

3)Artemis Dclre1b

Rattus norvegicus DNA cross-link repair 1B (Dclre1b), mRNA

=SNM1 homolog B; DNA cross-link repair 1B protein

- **Référence NCBI :** BC098939
- **Taille :930 NT**
- **Séquence NT :**

```
atgaacggg gtcgtaatcc cccaaacacc catcgctgtg
 241 gattttttgga gcctgcgcgcg tgctgggtacc gcgcggctct tcttcttatc ccacatgcac
 301 tgtgaccaca cgggtgggcct gtctagcaact tgggcacggc ccctctactg ctctcccatc
 361 actgcccacc tcttgcatcg tcgcctgcag gtgtctaagc agtggatccg agctctggag
 421 attggtgaga gccatgtatt acttctagat gaaattggac aagaaaccat gactgtaacc
 481 ctcatagatg ccaatcactg tcttggttct gtcatgtttc tctttgaagg atactttgga
 541 acaattctct acacaggtga ttttcgatat acaccgtcca tgctgaagga gctgctctg
 601 aactagggga aacagattca tactttatat ctagacaaca ccaattgcaa ccagccctt
 661 gttcttcctt cccgacagga agctactcaa cagattatcc agctaataccg acagttcccc
 721 caacacaaca taaagattgg cctctatagt ctaggaaaag aatcactgct ggagcagcta
 781 gcccttgagt ttcagacctg ggtggtattg agtcctcaac gcctggagtt ggtacagctg
 841 ctgggcctgg cagacgtggt cacagtggag gaagaagctg ggcgaatcca cgctgtggac
 901 cacatggaaa tctgccattc ggccatgctt cagtggaaacc agaccacccc caccattgct
 961 attttcccca caagccggaa aatacgaagc cctcacccca gcactacag catcccttac
1021 tctgaccatt catcctactc tgagcttcga gcatttggtg cagctctgag gccttgccag
1081 gtggtgcca tagtccgtga acagccttgt ggagagtttt ttcaggata g
```

- **Protéine AAH98939**

```
MNGVVIPQTPIAVDFWSLRRAGTARLFFLSHMHCDHTVGLSSTW
ARPLYCSPITAHLLHRRQLQVSKQWIRALEIGESHVLLLDEIGQETMTVTLLIDANHCPG
SVMFLFEGYFGTILYTGDFRYTPSMLKEPALTLGKQIHTLYLDNTNCNPALVLPSRQE
ATQQIIQLIRQFPQHNIKIGLYSLGKESLLEQLALEFQTWVVLSPQRLELVQLLGLAD
VFTVEEEAGRIHAVDHMEICHSA MLQWNQTHPTIAIFPTSRKIRSPHPSIYSIPYSDH
SSYSELRAFVAALRPCQVVPVIREQPCGEFFSG
```

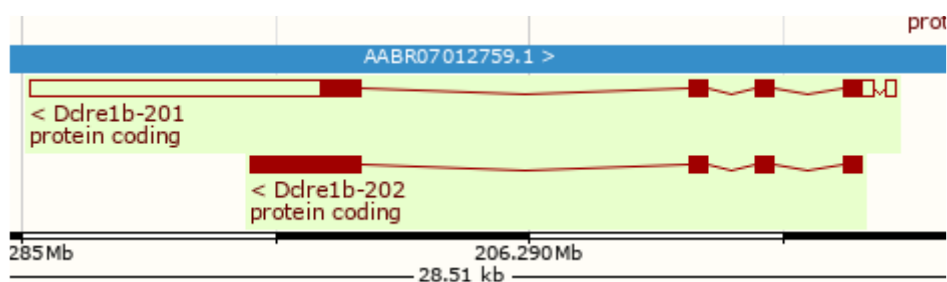
- **Amorces synthétisées :**

Dclre1b_AscI_Fwd

tataGGCGGCCa atgaacggg gtcgtaatcc ccc

Dclre1b_NotI_Rev

ttaaGCGCCGCa ctatcctgaaaaaactctccac

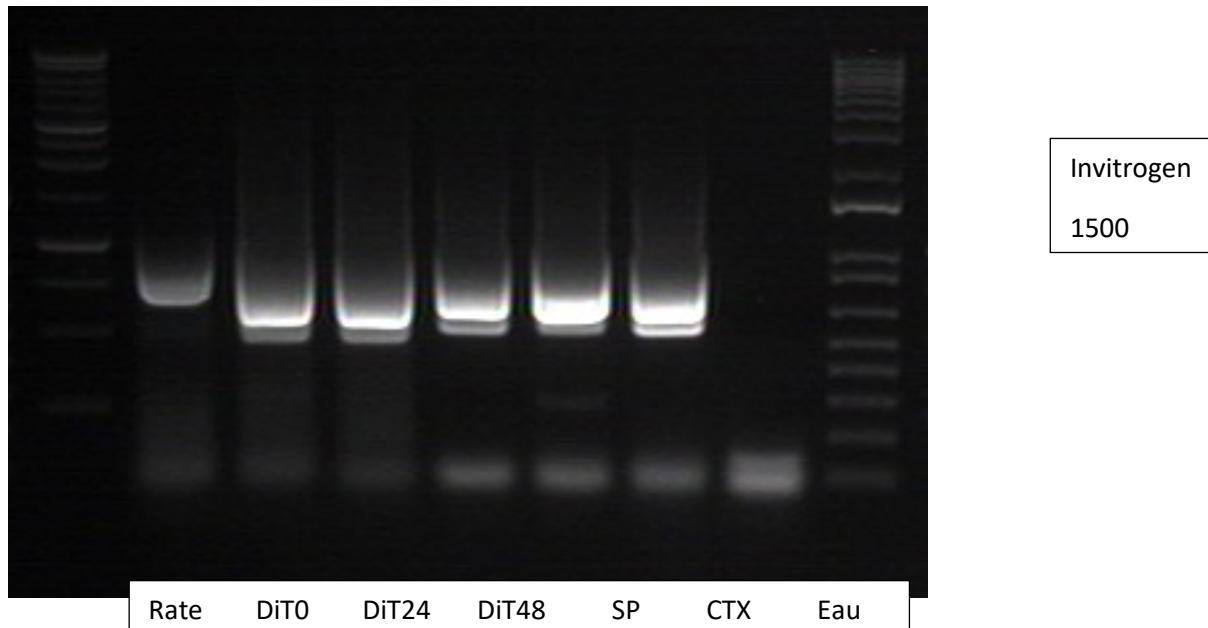


NM_001025687, protéine 5' exonuclease Apollo : [NP_001020858.2](#) : 1626NT contre 930NT, protéine 541aa contre 309aa : le début de la séquence est la même . La mutation en 241 C>T présente dans tous les clones y est retrouvée

[illegible]

- **Expériences :**

- PCR 20/07 : sur **les 7 conditions** cycle Q5-TM 60°C-Enhancer 0- 2min 30 d'élongation



- 08/09 : extraction sur gel et purification
- 14/09 : digestion, dosage
- 15/09 ligation dans FB
- Pause, vecteur refait
- 14/10 miniprep Dclre1 DiT0 ok , le reste 0
- 16/10 ligation
- 20/10 piquage colonies
- Miniprep le 21/10 : rien ne marche même avec nouveau vecteur
- En parallele le 19/10 : redigestion des PCR (au cas où pb de digestion des inserts aussi), et ligation
- 21/10 transformation insert redigérés + vecteur refait et redigéré
- Miniprep le 23/10 : FlagBirA Dclre1b rate, DiT24h, DiT48h , SP et CTX OK : à séquencer
- 28/10 : envoi au séquençage

Beaucoup de formes tronquées bizarres

- 24/11 : purification de PCR digérées sur gel : il y a effectivement des bandes : à différentes taille : nouvelle extraction et purification

o FlagBirA Dclre1b rate clone B : NOUVEAUX CLONES

➤ B3Fwd rate 916NT

ATGAACGGGGTCGTAATCCCCCAAACACCCATCGCTGTGGATTTTTGGAGCCTGCGCCGTGCTGGTACCGCGCG
GCTCTTCTTCTTATCCCACATGCACTGTGACCACACGGTGGGCCTGTCTAGCACTTGGGCACGGCCCCTCTACTGC
TCTCCCATCACTGCCCACCTCTTGATCGTCGCTGCAGGTGTCTAAGCAGTGGATCCGAGCTCTGGAGATTGGT
GAGAGCCATGTATTACCTCTAGATGAAATTGGACAAGAAACCATGACTGTAACCCTCATAGATGCCAATCACTGTC
CTGGTTCTGTCATGTTTCTCTTTGAAGGATACTTTGGAACAATTCTCTACACAGGTGATTTTCGATATACACCGTCC
ATGCTGAAGGAGCCTGCTCTGACACTAGGGAAACAGATTCTACTTTATATCTAGACAACACCAATTGCAACCCAG
CCCTTGTCTCTCTTCCCGACAGGAAGCTACTCAACAGATTATCCAGCTAATCCGACAGTTCCCCCAACACAACAT
AAAGATTGGCCTCTATAGTCTAGGAAAAGAATCACTGCTGGAGCAGCTAGCCCTTGAGTTTCAGACCTGGGTGGT
ATTGAGTCCTCAACGCCTGGAGTTGGTACAGCTGCTGGGCCTGGCAGAcGTGTTACAGTGGAGGAAGAAGCT
GGGCGAATCCACGCTGTGGACCACATGGAAATCTGCCATTCGGCCATGCTTCAGTGGAACCAGACCCACCCAC
CATTGCTATTTTCCCCACAAGCCGAAATACGAAGCCCTACCCCAGCATCTACaGCATCCCTTNNCTGACCAT
TCATCCTACTCTGAGCTTCNAGCATTNGTNCANCTCTNNNNCTTGNCAAGNGGTGCCNATAGTCCGTNANANN
NNNNNGNNANTTTTTT

➤ BGHRev rate 307NT

GGNANNANTNCANCNGNNNNNANNGACANNNGNNNNCNNTGNNCNCNNNNNNNGNNNNNNNNNN
NNCNNNNNNNCNNNNCAANNCCNN
NNNNTNTNCNNCNCNAGCNGGNNNANNGAAGCCCTACCCCAGCATCTACAGCATCCCTTACTCTGACCAT
CATCCTACTCTGAGCTTCGAGCATTGTGTCAGCTCTGAGGCCTTGCCAGGTGGTGCCCATAGTCCGTGAACAGC
CTGTGGAGAGTTTTTTTCAGGATAG

