

15) Pol L

D'après les amorces d'Alice :

- Taille 1824 NT
- NM_001014168

CGTTT

TCATTGGCTCCCCATGAAAGGTCCAGATCCAGCGCACTTCA

ATGGACCCCAAGGC

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ATCAGCGACAGCGTGCCTGTCTTAGAGCTCTTCTCCAACATCTGGGAGCCGGGACGAAG
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GGCTCTGCCCACTTCAACCGGTCCATGAGAGCTCTGGCCAAGACCAAGGGCATGAGCCTG
TCAGAGCATGCCCTTAGTGCTGTGTGGTCCGGAACAGCCAAGGTGTCAAGGTTCGGGGCT
GGACAAGTGTGCCACCCCCACAGAGAAGGACGCTCTTCAAGCTCTTAGGCCTGCCCTAC
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GAACTAACTGCCTCATCTGCGACCCCTT

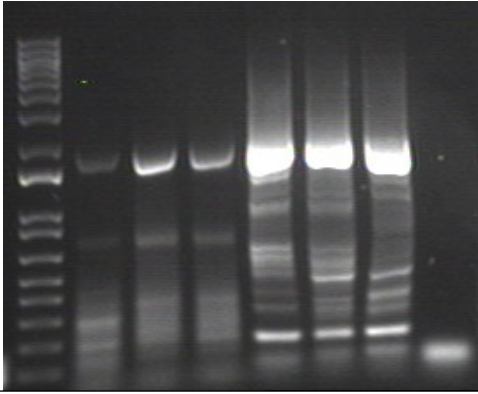
AGCTTTGCCTCACTCTGTCCTGACCACTTG

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GCCTGCCAGCTCTCTCTGGACAGGATCATGCTGCGGTCCCTCTGCTCCCTCTGCTCC
CTGTTCAAGCACAGCAGGTGGCTGGTTTCAAGCTGGTTTCCCTGTACTGCAGGCCTGGTTT
CCTGTACTGAAGGCTGAGCTTCCCTTTCCACCCCAAGACTGATGTAGACATAGGGGGTC
AGGAGAGGCTGCAGGAAGAGAGGGAGGAGCTGTGGGCCAGCATCTTCTTCGGGCCTTC
ACGGTAGAGAAAGCTATGTGGATTCCCTCACCCGCCCACTTCTGTGCAGCTGGAGCTGC
TGGGGGTGGCTGCCAGACTCTGTGAGAGTGGCTTCTAAGGGCCCTGGAGCCTAATAAA
GTGCTTCTGACATTG

MDPQGILKAFPKRKKIHADPSSNALAKIPKREAGDARGWLSSLRAHIMPTGIGRARAELFEKQIIQHGGQVCSAQA
PGVTHIVVDEGM DYERALLRLPQLPPGAQLVKS AWLSLCLQEKKLTDT DGFSLSSPKRSLNEPQPSKSGQDASAP
GTQGVLPRTTSLSPCTR AVSPPPKA EPPKTQTQLSSEDEASDGE GPQVSSADLQALISGHYPTPPGEDGGPDPA
PEALGK WVCAQPSQKATNYNLHITEKLEVLAKAYNVQGD KWRLALGYAKAINALKSFHKPVSSYQEAC SIPGVGRR
MAEKVMEILESGLRLKLDHISDSVPVLELFSNIWGAGTKTAQM WYHQGFRSLEDIRGLASLTAQQAIGLKH YDDFL
DRMPREEAAEIEQMVRVSAQAFNPGLLCVACGSFRRGKVTCGDVDVLITHPDGRSHQGIFSPLLDSL RQQGFLTDD
LVSQEENGQQQKYLGVCR LPGAQRHRRLDIIVVPYSEFACALLYFTGSAHFNRS MRALAKTKGMSLSEHALSAAV
VRNSQGVKVGAGQVLPTPEKDVFKLLGLPYREPAERDW-

- Expériences :

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



Rate	DiT0	DiT24	DiT48	SP	CTX	Eau
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➤ Résultats séquençages

