

8)Nhej1

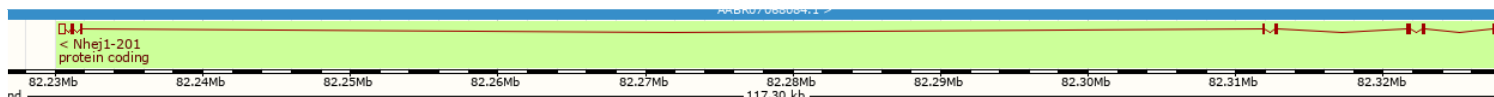
Nhej1= Xlf= protein cernunnos= XRCC4-like factor

Référence NCBI : [NM_001014217](#)

- **Taille 915 NT NT**

- **Séquence NT :**

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atgga ggaactagag
121 caaggcctgt tgatgcagcc atgggcatgg ttacaacttg ctgagaactc actcttggcc
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241 catgaacagg tggacacttt ggaggtcagc cagcgagcca aggagctgaa caagcgctc
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721 gcatgtgctg ttgggtgatg aaggccatth gccatgaatc tgcagagcct gtatgtggca
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```



- **Séquence prot :**

NP_001014239

```
MEELEQGLLMQPWAWLQLAENSLAKASITKHGYALLISDLQQV
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AALLRMKDLEIQAYQESGAVLSRGRLKTEPFEENSFLEQFMVEKLPEACAVGDGRPF
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- **Amorces synthétisées :**

Nhej1_AscI_Fwd

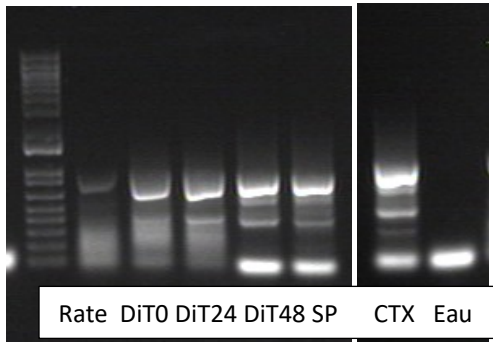
tataGGCGGCCa atgga ggaactagagcaaggcc

Nhej1_NotI_Rev

ttaaGCGGCCGCa ctaactgaagagtcctg

- **Expériences :**

- PCR 10/07 : sur **les 7 conditions** cycle Q5-TM 60°C-Enhancer 0- 2min 30 d'élongation



Bandes RATE, DiT0, DiT24h, DiT48h, SP et CTX Ok

- Sep/Oct : soucis clonage : Vecteur ? PCR mal digérée ?
- 08/09 : purification le 09/09
- 09/09 : test pCR 4Blunt pour Nhej1 **rate**, mini le 11/09 : **OK**
- 14/09 : digestion et purification de 10ul de DiT0, 24h, 48h, SP et CTX
- 15/09 : ligation dans FB marche pas
- 06/10 : religation dans nouv vecteur pour DiT0, DiT24, DiT48, SP et CTX
- 09/10 : miniprep **DiT0 et 48h OK**
- 16/10 redigestion DiT24h, SP et CTX
- 22/10 : mini : **OK**
- 28/10 envoi au séquençage

- Résultats séquençages

- pCR4Blunt Nhej1 rate clone A

- Fwd rate 1047NT : mauvais séquençage au début

TTAGCGgCCGCGAATTCGCCCTTTATAGGCGCGCCAATGGGGAACTAGAGCAAGGCCTGTTGATGCAGCCATGG
GCATGGTTACAACCTTGCTGAGAACTCACTCTTGGCCAAGGCTTCTATCACCAGCATGGTTATGCCTTGCTGATT
CGGATCTTCAACAGGTGTGGCATGAACAGGTGGACACTTTGGAGGTCAGCCAGCGAGCCAAGGAGCTGAACAA
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CACCAGGATGCTGCTCACCTAGCAAAGCCACTTTCTCCTGTGATCGTGGAGAGGAGGTATTGATCCTGAGGGTG
CGGAGTGAGCTCTCTGGTCTCCCCTTCAATTGGCATTTCCTGTCTTCCAGCTAGTTCTTTACTGGTCTCTCAGCA
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GAACAGCANATCTCTCCCACTCCAACCCTCTCANAGCCTGAATGTGAGCCTATGGCTGCTTCNNNCCTGTGCATA
NAGCTCANCTGGTAAAGGNCAAGANGAAGAANCCANGGGACTCTTCAGTTANTGCGGNCGCTTAANNNGCN
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NTTNCNG

- 968NT 25/11

CGGCCGCGAATTCGCCCTTTATAGGCGCGCCAATGGGGAACTAGAGCAAGGCCTGTTGATGCAGCCATGGGCAT
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TGNNGCCGCTNAANNNGCAATTCGTTTAAACCTGCNNNNNTNGTCCCTTTNNNGANGG

- Rev rate 976NT

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➤ Synthèse séquençage rate : 914NT

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 GGTCCAAGCCAGGCAGAAGCATAAAGGCTCTGGAGAGCCTCAGACATCAAGCAGCACCTC
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Le début du séquençage est mauvais

➤ Blast contre banque rat :

	Description	Common Name	Score	Score	Cover	value	Ident	Len	Accession
✓	PREDICTED: Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1), transcript variant X5, mRNA	Norway rat	1683	1683	100%	0.0	99.89%	1647	XM_006245242.3
✓	PREDICTED: Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1), transcript variant X4, mRNA	Norway rat	1683	1683	100%	0.0	99.89%	1878	XM_006245241.3
✓	PREDICTED: Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1), transcript variant X2, mRNA	Norway rat	1683	1683	100%	0.0	99.89%	1707	XM_017596524.1
✓	PREDICTED: Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1), transcript variant X1, mRNA	Norway rat	1683	1683	100%	0.0	99.89%	1972	XM_017596523.1
✓	PREDICTED: Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1), transcript variant X3, mRNA	Norway rat	1683	1683	100%	0.0	99.89%	1491	XM_006245240.1
✓	Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1), mRNA	Norway rat	1683	1683	100%	0.0	99.89%	1445	NM_001014217.1
✓	PREDICTED: Rattus rattus non-homologous end joining factor 1 (Nhej1), mRNA	black rat	1622	1622	100%	0.0	98.69%	1782	XM_032901378.1
✓	PREDICTED: Arvicanthis niloticus non-homologous end joining factor 1 (Nhej1), transcript variant X2, mRNA	African grass rat	1397	1397	99%	0.0	94.39%	1321	XM_034498442.1
✓	PREDICTED: Arvicanthis niloticus non-homologous end joining factor 1 (Nhej1), transcript variant X1, mRNA	African grass rat	1397	1397	99%	0.0	94.39%	1319	XM_034498441.1

➤ Différence Séquençage/CDS au niveau NT :

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CDS	ATGGAGGAAC TAGAGCAGGCTGTTGATGCAGCCATGGGCATGGTTACAACCTTGCTGAGAACTCAGCTTTGGCCAGGCTTCTATCACCAGCATGGTTATGCCCTTGCTGATTTCCGATCTTCACACGG														
Consensus	ATGG_GGAAC TAGAGCAGGCTGTTGATGCAGCCATGGGCATGGTTACAACCTTGCTGAGAACTCAGCTTTGGCCAGGCTTCTATCACCAGCATGGTTATGCCCTTGCTGATTTCCGATCTTCACACGG														
	131	140	150	160	170	180	190	200	210	220	230	240	250	260	
seq	TGTGGCATGAACAGGTGGACACTTTGAGGTCAGCCAGCGAGCCAGGAGCTGAACAGCGCTCAGCCGCTCCCTGAGCTTTCTCCATCACTTGGATGAAGTGCTTCGCCACTGTTTAAAGATTC														
CDS	TGTGGCATGAACAGGTGGACACTTTGAGGTCAGCCAGCGAGCCAGGAGCTGAACAGCGCTCAGCCGCTCCCTGAGCTTTCTCCATCACTTGGATGAAGTGCTTCGCCACTGTTTAAAGATTC														
Consensus	TGTGGCATGAACAGGTGGACACTTTGAGGTCAGCCAGCGAGCCAGGAGCTGAACAGCGCTCAGCCGCTCCCTGAGCTTTCTCCATCACTTGGATGAAGTGCTTCGCCACTGTTTAAAGATTC														
	261	270	280	290	300	310	320	330	340	350	360	370	380	390	
seq	TGCCACCCAGGATGCTGCTCAGCTAGCAAGCCACTTTCTCCTGTGATCGTGAGAGGAGGATTGATCCTGAGGGTGCGGAGTGAGCTCTCTGCTCCTCCCTCAATTGGCATTTCCACTGCTTCCA														
CDS	TGCCACCCAGGATGCTGCTCAGCTAGCAAGCCACTTTCTCCTGTGATCGTGAGAGGAGGATTGATCCTGAGGGTGCGGAGTGAGCTCTCTGCTCCTCCCTCAATTGGCATTTCCACTGCTTCCA														
Consensus	TGCCACCCAGGATGCTGCTCAGCTAGCAAGCCACTTTCTCCTGTGATCGTGAGAGGAGGATTGATCCTGAGGGTGCGGAGTGAGCTCTCTGCTCCTCCCTCAATTGGCATTTCCACTGCTTCCA														
	391	400	410	420	430	440	450	460	470	480	490	500	510	520	
seq	GCTAGTTCTTTACTGGTCTCTCAGCATTTGATTTGCTCTGATGGGTGTGAGCTTGGCATTGCACAGTCATGTGAGGGAGCTAGCAGCATTGCTTCGGATGAAGGACCTTGAGATCCAGGCTACACGG														
CDS	GCTAGTTCTTTACTGGTCTCTCAGCATTTGATTTGCTCTGATGGGTGTGAGCTTGGCATTGCACAGTCATGTGAGGGAGCTAGCAGCATTGCTTCGGATGAAGGACCTTGAGATCCAGGCTACACGG														
Consensus	GCTAGTTCTTTACTGGTCTCTCAGCATTTGATTTGCTCTGATGGGTGTGAGCTTGGCATTGCACAGTCATGTGAGGGAGCTAGCAGCATTGCTTCGGATGAAGGACCTTGAGATCCAGGCTACACGG														
	521	530	540	550	560	570	580	590	600	610	620	630	640	650	
seq	AGAGTGGGGCTGTGCTGAGCCGAGGTCGATTGAGACAGAGCCATTTGAGAGAAATTCCTTCTGGACAGTTTATGGTAGAGAAATTGCCAGAGGCATGTGCTGTTGGTGATGGAGGCCATTTGCCAT														
CDS	AGAGTGGGGCTGTGCTGAGCCGAGGTCGATTGAGACAGAGCCATTTGAGAGAAATTCCTTCTGGACAGTTTATGGTAGAGAAATTGCCAGAGGCATGTGCTGTTGGTGATGGAGGCCATTTGCCAT														
Consensus	AGAGTGGGGCTGTGCTGAGCCGAGGTCGATTGAGACAGAGCCATTTGAGAGAAATTCCTTCTGGACAGTTTATGGTAGAGAAATTGCCAGAGGCATGTGCTGTTGGTGATGGAGGCCATTTGCCAT														
	651	660	670	680	690	700	710	720	730	740	750	760	770	780	
seq	GAATCTGCAGAGCTGTATGTGGCAGTCACAAAGCAGAGGTCAGGCCAGGCGAGAGCATAAAGGCTCTGGAGAGCTCAGACATCAGCAGCAGCTCCCTCAGGAACTGTATAGCCAGCTTCAGAAC														
CDS	GAATCTGCAGAGCTGTATGTGGCAGTCACAAAGCAGAGGTCAGGCCAGGCGAGAGCATAAAGGCTCTGGAGAGCTCAGACATCAGCAGCAGCTCCCTCAGGAACTGTATAGCCAGCTTCAGAAC														
Consensus	GAATCTGCAGAGCTGTATGTGGCAGTCACAAAGCAGAGGTCAGGCCAGGCGAGAGCATAAAGGCTCTGGAGAGCTCAGACATCAGCAGCAGCTCCCTCAGGAACTGTATAGCCAGCTTCAGAAC														
	781	790	800	810	820	830	840	850	860	870	880	890	900	910	
seq	CAGCCAGAACAGCAGATCTCTCCACTCCACCCCTCTCAGAGCCTGAATGTGAGCCTATGGCTGCTTCAGGCCCTGTGCATAGAGCTCAGCTGGTAAGGCCAGAGGAGAGGCCAGGGGACTCTTCA														
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Consensus	CAGCCAGAACAGCAGATCTCTCCACTCCACCCCTCTCAGAGCCTGAATGTGAGCCTATGGCTGCTTCAGGCCCTGTGCATAGAGCTCAGCTGGTAAGGCCAGAGGAGAGGCCAGGGGACTCTTCA														
	911	915													
seq	---														
CDS	GTTAG														
Consensus	GTTAG														

Début mauvais qvec A qui manque en position5, alors que c'est dans l'amorce .

