mRNA Sequencing of Limbal Epithelial Cells and mRNA/miRNA Profiling of Limbal Stromal cells in PAX6-related Congenital Aniridia

Table S4. Deregulated miRNAs of AN-LECs out of the Top 40 with strong evidenced target genes (**a**) and the resulting enriched pathways identified using geneTrail online software tool (https://genetrail.bioinf.uni-sb.de/) (**b**) and enriched pathways of target genes of deregulated miRNAs of AN-LSCs, observed by the KEGG database. Genes in bold are double or multiple mentions.

a)

downregulated miRNAs in AN-LSCs	*strong evidenced target genes*
hsa-miR-193a-3p	**KRAS; MCL1**; E2F6; PRAP1; **CCND1; ERBB2**; SLC7A5; PLAU; **TGFB2; PTEN**; RAB27B; SELENON; **ERBB4; E2F1**; SRSF2; TYMS; RPS6KB2; **HMGB1**; HYOU1; **MMP14**
hsa-miR-452-5p	FGFR3; **CCND1; PTEN**; THRB; TACC3; MAFB; BTK; PDCD10; **SMAD2**
hsa-miR-29a-5p	**PTEN**; HDAC9; **COL3A1**; **SPARC**; TAB1; **DKK1; GSK3B**; ST2
hsa-miR-106a-5p	APP; **E2F1; CDKN1A**; HIPK3; MYLIP; RB1; **RUNX1; VEGFA**; ARID4B; CYP19A1; IL10; **TGFBR2; FAS**; SIRPA; **PTEN**; SLC2A3; BMP2**; STAT3; CCND1**; TIMP2**; CASP7**; BCL10; RUNX3; ATM; ULK1; MAPK9; HIF1A; RBL2; **CXCL8**; MFN2; **APC**; MYB; MGST2; ATG7; ERCC1; RND3; **RARB; CDX2; HMGA2**
hsa-miR-218-5p	RICTOR; LAMB3; **LASP1**; IKBKB; **SP1**; VOPP1; BIRC5; GJA1; ROBO1; **HMGB1**; SOST; SFRP2; DKK2; TOB1; **CDK6; BMI1**; LEF1; HOXB3; OTUD7B; MITF; GLI2; **PDGFRA**; TFF1; RUNX2; **CDH2**; **EGFR**; SH3GL1; RET; POU2F2; RPS6KA3; LGR4; **SMO; E2F2**; HMOX1; KIT; WASF3; **VPS51; MMP2; RPS6KB1**; BCL9
hsa-miR-9-5p	**PRDM1; ETS1; MMP13**; REST; CDH1; RAB34; **BACE1; NFKB1**; NR2E1; FOXO1; **NTRK3**; SIRT1; ONECUT2; SRF; **CDX2**; AP3B1; CCNG1; TGFBI; ID2; **CCND1**; FOXO3; SOCS5; **CD34**; XRN2; CHMP2B; STMN1; **ABCC1**; CREB1; KLF17; PPARA; NF1; FOXP1; **ELAVL1**; DICER1; MALAT1; PRTG; **CXCR4**; ACAT1; MIRLET7D; DRD2; **HDAC4**; **TGFBR2**; MTHFD1; **BCL2L11**; CUL4A; **IL6; ATG5; BCL2; GSK3B; PDGFRB**; IGF2BP1; NRP1; TM4SF1; **NOTCH1**; CYP4Z1; SOX7; FOXG1A; IGF2BP3; **UHRF1**; CBX7; CAMKK2; **RUNX1**; PRKAA1; **STARD13**; GALNT4; TNFAIP8; **MYOCD**; NOX4; SRSF1; HES1**; NOTCH2**; GDNF; STAU1; KPNB1; DYRK1B; **DKK1**; ZC3H12A; BECN1; RAP2A
hsa-miR-4516	**STAT3**
hsa-miR-1246	DYRK1A; PRKAR1A; NFIB; AXIN2; **GSK3B**
hsa-miR-301b-3p	TP63; **BCL2L11**; NR3C2; **PTEN**
hsa-miR-29b-3p	**ESR1**; TGFB3; **HDAC4**; CTNNBIP1; COL5A3; COL4A2; COL1A1; **CDK6; BACE1**; SFPQ; DNAJB11; **MCL1**; TET1; TCL1A; **SP1**; DNMT3B; DNMT3A; **BCL2**; DNMT1; S100B; **VEGFA**; FGG; FGA; **FGB**; MMP15; MMP24; GRN; **COL3A1**; COL4A1; **MMP2**; ADAM12; NID1; BMP1; **PTEN; HMGA2; TGFB2; TGFB1**; NCOA3; PPP1R13B; NASP; CDC42; **GSK3B**; DUSP2; **PIK3CG**; **NKIRAS2**; TBX21**; IFNG**; RAX; TDG; FOS; PIK3R1; MYCN; SNAI3; **CCND2**; SERPINH1; AKT2; PER1; LAMC1; AQP4; **LAMC2** ITGA6; COL5A2; COL10A1**; SPARC**; FBN1; LOX; **PDGFRB**; IL32; GATA3; **PDGFRA**; PDGFC; PDGFB;