➤ Synthèse séquençage rate 930NT

ATGAACGGGGTCGTAATCCCCCAAACACCCATCGCTGTGGATTTTTGGAGCCTGCGCCGT	60
GCTGGTACCGCGCGGCTCTTCTTCTTATCCCACATGCACTGTGACCACACGGTGGGCCTG	120
TCTAGCACTTGGGCACGGCCCCTCTACTGCTCTCCCATCACTGCCCACCTCTTGATCGT	180
CGCCTGCAGGTGTCTAAGCAGTGGATCCGAGCTCTGGAGATTGGTGAGAGCCATGTATTA	240
CCTCTAGATGAAATTGGACAAGAAACCATGACTGTAACCCTCATAGATGCCAATCACTGT	300
CCTGGTTCTGTCATGTTTCTCTTTGAAGGATACTTTGGAACAATTCTCTACACAGGTGAT	360
TTTCGATATACACCGTCCATGCTGAAGGAGCCTGCTCTGACACTAGGGAAACAGATTCAT	420
ACTTTATATCTAGACAACACCAATTGCAACCCAGCCCTTGTTCTTCTTCCCGACAGGAA	480
GCTACTCAACAGATTATCCAGCTAATCCGACAGTTCCCCCAACACAACATAAAGATTGGC	540
CTCTATAGTCTAGGAAAAGAATCACTGCTGGAGCAGCTAGCCCTTGAGTTTCAGACCTGG	600
GTGGTATTGAGTCCTCAACGCCTGGAGTTGGTACAGCTGCTGGGCCTGGCAGAcGTGTTT	660
ACAGTGGAGGAAGAAGCTGGGCGAATCCACGCTGTGGACCACATGGAAATCTGCCATTCTG	720
GCCATGCTTCAGTGGAACCAGACCCACCCACCATTTGCTATTTTCCCCACAAGCCGAAA	780
ATACGAAGCCCTACCCCAGCATCTACAGCATCCCTTACTCTGACCATTCATCCTACTCT	840
GAGCTTCGAGCATTGTGTCAGCTCTGAGGCCTTGCCAGGTGGTGCCCATAGTCCGTGAA	
CAGCCTTGTTGGAGAGTTTTTTTCAGGATAG	

MNGVVIPQTPIAVDFWSLRRAGTARLFFLSHMHCDHTVGLSSTWARPLYCSPITAHLLHRRQLQVSKQWIRALEIGES
HVLPLDEIGQETMTVTLIDANHCPGSVMFLFEGYFGTILYTGDFRYTPSMLKEPALTLGKQIHTLYLDNTNCNPALVL

➤ **Différence au niveau NT :**

Mutation en 242 C<T

	Name	Score	Score	Score	Value	Rank	Len		
✓	Rattus norvegicus DNA cross-link repair 1B_PSO2 homolog (S_cerevisiae)_mRNA (cDNA clone MGC:114481 IMAGE:...	Norway rat	1712	1712	100%	0.0	99.89%	4013	BC098939.1
✓	Rattus norvegicus DNA cross-link repair 1B (Dclre1b)_transcript variant 2_mRNA	Norway rat	1711	1711	100%	0.0	99.89%	3963	NM_001025687.2
✓	Rattus norvegicus DNA cross-link repair 1B (Dclre1b)_transcript variant 1_mRNA	Norway rat	1711	1711	100%	0.0	99.89%	4086	NM_001389222.1
✓	PREDICTED: Rattus norvegicus DNA cross-link repair 1B (Dclre1b)_transcript variant X3_mRNA	Norway rat	719	1377	80%	0.0	99.75%	3892	XM_006233080.3

➤ **Différence au niveau PROT :**

1102030405060708090100110120130

seqMNGVYIPQTPLAYDFWSLRRAGTARLFFLSHMHCHDTYGLSSTHARPLYCSPITAHLLHRRLLQVSKQHIRALEIGESHVLP

refMNGVYIPQTPLAYDFWSLRRAGTARLFFLSHMHCHDTYGLSSTHARPLYCSPITAHLLHRRLLQVSKQHIRALEIGESHVLP

ConsensusMNGVYIPQTPLAYDFWSLRRAGTARLFFLSHMHCHDTYGLSSTHARPLYCSPITAHLLHRRLLQVSKQHIRALEIGESHVLP

131140150160170180190200210220230240250260

seqPALTLGKQIHTLYLDNTNCNPALVLP

refPALTLGKQIHTLYLDNTNCNPALVLP

ConsensusPALTLGKQIHTLYLDNTNCNPALVLP

261270280290300309

seqIRSPHPSIYSIPYSDHSSYSELRAFVAALRPCQVVPVIREQPCGEFFSG

refIRSPHPSIYSIPYSDHSSYSELRAFVAALRPCQVVPVIREQPCGEFFSG

ConsensusIRSPHPSIYSIPYSDHSSYSELRAFVAALRPCQVVPVIREQPCGEFFSG

Mutation en 81 P<L

		Name	Score	Score	Cover	value	Ident	Len	Accession
✓	5' exonuclease Apollo [Rattus norvegicus]	Norway_rat	638	638	99%	0.0	100.00%	541	NP_001020858.2
✓	DNA cross-link repair 1B, PSO2 homolog (S. cerevisiae) [Rattus norvegicus]	Norway_rat	637	637	100%	0.0	99.68%	309	AAH98939.1
✓	RecName: Full=5' exonuclease Apollo; AltName: Full=DNA cross-link repair 1B protein; AltName: Full=SNM1 homolo...	Norway_rat	634	634	99%	0.0	99.67%	541	Q4KLY6.2
✓	PREDICTED: 5' exonuclease Apollo isoform X2 [Rattus norvegicus]	Norway_rat	407	407	99%	1e-140	70.03%	480	XP_006233142.1
✓	DNA cross-link repair 1B, PSO2 homolog (S. cerevisiae), isoform CRA_b [Rattus norvegicus]	Norway_rat	378	378	58%	4e-133	100.00%	221	EDL85473.1

o **FlagBirA Dclre1b DiT0 clone A : NOUVEAUX CLONES**

➤ **B3Fwd 1000NT**

ATGAACGGGGTCGTAATCCCCAAACACCCATCGCTGTGGATTTTGGAGCCTGCGCCGTGCTGGTACCGCGCG
GCTCTTCTTCTATCCCACATGCACTGTGACCACACGGTGGGCCTGTCTAGCACTTGGGCACGGCCCCTCTACTGC
TCTCCCATCACTGCCACCTCTTGCATCGTCGCTGCAGGTGTCTAAGCAGTGGATCCGAGCTCTGGAGATTGGT
GAGAGCCATGTATTACCTCTAGATGAAATTGGACAAGAAACCATGACTGTAACCCTCATAGATGCCAATCACTGTC
CTGGTTCTGTCATGTTTCTCTTTGAAGGATACTTTGGAACAATTCTCTACACAGGTGATTTTCGATATACACCGTCC
ATGCTGAAGGAGCCTGCTCTGACACTAGGGAAACAGATTCTACTTTATATCTAGACAACACCAATTGCAACCCAG
CCCTTGTCTCTCTTCCCGACAGGAAGCTACTCAACAGATTATCCAGCTAATCCGACAGTTCCCCAACACAACAT
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ATTGAGTCCTCAACGCCTGGAGTTGGTACAGCTGCTGGGCCTGGCAGACGTGTTTACAGTGGAGGAAGAAGCT
GGGCGAATCCACGCTGTGGACCACATGGAAATCTGCCATTGCGGcCATGCTTCaGTGAACCAGACCCACCCACC
ATTGCTATTTTCCCCACAAGCCGGAAAATACGAAGCCNTACCCAGCATCTACAGCATCCCTTACTCTGACCATTC
ATCCTACTCTGAGCTTCNAGCATTTGTTGCANCTCTNAGGNNNNGNCNGNGNNGCCNNNNNTNCGNNNNAG
CNTNNNGNNANTTTTTTNNNNNTANTGNNNNNNNTNCTNNANTCNNNNNGGNCNNNTNAANCCCNNTGA
TCANCNCNNCTGNNCNNCNANNNCNNCCAT

➤ **BGHRev 168NT**

TTNCNCCNNNGNNGGNNNNANNNGNANCCCTACCCAGCATCTACAGCATCCCTTACTCTGACCATTCATCCTA
CTCTGAGCTTCGAGCATTTGTTGCAGCTCTGAGGCCTTGCCAGGTGGTGCCCATAGCCGTGAACAGCCTTGTTG
AGAGTTTTTTTCAGGATAG

➤ **Synthèse séquençage 930NT**

ATGAACGGGGTCGTAATCCCCAAACACCCATCGCTGTGGATTTTGGAGCCTGCGCCGT	60
GCTGGTACCGCGCGGCTCTTCTTATCCACATGCACTGTGACCACACGGTGGGCCTG	120
TCTAGCACTTGGGCACGGCCCCTCTACTGCTCTCCCATCACTGCCACCTCTTGCATCGT	180
CGCCTGCAGGTGTCTAAGCAGTGGATCCGAGCTCTGGAGATTGGTGAGAGCCATGTATTA	240
CCTCTAGATGAAATTGGACAAGAAACCATGACTGTAACCCTCATAGATGCCAATCACTGT	300
CCTGGTTCTGTCATGTTTCTCTTTGAAGGATACTTTGGAACAATTCTCTACACAGGTGAT	360
TTTCGATATACACCGTCCATGCTGAAGGAGCCTGCTCTGACACTAGGGAACAGATTTCAT	420
ACTTTATATCTAGACAACACCAATTGCAACCCAGCCCTTGTCTCTCTTCCCGACAGGAA	480
GCTACTCAACAGATTATCCAGCTAATCCGACAGTTCCCCAACACAACATAAAGATTGGC	540
CTCTATAGTCTAGGAAAAGAATCACTGCTGGAGCAGCTAGCCCTTGAGTTTCAGACCTGG	600
GTGGTATTGAGTCTCAACGCCTGGAGTTGGTACAGCTGCTGGGCCTGGCAGACGTGTTT	660
ACAGTGGAGGAAGAAGCTGGGCGAATCCACGCTGTGGACCATGGAATCTGCCATTTCG	720
GcCATGCTTCaGTGAACCAGACCCACCCACCATTGCTATTTTCCCCACAAGCCGAAA	780
ATACGAAGCCCTACCCAGCATCTACAGCATCCCTTACTCTGACCATTCATCCTACTCT	840
GAGCTTCGAGCATTTGTTGCAGCTCTGAGGCCTTGCCAGGTGGTGCCCATAGTCCGTGAA	900
CAGCCTTGTTGGAGAGTTTTCAGGATAG-----	930