➤ Différence au niveau PROT :

Flag BirA Nhej1 rate (clone A) : début de séquence toujours bizarre

○ pCR4Blunt Nhej1 rate clone B

➤ Fwd 928NT

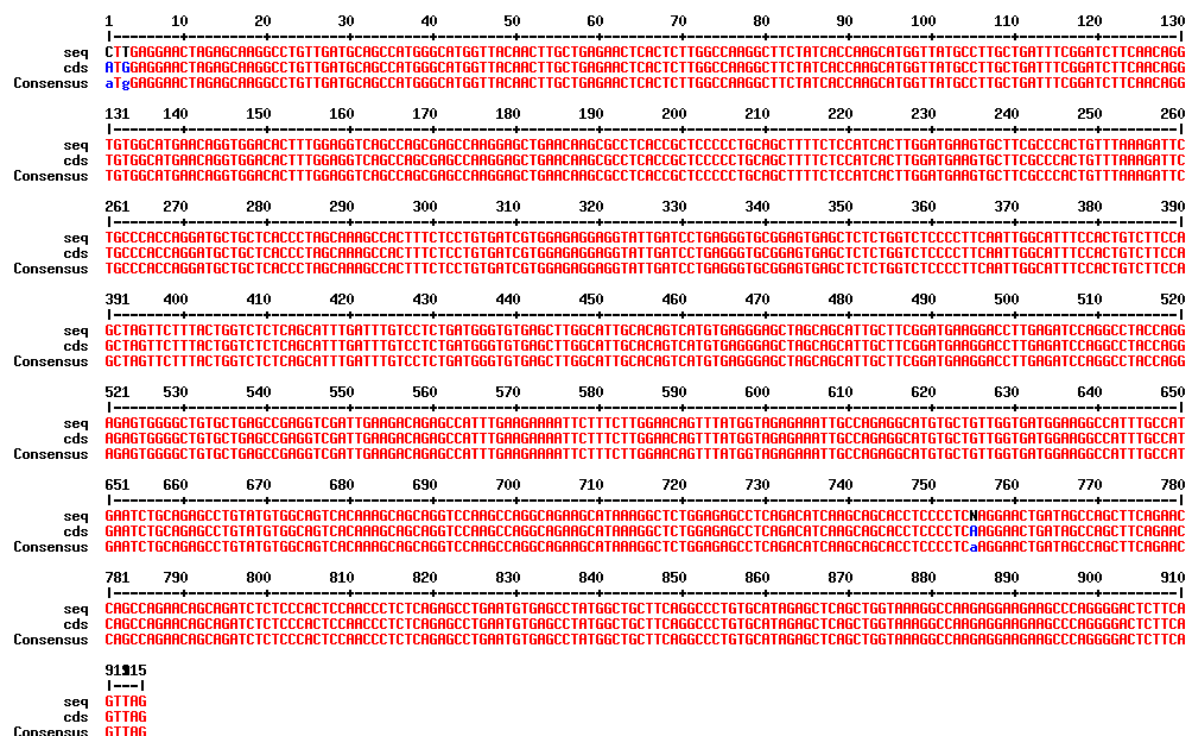
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AG

➤ **Synthèse séquençage rate :**

CTTGAGGAAGCTAGAGCAAGGCCTGTTGATGCAGCCATGGGCATGGTTACAACCTTG	55
CTGAGAAGCTCACTCTTGGCCAAAGGCTTCTATCACCAAGCATGGTTATGCCTTGCTGATTT	115
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TGCTTCGCCCACTGTTTAAAGATTCTGCCCAACAGGATGCTGCTCACCCTAGCAAAGCCA	295
CTTTCTCCTGTGATCGTGGAGAGGAGGTATTGATCCTGAGGGTGCGGAGTGAGCTCTCTG	355
GTCTCCCCTTCAATTGGCATTGTCATGCTCTCCAGTAGTCTTTACTGGTCTCTCAGC	415
ATTTGATTTGTCTCTGATGGGTGTGAGCTTGGCATTCGACAGTCATGTGAGGAGCTAG	475
CAGCATTGCTTCGGATGAAGGACCTTGAGATCCAGGCCTACCAGGAGAGTGGGGCTGTGC	525
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GCTCTGGAGAGCCTCAGACATCAAGCAGCACCTCCCGCTCNAGGAAGTGATAGCCAGCTTC	775
AGAACCAGCCAGAAACAGCAGATCTCTCCACTCCAACCTCTCAGAGCCTGAATGTGAGC	835
CTATGGCTGCTTCAGGCCCTGTGCATAGAGCTCAGCTGGTAAAGGCCAAGAGGAAGAAGC	895
CCAGGGGACTCTTCAGTTAG-----	915



Comme pour clone A, le début de séquence est mauvais alors qu'il s'agit de la partie qui est dans l'amorce : nouvelle ligation et transformation le 07/12

o **FlagBirA Nhej1 DiT0 clone A**

➤ **B3Fwd DiT0 848NT**

ATGGAGGAACTAGAGCAAGGCCTGTTGATGCAGCCATGGGCATGGTTACAACCTTGCTGAGAACTCACTCTTGGC
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ANANCTGAANGNGAGCCTATGGCTGCTTC

➤ **BGHRev DiT0 915NT**

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GCCTGAATGTGAGCCTATGGCTGCTTCAGGCCCTGTGCATAGAGCTCAGCTGGTAAAGGCCAAGAGGAAGAAG
CCCAGGGGACTCTTCAGTTAG

➤ **Synthèse séquençage DiT0 : 915NT**

ATGGAGGAACTAGAGCAAGGCCTGTTGATGCAGCCATGGGCATGGTTACAACCTTGCTGAG	60
AACTCACTCTTGGCCAAGGCTTCTATCACCAAGCATGGTTATGCCTTGCTGATTTTCGGAT	120
CTTCAACAGGTGTGGCATGAACAGGTGGACACTTTGGAGGTCAGCCAGCGAGCCAAGGAG	180
CTGAACAAGCGCCTCACCGCTCCCCCTGCAGCTTTTCTCCATCACTTGGATGAAGTGCTT	240
CGCCCCTGTTTAAAGATTCTGCCACCAGGATGCTGCTCACCTAGCAAAGCCACTTTC	300
TCCTGTGATCGTGGAGAGGAGGTATTGATCCTGAGGGTGCGGAGTGAGCTCTCTGGTCTC	360
CCCTTCAATTGGCATTTCCACTGTCTTCCAGCTAGTTCTTTACTGGTCTCTCAGCATTG	420
ATTTGTCCTCTGATGGGTGTGAGCTTGGCATTGCACAGTCATGTGAGGGAGCTAGCAGCA	480
TTGCTTCGGATGAAGGACCTTGAGATCCAGGCCTACCAGGAGAGTGGGGCTGTGCTGAGC	540
CGAGGTGATTGAAGACAGAGCCATTTGAAGAAAATTCTTTCTTGGAACAGTTTATGGTA	600
GAGAAATTGCCAGAGGCATGTGCTGTTGGTGATGGAAGGCCATTTGCCATGAATCTGCAG	660
AGCCTGTATGTGGCAGTCACAAAGCAGCAGGTCCAAGCCAGGCAGAAAGCATAAAGGCTCT	
GGAGAGCCTCAGACATCAAGCAGCAGCTCCCCTCAAGGAACTGATAGCCAGCTTCAGAAC	
CAGCCAGAACAGCAGATCTCTCCCCTCAACCCTCTCAGAGCCTGAATGTGAGCCTATG	
GCTGCTTCAGGCCCTGTGCATAGAGCTCAGCTGGTAAAGGCCAAGAGGAAGAAGCCCAGG	
GGACTCTTCAGTTAG	

MEELEQGLLMQPWAWLQLAENSLAKASITKHGYALLISDLQQVWHEQVDTLEVSQRAKELNKRLTAPPAFLHH
LDEVLRPLFKDSAHDAAHPSKATFSCDRGEEVLILRVSELSGLPFNWHFCLPASSLLVSQHLCPLMGVSLALHS

HVRELAALLRMKDLEIQAYQESGAVLSRGLKTEPFEENSFLEQFMVEKLPEACAVGDGRPFAMNLQSLYVAVTKQ
QVQARQKHKGSGEPQTSSSTSPQGTDSQLQNPQEQQISPTPTLSEPECEPMAASGPVHRAQLVKAKRKKPRGLFS-

➤ Blast contre banque rat :

	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
✓	PREDICTED: Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1), transcript variant X5, mRNA	1690	1690	100%	0.0	100.00%	XM_006245242.3
✓	PREDICTED: Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1), transcript variant X4, mRNA	1690	1690	100%	0.0	100.00%	XM_006245241.3
✓	PREDICTED: Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1), transcript variant X2, mRNA	1690	1690	100%	0.0	100.00%	XM_017596524.1
✓	PREDICTED: Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1), transcript variant X1, mRNA	1690	1690	100%	0.0	100.00%	XM_017596523.1
✓	PREDICTED: Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1), transcript variant X3, mRNA	1690	1690	100%	0.0	100.00%	XM_006245240.1
✓	Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1), mRNA	1690	1690	100%	0.0	100.00%	NM_001014217.1
✓	Rattus norvegicus BAC CH230-189D6 () complete sequence	429	1136	65%	3e-118	100.00%	AC121001.5

➤ Différence Séquencage/CDS au niveau NT :

sequence CDS Consensus	1 131 140 150 160 170 180 190 200 210 220 230 240 250 260	ATGGAGGAACTAGAGCAGGCGCTGTTGATGCAGCCATGGGCGATGGTTACAACTTGTCTGAGAACTCACTCTTGGCCAGGCTTCTATCACCAGCATGGTTATGCTTGGTATTTCCGATCTTCACAGG ATGGAGGAACTAGAGCAGGCGCTGTTGATGCAGCCATGGGCGATGGTTACAACTTGTCTGAGAACTCACTCTTGGCCAGGCTTCTATCACCAGCATGGTTATGCTTGGTATTTCCGATCTTCACAGG ATGGAGGAACTAGAGCAGGCGCTGTTGATGCAGCCATGGGCGATGGTTACAACTTGTCTGAGAACTCACTCTTGGCCAGGCTTCTATCACCAGCATGGTTATGCTTGGTATTTCCGATCTTCACAGG
sequence CDS Consensus	261 270 280 290 300 310 320 330 340 350 360 370 380 390	TGTGGCATGACAGGTGGACACTTTGGAGGTGAGCCAGGCGAGCCAGGAGCTGACAGGCGCTTCCCGCTCCCCCTGCAGCTTTTCTCCATCACTTGGATGAGTGCTTCGCCCACTGTTTAAGATT TGTGGCATGACAGGTGGACACTTTGGAGGTGAGCCAGGCGAGCCAGGAGCTGACAGGCGCTTCCCGCTCCCCCTGCAGCTTTTCTCCATCACTTGGATGAGTGCTTCGCCCACTGTTTAAGATT TGTGGCATGACAGGTGGACACTTTGGAGGTGAGCCAGGCGAGCCAGGAGCTGACAGGCGCTTCCCGCTCCCCCTGCAGCTTTTCTCCATCACTTGGATGAGTGCTTCGCCCACTGTTTAAGATT
sequence CDS Consensus	391 400 410 420 430 440 450 460 470 480 490 500 510 520	TGCCCAACAGGATGCTGCTACCCCTAGCAGAGCCACTTTCTCTGATGCTGGAGAGGAGATTGATCTGAGGCTGCGGAGTGAGCTCTCTGGTCTCCCTTCATTGGCATTTCCACTGCTTCCA TGCCCAACAGGATGCTGCTACCCCTAGCAGAGCCACTTTCTCTGATGCTGGAGAGGAGATTGATCTGAGGCTGCGGAGTGAGCTCTCTGGTCTCCCTTCATTGGCATTTCCACTGCTTCCA TGCCCAACAGGATGCTGCTACCCCTAGCAGAGCCACTTTCTCTGATGCTGGAGAGGAGATTGATCTGAGGCTGCGGAGTGAGCTCTCTGGTCTCCCTTCATTGGCATTTCCACTGCTTCCA
sequence CDS Consensus	521 530 540 550 560 570 580 590 600 610 620 630 640 650	GATGTTGGGCTGTGCTGAGCCAGGCTGATTGAGACAGAGCCATTGAGAGAAATCTTCTTGGAGAGCTTATGGTAGAGAAATGCCAGAGGCACTGTGCTTGGTATGGAGGCACTTGGCAT GATGTTGGGCTGTGCTGAGCCAGGCTGATTGAGACAGAGCCATTGAGAGAAATCTTCTTGGAGAGCTTATGGTAGAGAAATGCCAGAGGCACTGTGCTTGGTATGGAGGCACTTGGCAT GATGTTGGGCTGTGCTGAGCCAGGCTGATTGAGACAGAGCCATTGAGAGAAATCTTCTTGGAGAGCTTATGGTAGAGAAATGCCAGAGGCACTGTGCTTGGTATGGAGGCACTTGGCAT
sequence CDS Consensus	651 660 670 680 690 700 710 720 730 740 750 760 770 780	GATCTGAGAGGCTGTATGTGGAGTCACAGAGCAGGCTCCAGGCGAGGAGCATAGAGGCTCTGGAGAGCTTACAGCATCAGCAGCAGCTCCCCCTCAGGAGCTGATAGCAGGCTTCAGAG GATCTGAGAGGCTGTATGTGGAGTCACAGAGCAGGCTCCAGGCGAGGAGCATAGAGGCTCTGGAGAGCTTACAGCATCAGCAGCAGCTCCCCCTCAGGAGCTGATAGCAGGCTTCAGAG GATCTGAGAGGCTGTATGTGGAGTCACAGAGCAGGCTCCAGGCGAGGAGCATAGAGGCTCTGGAGAGCTTACAGCATCAGCAGCAGCTCCCCCTCAGGAGCTGATAGCAGGCTTCAGAG
