

SEQUENCE LISTING

<110> National University of Singapore

<120> Engineered Immune Cells

<130> S61014169

<160> 43

<170> PatentIn version 3.5

<210> 1

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> Intracellular signalling domain

<400> 1

Arg	Ser	Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr
1				5				10					15		

Pro	Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro
			20					25					30		

Pro	Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Ser
		35					40	

<210> 2

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Anti-CD19 scFV domain

<400> 2

Asp	Ile	Gln	Met	Thr	Gln	Thr	Thr	Ser	Ser	Leu	Ser	Ala	Ser	Leu	Gly
1				5				10					15		

Asp	Arg	Val	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Gln	Asp	Ile	Ser	Lys	Tyr
			20					25					30		

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Gly Gly Gly Ser
100 105 110

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu
115 120 125

Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Val Thr Cys
130 135 140

Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg
145 150 155 160

Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser
165 170 175

Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu Thr Ile Ile
180 185 190

Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln
195 200 205

Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly
210 215 220

Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val
225 230 235 240

Ser Ser

<210> 3
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> scFV capable of binding to LMP2A peptide - MHC complex

<400> 3

Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1 5 10 15

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ser Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Ile
50 55 60

Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65 70 75 80

Lys Met Asn Ser Leu Gln Ala Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
85 90 95

Arg Asn Trp Val Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Thr Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met
130 135 140

Ser Thr Ser Val Gly Asp Arg Val Ser Val Thr Cys Arg Ala Ser Gln
145 150 155 160

Asn Val Phe Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
165 170 175

Pro Lys Ala Leu Ile Tyr Ser Thr Ser Tyr Arg Tyr Ser Gly Val Pro
180 185 190

Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
195 200 205

Ser Asn Val Gln Ser Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr
210 215 220

Ile Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
225 230 235 240

<210> 4
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> signal peptide

<400> 4

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro
20

<210> 5
<211> 1563
<212> DNA
<213> Artificial Sequence

<220>

<223> CD28-CAR

<400> 5

atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg	60
ccggacatcc agatgacca gaccacaagc tccctgtctg ccagcctggg cgacagggtg	120
acaatctctt gccgcgccag ccaggacatc tccaagtacc tgaactggta tcagcagaag	180
cctgacggca ccgtgaagct gctgatctac cacacatctc ggctgcacag cggcgtgccca	240
tccaggttct ccggctctgg cagcggcacc gactattctc tgacaatcag caacctggag	300
caggaggaca tcgccaccta cttctgccag cagggaata ccctgcccta tacat ttggc	360
ggcggcacca agctggagat cacaggagga ggaggcagcg gcggaggagg ctccggcggc	420
ggcggctctg aggtgaagct gcaggagtcc ggaccaggcc tgggtggcacc atcccagtct	480
ctgagcgtga cctgtacagt gagcggcgtg tccctgcctg actacggcgt gtcctggatc	540
agacagcccc ctagaaaggg cctggagtgg ctgggcgtga tctggggcag cgagacaaca	600
tactataatt ccgccctgaa gtctcggctg accatcatca aggataactc caagtctcag	660
gtgtttctga agatgaatag cctgcagacc gacgatacag ccatctacta ttgtgccaaag	720
cactactatt acgggggggag ttatgctatg gattattggg ggacggggcac cagcgtcact	780
gtctcatcac gggcggccgc acatcatcat caccaccatc acggggccgc agaacaaaaa	840
ctcatctcag aagaggatcg tacgaagccc accacgacgc cagcgccgcg accaccaaca	900
ccggcgccca ccatcgctc gcagcccctg tccctgcgcc cagaggcgtg ccggccagcg	960
gcggggggcg cagtacacac gagggggctg gacttcgcct gtgatacgcg tttttgggtg	1020
ctggtggtgg ttggtggagt cctggcttgc tatagcttgc tagtaacagt ggcctttatt	1080
at tttctggg tgaggagtaa gaggagcagg ctctgcaca gtgactacat gaacatgact	1140
ccccgccgcc ccggggccac ccgcaagcat taccagccct atgccccacc acgcgacttc	1200
gcagcctatc gctccggatc cagagtgaag ttcagcagga gcgcagacgc ccccgctac	1260
cagcagggcc agaaccagct ctataacgag ctcaatctag gacgaagaga ggagtacgat	1320
gttttggaca agagacgtgg ccgggaccct gagatggggg gaaagccgca gagaaggaag	1380