MNGVVIPQTPIAVDFWSLRRAGTARLFFLSHMHCDHTVGLSSTWARPLYCSPITAHLLHRRQLQVSKQWIRALEIGES
HVLPLDEIGQETMTVTLIDANHCPGSVMFLFEGYFGTILYTGDFRYTPSMLKEPALTLGKQIHTLYLDNTNCNPALVL
PSRQEATQQIIQLIRQPQHNIKIGLYSLGKESLLEQLALEFQTWVVLSPQRLELVQLLGLADVFTVEEEAGRIHAVDH
MEICHSAMLQWNQHTPTIAIFPSTRKIRSPHSIYSIPYSDHSSYSELRAFVAALRPCQVVPVIREQPCGEFFSG-

➤ Différence au niveau NT :

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq	ATGACG666GCGTATCCCCARACCCCATCGCTGTGGATTTTGGAGCCTGCGCCGTGCTGGTACCGCGCGGCTCTTCTTATCCACATGCACTGTGACCAACG66TGGGCTGTCTAGCACTT													
cds	ATGACG666GCGTATCCCCARACCCCATCGCTGTGGATTTTGGAGCCTGCGCCGTGCTGGTACCGCGCGGCTCTTCTTATCCACATGCACTGTGACCAACG66TGGGCTGTCTAGCACTT													
Consensus	ATGACG666GCGTATCCCCARACCCCATCGCTGTGGATTTTGGAGCCTGCGCCGTGCTGGTACCGCGCGGCTCTTCTTATCCACATGCACTGTGACCAACG66TGGGCTGTCTAGCACTT													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq	GGGACG66CCCTCTACTGCTCTCCCATCACTGCCACCTCTTGCATCGTCGCCCTGAGGTTGCTTAAGCAGTGGATCCGAGCTCTGGAGATTGGTGAAGCCATGATTACCTCTAGATGAATTGGACA													
cds	GGGACG66CCCTCTACTGCTCTCCCATCACTGCCACCTCTTGCATCGTCGCCCTGAGGTTGCTTAAGCAGTGGATCCGAGCTCTGGAGATTGGTGAAGCCATGATTACCTCTAGATGAATTGGACA													
Consensus	GGGACG66CCCTCTACTGCTCTCCCATCACTGCCACCTCTTGCATCGTCGCCCTGAGGTTGCTTAAGCAGTGGATCCGAGCTCTGGAGATTGGTGAAGCCATGATTACCTCTAGATGAATTGGACA													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq	AGAACCATGACTGTAACTCATAGATGCCAATCACTGTCTG6TTCTGTCATGTTTCTCTTTGAAGGATACCTTGGACATTTCTACACAGGTGATTTTCGATATACACCCGATGCTGAAGGAG													
cds	AGAACCATGACTGTAACTCATAGATGCCAATCACTGTCTG6TTCTGTCATGTTTCTCTTTGAAGGATACCTTGGACATTTCTACACAGGTGATTTTCGATATACACCCGATGCTGAAGGAG													
Consensus	AGAACCATGACTGTAACTCATAGATGCCAATCACTGTCTG6TTCTGTCATGTTTCTCTTTGAAGGATACCTTGGACATTTCTACACAGGTGATTTTCGATATACACCCGATGCTGAAGGAG													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
seq	CCTGCTTGACACTAGGGAACAGATTCTATCTTTATATCTAGACACACCAATTCGACACCCAGCCCTGTTCTTCTTCCCGACAGGAGCTACTCAGACGATTATCCAGCTATCCGACAGTTCCCCC													
cds	CCTGCTTGACACTAGGGAACAGATTCTATCTTTATATCTAGACACACCAATTCGACACCCAGCCCTGTTCTTCTTCCCGACAGGAGCTACTCAGACGATTATCCAGCTATCCGACAGTTCCCCC													
Consensus	CCTGCTTGACACTAGGGAACAGATTCTATCTTTATATCTAGACACACCAATTCGACACCCAGCCCTGTTCTTCTTCCCGACAGGAGCTACTCAGACGATTATCCAGCTATCCGACAGTTCCCCC													
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
seq	AACACACATAAAGATTGGCTCTATAGTCTAGGAAAGAGATCACTGCTGGAGCAGTAGCCCTTGAGTTTCAGACCTGGGTGGATTGAGTCTTCACAGCCTGGAGTTGGTACAGCTGCTGGGCTGGC													
cds	AACACACATAAAGATTGGCTCTATAGTCTAGGAAAGAGATCACTGCTGGAGCAGTAGCCCTTGAGTTTCAGACCTGGGTGGATTGAGTCTTCACAGCCTGGAGTTGGTACAGCTGCTGGGCTGGC													
Consensus	AACACACATAAAGATTGGCTCTATAGTCTAGGAAAGAGATCACTGCTGGAGCAGTAGCCCTTGAGTTTCAGACCTGGGTGGATTGAGTCTTCACAGCCTGGAGTTGGTACAGCTGCTGGGCTGGC													
	651	660	670	680	690	700	710	720	730	740	750	760	770	780
seq	AGACGTGTTACAGTGGAGGAGAGCTGGGCGAATCCAGCTGTGGACACATGGAATCTGCCATTGGCCATGCTTCAGTGGACACAGACCCACCCACCATGCTATTTTCCACAGCCGGA													
cds	AGACGTGTTACAGTGGAGGAGAGCTGGGCGAATCCAGCTGTGGACACATGGAATCTGCCATTGGCCATGCTTCAGTGGACACAGACCCACCCACCATGCTATTTTCCACAGCCGGA													
Consensus	AGACGTGTTACAGTGGAGGAGAGCTGGGCGAATCCAGCTGTGGACACATGGAATCTGCCATTGGCCATGCTTCAGTGGACACAGACCCACCCACCATGCTATTTTCCACAGCCGGA													
	781	790	800	810	820	830	840	850	860	870	880	890	900	910
seq	ATACGAGCCCTCACCCAGCATCTACAGCATCCCTTACTCTGACCATTCATCTACTCTGAGCTTCGAGCATTTGTTGACGCTCTGAGGCTTGCCAGGTGGTGGCCATAGTCCGTAACAGCCTTG													
cds	ATACGAGCCCTCACCCAGCATCTACAGCATCCCTTACTCTGACCATTCATCTACTCTGAGCTTCGAGCATTTGTTGACGCTCTGAGGCTTGCCAGGTGGTGGCCATAGTCCGTAACAGCCTTG													
Consensus	ATACGAGCCCTCACCCAGCATCTACAGCATCCCTTACTCTGACCATTCATCTACTCTGAGCTTCGAGCATTTGTTGACGCTCTGAGGCTTGCCAGGTGGTGGCCATAGTCCGTAACAGCCTTG													
	911	920	930											
seq	GAGAGTTTTTTCAGGATAG													
cds	GAGAGTTTTTTCAGGATAG													
Consensus	GAGAGTTTTTTCAGGATAG													

Mutation en 242 C<T

➤ Blast contre banque de rat

	Description	Name	Score	Score	Cover	value	Ident	Len	Accession
☒	Rattus norvegicus DNA cross-link repair 1B_PSO2 homolog (S_cerevisiae) mRNA (cDNA clone MGC:114481 IMAGE...	Norway rat	1712	1712	100%	0.0	99.89%	4013	BC098939.1
☒	Rattus norvegicus DNA cross-link repair 1B (Dclre1b), transcript variant 2 mRNA	Norway rat	1711	1711	100%	0.0	99.89%	3963	NM_001025687.2
☒	Rattus norvegicus DNA cross-link repair 1B (Dclre1b), transcript variant 1 mRNA	Norway rat	1711	1711	100%	0.0	99.89%	4086	NM_001389222.1
☒	PREDICTED: Rattus norvegicus DNA cross-link repair 1B (Dclre1b), transcript variant X3 mRNA	Norway rat	719	1377	80%	0.0	99.75%	3892	XM_006233080.3

➤ Différence au niveau PROT :

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq	MNGVYIPQTPIAVDFWSLRRAGTARLFFLSHMHCDHTVGLSSTHARPLYCSPITAHLLHRLQVSKQHIRALEIGESHVLP LDEIGQETHVTYTLIDANHCPGSMFLFEGYFGTILYTGDFRYTPSMLKE													
ref	MNGVYIPQTPIAVDFWSLRRAGTARLFFLSHMHCDHTVGLSSTHARPLYCSPITAHLLHRLQVSKQHIRALEIGESHVLLDEIGQETHVTYTLIDANHCPGSMFLFEGYFGTILYTGDFRYTPSMLKE													
Consensus	MNGVYIPQTPIAVDFWSLRRAGTARLFFLSHMHCDHTVGLSSTHARPLYCSPITAHLLHRLQVSKQHIRALEIGESHVLLDEIGQETHVTYTLIDANHCPGSMFLFEGYFGTILYTGDFRYTPSMLKE													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq	PALTLGKQIHTLYLONTNCPALVLP SRQATQQIIQLIRQFPQHNIKIGLYSLGKESLLEQLALEFQTAVVYLS PQRLLEYQLGLADVFTVEEAGRIHAYDHMEICHSAHLQANQTHPTIAIFPISRK													
ref	PALTLGKQIHTLYLONTNCPALVLP SRQATQQIIQLIRQFPQHNIKIGLYSLGKESLLEQLALEFQTAVVYLS PQRLLEYQLGLADVFTVEEAGRIHAYDHMEICHSAHLQANQTHPTIAIFPISRK													
Consensus	PALTLGKQIHTLYLONTNCPALVLP SRQATQQIIQLIRQFPQHNIKIGLYSLGKESLLEQLALEFQTAVVYLS PQRLLEYQLGLADVFTVEEAGRIHAYDHMEICHSAHLQANQTHPTIAIFPISRK													
	261	270	280	290	300	309								
seq	IRSPHPSIYSIPYSDHSSYSELRAFYAALRPCQVYPIVREQPCGEFFSG													
ref	IRSPHPSIYSIPYSDHSSYSELRAFYAALRPCQVYPIVREQPCGEFFSG													
Consensus	IRSPHPSIYSIPYSDHSSYSELRAFYAALRPCQVYPIVREQPCGEFFSG													

