

10)Rag1

Rattus norvegicus recombination activating 1 (Rag1), mRNA

recombination activation protein 1; recombination activating gene

- **Référence NCBI :** NM_053468
- **Taille 3123 NT**
- **Séquences protéique / NT :**

MAVPLPSTLRLSSAPDEIQHPHIKFSEWKFLFRVRSFEKAPEE
AQKEKDSSEGGKPCLEQSPVVLDPKGGQNSVLTQRAKLHPKFSSKFHVDGKSSDKAI
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601	ccacccact	gaattctgcc	ataactgttg	gagcattatg	cacaggaagt	tcggcagtg
661	tcacagtcag	gtctactgcc	caaggaatgt	gaccgtggag	tggcaccctc	acacaccgtc
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2461 ttccatagat gcgcttcaact gtgacattgg aaatgcagct gaattctata agattttcca
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- **Amorces synthétisées :**

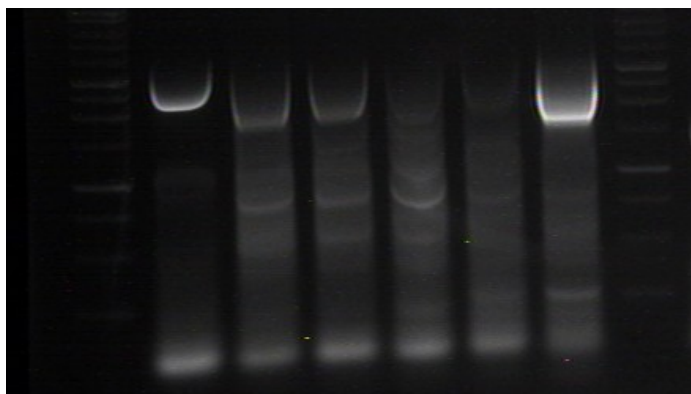
Rag1_AscI_Fwd

tataGGCGCGCCa atggct gtccccttgc catctaccc

Rag1_NotI_Rev

ttaaGCGGCCGCa ttaaaactccattgaatcttggc

- **Expériences :**
- 29/10 PCR pfu 60°C pfu 50ul 40 cycles
 - rate/DiTO/Di24hLPS : les miens de fevrier
 - 48h mix/SP/CTX faits le 28/10



➤ Résultats séquençages

○ FlagBirA Rag1 rate clone A

➤ B3Fwd 891NT

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CGAGTGGAATTTAAGCTGTTTAGGGTGAGATCCTTTGAAAAGGCACCCGAAGAAGCACAAAAAGAGAAGGAT
TCCTCAGAAGGGAAACCTTGCTCTCGAGCAGTCTCCAGTAGTTCTAGATAAGCCTGGGGGTCAGAATTCAGTTCTG
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➤ BGHRRev 1011NT

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➤ Int Fwd1

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➤ **Int Fwd2**

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➤ **Int Rev1**

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➤ **Int Rev2**

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➤ **Synthèse séquençage**

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 NALKNSGFTMNSKETLGDSL DIEDSLESQDSMEF-

➤ **Blast contre banque de rat**

	Description	Scientific Name	Score	Score	Cover	value	Ident	Len	Accession
✓	Rattus norvegicus recombination activating 1 (Rag1) mRNA	Rattus norvegicus	5705	5705	100%	0.0	99.55%	6536	NM_053468.2
✓	Rattus norvegicus recombination activating gene 1 (RAG1) gene, partial cds	Rattus norvegicus	2390	4598	82%	0.0	99.77%	3002	AY294938.1
✓	Rattus norvegicus rag1 gene, partial cds isolate HS131/KT2830	Rattus norvegicus	1832	1832	32%	0.0	99.60%	1002	AB164045.1
✓	Rattus norvegicus recombination activating protein 1 (Rag1) gene, partial cds	Rattus norvegicus	1419	1419	24%	0.0	100.00%	768	AY011884.1
✓	Rattus norvegicus mRNA for recombination activation protein (RAG1), partial	Rattus norvegicus	881	881	15%	0.0	98.79%	513	AJ006070.1

