Targeted Exome Sequencing of Congenital Cataracts Related Genes: Broadening the Mutation Spectrum and Genotype–Phenotype Correlations in 27 Chinese Han Families

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Supplementary Information

Gene	Inheritance	Genomic DNA	mRNA	Protein
EPHA2	AD/AR	NC_000001.10	NM_004431.3	NP_004422.2
FOXE3	AD/AR	NC_000001.10	NM_012186.2	NP_036318.1
GJA8	AD/AR	NC_000001.10	NM_005267.4	NP_005258.2
CRYGD	AD	NC_000002.11	NM_006891.3	NP_008822.2
CRYGC	AD	NC_000002.11	NM_020989.3	NP_066269.1
CRYGB	AD	NC_000002.12	NM_005210.3	NP_005201.2
CRYGA	N/A	NC_000002.12	NM_014617.3	NP_055432.2
CRYBA2	AD	NC_000002.12	NM_057093.1	NP_476434.1
KCNJ13	AD	NC_000002.12	NM_002242.4	NP_002233.2
FYCO1	AR	NC_000003.11	NM_024513.3	NP_078789.2
BFSP2	AD/AR	NC_000003.11	NM_003571.2	NP_003562.1
CRYGS	AD	NC_000003.11	NM_017541.2	NP_060011.1
EZR	N/A	NC_000006.12	NM_003379.4	NP_003370.2
GCNT2	AR	NC_000006.11	NM_001491.2	NP_001482.1
EYA1	AD	NC_000008.10	NM_000503.4	NP_000494.2
TDRD7	AR	NC_000009.11	NM_014290.2	NP_055105.2
SLC16A12	AD	NC_000010.10	NM_213606.3	NP_998771.3
PITX3	AD/AR	NC_000010.10	NM_005029.3	NP_005020.1
VIM	AD	NC_000010.10	NM_003380.3	NP_003371.2
PAX6	AD	NC_000011.10	NM_001258463.1	NP_001245392.1
CRYAB	AD	NC_000011.9	NM_001885.1	NP_001876.1
MIP	AD	NC_000012.11	NM_012064.3	NP_036196.1
GJA3	AD	NC_000013.10	NM_021954.3	NP_068773.2
VSX2	AR	NC_000014.9	NM_182894.2	NP_878314.1
MIR184	AD	NC_000015.10	N/A	N/A
HSF4	AD/AR	NC_000016.9	NM_001040667.2	NP_001035757.1
MAF	AD	NC_000016.9	NM_005360.4	NP_005351.2
TMEM114	AD	NC_000016.9	NM_001146336.1	NP_001139808.1
CRYBA1	AD	NC_000017.10	NM_005208.4	NP_005199.2
FTL	AD	NC_000019.9	NM_000146.3	NP_000137.2
LIM2	AR	NC_000019.9	NM_030657.3	NP_085915.2
CHMP4B	AD	NC_000020.10	NM_176812.4	NP_789782.1
BFSP1	AR	NC_000020.10	NM_001278607.1	NP_001265536.1
CRYAA	AD/AR	NC_000021.8	NM_000394.2	NP_000385.1
CRYBB2	AD	NC_000022.10	NM_000496.2	NP_000487.1
CRYBB3	AD/AR	NC_000022.10	NM_000496.2	NP_000487.1
CRYBB1	AD/AR	NC_000022.10	NM_001887.3	NP_001878.1
CRYBA4	AD	NC_000022.10	NM_001886.2	NP_001877.1
NHS	XL	NC_000023.10	NM_198270.2	NP_938011.1
TGFB2	N/A	NC_000001.11	NM_001135599.2	NP_001129071.1

CYP27A1	AR	NC_000002.12	NM_000784.3	NP_000775.1
SIL1	AR	NC_000005.10	NM_001037633.1	NP_001032722.1
GALT	AR	NC_000009.11	NM_000155.3	NP_000146.2
FAM126A	AR	NC_000007.14	NM_032581.3	NP_115970.2
WT1	N/A	NC_000011.10	NM_000378.4	NP_000369.3
COL2A1	AD	NC_000012.12	NM_001844.4	NP_001835.3
GFER	AR	NC_000016.10	NM_005262.2	NP_005253.3
GALK1	AR	NC_000017.10	NM_000154.1	NP_000145.1
CTDP1	AR	NC_000018.10	NM_004715.4	NP_004706.3
DNM2	N/A	NC_000019.10	NM_001005360.2	NP_001005360.1
DMPK	AD	NC_000019.10	NM_001081563.2	NP_001075032.1
ERCC1	N/A	NC_000019.10	NM_001983.3	NP_001974.1
MYH9	AD	NC_000022.11	NM_002473.5	NP_002464.1
OCRL1	N/A	NC_000023.11	NM_000276.3	NP_000267.2

Note: AD = autosomal dominant; AR = autosomal recessive; XL = X-linked.