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☒	5' exonuclease Apollo [Rattus norvegicus]	Norway rat	638	638	99%	0.0	100.00%	541	NP_001020858.2
☒	DNA cross-link repair 1B_PSO2 homolog (S. cerevisiae) [Rattus norvegicus]	Norway rat	637	637	100%	0.0	99.68%	309	AAH98939.1
☒	RecName: Full=5' exonuclease Apollo; AltName: Full=DNA cross-link repair 1B protein; AltName: Full=SNM1 homolo...	Norway rat	634	634	99%	0.0	99.67%	541	Q4KLY6.2
☒	PREDICTED: 5' exonuclease Apollo isoform X2 [Rattus norvegicus]	Norway rat	407	407	99%	1e-140	70.03%	480	XP_006233142.1

o FlagBirA Dclre1b DiT24h clone A : NOUVEAUX CLONES

➤ B3Fwd 919NT

ATGAACGGGGTCGTAATCCCCAAACACCCATCGCTGTGGATTTTTGGAGCCTGCGCCGTGCTGGTACCGCGCGGCTCTTC
TTCTTATCCCATGCACTGTGACCACACGGTGGGCCTGTCTAGCACTTGGGCACGGCCCCCTCTACTGCTCTCCCATCACTG
CCCACCTCTTGCATCGTCGCCTGCAGGTGTCTAAGCAGTGGATCCGAGCTCTGGAGATTGGTGAGAGCCATGTATTACCTC
TAGATGAAATTGGACAAGAAACCATGACTGTAACCCTCATAGATGCCAATCACTGCTCTGGTTCTGTCATGTTTCTCTTTGA
AGGATACTTTGGAACAATTCTCTACACAGGTGATTTTCGATATACACCGTCCATGCTGAAGGAGCCTGCTCTGACACTAGG
GAAACAGATTTCATACTTTATCTAGACAACACCAATTGCAACCCAGCCCTTGTTCTTCTTCCCGACAGGAAGCTACTCAA
CAGATTATCCAGCTAATCCGACAGTTCCCCAACACAACATAAAGATTGGCCTCTATAGTCTAGGAAAAGAATCACTGCTG
GAGCAGCTAGCCCTTGAGTTTCAGACCTGGGTGGTATTGAGTCTCAACGCCTGGAGTTGGTACAGCTGCTGGGCCTGGC
AGACGTGTTACAGTGgAGGAAGAAGCTGGGCGAATCCACGCTGTGGACCACATGgAAATCTGCCATTCGgCATGCTTCA
GTGGAACCAGACCCACCCACCATTTGCTATTTTCCCCACAAGCCGAAAAATACGAAGCCCTCACCCACGATCTACAGCAT
CCCTTACTCTGAcCATTATCCTACTCTGAgCTTCNAGCANTNNTNNANCTNTGAGGNNNTGCCNGGNGNGNCNATNNTC
CNNNAACANCNTNNGNAGTTTTTTN

➤ BGHRev 217NT

CCNNNCNNCCNNCNNTNNTCNNNCNAGNCCCACCCACCANNCNATTTTCNNCACAAGCCGGAAAAANN
NGAAGCCCTCACCCAGCATCTACAGCATCCCTTACTCTGACCATTATCCTACTCTGAGCTTCGAGCATTTGTTGG
AGCTCTGAGGCCCTTGCCAGGTGGTGCCCATAGTCCGTGAACAGCCTTGTTGGAGAGTTTTTTTCAGGATAG

➤ Synthèse séquençage 930NT

ATGAACGGGGTCGTAATCCCCAAACACCCATCGCTGTGGATTTTTGGAGCCTGCGCCGT 60
GCTGGTACCGCGCGGCTCTTCTTCTTATCCCATGCACTGTGACCACACGGTGGGCCTG 120
TCTAGCACTTGGGCACGGCCCCCTCTACTGCTCTCCCATCACTGCCCACCTCTTGCATCGT 180
CGCCTGCAGGTGTCTAAGCAGTGGATCCGAGCTCTGGAGATTGGTGAGAGCCATGTATTA 240
CCTCTAGATGAAATTGGACAAGAAACCATGACTGTAACCCTCATAGATGCCAATCACTGT 300
CCTGGTTCTGTCATGTTTCTCTTTGAAGGATACTTTGGAACAATTCTCTACACAGGTGAT 360
TTTCGATATACACCGTCCATGCTGAAGGAGCCTGCTCTGACACTAGGGAAACAGATTCAT 420
ACTTTATATCTAGACAACACCAATTGCAACCCAGCCCTTGTTCTTCTTCCCGACAGGAA 480
GCTACTCAACAGATTATCCAGCTAATCCGACAGTTCCCCAACACAACATAAAGATTGGC 540
CTCTATAGTCTAGGAAAAGAATCACTGCTGGAGCAGCTAGCCCTTGAGTTTCAGACCTGG 600
GTGGTATTGAGTCTCAACGCCTGGAGTTGGTACAGCTGCTGGGCCTGGCAGACGTGTTC 660
ACAGTGgAGGAAGAAGCTGGGCGAATCCACGCTGTGGACCACATGgAAATCTGCCATTCG 720
GcCATGCTTCAGTGGAACCAGACCCACCCACCATTTGCTATTTTCCCCACAAGCCGAAA 780
ATACGAAGCCCTCACCCACGATCTACAGCATCCCTTACTCTGAcCATTATCCTACTCT 840
GAGCTTCGAGCATTTGTTGCAGCTCTGAGGCCTTGCCAGGTGGTGCCCATAGTCCGTGAA
CAGCCTTGTTGGAGAGTTTTTTTCAGGATAG

MNGVVIPQTPIAVDFWSLRRAGTARLFFLSHMHCDHTVGLSSTWARPLYCSPITAHLLHRRQLQVSKQWIRALEIGES
HVLPLDEIGQETMTVTLIDANHCPGSMFLFEGYFGTILYTGDFRYTPSMLKEPALTLGKQIHTLYLDNTNCNPALVL
PSRQEATQQIIQLIRQPQHNIKIGLYSLGKESLLEQLALEFQTWVVLSPQRLELVQLLGLADVFTVEEEAGRIHAVDH
MEICHSAMLQWNQHTPTIAIFPTSRKIRSPHSIYSIPYSDHSSYSELRAFVAALRPCQVVPVIREQPCGEFFSG-

➤ Différence au niveau NT :

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

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

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

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

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

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

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

911 920 930
 seq GAGAGTTTTTTTCAGGATAG
 cds GAGAGTTTTTTTCAGGATAG
 Consensus GAGAGTTTTTTTCAGGATAG

Mutation en 242 C<T

➤ Blast contre banque de rat

Rattus norvegicus DNA cross-link repair 1B_PSO2 homolog (S_cerevisiae). mRNA (cDNA clone MGC:114481 IMAGE:...	Norway rat	1712	1712	100%	0.0	99.89%	4013	BC098939.1
Rattus norvegicus DNA cross-link repair 1B (Dclre1b). transcript variant 2. mRNA	Norway rat	1711	1711	100%	0.0	99.89%	3963	NM_001025687.2
Rattus norvegicus DNA cross-link repair 1B (Dclre1b). transcript variant 1. mRNA	Norway rat	1711	1711	100%	0.0	99.89%	4086	NM_001389222.1
PREDICTED: Rattus norvegicus DNA cross-link repair 1B (Dclre1b). transcript variant X3. mRNA	Norway rat	719	1377	80%	0.0	99.75%	3892	XM_006233080.3

➤ Différence au niveau PROT :

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

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

261 270 280 290 300 309
 seq IRSHPHSIYSIPYSDHSSYSELRAFVAALRPCQVVPVIVREQPCGEFFSG
 ref IRSHPHSIYSIPYSDHSSYSELRAFVAALRPCQVVPVIVREQPCGEFFSG
 Consensus IRSHPHSIYSIPYSDHSSYSELRAFVAALRPCQVVPVIVREQPCGEFFSG

☒	5' exonuclease Apollo [Rattus norvegicus]	Norway rat	638	638	99%	0.0	100.00%	541	NP_001020858.2
☒	DNA cross-link repair 1B, PSO2 homolog (S. cerevisiae) [Rattus norvegicus]	Norway rat	637	637	100%	0.0	99.68%	309	AAH98939.1
☒	RecName: Full=5' exonuclease Apollo; AltName: Full=DNA cross-link repair 1B protein; AltName: Full=SNM1 homolo...	Norway rat	634	634	99%	0.0	99.67%	541	Q4KLY6.2
☒	PREDICTED: 5' exonuclease Apollo isoform X2 [Rattus norvegicus]	Norway rat	407	407	99%	1e-140	70.03%	480	XP_006233142.1
☒	DNA cross-link repair 1B, PSO2 homolog (S. cerevisiae) isoform CRA_b [Rattus norvegicus]	Norway rat	378	378	58%	4e-133	100.00%	221	EDL85473.1
☒	DNA cross-link repair 1B, PSO2 homolog (S. cerevisiae) isoform CRA_c [Rattus norvegicus]	Norway rat	372	372	58%	4e-128	100.00%	415	EDL85474.1
☒	DNA cross-link repair 1A protein [Rattus norvegicus]	Norway rat	167	167	94%	7e-46	33.64%	1026	NP_001099671.1
☒	PREDICTED: DNA cross-link repair 1A protein isoform X2 [Rattus norvegicus]	Norway rat	144	144	70%	8e-38	37.67%	927	XP_008758745.1

o FlagBirA Dclre1b DiT48h clone A : NOUVEAUX CLONES

➤ B3Fwd 973NT

ATGAACGGGGTCGTAATCCCCCAAACACCCATCGCTGTGGATTTTGGAGCCTGCGCCGTGCTGGTACCGCGCG
GCTCTTCTTCTTATCCCACATGCACTGTGACCACACGGTGGCCTGTCTAGCACTTGGGCACGGCCCCTCTACTGC
TCTCCCATCACTGCCCCACCTCTTGCATCGTCGCTGCAGGTGTCTAAGCAGTGGATCCGAGCTCTGGAGATTGGT
GAGAGCCATGTATTACCTCTAGATGAAATTGGACAAGAAACCATGACTGTAACCCTCATAGATGCCAATCACTGTC
CTGGTTCTGTCATGTTTCTCTTTGAAGGATACTTTGGAACAATTCTCTACACAGGTGATTTTCGATATACACCGTCC
ATGCTGAAGGAGCCTGCTCTGACACTAGGGAAACAGATTCATACTTTATATCTAGACAACACCAATTGCAACCCAG
CCCTTGTTCTTCTTCCCCGACAGGAAGCTACTCAACAGATTATCCAGCTAATCCGACAGTTCCCCCAACACAACAT
AAAGATTGGCCTCTATAGTCTAGGAAAAGAATCACTGCTGGAGCAGCTAGCCCTTGAGTTTCAGACCTGGGTGGT
ATTGAGTCCTCAACGCCTGGAGTTGGTACAGCTGCTGGGcCTGGCAGACGTGTTTCACAGTGgAGGAAGAAGCTG
GGCGAATCCaCGCTGTGGACCACATGGAAATCTGCCATTGGGcCATGCTTCAGTGGAACCAGACCCACCCACCA
TTGCTATTTTCCCCACAAGCcGNAATAACNAAGCCCTCACCCAGCATCTACNNNATCCNTACTCTGANNATTC
ATCCTACTNTGAGCTTCNAGCATTTGTTGCAGNTCNNAGGCCTTGCNAGGNGNNGCCNTAGNCCNNNNANNN
CNTNNGNNANTTTTTNNNNGNNNNNGNNNNNNNNNACTCGAGTCTANANGGNCNNNTNAANCNNNTGAT
CA