sequence CDS Consensus	781 790 800 810 820 830 840 850 860 870 880 890 900 910	CAGCCAGAGCAGCAGATCTCTCCACTCCAGCCCTCTCAGAGCCTGATGTGAGCTATGGCTGCTCAGGCGCTGTGCATAGAGCTCAGCTGGTAAGGCCAGAGGAGGAGGCCAGGGGACTCTTCA CAGCCAGAGCAGCAGATCTCTCCACTCCAGCCCTCTCAGAGCCTGATGTGAGCTATGGCTGCTCAGGCGCTGTGCATAGAGCTCAGCTGGTAAGGCCAGAGGAGGAGGCCAGGGGACTCTTCA CAGCCAGAGCAGCAGATCTCTCCACTCCAGCCCTCTCAGAGCCTGATGTGAGCTATGGCTGCTCAGGCGCTGTGCATAGAGCTCAGCTGGTAAGGCCAGAGGAGGAGGCCAGGGGACTCTTCA
sequence CDS Consensus	91115 ---	GTTAG GTTAG GTTAG

➤ Différence au niveau PROT :

sequence refprot Consensus	1 10 20 30 40 50 60 70 80 90 100 110 120 130	MEELEQGLLQAPARHLQLAENSLAKASITKHGYALLISDLQQVHNEQVDTLEVSQAKELNKRLTAPPARFLAHLDEVLRLPLFKDSAHQDAHPKSRATSCORGEVLLILRVSELSGLPFMHHFCLP MEELEQGLLQAPARHLQLAENSLAKASITKHGYALLISDLQQVHNEQVDTLEVSQAKELNKRLTAPPARFLAHLDEVLRLPLFKDSAHQDAHPKSRATSCORGEVLLILRVSELSGLPFMHHFCLP MEELEQGLLQAPARHLQLAENSLAKASITKHGYALLISDLQQVHNEQVDTLEVSQAKELNKRLTAPPARFLAHLDEVLRLPLFKDSAHQDAHPKSRATSCORGEVLLILRVSELSGLPFMHHFCLP
sequence refprot Consensus	131 140 150 160 170 180 190 200 210 220 230 240 250 260	ASSLLYSQHLICPLMGVSLALSHVRELAALLRMKOLEIQAYQESGAVLSRGLKTEPFEENSFLEQFMVEKLPEACAVGDGRPFAMNLQSLYYAVTKQVQARQKHKGSGEPQTSSSTSPQGTDSQLN ASSLLYSQHLICPLMGVSLALSHVRELAALLRMKOLEIQAYQESGAVLSRGLKTEPFEENSFLEQFMVEKLPEACAVGDGRPFAMNLQSLYYAVTKQVQARQKHKGSGEPQTSSSTSPQGTDSQLN ASSLLYSQHLICPLMGVSLALSHVRELAALLRMKOLEIQAYQESGAVLSRGLKTEPFEENSFLEQFMVEKLPEACAVGDGRPFAMNLQSLYYAVTKQVQARQKHKGSGEPQTSSSTSPQGTDSQLN
sequence refprot Consensus	261 270 280 290 300 304	OPEEQISPTPTLSEPECEPMAASGPVHRAQLVKAKRKKPRGLFS OPEEQISPTPTLSEPECEPMAASGPVHRAQLVKAKRKKPRGLFS OPEEQISPTPTLSEPECEPMAASGPVHRAQLVKAKRKKPRGLFS

Flag BirA Nhej1 DiT0 (clone A) : OK

o FlagBirA Nhej1 DiT24hLPS clone B

➤ B3Fwd DiT24h 779NT

ATGGAGGAACTAGAGCAAGGCCTGTTGATGCAGCCATGGGCATGGTTACAACCTTGCTGAGAACTCACTCTTGGC
CAAGGCTTCTATCACCAAGCATGGTTATGCCTTGCTGATTTCCGATCTTCAACAGGTGTGGCATGAACAGGTGGA
CACTTTGGAGGTCAGCCAGCGAGCCAAGGAGCTGAACAAGCGCCTACCGCTCCCCCTGCAGCTTTTCTCCATC
ACTTGGATGAAGTGCTTCGCCCCTGTTTAAAGATTCTGCCACCAGGATGCTGCTCACCTAGCAAAGCCACTT
TCTCCTGTGATCGTGGAGAGGAGGTATTGATCCTGAGGGTGCGGAGTGAGCTCTCTGGTCTCCCCTTCAATTGGC
ATTTCCACTGTCTTCCAGCTAGTTCTTTACTGGTCTCTCAGCATTTGATTTGTCCTCTGATGGGTGTGAGCTTGGCA
TTGCACAGTCATGTGAGGGAGCTAGCAGCATTGCTTCGGATGAAGGACCTTGAGATCCAGGCCTACCAGGAGAG
TGGGGCTGTGCTGAGCCGAGGTGATTGAAGACAGAGCCATTTGAAGAAAATTCTTTCTTGAACAGTTTATGG
TAGAGAAATTGCCAGAGGCATGTGCTGTTGGTGATGGAAGGcCATTTGCCATGAATCTGCAGAGCCTGTATGTGG
CAGTCACAAAGCAGCANGTCCAAGCCAGGCAGAAGCATAAAGGCTCTGGANAGCCTCANACATCAAGCAGCAC
CTCCCCTCAAGGAACTGATAGCCAGCTTCANAA

➤ BGHRev DiT24h 915NT

ATGGAGGAACTAGAGCAAGGCCTGTTGATGCAGCCATGGGCATGGTTACAACCTTGCTGAGAACTCANTCTTGGC
CAAGGCTTCTATCACCAAGCATGGTTATGCCTTGCTGATTTCCGATCTTCAACAGGTGTGGCATGAACAGGTGGA
CACTTTGGAGGTCAGCCAGCGAGCCAAGGAGCTGAACAAGCGCCTACCGCTCCCCCTGCAGCTTTTCTCCATC
ACTTGGATGAAGTGCTTCGCCCCTGTTTAAAGATTCTGCCACCAGGATGCTGCTCACCTAGCAAAGCCACTT
TCTCCTGTGATCGTGGAGAGGAGGTATTGATCCTGAGGGTGCGGAGTGAGCTCTCTGGTCTCCCCTTCAATTGGC
ATTTCCACTGTCTTCCAGCTAGTTCTTTACTGGTCTCTCAGCATTTGATTTGTCCTCTGATGGGTGTGAGCTTGGCA
TTGCACAGTCATGTGAGGGAGCTAGCAGCATTGCTTCGGATGAAGGACCTTGAGATCCAGGCCTACCAGGAGAG
TGGGGCTGTGCTGAGCCGAGGTGATTGAAGACAGAGCCATTTGAAGAAAATTCTTTCTTGAACAGTTTATGG
TAGAGAAATTGCCAGAGGCATGTGCTGTTGGTGATGGAAGGCCATTTGCCATGAATCTGCAGAGCCTGTATGTGG
CAGTCACAAAGCAGCAGGTCCAAGCCAGGCAGAAGCATAAAGGCTCTGGAGAGCCTCAGACATCAAGCAGCAC
CTCCCCTCAAGGAACTGATAGCCAGCTTCAGAACCAGCCAGAACAGCAGATCTCTCCACTCCAACCCTCTCAGA
GCCTGAATGTGAGCCTATGGCTGCTTCAGGCCCTGTGCATAGAGCTCAGCTGGTAAAGGCCAAGAGGAAGAAG
CCCAGGGGACTCTTCAGTTAG

➤ Synthèse séquençage DiT24hLPS : 915NT

ATGGAGGAACTAGAGCAAGGCCTGTTGATGCAGCCATGGGCATGGTTACAACCTTGCTGAG	60
AACCTACTCTTGCCCAAGGCTTCTATCACCAAGCATGGTTATGCCCTTGCTGATTTCCGAT	120
CTTCAACAGGTGTGGCATGAACAGGTGGACACTTTGGAGGTCAGCCAGCGAGCCAAGGAG	180
CTGAACAAGCGCCTACCGCTCCCCCTGCAGCTTTTCTCCATCACTTGGATGAAGTGCTT	240
CGCCCCTGTTTAAAGATTCTGCCACCAGGATGCTGCTCACCTAGCAAAGCCACTTTC	300
TCCTGTGATCGTGGAGAGGAGGTATTGATCCTGAGGGTGCGGAGTGAGCTCTCTGGTCTC	360
CCCTTCAATTGGCATTTCCACTGTCTTCCAGCTAGTTCTTTACTGGTCTCTCAGCATTTG	420
ATTTGTCCTCTGATGGGTGTGAGCTTGGCATTGCACAGTCATGTGAGGGAGCTAGCAGCA	480
TTGCTTCGGATGAAGGACCTTGAGATCCAGGCCTACCAGGAGAGTGGGGCTGTGCTGAGC	540
CGAGGTGATTGAAGACAGAGCCATTTGAAGAAAATTCTTTCTTGAACAGTTTATGGTA	600
GAGAAATTGCCAGAGGCATGTGCTGTTGGTGATGGAAGGCCATTTGCCATGAATCTGCAG	660
AGCCTGTATGTGGCAGTCACAAAGCAGCAGGTCCAAGCCAGGCAGAAGCATAAAGGCTCT	
GGAGAGCCTCAGACATCAAGCAGCACCTCCCCTCAAGGAACTGATAGCCAGCTTCAGAAC	
CAGCCAGAACAGCAGATCTCTCCACTCCAACCCTCTCAGAGCCTGAATGTGAGCCTATG	
GCTGCTTCAGGCCCTGTGCATAGAGCTCAGCTGGTAAAGGCCAAGAGGAAGAAGCCAGG	
GGACTCTTCAGTTAG	

MEELEQGLLMQPWAWLQLAENSLAKASITKHGYALLISDLQQVWHEQVDTLEVSQRAKELNKRLTAPPAFLHH
LDEVLRPLFKDSAHQDAHPSKATFSCDRGEEVLILRVSELSGLPFNWHFCHLPASSLLVSQHLICPLMGVSLALHS

HVRELAALLRMKDLQAYQESGAVLSRGLKTEPFEENSFLEQFMVEKLPEACAVGDGRPFAMNLQSLYVAVTKQ
QVQARQKHKGSGEPQTSSSTSPQGTDSQLQNPQEQQISPTPTLSEPECEPMAASGPVHRAQLVKAKRKKPRGLFS-

➤ Blast contre banque rat :

✓	PREDICTED: Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1)_transcript variant X5_mRNA	1690	1690	100%	0.0	100.00%	XM_006245242.3
✓	PREDICTED: Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1)_transcript variant X4_mRNA	1690	1690	100%	0.0	100.00%	XM_006245241.3
✓	PREDICTED: Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1)_transcript variant X2_mRNA	1690	1690	100%	0.0	100.00%	XM_017596524.1
✓	PREDICTED: Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1)_transcript variant X1_mRNA	1690	1690	100%	0.0	100.00%	XM_017596523.1
✓	PREDICTED: Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1)_transcript variant X3_mRNA	1690	1690	100%	0.0	100.00%	XM_006245240.1
✓	Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1)_mRNA	1690	1690	100%	0.0	100.00%	NM_001014217.1
✓	Rattus norvegicus BAC CH230-189D6 () complete sequence	429	1136	65%	3e-118	100.00%	AC121001.5

➤ Différence Séquencage/CDS au niveau NT :

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