➤ **Différence au niveau NT**

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq	ATGGCTGTCCTCCATCCATCCCTGAGCTCAGTTTCTGCACCTGATGAARATCAGCACCAGCAGATCAATTTTCCAGTGGAAATTAAGCTGTTTAGGGTGAATCTTTGGAAAGGACCCGAG													
cds	ATGGCTGTCCTCCATCCATCCCTGAGCTCAGTTTCTGCACCTGATGAARATCAGCACCAGCAGATCAATTTTCCAGTGGAAATTAAGCTGTTTAGGGTGAATCTTTGGAAAGGACCCGAG													
Consensus	ATGGCTGTCCTCCATCCATCCCTGAGCTCAGTTTCTGCACCTGATGAARATCAGCACCAGCAGATCAATTTTCCAGTGGAAATTAAGCTGTTTAGGGTGAATCTTTGGAAAGGACCCGAG													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq	AAGCACAARAAGAGAGAGGATCTCTCAGAGGGAAACCTTGTCTCGAGCAGCTCCAGTAGTCTCAGATAGGCTTGGGGTCAGAAATTCAGTCTGACTCAGCAGCATTAAGATCCATCTTAATTTTC													
cds	AAGCACAARAAGAGAGAGGATCTCTCAGAGGGAAACCTTGTCTCGAGCAGCTCCAGTAGTCTCAGATAGGCTTGGGGTCAGAAATTCAGTCTGACTCAGCAGCATTAAGATCCATCTTAATTTTC													
Consensus	AAGCACAARAAGAGAGAGGATCTCTCAGAGGGAAACCTTGTCTCGAGCAGCTCCAGTAGTCTCAGATAGGCTTGGGGTCAGAAATTCAGTCTGACTCAGCAGCATTAAGATCCATCTTAATTTTC													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq	AAGAAATTCATGTTGATGGAGTCAAGCAGCAAGACATTCACAGCCAGCTTGAACACTTGTGCGCATCTGTGCAATCACTCAGAGTGACGGCAGCCAGGAGATACCCAGTCCACGGG													
cds	AAGAAATTCATGTTGATGGAGTCAAGCAGCAAGACATTCACAGCCAGCTTGAACACTTGTGCGCATCTGTGCAATCACTCAGAGTGACGGCAGCCAGGAGATACCCAGTCCACGGG													
Consensus	AAGAAATTCATGTTGATGGAGTCAAGCAGCAAGACATTCACAGCCAGCTTGAACACTTGTGCGCATCTGTGCAATCACTCAGAGTGACGGCAGCCAGGAGATACCCAGTCCACGGG													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
seq	CCGCTGGAGCTTAARACTTAAGCCTTTTCCAGAGAGGAAAGAGATCAGCTCTGCGCAGATCTCATTTGCCAGAGTTTCCGGATTGATGTGAGTCAAGATGTTGACTCCATCACCCCTGAT													
cds	CCGCTGGAGCTTAARACTTAAGCCTTTTCCAGAGAGGAAAGAGATCAGCTCTGCGCAGATCTCATTTGCCAGAGTTTCCGGATTGATGTGAGTCAAGATGTTGACTCCATCACCCCTGAT													
Consensus	CCGCTGGAGCTTAARACTTAAGCCTTTTCCAGAGAGGAAAGAGATCAGCTCTGCGCAGATCTCATTTGCCAGAGTTTCCGGATTGATGTGAGTCAAGATGTTGACTCCATCACCCCTGAT													
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
seq	TCTGCCATATCTGTTGGAGCATATGACAGAGAGATTCGCGAGTGTCTCAGCTCAGGTCTACTGCCAGAGGATGTAGCTGGAGTGGACCCCCACACACCGCTCTGTGACATCTGCTTACTGCCCA													
cds	TCTGCCATATCTGTTGGAGCATATGACAGAGAGATTCGCGAGTGTCTCAGCTCAGGTCTACTGCCAGAGGATGTAGCTGGAGTGGACCCCCACACACCGCTCTGTGACATCTGCTTACTGCCCA													
Consensus	TCTGCCATATCTGTTGGAGCATATGACAGAGAGATTCGCGAGTGTCTCAGCTCAGGTCTACTGCCAGAGGATGTAGCTGGAGTGGACCCCCACACACCGCTCTGTGACATCTGCTTACTGCCCA													
	651	660	670	680	690	700	710	720	730	740	750	760	770	780
seq	TGGGGACTGAGAGGAGAGAGACATCGCCCAACCTGACGCTCAGCAGAGAACTTAARAACTGTGCTCAGCATGCTAGACGGGACCGTCGACAGAGAACTCAGCTAGGGTCAGCAGAGAGGTCATG													
cds	TGGGGACTGAGAGGAGAGAGACATCGCCCAACCTGACGCTCAGCAGAGAACTTAARAACTGTGCTCAGCATGCTAGACGGGACCGTCGACAGAGAACTCAGCTAGGGTCAGCAGAGAGGTCATG													
Consensus	TGGGGACTGAGAGGAGAGAGACATCGCCCAACCTGACGCTCAGCAGAGAACTTAARAACTGTGCTCAGCATGCTAGACGGGACCGTCGACAGAGAACTCAGCTAGGGTCAGCAGAGAGGTCATG													
	781	790	800	810	820	830	840	850	860	870	880	890	900	910
seq	AAGAGATCTCCAGCTGAGTAGATTCATCTCAGTACCAAGCTCTCTGAGTAGACTTCCAGCAGCATTTTGAATCCATCTCTGCCAGATATGTAGACACATTTGGCCGATCCGGTGGAGACCA													
cds	AAGAGATCTCCAGCTGAGTAGATTCATCTCAGTACCAAGCTCTCTGAGTAGACTTCCAGCAGCATTTTGAATCCATCTCTGCCAGATATGTAGACACATTTGGCCGATCCGGTGGAGACCA													
Consensus	AAGAGATCTCCAGCTGAGTAGATTCATCTCAGTACCAAGCTCTCTGAGTAGACTTCCAGCAGCATTTTGAATCCATCTCTGCCAGATATGTAGACACATTTGGCCGATCCGGTGGAGACCA													
	911	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040
seq	CCTGAGGACCTGTTCTGAGATATGATCTCTCCGGTCTCAGGCTCATGGGAGCATTTGCTCTGCGCATATCCATGCTTCCCTAGCTGAGAGTCCGGTCAGTCTTTCTGAGCAT													
cds	CCTGAGGACCTGTTCTGAGATATGATCTCTCCGGTCTCAGGCTCATGGGAGCATTTGCTCTGCGCATATCCATGCTTCCCTAGCTGAGAGTCCGGTCAGTCTTTCTGAGCAT													
Consensus	CCTGAGGACCTGTTCTGAGATATGATCTCTCCGGTCTCAGGCTCATGGGAGCATTTGCTCTGCGCATATCCATGCTTCCCTAGCTGAGAGTCCGGTCAGTCTTTCTGAGCAT													
	1041	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170
seq	CTTGATCTCTGATGGTGAAGTCTCTGCCAGAGTGCATGAGGAGTAGTCTGGAARATATACCCATGTCTCAGGCCACAGAGATCTAAGAGACTTTGGTCATATTAAGGGGGG													
cds	CTTGATCTCTGATGGTGAAGTCTCTGCCAGAGTGCATGAGGAGTAGTCTGGAARATATACCCATGTCTCAGGCCACAGAGATCTAAGAGACTTTGGTCATATTAAGGGGGG													
Consensus	CTTGATCTCTGATGGTGAAGTCTCTGCCAGAGTGCATGAGGAGTAGTCTGGAARATATACCCATGTCTCAGGCCACAGAGATCTAAGAGACTTTGGTCATATTAAGGGGGG													
	1171	1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
seq	CGGCTCGCAGCATCTCTGCTACTGAGCGCAGAGGGCTCAGAAACATCGGCTGAGGGAGCTCAGATTCAGTCAAGAAATTTGAGACAAAGAGAGGTTGAGATGTGAGTCTGAGCT													
cds	CGGCTCGCAGCATCTCTGCTACTGAGCGCAGAGGGCTCAGAAACATCGGCTGAGGGAGCTCAGATTCAGTCAAGAAATTTGAGACAAAGAGAGGTTGAGATGTGAGTCTGAGCT													
Consensus	CGGCTCGCAGCATCTCTGCTACTGAGCGCAGAGGGCTCAGAAACATCGGCTGAGGGAGCTCAGATTCAGTCAAGAAATTTGAGACAAAGAGAGGTTGAGATGTGAGTCTGAGCT													
	1301	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430
seq	TGTTCTGCTGACATGAGGCGAAGGAGATGAGCAGACAGAGCTGATGAGCTCAGGCGCATATGACAGGCCGGGGCTCCGGTCTTCAGCAGCTGTTTGTGTCATCCGTTGATACCTTCTCCAG													
cds	TGTTCTGCTGACATGAGGCGAAGGAGATGAGCAGACAGAGCTGATGAGCTCAGGCGCATATGACAGGCCGGGGCTCCGGTCTTCAGCAGCTGTTTGTGTCATCCGTTGATACCTTCTCCAG													
Consensus	TGTTCTGCTGACATGAGGCGAAGGAGATGAGCAGACAGAGCTGATGAGCTCAGGCGCATATGACAGGCCGGGGCTCCGGTCTTCAGCAGCTGTTTGTGTCATCCGTTGATACCTTCTCCAG													
	1431	1440	1450	1460	1470	1480	1490	1500	1510	1520	1530	1540	1550	1560
seq	CTGTAGCCATACCATAGATGACAGGAGGCTGAAGACTATCACTGGAGGAGCATTTTACACCTTTGACGCTCTTGCATGCTGAGAGGCTCTCTACAGGCTACACCCCTTTGATGGAGC													
cds	CTGTAGCCATACCATAGATGACAGGAGGCTGAAGACTATCACTGGAGGAGCATTTTACACCTTTGACGCTCTTGCATGCTGAGAGGCTCTCTACAGGCTACACCCCTTTGATGGAGC													
Consensus	CTGTAGCCATACCATAGATGACAGGAGGCTGAAGACTATCACTGGAGGAGCATTTTACACCTTTGACGCTCTTGCATGCTGAGAGGCTCTCTACAGGCTACACCCCTTTGATGGAGC													
	1561	1570	1580	1590	1600	1610	1620	1630	1640	1650	1660	1670	1680	1690
seq	CCCCCTCGAAGACCTGCTCTCCAGACTGACGCTGGAATATTGATGGCTCTTGACCTTGCTCTCCGTAGATGAATACCAAGTGGACACAACTGCAAGAGGCTTCGCTATGACTTGCCTTGG													
cds	CCCCCTCGAAGACCTGCTCTCCAGACTGACGCTGGAATATTGATGGCTCTTGACCTTGCTCTCCGTAGATGAATACCAAGTGGACACAACTGCAAGAGGCTTCGCTATGACTTGCCTTGG													