➤ BGHRev 217NT

CNNNNNNNCNNNCNCNNNNNNNCNNNNNNNNNCACCCACCNNNNNtATTTNCCCCACAAGCCGGAAANTA
CGAAGCCCTCACCCAGCATCTACAGCATCCCTTACTCTGACCATTATCCTACTCTGAGCTTCGAGCATTTGTTGC
AGCTCTGAGGCCTTGCCAGGTGGTGCCCATAGTCCGTGAACAGCCTTGTGGAGAGTTTTTTTCAGGATAG

➤ Synthèse séquençage 930NT

ATGAACGGGGTCGTAATCCCCCAAACACCCATCGCTGTGGATTTTGGAGCCTGCGCCGT	60
GCTGGTACCGCGGGCTCTTCTTATCCCACATGCACTGTGACCACACGGTGGCCTG	120
TCTAGCACTTGGGCACGGCCCCTCTACTGCTCTCCCATCACTGCCCCACCTCTTGCATCGT	180
CGCCTGCAGGTGTCTAAGCAGTGGATCCGAGCTCTGGAGATTGGTGAGAGCCATGTATTA	240
CCTCTAGATGAAATTGGACAAGAAACCATGACTGTAACCCTCATAGATGCCAATCACTGT	300
CCTGGTTCTGTCATGTTTCTTGAAGGATACTTTGGAACAATTCTCTACACAGGTGAT	360
TTTCGATATACACCGTCCATGCTGAAGGAGCCTGCTCTGACACTAGGGAAACAGATTCAT	420
ACTTTATATCTAGACAACACCAATTGCAACCCAGCCCTGTTCTCTCCTTCCCGACAGGAA	480
GCTACTCAACAGATTATCCAGCTAATCCGACAGTTCCCCCAACACAACATAAAGATTGGC	540
CTCTATAGTCTAGGAAAAGAATCACTGCTGGAGCAGCTAGCCCTTGAGTTTCAGACCTGG	600
GTGGTATTGAGTCCTCAACGCCTGGAGTTGGTACAGCTGCTGGGcCTGGCAGACGTGTTTC	660
ACAGTGgAGGAAGAAGCTGGGCGAATCCaCGCTGTGGACCACATGGAAATCTGCCATTTCG	720
GcCATGCTTCAGTGGAACCAGACCCACCCACCATGCTATTTTCCCCACAAGCcGAAA	780
ATACGAAGCCCTCACCCAGCATCTACAGCATCCCTTACTCTGACCATTATCCTACTCT	
GAGCTTCGAGCATTTGTTGCAGCTCTGAGGCCTTGCCAGGTGGTGCCCATAGTCCGTGAA	
CAGCCTTGTTGGAGAGTTTTTTTCAGGATAG	

MNGVVIPQTPIAVDFWSLRRAGTARLFFLSHMHCDHTVGLSSTWARPLYCSPITAHLLHRRQLQVSKQWIRALEIGESHVLPDEI
GQETMTVTLIDANHCPGSVMFLFEGYFGTILYTGDFRYTPSMLKEPALTLGKQIHTLYLDNTNCNPALVLPQRQEATQQIILIRQ
FPQHNIKIGLYSLGESLLEQLALEFQTVVVLSPQRLELVQLGLADVFTVEEEAGRIHAVDHMEICHSAMLQWNQTHPTIAIFP
TSRKIRSPHPSIYSIPYSDHSSYSELRAFVAALRPCQVVPVIREQPCGEFFSG-



➤ **Différence au niveau NT :**

	131 140 150 160 170 180 190 200 210 220 230 240 250 260																									
seq	ATGACACGGGGTCGTATCCCCCAACACCCATCGCTGTGGATTTTGGAGCCTGCGCCGTGCTGGTACCGCGCGGCTCTTCTTCTATCCACATGCACTGTGACACACGGTGGGCCGTCTAGCACTT																									
cds	ATGACACGGGGTCGTATCCCCCAACACCCATCGCTGTGGATTTTGGAGCCTGCGCCGTGCTGGTACCGCGCGGCTCTTCTTCTATCCACATGCACTGTGACACACGGTGGGCCGTCTAGCACTT																									
Consensus	ATGACACGGGGTCGTATCCCCCAACACCCATCGCTGTGGATTTTGGAGCCTGCGCCGTGCTGGTACCGCGCGGCTCTTCTTCTATCCACATGCACTGTGACACACGGTGGGCCGTCTAGCACTT																									
	261 270 280 290 300 310 320 330 340 350 360 370 380 390																									
seq	GGGACACGGCCCTCTACTGTCTCCCATCACTGCCACCTCTTGATCGTGCCTGCAGGTGCTTAGCAGTGGATCCGAGCTCTGGAGATTGGTGAAGACCATGTATTACCTCTAGATGAATTGGACA																									
cds	GGGACACGGCCCTCTACTGTCTCCCATCACTGCCACCTCTTGATCGTGCCTGCAGGTGCTTAGCAGTGGATCCGAGCTCTGGAGATTGGTGAAGACCATGTATTACCTCTAGATGAATTGGACA																									
Consensus	GGGACACGGCCCTCTACTGTCTCCCATCACTGCCACCTCTTGATCGTGCCTGCAGGTGCTTAGCAGTGGATCCGAGCTCTGGAGATTGGTGAAGACCATGTATTACCTCTAGATGAATTGGACA																									
	391 400 410 420 430 440 450 460 470 480 490 500 510 520																									
seq	AGAAACCATGACTGTAAACCTCATAGATGCCAATCACTGTCTGGTCTGTCATGTTCTCTTTGAGGATACCTTGGACCAATCTCTACACAGGTGATTTTCATATACACCGTCCATGCTGAAGGAG																									
cds	AGAAACCATGACTGTAAACCTCATAGATGCCAATCACTGTCTGGTCTGTCATGTTCTCTTTGAGGATACCTTGGACCAATCTCTACACAGGTGATTTTCATATACACCGTCCATGCTGAAGGAG																									
Consensus	AGAAACCATGACTGTAAACCTCATAGATGCCAATCACTGTCTGGTCTGTCATGTTCTCTTTGAGGATACCTTGGACCAATCTCTACACAGGTGATTTTCATATACACCGTCCATGCTGAAGGAG																									
	521 530 540 550 560 570 580 590 600 610 620 630 640 650																									
seq	CCTGCTCTGCACTAGGGAACAGATTCTACTTTATATCTAGACACACCAATTGCACCCAGCCCTTGTTCTTCTCTCCGACAGGAGCTACTCAACAGATTATCCAGCTAATCCGACAGTTCCTCC																									
cds	CCTGCTCTGCACTAGGGAACAGATTCTACTTTATATCTAGACACACCAATTGCACCCAGCCCTTGTTCTTCTCTCCGACAGGAGCTACTCAACAGATTATCCAGCTAATCCGACAGTTCCTCC																									
Consensus	CCTGCTCTGCACTAGGGAACAGATTCTACTTTATATCTAGACACACCAATTGCACCCAGCCCTTGTTCTTCTCTCCGACAGGAGCTACTCAACAGATTATCCAGCTAATCCGACAGTTCCTCC																									
	651 660 670 680 690 700 710 720 730 740 750 760 770 780																									
seq	AACACACATTAAGATTGGCCCTATAGTCTAGGAAAGAAATCACTGCTGGAGCAGCTAGCCCTTGAGTTTCAGACCTGGGTGGTATTGAGTCCCTCAGCGCTGGAGTTGGTACAGCTGCTGGGCCCTGGC																									
cds	AACACACATTAAGATTGGCCCTATAGTCTAGGAAAGAAATCACTGCTGGAGCAGCTAGCCCTTGAGTTTCAGACCTGGGTGGTATTGAGTCCCTCAGCGCTGGAGTTGGTACAGCTGCTGGGCCCTGGC																									
Consensus	AACACACATTAAGATTGGCCCTATAGTCTAGGAAAGAAATCACTGCTGGAGCAGCTAGCCCTTGAGTTTCAGACCTGGGTGGTATTGAGTCCCTCAGCGCTGGAGTTGGTACAGCTGCTGGGCCCTGGC																									
	781 790 800 810 820 830 840 850 860 870 880 890 900 910																									
seq	ATACGAGGCCCTCACCCAGCATCTACAGCATCCCTTACTCTGACCATTCATCTACTCTGAGCTCTGAGCATTTGTTGACGCTCTGAGGCCCTTGCCAGGTTGGTGCCCATAGTCCGTGAACAGCCTTTGTG																									
cds	ATACGAGGCCCTCACCCAGCATCTACAGCATCCCTTACTCTGACCATTCATCTACTCTGAGCTCTGAGCATTTGTTGACGCTCTGAGGCCCTTGCCAGGTTGGTGCCCATAGTCCGTGAACAGCCTTTGTG																									
Consensus	ATACGAGGCCCTCACCCAGCATCTACAGCATCCCTTACTCTGACCATTCATCTACTCTGAGCTCTGAGCATTTGTTGACGCTCTGAGGCCCTTGCCAGGTTGGTGCCCATAGTCCGTGAACAGCCTTTGTG																									
	911 920 930																									
seq	GAGAGTTTTTTTCAGGATAG																									
cds	GAGAGTTTTTTTCAGGATAG																									
Consensus	GAGAGTTTTTTTCAGGATAG																									

Mutation en 242 C<T

➤ **Blast contre banque de rat**

	Description	Common Name	max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
Rattus norvegicus DNA cross-link repair 1B, PSO2 homolog (S. cerevisiae), mRNA (cDNA clone MGC:114481 IMAGE:...		Norway rat	1712	1712	100%	0.0	99.89%	4013	BC098939.1
Rattus norvegicus DNA cross-link repair 1B (Dclre1b), transcript variant 2, mRNA		Norway rat	1711	1711	100%	0.0	99.89%	3963	NM_001025687.2
Rattus norvegicus DNA cross-link repair 1B (Dclre1b), transcript variant 1, mRNA		Norway rat	1711	1711	100%	0.0	99.89%	4086	NM_001389222.1
PREDICTED: Rattus norvegicus DNA cross-link repair 1B (Dclre1b), transcript variant X3, mRNA		Norway rat	719	1377	80%	0.0	99.75%	3892	XM_006233080.3