sequence	ATGGAGGAAC TAGAGCAGGCC TGTGATGAGCCATGGGCATGGTTACAACTTGTCTGAGAACTCACTCTTGGCCAGGCTTCTATCACCAGCATGGTTATGCTTGCATTTCGGATCTTCACAGG													
CDS	ATGGAGGAAC TAGAGCAGGCC TGTGATGAGCCATGGGCATGGTTACAACTTGTCTGAGAACTCACTCTTGGCCAGGCTTCTATCACCAGCATGGTTATGCTTGCATTTCGGATCTTCACAGG													
Consensus	ATGGAGGAAC TAGAGCAGGCC TGTGATGAGCCATGGGCATGGTTACAACTTGTCTGAGAACTCACTCTTGGCCAGGCTTCTATCACCAGCATGGTTATGCTTGCATTTCGGATCTTCACAGG													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
sequence	TGTGGCATGAACAGGTGGACACTTTGGAGGTCAGCCAGCGAGCCAGGAGCTGAACAGCGCCTCACCCTCCCTTCAGCTTTTCTCCATCACTTGGATGAAGTGCTTCGCCACTGTTAAAGATTCT													
CDS	TGTGGCATGAACAGGTGGACACTTTGGAGGTCAGCCAGCGAGCCAGGAGCTGAACAGCGCCTCACCCTCCCTTCAGCTTTTCTCCATCACTTGGATGAAGTGCTTCGCCACTGTTAAAGATTCT													
Consensus	TGTGGCATGAACAGGTGGACACTTTGGAGGTCAGCCAGCGAGCCAGGAGCTGAACAGCGCCTCACCCTCCCTTCAGCTTTTCTCCATCACTTGGATGAAGTGCTTCGCCACTGTTAAAGATTCT													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
sequence	TGCCACACAGGATGCTGCTCACCCTAGCAAGGCCACTTTCTCCTGTGATCGTGGAGAGGAGGATTGATCCTGAGGGTGCGGAGTGAGCTCTCTGGTCTCCCTTCATTGGCATTTCACATGCTTTCCA													
CDS	TGCCACACAGGATGCTGCTCACCCTAGCAAGGCCACTTTCTCCTGTGATCGTGGAGAGGAGGATTGATCCTGAGGGTGCGGAGTGAGCTCTCTGGTCTCCCTTCATTGGCATTTCACATGCTTTCCA													
Consensus	TGCCACACAGGATGCTGCTCACCCTAGCAAGGCCACTTTCTCCTGTGATCGTGGAGAGGAGGATTGATCCTGAGGGTGCGGAGTGAGCTCTCTGGTCTCCCTTCATTGGCATTTCACATGCTTTCCA													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
sequence	GCTAGTCTCTTACTGGTCTCTCAGCATTTGATTTGTCTCTGATGGGTGTGAGCTTGGCATTGCACAGTCATGTGAGGGAGCTAGCAGCATTTGCTCGGATGAAGGACCTTGAGATCCAGGCTTACAGG													
CDS	GCTAGTCTCTTACTGGTCTCTCAGCATTTGATTTGTCTCTGATGGGTGTGAGCTTGGCATTGCACAGTCATGTGAGGGAGCTAGCAGCATTTGCTCGGATGAAGGACCTTGAGATCCAGGCTTACAGG													
Consensus	GCTAGTCTCTTACTGGTCTCTCAGCATTTGATTTGTCTCTGATGGGTGTGAGCTTGGCATTGCACAGTCATGTGAGGGAGCTAGCAGCATTTGCTCGGATGAAGGACCTTGAGATCCAGGCTTACAGG													
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
sequence	AGAGTGGGGCTGTGCTGAGCCGAGGTCGATTGAAGACAGAGCCATTGAAGAAATCTTTCTTGGACAGTTTATGGTAGAGAAATGCCAGAGGCATGTGCTGTTGGTGAAGAGGCCATTTGCCAT													
CDS	AGAGTGGGGCTGTGCTGAGCCGAGGTCGATTGAAGACAGAGCCATTGAAGAAATCTTTCTTGGACAGTTTATGGTAGAGAAATGCCAGAGGCATGTGCTGTTGGTGAAGAGGCCATTTGCCAT													
Consensus	AGAGTGGGGCTGTGCTGAGCCGAGGTCGATTGAAGACAGAGCCATTGAAGAAATCTTTCTTGGACAGTTTATGGTAGAGAAATGCCAGAGGCATGTGCTGTTGGTGAAGAGGCCATTTGCCAT													
	651	660	670	680	690	700	710	720	730	740	750	760	770	780
sequence	GAATCTGACAGGCTGTATGTGGCAGTCACAAAGCAGCAGGTCAGCCAGGCGAGGAGCATAAAGGCTCTGGAGAGCCTCAGACATCAGCAGCACCTCCCTCAGGAACTGATAGCCAGCTTCAGAAC													
CDS	GAATCTGACAGGCTGTATGTGGCAGTCACAAAGCAGCAGGTCAGCCAGGCGAGGAGCATAAAGGCTCTGGAGAGCCTCAGACATCAGCAGCACCTCCCTCAGGAACTGATAGCCAGCTTCAGAAC													
Consensus	GAATCTGACAGGCTGTATGTGGCAGTCACAAAGCAGCAGGTCAGCCAGGCGAGGAGCATAAAGGCTCTGGAGAGCCTCAGACATCAGCAGCACCTCCCTCAGGAACTGATAGCCAGCTTCAGAAC													
	781	790	800	810	820	830	840	850	860	870	880	890	900	910
sequence	CAGCCAGAACAGCAGATCTCTCCACTCCACCCCTCTCAGAGCCTGAATGTGAGCCTATGGCTGCTTCAGGCCCTGTGCATAGAGCTCAGCTGGTAAGGCCAAGAGGAGAGGCCAGGGGACTTTCA													
CDS	CAGCCAGAACAGCAGATCTCTCCACTCCACCCCTCTCAGAGCCTGAATGTGAGCCTATGGCTGCTTCAGGCCCTGTGCATAGAGCTCAGCTGGTAAGGCCAAGAGGAGAGGCCAGGGGACTTTCA													
Consensus	CAGCCAGAACAGCAGATCTCTCCACTCCACCCCTCTCAGAGCCTGAATGTGAGCCTATGGCTGCTTCAGGCCCTGTGCATAGAGCTCAGCTGGTAAGGCCAAGAGGAGAGGCCAGGGGACTTTCA													
	911	15												
sequence	GTTAG													
CDS	GTTAG													
Consensus	GTTAG													

➤ Différence au niveau PROT :

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
sequencage	MEELEQGLLHQPAHMLQAENSLAKASITKHGYALLISDLQQVWHEQVDTLEVSQRAKELNKRLTAPPAFLHHLDEVLRPLFKDSAHQDAHPSKATFSCDRGEEVILIRVRSLSGLPFNNHFLCLP													
ref^prot	MEELEQGLLHQPAHMLQAENSLAKASITKHGYALLISDLQQVWHEQVDTLEVSQRAKELNKRLTAPPAFLHHLDEVLRPLFKDSAHQDAHPSKATFSCDRGEEVILIRVRSLSGLPFNNHFLCLP													
Consensus	MEELEQGLLHQPAHMLQAENSLAKASITKHGYALLISDLQQVWHEQVDTLEVSQRAKELNKRLTAPPAFLHHLDEVLRPLFKDSAHQDAHPSKATFSCDRGEEVILIRVRSLSGLPFNNHFLCLP													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
sequencage	ASLLYSQHLICPLMGVSLALSHVRELALLRMKOLEIQAYQESGAVLSRGRLKTEPFEENSFLQFHYEKLPEACRYGEGRPFAHNLQSLYYAVTKQVQARQKHKGSGEPQTSSTSPQGTDSQLQN													
ref^prot	ASLLYSQHLICPLMGVSLALSHVRELALLRMKOLEIQAYQESGAVLSRGRLKTEPFEENSFLQFHYEKLPEACRYGEGRPFAHNLQSLYYAVTKQVQARQKHKGSGEPQTSSTSPQGTDSQLQN													
Consensus	ASLLYSQHLICPLMGVSLALSHVRELALLRMKOLEIQAYQESGAVLSRGRLKTEPFEENSFLQFHYEKLPEACRYGEGRPFAHNLQSLYYAVTKQVQARQKHKGSGEPQTSSTSPQGTDSQLQN													
	261	270	280	290	300	304								
sequencage	QPEQQTSPPTTLSEPECEPHASGPPVHRAQLVKAKRKKPRGLFS													
ref^prot	QPEQQTSPPTTLSEPECEPHASGPPVHRAQLVKAKRKKPRGLFS													
Consensus	QPEQQTSPPTTLSEPECEPHASGPPVHRAQLVKAKRKKPRGLFS													

Flag BirA Nhej1 DiT24hLPS (clone B) OK

o FlagBirA Nhej1 DiT48hMix clone A

➤ B3Fwd DiT48hMix 848NT

ATGGAGGAACTAGAGCAAGGCCTGTTGATGCAGCCATGGGCATGGTTACAACCTTGCTGAGAACTCACTCTTGGC
CAAGGCTTCTATCACCAGCATGGTTATGCCTTGCTGATTTTCGGATCTTCAACAGGTGTGGCATGAACAGGTGGA
CACTTTGGAGGTCAGCCAGCGAGCCAAGGAGCTGAACAAGCGCCTCACCGCTCCCCCTGCAGCTTTTCTCCATC
ACTTGGATGAAGTGCTTCGCCACTGTTTAAAGATTCTGCCACCAGGATGCTGCTCACCTAGCAAAGCCACTT
TCTCCTGTGATCGTGGAGAGGAGGTATTGATCCTGAGGGTGCGGAGTGAGCTCTCTGGTCTCCCCTTCAATTGGC
ATTTCCACTGTCTTCCAGCTAGTTCTTTACTGGTCTCTCAGCATTTGATTTGTCCTCTGATGGGTGTGAGCTTGGCA
TTGCACAGTCATGTGAGGGAGCTAGCAGCATTGCTTCGGATGAAGGACCTTGAGATCCAGGCCTACCAGGAGAG
TGGGGCTGTGCTGAGCCGAGGTGCGATTGAAGACAGAGCCATTTGAAGAAAATTCTTTCTTGAACAGTTTATGG
TAGAGAAATTGCCAGAGGCATGTGCTGTTGGTGATGGAAGGcCATTGGCCATGAATCTGCAGAGCCTGTATGTGG
CAGTCACAAAGCAGCANGTCCAAGCCAGGCANAAGCATAAAGGCTCTGGAGAGCCTCANACATCAAGCAGCAC
CTCCCCTCNAGGAACTGATAGCCAGCTTCANAACCAGCCANAACAGCANNTCTCTCCCACTCCAACCCTCTCAN
ANCCTGAATGTGANCTATGGCTGCTTC

➤ BGHRev DiT48hMix 915NT

ATGGAGGAACTAGAGCAAGNCCTGTTGATGCAGCCATGGGCATGGTTACAACCTTGCTGAGAACTCANTNTTGGC
CAAGGCTTCTATCACCAGCATGGTTATGCCTTGCTGATTTTCGGATCTTCAACAGGTGTGGCATGAACAGGTGGA
CACTTTGGAGGTCAGCCAGCGAGCCAAGGAGCTGAACAAGCGCCTCACCGCTCCCCcTGCAGCTTTTCTCCATC
