Retinal biomarkers and pharmacological targets for Hermansky-Pudlak syndrome 7

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Table 1S. Pathways dysregulated in the Dys$^{-/-}$ retina – Tarbase prediction (miR-101-3p, miR-186-5p, miR-382-5p)

KEGG pathway	p-value	#genes	#miRNAs
Protein processing in endoplasmic reticulum	5.23E-07	45	3
Endocytosis	5.23E-07	55	3
Adherens junction	5.23E-07	24	3
Lysine degradation	1.12E-06	14	3
TGF-beta signaling pathway	6.39E-06	22	2
Proteoglycans in cancer	4.00E-05	43	3
Adrenergic signaling in cardiomyocytes	0.000451986	30	3
Colorectal cancer	0.001121462	18	3
Thyroid hormone signaling pathway	0.001124907	27	3
Renal cell carcinoma	0.001124907	18	3
Hippo signaling pathway	0.001608411	35	3
N-Glycan biosynthesis	0.002511303	8	3
Long-term potentiation	0.003314069	20	2
Citrate cycle (TCA cycle)	0.005242178	10	3
Rap1 signaling pathway	0.005253159	41	3
Bacterial invasion of epithelial cells	0.005821178	20	3
Axon guidance	0.008547487	27	3
Gap junction	0.008547487	17	3
Long-term depression	0.008962452	14	2
Pathways in cancer	0.008962452	74	3
Regulation of actin cytoskeleton	0.009031618	40	3
Ubiquitin mediated proteolysis	0.010973081	33	3
Sphingolipid signaling pathway	0.013210665	30	3
cAMP signaling pathway	0.014889036	40	3
mRNA surveillance pathway	0.016670219	25	3
GnRH signaling pathway	0.016670219	21	3
mTOR signaling pathway	0.016825723	16	2

Dorso-ventral axis formation	0.023078633	9	3
MAPK signaling pathway	0.023078633	48	3
Endometrial cancer	0.0298516	14	3
Insulin signaling pathway	0.029975051	30	2
Neurotrophin signaling pathway	0.029975051	26	3
Melanogenesis	0.035735426	21	2
Focal adhesion	0.035735426	40	3
Steroid biosynthesis	0.036787678	4	2
Central carbon metabolism in cancer	0.037481481	13	3

Figure 1S. MiR-101-3p and miR-186-5p can control melanogenesis. Yellow genes are targets of miR-101-3p and miR-186-5p. This picture is the output of Diana miRPath software and recalls the KEGG pathway deposited in the database (KEGG permission n° 190309): https://www.genome.jp/kegg/pathway.html