aaccctcagg aaggcctgta caatgaactg cagaaagata agatggcgga ggcctacagt	1440
gagattggga tgaaaggcga gcgccggagg ggcaaggggc acgatggcct ttaccagggt	1500
ctcagtacag ccaccaagga cacctacgac gcccttcaca tgcaggccct gccccctcgc	1560
taa	1563

<210> 6
 <211> 520
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD28 CAR

<400> 6

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5					10					15	

His	Ala	Ala	Arg	Pro	Asp	Ile	Gln	Met	Thr	Gln	Thr	Thr	Ser	Ser	Leu
			20					25					30		

Ser	Ala	Ser	Leu	Gly	Asp	Arg	Val	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Gln
		35					40					45			

Asp	Ile	Ser	Lys	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Asp	Gly	Thr
	50					55					60				

Val	Lys	Leu	Leu	Ile	Tyr	His	Thr	Ser	Arg	Leu	His	Ser	Gly	Val	Pro
65				70						75				80	

Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Ser	Leu	Thr	Ile
			85						90					95	

Ser	Asn	Leu	Glu	Gln	Glu	Asp	Ile	Ala	Thr	Tyr	Phe	Cys	Gln	Gln	Gly
			100					105					110		

Asn	Thr	Leu	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Thr
		115					120					125			

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
130 135 140

Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser
145 150 155 160

Leu Ser Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly
165 170 175

Val Ser Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly
180 185 190

Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser
195 200 205

Arg Leu Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys
210 215 220

Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys
225 230 235 240

His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly
245 250 255

Thr Ser Val Thr Val Ser Ser Arg Ala Ala Ala His His His His His
260 265 270

His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Arg Thr
275 280 285

Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
290 295 300

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
305 310 315 320

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Thr
325 330 335

Arg Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
340 345 350

Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
355 360 365

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
370 375 380

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
385 390 395 400

Ala Ala Tyr Arg Ser Gly Ser Arg Val Lys Phe Ser Arg Ser Ala Asp
405 410 415

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
420 425 430

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
435 440 445

Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu
450 455 460

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
465 470 475 480

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
485 490 495

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
500 505 510

His Met Gln Ala Leu Pro Pro Arg
515 520

<210> 7
<211> 1689
<212> DNA
<213> Artificial Sequence

<220>
<223> CD137/CD28-CAR

<400> 7
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60
ccgcagggtgc agctgaagca gtcaggacct ggcctagtgc agccctcaca gagcctgtcc 120
atcacctgca cagtctctgg tttctcatta actaactatg gtgtacactg ggttcgccag 180
tctccaggaa agggctctgga gtggctggga gtgatatgga gtggtggaag cacagactat 240
aatgcagctt tcatatccag attgagcatc agcaaggaca attccaagag ccaagttttc 300
tttaaaatga acagtctgca agctaattgac acagccatat attactgtgc cagaaattgg 360
gtcccttact actttgacta ctggggccaa ggcaccacgg tcaccgtatc gagcgggtgga 420
ggcggttcag gcgagggtgg cagcggcggt ggcgggtcga cggacattgt gatgaccag 480
tctcaaaaat tcatgtccac atcagttgga gacagggtca gcgtcacctg cagggccagt 540
cagaatgtgt ttactaatgt agcctggat caacagaaac cagggaagc tcctaaagca 600
ctgatttact cgacatccta ccggtacagt ggagtccctg atcgcttcac aggcagtgga 660
tctgggacag atttcactct caccatcagc aatgtgcagt ctgaagactt ggcagagtat 720
ttctgtcagc aatatatcag ctatcctctc acgttcggtg ctgggaccaa gctggagctg 780
aaacgggcgg ccgcacatca tcatcaccac catcacgggg ccgcagaaca aaaactcatc 840
tcagaagagg atcgtagaa gcccaccacg acgccagcgc cgcgaccacc aacaccggcg 900
cccaccatcg cgtcgcagcc cctgtccctg cgccagagg cgtgccggcc agcggcgggg 960
ggcgcagtac acacgagggg gctggacttc gcctgtgata cgcgtttttg ggtgctggtg 1020
gtggttggtg gagtccctggc ttgctatagc ttgctagtaa cagtggcctt tattattttc 1080
tgggtgagga gtaagaggag caggctcctg cacagtgact acatgaacat gactccccgc 1140
cgccccgggc ccaccgcaa gcattaccag ccctatgccc caccacgcga cttcgcagcc 1200