ACTTGGATGAAGTGCTTCGCCACTGTTTAAAGATTCTGCCACCAGGATGCTGCTCACCTAGCAAAGCCACTT
TCTCCTGTGATCGTGGAGAGGAGGTATTGATCCTGAGGGTGCGGAGTGAGCTCTCTGGTCTCCCCTTCAATTGGC
ATTTCCACTGTCTTCCAGCTAGTTCTTTACTGGTCTCTCAGCATTTGATTTGTCCTCTGATGGGTGTGAGCTTGGCA
TTGCACAGTCATGTGAGGGAGCTAGCAGCATTGCTTCGGATGAAGGACCTTGAGATCCAGGCCTACCAGGAGAG
TGGGGCTGTGCTGAGCCGAGGTGCGATTGAAGACAGAGCCATTTGAAGAAAATTCTTTCTTGAACAGTTTATGG
TAGAGAAATTGCCAGAGGCATGTGCTGTTGGTGATGGAAGGCCATTGGCCATGAATCTGCAGAGCCTGTATGTGG
CAGTCACAAAGCAGCAGGTCCAAGCCAGGCAGAAGCATAAAGGCTCTGGAGAGCCTCAGACATCAAGCAGCAC
CTCCCCTCAAGGAACTGATAGCCAGCTTCAGAACCAGCCAGAACAGCAGATCTCTCCCACTCCAACCCTCTCAGA
GCCTGAATGTGAGCCTATGGCTGCTTCAGGCCCTGTGCATAGAGCTCAGCTGGTAAAGGCCAAGAGGAAGAAG
CCCAGGGGACTCTTCAGTTAG

➤ Synthèse séquencage DiT48hMix : 915NT

ATGGAGGAACTAGAGCAAGGCCTGTTGATGCAGCCATGGGCATGGTTACAACCTTGCTGAG	60
AACTCACTCTTGGCCAAGGCTTCTATCACCAGCATGGTTATGCCTTGCTGATTTTCGGAT	120
CTTCAACAGGTGTGGCATGAACAGGTGGACACTTTGGAGGTGTCAGCCAGCGAGCCAAGGAG	180

240
300
360
420
480
540
600

MEELEQGLLMQPWAWLQLAENSLAKASITKHGYALLISDLQQVWHEQVDTLEVSQRAKELNKRLTAPPAFLHH
LDEVLRPLFKDSAHQDAAHPSKATFSCDRGEEVLILRVSELSGLPFNWHFHCLPASSLLVSQHLICPLMGVSLAHS
HVRELAALLRMKDLEIQAYQESGAVLSRGRKTEPFEENSFLEQFMVEKLPEACAVGDGRPFAMNQLSLYAVTKQ
QVQARQKHKGSGEPQTSSSTSPQGTDSQLQNQPEQQISPTPTLSEPECEPMAASGPVHRAQLVKAKRKKPRGLFS-

➤ **Blast contre banque rat :**

	Description	Score	Score	Cover	value	Ident	Accession
✓	PREDICTED: Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1)_transcript variant X5_mRNA	1690	1690	100%	0.0	100.00%	XM_006245242.3
✓	PREDICTED: Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1)_transcript variant X4_mRNA	1690	1690	100%	0.0	100.00%	XM_006245241.3
✓	PREDICTED: Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1)_transcript variant X2_mRNA	1690	1690	100%	0.0	100.00%	XM_017596524.1
✓	PREDICTED: Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1)_transcript variant X1_mRNA	1690	1690	100%	0.0	100.00%	XM_017596523.1
✓	PREDICTED: Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1)_transcript variant X3_mRNA	1690	1690	100%	0.0	100.00%	XM_006245240.1
✓	Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1)_mRNA	1690	1690	100%	0.0	100.00%	NM_001014217.1
✓	Rattus norvegicus BAC CH230-189D6 () complete sequence	429	1136	65%	3e-118	100.00%	AC121001.5

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

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
sequence	ATGGAGGAACTAGAGCARGGCCTGTTGATGCAGCCATGGGCATGGTTACAACTTGTCTGAGAACTCACTCTTGGCCARGGCTTCTATCACCAGCATGTTATGCCTTGCTGATTTCGGATCTTCAACAGG													
CDS	ATGGAGGAACTAGAGCARGGCCTGTTGATGCAGCCATGGGCATGGTTACAACTTGTCTGAGAACTCACTCTTGGCCARGGCTTCTATCACCAGCATGTTATGCCTTGCTGATTTCGGATCTTCAACAGG													
Consensus	ATGGAGGAACTAGAGCARGGCCTGTTGATGCAGCCATGGGCATGGTTACAACTTGTCTGAGAACTCACTCTTGGCCARGGCTTCTATCACCAGCATGTTATGCCTTGCTGATTTCGGATCTTCAACAGG													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
sequence	TGTGGCATGAACAGGTGGACACTTTGGAGGTCAGCCAGCGAGCCARAGGAGCTGAACAGCGCCCTACCGCTCCCCCTGCAGCTTTTCTCCATCACTTGGATGAAGTGCTTCGCCCACTGTTTAAAGATTCT													
CDS	TGTGGCATGAACAGGTGGACACTTTGGAGGTCAGCCAGCGAGCCARAGGAGCTGAACAGCGCCCTACCGCTCCCCCTGCAGCTTTTCTCCATCACTTGGATGAAGTGCTTCGCCCACTGTTTAAAGATTCT													
Consensus	TGTGGCATGAACAGGTGGACACTTTGGAGGTCAGCCAGCGAGCCARAGGAGCTGAACAGCGCCCTACCGCTCCCCCTGCAGCTTTTCTCCATCACTTGGATGAAGTGCTTCGCCCACTGTTTAAAGATTCT													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
sequence	TGCCCAACAGGATGCTGCTACCCATGCAAAAGCCACTTTCTCCTGTGATCGTGGAGAGGAGGATTGATCTCGAGGGTGCAGAGTGAGCTCTCTGGTCTCCCTTCATTGGCATTTCACACTGCTCTTCA													
CDS	TGCCCAACAGGATGCTGCTACCCATGCAAAAGCCACTTTCTCCTGTGATCGTGGAGAGGAGGATTGATCTCGAGGGTGCAGAGTGAGCTCTCTGGTCTCCCTTCATTGGCATTTCACACTGCTCTTCA													
Consensus	TGCCCAACAGGATGCTGCTACCCATGCAAAAGCCACTTTCTCCTGTGATCGTGGAGAGGAGGATTGATCTCGAGGGTGCAGAGTGAGCTCTCTGGTCTCCCTTCATTGGCATTTCACACTGCTCTTCA													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
sequence	GCTAGTCTTTACTGGTCTCTCAGCATTTGATTGTCTCTGATGGGTGTGAGCTTGGCATTGCACAGTCATGTGAGGGAGCTAGCAGCATTGCTTCGGATGAAGGACCTTGAGATCCAGGCCATACCAGG													
CDS	GCTAGTCTTTACTGGTCTCTCAGCATTTGATTGTCTCTGATGGGTGTGAGCTTGGCATTGCACAGTCATGTGAGGGAGCTAGCAGCATTGCTTCGGATGAAGGACCTTGAGATCCAGGCCATACCAGG													
Consensus	GCTAGTCTTTACTGGTCTCTCAGCATTTGATTGTCTCTGATGGGTGTGAGCTTGGCATTGCACAGTCATGTGAGGGAGCTAGCAGCATTGCTTCGGATGAAGGACCTTGAGATCCAGGCCATACCAGG													
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
sequence	AGAGTGGGGCTGTGCTGAGCCGAGGTCGATTGAGACAGAGCCATTGAGAGAAATTCCTTCTTGGACAGTTTATGGTAGAGAAATGCCAGAGGCATGTGCTGTTGGTGATGGAGGCCATTGGCCAT													
CDS	AGAGTGGGGCTGTGCTGAGCCGAGGTCGATTGAGACAGAGCCATTGAGAGAAATTCCTTCTTGGACAGTTTATGGTAGAGAAATGCCAGAGGCATGTGCTGTTGGTGATGGAGGCCATTGGCCAT													
Consensus	AGAGTGGGGCTGTGCTGAGCCGAGGTCGATTGAGACAGAGCCATTGAGAGAAATTCCTTCTTGGACAGTTTATGGTAGAGAAATGCCAGAGGCATGTGCTGTTGGTGATGGAGGCCATTGGCCAT													
	651	660	670	680	690	700	710	720	730	740	750	760	770	780
sequence	GAATCTGCAGAGCCTGTATGTGGCAGTCAACAAGCAGCAGGTCACAGCCAGGCAGAGCATAAAGGCTCTGGAGAGCCTCAGACATCAAGCAGCACCCTCCCTCAGGAACCTGATAGCCAGCTTCAGAAC													
CDS	GAATCTGCAGAGCCTGTATGTGGCAGTCAACAAGCAGCAGGTCACAGCCAGGCAGAGCATAAAGGCTCTGGAGAGCCTCAGACATCAAGCAGCACCCTCCCTCAGGAACCTGATAGCCAGCTTCAGAAC													
Consensus	GAATCTGCAGAGCCTGTATGTGGCAGTCAACAAGCAGCAGGTCACAGCCAGGCAGAGCATAAAGGCTCTGGAGAGCCTCAGACATCAAGCAGCACCCTCCCTCAGGAACCTGATAGCCAGCTTCAGAAC													
	781	790	800	810	820	830	840	850	860	870	880	890	900	910
sequence	CAGCCAGAACAGCAGATCTCTCCACTCCAAACCTCTCAGAGCCTGAATGTGAGCCTATGGCTGCTTCAGGCCCTGTGCATAGAGCTCAGCTGGTAAGGCCAAGAGGAAAGAGGCCAGGGGACTCTTCA													
CDS	CAGCCAGAACAGCAGATCTCTCCACTCCAAACCTCTCAGAGCCTGAATGTGAGCCTATGGCTGCTTCAGGCCCTGTGCATAGAGCTCAGCTGGTAAGGCCAAGAGGAAAGAGGCCAGGGGACTCTTCA													
Consensus	CAGCCAGAACAGCAGATCTCTCCACTCCAAACCTCTCAGAGCCTGAATGTGAGCCTATGGCTGCTTCAGGCCCTGTGCATAGAGCTCAGCTGGTAAGGCCAAGAGGAAAGAGGCCAGGGGACTCTTCA													
	91915 ---													
sequence	GTTAG													
CDS	GTTAG													
Consensus	GTTAG													

➤ **Différence au niveau PROT :**

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