○ pCR4Blunt Pol L rate (cloneD)

➤ Fwd rate 1013NT SEQUENCE AOUT

ATGGAGATCCTGGAGAGTGGGCATCTGCGGAAGCTGGACCACATCAGCGACAGCGTGCCTGTCTTAGAGNTCTT
CTCCAACATCTGGGGAGCCGGGACGAAGACTGCCAGATGTGGTACCATCAGGGCTTCCGAAGCtTAGAAGATA
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CCGGTCCCACAGGGCATCTTCAGCCCACTCCTCGACAGCCTTCGGCAGCAAGGGTTCCTCACAGATGACTTGG
TGAGCCAGGAGGAGAATGGCCAGCAGCAGAAATACCTGGGTGTGTGCCGGCTCCAGGGGGCCGGGCAGCGCC
ACCGGCGACTGGACATCATCGTGGTGCCCTACAGTGAGTTTGCCTGTGCCCTGCTCTACTTCACCGGCTCTGCCC
ACTTCAACCGGTCCATGAGAGCTCTGGCCAAGACCAAGGGCATGAGCCTGTCAGAGCATGCCCTTAGTGCTGCT
GTGGTCCGGAACAGCCAAGGTGTCAAGGTCGGGGCTGGACAAGTGCTGCCCCACCCCCACAGAGAAGGACGTC
TTCAAGCTCTTAGGCCTGCCCTACCGAGAACCGGCTGAACGGGACTGGTGACGTAGGGTTTGGGCAAGGGAAG
CCACGTTGGATGAATACTGCCTCATCGCCACCCTCTT

➤ Rev 986NT SEQUENCE AOUT

AAAGGGNCTAGTCCTGCAGGTTTAAACGAATTCGCCCTTTCATTGGCTCCCATGAAAGGTCCAGATCCAGCGCAC
TTCAATGGACCCCCAGGGCATCCTGAAGGCATTTCCCAAGCGAAAGAAAATTCATGCAGATCCATCATCAAACGC
ACTTGCAAAGATTCCCAAAGGGAGGCAGGAGATGCTAGAGGATGGCTGAGCTCCCTGAGGGCCCCACATTATG
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TGCCAGGCCCCAGGAGTCACTCACATTGTGGTGGATGAAGGCATGGACTATGAACGGGCTCTCCGGCTCCTCA
GACTGCCCCAGCTGCCCCCTGGTGCTCAGCTGGTGAAGTCAGCCTGGCTGAGCTTGTGTCTACAGGAGAAAAAG
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TGGCAGANAANNNCATGGAGATCCTGGAGAGTGGGCATCTGCGGAAGCTGGANCACATCAGCGACAGCGTGC
CTGTCTTANAGCTCTTCTT

➤ Int Fwd Nov 26

GTGNNGGGGNAGGGCCCCAGGTTAGCTCAGCAGATCTGCAAGCCTTGATCAGTGGGCACTACCCCACTCCCC
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GAATGGCAGAGAAGGTCATGGAGATCCTGGAGAGTGGGCATCTGCGGAAGCTGGACCACATCAGCGACAGCGT
GCCTGTCTTAGAGCTCTTCTCCAACATCTGGGGAGCCGGGACGAAGACTGCCAGATGTGGTACCATCAGGGCT
TCCGAAGCCTAGAAGATATCCGAGGCCTGGCCTCCCTGACCGCTCAGCAGGCCATTGGCTTGAAGCACTATGATG
ACTTCTGGACCGCATGCCAGGGAGGAGGCTGCAGAAATTGAGCAGATGGTCCGAGTATCAGCCCAGGCCTTC
AACCCTGGGCTGCTGTGTGTGGCCTGTGGCTCTTTCCGTCGAGGGAAGGTGACCTGTGGGGATGTAGATGTACT
TATTACTCACCCCCGACGGCCGGTCCCACAGGGCATCTTCAGCCCACTCCTCGACAGCCTTCGGCAGCAAGGGTT
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CACAGAGAAGGACGTCTTCAAGCTCTTAGNNCTGCCCTACCGANAACCGGCTGAACGGGACTGGTGACGTNGG
NNTNGGCAAGGAAGCCACGTTGGATGAACTNACTGCCTCATCNNNCCCTNNTNAGGNGAANTCNCNGCNG
CTAAANTCANNCCNCCNATNNNGAGTCNNNTNNANTNANNGGNGNCNNTNNNANNTCNNGNNTGGAAA
NCCT

