

# Supplementary Materials:

**Table S1** Frequency and combination of medications used in eyes included in RNA sequencing. PGA: prostaglandin analogues. BB: beta-blockers. CAIs: carbonic anhydrase inhibitors. AA: alpha agonists.

PGA-BB-CAI-AA	Frequency	Percentage
1-1-0-0	9	27.3
0-1-1-0	5	15.2
1-1-1-0	5	15.2
0-0-0-1	3	9.1
0-1-0-1	3	9.1
0-1-0-0	2	6.1
0-1-1-1	2	6.1
1-1-1-1	2	6.1
1-0-0-0	1	3.0
1-1-0-1	1	3.0
<b>Total</b>	<b>33</b>	<b>100.0</b>

**Table S2.** List of 60 genes altered in the conjunctiva of treated patients compared to healthy conjunctiva by RNA sequencing.

ID gene	Gene Name	log Fold Change	p Value	GO Molecular Function	GO Biological Process
ENSG00000106278.11	<i>PTPRZ1</i>	1.893	0.002	Transmembrane receptor protein tyrosine phosphatase activity	Regulation of oligodendrocyte progenitor proliferation
ENSG00000114013.15	<i>CD86</i>	1.770	0.001	Signaling receptor binding and coreceptor activity	Immune system
ENSG00000112799.8	<i>LY86</i>	1.548	0.001	Sensor component	Immune system
ENSG00000095970.16	<i>TREM2</i>	1.523	0.003	Scaffold protein binding	Amyloid-beta clearance and immune system
ENSG00000175857.8	<i>GAPT</i>	1.484	0.005	Scaffold protein binding	Immune system
ENSG00000140678.16	<i>ITGAX</i>	1.471	0.009	Signaling receptor activity	Cell adhesion and immune system
ENSG00000043591.5	<i>ADRB1</i>	1.446	0.004	Nucleotide binding regulatory protein-coupled receptor	Adrenergic receptor signaling pathway and response to cold, fear.
ENSG00000010671.15	<i>BTB</i>	1.415	0.002	Non-membrane spanning protein tyrosine kinase activity	Immune system
ENSG00000136869.14	<i>TLR4</i>	1.409	0.000	Amyloid-beta binding and LPS sensor activity	Immune system

ENSG00000186818.12	LILRB4	1.336	0.001	Antigen binding and signaling receptor activity	Immune system
ENSG00000169896.17	ITGAM	1.326	0.005	Cargo receptor activity	Cell adhesion and immune system
ENSG00000011600.11	TYROBP	1.311	0.000	Signaling receptor binding	Actin cytoskeleton organization and immune system
ENSG00000158869.10	FCER1G	1.196	0.010	IgE receptor activity	Immune system and mast cell activation
ENSG00000000938.12	FGR	1.195	0.006	Fc-γ receptor I complex binding	Immune system
ENSG00000101336.13	HCK	1.187	0.004	Tyrosine kinase activity and signaling receptor binding	Cell adhesion and immune system
ENSG00000104903.4	LYL1	1.175	0.000	Transcription factor activity	B cell differentiation and blood vessel maturation
ENSG00000157017.15	GHRL	1.170	0.001	Hormone activity	Adult feeding behavior
ENSG00000153071.14	DAB2	1.167	0.008	GTPase activator activity	Cellular response to LPS, TNF and cellular response to unfolded protein
ENSG00000175899.14	A2M	1.166	0.007	Endopeptidase inhibitor activity	Extracellular matrix disassembly
ENSG00000213203.2	GIMAP1	1.163	0.000	GTP binding activity	UK
ENSG00000038945.14	MSR1	1.159	0.008	Cargo receptor activity	Phagocytosis, engulfment
ENSG00000134516.16	DOCK2	1.139	0.002	T-cell receptor binding	Actin remodelling and phagocytosis
ENSG00000137491.14	SLCO2B1	1.134	0.006	Organic anion transmembrane transporter activity	Solute transport membranes
ENSG00000203747.10	FCGR3A	1.092	0.007	IgG binding	Immune system
ENSG00000100097.11	LGALS1	1.091	0.000	Carbohydrate binding	Apoptotic process and cellular response to glucose stimulus
ENSG00000204482.10	LST1	1.086	0.002	Leukocyte specific transcript 1	Cell morphogenesis and immune system
ENSG00000155926.13	SLA	0.968	0.003	Signaling receptor binding	Cell differentiation and regulation of cell population proliferation
ENSG00000079215.13	SLC1A3	0.955	0.003	Glutamate binding	Response to light stimulus and response to wounding
ENSG00000136286.15	MYO1G	0.954	0.004	Actin and calmodulin binding	Cell gliding and cell-substrate adhesion
ENSG00000250312.7	ZNF718	0.896	0.009	DNA binding and metal ion binding	Regulation of transcription and DNA-templated
ENSG00000264230.8	ANXA8L1	-1.153	0.009	Calcium-dependent phospholipid binding	Endosome organization
ENSG00000156414.18	TDRD9	-1.159	0.003	RNA helicase activity	Cell differentiation and gene silencing
ENSG00000135318.11	NT5E	-1.162	0.008	Nucleotide binding	Leukocyte cell-cell adhesion and negative regulation of inflammatory response
ENSG00000181449.3	SOX2	-1.226	0.004	Transcription activator activity	Cell differentiation and cell fate commitment
ENSG00000164627.17	KIF6	-1.266	0.002	Microtubule binding	Microtubule-based movement
ENSG00000132429.9	POPDC3	-1.272	0.004	cAMP binding	Tissue development and differentiation
ENSG00000128578.9	STRIP2	-1.289	0.000	Striatin interacting protein	Cell migration and cytoskeleton organization
ENSG00000118971.7	CCND2	-1.302	0.010	Cyclin-dependent protein serine/threonine kinase	Cell division

