

11)Rag2

Rattus norvegicus recombination activating 2 (Rag2), mRNA

recombination activating protein 2; recombination activating gene 2

- **Référence NCBI :** [NM_001100528](#)

- **Taille 1584 NT**

- **Séquences protéique / NT :**

- [NP_001093998.1](#)

MSLQMVTVGHNIALIQPGFSLMNFDDGQVFFFGQKGWPKRSCPTG
VFHFDIKQNHKLKPAVFSKDSCYLPPLRYPATCSYKGSTDSKQYIIHGGKTPNNE
LSDKIYIMSVACKNNKKVTFRCTEKDLVGDVPEARYGHSIDVVYSRGKSVGVLFGGRSYMPSTQRTTE
KWNSVADCLPHVFLVDFEFGCATSYILPELQDGLSFHVSIRNDTIYI
LGGHSLASNIRPANLYRIRVDLPLGTPAVNCTVLPGGISVSSAIVTQTNNDEFVIVGG
YQLENQKRMVCSIVSLGDNRIEISEMETPDWTPDIKHSKIWFSGNMGNQTVFLGIPGD
NKQAMSEAFYFYMLRCSNEDNSSEEQKIVSNSQSTEDAGDSTPFEDSEEFCSAEAIS
FDGDDEFDTYNEDDEDESVTGYWITCSPTCDVDINTWVPFYSTELNKPAMIYCSHGDGHVHAQCM
DLEERTLIHLSEGSNKYYCNEHVRIARALQTPKRNLPKPPMKSLHKK GSGKVLTPAKKSFLRRLFD

atgt ccctgcagat gggtacagt

241	ggtcataaca	tagccttaat	tcaaccaggc	ttctcactga	tgaattttga	tgggtcaagtt
301	tttttctttg	gccaaaaagg	ctggcctaag	agatccctgcc	ctactggagt	ctttcatattt
361	gatataaaac	aaaatcatct	caaaactgaag	cctgcagttt	tctctaaaga	ttcctgctac
421	ctcccacctc	ttcgttaccc	agctacttgc	tcgtacaaaag	gcagcacaga	ctctgacaag
481	catcaatata	tcattccacg	agggaaaacg	ccaaacaatg	agctttccga	taagatttat
541	atcatgtctg	tcgcttgcaa	gaataacaaa	aaagttactt	tccgttgtag	agagaaagac
601	ttagtaggag	atgtccctga	agccagatat	ggccattcca	ttgacgtggt	atatagccga
661	ggaaaaaagt	ttggtgttct	ctttggagga	cgggtcatata	tgccttctac	ccaaagaacc
721	acagaaaaat	ggaatagtgt	agctgattgc	ctaccccatg	ttttcttggt	agattttgaa
781	tttgggtgtg	caacgtcata	tattctccca	gaacttcagg	acgggctgtc	ttttcatggt
841	tctattgcca	gaaatgatac	catttatatt	ttgggaggac	actcacttgc	cagtaacata
901	cgtcctgcta	acttgtagat	aataagagta	gatcttcccc	tgggtacccc	agcagtgaat
961	tgcactgtct	tgccaggagg	aatctctgtc	tccagtgcga	ttgtcactca	aacaaataat
1021	gatgaatttg	ttattgttgg	tgggtatcag	ctggaaaatc	aaaaaaggat	ggtgtgtagc
1081	attgtctctc	taggggacaa	caggattgaa	attagtgaga	tggagacccc	agactggacc
1141	ccagatatta	agcatagcaa	aatatggttt	ggaagcaaca	tgggaaacgg	gactgttttc
1201	cttggcatac	caggagacaa	caagcaggct	atgtcagaag	cattctatct	ctatatgttg
1261	agatgctctg	aagataatcc	gagtgaggag	cagaaaattg	tctcaaacag	tcagacatca
1321	actgaagatg	ccggggactc	cactcccttt	gaagactcgg	aagaattttg	tttcagtgtc
1381	gaagcaatca	gctttgatgg	tgatgatgaa	tttgacactt	acaatgaaga	tgatgaagat
1441	gatgaatctg	taaccggcta	ctggataacg	tgttccccta	cttgtgatgt	ggacatcaat
1501	acttgggttc	cattctattc	aactgagctc	aataaaccgg	ccatgatcta	ttgtttctcat
1561	ggggatggac	actgggtgca	tgcccagtgc	atggatctgg	aagaacgcac	actcatccac
1621	ttgtcagaag	gaagcaacaa	atattactgc	aatgagcatg	tgcggatagc	aagagcatta
1681	caaactccca	aaagaaacct	ccccttacaa	aagcccccaa	tgaatccct	ccacaaaaaa
1741	ggctccggga	aagtcttgac	tcctgccaag	aaatcctttc	ttaggaggtt	gtttgattag

- **Amorces synthétisées :**

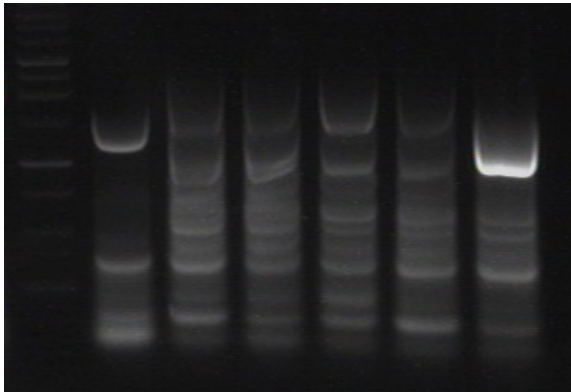
Rag2_AscI_Fwd

tataGGCGCGCCa atgt cctgcagat gggtacagtgg

Rag2_NotI_Rev

ttaaGCGGCCGCa ctaatcaaacaacctcctaagaaag

- **Expériences :**
 - 29/10 PCR pfu 60°C pfu 50ul 40 cycles
 - rate/DiT0/DiT24hLPS : les miens de fevrier
 - 48h mix/SP/CTX faits le 28/10



➤ Résultats séquençages

○ FlagBirA Rag2 rate clone B

➤ B3Fwd 846NT

ATGTCCTGCAGATGGTTACAGTGGGTCATAACATAGCCTTAATTCAACCAGGCTTCTCACTGATGAATTTTGA
TGGTCAAGTTTTTTCTTTGGCCAAAAGGCTGGCCTAAGAGATCCTGCCCTACTGGAGTCTTTCATTTTGATAT
AAAACAAAATCATCTCAAACCTGAAGCCTGCAGTTTTCTCTAAAGATTCTGCTACCTCCACCTCTTCGTTACCC
AGCTACTTGCTCGTACAAAGGCAGCACAGACTCTGACAAGCATCAATATATCATCCACGGAGGGAAAACGCCA
ACAATGAGCTTTCCGATAAGATTTATATCATGTCTGTCTGCAAGAATAACAAAAAAGTTACTTTCCGTTGT
ACAGAGAAAGACTTAGTAGGAGATGTCCTGAAGCCAGATATGGCCATTCCATTGACGTGGTATATAGCCGAG
GAAAAAGTGTGGTGTCTCTTTGGAGGACGGTCATACATGCCTTCTACCCAAAGAACCACAGAAAAATGGAA
TAGTGTAGCTGATTGCCTACCCCATGTTTTCTTGGTAGATTTGAATTTGGGTGTGCAACGTCATATATTCTCCC
AGAAGTTTCTAGGACGGGCTGTCTTTTCATGTTTCTATTGCCAGAAATGATACCATTTATATTTGGGAGGACACTC
ACTTGCCAGTAACATACGTCCTGCTAACTTGTATAGAATAAGAGTAGATCTTCCCTGGGTACCCAGCAGTGA
ATTGcACTGTCTTGCCaGGAGGAATCTCTGTCTCCAGTGCANTGTCACTCNNCAATAATGATGAATTTGTTATTG
NTGGTGGTNATCANCTGGAAATCAAAAAG

➤ BGHRev 943NT

TGATACCATTATATTTNGGGAGGNCNNTCACTTGCCAGTNACNTANGTCNTGCTNACTTGTATAGANTAAGAG
TAGATNTTNNNTGGNNACCCCANCACTGANTNGCACTNNNTNNcAGGAGGAaTNTCTNTCTCCANTGCAATT
GTCaCTCAAACAAATANTGATGAATTTGTTATTGTTGNTGGTNATCAGCTGNAAAaTCAAAAAGGANGGTGT
GTAGCATTGTCTCTctAgGNACaAaCAGGATTGNAATTAGTGANATGNNGACcCCAGACTNGACCCAGATATT
AANCATAGCAAAATATGGTTTGAAGCAACATGGGAAACGGGACTGTTTTCTTGGCATAcCAGGAGACAACA
AGCAGGcTATGTCAGAAGCATTCTATTTCTANAtGNTGAGATGCTcTGAAGATAATtcGAGTGAGGAGCAGAAA
ATtGTCTCAAACAGTCAGACATCAACTGAAGATGCCGGGGACTCCACTCCCTTTGAAGACTCGGAAGAATTTTG
TTTCACTGCTGAAGCAATCAGCTTTGATGGTGATGATGAATTTGACACTTACAATGAAGATGATGAAGATGAT
GAATCTGTAACCGGCTACTGGATAACGTGTTCCCTACNTGTGATGTGGACATCAATACTTGGGTTCCATTCTA
TTCAACTGAGCTCAATAAACCCGCCATGATCTATTGTTCTCATGGGGATGGACACTGGGTGCATGCCAGTGCA
TGGATCTGGAAGAACGCACACTCATCCACTTGTCAGAATGAAGCAACAAATATTACTGCAATGAGCATGTGCG
GATAGCAAGAGCATTACAACTCCCAAAAGAAACCTCCCCTTACAAAAGCCCCCAATGAAATCCCTCCACAAAA
AAGGCTCCGGGAAAGTCTTGACTCCTGCCAAGAAATCCTTTCTTAGGAGGTTGTTgATTAG

➤ Seq int 21/12

CTTGcNGGAGGATCTCTGTCTCCaGTGCAATTGTCACTCAAACAAATAATGATGAATTTGTTATTGTTGGTGGT
TATCAGCTGGAAAATCAAAAAGGATGGTGTGTAGCATTGTCTCTCTAGGGGACAACAGGATTGAAATTAGTG
AGATGGAGACCCCACTGGACCCCAAGATATTAAGCATAGCAAAATATGGTTTGAAGCAACATGGGAAACG
GGACTGTTTTCTTGGCATAcCAGGAGACAACAAGCAGGCTATGTCAGAAGCATTCTATTTCTATATGTTGAGA
TGCTCTGAAGATAATTCGAGTGAGGAGCAGAAAATTGTCTCAAACAGTCAGACATCAACTGAAGATGCCGGG
GACTCCACTCCCTTTGAAGACTCGGAAGAATTTGTTTCACTGCTGAAGCAATCAGCTTTGATGGTGATGATGA
ATTTGACACTTACAATGAAGATGATGAAGATGATGAATCTGTAACCGGCTACTGGATAACGTGTTCCCTACTT
GTGATGTGGACATCAATACTTGGGTTCCATTCTATTCAACTGAGCTCAATAAACCCGCCATGATCTATTGTTCTC
ATGGGGATGGACACTGGGTGCATGCCAGTGCATGGATCTGGAAGAACGCACACTCATCCACTGTGAGAAT

GAAGCAACAAATATTACTGCAATGAGCATGTGCGGATAGCAAGAGCATTACAAACTCCCCAAAAGAAACCTCCC
 CTTACAAAAGCCCCCAATGAAATCCCTCCACAAAAAANGcTCCGGGAAAAGTCTTGACTCCTGCCAAGAAATCCT
 TTCTTANGANGNTGTTTGATTAGTGCGGCCGCTAACTCGAGTCTAGAGGGCCCGTTTAAACCCGCTGATCAG
 CCTCNACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTGNCCCTCCCCNNGCCTTCCTTGANCCNNGAAGNN
 NNNNCTCCNNCTGTCCTTCTCTAATAAATGANGAAATTGCNTCNNATTGTCTGANTNNNGTCATNCTATNNG
 GGGGGGNGGGGNNNGGGNNGNNNNNCNAGGGGNNNGNA

➤ Synthèse séquençage

ATGTCCCTGCAGATGGTTACAGTGGGTCATAACATAGCCTTAATTCAACCAGGCTTCTCA	60
CTGATGAATTTTGTGATGGTCAAGTTTTTTCTTTGGCCAAAAAGGCTGGCCTAAGAGATCC	120
TGCCCTACTGGAGTCTTTCATTTTGATATAAAACAAAATCATCTCAAACCTGAAGCCTGCA	180
GTTTTCTCTAAAGATTCTGTACCTCCCACCTCTTCGTTACCCAGCTACTTGCTCGTAC	240
AAAGGCAGCACAGACTCTGACAAGCATCAATATATCATCCACGGAGGGAAAACGCCAAC	300
AATGAGCTTTCCGATAAGATTTATATCATGTCTGTCGCTTGCAAGAATAACAAAAAGTT	360
ACTTTCGGTTGTACAGAGAAAGACTTAGTAGGAGATGTCCCTGAAGCCAGATATGGCCAT	420
TCCATTGACGTGGTATATAGCCGAGGAAAAAGTGTGGTGTCTCTTTGGAGGACGGTCA	480
TACATGCCTTCTACCCAAAGAACCACAGAAAAATGGAATAGTGTAGCTGATTGCCTACCC	540
CATGTTTTCTTGGTAGATTTTGAATTTGGGTGTGCAACGTCATATATTCTCCCAGAACTT	600
CAGGACGGGCTGTCTTTTCATGTTTCTATTGCCAGAAATGATACCATTATATTTTGGGA	660
GGACACTCACTTGCCAGTAACATACGCTCTGCTAACTTGTATAGAATAAgAGTAGATCTT	720
CCCCTGGGTAcCCCAGCAGTGAATTGcACTGTCTTGCCaGGAGGAATCTCTGTCTCCAGT	780
GCAATTGTCAcTCAAACAAATAATGATGAATTTGTTATTGTTGGTGGTTATCAGCTGGaA	
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GAGATGGAGACCCAGACTGGACCCAGATATTAAGCATAGCAAAATATGGTTTGGAAAGC	
AACATGGGAACGGGACTGTTTTCTTGGCATAcCAGGAGACAACAAGCAGGcTATGTCA	
GAAGCATTCTATTTCTATATGTTGAGATGCTCTGAAAGATAAATTCGAGTGAGGAGCAGAAA	
AttGCTCTCAAACAGTCAGACATCAACTGAAGATGCCGGGGACTCCACTCCCTTTGAAGAC	
TCGGAAGAATTTTGTTCAGTGCTGAAGCAATCAGCTTTGATGGTGTATGATGAATTTGAC	1200
ACTTACAATGAAGATGATGAAGATGATGAATCTGTAACCGGCTACTGGATAACGTGTTCC	1260
CCTACTTGTGATGTGGACATCAATACTTGGGTTCATTCTATTCAACTGAGCTCAATAAA	1320
CCCGCATGATCTATTGTTCTCATGGGGATGGACACTGGGTGCATGCCAGTGCATGGAT	1380
CTGGAAGAAGCAGCACTCATCCACTTGTGAGAAcGAAGCAACAAATATTACTGCAATGAG	1440
CATGTGCGGATAGCAAGAGCATTACAAACTCCCAAAAGAAACCTCCCCTTACAAAAGCCC	1500
CCAATGAAATCCCTCCACAAAAAANGcTCCGGGAAAGTCTTGACTCCTGCCAAGAAATCC	1560
TTTCTTAGGAGGTTGTTtgATTAG	1584

