

13)Xrcc5 (Ku80)

Rattus norvegicus X-ray repair cross complementing 5 (Xrcc5), mRNA

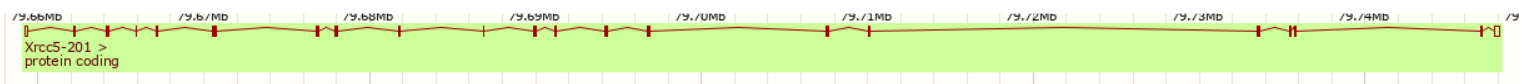
Xrcc5 Ku80 X-ray repair cross complementation (double-strand-break rejoining; Ku autoantigen, 80kD);X-ray repair complementing defective repair in Chinese hamster cells 5

- **Référence NCBI :** NM_177419

- **Taille 2199 NT**

- **Séquence NT :**

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 121 cagctgttgt gctgtgtatg gatgtggggg ttgccatggg taactccttt cctggtgaag
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 301 ttgctggcaa ggaccagtat cagaacatca cagtgcacag gcacctgatg ctaccagatt
 361 ttgatttgct ggaagacatc ggaaacaaaa tccaaccaag ttctcaacaa gccgacttcc
 421 tggacgccct gattgtgtgc atggatttga ttcagcgtga aaccatagga aagaagtgtg
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- Séquence protéique

NP_803154

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- Amorces synthétisées :

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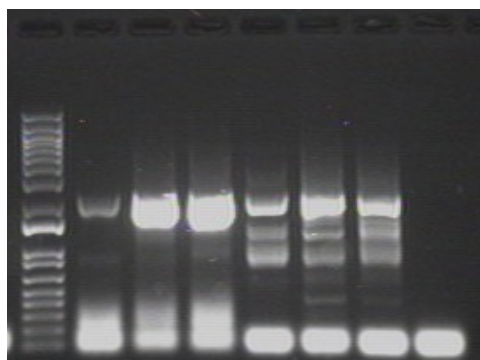
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Xrcc5_NotI_Rev

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- Expériences :

- PCR 10/07 : sur **les 7 conditions** cycle Q5-TM 56°C-Enhancer 10- 2min 30 d'élongation



Rate DiT0 DiT24 DiT48 SP CTX Eau

- Résultats séquençages

- FlagBirA rate clone B

- B3Fwd rate 825NT

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- BGHRev rate 973NT

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DLLDMI-

- Rev du 25/11

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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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➤ **Blast contre banque rat :**

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☒	Rattus norvegicus X-ray repair cross complementing 5 (Xrcc5). mRNA	Norway rat	4050	4050	100%	0.0	99.91%	2545	NM_177419.2
☒	Rattus norvegicus X-ray repair complementing defective repair in Chinese hamster cells 5. mRNA (cDNA clone MGC.72979...	Norway rat	4050	4050	100%	0.0	99.91%	2548	BC061576.1
☒	Rattus norvegicus mRNA for Xrcc5. partial cds	Norway rat	3480	3480	93%	0.0	97.22%	2100	AB066103.1

➤ **Différence Séquencage/CDS au niveau NT :**

➤ Différence au niveau PROT :

seq

refprot

Consensus

110120130

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AIYRYAYDKRANPQVGVAFPFIKDAYECLVYVQLPFMEDLRQYMFSSLKNNKKCTPTEAQLSAIDDLIDSHSLVKKNEEEDIEDLFPTSKIPNPEFQRLYQCLLHRAHLQERLPPIQQHILNMLDPPT

521530540550560570580590600610620630640650

EMKAKCEIPLSKYKTLFPLTEVYKKKQDQVTAQDVFQDNIEEGPAKKYKTEKEEGHISISSLAEGNVTYKVSYPNPFVFRVLRQKIASFEEASLQLMSHIEQFLDTNETLYFMKSMDCIKALREEAIQF

651660670680690700710720730732

SEEQRFNSFLEGLREKVEIKQLNHFWIEIYVQDGTITLTKDESPGSSVTAEEATKFLTPKDKAKEDTTGLEEGGDDVOLLDMI

Mutation aa 639

	Description	Common Name	Score	Score	Cover	value	Ident	Len	Accession
✓	X-ray repair complementing defective repair in Chinese hamster cells 5, isoform CRA_a [Rattus norvegicus]	Norway rat	1508	1508	100%	0.0	99.86%	732	EDL75243.1
✓	X-ray repair cross-complementing protein 5 [Rattus norvegicus]	Norway rat	1506	1506	100%	0.0	99.86%	732	NP_803154.1
✓	X-ray repair cross-complementing protein 5 [Rattus rattus]	black rat	1487	1487	100%	0.0	98.50%	732	XP_032757208.1
✓	X-ray repair cross-complementing protein 5 [Avicantis niloticus]	African grass rat	1459	1459	100%	0.0	96.17%	732	XP_034354459.1

Flag BirA Xrcc5 rate (clone B) OK

o **FlagBirA DiT0 clone B**

➤ **B3Fwd DiT0 836NT**

ATGGCGTGGTCCGGTAATAAGGCAGCTGTTGTGCTGTGTATGGATGTGGGGGTTGCCATGGGTAACCTCTTCCT
GGTGAAGAATCCCCACTTGAACAGGCCAAGAAAGTGATGACTATGTTTGTCCAACGACAGGTGTTTTCGGAGAG
CAAGGATGAGATCGCCTTAGTCCTCTATGGTACAGAGAGCACTGATAACGCCCTTGCTGGCAAGGACCAGTATCA
GAACATCACAGTGCACAGGCACCTGATGCTACCAGATTTTTGATTTGCTGGAAGACATCGGAAACAAAATCCAACC
AAGTTCTCAACAAGCCGACTTCCTGGACGCCCTGATTGTGTGCATGGATTTGATTACGCGTGAAACCATAGGAAA
GAAGTTTGGGAAGAAGCATATTGAAGTGTTCACTGATCTCAGCAGCCCATTCAGCCAAGACCAACTGGACATTAT
AATTTGTAACTGAAGAAGTCCGGCATCTCCCTGCAGTTCTTTCTGCCTTTTCCAATCGACAAGAATGGTGAGCCT
GGGGAGACAGAAGACCACGACTCCaGCTTCGACCACTGTGCACCCCTCTTCCCTCAAAAAGGACTTACTGAGCA
GCAAAAGGAAGGCATCCACATGGTGACGAGGGTGATGCTGTCTTTAGAAGGNAAAGATGGTCTGGATGAAATT
TATTCCTTCAGCGAGAGTCTTCAGCAACTGTGCATCTTTAANAANANTGAGAGGCGGTCCTTGCCCTNGNCCTG
CCAAGTACCATCGGCCCAACTTGTCTATANNNTCGTAGCCTATAAATCGATTGNACNGGANAAATTTAAAANA
GTTGGGTAGTTGTGG

➤ **BGHRev DiT0 966NT**

GGATGCCTATGAGTGTTTAGNTTANGNGCAGCTNCCNTTCATGGAAGACNNGCGGCNATACATGTTTTNCNCAC
TGAAAAACAATAAGAAGTGACCCCCACAGAGGCACAGCTGAGTGCGATCGATGATNTGATTGATTCCATGAGC
TTGGTAAAGAAAAACGAGGAAGAAGACATCATCGAAGACTTGTTTTCCAACNTCCAAAATTCCAAATCNTGAATTT
CAGCGGTTGTACCAGTGTCTGCTGCACAGANCTTACATCTCCAGGAGCGGCTGCCCCCAATTCAGCAGCACATT
TTGAATATGCTGGATCCCCCACTGAGATGAAAGCAAAATGTGAGATTCCACTCTCTAAAGTAAAGACCCTTTTCC
CTCTGACGGAAGTCGTTAAGAAAAAGGACCAAGTGACTGCTCAGGACGTTTTCCAAGACAATATTGAAGAGGG
GCCCCGTGCTAAAAATACAAGACTGAGAAAGAAGAAGGTCACATCAGCATCTCCAGCCTGGCAGAAGGGAAT
GTCACCAAGGTTGGAAGTGTGAATCCTGTTGAAAACCTCCGTGTCCTAGTAAGACAGAAGATTGCCAGCTTTGA
GGAAGCGAGTCTCCAGCTAATGAGTCACATTGAACAGTTTTTGGATACCAATGAAACACTGTATTTTATGAAAAGT
ATGGACTGCATCAAAGCTCTCCGGGAGGAAGCCATTAGTTTTTCAAGAGCAGCGTTTTCAACAGTTTCTGGA
AGGCCTTCGAGAGAAAGTGGAATTAACAATTAAATCATTTCTGGGAAATTGTCGTGCAGGATGGAATTNCTCT
GATACCAAAGACGAAAGCCCAGGAAGCTCTGTACAGCTGAGGAGGCCACGAAGTTTCTGACCCCCAAAGAC
AAAGCAAAAGAAGACACAACAGGACTTGAAGAAGGTGGTGATGTGGATGATTTACNGGACATGATATAG

➤ **Rev du 27/11**

TANNNNANGACAAAGAGCTAATCCTCAAGTNGGNGTANCNTTCCCTTTCATTAAGGATNCCTATGAGTGTTTAG
TTTATGTGCAGCTNCCTTTCATGGAAGACTNGCGGCAATACATGTTTTCCCTCACTGAAAANCAATAAGAAGTGCA
CCCCACAGAGGCACAGCTGAGTGCGATCGATGATCTGATTGATTCCATGAGCTTGGTAAAGAAAAACGAGGAA
GAAGACATCATCGAAGACTTGTTTTCCAACCTCCAAAATTCCAAATCCTGAaNtcAGCGTTGTACCAGTGTCTGCT
GCACAGAgCCTTACATCTCCAGGAGCGGCTGCCCCCAATTCAGCAGCACATTTTGAATATGCTGGATCCCCCACT
GAGATGAAAGCAAAATGTGAGATTCCACTCTCTAAAGTAAAGACCCTTTTCCCTCTGACGGAAGTCGTTAAGAAA
AAGGACCAAGTGACTGCTCAGGACGTTTTCCAAGACAATATTGAAGAGGGGCCCCGTGCTAAAAATACAAGAC
TGAGAAAGAAGAAGGTCACATCAGCATCTCCAGCCTGGCAGAAGGGAATGTCACCAAGGTTGGAAGTGTGAAT
CCTGTTGAAAACCTCCGTGTCCTAGTAAGACAGAAGATTGCCAGCTTTGAGGAAGCGAGTCTCCAGCTAATGAGT
CACATTGAACAGTTTTTGGATACCAATGAAACACTGTATTTTATGAAAAGTATGGACTGCATCAAAGCTCTCCGGG
AGGAAGCCATTAGTTTTTCAAGAGCAGCGTTTCAACAGTTTCTGGAAGGCCTTCGAGAGAAAGTGGAAT
TAAACAATTAAATCATTTCTGGGAAATTGTCGTGCAGGATGGAATTACTCTGATCACCAAAGACGAAAGCCCAGG
AAGCTCTGTACAGCTGAGGAGGCCACGAAGTTCTGACCCCCAAAGACAAAGCAAAAGAAGACACAACAGG
ACTTGAAGAAGGTGGTGATGTGGATGATTTACTGGACATGATATAG

➤ Fwd1

GNNGGNATCNNCNTGGTGACGAGGGTGATGCTGTCTTTAGAAAGGCAAAGATGGTCTGGATGAAATTTATTCCTT
CAGCGAGAGTCTTCAGCAACTGTGCATCTTTAAGAAGATTGAGAGGCGGTCCTTGCCCTGGCCCTGCCAACTGA
CCATCGGCCCAACTTGTCTATAAGGATCGTAGCCTATAAATCGATTGTACAGGAGAAATTTAAAAAGAGTTGGGT
AGTTGTGGACGCAAGAAGCTCTAAAGAAGGAAGATATACAAAAAGAGACTGTTTATTGCCTAAATGACGATGATG
AAACTGAAGTTTCCAAAGAGGACACTATTCAAGGGTTCGCTATGGAAGCGACATCATTCCTTTTTCTAAAGTGG
ATGAGGAACAAATGAAATATAAATCGGAGGGGAAGTGCTTCTGTCTGTTCTGGGGTTCTGTAAATCTTCTCAGGTTC
ATAGAAGATTCTTCATGGGACATCAAGTTCTGAAGGTCTTCGAGCGAAGGATGATGAGGCAGCAGCTGTTGCA
CTTTCTCCCTAGTTCACGCTTTGGATGAGTTAAACATGGTCGCTATCGTCCGCTACGCCTATGACAAAAGAGCTA
ATCCTCAAGTTGGTGTAGCCTTCCCTTTCATTAAGGATGCCTATGAGTGTTTAGTTTATGTGCAGCTGCCTTTCATG
GAAGACTTGCGGCAATACATGTTTTCTCACTGAAAAACAATAAGAAGTGCACCCCCACAGAGGCACAGCTGAg
TGCGATCGATGATCTGATTGATTCCATGAGCTTGGTAAAGAAAAACGAGGAAGAAGACATCATCGAAGACTTGTT
TCCNACCTCCAAAATTCCAAATCCTGAATTCAGCGGTTGTACCAAGTGTCTGCTGCACAGAGCCTTACATCTCCNG
GAGCGGCTGCCCCNATTCANCAGCACATTTTGAATATGCTGGATCCCCCACTGAGNTGAAAGCAAATGNGAN
ATTCNCTCTCTNAAGTAANACCCTTTCCNNNNGANGG

➤ Fwd2

TCTTNANAAGANTGAGAGGNGGTCCTTGCCCTGGCCCTGCCAACTGACCATCGGCCCAACTTGTCTATAAGGA
TCGTAGCCTATAAATCGATTGTACAGGAGAAATTTAAAAAGAGTTGGGTAGTTGTGGACGCAAGAAGCTCTAAAGA
AGGAAGATATACAAAAAGAGACTGTTTATTGCCTAAATGACGATGATGAAACTGAAGTTTCCAAAGAGGACACTA
TTCAAGGGTTCGCTATGGAAGCGACATCATTCCTTTTTCTAAAGTGGATGAGGAACAAATGAAATATAAATCGG
AGGGGAAGTGCTTCTGTCTGTTCTGGGGTTCTGTAAATCTTCTCAGGTTTCATAGAAGATTCTTCATGGGACATCAAGT
TCTGAAGGTCTTCGAGCGAAGGATGATGAGGCAGCAGCTGTTGCACTTTCTTCCCTAGTTCACGCTTTGGATGA
GTTAAACATGGTCGCTATCGTCCGCTACGCCTATGACAAAAGAGCTAATCCTCAAGTTGGTGTAGCCTTCCCTTTC
ATTAAGGATGCCTATGAGTGTTTAGTTTATGTGCAGCTGCCTTTCATGGAAGACTTGCGGCAATACATGTTTTCTC
ACTGAAAAACAATAAGAAGTGCACCCCCACAGAGGCACAGCTGAGTGCGATCGATGATCTGATTGATTCCATGA
GCTTGGTAAAGAAAAACGAGGAAGAAGACATCATCGAAGACTTGTTTCCAACCTCCAAAATTCCaAATCCTGAAT
TTCAGCGGTTGTACCAAGTGTCTGCTGCACAGAGCCTTACATCTCCNGGAGCGGCTGCCCCCAATTCAGCAGCACA
TTTTGAATATGCTGGNTCCCCCACTGAGATGAAAGCAAATGTGAGATTCCNCTCTCTAAAGTAAAGACCCTTTT
CCCTCTGANGGAAGTCGTTAANAAAAAGGANCNAGTGACTGCTCNNNNNTTTCCNANACAATATTGAANAG
GGGCCCCGCTGCTAAAAANNAN

➤ Rev1

AGCATNNGAANNNTNNNTGATNTCAGCANCCCNTCANCNNNNCCNNNTGNNCNTNTNANNNNANCNGNN
GAAGTNCGGCANCTCCNNGCAGTTNNTTNNNCCTTTTCCATNGACAAGAATGNTGAGCCTNGGGAGACAGAA
GACCNCGACTCCAGCTTCGACCACTGTGCACCCTCTNCCCTCAAAAAGGACTTANTGAGCAGCAAAAGGAAG
GCATCCACATGGTGACGAGGGTGATGCTGTCTTTAGAAAGGCAAAGATGGTCTGGATGAAATTTATTCNTTCAGCG
AGAGTCTTCAGCAACTGTGCATCTTTAAGAAGATTGAGAGGCGGTCCTTGCCCTGGCCCTGCCAACTGACCATCG
GCCCCAACTTGTCTATAAGGATCGTAGCCTATAAATCGATTGTACAGGAGAAATTTAAAAAGAGTTGGGTAGTTGT
GGACGCAAGAAGCTCTAAAGAAGGAAGATATACAAAAAGAGACTGTTTATTGCCTAAATGACGATGATGAAACTG
AAGTTTCCAAAGAGGACACTATTCAAGGGTTCGCTATGGAAGCGACATCATTCCTTTTTCTAAAGTGGATGAGG
AACAAATGAAATATAAATCGGAGGGGAAGTGCTTCTGTCTGTTCTGGGGTTCTGTAAATCTTCTCAGGTTTCATAGAA
GATTCTTCATGGGACATCAAGTTCTGAAGGTCTTCGAGCGAAGGATGATGAGGCAGCAGCTGTTGCACTTTCTT
CCCTAGTTCACGCTTTGGATGAGTTAAACATGGTCGCTATCGTCCGCTACGCCTATGACAAAAGAGCTAATCCTCA
AGTTGGTGTAGCCTTCCCTTTCATTAAGGATGCCTATGAGTGTTTAGTTTATGTGCAGCTGCCTTTCATGGAAGAC
TTGCGGCAATACATGTTTTCTCACTGAAAAACAATAAGAAGTGCACCCCCACAGAGGCACAGCTGAGTGCGATC

GATGATCTGATTGATTCCATGAGCTTGGTAAAGAAAAACGAGGAAGAAGACATCATCGAAGACTTGTTTCCAACC
TCCAAAATTCCAANTCCTGAATTCAGCGGT

➤ Rev2

CNTNGNAANNAAANCCNACNAANTNTCANAANNCCNACTNCTGGACNCCNGATTGTGTGCANGNANTGATTC
AGCGTGAAACCATAGGAAAGAAGTTTGGGAAGAAGCATATNGAAGTGTTCACTGANNTCAGCAGCCCATTTCAG
CCAAGACCAACTGGACATTATAATTNGTANCNTGAAGAAGTCNGGCATCTNCCNGCAGTTCTTTCTNCCTTTTCC
NATCGACAAGAATGGTGAGCCTNNGGAGACAGAAGACCACGACTCCAGCTTCGACCACTGTGCACCCTCCTTCC
CTCAAAAAGGACTTACTGAGCAGCAAAAGGAAGGCATCCACATGGTGACGAGGGTGATGCTGTCTTTAGAAGG
CAAAGATGGTCTGGATGAAATTTATTCCTTCAGCGAGAGTCTTCAGCAACTGTGCATCTTTAAGAAGATTGAGAG
GCGGTCCTTGCCCTGGCCCTGCCAACTGACCATCGGCCCAACTTGCTATAAGGATCGTAGCCTATAAATCGATT
GTACAGGAGAAATTTAAAAAGAGTTGGGTAGTTGTGGACGCAAGAACTCTAAAGAAGGAAGATATACAAAAAG
AGACTGTTTATTGCCTAAATGACGATGATGAACTGAAGTTTCCAAAGAGGACACTATTCAAGGGTTCCGCTATG
GAAGCGACATCATTCTTTTTCTAAAGTGGATGAGGAACAAATGAAATATAAATCGGAGGGGAAGTGCTTCTCTG
TTCTGGGGTTCTGTAAATCTTCTCAGGTTTCATAGAAGATTCTTCATGGGACATCAAGTTCTGAAGGTCTTCGCAGC
GAAGGATGATGAGGCAGCAGCTGTTGCACTTTCTCCCTAGTTCACGCTTTGGATGAGTTAAACATGGTCGCTAT
CGTCCGCTACGCCTATGACAAAAGAGCTAATCCTCAAGTTGGTGTAGCCTTCCCTTTCATTAAGGATGCCTATGAG
TGTTTAGTTTATGTGCAGCTGCCTTTCATGGAAGACTTGCGGCAATACATGTTTTCTCActGAAAAACAATAAGA
AGTGACCCCCNCAG