Table S1. 54 genes related to inherited cataracts

SNV ID	Gene	Family ID	mRNA	cDNA	Amino acid
SNV01	CRYBA4	1	NM_001886	c.26C>T	p.A9V
SNV02	CRYGS	4	NM_017541	c.53G>A	p.G18D
SNV03	CRYAA	4	NM_000394	c.312+4A>G	
SNV04	MYH9	5	NM_002473	c.1270C>T	p.R424W
SNV05	CRYBA1	5	NM_005208	c.269_271del	p.90_91del
SNV06	HSF4	6	NM_001538	c.-497-8C>G	
SNV07	CRYGS	7	NM_017541	c.224G>T	p.G75V
SNV08	MYH9	8	NM_002473	c.3754G>A	p.A1252T
SNV09	HSF4	9	NM_001040667	c.347G>A	p.R116H
SNV10	CRYBA1	9	NM_005208	c.607C>T	p.Q203X
SNV11	EZR	10	NM_003379	c.1597-7insTAAT	
SNV12	EZR	10	NM_003379	c.1439C>T	p.P480L
SNV13	MYH9	13	NM_00247	c.2900T>C	p.V967A
SNV14	VIM	14	NM_003380	c.623A>G	p.Q208R
SNV15	MIP	15	NM_012064	c.607-1G>A	
SNV16	CRYBB2	16	NM_000496	c.463C>T	p.Q155X
SNV17	CRYBB2	17	NM_000496	c.452G>A	p.W151X
SNV18	GJA3	17	NM_021954	c.304A>C	p.M102L
SNV19	FYCO1	18	NM_024513	c.3215C>T	p.A1072V
SNV20	CRYBA2	18	NM_057093	c.343A>G	p.N115D
SNV21	BFSP1	19	NM_001278607.1	c.625+3A>G	
SNV22	GJA8	20	NM_005267	c.98G>A	p.R33Q
SNV23	OCRL	21	NM_001587	c.430G>T	p.V144F
SNV24	CRYGD	22	NM_006891	c.70C>A	p.P24T
SNV25	EPHA2	22	NM_004431	c.1339C>T	p.R447C
SNV26	PAX6	24	NM_001258462	c.795delA	p.E265fs
SNV27	CRYGD	26	NM_006891	c.43C>A	p.R15S
SNV28	PAX6	27	NM_001258462	c.342G>A	p.W114X
SNV29	LIM2	28	NM_030657	c.514C>T	p.R172C
SNV30	SIL1	28	NM_022464	c.1115G>A	p.G372D

Table S2. Potential pathogenic mutations in 27 Chinese families with congenital cataract.

