

Supplemental Table S1. Summary of tandem mini genes (TMGs)

TMG	Gene No	mutation	reference number of mRNA	protein change	Sequence
TMG1	1	missense mutation	NM_194315.1	p.Gly243Arg	NLAGLQQANRHRHLLGGALANLFVI
TMG1	2	missense mutation	NM_001289862.1	p.Ala1016Thr	PPMKNPSTASTLSTGSPMKNPS
TMG1	3	missense mutation	NM_015074.3	p.Thr421Ile	TSVTSIQERIMSPJGGEEAIERLKE
TMG1	4	missense mutation	NM_004958.3	p.Leu1550Val	RDTHDGAFYRAVVALHQDLFLAQQ
TMG1	5	missense mutation	NM_006474.4	p.Gln59Pro	LGLWPRCFLIFPLRILLGPQESN
TMG1	6	missense mutation	NM_016252.3	p.Glu861Lys	DLSVHKKHCSDSKGKEFKESHVSQP
TMG1	7	missense mutation	NM_018202.5	p.Gln530Arg	KKLTMDMKVKEDRIRELELKVQELR
TMG1	8	missense mutation	NM_182578.3	p.Arg44Thr	SAFGSSTDSMFSTFLPEKTDLKDYA
TMG1	9	missense mutation	NM_005547.2	p.Gln172Arg	EGHLKHLEQQEGRLLKHPQQEQGLE
TMG1	10	missense mutation	NM_003126.2	p.Arg1076Cys	YRSLLDRAEERRCRLLRQYNEFLLA
TMG1	11	missense mutation	NM_012231.4	p.Leu1703Val	SDVIPPTPKTTPVFMTPPLTPPNEA
TMG2	12	missense mutation	NM_001171603.1	p.Ala92Val	QENEKPLPENMDVFEKVRTKLETQP
TMG2	13	missense mutation	NM_001282597.1	p.Ala365Glu	TGRKEKGDPLNIEIDKMTKKTRDLR
TMG2	14	missense mutation	NM_015348.1	p.Thr264Asn	LHLELPTGQQGGNRKLWEIPPYETK
TMG2	15	missense mutation	NM_032143.3	p.Arg787Ser	SFQLKQYRSLILSFVREWSSLTAMK
TMG2	16	missense mutation	NM_022648.4	p.Ser1309Tyr	SPSLGRHLGGSGYVVPSPCLDRHV
TMG2	17	missense mutation	NM_015512.4	p.Lys1868Asn	HGLMLVGPTGSGNSTCYRVLAAAMT
TMG2	18	missense mutation	NM_015136.2	p.Thr1365Met	SGECHCHEGFHGMACEVCELGRYGP
TMG2	19	missense mutation	NM_005929.5	p.Arg284Gln	HLARVPAHAVVQADTDGGLIFRLL
TMG2	20	missense mutation	NM_001039127.5	p.Ser312Leu	EHKRIHAGEKRFLLCEECGNVFTSS
TMG2	21	missense mutation	NM_006259.2	p.Leu437Arg	KLKSKALSLEMIQRKEKVARFSSSSP
TMG2	22	missense mutation	NM_018717.4	p.Ala1020Val	ANTGTVRTLNPAVMGRQMMPPLPGQ
TMG3	23	missense mutation	NM_007193.4	p.Glu141Lys	EAYCLQYSNNLQKDIYSETSGHFRD
TMG3	24	missense mutation	NM_018429.2	p.Glu162Gln	KLREMLKEELRKQKQKQWKNKYAINE
TMG3	25	missense mutation	NM_022897.3	p.Leu49Arg	LIDSPECLSKCQRLLQEQGTTSYAQL
TMG3	26	missense mutation	NM_024872.2	p.Gly95Asp	KVWALLYAGGSPDVARLESWEVRDG
TMG3	27	missense mutation	NM_024872.2	p.Ala90Ser	KKCWRKVWALLYSGGPGSVARLESW
TMG3	28	missense mutation	NM_004666.2	p.Gly335Val	IEALSSGNKEFKVTVFFDEFVFKL
TMG3	29	missense mutation	NM_001042683.2	p.Arg1220Pro	REAVKNLEGPPSPNVIESATVCHLR
TMG3	30	missense mutation	NM_025059.3	p.Gly662Ser	LADFREVYSQMLSLNVTSLALPDYE
TMG3	31	missense mutation	NM_152701.4	p.Ile4594Thr	TMLITIMPRLLAISKAKNLQNIYD
