

Supplemental table 1. Used Primers

Gene	Primer sequence	Product length [bp]	Accession number
<i>Rln</i>	forward, 5'-aggcaagccactgaagttgt-3' reverse, 5'-tccctcttttccgtgaatg-3'	284	NM_011272
<i>Rxfp1</i>	forward, 5'-ggagacaacaatgggtgggc-3' reverse, 5'-tcgactgaggtgattgtcttc-3'	transcript variant 1: 450 transcript variant 3: 344	NM_212452 XR_375538 XM_006501629
<i>Rxfp2</i>	forward, 5'-gacaaccatatttggcacagtcc-3' reverse, 5'-gtcttgaatatcccaggcc-3'	364	NM_080468
<i>Gapdh</i>	forward, 5'-tgatgacatcaagaaggtgg-3' reverse, 5'-tttcttactccttgaggcc-3'	250	XM_017321385

Supplemental table 2. RealTime ready Custom Panel

Type	Assay ID	Gene Symbol
Designer Assay	---	<i>Aqp1</i>
Catalog Assay	311400	<i>Aqp3</i>
Catalog Assay	311387	<i>Aqp4</i>

Catalog Assay	316493	<i>Aqp5</i>
Catalog Assay	300612	<i>Col1a1</i>
Catalog Assay	300611	<i>Col1a2</i>
Catalog Assay	300758	<i>Mmp2</i>
Catalog Assay	313931	<i>Mmp9</i>
Designer Assay	---	<i>Mmp13</i>
Catalog Assay	312477	<i>Timp1</i>
Catalog Assay	300926	<i>Timp2</i>
Catalog Assay	310719	<i>Vim</i>
Catalog Assay	300896	<i>Tjp1</i>
Reference Gene	307884	<i>Gapdh</i>
Reference Gene	307906	<i>Rn18s</i>

Supplemental table 3. Relative gene expression in cornea from wildtype (Rln^{+/+}) and Rln^{-/-} knockout mice. Five independent cornea samples (n = 5) for each group were analyzed by RealTime ready Custom Panel. All data were normalized to *Gapdh* gene expression and presented as mean ± SEM. Statistical significance were calculated as described between wildtype and Rln^{-/-} group.

gene	wildtype		Rln ^{-/-}		p-value
	Mean	SEM	Mean	SEM	
AQP1	1,435	0,3932	1,845	0,5775	0,566

AQP3	1,042	0,1098	1,315	0,2567	0,344
AQP4	0,786	0,2633	2,447	0,6553	0,030
AQP5	1,022	0,0806	0,821	0,1304	0,211
COL1A1	1,336	0,5123	1,973	0,7324	0,500
COL1A2	1,131	0,2156	0,512	0,1179	0,025
VIM	0,433	0,1178	0,249	0,0496	0,139
TJP1	0,759	0,2658	0,777	0,2652	0,962
MMP2	1,578	0,5319	2,824	0,7167	0,184
MMP9	1,107	0,2356	0,0089	0,0012	<0,0001
MMP13	1,066	0,3683	0,4246	0,1559	0,177
TIMP1	1,442	0,4414	0,2350	0,0596	0,006
TIMP2	1,051	0,1188	0,6477	0,1270	0,029

Supplemental table 4. Relative gene expression in retina from wildtype (Rln^{+/+}) and Rln^{-/-} knockout mice. Five independent cornea samples (n = 5) for each group were analyzed by RealTime ready Custom Panel. All data were normalized to *Gapdh* gene expression and presented as mean ± SEM. Statistical significance were calculated as described between wildtype and Rln^{-/-} group.

gene	wildtype		Rln ^{-/-}		p-value
	Mean	SEM	Mean	SEM	
<i>AQP1</i>	1,139	0,2938	0,961	0,1918	0,886
<i>AQP3</i>	0,348	0,0901	1,477	0,6999	0,116
<i>AQP4</i>	1,107	0,2735	1,144	0,3344	1,000
<i>AQP5</i>	0,490	0,0611	0,399	0,0300	0,286
<i>COL1A1</i>	1,802	0,8172	1,179	0,6243	0,566
<i>COL1A2</i>	0,656	0,1416	0,728	0,2252	0,905
<i>VIM</i>	1,020	0,1048	1,113	0,1055	0,553
<i>TJP1</i>	2,570	1,0180	4,021	0,7680	0,314
<i>MMP2</i>	1,038	0,1358	1,045	0,1914	0,975
<i>MMP9</i>	1,706	0,5087	2,115	0,7582	0,666
<i>MMP13</i>	1,727	1,0850	1,078	0,5569	1,000
<i>TIMP1</i>	1,567	0,5798	1,088	0,7869	0,686
<i>TIMP2</i>	1,273	0,4847	2,771	0,4448	0,081

Supplemental table 5. Relative gene expression in uvea from wildtype (Rln^{+/+}) and Rln^{-/-} knockout mice. Five independent cornea samples (n = 5) for each group were analyzed by RealTime ready Custom Panel. All data were normalized to *Gapdh* gene expression and presented as mean ± SEM. Statistical significance were calculated as described between wildtype and Rln^{-/-} group. Not detectable (n.d.)

gene	wildtype		Rln ^{-/-}		p-value
	Mean	SEM	Mean	SEM	
AQP1	1,079	0,2207	0,3788	0,0847	0,018
AQP3	1,006	0,0664	0,7356	0,2294	0,343
AQP4	1,022	0,1016	0,6407	0,0645	0,013
AQP5	1,419	0,6944	0,1769	0,0302	0,029
COL1A1	1,135	0,2897	0,4701	0,1467	0,075
COL1A2	1,317	0,3544	0,4974	0,3112	0,151
VIM	1,220	0,3220	0,4312	0,2209	0,032
TJP1	1,168	0,3070	0,2650	0,0906	0,022
MMP2	1,144	0,2926	0,7612	0,1280	0,265
MMP9	1,000	0,0173	3,790	1,503	0,133
MMP13	n.d.		n.d.		
TIMP1	n.d.		n.d.		
TIMP2	1,176	0,2866	0,7307	0,3847	0,381