A			Catalytic	Domain	Regulatory	Domain	Regulatory Dom	ain
	DI		Dlla	DIIb	DIII		DIV	
B								
-	zCAPN5a	1	MFSSVKPFEG	Gefsalrkoco	QNHTLFEDPVFRAED)SLFLQGNI	RLGKVTWKRPKDLCED	60
	zCAPN5b	1	MFSSAKAFEG	Ghystlkrocl	QSGALFEDPLFPAVDI)SLFYQGNI	RIGRVHWKRPEELCDD	60
	hCAPN5	1	MFSCVKPYEI	Conysalrrdcr	RRKVLFEDPLFPATDI)SLYYKGTI	PGPAVRWKRPKGICED	60
	zCAPN5a	61	PHLFVNGIS	AHDLNQGQLGNC	WFVAACSSLASREALW	NQKVIPDWI	KDQEWDKNKPESYAGI	120
	zCAPN5b	61	PHLFVDGIS	AHDLHQGQLGNC	WFVAACSSLASRESLW	NQKVIPDWI	KEQEWDPEKADSYAGI	120
	hCAPN5	61	PRLFVDGIS	SHDLHQGQVGNC	WFVAACSSLASRESLW	NQKVIPDWI	KEQEWDPEKPNAYAGI	120
	zCAPN5a zCAPN5b hCAPN5	121 121 121	Loop 1 FHFRFWRFGI FHFRFWRFGI FHFHFWRFGI	WVGVVIDDRLP WVDVVIDDRLP WVDVVIDDRLP	TANGKLIYCHSNDSNE TVDNQLVYCHSNDSNE TVNNQLIYCHSNSRNE	SFWSALVEI SFWSALVEI SFWCALVEI	KAYAKMCGCYEALDGG KAYAKVYGCYEALDGG KAYAKLAGCYQALDGG	180 180 180
	zCAPN5a	181	NTADALVDF1	rggvsepmdlle	GKFAQDEEARHQLFDH	RVLKVHNR(GGLISCSIRATTQADM	240
	zCAPN5b	181	NTADALVDF1	rggvsepmdlle	GQFAQDETARNQLFEH	RVLKVHNRI	DGLISCSIRATTVEDM	240
	hCAPN5	181	NTADALVDF1	rggvsepidlte	GDFANDETKRNQLFEH	RMLKVHSR(GGLISASIRAVTAADM	240
	zCAPN5a zCAPN5b hCAPN5	241 241 241	EARLDCGI VE EARLDCGI VE EARLACGI VE	KGHAYAVTDVRK KGHAYAVTDVRK KGHAYAVTDVRK	vrlgsgllaffkseki vrlghgllayfkseki vrlghgllaffkseki	SMIRMRNI HMIRMRNI JDMIRIRNI	Loop 2 PWGQRGWNGAWSDSSE PWGEKEWSGPWSDSSE PWGEREWNGPWSDTSE	300 300 300
	zCAPN5a zCAPN5b hCAPN5	301 301 301	LOOP 2 EWKRVSKGE EWKKVSKSE EWQKVSKSE	RERLGVTVEDDG REKLGVTVQDDG REKMGVTVQDDG	EFWMDFDDFCKHFTDI EFWMNFEDFCHYFTDI EFWMTFEDVCRYFTDI	LILCRLIN LILCRLIN LIKCRVIN	.00p 3 TSYLSIHKTWEEEVMR TSYLSIHKTWEEEVMR TSHLSIHKTWEEARLH	360 360 360
	zCAPN5a	361	GCWSRHDDPI	LRNRSGGCINHK	TTFLQNPQYVFDVTK#	AEDEVLICI	LQQQDKRARAKGE	417
	zCAPN5b	361	GLWLHRDEPI	LRNRAGGCINHK	TTFLQNPQYVFDVRK\	/EDEVLICI	LQQKERRATPKEGKGE	420
	hCAPN5	361	GAWTLHEDPF	RQNRGGGCINHK	DTFFQNPQYIFEVKK#	?EDEVLICI	LQQRPKRSTRREGKGE	420
	zCAPN5a	418	NMAIGFDIQF	RVELNRIYRMHS	IQKSVGSSIYINSRS\	/FLRKDLKI	EGRYVIVPSTFDPGMP	477
	zCAPN5b	421	NLAIGFDIHF	RVELNRKYRMHS	AQQKVAGSIYINSRC\	/FLRKELKI	EGRYVIIPTTFDPGQQ	480
	hCAPN5	421	NLAIGFDIYF	RVEENRQYRMHS	LQHKAASSIYINSRS\	/FLRTDQPI	EGRYVIIPTTFEPGHT	480
	zCAPN5a	478	GDFLLRIFTI	OVPSDCKELTVD	EPPQTCWTSCCGYPKI	LVTQVHVII	RADGLKALDGDGSSDP	537
	zCAPN5b	481	GEFLLRVFTI	OVPSDCKELTLD	EPPQTCWTGMCGYPQI	LVTQVHVLS	SAEGLQGQDANGASDP	540
	hCAPN5	481	GEFLLRVFTI	OVPSNCRELRLD	EPPHTCWSSLCGYPQI	LVTQVHVLS	GAAGLKDSPTGANS	538
	zCAPN5a	538	YIIISCEGER	KVRSPVHKDTQS	PDFDVKAVFYRKKPK()PIRIQIYI	NKNLLSDSFMGQVTLN	597
	zCAPN5b	541	YVIITCEGER	KVRSPVHKDTRC	PNFDIKGIFYRKKPK	GIHIEIYI	NKNVIVDTFLGQVTLF	600
	hCAPN5	539	YVIIKCEGDR	KVRSAVQKGTST	PEYNVKGIFYRKKLS()PITVQVWI	NHRVLKDEFLGQVHLK	598
	zCAPN5a zCAPN5b hCAPN5	598 601 599	GDLSDLQQLH SDPNDRQEQH ADPDNLQALH	itlrlqdkgsrk itvylkdkgsrq itlhlrdrnsrq	NNDLPGLLSVSLTTSI DNNLPGTLTVRVITCI PSNLPGTVAVHILSSI	ovltni (Ppltni (Islmav (539 542 540	

Supplemental figure 1. High level of conservation among zebrafish orthologs of CAPN5. (A) CAPN5 is composed of four domains; DI (yellow), DII (red), DIII (light blue) and DIV (purple). Four of the identified mutations are location in DII (green) and one in DIII. (B) Primary Protein alignment of the zebrafish CAPN5 orthologs and human CAPN5 shows high conservation in the catalytic residues (blue) as well as the identified mutations (green). High conservation can also be seen amongst the gated loops of DII (black boxes).



capn1a capn1b capn2a capn2b

Supplementary Figure 2. Expression of *capn1* and *capn2* in response to acute light damage. qPCR for *capn1a/b* and *capn2a/b* during and following light damage. A significant decrease in expression of *capn2a/b* was observed during light damage and a significant increase was observed after light damage. *Capn1a/b* expression did not change during LD. RT, reverse transcriptase; NT, no template control; p>0.05 (*).

Supplemental Table 1. Primer sequences used for RT-PCR and qPCR. RT-PCR primers were also used to design WISH and FISH probes.

Supplemental Table 2. Antibodies used for immunohistochemistry (IHC).