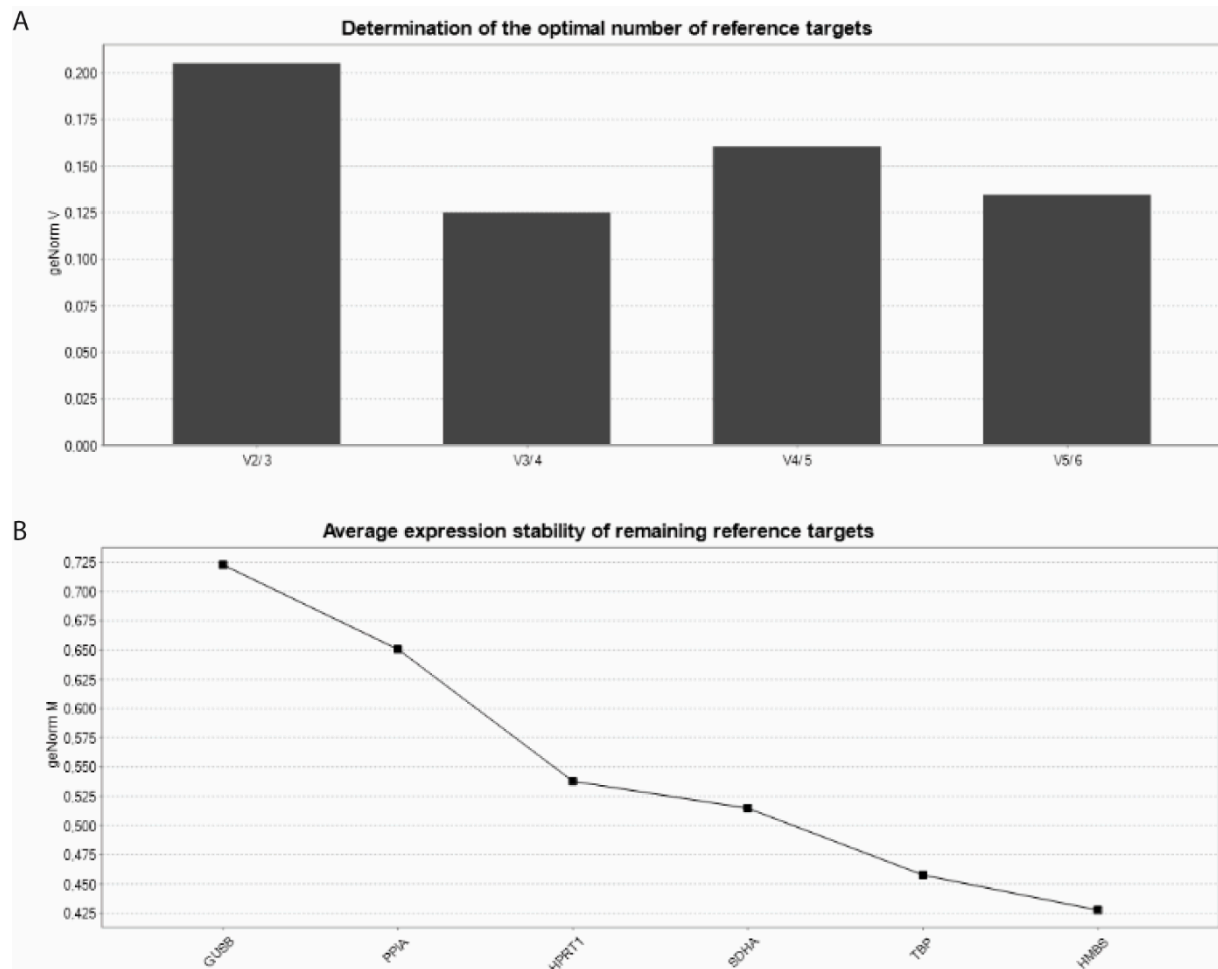


Supplementary data



Supplementary Figure S1: GeNorm analysis to determine the optimal number and most stable reference genes. A. GeNorm V analysis showing that the optimal number of reference genes to use is three ($V < 0.150$). B. GeNorm M analysis determining the stability of the six tested reference genes. *HMBS*, *TBP*, and *SDHA* are the most stably expressed in RPE-1 cells (lowest M values).

Supplementary Table S1: PCR primers.

	F-primer (5'-3')	R-primer (5'-3')
NR2E3 mutagenesis primers		
NR2E3_c.166G>A	CAGCAGCAGCaGGAAGCACTATGGC	TCTCCGCACACGCGGCAC
NR2E3 vector sequencing primers		
ORF_NR2E3_1	GGACTTTCCAAAATGTCG	/
ORF_NR2E3_2	CAGGTCCACCTGGACAGCAT	/
ORF_NR2E3_3	GAGTGAACTCTTTCTCCT	/
ORF_NR2E3_4	/	GGGTGGTCGGAACAGGATTA
qPCR GeNorm analysis		
HMBS_expr	GCCCTGGAGAAGAATGAA	GGTGAAAGACAACAGCATC
SDHA_expr	TGGGAACAAGAGGGCATCTG	CCACCACTGCATCAAATTCATG
HPRT1_expr	GACCAGTCAACAGGGGACAT	CCTGACCAAGGAAAGCAAAG
PPIA_expr	AGACAAGGTCCCAAAGAC	ACCACCCTGACACATAAA
GUSB_expr	AGCCAGTTCCTCATCAATGG	GGTAGTGGCTGGTACGGAAA
TBP_expr	CACGAACCACGGCACTGATT	TTTTCTTGCTGCCAGTCTGGAC
NR2E3_expr	GTGGACCCACGGAGTT	CTCAGCATCACTTGGGACTG