

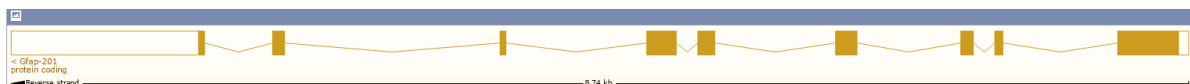
6)Gfap

Rattus norvegicus glial fibrillary acidic protein (Gfap), mRNA

intermediate filament; glial fibrillary acidic protein alpha; glial fibrillary acidic protein delta

- **Référence NCBI :** NM_017009
- **Taille 1293 NT**
- **Séquence NT :**

```
atggagcgg agacgtatca cctctgcacg ccgctcctat gcctcctccg agacgatggt
  61 caggggccat ggtcctacca gacacctggg taccattccg cgctctccc tgtctcgaat
 121 gacgcctcca ctccctgccg gggtagactt ctccctggcc ggggcgctca atgccggctt
 181 caaagagact cgggccagcg agcgtgcgga gatgatggag ctcaatgacc gctttgctag
 241 ctacatcgag aaggtccgct tcctggaaca gcaaaacaag gcgctggcag ctgagctgaa
 301 ccagcttcga gccaaaggag ccaccaaaact ggctgacgtt taccaggcag aacttcggga
 361 gctgcggctg cgtctggacc agcttactac caacagtgcc cgctggagg tggagagggg
 421 caatctcaca caggacctcg gcacctgag gcagaagctc caagatgaaa ccaacctgag
 481 gctggaggcg gagaacaacc ttggtgtgta cagacaggag gcggatgaag ccaccttggc
 541 tcgtgtggat ctggagagga aggttgagtc gctggaggag gagatccagt tcttgaggaa
 601 gatccatgag gaggaagttc gagaactcca ggagcagctg gccacgagc aggtccacgt
 661 ggagatggat gtggccaagc cagacctcac agcggctctg agagagattc gcactcagta
 721 cgaggcagtg gccaccagta acatgcaaga aacagaagag tggatcgggt ccaagtttgc
 781 agacctcaca gacgttgctt cccgcaacgc agagctgctc cgccaggcca agcacgaggc
 841 taatgactat cgccgccaac tgcaggcctt gacctgcgac cttgagtcct tgcgcggcac
 901 gaacgagtc ttggagaggc aaatgcgcga acaggaggag cgccacgcgc gggagtcggc
 961 gagttaccag gaggcactcg ctcggtgga ggaggagggc caaagcctca aggaggagat
1021 ggcccgccac ctgcaggagt accaggatct actcaacggt aagctagccc tggacatcga
1081 gatcgccacc tacaggaaat tgctggaggg cgaagaaaac cgcatcacca ttcctgtaca
1141 gactttctcc aacctccaga tccgagaaac cagcctggac accaaatctg tgtcagaagg
1201 ccacctcaag aggaacatcg tggtaaagac ggtggagatg cgggatggcg aggtcattaa
1261 ggagtcgaag caggagcaca aggatgtgat gtga
```



- **Séquence prot :** NP_058705

```
MERRRITSARRSYASSETMVRGHGPTRHLGTIPRLSLSRMTPPL
PARVDFSLAGALNAGFKETRASERAEMMELNDRFASYIEKVRFLQNNKALAAELN
QLRAKEPTKLADVYQAE LRELRLRLDQLTTNSARLEVERDNL TQDLGTLRQKLQDET
NLRLEAENNLAVYRQEAD EATLARVDLERKVESLEEEIQFLRKIHEEEVRELQEQLAQ
QQVHVEMDVAKPDLTAALREIRTQYEA VATSNMQETEEWYRSKFADLTDVASRNA
ELLRQAKHEANDYRRQLQALTCDLESLRG TNESLERQMREQEERHARESASYQEAL
ARLEEEGQSLKEEMARHLQEYQDLLNVKLALDIEIATYRKLL EGEENRITIPVQTFSNL
QIRETSLDTKSVSEGLKRNIVVKTVEMRDGEVIKESKQEHKDVM
```

- **Amorces synthétisées :**

Gfap_AscI_Fwd

tataGGCGCGCCa atggagcgg agacgtatca cctctg

Gfap_NotI_Rev

ttaaGCGGCGCa tcacatcacatccttgtgtcctgc

- **Expériences :**

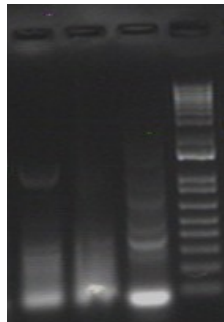
- PCR 06/07 et 07/07: -sur **rate** cycle Q5-Enhancer 0/10-TM 56°C - 2min 30 d'élongation

-sur **rate** cycle Q5-Enhancer 0/10-TM 60°C - 2min 30

d'élongation et pfu 60°C



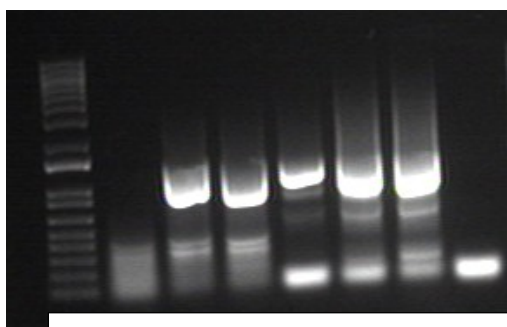
Rate 56°C Enhancer 0/10



Rate Enhancer 0 Enhancer10 pfu 60°C
60°C 60°C

Meilleures conditions : cycle Q5, TM 60°C Enhancer 0

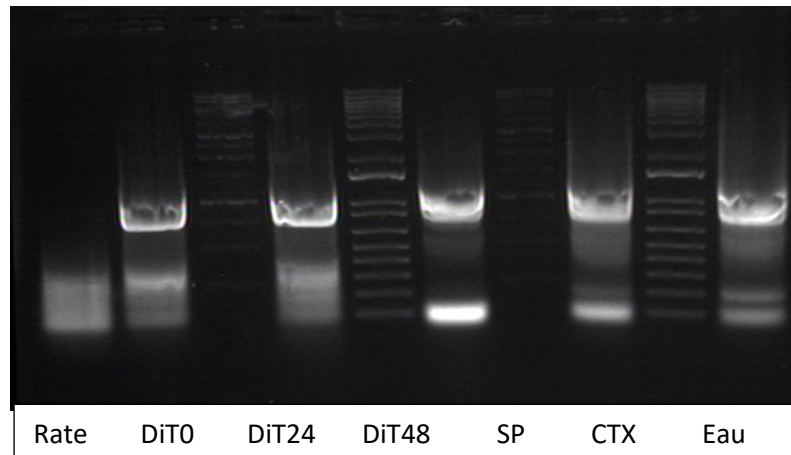
- PCR 10/07 : sur **les 7 conditions** cycle Q5-TM 60°C-Enhancer 0- 2min 30 d'élongation



Rate DiT0 DiT24 DiT48 SP CTX Eau

Bandes DiT0, DiT24h, DiT48h, SP et CTX Ok

- 21/07 : Extraction sur gel



- **Conclusion Jul 2020 :**
 - **Bandes extraites et purifiées à sous cloner**
 - **faire « beau gel » pour publi**
- [Sep/Oct : soucis clonage : Vecteur ? PCR mal digérée ?](#)
- [08/09 : 10ul digérés et purification le 09/09](#)
- [14/09 : ligation dans FB](#)
- [16/09 : essai miniprep : DiT0, 24h et 48h OK](#)
- [06/10 : religation dans nouv vecteur pour SP et CTX](#)
- [09/10 : miniprep SP et CTX OK](#)
- [28/10 envoi au séquençage](#)

- Résultats séquençages

- FlagBirA Gfap DiT0 clone A

- B3Fwd DiT0 810NT

ATGGAGCGGAGACGTATCACCTCTGCACGCCGCTCCTATGCCTCCTCCGAGACGATGGTCAGGGGCCATGGTCCT
ACCAGACACCTGGGTACCATTCCGCGCCTCTCCCTGTCTCGAATGACGCCTCCACTCCCTGCCAGGGTAGACTTCT
CCCTGGCCGGGGCGCTCAATGCCGGCTTCAAAGAGACTCGGGCCAGCGAGCGCGGAGATGATGGAGCTCA
ATGACCGCTTTGCTAGCTACATCGAGAAGGTCCGCTTCTGGAACAGCAAAACAAGGCGCTGGCAGCTGAGCTG
AACCAGCTTCGAGCCAAGGAGCCACCAAACCTGGCTGACGTTTACCAGGCAGAACTTCGGGAGCTGCGGCTGC
GTCTGGACCAGCTTACTACCAACAGTGCCCGGCTGGAGGTGGAGAGGGACAATCTCACACAGGACCTCGGCAC
CCTGAGGCAGAAGCTCCAAGATGAAACCAACCTGAGGCTGGAGGCGGAGAACAACCTGGCTGTGTACAGACA
GGAGGCGGATGAAGCCACCTTGGCTCGTGTGGATCTGGAGAGGAAGGTTGAGTCGCTGGAGGAGGAGATCCA
GTTCTTGAgGAAGATCCATGAgGAGGAAGTTCGAGAACTCCAGGAGCAGCTGGcCCAGCAGCAGGTCCNCGTG
GAGATGGATGTGGCCAAGCCAGACCTCACAGCGGCTCTGANAGAGANTCGCACTCAGTACGAGGCAGTGGCCA
CCAGTAACATGCAANAAACAGAANAGTGGTATCGGTCCAAGTTTCANANCTCACAGACGTTGCTTCCCGCNAC
GCA

- BGHRev DiT0 876NT

AGCCCAACAACTNGNTGACGTTNNCAGGCAGAACTTCGGGAGCTGCGNNTGCGTNTGGACCAGCTTACTACC
AACAGTGCCCGGCTGGAGGTGGAGAGGGACAATCTCACACAGGACNTNGGCACCCNGAGGCAGAAGNTCCA
AGATGAAACCAACcTGAGGCTGGAGGCGGAGAACAACTGGCTGTGTACAGACAGGAGGCGGATGAAGCCAC
cTTGGCTCGTGTGGATCTGGAGAGGAAGGTTGAGTCGCTGGAGGAGGAGATCCAGTTCTTGAGGAAGATCCAT
GAGGAGGAAGTTTCGAGAACTCCAGGAGCAGCTGGCCAGCAGCAGGTCCACGTGGAGATGGATGTGGCCAA
CCAGACCTCACAGCGGCTCTGAGAGAGATTGCACTCAGTACGAGGCAGTGGCCACCAGTAACATGCAAGAAA
CAGAAGAGTGGTATCGGTCCAAGTTTGCAGACCTCACAGACGTTGCTTCCCGCAACGCAGAGCTGCTCCGCCAG
GCCAAGCACGAGGCTAATGACTATCGCCGCCAACTGCAGGCCTTGACCTGCGACCTTGAGTCCTTGCGCGGCAC
GAACGAGTCCTTGAGAGGCCAAATGCGCGAACAGGAGGAGCGCCACGCGCGGGAGTCGGCGAGTTACCAGG
AGGCACTCGCTCGGCTGGAGGAGGAGGGCCAAAGCCTCAAGGAGGAGATGGCCCGCCACCTGCAGGAGTACC
AGGATCTACTCAACGTTAAGCTAGCCCTGGACATCGAGATGCCACCTACAGGAAATTGCTGGAGGGCGAAGAA
AACCGCATCACCATTCCTGTACAGACTTTCTCCAACCTCCAGATCCGAGAAACCAGCCTGGACACCAAATCTGTGT
CAGAAGGCCACCTCAAGAGGAACATCGTGGTAAAGACGGTGGAGATGCGGGATGGCGAGGTCATTAAGGAGT
CGAAGCAGGAGCACAAGGATGTGATGTGA

- Synthèse séquençage DiT0 : 1293NT

ATGGAGCGGAGACGTATCACCTCTGCACGCCGCTCCTATGCCTCCTCCGAGACGATGGTC	60
AGGGGCCATGGTCCTACCAGACACCTGGGTACCATTCCGCGCCTCTCCCTGTCTCGAATG	120
ACGCTCCACTCCCTGCCAGGGTAGACTTCTCCCTGGCCGGGGCGCTCAATGCCGGCTTC	180
AAAGAGACTCGGGCCAGCGAGCGCGCGGAGATGATGGAGCTCAATGACCGCTTTGCTAGC	240
TACATCGAGAAGGTCCGCTTCTTGGAAACAGCAAAACAAGGCGCTGGCAGCTGAGCTGAAC	300
CAGCTTCGAGCCAAGGAGCCACCAAACCTGGCTGACGTTTACCAGGCAGAACTTCGGGAG	360
CTGCGGCTGCGTCTGGACCAGCTTACTACCAACAGTGCCCGGCTGGAGGTGGAGAGGGAC	420
AATCTCACACAGGACCTCGGCACCCCTGAGGCAGAAGCTCCAAGATGAAACCAACCTGAGG	480
CTGGAGGCGGAGAACAACTGGCTGTGTACAGACAGGAGGCGGATGAAGCCACCTTGGCT	540
CGTGTGGATCTGGAGAGGAAGGTTGAGTCGCTGGAGGAGGAGATCCAGTTCTTGAGGAAG	600
ATCCATGAGGAGGAAGTTCGAGAACTCCAGGAGCAGCTGGCCAGCAGCAGGTCCACGTG	
GAGATGGATGTGGCCAAGCCAGACCTCACAGCGGCTCTGAGAGAGATTGCACTCAGTAC	
GAGGCAGTGGCCACAGTAACATGCAAGAAACAGAAGAGTGGTATCGGTCCAAGTTTGA	
GACCTCACAGACGTTGCTTCCCGCAACGCAGAGCTGCTCCGCCAGGCCAAGCACGAGGCT	
AATGACTATCGCCGCCAACTGCAGGCCTTGACCTGCGACCTTGAGTCCTTGCGCGGCACG	
AACGAGTCCTTGAGAGGCCAAATGCGCGAACAGGAGGAGCGCCACGCGGGGAGTCGGCG	