tatcgctccg gatccaaacg gggcagaaaag aaactcctgt atatattcaa acaaccat	1260
atgagaccag tacaaactac tcaagaggaa gatggctgta gctgccgatt tccagaagaa	1320
gaagaaggag gatgtgaact gggatccaga gtgaagttca gcaggagcgc agacgcccc	1380
gcgtaccagc agggccagaa ccagctctat aacgagctca atctaggacg aagagaggag	1440
tacgatgttt tggacaagag acgtggccgg gaccctgaga tggggggaaa gccgcagaga	1500
aggaagaacc ctcaggaagg cctgtacaat gaactgcaga aagataagat ggcgagggcc	1560
tacagtgaga ttgggatgaa aggcgagcgc cggaggggca aggggcacga tggcctttac	1620
cagggtctca gtacagccac caaggacacc tacgacgcc ttcacatgca ggccctgccc	1680
cctcgctaa	1689

<210> 8
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD137/CD28-CAR

<400> 8

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5					10					15	

His	Ala	Ala	Arg	Pro	Gln	Val	Gln	Leu	Lys	Gln	Ser	Gly	Pro	Gly	Leu
			20					25					30		

Val	Gln	Pro	Ser	Gln	Ser	Leu	Ser	Ile	Thr	Cys	Thr	Val	Ser	Gly	Phe
		35					40					45			

Ser	Leu	Thr	Asn	Tyr	Gly	Val	His	Trp	Val	Arg	Gln	Ser	Pro	Gly	Lys
	50					55					60				

Gly	Leu	Glu	Trp	Leu	Gly	Val	Ile	Trp	Ser	Gly	Gly	Ser	Thr	Asp	Tyr
65					70					75				80	

Asn Ala Ala Phe Ile Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys
85 90 95

Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Ala Asn Asp Thr Ala
100 105 110

Ile Tyr Tyr Cys Ala Arg Asn Trp Val Pro Tyr Tyr Phe Asp Tyr Trp
115 120 125

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Thr Asp Ile Val Met Thr Gln
145 150 155 160

Ser Gln Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Val Thr
165 170 175

Cys Arg Ala Ser Gln Asn Val Phe Thr Asn Val Ala Trp Tyr Gln Gln
180 185 190

Lys Pro Gly Gln Ala Pro Lys Ala Leu Ile Tyr Ser Thr Ser Tyr Arg
195 200 205

Tyr Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
210 215 220

Phe Thr Leu Thr Ile Ser Asn Val Gln Ser Glu Asp Leu Ala Glu Tyr
225 230 235 240

Phe Cys Gln Gln Tyr Ile Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr
245 250 255