Consensus	CCCCCTCGAAGACCTGCTCTCCAGACTGACGCTGGAATATTGATGGCTCTTGACCTTGCTCTCCGTAGATGAATACCAAGTGGACACAACTGCAAGAGGCTTCGCTATGACTTGCCTTGG													
	1691	1700	1710	1720	1730	1740	1750	1760	1770	1780	1790	1800	1810	1820
seq	TGTTGCTTGTATGGATGGAGGAGACATCTTGAGCGCATGAGATCCAGAGATCTGATGACTAGCTGAGTGGTCTCTCAGCGTGGTGGTAAGAGATCTGTGATGGATGGGGATGTGAGTGA													
cds	TGTTGCTTGTATGGATGGAGGAGACATCTTGAGCGCATGAGATCCAGAGATCTGATGACTAGCTGAGTGGTCTCTCAGCGTGGTGGTAAGAGATCTGTGATGGATGGGGATGTGAGTGA													
Consensus	TGTTGCTTGTATGGATGGAGGAGACATCTTGAGCGCATGAGATCCAGAGATCTGATGACTAGCTGAGTGGTCTCTCAGCGTGGTGGTAAGAGATCTGTGATGGATGGGGATGTGAGTGA													
	1821	1830	1840	1850	1860	1870	1880	1890	1900	1910	1920	1930	1940	1950
seq	GAGGACGCGAGTGGGCTCCAGCTCAGAGAAAGGAGTTCGGTCTCTCTCAGCGTATGAGATTAAGTCTGAGCATGGCTCTCAGAGCTGAGATATTGAGGAGCCAGAGCCATCTGAGCTG													
cds	GAGGACGCGAGTGGGCTCCAGCTCAGAGAAAGGAGTTCGGTCTCTCTCAGCGTATGAGATTAAGTCTGAGCATGGCTCTCAGAGCTGAGATATTGAGGAGCCAGAGCCATCTGAGCTG													
Consensus	GAGGACGCGAGTGGGCTCCAGCTCAGAGAAAGGAGTTCGGTCTCTCTCAGCGTATGAGATTAAGTCTGAGCATGGCTCTCAGAGCTGAGATATTGAGGAGCCAGAGCCATCTGAGCTG													
	1951	1960	1970	1980	1990	2000	2010	2020	2030	2040	2050	2060	2070	2080
seq	TGTTGAGGACCTTGCTTATGCTGGCAGATGAGTCTGACCCAGAGACATTAAGTCTCTCAGCGCTCTATGCTGAGGAGGAGGCGCATGAGGAGCTGAGTTCGCTGGAGATGGGAGCA													
cds	TGTTGAGGACCTTGCTTATGCTGGCAGATGAGTCTGACCCAGAGACATTAAGTCTCTCAGCGCTCTATGCTGAGGAGGAGGCGCATGAGGAGCTGAGTTCGCTGGAGATGGGAGCA													
Consensus	TGTTGAGGACCTTGCTTATGCTGGCAGATGAGTCTGACCCAGAGACATTAAGTCTCTCAGCGCTCTATGCTGAGGAGGAGGCGCATGAGGAGCTGAGTTCGCTGGAGATGGGAGCA													
	2081	2090	2100	2110	2120	2130	2140	2150	2160	2170	2180	2190	2200	2210
seq	TCCCGAGGATTTAATTTATCTTCAGGGGACCTGGATATGACGAGAACTTGTACGGGAGTAGAGGCTTGGAGGCTTCTGGCTCAGTCTACATTTGTACACTTTGTGATGCCACCGCTGGAGC													
cds	TCCCGAGGATTTAATTTATCTTCAGGGGACCTGGATATGACGAGAACTTGTACGGGAGTAGAGGCTTGGAGGCTTCTGGCTCAGTCTACATTTGTACACTTTGTGATGCCACCGCTGGAGC													
Consensus	TCCCGAGGATTTAATTTATCTTCAGGGGACCTGGATATGACGAGAACTTGTACGGGAGTAGAGGCTTGGAGGCTTCTGGCTCAGTCTACATTTGTACACTTTGTGATGCCACCGCTGGAGC													
	2211	2220	2230	2240	2250	2260	2270	2280	2290	2300	2310	2320	2330	2340
seq	CTCCCAAAATCTTGCTTCCATCTCAATACCCAGAGACACCGCCAGAGATCTGCAGCGCTATGAGGCTTGGCGGTCCAAATCCCATTATCAGAGTCAGTGGAGAAACTCCGGACCCGGTGAAGAGATCTCT													
cds	CTCCCAAAATCTTGCTTCCATCTCAATACCCAGAGACACCGCCAGAGATCTGCAGCGCTATGAGGCTTGGCGGTCCAAATCCCATTATCAGAGTCAGTGGAGAAACTCCGGACCCGGTGAAGAGATCTCT													
Consensus	CTCCCAAAATCTTGCTTCCATCTCAATACCCAGAGACACCGCCAGAGATCTGCAGCGCTATGAGGCTTGGCGGTCCAAATCCCATTATCAGAGTCAGTGGAGAAACTCCGGACCCGGTGAAGAGATCTCT													
	2341	2350	2360	2370	2380	2390	2400	2410	2420	2430	2440	2450	2460	2470
seq	GCCAAATCTTCATCGAGACATGCCCTCCATAGATGGCTCAGCTGCATCTGGATATGGATACGACTGAATCTATAGAAATTTCCAGCTGGAGTAGGGGAGGTATATAAAATCCCAATGCCCTTAAG													
cds	GCCAAATCTTCATCGAGACATGCCCTCCATAGATGGCTCAGCTGCATCTGGATATGGATACGACTGAATCTATAGAAATTTCCAGCTGGAGTAGGGGAGGTATATAAAATCCCAATGCCCTTAAG													
Consensus	GCCAAATCTTCATCGAGACATGCCCTCCATAGATGGCTCAGCTGCATCTGGATATGGATACGACTGAATCTATAGAAATTTCCAGCTGGAGTAGGGGAGGTATATAAAATCCCAATGCCCTTAAG													
	2471	2480	2490	2500	2510	2520	2530	2540	2550	2560	2570	2580	2590	2600
seq	AAGAAAGGAGAGAGATGCGAGGCGCACTTGACAAACATCTGCGGAAAGAGATGAATTAARACCATCTAGAGATGATGACCACTTGGCCGGAGCTTATAGCCCAAGAGACTGTGGACGAGTNG													
cds	AAGAAAGGAGAGAGATGCGAGGCGCACTTGACAAACATCTGCGGAAAGAGATGAATTAARACCATCTAGAGATGATGACCACTTGGCCGGAGCTTATAGCCCAAGAGACTGTGGACGAGTNG													
Consensus	AAGAAAGGAGAGAGATGCGAGGCGCACTTGACAAACATCTGCGGAAAGAGATGAATTAARACCATCTAGAGATGATGACCACTTGGCCGGAGCTTATAGCCCAAGAGACTGTGGACGAGTNG													
	2601	2610	2620	2630	2640	2650	2660	2670	2680	2690	2700	2710	2720	2730
seq	TGAGTATATCTCTCTCAGGAGAGGACCGAGACTCTCAGGAGGCTGATGGAACTTTACTGAGATGAGACCGGGTGGCGCTCATCTAGTCTCTCTGATAGAGTGGCCGGAGTCCCTTTGCTAGTACAGT													
cds	TGAGTATATCTCTCTCAGGAGAGGACCGAGACTCTCAGGAGGCTGATGGAACTTTACTGAGATGAGACCGGGTGGCGCTCATCTAGTCTCTCTGATAGAGTGGCCGGAGTCCCTTTGCTAGTACAGT													
Consensus	TGAGTATATCTCTCTCAGGAGAGGACCGAGACTCTCAGGAGGCTGATGGAACTTTACTGAGATGAGACCGGGTGGCGCTCATCTAGTCTCTCTGATAGAGTGGCCGGAGTCCCTTTGCTAGTACAGT													
	2731	2740	2750	2760	2770	2780	2790	2800	2810	2820	2830	2840	2850	2860
seq	TTCACTCNCAGCTTTTCGTGAGCTCTCTCCACAGTTCAAATACGATACAGGGCCAAATCCCAATCTCTTCAAAACCTTGGCACAGCTCCCTGAATATTAGAGGGATGGCTCTATTG													
cds	TTCACTCNCAGCTTTTCGTGAGCTCTCTCCACAGTTCAAATACGATACAGGGCCAAATCCCAATCTCTTCAAAACCTTGGCACAGCTCCCTGAATATTAGAGGGATGGCTCTATTG													
Consensus	TTCACTCNCAGCTTTTCGTGAGCTCTCTCCACAGTTCAAATACGATACAGGGCCAAATCCCAATCTCTTCAAAACCTTGGCACAGCTCCCTGAATATTAGAGGGATGGCTCTATTG													
	2861	2870	2880	2890	2900	2910	2920	2930	2940	2950	2960	2970	2980	2990
seq	GGGATCCGNCAGTGGGCGCATGATCTGGTACAAACGTTTATGGGCTCTCCGAARAGGATGCGAGGCGCTCCAGTGTGATGATGAGAGATGCTCTGAACACCACTGGCTGTATCTTCAA													
cds	GGGATCCGNCAGTGGGCGCATGATCTGGTACAAACGTTTATGGGCTCTCCGAARAGGATGCGAGGCGCTCCAGTGTGATGATGAGAGATGCTCTGAACACCACTGGCTGTATCTTCAA													
Consensus	GGGATCCGNCAGTGGGCGCATGATCTGGTACAAACGTTTATGGGCTCTCCGAARAGGATGCGAGGCGCTCCAGTGTGATGATGAGAGATGCTCTGAACACCACTGGCTGTATCTTCAA													
	2991	3000	3010	3020	3030	3040	3050	3060	3070	3080	3090	3100	3110	3120
seq	ATNCTCCAGAGTTTATGATGCCATATGATTAARAACTCTGGGTTACCATGACTCAAGAGAGACTTTAGGGGACTTTGGAACTTAGGAGCTCTCTGGAAAGCCAGAGATCAATGAGGTTT													
cds	ATNCTCCAGAGTTTATGATGCCATATGATTAARAACTCTGGGTTACCATGACTCAAGAGAGACTTTAGGGGACTTTGGAACTTAGGAGCTCTCTGGAAAGCCAGAGATCAATGAGGTTT													
Consensus	ATNCTCCAGAGTTTATGATGCCATATGATTAARAACTCTGGGTTACCATGACTCAAGAGAGACTTTAGGGGACTTTGGAACTTAGGAGCTCTCTGGAAAGCCAGAGATCAATGAGGTTT													
	3121	3130	3140	3150	3160	3170	3180	3190	3200	3210	3220	3230	3240	3250
seq	ATCTCCAGAGTTTATGATGCCATATGATTAARAACTCTGGGTTACCATGACTCAAGAGAGACTTTAGGGGACTTTGGAACTTAGGAGCTCTCTGGAAAGCCAGAGATCAATGAGGTTT													
cds	ATCTCCAGAGTTTATGATGCCATATGATTAARAACTCTGGGTTACCATGACTCAAGAGAGACTTTAGGGGACTTTGGAACTTAGGAGCTCTCTGGAAAGCCAGAGATCAATGAGGTTT													
Consensus	ATCTCCAGAGTTTATGATGCCATATGATTAARAACTCTGGGTTACCATGACTCAAGAGAGACTTTAGGGGACTTTGGAACTTAGGAGCTCTCTGGAAAGCCAGAGATCAATGAGGTTT													