MSLQMVTVGHNIALIQPGFSLMNFQGVFFFGQKGWPKRSCPTGVFHFQDIKQNHKLKPAVFSKSDCYLPPLRYP
 ATCSYKGSTDSKHKYIIHGGKTPNNELSDKIYIMSVACKNNKKVTRFCTEKDLVGDVPEARYGHSIDVVYSRGKSV
 GVLFGGRSYMPSTQRTTEKWNSVADCLPHVFLVDFFEGCATSYILPELQDGLSFHVSIRNDTIYILGGHSLASNIRP
 ANLYRIRVDLPLGTPAVNCTVLPGGISVSSAIVTQTNNDEFVIVGGYQLENQKRMVCSIVSLGDNRIEISEMETPDW
 TPDIKHSKIWFSGNMNGTVFLGIPGDNKQAMSEAFYFMYLRCEDNSSEEQKIVSNSQTSTEDAGDSTPFEDSEE
 FCFSAEAIISFDGDDFDTYNEDDEDESVTGYWITCSPTCDVDINTWVPFYSTELNKPAMIYCSHGDGHVVAHQ
 MDLEERTLIHLSE-SNKYYCNEHVRIARALQTPKRNLPQKPPMKSLHKKXSGKVLTPAKKSFLRLFD-

➤ Blast contre banque de rat

✓	Rattus norvegicus recombination activating 2 (Rag2) mRNA	Rattus norvegicus	2916	2916	100%	0.0	99.87%	3546	NM_001100528.2
✓	Rattus norvegicus RAG2 (RAG2) gene partial cds	Rattus norvegicus	1701	1701	58%	0.0	100.00%	921	AY303209.1
✓	Rattus norvegicus recombination activating protein 2 (Rag2) gene partial cds	Rattus norvegicus	815	815	28%	0.0	99.77%	444	AY011941.1

➤ Différence au niveau NT

1 10 20 30 40 50 60 70 80 90 100 110 120 130
Fud
cds
Consensus
ATGTCCTCGAGATGGTTACAGTGGGTCATACATAGCCTTATTCACACAGGCTTCTCATGTATGATTTTGTATGGTCAGTATTTTCTTTGGCCAAAGAGGCTGGCTACAGAGATCTGCCCCACTG
ATGTCCTCGAGATGGTTACAGTGGGTCATACATAGCCTTATTCACACAGGCTTCTCATGTATGATTTTGTATGGTCAGTATTTTCTTTGGCCAAAGAGGCTGGCTACAGAGATCTGCCCCACTG
ATGTCCTCGAGATGGTTACAGTGGGTCATACATAGCCTTATTCACACAGGCTTCTCATGTATGATTTTGTATGGTCAGTATTTTCTTTGGCCAAAGAGGCTGGCTACAGAGATCTGCCCCACTG
131 140 150 160 170 180 190 200 210 220 230 240 250 260
Fud
cds
Consensus
GAGTCTTTTATTTGATATAAACAAGATCATCTCAACCTGAGGCTGAGCTTTCTCAAGATTCCTGCTACCTCCCACTCTCTGTTACCCAGCTTCTGCTACAGAGGAGCAGACAGACTCTGA
GAGTCTTTTATTTGATATAAACAAGATCATCTCAACCTGAGGCTGAGCTTTCTCAAGATTCCTGCTACCTCCCACTCTCTGTTACCCAGCTTCTGCTACAGAGGAGCAGACAGACTCTGA
GAGTCTTTTATTTGATATAAACAAGATCATCTCAACCTGAGGCTGAGCTTTCTCAAGATTCCTGCTACCTCCCACTCTCTGTTACCCAGCTTCTGCTGCTACAGAGATACAAAAGTACTTTCGTTGACAGAGAGAGACTTAGTA
261 270 280 290 300 310 320 330 340 350 360 370 380 390
Fud
cds
Consensus
CARGCATCATATATCATCCACGGAGGGAAGACGCCAARCATGAGCTTCCGATAGATTTATATCATGCTGCTGCTGCTGACAGATACAAAAGTACTTTCGTTGACAGAGAGAGACTTAGTA
CARGCATCATATATCATCCACGGAGGGAAGACGCCAARCATGAGCTTCCGATAGATTTATATCATGCTGCTGCTGCTGACAGATACAAAAGTACTTTCGTTGACAGAGAGAGACTTAGTA
CARGCATCATATATCATCCACGGAGGGAAGACGCCAARCATGAGCTTCCGATAGATTTATATCATGCTGCTGCTGCTGACAGATACAAAAGTACTTTCGTTGACAGAGAGAGACTTAGTA
391 400 410 420 430 440 450 460 470 480 490 500 510 520
Fud
cds
Consensus
GGAGATGTCCTGAGGCGAGATATGGCCATTCCATTGACGTGGTATATAGCCGAGGAAAGAGTGTGGTGTCTCTTTGGAGGACGCTCATACATGCTTCTACCCAGAGACCCAGAGAAATGGATA
GGAGATGTCCTGAGGCGAGATATGGCCATTCCATTGACGTGGTATATAGCCGAGGAAAGAGTGTGGTGTCTCTTTGGAGGACGCTCATACATGCTTCTACCCAGAGACCCAGAGAAATGGATA
GGAGATGTCCTGAGGCGAGATATGGCCATTCCATTGACGTGGTATATAGCCGAGGAAAGAGTGTGGTGTCTCTTTGGAGGACGCTCATACATGCTTCTACCCAGAGACCCAGAGAAATGGATA
521 530 540 550 560 570 580 590 600 610 620 630 640 650
Fud
cds
Consensus
GTGTAGCTATTTGCTACCCCATGTTTCTTGGTAGATTTGATTTTGGGTTGGACAGCTCATATATTCCTCCAGACTTCAGAGAGGAGCTGCTTTTCTATGTTCTATTTGCCAGAAATGATACATTTA
GTGTAGCTATTTGCTACCCCATGTTTCTTGGTAGATTTGATTTTGGGTTGGACAGCTCATATATTCCTCCAGACTTCAGAGAGGAGCTGCTTTTCTATGTTCTATTTGCCAGAAATGATACATTTA
GTGTAGCTATTTGCTACCCCATGTTTCTTGGTAGATTTGATTTTGGGTTGGACAGCTCATATATTCCTCCAGACTTCAGAGAGGAGCTGCTTTTCTATGTTCTATTTGCCAGAAATGATACATTTA
651 660 670 680 690 700 710 720 730 740 750 760 770 780
Fud
cds
Consensus
TATTTTGGAGGACACTCCTTGCAGTAACTACGCTCTGCTACTTGTATAGATAGAGTAGATCTTCCCTGGGTACCCAGAGCTGATTCGACTGTCTTGCAGAGAGATCTCTGCTCCAGT
TATTTTGGAGGACACTCCTTGCAGTAACTACGCTCTGCTACTTGTATAGATAGAGTAGATCTTCCCTGGGTACCCAGAGCTGATTCGACTGTCTTGCAGAGAGATCTCTGCTCCAGT
TATTTTGGAGGACACTCCTTGCAGTAACTACGCTCTGCTACTTGTATAGATAGAGTAGATCTTCCCTGGGTACCCAGAGCTGATTCGACTGTCTTGCAGAGAGATCTCTGCTCCAGT
781 790 800 810 820 830 840 850 860 870 880 890 900 910
Fud
cds
Consensus
GCATTGTGACTCAACCAATATGATGAATTTGTTATTTGGTGGTTATCAGCTGGAAGATCAAAAAGGATGGTGTGTAGCATTTGCTCTTAGGGGACACAGGATTGAATTTAGTGAGATGGAGA
GCATTGTGACTCAACCAATATGATGAATTTGTTATTTGGTGGTTATCAGCTGGAAGATCAAAAAGGATGGTGTGTAGCATTTGCTCTTAGGGGACACAGGATTGAATTTAGTGAGATGGAGA
GCATTGTGACTCAACCAATATGATGAATTTGTTATTTGGTGGTTATCAGCTGGAAGATCAAAAAGGATGGTGTGTAGCATTTGCTCTTAGGGGACACAGGATTGAATTTAGTGAGATGGAGA
911 920 930 940 950 960 970 980 990 1000 1010 1020 1030 1040
Fud
cds
Consensus
CCCCAGACTGGACCCAGATATTAGCATAGCAAAATATGGTTTGGAGCACATGGGAACGGGACTGTTTCTTGGCATACCCAGAGACACACAGGAGGCTATGTCAGAGCATCTTATTTCTATAT
CCCCAGACTGGACCCAGATATTAGCATAGCAAAATATGGTTTGGAGCACATGGGAACGGGACTGTTTCTTGGCATACCCAGAGACACACAGGAGGCTATGTCAGAGCATCTTATTTCTATAT
CCCCAGACTGGACCCAGATATTAGCATAGCAAAATATGGTTTGGAGCACATGGGAACGGGACTGTTTCTTGGCATACCCAGAGACACACAGGAGGCTATGTCAGAGCATCTTATTTCTATAT
1041 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170
Fud
cds
Consensus
GTTGAGATGCTCTGAGATATTCGAGTGAGGAGCAGAAATTTGCTCAACAGTCAGACATCAGTGAGATGCCGGGACTCCACTCCCTTTGAGAGCTCGAGAGAAATTTGTTTCAGTGCTGAGACA
GTTGAGATGCTCTGAGATATTCGAGTGAGGAGCAGAAATTTGCTCAACAGTCAGACATCAGTGAGATGCCGGGACTCCACTCCCTTTGAGAGCTCGAGAGAAATTTGTTTCAGTGCTGAGACA
GTTGAGATGCTCTGAGATATTCGAGTGAGGAGCAGAAATTTGCTCAACAGTCAGACATCAGTGAGATGCCGGGACTCCACTCCCTTTGAGAGCTCGAGAGAAATTTGTTTCAGTGCTGAGACA
1171 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
Fud
cds
Consensus
ATCAGCTTTGATGGTGATGAATTTGACACTTACATGAGATGATGAGATGATGATCTGTACCCGGCTACTGGATACGTTTCCCTACTTTGATGTGGACATCAATACTTGGGTTCCATTCT
ATCAGCTTTGATGGTGATGAATTTGACACTTACATGAGATGATGAGATGATGATCTGTACCCGGCTACTGGATACGTTTCCCTACTTTGATGTGGACATCAATACTTGGGTTCCATTCT
ATCAGCTTTGATGGTGATGAATTTGACACTTACATGAGATGATGAGATGATGATCTGTACCCGGCTACTGGATACGTTTCCCTACTTTGATGTGGACATCAATACTTGGGTTCCATTCT
1301 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430
Fud
cds
Consensus
ATTCACCTGAGCTCARTAAACCCGCGATGATCTATTGTTCTCATGGGATGGACACTGGGTCATGCCAGTGATGGATCTGGAGAGCAGCAGCTCATCCACTTGTGAGATGAGCAGCAATATTA
ATTCACCTGAGCTCARTAAACCCGCGATGATCTATTGTTCTCATGGGATGGACACTGGGTCATGCCAGTGATGGATCTGGAGAGCAGCAGCTCATCCACTTGTGAGAGGAGCAGCAATATTA
ATTCACCTGAGCTCARTAAACCCGCGATGATCTATTGTTCTCATGGGATGGACACTGGGTCATGCCAGTGATGGATCTGGAGAGCAGCAGCTCATCCACTTGTGAGAGGAGCAGCAATATTA
1431 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560
Fud
cds
Consensus
CTGCATGAGCATGTGCGGATGCAAGAGCATTACAACTCCCAAGAGAACTCCCTTACAAAGCCCCARTGAATCCCTCCACAAAAGAGCTCCGGGAAGTCTGACTCCTGCCAGAAATCC
CTGCATGAGCATGTGCGGATGCAAGAGCATTACAACTCCCAAGAGAACTCCCTTACAAAGCCCCARTGAATCCCTCCACAAAAGAGCTCCGGGAAGTCTGACTCCTGCCAGAAATCC
CTGCATGAGCATGTGCGGATGCAAGAGCATTACAACTCCCAAGAGAACTCCCTTACAAAGCCCCARTGAATCCCTCCACAAAAGAGCTCCGGGAAGTCTGACTCCTGCCAGAAATCC
1561 1570 15801584
Fud
cds
Consensus
TTTCTTAGAGGTTGTTGATTAG
TTTCTTAGAGGTTGTTGATTAG
TTTCTTAGAGGTTGTTGATTAG

Rag2 rate : Toujours mutation en 1414 T<G avec séquençage interne:
introduit un stop

➤ Différence au niveau PROT :

	Description	Source	Score	Score	Cover	value	Ident	Len	Accession
✓	V(D)J recombination-activating protein 2 [Rattus norvegicus]	Rattus norvegicus	1096	1096	100%	0.0	99.62%	527	NP_001093998.1
✓	RAG2 [Rattus norvegicus]	Rattus norvegicus	644	644	58%	0.0	100.00%	307	AAQ77003.1
✓	recombination activating protein 2 [Rattus norvegicus]	Rattus norvegicus	310	310	28%	3e-104	100.00%	148	AAG38684.1

Stop en 472

	1	10	20	30	40	50	60	70	80	90	100	110	120	130	
seq	NSLQMYTYGHNIALIQPGFSLNFDGQVFFFGQKGHPKRSCPTGVFHFIDIKQNLKLPKPVFSKDSCYLPPLRYPATCSYKGSTDSOKHQYIIHGKTPNNELSDKIYINSVACKNNKKVTFRCTEKDLV														
ref	NSLQMYTYGHNIALIQPGFSLNFDGQVFFFGQKGHPKRSCPTGVFHFIDIKQNLKLPKPVFSKDSCYLPPLRYPATCSYKGSTDSOKHQYIIHGKTPNNELSDKIYINSVACKNNKKVTFRCTEKDLV														
Consensus	NSLQMYTYGHNIALIQPGFSLNFDGQVFFFGQKGHPKRSCPTGVFHFIDIKQNLKLPKPVFSKDSCYLPPLRYPATCSYKGSTDSOKHQYIIHGKTPNNELSDKIYINSVACKNNKKVTFRCTEKDLV														
	131	140	150	160	170	180	190	200	210	220	230	240	250	260	
seq	GDVPEARYGHSIDVYVSRGKSVGLFGGRSYMPSTQRTTEKMSVADCLPHVFLVDFFGCATSYILPELQGLSFHVSIARNDTIYILGGHSLASNIRPAMLYRIRVDLPLGTPAVNCTVLPGGISVSS														
ref	GDVPEARYGHSIDVYVSRGKSVGLFGGRSYMPSTQRTTEKMSVADCLPHVFLVDFFGCATSYILPELQGLSFHVSIARNDTIYILGGHSLASNIRPAMLYRIRVDLPLGTPAVNCTVLPGGISVSS														
Consensus	GDVPEARYGHSIDVYVSRGKSVGLFGGRSYMPSTQRTTEKMSVADCLPHVFLVDFFGCATSYILPELQGLSFHVSIARNDTIYILGGHSLASNIRPAMLYRIRVDLPLGTPAVNCTVLPGGISVSS														
	261	270	280	290	300	310	320	330	340	350	360	370	380	390	
seq	RIYVTQNNDEFYIVGGYQLENQKRMYCSIVSLGONRIEISEMETPDWTPDIKHSKIWFSGNMGNITVFLGIPGONKQAMSEAFYFYLRCSEDNSSEEQKIVSNSQSTSTEDAGDSTPFEDSEEFCSAER														
ref	RIYVTQNNDEFYIVGGYQLENQKRMYCSIVSLGONRIEISEMETPDWTPDIKHSKIWFSGNMGNITVFLGIPGONKQAMSEAFYFYLRCSEDNSSEEQKIVSNSQSTSTEDAGDSTPFEDSEEFCSAER														
Consensus	RIYVTQNNDEFYIVGGYQLENQKRMYCSIVSLGONRIEISEMETPDWTPDIKHSKIWFSGNMGNITVFLGIPGONKQAMSEAFYFYLRCSEDNSSEEQKIVSNSQSTSTEDAGDSTPFEDSEEFCSAER														
	391	400	410	420	430	440	450	460	470	480	490	500	510	520	
seq	ISFDGDDDEFDYNEDDEDESVTGYWITCSPTCOVDINTWVPFYSTELNKPAMIYCSHGDDGHVHAQCNDLEERTLIHLSE-SNKYYCNEHYRIARALQTPKRNLPQKPPHKS LHKXSGKVLTPAKKS														
ref	ISFDGDDDEFDYNEDDEDESVTGYWITCSPTCOVDINTWVPFYSTELNKPAMIYCSHGDDGHVHAQCNDLEERTLIHLSE6SNKYCNEHYRIARALQTPKRNLPQKPPHKS LHKK6SGKVLTPAKKS														
Consensus	ISFDGDDDEFDYNEDDEDESVTGYWITCSPTCOVDINTWVPFYSTELNKPAMIYCSHGDDGHVHAQCNDLEERTLIHLSE_SNKYYCNEHYRIARALQTPKRNLPQKPPHKS LHK6SGKVLTPAKKS														
	521	527													

seq	FLRRLFD														
ref	FLRRLFD														
Consensus	FLRRLFD														

Rag2 rate : mutation en 1414 T<G : introduit un stop en 472

ATGTCCCTGCAGATGGTTACAGTGGGTCATAACATAGCCTTAATTCAACCAGGCTTCTCACTGATGAATTTTGA
 TGGTCAAGTTTTTTCTTTGGCCAAAAAGGCTGGCCTAAGAGATCCTGCCCTACTGGAGTCTTTCATTTTGATAT
 AAAACAAAATCATCTCAAACCTGAAGCCTGCAGTTTTCTCTAAAGATTCCTGCTACCTCCCACCTCTTCGTTACCC
 AGCTACTTGCTCGTACAAAGGCAGCACAGACTCTGACAAGCATCAATATATCATCCACGGAGGGAAAAACGCCA
 AACAATGAGCTTTCCGATAAGATTTATATCATGTCTGTCTGCTTGAAGAATAACAAAAAAGTTACTTTCCGTTGT
 ACAGAGAAAGACTTAGTAGGAGATGTCCCTGAAGCCAGATATGGCCATTCCATTGACGTGGTATATAGCCGAG
 GAAAAAGTGTGGTGTCTCTTTGGAGGACGGTCATACATGCCTTCTACCCAAAGAACCACAGAAAAATGGAA
 TAGTGTAGCTGATTGCCTACCCCATGTTTTCTTGGTAGATTTTGAATTTGGGTGTGCAACGTCATATATTCTCCC
 AGAAGTTCAgGACGGGCTGTCTTTTCATGTTTCTATTGCCAGAAATGATACCATTATATTTTGGGAGGACACTC
 ACTTGCCAGTAACATACGTCCTGCTAACTTGTATAGAATAAGAGTAGATCTTCCCCTGGGTACCCAGCAGTGA
 ATTGCACTGTCTTGCCAGGAGGAATCTCTGTCTCCAGTGCAATTGTCACTCAAACAAATAATGATGAATTTGNT
 ATTN GTTGGTGGTNATCAGCTGGAAAATCAAAAAGNANGNNNNGNANCAT