AGTTACCAGGAGGCACTCGCTCGGCTGGAGGAGGAGGGCCAAAGCCTCAAGGAGGAGATG
 GCCCCCACCTGCAGGAGTACCAGGATCTACTCAACGTTAAGCTAGCCCTGGACATCGAG
 ATCGCCACCTACAGGAAATTGCTGGAGGGCGAAGAAAACCGCATCACCATTCTGTACAG
 ACTTTCTCCAACCTCCAGATCCGAGAAACCAGCCTGGACACCAAATCTGTGTCAGAAGGC
 CACCTCAAGAGGAACATCGTGGTAAAGACGGTGGAGATGCGGGATGGCGAGGTCATTAAG
 GAGTCGAAGCAGGAGCACAAGGATGTGATGTGA

MERRRITSARRSYASSETMVRGHGPTRHLGTIPRLSLSRMTPPLPARVDFSLAGALNAGFKETRASERAEMMELND
 RFASYIEKVRFLEQQNKALAAELNQLRAKEPTKLADVYQAELELRLRLDQLTTNSARLEVERDNLTDGLTLRQKLQ
 DETNLRLEAENNLAVYRQEADATLARVDLERKVESLEEEIQFLRKIHVEEVRELQEQLAQQVHVEMDVAKPDLTA
 ALREIRTQEAVATSNMQETEEWYRSKFADLTDVASRNAELLRQAKHEANDYRRQLQALTCDLESLRGTNESLERQ
 MREQEERHARESASYQEALARLEEEGQSLKEEMARHLQEYQDLLNVKLALDIEIATYRKLEGEENRITIPVQTFSNL
 QIRETSLDTKSVSEGLKRNIVVKTVMRMDGEVIKESKQEHKDV-

➤ **Blast contre banque rat :**

	Description	Match Score	Query Score	Query Cover	E- value	Query Ident	Accession
✓	Rattus norvegicus glial fibrillary acidic protein (GFAP) mRNA sequence	2388	2388	100%	0.0	100.00%	L27219.1
✓	Rattus norvegicus glial fibrillary acidic protein (Gfap) mRNA	2383	2383	100%	0.0	99.92%	NM_017009.2
✓	Rattus norvegicus Sprague Dawley glial fibrillary acidic protein mRNA complete cds	2366	2366	100%	0.0	99.69%	U03700.1
✓	Rattus norvegicus glial fibrillary acidic protein beta (Gfap) mRNA partial cds alternatively spliced	1836	1836	76%	0.0	100.00%	EF094476.1
✓	R.norvegicus partial gfap gene for glial fibrillary acidic protein	843	843	35%	0.0	100.00%	Z48978.1
✓	Rattus norvegicus glial fibrillary acidic proteins alpha and delta (GFAP) gene alternatively spliced products complete cds	843	2431	100%	0.0	100.00%	AF028784.1
✓	Rattus norvegicus glial fibrillary acidic protein epsilon (Gfap) mRNA partial cds alternatively spliced	704	704	29%	0.0	99.74%	EF094477.1
✓	PREDICTED: Rattus norvegicus keratin 7 (Krt7), transcript variant X2, mRNA	89.8	89.8	8%	7e-16	81.90%	XM_003754353.4
✓	PREDICTED: Rattus norvegicus keratin 7 (Krt7), transcript variant X1, mRNA	89.8	89.8	8%	7e-16	81.90%	XM_017603516.1
✓	Rattus norvegicus GFAP kappa mRNA partial cds alternatively spliced	82.4	82.4	3%	1e-13	100.00%	DQ979831.1

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

1 10 20 30 40 50 60 70 80 90 100 110 120 130
sequence
CDS
Consensus
ATGAGGCGGAGACGATACCTCTGCACGCCGCTCTATGCCCTCTCCGAGACGATGGTCAGGGGCCATGGTCTACCGAGACCTTGGGTACCATTCGCCGCTCTCCCTGTGTCGAAATGACGCTCCAC
ATGAGGCGGAGACGATACCTCTGCACGCCGCTCTATGCCCTCTCCGAGACGATGGTCAGGGGCCATGGTCTACCGAGACCTTGGGTACCATTCGCCGCTCTCCCTGTGTCGAAATGACGCTCCAC
ATGAGGCGGAGACGATACCTCTGCACGCCGCTCTATGCCCTCTCCGAGACGATGGTCAGGGGCCATGGTCTACCGAGACCTTGGGTACCATTCGCCGCTCTCCCTGTGTCGAAATGACGCTCCAC
131 140 150 160 170 180 190 200 210 220 230 240 250 260
sequence
CDS
Consensus
TCCCTGCCAGGATAGACTTCTCCCTGGCCGGGGCGCTCAATGCCGGCTTCAGAGAGACTCGGGCCAGCGAGCTGCGGAGATGATGGAGCTCAATGACCGCTTTGCTAGCTACATCGAGAGGTCGCGTT
TCCCTGCCAGGATAGACTTCTCCCTGGCCGGGGCGCTCAATGCCGGCTTCAGAGAGACTCGGGCCAGCGAGCTGCGGAGATGATGGAGCTCAATGACCGCTTTGCTAGCTACATCGAGAGGTCGCGTT
TCCCTGCCAGGATAGACTTCTCCCTGGCCGGGGCGCTCAATGCCGGCTTCAGAGAGACTCGGGCCAGCGAGCTGCGGAGATGATGGAGCTCAATGACCGCTTTGCTAGCTACATCGAGAGGTCGCGTT
261 270 280 290 300 310 320 330 340 350 360 370 380 390
sequence
CDS
Consensus
CCTGGAGACGCAAAACAGGCGCTGGCAGCTGAGCTGAACAGCTTCGAGCCAGGAGGCCACCAAACTGGCTGACGCTTTACAGGCAGAGACTTCGGAGCTGCGGCTGCGCTGGACCACTTACTACC
CCTGGAGACGCAAAACAGGCGCTGGCAGCTGAGCTGAACAGCTTCGAGCCAGGAGGCCACCAAACTGGCTGACGCTTTACAGGCAGAGACTTCGGAGCTGCGGCTGCGCTGGACCACTTACTACC
CCTGGAGACGCAAAACAGGCGCTGGCAGCTGAGCTGAACAGCTTCGAGCCAGGAGGCCACCAAACTGGCTGACGCTTTACAGGCAGAGACTTCGGAGCTGCGGCTGCGCTGGACCACTTACTACC
391 400 410 420 430 440 450 460 470 480 490 500 510 520
sequence
CDS
Consensus
AACAGTGCCCGGCTGAGAGTGGAGAGGACCAATCTCACACAGGACCTCGGACCCCTGAGGCGAGAGCTCCAGATGAACACCACTGAGGCTGGAGGCGGAGACCACTGGCTGTGTACAGACAGGAGG
AACAGTGCCCGGCTGAGAGTGGAGAGGACCAATCTCACACAGGACCTCGGACCCCTGAGGCGAGAGCTCCAGATGAACACCACTGAGGCTGGAGGCGGAGACCACTGGCTGTGTACAGACAGGAGG
AACAGTGCCCGGCTGAGAGTGGAGAGGACCAATCTCACACAGGACCTCGGACCCCTGAGGCGAGAGCTCCAGATGAACACCACTGAGGCTGGAGGCGGAGACCACTGGCTGTGTACAGACAGGAGG
521 530 540 550 560 570 580 590 600 610 620 630 640 650
sequence
CDS
Consensus
CGGATGAGGCCACCTTGGCTCGTGTGGATCTGAGAGGAGAGGTTGAGTCGCTGGAGGAGAGATCAAGTCTTGGAGGAGATCCATGAGGAGGAGTTCGAGACTCCAGGAGCAGCTGGCCACGACGA
CGGATGAGGCCACCTTGGCTCGTGTGGATCTGAGAGGAGAGGTTGAGTCGCTGGAGGAGAGATCAAGTCTTGGAGGAGATCCATGAGGAGGAGTTCGAGACTCCAGGAGCAGCTGGCCACGACGA
CGGATGAGGCCACCTTGGCTCGTGTGGATCTGAGAGGAGAGGTTGAGTCGCTGGAGGAGAGATCAAGTCTTGGAGGAGATCCATGAGGAGGAGTTCGAGACTCCAGGAGCAGCTGGCCACGACGA
651 660 670 680 690 700 710 720 730 740 750 760 770 780
sequence
CDS
Consensus
GGTCACGCTGGAGATGGATGTGGCCAGCCAGACCTCACAGCGGCTCTGAGAGAGATTCCGACTCAGTACGAGGAGTGGCCACCACTGACATGCAAGAACAGAGAGTGGTATCGGTCAGGTTTGA
GGTCACGCTGGAGATGGATGTGGCCAGCCAGACCTCACAGCGGCTCTGAGAGAGATTCCGACTCAGTACGAGGAGTGGCCACCACTGACATGCAAGAACAGAGAGTGGTATCGGTCAGGTTTGA
GGTCACGCTGGAGATGGATGTGGCCAGCCAGACCTCACAGCGGCTCTGAGAGAGATTCCGACTCAGTACGAGGAGTGGCCACCACTGACATGCAAGAACAGAGAGTGGTATCGGTCAGGTTTGA
781 790 800 810 820 830 840 850 860 870 880 890 900 910
sequence
CDS
Consensus
GACCTCAGACGCTTGTCTCCCGAACGCGAGAGCTGCTCCGCGAGGCCAGGACGAGGCTTAATGACTATCGCCGCACCTGACGAGCTTGACCTGCGACCTTGAGTCTTGGCGGCGACGACGAGTCT
GACCTCAGACGCTTGTCTCCCGAACGCGAGAGCTGCTCCGCGAGGCCAGGACGAGGCTTAATGACTATCGCCGCACCTGACGAGCTTGACCTGCGACCTTGAGTCTTGGCGGCGACGACGAGTCT
GACCTCAGACGCTTGTCTCCCGAACGCGAGAGCTGCTCCGCGAGGCCAGGACGAGGCTTAATGACTATCGCCGCACCTGACGAGCTTGACCTGCGACCTTGAGTCTTGGCGGCGACGACGAGTCT
911 920 930 940 950 960 970 980 990 1000 1010 1020 1030 1040
sequence
CDS
Consensus
TGGAGAGGCAATGCGCGACAGGAGGAGCGCCACGCGCGGAGTCCGCGAGTTACAGAGGACACTCGCTCGGCTGGAGGAGGAGGCCAAGGCTCAGAGGAGAGATGGCCGCGACCTGACAGAGTA
TGGAGAGGCAATGCGCGACAGGAGGAGCGCCACGCGCGGAGTCCGCGAGTTACAGAGGACACTCGCTCGGCTGGAGGAGGAGGCCAAGGCTCAGAGGAGAGATGGCCGCGACCTGACAGAGTA
TGGAGAGGCAATGCGCGACAGGAGGAGCGCCACGCGCGGAGTCCGCGAGTTACAGAGGACACTCGCTCGGCTGGAGGAGGAGGCCAAGGCTCAGAGGAGAGATGGCCGCGACCTGACAGAGTA
1041 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170
sequence
CDS
Consensus
CCAGGATCTACTCAGCTTACGCTAGCCTTGGACATCGAGATCGCCACCTACAGGAATTTGCTGGAGGCGAGAGAAACCGATCACCATTCTCTGACAGCTTTCTCCACCTCCAGATCCGAGARAC
CCAGGATCTACTCAGCTTACGCTAGCCTTGGACATCGAGATCGCCACCTACAGGAATTTGCTGGAGGCGAGAGAAACCGATCACCATTCTCTGACAGCTTTCTCCACCTCCAGATCCGAGARAC
CCAGGATCTACTCAGCTTACGCTAGCCTTGGACATCGAGATCGCCACCTACAGGAATTTGCTGGAGGCGAGAGAAACCGATCACCATTCTCTGACAGCTTTCTCCACCTCCAGATCCGAGARAC
1171 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 129#293
sequence
CDS
Consensus
AGCCTGGACACCAATCTGTGTGAGAGGCGACCTCAGAGGAGACATCGTGGTAAGACGGTGGAGATCGGGATGGCGAGGCTATTAGGAGTCCAGACGAGGACACAGGATGTGATGTGA
AGCCTGGACACCAATCTGTGTGAGAGGCGACCTCAGAGGAGACATCGTGGTAAGACGGTGGAGATCGGGATGGCGAGGCTATTAGGAGTCCAGACGAGGACACAGGATGTGATGTGA
AGCCTGGACACCAATCTGTGTGAGAGGCGACCTCAGAGGAGACATCGTGGTAAGACGGTGGAGATCGGGATGGCGAGGCTATTAGGAGTCCAGACGAGGACACAGGATGTGATGTGA

En position 204 : C<T

➤ Différence au niveau PROT :

1 10 20 30 40 50 60 70 80 90 100 110 120 130
sequence
CDS
Consensus
MEARRRITSARRSYASSETHYVRGNGPTRHLGTIPRLSLSRHTPPLPARVDFSLAGALNAGFKETRASERAHEMELNDRFASYIEKYRFLQGNKALAEELNQLRAKEPTKLADYVQRELRELRLDQLTT
MEARRRITSARRSYASSETHYVRGNGPTRHLGTIPRLSLSRHTPPLPARVDFSLAGALNAGFKETRASERAHEMELNDRFASYIEKYRFLQGNKALAEELNQLRAKEPTKLADYVQRELRELRLDQLTT
MEARRRITSARRSYASSETHYVRGNGPTRHLGTIPRLSLSRHTPPLPARVDFSLAGALNAGFKETRASERAHEMELNDRFASYIEKYRFLQGNKALAEELNQLRAKEPTKLADYVQRELRELRLDQLTT
131 140 150 160 170 180 190 200 210 220 230 240 250 260
sequence
CDS
Consensus
NSARLEVERDNLTDQLGTLRQKLQDETNLRLERENNLAYRQDEADTLARVLDLRYKVESLEEEIQFLRKIHIEEYRELQEQLAQQVHVEMDVAKPDLTAALREIRTQYEVATSNMQETEENYRSKFA
NSARLEVERDNLTDQLGTLRQKLQDETNLRLERENNLAYRQDEADTLARVLDLRYKVESLEEEIQFLRKIHIEEYRELQEQLAQQVHVEMDVAKPDLTAALREIRTQYEVATSNMQETEENYRSKFA
NSARLEVERDNLTDQLGTLRQKLQDETNLRLERENNLAYRQDEADTLARVLDLRYKVESLEEEIQFLRKIHIEEYRELQEQLAQQVHVEMDVAKPDLTAALREIRTQYEVATSNMQETEENYRSKFA
261 270 280 290 300 310 320 330 340 350 360 370 380 390
sequence
CDS
Consensus
DLTDVASRNHELLRQAKHEANDYRRLQALTCOLESLRGTNESLERQHQREQEERHARESASYQEARLARLEEGQSLKEEMARHLQEYQDLLNVKALDIEATYRKLLGEENRITIPVQTFSNLQIRET
DLTDVASRNHELLRQAKHEANDYRRLQALTCOLESLRGTNESLERQHQREQEERHARESASYQEARLARLEEGQSLKEEMARHLQEYQDLLNVKALDIEATYRKLLGEENRITIPVQTFSNLQIRET
DLTDVASRNHELLRQAKHEANDYRRLQALTCOLESLRGTNESLERQHQREQEERHARESASYQEARLARLEEGQSLKEEMARHLQEYQDLLNVKALDIEATYRKLLGEENRITIPVQTFSNLQIRET
391 400 410 420 430
sequence
CDS
Consensus
SLDTKSVSSEGLKRNIVYKTVEMRDGEVTKESQKQKHQVH
SLDTKSVSSEGLKRNIVYKTVEMRDGEVTKESQKQKHQVH
SLDTKSVSSEGLKRNIVYKTVEMRDGEVTKESQKQKHQVH