ENSG00000141314.12	<i>RHBDL3</i>	-1.344	0.001	Calcium ion binding and endopeptidase activity	UK
ENSG00000110975.8	<i>SYT10</i>	-1.373	0.009	Clathrin binding	Exocytosis
ENSG00000164949.7	<i>GEM</i>	-1.446	0.006	GTPase activity and calcium channel regulator activity	Immune system and mitotic cell cycle
ENSG00000203710.11	<i>CR1</i>	-1.452	0.001	Complement component	Complement activation
ENSG00000119508.17	<i>NR4A3</i>	-1.467	0.004	Steroid hormone receptor activity	Cellular response to catecholamine and corticotropin-releasing hormone stimulus
ENSG00000135046.13	<i>ANXA1</i>	-1.469	0.004	Cadherin binding and single-stranded RNA binding	Immune system and inflammatory response
ENSG00000142149.8	<i>HUNK</i>	-1.469	0.002	Protein serine/threonine kinase activity	Signal transduction
ENSG00000128422.16	<i>KRT17</i>	-1.469	0.006	Structural constituent of cytoskeleton and MHC class II protein binding	Cornification and epidermis development
ENSG00000137440.4	<i>FGFBP1</i>	-1.480	0.004	Fibroblast growth factor binding	Regulation of fibroblast growth factor receptor signaling pathway
ENSG00000164687.10	<i>FABP5</i>	-1.494	0.001	Lipid binding and retinoic acid binding	Epidermis development
ENSG00000135919.12	<i>SERPINE2</i>	-1.504	0.006	Signaling receptor binding	Secretion by cell and sensory perception
ENSG00000182950.2	<i>ODF3L1</i>	-1.547	0.001	UK	UK
ENSG00000153234.13	<i>NR4A2</i>	-1.570	0.000	Steroid hormone receptor activity	Cellular response to catecholamine and corticotropin-releasing hormone stimulus
ENSG00000160223.17	<i>ICOSLG</i>	-1.604	0.002	Signaling receptor binding	Immune system
ENSG00000112276.13	<i>BVES</i>	-1.711	0.001	Structural molecule activity	Epithelial cell-cell adhesion
ENSG00000163735.6	<i>CXCL5</i>	-1.733	0.004	Chemokine activity	Immune system
ENSG00000100234.11	<i>TIMP3</i>	-1.871	0.001	Metalloendopeptidase inhibitor activity	Cellular response to organic substance and negative regulation of metalloendopeptidase activity
ENSG00000123243.14	<i>ITIH5</i>	-1.903	0.001	Endopeptidase inhibitor activity	Collagen-containing extracellular matrix
ENSG00000183833.16	<i>MAATS1</i>	-2.061	0.001	Cilium movement	UK
Ensg00000275993.2	<i>Sik1b</i>	-2.070	0.000	Serine/threonine kinase activity	Intracellular signal transduction and protein phosphorylation
Ensg00000136244.11	<i>Il6</i>	-2.103	0.003	Cytokine binding	Immune system
Ensg00000183092.16	<i>Begain</i>	-2.204	0.000	Kinase activity	Neuropathic pain and interaction at synapses

**Table S3.** List of 60 genes most significantly altered in the conjunctiva of dry eye patients compared to healthy conjunctiva by RNA sequencing.

ID gene	Gene Name	log Fold Change	p Value	GO Molecular Function	GO Biological Process
ENSG00000090104.11	<i>RGS1</i>	2.779	0.001	GTPase activator activity and calmodulin binding	G protein-coupled receptor signaling pathway and immune response
ENSG00000147604.13	<i>RPL7</i>	2.355	0.001	Nucleic acid binding and protein homodimerization activity	RNA catabolic process, nonsense-mediated decay
ENSG00000144199.11	<i>FAHD2B</i>	2.259	0.000	Hydrolase activity mitochondria	ROS formation in respiratory chains
ENSG00000186847.5	<i>KRT14</i>	2.174	0.007	Structural constituent of cytoskeleton	Aging and cornification
ENSG00000169413.2	<i>RNASE6</i>	2.155	0.002	Nucleic acid binding and ribonuclease activity	Innate immune response and RNA catabolic process
ENSG00000123560.13	<i>PLP1</i>	2.125	0.005	Major myelin protein	Astrocyte development and inflammatory response
ENSG00000197410.13	<i>DCHS2</i>	2.052	0.002	Calcium ion binding	Homophilic cell adhesion via plasma membrane adhesion molecules
ENSG00000198712.1	<i>MT-CO2</i>	1.993	0.006	Copper ion binding and cytochrome-c oxidase activity	Mitochondrial electron transport
ENSG00000198189.10	<i>HSD17B11</i>	1.962	0.001	Steroid dehydrogenase activity	Androgen catabolic process and estrogen biosynthetic process
ENSG00000198727.2	<i>MT-CYB</i>	1.848	0.007	Metal ion binding and cytochrome-c oxidase activity	Mitochondrial electron transport and response to stress and ion
ENSG00000087076.8	<i>HSD17B14</i>	1.831	0.009	Steroid dehydrogenase activity	Androgen catabolic process and estrogen biosynthetic process
ENSG00000136160.15	<i>EDNRB</i>	1.786	0.009	Endothelin receptor activity	Aging, proliferation and pain reception
ENSG00000150594.6	<i>ADRA2A</i>	1.753	0.005	Adrenergic receptor activity	Proliferation and wound healing
ENSG00000158869.10	<i>FCER1G</i>	1.698	0.001	IgE receptor activity	Immune system and mast cell activation
ENSG00000269028.3	<i>MTRNR2L12</i>	1.667	0.002	Receptor antagonist activity	Negative regulation of execution phase of apoptosis
ENSG00000113140.10	<i>SPARC</i>	1.551	0.009	Extracellular matrix binding	Proliferation, migration, and cell differentiation
ENSG00000131153.8	<i>GIN52</i>	1.529	0.000	DNA duplex unwinding	DNA replication
ENSG00000091136.13	<i>LAMB1</i>	1.527	0.004	Extracellular matrix structural constituent and integrin binding	Cell adhesion and proliferation
ENSG00000165568.17	<i>AKR1E2</i>	1.505	0.006	Oxidoreductase activity	Oxidation-reduction process
ENSG00000089685.14	<i>BIRC5</i>	1.499	0.005	Chaperone binding	Cell proliferation and preventing apoptosis
ENSG00000276600.4	<i>RAB7B</i>	1.496	0.004	GTPase activity	inflammation and vesicle trafficking
ENSG00000115041.12	<i>KCNIP3</i>	1.491	0.003	Calcium ion binding	Intracellular protein transport and apoptosis
ENSG00000124664.10	<i>SPDEF</i>	1.464	0.008	DNA-binding transcription factor activity	Goblet cells differentiation
ENSG00000011028.13	<i>MRC2</i>	1.436	0.004	Collagen binding and transmembrane signaling receptor activity	Collagen catabolic process and endocytosis
ENSG00000176153.11	<i>GPX2</i>	1.430	0.003	Electron transfer activity	Cellular response to oxidative stress
ENSG00000136522.13	<i>MRPL47</i>	1.428	0.001	Structural constituent of ribosome	Mitochondrial translation
ENSG00000150201.14	<i>FXYD4</i>	1.395	0.004	ATPase binding	Ion channel regulator activity
ENSG00000163453.11	<i>IGFBP7</i>	1.360	0.005	Insulin-like growth factor binding	Cell adhesion and response to retinoic acid