TGATTGNNTNCCCNANNNNTTNNNTGGNAGNTTGGANTTNGGNTNNGCAACGTNATATNTTNTCCCNNAANT
 CAGGNCGGGNGNCTTTNCANGTTTNTATNNCCAGAAATGATACCATTNATANTTNGNGAGGACANTCACTT
 GCCAGTNACATANGTCTGCTAACNNGTANAGAATAAGAGTANATNTTNCCTGGNTANCCAGCAGTGAAT
 TGCACTNTCTTGCCAGGAGGANNNTCTGTCTNCAGTGCAATTGTCACTCAAACAAATAATGATGAATTTGTTAT
 TGTTGGTGGTTATCAGCNGGAAAATCAAAAAGGATGGTGTGTAGCATTGTCTCTAGGGGACAACAGGATT
 GAAATTAGTGAGATGGAGACCCAGACTGGACCCAGATATTAAGCATAGCAAAATATGGTTTGAAGCAAC
 ATGGGAAACGGGACTGTTTTCTTGGCATACCAGGAGACAACAAGCAGGCTATGTCAGAAGCATTCTATTCT
 ATATGTTGAGATGCTCTGAAGATAATTCGAGTGAGGAGCAGAAAATTGTCTCAAACAGTCAGACATCAACTGA
 AGATGCCGGGGACTCCACTCCCTTGAAGACTCGGAAGAATTTTGTTCAGTGCTGAAGCAATCAGCTTTGATG
 GTGATGATGAATTTGACACTTACAATGAAGATGATGAAGATGATGAATCTGTAACCGGCTACTGGATAACGTG
 TCCCCCTACTTGATGTGGACATCAATACTTGGGTTCCATTCTATTCAACTGAGCTCAATAAACCCGCCATGAT
 CTATTGTTCTCATGGGGATGGACACTGGGTGCATGCCAGTGCATGGATCTGGAAGAACGCACACTCATCCAC
 TTGTCAGAAGGAAGCAACAAATATTACTGCAATGAGCATGTGCGGATAGCAAGAGCATTACAAACTCCCCAAA
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 AAGAAATCCTTTCTTAGGAGGTTGTTTGATTAG

ATGTCCCTGCAGATGGTTACAGTGGGTCATAACATAGCCTTAATTCAACCAGGCTTCTCA	60
CTGATGAATTTTGATGGTCAAGTTTTTTCTTTGGCCAAAAAGGCTGGCCTAAGAGATCC	120
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GTTTCTCTAAAGATTCCTGCTACCTCCCACCTCTTCGTTACCCAGCTACTTGCTCGTAC	240
AAAGGCAGCAGACTCTGACAAGCATCAATATATCATCCACGGAGGGAAAAACGCCAAAC	300
AATGAGCTTTCCGATAAGATTTATATCATGTCTGTCTGCTTGAAGAATAACAAAAAAGTT	360
ACTTTCCGTTGTACAGAGAAAGACTTAGTAGGAGATGTCCCTGAAGCCAGATATGGCCAT	420
TCCATTGACGTGGTATATAGCCGAGGAAAAAGTGTGGTGTCTCTTTGGAGGACGGTCA	480
TACATGCCTTCTACCCAAAGAACCACAGAAAAATGGAATAGTGTAGCTGATTGCCTACCC	540
CATGTTTTCTTGGTAGATTTTGAATTTGGGTGTGCAACGTCATATATTCTCCAGAACTT	600
CAGGACGGGCTGTCTTTTCATGTTTCTATTGCCAGAAATGATACCATTATATTTGGGA	660
GGACACTCACTTGCCAGTAACATACGTCCTGCTAACTTGTATAGAATAAGAGTAGATCTT	720
cds ggacactcacttgccagtaacatacgtcctgctaacttgtatagaataagagtagatcctt	720

rev NCCCTGGNTANCCAGCAGTGAATTGCACTNTCTTGCCAGGAGGANNNTCTGTCTNCAGT	251
fwd CCCTTGGGTACCCAGCAGTGAATTGCACTGTCTTGCCAGGAGGAATCTCTGTCTCCAGT	780
cds ccccctgggtacccagcagtggaattgcaactgtccttgccaggaggaatctctgtctccagt	780

rev GCAATTGTCACTCAAACAAATAATGATGAATTTGTTATTGTTGGTGG- TTATCAGCNGGA	310
fwd GCAATTGTCACTCAAACAAATAATGATGAATTTGNTATTNGTTGGTGGTNATCAGCTGGA	840
cds gcaattgtcactcaacaaataatgatgaatttgttattgttgggtggtt-atcagctgga	839

rev AAATCAAAAAGGATGGTGTGTAGCATTGTCTCTAGGGGACAACAGGATTGAAATTAG	370
fwd AAATCAAAA-AAGNANGNNNGNANCAT-----	866

cds	aaatcaaaaaggatggtgtgtagcattgtctctctaggggacaacaggattgaaattag ***** * * * * * * *	899
rev	TGAGATGGAGACCCAGACTGGACCCAGATATTAAGCATAGCAAAATATGGTTTGAAG	430
fwd	-----	866
cds	tgagatggagaccccagactggaccccagatattaagcatagcaaaatatggtttggaag	959
rev	CAACATGGGAAACGGGACTGTTTTCTTGGCATAACCAGGAGACAACAAGCAGGCTATGTC	490
fwd	-----	866
cds	caacatgggaaacgggactgttttccttggcataccaggagacaacaagcaggctatgtc	1019
rev	AGAAGCATTCTATTTCTATATGTTGAGATGCTCTGAAGATAATTCGAGTGAGGAGCAGAA	550
fwd	-----	866
cds	agaagcattctatttctatatgttgagatgctctgaagataattcgagtgaggagcagaa	1079
rev	AATTGTCTCAAACAGTCAGACATCAACTGAAGATGCCGGGGACTCCACTCCCTTTGAAGA	610
fwd	-----	866
cds	aattgtctcaaacagtcagacatcaactgaagatgccggggactccactccctttgaaga	1139
rev	CTCGGAAGAATTTTGTTCAGTGCTGAAGCAATCAGCTTTGATGGTGATGATGAATTTGA	670
fwd	-----	866
cds	ctcgaagaattttgtttcagtgctgaagcaatcagctttgatggtgatgatgaatttga	1199
rev	CACTTACAATGAAGATGATGAAGATGATGAATCTGTAACCGGCTACTGGATAACGTGTTC	730
fwd	-----	866
cds	cacttacaatgaagatgatgaagatgatgaatctgtaaccggctactggataacgtgttc	1259
rev	CCCTACTTGTGATGTGGACATCAATACTTGGGTTCCATTCTATTCAACTGAGCTCAATAA	790
fwd	-----	866
cds	ccctacttgtgatgtggacatcaatacttgggttcattctattcaactgagctcaataa	1319
rev	ACCCGCCATGATCTATTGTTCTCATGGGGATGGACACTGGGTGCATGCCAGTGCATGGA	850
fwd	-----	866
cds	accgcgatgatctattgttctcatggggatggacactgggtgcatgccagtgcatgga	1379
rev	TCTGGAAGAACGCACACTCATCCACTTGTGAGAAGGAAGCAACAAATATTACTGCAATGA	910
fwd	-----	866
cds	tctggaagaacgcacactcatccacttgtcagaaggaagcaacaaatattactgcaatga	1439
rev	GCATGTGCGGATAGCAAGAGCATTACAAACTCCCAAAAGAAACCTCCCCTTACAAAAGCC	970
fwd	-----	866
cds	gcatgtgcgatagcaagagcattacaaactcccaaaagaacctccccttacaaaagcc	1499
rev	CCCAATGAAATCCCTCCACAAAAAAGGCTCCGGGAAAGTCTTGACTCCTGCCAAGAAATC	1030
fwd	-----	866
cds	cccaatgaaatccctccacaaaaaggctccgggaaagtcttgactcctgccaagaaatc	1559
rev	CTTTCTTAGGAGGTGTTTGATTAG	1055
fwd	-----	866
cds	ctttcttaggaggttgtttgattag	1584

o **FlagBirA Rag2 DiT0 clone A**

➤ **B3Fwd 877NT**

ATGTCCTGCAGATGGTTACAGTGGGTCATAACATAGCCTTAATTCAACCAGGCTTCTCACTGATGAA
TTTTGATGGTCAAGTTTTTTCTTTGGCCAAAAAGGCTGGCCTAAGAGATCCTGCCCTACTGGAGTCTT
TCATTTTGATATAAAACAAAATCATCTCAAAGTGAAGCCTGCAGTTTTCTCTAAAGATTCCTGCTACCT
CCCACCTCTTCGTTACCCAGCTACTTGCTCGTACAAAGGCAGCACAGACTCTGACAAGCATCAATATAT
CATCCACGGAGGGAAAACGCCAAACAATGAGCTTTCCGATAAGATTTATATCATGTCTGTCTGCTGCA
AGAATAACAAAAAAGTTACTTTCCGTTGTACAGAGAAAGACTTAGTAGGAGATGTCCCTGAAGCCAG
ATATGGCCATTCCATTGACGTGGTATATAGCCGAGGAAAAAGTGTGGTGTCTCTTTGGAGGACGG
TCATACATGCCTTCTACCCAAAGAACCACAGAAAAATGGAATAGTGTAGCTGATTGCCTACCCCATGT
TTTCTTGGTAGATTTTGAATTTGGGTGTGCAACGTCAATATTCTCCAGAACTTCAGGACGGGCTGTG
TTTTCATGTTTCTATTGCCAGAAATGATACCTTTATATTTTGGGAGGACACTCACTTGCCAGTAACAT
ACGTCCTGCTAAGTGTATAGAATAAGAGTAGATCTTCCCTGGGTACCCAGCAGTGAATTGCACTG
TCTTGCCAGGAGGAATCTCTGTCTCCAGTGCAATTGtCACTCAACAAATAATGATGAATTTGTtATTGt
NGGTGGTNATCANCTGGAAATCAAAAANGATGNNGTGTANCATTGTCTCNCTNNGG

➤ **BGHRev**

GAANNANACNATNNANANNNNNGGGNNNNNNNNNTGNCAGNNNCNNNNNNNNNTANN
NNGNANNGNATNAGAGTANNNCTTNCNNTGGGTANCCNNNNNGNNNNNNNNNTNTNNNNNN
NNNNNNNANNATNNNNNNNCANNNNNNNNNNNANNNANNNAAANNNNNGNANTNNNNNT
GNNNGNGNNNNNNNNNNNNNAATNAANNNGGATNGTGTNNNGCNNTGTCTCTNTNGGGNN
NNNNNGATTGAAATTANTGAGATGGAGANNNCAGANNGGACCNCAGATANNNNGCATANCNN
AATNTGGGTTTGGAAGCAACANNNNNAANGNGANNGTNTCNTNGGNANANCAGGNGNCNACA
AGCAGGNNANNNNNGNAGCATTCTATTTNTATNNNTGAGNNGCTNTGNNGNNTNNNNNN
NNGNGNNNNNNNGTNTCAAGCNNNNNGNCANNANTGAANNNNNCGNGGACTCCGNNCCCN
NNNNNCNNGGANGANNNTGTTCANNGNNGAAGCAATCAGCTNNNNNNGNNANGANGAATTN
NNCNNNNACAATGAAGNNGANGAAGATGATGANNNNNGNNNCCGGCTNNNGGATANCCTGTTCC
CCTNCNTNNNNNNNGACATCNNTNCTTGGGTTCNNNNCNNTCNNTGAGNTCAATAAACCCGC
CATGATCTATNGTTCTCATGGNGNNGGNCANNGGGNGCATGCCNGTNCATGGATNNGGAAGAAC
GCACACTCATCCACTNGTNNGNAGGAAGCAACAAATANNNCNGNNNGAGCATGNGCGGATAGC
AAGAGCATTACAAAACCCAAAAGAAACCTCCCCTTACAAAAGCCCCAATGAAATCCCTCCACAAAA
AAGGCTCCGGGAAAGTCTTGACTCCNGNCAAGAAATCCTTTCTAGGAGGTTGTTTGATTAG

➤ **BGHRev 918NT : reséquençage du 21/12**

TCACTTNCCAGNNNCNTNCGNNNNNNNANTTGNNTNGAATAAGAGTAGATNTTNCNNTNNNTACC
CCANCAGNGAATTGCACTGTCTTNNCNGGAGGANNNNNTGTNTNCCNGTGCAANTGTCACTCAAAC
AAATAATGATGAATTTGTTANNTNNGNNNTTATCAGNTGGAAANTCAAAAAGGANGGTGTGTA
GCANNGTCTCTNTAGGGGACAACNGGATTGAAATTAGTGAGATGGAGACCCAGACTGGACCCAG
ATATTAAGCATAGCAAAAATATGGTNNNGAAGCAACATGGGAAACGGGACTGTTTCTNNGGCATACC
AGGAGACAACAAGCAGGNTATGTCAGAAGCATTCTATTTCTATATGTTGAGATGCTCTGAAGATAAT
TCGAGTGAGGAGCAGAAAATTGTCTCAAACAGTCAGACATCAACTGAAGATGCCGGGGACTCCACTC

CCTTTGAAGACTCGGAAGAATTTTGTTCAGTGCTGAAGCAATCAGCTTTGATGGTGATGATGAATTT
GACACTTACAATGAAGATGATGAAGATGATGAATCTGTAACCGGCTACTGGATAACGTGTTCCCCTAC
TTGTGATGTGGACATCAATACTTGGGTTCATTCTATTCAACTGAGCTCAATAAACCCGCCATGATCTA
TTGTTCTCATGGGGATGGACACTGGGTGCATGCCAGTGATGGATCTGGAAGAACGCACACTCATC
CACTTGTGAGAAGGAAGCAACAAATATTACTGCAATGAGCATGTGCGGATAGCAAGAGCATTACAAA
CTCCAAAAGAAACCTCCCCTTACAAAAGCCCCCAATGAAATCCCTCCACAAAAAAGGCTCCGGGAAA
GTCTTGACTCCTGCCAAGAAATCCTTTCTAGGAGGTTGTTTGATTAG

