

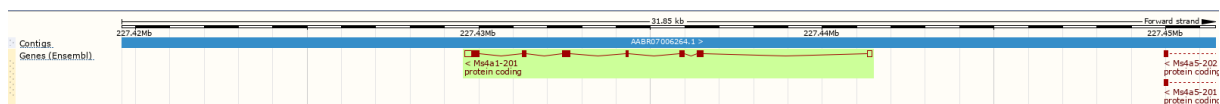
Rattus norvegicus membrane spanning 4-domains A1 (Ms4a1), mRNA = B-lymphocyte antigen CD20

- **Référence NCBI :** NM_001107578 [ENSRNOT00000028433.7](#)
- **Taille 894 NT**
- **Séquences protéique / NT :**

MTTPRNSVSGPFPTEPTKGPLAMQPAQKVIPRRPSSLVGPTQSF
FMRESKALGAVQIMNGLFHISLGGLLMIPTGVFAPICLSVWYPLWGGIMYIISGSLA
AAAEKTSRKSLATKVIMSSLSLFAAISGIILSIMDILNITVSHFLKMERLELIKTPKL
YVDIYNCEPSNSSEKNSPSTQYCNSVQSVFLGILSVMLISAFFQKLVTAGVVENEWKR
VCSRPKSNVLLSAGEKKEQTIKMKEEIIELSGVSSQPKNEEEIEIIPVQEEEEEEAE
INFPAPPOEQESLPVENEISP

at gacaacaccc agaaattcag tgagtggacc tttcccaaca

61	gagcctacaa	aaggaccctt	cgccatgcaa	cctgctcaaa	aagtaatccc	cagaagacca
121	tcttcaactgg	tgggccccac	acaaagcttc	ttcatgaggg	aatcaaaggc	tttgggggct
181	gtccagatca	tgaatggcct	cttccacatt	tccctggggg	gactgctgat	gatccccaca
241	ggagtttttg	cacccatctg	tttgagtgtg	tggtaacctc	tgtggggagg	cattatgtac
301	atcatttcag	gatcactcct	ggcagctgca	gcagagaaaa	cctccaggaa	gagtttggca
361	acgaaagtga	taatgagctc	tctaagcctc	tttgctgcca	tttctggaat	aattctttca
421	atcatggaca	tacttaacat	tacagtttct	catttttttaa	aaatggagag	actggaactg
481	attaaaaactc	ccaagctata	tgttgatata	tacaactgtg	agccatccaa	ttcctcagag
541	aaaaaactccc	catctacaca	gtactgtaac	agcgtgcagt	ctgtgttctt	gggcattctg
601	tcggtgatgc	tgatctctgc	cttcttccag	aagctcgtga	cagccgggtg	tgtagagaat
661	gagtggaaaa	gagtgtgctc	caggcccaaa	tctaattgtg	ttctgctgtc	agctggagaa
721	aaaaaaagagc	agacaattaa	aatgaaaagaa	gaaatcattg	agctaagtgg	agtatcttcc
781	caacaaaaga	atgaaagagga	aattgaaatt	attccagtc	aggaggaaga	agaagaagaa
841	gcagaaaataa	acttcccagc	acctcccaa	gagcaggaat	ccttgccagt	ggaaaatgag
901	atctctcctt	aa				



- Amorces synthétisées :

Ms4a1 Ascl Fwd

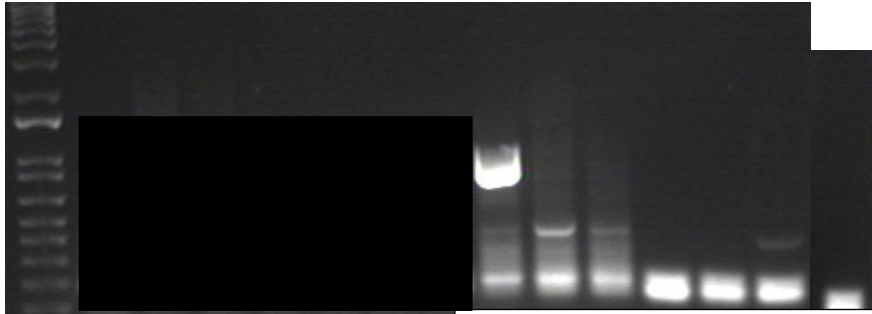
tataGGCGGCCa at gacaacaccc agaaattcag tg

Ms4a1_NotI_Rev

ttaaGCGCCGCa ttaaggagagatctcattttccac

- Expériences :

- PCR 08/07 : sur **les 7 conditions** cycle Q5-TM 56°C-Enhancer 5- 2min 30 d'élongation



Bande RATE

Rate DiT0 DiT24 DiT48 SP CTX Eau

- 21/07 : Extraction sur gel et purification bande rate :
- 22/07 : Réaction Zéro Blunt TOPO
- 24/07 Miniprep