➤ **Int Rev Nov 26**

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GNAGCATCCCAGGAGNNGGCAGGCGAATGGCAGAGAAGGTCATGNAGATCCTGGAGAGTGGGCANNTGCGG
AAGNTGGACCACATCAGNGNCAGCGTGCCTGTCTTAGAGCTCTTCTCAACATCTGGGGAGCCGGGNGCAAGN
CTGCCCAGATGTGGTACCATCAGNGCTCNGAAG

➤ **Synthèse séquençage rate : NT**

ATGGACCCCCAGGGCATCCTGAAGGCATTTCCCAAGCGAAA 81
GAAAATTCATGCAGATCCATCATCAAACGCACTTGCAAAGATTCCCAAAAGGGAGGCAGG 141
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AGCCCGGGCTGAACCTTTTGAAGAAGCAGATTATCCAGCATGGTGGCCAGGTGTGCTCTGC 261
CCAGGCCCCAGGAGTCACTCACATTGTGGTGGATGAAGGCATGGACTATGAACGGGCTCT 321
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QLSSEDEASDGEQPQVSSADLQALISGHYPTPPGEDGGPDPAEALGGL-
HPRSQAQNGREGHDPGEWASAEAGPHQRQRACLRALQLHLSRDEDCPDVVPGLPKPRRYPRPLDRSAGHWLEAL--
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LGEPPGEWPAAEIPGCVPAAPRGRAAPPATGHHRGALQ-VCLCPALLHRLCPLQPVHESSGQDQGHEPVRACP-
CCCCPEQPRCQGRGWTSAAPHREGRLQALRPALPRTG-TGLV

○ **Blast contre banque rat :**

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

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
✓	PREDICTED: <i>Rattus norvegicus</i> polymerase (DNA) lambda (Poll) transcript variant X1 mRNA	Norway rat	1548	2639	92%	0.0	100.00%	2210	XM_006231545.3
✓	<i>Rattus norvegicus</i> DNA polymerase lambda (Poll) mRNA	Norway rat	1548	2844	100%	0.0	100.00%	2320	NM_001014168.1
✓	PREDICTED: <i>Rattus norvegicus</i> polymerase (DNA) lambda (Poll) transcript variant X2 mRNA	Norway rat	1546	1664	58%	0.0	100.00%	1433	XM_017589456.1