➤ **Différence au niveau PROT :**

1 10 20 30 40 50 60 70 80 90 100 110 120 130

ref MNGVVLPQTPIAVDFWSLRAGTARLFFLSMHCHDHTVGLSSTWAPRLCYCSPTIAHLLHRRLLQVSKQIRALEIGESHVLLDEIGQETHVTYLIDANHCPGSMYHFLFEGYFGTILYTGDFRYTPSMHKE

seq MNGVVLPQTPIAVDFWSLRAGTARLFFLSMHCHDHTVGLSSTWAPRLCYCSPTIAHLLHRRLLQVSKQIRALEIGESHVLPDEIGQETHVTYLIDANHCPGSMYHFLFEGYFGTILYTGDFRYTPSMHKE

Consensus MNGVVLPQTPIAVDFWSLRAGTARLFFLSMHCHDHTVGLSSTWAPRLCYCSPTIAHLLHRRLLQVSKQIRALEIGESHVLLDEIGQETHVTYLIDANHCPGSMYHFLFEGYFGTILYTGDFRYTPSMHKE

	Description	Common Name	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession	
✓	5' exonuclease Apollo [Rattus norvegicus]	Norway rat	638	638	99%	0.0	100.00%	541	NP_001020858.2
✓	DNA cross-link repair 1B_PSO2 homolog (S_cerevisiae) [Rattus norvegicus]	Norway rat	637	637	100%	0.0	99.68%	309	AAH98939.1
✓	RecName: Full=5' exonuclease Apollo; AltName: Full=DNA cross-link repair 1B protein; AltName: Full=SNM1 homolog [Rattus norvegicus]	Norway rat	634	634	99%	0.0	99.67%	541	Q4KLY6.2
✓	PREDICTED: 5' exonuclease Apollo isoform X2 [Rattus norvegicus]	Norway rat	407	407	99%	1e-140	70.03%	480	XP_006233142.1

o FlagBirA Dclre1b SP clone A : NOUVEAUX CLONES

➤ B3Fwd 918NT

ATGAACGGGGTCGTAATCCCCCAAACACCCATCGCTGTGGATTTTTGGAGCCTGCGCCGTGCTGGTACCGCGCG
GCTCTTCTTCTATCCCACATGCACTGTGACCACACGGTGGGCCTGTCTAGCACTTGGGCACGGCCCCCTCTACTGC
TCTCCCATCACTGCCCCACCTCTTGCATCGTCGCCTGCAGGTGTCTAAGCAGTGGATCCGAGCTCTGGAGATTGGT
GAGAGCCATGTATTACCTCTAGATGAAATTGGACAAGAAACCATGACTGTAACCCTCATAGATGCCAATCACTGTC
CTGGTTCTGTCATGTTTCTCTTTGAAGGATACTTTGGAACAATTCTCTACACAGGTGATTTTCGATATACACCGTCC
ATGCTGAAGGAGCCTGCTCTGACACTAGGGAAACAGATTCATACTTTATATCTAGACAACACCAATTGCAACCCAG
CCCTTGTTCTTCTTCCCCGACAGGAAGCTACTCAACAGATTATCCAGCTAATCCGACAGTTCCCCCAACACAACAT
AAAGATTGGCCTCTATAGTCTAGGAAAAGAATCACTGCTGGAGCAGCTAGCCCTTGAGTTTCAGACCTGGGTGGT
ATTGAGTCCTCAACGCCTGGAGTTGGTACAGCTGCTGGGCCTGGCAGACGTGTTTCAGTGGAAGGAAGAAGCT
GGGCGAATCCACGCTGTGGACACATGGAAATCTGCCATTGCGCCATGCTTCAGTGGAACAGACCCACCCACC
ATTGCTATTTTCCCACAAGCCGGAAAATACGAAGCCCTCACCCAGCATCTACAGCATCCCTTACTCTGACCATT
ATCCTACTCTGAGCTTCNAGCATTTGNTGCANCTCTGANGNNTTGNCAGNNGNTGNCCATANNCCGTGANNAN
NNNNNGNNANTTTTT

➤ BGHRev 182NT

NNNGNCGGANNNNNNGAAGCCCTCACCCAGCATCTACAGCATCCCTTACTCTGACCATTATCCTACTCTGAG
CTTCGAGCATTTGTTGCAGCTCTGAGGCCTTGCCAGGTGGTGCCCATAGTCCGTGAACAGCCTGTGGAGAGTT
TTTTTCAGGATAGTGCGGCCGgCtaACTCGANTC

➤ Synthèse séquençage 930NT

ATGAACGGGGTCGTAATCCCCCAAACACCCATCGCTGTGGATTTTTGGAGCCTGCGCCGT	60
GCTGGTACCGCGCGGCTCTTCTTCTTATCCCACATGCACTGTGACCACACGGTGGGCCTG	120
TCTAGCACTTGGGCACGGCCCCCTCTACTGCTCTCCCATCACTGCCACCTCTTGCATCGT	180
CGCCTGCAGGTGTCTAAGCAGTGGATCCGAGCTCTGGAGATTGGTGAGAGCCATGTATTA	240
CCTCTAGATGAAATTGGACAAGAAACCATGACTGTAACCCTCATAGATGCCAATCACTGT	300
CCTGGTTCTGTCATGTTTCTCTTTGAAGGATACTTTGGAACAATTCTCTACACAGGTGAT	360
TTTCGATATACACCGTCCATGCTGAAGGAGCCTGCTCTGACACTAGGGAAACAGATTCAT	420
ACTTTATATCTAGACAACACCAATTGCAACCCAGCCCTTGTCTTCTTCTTCCCCGACAGGAA	480
GCTACTCAACAGATTATCCAGCTAATCCGACAGTTCCCCCAACACAACATAAAGATTGGC	540
CTCTATAGTCTAGGAAAAGAATCACTGCTGGAGCAGCTAGCCCTTGAGTTTCAGACCTGG	600
GTGGTATTGAGTCCTCAACGCCTGGAGTTGGTACAGCTGCTGGGCCTGGCAGACGTGTTT	660
ACAGTGGAAGGAAGAAGCTGGGCGAATCCACGCTGTGGACACATGGAAATCTGCCATTG	720
GCCATGCTTCAGTGGAACAGACCCACCCACCATTGCTATTTTCCCACAAGCCGGAAA	780
ATACGAAGCCCTCACCCAGCATCTACAGCATCCCTTACTCTGACCATTATCCTACTCT	840
GAGCTTCGAGCATTTGTTGCAGCTCTGAGGCCTTGCCAGGTGGTGCCCATAGTCCGTGAA	900
CAGCCTTGTGGAGAGTTTTTTTCAGGATAG	930

MNGVVIPQTPIAVDFWSLRRAGTARLFFLSHMHCDHTVGLSSTWARPLYCSPITAHLLHRRQLQVSKQWIRALEIGES
HVLPLDEIGQETMTVTLIDANHCPGSVMFLFEGYFGTILYTGDFRYTPSMLKEPALTLGKQIHTLYLDNTNCNPALVL
PSRQEATQQIIQLIRQPQHNIKIGLYSLGKESLLEQLALEFQTWVVLSPQRLELVQLLGLADVFTVEEEAGRIHAVDH
MEICHSAMLQWNQHTPTIAIFPISRKIRSPHSIYSIPYSDHSSYSELRAFVAALRPCQVVPVIREQPCGEFFSG-