➤ Différence au niveau PROT :

☒	V(D)J recombination-activating protein 1 [Rattus norvegicus]	Rattus norvegicus	2145	2145	100%	0.0	99.04%	1040	NP_445920.1
☒	recombination activating gene 1 [Rattus norvegicus]	Rattus norvegicus	904	1741	82%	0.0	99.54%	1000	AAQ63060.1
☒	rag1 [Rattus norvegicus]	Rattus norvegicus	687	687	32%	0.0	99.40%	333	BAD38670.1
☒	recombination activating protein 1 [Rattus norvegicus]	Rattus norvegicus	532	532	24%	0.0	100.00%	256	AAG38402.1
☒	RAG1 [Rattus norvegicus]	Rattus norvegicus	339	339	15%	6e-110	98.18%	165	CAA06842.1
☒	E3 ubiquitin-protein ligase RNF166 [Rattus norvegicus]	Rattus norvegicus	51.2	51.2	9%	3e-06	34.62%	237	NP_001002279.1

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq	RAYPLPSTLRLSSAPDEIQPHIKFSEAKFLFRVRSFEKAPEEAQKEKDSSEGPCLQSPVYLDKPGGQNSVLTORALKLHPKFSKKFHVDGKSSDKAIHQARLRHFCRTICGNHFKSGDHNRRYPVHG													
ref	RAYPLPSTLRLSSAPDEIQPHIKFSEAKFLFRVRSFEKAPEEAQKEKDSSEGPCLQSPVYLDKPGGQNSVLTORALKLHPKFSKKFHVDGKSSDKAIHQARLRHFCRTICGNHFKSGDHNRRYPVHG													
Consensus	RAYPLPSTLRLSSAPDEIQPHIKFSEAKFLFRVRSFEKAPEEAQKEKDSSEGPCLQSPVYLDKPGGQNSVLTORALKLHPKFSKKFHVDGKSSDKAIHQARLRHFCRTICGNHFKSGDHNRRYPVHG													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq	PYDAKTQSLFRKKEKRYTSPDLIARYFRIDVKSQVDSIHPTEFCNCHCSIHHRKFGSAHSQVYCPRNVTVEWHPHTPSCDICTFAHRGLKRRKHQPNVQLSKKLKTVLNHARRDRRKRTQARYSSKEVH													
ref	PYDAKTQSLFRKKEKRYTSPDLIARYFRIDVKSQVDSIHPTEFCNCHCSIHHRKFGSAHSQVYCPRNVTVEWHPHTPSCDICTFAHRGLKRRKHQPNVQLSKKLKTVLNHARRDRRKRTQARYSSKEVH													
Consensus	PYDAKTQSLFRKKEKRYTSPDLIARYFRIDVKSQVDSIHPTEFCNCHCSIHHRKFGSAHSQVYCPRNVTVEWHPHTPSCDICTFAHRGLKRRKHQPNVQLSKKLKTVLNHARRDRRKRTQARYSSKEVH													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq	KKISNCSKIHLSTKLLAYDFPAHFVKSISQICEHILADPYETTCKHLFCRICILRCLKYMGSYCPSCRYPCFPTDLQSPVKSFLSILNSLHYKCPAQECNEEVSLEKYNAHVSSHESKETLVHINKGG													
ref	KKISNCSKIHLSTKLLAYDFPAHFVKSISQICEHILADPYETTCKHLFCRICILRCLKYMGSYCPSCRYPCFPTDLQSPVKSFLSILNSLHYKCPAQECNEEVSLEKYNAHVSSHESKETLVHINKGG													
Consensus	KKISNCSKIHLSTKLLAYDFPAHFVKSISQICEHILADPYETTCKHLFCRICILRCLKYMGSYCPSCRYPCFPTDLQSPVKSFLSILNSLHYKCPAQECNEEVSLEKYNAHVSSHESKETLVHINKGG													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
seq	RPROHLLSLTRRAQKHRLRELKIQVKEFADKEEGGVKSYCLTLFLLALRARNEHRAQDELEAIMQGRGSLQPAYCLAIRYNTFLSCSYQYKHYRTYKAITGRQIFQPLHALRNAEKALLPGYHPFEHQ													
ref	RPROHLLSLTRRAQKHRLRELKIQVKEFADKEEGGVKSYCLTLFLLALRARNEHRAQDELEAIMQGRGSLQPAYCLAIRYNTFLSCSYQYKHYRTYKAITGRQIFQPLHALRNAEKALLPGYHPFEHQ													
Consensus	RPROHLLSLTRRAQKHRLRELKIQVKEFADKEEGGVKSYCLTLFLLALRARNEHRAQDELEAIMQGRGSLQPAYCLAIRYNTFLSCSYQYKHYRTYKAITGRQIFQPLHALRNAEKALLPGYHPFEHQ													
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
seq	PPLKNVSSRTDVGIIDGLSGLASSYDEYPVDTIAKFRYDSALYSALMDHEEDILDGHRSDQLDDYVSGPFTVYVVKESCDGMDGVSEKHGSGPAYPEKAVRFSFTYHRYTVEHGSDNYKIFEEPKPNSEL													
ref	PPLKNVSSRTDVGIIDGLSGLASSYDEYPVDTIAKFRYDSALYSALMDHEEDILDGHRSDQLDDYVSGPFTVYVVKESCDGMDGVSEKHGSGPAYPEKAVRFSFTYHRYTVEHGSDNYKIFEEPKPNSEL													
Consensus	PPLKNVSSRTDVGIIDGLSGLASSYDEYPVDTIAKFRYDSALYSALMDHEEDILDGHRSDQLDDYVSGPFTVYVVKESCDGMDGVSEKHGSGPAYPEKAVRFSFTYHRYTVEHGSDNYKIFEEPKPNSEL													
	651	660	670	680	690	700	710	720	730	740	750	760	770	780
seq	CCKPLCLMLADESDHETLTAILSPLIAERAMKSSELLLEHGGIPRTFKIFRGTGYDEKL VREVEGLEASGSVYICTLCOATRLERSQNLVFHSITRSHAENLQRYEYVARSNPYHESVEELRDYKGVGS													
ref	CCKPLCLMLADESDHETLTAILSPLIAERAMKSSELLLEHGGIPRTFKIFRGTGYDEKL VREVEGLEASGSVYICTLCOATRLERSQNLVFHSITRSHAENLQRYEYVARSNPYHESVEELRDYKGVGS													
Consensus	CCKPLCLMLADESDHETLTAILSPLIAERAMKSSELLLEHGGIPRTFKIFRGTGYDEKL VREVEGLEASGSVYICTLCOATRLERSQNLVFHSITRSHAENLQRYEYVARSNPYHESVEELRDYKGVGS													
	781	790	800	810	820	830	840	850	860	870	880	890	900	910
seq	AKPFIETVPSIDALHCDIGNAREFYKIFQLEIGEYVKNPNASKEERKRQATLDKHLAKRKNLKPINRWNGNFARKLATQETVDAYCELIPSEERHEALRELMDLYLKNKPVWRSSCPAKECPESLCQYS													
ref	AKPFIETVPSIDALHCDIGNAREFYKIFQLEIGEYVKNPNASKEERKRQATLDKHLAKRKNLKPINRWNGNFARKLATQETVDAYCELIPSEERHEALRELMDLYLKNKPVWRSSCPAKECPESLCQYS													
Consensus	AKPFIETVPSIDALHCDIGNAREFYKIFQLEIGEYVKNPNASKEERKRQATLDKHLAKRKNLKPINRWNGNFARKLATQETVDAYCELIPSEERHEALRELMDLYLKNKPVWRSSCPAKECPESLCQYS													
	911	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040
seq	FNXQRFALLSTFKYRYEGKITNYFAKTLAHVPEIITERDGSIGAWASEGNESGNKFRRFRKXNARQSKCYEMEDVYLKHHMLYKSKXLQKFMAHNAHNAKNSGFTMNSKETLGDSLDTEDSLESQDSHEF													
ref	FNXQRFALLSTFKYRYEGKITNYFAKTLAHVPEIITERDGSIGAWASEGNESGNKFRRFRKXNARQSKCYEMEDVYLKHHMLYKSKXLQKFMAHNAHNAKNSGFTMNSKETLGDSLDTEDSLESQDSHEF													
Consensus	FNXQRFALLSTFKYRYEGKITNYFAKTLAHVPEIITERDGSIGAWASEGNESGNKFRRFRKXNARQSKCYEMEDVYLKHHMLYKSKXLQKFMAHNAHNAKNSGFTMNSKETLGDSLDTEDSLESQDSHEF													

En 509 A>V

○ **FlagBirA Rag1 CTX clone B**

➤ **B3Fwd 868NT**

ATGGCTGTCCCCTTGCCATCTACCCTGAGACTCAGTTCTGCACCTGATGAAATTCAGCACCCGCACATCAAATTTTC
CGAGTGGAATTTAAGCTGTTTAGGGTGAGATCCTTTGAAAAGGCACCCGAAGAAGCACAAAAAGAGAAGGAT
TCCTCAGAAGGGAAACCTTGCTCTGAGCAGTCTCCAGTAGTTCTAGATAAGCCTGGGGGTCAGAATTCAGTTCTG
ACTCAACGAGCATTGAACTCCATCCTAAATTTCAAAGAAATTCATGTTGATGGGAAGTCAAGCGACAAAGCA
ATCACCAAGCCAGGCTTAGACACTTCTGCCGATCTGTGGCAATCACTTCAAGAGTGACGGGCACAACCGGAG
ATACCCAGTCCACGGGCCCCGTGGACGCTAAACTCAAAGCCTTTCCGAAAGAAGGAAAAAAGAGTCACGTCCT
GGCCAGATCTCATTGCCAGAGTTTTCCGATTGATGTGAAGTCAGATGTTGACTCCATCCACCCCACTGAATTCTG
CCATAACTGTTGGAGCATTATGCACAGGAAGTTCCGGCAGTGCTCACAGTCAGGTCTACTGCCCAAGGAATGTGAC
CGTGAGTGGCACCCCAACACACCGTCCTGTGACATCTGCTTACTGCCCATCGGGGACTGAAGAGGAAGAGAC
ATCAGCCCAACGTGCAGCTCagCAAGAACTAAAACTGtGCTCAACCATGCTAGACGGGACCGTCGCAAGAgA
ACTCagcTAGGGTCAGCAGCAAGNAGGTCATGAANAANATCTCCAAGTCAGTAAGANTCATCTCANTACCAAG
CTTCTTGCAANNANACTTCCCAGCACACTTTGNGAANTCCATCTCCNG

➤ **BGHRev**

TCTTNCANTCCATAACCAGAANCCACGCCGAGANTNTGCAGCGCTATGAGNTCNGGCGNTCCAATCCNNATC
ACGAGTCNGTGGAAGAACTCCGNGACCGGTGNNNGGAGTCTNTGCCAAACNNtTCATCGAGACAGTcCcTT
CCATAGATGCGCTTCACTGTGACATTGGAaNTGCAGCTGAATTcTATAAGATTTTCCAGCNGgANATAGGGNA
AGTGTATaAAAATCCCAATGCCTCTAAAGAGGAAAGGgAAGAGANGGCAGGCCACCTTGACAAACANcTGCG
GAAAAGGATGAACCTAAAACCAATCATGAGGATGAATGGCAACTTTGCCGGAAGCTTATGACCCAAGAGACT
GTGGACGCAGTTTGTGAGTTAATTCCTTCTGAGGAGAGGCaGAAGCTCTCAGGGAGcTGATGGACCTTTACCT
GAAGATGAAACCGGTGTGGCGCTCATCATGTCCTGCTAAAGAGTGCCCGGAGTCCCTTTGTGAGTACAGTTTC
AACTCACAGCGTTTTGCTGAGCTCCTCTCCACCAAGTTCAAATACAGATACGAGGGCAAAATCACCAATTACTT
TCACAAAACCTTGGCACACGTCCCTGAAATTATTGAAAGGGATGGCTCTATTGGGGCATGGGCAAGTGAGGG
CAATGAATCTGGTAACAACTGTTTAGGCGCTTCGGGAAAATGAATGCCAGGCAGTCCAAGTGCTATGAGATG
GAAGATGTCCTGAAACACCACTGGCTGTATACTTCAAATACCTCCAGAAGTTTATGAATGCCATAATGCATT
AAAAAACTCTGGGTTTACCATGAACTCAAAGGAGACTTTAGGGGACTCTTTGGACATTGAGGACTCTCTGGAA
AGCCAAGATTCAAtGGAGTTTTAA

➤ **Seq int fwd1**

TCTGCTTNACTGCCNNTCGGGGNNTGAAGAGGAAGAGACATCAGCCCAACGTGCAGCTCAGCAAGAACTAA
AAACTGTGCTCAACCATGCTAGACGGGACCGTCGCAAGAGAACTCAGGCTAGGGTCAGCAGCAAGGAGGTCA
TGAAGAAGATCTCCAAGTGCAGTAAGATTCATCTCAGTACCAAGCTTCTTGAGTAGACTTCCAGCACACTTT
GTGAAATCCATCTCCTGCCAGATATGTGAACACATTCTGGCCGATCCGGTGAGACCACCTGTAAGCACCTGTT
CTGTAGAATATGCATTCTCCGGTGCCTCAAGGTCATGGGCAGCTATTGTCCCTCGTGCCGATATCCATGCTTCCC
TACTGACCTGCAGAGTCCGGTCAAGTCTTTCTGAGCATCTTGAATTCTCTGATGGTGAAGTGTCTGCCAAG
AGTGCAATGAGGAAGTAAGTCTGGAAAAATATAACCACCATGTCTCAAGCCACAAAGAATCTAAAGAGACTTT
GGTGATATTAATAAAGGGGGCCGGCTCGCCAGCATCTCCTGTCACTGACGCGAAGGGCTCAGAAACATCG
GCTGAGGGAGCTCAAGATTCAAGTCAAAGAATTTGCAGACAAAGAAGGTGGAGATGTGAAGTCTGTGTG
CTTGACGTTGTTCTGCTGGCACTGAGGGCAAGGAATGAGCACAGACAAGCTGATGAGCTCGAGGCCATCAT
GCAAGGCCGGGGCTCCGGTCTTCAACAGCTGTTTGCTTGGCCATCCGTGTCAATACCTTCTCAGCTGTAGCC
AATACCATAAGATGTACAGGACGGTGAAAGCTATCACTGGGAGGCAGATTTTTCAACCTTTGCACGCTCTTCGC
AATGCTGANAAGGNCCTCTACCAGGCTACCACCCCTTTGAGTGGCAGCCCCCTCTGAANAACGTGTCTCCA
NAACTGACGTTGGAATTANTGATGGGCTCTCTGGACTTGCTCCTCCGNANATGANTACCCNGNNGNNNNNA
NTGCAANNNNNTNCNNCTNTGACTCTNCTNNNNGTCTGCTTTGNNNGANNNGANNAAGANNTNT