sequence	MEELEQGLLMQPHAWLQLAENSLAKASITKHGYALLISDLQQVWHEQVDTLEYSQRAKELNKRLTAPPAFLHHLDEYLRPLFKOSAHQDAHPSKATFSCDRGEEVLILRVRSELSGLPFNHHFHCPL													
refprot	MEELEQGLLMQPHAWLQLAENSLAKASITKHGYALLISDLQQVWHEQVDTLEYSQRAKELNKRLTAPPAFLHHLDEYLRPLFKOSAHQDAHPSKATFSCDRGEEVLILRVRSELSGLPFNHHFHCPL													
Consensus	MEELEQGLLMQPHAWLQLAENSLAKASITKHGYALLISDLQQVWHEQVDTLEYSQRAKELNKRLTAPPAFLHHLDEYLRPLFKOSAHQDAHPSKATFSCDRGEEVLILRVRSELSGLPFNHHFHCPL													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
sequence	ASSLLVSQHLICPLMGVSLALHSHVRELAALLRMKDLEIQAYQESGAVLSRGRLKTEPFEEENSFLEQFMVEKLPEACAYGDGRPFAMNLQSLYYAVYTKQQVQARQKHKGSGEPQTSSTSPQGTDSQLQN													
refprot	ASSLLVSQHLICPLMGVSLALHSHVRELAALLRMKDLEIQAYQESGAVLSRGRLKTEPFEEENSFLEQFMVEKLPEACAYGDGRPFAMNLQSLYYAVYTKQQVQARQKHKGSGEPQTSSTSPQGTDSQLQN													
Consensus	ASSLLVSQHLICPLMGVSLALHSHVRELAALLRMKDLEIQAYQESGAVLSRGRLKTEPFEEENSFLEQFMVEKLPEACAYGDGRPFAMNLQSLYYAVYTKQQVQARQKHKGSGEPQTSSTSPQGTDSQLQN													
	261	270	280	290	300	304								
sequence	QPEQISPTPTLSEPECEPHARSGPVHRAQLVKAKRKKPRGLFS													
refprot	QPEQISPTPTLSEPECEPHARSGPVHRAQLVKAKRKKPRGLFS													
Consensus	QPEQISPTPTLSEPECEPHARSGPVHRAQLVKAKRKKPRGLFS													

Flag BirA Nhej1 DiT48hMix (clone A) OK

o FlagBirA Nhej1 SP clone C

➤ B3Fwd SP 854NT

ATGGAGGAACTAGAGCAAGGCCTGTTGATGCAGCCATGGGCATGGTTACAACCTTGCTGAGAACTCACTCTTGGC
CAAGGCTTCTATACCAAGCATGGTTATGCCTTGCTGATTTTCGGATCTTCAACAGGTGTGGCATGAACAGGTGGA
CACTTTGGAGGTCAGCCAGCGAGCCAAGGAGCTGAACAAGCGCCTACCGCTCCCCCTGCAGCTTTTCTCCATC
ACTTGGATGAAGTGCTTCGCCCCTGTTTAAAGATTCTGCCACCAGGATGCTGCTCACCTAGCAAAGCCACTT
TCTCCTGTGATCGTGGAGAGGAGGTATTGATCCTGAGGGTGCGGAGTGAGCTCTCTGGTCTCCCTTCAATTGGC
ATTTCCACTGTCTTCCAGCTAGTTCTTTACTGGTCTCTCAGCATTTGATTTGTCCTCTGATGGGTGTGAGCTTGGCA
TTGCACAGTCATGTGAGGGAGCTAGCAGCATTGCTTCGGATGAAGGACCTTGAGATCCAGGCCTACCAGGAGAG
TGGGGCTGTGCTGAGCCGAGGTCGATTGAAGACAGAGCCATTTGAAGAAAATTCTTTCTTGAACAGTTTATGG
TAGAGAAATTGCCAGAGGCATGTGCTGTTGGTGATGGAAGGcCATTTGCCATGAATCTGCAGAGCCTGTATGTGG
CAGTCACAAAGCAGCANNCCAAGCCAGGCAGAGCATAAAGGNTCTGGAGAGCCTCANACATCAAGCAGCAC
CTCCCCCANGGAAGTATAGCCAGCTTCNNAACCAGCCAGAGANAGCANATCTCTCCCACTCCAACCCTCTCAN
ANCCTGAATGTGANCTATGGCTGCTTCNNCNTN

➤ BGHRev SP 915NT

ATGGAGGAACTAGAGCAAGGCCTGTTGATGCAGCCATGGGCATGGTTACAACCTTGCTGAGAACTCACTCTTGGC
CAAGGCTTCTATACCAAGCATGGTTATGCCTTGCTGATTTTCGGATCTTCAACAGGTGTGGCATGAACAGGTGGA
CACTTTGGAGGTCAGCCAGCGAGCCAAGGAGCTGAACAAGCGCCTACCGCTCCCCCTGCAGCTTTTCTCCATC
ACTTGGATGAAGTGCTTCGCCCCTGTTTAAAGATTCTGCCACCAGGATGCTGCTCACCTAGCAAAGCCACTT
TCTCCTGTGATCGTGGAGAGGAGGTATTGATCCTGAGGGTGCGGAGTGAGCTCTCTGGTCTCCCTTCAATTGGC
ATTTCCACTGTCTTCCAGCTAGTTCTTTACTGGTCTCTCAGCATTTGATTTGTCCTCTGATGGGTGTGAGCTTGGCA
TTGCACAGTCATGTGAGGGAGCTAGCAGCATTGCTTCGGATGAAGGACCTTGAGATCCAGGCCTACCAGGAGAG
TGGGGCTGTGCTGAGCCGAGGTCGATTGAAGACAGAGCCATTTGAAGAAAATTCTTTCTTGAACAGTTTATGG
TAGAGAAATTGCCAGAGGCATGTGCTGTTGGTGATGGAAGGCCATTTGCCATGAATCTGCAGAGCCTGTATGTGG
CAGTCACAAAGCAGCAGGTCCAAGCCAGGCAGAGCATAAAGGCTCTGGAGAGCCTCAGACATCAAGCAGCAC
CTCCCCCAAGGAAGTATAGCCAGCTTCAGAACCAGCCAGAGCAGATCTCTCCCACTCCAACCCTCTCAGA
GCCTGAATGTGAGCCTATGGCTGCTTCAGGCCCTGTGCATAGAGCTCAGCTGGTAAAGGCCAAGAGGAAGAAG
CCCAGGGGACTCTTCAGTTAG

➤ Synthèse séquençage SP: 915NT

ATGGAGGAACTAGAGCAAGGCCTGTTGATGCAGCCATGGGCATGGTTACAACCTTGCTGAG	60
AACTCACTCTTGGCCAAGGCTTCTATACCAAGCATGGTTATGCCTTGCTGATTTTCGGAT	120
CTTCAACAGGTGTGGCATGAACAGGTGGACACTTTGGAGGTGAGCCAGCGAGCCAAGGAG	180
CTGAACAAGCGCCTACCGCTCCCCCTGCAGCTTTTCTCCATCACTTGGATGAAGTGCTT	240
CGCCCCTGTTTAAAGATTCTGCCACCAGGATGCTGCTCACCTAGCAAAGCCACTTTC	300
TCCTGTGATCGTGGAGAGGAGGTATTGATCCTGAGGGTGCGGAGTGAGCTCTCTGGTCTC	360
CCCTTCAATTGGCATTTCCTACTGTCTTCCAGCTAGTTCTTTACTGGTCTCTCAGCATTG	420
ATTTGTCTCTGATGGGTGTGAGCTTGGCATTGCACAGTCATGTGAGGGAGCTAGCAGCA	480
TTGCTTCGGATGAAGGACCTTGAGATCCAGGCCTACCAGGAGAGTGGGGCTGTGCTGAGC	540
CGAGGTCGATTGAAGACAGAGCCATTTGAAGAAAATTCTTTCTTGAACAGTTTATGGTA	600
GAGAAATTGCCAGAGGCATGTGCTGTTGGTGATGGAAGGCCATTTGCCATGAATCTGCAG	660
AGCCTGTATGTGGCAGTCACAAAGCAGCAGGTCCAAGCCAGGCAGAGCATAAAGGCTCT	
GGAGAGCCTCAGACATCAAGCAGCACCTCCCCCTCAAGGAAGTATAGCCAGCTTCAGAAC	
CAGCCAGAACAGCAGATCTCTCCCACTCCAACCCTCTCAGAGCCTGAATGTGAGCCTATG	
GCTGCTTCAGGCCCTGTGCATAGAGCTCAGCTGGTAAAGGCCAAGAGGAAGAAGCCAGG	
GGACTCTTCAGTTAG	

MEELEQGLLMQPWAWLQLAENSLAKASITKHGYALLISDLQQVWHEQVDTLEVSQRAKELNKRLTAPPAFLHH
LDEVLRPLFKDSAHDAAHPSKATFSCDRGEEVLILRVSELSGLPFNWHFCLPASSLLVSQHLCPLMGVSLALHS

HVRELAALLRMKDLEIQAYQESGAVLSRGRKTEPFEENSFLEQFMVEKLPEACAVGDGRPFAMNLSLYVAVTKQ
QVQARQKHKGSGEPQTSSSTSPQGTDSQLQNQPEQQISPTPTLSEPECEPMAASGPVHRAQLVKAKRKKPRGLFS-

➤ **Blast contre banque rat :**

	Description	Score	Score	Cover	value	Ident	Accession
✓	PREDICTED: Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1)_transcript variant X5_mRNA	1690	1690	100%	0.0	100.00%	XM_006245242.3
✓	PREDICTED: Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1)_transcript variant X4_mRNA	1690	1690	100%	0.0	100.00%	XM_006245241.3
✓	PREDICTED: Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1)_transcript variant X2_mRNA	1690	1690	100%	0.0	100.00%	XM_017596524.1
✓	PREDICTED: Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1)_transcript variant X1_mRNA	1690	1690	100%	0.0	100.00%	XM_017596523.1
✓	PREDICTED: Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1)_transcript variant X3_mRNA	1690	1690	100%	0.0	100.00%	XM_006245240.1
✓	Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1)_mRNA	1690	1690	100%	0.0	100.00%	NM_001014217.1
✓	Rattus norvegicus BAC CH230-189D6 ()_complete sequence	429	1136	65%	3e-118	100.00%	AC121001.5

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

Genomic map of the G6PD gene on chromosome 10. The map shows the gene structure with exons represented by boxes and introns by lines with arrows. The gene is divided into 10 exons, numbered 1 to 10. The sequence of the gene is shown in the bottom track, with the sequence of the G6PD gene (G6PD) and the sequence of the G6PD gene (G6PD) shown. The sequence of the G6PD gene (G6PD) is shown in the bottom track, with the sequence of the G6PD gene (G6PD) shown. The sequence of the G6PD gene (G6PD) is shown in the bottom track, with the sequence of the G6PD gene (G6PD) shown.

