

List of Primers

Primer name	Primer sequence 5'	Purpose
SacII-Gly-mCatZ	GAGGCTCCGCGGTGGACTGCCCAAGAGCTGGGACTG	
SacII-Gly-mCatV	GAGGCTCCGCGGTGGACTACCCAAGTCTGTGGATTGGAGAAAG	
SacII-Gly-mCatL	GAGGCTCCGCGGTGGAGCCCCCAGATCTGTGGATTGGAGAG	
SacII-Gly-mCatC	GAGGCTCCGCGGTGGATTGCCAACATCTTGGGACTGGAGAAATG	
SacII-Gly-mCatK	GAGGCTCCGCGGTGGAGCCCCCGATTCTGTGGATTATAGAAAGAAAG	
StrepTag-XbaI-rev	gtcatctctagatcatttctcaaattgtggaatgactccagc	
fw-CatZ KtoP	cggtggactgccccgagctgggactgg	K3P mutagenesis of CTSZ ₍₁₋₂₂₎ reporter
rev-CatZ KtoP	ccagtcccagctcggggagctccaccg	K3P mutagenesis of CTSZ ₍₁₋₂₂₎ reporter
fw_CatZ KtoG	cggtggactgccccgagctgggactgg	K3G mutagenesis of CTSZ ₍₁₋₂₂₎ reporter
Rev_CatZ KtoG	ccagtcccagctccccgagctccaccg	K3G mutagenesis of CTSZ ₍₁₋₂₂₎ reporter
fw_CatZdLP	gctccgcggtggaagagctgggact	ΔLP mutagenesis of CTSZ ₍₁₋₂₂₎ reporter
rev_CatZdLP	agtcccagctcttccaccgcggagc	ΔLP mutagenesis of CTSZ ₍₁₋₂₂₎ reporter

qRT-PCR primer:

Target gene		Sequence (5'- 3')
Human β-Actin	fwd	AGCACTGTGTTGGCGTACAG
	rev	CTCTTCCAGCCTTCCTTCCT
Human CTSB	fwd	TGTAATGGTGGCTATCCTGCTGAG
	rev	TCCGTAGTGCTTGTCTGTTTGTAG
Human CTSC	fwd	TCAACTGCTCGGTTATGGGAC
	rev	CTCGTTGCAGTAAGTGGTCAC
Human CTSD	fwd	ATTCCCGAGGTGCTCAAGAA
	rev	AAGCGATGTCCAGCAGTTTG
Human CTSL1	fwd	GAATCCTACACTCATCCTTGCTGCC
	rev	ACACTGCTCTCCTCCATCCTTCTTC
Human CTSV	fwd	TCCGTGAGCCTCTGTTTCTT
	rev	CTAGCCATGAAGCCACCATT

Human CTSZ	fwd	GCATCCCTGACGAGACCTG
	rev	TTCCACAGCTGATGGGACC
Human StfB	fwd	CCTGTGTTTAAGGCCGTGTC
	rev	AGGTCAGCTCATCATGCTTG

Peptide	Source	Theor. MW	Sequence	Purity in %
BRCA2 ₍₁₋₄₀₎	GeneScript	4587.24	MPIGSKERPTFFEIFKTRCNKADLGPISLNWFEEELSSEAP	85.0 %
Syk ₍₁₋₃₁₎	GeneScript	3448.78	MASSGMADSANHLPFFFGNITREEAEDYLVQ	85.5 %
LGMN ₍₁₋₂₂₎	GeneScript	2261,48	VPIDDPEDGGKHWVIVAGSNG	98.8 %
LIPA ₍₁₋₂₂₎	GeneScript	2379,71	GPKPVVFLQHGLLADSSNWVTN	83.8 %
CTSA ₍₁₋₂₂₎	GeneScript	2557,86	APDQDEIQRLPGLAKQPSFRQY	92.3 %
CTSB ₍₁₋₂₂₎	GeneScript	2600,94	LPASFDAREQWPQCPTIKEIRD	89.9 %
CTSC ₍₁₋₂₂₎	GeneScript	2622,94	LPTSWDWRNVHGINFVSPVRNQ	98.5 %
CTSD ₍₁₋₂₂₎	GeneScript	2427,76	GPIPEVLKKNYMDAQYYGEIGIG	89.6 %
CTSH ₍₁₋₂₂₎	GeneScript	2474,81	YPPSVDWRKKGNFVSPVKNQGA	90.7 %
CTSK ₍₁₋₁₃₎	GeneScript	1497.67	APDSVDYRKKGYV	91.3 %
CTSL1 ₍₁₋₂₂₎	GeneScript	2518,84	APRSVDWREKGYVTPVKNQQQC	94.5 %
CTSO ₍₁₋₂₂₎	GeneScript	2761,23	LPLRFDWRDKQVVTQVRNQQMC	93.2 %
CTSS ₍₁₋₂₂₎	GeneScript	2499,80	LPDSVDWREKGCVTEVKYQGSC	77.9 %
CTSV ₍₁₋₂₂₎	GeneScript	2603,09	LPKSVDWRRKKGYVTPVKNQKQC	95.9 %
CTSW ₍₁₋₂₂₎	GeneScript	2489,88	VPFSCDWRKVASAISPIKDQKN	95.8 %
CTSZ ₍₁₋₂₂₎	GeneScript	2619,89	LPKSWDWRNVNVDGVNYASITRNQ	93.0 %
CTSZ ΔLP	GeneScript	2409.61	KSWDWRNVNVDGVNYASITRNQ	99.9 %
CTSZ P2G	GeneScript	2579.82	L G KSWDWRNVNVDGVNYASITRNQ	95.9 %
CTSZ K3P	GeneScript	2588,83	LP P SWDWRNVNVDGVNYASITRNQ	94.1 %
CTSZ K3G	GeneScript	2548,76	LP G SWDWRNVNVDGVNYASITRNQ	81.5 %
CTSZ L1A	GeneScript	2577,81	A P KSWDWRNVNVDGVNYASITRNQ	93.4 %
CTSZ K3A	GeneScript	2562,79	LP A SWDWRNVNVDGVNYASITRNQ	94.7 %
CTSZ S4A	GeneScript	2603,89	LPK A WDWRNVNVDGVNYASITRNQ	94.8 %
CTSZ W5A	GeneScript	2504,75	LPK S ADWRNVNVDGVNYASITRNQ	94.4 %
CTSZ D6A	GeneScript	2575,88	LPKSW A WRNVNVDGVNYASITRNQ	97.1 %
CTSZ W7A	GeneScript	2504,75	LPKSWD A RNVNVDGVNYASITRNQ	92.1 %
CTSZ R8A	GeneScript	2534,78	LPKSWDW A NVDGVNYASITRNQ	93.0 %
CTSZ N9A	GeneScript	2576,86	LPKSWDW R AVNVDGVNYASITRNQ	82.7 %