

Tube 3
 #457 = 10
 #458 = 11
 Rab11 WT
 S25N

Séquençage des clones 457 et 458
 pCMV-intron-myc-hRab11 WT and DN (S25N)
 Résultats reçus le 16 octobre 2008
 Acc number: AF000231

(see map next)

			BamHI	
	1			50
clone457mineFWD	(1)	-----GGATCTGTCTAGAGGATCCACCATGGGCACCC		
clone458mineFWD	(1)	GAAACTCATCTCTGAAGAGGATCTGTCTAGAGGATCCACCATGGGCACCC		
hRab11	(1)	-----ATGGGCACCC		
Consensus	(1)	GGATCTGTCTAGAGGATCCACCATGGGCACCC		
	51			100
clone457mineFWD	(33)	GCGACGACGAGTACGACTACCTCTTTAAAGTTGTCCTTATTGGAGATTCT		
clone458mineFWD	(51)	GCGACGACGAGTACGACTACCTCTTTAAAGTTGTCCTTATTGGAGATTCT		
hRab11	(11)	GCGACGACGAGTACGACTACCTCTTTAAAGTTGTCCTTATTGGAGATTCT		
Consensus	(51)	GCGACGACGAGTACGACTACCTCTTTAAAGTTGTCCTTATTGGAGATTCT		
	101	AGT=S AAT=N		150
clone457mineFWD	(83)	GGTGTGGAAAGAGTAATCTCCTGTCTCGATTTACTCGAAATGAGTTTAA		
clone458mineFWD	(101)	GGTGTGGAAAGAGTAATCTCCTGTCTCGATTTACTCGAAATGAGTTTAA		
hRab11	(61)	GGTGTGGAAAGAGTAATCTCCTGTCTCGATTTACTCGAAATGAGTTTAA		
Consensus	(101)	GGTGTGGAAAGAGTAATCTCCTGTCTCGATTTACTCGAAATGAGTTTAA		
	151			200
clone457mineFWD	(133)	TCTGGAAAGCAAGAGCACCATTGGAGTAGAGTTTGCACAAGAAGCATCC		
clone458mineFWD	(151)	TCTGGAAAGCAAGAGCACCATTGGAGTAGAGTTTGCACAAGAAGCATCC		
hRab11	(111)	TCTGGAAAGCAAGAGCACCATTGGAGTAGAGTTTGCACAAGAAGCATCC		
Consensus	(151)	TCTGGAAAGCAAGAGCACCATTGGAGTAGAGTTTGCACAAGAAGCATCC		
	201			250
clone457mineFWD	(183)	AGGTTGATGGAAAAACAATAAAGGCACAGATATGGGACACAGCAGGGCAA		
clone458mineFWD	(201)	AGGTTGATGGAAAAACAATAAAGGCACAGATATGGGACACAGCAGGGCAA		
hRab11	(161)	AGGTTGATGGAAAAACAATAAAGGCACAGATATGGGACACAGCAGGGCAA		
Consensus	(201)	AGGTTGATGGAAAAACAATAAAGGCACAGATATGGGACACAGCAGGGCAA		
	251			300
clone457mineFWD	(233)	GAGCGATATCGAGCTATAACATCAGCATATTTATCGTGGAGCTGTAGGTGC		
clone458mineFWD	(251)	GAGCGATATCGAGCTATAACATCAGCATATTTATCGTGGAGCTGTAGGTGC		
hRab11	(211)	GAGCGATATCGAGCTATAACATCAGCATATTTATCGTGGAGCTGTAGGTGC		
Consensus	(251)	GAGCGATATCGAGCTATAACATCAGCATATTTATCGTGGAGCTGTAGGTGC		
	301			350
clone457mineFWD	(283)	CTTATTGGTTTATGACATTGCTAAACATCTCACATATGAAAATGTAGAGC		
clone458mineFWD	(301)	CTTATTGGTTTATGACATTGCTAAACATCTCACATATGAAAATGTAGAGC		
hRab11	(261)	CTTATTGGTTTATGACATTGCTAAACATCTCACATATGAAAATGTAGAGC		
Consensus	(301)	CTTATTGGTTTATGACATTGCTAAACATCTCACATATGAAAATGTAGAGC		
	351			400
clone457mineFWD	(333)	GATGGCTGAAAGAAGTGAAGATCATGCTGATAGTAAATTTGTTATCATG		
clone458mineFWD	(351)	GATGGCTGAAAGAAGTGAAGATCATGCTGATAGTAAATTTGTTATCATG		
hRab11	(311)	GATGGCTGAAAGAAGTGAAGATCATGCTGATAGTAAATTTGTTATCATG		
Consensus	(351)	GATGGCTGAAAGAAGTGAAGATCATGCTGATAGTAAATTTGTTATCATG		
	401			450
clone457mineFWD	(383)	CTTGTGGGCAATAAGAGTGAATCTACGTCATCTCAGGGCAGTTCCTACAGA		
clone458mineFWD	(401)	CTTGTGGGCAATAAGAGTGAATCTACGTCATCTCAGGGCAGTTCCTACAGA		
hRab11	(361)	CTTGTGGGCAATAAGAGTGAATCTACGTCATCTCAGGGCAGTTCCTACAGA		
Consensus	(401)	CTTGTGGGCAATAAGAGTGAATCTACGTCATCTCAGGGCAGTTCCTACAGA		
	451			500
clone457mineFWD	(433)	TGAAGCAAGAGCTTTTGCAGAAAAGAATGGTTTGTCAATTCATTGAAACTT		
clone458mineFWD	(451)	TGAAGCAAGAGCTTTTGCAGAAAAGAATGGTTTGTCAATTCATTGAAACTT		
hRab11	(411)	TGAAGCAAGAGCTTTTGCAGAAAAGAATGGTTTGTCAATTCATTGAAACTT		
Consensus	(451)	TGAAGCAAGAGCTTTTGCAGAAAAGAATGGTTTGTCAATTCATTGAAACTT		