- [Sep/Oct : soucis clonage : Vecteur ? PCR mal digérée ?](#)
- [Essais miniprep 16/09 09/10](#)
- [19/10 : redigestion de la PCR](#)
- [20/10 transformation](#)

Rate

[2/10 mini prep FlagBirA_CD20 rate OK à séquencer](#)

- [28/10 envoi au séquençage](#)

- **Sequencage : clone FlagBirA CD20 rate A**

- **B3Fwd Séquencage**

ATGACAACACCCAGAAATTCAGTGAGTGGACCTTTCCCAACAGAGCCTACAAAAGGACCCCTCGCCATGCAAC
CTGCTCAAAAAGTAATCCCCAGAAGACCATCTTCACTGGTGGGCCCCACACAAAGCTTCTTCATGAGGGAATCA
AAGGCTTTGGGGGCTGTCCAGATCATGAATGGCCTCTTCCACATTTCCCTGGGGGGACTGCTGATGATCCCCAC
AGGAGTTTTTGCACCCATCTGTTTGAGTGTATGGTACCCTCTGTGGGGAGGCATTATGTACATCATTTTCAGGAT
CACTCCTGGCAGCTGCAGCAGAGAAAACCTCCAGGAAGAGTTTGGTCAAAGCGAAAAGTGATAATGAGCTCTCT
AAGCCTCTTTGCTGCCATTTCTGGAATAATTCTTTCAATCATGGACATACTTAACATTACAGTTTCTCATTTTTTA
AAAATGGAGAGACTGGAAGTATTAAAACTCCCAAGCTATATGTTGATATCTACAAGTGTGAGCCATCCAATTC
CTCAGAGAAAAACTCCCCATCTACACAGTACTGTAACAGCGTGCAGTCTGTGTTCTTGGGCATTCTGTGCGGTGA
TGCTGATCTCTGCCTTCTTCCAGAGCTCGTGACAGCCGGTGTGTAGAGAATGAGTGGAAAAGAGTGTGCTC
CAGGCCCCAATCTAATGTGGTTCTGCTGTCAGCTGGAGAAAAAAAAGANCANACAATTAATAATGAAAGAAGA
AATCATTGAGCTAAGTGGAGTATCTTCCCANCCAAAGAATGAANAGGAAATTGAAATTATTCCNGTGCNGNA
GGAAGAA

- **BGHRev Séquencage**

ATGACAACACCCAGAAATTCAGTGAGTGGACCTTTCCCAACAGAGCNTACAAAAGGACCCCTCGCCATGCAact
GCTCAAAAAGTAATCCCCAGAAGACCATCTTCACTGGTGGGCCCCACACAAAGcTTCTTCATGAGGGAATCAAA
GGCTTTGGGGGCTGTCCAGATCATGAATGGCcTCTTCCACATTTCCCTGGGGGGACTGCTGATGATCCCCACAG
GAGTTTTTGCACCCATCTGTTTGAGTGTATGGTACCCTCTGTGGGGAGGCATTATGTACATCATTTTCAGGATCA
CTCCTGGCAGCTGCAGCAGAGAAAACCTCCAGGAAGAGTTTGGTCAAAGCGAAAAGTGATAATGAGCTCTCTAA
GCCTCTTTGCTGCCATTTCTGGAATAATTCTTTCAATCATGGACATACTTAACATTACAGTTTCTCATTTTTTAA
AATGGAGAGACTGGAAGTATTAAAACTCCCAAGCTATATGTTGATATCTACAAGTGTGAGCCATCCAATTCCT
CAGAGAAAAACTCCCCATCTACACAGTACTGTAACAGCGTGCAGTCTGTGTTCTTGGGCATTCTGTGCGGTGATG
CTGATCTCTGCCTTCTTCCAGAAGCTCGTGACAGCCGGTGTGTAGAGAATGAGTGGAAAAGAGTGTGCTCCA
GGCCCAATCTAATGTGGTTCTGCTGTCAGCTGGAGAAAAAAAAGAGCAGACAATTAATAATGAAAGAAGAAA
TCATTGAGCTAAGTGGAGTATCTTCCCAACCAAAGAATGAAGAGGAAATTGAAATTATTCCAGTGCAGGAGGA
AGAAGAAGAAGAAGCAGAAATAAACTTCCCAGCACCTCCCCAAGAGCAGGAATCCTTGCCAGTGGAAAATGA
GATCTCTCCTTAA