➤ **Différence au niveau PROT :**

	1	10	20	30	40	50	60	70	80	90	100	110	120	130	
sequence	MEELEQGLMQPHAHQLAENSLAKASITKHGYALLISDLQQVWHEQYDTLEYSQRAKELNKRLTAPPAFLHHLDEVLRPLFKDSAHQDRAHPSKATFSCDRGEEVLILRVSELSGLPFNAHFHCLP														
refprot	MEELEQGLMQPHAHQLAENSLAKASITKHGYALLISDLQQVWHEQYDTLEYSQRAKELNKRLTAPPAFLHHLDEVLRPLFKDSAHQDRAHPSKATFSCDRGEEVLILRVSELSGLPFNAHFHCLP														
Consensus	MEELEQGLMQPHAHQLAENSLAKASITKHGYALLISDLQQVWHEQYDTLEYSQRAKELNKRLTAPPAFLHHLDEVLRPLFKDSAHQDRAHPSKATFSCDRGEEVLILRVSELSGLPFNAHFHCLP														
	131	140	150	160	170	180	190	200	210	220	230	240	250	260	
sequence	ASSLLVSQHLICPLMGVSLALHSHVRELAALLRNKDLEIQAYQESGAYLSRGRLKTEPFEENSFLEQFHYEKLPEACAYGDGRPFAMNLQSLYYAVTKQQVQARQKHKGSGEPQTSSTSPQGTDSQLQN														
refprot	ASSLLVSQHLICPLMGVSLALHSHVRELAALLRNKDLEIQAYQESGAYLSRGRLKTEPFEENSFLEQFHYEKLPEACAYGDGRPFAMNLQSLYYAVTKQQVQARQKHKGSGEPQTSSTSPQGTDSQLQN														
Consensus	ASSLLVSQHLICPLMGVSLALHSHVRELAALLRNKDLEIQAYQESGAYLSRGRLKTEPFEENSFLEQFHYEKLPEACAYGDGRPFAMNLQSLYYAVTKQQVQARQKHKGSGEPQTSSTSPQGTDSQLQN														
	261	270	280	290	300	304									
sequence	QPEQQISPTPTLSEPECEPHASGPVHRAQLVKAKRKKPRGLFS														
refprot	QPEQQISPTPTLSEPECEPHASGPVHRAQLVKAKRKKPRGLFS														
Consensus	QPEQQISPTPTLSEPECEPHASGPVHRAQLVKAKRKKPRGLFS														

Flag BirA Nhej1 SP (clone C) OK

○ **FlagBirA Nhej1 CTX clone A**

➤ **B3Fwd CTX 916NT**

ATGGAGGAACTAGAGCAAGGCCTGTTGATGCAGCCATGGGCATGGTTACAACCTTGCTGAGAACTCACTCTTGGC
CAAGGCTTCTATACCAAGCATGGTTATGCCTTGCTGATTTTCGGATCTTCAACAGGTGTGGCATGAACAGGTGGA
CACTTTGGAGGTCAGCCAGCGAGCCAAGGAGCTGAACAAGCGCCTACCGCTCCCCCTGCAGCTTTTCTCCATC
ACTTGGATGAAGTGCTTCGCCCCTGTTTAAAGATTCTGCCACCAGGATGCTGCTCACCTAGCAAAGCCACTT
TCTCCTGTGATCGTGGAGAGGAGGTATTGATCCTGAGGGTGCGGAGTGAGCTCTCTGGTCTCCCCTTCAATTGGC
ATTTCCACTGTCTTCCAGCTAGTTCTTTACTGGTCTCTCAGCATTGATTTGTCCTCTGATGGGTGTGAGCTTGGCA
TTGCACAGTCATGTGAGGGAGCTAGCAGCATTGCTTCGGATGAAGGACCTTGAGATCCAGGCCTACCAGGAGAG
TGGGGCTGTGCTGAGCCGAGGTCGATTGAAGACAGAGCCATTTGAAGAAAATTCTTTCTTGGAACAGTTTATGG
TAGAGAAATTGCCAGAGGCATGTGCTGTTGGTGATGGAAGGcCATTGTCATGAATCTGCAGAGCCTGTATGTGG
CAGTCACAAAGCAGCAGGTCCAAGCCAGGCAGAAGCATAAAGGCTCTGGAGAGCCTCANACATCAAGCAGCAC
CTCCCCCTNAGGAACTGATAGCCAGCTTCAGAANNAGCCAGAACAGCANATCTCTCCCACTCCNNCCCTCTCAN
ANCCTGAATGTGANCTATGGNTGCTTCNNNCNTGNGCATANAGCTCANCTNGNAAAGGNNANNNNNANNNN
CNNNGGNNNCNTNANTNANTGNNNNNNNNNNCTCGNNNCTANAGGNCNNNTNAAAC

➤ **BGHRev CTX 915NT**

ATGGAGGAACTAGAGCAAGGCCTGTTGATGCAGCCATGGGCATGGTTACAACCTTGCTGAGAACTCACTCTTGGC
CAAGGCTTCTATACCAAGCATGGTTATGCCTTGCTGATTTTCGGATCTTCAACAGGTGTGGCATGAACAGGTGGA
CACTTTGGAGGTCAGCCAGCGAGCCAAGGAGCTGAACAAGCGCCTACCGCTCCCCCTGCAGCTTTTCTCCATC
ACTTGGATGAAGTGCTTCGCCCCTGTTTAAAGATTCTGCCACCAGGATGCTGCTCACCTAGCAAAGCCACTT
TCTCCTGTGATCGTGGAGAGGAGGTATTGATCCTGAGGGTGCGGAGTGAGCTCTCTGGTCTCCCCTTCAATTGGC
ATTTCCACTGTCTTCCAGCTAGTTCTTTACTGGTCTCTCAGCATTGATTTGTCCTCTGATGGGTGTGAGCTTGGCA
TTGCACAGTCATGTGAGGGAGCTAGCAGCATTGCTTCGGATGAAGGACCTTGAGATCCAGGCCTACCAGGAGAG
TGGGGCTGTGCTGAGCCGAGGTCGATTGAAGACAGAGCCATTTGAAGAAAATTCTTTCTTGGAACAGTTTATGG
TAGAGAAATTGCCAGAGGCATGTGCTGTTGGTGATGGAAGGCCATTTGCCATGAATCTGCAGAGCCTGTATGTGG
CAGTCACAAAGCAGCAGGTCCAAGCCAGGCAGAAGCATAAAGGCTCTGGAGAGCCTCAGACATCAAGCAGCAC
CTCCCCCTCAAGGAACTGATAGCCAGCTTCAGAACCAGCCAGAACAGCAGATCTCTCCCACTCCAACCCTCTCAGA
GCCTGAATGTGAGCCTATGGCTGCTTCAGGCCCTGTGCATAGAGCTCAGCTGGTAAAGGCCAAGAGGAAGAAG
CCAGGGGACTCTTCAGTTAG

➤ **Synthèse séquençage CTX: 915NT**

ATGGAGGAACTAGAGCAAGGCCTGTTGATGCAGCCATGGGCATGGTTACAACCTTGCTGAG	60
AACTCACTCTTGGCCAAGGCTTCTATACCAAGCATGGTTATGCCTTGCTGATTTTCGGAT	120
CTTCAACAGGTGTGGCATGAACAGGTGGACACTTTGGAGGTCAGCCAGCGAGCCAAGGAG	180
CTGAACAAGCGCCTACCGCTCCCCCTGCAGCTTTTCTCCATCACTTGGATGAAGTGCTT	240
CGCCCCTGTTTAAAGATTCTGCCACCAGGATGCTGCTCACCTAGCAAAGCCACTTTC	300
TCCTGTGATCGTGGAGAGGAGGTATTGATCCTGAGGGTGCGGAGTGAGCTCTCTGGTCTC	360
CCCTTCAATTGGCATTTCCACTGTCTTCCAGCTAGTTCTTTACTGGTCTCTCAGCATTG	420
ATTTGTCCTCTGATGGGTGTGAGCTTGGCATTGCACAGTCATGTGAGGGAGCTAGCAGCA	480
TTGCTTCGGATGAAGGACCTTGAGATCCAGGCCTACCAGGAGAGTGGGGCTGTGCTGAGC	540
CGAGGTCGATTGAAGACAGAGCCATTTGAAGAAAATTCTTTCTTGGAACAGTTTATGGTA	600
GAGAAATTGCCAGAGGCATGTGCTGTTGGTGATGGAAGGcCATTGTCATGAATCTGCAG	660
AGCCTGTATGTGGCAGTCACAAAGCAGCAGGTCCAAGCCAGGCAGAAGCATAAAGGCTCT	720
GGAGAGCCTCAGACATCAAGCAGCACCTCCCCCTCAAGGAACTGATAGCCAGCTTCAGAAC	
CAGCCAGAACAGCAGATCTCTCCCACTCCAACCCTCTCAGAGCCTGAATGTGAGCCTATG	
GCTGCTTCAGGCCCTGTGCATAGAGCTCAGCTGGTAAAGGCCAAGAGGAAGAAGCCCAGG	
GGACTCTTCAGTTAG	

MEELEQGLLMQPWAWLQLAENSLAKASITKHGYALLISDLQQVWHEQVDTLEVSQRAKELNKRLTAPPAFLHH
LDEVLRPLFKDSAHQDAAHPSKATFSCDRGEEVLILRVRELSGLPFNWFHCLPASSLLVSQHLCPLMGVSLALHS

HVRELAALLRMKDLEIQAYQESGAVLSRGLKTEPFEENSFLEQFMVEKLPEACAVGDGRPFAMNLQSLYVAVTKQ
QVQARQKHKGSGEPQTSSSTSPQGTDSQLQNPQEQQISPTPTLSEPECEPMAASGPVHRAQLVKAKRKKPRGLFS-

➤ Blast contre banque rat :

✓	PREDICTED: Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1) transcript variant X5 mRNA	1690	1690	100%	0.0	100.00%	XM_006245242.3
✓	PREDICTED: Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1) transcript variant X4 mRNA	1690	1690	100%	0.0	100.00%	XM_006245241.3
✓	PREDICTED: Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1) transcript variant X2 mRNA	1690	1690	100%	0.0	100.00%	XM_017596524.1
✓	PREDICTED: Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1) transcript variant X1 mRNA	1690	1690	100%	0.0	100.00%	XM_017596523.1