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq	MDPQGILKAFPKRRKIHADPSNNALAKTPKREAGDARGULSSLRAHIMPTGIGRRARALFEKQIIQHGGQVCSAQAPGVTHIYVDEGHDYERALLRLPQLPPGAQLVKSAMLSLCLQEKKLTDTGFS													
ref	MDPQGILKAFPKRRKIHADPSNNALAKTPKREAGDARGULSSLRAHIMPTGIGRRARALFEKQIIQHGGQVCSAQAPGVTHIYVDEGHDYERALLRLPQLPPGAQLVKSAMLSLCLQEKKLTDTGFS													
Consensus	MDPQGILKAFPKRRKIHADPSNNALAKTPKREAGDARGULSSLRAHIMPTGIGRRARALFEKQIIQHGGQVCSAQAPGVTHIYVDEGHDYERALLRLPQLPPGAQLVKSAMLSLCLQEKKLTDTGFS													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq	LSSPKRSLNEPQPSKSGQDASAPGTQGVLPRTTSLSPPECTRAYSPPPKAEKPKPTQTQLSSEDEASDGGGPVSSADLQALISGHYPTPPGEDGGDPDAPEARLGG---LHPFSMQANGREGHGDPEGWA													
ref	LSSPKRSLNEPQPSKSGQDASAPGTQGVLPRTTSLSPPECTRAYSPPPKAEKPKPTQTQLSSEDEASDGGGPVSSADLQALISGHYPTPPGEDGGDPDAPEARLGGKWCYQPSQKATHYMLHTEKLEY													
Consensus	LSSPKRSLNEPQPSKSGQDASAPGTQGVLPRTTSLSPPECTRAYSPPPKAEKPKPTQTQLSSEDEASDGGGPVSSADLQALISGHYPTPPGEDGGDPDAPEARLGG...aQFSqqaAnnr#gHgedeeea													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq	SAEAGPHQROR---ACLRLALLQLHLSRDEDC---PDVPSGLPKPRYPRIPLGLPDR---SAGHWLEALLPGPHAQGGGCKRNDGPGSTSPGLQPHARYCGLWLFPSREGDLHGCRCTYYSPRRPVP													
ref	LAKAYNVQDKKARALGYAKANLAKSFHKPVSSYQACISPGVGRRAHAEKVMETLESLSDSVPVLELFSNHWGAKTKTAQ---HMVHQGFRLSEDLRGLASLTAQAGLKGYYDFLDLRMPREE													
Consensus	LaeAgnhQRr.....aaLralqhlgSr#EaC...PdvgrrgaeKprirrlpGhLrr...hagdslealelgnpaGaeGcrnA#.nsihqGlrplaa!rGLallpar#adglgcrddldrrrrree													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
seq	PGHILPTPPDPSAARYPHRLGEPGGEWAAREITPGCVAPPRGRRAPPATGHRGALQVCLPALLHLRLCPLQPVHESSSGQDQGHFVRACP---CCCGPEPRCGGRGATSAAIHPRERGLQA													
ref	AREIEQVYVSAQAFNPGLLCYACGSFRAGKYT---CGVDYILITHPDGRSHQGIFSPLLDSLRLQGGFLTDDLVSQEENGQQQKYLGVCRPLPGAGQRHRRLDIIYVVPSEFACALLYFTGSAHFNRSNRALA													
Consensus	aaei#qprRpaafanrFgrLceacGefrae!p.CgdaddrgraaPdargHqralqldcldlaqgrLcddqpsqEenGQ#QghgVracP.....cccgpe#fagCagrfgTgaAhfnRegRaqA													
	521	530	540	550	560	570	575							
seq	LRPLAPRTGTGLV													
ref	KTKGMSLSEHALSAARYVNSQGVYVAGQVLPPTPEKDYFKLLGLPYREAPERDW													
Consensus	lrka!prsehalS													

pCR4Blunt Pol L rate (clone D) mauvais : délétion au milieu
qui mène à des stop précoces

○ **pCR4Blunt DiT0 clone E**

➤ **Fwd DiT0 976NT SEQUENCAGE AOUT**

TCATTGGCTCCCATGAAAGGTCCAGATCCAGCGCACTTCA

ATGGACCCCCAGGGCATCCTGAAGGCATTTCCCAAGCGAAAGAAAATTCATGCAGATCCATCATCAAACGCACTT
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CTGGCATTGGGCGAGCCCCGGGCTGAACCTTTTGAGAAGCAGATTATCCAGCATGGTGGCCAGGTGTGCTCTGCC
CAGGCCCCAGGAGTCACTCACATTGTGGTGGATGAAGGCATGGACTATGAACGGGCTCTCCGGCTCCTCAGACT
GCCCCAGCTGCCCCCTGGTGCTCAGCTGGTGAAGTCAGCCTGGCTGAGCTTGTGTCTACAGGAGAAAAAGCTGA
CAGACACGGACGGATTACGCCTTTCCAGCCCTAAGAGGTCCTTGAATGAACCACAGCCCAGCAAGTCAGGCCAA
GATGCTTCTGCTCCTGGCACTCAGGGGGTTCTACCCAGGACAACGCTCTCTCTTTCCCCTCCTGTACCAGAGCTG
TATCTCTCCCCCAAAGGCAGAAAAGCCACCAAAACCCAAACCCAGCTCAGCTCAGAGGATGAAGCCAGTGAT
GGGGAAGGGCCCCAGGTTAGCTCAGCAGATCTGCAAGCCTTGATCAGTGGGCACTACCCCACTCCCCCTGGGG
AAGATGGTGGGCCTGACCCAGCCCCAGAAGCTCTGGGTAAgtgNNNTGTGCACAGCCCTCAAGCCAGAAGGNA
ACTAATTACNACCTGCACATCACAGANAAGCTCGAAGTGCTGGCTAAAGCCTACAATGTCCANGGAGANAAGTG
GANGGNTCTGGGCTATGCNAAGGNCATCAACGCCCTCAANANCTTCCACAAGCCTGTCAGTTCTACCANNAG
GCCTGTAGCATCCNNGNANTTGGCAGGNNAATGGCANANNNNCATGGANATNCTNGNNAAGTGGNNNTCTGN
NNANNTNACNNCNTCA