Pas de diff au niveau prot

		Score	Score	Cover	value	Ident	
✓	glial fibrillary acidic protein [Rattus norvegicus]	862	862	100%	0.0	100.00%	NP_058705.2
✓	glial fibrillary acidic protein [Rattus norvegicus]	861	861	100%	0.0	99.77%	AAA20540.1
✓	glial fibrillary acidic protein delta [Rattus norvegicus]	780	780	93%	0.0	96.35%	AAD01874.2
✓	glial fibrillary acidic protein beta [Rattus norvegicus]	660	660	76%	0.0	100.00%	ABK91944.1

Flag BirA Gfap DiT0 (clone A) : NT en 204 C>T mais
n'engendrant pas de diff au niv prot donc OK

○ FlagBirA Gfap DiT24hLPS clone A

➤ B3Fwd DiT24hLPS 837NT

ATGGAGCGGAGACGTATCACCTCTGCACGCCGCTCCTATGCCTCCTCCGAGACGATGGTCAGGGGCCATGGTCCT
ACCAGACACCTGGGTACCATTCCGCGCCTCTCCCTGTCTCGAATGACGCCTCCACTCCCTGCCAGGGTAGACTTCT
CCCTGGCCGGGGCGCTCAATGCCGGCTTCAAAGAGACTCGGGCCAGCGAGCGCGGAGATGATGGAGCTCA
ATGACCGCTTTGCTAGCTACATCGAGAAGGTCCGCTTCTGGAACAGCAAAACAAGGCGCTGGCAGCTGAGCTG
AACCAGCTTCGAGCCAAGGAGCCACCAAACCTGGCTGACGTTTACCAGGCAGAACTTCGGGAGCTGCGGCTGC
GTCTGGACCAGCTTACTACCAACAGTGCCCCGCTGGAGGTGGAGAGGGACAATCTCACACAGGACCTCGGCAC
CCTGAGGCAGAAGCTCCAAGATGAAACCAACCTGAGGCTGGAGGCGGAGAACAACCTGGCTGTGTACAGACA
GGAGGCGGATGAAGCCACCTTGGCTCGTGTGGATCTGGAGAGGAAGGTTGAGTCGCTGGAGGAGGAGATCCA
GTTCTTGAGGAAGATCCATGAGGAGGAAGTTCGAGAACTCCAGGAGCAGCTGGCCCAGCAGCAgTCCACGTG
GANATGGATGTGGCCAAGCCAGACCTCACAGCGGCTCTGANAGAGATTGCACTCAGTACGAGGCAGTGGCNA
CCAGTAACATGCAAGAAACAGAANAGTGGTATCGGTCCNAGTTTGCANANCTCACAGACGTTGCTTCCCGCAAC
GCANANCTGCTCCGCCAGGCCAAGCACGAG

➤ BGHRev DiT24hLPS 942NT

ACTTNNAGCTGCGGNTGCNTCTGGACCAGCTTACTACCANCAGTGCCCCGCTGGAGGTGGAGAGGGACAA
TCTCACACAGGACNTCGGCACCCTGAGGCAGAAGNTCCAAGATGAAACCANctGAGGCTGGAGGCGGAGAAC
AACCTGGCTGTGTACAGACAGGAGGCGGATGAAGCCACCTTGGCTCGTGTGGATCTGGAGAGGAAGGTTGAGT
CGCTGGAGGAGGAGATCCAGTTCTTGAGGAAGATCCATGAGGAGGAAGTTCGAGAACTCCAGGAGCAGCTGG
CCCAGCAGCAGGTCCACGTGGAGATGGATGTGGCCAAGCCAGACCTCACAGCGGCTCTGAGAGAGATTTCGCAC
TCAGTACGAGGCAGTGGCCACCAGTAACATGCAAGAAACAGAAGAGTGGTATCGGTCCAAGTTTGCAGACCTCA
CAGACGTTGCTTCCCGCAACGCAGAGCTGCTCCGCCAGGCCAAGCACGAGGCTAATGACTATCGCCGCCAACTG
CAGGCCTTGACCTGCGACCTTGAGTCCTTGCGCGGCACGAACGAGTCCTTGGAGAGGCCAAATGCGCGAACAGG
AGGAGCGCCACGCGCGGGAGTCGGCGAGTTACCAGGAGGCACTCGCTCGGCTGGAGGAGGAGGGCCAAAGC
CTCAAGGAGGAGATGGCCCCCACCTGCAGGAGTACCAGGATCTACTCAACGTTAAGCTAGCCCTGGACATCGA
GATCGCCACCTACAGGAAATTGCTGGAGGGCGAAGAAAACCGCATCACCATTCTGTACAGACTTTCTCCAACCT
CCAGATCCGAGAAACCAGCTGGACACCAATCTGTGTGAGAAGGCCACCTCAAGAGGAACATCGTGGTAAAG
ACGGTGGAGATGCGGGATGGCGAGGTCATTAAGGAGTCAAGCAGGAGCACAAAGGATGTGATGTGA

➤ Synthèse séquençage DiT24hLPS : 1293NT

ATGGAGCGGAGACGTATCACCTCTGCACGCCGCTCCTATGCCTCCTCCGAGACGATGGTC	60
AGGGGCCATGGTCTTACCAGACACCTGGGTACCATTCCGCGCCTCTCCCTGTCTCGAATG	120
ACGCTCCACTCCCTGCCAGGGTAGACTTCTCCCTGGCCGGGGCGCTCAATGCCGGCTTC	180
AAAGAGACTCGGGCCAGCGAGCGCGCGGAGATGATGGAGCTCAATGACCGCTTTGCTAGC	240
TACATCGAGAAGGTCCGCTTCTTGGAAACAGCAAAACAAGGCGCTGGCAGCTGAGCTGAAC	300
CAGCTTCGAGCCAAGGAGCCACCAAACCTGGCTGACGTTTACCAGGCAGAACTTCGGGAG	360
CTGCGGCTGCGTCTGGACCAGCTTACTACCAACAGTGCCCCGCTGGAGGTGGAGAGGGAC	420
AATCTCACACAGGACCTCGGCACCCTGAGGCAGAAGCTCCAAGATGAAACCAACCTGAGG	480
CTGGAGGCGGAGAACAACCTGGCTGTGTACAGACAGGAGGCGGATGAAGCCACCTTGGCT	540
CGTGTGGATCTGGAGAGGAAGGTTGAGTCGCTGGAGGAGGAGATCCAGTTCTTGAGGAAG	600
ATCCATGAGGAGGAAGTTCGAGAACTCCAGGAGCAGCTGGCCCAGCAGCAgGTCCACGTG	660
GAGATGGATGTGGCCAAGCCAGACCTCACAGCGGCTCTGAGAGAGATTGCACTCAGTAC	
GAGGCAGTGGCCACAGTAACATGCAAGAAACAGAAGAGTGGTATCGGTCCAAGTTTGCA	
GACCTCACAGACGTTGCTTCCCGCAACGCAGAGCTGCTCCGCCAGGCCAAGCACGAGGCT	
AATGACTATCGCCGCCAACTGCAGGCTTGACCTGCGACCTTGAGTCCTTGCGCGGCACG	
AACGAGTCCTTGAGAGGCAATGCGCGAACAGGAGGAGCGCCACGCGCGGGAGTCGGCG	
AGTTACCAGGAGGCACTCGCTCGGCTGGAGGAGGAGGGCCAAAGCCTCAAGGAGGAGATG	

GCCCCGCACCTGCAGGAGTACCAGGATCTACTCAACGTTAAGCTAGCCCTGGACATCGAG
ATCGCCACCTACAGGAAATTGCTGGAGGGCGAAGAAAACCGCATCACCATTCTGTACAG
ACTTTCTCCAACCTCCAGATCCGAGAAACCAGCCTGGACACCAAATCTGTGTCAGAAGGC
CACCTCAAGAGGAACATCGTGGTAAAGACGGTGGAGATGCGGGATGGCGAGGTCATTAAAG
GAGTCGAAGCAGGAGCACAAGGATGTGATGTGA

MERRRITSARRSYASSETMVRGHGPTRHLGTIPRLSLSRMTPPLPARVDFSLAGALNAGFKETRASERAEMMELND
RFASYIEKVRFLEQQNKALAAELNQLRAKEPTKLADVYQAE LRELRLRLDQLTTNSARLEVERDNLTDLGLTLRQKLQ
DETNRLEAENNLAVYRQEAD EATLARVDLERKVESLEEEIQFLRKIHEEEVRELQEQLAQQVHVEMDVAKPDLTA
ALREIRTQYEAVATSNMQETEEWYRSKFADLTDVASRNAELLRQAKHEANDYRRQLQALTCDLESLRGTNESLERQ
MREQEERHARESASYQEALARLEEEGQSLKEEMARHLQEYQDLLNVKLALDIEIATYRKLLEGEENRITIPVQTFSNL
QIRETSLDTKSVSEGLKRNIVVKTVEMRDGEVIKESKQEHKDVM-

➤ **Blast contre banque rat :**

➤ **Différence**

Séquencage/CDS au niveau NT :