➤ Synthèse séquençage DiTO

ATGGCGTGGTCCGGTAATAAGGCAGCTGTTGTGCTGTGTATGGATGTGGGGTTGCCATG	60
GGTAACTCCTTTTCCTGGTGAAGAATCCCCACTTGAACAGGCCAAGAAAGTGATGACTATG	120
TTTGTCCAACGACAGGTGTTTTTCGGAGAGCAAGGATGAGATCGCCTTAGTCCTCTATGGT	180
ACAGAGAGCACTGATAACGCCCTTGCTGGCAAGGACCAGTATCAGAACATCACAGTGAC	240
AGGCACCTGATGCTACCAGATTTTGATTTGCTGGAAGACATCGGAAACAAAATCCAACCA	300
AGTTCTCAACAAGCCGACTTCTGGACGCCCTGATTGTGTGCATGGATTGATTACAGCGT	360
GAAACCATAGGAAAGAGTTTGGGAAGAAGCATATTGAAAGTGTTCATGATCTCAGCAGC	420
CCATTTCAGCCAAGACCAACTGGACATTATAATTTGTAACCTGAAGAAGTCCGGCATCTCC	480
CTGCAGTTCTTTCTGCCTTTTCCAATCGACAAGAATGGTGAGCCTGGGGAGACAGAAGAC	540
CACGACTCCAGCTTCGACCACTGTGCACCCTCCTTCCCTCAAAAAGGACTTACTGAGCAG	600
CAAAAGGAAGGCATCCACATGGTGACGAGGGTGATGCTGTCTTTAGAAGGCAAGATGGT	660
CTGGATGAAATTTATTCCTTCAGCGAGAGTCTTCAGCAACTGTGCATCTTTAAGAAGATT	720
GAGAGGCGGTCTTGGCCTGGCCCTGCCAACTGACCATCGGCCCAACTTGCTCTATAAGG	780
ATCGTAGCCTATAAATCGATTGTACAGGAGAAATTTAAAAAGAGTTGGGTAGTTGTGGAC	840
GCAAGAAGCTCTAAAGAAGGAAGATATACAAAAGAGACTGTTTATTGCCTAAATGACGAT	900
GATGAAAGCTGAAGTTTCCAAAGAGGACACTATTCAAGGGTTCCGCTATGGAAGCGACATC	960
ATTCCTTTTTCTAAAGTGGATGAGGAACAAATGAAATATAAATCGGAGGGGAAGTGCTTC	1020
TCTGTTCTGGGGTTCTGTAAATCTTCTCAGGTTTCATAGAAGATTCTTCATGGGACATCAA	1080
GTTCTGAAGGTCTTCGCAGCGAAGGATGATGAGGCAGCAGCTGTTGCACTTTCTTCCCTA	1140
GTTACGCTTTTGATGAGTTAAACATGGTCGCTATCGTCCGCTACGCCTATGACAAAAGA	1200
GCTAATCCTCAAGTTGGTGTAGCCTTCCCTTTTCATTAAGGATGCCTATGAGTGTTTAGTT	1260
TATGTGCAGCTGCCTTTCATGGAAGACTTGCGGCAATACATGTTTTCTCActGAAAAAC	1320
AATAAGAAGTGACCCCCACAGAGGCACAGCTGAGTGCGATCGATGATCTGATTGATTCC	1380
ATGAGCTTGGTAAAGAAAAACGAGGAAGAAGACATCATCGAAGACTTGTTTCCAACCTCC	1440
AAAATTCCAATCCTGAATTTTCAGCGGTTGTACCAGTGTCTGCTGCACAGAGCCTTACAT	1500
CTCCAGGAGCGGCTGCCCCAATTCAGCAGCACATTTTGAATATGCTGGATCCCCCACT	1560
GAGATGAAAGCAAAATGTGAGATTCCACTCTCTAAAGTAAAGACCCTTTTCCCTCTGACG	1620
GAAGTCGTTAAGAAAAAGGACCAAGTGACTGCTCAGGACGTTTTCGAAGACAATATTGAA	1680
GAGGGGCCCCGCTGCTAAAAAATACAAGACTGAGAAAGAAGAGTACATCAGCATCTCC	1740
AGCCTGGCAGAAGGAATGTACCAAGGTTGGAAGTGTGAATCCTGTTGAAAAGTTCCGT	1800
GTCTAGTAAGACAGAAGATTGCCAGCTTTGAGGAAGCGAGTCTCCAGCTAATGAGTCAC	1860
ATTGAACAGTTTTTTGGATACCAATGAAACACTGTATTTTATGAAAAGTATGGACTGCATC	1920
AAAGCTCTCCGGGAGGAAGCCATTTCAGTTTTCAGAAGAGCAGCGTTTCAACAGTTTCCTG	1980
GAAGGCCTTCGAGAGAAAGTGAAATTAACAATTAATCATTCTGGGAAATTGTCGTG	2040
CAGGATGGAATTACTCTGATCACCAAGACGAAAGCCAGGAAGCTCTGTACAGCTGAG	2100

GAGGCCACGAAGTTCCTGACCCCCAAAGACAAAGCAAAAGAAGACACAACAGGACTTGAA
GAAGGTGGTGATGTGGATGATTTACTGGACATGATATAG

2160
2199

MAWSGNKAAVVLCDMDVGVAMGNSFPGEESPLEQAKKVM TMFVQRQVFSESKDEIALVLYGTESTDNALAGKD
QYQNITVHRHMLPDPFDLLEDIGNKIQPSSQQADFLDALIVCMDLIQRETIGKKFGKKHIEVFTDLSSPFSQDQLDIIIC
NLKKSISLQFFLPFPIDKNGEPGETEDHDSSFDHCAPSFPQKGLTEQQKEGIH MVTRVMLSLEGKDGLDEIYSFSES
LQQLCIFKKIERRSLPWPCQLTIGPNLSIRIVAYKSIVQEKFKKSWVVVDARTLKKEDIQKETVYCLNDDDETEVSKEDT
IQGFRYGSDIIPFSKVDEEQMKYKSEGKCFSVLGFCKSSQVHRRFFMGHQVLKVFAAKDDEAAVALSSLVHALDEL
NMVAIVRYAYDKRANPQVGVAFFPIKDAYECLVYVQLPFMEDLRQYMFSSLKNNKKCTPTEAQLSAIDDLIDMSL
VKKNEEEDIIEDLFPTSKIPNPEFQRLYQCLLHRAHLQERLPPIQQHILNMLDPPTMKAKCEIPLSKVKTLFPLTEVV
KKKDQVTAQDVFQDNIEEGPAAKKYKTEKEEGHISISSLAEGNVTKVGSVNPVENFRVLVRQKIASFEEASLQLMSHI
EQFLDTNETLYFMKSMDCIKALREEAIQFSEEQRFN SFLEGLREKVEIKQLNHFWEIVVQDGITLITKDESPGSSVTAE
EATKFLTPKDKAKEDTTGLEEGGDVDDLDMI-

➤ **Blast DiT0 contre banque rat :**

	Description	Name	Score	Score	Cover	value	Ident	Len	Accession
2	Rattus norvegicus X-ray repair cross complementing 5 (Xrcc5)_mRNA	Norway rat	4050	4050	100%	0.0	99.91%	2545	NM_177419.2
2	Rattus norvegicus X-ray repair complementing defective repair in Chinese hamster cells 5_mRNA (cDNA clone MGC:72979...)	Norway rat	4050	4050	100%	0.0	99.91%	2548	BC061576.1
2	Rattus norvegicus mRNA for Xrcc5_partial cds	Norway rat	3480	3480	93%	0.0	97.22%	2100	AB066103.1

➤ **Différence Séquencage DiT0/CDS au niveau NT :**

1 10 20 30 40 50 60 70 80 90 100 110 120 130
seq ATGGCGTGGTCCGGTAATAGGCAGCTGTTGTGCTGTATGGATGTGGGGTTGCCATGGGTAACTCCTTTCTGGTGAAGATCCCACCTTGACAGGGCCAGAAAGTGATGACTATGTTTGTCCAA
cds ATGGCGTGGTCCGGTAATAGGCAGCTGTTGTGCTGTATGGATGTGGGGTTGCCATGGGTAACTCCTTTCTGGTGAAGATCCCACCTTGACAGGGCCAGAAAGTGATGACTATGTTTGTCCAA
Consensus ATGGCGTGGTCCGGTAATAGGCAGCTGTTGTGCTGTATGGATGTGGGGTTGCCATGGGTAACTCCTTTCTGGTGAAGATCCCACCTTGACAGGGCCAGAAAGTGATGACTATGTTTGTCCAA

131 140 150 160 170 180 190 200 210 220 230 240 250 260
seq GACAGGTGTTTTCCGAGAGCAGGATGAGATCGCCTTAGTCCTCTATGTTACAGAGGACCTGATACGCCCTTGCTGGCAGGACCAAGTACAGACATCACAGTGCACAGGACCTGATGCTACCA
cds GACAGGTGTTTTCCGAGAGCAGGATGAGATCGCCTTAGTCCTCTATGTTACAGAGGACCTGATACGCCCTTGCTGGCAGGACCAAGTACAGACATCACAGTGCACAGGACCTGATGCTACCA
Consensus GACAGGTGTTTTCCGAGAGCAGGATGAGATCGCCTTAGTCCTCTATGTTACAGAGGACCTGATACGCCCTTGCTGGCAGGACCAAGTACAGACATCACAGTGCACAGGACCTGATGCTACCA

261 270 280 290 300 310 320 330 340 350 360 370 380 390
seq TTTTGATTGCTGGAGACATCGGAACAAATCCACCAAGTTCTCAGCAGCCGACTTCTGGACGCCCTGATTGTGTGCATGATTGATTGACGCTGAACCATAGGAAGAGATTGGGAAGAG
cds TTTTGATTGCTGGAGACATCGGAACAAATCCACCAAGTTCTCAGCAGCCGACTTCTGGACGCCCTGATTGTGTGCATGATTGATTGACGCTGAACCATAGGAAGAGATTGGGAAGAG
Consensus TTTTGATTGCTGGAGACATCGGAACAAATCCACCAAGTTCTCAGCAGCCGACTTCTGGACGCCCTGATTGTGTGCATGATTGATTGACGCTGAACCATAGGAAGAGATTGGGAAGAG

391 400 410 420 430 440 450 460 470 480 490 500 510 520
seq CATATTGAAGTGTTCACATGATCTCAGCAGCCCATTCAGCAGAGCAACTGGACATTATTAATTTGTACCTGAGAGAGTCGGCATCTCCCTGCAGTCTTCTGCTTTTCCATCGACAGAGATGGT
cds CATATTGAAGTGTTCACATGATCTCAGCAGCCCATTCAGCAGAGCAACTGGACATTATTAATTTGTACCTGAGAGAGTCGGCATCTCCCTGCAGTCTTCTGCTTTTCCATCGACAGAGATGGT
Consensus CATATTGAAGTGTTCACATGATCTCAGCAGCCCATTCAGCAGAGCAACTGGACATTATTAATTTGTACCTGAGAGAGTCGGCATCTCCCTGCAGTCTTCTGCTTTTCCATCGACAGAGATGGT

521 530 540 550 560 570 580 590 600 610 620 630 640 650
seq AGCCTGGGGAGACAGAGACACGACTCCAGCTTCGACCACTGTGCACCTCCTTCCCTCAAAAGGACTTACTGAGCAGCAAAAGGAGGACATCCACATGGTGACGAGGGTGATGCTGTCTTAGAGG
cds AGCCTGGGGAGACAGAGACACGACTCCAGCTTCGACCACTGTGCACCTCCTTCCCTCAAAAGGACTTACTGAGCAGCAAAAGGAGGACATCCACATGGTGACGAGGGTGATGCTGTCTTAGAGG
Consensus AGCCTGGGGAGACAGAGACACGACTCCAGCTTCGACCACTGTGCACCTCCTTCCCTCAAAAGGACTTACTGAGCAGCAAAAGGAGGACATCCACATGGTGACGAGGGTGATGCTGTCTTAGAGG

651 660 670 680 690 700 710 720 730 740 750 760 770 780
seq CAAGAGTGGTCTGGATGAATTTATCTTCAGCGAGAGCTTCAGCACTGTGCATCTTTAAGAGATTGAGAGGCGGCTTGCCTTGCCCTGCCCCGCACTGACCATCGCCCCCACTTGTCTATAGG
cds CAAGAGTGGTCTGGATGAATTTATCTTCAGCGAGAGCTTCAGCACTGTGCATCTTTAAGAGATTGAGAGGCGGCTTGCCTTGCCCTGCCCCGCACTGACCATCGCCCCCACTTGTCTATAGG
Consensus CAAGAGTGGTCTGGATGAATTTATCTTCAGCGAGAGCTTCAGCACTGTGCATCTTTAAGAGATTGAGAGGCGGCTTGCCTTGCCCTGCCCCGCACTGACCATCGCCCCCACTTGTCTATAGG

781 790 800 810 820 830 840 850 860 870 880 890 900 910
seq ATCGTAGCCTATTAATCGATTGTACAGGAGAAATTTAAAGAGGTTGGGTAGTTGTGGACGCAAGACTCTAAGAGAGGAGATATACAAAGAGAGCTGTTATTGCTTAATGACGATGATGAACCTG
cds ATCGTAGCCTATTAATCGATTGTACAGGAGAAATTTAAAGAGGTTGGGTAGTTGTGGACGCAAGACTCTAAGAGAGGAGATATACAAAGAGAGCTGTTATTGCTTAATGACGATGATGAACCTG
Consensus ATCGTAGCCTATTAATCGATTGTACAGGAGAAATTTAAAGAGGTTGGGTAGTTGTGGACGCAAGACTCTAAGAGAGGAGATATACAAAGAGAGCTGTTATTGCTTAATGACGATGATGAACCTG

911 920 930 940 950 960 970 980 990 1000 1010 1020 1030 1040
seq ARGTTTCCAAAGAGGACATATTCAAGGGTCCGCTATGGAGCGACATCTTCTTTCTAAGTGGATGAGGAAACAAATGAATATTAATCGAGGGGAGTGCTTCTGTTCTCGGGTCTCTGA
cds ARGTTTCCAAAGAGGACATATTCAAGGGTCCGCTATGGAGCGACATCTTCTTTCTAAGTGGATGAGGAAACAAATGAATATTAATCGAGGGGAGTGCTTCTGTTCTCGGGTCTCTGA
Consensus ARGTTTCCAAAGAGGACATATTCAAGGGTCCGCTATGGAGCGACATCTTCTTTCTAAGTGGATGAGGAAACAAATGAATATTAATCGAGGGGAGTGCTTCTGTTCTCGGGTCTCTGA

1041 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170
seq ATCTTCTCAGGTTTCATAGAGATTCTTCATGGGACATCAAGTTCTGAGGCTCTCGCAGCGAGGATGATGAGGACAGCTGTTGCATCTTCTTCCCTAGTTCACGCTTTGGATGAGTTAACATGGTC
cds ATCTTCTCAGGTTTCATAGAGATTCTTCATGGGACATCAAGTTCTGAGGCTCTCGCAGCGAGGATGATGAGGACAGCTGTTGCATCTTCTTCCCTAGTTCACGCTTTGGATGAGTTAACATGGTC
Consensus ATCTTCTCAGGTTTCATAGAGATTCTTCATGGGACATCAAGTTCTGAGGCTCTCGCAGCGAGGATGATGAGGACAGCTGTTGCATCTTCTTCCCTAGTTCACGCTTTGGATGAGTTAACATGGTC

1171 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
seq GCTATCGTCCGCTACGCTATGACAAAGAGCTAATCCTCAAGTTGGGTAGGCTTCCCTTTTCATTAGGATGCTATGAGTGTTTAGTTTATGTGACAGCTGCCCTTCATGGAGACTTGGCGCAATACA
cds GCTATCGTCCGCTACGCTATGACAAAGAGCTAATCCTCAAGTTGGGTAGGCTTCCCTTTTCATTAGGATGCTATGAGTGTTTAGTTTATGTGACAGCTGCCCTTCATGGAGACTTGGCGCAATACA
Consensus GCTATCGTCCGCTACGCTATGACAAAGAGCTAATCCTCAAGTTGGGTAGGCTTCCCTTTTCATTAGGATGCTATGAGTGTTTAGTTTATGTGACAGCTGCCCTTCATGGAGACTTGGCGCAATACA

1301 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430
seq TGTTTTCTCCTCACTGAARAAACAAATAGAGGTGACCCCCACAGAGGACAGCTGAGTGCGATCGATGATCTGATTGATTCCATGAGCTTGGTAAGAAACAGAGGAGAGACATCATCGAGACTTGT
cds TGTTTTCTCCTCACTGAARAAACAAATAGAGGTGACCCCCACAGAGGACAGCTGAGTGCGATCGATGATCTGATTGATTCCATGAGCTTGGTAAGAAACAGAGGAGAGACATCATCGAGACTTGT
Consensus TGTTTTCTCCTCACTGAARAAACAAATAGAGGTGACCCCCACAGAGGACAGCTGAGTGCGATCGATGATCTGATTGATTCCATGAGCTTGGTAAGAAACAGAGGAGAGACATCATCGAGACTTGT

1431 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560
seq TCCACCTCCAAATTCCAATCCTGATTTCAGCGGTTGACAGGTGCTGCTGACAGAGGCTTACATCTCCAGGAGCGGCTGCCCCCAATTACAGCAGCACATTTGAATATGCTGGATCCCCCACT
cds TCCACCTCCAAATTCCAATCCTGATTTCAGCGGTTGACAGGTGCTGCTGACAGAGGCTTACATCTCCAGGAGCGGCTGCCCCCAATTACAGCAGCACATTTGAATATGCTGGATCCCCCACT
Consensus TCCACCTCCAAATTCCAATCCTGATTTCAGCGGTTGACAGGTGCTGCTGACAGAGGCTTACATCTCCAGGAGCGGCTGCCCCCAATTACAGCAGCACATTTGAATATGCTGGATCCCCCACT

1561 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690
seq GAGATGAAGCAAAATGTGAGATTCCACTCTCTAAGGTAAAGACCTTTCCCTCTGACGGAGTCTTGAAGAAAGGACCAAGTGACTGCTCAGGACGTTTCCAGACAAATATTGAGAGGGGGCCG
cds GAGATGAAGCAAAATGTGAGATTCCACTCTCTAAGGTAAAGACCTTTCCCTCTGACGGAGTCTTGAAGAAAGGACCAAGTGACTGCTCAGGACGTTTCCAGACAAATATTGAGAGGGGGCCG
Consensus GAGATGAAGCAAAATGTGAGATTCCACTCTCTAAGGTAAAGACCTTTCCCTCTGACGGAGTCTTGAAGAAAGGACCAAGTGACTGCTCAGGACGTTTCCAGACAAATATTGAGAGGGGGCCG

1691 1700 1710 1720 1730 1740 1750 1760 1770 1780 1790 1800 1810 1820
seq CTGCTAAAAATACAGACTGAGAAAGAGAGGTCACATCAGCATCTCCAGCTGGCAGAGGGGATGTCCACAGGTTGGAGTGTGAATCTGTTGAACCTTCCGTGCTAGTAGACAGAGAT
cds CTGCTAAAAATACAGACTGAGAAAGAGAGGTCACATCAGCATCTCCAGCTGGCAGAGGGGATGTCCACAGGTTGGAGTGTGAATCTGTTGAACCTTCCGTGCTAGTAGACAGAGAT
Consensus CTGCTAAAAATACAGACTGAGAAAGAGAGGTCACATCAGCATCTCCAGCTGGCAGAGGGGATGTCCACAGGTTGGAGTGTGAATCTGTTGAACCTTCCGTGCTAGTAGACAGAGAT

1821 1830 1840 1850 1860 1870 1880 1890 1900 1910 1920 1930 1940 1950
seq TGCCAGCTTTGAGGAGCGAGCTCCAGCTAATGAGTCACATTGAACAGTTTTTGGATACCAATGAACACTGTATTTTATGAAGATATGGACTGCATCAAGCTCTCCGGAGGAGGACATTACGTTT
cds TGCCAGCTTTGAGGAGCGAGCTCCAGCTAATGAGTCACATTGAACAGTTTTTGGATACCAATGAACACTGTATTTTATGAAGATATGGACTGCATCAAGCTCTCCGGAGGAGGACATTACGTTT
Consensus TGCCAGCTTTGAGGAGCGAGCTCCAGCTAATGAGTCACATTGAACAGTTTTTGGATACCAATGAACACTGTATTTTATGAAGATATGGACTGCATCAAGCTCTCCGGAGGAGGACATTACGTTT

1951 1960 1970 1980 1990 2000 2010 2020 2030 2040 2050 2060 2070 2080
seq TCAGAGAGCAGCGTTTCAACAGTTTCTTGGAGGCTTCGAGAGAAAGTGGAAATTAACATTAATCAATTTCTGGGAATTGTCTGTCAGGATGGAAATTAATCTGATCACCAGAGCAGAAAGCCAG
cds TCAGAGAGCAGCGTTTCAACAGTTTCTTGGAGGCTTCGAGAGAAAGTGGAAATTAACATTAATCAATTTCTGGGAATTGTCTGTCAGGATGGAAATTAATCTGATCACCAGAGCAGAAAGCCAG
Consensus TCAGAGAGCAGCGTTTCAACAGTTTCTTGGAGGCTTCGAGAGAAAGTGGAAATTAACATTAATCAATTTCTGGGAATTGTCTGTCAGGATGGAAATTAATCTGATCACCAGAGCAGAAAGCCAG

2081 2090 2100 2110 2120 2130 2140 2150 2160 2170 2180 2190 2199
seq GAGACTCTGTACAGCTGAGGAGGCGCAGAGTTCTGACCCCAAGAGCAAGCAAGAGAGACACACAGGACTTGAGAGGTTGGTGTGATGTGGATGATTACTGGACATGATATAG
cds GAGACTCTGTACAGCTGAGGAGGCGCAGAGTTCTGACCCCAAGAGCAAGCAAGAGAGAGACACACAGGACTTGAGAGGTTGGTGTGATGTGGATGATTACTGGACATGATATAG
Consensus GAGACTCTGTACAGCTGAGGAGGCGCAGAGTTCTGACCCCAAGAGCAAGCAAGAGAGAGACACACAGGACTTGAGAGGTTGGTGTGATGTGGATGATTACTGGACATGATATAG

mutations 1915 T<C et A<G en 1956

➤ Différence Séquençage DiT0/CDS au niveau PROT :

