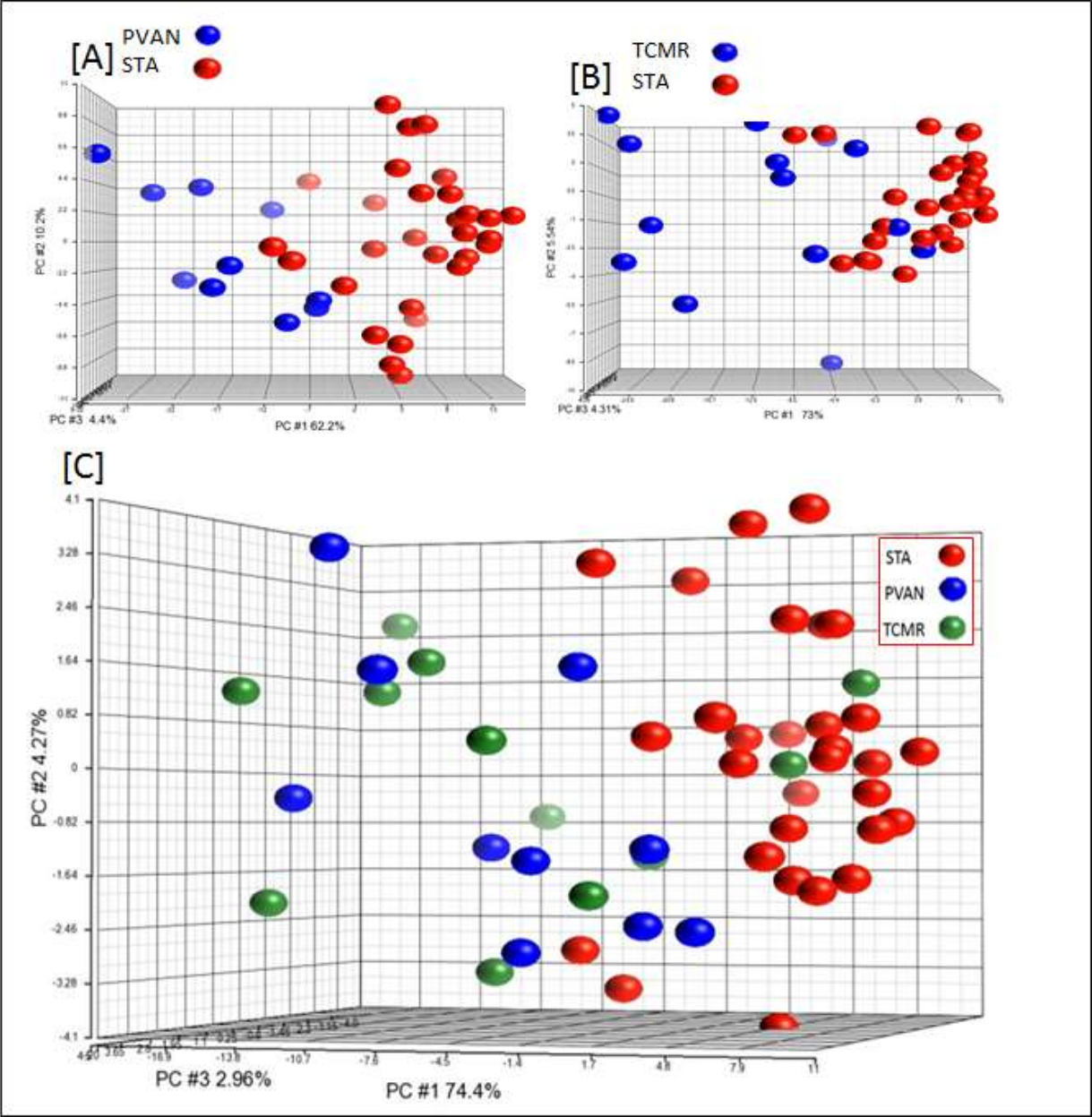


**Figure S1, SDC.** [LEGEND] Principle component analysis (PCA) demonstrates overall similarity in between PVAN and TCMR gene expression. Using Principle Component Analysis (PCA) and taking into account the 150 top ranked genes based on a FDR adjusted p-value ( $p < 0.05$  and 2-fold increase expression), a significant clustering [A] PVAN, [B] TCMR and [C] PVAN and TCMR samples was observed when compared to normal (STA) samples.