ENSG00000198677.11	TTC37	1.320	0.006	Catabolism of deadenylated mRNA	RNA catabolic process
ENSG00000135547.8	HEY2	1.305	0.003	DNA-binding transcription factor activity	Embryonic development
ENSG00000107201.9	DDX58	-0.748	0.008	Double-stranded RNA binding and RNA helicase	Innate immune response
ENSG00000137492.7	THAP12	-0.758	0.000	Transcription factor activity	Negative regulation of cell population proliferation
ENSG00000155090.14	KLF10	-0.760	0.004	Transcription factor activity	Negative regulation of cell population proliferation
ENSG00000135049.15	AGTPBP1	-0.775	0.006	Metalloprotease activity and tulin binding	Eye photoreceptor cell differentiation and mitochondrion organization
ENSG00000135317.12	SNX14	-0.781	0.006	Phosphatidylinositol-3,5-bisphosphate binding	Autophagosome maturation
ENSG00000152601.17	MBNL1	-0.786	0.001	Double-stranded RNA binding	Myoblast differentiation and nervous system development
ENSG00000154114.12	TBCEL	-0.788	0.008	Alpha-tubulin binding	Microtubule cytoskeleton organization
ENSG00000114480.12	GBE1	-0.803	0.003	Glucan branching enzyme activity	Carbohydrate metabolic process
ENSG00000165322.17	ARHGAP12	-0.807	0.001	GTPase activator activity	Actin filament organization and morphogenesis of an epithelial sheet
ENSG00000196263.7	ZNF471	-0.826	0.010	DNA binding and metal ion binding	Regulation of transcription
ENSG00000115339.13	GALNT3	-0.827	0.007	Calcium ion binding and carbohydrate binding	Carbohydrate metabolic process and fibroblast growth factor receptor signaling pathway
ENSG00000140450.8	ARRDC4	-0.831	0.005	Protein binding. bridging involved in substrate recognition for ubiquitination	Extracellular vesicle biogenesis and positive regulation of ubiquitin-protein transferase activity
ENSG00000119938.8	PPP1R3C	-0.845	0.008	Glycogen binding	Glycogen biosynthetic process
ENSG00000180530.10	NRIP1	-0.853	0.006	Hormone receptor binding	Regulation of transcription
ENSG00000150457.8	LATS2	-0.853	0.004	ATP binding Source and metal ion binding	Cell division and hippo pathway
ENSG00000179941.7	BBS10	-0.885	0.006	ATP binding and RNA polymerase II repressing transcription factor binding	Photoreceptor cell maintenance and visual perception
ENSG00000239305.6	RNF103	-0.898	0.004	E3 ubiquitin-protein ligase	Central nervous system development
ENSG00000096717.11	SIRT1	-0.901	0.009	NAD-dependent histone deacetylase activity	Angiogenesis and response to damage
ENSG00000261210.7	CLEC19A	-0.910	0.004	Carbohydrate binding	UK
ENSG00000196542.8	SPTSSB	-0.949	0.000	Serine palmitoyltransferase	Lipid metabolic process
ENSG00000185947.14	ZNF267	-0.956	0.006	DNA-binding transcription factor activity	UK
ENSG00000105855.9	ITGB8	-0.965	0.010	Extracellular matrix protein binding	Cell adhesion and migration
ENSG00000176208.8	ATAD5	-0.976	0.000	ATP binding and DNA binding	Regulation of mitotic cell cycle phase transition
ENSG00000273604.1	EPOP	-1.177	0.001	Chromatin binding	Regulation of transcription
ENSG00000148516.21	ZEB1	-1.273	0.007	DNA-binding transcription factor activity	Embryonic camera-type eye morphogenesis
ENSG00000169282.17	KCNAB1	-1.342	0.005	Voltage-gated ion channels subunit	Oxidation-reduction process
ENSG00000050344.8	NFE2L3	-1.409	0.005	DNA-binding transcription factor activity	Positive regulation of transcription
ENSG00000107249.22	GLIS3	-1.413	0.005	DNA binding and metal ion binding	Transcription factor involved in eye development
ENSG00000183092.16	BEGAIN	-1.720	0.004	Kinase activity	Neuropathic pain and interaction at synapses
ENSG00000154548.8	SRSF12	-1.872	0.000	Nucleic acid binding	Regulation of mRNA splicing