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq	MAHSGNKRAVYVLCMDVGVAMGNSFPGEESPLEQAKKYVTHMFVQRQVFSSEKDEIALVLYGTESTDNALAGKQDYQNTIVHRHMLPDPDLLEDIGNKIQPSSQAQDFLDALIVCHDLIQRETTIGKFGKK													
ref	MAHSGNKRAVYVLCMDVGVAMGNSFPGEESPLEQAKKYVTHMFVQRQVFSSEKDEIALVLYGTESTDNALAGKQDYQNTIVHRHMLPDPDLLEDIGNKIQPSSQAQDFLDALIVCHDLIQRETTIGKFGKK													
Consensus	MAHSGNKRAVYVLCMDVGVAMGNSFPGEESPLEQAKKYVTHMFVQRQVFSSEKDEIALVLYGTESTDNALAGKQDYQNTIVHRHMLPDPDLLEDIGNKIQPSSQAQDFLDALIVCHDLIQRETTIGKFGKK													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq	HIEVFTDLSPPFSQDQLDIIICNLKKSGLSQFLFPFDKNGEPGETEDHSSFDHCAPSPFQKGLTEQQKEGIHMYTRYMLSLGKDGLEIYFSSESLLQQLCIFKKIERRSLPWPQQLTIGPMLSIR													
ref	HIEVFTDLSPPFSQDQLDIIICNLKKSGLSQFLFPFDKNGEPGETEDHSSFDHCAPSPFQKGLTEQQKEGIHMYTRYMLSLGKDGLEIYFSSESLLQQLCIFKKIERRSLPWPQQLTIGPMLSIR													
Consensus	HIEVFTDLSPPFSQDQLDIIICNLKKSGLSQFLFPFDKNGEPGETEDHSSFDHCAPSPFQKGLTEQQKEGIHMYTRYMLSLGKDGLEIYFSSESLLQQLCIFKKIERRSLPWPQQLTIGPMLSIR													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq	IVAYKSIYQEKFKKSHVYVDARTLKKEIDQKETVYCLNDDDETEVSKEDTIQGFYRGSIIIPFSKYDVEEQHKYKSEGKCFSVLGFCCKSSQVHRRFFHGHQVLKYFAAKDDEAAAVLSSLYHALDELNMV													
ref	IVAYKSIYQEKFKKSHVYVDARTLKKEIDQKETVYCLNDDDETEVSKEDTIQGFYRGSIIIPFSKYDVEEQHKYKSEGKCFSVLGFCCKSSQVHRRFFHGHQVLKYFAAKDDEAAAVLSSLYHALDELNMV													
Consensus	IVAYKSIYQEKFKKSHVYVDARTLKKEIDQKETVYCLNDDDETEVSKEDTIQGFYRGSIIIPFSKYDVEEQHKYKSEGKCFSVLGFCCKSSQVHRRFFHGHQVLKYFAAKDDEAAAVLSSLYHALDELNMV													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
seq	AIYRYAYDKRANPQVGVAFPIKDAYECLVYVQLPFMEDLRQYMFSSLKNNKCTPTERQLSAIDDLIDSHSLYKKNNEEDIIEDLFPTSKIPNPEFQRLYQCLLHRAHLQERLPPQQHILNMLDPPT													
ref	AIYRYAYDKRANPQVGVAFPIKDAYECLVYVQLPFMEDLRQYMFSSLKNNKCTPTERQLSAIDDLIDSHSLYKKNNEEDIIEDLFPTSKIPNPEFQRLYQCLLHRAHLQERLPPQQHILNMLDPPT													
Consensus	AIYRYAYDKRANPQVGVAFPIKDAYECLVYVQLPFMEDLRQYMFSSLKNNKCTPTERQLSAIDDLIDSHSLYKKNNEEDIIEDLFPTSKIPNPEFQRLYQCLLHRAHLQERLPPQQHILNMLDPPT													
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
seq	EMKAKCEIPLSKYKTLFPLTEVYVKKQDVTAQDYFQDNIEEGPAKKYKTEKEEGHISISSLAEGNVTYKGSYNPNVENFRVLYRQKIASFEASLQLMSHIEQFLDTNETLYFMKSHDCKIKALREEAIOF													
ref	EMKAKCEIPLSKYKTLFPLTEVYVKKQDVTAQDYFQDNIEEGPAKKYKTEKEEGHISISSLAEGNVTYKGSYNPNVENFRVLYRQKIASFEASLQLMSHIEQFLDTNETLYFMKSHDCKIKALREEAIOF													
Consensus	EMKAKCEIPLSKYKTLFPLTEVYVKKQDVTAQDYFQDNIEEGPAKKYKTEKEEGHISISSLAEGNVTYKGSYNPNVENFRVLYRQKIASFEASLQLMSHIEQFLDTNETLYFMKSHDCKIKALREEAIOF													
	651	660	670	680	690	700	710	720	730	732				
seq	SEEQRFNSFLEGLREKVEIKQLNHFMIEYVQDGITLITKDESPGSSVTAERTKFLTPKDKAKEDTTGLEEGGDDVOLLDMI													
ref	SEEQRFNSFLEGLREKVEIKQLNHFMIEYVQDGITLITKDESPGSSVTAERTKFLTPKDKAKEDTTGLEEGGDDVOLLDMI													
Consensus	SEEQRFNSFLEGLREKVEIKQLNHFMIEYVQDGITLITKDESPGSSVTAERTKFLTPKDKAKEDTTGLEEGGDDVOLLDMI													

Comme rate mutation en 639

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
✓	X-ray repair complementing defective repair in Chinese hamster cells 5, isoform CRA_a [Rattus norvegicus]	Norway rat	1508	1508	100%	0.0	99.86%	732	EDL75243.1
✓	X-ray repair cross-complementing protein 5 [Rattus norvegicus]	Norway rat	1506	1506	100%	0.0	99.86%	732	NP_803154.1
✓	Xrcc5 [Rattus norvegicus]	Norway rat	1359	1359	93%	0.0	96.63%	683	BAB83859.1
✓	X-ray repair complementing defective repair in Chinese hamster cells 5, isoform CRA_b [Rattus norvegicus]	Norway rat	471	471	31%	1e-163	99.56%	228	EDL75244.1

Flag BirA Xrcc5 DiT0 (cloneB) OK, mutation d'1aa en 639 comme rate

○ FlagBirA DiT24hLPS clone C

➤ B3Fwd DiT24h 834NT

ATGGCGTGGTCCGGTAATAAGGCAGCTGTTGTGCTGTGTATGGATGTGGGGGTTGCCATGGGTAACCTCTTCCT
GGTGAAGAATCCCCACTTGAACAGGCCAAGAAAGTGATGACTATGTTTGTCCAACGACAGGTGTTTTCGGAGAG
CAAGGATGAGATCGCCTTAGTCCTCTATGGTACAGAGAGCACTGATAACGCCCTTGCTGGCAAGGACCAGTATCA
GAACATCACAGTGCACAGGCACCTGATGCTACCAGATTTTTGATTTGCTGGAAGACATCGAAACAAAATCCAACC
AAGTTCTCAACAAGCCGACTTCCTGGACGCCCTGATTGTGTGCATGGATTTGATTCAGCGTGAAACCATAGGAAA
GAAGTTTGGGAAGAAGCATATTGAAGTGTTCACTGATCTCAGCAGCCCATTCAGCCAAGACCAACTGGACATTAT
AATTTGTAACCTGAAGAAGTCCGGCATCTCCCTGCAGTTCTTTCTGCCTTTTCCAATCGACAAGAATGGTGAGCCT
GGGGAGACAGAAGAcCACGACTCCaGCTTCGACCACTGTGCACCCTCCTTCCCTCAAAAAGGACTTACTGAGCA
GCAAAAGGAANGCATCCACATGGTGACGAGGGTGATGCTGTCTTTAGAAGGNAAAGATGGTCTGGATGAAATT
TATTCCTTCAGCGAGAGTCTTCAGCAACTGTGCATCTTTAANAANNNTGAGAGGCGGTCCTTGCCCTNNNCCTG
CCAAGTACCATCNGCCCNNACTTGTCTATNAGNATCGTANCCTATAAATCGATTGNACNGNANAAATTTAAAAAN
ANTTGGGTAGTTG

➤ BGHRev DiT24h 1004NT

AANNAGNTAATCCTCNAGTNGNNGTANCCCTTCNNNTTCATTAAGGATGCCTATGAGTGTTTAGTNNATGNGCAG
CTNCNTTTCATGGAAGACNNNCGGCAATACANGTTTTCTNTCACTGAAAANCAATAAGAAGTGACCCCCACAG
AGGCACAGCTGAGTGCGATCGATGATCTGATTGATTCCATGAGCTTGGTAAAGAAAAACGAGGNAGAAGACATC
ATCGAAGACTTGTTCANCTCCAAAATTNCAAaTCNTGAATTTAGCGGTTGTACCAGTGTCTGCTGCACAGA
GCCTTACATCTCCAGGAGCGGCTGCCCcCAATTCAGCAGCACATTTGAATATGCTGGATCCCCCACTGAGATGA
AAGCAAAATGTGAGATTCCACTCTCTAAAGTAAAGACCCTTTTCCCTCTGACGGAAGTCGTTAAGAAAAAGGACC
AAGTGACTGCTCAGGACGTTTTCCAAGACAATATTGAAGAGGGGGCCGCTGCTAAAAAATACAAGACTGAGAAA
GAAGAAGGTCACATCAGCATCTCCAGCCTGGCAGAAGGGAATGTCACCAAGGTTGGAAGTGTGAATCCTGTTGA
AACTTCCGTGTCCTAGTAAGACAGAAGATTGCCAGCTTTGAGGAAGCGAGTCTCCAGCTAATGAGTCACATTGA
ACAGTTTTTGGATACCAATGAAACACTGTATTTATGAAAAGTATGGACTGCATCAAAGCTCTCCGGGAGGAAGC
CATTCAATTTTGAAGAGCAGCGTTTCAACAGTTTCTGGAAGGCCTTCGAGAGAAAGTGGAATTAACAAT
TAAATCATTTCTGGGAAATTGTCGTGCAGGATGGAATTACTCTGATCACCAAAGACGAAAGCCCAGGAAGCTCTG
TCACAGCTGAGGAGGCCACGAAGTTCCTGACCCCCAAAGACAAAGCAAAAGAAGACACAACAGGACTTGAAG
AAGGTGGTGATGTGGATGATTACNGGACATGATATAG

➤ Séquençage du 27/11 BGHRev DiT24h

TNCTCAAGTNGGTGTANNTCCCTTTCATTAAGGATGCCTATGAGTNTTATGTTTATGTGCAGCTNCCTTTCATGG
AAGACNNGCGGCAATACATGTTTTCTCACTGAAAANCAATAAGAAGTNCACCCCCANAGAGGCACAGCTGAG
TGCGATCGATGATCTGATTGATTCCATGAGCTTGGTAAAGAAAAACGAGGAAGAAGACATCATCGAAGACTTGT
TCCAACCTCCAAAATTCCAAATCNTGAATTTAGCGGTTGTACCAGTGTCTGCTGCACAGAGCCTTACATCTCCAG
GAGCGGCTGCCCCAATTCAGCAGCACATTTTGAATATGCTGGATCCCCCACTGAGATGAAAGCAAAATGTGAG
ATTCACTCTCTAAAGTAAAGACCCTTTTCCCTCTGACGGAAGTCGTTAAGAAAAAGGACCAAGTGACTGCTCAG
GACGTTTTTCCAAGACAATATTGAAGAGGGGGCCGCTGCTAAAAAATACAAGACTGAGAAAGAAGAAGGTCACAT
CAGCATCTCCAGCCTGGCAGAAGGGAATGTCACCAAGGTTGGAAGTGTGAATCCTGTTGAAAACCTCCGTGTCC
TAGTAAGACAGAAGATTGCCAGCTTTGAGGAAGCGAGTCTCCAGCTAATGAGTCACATTGAACAGTTTTTGGATA
CCAATGAAACACTGTATTTATGAAAAGTATGGACTGCATCAAAGCTCTCCGGGAGGAAGCCATTAGTTTTAG
AAGAGCAGCGTTTCAACAGTTTCTGGAAGGCCTTCGAGAGAAAGTGGAATTAACAATTAATCATTTCTGG
GAAATTGTCGTGCAGGATGGAATTACTCTGATCACCAAAGACGAAAGCCCAGGAAGCTCTGTACAGCTGAGGA
GGCCACGAAGTTCCTGACCCCCAAAGACAAAGCAAAAGAAGACACAACAGGACTTGAAGAAGGTGGTGATGT
GGATGATTACTGGACATGATATAG

➤ Fwd1

ANGNATCCNCNTGGTGACGAGGGTGATGCTGTCTTTAGAAGGCAAAGATGGTCTGGATGAAATTTATTCCTTCA
GCGAGAGTCTTCAGCAACTGTGCATCTTTAAGAAGATTGAGAGGCGGTCCTTGCCCTGGCCCTGCCAACTGACC
ATCGGCCCAACTTGTCTATAAGGATCGTAGCCTATAAATCGATTGTACAGGAGAAATTTAAAAAGAGTTGGGTAG
TTGTGGACGCAAGAACTCTAAAGAAGGAAGATATACAAAAAGAGACTGTTTATTGCCTAAATGACGATGATGAAA
CTGAAGTTTCCAAGAGGACACTATTCAAGGGTTCCGCTATGGAAGCGACATCATTCCTTTTTCTAAAGTGGATG
AGGAACAAATGAAATATAAATCGGAGGGGAAGTGCTTCTCTGTTCTGGGGTTCTGTAAATCTTCTCAGGTTCTATA
GAAGATTCTTCATGGGACATCAAGTTCTGAAGGTCTTCGAGCGAAGGATGATGAGGCAGCAGCTGTTGCACTT
TCTCCCTAGTTTACGCTTTGGATGAGTTAAACATGGTCGCTATCGTCCGCTACGCCTATGACAAAAGAGCTAATC
CTCAAGTTGGTGTAGCCTTCCCTTTCATTAAGGATGCCTATGAGTGTTTAGTTTATGTGCAGCTGCCTTTCATGGAA
GACTTGCGGCAATACATGTTTTCTCACTGAAAAACAATAAGAAGTGCACCCCCACAGAGGCACAGCTGAgTGC
GATCGATGATCTGATTGATTCCATGAGCTTGGTAAAGAAAAACGAGGAAGAAGACATCATCGAAGACTTGTTTTCC
AACCTCCAAAATTCCAAATCCTGAATTCAGCGGTTGTACCAGTGTCTGCTGCACAGAGCCTTACATCTCCNGGA
GCGGCTGCCCCCNATTCAGCAGCACATTTTGAATATGCTGGATCCCCCACTGAGATGAAAGCAAATGTGANAT
TNCNCTCTCTAAAGTNAAGANCNTTTTNCCTNNGA

➤ Fwd2

TCTTTANAANANTGAGAGGNGGTCCTTGCCCTGGCCCTGCCAACTGACCATCGGCCCAACTTGTCTATAAGGAT
CGTAGCCTATAAATCGATTGTACAGGAGAAATTTAAAAAGAGTTGGGTAGTTGTGGACGCAAGAACTCTAAAGA
AGGAAGATATACAAAAAGAGACTGTTTATTGCCTAAATGACGATGATGAACTGAAGTTTCCAAAGAGGACACTA
TTCAAGGGTTCGCTATGGAAGCGACATCATTCCTTTTTCTAAAGTGGATGAGGAACAAATGAAATATAAATCGG
AGGGGAAGTGCTTCTCTGTTCTGGGGTTCTGTAAATCTTCTCAGGTTTCATAGAAGATTCTTCATGGGACATCAAGT
TCTGAAGGTCTTCGAGCGAAGGATGATGAGGCAGCAGCTGTTGCACTTTCTCCCTAGTTTACGCTTTGGATGA
GTTAAACATGGTCGCTATCGTCCGCTACGCCTATGACAAAAGAGCTAATCCTCAAGTTGGTGTAGCCTTCCCTTTC
ATTAAGGATGCCTATGAGTGTTTAGTTTATGTGCAGCTGCCTTTCATGGAAGACTTGCGGCAATACATGTTTTCTC
ACTGAAAAACAATAAGAAGTGCACCCCCACAGAGGCACAGCTGAGTGCGATCGATGATCTGATTGATTCCATGA
GCTTGGTAAAGAAAAACGAGGAAGAAGACATCATCGAAGACTTGTTTCCAACCTCCAAAATTCCAAATCCTGAAT
TTCAGCGGTTGTACCAGTGTCTGCTGCACAGAGCCTTACATCTCCAGGANCGGCTGCCCCCAATTCAGCAGCACA
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TCCCTCTGACGGAAGTCGTTNANAAAAAGGANCNAGTGACTGCTCNNNNGTTTTCCAAGANAATATTGAANAN
GGGCCGCTGCTANAANTACANACTGANAAGANAANNACATCAGCATCTNCNNNCTGNNNAGNAA

➤ Rev1

TGATNNCAGCAGCCCATTANCNANANCNNCTGNNCATNNTAATTNGNANCNGAAGAANTNCGGCATNTCCN
NGCAGTTCTTTCTGCNTTTTNCANTCGACAAGAAATGGTGAGCCTGGGGAGACAGAAGACCACGACTCCAGCTT
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CACTATTCAAGGGTTCCGCTATGGAAGCGACATCATTCCTTTTTCTAAAGTGGATGAGGAACAAATGAAATATAAA
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CCTCACTGAAAAACAATAAGAAGTGCACCCCCACAGAGGCACAGCTGAGTGCGATCGATGATCTGATTGATTCCA

TGAGCTTGGTAAAGAAAAACGAGGAAGAAGACATCATCGAAGACTTGTTCCTCAaNTCCAAAATTCCAANTCCN
GAANTCAGCGG

➤ Rev2

GNNCNGATGCTNCCAGATTTGATTNNTGNANNNNNNTNGNAANNAATCCNACNANNTNTNANNAGCCGANTC
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AGTGTTCACTGATNTCAGCAGCCCATTACGCCAAGACCAACTGGACATTATAATTTGTAACNNGAAGAANTCCGG
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CAACTGTGCATCTTTAAGAAGATTGAGAGGCGGTCTTGCCCTGGCCCTGCCAACTGACCATCGGCCCAACTTG
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CTTTGGATGAGTTAAACATGGTCGCTATCGTCCGCTACGCCTATGACAAAAGAGCTAATCCTCAAGTTGGTGTAGC
CTTCCCTTTCATTAAGGATGCCTATGAGTGTTTAGTTTATGTGCAGCTGCCTTTCATGGAAGACTTGCGGCAATACA
TGTTTTCCTCACTGAAAAACAATAAGAAGTGCNCCCCCACAGAGG

➤ Synthèse séquençage

ATGGCGTGGTCCGGTAATAAGGCAGCTGTTGTGCTGTGTATGGATGTGGGGGTTGCCATG	60
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AGTTCTCAACAAGCCGACTTCTTGGACGCCCTGATTGTGTGCATGGATTGATTACGCGT	360
GAAACCATAGGAAAGAAGTTTGGGAAGAAGCATATTGAAGTGTTCAGTCTCAGCAGC	420
CCATTTCAGCCAAGACCAACTGGACATTATAATTTGTAACTGAAGAAGTCCGGCATCTCC	480
CTGCAGTTCTTTCTGCCTTTTCCAATCGACAAGAATGGTGAGCCTGGGGAGACAGAAGAC	540
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CAAAAGGAAGGCATCCACATGGTGACGAGGGTGATGCTGTCTTTAGAAGGCAAGATGGT	660
CTGGATGAAATTTATTCCTTCAGCGAGAGTCTTCAGCAACTGTGCATCTTTAAGAAGATT	720
GAGAGGCGGTCTTGGCCCTGGCCCTGCCAACTGACCATCGGCCCAACTTGTCTATAAGG	780
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GATGAAACTGAAGTTTCAAAGAGGACACTATTCAAGGGTTCGCTATGGAAGCGACATC	960
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GTTCTGAAGGTCTTCGACGCAAGGATGATGAGGCAGCAGCTGTTGCACTTTCTTCCCTA	1140
GTTACGCTTTGGATGAGTTAAACATGGTCGCTATCGTCCGCTACGCCTATGACAAAAGA	1200
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AAAATTCCAATCTGAATTTTCAGCGGTTGTACCAGTGTCTGCTGCACAGAGCCTTACAT	1500
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GTCTAGTAAGACAGAAGATTGCCAGCTTTGAGGAAGCGAGTCTCCAGCTAATGAGTCAC	1860
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GAAGGCCTTCGAGAGAAAAGTGAAATTAACAATTAATCAATTTCTGGGAAATTGTCTGTG	2040
CAGGATGGAATTACTCTGATCACCAAAGACGAAAGCCCAGGAAGCTCTGTACAGCTGAG	2100
GAGGCCACGAAGTTCTGACCCCCAAAGACAAAGCAAAAGAAGACACAACAGGACTTGAA	2160
GAAGTGTTGATGTGGATGATTTACTGGACATGATATAG	2199

MAWSGNKAAVVLCDVGVAMGNSFPGEESPLEQAKKVM TMFVQRQVFSESKDEIALVLYGTESTDNALAGKD
 QYQNITVHRHMLPDLFDLLEDIGNKIQPSSQQADFLDALIVCMDLIQRETIGKKFGKKHIEVFTDLSSPFSQDQLDIIC
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 EATKFLTPKDKAKEDTTGLEEGGDVDDLLDMI-

➤ Blast contre banque rat :

	Name	Score	Score	Cover	Value	Ident	Len	
Rattus norvegicus X-ray repair cross complementing 5 (Xrcc5), mRNA	Norway rat	4050	4050	100%	0.0	99.91%	2545	NM_177419.2
Rattus norvegicus X-ray repair complementing defective repair in Chinese hamster cells 5, mRNA (cDNA clone MGC:72979...)	Norway rat	4050	4050	100%	0.0	99.91%	2548	BC061576.1
Rattus norvegicus mRNA for Xrcc5, partial cds	Norway rat	3480	3480	93%	0.0	97.22%	2100	AB066103.1

➤ Différence Séquencage/CDS au niveau NT :