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
sequencage	ATGGAGCGAGAGCTATCACTCTGCACGCCGCTCCTATGCCCTCCGAGACGATGGTCAGGGGCGATGGCTTACCAGACACCTGGGTACCATTCGCGCCTCTCCCTGTCTCGAATGACGCTCCAC													
CDS	ATGGAGCGAGAGCTATCACTCTGCACGCCGCTCCTATGCCCTCCGAGACGATGGTCAGGGGCGATGGCTTACCAGACACCTGGGTACCATTCGCGCCTCTCCCTGTCTCGAATGACGCTCCAC													
Consensus	ATGGAGCGAGAGCTATCACTCTGCACGCCGCTCCTATGCCCTCCGAGACGATGGTCAGGGGCGATGGCTTACCAGACACCTGGGTACCATTCGCGCCTCTCCCTGTCTCGAATGACGCTCCAC													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
sequencage	TCCCTGCCAGGGTAGACTTCTCCCTGGCCGGGGCGCTCAATGCCGGCTTCAGAGAGACTCGGGCCAGCGAGC CGCGGAGATGATGGAGCTCAATGACCGCTTTGCTAGCTACATCGAGAGGGTCCGCTT													
CDS	TCCCTGCCAGGGTAGACTTCTCCCTGGCCGGGGCGCTCAATGCCGGCTTCAGAGAGACTCGGGCCAGCGAGC CGCGGAGATGATGGAGCTCAATGACCGCTTTGCTAGCTACATCGAGAGGGTCCGCTT													
Consensus	TCCCTGCCAGGGTAGACTTCTCCCTGGCCGGGGCGCTCAATGCCGGCTTCAGAGAGACTCGGGCCAGCGAGC CGCGGAGATGATGGAGCTCAATGACCGCTTTGCTAGCTACATCGAGAGGGTCCGCTT													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
sequencage	CCTGGARACGCAAAACAGGCGCTGGCAGCTGAGCTGAACAGCTTCGAGCCAGGAGGCCACCAAACTGGCTGACGTTTACCAGGACAGACTTCGGAGCTGCGGCTGGAGCAGCTTACTACC													
CDS	CCTGGARACGCAAAACAGGCGCTGGCAGCTGAGCTGAACAGCTTCGAGCCAGGAGGCCACCAAACTGGCTGACGTTTACCAGGACAGACTTCGGAGCTGCGGCTGGAGCAGCTTACTACC													
Consensus	CCTGGARACGCAAAACAGGCGCTGGCAGCTGAGCTGAACAGCTTCGAGCCAGGAGGCCACCAAACTGGCTGACGTTTACCAGGACAGACTTCGGAGCTGCGGCTGGAGCAGCTTACTACC													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
sequencage	AACAGTGGCCGGTGGAGGTTGGAGAGGGACAAATCTCACACAGGAGCTCGGACCCCTGAGGCGAGAGCTCCAGATGAACCAACCTGAGGCTGGAGGCGGAGAACCACTGGCTGTGTACACAGGAGG													
CDS	AACAGTGGCCGGTGGAGGTTGGAGAGGGACAAATCTCACACAGGAGCTCGGACCCCTGAGGCGAGAGCTCCAGATGAACCAACCTGAGGCTGGAGGCGGAGAACCACTGGCTGTGTACACAGGAGG													
Consensus	AACAGTGGCCGGTGGAGGTTGGAGAGGGACAAATCTCACACAGGAGCTCGGACCCCTGAGGCGAGAGCTCCAGATGAACCAACCTGAGGCTGGAGGCGGAGAACCACTGGCTGTGTACACAGGAGG													
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
sequencage	CGGATGAAGCCACCTTTGGCTCGTGTGGATCTGGAGAGGAGGTTGAGTCGCTGGAGAGGAGATCCAGTCTTTCAGGAGAGATCCATGAGGAGGAGTTTCAGAGACTCCAGGAGCAGCTGGCCAGCAGCA													
CDS	CGGATGAAGCCACCTTTGGCTCGTGTGGATCTGGAGAGGAGGTTGAGTCGCTGGAGAGGAGATCCAGTCTTTCAGGAGAGATCCATGAGGAGGAGTTTCAGAGACTCCAGGAGCAGCTGGCCAGCAGCA													
Consensus	CGGATGAAGCCACCTTTGGCTCGTGTGGATCTGGAGAGGAGGTTGAGTCGCTGGAGAGGAGATCCAGTCTTTCAGGAGAGATCCATGAGGAGGAGTTTCAGAGACTCCAGGAGCAGCTGGCCAGCAGCA													
	651	660	670	680	690	700	710	720	730	740	750	760	770	780
sequencage	GGTCCACGTGGAGATGGATGTGGCCAGGCGAGACCTCACAGCGGCTCTGAGAGAGATTTCGCACTCAGTACGAGGCGAGTGGCCACAGTACATGCAGAAACAGAGAGTGGTATCGGTCGAAGTTTGA													
CDS	GGTCCACGTGGAGATGGATGTGGCCAGGCGAGACCTCACAGCGGCTCTGAGAGAGATTTCGCACTCAGTACGAGGCGAGTGGCCACAGTACATGCAGAAACAGAGAGTGGTATCGGTCGAAGTTTGA													
Consensus	GGTCCACGTGGAGATGGATGTGGCCAGGCGAGACCTCACAGCGGCTCTGAGAGAGATTTCGCACTCAGTACGAGGCGAGTGGCCACAGTACATGCAGAAACAGAGAGTGGTATCGGTCGAAGTTTGA													
	781	790	800	810	820	830	840	850	860	870	880	890	900	910
sequencage	GACCTCACAGAGCTTGTCTCCCGAAGCGAGAGCTGTCTCCGCGAGGCGAGGACGAGGCTTAATGACTATCGCCGCCAATCGAGGCTTGAACCTGCGACCTTGAAGTCTTGGCGGCGAGAGAGTCT													
CDS	GACCTCACAGAGCTTGTCTCCCGAAGCGAGAGCTGTCTCCGCGAGGCGAGGACGAGGCTTAATGACTATCGCCGCCAATCGAGGCTTGAACCTGCGACCTTGAAGTCTTGGCGGCGAGAGAGTCT													
Consensus	GACCTCACAGAGCTTGTCTCCCGAAGCGAGAGCTGTCTCCGCGAGGCGAGGACGAGGCTTAATGACTATCGCCGCCAATCGAGGCTTGAACCTGCGACCTTGAAGTCTTGGCGGCGAGAGAGTCT													
	911	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040
sequencage	TGGAGAGGCAAAATGCGCGARACAGGAGGAGCGCCACGCGCGGAGTTCGCGAGTTACAGGAGGCACTCGCTCGGCTGGAGAGGAGGCGCCAAAGCTTCAGGAGGAGATGGCCGCCACCTGCAGAGTA													
CDS	TGGAGAGGCAAAATGCGCGARACAGGAGGAGCGCCACGCGCGGAGTTCGCGAGTTACAGGAGGCACTCGCTCGGCTGGAGAGGAGGCGCCAAAGCTTCAGGAGGAGATGGCCGCCACCTGCAGAGTA													
Consensus	TGGAGAGGCAAAATGCGCGARACAGGAGGAGCGCCACGCGCGGAGTTCGCGAGTTACAGGAGGCACTCGCTCGGCTGGAGAGGAGGCGCCAAAGCTTCAGGAGGAGATGGCCGCCACCTGCAGAGTA													
	1041	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170
sequencage	CCAGGATCTACTCAACGTTAAGCTAGCCCTGGACATCGAGATCGCCACCTACAGGAATGCTGGAGGGCGAGGAARACCGCATCACCATTCTCTACAGACTTCTCCACCTCCAGATCCGAGAAAC													
CDS	CCAGGATCTACTCAACGTTAAGCTAGCCCTGGACATCGAGATCGCCACCTACAGGAATGCTGGAGGGCGAGGAARACCGCATCACCATTCTCTACAGACTTCTCCACCTCCAGATCCGAGAAAC													
Consensus	CCAGGATCTACTCAACGTTAAGCTAGCCCTGGACATCGAGATCGCCACCTACAGGAATGCTGGAGGGCGAGGAARACCGCATCACCATTCTCTACAGACTTCTCCACCTCCAGATCCGAGAAAC													
	1171	1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1293
sequencage	AGCCTGGACACCAATCTGTGTACAGAGGCGACCTCAGAGGAGACATCGTGGTAAGAGCGGTGGAGATCGGGATGGCGAGGTCATTAGGAGTCGAGCAGGAGCACAGGATGTGATGTGA													
CDS	AGCCTGGACACCAATCTGTGTACAGAGGCGACCTCAGAGGAGACATCGTGGTAAGAGCGGTGGAGATCGGGATGGCGAGGTCATTAGGAGTCGAGCAGGAGCACAGGATGTGATGTGA													
Consensus	AGCCTGGACACCAATCTGTGTACAGAGGCGACCTCAGAGGAGACATCGTGGTAAGAGCGGTGGAGATCGGGATGGCGAGGTCATTAGGAGTCGAGCAGGAGCACAGGATGTGATGTGA													

Comme pour DiT0, C>T en 204

➤ Différence au niveau PROT :

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
sequencage	MERRRITSARRSYASSETHYRGHPTRHLGTIPRLSLSRMTPLPARVDFSLAGALNAGFKETRASERAEHMLNDRFASYIEKVRFLEQQNKALAEHLNQLRAKEPTKLADYVQRELRELRLRLDQLTT													
ref	MERRRITSARRSYASSETHYRGHPTRHLGTIPRLSLSRMTPLPARVDFSLAGALNAGFKETRASERAEHMLNDRFASYIEKVRFLEQQNKALAEHLNQLRAKEPTKLADYVQRELRELRLRLDQLTT													
Consensus	MERRRITSARRSYASSETHYRGHPTRHLGTIPRLSLSRMTPLPARVDFSLAGALNAGFKETRASERAEHMLNDRFASYIEKVRFLEQQNKALAEHLNQLRAKEPTKLADYVQRELRELRLRLDQLTT													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
sequencage	NSARLEVERDNLTDQLGTLRQKLQDETNLRLAEENNLAYYRQEADEATLARVDLERKVESLEEIIQFLRKIEHEEYRELQEQLAQQVHVENDVAKPDLTAALREIRTQYERAVATSNMQETEEHYRSKFA													
ref	NSARLEVERDNLTDQLGTLRQKLQDETNLRLAEENNLAYYRQEADEATLARVDLERKVESLEEIIQFLRKIEHEEYRELQEQLAQQVHVENDVAKPDLTAALREIRTQYERAVATSNMQETEEHYRSKFA													
Consensus	NSARLEVERDNLTDQLGTLRQKLQDETNLRLAEENNLAYYRQEADEATLARVDLERKVESLEEIIQFLRKIEHEEYRELQEQLAQQVHVENDVAKPDLTAALREIRTQYERAVATSNMQETEEHYRSKFA													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
sequencage	DLTDVARSNRELLRQAKHEANDYRRQLQALTCOLESLRGTMESLERQMRQEERHARESASYQEARLEEEGASLKEENARHLQEYQDLLWYKALDIEATYRKLLGGEENRITIPYQTFSNLQIRET													
ref	DLTDVARSNRELLRQAKHEANDYRRQLQALTCOLESLRGTMESLERQMRQEERHARESASYQEARLEEEGASLKEENARHLQEYQDLLWYKALDIEATYRKLLGGEENRITIPYQTFSNLQIRET													
Consensus	DLTDVARSNRELLRQAKHEANDYRRQLQALTCOLESLRGTMESLERQMRQEERHARESASYQEARLEEEGASLKEENARHLQEYQDLLWYKALDIEATYRKLLGGEENRITIPYQTFSNLQIRET													
	391	400	410	420	430									
sequencage	SLDTKSVSEGHLLKRNIVVKTVEHMDGEVTKESKQEHKQVM													
ref	SLDTKSVSEGHLLKRNIVVKTVEHMDGEVTKESKQEHKQVM													
Consensus	SLDTKSVSEGHLLKRNIVVKTVEHMDGEVTKESKQEHKQVM													

Pas de diff au niveau prot

Flag BirA Gfap DiT24hLPS (clone A) : NT en 204 C>T mais n'engendrant pas de diff au niv prot donc OK

○ **FlagBirA Gfap DiT48hMix clone A**

➤ **B3Fwd DiT48hMix 851NT**

ATGGAGCGGAGACGTATCACCTCTGCACGCCGCTCCTATGCCTCCTCCGAGACGATGGTCAGGGGCCATGGTCCT
ACCAGACACCTGGGTACCATTCCGCGCCTCTCCCTGTCTCGAATGACGCCTCCACTCCCTGCCAGGGTAGACTTCT
CCCTGGCCGGGGCGCTCAATGCCGGCTTCAAAGAGACTCGGGCCAGCGAGCGCGGAGATGATGGAGCTCA
ATGACCGCTTTGCTAGCTACATCGAGAAGGTCCGCTTCTGGAACAGCAAAACAAGGCGCTGGCAGCTGAGCTG
AACCAGCTTCGAGCCAAGGAGCCACCAAACCTGGCTGACGTTTACCAGGCAGAACTTCGGGAGCTGCGGCTGC
GTCTGGACCAGCTTACTACCAACAGTGCCCCGCTGGAGGTGGAGAGGGACAATCTCACACAGGACCTCGGCAC
CCTGAGGCAGAAAGCTCCAAGATGAAACCAACCTGAGGCTGGAGGCGGAGAACAACCTGGCTGTGTACAGACA
GGAGGCGGATGAAGCCACCTTGCTCGTGTGGATCTGGAGAGGAAGTTGAGTCGCTGGAGGAGGAGATCCA
GTTCTTGAGGAAGATCCATGAGGAGGAAGTTGAGAACTCCAGGAGCAGCTGGcCCAGCAGCAgGTCCACGTG
GAGATGGATGTGGCCAAGCCAGANCTCACAGCGGCTCTGANAGAGATTGCACTCAGTACGAGGCAGTGGCCA
CCAGTAACATGCAAGAAACAGAAANANTGGTATCGGTCCAAGTTTGCANANNTCACAGACGTTGCTTCCCGCAAC
GCANANCTGCTCCGCCAGGCCAAGCACGAGGCTAATGACTATCG

➤ **BGHTRev DiT48hMix 973NT**

CCCANCNANNTNGCTGACGTTNNCAGNCAGNANTTNNGNAGNTGNNGNTGCGTNTGGACCAGCTTACTACC
AACAGTNCNGGCGNGGAGGTGGAGAGGGACAATNTCACACAGGACCTCGGCANCTGAGGCAGAAAGNTCCA
AGATGAAACCANctGAGGCTGGAGGCGGAGAACAACctGGCTGTGTACAGACAGGAGGCGGATGAAGCCACcT
TGGCTCGTGTGGATCTGGAGAGGAAGGTTGAGTCGCTGGAGGAGGAGATCCAGTTCTTGAGGAAGATCCATGA
GGAGGAAGTTGAGAACTCCAGGAGCAGCTGGCCAGCAGCAGGTCCACGTGGAGATGGATGTGGCCAAGCC
AGACCTCACAGCGGCTCTGAGAGAGATTGCACTCAGTACGAGGCAGTGGCCACCAGTAACATGCAAGAAACA
GAAGAGTGGTATCGGTCCAAGTTTGACAGACCTCACAGACGTTGCTTCCCGCAACGCAGAGCTGCTCCGCCAGGC
CAAGCACGAGGCTAATGACTATCGCCGCAACTGCAGGCCTTGACCTGCGACCTTGAGTCCTTGCGCGGCACGA
ACGAGTCCTTGAGAGGCAAATGCGCGAACAGGAGGAGCGCCACGCGCGGGAGTCGGCGAGTTACCAGGAG
GCACTCGCTCGGCTGGAGGAGGAGGGCCAAAGCCTCAAGGAGGAGATGGCCCGCCACCTGCAGGAGTACCAG
GATCTACTCAACGTTAAGCTAGCCCTGGACATCGAGATCGCCACCTACAGGAAATTGCTGGAGGGCGAAGAAAA
CCGCATCACCATTCTGTACAGACTTTCTCCAACCTCCAGATCCGAGAAACCAGCCTGGACACCAAATCTGTGTCA
GAAGGCCACCTCAAGAGGAACATCGTGGTAAAGACGGTGGAGATGCGGGATGGCGAGGTCATTAAGGAGTCG
AAGCAGGAGCACAAGGATGTGATGTGA

➤ **Synthèse séquençage DiT48hMix : 1293NT**

ATGGAGCGGAGACGTATCACCTCTGCACGCCGCTCCTATGCCTCCTCCGAGACGATGGTC	60
AGGGGCCATGGTCCTACCAGACACCTGGGTACCATTCCGCGCCTCTCCCTGTCTCGAATG	120
ACGCCTCCACTCCCTGCCAGGGTAGACTTCTCCCTGGCCGGGGCGCTCAATGCCGGCTTC	180
AAAGAGACTCGGGCCAGCGAGCGCGCGGAGATGATGGAGCTCAATGACCGCTTTGCTAGC	240
TACATCGAGAAGGTCCGCTTCTGGAACAGCAAAACAAGGCGCTGGCAGCTGAGCTGAAC	300
CAGCTTCGAGCCAAGGAGCCACCAAACCTGGCTGACGTTTACCAGGCAGAACTTCGGGAG	360
CTGCGGCTGCGTCTGGACCAGCTTACTACCAACAGTGCCCCGCTGGAGGTGGAGAGGGAC	420
AATCTCACACAGGACCTCGGCACCTGAGGCAGAAGCTCCAAGATGAAACCAACCTGAGG	480
CTGGAGGCGGAGAACAACCTGGCTGTGTACAGACAGGAGGCGGATGAAGCCACCTTGCT	540
CGTGTGGATCTGGAGAGGAAGGTTGAGTCGCTGGAGGAGGAGATCCAGTTCTTGAGGAAG	600
ATCCATGAGGAGGAAGTTGAGAACTCCAGGAGCAGCTGGcCCAGCAGCAgGTCCACGTG	660
GAGATGGATGTGGCCAAGCCAGACCTCACAGCGGCTCTGAGAGAGATTGCACTCAGTAC	
GAGGCAGTGGCCACCAGTAACATGCAAGAAACAGAAAGTGGTATCGGTCCAAGTTTGCA	
GACCTCACAGACGTTGCTTCCCGCAACGCAGAGCTGCTCCGCCAGGCCAAGCACGAGGCT	
AATGACTATCGCCGCAACTGCAGGCCTTGACCTGCGACCTTGAGTCCTTGCGCGGCACG	
AACGAGTCCTTGAGAGGCAAATGCGCGAACAGGAGGAGCGCCACGCGCGGGAGTCGGCG	
AGTTACCAGGAGGCACTCGCTCGGCTGGAGGAGGAGGGCCAAAGCCTCAAGGAGGAGATG	
GCCCCCACCTGCAGGAGTACCAGGATCTACTCAACGTTAAGCTAGCCCTGGACATCGAG	