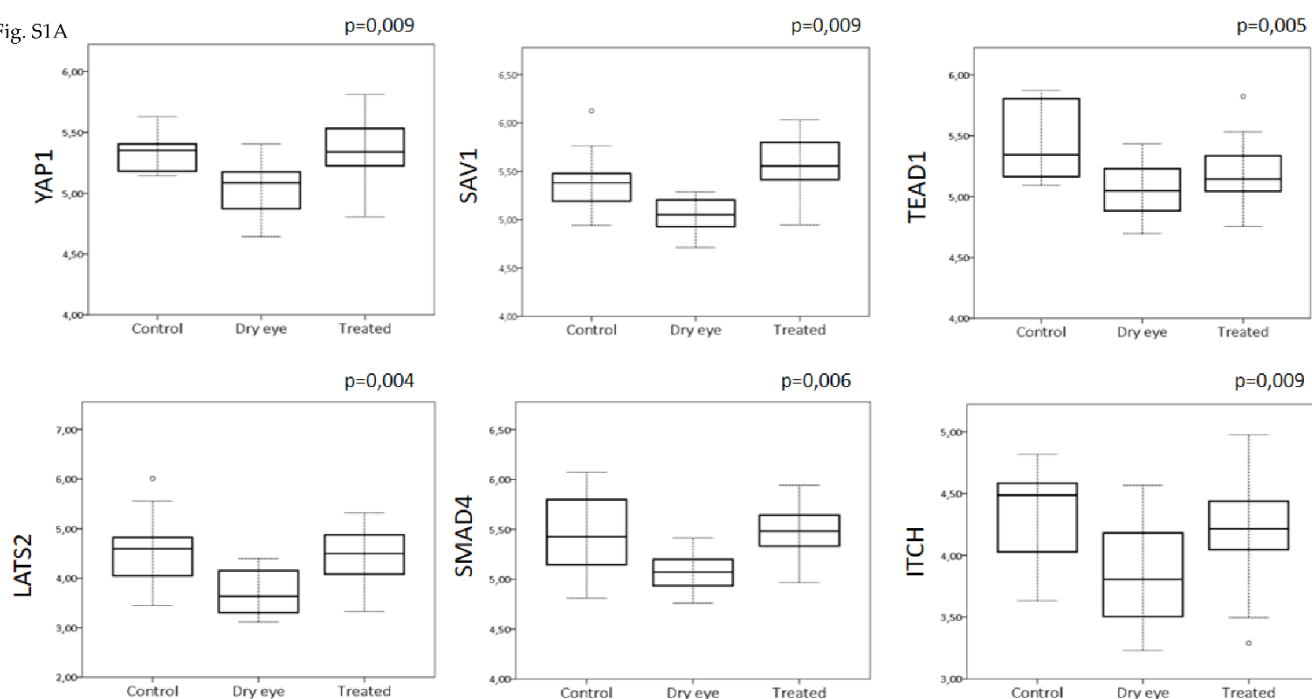
**Table S4.** List of 60 genes most significantly altered in the conjunctiva of dry eye patients compared to healthy conjunctiva by RNA sequencing.

ID gene	Gene Name	Log FC	p Value	GO Molecular Function	GO Biological Process
ENSG00000187242.5	<i>KRT12</i>	2.505	0.0078	Structural molecule activity	Cornification and keratinization
ENSG00000154548.8	<i>SRSF12</i>	1.866	0.0000	Nucleic acid binding	Regulation of mRNA splicing
ENSG00000179636.14	<i>TPPP2</i>	1.599	0.0050	Tubulin binding	Cell differentiation
ENSG00000106278.11	<i>PTPRZ1</i>	1.527	0.0072	Transmembrane receptor protein tyrosine phosphatase activity	Regulation of oligodendrocyte progenitor proliferation
ENSG00000043591.5	<i>ADRB1</i>	1.435	0.0066	Nucleotide binding regulatory protein-coupled receptor	Adrenergic receptor signaling pathway and response to cold, fear.
ENSG00000050344.8	<i>NFE2L3</i>	1.400	0.0020	DNA-binding transcription factor activity	Positive regulation of transcription
ENSG00000238083.7	<i>LRRC37A2</i>	1.378	0.0059	Leucine-rich repeat-containing protein	UK
ENSG00000136867.10	<i>SLC31A2</i>	1.371	0.0034	Copper ion transmembrane transporter activity	Cellular copper ion homeostasis
ENSG00000114346.13	<i>ECT2</i>	1.312	0.0045	GTPase activator activity	Bicellular tight junction assembly and cell morphogenesis
ENSG00000105327.17	<i>BBC3</i>	1.224	0.0002	Cysteine-type endopeptidase activity involved in apoptotic process	Cellular response to damage
ENSG00000058866.14	<i>DGKG</i>	1.185	0.0069	Diacylglycerol kinase activity Source: BHF-UCL	Glycerolipid metabolic process
ENSG00000188051.6	<i>TMEM221</i>	1.158	0.0024	Non-membrane spanning protein tyrosine kinase activity	Immune system
ENSG00000010671.15	<i>BTK</i>	1.150	0.0093	Transcription factor activity	Cell differentiation
ENSG00000123095.5	<i>BHLHE41</i>	1.145	0.0002	Transcription factor activity	Animal organ morphogenesis and animal organ morphogenesis
ENSG00000104154.6	<i>SLC30A4</i>	1.136	0.0020	Zinc ion transmembrane transporter activity	Zinc ion homeostasis and response to toxic substance
ENSG00000196542.8	<i>SPTSSB</i>	1.132	0.0000	Ceramide biosynthetic process serine C-palmitoyltransferase activity	Sphingolipid metabolism and in Lipid metabolism
ENSG00000164440.14	<i>TXLNB</i>	1.104	0.0083	Syntaxin binding	UK
ENSG00000114805.17	<i>PLCH1</i>	1.098	0.0009	Calcium-dependent phospholipase C activity	Lipid catabolic process and release of calcium ion into cytosol
ENSG00000241106.7	<i>HLA-DOB</i>	1.091	0.0084	MHC class II protein complex binding	Immune system
ENSG00000183018.8	<i>SPNS2</i>	1.034	0.0007	Sphingolipid transporter activity	Lipid transport, immune cells homeostasis and regulation of eye pigmentation
ENSG00000105855.9	<i>ITGB8</i>	1.028	0.0018	Extracellular matrix protein binding	Cell adhesion and migration
ENSG00000074527.11	<i>NTN4</i>	1.027	0.0060	Laminin-1 binding	Substrate adhesion-dependent cell spreading and tissue development
ENSG00000113328.18	<i>CCNG1</i>	1.021	0.0089	Cyclin-dependent protein serine/threonine kinase	Cell division