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq	ATGGCGTGGTCCGGTAATAGGCAGCTGTTGTGCTGTGATGGATGTGGGGTGGCATGGGTAACTCCTTTCCCTGGTGAGAGATCCCACCTTGACAGGGCCAGAGAGTGATGACTATGTTTGTCCAC													
cds	ATGGCGTGGTCCGGTAATAGGCAGCTGTTGTGCTGTGATGGATGTGGGGTGGCATGGGTAACTCCTTTCCCTGGTGAGAGATCCCACCTTGACAGGGCCAGAGAGTGATGACTATGTTTGTCCAC													
Consensus	ATGGCGTGGTCCGGTAATAGGCAGCTGTTGTGCTGTGATGGATGTGGGGTGGCATGGGTAACTCCTTTCCCTGGTGAGAGATCCCACCTTGACAGGGCCAGAGAGTGATGACTATGTTTGTCCAC													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq	GACAGGTGTTTTCCGGAGCAGAGATGAGATCGCCTTAGTCCTCTATGGTACAGAGAGCCTGATACGCCCTTGCTGGCAGGACCACTATCAGACATCAGAGTGCACAGGCACCTGATGCTACACGA													
cds	GACAGGTGTTTTCCGGAGCAGAGATGAGATCGCCTTAGTCCTCTATGGTACAGAGAGCCTGATACGCCCTTGCTGGCAGGACCACTATCAGACATCAGAGTGCACAGGCACCTGATGCTACACGA													
Consensus	GACAGGTGTTTTCCGGAGCAGAGATGAGATCGCCTTAGTCCTCTATGGTACAGAGAGCCTGATACGCCCTTGCTGGCAGGACCACTATCAGACATCAGAGTGCACAGGCACCTGATGCTACACGA													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq	TTTTGATTGTGCTGGAGACATCGGAACAAATCCACCAAGTTCTCACACAGCCGACTTCTGGACGCCCTGATTGTGTGCATGGATTGATTACGGCTGAACCAATGGAAGAAGATTGGGAAGAAG													
cds	TTTTGATTGTGCTGGAGACATCGGAACAAATCCACCAAGTTCTCACACAGCCGACTTCTGGACGCCCTGATTGTGTGCATGGATTGATTACGGCTGAACCAATGGAAGAAGATTGGGAAGAAG													
Consensus	TTTTGATTGTGCTGGAGACATCGGAACAAATCCACCAAGTTCTCACACAGCCGACTTCTGGACGCCCTGATTGTGTGCATGGATTGATTACGGCTGAACCAATGGAAGAAGATTGGGAAGAAG													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
seq	CATATTGAAGTGTCTCACTGATCTCAGCAGCCCATTCAGCCAGACCACTGGACATTATAATTGTGATCTGAGAGAGTCCGGCATCTCCCTGCAGTCTTTCTGCCCTTTCCATCTGCACAGAGATGGTG													
cds	CATATTGAAGTGTCTCACTGATCTCAGCAGCCCATTCAGCCAGACCACTGGACATTATAATTGTGATCTGAGAGAGTCCGGCATCTCCCTGCAGTCTTTCTGCCCTTTCCATCTGCACAGAGATGGTG													
Consensus	CATATTGAAGTGTCTCACTGATCTCAGCAGCCCATTCAGCCAGACCACTGGACATTATAATTGTGATCTGAGAGAGTCCGGCATCTCCCTGCAGTCTTTCTGCCCTTTCCATCTGCACAGAGATGGTG													
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
seq	AGCCTGGGGAGACAGAGACCCAGCACTCCAGCTTCGACCACTGTGCACCTCCCTCCCTCAAAAGAGACTTACTGAGCAGCAAAAGGAGGCACTCCACATGGTGAACGAGGTGATGCTGTCTTAGAAGG													
cds	AGCCTGGGGAGACAGAGACCCAGCACTCCAGCTTCGACCACTGTGCACCTCCCTCCCTCAAAAGAGACTTACTGAGCAGCAAAAGGAGGCACTCCACATGGTGAACGAGGTGATGCTGTCTTAGAAGG													
Consensus	AGCCTGGGGAGACAGAGACCCAGCACTCCAGCTTCGACCACTGTGCACCTCCCTCCCTCAAAAGAGACTTACTGAGCAGCAAAAGGAGGCACTCCACATGGTGAACGAGGTGATGCTGTCTTAGAAGG													
	651	660	670	680	690	700	710	720	730	740	750	760	770	780
seq	CAAGATGGTCTGGATGAATTTATTCCCTCAGCAGAGTCTTCAGCACTGTGCATCTTTAAGAGAGATGAGAGGCGGCTCTGCCCTGGCCCTGCCCACTGACCATCGGCCCACTTTGTCTATAGG													
cds	CAAGATGGTCTGGATGAATTTATTCCCTCAGCAGAGTCTTCAGCACTGTGCATCTTTAAGAGAGATGAGAGGCGGCTCTGCCCTGGCCCTGCCCACTGACCATCGGCCCACTTTGTCTATAGG													
Consensus	CAAGATGGTCTGGATGAATTTATTCCCTCAGCAGAGTCTTCAGCACTGTGCATCTTTAAGAGAGATGAGAGGCGGCTCTGCCCTGGCCCTGCCCACTGACCATCGGCCCACTTTGTCTATAGG													
	781	790	800	810	820	830	840	850	860	870	880	890	900	910
seq	ATCGTAGCTATATAATCATTGTACAGGAGAAATTTAAAGAGAGTTGGGTAGTTGTGGACGAGAGACTTAAGAGAGGAGATATACAAAGAGAGACTGTTTATTGCTTAATGACGATGATGAACCTG													
cds	ATCGTAGCTATATAATCATTGTACAGGAGAAATTTAAAGAGAGTTGGGTAGTTGTGGACGAGAGACTTAAGAGAGGAGATATACAAAGAGAGACTGTTTATTGCTTAATGACGATGATGAACCTG													
Consensus	ATCGTAGCTATATAATCATTGTACAGGAGAAATTTAAAGAGAGTTGGGTAGTTGTGGACGAGAGACTTAAGAGAGGAGATATACAAAGAGAGACTGTTTATTGCTTAATGACGATGATGAACCTG													
	911	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040
seq	AAGTTTCCAAAGAGGACACTATTCCAGGGTTCGCTATGGAGCGACATCACTCTTTTCTTAAGTGGATGAGGACCAATGAATATAAATCGAGGGGAGTGCTTTCTGTTCTG6GGTCTGTAA													
cds	AAGTTTCCAAAGAGGACACTATTCCAGGGTTCGCTATGGAGCGACATCACTCTTTTCTTAAGTGGATGAGGACCAATGAATATAAATCGAGGGGAGTGCTTTCTGTTCTG6GGTCTGTAA													
Consensus	AAGTTTCCAAAGAGGACACTATTCCAGGGTTCGCTATGGAGCGACATCACTCTTTTCTTAAGTGGATGAGGACCAATGAATATAAATCGAGGGGAGTGCTTTCTGTTCTG6GGTCTGTAA													
	1041	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170
seq	ATCTTCTCAGGTTTCATAGAGATCTTCATGGGACATCAGTTCAGAGGTTCTCGACGAGAGGATGATGAGGACAGCTGTTGCACCTTTCTCCCTAGTTACAGCTTTGGATGAGTTAAACATGGTC													
cds	ATCTTCTCAGGTTTCATAGAGATCTTCATGGGACATCAGTTCAGAGGTTCTCGACGAGAGGATGATGAGGACAGCTGTTGCACCTTTCTCCCTAGTTACAGCTTTGGATGAGTTAAACATGGTC													
Consensus	ATCTTCTCAGGTTTCATAGAGATCTTCATGGGACATCAGTTCAGAGGTTCTCGACGAGAGGATGATGAGGACAGCTGTTGCACCTTTCTCCCTAGTTACAGCTTTGGATGAGTTAAACATGGTC													
	1171	1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
seq	GCTATCGTCGCTACGCTATGACAAAGAGCTAATCTCAGTTGGGTAGTCTCCCTTTCATTAGGAGTGCTATGAGTGTAGTTATGTTATGTCGAGCTGCCCTTCATGGAGACTTGGGCAATACA													
cds	GCTATCGTCGCTACGCTATGACAAAGAGCTAATCTCAGTTGGGTAGTCTCCCTTTCATTAGGAGTGCTATGAGTGTAGTTATGTTATGTCGAGCTGCCCTTCATGGAGACTTGGGCAATACA													
Consensus	GCTATCGTCGCTACGCTATGACAAAGAGCTAATCTCAGTTGGGTAGTCTCCCTTTCATTAGGAGTGCTATGAGTGTAGTTATGTTATGTCGAGCTGCCCTTCATGGAGACTTGGGCAATACA													
	1301	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430
seq	TGTTTTCCCTCCTGAAAGCAATAGAGAGTGCACCCCCACAGAGGCACAGCTGAGTGCATCGATGATCGATTGATTCCATGAGCTTGGTAAGAAACAGGAGAGAGACATCATCGAGAGCTTGT													
cds	TGTTTTCCCTCCTGAAAGCAATAGAGAGTGCACCCCCACAGAGGCACAGCTGAGTGCATCGATGATCGATTGATTCCATGAGCTTGGTAAGAAACAGGAGAGAGACATCATCGAGAGCTTGT													
Consensus	TGTTTTCCCTCCTGAAAGCAATAGAGAGTGCACCCCCACAGAGGCACAGCTGAGTGCATCGATGATCGATTGATTCCATGAGCTTGGTAAGAAACAGGAGAGAGACATCATCGAGAGCTTGT													
	1431	1440	1450	1460	1470	1480	1490	1500	1510	1520	1530	1540	1550	1560
seq	TCCACCTCCAAATTCCAATCTGATTTTCAGCGGTTGACAGTGTCTGCTGCACAGAGCTTACATCTCCAGGAGCGGCTGCCCCCAATTCAGCAGCACATTTTGATATGCTGGATCCCCCACT													
cds	TCCACCTCCAAATTCCAATCTGATTTTCAGCGGTTGACAGTGTCTGCTGCACAGAGCTTACATCTCCAGGAGCGGCTGCCCCCAATTCAGCAGCACATTTTGATATGCTGGATCCCCCACT													
Consensus	TCCACCTCCAAATTCCAATCTGATTTTCAGCGGTTGACAGTGTCTGCTGCACAGAGCTTACATCTCCAGGAGCGGCTGCCCCCAATTCAGCAGCACATTTTGATATGCTGGATCCCCCACT													
	1561	1570	1580	1590	1600	1610	1620	1630	1640	1650	1660	1670	1680	1690
seq	GAGATGAAGCAAAATGTGAGATTCACCTCTCTAAGTAAAGACCTTTTCCCTCTGACGGAGTGGTAAAGAAAGGACCAAGTGACTGCTCAGGACGTTTCCAGACAAATTTGAAGAGGGGCCCG													
cds	GAGATGAAGCAAAATGTGAGATTCACCTCTCTAAGTAAAGACCTTTTCCCTCTGACGGAGTGGTAAAGAAAGGACCAAGTGACTGCTCAGGACGTTTCCAGACAAATTTGAAGAGGGGCCCG													
Consensus	GAGATGAAGCAAAATGTGAGATTCACCTCTCTAAGTAAAGACCTTTTCCCTCTGACGGAGTGGTAAAGAAAGGACCAAGTGACTGCTCAGGACGTTTCCAGACAAATTTGAAGAGGGGCCCG													
	1691	1700	1710	1720	1730	1740	1750	1760	1770	1780	1790	1800	1810	1820
seq	CTGCTAAAGAAATACAGACTGAGAGAGAGAGGTGCATCTCAGCATCTCCAGCTGGCAGAGGGGATGTACCAAGGTTGAGAGTGTGAATCCGTTGAAAGACTCCGCTGTCTAGTAGACAGAGAT													
cds	CTGCTAAAGAAATACAGACTGAGAGAGAGAGGTGCATCTCAGCATCTCCAGCTGGCAGAGGGGATGTACCAAGGTTGAGAGTGTGAATCCGTTGAAAGACTCCGCTGTCTAGTAGACAGAGAT													
Consensus	CTGCTAAAGAAATACAGACTGAGAGAGAGAGGTGCATCTCAGCATCTCCAGCTGGCAGAGGGGATGTACCAAGGTTGAGAGTGTGAATCCGTTGAAAGACTCCGCTGTCTAGTAGACAGAGAT													
	1821	1830	1840	1850	1860	1870	1880	1890	1900	1910	1920	1930	1940	1950
seq	TGCCAGCTTTGAGGAGCGAGTCTCCAGCTAATGAGTCACATGACAGTTTTTGGATACCAATGAACACCTGATTTTATGAAGATATGGACTGCATCAAGCTCTCCGGGAGGAGCAATTCAGTTTT													
cds	TGCCAGCTTTGAGGAGCGAGTCTCCAGCTAATGAGTCACATGACAGTTTTTGGATACCAATGAACACCTGATTTTATGAAGATATGGACTGCATCAAGCTCTCCGGGAGGAGCAATTCAGTTTT													
Consensus	TGCCAGCTTTGAGGAGCGAGTCTCCAGCTAATGAGTCACATGACAGTTTTTGGATACCAATGAACACCTGATTTTATGAAGATATGGACTGCATCAAGCTCTCCGGGAGGAGCAATTCAGTTTT													
	1951	1960	1970	1980	1990	2000	2010	2020	2030	2040	2050	2060	2070	2080
seq	TCAGAGAGCAGCGTTTCACACAGTTTCTGGAGGGCTTCGAGAGAAAGTGGAAATTAACCAATTAATCATTTCTGGGAATTTGCTGTCAGGATGGAAATTAATCTGATCACCAGAGCAGAAAGCCAG													
cds	TCAGAGAGCAGCGTTTCACACAGTTTCTGGAGGGCTTCGAGAGAAAGTGGAAATTAACCAATTAATCATTTCTGGGAATTTGCTGTCAGGATGGAAATTAATCTGATCACCAGAGCAGAAAGCCAG													
Consensus	TCAGAGAGCAGCGTTTCACACAGTTTCTGGAGGGCTTCGAGAGAAAGTGGAAATTAACCAATTAATCATTTCTGGGAATTTGCTGTCAGGATGGAAATTAATCTGATCACCAGAGCAGAAAGCCAG													
	2081	2090	2100	2110	2120	2130	2140	2150	2160	2170	2180	2190	2199	
seq	GAGGCTCTGTACAGCTGAGGAGGCCAGGATTTCTGACCCCCAAGACAAAGCAAAAGAGACACACAGGACTTGAGAGGGTGGTGTGATGGATGATTACTGGACATGATATAG													
cds	GAGGCTCTGTACAGCTGAGGAGGCCAGGATTTCTGACCCCCAAGACAAAGCAAAAGAGACACACAGGACTTGAGAGGGTGGTGTGATGGATGATTACTGGACATGATATAG													
Consensus	GAGGCTCTGTACAGCTGAGGAGGCCAGGATTTCTGACCCCCAAGACAAAGCAAAAGAGACACACAGGACTTGAGAGGGTGGTGTGATGGATGATTACTGGACATGATATAG													

mutation T<C en 1915 G<A 1956

➤ Différence Séquençage/CDS au niveau PROT :

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
✓	X-ray repair complementing defective repair in Chinese hamster cells 5, isoform CRA_a [Rattus norvegicus]	Norway rat	1508	1508	100%	0.0	99.86%	732	EDL75243.1
✓	X-ray repair cross-complementing protein 5 [Rattus norvegicus]	Norway rat	1506	1506	100%	0.0	99.86%	732	NP_803154.1
✓	Xrcc5 [Rattus norvegicus]	Norway rat	1359	1359	93%	0.0	96.63%	683	BAB83859.1
✓	X-ray repair complementing defective repair in Chinese hamster cells 5, isoform CRA_b [Rattus norvegicus]	Norway rat	471	471	31%	1e-163	99.56%	228	EDL75244.1

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq	MAHSGNKAAYVLCMDVGVAMGNSFPGEESPLEQAKKVMTMFVQRQVFSESKDEIALVLYGTESTDNALAGKDQYQNITYVHRHLMLPDFDLLEDIGNKIQPSQQADFLOALIVCHDLIQRETIGKKFGKK													
ref	MAHSGNKAAYVLCMDVGVAMGNSFPGEESPLEQAKKVMTMFVQRQVFSESKDEIALVLYGTESTDNALAGKDQYQNITYVHRHLMLPDFDLLEDIGNKIQPSQQADFLOALIVCHDLIQRETIGKKFGKK													
Consensus	MAHSGNKAAYVLCMDVGVAMGNSFPGEESPLEQAKKVMTMFVQRQVFSESKDEIALVLYGTESTDNALAGKDQYQNITYVHRHLMLPDFDLLEDIGNKIQPSQQADFLOALIVCHDLIQRETIGKKFGKK													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq	HIEVFTDLSSPFSQDQLDIIICNLKKSGLSQFFLPFPIDKNGEPGETEDHSSFDHCAPSPQKGLTEQQKEGIHMVTRYMLSLGKDGDLDEIYSFSESQQLCIFKKIERRSLPWPQCLTIGPNLSIR													
ref	HIEVFTDLSSPFSQDQLDIIICNLKKSGLSQFFLPFPIDKNGEPGETEDHSSFDHCAPSPQKGLTEQQKEGIHMVTRYMLSLGKDGDLDEIYSFSESQQLCIFKKIERRSLPWPQCLTIGPNLSIR													
Consensus	HIEVFTDLSSPFSQDQLDIIICNLKKSGLSQFFLPFPIDKNGEPGETEDHSSFDHCAPSPQKGLTEQQKEGIHMVTRYMLSLGKDGDLDEIYSFSESQQLCIFKKIERRSLPWPQCLTIGPNLSIR													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq	IVAYKSIVQEFKKSWMVVDARTLKKEDIQKETVYCLNDDDETEVSKEDTIQGFYRGSDIIPFSKYDDEEQMKYKSEGKCFSVLGFCSSQVHRRFFMNGHQLKVFAAKDDEAAVALSSLVHALDELNMV													
ref	IVAYKSIVQEFKKSWMVVDARTLKKEDIQKETVYCLNDDDETEVSKEDTIQGFYRGSDIIPFSKYDDEEQMKYKSEGKCFSVLGFCSSQVHRRFFMNGHQLKVFAAKDDEAAVALSSLVHALDELNMV													
Consensus	IVAYKSIVQEFKKSWMVVDARTLKKEDIQKETVYCLNDDDETEVSKEDTIQGFYRGSDIIPFSKYDDEEQMKYKSEGKCFSVLGFCSSQVHRRFFMNGHQLKVFAAKDDEAAVALSSLVHALDELNMV													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
seq	AIVRYAYDKRANPQVGVAFFPIKDAYECLVYVQLPFMEDLRQYMFSSLKNNKKCTPTEAQLSAIDDLIDSMSLVKNEEEDIEDLFPTSKIPNPEFQRLYQCLLHRALHLQERLPPIQHILNMLDPPT													
ref	AIVRYAYDKRANPQVGVAFFPIKDAYECLVYVQLPFMEDLRQYMFSSLKNNKKCTPTEAQLSAIDDLIDSMSLVKNEEEDIEDLFPTSKIPNPEFQRLYQCLLHRALHLQERLPPIQHILNMLDPPT													
Consensus	AIVRYAYDKRANPQVGVAFFPIKDAYECLVYVQLPFMEDLRQYMFSSLKNNKKCTPTEAQLSAIDDLIDSMSLVKNEEEDIEDLFPTSKIPNPEFQRLYQCLLHRALHLQERLPPIQHILNMLDPPT													
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
seq	EMKAKCEIPLSKYKTLFPLTEVYKKKQDYTAQDVFDNIIEGPAARKKYKTEKEEGHISISSLAEGNVTYKGSYNPVENFRVLVRQKIASFEERASLQLMSHIEQFLDTNETLYFMKSHDRIKALREERAIQF													
ref	EMKAKCEIPLSKYKTLFPLTEVYKKKQDYTAQDVFDNIIEGPAARKKYKTEKEEGHISISSLAEGNVTYKGSYNPVENFRVLVRQKIASFEERASLQLMSHIEQFLDTNETLYFMKSHDRIKALREERAIQF													
Consensus	EMKAKCEIPLSKYKTLFPLTEVYKKKQDYTAQDVFDNIIEGPAARKKYKTEKEEGHISISSLAEGNVTYKGSYNPVENFRVLVRQKIASFEERASLQLMSHIEQFLDTNETLYFMKSHDRIKALREERAIQF													
	651	660	670	680	690	700	710	720	730	740	750	760	770	780
seq	SEEQRFSNLEGLREKVEIKQLNHFMEIYVQDGITLITKDESPGSSVTAEEATKFLTPKDKAKEDTTGLEEGGDVDDLLDHI													
ref	SEEQRFSNLEGLREKVEIKQLNHFMEIYVQDGITLITKDESPGSSVTAEEATKFLTPKDKAKEDTTGLEEGGDVDDLLDHI													
Consensus	SEEQRFSNLEGLREKVEIKQLNHFMEIYVQDGITLITKDESPGSSVTAEEATKFLTPKDKAKEDTTGLEEGGDVDDLLDHI													

comme rate mutation en 639

Flag BirA Xrcc5 DiT24hLPS (clone B)OK, même mutation en 639 que rate et DiT0

○ **FlagBirA DiT48hMix clone A**

➤ **B3Fwd DiT48h 852NT**

ATGGCGTGGTCCGGTAATAAGCTGTTGTGCTGTGTATGGATGTGGGGGTTGCCATGGGTAACCTTTCTGGTG
AAGAATCCCCACTTGAACAGGCCAAGAAAGTGATGACTATGTTTGTCCAACGACAGGTGTTTTCGGAGAGCAAG
GATGAGATCGCCTTAGTCCTCTATGGTACAGAGAGCACTGATAACGCCCTTGCTGGCAAGGACCAGTATCAGAAC
ATCACAGTGCACAGGCACCTGATGCTACCAGATTTTGATTTGCTGGAAGACATCGGAAACAAAATCCAACCAAGT
TCTCAACAAGCCGACTTCCTGGACGCCCTGATTGTGTGCATGGATTTGATTACAGCGTGAAACCATAGGAAAGAAG
TTTGGGAAGAAGCATATTGAAGTGTTCACCTGACCTCAGCAGCCCATTCAGCCAAGACCAACTGGACATTATAATT
TGTAACCTGAAGAAGTCCGGCATCTCCCTGCAGTTCTTTCTGCCTTTTCCAATCGACAAGAATGGTGAGCCTGGG
GAGACAGAAGACCAGACTCCaGCTTCGACCACTGTGCACCCTCTCCCTCAAAAAGGACTTACTGAGCAGCa
AAAGGAAGGCATCCACATGGTGACGAGGGTGATGCTGTCTTTAGAAGGNAAAGATGGTCTGGATGAAATTTATT
CCTTCAGCGAGAGTCTTCAGCAACTGTGCGTCTTTAANAANATTGAGAGGCGGTCCTTGCCCTNGNCCTGCCAA
CTGACCATCGGCCCCAACTTGTCTANNNNNTCGTANCCTATAAATCGATTGNACNGGANANTTTAAANANTTG
GGTAGTTGTGGNNNNANANTCTAANNAGGAAG

➤ **BGHRev DiT48h 1073NT**

TGCACTTTNNNNCNTNGTNCATGCTTNGNATGAGTNNANCATNGTNNCNANNNTNNNNNTANNNNATGNCAA
ANNGNTAATCCTCAAGTTGGTGTANCNTCCNNTTCATTAAGGATGCCTANGAGTGTTTAGTTTATGTGCAGCTN
CCTTCATGGAAGACTNGCGNCAATACATGTTTTCTCANTGAAAAACAATAAGAAGTGCACCCCCACAGAGGC
ACAGNTGAGTGCGATCGATGATCTGATTGATTCCATGAGCTTGGTAAAGNAAAACCAGGAAGAAGACATCATNG
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AAGGTCACATCAGCATCTCCAGCCTGGCAGAAGGGAATGTCACCAAGGTTGGAAGTGTGAATCCTGTTGAAAAC
TTCCGTGTCCTAGTAAGACAGAAGATTGCCAGCTTTGAGGAAGCGAGTCTCCAGCTAATGAGTCACATTGAACA
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AGCTGAGGAGGCCACGAAGTTCCTGACCCCCAAAGACAAAGCAAAGAAGACACAACAGGACTTGAAGAAGG
TGGTGATGTGGATGATTTACTGGACATGATATAG

➤ **BGHRev du 25/11**

GNCAANGAGNNNATNNTCAAGTTGGNGTANNTTCNNTNCATTAAGGANGCCTATGAGTGTTTAGTTTATGTGC
AGCTNCCTTTTCATGGAAGACNNGCGCAATACATGTTTTCTCACTGAAAAACAATAAGAAGTGCACCCCCACA
GAGGCACAGCTGAGTGCGATCGATGATCTGATTGATTCCATGAGCTTGGTAAAGAAAAACCAGGAAGAAGACAT
CATCGAAGACTTGTTTCCAACCTCCAAAATTCCAAATCNTGAATTCAGCGTTGTACCAGTGTCTGCTGCACAGA
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TCACAGCTGAGGAGGCCACGAAGTTCCTGACCCCCAAAGACAAAGCAAAGAAGACACAACAGGACTTGAAG
AAGGTGGTGTATGTGGATGATTTACTGGACATGATATAG