- **Synthèse séquencage 897NT**

ATGACAACACCCAGAAATTCAGTGAGTGGACCTTTCCCAACAGAGCCTACAAAAGGACCC	60
CTCGCCATGCAACCTGCTCAAAAAGTAATCCCCAGAAGACCATCTTCACTGGTGGGCCCC	120
ACACAAAGCTTCTTCATGAGGGAATCAAAGGCTTTGGGGGCTGTCCAGATCATGAATGGC	180
CTCTTCCACATTTCCCTGGGGGGACTGCTGATGATCCCCACAGGAGTTTTTGCACCCATC	240
TGTTTGAGTGTATGGTACCCTCTGTGGGGAGGCATTATGTACATCATTTTCAGGATCACTC	300
CTGGCAGCTGCAGCAGAGAAAACCTCCAGGAAGAGTTTGGTCAAAGCGAAAAGTGATAATG	360
AGCTCTCTAAGCCTCTTTGCTGCCATTTCTGGAATAATTCTTTCAATCATGGACATACTT	420
AACATTACAGTTTCTCATTTTTTAAAAATGGAGAGACTGGAAGTATTAAAACTCCCAAG	480
CTATATGTTGATATCTACAAGTGTGAGCCATCCAATTCCTCAGAGAAAAACTCCCCATCT	540
ACACAGTACTGTAACAGCGTGCAGTCTGTGTTCTTGGGCATTCTGTGCGGTGATGCTGATC	600
TCTGCCTTCTTCCAGAGCTCGTGACAGCCGGTGTGTAGAGAATGAGTGGAAAAGAGTG	660
TGCTCCAGGCCCCAATCTAATGTGGTTCTGCTGTCAGCTGGAGAAAAAAAAGAGCAGACA	720
ATTAATAATGAAAGAAGAAATCATTGAGCTAAGTGGAGTATCTTCCCAACCAAAGAATGAA	780
GAGGAAATTGAAATTATTCCAGTGCAGGAGGAAGAAGAAGAAGCAGAAATAAACTTC	837
CCAGCACCTCCCCAAGAGCAGGAATCCTTGCCAGTGGAAAATGAGATCTCTCCTTAA	897

MTTPRNSVSGPFPTEPTKGPLAMQPAQKVIPRRPSSLVGPTQSFFMRESKALGAVQIMNGLFHISLGGLLMIPTGV
FAPICLSVWYPLWGGIMYIISGSLAAAAEKTSRKSLVKAKVIMSSLSLFAAISGIILSIMDILNITVSHFLKMERLELIKTP

KLYVDIYNCEPSNSSEKNSPSTQYCNSVQSVFLGILSVMLISAFFQKLVTAGVVENEWKRVCSRPKSNVVLLSAGEKK
EQTIKMKEIIELSGVSSQPKNEEEIEIPVQEEEEEEAEINFPAPPQEQESLPVENEISP-

➤ Blast contre banque rat :

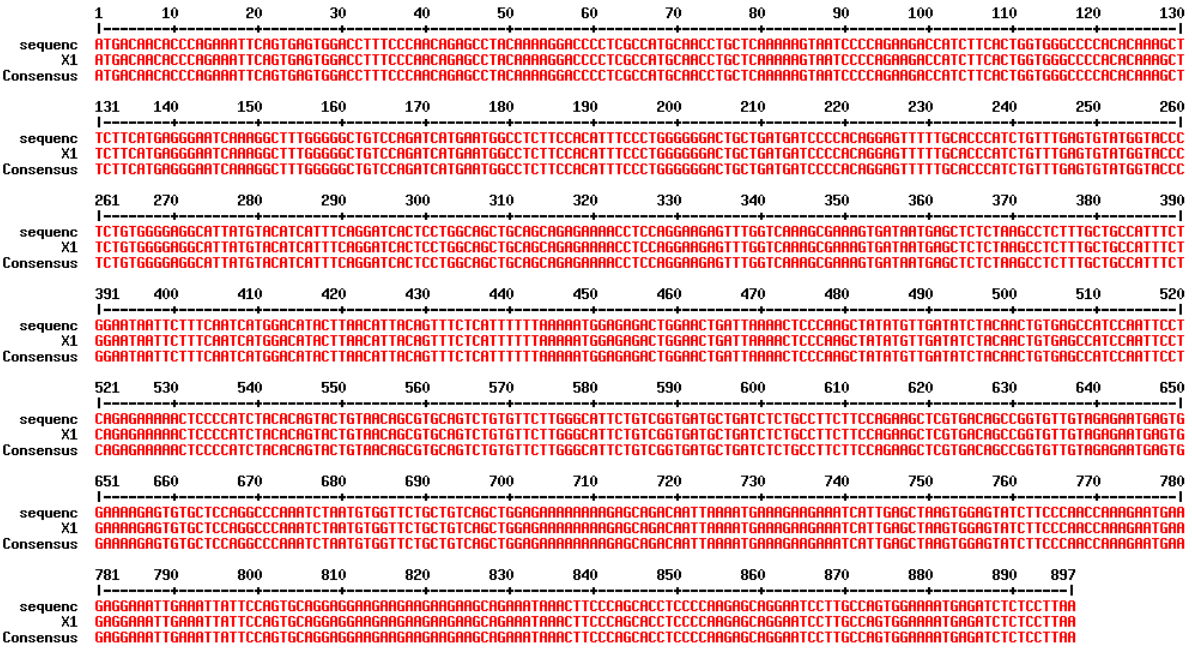
✓	PREDICTED: Rattus norvegicus membrane spanning 4-domains A1 (Ms4a1) , transcript variant X1 , mRNA	1657	1657	100%	0.0	100.00%	XM_006231089.3
✓	Rattus norvegicus membrane spanning 4-domains A1 (Ms4a1) , mRNA	1637	1637	100%	0.0	99.67%	NM_001107578.1
✓	Rattus norvegicus TL0AEA4YK03 mRNA sequence	1589	1589	100%	0.0	98.66%	FQ225563.1
✓	Rattus norvegicus TL0AEA2YD20 mRNA sequence	1554	1554	100%	0.0	97.89%	FQ226425.1
✓	Rattus norvegicus TL0AEA5YJ12 mRNA sequence	1552	1552	94%	0.0	99.65%	FQ235337.1
✓	Rattus norvegicus cDNA clone IMAGE:7387276	1066	1662	100%	0.0	100.00%	BC098745.1
✓	Rattus norvegicus TL0AEA64YD18 mRNA sequence	243	243	14%	3e-62	99.25%	FQ232846.1