ATCGCCACCTACAGGAAATTGCTGGAGGGCGAAGAAAACCGCATCACCATTCTGTACAG
 ACTTTCTCCAACCTCCAGATCCGAGAAACCAGCCTGGACACCAAATCTGTGTCAGAAGGC
 CACCTCAAGAGGAACATCGTGGTAAAGACGGTGGAGATGCGGGATGGCGAGGTCATTAAG
 GAGTCGAAGCAGGAGCACAAGGATGTGATGTGA

MERRRITSARRSYASSETMVRGHGPTRHLGTIPRLSLSRMTPPLPARVDFSLAGALNAGFKETRASERAEMMELND
 RFASYIEKVRFLQEQNKALAAELNQLRAKEPTKLADVYQAELELRLRLDQLTTNSARLEVERDNLTDLGLTLRQKLQ
 DETNLRLEAENNLAVYRQEADEATLARVDLERKVESLEEEIQFLRKIHVEEVRELQEQLAQQQVHVEMDVAKPDLTA
 ALREIRTQYEAVATSNMQETEEWYRSKFADLTDVASRNAELLRQAKHEANDYRRQLQALTCDLESRLRGTNESLERQ
 MREQEERHARESASYQEALARLEEEGQSLKEEMARHLQEYQDLLNVKLALDIEIATYRKLLERGEENRITIPVQTFSNL
 QIRETSLDTKSVSEGLKRNIVVKTVMRDGEVIKESKQEHKDVM-

➤ **Blast contre banque rat :**

	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
✓	Rattus norvegicus glial fibrillary acidic protein (GFAP) mRNA sequence	2388	2388	100%	0.0	100.00%	L27219.1
✓	Rattus norvegicus glial fibrillary acidic protein (Gfap) mRNA	2383	2383	100%	0.0	99.92%	NM_017009.2
✓	Rattus norvegicus Sprague Dawley glial fibrillary acidic protein mRNA, complete cds	2366	2366	100%	0.0	99.69%	U03700.1
✓	Rattus norvegicus glial fibrillary acidic protein beta (Gfap) mRNA, partial cds, alternatively spliced	1836	1836	76%	0.0	100.00%	EF094476.1
✓	R.norvegicus partial gfap gene for glial fibrillary acidic protein	843	843	35%	0.0	100.00%	Z48978.1
✓	Rattus norvegicus glial fibrillary acidic proteins alpha and delta (GFAP) gene, alternatively spliced products, complete cds	843	2431	100%	0.0	100.00%	AF028784.1
✓	Rattus norvegicus glial fibrillary acidic protein epsilon (Gfap) mRNA, partial cds, alternatively spliced	704	704	29%	0.0	99.74%	EF094477.1
✓	PREDICTED: Rattus norvegicus keratin 7 (Krt7), transcript variant X2, mRNA	89.8	89.8	8%	7e-16	81.90%	XM_003754353.4
✓	PREDICTED: Rattus norvegicus keratin 7 (Krt7), transcript variant X1, mRNA	89.8	89.8	8%	7e-16	81.90%	XM_017603516.1
✓	Rattus norvegicus GFAP kappa mRNA, partial cds, alternatively spliced	82.4	82.4	3%	1e-13	100.00%	DQ979831.1

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

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
sequence	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----													
CDS	ATGGAGCGGAGGATATCACTCTGACGCGCGCTCTATGCTCTCCGAGACGATGGTCAGGGGCCATGGTCTTACGACACCTGGGTACCATTCGCGGCTCTCCTTGTCTGARTAGCGCTCCAC													
Consensus	ATGGAGCGGAGGATATCACTCTGACGCGCGCTCTATGCTCTCCGAGACGATGGTCAGGGGCCATGGTCTTACGACACCTGGGTACCATTCGCGGCTCTCCTTGTCTGARTAGCGCTCCAC													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
sequence	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----													
CDS	TCCCTGCCAGGGTAGACTTCTCCCTGGCGGGGCGCTCAATGCCGGCTTCAAGAGAGCTCGGGCCAGCGAGCGCGGAGATGATGGAGCTCAATGACCGTTTCTAGCTACATCAGAGAGGTCGCGTT													
Consensus	TCCCTGCCAGGGTAGACTTCTCCCTGGCGGGGCGCTCAATGCCGGCTTCAAGAGAGCTCGGGCCAGCGAGCGCGGAGATGATGGAGCTCAATGACCGTTTCTAGCTACATCAGAGAGGTCGCGTT													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
sequence	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----													
CDS	CCTGGARACGCAAAACAGGCGCTGGCAGCTGAGCTGACACAGCTTCGAGCCAGGAGGCCACCAAACTGGCTGACGTTTACAGGCAGAACTTCGGAGCTGCGGCTGCGCTTGGACAGCTTACTACC													
Consensus	CCTGGARACGCAAAACAGGCGCTGGCAGCTGAGCTGACACAGCTTCGAGCCAGGAGGCCACCAAACTGGCTGACGTTTACAGGCAGAACTTCGGAGCTGCGGCTGCGCTTGGACAGCTTACTACC													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
sequence	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----													
CDS	AACAGTGCCCGGCTGGAGGTGGAGAGGGACARTCTCACACAGGACCTCGGACCCCTGAGGCAGAGCTCCAGATGAAACACACCTGAGGCTGGAGGCGGAGAACACCTGGCTGTGTACACAGCAGGAG													
Consensus	AACAGTGCCCGGCTGGAGGTGGAGAGGGACARTCTCACACAGGACCTCGGACCCCTGAGGCAGAGCTCCAGATGAAACACACCTGAGGCTGGAGGCGGAGAACACCTGGCTGTGTACACAGCAGGAG													
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
sequence	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----													
CDS	CGGATGAGACACCTTGGCTCGTGTGGATCTGGAGGAGAGGTTGAGTCGCTGGAGGAGGAGATCCAGTTCTTGAGGAGATCCATGAGGAGGAGTTTCGAGACTCCAGAGACAGCTGGCCAGCAGCA													
Consensus	CGGATGAGACACCTTGGCTCGTGTGGATCTGGAGGAGAGGTTGAGTCGCTGGAGGAGGAGATCCAGTTCTTGAGGAGATCCATGAGGAGGAGTTTCGAGACTCCAGAGACAGCTGGCCAGCAGCA													
	651	660	670	680	690	700	710	720	730	740	750	760	770	780
sequence	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----													
CDS	GGTCACGCTGGAGATGGATGTGGCCAGGCGAGACCTCACAGCGGCTCTGAGAGAGATTCGACTCAGTACGAGGCGAGTGGCCACGATACATGCAGAAACAGAGAGTGGATCGGTCAGGTTTGCA													
Consensus	GGTCACGCTGGAGATGGATGTGGCCAGGCGAGACCTCACAGCGGCTCTGAGAGAGATTCGACTCAGTACGAGGCGAGTGGCCACGATACATGCAGAAACAGAGAGTGGATCGGTCAGGTTTGCA													
	781	790	800	810	820	830	840	850	860	870	880	890	900	910
sequence	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----													
CDS	GACCTCACAGACGTTGGTTCGCCAGACGACAGCTGCTCCGCCAGGCCAGACGAGGCTTAATGACTATCGCCGCCACTGACGGCTTGAACCTGCGACCTTGAGTCTTGGCGGGACGACAGGTTGCT													
Consensus	GACCTCACAGACGTTGGTTCGCCAGACGACAGCTGCTCCGCCAGGCCAGACGAGGCTTAATGACTATCGCCGCCACTGACGGCTTGAACCTGCGACCTTGAGTCTTGGCGGGACGACAGGTTGCT													
	911	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040
sequence	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----													
CDS	TGGAGAGGCAATGCGCGACAGGAGGAGCGCCAGCGCGGGAGTCCGCGAGTTACAGGAGGCACTCGCTCGGCTGGAGGAGGAGGCGCCAGAGCTCAGGAGGAGATGGCCGCCACCTCGAGGAGTA													
Consensus	TGGAGAGGCAATGCGCGACAGGAGGAGCGCCAGCGCGGGAGTCCGCGAGTTACAGGAGGCACTCGCTCGGCTGGAGGAGGAGGCGCCAGAGCTCAGGAGGAGATGGCCGCCACCTCGAGGAGTA													
	1041	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170
sequence	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----													
CDS	CCAGGATCTACTCAACGTTAGCTAGCCCTGGACATCGAGATGCCACCTACAGGAATTTGCTGGAGGGCGAGAAACCGCATCACCATTCTCTACAGACTTTCTCCACCTCCAGATCCGAGAAAC													
Consensus	CCAGGATCTACTCAACGTTAGCTAGCCCTGGACATCGAGATGCCACCTACAGGAATTTGCTGGAGGGCGAGAAACCGCATCACCATTCTCTACAGACTTTCTCCACCTCCAGATCCGAGAAAC													
	1171	1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1293
sequence	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----													
CDS	AGCCTGGACACCAATCTGTGTGAGAGGCGACCTCAGAGGAGACATCGTGGTAAGAGCGTGGAGATCGGGATGGCAGGTCATTAGGAGCTCAGACAGGAGCAGAGGATGTGATGTA													
Consensus	AGCCTGGACACCAATCTGTGTGAGAGGCGACCTCAGAGGAGACATCGTGGTAAGAGCGTGGAGATCGGGATGGCAGGTCATTAGGAGCTCAGACAGGAGCAGAGGATGTGATGTA													

Comme pour DiT0 et DiT24hLPS C>T en 204

➤ Différence au niveau PROT :

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
sequence	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----													
refprot	MERRRITSARRSYSSSETHYRGHPTRIHGTIPRLSLSRHTPPLPARVDFSLAGALNAGFKETRASERHEHMLNDRFASYIEKVRFLQGNKALARELNQRAKEPTKLADYVQAEARELRLRLDQLTT													
Consensus	MERRRITSARRSYSSSETHYRGHPTRIHGTIPRLSLSRHTPPLPARVDFSLAGALNAGFKETRASERHEHMLNDRFASYIEKVRFLQGNKALARELNQRAKEPTKLADYVQAEARELRLRLDQLTT													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
sequence	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----													
refprot	NSARLEVERDNLTDQLGTLRQKLQDETNLRLARENNLAVYRQDEATLARYDLERKYESLEEETQFLRKIHEEEVRELQEQLRQQQVYVHMDYAKPDLTRALREIRTQYEVATSNNOCTEEHYRSKFA													
Consensus	NSARLEVERDNLTDQLGTLRQKLQDETNLRLARENNLAVYRQDEATLARYDLERKYESLEEETQFLRKIHEEEVRELQEQLRQQQVYVHMDYAKPDLTRALREIRTQYEVATSNNOCTEEHYRSKFA													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
sequence	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----													
refprot	DLTDVARSNAELLRQAKHEANDYRRQLQALTCOLESLRGTHESLERQMRQEERHARESASYQEARLAREEGQSLKEENARHLQEYQDLLNVKLRALDTEIATYRKLLEGENRITIPVQTFSNLQIRET													
Consensus	DLTDVARSNAELLRQAKHEANDYRRQLQALTCOLESLRGTHESLERQMRQEERHARESASYQEARLAREEGQSLKEENARHLQEYQDLLNVKLRALDTEIATYRKLLEGENRITIPVQTFSNLQIRET													
	391	400	410	420	430									
sequence	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----													
refprot	SLDTKSYSEGLHKNIVYKTVEMRDGEVYKESKQEHKQVH													
Consensus	SLDTKSYSEGLHKNIVYKTVEMRDGEVYKESKQEHKQVH													

Pas de diff au niveau prot

Flag BirA Gfap DiT48hMix (clone A) : NT en 204 C>T mais
n'engendrant pas de diff au niv prot donc OK

o **FlagBirA Gfap SP clone A**

➤ **B3Fwd SP 862NT**

ATGGAGCGGAGACGTATCACCTCTGCACGCCGCTCCTATGCCTCCTCCGAGACGATGGTCAGGGGCCATGGTCCT
ACCAGACACCTGGGTACCATTCCGCGCCTCTCCCTGTCTCGAATGACGCCTCCACTCCCTGCCAGGGTAGACTTCT
CCCTGGCCGGGGCGCTCAATGCCGGCTTCAAAGAGACTCGGGCCAGCGAGCGCGGAGATGATGGAGCTCA
ATGACCGCTTTGCTAGCTACATCGAGAAGGTCCGCTTCTGGAACAGCAAAACAAGGCGCTGGCAGCTGAGCTG
AACCAGCTTCGAGCCAAGGAGCCCACCAAACCTGGCTGACGTTTACCAGGCAGAACTTCGGGAGCTGCGGCTGC
GTCTGGACCAGCTTACTACCAACAGTGCCCCGCTGGAGGTGGAGAGGGACAATCTCACACAGGACCTCGGCAC
CCTGAGGCAGAAGCTCCAAGATGAAACCAACCTGAGGCTGGAGGCGGAGAACAACCTGGCTGTGTACAGACA
GGAGGCGGATGAAGCCACCTTGGCTCGTGTGGATCTGGAGAGGAAGGTTGAGTCGCTGGAGGAGGAGATCCA
GTTCTTGAGGAAGATCCATGAGGAGGAAGTTCGAGAACTCCAGGAGCAGCTGGCCCAGCAGCAgTCCACGTG
GAGATGGATGTGGCCAAGCCAGACCTCACAGCGGCTCTGAGAGAGATTCGCACTCANTACGAGGCAGTGGCCA
CCAGTAACATGCAAGAAACANAANAGTGGTATCGGTCCAAGTTTGCANACCTCACAGACGTTGCTTCCCGCAAC
GCANANCTGCTCCGNCAGGCCAAGCACGAGGCTAATGACTATCGCCGCCAACTGC