➤ **Fwd1**

GGNATCCNCATGGTGACGAGGGTGA~~t~~GCTGTCTTTAGAAGGCCAAAGATGGTCTGGATGAAATTTATTCCTTCA
GCGAGAGTCTTCAGCAACTGTGCGTCTTTAAGAAGATTGAGAGGCGGTCCTTGCCCTGGCCCTGCCAACTGAC
CATCGGCCCCAACTTGTCTATAAGGATCGTAGCCTATAAATCGATTGTACAGGAGAAATTTAAAAAGAGTTGG
GTAGTTGTGGACGCAAGAACTCTAAAGAAGGAAGATATACAAAAGAGACTGTTTATTGCCTAAATGACGATG
ATGAAACTGAAGTTTCCAAAGAGGACACTATTCAAGGGTTCCGCTATGGAAGCGACATCATTCTTTTTCTAAA
GTGGATGAGGAACAAATGAAATATAAATCGGAGGGGAAGTGCTTCTCTGTTCTGGGGTTCTGTAAATCTTCTC
AGGTTTCATAGAAGATTCTTCATGGGACATCAAGTTCTGAAGGTCTTCGAGCGAAGGATGATGAGGCAGCAG
CTGTTGCACTTTCTCCCTCGTTCATGCTTTGGATGAGTTAAACATGGTCGCCATCGTCCGCTACGCCTATGACA
AAAGAGCTAATCCTCAAGTTGGTGTAGCCTTCCCTTTCATTAAGGATGCCTATGAGTGTTTAGTTTATGTGCAG
CTGCCTTTCATGGAAGACTTGCGGCAATACATGTTTTCTCACTGAAAAACAATAAGAAGTGCACCCCCACAGA
GGCACAGCTGA~~g~~TGCGATCGATGATCTGATTGATTCCATGAGCTTGGTAAAGAAAAACCAGGAAGAAGACATC
ATCGAAGACTTGTTCCNACCTCCAAAATTCCAAATCCTGAATTTACGCGGTTGTACCAGTGTCTGCTGCACAG
ANCCTTACATCTCCNGGANCGGCTGCCCCNATTCAGCANACATTTTGAATATGCTGGNTCCCCCACTGAN
ATGAAAGCAAATGNGANANTCCNCTCTCTNAGTAANANCNTTTTNCNNNNNANGGNNNTCNNNNAAANNN
NCAGTGACTGNTCNNNNGTTTTCCANANANANNANANGNNNNNTGCTAAAA

➤ **Fwd2**

TGAGAGNNGNCCTTGCCCTGGCCCTGCCAACTGACCATCGGCCCCAACTTGTCTATAAGGATCGTAGCCTAT
AAATCGATTGTACAGGAGAAATTTAAAAAGAGTTGGGTAGTTGTGGACGCAAGAACTCTAAAGAAGGAAGAT
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GGTTCGCTATGGAAGCGACATCATTCTTTTTCTAAAGTGGATGAGGAACAAATGAAATATAAATCGGAGGG
GAAGTGCTTCTCTGTTCTGGGGTTCTGTAAATCTTCTCAGGTTTCATAGAAGATTCTTCATGGGACATCAAGTTCT
GAAGGTCTTCGAGCGAAGGATGATGAGGCAGCAGCTGTTGCACTTTCTCCCTCGTTCATGCTTTGGATGAGT
TAAACATGGTCGCCATCGTCCGCTACGCCTATGACAAAAGAGCTAATCCTCAAGTTGGTGTAGCCTTCCCTTTC
ATTAAGGATGCCTATGAGTGTTTAGTTTATGTGCAGCTGCCTTTCATGGAAGACTTGCGGCAATACATGTTTTCT
CTCACTGAAAAACAATAAGAAGTGCACCCCCACAGAGGCACAGCTGAGTGCGATCGATGATCTGATTGATTCC
ATGAGCTTGGTAAAGAAAAACCAGGAAGAAGACATCATGAAGAcTTGTTTCCaACCTCCAAAATTCCAAATCC
TGAATTTACGCGGTTGTACCAGTGTCTGCTGCACAGAGCCTTACATCTCCAGGAGCGGCTGCCCCNATTCAGC
AGCACATTTTGAATATGCTGGATCCCCCACTGAGATGAAAGCAAATGNGAGATTCCACTCTCTAAAGTAAA
GACCCTTTCCCTCTGACGGAAGTCGTTAANAAAAANNANCNAGTGACTGNTCNNNNNTTTTCCAAGACAAT
AATGAANNNGGGNCCGCTGCTAAAAANNC

➤ **Rev1**

GNCTCAGNANCCNNTNNNCNANNCNNNNNTNGACNTATAATTNNNNNNGAAGAANTNCNNCNNTCCNGC
AGNNNTTNTNCTTNCCAATNGACAAGAATGGTGAGCNTNGGGAGACAGAAGNCCACGANTCCAGCTTCGN
CCACTGTGCACCCTCCTTCCCTCAAAAAGGACTTANTGAGCAGCAAAAGGAAGGCATNCACATGGTGACGAG
GGTGATGCTGTCTTTAGAAGGCCAAAGATGGTCTGGATGAAATTTATTCNTTCAGCGAGAGTCTTCAGCAACTG
TGCGTCTTTAAGAAGATTGAGAGGCGGTCCTTGCCCTGGCCCTGCCAACTGACCATCGGCCCCAACTTGTCTAT
AAGGATCGTAGCCTATAAATCGATTGTACAGGAGAAATTTAAAAAGAGTTGGGTAGTTGTGGACGCAAGAAC
TCTAAAGAAGGAAGATATACAAAAGAGACTGTTTATTGCCTAAATGACGATGATGAAACTGAAGTTTCCAAA
GAGGACACTATTCAAGGGTTCCGCTATGGAAGCGACATCATTCTTTTTCTAAAGTGGATGAGGAACAAATGA

AATATAAATCGGAGGGGAAGTGCTTCTCTGTTCTGGGGTTCTGTAAATCTTCTCAGGTTTCATAGAAGATTCTTC
ATGGGACATCAAGTTCTGAAGGTCTTCGCAGCGAAGGATGATGAGGCAGCAGCTGTTGCACTTTCTCCCTCG
TTCATGCTTTGGATGAGTTAAACATGGTCGCCATCGTCCGCTACGCCTATGACAAAAGAGCTAATCCTCAAGTT
GGTGTAGCCTTCCCTTTTCTTAAGGATGCCTATGAGTGTTTAGTTTATGTGCAGCTGCCTTTTCATGGAAGACTTG
CGGCAATACATGTTTTCTCTACTGAAAAACAATAAGAAGTGACCCCCACAGAGGCACAGCTGAGTGCGATCG
ATGATCTGATTGATTCCATGAGCTTGGTAAAGAAAAACCAGGAAGAAGACATCATCGAAGACTTGTTTCCAacC
TCCAAAATTCCAANTCCNGANNTCAGC

➤ **Rev2**

TTGNNNNANNNCATNNNNANNNAAAANCCNNCNAANTNTNNNNCNANNCNNNTTNNNGNACGCCCNGANNGTG
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TGCACCCTCCTTCCCTCAAAAAGGACTTACTGAGCAGCAAAAAGGAAGGCATCCACATGGTGACGAGGGTGATGC
TGTCTTTAGAAGGCAAAGATGGTCTGGATGAAATTTATTCCTTCAGCGAGAGTCTTCAGCAACTGTGCGTCTTTAA
GAAGATTGAGAGGCGGTCTTGCCCTGGCCCTGCCAACTGACCATCGGCCCAACTTGCTCTATAAGGATCGTAGC
CTATAAATCGATTGTACAGGAGAAATTTAAAAAGAGTTGGGTAGTTGTGGACGCAAGAAGTCTAAAGAAGGAAG
ATATACAAAAAGAGACTGTTTATTGCCTAAATGACGATGATGAACTGAAGTTTCCAAAGAGGACACTATTCAAG
GGTTCCGCTATGGAAGCGACATCATTCTTTTTCTAAAGTGGATGAGGAACAAATGAAATATAAATCGGAGGGGA
AGTGCTTCTCTGTTCTGGGGTTCTGTAAATCTTCTCAGGTTTCATAGAAGATTCTTCATGGGACATCAAGTTCTGAA
GGTCTTCGCAGCGAAGGATGATGAGGCAGCAGCTGTTGCACTTTCTTCCCTCGTTCATGCTTTGGATGAGTTAAA
CATGGTCGCCATCGTCCGCTACGCCTATGACAAAAGAGCTAATCCTCAAGTTGGTGTAGCCTTCCCTTTCATTAAG
GATGCCTATGAGTGTTTAGTTTATGTGCAGCTGCCTTTCATGGAAGACTTGCGGCAATACATGTTTTCTCTACTGAA
AAACAATAAGAAGTGCNCCCCCNCA

➤ **Blast DiT48h contre banque rat :**

ATGGCGTGGTCCGTAATAAG	CTGTTGTGCTGTGTATGGATGTGGGGTTGCCATG 60	
GGTAACTCCTTTCCCTGGTGAAGAATCCCCACTTGAACAGGCCAAGAAAGTGATGACTATG		120
TTTGTCCAACGACAGGTGTTTTCGGAGAGCAAGGATGAGATCGCCTTAGTCCTCTATGGT		180
ACAGAGAGCACTGATAACGCCCTTGCTGGCAAGGACCAGTATCAGAACATCACAGTGAC		240
AGGCACCTGATGCTACCAGATTTTGATTGCTGGAAGACATCGGAAACAAAATCCAACCA		300
AGTTCTCAACAAGCCGACTTCCTGGACGCCCTGATTGTGTGCATGGATTGATTACGCGT		360
GAAACCATAGGAAAGAAGTTTGGGAAGAAGCATATTGAAGTGTTCACTGACCTCAGCAGC		420
CCATTAGCCAAGACCAACTGGACATTATAATTTGTAACCTGAAGAAGTCCGGCATCTCC		480
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CACGACTCCAGCTTCGACCACTGTGCACCCTCCTTCCCTCAAAAAGGACTTACTGAGCAG		600
CAAAAGGAAGGCATCCACATGGTGACGAGGGTGATGCTGTCTTTAGAAGGCAAAGATGGT		660
CTGGATGAAATTTATTCCTTCAGCGAGAGTCTTCAGCAACTGTGCGTCTTTAAGAAGATT		720
GAGAGGCGGTCTTGCCCTGGCCCTGCCAACTGACCATCGGCCCAACTTGCTCTATAAGG		780
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GCAAGAACTCTAAAGAAGGAAGATATACAAAAGAGACTGTTTATTGCCTAAATGACGAT		900
GATGAAACTGAAGTTTCCAAAGAGGACACTATTCAAGGGTTCCGCTATGGAAGCGACATC		960
ATTCTTTTCTAAAGTGGATGAGGAACAAATGAAATATAAATCGGAGGGGAAGTGCTTC		1020
TCGTGTTCTGGGGTTCTGTAAATCTTCTCAGGTTTCATAGAAGATTCTTCATGGGACATCAA		1080
GTTCTGAAGGTCTTCGCAGCGAAGGATGATGAGGCAGCAGCTGTTGCACTTTCTTCCCTC		1140
GTTTCATGCTTTGGATGAGTTAAACATGGTCGCCATCGTCCGCTACGCCTATGACAAAAGA		1200
GCTAATCCTCAAGTTGGTGTAGCCTTCCCTTTCATTAAGGATGCCTATGAGTGTTTAGTT		1260
TATGTGCAGCTGCCTTTCATGGAAGACTTGCGGCAATACATGTTTTCTCTACTGAAAAAC		1320
AATAAGAAGTGACCCCCACAGAGGCACAGCTGAGTGCGATCGATGATCTGATTGATTCC		1380
ATGAGCTTGGTAAAGAAAAACCAGGAAGAAGACATCATCGAAGACTTGTTTCCAACCTCC		1440
AAAAATCCAAATCCTGAATTCAGCGGTTGTACCAGTGTCTGCTGCACAGAGCCTTACAT		1500
CTCCAGGAGCGGCTGCCCCCAATTCAGCAGCACATTTGAATATGCTGGATCCCCCACT		1560
GAGATGAAAGCAAAATGTGAGATTCCACTCTCTAAAGTAAAGACCTTTTCCCTCTGACG		1620
GAAGTCGTTAAGAAAAAGGACCAAGTGACTGCTCAGGACGTTTTCCAAGACAATAATGAA		1680
GAGGGGCCCCGTGCTAAAAAATACAAGACTGAGAAAGAAGAAGGTCACATCAGCATCTCC		1740
AGCCTGGCAGAAGGGAATGTCACCAAGGTTGGAAGTGTAATCCTGTTGAAAACCTCCGT		1800

		1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq		ATGGCGTGGTCCGGTARTAAAG...CTGTGTGCTGTGATGGATGTGGGGGTTGCCATGGGTACTCTTCTTGGTGARGAATCCCCATTGACACGGCCAGGAAGATGATGACTATGTTTGTCCAC													
Consensus		ATGGCGTGGTCCGGTARTAAAG...CTGTGTGCTGTGATGGATGTGGGGGTTGCCATGGGTACTCTTCTTGGTGARGAATCCCCATTGACACGGCCAGGAAGATGATGACTATGTTTGTCCAC													
		131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq		GACAGGTGTTTTCGGAGAGCAGGATGAGATGCCCTAGTCTTCATGGTACAGAGAGCATTGATAGCGCCCTTGTGCGAGGAGCCAGTATCAGACATCACAGTGCACAGGACCTTGATGCTACCGA													
Consensus		GACAGGTGTTTTCGGAGAGCAGGATGAGATGCCCTAGTCTTCATGGTACAGAGAGCATTGATAGCGCCCTTGTGCGAGGAGCCAGTATCAGACATCACAGTGCACAGGACCTTGATGCTACCGA													
		261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq		TTTTGATTTCCTGGAGACATCGGAACAAATCCACACAGTTCTACACAGGCCAGTCTCCGAGGCCCTGATGTGTGTCATGGATTTGATTTCAGCGTGAACCATAGGAAGAGATTTGGGAGAGAG													
Consensus		TTTTGATTTCCTGGAGACATCGGAACAAATCCACACAGTTCTACACAGGCCAGTCTCCGAGGCCCTGATGTGTGTCATGGATTTGATTTCAGCGTGAACCATAGGAAGAGATTTGGGAGAGAG													
		391	400	410	420	430	440	450	460	470	480	490	500	510	520
seq		CATATTGAAGTGTCTACCTGACCTCAGCAGGCCCATTCAGCCAGAGCCACTGGACATTATATTTGTARCTTGAAAGATCCGCGCATCTCCCTCGAGTTCTTTTCGCTTTTCCAACTGCACAGAGATGGTG													
Consensus		CATATTGAAGTGTCTACCTGACCTCAGCAGGCCCATTCAGCCAGAGCCACTGGACATTATATTTGTARCTTGAAAGATCCGCGCATCTCCCTCGAGTTCTTTTCGCTTTTCCAACTGCACAGAGATGGTG													
		521	530	540	550	560	570	580	590	600	610	620	630	640	650
seq		AGCCTGGGGAGACAGAGACCAGCTCAGCTTCGACACTGTGCACCTCTCTCCCTCAAAAGAGACTTACTGACAGCAGAAAGGAGGCATCCACATGGTGACAGGGGTGATGCTGCTTTAGAGAG													
Consensus		AGCCTGGGGAGACAGAGACCAGCTCAGCTTCGACACTGTGCACCTCTCTCCCTCAAAAGAGACTTACTGACAGCAGAAAGGAGGCATCCACATGGTGACAGGGGTGATGCTGCTTTAGAGAG													
		651	660	670	680	690	700	710	720	730	740	750	760	770	780
seq		CAARGATGGTCTGGATGAATTTATCTCTCAGCGAGAGTCTCAGACACTGTGCTGCTTTAARGAGATTGAGAGGCGGTCTTGCCCTGGCCCTGCCACTGACCATCGGCCCACTTGCTCTATAGG													
Consensus		CAARGATGGTCTGGATGAATTTATCTCTCAGCGAGAGTCTCAGACACTGTGCTGCTTTAARGAGATTGAGAGGCGGTCTTGCCCTGGCCCTGCCACTGACCATCGGCCCACTTGCTCTATAGG													
		781	790	800	810	820	830	840	850	860	870	880	890	900	910
seq		ATCTAGCCTATTAATCGATTGTACAGGGAATTTAAAGAGAGTTGGGATGTTGGAGCCAGAGACTTAAAGAGGAGAGATATCAAAAGAGAGCTGTTATTGCTTAATGACATGATGAACCTG													
Consensus		ATCTAGCCTATTAATCGATTGTACAGGGAATTTAAAGAGAGTTGGGATGTTGGAGCCAGAGACTTAAAGAGGAGAGATATCAAAAGAGAGCTGTTATTGCTTAATGACATGATGAACCTG													
		911	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040
seq		ARGTTTCCAAAGAGGACATATTCAAGGTTCCGCTATGGAGCGACATCATCTCTTTCTAARGTGGATGAGGACAAATGAATATTAATCGAGGGGAGTGCTCTCTGTTCTGGGGTCTGTAA													
Consensus		ARGTTTCCAAAGAGGACATATTCAAGGTTCCGCTATGGAGCGACATCATCTCTTTCTAARGTGGATGAGGACAAATGAATATTAATCGAGGGGAGTGCTCTCTGTTCTGGGGTCTGTAA													
		1041	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170
seq		ATCTCTCAGGTTCTATAGAGATCTTCATGGGACATCAGTCTCGARGCTTCGCGAGGAGGATGATGAGGCAGCAGCTGTGCATCTTCTCCCTCGTTCATGCTTTGGATGAGTTAARCATGGTCT													
Consensus		ATCTCTCAGGTTCTATAGAGATCTTCATGGGACATCAGTCTCGARGCTTCGCGAGGAGGATGATGAGGCAGCAGCTGTGCATCTTCTCCCTCGTTCATGCTTTGGATGAGTTAARCATGGTCT													
		1171	1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
seq		GCTATCGTCCGCTAGCTGATGACAAAGAGCTAATCCTCAGTGGTGGTAGGCTTCCCTTCATTAAAGATGCCATGAGTGTAGTTTATGTGTCAGCTGCCCTTCATGAGAGCTTGGCCATACA													
Consensus		GCTATCGTCCGCTAGCTGATGACAAAGAGCTAATCCTCAGTGGTGGTAGGCTTCCCTTCATTAAAGATGCCATGAGTGTAGTTTATGTGTCAGCTGCCCTTCATGAGAGCTTGGCCATACA													
		1301	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430
seq		TGTTTTCTCACTAGAAACAAATAGAGAGTGACCCCCACAGAGGCACAGCTGAGTGGCGATCGATGATCTGATTGATTCATGAGCTTGGTAAAGAAAACAGGAGAGAGACATCATCGAGACTTTGT													
Consensus		TGTTTTCTCACTAGAAACAAATAGAGAGTGACCCCCACAGAGGCACAGCTGAGTGGCGATCGATGATCTGATTGATTCATGAGCTTGGTAAAGAAAACAGGAGAGAGACATCATCGAGACTTTGT													
		1431	1440	1450	1460	1470	1480	1490	1500	1510	1520	1530	1540	1550	1560
seq		TCCACCTCCAAATTCCAAATCCTGAATTCAGCGGTTGACCAAGTGTCTGCTGCACAGGCTTACATCTCCAGAGCGGCTGCCCCCAATTCAGCAGCAATTTTGATATGCTGGATCCCCCACT													
Consensus		TCCACCTCCAAATTCCAAATCCTGAATTCAGCGGTTGACCAAGTGTCTGCTGCACAGGCTTACATCTCCAGAGCGGCTGCCCCCAATTCAGCAGCAATTTTGATATGCTGGATCCCCCACT													
		1561	1570	1580	1590	1600	1610	1620	1630	1640	1650	1660	1670	1680	1690
seq		GGATGAGAGCAAAATGTGATATCCCTCTTAAGATAGAGACCTTTTCCCTTGACGGAGTCTGTAGAAAGAGGACAGTAGCTGCTCAGAGCTTTTCCAGAGCATATAGAGAGGGGCCCG													
Consensus		GGATGAGAGCAAAATGTGATATCCCTCTTAAGATAGAGACCTTTTCCCTTGACGGAGTCTGTAGAAAGAGGACAGTAGCTGCTCAGAGCTTTTCCAGAGCATATAGAGAGGGGCCCG													
		1691	1700	1710	1720	1730	1740	1750	1760	1770	1780	1790	1800	18	

Flag BirA Xrcc5 DiT48hMix (cloneB) 5NT manquent au début de la séquence

○ FlagBirA SP clone B

➤ B3Fwd 842NT

ATGGCGTGGTCCGGTAATAAGGCAGCTGTTGTGCTGTGTATGGATGTGGGGGTTGCCATGGGTAACCTCTTCCT
GGTGAAGAATCCCCACTTGAACAGGCCAAGAAAGTGATGACTATGTTTGTCCAACGACAGGTGTTTTCGGAGAG
CAAGGATGAGATCGCCTTAGTCCTCTATGGTACAGAGAGCACTGATAACGCCCTTGCTGGCAAGGACCAGTATCA
GAACATCACAGTGCACAGGCACCTGATGCTACCAGATTTTGATTGCTGGAAGACATCGGAAACAAAATCCAACC
AAGTTCTCAACAAGCCGACTTCCTGGACGCCCTGATTGTGTGCATGGATTTGATTCAGCGTGAAACCATAGGAAA
GAAGTTTGGGAAGAAGCATATTGAAGTGTCACTGATCTCAGCAGCCCATTGAGCCAAGACCAACTGGACATTAT
AATTTGTAACCTGAAGAAGTCCGGCATCTCCCTGCAGTTCTTTCTGCCTTTTCCAATCGACAAGAATGGTGAGCCT
GGGGAGACAGAAGACCACGACTCCaGCTTCGACCACTGTGCACCCTCCTTCCTCaAAAAGGACTTACTGAGCA
GCAAAAGGAAGGCATCCACATGGTGACGAGGGTGATGCTGTCTTTAGAAGGCAAAGATGGTCTGGATGAAATTT
ATTCCTTCNGCGAGAGTCTTCAGCAACTGTGCATCTTTAANAAGANTGAGAGGNGGTCCTTGCCCTNGNCCTGC
CAACTGACCATCNGCCCNACTTGCTATAAGNATCGTANCCTATAANTCGATNGNACNGGANAAATTTAAAN
AGTTGGGTAGTNGTNGNNGCA