		501		550
clone457mineFWD	(483)	CGGCCCTAGACTCTACAAATGTAGAAGCTGCTTTTCAGACAATTTTAACA		
clone458mineFWD	(501)	CGGCCCTAGACTCTACAAATGTAGAAGCTGCTTTTCAGACAATTTTAACA		
hRab11	(461)	CGGCCCTAGACTCTACAAATGTAGAAGCTGCTTTTCAGACAATTTTAACA		
Consensus	(501)	CGGCCCTAGACTCTACAAATGTAGAAGCTGCTTTTCAGACAATTTTAACA		
		551		600
clone457mineFWD	(533)	GAGATTTACCGCATTGTTTCTCAGAAGCAAATGTCAGACAGACGCGAAAA		
clone458mineFWD	(551)	GAGATTTACCGCATTGTTTCTCAGAAGCAAATGTCAGACAGACGCGAAAA		
hRab11	(511)	GAGATTTACCGCATTGTTTCTCAGAAGCAAATGTCAGACAGACGCGAAAA		
Consensus	(551)	GAGATTTACCGCATTGTTTCTCAGAAGCAAATGTCAGACAGACGCGAAAA		
		601		650
clone457mineFWD	(583)	TGACATGTC TCCAAGCAACAATGTGGTTCCTATTCATGTTCCACCAACCA		
clone458mineFWD	(601)	TGACATGTC TCCAAGCAACAATGTGGTTCCTATTCATGTTCCACCAACCA		
hRab11	(561)	TGACATGTC TCCAAGCAACAATGTGGTTCCTATTCATGTTCCACCAACCA		
Consensus	(601)	TGACATGTC TCCAAGCAACAATGTGGTTCCTATTCATGTTCCACCAACCA		
		651		700
clone457mineFWD	(633)	CTGAAAACAAGCCAAAGGTGCAGTGCTGTCAGAACATCTAACTCGAGCAT		
clone458mineFWD	(651)	CTGAAAACAAGCCAAAGGTGCAGTGCTGTCAGAACATCTAACTCGAGCAT		
hRab11	(611)	CTGAAAACAAGCCAAAGGTGCAGTGCTGTCAGAACATCTAA-----		
Consensus	(651)	CTGAAAACAAGCCAAAGGTGCAGTGCTGTCAGAACATCTAACTCGAGCAT		
		701		750
clone457mineFWD	(683)	GCATCTAGAGGGCCCTATTCTATAGTGTACCTAAATGCTAGAGCTCGCT		
clone458mineFWD	(701)	GCATCTAGAGGGCCCTATTCTATAGTGTACCTAAATGCTAGAGCTCGCT		
hRab11	(652)	-----		
Consensus	(701)	GCATCTAGAGGGCCCTATTCTATAGTGTACCTAAATGCTAGAGCTCGCT		
		751		789
clone457mineFWD	(733)	GNNNAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTG		
clone458mineFWD	(751)	GATCAGCCT-----		
hRab11	(652)	-----		
Consensus	(751)	G AGCCT		

== Enzymes that DO NOT MAP to this sequence:

AarI	AatII	AbsI	Acc65I	AclI	AfeI	AflIII	AgeI	AhdI	AjuI
AjuI	AleI	AlfI	AloI	AloI	AlwNI	ApaLI	AscI	AseI	AsiSI
AvrII	BaeI	BaeI	BarI	BarI	BbeI	BbsI	BbvCI	BcgI	BcgI
BclIV	BglI	BglII	BlpI	BmgBI	BmrI	BmtI	BplI	BpmI	Bpu10I
BpuEI	BsaI	BsaBI	BsaXI	BsaXI	BseRI	BseYI	BsiWI	BsmI	BsmBI
BspEI	BspHI	BspMI	BsrBI	BsrGI	BsshII	BsssI	BstAPI	BstBI	BstEII
HstZ17I	Hsu36I	Clal	CspCI	CspCI	DraIII	DrdI	EagI	EciI	EcoNI
EcoRI	FseI	FspI	FspAI	GsaI	HindIII	HpaI	KasI	KpnI	MauBI
MfeI	MluI	MreI	MscI	NaeI	NarI	NgoMIV	NheI	NmeAIII	NotI
NruI	PacI	PasI	PflMI	PfoI	PmeI	PmlI	PpiI	PpiI	PshAI
PsiI	PsrI	PsrI	PstI	PvuI	PvuII	RsrII	SacII	Sall	SanDI
SapI	SbfI	ScaI	SexAI	SfiI	SfoI	SgrAI	SgrDI	SmaI	SnaBI
SpeI	SrfI	SspI	StuI	SwaI	TaqII	TaqII	TstI	TstI	Tth111I
XcmI	XmaI	XmnI	ZraI						