➤ Synthèse séquençage

ATGTCCCTGCAGATGGTTACAGTGGGTCATAACATAGCCTTAATTCAACCAGGCTTCTCA	60
CTGATGAATTTTGTGGTCAAGTTTTTTCTTTGGCCAAAAAGGCTGGCCTAAGAGATCC	120
TGCCCTACTGGAGTCTTTCATTTTGATATAAAACAAAATCATCTCAAAGCTGAAGCCTGCA	180
GTTTTCTCTAAAGATTCTGTACCTCCACCTCTTCGTTACCCAGCTACTTGCTCGTAC	240
AAAGGCAGCACAGACTCTGACAAGCATCAATATATCATCCACGGAGGGAAAAACGCCAAC	300
AATGAGCTTTCCGATAAGATTTATATCATGTCTGTCTGCTTGAAGAATAACAAAAAGTT	360
ACTTTCGGTGTACAGAGAAAGACTTAGTAGGAGATGTCCCTGAAGCCAGATATGGCCAT	420
TCCATTGACGTGGTATATAGCCGAGGAAAAAGTGTGGTGTCTCTTTGGAGGACGGTCA	480
TACATGCCTTCTACCCAAAGAACCACAGAAAAATGGAATAGTGTAGCTGATTGCCTACCC	540
CATGTTTTCTTGGTAGATTTTGAATTTGGGTGTGCAACGTCATATATTCTCCAGAACTT	600
CAGGACGGGCTGTCTTTTCATGTTTCTATTGCCAGAAATGATACCATTATATTTTGGGA	660
GGACACTCACTTGCCAGTAACATACGTCCTGCTAACTTGTATAGAATAAGAGTAGATCTT	720
CCCCTGGGTACCCAGCAGTGAATTGCACTGTCTTGCCAGGAGGAATCTCTGTCTCCAGT	780
GCAATTGTCACTCAAACAAATAATGATGAATTTGTTATTGTNGGTGGTTATCAGCTGGA	
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TGAGATGGAGACCCAGACTGGACCCAGATATTAAGCATAGCAAAATATGGTTTGGAAAG	
CAACATGGGAAACGGGACTGTTTTCTNNGGCATACCAGGAGACAACAAGCAGGNTATGTC	
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CTCGGAAGAATTTTGTTCAGTGTGAAGCAATCAGCTTTGATGGTGATGATGAATTTGA	
CACCTACAATGAAGATGATGAAGATGATGAATCTGTAACCGGCTACTGGATAACGTGTTT	
CCCTACTTGTGATGTGGACATCAATACTTGGGTTCATTCTATTCAACTGAGCTCAATAA	
ACCCGCCATGATCTATTGTTCTCATGGGGATGGACACTGGGTGCATGCCAGTGATGGA	
TCTGGAAGAACGCACACTCATCCACTTGTGAGAAGGAAGCAACAAATATTACTGCAATGA	
GCATGTGCGGATAGCAAGAGCATTACAACTCCCAAAAGAAACCTCCCCTTACAAAAGCC	
CCCAATGAAATCCCTCCACAAAAAAGGCTCCGGGAAAGTCTTGACTCCTGCCAAGAAATC	
CTTCTTAGGAGGTTGTTTGATTAG	

MSLQMVTVGHNIALIQPGFSLMNFDGQVFFGQKGWPKRSCPTGVFHFQKQHLKPAVFSKDSCLPPLRYPATCSYKGS
TDSKHKYIIHGGKTPNNELSDKIYIMSVACKNNKKVTRFCTEKDLVGDVPEARYGHSIDVVYSRGSVGVLFGGRSYMPSTQR
TTEKWNSVADCLPHVFLVDFFGCATSYILPELQDGLSFHVSIARNDTIYILGGHSLASNIRPANLYRIRVDLPLGTPAVNCTVLP
GISVSSAIVTQTNNEDEFVIXGGYQLENQKRMVCSIVSLGDNRIEISEMETPDWTPDIKHSKIWFSGNMGNVTGFXGIPGDNKQX
MSEAFYFMYMLRCSNSEEQKIVSNSQSTEDAGDSTPFEDSEFCFSAEISFDGDDDEFDTYNEDDEDESVTGYWITCSPTC
DVDINTWVPFYSTELNKPAMIYCSHGDGHVHAQCMDLEERTLIHLSEGSNKYYCNEHVRIARALQTPKRNLPQKPPMKSLH
KKGSGKVLTPAKKSFLRRFLD-

➤ Blast contre banque de rat

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
✓	Rattus norvegicus recombination activating 2 (Rag2) mRNA	Rattus norvegicus	2915	2915	100%	0.0	99.81%	3546	NM_001100528.2
✓	Rattus norvegicus RAG2 (RAG2) gene partial cds	Rattus norvegicus	1690	1690	58%	0.0	99.67%	921	AY303209.1
✓	Rattus norvegicus recombination activating protein 2 (Rag2) gene partial cds	Rattus norvegicus	815	815	28%	0.0	99.77%	444	AY011941.1

➤ Différence au niveau NT

1 10 20 30 40 50 60 70 80 90 100 110 120 130

seq
cds
Consensus
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
ATGTCCTTGCAGATGGTTACAGTGGGTCATACATAGCCTTAATTCACCCAGGCTTCTCAGTATGATTTTGTATGGTCAGGTTTTTTCTTTGGCCAAAAGAGGCTGGCTTAGAGATCTCGCCCTACTG
ATGTCCTTGCAGATGGTTACAGTGGGTCATACATAGCCTTAATTCACCCAGGCTTCTCAGTATGATTTTGTATGGTCAGGTTTTTTCTTTGGCCAAAAGAGGCTGGCTTAGAGATCTCGCCCTACTG
ATGTCCTTGCAGATGGTTACAGTGGGTCATACATAGCCTTAATTCACCCAGGCTTCTCAGTATGATTTTGTATGGTCAGGTTTTTTCTTTGGCCAAAAGAGGCTGGCTTAGAGATCTCGCCCTACTG

131 140 150 160 170 180 190 200 210 220 230 240 250 260

seq
cds
Consensus
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
GAGCTTTTCATTTTGATATAAAACAAATCATCTCAAACTGAGGCTGCAGTTTTCTTAAGATTCCTGCTACCTCCACCTCTTCGTTACCCAGCTACTTGTCTGACAAAGGCGACACAGACTCTGA
GAGCTTTTCATTTTGATATAAAACAAATCATCTCAAACTGAGGCTGCAGTTTTCTTAAGATTCCTGCTACCTCCACCTCTTCGTTACCCAGCTACTTGTCTGACAAAGGCGACACAGACTCTGA
GAGCTTTTCATTTTGATATAAAACAAATCATCTCAAACTGAGGCTGCAGTTTTCTTAAGATTCCTGCTACCTCCACCTCTTCGTTACCCAGCTACTTGTCTGACAAAGGCGACACAGACTCTGA

261 270 280 290 300 310 320 330 340 350 360 370 380 390

seq
cds
Consensus
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
CAGCATCATATATCATCCAGGGGAAACGCCAARCAATGAGCTTTCCGATAGATTATATCATGTCTGCTGCTTCGAGATACAAAAAGTTACTTTCCGTTGTACAGAGAAAGACTTAGTA
CAGCATCATATATCATCCAGGGGAAACGCCAARCAATGAGCTTTCCGATAGATTATATCATGTCTGCTGCTTCGAGATACAAAAAGTTACTTTCCGTTGTACAGAGAAAGACTTAGTA
CAGCATCATATATCATCCAGGGGAAACGCCAARCAATGAGCTTTCCGATAGATTATATCATGTCTGCTGCTTCGAGATACAAAAAGTTACTTTCCGTTGTACAGAGAAAGACTTAGTA

391 400 410 420 430 440 450 460 470 480 490 500 510 520

seq
cds
Consensus
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
GGAGATGTCCTTGAGCCAGATATGGCATTCCATTGACGTGGTATATAGCCGAGGAAAGATGTTGGTGTCTCTTTGGAGGCGGTACATACGCTCTTACCCAAAGAACCCAGAAATGGATA
GGAGATGTCCTTGAGCCAGATATGGCATTCCATTGACGTGGTATATAGCCGAGGAAAGATGTTGGTGTCTCTTTGGAGGCGGTACATACGCTCTTACCCAAAGAACCCAGAAATGGATA
GGAGATGTCCTTGAGCCAGATATGGCATTCCATTGACGTGGTATATAGCCGAGGAAAGATGTTGGTGTCTCTTTGGAGGCGGTACATACGCTCTTACCCAAAGAACCCAGAAATGGATA

521 530 540 550 560 570 580 590 600 610 620 630 640 650

seq
cds
Consensus
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
GTGTAGCTGATGCTTACCCCATGTTTCTTGGTAGATTGGATTGGGTGTGCAGCTCATATCTCCAGAACCTCAGGACGGCTGTCTTTTCATGTTCTATTGCCAGAAATGATACCATTTA
GTGTAGCTGATGCTTACCCCATGTTTCTTGGTAGATTGGATTGGGTGTGCAGCTCATATCTCCAGAACCTCAGGACGGCTGTCTTTTCATGTTCTATTGCCAGAAATGATACCATTTA
GTGTAGCTGATGCTTACCCCATGTTTCTTGGTAGATTGGATTGGGTGTGCAGCTCATATCTCCAGAACCTCAGGACGGCTGTCTTTTCATGTTCTATTGCCAGAAATGATACCATTTA

651 660 670 680 690 700 710 720 730 740 750 760 770 780

seq
cds
Consensus
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
TATTTTGGAGGACACTCACTTGGCAGTACATAGCTCTGCTACTTGTATAGATATAGAGTAGATCTTCCCTGGGTACCCAGCAGTGAATTGCATGCTGTGCCAGAGGGAATCTCTGTCCAGT
TATTTTGGAGGACACTCACTTGGCAGTACATAGCTCTGCTACTTGTATAGATATAGAGTAGATCTTCCCTGGGTACCCAGCAGTGAATTGCATGCTGTGCCAGAGGGAATCTCTGTCCAGT
TATTTTGGAGGACACTCACTTGGCAGTACATAGCTCTGCTACTTGTATAGATATAGAGTAGATCTTCCCTGGGTACCCAGCAGTGAATTGCATGCTGTGCCAGAGGGAATCTCTGTCCAGT

781 790 800 810 820 830 840 850 860 870 880 890 900 910

seq
cds
Consensus
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
GCARTTGTCTCAACCAATATATGATGATTTGTTATTGTTGGTGGTTATCAGCTGGAAATCAAAAAGGATGGTGTGTAGCTTGTCTCTAGGGGACACAGGATTGAATTAGTGAGATGGAGA
GCARTTGTCTCAACCAATATATGATGATTTGTTATTGTTGGTGGTTATCAGCTGGAAATCAAAAAGGATGGTGTGTAGCTTGTCTCTAGGGGACACAGGATTGAATTAGTGAGATGGAGA
GCARTTGTCTCAACCAATATATGATGATTTGTTATTGTTGGTGGTTATCAGCTGGAAATCAAAAAGGATGGTGTGTAGCTTGTCTCTAGGGGACACAGGATTGAATTAGTGAGATGGAGA

911 920 930 940 950 960 970 980 990 1000 1010 1020 1030 1040

seq
cds
Consensus
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
CCCCAGCTGGACCCAGATATTAGCATAGCAAAATATGTTTGGAGCAACATGGGAACGGGACTGTTTCCCTTGGCATACAGGAGACACACAGCAGGNTATGTACAGGACTTATTTCTATAT
CCCCAGCTGGACCCAGATATTAGCATAGCAAAATATGTTTGGAGCAACATGGGAACGGGACTGTTTCCCTTGGCATACAGGAGACACACAGCAGGNTATGTACAGGACTTATTTCTATAT
CCCCAGCTGGACCCAGATATTAGCATAGCAAAATATGTTTGGAGCAACATGGGAACGGGACTGTTTCCCTTGGCATACAGGAGACACACAGCAGGNTATGTACAGGACTTATTTCTATAT

1041 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170

seq
cds
Consensus
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
GTTGAGATGCTCTGAGATATTTGAGTGAGGAGCAGAAATTTGCTCAACAGCTCAGACATCACTGAGATGCCGGGACTCCACTCCCTTTGAGAGCTCGGAGAGATTTTGTTCAGTGCTGAGGCA
GTTGAGATGCTCTGAGATATTTGAGTGAGGAGCAGAAATTTGCTCAACAGCTCAGACATCACTGAGATGCCGGGACTCCACTCCCTTTGAGAGCTCGGAGAGATTTTGTTCAGTGCTGAGGCA
GTTGAGATGCTCTGAGATATTTGAGTGAGGAGCAGAAATTTGCTCAACAGCTCAGACATCACTGAGATGCCGGGACTCCACTCCCTTTGAGAGCTCGGAGAGATTTTGTTCAGTGCTGAGGCA

1171 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300

seq
cds
Consensus
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
ATCAGCTTTGATGGTATGATGATTTTGCACCTTACATGAGATGATGAGATGATGATCTGTATCCGGCTACTGGATATCGTGTCCCTACTTGTGATGTGGACATCAATACTTGGTTCCTATTCT
ATCAGCTTTGATGGTATGATGATTTTGCACCTTACATGAGATGATGAGATGATGATCTGTATCCGGCTACTGGATATCGTGTCCCTACTTGTGATGTGGACATCAATACTTGGTTCCTATTCT
ATCAGCTTTGATGGTATGATGATTTTGCACCTTACATGAGATGATGAGATGATGATCTGTATCCGGCTACTGGATATCGTGTCCCTACTTGTGATGTGGACATCAATACTTGGTTCCTATTCT

1301 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430

seq
cds
Consensus
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
ATTCACCTGAGCTCAATAAACCCGCATGATCTATTGTTCTCATGGGATGGACACTGGGTGATGCCAGTGCATGGATCTGGAGAGCGACACTCATCCACTTGTACAGAGGAGCAGCAAAATATTA
ATTCACCTGAGCTCAATAAACCCGCATGATCTATTGTTCTCATGGGATGGACACTGGGTGATGCCAGTGCATGGATCTGGAGAGCGACACTCATCCACTTGTACAGAGGAGCAGCAAAATATTA
ATTCACCTGAGCTCAATAAACCCGCATGATCTATTGTTCTCATGGGATGGACACTGGGTGATGCCAGTGCATGGATCTGGAGAGCGACACTCATCCACTTGTACAGAGGAGCAGCAAAATATTA

1431 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560

seq
cds
Consensus
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
CTGCARTGAGCATGTGCGGATAGCAGAGCATTACAACTCCCAAAGAAACCTCCCTTACAAAGCCCCARTGAATCCCTCCACAAAAGGCTCCGGGAAGTCTTGACTCTTGCACAGAAATCC
CTGCARTGAGCATGTGCGGATAGCAGAGCATTACAACTCCCAAAGAAACCTCCCTTACAAAGCCCCARTGAATCCCTCCACAAAAGGCTCCGGGAAGTCTTGACTCTTGCACAGAAATCC
CTGCARTGAGCATGTGCGGATAGCAGAGCATTACAACTCCCAAAGAAACCTCCCTTACAAAGCCCCARTGAATCCCTCCACAAAAGGCTCCGGGAAGTCTTGACTCTTGCACAGAAATCC

1561 1570 15801584

seq
cds
Consensus
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
TTTCTTAGGAGGTTGTTGATTAG
TTTCTTAGGAGGTTGTTGATTAG
TTTCTTAGGAGGTTGTTGATTAG

➤ **Blast contre banque de rat**

			Score	Score	Cover	value	ident	Len	
✓	V(D)J recombination-activating protein 2 [Rattus norvegicus]	Rattus norvegicus	1099	1099	100%	0.0	99.43%	527	NP_001093998.1
✓	RAG2 [Rattus norvegicus]	Rattus norvegicus	637	637	58%	0.0	99.02%	307	AAQ77003.1
✓	recombination activating protein 2 [Rattus norvegicus]	Rattus norvegicus	309	309	28%	5e-104	100.00%	148	AAG38684.1