✓	PREDICTED: Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1) transcript variant X3 mRNA	1690	1690	100%	0.0	100.00%	XM_006245240.1
✓	Rattus norvegicus nonhomologous end-joining factor 1 (Nhej1) mRNA	1690	1690	100%	0.0	100.00%	NM_001014217.1
✓	Rattus norvegicus BAC CH230-189D6 () complete sequence	429	1136	65%	3e-118	100.00%	AC121001.5

➤ Différence Séquencage/CDS au niveau NT :

sequence	ATGGAGGAACTAGAGCAGGCGCTGTGATGACGCATGGGATGTTACAACTTGCTGAGAACTCACTCTTGGCCAGGCTTCTATCACCAGCATGGTTATGCCTTGCTGATTTCGGATCTTCACAGG	131	140	150	160	170	180	190	200	210	220	230	240	250	260
CDS	ATGGAGGAACTAGAGCAGGCGCTGTGATGACGCATGGGATGTTACAACTTGCTGAGAACTCACTCTTGGCCAGGCTTCTATCACCAGCATGGTTATGCCTTGCTGATTTCGGATCTTCACAGG														
Consensus	ATGGAGGAACTAGAGCAGGCGCTGTGATGACGCATGGGATGTTACAACTTGCTGAGAACTCACTCTTGGCCAGGCTTCTATCACCAGCATGGTTATGCCTTGCTGATTTCGGATCTTCACAGG														
sequence	TGTGGCATGAAACAGGTGGACACTTTGGAGGTGAGCAGCAGCCAGGAGCTGAAACAGCGCTCACCGCTCCCGCTGCAGCTTTTCTCCATCACTTGGATGAAGTGCTTCGCCCACTGTTTAAAGATT	261	270	280	290	300	310	320	330	340	350	360	370	380	390
CDS	TGTGGCATGAAACAGGTGGACACTTTGGAGGTGAGCAGCAGCCAGGAGCTGAAACAGCGCTCACCGCTCCCGCTGCAGCTTTTCTCCATCACTTGGATGAAGTGCTTCGCCCACTGTTTAAAGATT														
Consensus	TGTGGCATGAAACAGGTGGACACTTTGGAGGTGAGCAGCAGCCAGGAGCTGAAACAGCGCTCACCGCTCCCGCTGCAGCTTTTCTCCATCACTTGGATGAAGTGCTTCGCCCACTGTTTAAAGATT														
sequence	TGCCACACAGGATGCTGCTCACCTAGCAAGCCACTTTCTCTGTGATCGTGGAGAGGAGGATTGATCCTGAGGGTGCGAGTGAGCTCTTGCTTCCCTTCATTGGCATTTCACATGCTTCCCA	391	400	410	420	430	440	450	460	470	480	490	500	510	520
CDS	TGCCACACAGGATGCTGCTCACCTAGCAAGCCACTTTCTCTGTGATCGTGGAGAGGAGGATTGATCCTGAGGGTGCGAGTGAGCTCTTGCTTCCCTTCATTGGCATTTCACATGCTTCCCA														
Consensus	TGCCACACAGGATGCTGCTCACCTAGCAAGCCACTTTCTCTGTGATCGTGGAGAGGAGGATTGATCCTGAGGGTGCGAGTGAGCTCTTGCTTCCCTTCATTGGCATTTCACATGCTTCCCA														
sequence	GCTAGTCTTTACTGGTCTCTCAGCATTTGATTTGTCTCTGATGGGTGTGAGCTTGGCATTGCACAGTCATGTGAGGGAGCTAGCAGCATTGCTTCGGATGAAGGACCTTGAGATCCAGGCTACACAGG	521	530	540	550	560	570	580	590	600	610	620	630	640	650
CDS	GCTAGTCTTTACTGGTCTCTCAGCATTTGATTTGTCTCTGATGGGTGTGAGCTTGGCATTGCACAGTCATGTGAGGGAGCTAGCAGCATTGCTTCGGATGAAGGACCTTGAGATCCAGGCTACACAGG														
Consensus	GCTAGTCTTTACTGGTCTCTCAGCATTTGATTTGTCTCTGATGGGTGTGAGCTTGGCATTGCACAGTCATGTGAGGGAGCTAGCAGCATTGCTTCGGATGAAGGACCTTGAGATCCAGGCTACACAGG														
sequence	AGAGTGGGGCTGTGCTGAGCCGAGGTGATTGAAGACAGAGCCATTGAGGAAATTTCTTCTTGAGACAGTTTATGGTAGAGAAATTGCCAGAGGCTATGCTGTTGGTGAAGGACCTTTGCCAT	651	660	670	680	690	700	710	720	730	740	750	760	770	780
CDS	AGAGTGGGGCTGTGCTGAGCCGAGGTGATTGAAGACAGAGCCATTGAGGAAATTTCTTCTTGAGACAGTTTATGGTAGAGAAATTGCCAGAGGCTATGCTGTTGGTGAAGGACCTTTGCCAT														
Consensus	AGAGTGGGGCTGTGCTGAGCCGAGGTGATTGAAGACAGAGCCATTGAGGAAATTTCTTCTTGAGACAGTTTATGGTAGAGAAATTGCCAGAGGCTATGCTGTTGGTGAAGGACCTTTGCCAT														
sequence	GATCTGACAGGCTGTATGTGACAGTCACAAAGCAGCAGGTCACAGCCAGGCGAGGATTAAGGCTCTGAGAGCCTCAGACATCAGCAGCACCTCCCGTCAGGAACTGATAGCCAGCTTCAGAAC	781	790	800	810	820	830	840	850	860	870	880	890	900	910
CDS	GATCTGACAGGCTGTATGTGACAGTCACAAAGCAGCAGGTCACAGCCAGGCGAGGATTAAGGCTCTGAGAGCCTCAGACATCAGCAGCACCTCCCGTCAGGAACTGATAGCCAGCTTCAGAAC														
Consensus	GATCTGACAGGCTGTATGTGACAGTCACAAAGCAGCAGGTCACAGCCAGGCGAGGATTAAGGCTCTGAGAGCCTCAGACATCAGCAGCACCTCCCGTCAGGAACTGATAGCCAGCTTCAGAAC														
sequence	CAGCCAGAACAGCAGATCTCTCCACTCCAACTCTCAGAGCTGATGTGAGCTTATGGCTGCTTCAGGCCCTGTGCATAGAGCTCAGCTGGTAAAGGCCAAGAGGAAAGGCCAGGGGACTCTTCA														
CDS	CAGCCAGAACAGCAGATCTCTCCACTCCAACTCTCAGAGCTGATGTGAGCTTATGGCTGCTTCAGGCCCTGTGCATAGAGCTCAGCTGGTAAAGGCCAAGAGGAAAGGCCAGGGGACTCTTCA														
Consensus	CAGCCAGAACAGCAGATCTCTCCACTCCAACTCTCAGAGCTGATGTGAGCTTATGGCTGCTTCAGGCCCTGTGCATAGAGCTCAGCTGGTAAAGGCCAAGAGGAAAGGCCAGGGGACTCTTCA														
91115	-----														
sequence	GTAG														
CDS	GTAG														
Consensus	GTAG														

➤ Différence au niveau PROT :

sequence	HEEEQLGLAQPAAHLQLAENSLAKASITKHGYALLISDLQVYVHEQYDTLEVSQRAKELNKL TAPPAFLAHLDEVLRLPLFKDSAHQDAHPSKATFSCDGEVYLILRVSEL SGLPFNAHFHCLP	1	10	20	30	40	50	60	70	80	90	100	110	120	130
refprot	HEEEQLGLAQPAAHLQLAENSLAKASITKHGYALLISDLQVYVHEQYDTLEVSQRAKELNKL TAPPAFLAHLDEVLRLPLFKDSAHQDAHPSKATFSCDGEVYLILRVSEL SGLPFNAHFHCLP														
Consensus	HEEEQLGLAQPAAHLQLAENSLAKASITKHGYALLISDLQVYVHEQYDTLEVSQRAKELNKL TAPPAFLAHLDEVLRLPLFKDSAHQDAHPSKATFSCDGEVYLILRVSEL SGLPFNAHFHCLP														
sequence	ASSLLVSQLICPLMGVSLALNSHVRELAALLRMKDLEIQAYQESGAVLSRGLKTEPFEENSFLEQFMVEKLPEACAVGDGRPFAMNLQSLYVAVTKQVQARQKHKGSGEPQTSSSTSPQGTDSQLQ	131	140	150	160	170	180	190	200	210	220	230	240	250	260
refprot	ASSLLVSQLICPLMGVSLALNSHVRELAALLRMKDLEIQAYQESGAVLSRGLKTEPFEENSFLEQFMVEKLPEACAVGDGRPFAMNLQSLYVAVTKQVQARQKHKGSGEPQTSSSTSPQGTDSQLQ														
Consensus	ASSLLVSQLICPLMGVSLALNSHVRELAALLRMKDLEIQAYQESGAVLSRGLKTEPFEENSFLEQFMVEKLPEACAVGDGRPFAMNLQSLYVAVTKQVQARQKHKGSGEPQTSSSTSPQGTDSQLQ														
sequence	QPEQISPTPTLSEPECEPMAASGPVHRAQLVKAKRKKPRGLFS	261	270	280	290	300	304								
refprot	QPEQISPTPTLSEPECEPMAASGPVHRAQLVKAKRKKPRGLFS														
Consensus	QPEQISPTPTLSEPECEPMAASGPVHRAQLVKAKRKKPRGLFS														

Flag BirA Nhej1 CTX (clone A) OK