**Table S1, SDC. A list of PVAN specific genes\***

<b>Gene Symbol</b>	<b>Gene name</b>	<b>Fold Increase</b>	<b>Adjusted P-value</b>
ADA	adenosine deaminase	2.2	1.58E-03
AGR2	anterior gradient homolog 2 ( <i>Xenopus laevis</i> )	2.1	1.46E-03
AGRN	agrin	2.1	6.69E-05
AIF1	allograft inflammatory factor 1	2.7	1.26E-04
ALS2CR8	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 8 [Source:HGNC Symbol;Acc:14435]	2.2	3.06E-05
AMACR	alpha-methylacyl-CoA racemase	2.1	7.40E-03
ANKRD19	ankyrin repeat domain 19	2.1	4.60E-04
AP2S1	adaptor-related protein complex 2, sigma 1 subunit	2.0	1.38E-03
APOBEC3G	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G	2.5	6.32E-04
APOC1	apolipoprotein C-I	4.1	3.55E-04
ARHGAP15	Rho GTPase activating protein 15	2.1	1.66E-03
ASL	argininosuccinate lyase	2.3	6.78E-03
ATN1	atrophin 1	2.1	4.54E-04
AURKAIP1	aurora kinase A interacting protein 1	2.1	4.14E-04
AVIL	advillin	2.4	6.06E-05
BCL2A1	BCL2-related protein A1	3.2	1.07E-04
BIN2	bridging integrator 2	2.0	1.17E-03
BIRC3	baculoviral IAP repeat-containing 3	2.2	5.13E-04
BST2	bone marrow stromal cell antigen 2	2.6	5.25E-05
BTN3A2	butyrophilin, subfamily 3, member A2	2.5	4.11E-04
C11orf2	chromosome 11 open reading frame2	2.0	7.00E-03
C11orf83	chromosome 11 open reading frame 83	2.2	8.00E-03
C1orf162	chromosome 1 open reading frame 162	2.7	3.93E-04
C1QA	complement component 1, q subcomponent, A chain	3.1	2.94E-05
C1QB	complement component 1, q subcomponent, B chain	4.4	4.86E-06
C1QC	complement component 1, q subcomponent, C chain	2.9	3.45E-05
C1S	complement component 1, s subcomponent	2.2	1.80E-03
C2	complement component 2	2.1	5.98E-04
C3	complement component 3	4.0	2.80E-04
C3AR1	complement component 3a receptor 1	2.0	2.62E-04
C4orf48	chromosome 4 open reading frame 48	2.4	1.07E-03
C9orf16	chromosome 9 open reading frame 16	2.1	2.13E-03
CARD16	caspase recruitment domain family, member 16	2.2	4.09E-05
CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	2.6	7.43E-05
CCDC109B	coiled-coil domain containing 109B	2.0	2.17E-03