➤ **BGHRRev SP 998NT**

TGAACNAGNNTNGAGCCNNGNANCCCACCAAACCTNGNTGACGTTTNCNGNCAGAACTTCNGGAGCTGCGG
CTGCNTCTGGACCAGCTTACTACCAACAGTGCCCCGCTGGAGGTGGAGAGGGACANTNTCACACAGGACNTCG
GCACCCTGAGGCAGAAGNTCCAAGATGAAACCAACNTGAGGCTGGAGGCGGAGAACAACCTGGCTGTGTACA
GACAGGAGGCGGATGAAGCCACcTTGGCTCGTGTGGATCTGGAGAGGAAGGTTGAGTCGCTGGAGGAGGAGA
TCCAGTTCTTGAGGAAGATCCATGAGGAGGAAGTTCGAGAACTCCAGGAGCAGCTGGCCCAGCAGCAGGTCCA
CGTGGAGATGGATGTGGCCAAGCCAGACCTCACAGCGGCTCTGAGAGAGATTTCGCACTCAGTACGAGGCAGTG
GCCACCAGTAACATGCAAGAAACAGAAGAGTGGTATCGGTCCAAGTTTGCAGACCTCACAGACGTTGCTTCCCG
CAACGCAGAGCTGCTCCGCCAGGCCAAGCACGAGGCTAATGACTATCGCCGCCAACTGCAGGCCTTGACCTGCG
ACCTTGAGTCCTTGCGCGGCACGAACGAGTCCTTGAGAGGCAAATGCGCGAACAGGAGGAGCGCCACGCGC
GGGAGTCGGCGAGTTACCAGGAGGCACTCGCTCGGCTGGAGGAGGAGGGCCAAAGCCTCAAGGAGGAGATG
GCCCCCACCTGCAGGAGTACCAGGATCTACTCAACGTTAAGCTAGCCCTGGACATCGAGATCGCCACCTACAGG
AAATTGCTGGAGGGCGAAGAAAACCGCATCACCATTCTGTACAGACTTTCTCCAACCTCCAGATCCGAGAAACC
AGCCTGGACACCAAATCTGTGTGAGAAGGCCACCTCAAGAGGAACATCGTGGTAAAGACGGTGGAGATGCGGG
ATGGCGAGGTCATTAAGGAGTCGAAGCAGGAGCACAAGGATGTGATGTGA

➤ **Synthèse séquençage SP : 1293NT**

ATGGAGCGGAGACGTATCACCTCTGCACGCCGCTCCTATGCCTCCTCCGAGACGATGGTC	60
AGGGGCCATGGTCCTACCAGACACCTGGGTACCATTCCGCGCCTCTCCCTGTCTCGAATG	120
ACGCCTCCACTCCCTGCCAGGGTAGACTTCTCCCTGGCCGGGGCGCTCAATGCCGGCTTC	180
AAAGAGACTCGGGCCAGCGAGCGCGCGGAGATGATGGAGCTCAATGACCGCTTTGCTAGC	240
TACATCGAGAAGGTCCGCTTCTGGAACAGCAAAACAAGGCGCTGGCAGCTGAGCTGAAC	300
CAGCTTCGAGCCAAGGAGCCCACCAAACCTGGCTGACGTTTACCAGGCAGAACTTCGGGAG	360
CTGCGGCTGCGTCTGGACCAGCTTACTACCAACAGTGCCCCGCTGGAGGTGGAGAGGGAC	420
AATCTCACACAGGACCTCGGCACCTGAGGCAGAAGCTCCAAGATGAAACCAACCTGAGG	480
CTGGAGGCGGAGAACAACCTGGCTGTGTACAGACAGGAGGCGGATGAAGCCACCTTGGCT	540
CGTGTGGATCTGGAGAGGAAGGTTGAGTCGCTGGAGGAGGAGATCCAGTTCTTGAGGAAG	600
ATCCATGAGGAGGAAGTTCGAGAACTCCAGGAGCAGCTGGCCCAGCAGCAgTCCACGTG	660
GAGATGGATGTGGCCAAGCCAGACCTCACAGCGGCTCTGAGAGAGATTTCGCACTCAGTAC	
GAGGCAGTGGCCACCAGTAACATGCAAGAAACAGAAGAGTGGTATCGGTCCAAGTTTGCA	
GACCTCACAGACGTTGCTTCCCGCAACGCAGAGCTGCTCCGCCAGGCCAAGCACGAGGCT	
AATGACTATCGCCGCAACTGCAGGCCTTGACCTGCGACCTTGAGTCCTTGCGCGGCACG	
AACGAGTCCTTGAGAGGCAATGCGCGAACAGGAGGAGCGCCACGCGCGGGAGTCGGCG	
AGTTACCAGGAGGCACTCGCTCGGCTGGAGGAGGAGGGCCAAAGCCTCAAGGAGGAGATG	
GCCCCCACCTGCAGGAGTACCAGGATCTACTCAACGTTAAGCTAGCCCTGGACATCGAG	

MERRRITSARRSYASSETMVRGHGPTRHLGTIPRLSLSRMTPPLPARVDFSLAGALNAGFKETRASERAEMMELN
DRFASYIEKVRFLQEQNKALAAELNQLRAKEPTKLADVYQAELELRLRLDQLTTNSARLEVERDNLTDQLGTLR
QKLQDETNRLEAENNLAVYRQEADATLARVDLERKVESLEEEIQFLRKIHHEEVRELQEQLAQQQVHVEMDVA
KPDLTAAALREIRTYEAVATSNMQEETEYWRSGFADLTVDASRNAELLRLQAKHEANDYRRQLQALTCDLSELRGT
NESLERQMRQEERHARESASYQEALARLEEGQSLKEEMARHLQEQDILLNKALDIEIATYRKLLEGEENRI
TIPVQTFSNLQIRETSLDTKSVSEGHLLKRNIVVKTVEMMRDGEVIKESKQEHKDVM-

➤ **Blast contre banque rat :**

	Description	max Score	total Score	Query Cover	E value	Per. Ident	Accession
	Rattus norvegicus glial fibrillary acidic protein (GFAP) mRNA sequence	2388	2388	100%	0.0	100.00%	L27219.1
	Rattus norvegicus glial fibrillary acidic protein (Gfap) mRNA	2383	2383	100%	0.0	99.92%	NM_017009.2
	Rattus norvegicus Sprague Dawley glial fibrillary acidic protein mRNA complete cds	2366	2366	100%	0.0	99.69%	U03700.1
	Rattus norvegicus glial fibrillary acidic protein beta (Gfap) mRNA partial cds alternatively spliced	1836	1836	76%	0.0	100.00%	EF094476.1
	R.norvegicus partial gfap gene for glial fibrillary acidic protein	843	843	35%	0.0	100.00%	Z48978.1
	Rattus norvegicus glial fibrillary acidic proteins alpha and delta (GFAP) gene alternatively spliced products complete cds	843	2431	100%	0.0	100.00%	AF028784.1
	Rattus norvegicus glial fibrillary acidic protein epsilon (Gfap) mRNA partial cds alternatively spliced	704	704	29%	0.0	99.74%	EF094477.1
	PREDICTED: Rattus norvegicus keratin 7 (Krt7) transcript variant X2 mRNA	89.8	89.8	8%	7e-16	81.90%	XM_003754353.4
	PREDICTED: Rattus norvegicus keratin 7 (Krt7) transcript variant X1 mRNA	89.8	89.8	8%	7e-16	81.90%	XM_017603516.1
	Rattus norvegicus GFAP kappa mRNA partial cds alternatively spliced	82.4	82.4	3%	1e-13	100.00%	DQ979831.1

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

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
sequence	ATGGAGCGGGAGCGTATCACCTCGACGCCGCTCCTATGCCCTCTCGAGGACGATGGTCAGGGGCATGGCTCTACGACAGACCTTGGGTACCATTCGCGGCTCTCCCTGTGTCGAGTAGCGGCTTCAC													
CDS	ATGGAGCGGGAGCGTATCACCTCGACGCCGCTCCTATGCCCTCTCGAGGACGATGGTCAGGGGCATGGCTCTACGACAGACCTTGGGTACCATTCGCGGCTCTCCCTGTGTCGAGTAGCGGCTTCAC													
Consensus	ATGGAGCGGGAGCGTATCACCTCGACGCCGCTCCTATGCCCTCTCGAGGACGATGGTCAGGGGCATGGCTCTACGACAGACCTTGGGTACCATTCGCGGCTCTCCCTGTGTCGAGTAGCGGCTTCAC													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
sequence	TCCCTGCCAGGATAGACTTCTCCCTGGCCGGGGCGCTCAATGCCGGCTTCAAGAGAGCTGGGCGACGAGCGCGCGGAGATGATGGAGCTCAATGACCGCTTTGTAGTACATCGAGAGGTCGCGTT													
CDS	TCCCTGCCAGGATAGACTTCTCCCTGGCCGGGGCGCTCAATGCCGGCTTCAAGAGAGCTGGGCGACGAGCGCGCGGAGATGATGGAGCTCAATGACCGCTTTGTAGTACATCGAGAGGTCGCGTT													
Consensus	TCCCTGCCAGGATAGACTTCTCCCTGGCCGGGGCGCTCAATGCCGGCTTCAAGAGAGCTGGGCGACGAGCGCGCGGAGATGATGGAGCTCAATGACCGCTTTGTAGTACATCGAGAGGTCGCGTT													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
sequence	CCTGGACAGCAAAACAGGCGCTGGCAGCTGAGCTGAAACAGCTTTCGAGCCAGAGGACCCCAACAACTGGCTGAGCTTTTACAGGCGAGACTTCGGAGCTGCGGCTGCGTCTGGACAGCTTACTACC													
CDS	CCTGGACAGCAAAACAGGCGCTGGCAGCTGAGCTGAAACAGCTTTCGAGCCAGAGGACCCCAACAACTGGCTGAGCTTTTACAGGCGAGACTTCGGAGCTGCGGCTGCGTCTGGACAGCTTACTACC													
Consensus	CCTGGACAGCAAAACAGGCGCTGGCAGCTGAGCTGAAACAGCTTTCGAGCCAGAGGACCCCAACAACTGGCTGAGCTTTTACAGGCGAGACTTCGGAGCTGCGGCTGCGTCTGGACAGCTTACTACC													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
sequence	AACAGTGCCTCGGCTGGAGGTGGAGGGGGACATCTCACACAGGACCTCGGCACCTTGAGGCGAGAGTCCAGATGAACACACCTTGAGCTGGAGGCGGGAGACACCTTGGCTGTGTACAGACAGGAG													
CDS	AACAGTGCCTCGGCTGGAGGTGGAGGGGGACATCTCACACAGGACCTCGGCACCTTGAGGCGAGAGTCCAGATGAACACACCTTGAGCTGGAGGCGGGAGACACCTTGGCTGTGTACAGACAGGAG													
Consensus	AACAGTGCCTCGGCTGGAGGTGGAGGGGGACATCTCACACAGGACCTCGGCACCTTGAGGCGAGAGTCCAGATGAACACACCTTGAGCTGGAGGCGGGAGACACCTTGGCTGTGTACAGACAGGAG													
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
sequence	CGGATGAGGCGACCTTGGCTCGTGTGGATTCGGAGAGGAGGTTGAGTCTGCGTGGAGGAGGAGATCCAGTTCTTGAGGAAGATCCATGAGGAGGAGTTCGAGACTCCAGAGGACAGCTGGCCAGCAGCA													
CDS	CGGATGAGGCGACCTTGGCTCGTGTGGATTCGGAGAGGAGGTTGAGTCTGCGTGGAGGAGGAGATCCAGTTCTTGAGGAAGATCCATGAGGAGGAGTTCGAGACTCCAGAGGACAGCTGGCCAGCAGCA													
Consensus	CGGATGAGGCGACCTTGGCTCGTGTGGATTCGGAGAGGAGGTTGAGTCTGCGTGGAGGAGGAGATCCAGTTCTTGAGGAAGATCCATGAGGAGGAGTTCGAGACTCCAGAGGACAGCTGGCCAGCAGCA													
	651	660	670	680	690	700	710	720	730	740	750	760	770	780
sequence	GGTCCAGCTGGAGATGGATGTGGCCAGGCGAGCTCACAGCGGCTCTGAGAGAGATTCCGACTCAGTACGAGGCGAGTGGCCACCGTAGATCGAGAAACAGAGAGTGGATATCGCTCCAGTTTGCA													
CDS	GGTCCAGCTGGAGATGGATGTGGCCAGGCGAGCTCACAGCGGCTCTGAGAGAGATTCCGACTCAGTACGAGGCGAGTGGCCACCGTAGATCGAGAAACAGAGAGTGGATATCGCTCCAGTTTGCA													
Consensus	GGTCCAGCTGGAGATGGATGTGGCCAGGCGAGCTCACAGCGGCTCTGAGAGAGATTCCGACTCAGTACGAGGCGAGTGGCCACCGTAGATCGAGAAACAGAGAGTGGATATCGCTCCAGTTTGCA													
	781	790	800	810	820	830	840	850	860	870	880	890	900	910
sequence	GACCTCACAGAGCTTGTCTTCCGACAGCAGAGCTGCTCCGCGAGGCGAGGCGAGGCTATGACTATCGCCGCACCTGAGCGGCTTGACCTGCGACCTTGAGTCTTTCGCGGCGACAGCAGGCTCT													
CDS	GACCTCACAGAGCTTGTCTTCCGACAGCAGAGCTGCTCCGCGAGGCGAGGCGAGGCTATGACTATCGCCGCACCTGAGCGGCTTGACCTGCGACCTTGAGTCTTTCGCGGCGACAGCAGGCTCT													
Consensus	GACCTCACAGAGCTTGTCTTCCGACAGCAGAGCTGCTCCGCGAGGCGAGGCGAGGCTATGACTATCGCCGCACCTGAGCGGCTTGACCTGCGACCTTGAGTCTTTCGCGGCGACAGCAGGCTCT													
	911	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040
sequence	TGGAGGAGCAATGCGCGAACAGGAGAGGCGCCAGCGCGGAGTCCGCGAGTTACCGAGAGGACACTTCGCTCGGCTGGAGGAGGAGGCGCAAGCTTCAGAGGAGAGATGGCCCGCACCTTCGAGGAGTA													
CDS	TGGAGGAGCAATGCGCGAACAGGAGAGGCGCCAGCGCGGAGTCCGCGAGTTACCGAGAGGACACTTCGCTCGGCTGGAGGAGGAGGCGCAAGCTTCAGAGGAGAGATGGCCCGCACCTTCGAGGAGTA													
Consensus	TGGAGGAGCAATGCGCGAACAGGAGAGGCGCCAGCGCGGAGTCCGCGAGTTACCGAGGAGGACACTTCGCTCGGCTGGAGGAGGAGGCGCAAGCTTCAGAGGAGAGATGGCCCGCACCTTCGAGGAGTA													
	1041	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170
sequence	CCAGGATCTACTCAAGCTTTAGCTAGCCCTGGACATCGAGATCGGCACCTACAGGAATTTGCTGGAGGCGAGAGAAACCGATCACCATTCTGTATACAGCTTTTCCARACCTCCAGATCCGAGAAACC													
CDS	CCAGGATCTACTCAAGCTTTAGCTAGCCCTGGACATCGAGATCGGCACCTACAGGAATTTGCTGGAGGCGAGAGAAACCGATCACCATTCTGTATACAGCTTTTCCARACCTCCAGATCCGAGAAACC													
Consensus	CCAGGATCTACTCAAGCTTTAGCTAGCCCTGGACATCGAGATCGGCACCTACAGGAATTTGCTGGAGGCGAGAGAAACCGATCACCATTCTGTATACAGCTTTTCCARACCTCCAGATCCGAGAAACC													
	1171	1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
sequence	AGCCTGGACACCAACTCTGTGTCAGAGGGCCACCTCAGAGGGAGACATCGTGGTAAAGACGGTGGAGATGCGGGATGGCGAGGCTATTAGGAGATCGAGCAGGAGACACAGGATGTGATGTGA													
CDS	AGCCTGGACACCAACTCTGTGTCAGAGGGCCACCTCAGAGGGAGACATCGTGGTAAAGACGGTGGAGATGCGGGATGGCGAGGCTATTAGGAGATCGAGCAGGAGACACAGGATGTGATGTGA													
Consensus	AGCCTGGACACCAACTCTGTGTCAGAGGGCCACCTCAGAGGGAGACATCGTGGTAAAGACGGTGGAGATGCGGGATGGCGAGGCTATTAGGAGATCGAGCAGGAGACACAGGATGTGATGTGA													