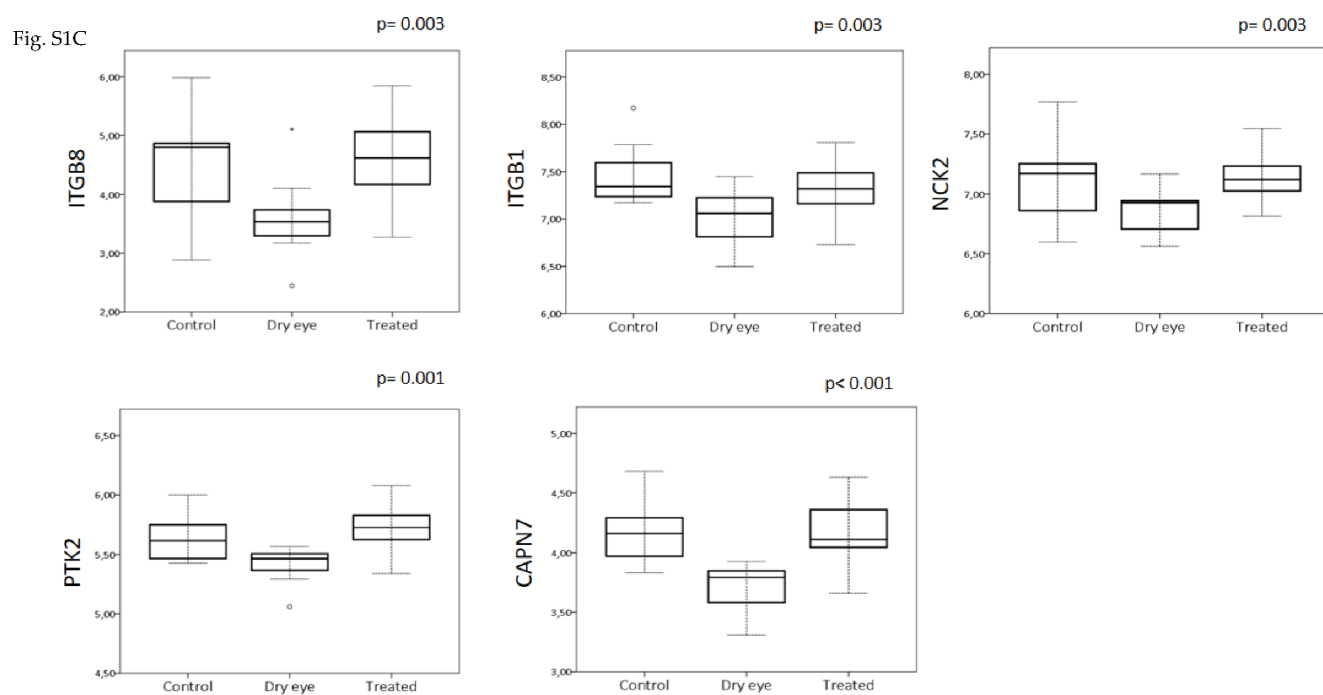
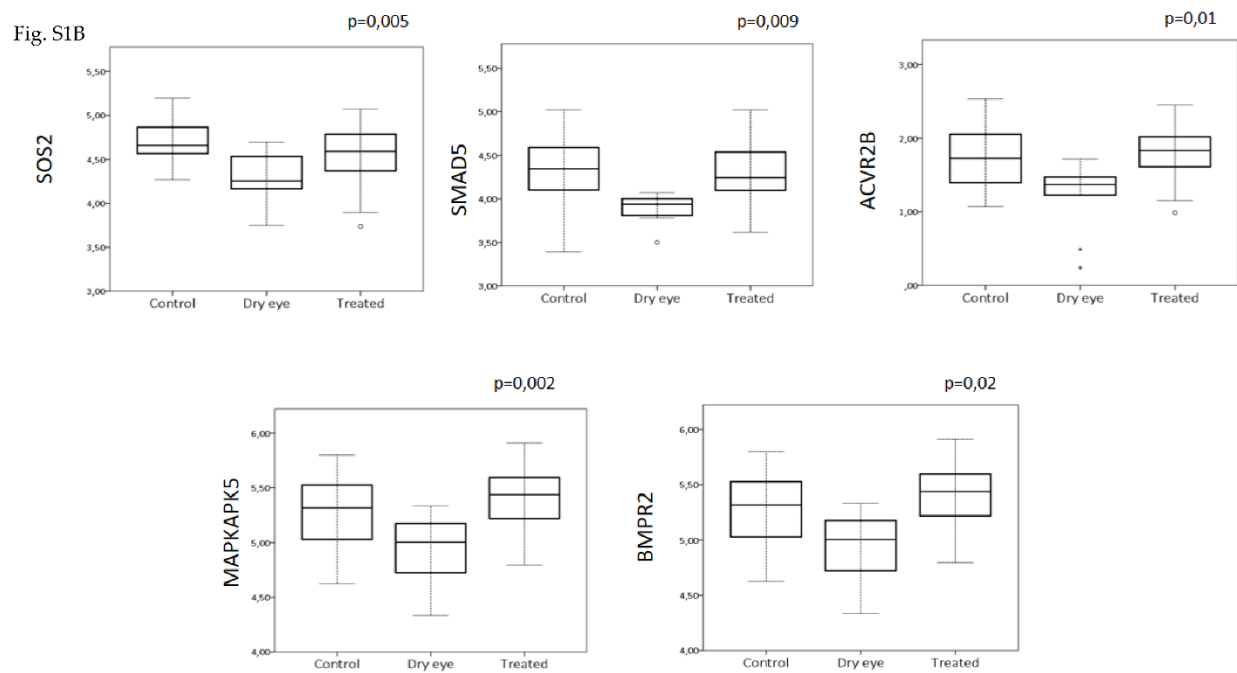
ENSG00000104043.14	<i>ATP8B4</i>	0.999	0.0046	ATPase-coupled intramembrane lipid transporter activity	Golgi organization and neutrophil degranulation
ENSG00000239305.6	<i>RNF103</i>	0.997	0.0004	Ubiquitin protein ligase activity	Endoplasmic reticulum mannose trimming and protein ubiquitination
ENSG00000273604.1	<i>EPOP</i>	0.965	0.0030	Chromatin binding	Regulation of transcription
ENSG00000137878.17	<i>GCOM1</i>	0.950	0.0006	Intracellular signal transduction	UK
ENSG00000115339.13	<i>GALNT3</i>	0.869	0.0011	Carbohydrate binding	Protein O-linked glycosylation via threonine
ENSG00000145375.7	<i>SPATA5</i>	0.867	0.0016	ATPase activity	Cell differentiation
ENSG00000198157.10	<i>HMG5</i>	-1.629	0.0005	Chromatin and RNA binding	Chromatin organization
ENSG00000112769.18	<i>LAMA4</i>	-1.645	0.0024	Extracellular matrix structural constituent	Cell adhesion and extracellular matrix organization
ENSG00000107165.12	<i>TYRP1</i>	-1.732	0.0040	Oxidoreductase activity	Regulation of melanin biosynthetic process
ENSG00000135919.12	<i>SERPINE2</i>	-1.746	0.0015	Serine-type endopeptidase inhibitor activity	Innervation and secretion by cell
ENSG00000150201.14	<i>FXD4</i>	-1.756	0.0000	ATPase binding and ion channel regulator activity	Ion transmembrane transport
ENSG00000206072.12	<i>SERPINB11</i>	-1.773	0.0038	Serine-type endopeptidase inhibitor activity	Negative regulation of endopeptidase activity
ENSG00000228253.1	<i>MT-ATP8</i>	-1.818	0.0001	Proton transmembrane transporter activity	Mitochondrial ATP synthesis coupled proton transport
ENSG00000197641.11	<i>SERPINB13</i>	-1.819	0.0000	Cysteine-type endopeptidase inhibitor activity	Negative regulation of keratinocyte apoptotic process
ENSG00000173114.12	<i>LRRN3</i>	-1.841	0.0009	UK	UK
ENSG00000198739.10	<i>LRRTM3</i>	-1.844	0.0072	Protein-protein interactions	UK
ENSG00000118402.5	<i>ELOVL4</i>	-1.862	0.0023	Fatty acid elongase activity	Fatty acid biosynthetic process
ENSG00000128422.16	<i>KRT17</i>	-1.874	0.0007	Structural constituent of cytoskeleton and MHC class II protein binding	Cornification and epidermis development
ENSG00000136522.13	<i>MRPL47</i>	-1.893	0.0000	Structural constituent of ribosome	Mitochondrial translation
ENSG00000206075.13	<i>SERPINB5</i>	-1.901	0.0000	Serine-type endopeptidase inhibitor activity	Extracellular matrix organization and regulation of epithelial cell proliferation
ENSG00000210082.2	<i>MT-RNR2</i>	-1.945	0.0000	Receptor antagonist activity and signaling receptor binding	Apoptotic process and cellular iron ion homeostasis
ENSG00000145423.4	<i>SFRP2</i>	-1.941	0.0038	Endopeptidase activator and fibronectin binding activity	Apoptotic process and negative regulation of epithelial cell proliferation
ENSG00000119508.17	<i>NR4A3</i>	-1.948	0.0001	Transcription activator activity	Cellular respiration and mast cell degranulation
ENSG00000198189.10	<i>HSD17B11</i>	-2.038	0.0000	Steroid dehydrogenase activity	Steroid metabolic process
ENSG00000142149.8	<i>HUNK</i>	-2.080	0.0000	Protein serine/threonine kinase activity	Signal transduction
ENSG00000138653.9	<i>NDST4</i>	-2.095	0.0012	Heparan sulfate N-acetylglucosaminyltransferase activity	Heparin biosynthetic process