➤ **Seq int fwd2**

TNAATAANGGGGGCCGGCCTCGCCNGCATCTCCTGTCACTGACGCGAAGGGCTCAGAAACATCGGCTGAGGGA
GCTCAAGATTCAAGTCAAAGAATTTGCAGACAAAGAAGAAGGTGGAGATGTGAAGTCTGTGTGCTTGACGTTGT
TCCTGCTGGCACTGAGGGCAAGGAATGAGCACAGACAAGCTGATGAGCTCGAGGCCATCATGCAAGGCCGGGG
CTCCGGTCTTCAACCAGCTGTTTGCTTGGCCATCCGTGTCAATACCTTCCTCAGCTGTAGCCAATACCATAAGATGT
ACAGGACGGTGAAAGCTATCACTGGGAGGCAGATTTTTCAACCTTTGCACGCTCTTCGCAATGCTGAGAAGGCC
CTCCTACCAGGCTACCACCCCTTTGAGTGGCAGCCCCCTCTGAAGAACGTGTCTCCAGAACTGACGTTGGAATT
ATTGATGGGCTCTCTGGACTTGCTCTCCGTAGATGAATACCCAGTGGACACAATTGCAAAGAGGTTCCGCTAT
GACTCTGCTTTGGTGTCTGCTTTGATGGACATGGAGGAAGACATCTTGACGGCATGAGATCCCAAGATCTTGAT
GACTACGTGAGTGGTCCCTTCACCGTGGTGGTAAAGGAATCGTGTGATGGAATGGGGGGATGTGAGTGANAAG
CACGGGANTGGGCCCNNNNNTCCNNNNNNNGNNNNNNNNNTCNCTNNNNNNNNCNGAGAGTTNCNGT
CNANNNGGCTCTCNNAANNTGNANNNNTNTNGAGGANCNNNNNNCCNNTTCNNANCTGN GTTGNANGC
CACNGTGNNTTATNNTGNNNNTGANTCTNANCNNNNNACANNNNCNGNTATNCTCNNCCCCNNCNTCNNT
NANNNGNANGCC

➤ **Seq int Rev1**

NTCNTNNNAGCATNTTGANTTCTNTGANNNTGAANNNTCCNGCCCANAGTGCAATGAGGAAGTAAGTNTG
GAAAAATATAACCACCATGTCTCAAGCCACAAAGANTNNAAGAGACTTTGGTGCATATTAATAAAGGGGGCNGN
CCTNGCCAGCATCTCCTGTCACTGACGCGAAGGGNTCAGAAACATCGGCTGAGGGAGCTCAAGATTCAAGTCA
AAGAATTTGCAGACAAAGAAGAAGGTGGAGATGTGAAGTCTGTGTGCTTGACGTTGTCNTGCTGGCACTGAG
GGCAAGGAATGAGCACAGACAAGCTGATGAGCTCGAGGCCATCATGCAAGGCCGGGGCTCCGGTCTTCAACCA
GCTGTTTGCTTGGCCATCCGTGTCAATACCTTCCTCAGCTGTAGCCAATACCATAAGATGTACAGGACGGTGAAAG
CTATCACTGGGAGGCAGATTTTTCAACCTTTGCACGCTCTTCGCAATGCTGAGAAGGCCCTCCTACCAGGCTACC
ACCCCTTTGAGTGGCAGCCCCCTCTGAAGAACGTGTCTCCAGAACTGACGTTGGAATTATTGATGGGCTCTCTG
GACTTGCTCTCCGTAGATGAATACCCAGTGGACACAATTGCAAAGAGGTTCCGCTATGACTCTGCTTTGGTGTG
TGCTTTGATGGACATGGAGGAAGACATCTTGACGGCATGAGATCCCAAGATCTTGATGACTACGTGAGTGGTCC
CTTACCGTGGTGGTAAAGGAATCGTGTGATGGAATGGGGGATGTGAGTGAGAAGCACGGGAGTGGGCCCCGC
AGTTCCAGAAAAGGCAGTTCGGTTCTTTTACCGTCATGAGAGTTACAGTCGAGCATGGCTCTCAGAACGTGA
AGATATTTGAGGAACCAAGCCCAATTCTGAACTGTGTTGCAAGCCACTGTGCCTTATGCTGGCAGATGAGTCTG
ACCACGAGACACTTACTGCTATTCTCAGCCCCCTCATCGNNNNNaGGGAGGCCATGAAGAGCAGTGAATTGCTG
CtGGAGANGGGAGGCNNCCCCANGA

➤ **Seq int Rev2**

GCANNCCNNNTGANNAANGNGTNCTCCAGNACTGACGTTGGAATTATNATNGGCTCTCTGGACTTGCCTCCTN
NGTAGATGANTACCCAGTNGACNCAATTGCAAAGAGGTTNCGCTANGANTNTGCTTTGGTGTNTGCTTTGATG
GACANGGAGGAAGACATCTTGACGGCATGAGATCCCAAGATCTTGATGACTACGTGAGTGGTCCNTTCACCGT
GGTGGTAAAGGAATCGTGTGATGGAATGGGGGATGTGAGTGAGAAGCACGGGAGTGGGCCCCGAGTTCCAGA
AAAGGCAGTTCGGTTCTTTTACCGTCATGAGAGTTACAGTCGAGCATGGCTCTCAGAACGTGAAGATATTGA
GGAACCAAGCCCAATTCTGAACTGTGTTGCAAGCCACTGTGCCTTATGCTGGCAGATGAGTCTGACCACGAGA
CACTTACTGCTATTCTCAGCCCCCTCATCGCTGAGAGGGAGGCCATGAAGAGCAGTGAATTGCTGCTGGAGATG
GGAGGCATCCCCAGGACTTTTAAATTTATCTTCAGGGGCACTGGATATGACGAGAACTTGTGAGGGAAGTAGA
AGGCTTGGAAGCTTCTGGCTCAGTCTACATTTGTACACTTTGTGATGCCACCCGTCTGGAAGCCTCCCAAATCTT
GTCTTCACTCCATAACCAGAAGCCACGCCGAGAATCTGCAGCGCTATGAGGTCTGGCGGTCCAATCCCTATCAC
GAGTCAGTGGAAGAACTCCGGGACCGGGTGAAAGGAGTCTCTGCCAAACCTTTCATCGAGACAGTCCCTTCCAT

AGATGCGCTTCACTGTGACATTGGAAATGCAGCTGAATTCTATAAGATTTTCCAGCTGGAGATAGGGGAAGTGTA
TAAAAATCCCAATGCCTCTAAAGAGGAAAGGAAGAGATGGCAGGCCACCTTGACAAACATCTGCGGAAAAGG
ATGAACTTAAACCAATCATGAGGATGAATGGCAACTTTGCCCGGAAGCTTATGACCCAAGAGACNGNNGACGC
AGTTNGNNAGTNA