== Total Number of Hits per Enzyme:

AcuI	1	BsgI	1	DraI	1	NcoI	1	PspXI	1
ApaI	1	BsrDI	1	EarI	1	NdeI	1	SacI	1
BamHI	1	HstXI	1	EcoICRI	1	NsiI	1	SphI	1
BclI	1	BtgZI	1	EcoRV	1	PciI	1	XbaI	2
BdaI	1	BtsI	1	FalI	1	PspOMI	1	XhoI	1

Linear Map of Sequence:

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      AcuI
      EarI~      XbaI  BamHI  NcoI                        DraI
1  aaactcatctctgaagaggatctgtctagaggatccacatgggcacccgcgacgacgagtacgactacctctttaagttgtccttatt 90
   ttgagtagagacttctctagacagatctcttagtggtaccctgggcgctgctgctcatgctgatggagaaattccaacaggaataa
   ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^
1  K L I S E E D L S R G S T M G T R D D E Y D Y L F K V V L I

      FalI
91  ggagattctgtgttggaaagagtaatctcctgtctcgatttactcgaatgagtttaactctgaaagcaagagcaccattggagtagag 180
   cctctaagaccacaacctttctcattagaggacagagctaaatgagctttactcaaattagacctttcgttctcgtggtaacctcatctc
   ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^
1  G D S G V G K S N L L S R F T R N E F N L E S K S T I G V E

      BstXI      EcoRV
181  tttgcaacaagaagcatccagttgatggaaaaacaataaaggcacagatgggacacagcagggaagagcgatctcgagctataaca 270
   aaacgttgttctctgttaggtccaactacctttttgttatttccggtgcttatccctgtgtgctcccgcttctcgctatagctcgatattgt
   ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^
1  F A T R S I Q V D G K T I K A Q I W D T A G Q E R Y R A I T

      BsrDI~      NdeI
271  tcagcatattatcgtaggactgtaggtgcttattggtttatgacattgctaaacatctcacatatgaaaatgtagagcgatggctgaaa 360
   agtcgtataatagcacctcgacatccacggaataaccaaatactgtaacgattgtagagtgatatactttacatctcgctaccgacttt
   ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^
1  S A Y Y R G A V G A L L V Y D I A K H L T Y E N V E R W L K

      BtgZI      BdaI
361  gaactgagagatcatgctgatagtaacattggtatcatgcttgtggccaataagagtgatctacgtcatctcagggcagtctoctacagat 450
   ctgactctctagtacgactatcattgtaacaatagtagcaaacacccgttattctcactagatgcagttagagccccgtcaaggatgtcta
   ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^
1  E L R D H A D S N I V I M L V G N K S D L R H L R A V P T D

451  gaagcaagagcttttgcagaaaagaatggtttgtcattcattgaaacttcggccctagactctacaaatgtagaagctgcttttcagaca 540
   cttcgttctcgaaaacgtcttttcttaccaaaacagtaagtaactttgaagccgggatctgagatggttacatcttgcagcaaaagctctgt
   ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^
1  E A R A F A E K N G L S F I E T S A L D S T N V E A A F Q T

      PciI
541  attttaacagagatttaccgcattgtttctcagaagcaaatgtcagacagacgcgaaaatgacatgctccaagcaacaatgtggttctct 630
   taaaattgtctcctaaatggcgtaacaaagactcttcgtttacagctgtgctggcgttttactgtacagaggttcggtgttacaccaagga
   ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^
1  I L T E I Y R I V S Q K Q M S D R R E N D M S P S N N V V P

      XhoI      XbaI
      PspXI      NsiI      ApaI
      BtsI      BsgI      SphI      PspOMI
631  attcatgtccaccaaccactgaaacaagccaaggtgcatgctgtcagaacatctaaactcgagcatgcatctagaggccctattct 720
   taagtacaaggtggtggtgactttgttcggtttccacgtcagcagctctgttagattgagctcgtacgttagatctcccggtataaga
   ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^
1  I H V P P T T E N K P K V Q C C Q N I * L E H A S R G P Y S

      BclI
      SacI
      EcoICRI
721  atagtgacacctaagtctagagctcgctgatcagcctcgactgtgccttctagttgccagccatctg 810
   tatcacagtgatttacgatctcgagcagctagtcggagctgacacggaagatcaacggctcggtagac
   ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^  ^
1  I V S P K C * S S L I S L D C A F * L P A I

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