➤ Différence au niveau PROT :

	1	10	20	30	40	50	60	70	80	90	100	110	120	130	
seq	-----														
ref	MSLQMYTVGHNIALIQPGFSLHNFQGVFFFGQKGHPKRSCPTGVFHFQDIQNHLLKLPVAFSKDSCYLPLRYPATCSYKGSTDSKQHYIIHGKTPNNELSDKIYIHSVACKNNKKVTFRCTEKDLV														
Consensus	MSLQMYTVGHNIALIQPGFSLHNFQGVFFFGQKGHPKRSCPTGVFHFQDIQNHLLKLPVAFSKDSCYLPLRYPATCSYKGSTDSKQHYIIHGKTPNNELSDKIYIHSVACKNNKKVTFRCTEKDLV														
	131	140	150	160	170	180	190	200	210	220	230	240	250	260	
seq	-----														
ref	GDVPEARYGHSIDVYYSRGKSVGVLFGGRSYMPSTQRTTEKMSVADCLPHVFLVDFEFGCATSYILPELQDGLSFHYSIARNDTIYILGGHSLASNIRPANLYRIRVDLPLGTPAVNCTVLPGGISVSS														
Consensus	GDVPEARYGHSIDVYYSRGKSVGVLFGGRSYMPSTQRTTEKMSVADCLPHVFLVDFEFGCATSYILPELQDGLSFHYSIARNDTIYILGGHSLASNIRPANLYRIRVDLPLGTPAVNCTVLPGGISVSS														
	261	270	280	290	300	310	320	330	340	350	360	370	380	390	
seq	-----														
ref	RIVTQTNNDEFVIXGGYQLENQKRHVCSIYSLGDNRIEISEMETPDWTPDIKHSKIIFGSGNHMGNGTVFXGIPGDNKQXMSSEAFYFYMLRCSEDNSSEEQKIVSNSQSTSEDAGDSTPFEDSEEFCSAEAR														
Consensus	RIVTQTNNDEFVIXGGYQLENQKRHVCSIYSLGDNRIEISEMETPDWTPDIKHSKIIFGSGNHMGNGTVFLGIPGDNKQAMSEAFYFYMLRCSEDNSSEEQKIVSNSQSTSEDAGDSTPFEDSEEFCSAEAR														
	391	400	410	420	430	440	450	460	470	480	490	500	510	520	
seq	-----														
ref	ISFDGDDDEFDTYNEDDEDDSVTGYWITCSPTCDVDINTWVPFYSTELNKPAMIYCSHGQGHVYHAQCHDLEERTLIHLSEGSNKYYCNEHVRIARALQTPKRNLPQKPPMKSLHKKGSQKVLTPAKKS														
Consensus	ISFDGDDDEFDTYNEDDEDDSVTGYWITCSPTCDVDINTWVPFYSTELNKPAMIYCSHGQGHVYHAQCHDLEERTLIHLSEGSNKYYCNEHVRIARALQTPKRNLPQKPPMKSLHKKGSQKVLTPAKKS														
	521	527													

seq	FLRRLFD														
ref	FLRRLFD														
Consensus	FLRRLFD														

○ **FlagBirA Rag2 DiT0 clone C**

➤ **B3Fwd 949NT**

ATGTCCCTGCAGATGGTTACAGTGGGTCATAACATAGCCTTAATTCAACCAGGCTTCTCACTGATGAATTTTGATG
GTCAAGTTTTTTCTTTGGCCAAAAAGGCTGGCCTAAGAGATCCTGCCCTACTGGAGTCTTTCATTTTGATATAAA
ACAAAATCATCTCAAAGCTGAAGCCTGCAGTTTTCTCTAAAGATTCCTGCTACCTCCCACCTCTTCGTTACCCAGCTA
CTTGCTCGTACAAAGGCAGCACAGACTCTGACAAGCATCAATATATCATCCACGGAGGGAAAAACGCCAAACAATG
AGCTTTCCGATAAGATTATATCATGTCTGTCGCTTGCAAGAATAACAAAAAGTTACTTTCGTTGTACAGAGAA
AGACTTAGTAGGAGATGTCCCTGAAGCCAGATATGGCCATTCCATTGACGTGGTATATAGTCGAGGAAAAAGTGT
TGGTGTCTCTTTGGAGGACGGTCATACATGCCTTCTACCCAAAGAACCACAGAAAAATGGAATAGTGTAGCTGA
TTGCCTACCCCATGTTTTCTTGGTAGATTTTGAATTTGGGTGTGCAACGTCATATATTCTCCAGAAGTTTCAGGACG
GGCTGTCTTTTCATGTTTCTATTGCCAGAAATGATACCTTTATATTTTGGGAGGACACTCACTTGCCAGTAACATA
CGTCTGCTAACTTGATAGAATAAGAGTAGATCTTCCCCTGGGTACCCAGCAGTGAATTGCACTGTCTTGCCAG
GAGGAATCTCTGTCTCCAGTGAATTGTCACTCAACAaTAATGAtGAATTTgNTATNNNNNTNGNNGGTNNNTCAGC
TGGAAATCAAAAAGGATGGTGTGNAGCATTGTCTCTCNNNGGGANNNNNNGNNNTGANNTANTGANNNGNA
NNNCCNNNCTGNNCCCCNGANNTTNNNNNTNGCNAANNNNNNTTG

➤ **BGHRev**

GNTTGGANGCNANATGGGAAANNNNAGTGNNNNNNNNGGCATNNCAGGAGNNNNNCNNNCNNNNNTANNT
CNNNAGCATNNTATTTNTATNNNNNTGANANGCTNNGNNGANNNNNNNGNGTNNNNNGCNNNNNNNTTNTNT
CAANCANNNNGACATCAACTGNAGANGCCGNGGANTNCACTCCCTNTGNNGACTNGNAAGNANTNNGTNN
CNNTGNNNNNAGCAATCAGCTTNNANNGNANNANNANNANTTGACACTNNCANTGAAGANGANNNAGATGN
NNNANNNNNNNCCNGCNNNTGGNTNACGTGTTCCCNACNTGTGANGTGGACANCNATACTTGGGTTCCAT
TCTATTNNNTNANNTCAATAAACCCNCCATGATNNANNGTTCTCATGGGGATGGACNCNGNGTGCATNCCCN
GNGCATGGATNNGGAAGAANNNNCNNTCATCCACTNGNCNGNNGGNGCAANNNNNNTNANNGCAATGA
GCATGTGCGNATAGCAAGAGCNNNCNAACTCCCAAAAGAAACCTCCCCTTACAAAAGCCCCCAATGAAATCCCT
CCACAAAAAAGGCTCCGGGAAAGTCTTGACTCCTGCCAAGAAATCCTTTCTTAGGAGGTTGTTTGATTAG

➤ **BGHRev 982NT reséquence 21/12**

GGANNGGNNNTNTTTNATGTTTNTATNNCNAAATGATNNNNNNNNNNNTNGNGAGGNCACACTCACNNNCC
AGTACCNNANNNNNNNNTANNTGNATAGNATNAGAGNAGATNTNNCNNNNGNTNNCCNCNNCAGNGA
ATTNCACTNTNTTGNACAGGNNNGGAATNTNTNTNTNAGNGCAATTGTCANTCAAACAAATNATGATGAATTTG
TNNTTGTNNGTGGNNNTCANNTGGAAANTCAAAAAAGGATGGTGNGTANCATNGTCTCTCTAGGGGACAACA
GGATTGAAATTAGTGAGATGGAGACCCAGNNNNNNNNCCAGATATTAAGCATAGCAANATATGGTTNGGAAG
CAACATGGGAAACGGGANTGTTTTNNNNNCATACCAGGAGACAACAAGCAGGCTATGTCAGAAGCATTCTAT
TTCTATATGTTGAGATGCTCTGAAGATAATTCGAGTGAGGAGCAGAAAATTGTCTCAAACAGTCAGACATCAACT
GAAGANGCCGGGGACTCCACTCCCTTTGAAGACTCGGAAGAATTTTGTTCAGTGCTGAAGCAATCAGCTTTGA
TGGTGATGATGAATTTGACACTTACAATGAAGATGATGAAGATGATGAATCTGTAACCGGCTACTGGATAACGTGT
TCCCCTACTTGTGATGTGGACATCAATACTTGGGTTCCATTCTATTCAACTGAGCTCAATAAACCCGCCATGATCTAT
TGTTCTCATGGGGATGGACACTGGGTGCATGCCAGTGCATGGATCTGGAAGAACGCACACTCATCCACTTGTC
GAAGGAAGCAACAAATATTACTGCAATGAGCATGTGCGGATAGCAANNNNNNTACAAACTCCCAAAAGAAACCT
CCCCTTACAAAAGCCCCCAATGAAATCCCTCCACAAAAAAGGCTCCGGGAAAGTCTTGACTCCTGCCAAGAAATC
CTTTCTTAGGAGGTTGTTTGATTAG

➤ **Seq int 21/12**

TCTTGCCNGGAGGAATCTCTGTCTCCAGTGCAATTGTCACTCAAACAAATAATGATGAATTTGTTATTGTTGGTGG
 TTATCAGCTGGAAAATCAAAAAGGATGGTGTGTAGCATTGTCTCTCTAGGGGACAACAGGATTGAAATTAGTGA
 GATGGAGACCCCAGACTGGACCCCAGATATTAAGCATAGCAAAATATGGTTTGGAAAGCAACATGGGAAACGGGA
 CTGTTTTCTTGGCATACCAGGAGACAACAAGCAGGCTATGTCAGAAGCATTCTATTTCTATATGTTGAGATGCTCT
 GAAGATAATTCGAGTGAGGAGCAGAAAATTGTCTCAAACAGTCAGACATCAACTGAAGATGCCGGGGACTCCAC
 TCCCTTTGAAGACTCGGAAGAATTTTGTTCAGTGCTGAAGCAATCAGCTTTGATGGTGATGATGAATTTGACAC
 TTACAATGAAGATGATGAAGATGATGAATCTGTAACCGGCTACTGGATAACGTGTTCCCTACTTGTGATGTGGAC
 ATCAATACTGGGTTCCATTCTATTCAACTGAGCTCAATAAACCCGCCATGATCTATTGTTCTCATGGGGATGGACA
 CTGGGTGCATGCCAGTGCGATGGATCTGGAAGAAGCACACTCATCCACTTGTGAGAAGGAAGCAACAAATATTA
 CTGCAATGAGCATGTGCGGATAGCAAGAGCATTACAACTCCCAAAGAAACCTCCCCTTACAAAAGCCCCAAT
 GAAATCCCTCCACAAAAAGGcTCCGGGAAAGTCTTGACTCCTGCCAAGAAATCCTTTCTNAGGANGTTGTTTGA
 TTAG

➤ **Synthèse séquençage**

ATGTCCTTCGAGATGGTTACAGTGGGTCATAACATAGCCTTAATTCAACCAGGCTTCTCA	60
CTGATGAATTTTGATGGTCAAGTTTTTTCTTTGGCCAAAAAGGCTGGCCTAAGAGATCC	120
TGCCCTACTGGAGTCTTTCATTTTGATATAAAACAAAATCATCTCAAACCTGAAGCCTGCA	180
GTTTTCTCTAAAGATTCTGCTACCTCCACCTCTTCGTTACCCAGCTACTTGCTCGTAC	240
AAAGGCAGCACAGACTCTGACAAGCATCAATATATCATCCACGGAGGGAAAACGCCAAAC	300
AATGAGCTTTCCGATAAGATTTATATCATGTCTGTCTGCTTGAAGAATAACAAAAAGTT	360
ACTTTCGGTTGTACAGAGAAAGACTTAGTAGGAGATGTCCCTGAAGCCAGATATGGCCAT	420
TCCATTGACGTGGTATATAGTCGAGGAAAAAGTGTGGTGTCTCTTTGGAGGACGGTCA	480
TACATGCCTTCTACCCAAAGAACCACAGAAAAATGGAATAGTGTAGCTGATTGCCTACCC	540
CATGTTTTCTTGGTAGATTTTGAATTTGGGTGTGCAACGTCATATATTCTCCAGAACTT	600
CAGGACGGGCTGTCTTTTCATGTTTCTATTGCCAGAAATGATACCATTATATTTTGGGA	660
GGACACTCACTTGCCAGTAACATACGCTCTGCTAAGTGTATAGAATAAGAGTAGATCTT	720
CCCCTGGGTACCCAGCAGTGAATTGCACTGTCTTGCCAGGAGGAATCTCTGTCTCCAGT	780
GCAATTGTCACTCAAACAAATAATGATGAATTTGTTATTGTTGGTGGTTATCAGCTGGAA	
AATCAAAAAGGATGGTGTGTAGCATTTGTCTCTTAGGGGACAACAGGATTGAAATTAGT	
GAGATGGAGACCCCAGACTGGACCCAGATATTAAGCATAGCAAAATATGGTTTGGAGC	
AACATGGGAAACGGGACTGTTTTCTTGGCATAACCAGGAGACAACAAGCAGGCTATGTCA	
GAAGCATTCTATTTCTATATGTTGAGATGCTCTGAAGATAATTGAGTGAGGAGCAGAAA	
ATTTGCTCAAACAGTCAGACATCAACTGAAGATGCCGGGGACTCCACTCCCTTTGAAGAC	
TCGGAAGAATTTTGTTCAGTGCTGAAGCAATCAGCTTTGATGGTGATGATGAATTTGAC	
ACTTACAATGAAGATGATGAAGATGATGAATCTGTAACCGGCTACTGGATAACGTGTTCC	
CCTACTTGTGATGTGGACATCAATACTTGGGTTCCATTCTATTCAACTGAGCTCAATAAA	
CCCGCCATGATCTATTGTTCTCATGGGGATGGACACTGGGTGCATGCCAGTGATGGAT	
CTGGAAGAAGCACACTCATCCACTTGTGAGAAGGAAGCAACAAATATTACTGCAATGAG	
CATGTGCGGATAGCAAGAGCATTACAACTCCCAAAGAAACCTCCCCTTACAAAAGCCC	
CCAATGAAATCCCTCCACAAAAAGGCTCCGGGAAAGTCTTGACTCCTGCCAAGAAATCC	
TTTCTTAGGAGGTTGTTTGATTAG	

MSLQMVTVGHNIALIQPGFSLMNFDDGQVFFFGQKGWPKRSCPTGVFHFQDIQNHLKLKPAVFSKSDCYLPLRYP
 ATCSYKGSTDSKDHQYIIHGGKTPNNELSDKIYIMSVACKNNKKVTFRCTEKDLVGDVPEARYGHSIDVVYSRGKSV
 GVLFGGRSYMPSTQRTTEKWNSVADCLPHVFLVDFFEGCATSYILPELQDGLSFHVSIRNDTIYLGGHSLASNIRP
 ANLYRIRVDLPLGTPAVNCTVLPGGISVSSAIVTQTNNDFFVIVGGYQLENQKRMVCSIVSLGDNRIEISEMETPDW
 TPDIKHSKIWFSGNMNGTVFLGIPGDNKQAMSEAFYFMYLRCEQKIVSNSQSTEDAGDSTPFEDSEE
 FCFSAEAIISFDGDDFDTYNEDDEDESVTGYWITCSPTCDVDINTWVPFYSTELNKPAMIYCSHGDGHVVAHQ
 MDLEERTLIHLSEGSNKYYCNEHVRIARALQTPKRNLPLQKPPMKSLHKKGSGKVLTPAKKSFLRRLFD-

➤ **Blast contre banque de rat**

Rattus norvegicus recombination activating 2 (Rag2). mRNA	Rattus norvegicus	2920	2920	100%	0.0	99.94%	3546	NM_001100528.1
Rattus norvegicus RAG2 (RAG2). gene, partial cds	Rattus norvegicus	1701	1701	58%	0.0	100.00%	921	AY303209.1
Rattus norvegicus recombination activating protein 2 (Rag2). gene, partial cds	Rattus norvegicus	809	809	28%	0.0	99.55%	444	AY011941.1