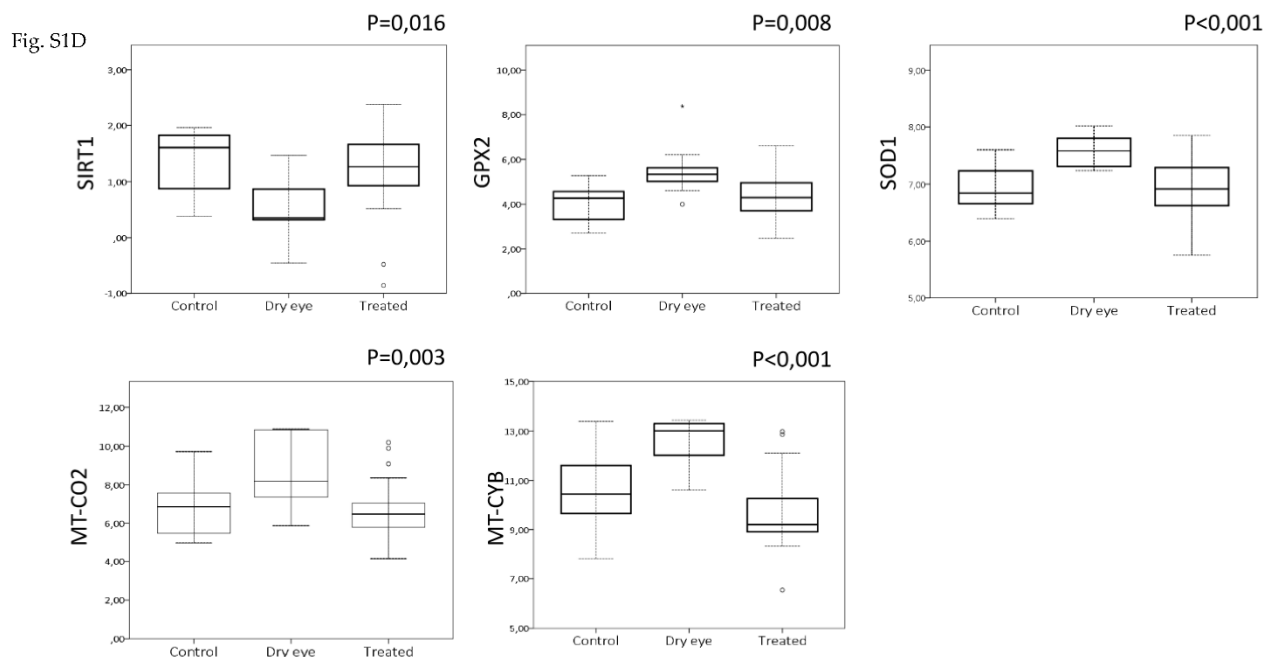
ENSG00000198712.1	<i>MT-CO2</i>	-2.116	0.0006	Copper ion binding and cytochrome-C oxidase activity	Mitochondrial electron transport
ENSG00000136160.15	<i>EDNRB</i>	-2.117	0.0001	Endothelin receptor activity	Aging, proliferation, and pain reception
ENSG00000198677.11	<i>TTC37</i>	-2.118	0.0000	Catabolism of deadenylated mRNA	RNA catabolic process
ENSG00000169429.10	<i>CXCL8 (IL8)</i>	-2.257	0.0001	Chemokine activity	Immune response
ENSG00000137440.4	<i>FGFBP1</i>	-2.379	0.0000	Fibroblast growth factor binding	Cell-cell signaling
ENSG00000164687.10	<i>FABP5</i>	-2.563	0.0000	Lipid binding and retinoic acid binding	Epidermis development
ENSG00000135046.13	<i>ANXA1</i>	-2.799	0.0000	Cadherin binding and single-stranded RNA binding	Immune system and inflammatory response
ENSG00000198727.2	<i>MT-CYB</i>	-2.836	0.0000	Metal ion binding and cytochrome-c oxidase activity	Mitochondrial electron transporter and response to stress and ion
ENSG00000169413.2	<i>RNASE6</i>	-2.941	0.0000	Nucleic acid binding and ribonuclease activity	Innate immune response and RNA catabolic process
ENSG00000090104.11	<i>RGS1</i>	-2.996	0.0000	GTPase activator activity and calmodulin binding	G protein-coupled receptor signaling pathway and immune response
ENSG00000147604.13	<i>RPL7</i>	-3.125	0.0000	Nucleic acid binding and protein homodimerization activity	RNA catabolic process, nonsense-mediated decay

