

Table S3. Tandem minigene (TMG) constructs

TMG	Mutated Gene	Mutated* Minigene Amino Acid Sequence	TMG Amino Acid Sequence
1	ALK	RVLKGGSVRKL R HAKQLVLELGEEA	RVLKGGSVRKL R HAKQLVLELGEEAQNAADSYSWVP
	CD93	QNAADSYSWVPE Q AESRAMENQYSP	E QAESRAMENQYSPTSFLSINSKEET G HLENGNKYPN
	ERBB2IP	TSFLSINSKEET G HLENGNKYPNLE	LEFIPLLVILFAV H TGLFISTQQQVTESDRPRKVRFR I V
	FCER1A	FIPLLVILFAV H TGLFISTQQQVT	SSHSGRVLKEVYEIYNESLFDLLS A LPYVGPSVTPMTG
	GRXCR1	ESDRPRKVRFR I VSSHSGRVLKEVY	KKLRDDYLASL H PRLHSIYVSEGYPDIKQELLRCDI I CK
	KIF9	EIYNESLFDLLS A LPYVGPSVTPMT	GGHSTVTDLQVGTKLDLRDDDKD N IERLRDCKKLAPI
	NAGS	GKKLRDDYLASL H PRLHSIYVSEGY	
	NLRP2	PDIKQELLRCDI I CKGGHSTVTDLQ	
	RAC3	VGTKLDRDDDKD N IERLRDCKKLAPI	
2	RAP1GDS1	VKLLGIHCQNA I TEMCLVAFGNLANLRKSSPGTSNK	VKLLGIHCQNA I TEMCLVAFGNLANLRKSSPGTSNK
	RASA1	NLRKSSPGTSNK C LRQVSSLVLHIE	C LRQVSSLVLHIELGRLHPCVMASL K AQSPIPNLYLTG
	RETSAT	LGRHPCVMASL K AQSPIPNLYLTG	LLPIHTLDVKST T LPAAVRCESRLMTMDNFGKHYYTL
	SEC24D	LLPIHTLDVKST T LPAAVRCESRL	K SEAPLYVGGMPVMTMDNFGKHYYTL K SEAPLYVGG
	SLIT1	MTMDNFGKHYYTL K SEAPLYVGGMPV	MPVHDGPFVFAEVN A NYITWLWHEDESRQAKEDFS
	TARBP1	AVDVEGMKTQYS V KQRTENVLRIFL	GYDF E TRLHVRIHAALASPAVRPGICPGPD G WRIPLG
	TGM6	HDGPFVFAEVN A NYITWLWHEDESR	PLPHEF
	TTC39C	QAKEDFSGYDF E TRLHVRIHAALAS	
	POU5F2	PAVRPGICPGPD G WRIPLGPLPHEF	
3	SEN3	VAQELFQGS D LV A EEAERPGEKAG	VAQELFQGS D LV A EEAERPGEKAGGTATTLTDLTN
	LHX9	GTATTLTDLTN P LSL	P LSLTHIRRIVPGAV S D G RM G SWR A P T LSVPASPLT
	KLHL6	THIRRIVPGAV S D G RM G SWR A P T LS	LLQSHFRQARVRHLSQEFGLWQIT P PGIPV H ESTAT
	AR	RHLSQEFGLWQIT P PGIPV H ESTAT L Q	L QHYSS G WAEK S KILSPDSKIQMVSSSQ K RALL C LIAL
	PDZD2	SPDSKIQMVSSSQ K RALL C LIAL S R K Q	L SR K Q T W K IR T CL R RV R Q K CF T LLSPQEAGAT K DE C E
	HLA-DOA	TLLSPQEAGAT K DE C E G E E GA A GS R DL	G E E GA A GS R DL S W V T E ETGMPNKASK Q GP G ST Q
	LONRF3	EETGMPNKASK Q GP G ST Q REG S LE I	R EG S LE I P L T N I Y K L L T S V W G L L R L W V W G P A L F T
		A FT S CV T SE I AM R LL	

*Red and bolded denotes mutated amino acids and neo-sequences encoded by point mutations, or nucleotide insertions or deletions. For splice-site donor mutations (*HLA-DOA* and *LONRF3*), we designed mutant minigene transcripts that continued into the downstream intron until the next stop codon, based on the assumption that the mutations prevented splicing at that site. The splice-site acceptor mutation in *DIP2C* was not assessed.