➤ Différence au niveau NT

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq	ATGTCCTGCGATGGTTACAGTGGGTCATACATAGCCTTAATTCACCCAGGCTTCTACTGATGATTTTGTATGGTCAGTCTTTTCTTTGGCCAAAGGGCTGGCTTAGAGATCCTGCCCTACTG													
cds	ATGTCCTGCGATGGTTACAGTGGGTCATACATAGCCTTAATTCACCCAGGCTTCTACTGATGATTTTGTATGGTCAGTCTTTTCTTTGGCCAAAGGGCTGGCTTAGAGATCCTGCCCTACTG													
Consensus	ATGTCCTGCGATGGTTACAGTGGGTCATACATAGCCTTAATTCACCCAGGCTTCTACTGATGATTTTGTATGGTCAGTCTTTTCTTTGGCCAAAGGGCTGGCTTAGAGATCCTGCCCTACTG													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq	GAGCTTTTCATTTTGATATATAAACAARATCATCTCAACCTGAGGCTTGAGCTTTTCTTAAGATTCTGCTACCTCCACCTCTTCGTTACCCAGCTACTTGCCTGACAAAGGCAGCAGACTCTGA													
cds	GAGCTTTTCATTTTGATATATAAACAARATCATCTCAACCTGAGGCTTGAGCTTTTCTTAAGATTCTGCTACCTCCACCTCTTCGTTACCCAGCTACTTGCCTGACAAAGGCAGCAGACTCTGA													
Consensus	GAGCTTTTCATTTTGATATATAAACAARATCATCTCAACCTGAGGCTTGAGCTTTTCTTAAGATTCTGCTACCTCCACCTCTTCGTTACCCAGCTACTTGCCTGACAAAGGCAGCAGACTCTGA													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq	CAGCATCATATATATCCACGAGGGGAACGCCAARCAATGAGCTTCCGATAGATTTATATCATGTCTGCTGCTGACAGARTACAAAAAGTTACTTCCGTTGTACAGAGAAAGACTTAGTA													
cds	CAGCATCATATATATCCACGAGGGGAACGCCAARCAATGAGCTTCCGATAGATTTATATCATGTCTGCTGCTGACAGARTACAAAAAGTTACTTCCGTTGTACAGAGAAAGACTTAGTA													
Consensus	CAGCATCATATATATCCACGAGGGGAACGCCAARCAATGAGCTTCCGATAGATTTATATCATGTCTGCTGCTGACAGARTACAAAAAGTTACTTCCGTTGTACAGAGAAAGACTTAGTA													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
seq	GGAGATGCTCCCTGAGGCGAGATATGGCCATTCCATTGACGTGGATATATAGCGAGGAAAGGTGGTGGTCTCTTTGGAGGACGGCTACATGCTCTTACCCAAAGAACCCAGAAATGGAA													
cds	GGAGATGCTCCCTGAGGCGAGATATGGCCATTCCATTGACGTGGATATATAGCGAGGAAAGGTGGTGGTCTCTTTGGAGGACGGCTACATGCTCTTACCCAAAGAACCCAGAAATGGAA													
Consensus	GGAGATGCTCCCTGAGGCGAGATATGGCCATTCCATTGACGTGGATATATAGCGAGGAAAGGTGGTGGTCTCTTTGGAGGACGGCTACATGCTCTTACCCAAAGAACCCAGAAATGGAA													
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
seq	GCTAGCTGATTCCTACCCCATGTTTTCTTGGTAGATTTGAATTTGGGTGTCAGAGCTCATATATCTCCAGAACTTCAGGACGGGCTGCTTTTCATGTTCTATTGCCAGAAATGATACCATTA													
cds	GCTAGCTGATTCCTACCCCATGTTTTCTTGGTAGATTTGAATTTGGGTGTCAGAGCTCATATATCTCCAGAACTTCAGGACGGGCTGCTTTTCATGTTCTATTGCCAGAAATGATACCATTA													
Consensus	GCTAGCTGATTCCTACCCCATGTTTTCTTGGTAGATTTGAATTTGGGTGTCAGAGCTCATATATCTCCAGAACTTCAGGACGGGCTGCTTTTCATGTTCTATTGCCAGAAATGATACCATTA													
	651	660	670	680	690	700	710	720	730	740	750	760	770	780
seq	TATTTGGAGGACACCTCACTTGGCAGTACATACGCTCTGCTAATCTGTATAGATAGAGATAGATCTTCCCTGGGTACCCAGCAGTGAATTCACCTGTCTGCCAGGAGAACTCTGTCTCCAGT													
cds	TATTTGGAGGACACCTCACTTGGCAGTACATACGCTCTGCTAATCTGTATAGATAGAGATAGATCTTCCCTGGGTACCCAGCAGTGAATTCACCTGTCTGCCAGGAGAACTCTGTCTCCAGT													
Consensus	TATTTGGAGGACACCTCACTTGGCAGTACATACGCTCTGCTAATCTGTATAGATAGAGATAGATCTTCCCTGGGTACCCAGCAGTGAATTCACCTGTCTGCCAGGAGAACTCTGTCTCCAGT													
	781	790	800	810	820	830	840	850	860	870	880	890	900	910
seq	GCATTTGCTCACTCAACAAATATGATGATTTGTTATTGTTGGTGGTTATCAGCTGGAAATCAAAAAGGATGGTGTGTAGCATTTGCTCTAGGGGACACAGGATTGAATTAGTGAGATGGAGA													
cds	GCATTTGCTCACTCAACAAATATGATGATTTGTTATTGTTGGTGGTTATCAGCTGGAAATCAAAAAGGATGGTGTGTAGCATTTGCTCTAGGGGACACAGGATTGAATTAGTGAGATGGAGA													
Consensus	GCATTTGCTCACTCAACAAATATGATGATTTGTTATTGTTGGTGGTTATCAGCTGGAAATCAAAAAGGATGGTGTGTAGCATTTGCTCTAGGGGACACAGGATTGAATTAGTGAGATGGAGA													
	911	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040
seq	CCCCAGACTGGACCCAGATATTAGCATAGCAAAATATGTTTGGAGACACATGGGAACGGGACTGTTTCTTGGCATACAGGAGACACAGCAGGCTATGTCAGAGCATCTATTCTATAT													
cds	CCCCAGACTGGACCCAGATATTAGCATAGCAAAATATGTTTGGAGACACATGGGAACGGGACTGTTTCTTGGCATACAGGAGACACAGCAGGCTATGTCAGAGCATCTATTCTATAT													
Consensus	CCCCAGACTGGACCCAGATATTAGCATAGCAAAATATGTTTGGAGACACATGGGAACGGGACTGTTTCTTGGCATACAGGAGACACAGCAGGCTATGTCAGAGCATCTATTCTATAT													
	1041	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170
seq	GTTGAGATGCTCTGAGATATTTGAGTGGAGGACGAAATTTGTCACACAGTCAGACATCACTGAGATGCCGGGACTCCACTCCCTTTGAGACTCGGAGGATTTGTTTCAGTGTCTGAGCA													
cds	GTTGAGATGCTCTGAGATATTTGAGTGGAGGACGAAATTTGTCACACAGTCAGACATCACTGAGATGCCGGGACTCCACTCCCTTTGAGACTCGGAGGATTTGTTTCAGTGTCTGAGCA													
Consensus	GTTGAGATGCTCTGAGATATTTGAGTGGAGGACGAAATTTGTCACACAGTCAGACATCACTGAGATGCCGGGACTCCACTCCCTTTGAGACTCGGAGGATTTGTTTCAGTGTCTGAGCA													
	1171	1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
seq	ATCAGCTTTGATGGTGATGATGATTTGACACTTACATGAGATGATGAGATGATGATCTGTACCCGGCTACTGGATACGCTGTTCCCTACTTGTGATGGACATCACTACTGGGTTCCATTCT													
cds	ATCAGCTTTGATGGTGATGATGATTTGACACTTACATGAGATGATGAGATGATGATCTGTACCCGGCTACTGGATACGCTGTTCCCTACTTGTGATGGACATCACTACTGGGTTCCATTCT													
Consensus	ATCAGCTTTGATGGTGATGATGATTTGACACTTACATGAGATGATGAGATGATGATCTGTACCCGGCTACTGGATACGCTGTTCCCTACTTGTGATGGACATCACTACTGGGTTCCATTCT													
	1301	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430
seq	ATTCAACTGAGCTCAATAAACCCGCCATGATCTATTGTTCTCATGGGATGGACCTGGGTGATGCCAGTGATGGATCTGGAGAGCGCACACTCATCCACTTGTGAGAGGAGGACCAAAATATTA													
cds	ATTCAACTGAGCTCAATAAACCCGCCATGATCTATTGTTCTCATGGGATGGACCTGGGTGATGCCAGTGATGGATCTGGAGAGCGCACACTCATCCACTTGTGAGAGGAGGACCAAAATATTA													
Consensus	ATTCAACTGAGCTCAATAAACCCGCCATGATCTATTGTTCTCATGGGATGGACCTGGGTGATGCCAGTGATGGATCTGGAGAGCGCACACTCATCCACTTGTGAGAGGAGGACCAAAATATTA													
	1431	1440	1450	1460	1470	1480	1490	1500	1510	1520	1530	1540	1550	1560
seq	CTGCATGAGCATGTGCGGATAGCAGAGCATTACAACTCCCAAGGAACCTCCCTTACAAAGGCCCAATGAATCCCTCCACAAAAGGCTCCGGGAAGTCTTGACTCTGCCAGGAATCC													
cds	CTGCATGAGCATGTGCGGATAGCAGAGCATTACAACTCCCAAGGAACCTCCCTTACAAAGGCCCAATGAATCCCTCCACAAAAGGCTCCGGGAAGTCTTGACTCTGCCAGGAATCC													
Consensus	CTGCATGAGCATGTGCGGATAGCAGAGCATTACAACTCCCAAGGAACCTCCCTTACAAAGGCCCAATGAATCCCTCCACAAAAGGCTCCGGGAAGTCTTGACTCTGCCAGGAATCC													
	1561	1570	1580	1584										
seq	TTTCTTAGGAGGTTGTTGATTAG													
cds	TTTCTTAGGAGGTTGTTGATTAG													
Consensus	TTTCTTAGGAGGTTGTTGATTAG													

Mutation en 441 :T<C

➤ Différence au niveau PROT :

110120130

seqref

Consensus

131140150160170180190200210220230240250260

seqref

Consensus

261270280290300310320330340350360370380390

seqref

Consensus

400410420430440450460470480490500510520

seqref

Consensus

521527

seqref

Consensus

Mutation silencieuse

	Description	Scientific Name	Score	Score	Cover	value	Ident	Len	Accession
?	V(D)J recombination-activating protein 2 [Rattus norvegicus]	Rattus norvegicus	1105	1105	100%	0.0	100.00%	527	NP_001093998.1
?	RAG2 [Rattus norvegicus]	Rattus norvegicus	644	644	58%	0.0	100.00%	307	AAQ77003.1
?	recombination activating protein 2 [Rattus norvegicus]	Rattus norvegicus	310	310	28%	4e-104	100.00%	148	AAG38684.1

Rag2 DiT0 clone C OK

○ **FlagBirA Rag2 CTX clone A**

➤ **B3Fwd 873NT**

ATGTCCCTGCAGATGGTTACAGTGGGTCATAACATAGCCTTAATTCAACCAGGCTTCTCACTGATGAATTTTGATG
GTCAAGTTTTTTTCTTTGGCCAAAAAGGCTGGCCTAAGAGATCCTGCCCTACTGGAGTCTTTCAATTTGATATAAA
ACAAAATCATCTCAAACCTGAAGCCTGCAGTTTTCTCTAAAGATTCTGCTACCTCCCACCTCTTCGTTACCCAGCTA
CTTGCTCGTACAAAGGCAGCACAGACTCTGACAAGCATCAATATATCATCCACGGAGGGAAAAACGCCAAACAATG
AGCTTTCCGATAAGATTTATATCATGTCTGCTGCTTGAAGAATAACAAAAAGTTACTTTCCGTTGTACAGAGAA
AGACTTAGTAGGAGATGTCCCTGAAGCCAGATATGGCCATTCCATTGACGTGGTATATAGCCGAGGAAAAAGTGT
TGGTGTCTCTTTGGAGGACGGTCATACATGCCTTCTACCCAAAGAACCACAGAAAAATGGAATAGTGTAGCTGA
TTGCCTACCCCATGTTTTCTTGGTAGATTTTGAATTTGGGTGTGCTACGTATATATTCTCCAGAACTTCAGGACG
GGCTGTCTTTTCATGTTTCTATTGCCAgaatGATACCATTATATTTTGGGAGGACACTCACTTGCCAGTAACATACG
TCCTGCTAACTTGATAGAATAAGAGTAGATCTTCCCCTGGGTACCCAGCAGTGAATTGCACTGTCTTGNACGGA
GGAATCTCTGTCTCCNGTGCAATTGTCACTCAAACAAATAATGATGAATTTGNTATTGNTGGTGGTNATCAGCTGG
AAAATCAAAAANGGANGGTGTGTANCATTGNCCTCT

➤ **BGHRev 1050NT**

GCTGNTNNNACCCANNTTTTNNNNNTAGNTTNAANNNGNTGTNNTACGTCANANNTNTCCCNANTTCA
GGACNGCTGTNTTTCANGNTTNTATNCCAGAAATGATACCATTATATTTGGGAGGACACTCACTNCCAGTAN
CATACGTNCTGNTAACTTGTATAGAATAAGAGTAGATCTTCCNTGGGTACCCAGCAGTGAATTGCACTGTCTTN
CCAGGAGGAATCTCTGTCTCCAGTGCAATTGTCACTCAAACAAATAATGATGAATTTGTTATTGTTGGTGGTTATCA
GCTGGAAAATCAAAAAAGGATGGTGTGTAGCATTGTCTCTAGGGGACAACAGGATTGAAATTAGTGAGATGG
AGACCCAGACTGGACCCAGATATTAAGCATAGCAAAATATGGTTTGAAGCAACATGGGAAACGGGACTGTT
TTCCTTGGCATACCAGGAGACAACAAGCAGGCTATGTCAGAAGCATTCTATTTCTATATGTTGAGATGCTCTGAAG
ATAATTCGAGTGAGGAGCAGAAAATTGTCTCAACAGTCAGACATCAACTGAAGATGCCGGGACTCCACTCCC
TTTGAAGACTCAGAAGAATTTTGTTCAGTGCTGAAGCAACCAGCTTGTATGGTGATGATGAATTTGACACTTAC
AATGAAGATGATGAAGATGATGAATCTGTAACCGGCTACTGGATAACGTGTTCCCCTACTTGTGATGTGGACATCA
ATACTTGGGTTCATTCTATTCAACTGAGCTCAATAAACCCGCCATGATCTATTGTTCTCATGGGGATGGACACTGG
GTGCATGCCAGTGATGGATCTGGAAGAACGCACACTCATCCACTTGTGAGAAGGAAGCAACAAATATTACTGC
AATGAGCATGTGCGGATAGCAAGAGCATTACAACTCCCAAAGAAACCTCCCCTTACAAAAGCCCCAATGAAA
TCCCTCCACAAAAAAGGCTCCGGGAAAGTCTTGACTCCNGCCAAGAAATCCTTTCTTAGGAGGTTGTTTGATTAG

➤ **Synthèse séquençage**

ATGTCCCTGCAGATGGTTACAGTGGGTCATAACATAGCCTTAATTCAACCAGGCTTCTCA	60
CTGATGAATTTTGATGGTCAAGTTTTTTTCTTTGGCCAAAAAGGCTGGCCTAAGAGATCC	120
TGCCCTACTGGAGTCTTTCATTTTGATATAAAACAAAATCATCTCAAACCTGAAGCCTGCA	180
GTTTTCTCTAAAGATTCTGCTACCTCCCACCTCTTCGTTACCCAGCTACTTGCTCGTAC	240
AAAGGCAGCACAGACTCTGACAAGCATCAATATATCATCCACGGAGGGAAAAACGCCAAAC	300
AATGAGCTTTCCGATAAGATTTATATCATGTCTGCTGCTTGAAGAATAACAAAAAGTT	360
ACTTTCGGTTGTACAGAGAAAGACTTAGTAGGAGATGTCCCTGAAGCCAGATATGGCCAT	420
TCCATTGACGTGGTATATAGCCGAGGAAAAAGTGTGGTGTCTCTTTGGAGGACGGTCA	480
TACATGCCTTCTACCCAAAGAACACAGAAAAATGGAATAGTGTAGCTGATTGCCTACCC	540
CATGTTTTCTTGGTAGATTTTGAATTTGGGTGTGCTACGTATATATTCTCCAGAACTT	600
CAGGACGGGCTGTCTTTTCATGTTTCTATTGCCAGAAATGATACCATTATATTTTGGGA	660
GGACACTCACTTGCCAGTAACATACGTCCTGCTAACTTGATAGAATAAGAGTAGATCTT	719
CCCCTGGGTACCCAGCAGTGAATTGCACTGTCTTGCAGGAGGAATCTCTGTCTCCAGT	779
GCAATTGTCACTCAAACAAATAATGATGAATTTGTTATTGTTGGTGGTTATCAGCTGGAA	840