➤ **Rev DiT0 928NT SEQUENCAGE AOUT**

CAANNNCNNGGNNGNNNAGNNGAGGGNTNTGGGNTATNCNAAGGCCATNAACGCCCTCAAGAGNTTCCAC
AAGCCNGTCAGTTNCNNCNGGAGNCCNGTAGCNTCCCAGGAGTTGGCAGGNGAATGGCAGAGAAGGTAT
GGAGATCNTGGAGAGTGGGCATNTGNGGAAGCTGGACCACATCAGCGACAGCGTGCCTGTCTTAGAGCTCTTC
TCCAACATCTGGGGAGCCGGGACGAAGACTGCCCAGATGTGGTACCATCAGGGCTTCcGAAGCcTAGAAGATAT
CCGAGGCCTGGCCTCCCTGACCGCTCAGCAGGCCATTGGCTTGAAGCACTATGATGACTTCCTGGACCGCATGCC
CAGGGAGGAGGCTGCAGAAATTGAGCAGATGGTCCGAGTATCAGCCCAGGCCTTCAACCCTGGGCTGCTGTGT
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CGGTCCCACAGGGCATCTTCAGCCCACTCCTCGACAGCCTTCGGCAGCAAGGGTTCTCACAGATGACTTGGT
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CCGGCGACTGGACATCATCGTGGTGCCCTACAGTGAGTTTGCCTGTGCCCTGCTCTACTTCACCGGCTCTGCCCA
CTTCAACCGGTCCATGAGAGCTCTGGCCAAGACCAAGGGCATGAGCCTGTCAGAGCATGCCCTTAGTGCTGCTG
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CAAGCTCTTAGGCCTGCCCTACCGAGAACCGGCTGAACGGGACTGGTGA

CGTAGGGTTTGGGCAAGGGAAGCCACGTTGGATGAACTAACTGCCTCATCTGCCACCCTCTTAAGGGCGAATTC
GTTTAAACCTGCAGGACTAGTCCCTTAGT

➤ **Int Fwd Nov26**

GGGGAAGGGCCCCaGGTTAGCTCAGCAGATCTGCAAGCCTTGATCAGTGGGCACTACCCCACTCCCCCTGGGGA
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TCCTCGACAGCCTTCGGCAGCAAGGGTTCCTCACAGATGANTTGGTGAGCCAGGAGGAGAATGGCCAGCAGCA
NNNNACCTGGGTGTGTGCCGGCTCCCAGGGGGCCGGGCAGCGCCACCGGCGACTGGACATCATCGTGGTGCCCT
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NANCAAGGGCATGAGCCTGTANANCATGCCCTTANTGCTGCTGTGGTCCNGANCANCNNNGNNGTNNNNTC
GGGGNNNNNNANTGCTNCCCNCCCC