➤ **Synthèse séquençage**

ATGGCTGTCCCTTGCCATCTACCCTGAGACTCAGTTCTGCACCTGATGAAATTCAGCAC	60
CCGCACATCAAATTTTCGAGTGGAATTTAAGCTGTTTAGGGTGAGATCCTTTGAAAAG	120
GCACCCGAAGAAGCACAAAAAGAGAAGGATTCCCTCAGAAGGGAAACCTTGCTCGAGCAG	180
TCTCCAGTAGTTCTAGATAAGCCTGGGGGTGAGAATTCAGTTCTGACTCAACGAGCATTG	240
AAACTCCATCCTAAATTTTCAAAGAAATTCATGTTGATGGGAAGTCAAGCGACAAAGCA	300
ATTCACCAAGCCAGGCTTAGACACTTCTGCCGATCTGTGGCAATCACTTCAAGAGTGAC	360
GGGCACAACCCGAGATACCCAGTCCACGGGCCCGTGGACGCTAAAACCTCAAAGCCTTTTC	420
CGAAAGAAGGAAAAAGAGTCAGTCCCTGGCCAGATCTCATGGCCAGAGTTTTCGGGATT	480
GATGTGAAGTCAGATGTTGACTCCATCCACCCACTGAATTCTGCCATAACTGTTGGAGC	540
ATTATGCACAGGAAGTTGGCGAGTGCTCACAGTCAGGTCTACTGCCCAAGGAATGTGACC	600
GTGGAGTGGCACCCCCACACCCGTCCTGTGACATCTGCTTTACTGCCCATCGGGGACTG	660
AAGAGGAAGAGACATCAGCCCAACGTGCAGCTCAgCAAGAAACTAAAACTGtGCTCAAC	720
CATGCTAGACGGGACCGTCGCAAGAGAAGTCAAGGCTAGGGTCAGCAGCAAGGAGGTCATG	780
AAGAAGATCTCCAAGTGCAGTAAGATTATCTCAGTACCAAGCTCTTGCAGTAGACTTC	840
CCAGCACACTTTGTGAAATCCATCTCCTGCCAGATATGTGAACACATCTTGCCCGATCCG	900
GTGGAGACACCTGTGTTGCTTGTGTAAGATATGCATTCTCCGGTGCCTCAAGGTC	960
ATGGGCAGCTATTGTCCCTCGTGCCGATATCCATGCTTCCCTACTGACCTGCAGAGTCCG	1020
GTCAAGTCTTTCTGAGCATCTTGAATTCTCTGATGGTGAAAGTCTCTGCCCAAGAGTGC	1080
AATGAGGAAGTAAGTCTGGAAAAATATAACCACCATGTCTCAAGCCACAAAGAATCTAAA	1140
GAGACTTTGGTGCAATTAATAAAGGGGGCCGCTCGCCAGCATCTCTGCTACTGACG	1200
CGAAGGGCTCAGAAACATCGGCTGAGGGAGCTCAAGATTCAAGTCAAAGAATTTGCAGAC	1260
AAAGAAGAAGGTGGAGATGTGAAGTCTGTGTGCTTGACGTTGTTCTGCTGGCACTGAGG	1320
GCAAGGAATGAGCACAGACAAGCTGATGAGCTCGAGGCCATCATGCAAGGCCGGGGCTCC	1380
GGTCTTCAACAGCTGTTTGTGCTTGGCCATCCGTGTCAATACCTTCTCAGCTGTAGCCAA	1440
TACCATAAGATGTACAGGACGGTGAAAGCTATCACTGGGAGGCAGATTTTCAACCTTTG	1500
CACGCTCTTCGCAATGCTGAGAAGGCCCTCCTACCAGGCTACCACCCCTTTGAGTGGCAG	1560
CCCCCTCTGAAGAACGTGCTCTCCAGAAGTACGTTGGAATTATTTGATGGGCTCTCTGGA	1620
CTTGCCCTCCCTCGTAGATGAATACCCAGTGGACACAATTGCAAAGAGGTTCCGCTATGAC	1680
TCTGCTTTGGTGCTGCTGCTTTGATGGACATGGAGGAAGACATCTTGGACGGCATGAGATCC	1740
CAAGATCTTGATGACTACGTGAGTGGTCCCTTACCCTGGTGGTAAAGGAATCGTGTGAT	1800
GGAAATGGGGGATGTGAGTGAGAAGCACGGGAGTGGGCCCGCAGTTCAGAAAAAGGCAGT	1859
TCGGTTCTCTTTACCGTCATGAGAGTTACAGTCGAGCATGGCTCTCAGAACGTGAAGAT	1919
ATTTGAGGAACCAAGACCAATTCTGAACTGTGTGCAAGCCACTGTGCCTTATGCTGG	1978
CAGATGAGTCTGACCACGAGACACTTACTGCTATTCTCAGCCCCCTCATCGCTGAGAGGG	2038
AGGCCATGAAGAGCAGTGAATTGCTGCTGGAGATGGGAGGCATCCCCAGGACTTTTAAAT	2098
TTATCTTCAGGGGCACCTGGATATGACGAGAAACTTGTCAAGGAAGTAGAAGGCTTGAAG	2158
CTTCTGGCTGAGTCTGCTTTGATGACCTTTGATGACCTTTGATGCCACCCGCTTGGAAAGCCTCCCAA	2218
ATCTTGTCTTCCACTCCATAACCAGAAGCCACGCCGAGAATCTGCAGCGCTATGAGGTCT	2278
GGCGGTCCAATCCCTATCACGAGTCAGTGGAAGAACTCCGGGACCGGGTGAAAGGAGTCT	2338
CTGCCAAACCTTTTCATCGAGACAGTCCCTTCCATAGATGCGCTTCACTGTGACATTGGAA	2398
ATGCAGCTGAATCTATTAAGATTTTCCAGCTGGAGATAGGGGAAGTGTATAAAAATCCCA	2458
ATGCCTCTAAAGAGGAAAGGAAGAGATGGCAGGCCACCTTGGACAAACATCTGCGGAAAA	2518
GGATGAACCTTAAACCAATCATGAGGATGAATGGCAACTTTGCCCGGAAGCTTATGACCC	2578
AAGAGACTGTGGACGCACTTTGTGAGTTAATTCCTTCTGAGGAGAGGCacGAAGCTCTCA	2638
GGGAGCTGATGGACCTTTACCTGAAGATGAAACCGGTGTGGCGCTCATCATGCTGCTGCTA	2698
AAGAGTGCCCGGAGTCCCTTTGTGAGTACAGTTTCAACTCACAGCGTTTCGCTGAGCTCC	2758
TCTCCACCAAGTTCAAATACAGATACGAGGGGCAAAATACCAATTACTTTCACAAAACCT	2818
TGGCACACGTCCTTGAATATTGAAAGGGATGGCTCTATTGGGGCATGGGCAAGTGAGG	2878
GCAATGAATCTGGTAACAAACTGTTTAGGCGCTTCCGGAAAATGAATGCCAGGCAGTCCA	2938
AGTGCTATGAGATGGAAGATGTCTGAAACACCACTGGCTGTATACTTCAAAAATACCTCC	2998
AGAAGTTTATGAATGCCATAATGCATTAAAAAACTCTGGGTTTACCATGAACCTCAAAGG	3058
AGACTTTAGGGGACTCTTTGGACATTGAGGACTCTCTGGAAAGCCAAGATTCAAtGGAGT	3118
TTTAA	3123

MAVPLPSTLRLSSAPDEIQHPHIKFSEWKFLFRVRSFEKAPEEAQKEKDSSEGGKPCLEQSPVVLDKPGGQNSVLTQR
ALKLHPKFSKKFHVDGKSSDKAIHQARLRHFCRICGNHFKSDGHNRRYPVHGPVDAKTQSLFRKKEKRVTSWPDLIA
RVFRIDVKSDVDSIHPTEFCHNCWSIMHRKFGSAHSQVYCPRNVTVVHHPHTPSCDICFTAHRGLKRKRHQPNVQ
LSKKLKTVLNHARRDRRKRTQARVSSKEVMKKISNCSKIHLSTKLLAVDFPAHFVKSISCQICEHILADPVETTCKHLFC
RICILRLKVMGSYPCSCRYPCFPTDLQSPVKSFLSILNSLMVKCPAQECNEEVSLKYNNHVVSSHKESKETLVHINKG
GRPRQHLLSLTRRAQKHRLRELKIQVKEFADKEEGGDVKSVCCLTLFLLALRARNEHRQADELEAIMQGRGSGLQPAV
CLAIRVNTFLSCSQYHKMYRTVKAITGRQIFQLHALRNAEKALLPGYHPFEWQPPLKNVSSRTDVGIIDGLSGLASS
VDEYPVDTIAKRFRYDSALVSALMDMEEDILDGMRSQDLDDYVSGPFTVVVKESCDGMGDVSEKHGSGPAVPEK

AVRFSFTVMRVTVEHGSQNVKIFEEPKNSELCKPLCLMLADESDHETLTAILSPLIAEREAMKSSSELLEMGGIPRT
FKFIFRGTGYDEKLVREVEGLEASGSVYICTLCDATRLEASQNLVHFHSITRSHAENLQRYEVWRSNPYHESVEELRDRV
KGVSAKPFIE TVPSIDALHCDIGNAAEFYKIFQLEIGEVYKNPNASKEERKRWQATLDKHLRKR MNLKPIMRMNGNF
ARKLMTQETVDAVCELIPSEERHEALRELM DLYLKMMPVWRSSCPAKECPESLCQYSFNSQRFAELLSTKFKYRYEGK
ITNYFHKTLAHVPEIIERDGSIGAWASEGNESGNKLFRRFRKM NARQSKCYEMEDVLKHHWLYTSKYLQKFMNAH
NALKNSGFTMNSKETLGDSL DIEDSLESQDSMEF-

➤ **Blast contre banque de rat**

☒	Rattus norvegicus recombination activating 1 (Rag1) mRNA	Rattus norvegicus	5746	5746	100%	0.0	99.87%	6536	NM_053468.2	
☒	Rattus norvegicus recombination activating gene 1 (RAG1) gene, partial cds	Rattus norvegicus	2390	4628	82%	0.0	99.77%	3002	AY294938.1	
☒	Rattus norvegicus rag1 gene, partial cds isolate: HS131/KT2830	Rattus norvegicus	1840	1840	32%	0.0	99.80%	1002	AB164045.1	
☒	Rattus norvegicus recombination activating protein 1 (Rag1) gene, partial cds	Rattus norvegicus	1419	1419	24%	0.0	100.00%	768	AY011884.1	
☒	Rattus norvegicus mRNA for recombination activation protein (RAG1), partial	Rattus norvegicus	881	881	15%	0.0	98.79%	513	AJ006070.1	