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AATCAAAAAAGGATGGTGTGTAGCATTGTCTCTCTAGGGGACAACAGGATTGAAATTAGT      900
GAGATGGAGACCCCAGACTGGACCCCAGATATTAAGCATAGCAAAATATGGTTTGAAGC      960
AACATGGGAAACGGGACTGTTTTCTTGGCATAACCAGGAGACAACAAGCAGGCTATGTCA      1020
GAAGCATTCATTTTCTATATGTTGAGATGCTCTGAAGATAATTTCAGTGAGGAGCAGAAA      1080
ATTGTCTCAAACAGTCAGACATCAACTGAAGATGCCGGGGACTCCACTCCCTTTGAAGAC      1140
TCAGAAGAATTTTGTTCAGTGCTGAAGCAACCAGCTTTGATGGTGATGATGAATTTGAC      1200
ACTTACAATGAAGATGATGAAGATGATGAATCTGTAACCGGCTACTGGATAACGTGTTCC      1260
CCTACTTGTGATGTGGACATCAATACTGGGTTCCATCTATTCAACTGAGCTCAATAAA      1320
CCCGCCATGATCTATTGTTCTCATGGGGATGGACACTGGGTGCATGCCCAGTGCATGGAT      1380
CTGGAAGAACGCACACTCATCCACTTGTGAGAAGGAAGCAACAAATATTACTGCAATGAG      1440
CATGTGCGGATAGCAAGAGCATTACAAACTCCCAAAAGAAACCTCCCCTTACAAAAGCCC      1500
CCAATGAAATCCCTCCACAAAAAAGGCTCCGGGAAAGTCTTGACTCCNGCCAAGAAATCC      1560
TTTCTTAGGAGGTTGTTTGATTAG  1584

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MSLQMVTVGHNIALIQPGFSLMNFDDGQVFFFGQKGWPKRSCPTGVFHFEDIKQNHLLKPAVFSKDCYL
 PPLRYPATCSYKGSTDSKHKQYIIHGGKTPNNELSDKIYIMSVACKNNKKVTFRCTEKDLVGDVPEARYGH
 SIDVVYSRGKSVGLVFGGRSYMPSTQRTTEKWNNSVADCLPHVFLVDFFEGCATSYILPELQDGLSFHVSIR
 NDTIYILGGHSLASNIRPANLYRIRVDLPLGTPAVNCTVLPGGISVSSAIVTQTNNDEFVIVGGYQLENQKR
 MVCSIVSLGDNRIEISEMETPDWTPDIKHSKIWFSGSNMGNGTVFLGIPGDNKQAMSEAFYFYMLRCSED
 NSSEEQKIVSNSQSTEDAGDSTPFEDSEEFCSAEATSFDGDDEFDTYNEDDEDESVTGYWITCSPTCD
 VDINTWVPFYSTELNKPAMIYCSHGDGHWVHAQCMDLEERTLIHLSEGSNKYYCNEHVRIARALQTPKR
 NLPLQKPPMKSLHKKGSGKVLTXAKKSFLRRLFD-

➤ **Blast contre banque de rat**

		Score	Score	Cover	value	Ident	Len	
2	Rattus norvegicus recombination activating 2 (Rag2) mRNA	Norway rat	2905	2905	100%	0.0	99.75%	3546 NM_001100528.2
2	Rattus norvegicus RAG2 (RAG2) gene, partial cds	Norway rat	1685	1685	58%	0.0	99.67%	921 AY303209.1
2	Rattus norvegicus recombination activating protein 2 (Rag2) gene, partial cds	Norway rat	821	821	28%	0.0	100.00%	444 AY011941.1

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq	ATGTCCTTCAGATGGTTACAGTGGGTCATACATAGCCTTAATTCACACAGGCTTCTACTGATGAAATTTGATGGTCAGGTTTTTCTTTGGCCAAAAGGCTGGCCTAGAGATCTCGCCCTACTG													
cds	ATGTCCTTCAGATGGTTACAGTGGGTCATACATAGCCTTAATTCACACAGGCTTCTACTGATGAAATTTGATGGTCAGGTTTTTCTTTGGCCAAAAGGCTGGCCTAGAGATCTCGCCCTACTG													
Consensus	ATGTCCTTCAGATGGTTACAGTGGGTCATACATAGCCTTAATTCACACAGGCTTCTACTGATGAAATTTGATGGTCAGGTTTTTCTTTGGCCAAAAGGCTGGCCTAGAGATCTCGCCCTACTG													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq	GAGTCTTTTCATTTTGATATAAACAAATCATCTCAAACTGAAGCTCGAGTTTTTCTTAAGATTCTGCTACCTCCCACTCTTCGTTACCCAGCTACTTGTCTGTACAAAGGCAGCAGACTCTGA													
cds	GAGTCTTTTCATTTTGATATAAACAAATCATCTCAAACTGAAGCTCGAGTTTTTCTTAAGATTCTGCTACCTCCCACTCTTCGTTACCCAGCTACTTGTCTGTACAAAGGCAGCAGACTCTGA													
Consensus	GAGTCTTTTCATTTTGATATAAACAAATCATCTCAAACTGAAGCTCGAGTTTTTCTTAAGATTCTGCTACCTCCCACTCTTCGTTACCCAGCTACTTGTCTGTACAAAGGCAGCAGACTCTGA													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq	CARGCATCAATATATCATCCACGGAGGGAARAGCCAAACATGAGCTTTCCGATAGATTATATCATGTCTGTGCGTTCGACAGATACAAAAAGTTACTTTCCGTTGTACAGAGAAAGACTTAGTA													
cds	CARGCATCAATATATCATCCACGGAGGGAARAGCCAAACATGAGCTTTCCGATAGATTATATCATGTCTGTGCGTTCGACAGATACAAAAAGTTACTTTCCGTTGTACAGAGAAAGACTTAGTA													
Consensus	CARGCATCAATATATCATCCACGGAGGGAARAGCCAAACATGAGCTTTCCGATAGATTATATCATGTCTGTGCGTTCGACAGATACAAAAAGTTACTTTCCGTTGTACAGAGAAAGACTTAGTA													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
seq	GGAGATGTCCTTGAAGCCAGATATGGCCATTCCATTGACGTGGTATATAGCCAGGAAAAAGTGTGGTGTTCTCTTTGGAGGACGGTCATACATGCCCTTACCCAAAGAACCCAGAAAAATGGAAAT													
cds	GGAGATGTCCTTGAAGCCAGATATGGCCATTCCATTGACGTGGTATATAGCCAGGAAAAAGTGTGGTGTTCTCTTTGGAGGACGGTCATACATGCCCTTACCCAAAGAACCCAGAAAAATGGAAAT													
Consensus	GGAGATGTCCTTGAAGCCAGATATGGCCATTCCATTGACGTGGTATATAGCCAGGAAAAAGTGTGGTGTTCTCTTTGGAGGACGGTCATACATGCCCTTACCCAAAGAACCCAGAAAAATGGAAAT													
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
seq	GTGTAGCTGATTGCCATCCCATGTTTCTTGGTAGATTTGAAATTTGGGTGTGCTACGTCATATATTTCCAGAACTTCAGGACGGGCTGTCTTTTCATGTTTCTATTGCCAGAAATGATACCATTTA													
cds	GTGTAGCTGATTGCCATCCCATGTTTCTTGGTAGATTTGAAATTTGGGTGTGCTACGTCATATATTTCCAGAACTTCAGGACGGGCTGTCTTTTCATGTTTCTATTGCCAGAAATGATACCATTTA													
Consensus	GTGTAGCTGATTGCCATCCCATGTTTCTTGGTAGATTTGAAATTTGGGTGTGCTACGTCATATATTTCCAGAACTTCAGGACGGGCTGTCTTTTCATGTTTCTATTGCCAGAAATGATACCATTTA													
	651	660	670	680	690	700	710	720	730	740	750	760	770	780
seq	TATTTTGGGAGGACACTCACTTGCAGTACATACGCTCTGCTAAGCTGTATAGATAGAGTAGACTTCCCTGGGTACCCAGCAGTGAAATGCACGTCTTGCACGAGGAAATCTCTGCTCCAGT													
cds	TATTTTGGGAGGACACTCACTTGCAGTACATACGCTCTGCTAAGCTGTATAGATAGAGTAGACTTCCCTGGGTACCCAGCAGTGAAATGCACGTCTTGCACGAGGAAATCTCTGCTCCAGT													
Consensus	TATTTTGGGAGGACACTCACTTGCAGTACATACGCTCTGCTAAGCTGTATAGATAGAGTAGACTTCCCTGGGTACCCAGCAGTGAAATGCACGTCTTGCACGAGGAAATCTCTGCTCCAGT													
	781	790	800	810	820	830	840	850	860	870	880	890	900	910
seq	GCAATTTGCACTCAACCAAAATATGATGAAATTTGTTATTGTTGGTGGTTATCAGCTGGAAGATCAAAAAGGATGGTGTGTAGCATTGTCTCTAGGGGACACAGGATTGAATTAGTGAGATGGAGA													
cds	GCAATTTGCACTCAACCAAAATATGATGAAATTTGTTATTGTTGGTGGTTATCAGCTGGAAGATCAAAAAGGATGGTGTGTAGCATTGTCTCTAGGGGACACAGGATTGAATTAGTGAGATGGAGA													
Consensus	GCAATTTGCACTCAACCAAAATATGATGAAATTTGTTATTGTTGGTGGTTATCAGCTGGAAGATCAAAAAGGATGGTGTGTAGCATTGTCTCTAGGGGACACAGGATTGAATTAGTGAGATGGAGA													
	911	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040
seq	CCCCAGACTGGACCCAGATATTAGCATAGCAAAATATGGTTTGGAGCAACATGGGAACGGGACTGTTTCTTGGCATACAGGAGACACACAGCAGGCTATGTGAGAGCATTCTATTCTATAT													
cds	CCCCAGACTGGACCCAGATATTAGCATAGCAAAATATGGTTTGGAGCAACATGGGAACGGGACTGTTTCTTGGCATACAGGAGACACACAGCAGGCTATGTGAGAGCATTCTATTCTATAT													
Consensus	CCCCAGACTGGACCCAGATATTAGCATAGCAAAATATGGTTTGGAGCAACATGGGAACGGGACTGTTTCTTGGCATACAGGAGACACACAGCAGGCTATGTGAGAGCATTCTATTCTATAT													
	1041	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170
seq	GTTGAGATGCTCTGAGATATATTCAGGTGAGGAGCAGAAATTTGCTCAACAGTCAGACATCACTGAGATGCCGGGACTCCACTCCCTTTGAGAGCTCAGAGAAATTTGTTTCAGTGCTGAGACA													
cds	GTTGAGATGCTCTGAGATATATTCAGGTGAGGAGCAGAAATTTGCTCAACAGTCAGACATCACTGAGATGCCGGGACTCCACTCCCTTTGAGAGCTCAGAGAAATTTTGTTCAGTGCTGAGACA													
Consensus	GTTGAGATGCTCTGAGATATATTCAGGTGAGGAGCAGAAATTTGCTCAACAGTCAGACATCACTGAGATGCCGGGACTCCACTCCCTTTGAGAGCTCAGAGAAATTTTGTTCAGTGCTGAGACA													
	1171	1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
seq	ACCAAGCTTTGATGGTGATGATGAAATTTGACACTTACAATGAGATGATGAGATGATGAATCTGTAAACGGCTACTGGATACGGTGTCCCTACTTGTGATGTGGACATCACTTGGGTTCCATTCT													
cds	ATCAGCTTTGATGGTGATGATGAAATTTGACACTTACAATGAGATGATGAGATGATGAATCTGTAAACGGCTACTGGATACGGTGTCCCTACTTGTGATGTGGACATCACTTGGGTTCCATTCT													
Consensus	ACCAAGCTTTGATGGTGATGATGAAATTTGACACTTACAATGAGATGATGAGATGATGAATCTGTAAACGGCTACTGGATACGGTGTCCCTACTTGTGATGTGGACATCACTTGGGTTCCATTCT													
	1301	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430
seq	ATTCAACTGAGCTCAATAAACCCGCATGATCTATTGTTCTCATGGGGATGGACACTGGGTGCATGCCAGTGCATGGATCTGGAGAGACGCACACTCATCCACTTGTGAGAGGAGGACACAAATATTA													
cds	ATTCAACTGAGCTCAATAAACCCGCATGATCTATTGTTCTCATGGGGATGGACACTGGGTGCATGCCAGTGCATGGATCTGGAGAGACGCACACTCATCCACTTGTGAGAGGAGGACACAAATATTA													
Consensus	ATTCAACTGAGCTCAATAAACCCGCATGATCTATTGTTCTCATGGGGATGGACACTGGGTGCATGCCAGTGCATGGATCTGGAGAGACGCACACTCATCCACTTGTGAGAGGAGGACACAAATATTA													
	1431	1440	1450	1460	1470	1480	1490	1500	1510	1520	1530	1540	1550	1560
seq	CTGCATGAGCATGTGCGGATAGCAGAGCATTACAACCTCCAAAAGAAACCTCCCTTACAAAAGCCCCAATGAATCCCTCCACAAAAGAGCTCCGGGAAGTCTTGACTCCnGCCAGAAATCC													
cds	CTGCATGAGCATGTGCGGATAGCAGAGCATTACAACCTCCAAAAGAAACCTCCCTTACAAAAGCCCCAATGAATCCCTCCACAAAAGAGCTCCGGGAAGTCTTGACTCTCGCCAGAAATCC													
Consensus	CTGCATGAGCATGTGCGGATAGCAGAGCATTACAACCTCCAAAAGAAACCTCCCTTACAAAAGCCCCAATGAATCCCTCCACAAAAGAGCTCCGGGAAGTCTTGACTCTCGCCAGAAATCC													
	1561	1570	1580	1584										
seq	TTTCTAGGAGGTTGTTTGATTAG													
cds	TTTCTAGGAGGTTGTTTGATTAG													
Consensus	TTTCTAGGAGGTTGTTTGATTAG													

Mutation en 576 T<A et 1143 A<G

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1      10      20      30      40      50      60      70      80      90      100     110     120     130
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
seq  HSLQHYTVGHNIALIQPGFSLNMFQGVFFFGQKGAPKRSCPTGVFHFQIKQNHLLKPAVFSKDSYLPPLRYPATCSYKGSTSDKHQYIIHGKTPNNELSDKIYINSYACKNNKKYTFRCTEKDLV
ref  HSLQHYTVGHNIALIQPGFSLNMFQGVFFFGQKGAPKRSCPTGVFHFQIKQNHLLKPAVFSKDSYLPPLRYPATCSYKGSTSDKHQYIIHGKTPNNELSDKIYINSYACKNNKKYTFRCTEKDLV
Consensus HSLQHYTVGHNIALIQPGFSLNMFQGVFFFGQKGAPKRSCPTGVFHFQIKQNHLLKPAVFSKDSYLPPLRYPATCSYKGSTSDKHQYIIHGKTPNNELSDKIYINSYACKNNKKYTFRCTEKDLV