CCDC93	coiled-coil domain containing 93	2.1	2.52E-05
CCL18	chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)	2.0	5.04E-03
CCL19	chemokine (C-C motif) ligand 19	4.7	2.18E-04
CCL2	chemokine (C-C motif) ligand 2	2.2	6.95E-03
CCL3	chemokine (C-C motif) ligand 3	2.7	1.03E-03
CCL5	chemokine (C-C motif) ligand 5	2.7	7.24E-05
CD14	CD14 molecule	2.0	7.37E-04
CD163	CD163 molecule	2.6	3.63E-04
CD2	CD2 molecule	2.2	6.20E-04
CD3D	CD3d molecule, delta (CD3-TCR complex)	3.3	2.89E-04
CD48	CD48 molecule	2.7	3.13E-04
CD52	CD52 molecule	6.0	6.69E-05
CD53	CD53 molecule	3.0	2.50E-04
CD69	CD69 molecule	2.3	1.98E-03
CDH6	Cadherin 6, type 2, K-cadherin (fetal kidney)	2.0	6.75E-04
CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	2.1	2.84E-03
<b>CFD</b>	<b>complement factor D (adipsin)</b>	<b>3.0</b>	<b>2.85E-03</b>
CHEK2	CHK2 checkpoint homolog (S. pombe)	2.0	1.58E-04
CHIC1	cysteine-rich hydrophobic domain 1	3.3	1.66E-06
CKS2	CDC28 protein kinase regulatory subunit 2	2.3	2.49E-04
CLEC2B	C-type lectin domain family 2, member B	2.7	2.03E-04
CNN1	calponin 1, basic, smooth muscle	2.2	7.42E-03
CORO1A	coronin, actin binding protein, 1A	2.5	4.73E-05
CSPG5	chondroitin sulfate proteoglycan 5 (neuroglycan C)	2.4	5.02E-06
CST7	cystatin F (leukocystatin)	2.1	4.75E-04
CSTA	cystatin A (stefin A)	3.8	2.94E-05
CTSS	cathepsin S	2.5	7.36E-04
CXCL10	chemokine (C-X-C motif) ligand 10	6.7	6.36E-06
CXCL13	chemokine (C-X-C motif) ligand 13	4.9	2.74E-05
CXCL6	chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)	2.2	7.39E-03
CXCL9	chemokine (C-X-C motif) ligand 9	6.2	3.60E-05
CYTIP	cytohesin 1 interacting protein	2.0	3.89E-04
DPP3	dipeptidyl-peptidase 3	3.0	6.34E-06
EDF1	endothelial differentiation-related factor 1	2.1	1.03E-03
EEF1D	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	2.0	8.74E-04
EIF3G	eukaryotic translation initiation factor 3, subunit G	2.2	2.49E-04
EVI2A	ecotropic viral integration site 2A	2.7	5.11E-04
F13A1	coagulation factor XIII, A1 polypeptide	2.2	4.52E-03
FAM101B	family with sequence similarity 101, member B	2.1	4.82E-05

FAM105B	family with sequence similarity 105, member B	3.4	3.98E-05
FAM26F	family with sequence similarity 26, member F	3.6	1.10E-04
FBXL15	F-box and leucine-rich repeat protein 15	2.0	2.63E-03
FCER1G	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide	2.6	4.98E-04
FCGR1A	Fc fragment of IgG, high affinity Ia, receptor (CD64)	2.4	2.94E-05
FCGR1B	Fc fragment of IgG, high affinity Ib, receptor (CD64)	2.5	1.27E-05
FGFR1	fibroblast growth factor receptor 1	3.5	8.76E-06
FKBP11	FK506 binding protein 11, 19 kDa	2.0	8.91E-04
GABBR1	Gamma-aminobutyric acid (GABA) B receptor, 1	4.3	2.52E-05
GBP1	guanylate binding protein 1, interferon-inducible, 67kDa	2.5	5.19E-06
GBP2	guanylate binding protein 2, interferon-inducible	3.2	5.02E-06
GBP5	guanylate binding protein 5	2.9	3.20E-05
GMFG	glia maturation factor, gamma	2.1	1.36E-03
GPR183	G protein-coupled receptor 183	2.1	1.18E-04
GPX4	glutathione peroxidase 4 (phospholipid hydroperoxidase)	2.3	4.83E-05
GYPC	glycophorin C (Gerbich blood group)	2.1	1.95E-04
GZMA	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)	3.1	1.26E-04
GZMB	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	2.4	1.66E-03
GZMK	granzyme K (granzyme 3; tryptase II)	3.3	1.75E-04
HBA2	hemoglobin, alpha 2	2.4	1.10E-03
HCLS1	hematopoietic cell-specific Lyn substrate 1	2.2	5.91E-03
HCP5	HLA complex P5	2.5	2.52E-05
HCST	hematopoietic cell signal transducer	2.3	7.23E-06
HOPX	HOP homeobox	2.9	4.41E-04
HPR	haptoglobin-related protein	2.1	5.25E-05
HSPD1	Heat shock 60kDa protein 1 (chaperonin)	2.3	2.05E-05
HTR6	5-hydroxytryptamine (serotonin) receptor 6	2.0	2.43E-05
ICAM2	intercellular adhesion molecule 2	2.0	5.03E-03
IDO1	indoleamine 2,3-dioxygenase 1	2.6	2.01E-05
IFI27	interferon, alpha-inducible protein 27	2.1	2.62E-03
<b>IFITM1</b>	<b>interferon induced transmembrane protein 1 (9-27)</b>	<b>2.5</b>	<b>1.17E-03</b>
IGHM	immunoglobulin heavy constant mu	5.7	3.30E-04
IGKJ5	immunoglobulin kappa joining 5 [Source:HGNC Symbol;Acc:5723]	3.1	6.90E-03
IGL@	Immunoglobulin lambda locus	3.3	7.79E-03
IL32	interleukin 32	2.5	5.35E-04
IL7R	interleukin 7 receptor	2.7	2.75E-04
IRF1	interferon regulatory factor 1	2.0	9.36E-04
ISG20	interferon stimulated exonuclease gene 20kDa	2.7	8.76E-06