➤ Différence au niveau NT :

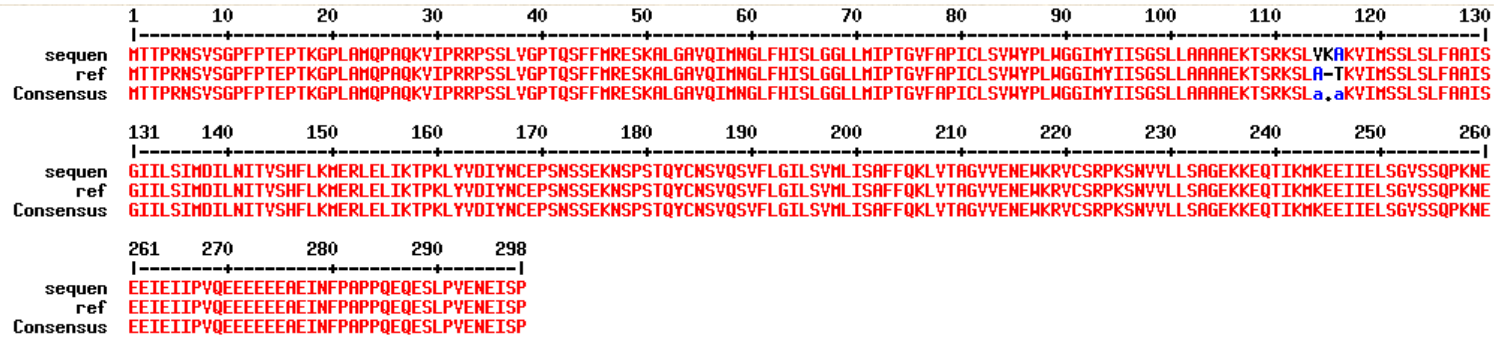
	1	10	20	30	40	50	60	70	80	90	100	110	120	130
sequenc	ATGACACACCCAGAAATTCAGTGAGTGGACCTTTCCACACAGAGCCTACAAAGGACCCCTCGCCATGCACCTGCTCAAAAGTATCCCCAGAGACCATCTTCAC													
CDS	ATGACACACCCAGAAATTCAGTGAGTGGACCTTTCCACACAGAGCCTACAAAGGACCCCTCGCCATGCACCTGCTCAAAAGTATCCCCAGAGACCATCTTCAC													
Consensus	ATGACACACCCAGAAATTCAGTGAGTGGACCTTTCCACACAGAGCCTACAAAGGACCCCTCGCCATGCACCTGCTCAAAAGTATCCCCAGAGACCATCTTCAC													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
sequenc	TCTTCATGAGGGAATCAAGGCTTTGGGGCTGTCAGATCATGAATGGCTCTTCCACATTTCCCTGGGGGACTGCTGATGATCCCAACAGAGTTTTCACCCATCTGTTT													
CDS	TCTTCATGAGGGAATCAAGGCTTTGGGGCTGTCAGATCATGAATGGCTCTTCCACATTTCCCTGGGGGACTGCTGATGATCCCAACAGAGTTTTCACCCATCTGTTT													
Consensus	TCTTCATGAGGGAATCAAGGCTTTGGGGCTGTCAGATCATGAATGGCTCTTCCACATTTCCCTGGGGGACTGCTGATGATCCCAACAGAGTTTTCACCCATCTGTTT													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
sequenc	TCTGTGGGGAGGCATTATGTACATCATTTTCAGGATCACTCTGGCAGCTGCAGCAGAGAAACCTCCAGGAGAGTTTGGTCAAGAGCGAAGTGATATGAGCTCTT													
CDS	TCTGTGGGGAGGCATTATGTACATCATTTTCAGGATCACTCTGGCAGCTGCAGCAGAGAAACCTCCAGGAGAGTTTGGTCAAGAGCGAAGTGATATGAGCTCTT													
Consensus	TCTGTGGGGAGGCATTATGTACATCATTTTCAGGATCACTCTGGCAGCTGCAGCAGAGAAACCTCCAGGAGAGTTTGGTCAAGAGCGAAGTGATATGAGCTCTT													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
sequenc	GGATAATCTTTTCATCATGGACATCTTAACATTACAGTTTCTCATTTTAAATAATGGAGAGCTGGAACGATTAAACCTCCAGCTATATGTTGATATCTACACTGTGAGCCATCCATTCT													
CDS	GGATAATCTTTTCATCATGGACATCTTAACATTACAGTTTCTCATTTTAAATAATGGAGAGCTGGAACGATTAAACCTCCAGCTATATGTTGATATCTACACTGTGAGCCATCCATTCT													