131    140    150    160    170    180    190    200    210    220    230    240    250    260
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
seq  GGVPEARYGHSIDVYVSRGKSVGVLFGGRSYMPSTQRTTEKMSVADCLPHVFLYDFEFGCATSYILPELQDGLSFHYSIARNDTIYILGGHSLASNIIRPANLYRIRYDLPLGTPAYNCTVLPGGISYSS
ref  GGVPEARYGHSIDVYVSRGKSVGVLFGGRSYMPSTQRTTEKMSVADCLPHVFLYDFEFGCATSYILPELQDGLSFHYSIARNDTIYILGGHSLASNIIRPANLYRIRYDLPLGTPAYNCTVLPGGISYSS
Consensus GGVPEARYGHSIDVYVSRGKSVGVLFGGRSYMPSTQRTTEKMSVADCLPHVFLYDFEFGCATSYILPELQDGLSFHYSIARNDTIYILGGHSLASNIIRPANLYRIRYDLPLGTPAYNCTVLPGGISYSS

261    270    280    290    300    310    320    330    340    350    360    370    380    390
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
seq  AIYVTQTNNDEFVIYGGYQLENQKRMYCSIVSLGDNRIEISEMETPDWTPDIKHSKIHFSGNMHNGTVFLGIPGDNKQAMSEAFYFYHLRCSEDNSSSEEQKIYVNSQTSSTEDAGDSTPFEDSEEFCSAEA
ref  AIYVTQTNNDEFVIYGGYQLENQKRMYCSIVSLGDNRIEISEMETPDWTPDIKHSKIHFSGNMHNGTVFLGIPGDNKQAMSEAFYFYHLRCSEDNSSSEEQKIYVNSQTSSTEDAGDSTPFEDSEEFCSAEA
Consensus AIYVTQTNNDEFVIYGGYQLENQKRMYCSIVSLGDNRIEISEMETPDWTPDIKHSKIHFSGNMHNGTVFLGIPGDNKQAMSEAFYFYHLRCSEDNSSSEEQKIYVNSQTSSTEDAGDSTPFEDSEEFCSAEA

391    400    410    420    430    440    450    460    470    480    490    500    510    520
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
seq  TSFDGDDFDTYNEDDEDDSYTGYHITCSPTCDVDINTWVPFYSTELNKPAMIYCSHGDDHVAHQCHOLEERTLIHLSEGSNKYYCNEHVRIARRALQTPKRNLPQKPPHKSLLHKKGGSKVLTAKKS
ref  TSFDGDDFDTYNEDDEDDSYTGYHITCSPTCDVDINTWVPFYSTELNKPAMIYCSHGDDHVAHQCHOLEERTLIHLSEGSNKYYCNEHVRIARRALQTPKRNLPQKPPHKSLLHKKGGSKVLTAKKS
Consensus TSFDGDDFDTYNEDDEDDSYTGYHITCSPTCDVDINTWVPFYSTELNKPAMIYCSHGDDHVAHQCHOLEERTLIHLSEGSNKYYCNEHVRIARRALQTPKRNLPQKPPHKSLLHKKGGSKVLTAKKS

521  527
|-----|
seq  FLRRRLFD
ref  FLRRRLFD
Consensus FLRRRLFD

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Mutation en 391 T<

	V(D)J recombination-activating protein 2 [Rattus norvegicus]	Norway rat	1101	1101	100%	0.0	99.62%	527	NP_001093998.1
	RAG2 [Rattus norvegicus]	Norway rat	643	643	58%	0.0	99.67%	307	AAQ77003.1
	recombination activating protein 2 [Rattus norvegicus]	Norway rat	310	310	28%	3e-104	100.00%	148	AAG38684.1

○ **FlagBirA Rag2 CTX clone B**

➤ **B3Fwd 963NT**

ATGTCCCTGCAGATGGTTACAGTGGGTCATAACATAGCCTTAATTCAACCAGGCTTCTCACTGATGAATTTTGATG
GTCAAGTTTTTTCTTTGGCCAAAAAGGCTGGCCTAAGAGATCCTGCCCTACTGGAGTCTTTCATTTTGATATAAA
ACAAAATCATCTCAAACCTGAAGCCTGCAGTTTTCTCTAAAGATTCCTGCTACCTCCCACCTCTTCGTTACCCAGCTA
CTTGCTCGTACAAAGGCAGCACAGACTCTGACAAGCATCAATATATCATCCACGGAGGGAAAAACGCCAAACAATG
AGCTTTCCGATAAGATTTATATCATGTCTGTCGCTTGCAAGAATAACAAAAAGTTACTTTCGGTTGTACAGAGAA
AGACTTAGTAGGAGATGTCCCTGAAGCCAGATATGGCCATTCCATTGACGTGGTATATAGCCGAGGAAAAAGTGT
TGGTGTCTCTTTGGAGGACGGTCATACATGCCTTCTACCCAAAGAACCACAGAAAAATGGAATAGTGTAGCTGA
TTGCCTACCCCATGTTTTCTTGGTAGATTTTGAATTTGGGTGTGCAACGTCATATATTCTCCAGAACTTCAGGACG
GGCTGTCTTTTCATGTTTCTATTGCCAGAAATGATACCATTTATATTTGGGAGGACACTCACTTGCCAGTAACATA
CGTCTGTCTAACTTGATAGAATAAGAGTAgATCTTCCCCTGGGTACCCAGCAGTGAATTGCACTGTCTTGCCAG
GANGAATCTCTGTCTCCAGTGAATTGTCACTCAAACAAATAATGATGAATTTNNTATTGTTGGTGGTTATCANCT
GGAAAAACAAAAANGATGGTGTGNANCATTGNCTCTCTNGGGANANNGGATNGAANNNTANNGANANGGAN
ANCCNNACNGGNNCNNNNNNNNANCNTAGCNAANNATNGTTNNNNGCNNNNNTGGNAAA

➤ **BGHRev 1082NT**

AAAAAANGNANNANNANNNNCNNNNNNNNCCNNNNNTTTNNTNGNANNNTTTNAATTTGGGNNN
NNAANNTNNANNNTTNTCCNNNANTTCANGANGGCTGTCTTTTCANGTTNNNNNNNNCNNNAAANNA
NNCCATTNANNTTNGGNGGNCNNTNCTTGCCAGTANCANNGTNTCTNNTAACTTGNATANAANANNNTN
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TGTCANTNANNCNAAANANNNNNNNAATTNNNTNNTGTNNGGTGGNTNTCAGCTGGAAAATCAAAAANGGATG
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NNNTATTAAGCATAGCANNNNANGGTTTNGGAAGCAACATGGGAAANNGGANNGTNTTCTNNGGCATNCCA
GGAGACAACAAGCAGGCTATGTCAGAAGCATTCTATTTCTATATGNTGAGATGCTNTGAAGATAATTNGAGTGAG
GNNCANNNAATTGTCTCAAACAGTCAGNCATCANCTGAAGANGCNGGGGACTCCACTCCCTTTGAAGACTCGG
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ATTCTATTCAANTGAGCTCAATAAACCCGCCATGATCTATTGTTCTCATGGGGATGGACACTGGGTGCATGCCAG
TGCATGGATCTGGAAGAACGCACACTCATCCACTTGTGAGAAGGAAGCAACAAATATTACTGCAATGAGCATGTG
CGGATAGCAAGAGCATTACAAACTCCAAAAAGAACTCCCTTACAAAAGCCCCAATGAAATCCCTCCACAAA
AAAGGCTCCGGGAAAGTCTTGACTCCTGCCAAGAAATCCTTTCTTAGGAGGTTGTTTGATTAG

➤ **Seq int du 21/12**

CTGTCTGCNNGGAGGATCTCTGTCTCCaGTGCAATTGTCACTCAAACAAATAATGAtGAATTTGTTATTGTTGGT
GGTTATCAGCTGGAAAATCAAAAAAGGATGGTGTGTAGCATTGTCTCTCTAGGGGACAACAGGATTGAAATTAGT
GAGATGGAGACCCAGACTGGACCCAGATATTAAGCATAGCAAATATGGTTTGGAAGCAACATGGGAAACGG
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 TTTGATTAGTGCGGNCGCCTAACTCGAGTCTAGAGGGCCCGTTTAAACCCGCTGATCAGCCTCNACTGTGCCTTC
 TAGTTGCCAGCCATCTGTTGNTTGGCCCTNCCCCNTGCCTTCCTTGACCCTGNAAGGNGCNCTCCNNCTGTCCTT
 TNCTAATAAATGAGNAAATTGCATCNCATTGTCTGAGTNGNGNCATNCTNTTCTGGGGGNNNGGG

➤ Synthèse séquençage

ATGTCCCTGCAGATGGTTACAGTGGGTCATAACATAGCCTTAATTCAACCAGGCTTCTCA	60
CTGATGAATTTTGTAGGTCAAGTTTTTTTCTTTGGCCAAAAAGGCTGGCCTAAGAGATCC	120
TGCCCTACTGGAGTCTTTCATTTTATATAAAAACAAAATCATCTCAAACCTGAAGCCTGCA	180
GTTTTCTCTAAAGATTCCTGCTACCTCCACCTCTTCGTTACCCAGCTACTTGCTCGTAC	240
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AGGACACTCACTTGCCAGTAACATACGTCCTGCTAACTTGTATAGAATAAGAGTAGATCT	719
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GCAATTGTCACCTCAACAAATAATGATGAATTTGTTATTGTTGGTGGTTATCAGCTGGAA	838
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ACTTACAATGAAGATGATGAAGATGATGAATCTGTAACCGGCTACTGGATAACGTGTTCC	
CCTACTTGTGATGTGGACATCAATACTTGGGTTCATTCTATTCAACTGAGCTCAATAAA	
CCCGCCATGATCTATTGTTCTCATGGGATGGACACTGGGTGCATGCCAGTGCATGGAT	
CTGGAAGAACGCACACTCATCCACTTGTGAGAAGGAAGCAACAAATATTACTGCAATGAG	
CATGTGCGGATAGCAAGAGCATTACAAACTCCCCAAAAGAAACCTCCCCTTACAAAAGCCC	
CCAATGAAATCCCTCCACAAAAAAGGCTCCGGGAAAGTCTTGACTCCTGCCAAGAAATCC	
TTTCTTAGGAGGTTGTTTGATTAG	

MSLQMVTVGHNIALIQPGFSLMNFDDGQVFFFGQKGWPKRSCPTGVFHFEDIKQNHKLKPAVFSKSDCYLPPLRYP
 ATCSYKGSTDSKDKHQYIIHGGKTPNNELSDKIYIMSVACKNNKKVTRFCTEKDLVGDVPEARYGHSIDVVYSRGKSV
 GVLFGGRSYMPSTQRTTEKWNSVADCLPHVFLVDVEFGCATSYLPELQDGLSFHVSIARNDTIYILGGHSLASNIRP
 ANLYRIRVDLPLGTPAVNCTVLPGGISVSSAIVTQTNNDFFVIVGGYQLENQKRMVCSIVSLGDNRIEISEMETPDW
 TPDIKHSKIWFSGNMGNVTFLGIPGDNKQAMSEAFYFMYLRCSEDNSSEEQKIVSNSQSTEDAGDSTPFEDSEE
 FCFSAEISFDGDDEFDTYNEDDEDESVTGYWITCSPTCDVDINTWVPFSTELNKPAMIYCSHGDGHVHAQC
 MDLEERTLIHLSEGSNKYYCNEHVRIARALQTPKRNLPLQKPPMKSLHKKGSGKVLTPAKKSFLRRLFD-

➤ Blast contre banque de rat

		Score	Score	Cover	Value	Ident	Len	
 Rattus norvegicus recombination activating 2 (Rag2)_mRNA	Rattus norvegicus	2926	2926	100%	0.0	100.00%	3546	NM_001100528.2
 Rattus norvegicus RAG2 (RAG2)_gene_partial cds	Rattus norvegicus	1701	1701	58%	0.0	100.00%	921	AY303209.1
 Rattus norvegicus recombination activating protein 2 (Rag2)_gene_partial cds	Rattus norvegicus	815	815	28%	0.0	99.77%	444	AY011941.1

Différence au niveau NT

TTCTTAGGAGGTGTTTGATTAG

➤ Différence au niveau prot

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq	MSLQMYTVGHNIALIQPGFSLMNFQGGVFFFGQKGPKRSCPTGVFHFQDIKQNHLLKLPAYFSKQSCYLPPLRYPATCSYKGSTDSOKHQYIIHGKTPNNELSDKIYIHSVACKNNKKYTFRCTEKDLV													
ref	MSLQMYTVGHNIALIQPGFSLMNFQGGVFFFGQKGPKRSCPTGVFHFQDIKQNHLLKLPAYFSKQSCYLPPLRYPATCSYKGSTDSOKHQYIIHGKTPNNELSDKIYIHSVACKNNKKYTFRCTEKDLV													
Consensus	MSLQMYTVGHNIALIQPGFSLMNFQGGVFFFGQKGPKRSCPTGVFHFQDIKQNHLLKLPAYFSKQSCYLPPLRYPATCSYKGSTDSOKHQYIIHGKTPNNELSDKIYIHSVACKNNKKYTFRCTEKDLV													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq	GDVPEARYGHSIDVYYSRGKSVGVLFGGRSYMPSTQRTTEKINSVADCLPHVFLVDFFEGCATSYILPELQDGLSFHYSIARNOTIYILGGHSLASNIRPANLYRIRVDPLGTPAVNCTVLPGGISVSS													
ref	GDVPEARYGHSIDVYYSRGKSVGVLFGGRSYMPSTQRTTEKINSVADCLPHVFLVDFFEGCATSYILPELQDGLSFHYSIARNOTIYILGGHSLASNIRPANLYRIRVDPLGTPAVNCTVLPGGISVSS													
Consensus	GDVPEARYGHSIDVYYSRGKSVGVLFGGRSYMPSTQRTTEKINSVADCLPHVFLVDFFEGCATSYILPELQDGLSFHYSIARNOTIYILGGHSLASNIRPANLYRIRVDPLGTPAVNCTVLPGGISVSS													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq	RIYVTQTNDEFVIYGGYQLENQKRMYCSIVSLGONRIEISEMETPDWTPDIKHSKIWFSGNMHNGTVFLGIPGONKQAMSEAFYFYLRCSEDSSEEQKIYSNSQTSSTEDAGDSTPFEDSEEFCSAEAR													
ref	RIYVTQTNDEFVIYGGYQLENQKRMYCSIVSLGONRIEISEMETPDWTPDIKHSKIWFSGNMHNGTVFLGIPGONKQAMSEAFYFYLRCSEDSSEEQKIYSNSQTSSTEDAGDSTPFEDSEEFCSAEAR													
Consensus	RIYVTQTNDEFVIYGGYQLENQKRMYCSIVSLGONRIEISEMETPDWTPDIKHSKIWFSGNMHNGTVFLGIPGONKQAMSEAFYFYLRCSEDSSEEQKIYSNSQTSSTEDAGDSTPFEDSEEFCSAEAR													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
seq	ISFDGDDDEFDTYNEDDEDDSVTGYMITCSPDCQVDINTAVPFYSTELNKPANIYCSHGDDHVAHQCMOLEERTLIHLSEGSNKYYCNEHYRIARALQTPKRNLPQKPPHKSLLHKKSGKVLTPAKKS													
ref	ISFDGDDDEFDTYNEDDEDDSVTGYMITCSPDCQVDINTAVPFYSTELNKPANIYCSHGDDHVAHQCMOLEERTLIHLSEGSNKYYCNEHYRIARALQTPKRNLPQKPPHKSLLHKKSGKVLTPAKKS													
Consensus	ISFDGDDDEFDTYNEDDEDDSVTGYMITCSPDCQVDINTAVPFYSTELNKPANIYCSHGDDHVAHQCMOLEERTLIHLSEGSNKYYCNEHYRIARALQTPKRNLPQKPPHKSLLHKKSGKVLTPAKKS													
	521	527												
seq	FLRRLLFD													
ref	FLRRLLFD													
Consensus	FLRRLLFD													

	Description	Scientific name	Score	Score	Cover	value	Ident	Len	Accession
☒	V(D)J recombination-activating protein 2 [Rattus norvegicus]	Rattus norvegicus	1105	1105	100%	0.0	100.00%	527	NP_001093998.1
☒	RAG2 [Rattus norvegicus]	Rattus norvegicus	644	644	58%	0.0	100.00%	307	AAQ77003.1
☒	recombination activating protein 2 [Rattus norvegicus]	Rattus norvegicus	310	310	28%	4e-104	100.00%	148	AAG38684.1

Rag2 CTX clone B parfait