➤ BGHRev 976NT

TCCNNTTCANNNNGGATGCCTATGAGNNTTTAGNNTATGNGCAGCTNCCTTTCATGNAAGACNNGCGNCNNT
NCATGTTTTCTCACTGAAAANCAATAAGAAGTGACCCCCACAGAGGCACAGCNNGTGCGATCGATGATCTG
ATTGATTCCATGAGCTNGGTAAAGAAAAACGNNNNNGAAGACATCATCGAAGACTTGTTTTCCANCCTCCAAAN
NTNCCAAATCNTGAATTTAGCGGTNGTACCAGTGNTGCTGCACAGANCNTTACATCTCCAGGAGCGGCTGCC
CCANTTCAGCAGCACATTTTGAATATGCNGGATCCCCCACTGAGATGAAAGCAAATGTGAGATTCCACTCTN
TAAAGTAAAGACCCTTTTCCCTNTGACGGAAGTCGTTAAGAAAAAGGACCAAGNGACTGCTCAGGACGTTTTN
CAAGACAATATTGAAGAGGGGCGCTGCTAAAAAATACAAGANTGAGAAAGAAGAAGGTCACATCAGCATCT
CCAGCCTGGCAGAAGGGAATGTCACCAAGGTTGGAAGTGTGAATCCTGTTGAAAACCTCCGTGTCCTAGTAAGA
CAGAAGATTGCCAGCNTTGAGGAAGCGAGTCTCCAGCTAATGAGTCACATTGAACAGTTTTTGGATACCAATGA
AACACTGTATTTTATGAAAAGTATGGAAGTGCATCAAAGCTCTCCGGGAGGAAGCCATTGATTTTTCAGAAGAGCA
GCGTTTCAACAGTTTCNTGGAAGGCCTTCGAGAGAAAGTGGAATTAACAATTAAATCATTCTGGGAAATTGT
CGTGAGGATGGAATTNCTGATCACCAAAGACGAAAGCCAGGAAGCTCTGTACAGCTGAGGAGGCCACG
AAGTTCCTGACCCCCAAAGACAAAGCAAAGANGACACAACAGGACTTGAAGAAGGTGGTGATGTGGANGAT
NTANNGGNCNNGATATAGT

➤ BGHRev du 25/11

GNATGANTAANCATNNTCGNNATCNTCCGNTACNNNANGNCAAAGAGNTANTCNTCAAGTTGGNNTANNTTC
CCTTTCATTAAGGANGCCTANGAGTGTTTAGTTTATGTGCAGCTNCCNTTCATGGAAGACTNGCGGCAATACATG
TTTTCTCNCTGAAAAACAATAAGAAGTGACCCCCACAGAGGCACAGCTGAGTGCGATCGATGATNTGATTGAT
TCCATGAGCTTGGTAAAGAAAAACGAGGAAGAAGACATCATNGAAGACTTGTTTCCAACCTCCAAAATTCCAAA
TCNTGAATTTAGCGGTTGTACCAAGTGTCTGCTGCACAGAGCCTTACATCTCCAGGAGCGGCTGCCCCAATTCA
GCAGCACATTTTGAATATGCTGGATCCCCCACTGAGATGAAAGCAAATGTGAGATTCCACTCTCTAAAGTAAA
GACCCTTTTCCCTCTGACGGAAGTCGTTAAGAAAAAGGACCAAGTGACTGCTCAGGACGTTTTTCCAAGACAATA
TTGAAGAGGGGCGCTGCTAAAAAATACAAGACTGAGAAAGAAGAAGGTCACATCAGCATCTCCAGCCTGGC

AGAAGGGAATGTCACCAAGGTTGGAAGTGTGAATCCTGTTGAAAACCTCCGTGTCCTAGTAAGACAGAAGATTG
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GGAATTACTCTGATCACCAAAGACGAAAGCCCAGGAAGCTCTGTACAGCTGAGGAGGCCACGAAGTTCCTGA
CCCCAAAGACAAAGCAAAGAAGACACAACAGGACTTGAAGAAGGTGGTGTATGTGGATGATTACTGGACAT
GATATAG

➤ **Fwd1**

ATCNNCNTGGTGACGAGGGTGATGCTGTCTTTAGAAGGCAAAGATGGTCTGGATGAAATTTATTCCTTCAGCGA
GAGTCTTCAGCAACTGTGCATCTTTAAGAAGATTGAGAGGCGGTCCTTGCCCTGGCCCTGCCAACTGACCATCGG
CCCCAACTTGTCTATAAGGATCGTAGCCTATAAATCGATTGTACAGGAGAAATTTAAAAAGAGTTGGGTAGTTGTG
GACGCAAGAACTCTAAAGAAGGAAGATATACAAAAAGAGACTGTTTATTGCCTAAATGACGATGATGAAACTGA
AGTTTCCAAAGAGGACACTATTCAAGGGTTCCGCTATGGAAGCGACATCATTCTTTTTCTAAAGTGGATGAGGA
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CGGCAATACATGTTTTCTCACTGAAAAACAATAAGAAGTGCACCCCCACAGAGGCACAGCTGAgTGCGATCGAT
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CNAAATTCCNAATCCTGAATTCAGCGGTTGTACCAGTGTCTGCTGCACAGANCCTTACATCTCCAGGAGCGGCT
GNCCCNATTTCAGCAGCACATTTTGAATATGCTGGNTNCCCCNCTGANATGAAAGCAAATGNGANANTNCAC
TCTCTAAGTNAAGANCCTTTTCCNNTGANNGANN CNNNANAAAAANNNNNNNTGACTGCTC

➤ **Fwd2**

TCTTTNANAAGANTGAGAGGNGGTCCTTGCCCTGGCCCTGCCAACTGACCATCGGCCCCAACTTGTCTATAAG
GATCGTAGCCTATAAATCGATTGTACAGGAGAAATTTAAAAAGAGTTGGGTAGTTGTGGACGCAAGAACTCTA
AAGAAGGAAGATATACAAAAAGAGACTGTTTATTGCCTAAATGACGATGATGAAACTGAAGTTTCCAAAGAG
GACACTATTCAAGGGTTCCGCTATGGAAGCGACATCATTCTTTTTCTAAAGTGGATGAGGAACAAATGAAAT
ATAAATCGGAGGGGAAGTGCTTCTGTCTGGGGTTCTGTAAATCTTCTCAGGTTTCATAGAAGATTCTTCATG
GGACATCAAGTTCTGAAGGTCTTCGCAGCGAAGGATGATGAGGCAGCAGCTGTTGCACTTTCTTCCCTAGTTC
ACGCTTTGGATGAGTTAAACATGGTCGCTATCGTCCGCTACGCCTATGACAAAAGAGCTAATCCTCAAGTTGGT
GTAGCCTTCCCTTTCATTAAGGATGCCTATGAGTGTTTAGTTTATGTGCAGCTGCCTTTCATGGAAGACTTGCG
GCAATACATGTTTTCTCACTGAAAAACAATAAGAAGTGCACCCCCACAGAGGCACAGCTGAGTGCGATCGAT
GATCTGATTGATTCCATGAGCTTGGTAAAGAAAAACGAGGAAGAAGAcATCATCGAAGACTTGTTTTCCAACCT
CCAAAATTCCAAATCCTGAATTCAGCGGTTGTACCAGTGTCTGCTGCACAGAGCCTTACATCTCCAGGAGCGG
CTGCCCCCAATTTCAGCAGCACATTTTGAATATGCTGGATCCCCCACTGAGATGAAAGCAAAATGNGAGANTC
CACTCTCTAAAGTAAAGACCCTTTTCCCTCTGACGGAAGTCGTTAANAAAAAGNACCAAGTGAAGTCTCNNNN
NTTTTNCAAGANAATATTGAAGAGGGGCCGCTGCTAAAAATACANACTGANAAAGANNNNNNCNCATCANN
NTCTNCNGNCTNNNNAGGA

➤ **Rev1**

TCCTNNNNAGNCNGNAGANNNTGATGNGNNNNNTCTTTNTCAGTNTGTATTTTTCAGCAGCGGGCCCCCTCTTC
AATATTNTCTTGNAANNNNNNGAGCAGTCACTTGGTNCTTTTTNTAACGACTTCCGTCAGAGGGAAAAGG
GTCTTTACTTTAGAGAGTGGANTCTCNCATTTTGCTTTTCATCTCAGTGGGGGGATCCAGCATATTCAAATGTG
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 TTCAGAACTTGATGTCCCATGAAGAATCTTCTATGAACCTGAGAAGATTTACAGAACCCAGAACAGAGAAGC
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 ACCCTTGAATAGTGTCTCTTTGGAACTTCAGTTTCATCATCGTCATTTAGGCAATAAACAGTCTCTTTTTGTAT
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 NTNAAAGA

➤ **Rev2**

TGANCAGNANNNGGAANGCATNCNCNNNGTGNNGANNGNANGCTGTNNTTAGANNGGCANNGNNGTN
 NNGNTGAANNNTNTTCNTTCAGNNNNNTNNNCAGCANNNNTNCNTCTTTAAGAAGNTNGNNNGNNGNN
 CNNNGCCNTGGCCTGNCANNNNNCCATCGGCCCAANTTGTCTATAAGNANNNTNGCCTATAANNNGN
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 GAGANTGTTTATTGCNTAAATGACGANGATGAACTGAAGTTTCCAAAGAGGACACTATTCAAGGGTTCCGCTAT
 GGAAGCGACATCATTCCTTTTTCTAAAGTGGATGAGGAACAAATGAAATATAAATCGGAGGGGAAGTGCTTCTCT
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 NGAAGGATGATGAGGCAGCAGCTGTTGCACTTTCTCCCTAGTTCACGCTTTGGATGAGTTAAACATGGTCGCTA
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 GTGTTTAGTTTATGTGCAGCTGCCTTTCATGGAAGACTTGCGGCAATACATGTTTTCTCACTGAAAAACAATAAG
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➤ **Synthèse séquençage**

ATGGCGTGGTCCGGTAATAAGGCAGCTGTTGTGCTGTGTATGGATGTGGGGGTTGCCATG	60
GGTAACTCCTTTCTGGTGAAGAATCCCCACTTGAACAGGCCAAGAAAGTGATGACTATG	120
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ACAGAGAGCACTGATAACGCCCTTGCTGGCAAGGACCAGTATCAGAACATCACAGTGCAC	240
AGGCACCTGATGCTACCAGATTTTGATTTGCTGGAAGACATCGGAAACAAAATCCAACCA	300
AGTTCTCAACAAGCCGACTTCTTGGACGCCCTGATTGTGTGCATGGATTGATTACGCGT	360
GAAACCATAGGAAAGAGTTTGGGAAGAAGCATATTGAAGTGTTCACTGATCTCAGCAGC	420
CCATTTCAGCCAAGACCAACTGGACATTATAATTTGTAACCTGAAGAAGTCCGGCATCTCC	480
CTGCAGTTCTTTCTGCCTTTTCCAATCGACAAGAATGGTGAGCCTGGGGAGACAGAAGAC	540
CACGACTCCaGCTTCGACCACTGTGCACCCTCCTTCCCTCAAAAAGGACTTACTGAGCAG	600
CAAAAGGAAGGCATCCACATGGTGACGAGGGTGATGCTGTCTTTAGAAGGCAAGATGGT	660
CTGGATGAAATTTATTCCTTCAGCGAGAGTCTTCAGCAACTGTGCATCTTTAAGAAGATT	720
GAGAGGCGGTCTTGGCCTGGCCCTGCCAACTGACCATCGGCCCAACTTGTCTATAAGG	780
ATCGTAGCCTATAAATCGATTGTACAGGAGAAATTTAAAAAGAGTTGGGTAGTTGTGGAC	840
GCAAGAACTCTAAAGAAGGAAGATATACAAAAGAGACTGTTTATTGCCTAAATGACGA	899
TGATGAACTGAAGTTTCCAAAGAGGACACTATTCAAGGGTTCGGCTA	947
TGGAAGCGACATCATTCCTTTTTCTAAAGTGGATGAGGAACAAATGAAATATAAAT	1003
CGGAGGGGAAGTGCTTCTCTGTTCTGGGGTCTGTAAATCTTCTCAGGTTTCATAGAAGAT	1063
TCTTCATGGGACATCAAGTTCTGAAGGTCTTCGAGCGAAGGATGATGAGGCAG	1117
CAGCTGTTGCACTTTCTCCCTAGTTCACGCTTTGGATGAGTTAAACATGGTCGCTAT	1175
CGTCCGCTACGCCTATGACAAAAGAGCTAATCCTCAAGTTGGTGTAGCCTTCCCTTTCAT	1235
TAAGGATGCCTATGAGTGTTTAGTTTATGTGCAGCTGCCTTTCATGGAAGACTTG	1290
CGGCAATACATGTTTTCTCACTGAAAAACAATAAGAAGTGCACCCCAAGAGGCACAG	1350
CTGAGTGCATCGATGATCTGATTGATTCCATGAGCTTGGTAAAGAAAAACGAGGAAGAA	1410
GACATCATCGAAGACTTGTTTCCAACCTCCAAAATTCAAAATCCTGAATTTAGCGGTTG	1470
TACCAGTGTCTGTGCACAGAGCCTTACATCTCCAGGAGCGGCTGCCCAATTTCAGCAG	1530
CACATTTTGAATATGCTGGATCCCCCACTGAGATGAAAGCAAAATGTGAGATTCCACTC	1590
TCTAAAGTAAAGACCTTTTCCCTCTGACGGAAGTCGTTAAGAAAAAGGACCAAGTACT	1650
GCTCAGGACGTTTTCCAAGACAATATTGAAGAGGGGCCGCTGCTAAAAATACAAGACT	1710

GAGAAAGAAGAAGGTCACATCAGCATCTCCAGCCTGGCAGAAGGGAATGTCACCAAGGTT	1770
GGAAGTGTGAATCCTGTTGAAAACCTCCGTGTCCTAGTAAGACAGAAGATTGCCAGCTTT	1830
GAGGAAGCGAGTCTCCAGCTAATGAGTCACATTGAACAGTTTTTTGGATACCAATGAAACA	1890
CTGTATTTTATGAAAAGTATGGACTGCATCAAAGCTCTCCGGGAGGAAGCCATTCAGTTT	1950
TCAGAAGAGCAGCGTTTCAACAGTTTCTGGAAGGCCTTCGAGAGAAAGTGGAATTAAA	2010
CAATTAAATCATTTCTGGGAAATTGTCGTGCAGGATGGAATTACTCTGATCACCAGAAC	2070
GAAAGCCCAGGAAGCTCTGTACAGCTGAGGAGGCCACGAAGTTCCTGACCCCCAAAGAC	2130
AAAGCAAAAGAAGACACAACAGGACTTGAAGAAGGTGGTGATGTGGATGATTTACTGGAC	2190
ATGATATAG	2199

MAWSGNKAAVVLCDVGVAMGNSFPGEESPLEQAKKVMTMFVQRQVFSESKDEIALVLYGTESTDNALAGKD
 QYQNITVHRHMLPDFDLLEDIGNKIQPSQQADFLDALIVCMDLIQRETIGKKFGKKHIEVFTDLSSPFSQDQLDIIC
 NLKKSIGSLQFFLPFPIDKNGEPGETEDHDSFSDHCAPSFPQKGLTEQQKEGIHMTVRVMLSLEGKDGLEIYSFSES
 LQQLCIFKKIERRSLPWPCLTIGPNLSIRIVAYSIVQEKFKKSWVVVDARTLKKEDIQKETVYCLNDDDETEVSKEDT
 IQGFRYGSIIIPFSKVDEEQMKYKSEKCFSVLGFCSSQVHRRFFMGHQVLKVFAAKDDEAAVALSSLVHALDEL
 NMVAIVRYAYDKRANPQVGVAFFIKDAYECLVYVQLPFMEDLRQYMFSSLKNNKCTPTEAQLSAIDDLIDMSL
 VKKNEEDIIEDLFPTSKIPNPEFQRLYQCLLHRLHLQERLPPIQQHILNMLDPPTMKAKCEIPLSKVKTFLPLTEVV
 KKKDQVTAQDVFQDNIEEGPAAKKYKTEKEEGHISISLAEGNVTKVGSVNPVENFRVLVRQKIASFEEASLQLMSHI
 EQFLDTNETLYFMKSMDCIKALREEAIQFSEEQRFNSFLEGLREKVEIKQLNHFWIIVQDGITLITKDESPGSSVTAE
 EATKFLTPKDKAKEDTTGLEEGGDVDDLLDMI-

➤ **Blast contre banque rat :**

	Description	Name	Score	Score	Cover	value	Ident	Len	Accession
✓	Rattus norvegicus X-ray repair cross complementing 5 (Xrcc5) mRNA	Norway rat	4050	4050	100%	0.0	99.91%	2545	NM_177419.2
✓	Rattus norvegicus X-ray repair complementing defective repair in Chinese hamster cells 5 mRNA (cDNA clone MGC:72979...)	Norway rat	4050	4050	100%	0.0	99.91%	2548	BC061576.1
✓	Rattus norvegicus mRNA for Xrcc5, partial cds	Norway rat	3480	3480	93%	0.0	97.22%	2100	AB066103.1

➤ **Différence Séquençage/CDS au niveau NT :**

Mutations : T<C en 1915 et A<G en 1956

		10	20	30	40	50	60	70	80	90	100	110	120	130	
seq		ATGGCGTGGTCCGGTAAATAGGCAGCTGTGTGCTGTGTATGGATGTGGGGTGGCCATGGGTAACTCCTTTCTGGTGAGAGATCCCACCTGAGCAGGCCAGAGAAGTGATGACTATGTTTGCCAAAC													
cds		ATGGCGTGGTCCGGTAAATAGGCAGCTGTGTGCTGTGTATGGATGTGGGGTGGCCATGGGTAACTCCTTTCTGGTGAGAGATCCCACCTGAGCAGGCCAGAGAAGTGATGACTATGTTTGCCAAAC													
Consensus		ATGGCGTGGTCCGGTAAATAGGCAGCTGTGTGCTGTGTATGGATGTGGGGTGGCCATGGGTAACTCCTTTCTGGTGAGAGATCCCACCTGAGCAGGCCAGAGAAGTGATGACTATGTTTGCCAAAC													
		131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq		GACAGGGTGTTTTCGGAGAGCAGGGATGAGATCGCCTTAGTCCTCTATGGTACAGAGAGCACTGATAGCGCCCTTGCTGGCAGAGGACCAAGTATCAGACATCAGAGTCACAGGCCACCTGATGCTACCAAG													
cds		GACAGGGTGTTTTCGGAGAGCAGGGATGAGATCGCCTTAGTCCTCTATGGTACAGAGAGCACTGATAGCGCCCTTGCTGGCAGAGGACCAAGTATCAGACATCAGAGTCACAGGCCACCTGATGCTACCAAG													
Consensus		GACAGGGTGTTTTCGGAGAGCAGGGATGAGATCGCCTTAGTCCTCTATGGTACAGAGAGCACTGATAGCGCCCTTGCTGGCAGAGGACCAAGTATCAGACATCAGAGTCACAGGCCACCTGATGCTACCAAG													
		261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq		TTTTGATTGTCTGGAGACATCGGAACAARAATCCAAACAGTCTTCACAGGCCGACCTTCCTGGAGCCCTGATTGTGTGCATGGATTGATTACGCGTGAACCATAGGAAGAAGTTTGGAGAGAG													
cds		TTTTGATTGTCTGGAGACATCGGAACAARAATCCAAACAGTCTTCACAGGCCGACCTTCCTGGAGCCCTGATTGTGTGCATGGATTGATTACGCGTGAACCATAGGAAGAAGTTTGGAGAGAG													
Consensus		TTTTGATTGTCTGGAGACATCGGAACAARAATCCAAACAGTCTTCACAGGCCGACCTTCCTGGAGCCCTGATTGTGTGCATGGATTGATTACGCGTGAACCATAGGAAGAAGTTTGGAGAGAG													
		391	400	410	420	430	440	450	460	470	480	490	500	510	520
seq		CATATTGAGTGTTCACGTGATCTCAGAGGCCATTACGACAGACCACTGGACATTATTAATTTGTAACCTGAGAGAGTCCGGCATCTCCCTGCAGTCTCTTCGCTTTTCCATTCGACAGAGATGGTG													
cds		CATATTGAGTGTTCACGTGATCTCAGAGGCCATTACGACAGACCACTGGACATTATTAATTTGTAACCTGAGAGAGTCCGGCATCTCCCTGCAGTCTCTTCGCTTTTCCATTCGACAGAGATGGTG													
Consensus		CATATTGAGTGTTCACGTGATCTCAGAGGCCATTACGACAGACCACTGGACATTATTAATTTGTAACCTGAGAGAGTCCGGCATCTCCCTGCAGTCTCTTCGCTTTTCCATTCGACAGAGATGGTG													
		521	530	540	550	560	570	580	590	600	610	620	630	640	650
seq		AGCCTGGGAGACAGAGAACCCAGCTCCAGCTTCGACCACTGTGCACCTCTCTCCCTCAAAAGGACTTACTGAGCAGCAAAAGGAGGACATCCACATGGTGACGAGGGTGATGCTGTCTTAGAGG													
cds		AGCCTGGGAGACAGAGAACCCAGCTCCAGCTTCGACCACTGTGCACCTCTCTCCCTCAAAAGGACTTACTGAGCAGCAAAAGGAGGACATCCACATGGTGACGAGGGTGATGCTGTCTTAGAGG													
Consensus		AGCCTGGGAGACAGAGAACCCAGCTCCAGCTTCGACCACTGTGCACCTCTCTCCCTCAAAAGGACTTACTGAGCAGCAAAAGGAGGACATCCACATGGTGACGAGGGTGATGCTGTCTTAGAGG													
		651	660	670	680	690	700	710	720	730	740	750	760	770	780
seq		CAAGAGTGGTCTGGATGAATTTATTCCTTCAGCGAGAGCTTCAGCACTGTGCATCTTAGAGAGATTGAGAGGCCGTCTTGCCCTGGCCCTGCCAATGACCATCGCCCACTTGTCTATAGG													
cds		CAAGAGTGGTCTGGATGAATTTATTCCTTCAGCGAGAGCTTCAGCACTGTGCATCTTAGAGAGATTGAGAGGCCGTCTTGCCCTGGCCCTGCCAATGACCATCGCCCACTTGTCTATAGG													
Consensus		CAAGAGTGGTCTGGATGAATTTATTCCTTCAGCGAGAGCTTCAGCACTGTGCATCTTAGAGAGATTGAGAGGCCGTCTTGCCCTGGCCCTGCCAATGACCATCGCCCACTTGTCTATAGG													
		781	790	800	810	820	830	840	850	860	870	880	890	900	910
seq		ATCGTAGCCTATAAATCGATTGTACAGGAGAAATTTAAAGAGAGTTGGGTAGTTGTGGACGCAAGACCTTAAGAGAGGAGATATACAAAGAGAGACTGTTTATTGCCTAATGACGATGATGAACCTG													
cds		ATCGTAGCCTATAAATCGATTGTACAGGAGAAATTTAAAGAGAGTTGGGTAGTTGTGGACGCAAGACCTTAAGAGAGGAGATATACAAAGAGAGACTGTTTATTGCCTAATGACGATGATGAACCTG													
Consensus		ATCGTAGCCTATAAATCGATTGTACAGGAGAAATTTAAAGAGAGTTGGGTAGTTGTGGACGCAAGACCTTAAGAGAGGAGATATACAAAGAGAGACTGTTTATTGCCTAATGACGATGATGAACCTG													
		911	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040
seq		AAGTTTCCAAGAGGACACTATTCAAGGGTCCGCTATGAGAGCGACATCATTCCTTTTCTAAGTGGATGAGGACAAATGAATATATAATCGAGGGGAGTGCTTCTCTGTTCTGGGGTCTGTAA													
cds		AAGTTTCCAAGAGGACACTATTCAAGGGTCCGCTATGAGAGCGACATCATTCCTTTTCTAAGTGGATGAGGACAAATGAATATATAATCGAGGGGAGTGCTTCTCTGTTCTGGGGTCTGTAA													
Consensus		AAGTTTCCAAGAGGACACTATTCAAGGGTCCGCTATGAGAGCGACATCATTCCTTTTCTAAGTGGATGAGGACAAATGAATATATAATCGAGGGGAGTGCTTCTCTGTTCTGGGGTCTGTAA													
		1041	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170
seq		ATCTTCTCAGGTCATAGAGATTCTTCATGGGACATCAGTTCTGARGGTCTCGCAGCAGAGATGATGAGGCAGCGCTGTGCACCTTTCTCCCTAGTTCAGCGTTTGGATGAGTTAAACATGGTC													
cds		ATCTTCTCAGGTCATAGAGATTCTTCATGGGACATCAGTTCTGARGGTCTCGCAGCAGAGATGATGAGGCAGCGCTGTGCACCTTTCTCCCTAGTTCAGCGTTTGGATGAGTTAAACATGGTC													
Consensus		ATCTTCTCAGGTCATAGAGATTCTTCATGGGACATCAGTTCTGARGGTCTCGCAGCAGAGATGATGAGGCAGCGCTGTGCACCTTTCTCCCTAGTTCAGCGTTTGGATGAGTTAAACATGGTC													
		1171	1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
seq		GCTATCGTCCGCTACGCCCTATGCAAAAGAGCTTAATCCTCAGTTGGGTAGCCTTCCCTTTTCATTAGGATGCCATGATGTTTGGTTTATGTGTCAGCTGCCCTTCATGGAGACTTCGGGCATACA													
cds		GCTATCGTCCGCTACGCCCTATGCAAAAGAGCTTAATCCTCAGTTGGGTAGCCTTCCCTTTTCATTAGGATGCCATGATGTTTGGTTTATGTGTCAGCTGCCCTTCATGGAGACTTCGGGCATACA													
Consensus		GCTATCGTCCGCTACGCCCTATGCAAAAGAGCTTAATCCTCAGTTGGGTAGCCTTCCCTTTTCATTAGGATGCCATGATGTTTGGTTTATGTGTCAGCTGCCCTTCATGGAGACTTCGGGCATACA													
		1301	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430
seq		TGTTTTCTCTACTGA AAAACATAGAG													