Consensus	GGATAATCTTTTCATCATGGACATCTTAACATTACAGTTTCTCATTTTAAATAATGGAGAGCTGGAACGATTAAACCTCCAGCTATATGTTGATATCTACACTGTGAGCCATCCATTCT													
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
sequenc	CAGAGAAAACCTCCCATCTACACAGTACTGTACAGCTGCAGTCTGTGTTCTTGGGCATTCTGTCGGTGATGCTGATCTCTGCCCTCTCCAGAGCTCGTGACAGCCGGTGTGTAGAGATGAGTG													
CDS	CAGAGAAAACCTCCCATCTACACAGTACTGTACAGCTGCAGTCTGTGTTCTTGGGCATTCTGTCGGTGATGCTGATCTCTGCCCTCTCCAGAGCTCGTGACAGCCGGTGTGTAGAGATGAGTG													
Consensus	CAGAGAAAACCTCCCATCTACACAGTACTGTACAGCTGCAGTCTGTGTTCTTGGGCATTCTGTCGGTGATGCTGATCTCTGCCCTCTCCAGAGCTCGTGACAGCCGGTGTGTAGAGATGAGTG													
	651	660	670	680	690	700	710	720	730	740	750	760	770	780
sequenc	GAAAGAGTGTGCTCCAGGCCAATCTAATGTGTTCTGCTGTCAGCTGGAGAAAAAAGAGCAGACAAATAAATGAAGAGAGAAATCATTGAGCTAAGTGGAGTATCTCCACCAAGAAATGAA													
CDS	GAAAGAGTGTGCTCCAGGCCAATCTAATGTGTTCTGCTGTCAGCTGGAGAAAAAAGAGCAGACAAATAAATGAAGAGAGAAATCATTGAGCTAAGTGGAGTATCTCCACCAAGAAATGAA													
Consensus	GAAAGAGTGTGCTCCAGGCCAATCTAATGTGTTCTGCTGTCAGCTGGAGAAAAAAGAGCAGACAAATAAATGAAGAGAGAAATCATTGAGCTAAGTGGAGTATCTCCACCAAGAAATGAA													
	781	790	800	810	820	830	840	850	860	870	880	890	897	
sequenc	GAGGAATTTGAATTTATTCAGTGCAGGAGGAGAGAGAGAGAGCAGAAATAAATCTCCAGACCTCCCAAGAGCAGGAATCCTTGCCAGTGGAAATGAGATCTCTCCTTAA													
CDS	GAGGAATTTGAATTTATTCAGTGCAGGAGGAGAGAGAGAGAGCAGAAATAAATCTCCAGACCTCCCAAGAGCAGGAATCCTTGCCAGTGGAAATGAGATCTCTCCTTAA													
Consensus	GAGGAATTTGAATTTATTCAGTGCAGGAGGAGAGAGAGAGAGCAGAAATAAATCTCCAGACCTCCCAAGAGCAGGAATCCTTGCCAGTGGAAATGAGATCTCTCCTTAA													