➤ **Int Rev Nov 26**

AGNCATTNNCNAGNNAANNAANTCATGCAGANCCATCATCNACGCACTGCAANGNTTCCCAAAGGGAGGCN
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ANTNTTGAGAAGCAGATTATCCAGCATGGTGGCCAGGTGTGNTCTGCCAGGCCCCAGGAGTCACTCACATTGT
GGTGGATGAAGGCATGGACTATGAACGGGCTCTCCGGCTCCTCAGACTGCCCCAGCTGCCCCCTGGTGcTCAGC
TGGTGAAGTCAGCCTGGCTGAGCTTGTGTCTACAGGAGAAAAAGCTGACAGACACGGACGGATTCAgCCTTTCC
AGCCcTAAGAGGTCTTGAATGAACCACAGCCCAGCAAGTCAGGCCAAGATGCTTCTGCTCCTGGCACTCAGGG
GGTTCTACCCAGGACAACGCTCTCTTTCCCTCCTTGACCAGAGCTGTATCTCTCCCCAAAGGCAGAAAAAG
CCACCAAAAACCCAAACCCAGCTCAGCTCAGAGGATGAAGCCAGTGATGGGGAAGGGCCCCAGGTTAGCTCAG
CAGATCTGCAAGCCTTGATCAGTGGGCACTACCCCACTCCCCCTGGGGAAGATGGTGGGCCTGACCCAGCCCCA
GAAGCTCTGGGTAAGTGGGTCTGTGCACAGCCCTCAAGCCAGAAGGCAACTAATTACAACCTGCACATCACAGA
GAAGCTCGAAGTGCTGGCTAAAGCCTACAATGTCCAGGGAGACAAGTGAGGGCTCTGGGCTATGCCAAGGCC
ATCAACGCCCTCAAGAGCTTCCACAAGCCTGTCAAGTTCCTACCAGGAGGCCTGTAGCATCCCAGGAGTTGGCAG
GCGAATGGCAGAGAAGGTCATGGAGATCCTGGAGAGTGGGCATCTGCGGAAGCTGGACCACATCAGCGACAG
CGTGCTGTCTTAGAGCTCTTCTCCAACATCTGGGGAGCCGGGACGAAGACTGCCCAGATGtGGTACCATCAGG
GNTCCGAANCCNAGAA

➤ **Synthèse séquençage DiT0 :**

ATGGACCCCCAGGGCATCCTGAAGGCATTTCCTCAAGCGAAAGAAAATTCATGCAGATCCA	60
TCATCAAACGCACTTGCAAAGATTCCCAAAAGGGAGGCAGGAGATGCTAGAGGATGGCTG	120
AGTCCCTGAGGGCCACATTATGCCCACTGGCATTGGGCGAGCCCGGGCTGAACCTTT	180
GAGAAGCAGATTATCCAGCATGGTGGCCAGGTGTGCTCTGCCAGGCCCCAGGAGTCACT	240
CACATTGTGGTGGATGAAGGCATGGACTATGAACGGGCTCTCCGGCTCCTCAGACTGCCC	300
CAGCTGCCCCCTGGTGCTCAGCTGGTGAAGTCAGCCTGGCTGAGCTTGTGTCTACAGGAG	360
AAAAAGCTGACAGACACGGACGGATTACGCTTTCCAGCCCTAAGAGGTCTTGAATGAA	420
CCACAGCCCAGCAAGTCAGGCCAAGATGCTTCTGCTCCTGGCACTCAGGGGGTTCTACCC	480
AGGACAACGCTCTCTTTTCCCTCCTTGACCAGAGCTGTATCTCTCCCCCAAAGGCA	540
GAAAAGCCACCAAAACCCAAACCCAGCTCAGCTCAGAGGATGAAGCCAGTGATGGGGAA	600
GGGCCCCAGGTTAGTTCAGCAGATCTGCAAGCCTTGATCAGTGGGCACTACCCCACTCCC	660
CCTGGGGAAGATGGTGGGCCTGACCCAGCCCCAGAAGCTCTGGGTAAGTGGGTCTGTGCA	
CAGCCCTCAAGCCAGAAGGCAACTAATTACAACCTGCACATCACAGAGAAGCTCGAAGTG	
CTGGCTAAAGCCTACAATGTCCAGGGAGACAAGTGAGGGGCTCTGGGCTATGCCAAGGCC	
ATCAACGCCCTCAAGAGCTTCCACAAGCCTGTCAAGTTCCTACCAGGAGGCCTGTAGCATC	
CCAGGAGTTGGCAGGCGAATGGCAGAGAAGGTATGGAGATCCTGGAGAGTGGGCATCTG	
CGGAAGCTGGACCACATCAGCGACAGCGTGCCTGTCTAGAGCTCTTCTCCAACATCTGG	
GGAGCCGGGACGAAGACTGCCCAGATGTGGTACCATCAGGGCTTCCGAAGCCTAGAAGAT	
ATCCGAGGCCTGGCCTCCCTGACCGCTCAGCAGGCCATTGGCTTGAAGCACTATGATGAC	
TTCTTGGACCGCATGCCAGGGAGGAGGCTGCAGAAATTGAGCAGATGGTCCGAGTATCA	
GCCCAGGCCTTCAACCCTGGGCTGTGTGTGTGGCCTGTGGCTCTTTCCGTCGAGGGAAG	
GTGACCTGTGGGGATGTAGATGTACTTATTACTACCCCGACGGCCGGTCCCACCAGGGC	
ATCTTCAGCCCACTCTCGACAGCCTTCGGCAGCAAGGGTTCCTCACAGATGACTTGGTG	
AGCCAGGAGGAGAATGGCCAGCAGCAGAAATACCTGGGTGTGTGCCGGCTCCCAGGGGCC	
GGGCAGCGCCACCGGCGACTGGACATCATCGTGGTGCCCTACAGTGAGTTTGCCTGTGCC	
CTGCTCTACTTCACCGGCTCTGCCCACTTCAACCGGTCCATGAGAGCTCTGGCCAAGACC	
AAGGCATGAGCCTGTACAGCATGCCCTTAGTGCTGCTGTGGTCCGGAACAGCCAAGGT	
GTCAAGGTCGGGGCTGGACAAGTGCTGCCACCCCCACAGAGAAGGACGCTCTTCAAGCTC	
TTAGGCTGCCCTACCGAGAACCGGCTGAACGGGACTGGTGA	