➤ **Différence au niveau NT**

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq	ATGGCTGTCCCTTGGCATTACCTCGAGCTCAGTTCTGCACCTGATGAATTCAGCACCCGACATCAAAATTTCCGAGTGGAAATTTAGCTGTTTAGGGTGAATCCTTTGAAGAGGCCACCGAG													
Consensus	ATGGCTGTCCCTTGGCATTACCTCGAGCTCAGTTCTGCACCTGATGAATTCAGCACCCGACATCAAAATTTCCGAGTGGAAATTTAGCTGTTTAGGGTGAATCCTTTGAAGAGGCCACCGAG													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq	AAGCACAAAGAGAGAGATTCCTCAGAGGGAAACCTTGTCTCAGCAGCTCTCCAGTAGTTCTAGTAGGCTGGGGTCAGATTCAGTCTGACTCAGCAGCATTGAAATCCATCTAAATTTTC													
Consensus	AAGCACAAAGAGAGAGATTCCTCAGAGGGAAACCTTGTCTCAGCAGCTCTCCAGTAGTTCTAGTAGGCTGGGGTCAGATTCAGTCTGACTCAGCAGCATTGAAATCCATCTAAATTTTC													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq	AAGAARATTCATGTTGATGGGAGTCAGGCACAAAGCAATTCACCAAGCCAGGCTAGACACTTCTGCCGATCTGTGGCARTCACTTCAGAGTGACGGGCACACCGAGATACCCAGTCCACGG													
Consensus	AAGAARATTCATGTTGATGGGAGTCAGGCACAAAGCAATTCACCAAGCCAGGCTAGACACTTCTGCCGATCTGTGGCARTCACTTCAGAGTGACGGGCACACCGAGATACCCAGTCCACGG													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
seq	CCCTGGAGCGTAAATCTAAGCTTTTCCGAAGAGGAAAGAAAGAGTCAGCTCTGGCCAGATCTATTGCCAGAGTTTCCGGATTGATGTGAAGTCAGATGTGACTCCATCACCCTCATGAT													
Consensus	CCCTGGAGCGTAAATCTAAGCTTTTCCGAAGAGGAAAGAAAGAGTCAGCTCTGGCCAGATCTATTGCCAGAGTTTCCGGATTGATGTGAAGTCAGATGTGACTCCATCACCCTCATGAT													
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
seq	TCTGCCATACCTGTTGGAGCATATGACACAGGAGTTGGCAGTGTCTCAGTCAGGCTTACTGCCAAGGATGTGACCTGGAGTGGACCCACACACCGCTCTTGACATCTGCTTTACTGCCA													
Consensus	TCTGCCATACCTGTTGGAGCATATGACACAGGAGTTGGCAGTGTCTCAGTCAGGCTTACTGCCAAGGATGTGACCTGGAGTGGACCCACACACCGCTCTTGACATCTGCTTTACTGCCA													
	651	660	670	680	690	700	710	720	730	740	750	760	770	780
seq	TCGGGGCTGAAGAGAGAGATCTAGCCACAGCTCAGCTCAGCAGAAATCAAAATCTGTCTCAACATGTAGACGGGACCTGCCAAGAGATCAAGCTAGGGTCAGCAGCAGAGAGGTCATG													
Consensus	TCGGGGCTGAAGAGAGAGATCTAGCCACAGCTCAGCTCAGCAGAAATCAAAATCTGTCTCAACATGTAGACGGGACCTGCCAAGAGATCAAGCTAGGGTCAGCAGCAGAGAGGTCATG													
	781	790	800	810	820	830	840	850	860	870	880	890	900	910
seq	AAGAAGATCTCCATCTCAGTAGATTCATCTCAGTACAGCTTCTTGCAGTAGACTTCCACACACATTTGTGAATCCATCTCTGCCAGATATGTGAACATTTTGGCCGATCCGGTGAAGACA													
Consensus	AAGAAGATCTCCATCTCAGTAGATTCATCTCAGTACAGCTTCTTGCAGTAGACTTCCACACACATTTGTGAATCCATCTCTGCCAGATATGTGAACATTTTGGCCGATCCGGTGAAGACA													
	911	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040
seq	CCTGAGACCATGTTCTGTAGATATGATCTCTCGGTGCTCAGGTCATGGGACGATTTGTCTCTGTCGATATCCATGCTTCCCTACTGACTGCGAGGTCGGTCAGTCTTTCTGAGCAT													
Consensus	CCTGAGACCATGTTCTGTAGATATGATCTCTCGGTGCTCAGGTCATGGGACGATTTGTCTCTGTCGATATCCATGCTTCCCTACTGACTGCGAGGTCGGTCAGTCTTTCTGAGCAT													
	1041	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170
seq	CTTGAATTTCTGTATGGTGAAGTCTCTGCCAAGAGTGCATGAGAGTAGTCTGGAAATATATACCAATGCTCTCAGGCCAAGAGATCTAAGAGACTTTGGTGCATATATTAAGAGGGG													
Consensus	CTTGAATTTCTGTATGGTGAAGTCTCTGCCAAGAGTGCATGAGAGTAGTCTGGAAATATATACCAATGCTCTCAGGCCAAGAGATCTAAGAGACTTTGGTGCATATATTAAGAGGGG													
	1171	1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
seq	CGGCTCTGCCAGCATCTCTGTCTACTGAGCGAGGGCTCAGAAATCTCGGTCAGGAGGCTCAGATTCAGTCAAGAGATTTGCAGCAGAGAGAGAGGTCGAGATGTGAGTCTGTGTGCTTGAGCT													
Consensus	CGGCTCTGCCAGCATCTCTGTCTACTGAGCGAGGGCTCAGAAATCTCGGTCAGGAGGACTCAGATTCAGTCAAGAGATTTGCAGCAGAGAGAGAGGTCGAGATGTGAGTCTGTGTGCTTGAGCT													
	1301	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430
seq	TGTTCCTGCTGGCCTGAGGGCAGGATGAGCAGAGCAGACTGATGAGCTCAGGGCCTATGACAGGCCGGGCTCGGCTCTCAGCAGCTGTTTGTCTGGCATCCGTTCAATACCTTCTCTCAG													
Consensus	TGTTCCTGCTGGCCTGAGGGCAGGATGAGCAGAGCAGACTGATGAGCTCAGGGCCTATGACAGGCCGGGCTCGGCTCTCAGCAGCTGTTTGTCTGGCATCCGTTCAATACCTTCTCTCAG													
	1431	1440	1450	1460	1470	1480	1490	1500	1510	1520	1530	1540	1550	1560
seq	CTGAGCCATACATATGATACAGCAGGTCAGAGCTATCATGGGAGGAGATTTTCACATCTTGACAGCTCTTCGATGCTGAGAGGCTCTCTACAGGCTACACCCCTTTGAGTGGG													
Consensus	CTGAGCCATACATATGATACAGCAGGTCAGAGCTATCATGGGAGGAGATTTTCACATCTTGACAGCTCTTCGATGCTGAGAGGCTCTCTACAGGCTACACCCCTTTGAGTGGG													
	1561	1570	1580	1590	1600	1610	1620	1630	1640	1650	1660	1670	1680	1690
seq	CCCCCTCTGAAGAGCTGTCTCCAGAGCTGAGCTTGAAATATATGATGGGCTCTTGAGCTTGCTCTCCGATATGATACCCAGTGAGACATTTGCAAGAGGTTCCGATATGACTTCTGTTGG													
Consensus	CCCCCTCTGAAGAGCTGTCTCCAGAGCTGAGCTTGAAATATATGATGGGCTCTTGAGCTTGCTCTCCGATATGATACCCAGTGAGACATTTGCAAGAGGTTCCGATATGACTTCTGTTGG													
	1691	1700	1710	1720	1730	1740	1750	1760	1770	1780	1790	1800	1810	1820
seq	TGTCTGCTTGTATGAGATGGAGAGAGATCTTGAGCGCATGAGATCCCAAGATCTTGTATGACTAGCTGAGTGGTCCCTTACCGCTGGTGGTAAGAGATCGTGTATGAGATGGGGATGTAGTGA													
Consensus	TGTCTGCTTGTATGAGATGGAGAGAGATCTTGAGCGCATGAGATCCCAAGATCTTGTATGACTAGCTGAGTGGTCCCTTACCGCTGGTGGTAAGAGATCGTGTATGAGATGGGGATGTAGTGA													
	1821	1830	1840	1850	1860	1870	1880	1890	1900	1910	1920	1930	1940	1950
seq	GAGACAGGGAGTGGGCCCCGAGTCCAGAAAGGAGCTTCGGTCTCTTTACCGCTCATGAGATTCAGCTCAGCATGGCTCTCAGAGCTGAGATATTGAGAGACCAAGCCCATTTCTGAGTGA													
Consensus	GAGACAGGGAGTGGGCCCCGAGTCCAGAAAGGAGCTTCGGTCTCTTTACCGCTCATGAGATTCAGCTCAGCATGGCTCTCAGAGCTGAGATATTGAGAGACCAAGCCCATTTCTGAGTGA													
	1951	1960	1970	1980	1990	2000	2010	2020	2030	2040	2050	2060	2070	2080
seq	TGTTCAGGCACGTGGCTTATGCTGGCAGATGAGTCTGACACAGAGCATTTACTGCTATCTCAGCCCCCTCATGCTGAGAGGGAGGATAGAGAGCATGATTTGCTGAGATGGAGGCA													
Consensus	TGTTCAGGCACGTGGCTTATGCTGGCAGATGAGTCTGACACAGAGCATTTACTGCTATCTCAGCCCCCTCATGCTGAGAGGGAGGATAGAGAGCATGATTTGCTGAGATGGAGGCA													
	2081	2090	2100	2110	2120	2130	2140	2150	2160	2170	2180	2190	2200	2210
seq	TCCCAAGGCTTTAATTTATCTCTCAGGGGACTGATATGACAGAGATTTGTACAGGAGTAGAGAGGCTTGAAGCTCTGGCTCAGCTACATTTGTACACTTTGTATGTCACCCGCTTGAGAC													
Consensus	TCCCAAGGCTTTAATTTATCTCTCAGGGGACTGATATGACAGAGATTTGTACAGGAGTAGAGAGGCTTGAAGCTCTGGCTCAGCTACATTTGTACACTTTGTATGTCACCCGCTTGAGAC													
	2211	2220	2230	2240	2250	2260	2270	2280	2290	2300	2310	2320	2330	2340
seq	CTCCAAATCTTTGCTCTCCTATACATACAGAGCAGCCGAGATCTGACAGCTATGAGGTCATGAGGTCATGGCGCTCATCTCCATCAGAGCTAGTGAAGATCTCCGAGCCGATGAAGAGATCTCT													
Consensus	CTCCAAATCTTTGCTCTCCTATACATACAGAGCAGCCGAGATCTGACAGCTATGAGGTCATGAGGTCATGGCGCTCATCTCCATCAGAGCTAGTGAAGATCTCCGAGCCGATGAAGAGATCTCT													
	2341	2350	2360	2370	2380	2390	2400	2410	2420	2430	2440	2450	2460	2470
seq	GCCAATCTTTATCAGAGACTGCTTCCATAGATGCTCTACTGTGATGATGGATTCAGATCTATAGATTTTCCAGCTGGAGATGGGAGGATGATATAAATCCCATGCTCTTAAG													
Consensus	GCCAATCTTTATCAGAGACTGCTTCCATAGATGCTCTACTGTGATGATGGATTCAGATCTATAGATTTTCCAGCTGGAGATGGGAGGATGATATAAATCCCATGCTCTTAAG													
	2471	2480	2490	2500	2510	2520	2530	2540	2550	2560	2570	2580	2590	2600
seq	AAGAAGAGAGAGATGGCAGGCACCTTGGCAAACTCTCGGAAGAGGATGATCTAATCAACCTCATGAGGATGATGGCACTTTGCCCGAGACTTATGACCCAGAGACTGTGACGCAATTTG													
Consensus	AAGAAGAGAGAGATGGCAGGCACCTTGGCAAACTCTCGGAAGAGGATGATCTAATCAACCTCATGAGGATGATGGCACTTTGCCCGAGACTTATGACCCAGAGACTGTGACGCAATTTG													
	2601	2610	2620	2630	2640	2650	2660	2670	2680	2690	2700	2710	2720	2730
seq	TGAATTTATCTCTCTGAGAGAGGACAGAGCTCTCAGGAGCTGATGGACCTTACTTGAAGATGAACCGGTTGGGCTCATCTGCTCTGCTAAGAGTGGCCGGAGTCCCTTTGTCATGACATG													
Consensus	TGAATTTATCTCTCTGAGAGAGGACAGAGCTCTCAGGAGCTGATGGACCTTACTTGAAGATGAACCGGTTGGGCTCATCTGCTCTGCTAAGAGTGGCCGGAGTCCCTTTGTCATGACATG													
	2731	2740	2750	2760	2770	2780	2790	2800	2810	2820	2830	2840	2850	2860
seq	TTCACTCAGAGCTTCTGCTGAGCTCTTCCACAGTTCAAATCAGATACGAGGCAAAATCACCATTACTTTCAAAACCTTGGCACAGCTCCCTGAATATTGAAGAGGATGGCTCTATTG													
Consensus	TTCACTCAGAGCTTCTGCTGAGCTCTTCCACAGTTCAAATCAGATACGAGGCAAAATCACCATTACTTTCAAAACCTTGGCACAGCTCCCTGAATATTGAAGAGGATGGCTCTATTG													
	2861	2870	2880	2890	2900	2910	2920	2930	2940	2950	2960	2970	2980	2990
seq	GGGATGGGCAAGTGGGCGATGATCTGATACAACTGTTTAGGCGCTCCGAATATGATGACGAGCAGTCAAGTGCTATGAGATGGAGATGCTTGAACACCTGAGCTATACCTCAAA													
Consensus	GGGATGGGCAAGTGGGCGATGATCTGATACAACTGTTTAGGCGCTCCGAATATGATGACGAGCAGTCAAGTGCTATGAGATGGAGATGCTTGAACACCTGAGCTATACCTCAAA													
	2991	3000	3010	3020	3030	3040	3050	3060	3070	3080	3090	3100	3110	3120
seq	ATACCTCCAGAGTTATGATGCCATATGCTATTAAGAACTCTGGTTTACCATGATCAAGAGAGACTTTAGGGGACTCTTTGGACATTGAGGACTCTCTGAAGAGCCAGATCATGAGGTT													
Consensus	ATACCTCCAGAGTTATGATGCCATATGCTATTAAGAACTCTGGGTTACCATGATCAAGAGAGACTTTAGGGGACTCTTTGGACATTGAGGACTCTCTGAAGAGCCAGATCATGAGGTT													