Il y a 3 NT en plus : 341, 344 et 345

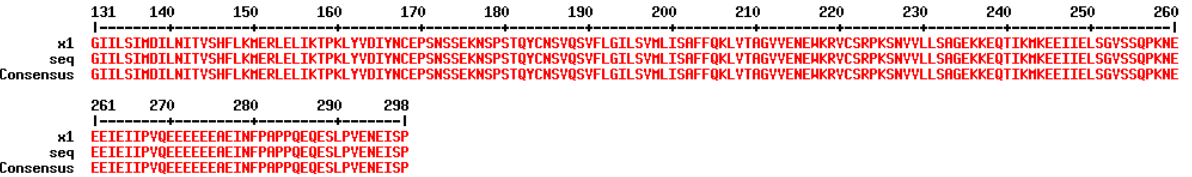
100% avec la forme X1 XM_006231089.3



➤ Différence au niveau PROT :



	Score	Score	Cover	value	ident	
PREDICTED: B-lymphocyte antigen CD20 isoform X1 [Rattus norvegicus]	597	597	100%	0.0	100.00%	XP_006231151.1
B-lymphocyte antigen CD20 [Rattus norvegicus]	587	587	100%	0.0	98.99%	NP_001101048.1



Prot X1 XP_006231151 100% d'homologie

FlagBirA CD20 rate clone A OK : correspond à l'isoforme X1
(3NT en plus par rapport au CDS ref)

- **Sequencage : clone FlagBirA CD20 rate C 25/11**

- **B3Fwd Séquencage 869NT**

ATGACAACACCCAGAAATTCAGTGAGTGGACCTTTCCCAACAGAGCCTACAAAAGGACCCCTCGCCA
TGCAACCTGCTCAAAAAGTAATCCCCAGAAGACCATCTTCACTGGTGGGCCCCACACAAAGCTTCTTC
ATGAGGGAATCAAAGGCTTTGGGGGCTGTCCAGATCATGAATGGCCTCTTCCACATTTCCCTGGGGG
GACTGCTGATGATCCCCACAGGAGTTTTTGCACCCATCTGTTTGAGTGTATGGTACCCTCTGTGGGGA
GGCATTATGTACATCATTTTCAGGATCACTCCTGGCAGCTGCAGCAGAGAAAACTCCAGGAAGAGTT
TGGTCAAAGCGAAAGTGATAATGAGCTCTCTAAGCCTCTTTGCTGCCATTTCTGGAATAATTCTTTCA
ATCATGGACATACTTAACATTACAGTTTCTCATTTTTTAAAAATGGAGAGACTGGAAGTATTAAAC
TCCCAAGCTATATGTTGATATCTACAACTGTGAGCCATCCAATTCCTCAGAGAAAACTCCCCATCTAC
ACAGTACTGTAACAGCGTGCAGTCTGTGTTCTTGGGCATTCTGTGCGTGATGCTGATCTCTGCCTTCT
TCCAGAAGCTCGTGACAGCCGGTGTGTAGAGAANGAGTGGAAAAGAGTGTGCTCCAGGCCCAAAT
CTAATGTGGTTCTGCTGTCAGCTGGAGAAAAAAGAGCANACAATTAATGAAANANGAAATCA
TTGAGCTAAGTGGAGTATCTTCCCNACCAAAGAATGAAGAGGAAATTGAAATTATTCCAGTGCAGGA
GGAAGAAGAANAANAAGCANANTAACTTCCANCNNCTNCCNNAGANCAGGANTCCTTG

- **BGHRev Séquencage 897NT**

NTGACAACACCCAGAAATTCAGTGAGNGGNCNTTTCCCAACAGANCNTACAAAAGGACCCCTCGCCATGCAN
CCTGCTCAAAAAGTAATCCCCAGAAGACCATCTTCACTGGTGGNCCCCACACAAAGNTTCTTCATGAGGGAAT
CAAAGGCTTTGGGGGCTGTCCAGATCATGAATGgCCTCTTCCACATTTCCctGGGGGGACTGCTGATGATCCCC
ACAGGAGTTTTTGCACCCATCTGTTTGAGTGTATGGTACCCTCTGTGGGGAGGCATTATGTACATCATTTTCAGG
ATCACTCCTGGCAGCTGCAGCAGAGAAAACTCCAGGAAGAGTTTGGTCAAAGCGAAAAGTGATAATGAGCTCT
CTAAGCCTCTTTGCTGCCATTTCTGGAATAATTCTTTCAATCATGGACATACTTAACATTACAGTTTCTCATTTTTT
AAAAATGGAGAGACTGGAAGTATTAAAACTCCCAAGCTATATGTTGATATCTACAACTGTGAGCCATCCAATT
CCTCAGAGAAAACTCCCCATCTACACAGTACTGTAACAGCGTGCAGTCTGTGTTCTTGGGCATTCTGTGCGTG
ATGCTGATCTCTGCCTTCTTCCAGAAGCTCGTGACAGCCGGTGTGTAGAGAATGAGTGGAAAAGAGTGTGCT
CCAGGCCCAAATCTAATGTGGTTCTGCTGTCAGCTGGAGAAAAAAGAGCAGACAATTAATGAAAGAAG
AAATCATTGAGCTAAGTGGAGTATCTTCCCAACCAAAGAATGAAGAGGAAATTGAAATTATTCCAGTGCAGGA
GGAAGAAGAAGAAGAAGCAGAAATAAACTTCCAGCACCTCCCCAAGAGCAGGAATCCTTGCCAGTGGAAAA
TGAGATCTCTCCTAA