ITGAL	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide)	2.0	5.82E-03
ITGB2	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	3.0	4.76E-04
KLC4	kinesin light chain 4	2.2	3.20E-05
KLRB1	killer cell lectin-like receptor subfamily B, member 1	2.0	4.50E-03
LAPTM5	lysosomal multispinning membrane protein 5	2.9	1.38E-04
LARP4	La ribonucleoprotein domain family, member 4	2.3	2.05E-05
LCP1	lymphocyte cytosolic protein 1 (L-plastin)	2.4	4.65E-03
LENEP	lens epithelial protein	2.5	2.94E-05
LMOD1	leiomodulin 1 (smooth muscle)	2.3	2.05E-05
LOC348262	hypothetical protein LOC348262	2.0	2.38E-03
LOC643187	hypothetical LOC643187	2.1	1.11E-04
LOC91316	Glucuronidase, beta/ immunoglobulin lambda-like polypeptide 1 pseudogene	2.2	7.73E-03
LSM7	LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae)	2.0	1.13E-04
LSP1	lymphocyte-specific protein 1	2.0	1.37E-03
LST1	leukocyte specific transcript 1	2.4	9.78E-04
LTB	lymphotoxin beta (TNF superfamily, member 3)	2.7	4.01E-05
<b>LTF</b>	<b>lactotransferrin</b>	<b>4.7</b>	<b>5.69E-04</b>
LYG1	lysozyme G-like 1	2.2	5.97E-03
MIR142	microRNA 142 [Source:HGNC Symbol;Acc:31529]	3.2	5.10E-04
MIRHG2	microRNA host gene 2 (non-protein coding)	2.2	2.22E-03
MMP7	matrix metalloproteinase 7 (matrilysin, uterine)	2.8	1.24E-03
MRPL54	mitochondrial ribosomal protein L54	2.2	4.68E-04
MRPL55	Mitochondrial ribosomal protein L55	2.1	2.13E-03
MS4A4A	membrane-spanning 4-domains, subfamily A, member 4	3.3	5.56E-05
MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	2.3	2.41E-03
N4BP1	NEDD4 binding protein 1	2.0	1.56E-03
NCAPH2	non-SMC condensin II complex, subunit H2	2.1	4.25E-04
NCKAP1L	NCK-associated protein 1-like	2.1	2.26E-04
NDUFA11	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 11, 14.7kDa	2.2	2.52E-03
NDUFA3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3, 9kDa	2.1	1.02E-03
NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase)	2.2	2.39E-03
NKAIN4	Na <sup>+</sup> /K <sup>+</sup> transporting ATPase interacting 4	3.8	4.83E-05
NKG7	natural killer cell group 7 sequence	2.9	5.84E-05
NLRC5	NLR family, CARD domain containing 5	2.5	5.47E-04
NNMT	Nicotinamide N-methyltransferase	4.3	5.84E-05
<b>NOSIP</b>	<b>nitric oxide synthase interacting protein</b>	<b>2.7</b>	<b>8.45E-04</b>