➤ Différence au niveau PROT :

☒	V(D)J recombination-activating protein 1 [Rattus norvegicus]	Rattus norvegicus	2168	2168	100%	0.0	99.90%	1040	NP_445920.1
☒	recombination activating gene 1 [Rattus norvegicus]	Rattus norvegicus	903	1760	82%	0.0	99.31%	1000	AAQ63060.1
☒	rag1 [Rattus norvegicus]	Rattus norvegicus	693	693	32%	0.0	100.00%	333	BAD38670.1

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq	HAYPLSTLRLSSAPDEIQPHIKFSEMKFLFRVRSFEKAPEEAQKEKDSSEGGKPCLEQSPVYLQKPGGQNSVLTQRALKLHPKFSKKFHYDGGKSSDKATHQARLRHFCRICGNHFKSDGHNRRYPYHG													
ref	HAYPLSTLRLSSAPDEIQPHIKFSEMKFLFRVRSFEKAPEEAQKEKDSSEGGKPCLEQSPVYLQKPGGQNSVLTQRALKLHPKFSKKFHYDGGKSSDKATHQARLRHFCRICGNHFKSDGHNRRYPYHG													
Consensus	HAYPLSTLRLSSAPDEIQPHIKFSEMKFLFRVRSFEKAPEEAQKEKDSSEGGKPCLEQSPVYLQKPGGQNSVLTQRALKLHPKFSKKFHYDGGKSSDKATHQARLRHFCRICGNHFKSDGHNRRYPYHG													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq	PYDAKQSLFRKKKEKRYTSMPLIARVFRIDVKSVDVSIHPTFECHNCUSIMHARKFGSAHSQVYCPNVTVEAHNPTPSCDICFTAHRGLKRRKHQPNVQLSKKLKTVLNHARRDRRKRTQARVSSKEVM													
ref	PYDAKQSLFRKKKEKRYTSMPLIARVFRIDVKSVDVSIHPTFECHNCUSIMHARKFGSAHSQVYCPNVTVEAHNPTPSCDICFTAHRGLKRRKHQPNVQLSKKLKTVLNHARRDRRKRTQARVSSKEVM													
Consensus	PYDAKQSLFRKKKEKRYTSMPLIARVFRIDVKSVDVSIHPTFECHNCUSIMHARKFGSAHSQVYCPNVTVEAHNPTPSCDICFTAHRGLKRRKHQPNVQLSKKLKTVLNHARRDRRKRTQARVSSKEVM													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq	KKISNCSKIHLSTKLLAVDFPAHFVKSISQICEHILADPVETTCCKILFCRICILRCLKVHGSYCPSCRYPCFPTDLQSPVKSFLSLNLSLVKCPAQECNEEVSLKYNHNVSSHKESKETLVHINKGG													
ref	KKISNCSKIHLSTKLLAVDFPAHFVKSISQICEHILADPVETTCCKILFCRICILRCLKVHGSYCPSCRYPCFPTDLQSPVKSFLSLNLSLVKCPAQECNEEVSLKYNHNVSSHKESKETLVHINKGG													
Consensus	KKISNCSKIHLSTKLLAVDFPAHFVKSISQICEHILADPVETTCCKILFCRICILRCLKVHGSYCPSCRYPCFPTDLQSPVKSFLSLNLSLVKCPAQECNEEVSLKYNHNVSSHKESKETLVHINKGG													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
seq	RPRQHLLSLTRRAQKHRLRELKIQVKEFADKEEGGVKSYCLTLFLALRARNEHRQADELAIHQGRGSGLQPAYCLAIRYNTFLSCSQYHKMYRTVKAITGRQIFQPLHALRNAEKaLLPGYHPFEMQ													
ref	RPRQHLLSLTRRAQKHRLRELKIQVKEFADKEEGGVKSYCLTLFLALRARNEHRQADELAIHQGRGSGLQPAYCLAIRYNTFLSCSQYHKMYRTVKAITGRQIFQPLHALRNAEKaLLPGYHPFEMQ													
Consensus	RPRQHLLSLTRRAQKHRLRELKIQVKEFADKEEGGVKSYCLTLFLALRARNEHRQADELAIHQGRGSGLQPAYCLAIRYNTFLSCSQYHKMYRTVKAITGRQIFQPLHALRNAEKaLLPGYHPFEMQ													
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
seq	PPLKNVSSRTDVGIDGLSGLASSVDEYYPVDTIAKRFYDSALYSALNOMEEDIDGHRSDQLDDYYSGPFTYVVKESCQDGMGVSEKHGSGPAPVPEKAVRFSFTVMHRTVEHGSQNVKIFEEPKNSEL													
ref	PPLKNVSSRTDVGIDGLSGLASSVDEYYPVDTIAKRFYDSALYSALNOMEEDIDGHRSDQLDDYYSGPFTYVVKESCQDGMGVSEKHGSGPAPVPEKAVRFSFTVMHRTVEHGSQNVKIFEEPKNSEL													
Consensus	PPLKNVSSRTDVGIDGLSGLASSVDEYYPVDTIAKRFYDSALYSALNOMEEDIDGHRSDQLDDYYSGPFTYVVKESCQDGMGVSEKHGSGPAPVPEKAVRFSFTVMHRTVEHGSQNVKIFEEPKNSEL													
	651	660	670	680	690	700	710	720	730	740	750	760	770	780
seq	CCPKLCLHADSDEHETLTAILSPLIAERERAMKSELLENGGIPRTFKFIFRGTYDEKLRYREVEGLEASGSVYICTLCOATRLERASQNLVHHSITRSHAENLQRYEVHRSNPNYESVEELDRVKGVS													
ref	CCPKLCLHADSDEHETLTAILSPLIAERERAMKSELLENGGIPRTFKFIFRGTYDEKLRYREVEGLEASGSVYICTLCOATRLERASQNLVHHSITRSHAENLQRYEVHRSNPNYESVEELDRVKGVS													
Consensus	CCPKLCLHADSDEHETLTAILSPLIAERERAMKSELLENGGIPRTFKFIFRGTYDEKLRYREVEGLEASGSVYICTLCOATRLERASQNLVHHSITRSHAENLQRYEVHRSNPNYESVEELDRVKGVS													
	781	790	800	810	820	830	840	850	860	870	880	890	900	910
seq	AKPFIETVPSIDALHCDIGNAREFYKIFQLEIGEYVKNPNASKEERKRQATLDKHLRKRHNLKPIMRNNGNFARKLMTQETVDAYCELIPSEERHEALRELMDLYLKMKPVMRSSCPAKECPESLCQYS													
ref	AKPFIETVPSIDALHCDIGNAREFYKIFQLEIGEYVKNPNASKEERKRQATLDKHLRKRHNLKPIMRNNGNFARKLMTQETVDAYCELIPSEERHEALRELMDLYLKMKPVMRSSCPAKECPESLCQYS													
Consensus	AKPFIETVPSIDALHCDIGNAREFYKIFQLEIGEYVKNPNASKEERKRQATLDKHLRKRHNLKPIMRNNGNFARKLMTQETVDAYCELIPSEERHEALRELMDLYLKMKPVMRSSCPAKECPESLCQYS													
	911	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040
seq	FNSQRFaELLSTKFKYRYEGKITNYFHKTLAHYPEIIERDGSIGAWASEGNEGSKLFRFRKMNARQSKCYEMEDVLKHHALYTSKYLQKFHNAHNAKNSGFTHNSKETLGOSLDIEDSLESQDSHEF													
ref	FNSQRFaELLSTKFKYRYEGKITNYFHKTLAHYPEIIERDGSIGAWASEGNEGSKLFRFRKMNARQSKCYEMEDVLKHHALYTSKYLQKFHNAHNAKNSGFTHNSKETLGOSLDIEDSLESQDSHEF													
Consensus	FNSQRFaELLSTKFKYRYEGKITNYFHKTLAHYPEIIERDGSIGAWASEGNEGSKLFRFRKMNARQSKCYEMEDVLKHHALYTSKYLQKFHNAHNAKNSGFTHNSKETLGOSLDIEDSLESQDSHEF													

Identique à rate : en 509 A>V

Amorces séquençage interne :

Rag1_int_590Fwd : ggaatgtgaccgtggagtgg

Rag1_int_1107Fwd : taaccacat gtctcaagcc

Rag1_int_2639_Rev : gtaaaggtccatcagctccc

Rag1_int_2116Rev : gacaagtttctgctcatatcc