- **Synthèse séquencage 897NT**

ATGACAACACCCAGAAATTCAGTGAGTGGACCTTTCCCAACAGAGCCTACAAAAGGACCC	60
CTCGCCATGCAACCTGCTCAAAAAGTAATCCCCAGAAGACCATCTTCACTGGTGGGCCCC	120
ACACAAAGCTTCTTCATGAGGGAATCAAAGGCTTTGGGGGCTGTCCAGATCATGAATGGC	180
CTCTTCCACATTTCCCTGGGGGACTGCTGATGATCCCCACAGGAGTTTTTGCACCCATC	240
TGTTTGAGTGTATGGTACCCTCTGTGGGGAGGCATTATGTACATCATTTTCAGGATCACTC	300
CTGGCAGCTGCAGCAGAGAAAACTCCAGGAAGAGTTTGGTCAAAGCGAAAAGTGATAATG	360
AGCTCTCTAAGCCTCTTTGCTGCCATTTCTGGAATAATTCTTTCAATCATGGACATACTT	420
AACATTACAGTTTCTCATTTTTTAAAAATGGAGAGACTGGAAGTATTAAAACTCCCAAG	480
CTATATGTTGATATCTACAACTGTGAGCCATCCAATTCCTCAGAGAAAACTCCCCATCT	540
ACACAGTACTGTAACAGCGTGCAGTCTGTGTTCTTGGGCATTCTGTGCGTGATGCTGATC	600
TCTGCCTTCTTCCAGAAGCTCGTGACAGCCGGTGTGTAGAGAATGAGTGGAAAAGAGTG	660
TGCTCCAGGCCCAAATCTAATGTGGTTCTGCTGTCAGCTGGAGAAAAAAGAGCAGACA	720

```

ATTAAATGAAAGAAGAAATCATTGAGCTAAGTGGAGTATCTTCCCAACCAAGAATGAA      780
GAGGAAATTGAAATTATTCCAGTGCAGGAGGAAGAAGAAGAAGCAGAAATAAACTTC      840
CCAGCACCTCCCCAAGAGCAGGAATCCTTGCCAGTGGAAAATGAGATCTCTCCTTAA      897

```

➤ Blast contre banque rat :

➤ Différence au niveau NT :

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq	-----													
cds	-----													
Consensus	-----													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq	-----													
cds	-----													
Consensus	-----													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq	-----													
cds	-----													
Consensus	-----													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
seq	-----													
cds	-----													
Consensus	-----													
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
seq	-----													
cds	-----													
Consensus	-----													
	651	660	670	680	690	700	710	720	730	740	750	760	770	780
seq	-----													
cds	-----													
Consensus	-----													
	781	790	800	810	820	830	840	850	860	870	880	890	897	
seq	-----													
cds	-----													
Consensus	-----													

FlagBirA CD20 rate clone C idem que clone A

- **Sequencage : clone FlagBirA CD20 rate D 25/11**

- **B3Fwd Séquencage 845NT**

ATGACAACACCCAGAAATTCAGTGAGTGGACCTTTCCCAACAGAGCCTACAAAAGGACCCCTCGCCATGCAAC
CTGCTCAAAAAGTAATCCCCAGAAGACCATCTTCACTGGTGGGCCCCACACAAAGCTTCTTCATGAGGGAATCA
AAGGCTTTGGGGGCTGTCCAGATCATGAATGGCCTCTTCCACATTTCCCTGGGGGGACTGCTGATGATCCCCAC
AGGAGTTTTTGCACCCATCTGTTTGAGTGTATGGTACCCTCTGTGGGGAGGCATTATGTACATCATTTTCAGGAT
CACTCCTGGCAGCTGCAGCAGAGAAAACCTCCAGGAAGAGTTTGGTCAAAGCGAAAAGTGATAATGAGCTCTCT
AAGCCTCTTTGCTGCCATTTCTGGAATAATTCTTTCAATCATGGACATACTTAACATTACAGTTTCTCATTTTTTA
AAAATGGAGAGACTGGAAGTATTAAAACTCCCAAGCTATATGTTGATATCTACAACTGTGAGCCATCCAATTC
CTCAGAGAAAAACTCCCCATCTACACAGTACTGTAACAGCGTGCAGTCTGTGTTCTTGGGCATTCTGTCGGTGA
TGCTGATCTCTGCCTTCTTCCAGAAGCTCGTGACAGCCGGTGTGTAGAGAATGAGTGGAAAAGAGTGTGCTC
CAGGCCNAATCTAATGTGGTTCTGCTGTCAGCTGGAGAAAAAAGAGCAGACAATTAATAAGAAAGA
AATCATTGAGCTAAGTGGAGTATCTCCCNACCNAAGAATGAAGAGGAAATTGAAATTATTCCNGTGCNGNN
GGAAGAAGAAGAAGAACNNAATAAACTTCCAGCA