PHPT1	phosphohistidine phosphatase 1	2.1	1.33E-04
PLAC8	placenta-specific 8	2.6	5.04E-04
PLTP	phospholipid transfer protein	2.3	3.83E-03
POLR2I	polymerase (RNA) II (DNA directed) polypeptide I, 14.5kDa	2.1	5.56E-04
PRF1	perforin 1 (pore forming protein)	2.0	7.19E-03
PSMB10	proteasome (prosome, macropain) subunit, beta type, 10	2.5	4.06E-06
PSMB8	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7)	2.3	2.01E-05
PSMB9	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional peptidase 2)	4.1	1.75E-05
PTGDS	prostaglandin D2 synthase 21kDa (brain)	2.3	8.82E-03
PTPRC	protein tyrosine phosphatase, receptor type, C	2.8	3.07E-04
PTPRCAP	protein tyrosine phosphatase, receptor type, C-associated protein	2.8	1.12E-03
PTTG1	pituitary tumor-transforming 1	2.2	3.12E-04
RAC2	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)	2.9	1.37E-03
RARRES1	retinoic acid receptor responder (tazarotene induced) 1	2.0	3.01E-03
RARRES3	retinoic acid receptor responder (tazarotene induced) 3	3.3	6.63E-05
RASSF5	Ras association (RalGDS/AF-6) domain family member 5	2.1	1.41E-03
RBMS3	RNA binding motif, single stranded interacting protein	2.3	1.78E-03
REG1A	regenerating islet-derived 1 alpha	2.4	4.83E-05
RGS2	regulator of G-protein signaling 2, 24kDa	2.3	2.30E-03
RNASEH2C	ribonuclease H2, subunit C	2.0	4.52E-03
<b>RPS15</b>	<b>ribosomal protein S15</b>	<b>2.8</b>	<b>7.84E-04</b>
S100A1	S100 calcium binding protein A1	3.1	3.06E-04
S100A8	S100 calcium binding protein A8	2.3	6.23E-04
SAA1	serum amyloid A1	3.1	4.06E-06
SAMD10	sterile alpha motif domain containing 10	2.3	6.69E-05
SCO2	SCO cytochrome oxidase deficient homolog 2 (yeast)	2.1	2.26E-04
SEC61A1	Sec61 alpha 1 subunit ( <i>S. cerevisiae</i> )	2.3	8.25E-06
SF3B5	splicing factor 3b, subunit 5, 10kDa	2.1	4.81E-04
SLA	Src-like-adaptor	2.2	3.76E-04
SLAMF7	SLAM family member 7	3.0	5.14E-04
SLAMF8	SLAM family member 8	2.6	9.94E-05
SLC1A3	solute carrier family 1 (glial high affinity glutamate transporter), member 3	2.1	8.39E-04
SNRPB	small nuclear ribonucleoprotein polypeptides B and B1	2.0	3.87E-03
SOD2	superoxide dismutase 2, mitochondrial	2.4	8.75E-05
SPA17	sperm autoantigenic protein 17	2.1	2.01E-05
STAB1	stabilin 1	2.0	2.14E-03
STAT1	signal transducer and activator of transcription 1, 91kDa	3.2	7.18E-06

STK17A	serine/threonine kinase 17a	2.6	5.02E-06
TAF10	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 30kDa	2.1	1.56E-03
TAP1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	2.9	6.63E-05
TIMM13	translocase of inner mitochondrial membrane 13 homolog (yeast)	2.4	3.93E-04
TIMP1	TIMP metalloproteinase inhibitor 1	2.8	9.63E-05
TKT	transketolase	2.0	6.72E-04
TMC8	transmembrane channel-like 8	2.4	5.80E-03
TMEM54	transmembrane protein 54	2.4	5.09E-04
TNFRSF25	tumor necrosis factor receptor superfamily, member 25	2.6	4.06E-06
TNFSF13B	tumor necrosis factor (ligand) superfamily, member 13b	2.6	5.02E-06
TNMD	tenomodulin	2.3	5.84E-05
TRA@	T cell receptor alpha locus	2.6	2.49E-04
TRAF3IP3	TRAF3 interacting protein 3	2.1	7.77E-04
TRAPPC5	trafficking protein particle complex 5	2.3	4.75E-03
TRBC1	T cell receptor beta constant 1	3.2	7.77E-04
TRMT61A	tRNA methyltransferase 61 homolog A ( <i>S. cerevisiae</i> )	2.1	8.76E-06
TYROBP	TYRO protein tyrosine kinase binding protein	4.2	1.99E-05
UBE2D4	ubiquitin-conjugating enzyme E2D 4 (putative)	2.8	4.06E-06
UBE2L6	ubiquitin-conjugating enzyme E2L 6	2.2	5.40E-05
WARS	tryptophanyl-tRNA synthetase	2.2	2.29E-03
WFDC2	WAP four-disulfide core domain 2	2.0	8.06E-03
WNK2	WNK lysine deficient protein kinase 2	2.0	1.39E-03
XCL1	chemokine (C motif) ligand 1	2.8	9.63E-05
ZNF511	zinc finger protein 511	2.1	2.02E-04

\*Genes validated with QPCR and IHC are listed with bold font.