➤ **Différence au niveau NT :**

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq	ATGAACGGGGTCGTARTCCCCAARACCCATCGCTGTGGATTTTGGAGCCTGCGCCGTGCTGGTACCGCGCGGCTCTTCTTCTATCCACATGCACCTGTGACCAACAGGGTGGGCTGTCTAGCACCT													
cds	ATGAACGGGGTCGTARTCCCCAARACCCATCGCTGTGGATTTTGGAGCCTGCGCCGTGCTGGTACCGCGCGGCTCTTCTTCTATCCACATGCACCTGTGACCAACAGGGTGGGCTGTCTAGCACCT													
Consensus	ATGAACGGGGTCGTARTCCCCAARACCCATCGCTGTGGATTTTGGAGCCTGCGCCGTGCTGGTACCGCGCGGCTCTTCTTCTATCCACATGCACCTGTGACCAACAGGGTGGGCTGTCTAGCACCT													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq	GGGACGGGCCCTCTACTGCTCTCCCATCACTGCCACCTCTTGCACTGTCGCCCTGACGGTGCTTAGCGAGTGGATCCGAGCTCTGGAGATTGGTGAGAGCCATGTATTACCTCTAGATGAATTTGGACA													
cds	GGGACGGGCCCTCTACTGCTCTCCCATCACTGCCACCTCTTGCACTGTCGCCCTGACGGTGCTTAGCGAGTGGATCCGAGCTCTGGAGATTGGTGAGAGCCATGTATTACCTCTAGATGAATTTGGACA													
Consensus	GGGACGGGCCCTCTACTGCTCTCCCATCACTGCCACCTCTTGCACTGTCGCCCTGACGGTGCTTAGCGAGTGGATCCGAGCTCTGGAGATTGGTGAGAGCCATGTATTACCTCTAGATGAATTTGGACA													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq	AGAACCATGACTGTACCCCTCATAGATGCCAATCACTGTCTGGTTCTGTCTATGTTCTCTTTGAGGGATACCTTGGAAACATTCCTACACAGGTGATTTTCGATATACACCGTCCATGCTGAGGGAG													
cds	AGAACCATGACTGTACCCCTCATAGATGCCAATCACTGTCTGGTTCTGTCTATGTTCTCTTTGAGGGATACCTTGGAAACATTCCTACACAGGTGATTTTCGATATACACCGTCCATGCTGAGGGAG													
Consensus	AGAACCATGACTGTACCCCTCATAGATGCCAATCACTGTCTGGTTCTGTCTATGTTCTCTTTGAGGGATACCTTGGAAACATTCCTACACAGGTGATTTTCGATATACACCGTCCATGCTGAGGGAG													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
seq	CTGTCTGTGACACTAGGGAAACAGATTCTACTTTATATCTAGACAAACCAATTGCARCCAGCCCTTGTTCTTCTCTTCCGACAGGAGAGCTACTCAACAGATTATCCAGCTAATCCGACAGTTCCCCC													
cds	CTGTCTGTGACACTAGGGAAACAGATTCTACTTTATATCTAGACAAACCAATTGCARCCAGCCCTTGTTCTTCTCTTCCGACAGGAGAGCTACTCAACAGATTATCCAGCTAATCCGACAGTTCCCCC													
Consensus	CTGTCTGTGACACTAGGGAAACAGATTCTACTTTATATCTAGACAAACCAATTGCARCCAGCCCTTGTTCTTCTCTTCCGACAGGAGAGCTACTCAACAGATTATCCAGCTAATCCGACAGTTCCCCC													
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
seq	AACACACATAAAGATTGGCCCTCTATAGCTTAGGAAAGAGATCACTGCTGGAGCAGCTAGCCCTTGAGTTTCAGACCTGGGTTGGATTGAGTCTTCAACGCCCTGGAGTTGGTACAGCTGCTGGGCTTGGC													
cds	AACACACATAAAGATTGGCCCTCTATAGCTTAGGAAAGAGATCACTGCTGGAGCAGCTAGCCCTTGAGTTTCAGACCTGGGTTGGATTGAGTCTTCAACGCCCTGGAGTTGGTACAGCTGCTGGGCTTGGC													
Consensus	AACACACATAAAGATTGGCCCTCTATAGCTTAGGAAAGAGATCACTGCTGGAGCAGCTAGCCCTTGAGTTTCAGACCTGGGTTGGATTGAGTCTTCAACGCCCTGGAGTTGGTACAGCTGCTGGGCTTGGC													
	651	660	670	680	690	700	710	720	730	740	750	760	770	780
seq	AGACGTGTTTCACAGTGGAGGAGAGAGCTGGGCGAATCCACGCTGTGGACACCATGGAATCTGCCATTTCGGCCATGCTTCAGTGGAACAGACCCACCCACCATTGCTATTTTCCCCACAGCCGGAAA													
cds	AGACGTGTTTCACAGTGGAGGAGAGAGCTGGGCGAATCCACGCTGTGGACACCATGGAATCTGCCATTTCGGCCATGCTTCAGTGGAACAGACCCACCCACCATTGCTATTTTCCCCACAGCCGGAAA													
Consensus	AGACGTGTTTCACAGTGGAGGAGAGAGCTGGGCGAATCCACGCTGTGGACACCATGGAATCTGCCATTTCGGCCATGCTTCAGTGGAACAGACCCACCCACCATTGCTATTTTCCCCACAGCCGGAAA													
	781	790	800	810	820	830	840	850	860	870	880	890	900	910
seq	ATACGAGGCCCTCACCCAGCATCTACAGCATCCCTTACTCTGACCAATTCTCTACTCTGAGCTTCGAGCATTTGTTGACAGCTCTGAGGCTTGGCAGGTGGTGCCCATAGTGCCTGACACGCTTTGTG													
cds	ATACGAGGCCCTCACCCAGCATCTACAGCATCCCTTACTCTGACCAATTCTCTACTCTGAGCTTCGAGCATTTGTTGACAGCTCTGAGGCTTGGCAGGTGGTGCCCATAGTGCCTGACACGCTTTGTG													
Consensus	ATACGAGGCCCTCACCCAGCATCTACAGCATCCCTTACTCTGACCAATTCTCTACTCTGAGCTTCGAGCATTTGTTGACAGCTCTGAGGCTTGGCAGGTGGTGCCCATAGTGCCTGACACGCTTTGTG													
	911	920	930											
seq	GAGAGTTTTTTTCAGGATAG													
cds	GAGAGTTTTTTTCAGGATAG													
Consensus	GAGAGTTTTTTTCAGGATAG													

Mutation en 242 C<T

➤ Blast contre banque de rat

		Name	Score	Score	Cover	value	Ident	Len	Accession
✓	Rattus norvegicus DNA cross-link repair 1B_PSO2 homolog (S_cerevisiae)_mRNA (cDNA clone MGC:114481 IMAGE:50220586)	Norway_rat	1712	1712	100%	0.0	99.89%	4013	BC098939.1
✓	Rattus norvegicus DNA cross-link repair 1B (Dclre1b)_transcript variant 2_mRNA	Norway_rat	1711	1711	100%	0.0	99.89%	3963	NM_001025687.2
✓	Rattus norvegicus DNA cross-link repair 1B (Dclre1b)_transcript variant 1_mRNA	Norway_rat	1711	1711	100%	0.0	99.89%	4086	NM_001389222.1
✓	PREDICTED: Rattus norvegicus DNA cross-link repair 1B (Dclre1b)_transcript variant X3_mRNA	Norway_rat	719	1377	80%	0.0	99.75%	3892	XM_006233080.3

➤ **Différence au niveau PROT :**

	Name	Score	Score	Cover	value	Ident	Len	Accession	
✓	5' exonuclease Apollo [Rattus norvegicus]	Norway_rat	638	638	99%	0.0	100.00%	541	NP_001020858.2
✓	DNA cross-link repair 1B_PSO2 homolog (S. cerevisiae) [Rattus norvegicus]	Norway_rat	637	637	100%	0.0	99.68%	309	AAH98939.1
✓	RecName: Full=5' exonuclease Apollo; AltName: Full=DNA cross-link repair 1B protein; AltName: Full=SNM1 homolog... [Rattus norvegicus]	Norway_rat	634	634	99%	0.0	99.67%	541	Q4KLY6.2
✓	PREDICTED: 5' exonuclease Apollo isoform X2 [Rattus norvegicus]	Norway_rat	407	407	99%	1e-140	70.03%	480	XP_006233142.1

Consensus PMLILGKQLHILFLYLTNLTNLPALVPSKQEAHQQLILQLKQFPQNMILIGLTSLGKESLLEQLHLEFQITAVVLSFQKLELVQLGLHUYFIVEEENGKLAHYDMEILASHNLQNNQTHPTLHLPFTSKK

261 270 280 290 300 309

ref IRSPHPHSIYSIPYSDHSSYSELRAFVAALRPCQVYPIVREQPCGEFFSG

seq IRSPHPHSIYSIPYSDHSSYSELRAFVAALRPCQVYPIVREQPCGEFFSG

Consensus IRSPHPHSIYSIPYSDHSSYSELRAFVAALRPCQVYPIVREQPCGEFFSG

o **FlagBirA Dclre1b CTX clone A : NOUVEAUX CLONES**

➤ **B3Fwd 966NT**

ATGAACGGGGTCGTAATCCCCCAAACACCCATCGCTGTGGATTTTGGAGCCTGCGCCGTGCTGGTACCGCGCG
GCTCTTCTTCTATCCCACATGCACTGTGACCACACGGTGGGCCTGTCTAGCACTTGGGCACGGCCCCTCTACTGC
TCTCCCATCACTGCCCCACCTCTTGCATCGTCGCTGCAGGTGTCTAAGCAGTGGATCCGAGCTCTGGAGATTGGT
GAGAGCCATGTATTACCTCTAGATGAAATTGGACAAGAAACCATGACTGTAACCCTCATAGATGCCAATCACTGTC
CTGGTTCTGTCATGTTTCTCTTTGAAGGATACTTTGGAACAATTCTCTACACAGGTGATTTTCGATATACACCGTCC
ATGCTGAAGGAGCCTGCTCTGACACTAGGGAAACAGATTCATACTTTATATCTAGACAACACCAATTGCAACCCAG
CCCTTGTTCTTCTTCCCCGACAGGAAGCTACTCAACAGATTATCCAGCTAATCCGACAGTTCCCCCAACACAACAT
AAAGATTGGCCTCTATAGTCTAGGAAAAGAATCACTGCTGGAGCAGCTAGCCCTTGAGTTTCAGACCTGGGTGGT
ATTGAGTCCTCAACGCCTGgAGTTGGTACAGCTGCTGGGCCTGGCAGACGTGTTACAGTGGAGGAAGAAGCT
GGGCGAATCCACGCTGTGGACCACATGGAAATCTGCcATTGCGCCATGCTTCAGTGGAACCAGACCCACCCACC
ATTGCTATTTTCCCACAAGCCGGAAAATACNAAGCCCTCACCCAGCATCTACNGCATCCCNNACTCTGANCATT
CATCCTACTCTGANCTTCNAGCATTGNNGCANCTNTGAGGCCTTGCCNGNNNTGNCNNNNANNCNNNNNN
NNCNTNNNGGNNANTTTTTTCAGGANNGTGNGNNNCNANTNNNNNTCTNNANGGNCNNNTNAANNCC

➤ **BGHRev 317NT**

CGNCCTNNNNNNNNNNNNNNNNNNNNCNCNCTNNNNNGCCNNNNNNNNNNNNNNNNNNNNCNCNNNNNNNNNNNN
NCNNNNNNNNNNNTNGNNNNNNNNNNCNCNNANATNNNNNNNNNNNNCNCNNNNNNNNANNCNCNCANANC
CACCCNCNCANNNTNTTTTTCCNCNCAAGCCGAAAATANGAAGCCCTCACCCAGCATCTACAGCATCCCTTA
CTCTGACCATTATCCTACTCTGAGCTTCGAGCATTTGTTGCAGCTCTGAGGCCTTGCCAGGTGGTGCCCATAGTC
CGTGAACAGCCTTGTTGGAGAGTTTTTTTCAGGATAG

➤ **Synthèse séquençage 930NT**

ATGAACGGGGTCGTAATCCCCCAAACACCCATCGCTGTGGATTTTGGAGCCTGCGCCGT	60
GCTGGTACCGCGCGGCTCTTCTTCTTATCCCACATGCACTGTGACCACACGGTGGGCCTG	120
TCTAGCACTTGGGCACGGCCCTCTACTGCTCTCCATCACTGCCCACCTCTTGCATCGT	180
CGCCTGCAGGTGTCTAAGCAGTGGATCCGAGCTCTGGAGATTGGTGAGAGCCATGTATTA	240
CCTCTAGATGAAATTGGACAAGAAACCATGACTGTAACCCTCATAGATGCCAATCACTGT	300
CCTGGTTCTGTCATGTTTCTTCTTTGAAGGATACTTTGGAACAATTCTCTACACAGGTGAT	360
TTTCGATATACACCGTCCATGCTGAAGGAGCCTGCTCTGACACTAGGGAACAGATTTCAT	420
ACTTTATATCTAGACAACACCAATTGCAACCCAGCCCTGTTCTTCTTCCCGACAGGAA	480
GCTACTCAACAGATTATCCAGCTAATCCGACAGTTCCCCCAACACAACATAAAGATTGGC	540
CTCTATAGTCTAGGAAAAGAATCACTGCTGGAGCAGCTAGCCCTTGAGTTTCAGACCTGG	600
GTGGTATTGAGTCTCAACGCCTGgAGTTGGTACAGCTGCTGGGCCTGGCAGACGTGTTTC	660
ACAGTGGAGGAAGAAGCTGGGCGAATCCACGCTGTGGACCACATGGAAATCTGCcATTTCG	720
GCCATGCTTCAGTGGAAACCAGACCCACCCACCATTTGCTATTTTCCCACAAGCCGAAA	780
ATACGAAGCCCTCACCCAGCATCTACAGCATCCCTTACTCTGACCATTCATCCTACTCT	
GAGCTTCGAGCATTTGTTGCAGCTCTGAGGCCTTGCCAGGTGGTGCCCATAGTCCGTGAA	
CAGCCTTGTTGGAGAGTTTTTTTCAGGATAG	