- **BGHRev Séquencage 897NT**

ANGACANCNCCCAGAAATTCAGTGAGTGGNCCTTTCCCAACAGANCNTACAAAAGGACCCCTCNCCATGCAN
CNTGCTCAAAAAGTAATCCCCAGAAGACCATCTTCACTGGTGGNCCCCACACAAAGCTTNTTCATGAGGGAAT
CAAAGGCTTTGGGGGCTGTCCAGATCATGAATGGCCTCTTCCACATTTCCcTGGGGGGACTGCTGATGATCCCC
ACAGGAGTTTTTGCACCCATCTGTTTGAGTGTATGGTACCCTCTGTGGGGAGGCATTATGTACATCATTTTCAGG
ATCACTCCTGGCAGCTGCAGCAGAGAAAACCTCCAGGAAGAGTTTGGTCAAAGCGAAAAGTGATAATGAGCTCT
CTAAGCCTCTTTGCTGCCATTTCTGGAATAATTCTTTCAATCATGGACATACTTAACATTACAGTTTCTCATTTTTT
AAAAATGGAGAGACTGGAAGTATTAAAACTCCCAAGCTATATGTTGATATCTACAACTGTGAGCCATCCAATT
CCTCAGAGAAAAACTCCCCATCTACACAGTACTGTAACAGCGTGCAGTCTGTGTTCTTGGGCATTCTGTCGGTG
ATGCTGATCTCTGCCTTCTTCCAGAAGCTCGTGACAGCCGGTGTGTAGAGAATGAGTGGAAAAGAGTGTGCT
CCAGGCCCAAATCTAATGTGGTTCTGCTGTCAGCTGGAGAAAAAAGAGCAGACAATTAATAAGAAAG
AAATCATTGAGCTAAGTGGAGTATCTTCCCAACCAAGAATGAAGAGGAAATTGAAATTATTCCAGTGCAGGA
GGAAGAAGAAGAAGAGCAGAAATAAACTTCCAGCACCTCCCCAAGAGCAGGAATCCTTGCCAGTGGAAAA
TGAGaTCTCTCTTAA

- **Synthèse séquencage 897NT**

ATGACAACACCCAGAAATTCAGTGAGTGGACCTTTCCCAACAGAGCCTACAAAAGGACCC	60
CTCGCCATGCAACCTGCTCAAAAAGTAATCCCCAGAAGACCATCTTCACTGGTGGGCCCC	120
ACACAAAGCTTCTTCATGAGGGAATCAAAGGCTTTGGGGGCTGTCCAGATCATGAATGGC	180
CTCTTCCACATTTCCCTGGGGGGACTGCTGATGATCCCCACAGGAGTTTTTGCACCCATC	240
TGTTTGAGTGTATGGTACCCTCTGTGGGGAGGCATTATGTACATCATTTTCAGGATCACTC	300
CTGGCAGCTGCAGCAGAGAAAACCTCCAGGAAGAGTTTGGTCAAAGCGAAAAGTGATAATG	360
AGCTCTCTAAGCCTCTTTGCTGCCATTTCTGGAATAATTCTTTCAATCATGGACATACTT	420
AACATTACAGTTTCTCATTTTTTAAAAATGGAGAGACTGGAAGTATTAAAACTCCCAAG	480
CTATATGTTGATATCTACAAGTGTGAGCCATCCAATTCCCTCAGAGAAAAACTCCCCATCT	540
ACACAGTACTGTAACAGCGTGCAGTCTGTGTTCTTGGGCATTCTGTCGGTGATGCTGATC	600
TCTGCCTTCTTCCAGAAGCTCGTGACAGCCGGTGTGTAGAGAATGAGTGGAAAAGAGTG	660
TGCTCCAGGCCCAAATCTAATGTGGTTCTGCTGTCAGCTGGAGAAAAAAGAGCAGACA	720
ATTAAAAATGAAAGAAGAAATCATTGAGCTAAGTGGAGTATCTTCCCAACCAAGAATGAA	780
GAGGAAATTGAAATTATTCCAGTGCAGGAGGAAGAAGAAGAAGCAGAAATAAACTTC	840
CCAGCACCTCCCCAAGAGCAGGAATCCTTGCCAGTGGAAAATGAGaTCTCTCTCTTAA	897

FlagBirA CD20 rate clone D idem que clone A et C