Fig. S1A

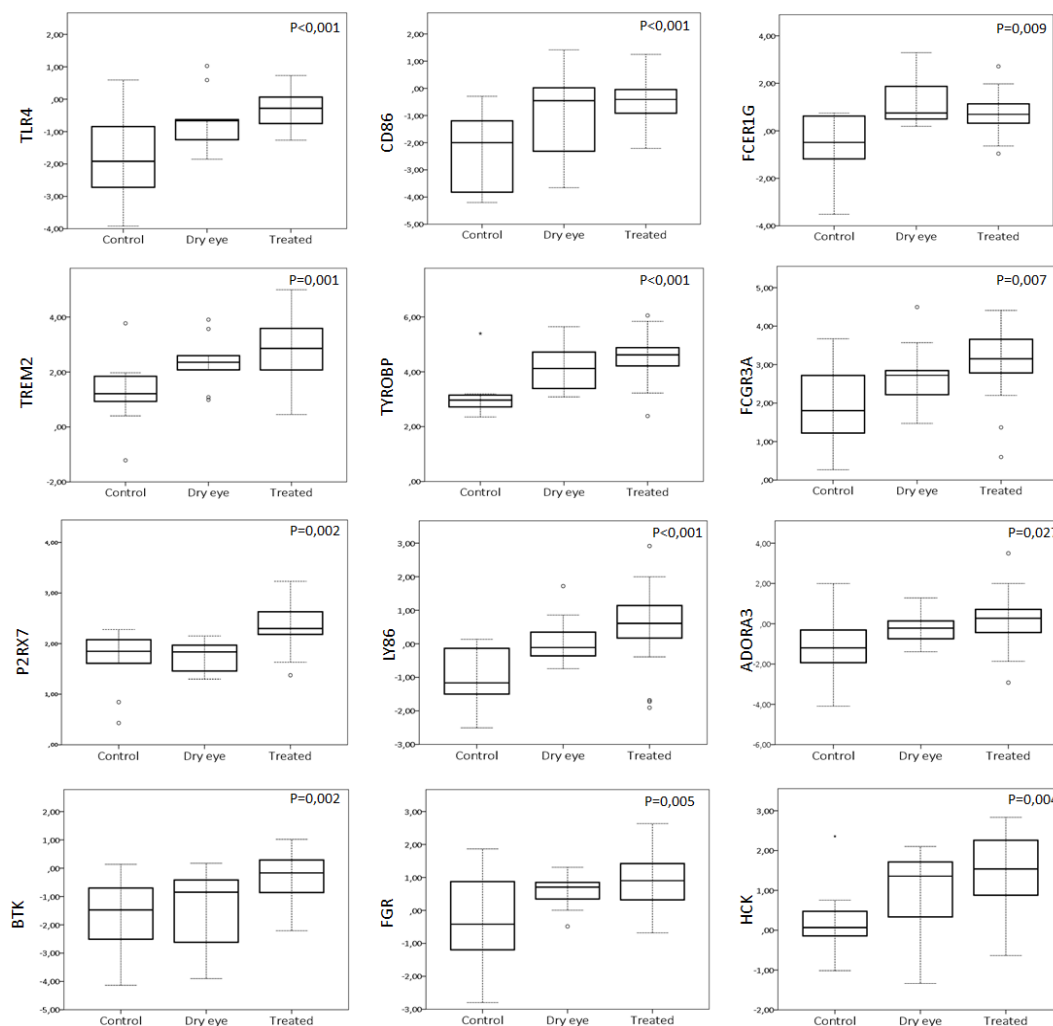








**Figure S1.** This figure shows gene expression levels dysregulated in dry eye syndrome patients related to the different pathways mentioned in the manuscript (immune system, cellular proliferation and differentiation, mitochondrial dysfunction, cellular movement and integrity and wound healing). A, Hippo signaling pathway-related gene expression. B, The TGF- $\beta$  signaling pathway-related gene expression. C, Gene expression related to the integrin signaling pathway. D, Gene expression regulating mitochondrial metabolism and redox equilibrium. These genes were obtained in the RNA sequencing.



**Figure S2.** This figure shows gene expression levels dysregulated in glaucoma treated patients related to the different pathways mentioned in the manuscript (host defense and immune system, cellular proliferation and differentiation). These genes were obtained in the RNA sequencing.