	PDGFA; MMP9; LOXL4; LOXL2; ITGB1; ANGPTL4**; LASP1**; PPIC; **TNFAIP3**; **TET2**; KIF1B; KDM2A; HMGCR; **STAT3**; MEN1; AKT3; LRP6**; ELAVL1**; PATZ1; **MYC**
miR-146a-5p	**CXCR4**; FADD; TLR2; CFH; IRAK2; IRAK1; **TRAF6; NFKB1**; **ROCK1**; BRCA2; BRCA1; **CXCL8**; FAF1; CCNA2; PA2G4; **ERBB4**; **EGFR**; MTA2; **SMAD4**; CD40LG; **FAS**; WASF2; TLR4; L1CAM; CD80; SLPI; **STAT1; UHRF1**; NUMB; SMN1; CARD10; COPS8; **ELAVL1**; ICAM1; **SMAD2**; PRKCE; PTGS2; CNOT6L; CCL5; PTGES2; SIKE1; CXCL12; SOS1; HOXD10; COX2; DUSP1; RAC1; **LAMC2**; RNF11; **CASP7**; BCLAF1; IS2; CPM; **NOTCH2; SOX2**; **IL6**; RHOA; **TGFB1; LFNG**; FANCM; MIF; **NOTCH1**; NFAT5; RHO; **RARB; CCND2; CCND1**; LRP2; NOS1; PLAUR
upregulated miRNAs in AN-LSCs	*strong evidenced target genes*
hsa-miR-493-3p	MIXI1; **RHOC**; MAP2K7; FZD4; **DKK1**
hsa-miR-758-3p	TLR7; TLR3
hsa-miR-127-5p	BLVRB; **SPP1**
hsa-miR-487b-3p	GRM3; SUZ12; **BMI1**; WNT5A; **MYC; KRAS**; MAGI2; THBS1
hsa-miR-299-5p	**CDKN1A; SPP1; ATG5**
hsa-miR-326	**SMO; GLI1**; CD9; **NOTCH1**; **NOTCH2; MSH3**; PKM; HOTAIR; NOB1; CD274; FGF1; BCL2L1; **FSCN1; SP1**
hsa-miR-485-5p	HIF3A; APOA5; FZD7; FLOT1; PPARGC1A; STC2; **HMGA2**
hsa-miR-381-5p	NEFL; **HES1**
hsa-miR-127-3p	**BLVRB; SPP1**
hsa-miR-370-3p	GADD45A; CTNNB1; MAP3K8; MGMT; CPT1A; **TGFBR2; FOXO1**; FOXM1; **NF1**; LIN28A; TCEAL1
hsa-miR-485-3p	**NTRK3; PPARGC1A**; PBRM1; SLC40A1; NFYB; MAT1A
hsa-miR-494-5p	**CXCR4; PTEN**; DPYD
hsa-miR-493-5p	**RHOC**; FUT4; GOLM1
hsa-miR-433-3p	**HIF1A**; MET; GRB2; **RUNX2**; FGF20; GBP2; CFTR; **KRAS; CREB1; TYMS;** AZIN1
hsa-miR-1247-5p	SOX9; MAP3K9

b)

Name	Expected number of genes	Observed number of genes	Adjusted p-value
PI3K-Akt signaling pathway	6.39	56	2.11E-031
MAPK signaling pathway	5.32	42	2.76E-022
Focal adhesion	3.60	35	3.45E-021
FoxO signaling pathway	2.37	30	4.76E-021
Cellular senescence	2.89	31	5.94E-020
Toll-like receptor signaling pathway	1.90	24	4.96E-017
TNF signaling pathway	2.02	21	1.31E-013
Hippo signaling pathway	2.77	23	4.70E-013
Signaling pathways regulating pluripotency of stem cells	2.53	21	4.82E-012
Wnt signaling pathway	2.89	22	6.50E-012
Jak-STAT signaling pathway	2.93	22	7.97E-012
NF-kappa B signaling pathway	1.84	18	1.69E-011
mTOR signaling pathway	2.77	21	2.02E-011
Rap1 signaling pathway	3.80	24	2.05E-011

Ras signaling pathway	4.10	25	2.14E-011
AMPK signaling pathway	2.17	19	2.17E-011
TGF-beta signaling pathway	1.70	17	4.31E-011
Cell cycle	2.24	18	2.44E-010
HIF1 signaling pathway	1.97	17	2.99E-010
IL-17 signaling pathway	1.70	16	3.30E-010
Chemokine signaling pathway	3.42	21	5.65E-010
Regulation of actin cytoskeleton	3.85	21	3.89E-009
Apoptosis	2.44	17	5.18E-009
NOD-like receptor signaling pathway	3.26	17	2.15E-007
P53 signaling pathway	1.30	11	5.43E-007
Axon guidance	3.27	16	1.11E-006
Gap junction	1.59	11	3.08E-006
Growth hormone synthesis. secretion and action	2.15	12	7.88E-006
Hedgehog signaling pathway	0.90	8	1.59E-005
ECM-receptor interaction	1.59	10	1.89E-005
Necroptosis	2.59	13	3.14E-005
cAMP signaling pathway	3.91	15	3.32E-005
Tight junction	3.04	13	4.14E-005
VEGF signaling pathway	1.06	8	4.41E-005
RIG-I-like receptor signaling pathway	1.26	8	1.30E-004
Cytokine-cytokine receptor interaction	5.34	15	8.05E-004
Cell adhesion molecules (CAMPs)	2.62	9	2.88E-003