➤ Différence Séquençage/CDS au niveau PROT :

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq	MAWSGNKAAVYVLCNDGVYAMGNSFPGEEESPLEQAKKYVTHFYQRQVFSKDEIALVLYGTESTDNALAGKQDYQNTIVHRHLHPDFDLLEDIGNKIQPSQQADFLDALIVCHDLIQRETIGKKFGKK													
ref	MAWSGNKAAVYVLCNDGVYAMGNSFPGEEESPLEQAKKYVTHFYQRQVFSKDEIALVLYGTESTDNALAGKQDYQNTIVHRHLHPDFDLLEDIGNKIQPSQQADFLDALIVCHDLIQRETIGKKFGKK													
Consensus	MAWSGNKAAVYVLCNDGVYAMGNSFPGEEESPLEQAKKYVTHFYQRQVFSKDEIALVLYGTESTDNALAGKQDYQNTIVHRHLHPDFDLLEDIGNKIQPSQQADFLDALIVCHDLIQRETIGKKFGKK													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq	HIEVF TDLSSPFSQDQLDIICNLKKS6ISLQFFLPFPIDKNGEPGETEDHDSFDFHCAPSPFPQKGLTEQQKEGIHMYTRYMLSEGGKDLDEIYFSSESLLQCLCFKKIERRSLPWPQCLTI6PMLSIR													
ref	HIEVF TDLSSPFSQDQLDIICNLKKS6ISLQFFLPFPIDKNGEPGETEDHDSFDFHCAPSPFPQKGLTEQQKEGIHMYTRYMLSEGGKDLDEIYFSSESLLQCLCFKKIERRSLPWPQCLTI6PMLSIR													
Consensus	HIEVF TDLSSPFSQDQLDIICNLKKS6ISLQFFLPFPIDKNGEPGETEDHDSFDFHCAPSPFPQKGLTEQQKEGIHMYTRYMLSEGGKDLDEIYFSSESLLQCLCFKKIERRSLPWPQCLTI6PMLSIR													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq	IVAYKSIYQEFKKSHVYVDARTLKKEDIQKETVYCLNDDDETEVSKEDTIQGFYRGSDIIPFSKYDVEQMKYKSEGKCFSVLGCKSSQVHRRFFMGHQVLKVFARKDOEAAHVALSSLVHALDELNMV													
ref	IVAYKSIYQEFKKSHVYVDARTLKKEDIQKETVYCLNDDDETEVSKEDTIQGFYRGSDIIPFSKYDVEQMKYKSEGKCFSVLGCKSSQVHRRFFMGHQVLKVFARKDOEAAHVALSSLVHALDELNMV													
Consensus	IVAYKSIYQEFKKSHVYVDARTLKKEDIQKETVYCLNDDDETEVSKEDTIQGFYRGSDIIPFSKYDVEQMKYKSEGKCFSVLGCKSSQVHRRFFMGHQVLKVFARKDOEAAHVALSSLVHALDELNMV													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
seq	AIVRYAYDKRANPQVGVAFFPIKDAYECLVYVQLPFMEDLRQYMFSSLKNNKKCTPTAQLSAIDDLIDSMVKKNEEEDITIEDLFPTSKIPNPEFQRLYQCLLHRLHLQERLPPIIQHILNMLDPPT													
ref	AIVRYAYDKRANPQVGVAFFPIKDAYECLVYVQLPFMEDLRQYMFSSLKNNKKCTPTAQLSAIDDLIDSMVKKNEEEDITIEDLFPTSKIPNPEFQRLYQCLLHRLHLQERLPPIIQHILNMLDPPT													
Consensus	AIVRYAYDKRANPQVGVAFFPIKDAYECLVYVQLPFMEDLRQYMFSSLKNNKKCTPTAQLSAIDDLIDSMVKKNEEEDITIEDLFPTSKIPNPEFQRLYQCLLHRLHLQERLPPIIQHILNMLDPPT													
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
seq	EMKAKCEIPLSKVKTLPFLTEVYKKKQVTAQDVFDNIEEGPAAKKYKTEKEEGHISISSLAEGNVTKVGSYNPYENFRVLYRQKIASFEASLQLMSHIEQFLDTNETLYFHKSHDCKIKALREERIQF													
ref	EMKAKCEIPLSKVKTLPFLTEVYKKKQVTAQDVFDNIEEGPAAKKYKTEKEEGHISISSLAEGNVTKVGSYNPYENFRVLYRQKIASFEASLQLMSHIEQFLDTNETLYFHKSHDCKIKALREERIQF													
Consensus	EMKAKCEIPLSKVKTLPFLTEVYKKKQVTAQDVFDNIEEGPAAKKYKTEKEEGHISISSLAEGNVTKVGSYNPYENFRVLYRQKIASFEASLQLMSHIEQFLDTNETLYFHKSHDCKIKALREERIQF													
	651	660	670	680	690	700	710	720	730	732				
seq	SEEQRFNSFLEGLREKVEIKQLNHFMEIVYQDGITLITKDESPGSSVTAEEATKFLTPDKAKEDTTGLEEGGDVDDLDMI													
ref	SEEQRFNSFLEGLREKVEIKQLNHFMEIVYQDGITLITKDESPGSSVTAEEATKFLTPDKAKEDTTGLEEGGDVDDLDMI													
Consensus	SEEQRFNSFLEGLREKVEIKQLNHFMEIVYQDGITLITKDESPGSSVTAEEATKFLTPDKAKEDTTGLEEGGDVDDLDMI													

Mutation en 639 C<R comme rate et Di

		Name	Score	Score	Cover	value	ident	Len	
☒	X-ray repair complementing defective repair in Chinese hamster cells 5 isoform CRA_a [Rattus norvegicus]	Norway rat	1508	1508	100%	0.0	99.86%	732	EDL75243.1
☒	X-ray repair cross-complementing protein 5 [Rattus norvegicus]	Norway rat	1506	1506	100%	0.0	99.86%	732	NP_803154.
☒	Xrcc5 [Rattus norvegicus]	Norway rat	1359	1359	93%	0.0	96.63%	683	BAB83859.1
☒	X-ray repair complementing defective repair in Chinese hamster cells 5 isoform CRA_b [Rattus norvegicus]	Norway rat	471	471	31%	1e-163	99.56%	228	EDL75244.1

Flag BirA SP (cloneB) OK

○ **FlagBirA CTX clone B**

➤ **B3Fwd 848NT**

ATGGCGTGGTCCGGTAATAAGGCAGCTGTTGTGCTGTGTATGGATGTGGGGGTTGCCATGG
GTAACCTCTTTTCTGGTGAAGAATCCCCACTTGAACAGGCCAAGAAAGTGATGACTATGTT
TGTCCAACGACAGGTGTTTTTCGGAGAGCAAGGATGAGATCGCCTTAGTCCTCTATGGTACA
GAGAGCACTGATAACGCCCTTGCTGGCAAGGACCAGTATCAGAACATCACAGTGACACAGG
CACCTGATGCTACCAGATTTTGATTTGCTGGAAGACATCGGAAACAAAATCCAACCAAGTT
CTCAACAAGCCGACTTCTGGACGCCCTGATTGTGTGCATGGATTTGATTTCAGCGTGAAAC
CATAGGAAAGAAGTTTGGGAAGAAGCATATTGAAGTGTTCACTGATCTCAGCAGCCCATTC
AGCCAAGACCAACTGGACATTATAATTTGTAACCTGAAGAAGTCCGGCATCTCCCTGCAGT
TCTTTCTGCCTTTTCCAATCGACAAGAATGGTGAGCCTGGGGAGACAGAAGACCACGACT
CCAGCTTCGACCACTGTGCACCCCTCCTTCCCTCAAAAAGGACTTACTGAGCAGCAAAAGG
AAGGCATCCACATGGTGACgAGGGTGATGCTGTCTTTAGAAGGCCAAAGATGGTCTGGATGA
AATTTATTCCTTCAGCGAGAGTCTTCAGCAACTGTGCATCTTTAAGAAGANTGAGAGGCCG
TCCTTGCCCTGNCCCTGCCAACTGACCATCGGCCCCAACTTGTCTATAAGGATCGTANCCTA
TAANTCGATTGNACNGNANAANTTAAAAGAGTTGGGTAGTNGTGGANGCANAACCTCT

➤ **BGHRV 1035NT**

ANNNTCGNTATCNNCNNNTANNNNNNGNNAANNNAGNTANTCCTCNGTTGGTGTANCC
TTCCCNNTTCATTAAGGATGCCTANGAGTGTTTAGTNTATGTGCAGCTNNCNTTCATGGAAGA
CTTGCGGCAATACATGTTTTCTCACTGAAAANCAATAAGAAGTGCACCCCCACAGAGGC
ACAGCTGAGTGCGATCGATGATCTGATTGATTCCATGAGCTTGGTAAAGAAAAACGAGGA
AGAAGACATCATCGAAGACTTGTTTTCCAACCTCCAAAATTCCAANTCNTGAATTTACGCGG
TTGTACCAGTGTCTGCTGCACAGAGCCTTACATCTCCAGGAGCGGCTGCCCCCAATTCAGC
AGCACATTTTGAATATGCTGGATCCCCCACTGAGATGAAAGCAAAATGTGAGATTCCACT
CTCTAAAGTAAAGACCCTTTTCCCTCTGACGGAAGTCGTTAAGAAAAAGGACCAAGTGAC
TGCTCAGGACGTTTTCCAAGACAATATTGAAGAGGGGCCGCTGCTAAAAAATACAAGAC
TGAGAAAGAAGAAGGTCACATCAGCATCTCCAGCCTGGCAGAAGGGAATGTCACCAAGG
TTGGAAGTGTGAATCCTGTTGAAAACCTCCGTGTCCTAGTAAGACAGAAGATTGCCAGCTT
TGAGGAAGCGAGTCTCCAGCTAATGAGTCACATTGAACAGTTTTTGGATACCAATGAAACA
CTGTATTTTATGAAAAGTATGGACTGCATCAAAGCTCTCCGGGAGGAAGCCATTGAGTTTTC
AGAAGAGCAGCGTTTTCAACAGTTTTCTGGAAGGCCTTCGAGAGAAAGTGGAATTAAC
AATTAAATCATTTCTGGGAAATTGTCGTGCAGGATGGAATTNCTCTGATCACCAAAGACGA
AAGCCCAGGAAGCTCTGTACAGCTGAGGAGGCCACGAAGTTCCTGACCCCCAAAGACA
AAGCAAAAGAAGACACAACAGGACTTGAAGAAGGTGGTGATGTGGATGATTACNGGAC
ATGATATAG

➤ **BGHRV du 25/111**

TTTCATNAAGGANNNNATGAGTGTTTAGTTTATGTGCAGCTNCCTTTTCATGGAAGACTNGC
GNCAATACATGTTTTCTCACTGAAAANCAATAAGAAGTGCACCCCCACAGAGGCACAGC
TGAGTGCGANCGATGATNTGATTGATTCCATGAGCTNGGTAAAGAAAAACGAGGAAGAAG
ACATCATCGAAGACTTGTTTTCCAACNTCCAAAATTCCAAATCcTGAATTTACGCGGTTGTAC
CAGTGTCTGCTGCACAGAGCCTTACATCTCCAGGAGCGGCTGCCCCCAATTCAGCAGCACA
TTTTGAATATGCTGGATCCCCCACTGAGATGAAAGCAAAATGTGAGATTCCACTCTCTAA
AGTAAAGACCCTTTTCCCTCTGACGGAAGTCGTTAAGAAAAAGGACCAAGTGACTGCTCA
GGACGTTTTCCAAGACAATATTGAAGAGGGGCCGCTGCTAAAAAATACAAGACTGAGAA
AGAAGAAGGTCACATCAGCATCTCCAGCCTGGCAGAAGGGAATGTCACCAAGGTTGGAA
GTGTGAATCCTGTTGAAAACCTCCGTGTCCTAGTAAGACAGAAGATTGCCAGCTTTGAGGA

AGCGAGTCTCCAGCTAATGAGTCACATTGAACAGTTTTTTGGATACCAATGAAACACTGTAT
TTTATGAAAAGTATGGACTGCATCAAAGCTCTCCGGGAGGAAGCCATTTCAGTTTTTCAGAAG
AGCAGCGTTTTCAACAGTTTCCTGGAAGGCCTTCGAGAGAAAGTGGAATTAACAATTAA
ATCATTCTCTGGGAAATTGTCGTGCAGGATGGAATTACTCTGATCACCAAAGACGAAAGCCC
AGGAAGCTCTGTACAGCTGAGGAGGCCACGAAGTTCCTGACCCCCAAAGACAAAGCAA
AAGAAGACACAACAGGACTTGAAGAAGGTGGTGATGTGGATGATTTACTGGACATGATAT
AG

➤ **Fwd1**

GNANGNATCNNCNTGGTGANGAGGNNGATGCTGTCTTTAGAAGGCAAAGATGGTCTGGATGAAATTTATTCCT
TCAGCGAGAGTCTTCAGCAACTGTGCATCTTTAAGAAGATTGAGAGGCGGTCTTGCCCTGGCCCTGCCAACTG
ACCATCGGCCCCAACTTGTCTATAAGGATCGTAGCCTATAAATCGATTGTACAGGAGAAATTTAAAAAGAGTTGGG
TAGTTGTGGACGCAAGAACTCTAAAGAAGGAAGATATACAAAAGAGACTGTTTATTGCCTAAATGACGATGATG
AAACTGAAGTTTTCAAAGAGGACACTATTCAAGGGTTCGCTATGGAAGCGACATCATTCCTTTTTCTAAAGTGG
ATGAGGAACAAATGAAATATAAATCGGAGGGGAAGTGCTTCTGTCTGGGGTTCTGTAAATCTTCTCAGGTTT
ATAGAAGATTCTTCATGGGACATCAAGTTCTGAAGGTCTTCGAGCGAAGGATGATGAGGCAGCAGCTGTTGCA
CTTTCTCCCTAGTTCACGCTTTGGATGAGTTAAACATGGTCGCTATCGTCCGCTACGCCTATGACAAAAGAGCTA
ATCCTCAAGTTGGTGTAGCCTTCCCTTTCATTAAGGATGCCTATGAGTGTTTAGTTTATGTGCAGCTGCCTTTCATG
GAAGACTTGCGGCAATACATGTTTTCTCACTGAAAAACAATAAGAAGTGCACCCCCACAGAGGCACAGCTGAg
TGCGATCGATGATCTGATTGATTCCATGAGCTTGGTAAAGAAAAACGAGGAAGAAGANATCATCGAAGANTTGT
TTCCNACCTCCAAAATTNCAATCCTGAATTCAGCGGTTGTACCAGTGTCTGCTGCACAGAGCCTTACATCTCCA
GGANCGGCTGCCCCCAATTCAGCAGCACATTTTGAATATGCTGGNTCCCCNNCTGANATGAAAGCAANNNGN
ANATTCCANTCTCTNNNTAAAGACNNTTNNCCTN

➤ **Fwd2**

TCTTTANNNNNTGAGAGGNGGTCCTTGCCCTGGCCCTGCCAACTGACCATCGGCCCCAAC
TTGTCTATAAGGATCGTAGCCTATAAATCGATTGTACAGGAGAAATTTAAAAAGAGTTGGGT
AGTTGTGGACGCAAGAACTCTAAAGAAGGAAGATATACAAAAGAGACTGTTTATTGCCT
AAATGACGATGATGAAACTGAAGTTTCAAAGAGGACACTATTCAAGGGTTCGCTATGGA
AGCGACATCATTCCTTTTTCTAAAGTGGATGAGGAACAAATGAAATATAAATCGGAGGGGA
AGTGCTTCTCTGTTCTGGGGTTCTGTAAATCTTCTCAGGTTTCATAGAAGATTCTTCATGGGA
CATCAAGTTCTGAAGGTCTTCGCAGCGAAGGATGATGAGGCAGCAGCTGTTGCACTTTCTT
CCCTAGTTCACGCTTTGGATGAGTTAAACATGGTCGCTATCGTCCGCTACGCCTATGACAAA
AGAGCTAATCCTCAAGTTGGTGTAGCCTTCCCTTTCATTAAGGATGCCTATGAGTGTTTAGT
TTATGTGCAGCTGCCTTTCATGGAAGACTTGCGGCAATACATGTTTTCTCACTGAAAAAC
AATAAGAAGTGCACCCCCACAGAGGCACAGCTGAGTGCGATCGATGATCTGATTGATTCCA
TGAGCTTGGTAAAGAAAAACGAGGAAGAAGACATCATCGAAGACTTGTTTCCaACCTCCA
AAATTCCAAATCCTGAATTTACGCGGTTGTACCAGTGTCTGCTGCACAGAGCCTTACATCTC
CNGGAGCGGCTGCCCCCAATTCAGCAGCACATTTTGAATATGCTGGATCCCCCCTGAGA
TGAAAGCAAAATGNGAGATTCCNCTCTCTAAAGTAAAGANCCTTTTCCCTCTGACGGAAG
TCNTTAAGAAAAAGGANCAAGTGACTGCTCNNNCGTTTTCCAAGACAATATTGAANAGGG
GNCCNCTGCTAAAAA

➤ **Rev1**

CNTNTNATTNNACCNGAAGAANTNNGNCATCTCNNGCAGTTNTTNTNCCTTTTNCATNGACAAGAATGGTGA
GCCTGGGGAGACAGAAGNCCACGACTCCAGCTTCGNCCNCTGTGCACCTCCTTCCCTCAAAAAGGACTTANT
GAGCAGCAAAAGGAAGGCATCCACATGGTGACGAGGGTGATGCTGTCTTTAGAAGGCAAAGATGGTCTGGAT
GAAATTTATTNNTCAGCGAGAGTCTTCAGCAACTGTGCATCTTTAAGAAGATTGAGAGGCGGTCTTGCCCT

GGCCCTGCCAACTGACCATCGGCCCAACTTGTCTATAAGGATCGTAGCCTATAAATCGATTGTACAGGAGAA
 ATTTAAAAAGAGTTGGGTAGTTGTGGACGCAAGAACTCTAAAGAAGGAAGATATACAAAAAGAGACTGTTTA
 TTGCCTAAATGACGATGATGAACTGAAGTTTCCAAAGAGGACACTATTCAAGGGTTCCGCTATGGAAGCGAC
 ATCATTCTTTTTCTAAAGTGGATGAGGAACAAATGAAATATAAATCGGAGGGGAAGTGCTTCTCTGTTCTGG
 GGTCTGTAAATCTTCTCAGGTTTCATAGAAGATTCTTCATGGGACATCAAGTTCTGAAGGTCTTCGCAGCGAAG
 GATGATGAGGCAGCAGCTGTTGCACTTTCTCCCTAGTTCACGCTTTGGATGAGTTAAACATGGTCGCTATCGT
 CCGCTACGCCTATGACAAAAAGAGCTAATCCTCAAGTTGGTGTAGCCTTCCCTTTCATTAAGGATGCCTATGAGT
 GTTTAGTTTATGTGCAGCTGCCTTTCATGGAAGACTTGCGGCAATACATGTTTTCTCACTGAAAAACAATAAG
 AAGTGCACCCCCACAGAGGCACAGCTGAGTGCGATCGATGATCTGATTGATTCCATGAGCTTGGTAAAGAAAA
 ACGAGGAAGAAGACATCATCGAAGACTTGTTTCCAACCTCCAAAATTCCAANNCCNGAANTCAGC

