicidin antimicrobial peptide	0.0413	7.9126	Up
<i>ISG20</i>	Interferon-stimulated protein	0.0307	3.1225	Up
<i>MPO</i>	Myeloperoxidase	0.0449	11.1979	Up
<i>SPIB</i>	Spi-B transcription factor	0.0273	5.4265	Up



Additional Figure 1. Functional enrichment analyses of DEGs associated with neurogenesis. (A) GO term categorisation. (B) KEGG pathway mapping. DEG: differentially expressed gene; GO: Gene Ontology; KEGG: Kyoto Encyclopedia of Genes and Genomes.