Lys Leu Glu Leu Lys Arg Ala Ala Ala His His His His His His His
260 265 270

Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Arg Thr Lys Pro
275 280 285

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
290 295 300

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
305 310 315 320

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Thr Arg Phe
325 330 335

Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu
340 345 350

Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg
355 360 365

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
370 375 380

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
385 390 395 400

Tyr Arg Ser Gly Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
405 410 415

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
420 425 430

Cys Ser Cys Arg Phe Pro Glu Glu Glu Gly Gly Cys Glu Leu Gly
435 440 445

Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
450 455 460

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
465 470 475 480

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
485 490 495

Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
500 505 510

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
515 520 525

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
530 535 540

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
545 550 555 560

Pro Arg

<210> 9
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> LCK gRNA1

<400> 9
gacccactgg ttacctacga 20

<210> 10
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> LCK gRNA2

<400> 10
gccgggaaaa gtgattcgag 20

<210> 11
<211> 20

<212> DNA
<213> Artificial Sequence

<220>
<223> LCK gRNA3

<400> 11
cgggacttcg accagaacca 20

<210> 12
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> LCK gRNA4

<400> 12
tggagcccgga accgtaagtg 20

<210> 13
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> LCK gRNA5

<400> 13
cggcggattg gagccttcgt 20

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> LCK gRNA6

<400> 14
gcggaccagt tcatgcaggc 20

<210> 15
<211> 20
<212> DNA
<213> Artificial Sequence

<220>		
<223>	LCK gRNA7	
<400>	15	
	cgttgtagta ccctgggtcg	20
<210>	16	
<211>	20	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	LCK gRNA8	
<400>	16	
	gggtgacaat ttccgtcagc	20
<210>	17	
<211>	19	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	LCK gRNA9	
<400>	17	
	cgtaagtggg gacccgtcg	19
<210>	18	
<211>	20	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	LCK gRNA10	
<400>	18	
	ctggagcccg aaccgtaagt	20
<210>	19	
<211>	20	
<212>	DNA	
<213>	Artificial Sequence	
<220>		

<223> LCK gRNA11

<400> 19

ggtgaatgtc ccgtagttaa

20

<210> 20

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> LCK gRNA12

<400> 20

gatcgttttc actgtcggtc

20

<210> 21

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> LCK gRNA13

<400> 21

ccgtaagtgg ggacccgtcg

20

<210> 22

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> LCK gRNA14

<400> 22

ccctctcacg acggagatct

20

<210> 23

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> LCK gRNA15

<400> 23
ctggcgccccg ggaacactca 20

<210> 24
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> LCK gRNA16

<400> 24
gtaagtggggg acccgtcgtg 20

<210> 25
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> LCK gRNA17

<400> 25
tgtgcccgtt gtagtaccct 20

<210> 26
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> LCK gRNA18

<400> 26
attacaccag tgagcccgac 20

<210> 27
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> LCK gRNA19

<400> 27
tggcctagca cgcctcattg 20

<210> 28
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> LCK gRNA20

<400> 28
cgtagagccg aaccagccgc 20

<210> 29
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> LCK gRNA21

<400> 29
atccgtaatc tggacaacgg 20

<210> 30
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> LCK gRNA22

<400> 30
gccctctcac gacggagatc 20

<210> 31
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> LCK gRNA23

<400> 31
atcgttttca ctgtcgggtcc 20

<210> 32
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> LCK gRNA24

<400> 32
gaacctgagc cgcaaggacg 20

<210> 33
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> LCK gRNA25

<400> 33
ccattatccc atagtccac 20

<210> 34
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> LCK gRNA26

<400> 34
gctcacaccc ggaagatgac 20

<210> 35
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> LCK gRNA27

<400> 35
ctcacggctc cttcctcatc 20

<210> 36
<211> 20

<212> DNA
<213> Artificial Sequence

<220>

<223> LCK gRNA28

<400> 36

aaggcgcagt ccctgaccac 20

<210> 37

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> LCK gRNA29

<400> 37

ctacgaaggc tccaatccgc 20

<210> 38

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> FYN gRNA1

<400> 38

agagttcaca cctccaaaga 20

<210> 39

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> FYN gRNA2

<400> 39

acggggacct tgcgtacgag 20

<210> 40

<211> 20

<212> DNA

<213> Artificial Sequence

<220>
<223> FYN gRNA3

<400> 40
ttgtcctttg gaaacccaag 20

<210> 41
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> FYN gRNA4

<400> 41
gtcccccgaa tcattccttg 20

<210> 42
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> FYN gRNA5

<400> 42
tggatactac attaccaccc 20

<210> 43
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> RNA sequence

<220>
<221> misc_feature
<222> (1)..(3)
<223> modified base with 2'-O-methyl 3' phosphorothioate

<220>
<221> misc_feature
<222> (97)..(99)
<223> modified base with 2'-O-methyl 3' phosphorothioate

<400> 43

gccgggaaaa guguuucgag guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100