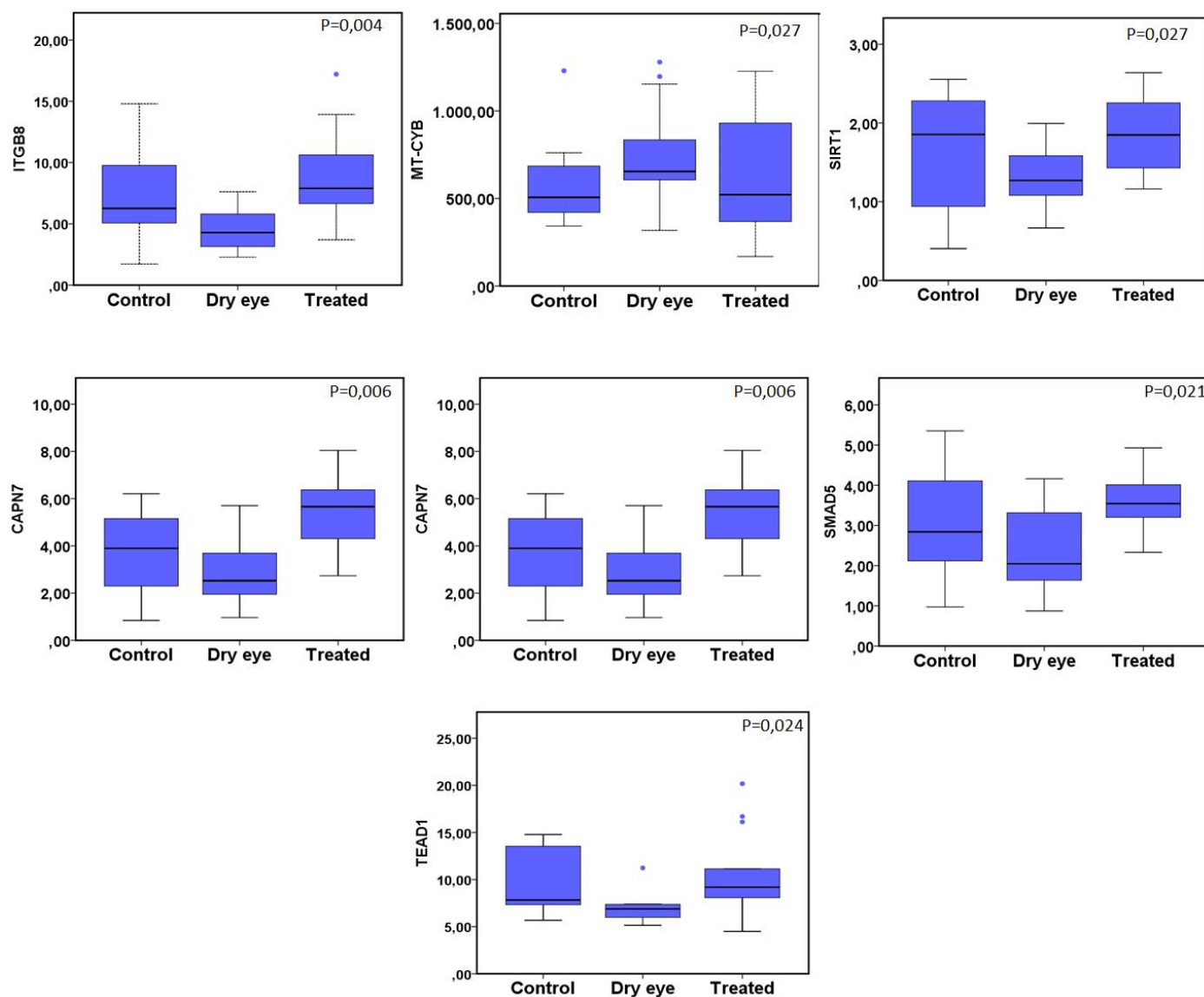


Figure S3. Validation of the gene expression in CIC samples from the dry eye syndrome patient group. 30 CIC samples out of 140 total CIC were selected for RNA validation.

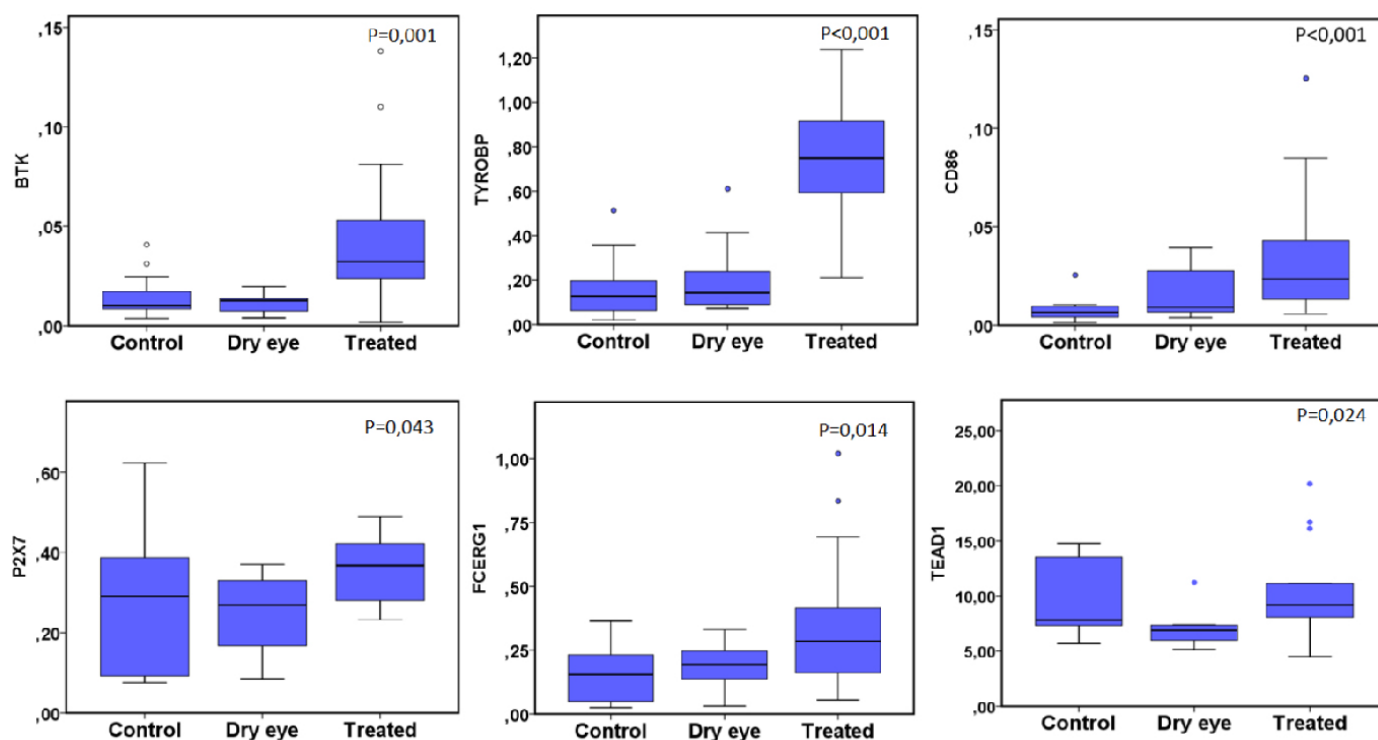


Figure S4. Validation of the gene expression in CIC samples from the treated glaucoma patient group. 30 CIC samples out of 140 total CIC were selected for RNA validation.