Supplementary Materials

Gel Lane	Study number	*CHM* variant	Predicted protein consequence	Predicted non-sense decay	Age at baseline	Half-Life (yr)	Standard deviations from mean half-life	Progression rate
1	PDRD011	non-contiguous dup exons 1-2 & 9-12	Two predicated RNA transcripts: r.[1511_*3450del; 117_1166del]	No	42	N/A	N/A	N/A
2	PDRD005	c.117_314del	R40_S105del	No	30	3.36	-1.10	Faster
3	PDRD014	c.179delA	K60Rfs*10	Yes	21	7.60	0.74	Slower
4	PDRD030	c.282delT	I95Ffs*31	Yes	17	3.52	-1.03	Faster
5	PDRD028	c.406_407insT	S136Ffs*9	Yes	N/A	N/A	N/A	N/A
6	PDRD022	c.492_493delGA	N165Cfs*8	Yes	22	7.49	0.69	Slower
7	PDRD012	c.655C>T	Q219X	Yes	45	3.54	-1.02	Faster
8	PDRD013	c.757C>T	R253X	Yes	53	3.74	-0.94	Faster
9	PDRD018	c.799C>T	R267X	Yes	53	4.21	-0.73	Faster
10	PDRD023	c.877C>T	R293X	Yes	38	3.94	-0.85	Faster
11	PDRD031	c.940+3delA	Splice donor site mutation – Intron 7 (+3)	No	36	14.07	3.54	Slower
12	PDRD029	c.941-2A>G	Splice acceptor site mutation – Intron 8 (-2)	Yes	33	3.46	-1.06	Faster
13	PDRD024	c.1083_1084insT	L362Sfs*56	Yes	47	6.01	0.05	Average
14	PDRD027	c.1099_1100ins TACC	R367Lfs*52	Yes	25	9.54	1.58	Slower
15	PDRD026	c.1780delC	L594Ffs*55	Yes	16	4.69	-0.52	Faster

Supplementary Table 1| Patients included in molecular studies. Patients with choroideremia from which analyses on donated fibroblast samples were conducted. Patients are listed order of loading in gel lanes in Figure 4A from left to right. Half-life of autofluorescence area shrinkage as calculated in Fig 1 is listed together with the standard deviations of the half-life from the cohort mean (SD) (5.86 ± 2.31). For further details regarding the non-contiguous exon duplication mutation in PDRD011, see Edwards et al.[30] Half-life was not calculated for PDRD011 as only two imaging time points were available, and PDRD028 was not included in area analysis due to poor image quality. Although the majority of transcripts for patient PDRD031 are predicted to undergo non-sense mediated decay, this patient has previously been shown to produce a low quantity of wildtype transcript,[7] and was therefore excluded from the analysis of compensatory *CHML* upregulation.

Gel Lane	Study Number	Gene
1	PDRD015	TOPORS
2	PDRD016	CAPN5
3	PDRD019	CEP290
4	PDRD004	RHO
5	PDRD006	TOPORS
6	PDRD003	USH2A
7	PDRD007	ABCA4
8	PDRD008	MAK
9	PDRD009	USH2A
10	PDRD021	RPGR
11	PDRD025	CDHR1
12	PDRD010	ABCA4
13	PDRD020	RPGR
14	PDRD017	IMPG2

Supplementary Table 2 | Control patients. Fibroblast samples used as controls in this study were donated by patients with an inherited retinal degeneration but a normal copy of *CHM*. Patients are listed in order of sample loading in Fig 4B from left to right.

Gel Lane	Study Number	*CHM* Variant
1	PDRD005	c.117_314del
2	PDRD011	Non-contiguous duplication exons 1-2 & exons 9-12
3	PDRD012	c.655C>T
4	PDRD013	c.757C>T
5	PDRD014	c.179delA
6	PDRD018	c.799C>T
7	PDRD022	c.492_493delGA
8	PDRD023	c.877C>T
9	PDRD024	c.1083dupT
10	PDRD026	c.1780delC
11	PDRD027	c.1099_1100insTACC
12	PDRD028	c.406_407insT
13	PDRD029	c.941-2A>G
14	PDRD030	c.282delT

Supplementary Table 3| Patients details from Fig 4C. Patients included in the western blot for REP2 in Fig 4C, listed order of sample loading from left to right.