Comme pour DiT0 et DiT24hLPS, DiT48hMis C>T en 204

		➤ Différence au niveau PROT :																																																										
		1	10	20	30	40	50	60	70	80	90	100	110	120	130																																													
sequencage		MERRRITSARRSYASSETHVRGHGPTRH LGTIPRLSLRHTPPLPARVDFSLAGALNAGFKETRASERAEHME LNDRFASYIEKVRFLEQQNKALAE LNLQRAKEPTKLADVYQAE LRELRLDLQLTT																																																										
refprot		MERRRITSARRSYASSETHVRGHGPTRH LGTIPRLSLRHTPPLPARVDFSLAGALNAGFKETRASERAEHME LNDRFASYIEKVRFLEQQNKALAE LNLQRAKEPTKLADVYQAE LRELRLDLQLTT																																																										
Consensus		MERRRITSARRSYASSETHVRGHGPTRH LGTIPRLSLRHTPPLPARVDFSLAGALNAGFKETRASERAEHME LNDRFASYIEKVRFLEQQNKALAE LNLQRAKEPTKLADVYQAE LRELRLDLQLTT																																																										
		131	140	150	160	170	180	190	200	210	220	230	240	250	260																																													
sequencage		NSARLEVERDNL TQDLGTLRQKLQDETNLRLAEENNLAVYRQEADEATLARVDLERKVESLEEEIQFLRKIH EEEYRELQEQLAQQYHVENDVAKPD LTAALREIRTQYEA VATSNHQETEEHYSKFA																																																										
refprot		NSARLEVERDNL TQDLGTLRQKLQDETNLRLAEENNLAVYRQEADEATLARVDLERKVESLEEEIQFLRKIH EEEYRELQEQLAQQYHVENDVAKPD LTAALREIRTQYEA VATSNHQETEEHYSKFA																																																										
Consensus		NSARLEVERDNL TQDLGTLRQKLQDETNLRLAEENNLAVYRQEADEATLARVDLERKVESLEEEIQFLRKIH EEEYRELQEQLAQQYHVENDVAKPD LTAALREIRTQYEA VATSNHQETEEHYSKFA																																																										
		261	270	280	290	300	310	320	330	340	350	360	370	380	390																																													
sequencage		DLTDVASRNAELLRQAKHEANDYRQLQALTCOLESLRG TNESLERQMRQEERHARESASYQEALARLEEEGQSLKEEMARHLQEYQDLLNVK LALDIEIATYRK LLEGEENRITIPVQTFSNLQIRET																																																										
refprot		DLTDVASRNAELLRQAKHEANDYRQLQALTCOLESLRG TNESLERQMRQEERHARESASYQEALARLEEEGQSLKEEMARHLQEYQDLLNVK LALDIEIATYRK LLEGEENRITIPVQTFSNLQIRET																																																										
Consensus		DLTDVASRNAELLRQAKHEANDYRQLQALTCOLESLRG TNESLERQMRQEERHARESASYQEALARLEEEGQSLKEEMARHLQEYQDLLNVK LALDIEIATYRK LLEGEENRITIPVQTFSNLQIRET																																																										
		391	400	410	420	430																																																						
sequencage		SLDTKSYSEGH LKRNIYVKTVEHRDGEYIKESKQEHKQVM																																																										
refprot		SLDTKSYSEGH LKRNIYVKTVEHRDGEYIKESKQEHKQVM																																																										
Consensus		SLDTKSYSEGH LKRNIYVKTVEHRDGEYIKESKQEHKQVM																																																										

Pas de diff au niveau prot

Flag BirA Gfap SP (clone A) : NT en 204 C>T mais
n'engendrant pas de diff au niv prot donc OK

o **FlagBirA Gfap CTX clone A**

➤ **B3Fwd CTX 850NT**

ATGGAGCGGAGACGTATCACCTCTGCACGCCGCTCCTATGCCTCCTCCGAGACGATGGTCAGGGGCCATGGTCCT
ACCAGACACCTGGGTACCATTCCGCGCCTCTCCCTGTCTCGAATGACGCCTCCACTCCCTGCCAGGGTAGACTTCT
CCCTGGCCGGGGCGCTCAATGCCGGCTTCAAAGAGACTCGGGCCAGCGAGCGCGGAGATGATGGAGCTCA
ATGACCGCTTTGCTAGCTACATCGAGAAGGTCCGCTTCTGGAACAGCAAAACAAGGCGCTGGCAGCTGAGCTG
AACCAGCTTCGAGCCAAGGAGCCCACCAAACCTGGCTGACGTTTACCAGGCAGAACTTCGGGAGCTGCGGCTGC
GTCTGGACCAGCTTACTACCAACAGTGCCCCGGCTGGAGGTGGAGAGGGACAATCTCACACAGGACCTCGGCAC
CCTGAGGCAGAAAGCTCCAAGATGAAACCAACCTGAGGCTGGAGGCGGAGAACAACCTGGCTGTGTACAGACA
GGAGGCGGATGAAGCCACCTTGGCTCGTGTGGATCTGGAGAGGAAGGTTGAGTCGCTGGAgGAGGAGATCCA
GTTCTTGAGGAAGATCCATGAgGAGGAAGTTCGAGAACTCCAGGAGCAGCTGGcCCAGCAGCAgGTCCACGTG
GAGATGGATGTGGCCAAGCCAGACCTCACAGCGGCTCTGANAGAGANTCGCACTCANTACGAGGCAGTGGCC
ACCAGTAACATGCAAGAAACAGAAAGTGGNATCGGTCCNAGTTTGCANANCTCACAGACGTTGCTTCCCGCA
ACGCANANCTGCTCCGCCAGGCCAAGCACGAGGCTANNGACTATC

➤ **BGHRev CTX 948NT**

GNCAGNACTTCNGGAGCTGCGGCTGCNTCTGGACCAGCTTACTACCAACAGTGCCCGGCTGGAGGTGGAGAG
GGACANTCTCACACAGGACCTNGGCACCTGAGGCAGAAGNTcCAAGATGAAACCAactGAGGCTGGAGGCGG
AGAACAACCTGGCTGTGTACAGACAGGAGGCGGATGAAGCCACCTTGGCTCGTGTGGATCTGGAGAGGAAGGT
TGAGTCGCTGGAGGAGGAGATCCAGTTCTTGAGGAAGATCCATGAGGAGGAAGTTTCGAGAACTCCAGGAGCA
GCTGGCCCAGCAGCAGGTCCACGTGGAGATGGATGTGGCCAAGCCAGACCTCACAGCGGCTCTGAGAGAGATT
CGCACTCAGTACGAGGCAGTGGCCACCAGTAACATGCAAGAAACAGAAGAGTGGTATCGGTCCAAGTTTGCAG
ACCTCACAGACGTTGCTTCCCGCAACGCAGAGCTGCTCCGCCAGGCCAAGCACGAGGCTAATGACTATCGCCGC
CAACTGCAGGCCTTGACCTGCGACCTTGAGTCCTTGC GCGGCACGAACGAGTCCTTGGAGAGGGCAAATGCGCG
AACAGGAGGAGCGCCACGCGCGGGAGTCGGCGAGTTACCAGGAGGCACTCGCTCGGCTGGAGGAGGAGGGC
CAAAGCCTCAAGGAGGAGATGGCCCGCACCTGCAGGAGTACCAGGATCTACTCAACGTTAAGCTAGCCCTGGA
CATCGAGATCGCCACCTACAGGAAATTGCTGGAGGGCGAAGAAAACCGCATCACCATTCTGTACAGACTTTCTC
CAACCTCCAGATCCGAGAAACCAGCCTGGACACCAAATCTGTGTCAGAAGGCCACCTCAAGAGGAACATCGTGG
TAAAGACGGTGGAGATGCGGGATGGCGAGGTCATTAAGGAGTCGAAGCAGGAGCACAAGGATGTGATGTGA

➤ **Synthèse séquençage CTX : 1293NT**

ATGGAGCGGAGACGTATCACCTCTGCACGCCGCTCCTATGCCTCCTCCGAGACGATGGTC	60
AGGGGCCATGGTCCTACCAGACACCTGGGTACCATTCCGCGCCTCTCCCTGTCTCGAATG	120
ACGCCTCCACTCCCTGCCAGGGTAGACTTCTCCCTGGCCGGGGCGCTCAATGCCGGCTTC	180
AAAGAGACTCGGGCCAGCGAGCGCGCGGAGATGATGGAGCTCAATGACCGCTTTGCTAGC	240
TACATCGAGAAGGTCCGCTTCTTGGAAACAGCAAAACAAGGCGCTGGCAGCTGAGCTGAAC	300
CAGCTTCGAGCCAAGGAGCCACCAAACCTGGCTGACGTTTACCAGGCAGAACTTCGGGAG	360
CTGCGGCTGCGTCTGGACCAGCTTACTACCAACAGTGCCCGGCTGGAGGTGGAGAGGGAC	420
AATCTCACACAGGACCTCGGCACCTGAGGCAGAAGCTCCAAGATGAAACCAACCTGAGG	480
CTGGAGGCGGAGAAACAACCTGGCTGTGTACAGACAGGAGGCGGATGAAGCCACCTTGGCT	540
CGTGTGGATCTGGAGAGGAAGGTTGAGTCGCTGGAgGAGGAGATCCAGTTCTTGAGGAAG	600
ATCCATGAGGAGGAAGTTCGAGAACTCCAGGAGCAGCTGGCCAGCAGCAGGTCCACGTG	
GAGATGGATGTGGCCAAGCCAGACCTCACAGCGGCTCTGAGAGAGATTGCACTCAGTAC	
GAGGCAGTGGCCACCAGTAACATGCAAGAAACAGAAGAGTGGTATCGGTCCAAGTTTGA	
GACCTCACAGACGTTGCTTCCCGCAACGCAGAGCTGCTCCGCCAGGCCAAGCACGAGGCT	
AATGACTATCGCCGCAACTGCAGGCCTTGACCTGCGACCTTGAGTCCTTGC GCGGCACG	
AACGAGTCCTTGGAGAGGCAAATGCGCGAACAGGAGGAGCGCCACGCGCGGGAGTCGGCG	
AGTTACCAGGAGGCACTCGCTCGGCTGGAGGAGGAGGGCCAAAGCCTCAAGGAGGAGATG	
GCCCGCCACCTGCAGGAGTACCAGGATCTACTCAACGTTAAGCTAGCCCTGGACATCGAG	
ATCGCCACCTACAGGAAATTGCTGGAGGGCGAAGAAAACCGCATCACCATTCTGTACAG	
ACTTTCTCCAACCTCCAGATCCGAGAAACCAGCCTGGACACCAAATCTGTGTCAGAAGGC	
CACCTCAAGAGGAACATCGTGGTAAAGACGGTGGAGATGCGGGATGGCGAGGTCATTAAG	

GAGTCGAAGCAGGAGCACAAAGGATGTGATGTGA

MERRRITSARRSYASSETMVRGHGPTRHLGTIPRLSLSRMTPPLPARVDFSLAGALNAGFKETRASERAEMMELND
RFASYIEKVRFLEQQNKALAAELNQLRAKEPTKLADVYQAE LRELRLRLDQLTTNSARLEVERDNLTDGLTLRQKLQ
DETNLRLAEENNLAVYRQEAD EATLARVDLERKVESLEEEIQFLRKIH EEEVRELQEQLAQQQVHVEMDVAKPDLTA
ALREIRTQYEAVATSNMQETE EWYRSKFADLTDVASRNAELLRQAKHEANDYRRQLQALTCDLES LRGTNESLERQM
REQEERHARESASYQEALARLEEEGQSLKEEMARHLQEYQDLLNVKLALDIEIATYRKLLGEENRITIPVQTF SNLQIR
ETSLDTKSVSEGH LKRNIVKTVEMRDGEVIKESKQEHKDVM-