TMG3	32	missense mutation	NM_001293626.1	p.Ser2204Pro	DTTSNSFSIMTTFSESTNAMNTTV
TMG3	33	missense mutation	NM_198495.2	p.Gly735Val	PPPPGTMGASRVYFPPRDFGPPH
TMG4	34	missense mutation	NM_003575.2	p.Met147Thr	DCEKTAVEFGNHTESKWAVLGTLLQ
TMG4	35	missense mutation	NM_198584.2	p.Ser207Thr	YPGSLTVPPLELTVTWIVLQKPINI
TMG4	36	missense mutation	NM_015902.5	p.Ala2014Val	ATLNDKDDDSLPLVETGQNHFFRRS
TMG4	37	missense mutation	NM_133497.3	p.Ala222Ser	LSERLKIQHELRSQAQVEAEELFR
TMG4	38	missense mutation	NM_002072.4	p.Thr96Ser	FTAMQAMIRAMD S LKIPYKYEHNKA
TMG4	39	missense mutation	NM_153698.1	p.Ser205Thr	RDRNRDLHKPINTVLQVLGVQHVNF
TMG4	40	missense mutation	NM_001340.3	p.Lys46Gln	ALLFPKQRPQTQRRSKQQRDNT
TMG4	41	missense mutation	NM_020824.3	p.Pro796Leu	KRMEERKASSTSLPGDSLASIPFID
TMG4	42	missense mutation	NM_032199.2	p.Leu690Met	LYSRGNPGIMSPMAKKKLLSQVSGA
TMG4	43	missense mutation	NM_017551.2	p.Pro779Leu	SKGYGIALQHGS L YRDLFSQRILEL
TMG4	44	missense mutation	NM_016341.3	p.Asp1667Asn	KKESRQIAPELSNLVIYQAVKFPFG
TMG5	45	missense mutation	NM_173791.3	p.Leu25Met	LGSFLTLLAQFFMLYRQPEPPADE
TMG5	46	missense mutation	NM_001244963.1	p.Arg1134Gly	GDESKKPLPSSSGTPTANANSFGFK
TMG5	47	missense mutation	NM_178570.2	p.Gln277Arg	CDCRARPLWAWFRARVSSSDVTCA
TMG5	48	missense mutation	NM_019021.3	p.Ile141Ser	DLRWCS T CSHSNSFEILVI
TMG5	49	missense mutation	NM_021957.3	p.Ala137Val	WNLD R WKGDLWEVCSVGIPYHDREA
TMG5	50	missense mutation	NM_003482.3	p.Asp3579Gly	VTEQSKIQKQLGQVVRKQKEHTNL
TMG5	51	missense mutation	NM_024902.2	p.Tyr189Asn	PLSVRLYRLGLANLAFTGPLAYSAL
TMG5	52	missense mutation	NM_002624.3	p.Leu12Arg	MAQSINITELNRPQLEMLKNQLDQ
TMG5	53	missense mutation	NM_175623.3	p.Tyr417His	KHRIKLGDSN Y HYISPFCRYRITS
TMG5	54	missense mutation	NM_014706.3	p.Ala671Gly	NVEVAAGPAGKCGAVDVEPPSKQKE
TMG5	55	missense mutation	NM_014868.4	p.Ile249Leu	ITRCGHIFCWACLLHYLSLSEKTSWS
TMG6	56	missense mutation	NM_018036.5	p.Gly1992Cys	HRLAHQPVDLRECVAKAYSVVKEGI
TMG6	57	missense mutation	NM_006291.2	p.Ala250Thr	LFPAEFGVAAAYTESYHQHFAAHLA
TMG6	58	missense mutation	NM_019074.3	p.Cys184Ser	RVICSDNYGDN S SRLCKKRNDFHG
TMG6	59	missense mutation	NM_022473.2	p.Leu1250Val	CPVYPVITARLSVPESTESFHEPSQ
TMG6	60	missense mutation	NM_004998.3	p.Tyr745Cys	RRNSINRNFIGDCIGMEEHPELQQF
TMG6	61	missense mutation	NM_144572.1	p.Lys450Asn	EQLGMLMETIQANDEVIILKSEGE
TMG6	62	missense mutation	NM_002952.3	p.Val112Leu	ASLKDEVLMKIMPLQKQTRAGQTRF
TMG6	63	missense mutation	NM_145254.1	p.Phe43Ile	GTLCPNSTLCSJPEM W YGVFLWAL
TMG6	64	missense mutation	NM_014853.2	p.Glu10Gln	MGSAEDAVKQKLLWNVKEVKQ