➤ Rev2

NTNGNAANAAATCCNACNAANTNTCANCAANCNGACTTCNTGGACGCCNGATTGTGTGCA
 TGGATTGATTCAGCGTGAAACCATAGGAAAGAAGTTNGGAAGAAGCATATTGAAGTGTTCT
 ACTGATNTCAGCAGCCCATNCAGCCAAGACCAACTGGACATTATAATTTGTANCNNGAAGA
 ANTCNNGGCATCTCCNTGCAGTTCTTTCTGCCTTTTNCAATCGACAAGAATGGTGAGCCTGG
 GGAGACAGAAGACCACGACTCCAGCTTCGACCACTGTGCACCCTCCTTCCCTCAAAAAGG
 ACTTACTGAGCAGCAAAAAGGAAGGCATCCACATGGTGACGAGGGTGATGCTGTCTTTAGA
 AGGCAAAGATGGTCTGGATGAAATTTATTCCTTCAGCGAGAGTCTTCAGCAACTGTGCATC
 TTTAAGAAGATTGAGAGGCGGTCCTTGCCCTGGCCCTGCCAACTGACCATCGGCCCAACT
 TGTCTATAAGGATCGTAGCCTATAAATCGATTGTACAGGAGAAATTTAAAAAGAGTTGGGTA
 GTTGTGGACGCAAGAAGCTCTAAAGAAGGAAGATATACAAAAAGAGACTGTTTATTGCCTA
 AATGACGATGATGAACTGAAGTTTCCAAAGAGGACACTATTCAAGGGTTCCGCTATGGAA
 GCGACATCATTCTTTTTCTAAAGTGGATGAGGAACAAATGAAATATAAATCGGAGGGGAA
 GTGCTTCTCTGTTCTGGGGTTCTGTAAATCTTCTCAGGTTTCATAGAAGATTCTTCATGGGAC
 ATCAAGTTCTGAAGGTCTTCGCAGCGAAGGATGATGAGGCAGCAGCTGTTGCACTTTCTTC
 CCTAGTTCACGCTTTGGATGAGTTAAACATGGTCGCTATCGTCCGCTACGCCTATGACAAAA
 GAGCTAATCCTCAAGTTGGTGTAGCCTTCCCTTTCATTAAGGATGCCTATGAGTGTTTAGTTT
 ATGTGCAGCTGCCTTTCATGGAAGACTTGCGGCAATACATGTTTTCTCACTGAAAAACAA
 TAAGAAGTGCNCCCCCNCA

➤ Synthèse séquençage

ATGGCGTGGTCCGGTAATAAGGCAGCTGTTGTGCTGTGTATGGATGTGGGGGTTGCCATG	60
GGTAACTCCTTTCTGGTGAAGAATCCCCACTTGAACAGGCCAAGAAAGTGATGACTATG	120
TTTGTCCAACGACAGGTGTTTTTCGGAGAGCAAGGATGAGATCGCCTTAGTCCTCTATGGT	180
ACAGAGAGCACTGATAACGCCCTTGCTGGCAAGGACCAGTATCAGAACATCACAGTGAC	240
AGGCACCTGATGCTACCAGATTTTGATTTGCTGGAAGACATCGGAAACAAAATCCAACCA	300
AGTTCTCAACAAGCCGACTTCCTGGACGCCCTGATTGTGTGCATGGATTGATTACAGCGT	360
GAAACCATAGGAAAGAGTTTGGGAAGAAGCATATTGAAGTGTTCACTGATCTCAGCAGC	420
CCATTACGCCAAGACCAACTGGACATTATAATTTGTAACCTGAAGAAGTCCGGCATCTCC	480
CTGCAGTTCTTTCTGCCTTTTCCAATCGACAAGAATGGTGAGCCTGGGGAGACAGAAGAC	540
CACGACTCCAGCTTCGACCACTGTGCACCCTCCTTCCCTCAAAAAGGACTTACTGAGCAG	600
CAAAAGGAAGGCATCCACATGGTGACGAGGGTGATGCTGTCTTTAGAAGGCAAGATGGT	660
CTGGATGAAATTTATTCCTTCAGCGAGAGTCTTCAGCAACTGTGCATCTTTAAGAAGATT	720
GAGAGCGGTCTTTGCCCTGGCCCTGCCAACTGACCATCGGCCCAACTTGTCTATAAGG	780
ATCGTAGCCTATAAATCGATTGTACAGGAGAAATTTAAAAAGAGTTGGGTAGTTGTGGAC	840
GCAAGAACTCTAAAGAAGGAAGATATACAAAAAGAGACTGTTTATTGCCTAAATGACGAT	900
GATGAACTGAAGTTTCCAAAGAGGACACTATTCAAGGGTTCCGCTATGGAAGCGACATC	960
ATTCCTTTTTCTAAAGTGGATGAGGAACAAATGAAATATAAATCGGAGGGGAAGTGCTTC	1020
TCTGTTCTGGGGTTCTGTAAATCTTCTCAGGTTTCATAGAAGATTCTTCATGGGACATCAA	1080
GTTCGAAAGTCTTCGCAGCGAAGGATGATGAGGCAGCAGCTGTTGCACTTTCTTCCCTA	1140
GTTACGCTTTGGATGAGTTAAACATGGTCGCTATCGTCCGCTACGCCTATGACAAAAAGA	1200
GCTAATCCTCAAGTTGGTGTAGCCTTCCCTTTCATTAAGGATGCCTATGAGTGTTTAGTT	1260
TATGTGCAGCTGCCTTTCATGGAAGACTTGCGGCAATACATGTTTTCTCACTGAAAAAC	1320

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AATAAGAAGTGCACCCCCACAGAGGCACAGCTGAGTGCATCGATGATCTGATTGATTCC      1380
ATGAGCTTGGTAAAGAAAAACGAGGAAGAAGACATCATCGAAGACTTGTTTCCAACCTCC      1440
AAAATTCCAAATCCTGAATTTACAGCGGTGTACCAGTGTCTGCTGCACAGAGCCTTACAT      1500
CTCCAGGAGCGGCTGCCCCCAATTCAGCAGCACATTTGAATATGCTGGATCCCCCACT      1560
GAGATGAAAGCAAAATGTGAGATTCCACTCTCTAAAGTAAAGACCCTTTTCCCTCTGACG      1620
GAAGTCGTTAAGAAAAAGGACCAAGTACTGCTCAGGACGTTTTTCCAAGACAATATTGAA      1680
GAGGGGCCCCGCTGCTAAAAAATACAAGACTGAGAAAGAAGAAGGTCACATCAGCATCTCC      1740
AGCCTGGCAGAAGGAATGTCACCAAGGTTGGAAGTGTGAATCCTGTGAAAACCTCCGT      1800
GTCCTAGTAAGACAGAAGATTGCCAGCTTTGAGGAAGCGAGTCTCCAGCTAATGAGTCAC      1860
ATTGAACAGTTTTTTGGATACCAATGAAACACTGTATTTTATGAAAAGTATGGACTGCATC      1920
AAAGCTCTCCGGGAGGAAGCAATTCAGTTTTTCAGAAGAGCAGCGTTTCAACAGTTTCCTG      1980
GAAGGCCTTCGAGAGAAAGTGGAAATTAAACAATTAATCATTTCTGGGAAATTGTCGTG      2040
CAGGATGGAATTACTCTGATCACCAAAGACGAAAGCCAGGAAGCTCTGTACAGCTGAG      2100
GAGGCCACGAAGTTCCTGACCCCCAAAGACAAAGCAAAAGAAGACACACAGGACTTGAA      2160
GAAGGTGGTGTATGTGGATGATTTACTGGACATGATATAG      2199

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MAWSGNKAAVVLCDVGVAMGNSFPGEESPLEQAKKVMTMFVQRQVFSESKDEIALVLYGTESTDNALAGKD
 QYQNITVHRHMLPDLFDLLEDIGNKIQSSQQADFLDALIVCMDLIQRETIGKKFGKKHIEVFTDLSSPFSQDQLDIIIC
 NLKKSIGSLQFFLPIDKNGEPGETEDHDSFDHCAPSFPQKGLTEQQKEGIHVMVTRVMLSLEGKDGLDEIYSFSES
 LQQLCIFKKIERRSLPWPCLTIGPNLSIRIVAYKSIVQEKFKKSXVVVDARTLKKEDIQKETVYCLNDDDETEVSKEDT
 IQGFRYGSIIIPFSKVDEEQMKYKSEGKCFSVLGFCXSSQVHRRFFMGHQVLKVFAAKDDEAAVALSSLVHALDEL
 NMVAIVRYAYDKRANPQVGVAFFIKDAYECLVYVQLPFMEDLRQYMFSSLKNNKKCTPTEAQLSAIDDLIDSMSL
 VKKNEEDIIEDLFPTSKIPNPEFQRLYQCLLHRAHLQERLPPIQQHILNMLDPPTMKAKCEIPLSKVKTLFPLTEVV
 KKKDQVTAQDVFQDNIEEPAKKYKTEKEEGHISISLAEGNVTKVGSVNPVENFRVLVRQKIASFEEASLQLMSHI
 EQFLDTNETLYFMKSMDCIKALREEAIQFSEEQRFNSFLEGLREKVEIKQLNHFWEIVVQDGITLITKDESPGSSVTAE
 EATKFLTPKDKAKEDTTGLEEGGDVDDLLDMI-

➤ **Blast contre banque rat :**

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☒	Rattus norvegicus X-ray repair cross complementing 5 (Xrcc5) mRNA	Norway rat	4050	4050	100%	0.0	99.91%	2545	NM_177419.2
☒	Rattus norvegicus X-ray repair complementing defective repair in Chinese hamster cells 5 mRNA (cDNA clone MGC.72979...)	Norway rat	4050	4050	100%	0.0	99.91%	2548	BC061576.1
☒	Rattus norvegicus mRNA for Xrcc5, partial cds	Norway rat	3480	3480	93%	0.0	97.22%	2100	AB066103.1

➤ **Différence Séquençage/CDS au niveau NT :**

		1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq	cds	ATGGCTGGTCCGGTAAATAGGCAGCTGTTGTGCTGTGTATGGATGTGGGGTGGCCATGGGTAACTCCTTCTCTGGTGAAGATCCCACCTTGACAGGCGCAGGAAGTGATGATCTGTTTGTCCAC													
Consensus		ATGGCTGGTCCGGTAAATAGGCAGCTGTTGTGCTGTGTATGGATGTGGGGTGGCCATGGGTAACTCCTTCTCTGGTGAAGATCCCACCTTGACAGGCGCAGGAAGTGATGATCTGTTTGTCCAC													
		131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq	cds	GACAGGTGTTTTCGGAGGACAGGATGAGATCGCTTATGTCCTTATGGTACAGAGGACCTGATACAGCCCTTCTGGCAGGAGCAGATATCAGACATCAGAGTGACAGGACCTGATGCTACCAAG													
Consensus		GACAGGTGTTTTCGGAGGACAGGATGAGATCGCTTATGTCCTTATGGTACAGAGGACCTGATACAGCCCTTCTGGCAGGAGCAGATATCAGACATCAGAGTGACAGGACCTGATGCTACCAAG													
		261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq	cds	TTTGTATTGCTGGAGACATCGGAACCAATCCACCAAGTCTCAGCAGGCGACTTCTGGAGCCCTGATTGTGTGATGATTGATTGACGCTGAACCATAGGAAGAGAGTTTGGGAAGAG													
Consensus		TTTGTATTGCTGGAGACATCGGAACCAATCCACCAAGTCTCAGCAGGCGACTTCTGGAGCCCTGATTGTGTGATGATTGATTGACGCTGAACCATAGGAAGAGAGTTTGGGAAGAG													
		391	400	410	420	430	440	450	460	470	480	490	500	510	520
seq	cds	CATATTGAGTGTCTACTGATCTCAGCAGCCATTACGACAGACCACTGGACATTATATTTGTACCTGAGAGAGTCGGGATCTCCCTGCGTTTCTTCTGCTTTTCCATCGACAGAGATGGTG													
Consensus		CATATTGAGTGTCTACTGATCTCAGCAGCCATTACGACAGACCACTGGACATTATATTTGTACCTGAGAGAGTCGGGATCTCCCTGCGTTTCTTCTGCTTTTCCATCGACAGAGATGGTG													
		521	530	540	550	560	570	580	590	600	610	620	630	640	650
seq	cds	AGCCTGGGAGACAGAGACACGACTCCAGCTTCAGCCACTGTGACCTCTCTCCCTCAAAAGGACTTACTGAGCAGCAAAAGGAGGAGATCCACATGGTGACAGGGTGATGCTGTCTTTAGAGG													
Consensus		AGCCTGGGAGACAGAGACACGACTCCAGCTTCAGCCACTGTGACCTCTCTCCCTCAAAAGGACTTACTGAGCAGCAAAAGGAGGAGATCCACATGGTGACAGGGTGATGCTGTCTTTAGAGG													
		651	660	670	680	690	700	710	720	730	740	750	760	770	780
seq	cds	CAAGATGGTCTGGATGAATTTATTCCTTCAGCGAGAGCTTCAGCACTGTGCATCTTAAAGAGATTGAGAGGCGGCTTGGCCCTGGCCCTGCCACTGACCATCGGCCCACTTGTCTATAGG													
Consensus		CAAGATGGTCTGGATGAATTTATTCCTTCAGCGAGAGCTTCAGCACTGTGCATCTTAAAGAGATTGAGAGGCGGCTTGGCCCTGGCCCTGCCACTGACCATCGGCCCACTTGTCTATAGG													
		781	790	800	810	820	830	840	850	860	870	880	890	900	910
seq	cds	ATCGTAGCCTATAATCGATTGTACAGGAGAAATTAAGAAGAGTTGGGTAGTTGTGGAGCGCAGAGACTTAAGAGAGGAGATATACAAAGAGAGCTGTTTATGCTTAATGACGATGATGAGACT													
Consensus		ATCGTAGCCTATAATCGATTGTACAGGAGAAATTAAGAAGAGTTGGGTAGTTGTGGAGCGCAGAGACTTAAGAGAGGAGATATACAAAGAGAGCTGTTTATGCTTAATGACGATGATGAGACT													
		911	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040
seq	cds	AAGTTTCCAGAGGAGCACTATTCAAGGTTCCGCTATGGAGCGACATCTCTTTTCTAAAGTGATGAGGACAAATGAATATATATTCGGAGGAGAGTGCTTCTCTGCTGGGTTCTGTAA													
Consensus		AAGTTTCCAGAGGAGCACTATTCAAGGTTCCGCTATGGAGCGACATCTCTTTTCTAAAGTGATGAGGACAAATGAATATATATTCGGAGGAGAGTGCTTCTCTGCTGGGTTCTGTAA													
		1041	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170
seq	cds	ATCTTCTCAGGTTCTATAGAGATTCTTCATGGGACATCAGTTCTGAAGGCTCTTCGAGCGAGGATGATGAGGCGAGCTGTTGCACCTTCTCCCTAGTTCAGGCTTGGATGAGTAAACATGGTC													
Consensus		ATCTTCTCAGGTTCTATAGAGATTCTTCATGGGACATCAGTTCTGAAGGCTCTTCGAGCGAGGATGATGAGGCGAGCTGTTGCACCTTCTCCCTAGTTCAGGCTTGGATGAGTAAACATGGTC													
		1171	1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
seq	cds	GCTATCGTCGCTACGCTTATGCAAAAGAGCTATCTCCAGTTGGTGTAGCTTCCCTTTCTAAGGATGCTATGAGTTTATGTTTATGTGACGCTGCTTTCATGGAGACTTGCAGCAATCA													
Consensus		GCTATCGTCGCTACGCTTATGCAAAAGAGCTATCTCCAGTTGGTGTAGCTTCCCTTTCTAAGGATGCTATGAGTTTATGTTTATGTGACGCTGCTTTCATGGAGACTTGCAGCAATCA													
		1301	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430
seq	cds	TGTTTTCTCCTACGAAACCAATAGAGAGTGACCCCAACAGAGGACAGCTGAGTGGCATGATGATCTGATTGATTCATGAGCTTGGTAAAGAAACAGGAGAGAGCATCATCAGAGACTTGT													
Consensus		TGTTTTCTCCTACGAAACCAATAGAGAGTGACCCCAACAGAGGACAGCTGAGTGGCATGATGATCTGATTGATTCATGAGCTTGGTAAAGAAACAGGAGAGAGCATCATCAGAGACTTGT													
		1431	1440	1450	1460	1470	1480	1490	1500	1510	1520	1530	1540	1550	1560
seq	cds	TCCACCTCCAAATCCAAATCCTGAATTCAGCGGTTGTACAGGTGTCTGCTGCACAGGCTTACATCTCCAGAGGCGGCTGCCCAATTCAGCAGCAATTTGAATATGCTGGATCCCCACT													
Consensus		TCCACCTCCAAATCCAAATCCTGAATTCAGCGGTTGTACAGGTGTCTGCTGCACAGGCTTACATCTCCAGAGGCGGCTGCCCAATTCAGCAGCAATTTGAATATGCTGGATCCCCACT													
		1561	1570	1580	1590	1600	1610	1620	1630	1640	1650	1660	1670	1680	1690
seq	cds	GAGATGAAGCAAAATGTGAGATCCACTCTCAAGTAAGAGCCTTTTCCCTCTGACGGAGTCTGTAAAGAAAGGACCAAGTGACTGCTCAGAGCTTTTCCAGACAAATTTGAAGAGGGGCGG													
Consensus		GAGATGAAGCAAAATGTGAGATCCACTCTCAAGTAAGAGCCTTTTCCCTCTGACGGAGTCTGTAAAGAAAGGACCAAGTGACTGCTCAGAGCTTTTCCAGACAAATTTGAAGAGGGGCGG													
		1691	1700	1710	1720	1730	1740	1750	1760	1770	1780	1790	1800	1810	1820
seq	cds	CTGCTAAAATAACAGACTGAGAAAGAGAGAGTGCACATCAGCATCTCCAGCTGGCAGAGGGAGATGACCAGAGTGGAGGTGATCTGTTGAAGACTTCGCGTCTAGTAGACAGAGAGT													
Consensus		CTGCTAAAATAACAGACTGAGAAAGAGAGAGTGCACATCAGCATCTCCAGCTGGCAGAGGGAGATGACCAGAGTGGAGGTGATCTGTTGAAGACTTCGCGTCTAGTAGACAGAGAGT													
		1821	1830	1840	1850	1860	1870	1880	1890	1900	1910	1920	1930	1940	1950
seq	cds	TGCCAGCTTTGAGGAGCGAGTCTCCAGCTARTAGTGCATTTGACAGTTTTGGATACCAATGAACACTGTATTTATGAAGAGTATGGACGATCAGAGCTTCCGGAGGAGGCATTTCAGTTT													
Consensus		TGCCAGCTTTGAGGAGCGAGTCTCCAGCTARTAGTGCATTTGACAGTTTTGGATACCAATGAACACTGTATTTATGAAGAGTATGGACGATCAGAGCTTCCGGAGGAGGCATTTCAGTTT													
		1951	1960	1970	1980	1990	2000	2010	2020	2030	2040	2050	2060	2070	2080
seq	cds	TCAGAGAGGACGCGTTTCACAGTTTCTCGAGGGCCTTCGAGAGAGTGGAAATTAACATTAAATCATTTCTGGAAATTTGTCGTGCAGGATGGAAATCTCTGATCACCAGAGCAGAGGCCAG													
Consensus		TCAGAGAGGACGCGTTTCACAGTTTCTCGAGGGCCTTCGAGAGAGTGGAAATTAACATTAAATCATTTCTGGAAATTTGTCGTGCAGGATGGAAATCTCTGATCACCAGAGCAGAGGCCAG													
		2081	2090	2100	2110	2120	2130	2140	2150	2160	2170	2180	2190	2199	
seq	cds	GARGCTCTGTACAGCTGAGGAGGCCAGAGTTCTGACCCCCAAGACCAAGACAAAGAGAGACACACAGGACTTGAGAGAGGTGGTGTGTGGATGATTTACTGGCATGATATAG													
Consensus		GARGCTCTGTACAGCTGAGGAGGCCAGAGTTCTGACCCCCAAGACCAAGACAAAGAGAGACACACAGGACTTGAGAGAGGTGGTGTGTGGATGATTTACTGGCATGATATAG													

➤ **Différence Séquençage/CDS au niveau PROT :**

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

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

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

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

521 530 540 550 560 570 580 590 600 610 620 630 640 650
seq EMKAKCEIPLSKYKTLFPLTEVYKKKQDYTAQDYFQDNIEEGPAAKKYKTEKEEGHISISSLAEGNVTYKGVSNPVENFRVLYRQKIASFEEASLQLMSHIEQFLDTNETLYFHKSHDRIKALREERAIQF
ref EMKAKCEIPLSKYKTLFPLTEVYKKKQDYTAQDYFQDNIEEGPAAKKYKTEKEEGHISISSLAEGNVTYKGVSNPVENFRVLYRQKIASFEEASLQLMSHIEQFLDTNETLYFHKSHDRIKALREERAIQF
Consensus EMKAKCEIPLSKYKTLFPLTEVYKKKQDYTAQDYFQDNIEEGPAAKKYKTEKEEGHISISSLAEGNVTYKGVSNPVENFRVLYRQKIASFEEASLQLMSHIEQFLDTNETLYFHKSHDRIKALREERAIQF

651 660 670 680 690 700 710 720 730 732
seq SEEQRFNSFLEGLREKVEIKQLNHFMIEIVYQDGITLITKDDESPGSSVTAERTKFLTPKDKAKEDTTGLEEGGQVDDLLDHI
ref SEEQRFNSFLEGLREKVEIKQLNHFMIEIVYQDGITLITKDDESPGSSVTAERTKFLTPKDKAKEDTTGLEEGGQVDDLLDHI
Consensus SEEQRFNSFLEGLREKVEIKQLNHFMIEIVYQDGITLITKDDESPGSSVTAERTKFLTPKDKAKEDTTGLEEGGQVDDLLDHI

Mutation en 639 C<R comme rate et Di et SP

	X-ray repair complementing defective repair in Chinese hamster cells 5, isoform CRA_a [Rattus norvegicus]	Norway rat	1508	1508	100%	0.0	99.86%	732	EDL75243.1
	X-ray repair cross-complementing protein 5 [Rattus norvegicus]	Norway rat	1506	1506	100%	0.0	99.86%	732	NP_003154.1
	Xrcc5 [Rattus norvegicus]	Norway rat	1359	1359	93%	0.0	96.63%	683	BAB83859.1
	X-ray repair complementing defective repair in Chinese hamster cells 5, isoform CRA_b [Rattus norvegicus]	Norway rat	471	471	31%	1e-163	99.56%	228	EDL75244.1

Flag BirA CTX (cloneB) ok

Renvoyer avec primer interne

Xrcc5_SeqInt_Fwd_1

Démarrage à 560 pour avoir 710

CACTGTGCACCCTCCTTCCC

Xrcc5_SeqInt_Fwd_2

Démarrage à 660 pour avoir 810

TCTGGATGAAATTTATCC

Xrcc5_SeqInt_Rev_1

Démarrage à 1370 pour avoir 1520

GGGGGCAGCCGCTCCTGG

Xrcc5_SeqInt_Rev2

Démarrage à 1390 pour avoir 1240

CCAAGCTCATGGAATCAATC