➤ Blast contre banque rat :

	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
✓	Rattus norvegicus glial fibrillary acidic protein (GFAP) mRNA sequence	2388	2388	100%	0.0	100.00%	L27219.1
✓	Rattus norvegicus glial fibrillary acidic protein (Gfap) mRNA	2383	2383	100%	0.0	99.92%	NM_017009.2
✓	Rattus norvegicus Sprague Dawley glial fibrillary acidic protein mRNA, complete cds	2366	2366	100%	0.0	99.69%	U03700.1
✓	Rattus norvegicus glial fibrillary acidic protein beta (Gfap) mRNA, partial cds, alternatively spliced	1836	1836	76%	0.0	100.00%	EF094476.1
✓	R norvegicus partial gfap gene for glial fibrillary acidic protein	843	843	35%	0.0	100.00%	Z48978.1
✓	Rattus norvegicus glial fibrillary acidic proteins alpha and delta (GFAP) gene, alternatively spliced products, complete cds	843	2431	100%	0.0	100.00%	AF028784.1
✓	Rattus norvegicus glial fibrillary acidic protein epsilon (Gfap) mRNA, partial cds, alternatively spliced	704	704	29%	0.0	99.74%	EF094477.1
✓	PREDICTED: Rattus norvegicus keratin 7 (Krt7), transcript variant X2, mRNA	89.8	89.8	8%	7e-16	81.90%	XM_003754353.4
✓	PREDICTED: Rattus norvegicus keratin 7 (Krt7), transcript variant X1, mRNA	89.8	89.8	8%	7e-16	81.90%	XM_017603516.1
✓	Rattus norvegicus GFAP kappa mRNA, partial cds, alternatively spliced	82.4	82.4	3%	1e-13	100.00%	DQ979831.1

➤ Différence Séquencage/CDS au niveau NT :

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
sequence	ATGGAGCGGAGACGTATCACTCTGCAACGCCGCTCCTATGCTCTCCAGAGACGATGGTCAGGGGCCATGGTCTACCAAGACACCTGGGTACCATTCGCGCCCTCTCCCTGTCTGAATGACGCTCCAC													
CDS	ATGGAGCGGAGACGTATCACTCTGCAACGCCGCTCCTATGCTCTCCAGAGACGATGGTCAGGGGCCATGGTCTACCAAGACACCTGGGTACCATTCGCGCCCTCTCCCTGTCTGAATGACGCTCCAC													
Consensus	ATGGAGCGGAGACGTATCACTCTGCAACGCCGCTCCTATGCTCTCCAGAGACGATGGTCAGGGGCCATGGTCTACCAAGACACCTGGGTACCATTCGCGCCCTCTCCCTGTCTGAATGACGCTCCAC													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
sequence	TCCCTGCCAGGGTAGACTTCTCCCTGGCCGGGGCGCTCAATGCGGGCTCAAGAGAGACTCGGGCAGCGAGCGCGGAGATGATGGAGCTCAATGACCGCTTGGTACGTACATCGAGAGGTCGGCTT													
CDS	TCCCTGCCAGGGTAGACTTCTCCCTGGCCGGGGCGCTCAATGCGGGCTCAAGAGAGACTCGGGCAGCGAGCGTGGGAGATGATGGAGCTCAATGACCGCTTGGTACGTACATCGAGAGGTCGGCTT													
Consensus	TCCCTGCCAGGGTAGACTTCTCCCTGGCCGGGGCGCTCAATGCGGGCTCAAGAGAGACTCGGGCAGCGAGCGCGGAGATGATGGAGCTCAATGACCGCTTGGTACGTACATCGAGAGGTCGGCTT													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
sequence	CTTGGACAGCAAAACAGGCGCTGGCAGCTGAGCTGAACAGCTTCGAGCCAGGAGGCCACCAACCTGGCTGACGTTTACCAGGCAGAACCTCGGGAGCTGCGGCTGCGCTGGACAGCTTACTACC													
CDS	CTTGGACAGCAAAACAGGCGCTGGCAGCTGAGCTGAACAGCTTCGAGCCAGGAGGCCACCAACCTGGCTGACGTTTACCAGGCAGAACCTCGGGAGCTGCGGCTGCGCTGGACAGCTTACTACC													
Consensus	ARCACTGCCCGGTGGAGGTGGAGAGGGACARTCTCACACAGGACCTCGGCACCTTGAGGCGAGAGCTCCAGATGAACACACCTGAGGCTGGAGGCGGAGAGACACCTGGCTGTGTACAGACAGGAGG													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
sequence	ARCACTGCCCGGTGGAGGTGGAGAGGGACARTCTCACACAGGACCTCGGCACCTTGAGGCGAGAGCTCCAGATGAACACACCTGAGGCTGGAGGCGGAGAGACACCTGGCTGTGTACAGACAGGAGG													
CDS	ARCACTGCCCGGTGGAGGTGGAGAGGGACARTCTCACACAGGACCTCGGCACCTTGAGGCGAGAGCTCCAGATGAACACACCTGAGGCTGGAGGCGGAGAGACACCTGGCTGTGTACAGACAGGAGG													
Consensus	ARCACTGCCCGGTGGAGGTGGAGAGGGACARTCTCACACAGGACCTCGGCACCTTGAGGCGAGAGCTCCAGATGAACACACCTGAGGCTGGAGGCGGAGAGACACCTGGCTGTGTACAGACAGGAGG													
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
sequence	CGGATGAAGCCACCTTGGCTCGTGTTGGATCTGGAGAGGAGGTTGAGTCGCTGGAGAGGAGATCCAGTTCTTGAGGAGATCCATGAGGAGGAGTTGAGAACCTCAGGAGACGTGGCCAGCAGCA													
CDS	CGGATGAAGCCACCTTGGCTCGTGTTGGATCTGGAGAGGAGGTTGAGTCGCTGGAGAGGAGATCCAGTTCTTGAGGAGATCCATGAGGAGGAGTTGAGAACCTCAGGAGACGTGGCCAGCAGCA													
Consensus	CGGATGAAGCCACCTTGGCTCGTGTTGGATCTGGAGAGGAGGTTGAGTCGCTGGAGAGGAGATCCAGTTCTTGAGGAGATCCATGAGGAGGAGTTGAGAACCTCAGGAGACGTGGCCAGCAGCA													
	651	660	670	680	690	700	710	720	730	740	750	760	770	780
sequence	GGTCCACGTGGAGATGGATGTGGCCAGCCAGACCTCACACAGGCTCTGAGAGAGATTGCGACTCAGTACGAGGACGTGGCCACCACTAACATGCAAGAAACAGAGAGTGGTATCGGTCCAGTTTGA													
CDS	GGTCCACGTGGAGATGGATGTGGCCAGCCAGACCTCACACAGGCTCTGAGAGAGATTGCGACTCAGTACGAGGACGTGGCCACCACTAACATGCAAGAAACAGAGAGTGGTATCGGTCCAGTTTGA													
Consensus	GGTCCACGTGGAGATGGATGTGGCCAGCCAGACCTCACACAGGCTCTGAGAGAGATTGCGACTCAGTACGAGGACGTGGCCACCACTAACATGCAAGAAACAGAGAGTGGTATCGGTCCAGTTTGA													
	781	790	800	810	820	830	840	850	860	870	880	890	900	910
sequence	GACCTCACAGACCTTGGCTCCCGCAACGACAGACTGCTCCGCGAGGCCAGCACAGGCTTATGACTATCGCCGCCACCTGACGGCTTGACCTGCGACCTTGAGTCTTGGCGGACAGACAGGCTCT													
CDS	GACCTCACAGACCTTGGCTCCCGCAACGACAGACTGCTCCGCGAGGCCAGCACAGGCTTATGACTATCGCCGCCACCTGACGGCTTGACCTGCGACCTTGAGTCTTGGCGGACAGACAGGCTCT													
Consensus	GACCTCACAGACCTTGGCTCCCGCAACGACAGACTGCTCCGCGAGGCCAGCACAGGCTTATGACTATCGCCGCCACCTGACGGCTTGACCTGCGACCTTGAGTCTTGGCGGACAGACAGGCTCT													
	911	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040
sequence	TGGAGAGGCAATGCGCGAACAGGAGGAGCGCCACGCGCGGGAGTCGGCGAGTTACAGGAGGCGACTCGCTCGGCTGGAGGAGGAGGGCCAAAGCCTCAGGAGGAGATGGCCCGCACCTGCAGAGTA													
CDS	TGGAGAGGCAATGCGCGAACAGGAGGAGCGCCACGCGCGGGAGTCGGCGAGTTACAGGAGGCGACTCGCTCGGCTGGAGGAGGAGGGCCAAAGCCTCAGGAGGAGATGGCCCGCACCTGCAGAGTA													
Consensus	TGGAGAGGCAATGCGCGAACAGGAGGAGCGCCACGCGCGGGAGTCGGCGAGTTACAGGAGGCGACTCGCTCGGCTGGAGGAGGAGGGCCAAAGCCTCAGGAGGAGATGGCCCGCACCTGCAGAGTA													
	1041	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170
sequence	CCAGGATCTACTCAGCGTTAGCTAGCCCTGGACATCGAGATCGCCACCTACAGGAARATGCTGGAGGGCGAGAGAAACCGCATCACCATTCTGTACAGACTTTCTCCACCTCCAGATCCGAGAAAC													
CDS	CCAGGATCTACTCAGCGTTAGCTAGCCCTGGACATCGAGATCGCCACCTACAGGAARATGCTGGAGGGCGAGAGAAACCGCATCACCATTCTGTACAGACTTTCTCCACCTCCAGATCCGAGAAAC													
Consensus	CCAGGATCTACTCAGCGTTAGCTAGCCCTGGACATCGAGATCGCCACCTACAGGAARATGCTGGAGGGCGAGAGAAACCGCATCACCATTCTGTACAGACTTTCTCCACCTCCAGATCCGAGAAAC													
	1171	1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	293
sequence	AGCCTGGACACCAATCTGTGTACAGAGGGCCACTCAGAGGAGACATCGTGGTAAGAGCGGTGGAGATGCGGGATGGCGAGGTCATTAGGAGTGCAGAGCAGGAGCAGAGGATGTGATGTGA													
CDS	AGCCTGGACACCAATCTGTGTACAGAGGGCCACTCAGAGGAGACATCGTGGTAAGAGCGGTGGAGATGCGGGATGGCGAGGTCATTAGGAGTGCAGAGCAGGAGCAGAGGATGTGATGTGA													
Consensus	AGCCTGGACACCAATCTGTGTACAGAGGGCCACTCAGAGGAGACATCGTGGTAAGAGCGGTGGAGATGCGGGATGGCGAGGTCATTAGGAGTGCAGAGCAGGAGCAGAGGATGTGATGTGA													

Comme pour DiT0 et DiT24hLPS, DiT48hMix, SP C>T en 204

➤ Différence au niveau PROT :

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
sequence	MERRITSARKSYRSETHYRGHPTRHLGTIPRLSLRMTPLPARVDFSLAGALNAGFKETRASERAEMELNDRFASYIEKVFLEQQNKALAEHLNQLRAKEPTKLADYVQRELRELRLDQLTT													
refprot	MERRITSARKSYRSETHYRGHPTRHLGTIPRLSLRMTPLPARVDFSLAGALNAGFKETRASERAEMELNDRFASYIEKVFLEQQNKALAEHLNQLRAKEPTKLADYVQRELRELRLDQLTT													
Consensus	MERRITSARKSYRSETHYRGHPTRHLGTIPRLSLRMTPLPARVDFSLAGALNAGFKETRASERAEMELNDRFASYIEKVFLEQQNKALAEHLNQLRAKEPTKLADYVQRELRELRLDQLTT													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
sequence	NSARLEYERDNLTDQLGTLRQKLQDETNLRLAEENNLAYYRQEDERTLARVDLERKVESLEEEIQFLRKIHIEEYVRELQELAQQVHVENDVAKPOLTAHLREIRTQYERAVTSNMQETEEHYRSKFA													
refprot	NSARLEYERDNLTDQLGTLRQKLQDETNLRLAEENNLAYYRQEDERTLARVDLERKVESLEEEIQFLRKIHIEEYVRELQELAQQVHVENDVAKPOLTAHLREIRTQYERAVTSNMQETEEHYRSKFA													
Consensus	NSARLEYERDNLTDQLGTLRQKLQDETNLRLAEENNLAYYRQEDERTLARVDLERKVESLEEEIQFLRKIHIEEYVRELQELAQQVHVENDVAKPOLTAHLREIRTQYERAVTSNMQETEEHYRSKFA													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
sequence	DLTDVSRNAELLRQAKIERANDYRRLQALTCOLESLRGTMESLERQMRDEERHARESASYQELARLEEGGSLKEEMARHLQEYQDLLNWKALDIEATYRKLLGEENRITIPYQTFSNLQIRET													
refprot	DLTDVSRNAELLRQAKIERANDYRRLQALTCOLESLRGTMESLERQMRDEERHARESASYQELARLEEGGSLKEEMARHLQEYQDLLNWKALDIEATYRKLLGEENRITIPYQTFSNLQIRET													
Consensus	DLTDVSRNAELLRQAKIERANDYRRLQALTCOLESLRGTMESLERQMRDEERHARESASYQELARLEEGGSLKEEMARHLQEYQDLLNWKALDIEATYRKLLGEENRITIPYQTFSNLQIRET													
	391	400	410	420	430									
sequence	SLDTKSYSEGHLLKRNIVVKTVEHMDGEVIKESKQEHKQVM													
refprot	SLDTKSYSEGHLLKRNIVVKTVEHMDGEVIKESKQEHKQVM													
Consensus	SLDTKSYSEGHLLKRNIVVKTVEHMDGEVIKESKQEHKQVM													

Pas de diff au niveau prot

Flag BirA Gfp CTX (clone A) : NT en 204 C>T mais
n'engendrant pas de diff au niv prot donc OK

- Conclusion séquencages

DiT0, T24hLPS, 48hMix, SP et CTX ont toutes NT en 204 C>T (forme décrite) mais n'engendrant pas de diff au niv prot avec ref prot donc OK