TMG6	65	missense mutation	NM_001372.3	p.Ser2752Arg	FDDIEDPVEQTQRPNLYCHANGIG
TMG7	66	missense mutation	NM_003771.4	p.Arg394Cys	VKARLEGEIATYCHLLEGEDCKLPP
TMG7	67	missense mutation	NM_004758.3	p.Arg1418His	RRGGGSPEKPPSHRRPPDPREHCSR
TMG7	68	missense mutation	NM_005121.2	p.Gln2136Pro	NQTS D VLRFVLEPYNALSWLTCDDPA
TMG7	69	missense mutation	NM_199242.2	p.Arg27Thr	LRQAIKIRRRRVTDLQDPPQMAPE
TMG7	70	missense mutation	NM_001941.4	p.Val458Phe	DIPRV T ALNRALFTVHVRDLDEGPE
TMG7	71	missense mutation	NM_020964.2	p.Glu264Asp	LVPFTKEQLKILDPG S WLENVESYL
TMG7	72	missense mutation	NM_144612.6	p.Arg2155Ser	RFFLETLELGELSKVRLEHDSSGYC
TMG7	73	missense mutation	NM_133475.1	p.Arg730Cys	SEKLQVELETRICGLEEALRQREFE
TMG7	74	missense mutation	NM_012335.3	p.Val23Leu	SHNVKQSGVDDMLLLPQITEDIAIA

TMG7	75	missense mutation	NM_020862.1	p.Thr46Lys	CPGRCICQNVAP <u>K</u> LTMLCAKTGLLF
TMG8	76	missense mutation	NM_052848.1	p.Asp86Asn	RLPVCSQQQGEPNLTEHEKVAILAQ
TMG8	77	missense mutation	NM_001256849.1	p.Met760Ile	SAKVYVYGD T DSV <u>I</u> CRFGVSSVAEAM
TMG8	78	missense mutation	NM_138578.1	p.Met159Thr	GGALCVESVDKETQVLVSRIAAWMA
TMG8	79	missense mutation	NM_018431.4	p.Ile159Val	PNLDVHGEALQV <u>T</u> YIEICLWDVQN
TMG8	80	missense mutation	NM_001256355.1	p.Ile111Met	PDNPPYDKGAFR <u>M</u> EINFPAYPFKP
TMG8	81	missense mutation	NM_001168465.1	p.Glu683Asp	LDGKSNLDDST <u>D</u> EVQSMDVSPVSK
TMG8	82	missense mutation	NM_007052.4	p.Leu365Val	IHIRAAGDWTEN <u>V</u> IRAFEQQYSPIP
TMG8	83	missense mutation	NM_024657.4	p.Thr849Asn	AEFQILKAELERN <u>K</u> EEKQELKECLK
TMG8	84	missense mutation	NM_001152.4	p.Val211Ile	KGMLPDPKNTH <u>I</u> ISWMIQTVTAV
TMG8	85	missense mutation	NM_001291527.1	p.Lys143Ile	VKEIRCLGRKYE <u>I</u> IFEMLEGVQGPT
TMG9	86	frameshift	NM_032789.3	p.Ala836fs	AENTGEFQEVVRL <u>R</u> HPPGRCPQQHPRRSCGAR VAPAAAA <u>V</u>
TMG9	87	frameshift	NM_001099661.1	p.Asp290del	AKKKHDKRSKRLE <u>E</u> EEEEEDNEGGEW
TMG9	88	frameshift	NM_003950.2	p.Asp362fs	KVRAGLFRSPGAWPPR <u>P</u> LRKGAAGAWAPTP LCSSDTKWGRLYWVEQGFPHFTSFLGPQNV TFGNRVVTTVTSGGHFGEGWALHPVWV <u>S</u>
TMG9	89	frameshift	NM_014643.3	p.Asp587_Glu588del	CAAADSPGSGLA <u>A</u> AEDSGEEGAPEP
TMG9	90	frameshift	NM_006181.2	p.Cys264fs	GGRCKCNGHASR <u>S</u> AGHTGPPDLRLSAWHRGP
TMG9	91	frameshift	NM_207380.2	p.Glu227fs	KGSWEPWSRPV <u>G</u> AGGGLGLCPVEAGAGADRP SPPRPAQRRTG
TMG9	92	frameshift	NM_000551.3	p.Lys159fs	FANITLPVYTL <u>K</u> SDASRLSGA
TMG9	93	frameshift	NM_018313.4	p.Met1331fs	SAKKEGSKRKIN <u>I</u> VATSCSAVR

Underlines indicate frameshifted amino acid sequence.