MNGVVIPQTPIAVDFWSLRRAGTARLFFLSHMHCDHTVGLSSTWARPLYCSPITAHLLHRRQLQVSKQWIRALEIGES
HVLPLDEIGQETMTVTLIDANHCPGSVMFLFEGYFGTILYTGDFRYTPSMLKEPALTLGKQIHTLYLDNTNCNPALVL
PSRQEATQQIIQLIRQPQHNIKIGLYSLGKESLLEQLALEFQTWVVLSPQRLELVQLLGLADVFTVEEEAGRIHAVDH
MEICHSAMLQWNQHTPTIAIFPSTRKIRSPHSIYSIPYSDHSSYSELRAFVAALRPCQVVPVIREQPCGEFFSG-

➤ Différence au niveau NT :

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq	ATGAACGGGGTCGTAAATCCCCAAACACCCATCGCTGTGGATTTTTGGAGCTGCGCCGTGCTGGTACCGCGCGGCTCTTCTTCTATCCACATGCACGTGTGACCCACAGGTGGGCTGTCTAGCACTT													
cds	ATGAACGGGGTCGTAAATCCCCAAACACCCATCGCTGTGGATTTTTGGAGCTGCGCCGTGCTGGTACCGCGCGGCTCTTCTTCTATCCACATGCACGTGTGACCCACAGGTGGGCTGTCTAGCACTT													
Consensus	ATGAACGGGGTCGTAAATCCCCAAACACCCATCGCTGTGGATTTTTGGAGCTGCGCCGTGCTGGTACCGCGCGGCTCTTCTTCTATCCACATGCACGTGTGACCCACAGGTGGGCTGTCTAGCACTT													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq	GGGCACGGCCCCCTACTGCTCTCCCATCACTGCCACCTCTTGCATCGTCGCTGCAGGTGTCTAGCAGTGGATCCGAGCTCTGGAGATTGGTGAGAGCCATGTATTACCTCTAGATGAATTTGGACA													
cds	GGGCACGGCCCCCTACTGCTCTCCCATCACTGCCACCTCTTGCATCGTCGCTGCAGGTGTCTAGCAGTGGATCCGAGCTCTGGAGATTGGTGAGAGCCATGTATTACCTCTAGATGAATTTGGACA													
Consensus	GGGCACGGCCCCCTACTGCTCTCCCATCACTGCCACCTCTTGCATCGTCGCTGCAGGTGTCTAGCAGTGGATCCGAGCTCTGGAGATTGGTGAGAGCCATGTATTACCTCTAGATGAATTTGGACA													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq	AGAAACCATGACTGTAAACCTCATAGATGCCAATCACTGTCCTGGTTCTGTCATGTTTCTCTTTGAAGGATACCTTGGAAACATTCCTACACAGGTGATTTTCATATACACCGTCCATGCTGAAGGAG													
cds	AGAAACCATGACTGTAAACCTCATAGATGCCAATCACTGTCCTGGTTCTGTCATGTTTCTCTTTGAAGGATACCTTGGAAACATTCCTACACAGGTGATTTTCATATACACCGTCCATGCTGAAGGAG													
Consensus	AGAAACCATGACTGTAAACCTCATAGATGCCAATCACTGTCCTGGTTCTGTCATGTTTCTCTTTGAAGGATACCTTGGAAACATTCCTACACAGGTGATTTTCATATACACCGTCCATGCTGAAGGAG													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
seq	CCTGCTCTGACACTAGGGAACAGATTTCATCTTTATATCTAGACACACCAATTGCAACCCAGCCCTTGTCTCTCTCCCGACAGGAAGCTACTCAACAGATTATCCAGCTAATCCGACAGTTCCCC													
cds	CCTGCTCTGACACTAGGGAACAGATTTCATCTTTATATCTAGACACACCAATTGCAACCCAGCCCTTGTCTCTCTCTCCCGACAGGAAGCTACTCAACAGATTATCCAGCTAATCCGACAGTTCCCC													
Consensus	CCTGCTCTGACACTAGGGAACAGATTTCATCTTTATATCTAGACACACCAATTGCAACCCAGCCCTTGTCTCTCTCTCTCCCGACAGGAAGCTACTCAACAGATTATCCAGCTAATCCGACAGTTCCCC													
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
seq	AACACACATAAAGATTGGCCTCTATAGTCTAGGAAAGAAATCACTGCTGGAGCAGTAGCCCTTGAGTTTCAGACCTGGGTGGTATTGAGTCTCAACGCCCTGGAGTTGGTACAGCTGCTGGCCCTGGC													
cds	AACACACATAAAGATTGGCCTCTATAGTCTAGGAAAGAAATCACTGCTGGAGCAGTAGCCCTTGAGTTTCAGACCTGGGTGGTATTGAGTCTCAACGCCCTGGAGTTGGTACAGCTGCTGGCCCTGGC													
Consensus	AACACACATAAAGATTGGCCTCTATAGTCTAGGAAAGAAATCACTGCTGGAGCAGTAGCCCTTGAGTTTCAGACCTGGGTGGTATTGAGTCTCAACGCCCTGGAGTTGGTACAGCTGCTGGCCCTGGC													
	651	660	670	680	690	700	710	720	730	740	750	760	770	780
seq	AGACGTGTTACAGTGGAGGAAGAGCTGGGCGAATCCACGCTGTGGACCATGGAATCTGCCATTGCGGCATGCTTCAGTGGAAACAGACCCACCCACCATTTGCTATTTTCCCCACAGCCGGA													
cds	AGACGTGTTACAGTGGAGGAAGAGCTGGGCGAATCCACGCTGTGGACCATGGAATCTGCCATTGCGGCATGCTTCAGTGGAAACAGACCCACCCACCATTTGCTATTTTCCCCACAGCCGGA													
Consensus	AGACGTGTTACAGTGGAGGAAGAGCTGGGCGAATCCACGCTGTGGACCATGGAATCTGCCATTGCGGCATGCTTCAGTGGAAACAGACCCACCCACCATTTGCTATTTTCCCCACAGCCGGA													
	781	790	800	810	820	830	840	850	860	870	880	890	900	910
seq	ATACGAAGCCCTACCCACAGCATCTACAGCATCCCTTACTCTGACCATTCATCTACTCTGAGCTTCGAGCATTGTTGACGCTCTGAGGCCCTTGCCAGGTGGTGGCCATAGTCCGTGAACAGCCTTG													
cds	ATACGAAGCCCTACCCACAGCATCTACAGCATCCCTTACTCTGACCATTCATCTACTCTGAGCTTCGAGCATTGTTGACGCTCTGAGGCCCTTGCCAGGTGGTGGCCATAGTCCGTGAACAGCCTTG													
Consensus	ATACGAAGCCCTACCCACAGCATCTACAGCATCCCTTACTCTGACCATTCATCTACTCTGAGCTTCGAGCATTGTTGACGCTCTGAGGCCCTTGCCAGGTGGTGGCCATAGTCCGTGAACAGCCTTG													
	911	920	930											
seq	GAGAGTTTTTTTCAGGATAG													
cds	GAGAGTTTTTTTCAGGATAG													
Consensus	GAGAGTTTTTTTCAGGATAG													

Mutation en 242 C>T

➤ Blast contre banque de rat

		Name	Score	Score	Score	Score	Score	Score	Score
✓	Rattus norvegicus DNA cross-link repair 1B_PSO2 homolog (S. cerevisiae)_mRNA (cDNA clone MGC:114481 IMAGE:...	Norway rat	1712	1712	100%	0.0	99.89%	4013	BC098939.1
✓	Rattus norvegicus DNA cross-link repair 1B (Dclre1b)_transcript variant 2_mRNA	Norway rat	1711	1711	100%	0.0	99.89%	3963	NM_001025687.2
✓	Rattus norvegicus DNA cross-link repair 1B (Dclre1b)_transcript variant 1_mRNA	Norway rat	1711	1711	100%	0.0	99.89%	4086	NM_001389222.1
✓	PREDICTED: Rattus norvegicus DNA cross-link repair 1B (Dclre1b)_transcript variant X3_mRNA	Norway rat	719	1377	80%	0.0	99.75%	3892	XM_006233080.3

➤ Différence au niveau PROT :

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

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
✓	5' exonuclease Apollo [Rattus norvegicus]	Norway rat	638	638	99%	0.0	100.00%	541	NP_001020858.2
✓	DNA cross-link repair 1B_PSO2 homolog (S. cerevisiae) [Rattus norvegicus]	Norway rat	637	637	100%	0.0	99.68%	309	AAH98939.1
✓	RecName: Full=5' exonuclease Apollo; AltName: Full=DNA cross-link repair 1B protein; AltName: Full=SNM1 homolog [Rattus norvegicus]	Norway rat	634	634	99%	0.0	99.67%	541	Q4KLY6.2
✓	PREDICTED: 5' exonuclease Apollo isoform X2 [Rattus norvegicus]	Norway rat	407	407	99%	1e-140	70.03%	480	XP_006233142.1
✓	DNA cross-link repair 1B_PSO2 homolog (S. cerevisiae)_isoform CRA_b [Rattus norvegicus]	Norway rat	378	378	58%	4e-133	100.00%	221	EDL85473.1

CONCLUSION :

Toutes le conditions correspondent à la même forme et au BC et AH mais J'aurais dû me baser sur le NM_001025687 protéine NP_001020858.2 qui est plus longue : voir s'il faut la faire

Dclre1b_202_NotI_Rev

ttaaGCGGCCGCa CTAGACATCATCCACTGTGTTC