SNV ID	Gene	Primers	
		F	R
SNV01	CRYBA4	5'-TGGAAGATGGCATTGGTGACA-3'	5'-GGATTCATGGGGACCTGAACC-3'
SNV02	CRYGS	5'-AATTAAGCCACCCAGCTCCT-3'	5'-AAGCAAGAGAAAGCGGACAG-3'
SNV03	CRYAA	5'-CACCTGACCATAGCCAAACAAC-3'	5'-TCTCCCAGGGTTGAAGGCA-3'
SNV04	MYH9	5'-AGATCTCGAAGCCGGCAATGT-3'	5'-TTGGCCAAGGCGACCTATGAG-3'
SNV05	CRYBA1	5'-GCCTTCTCCCCAAGGCCATA-3'	5'-CCCTCATATGCACGGAAGTGG-3'
SNV06	HSF4	5'-CCCGCGCCTGCGCACCTATAC-3'	5'-GTACCCCGCGCGTTCCCTGTC-3'
SNV07	CRYGS	5'-TCTTCAAAACACTCAAGAGGCAGAGA-3'	5'-TGTCAGAAAGCAATGTTGTAAGGTGA-3'
SNV08	MYH9	5'-TCCTTGGTGAGCTTGCTGGAC-3'	5'-GACCAGCCAGCCTTGTGTCAG-3'
SNV09	HSF4	5'-GGCACCGCTCACCCTCCTGGT-3'	5'-CGCAGGAGCAAGGCAGGCAGT-3'
SNV10	CRYBA1	5'-ATCTCCCCCAGACATGCCTCT-3'	5'-TGTGGATTTCAGCAGCTAACATTTG-3'
SNV11	EZR	5'-TCTAGTGAGGGCATCCG-3'	5'-TTCCGTAATTCAATCAGTCC-3'
SNV12	EZR	5'-CAGGACAGAGGGAGGTGA-3'	5'-ACATTAAGCAGCATTGGTCTA-3'
SNV13	MYH9	5'-CTCCAGGGAGCACTTGCAGTT-3'	5'-TCTGCGTCCTGCCTGTTTCAT-3'
SNV14	VIM	5'-GGAGCGAGACAAAGGGATGGT-3'	5'-TGTGGTCTTCCCGCCACTAGA-3'
SNV15	MIP	5'-GCTTCTACAGGGCCTGGGTGT-3'	5'-TTCCACTAAGGTGGCTGGAAAAA-3'
SNV16	CRYBB2	5'-CACCCTTCCTAGTGGCTTATGGATG-3'	5'-GGACTGCACCTGGGGGTGA-3'
SNV17	CRYBB2	5'-AGTGGCTTATGGATGCTCTATCTCT-3'	5'-AAGTCGCTGCTGTCCTTGTAGT-3'
SNV18	GJA3	5'-GCCCACCTCGAACAGCGTCTTGA-3'	5'-GGAGGACGTGTGGGGCGATGA-3'
SNV19	FYCO1	5'-GTGGCATGCTTCCAGCAGAA-3'	5'-TGGCACACCAGCCACTTTATG-3'
SNV20	CRYBA2	5'-TTTCCTCCACCCCCTCATGTT-3'	5'-TGCCTGTGGGTCCTAGACAGC-3'
SNV21	BFSP1	5'-AGCCACTCTGCACTGGACACC-3'	5'-TTTCTGCCAGGCTGACCTCTG-3'
SNV22	GJA8	5'-CAGATATTGACTCAGGGTTG-3'	5'-GATGATGTGGCAGATGTAGG-3'
SNV23	OCRL	5'-CAGTGTCATGGCAAGCACAGC-3'	5'-ACTGGTCAGTGGGCCTGGACT-3'
SNV24	CRYGD	5'-TGCTTGAAACCATCCAGTGAGTG-3'	5'-GCGACCAAAACCCACAACAAG-3'
SNV25	EPHA2	5'-TGCCTGCTCGTAGGCAGCTT-3'	5'-CTCTGCTGTGCTGCCTTGGG-3'
SNV26	PAX6	5'-TCTCCATTTGGCCCTTCGATTA-3'	5'-GGGAGGTGGGAACCAGTTTGA-3'
SNV27	CRYGD	5'-CCTCGCCTTGTCCCGC-3'	5'-TTAACTTTTGCTTGAAACCATCCA-3'
SNV28	PAX6	5'-TTCCTCTCTGTTCCCCCAGGT-3'	5'-ATGCAGGTGTCCAACGGATGT-3'
SNV29	LIM2	5'-GTGGGACTCATGTGGGACACC-3'	5'-CCCAAACCTATCCCCCAATCA-3'
SNV30	SIL1	5'-AGCCAGCACTGCCAAGATGTC-3'	5'-CCTCGTGCCTTCCTGTCTGAA-3'

Table S3. Primers used to amplify and sequence the variants regions in this study.

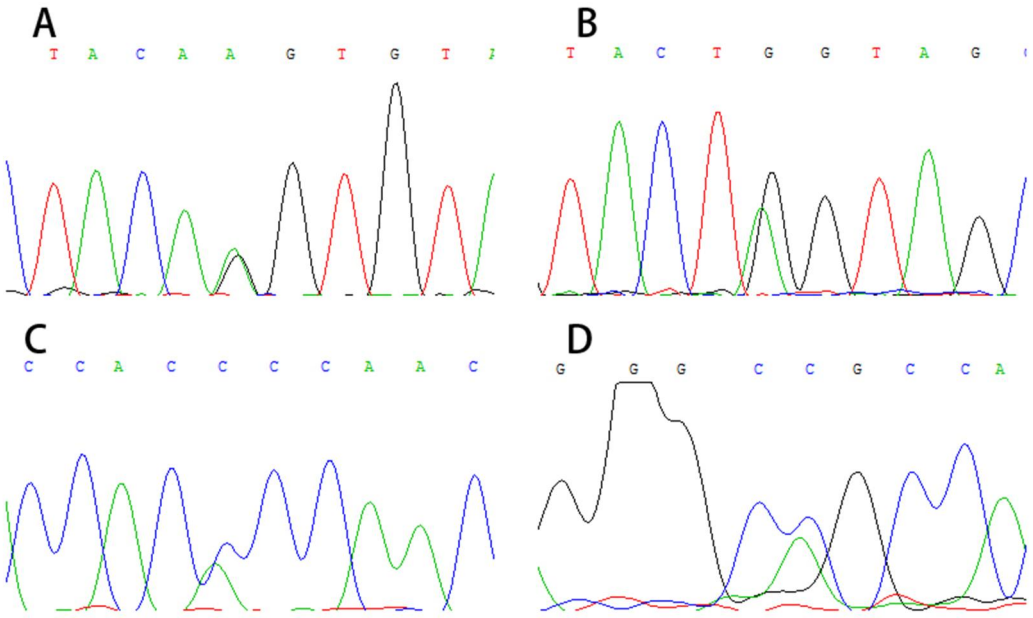

Figure S1. Sequencing results of four recurrent disease-causing mutations. (A) Forward sequencing showed c.607-1G>A mutation of MIP gene in patients from family 15. (B) Reverse sequencing showed c.463C>T mutation of CRYBB2 gene in patients from family 16. (C) Forward sequencing showed c.70C>A mutation of CRYGD gene in patients from family 22. (D) Forward sequencing showed c.43C>A mutation of CRYGD gene in patients from family 26.

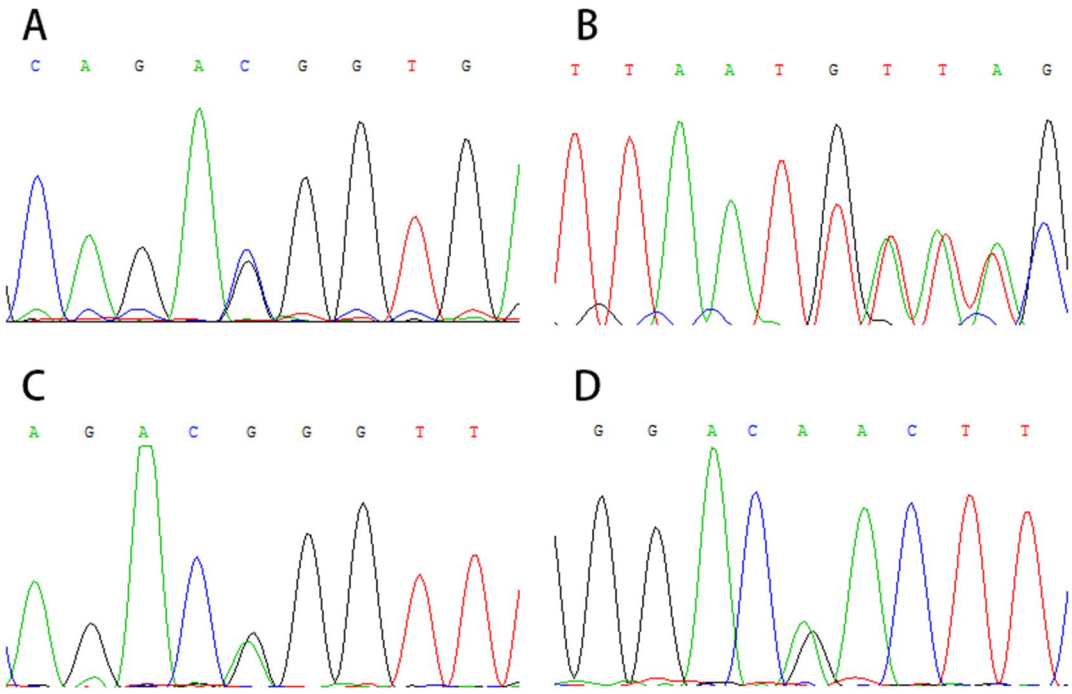

Figure S2. Sequencing results of four four pathogenic mutations could not be strongly associated with congenital cataracts. (A) Forward sequencing showed c.-497-8C>G mutation of HSF4 gene in patients from family 6. (B) Forward sequencing showed c.1597-7insTAAT mutation

of EZR gene in patients from family 10. (C) Forward sequencing showed c.623A>G mutation of VIM gene in patients from family 14. (D) Forward sequencing showed c.343A>G mutation of CRYBA2 gene in patients from family 18.