MDPQGILKAFPKRKKIHADPSSNALAKIPKREAGDARGWLSSLRAHIMPTGIGRARAELFEKQIIQHGGQVCSAQAPGVTHIVV
 DEGMDYERALLRLPQLPPGAQLVKSAWLSLCLQEKKLTDTDGFSLSPPKRSLENEPQPSKSGQDASAPGTQGVLPRTTSLSP
 CTRAVSPPPKAEKPKKTQTQLSSEDEASDGEQPQVSSADLQALISGHYPTPPGEDGGPDPAPEALGKWVCAQPSSQKATNYNL
 HITEKLEVLAKAYNVQGDKWALGYAKAINALKSFHKPVSSYQEACSIPIGVGRRMAEKVMEILESGLRKLDDHISDSVPVLELFS
 NIWGAGTKTAQMWHYHQGFRSLEDIRGLASLTAQQAIGLKHYYDFLDMPREEAAEIEQMVRVSAQAFNPGLLCVACGSFRRG
 KVTCGDVDVLITHPDGRSHQGIFSPLLDSLRLQGGFLTDLLVSQEENGQQQKYLGVCRPGAGQRHRRLDIIVVPYSEFACALLYF
 TGSAHFNRSMRALAKTKGMSLSEHALSAAVVRNSQGVKVGAGQVLPTPEKDVFKLLGLPYREPAERDW-

○ Blast contre banque rat :

☒	Rattus norvegicus DNA polymerase lambda (Poll) mRNA	Norway rat	3175	3175	100%	0.0	99.94%	2320	NM_001014168.1
☒	PREDICTED: Rattus norvegicus polymerase (DNA) lambda (Poll) transcript variant X1 mRNA	Norway rat	2970	2970	93%	0.0	99.94%	2210	XM_006231545.3
☒	PREDICTED: Rattus norvegicus polymerase (DNA) lambda (Poll) transcript variant X2 mRNA	Norway rat	1546	1664	52%	0.0	100.00%	1433	XM_017589456.1

○ Différence Séquençage/CDS au niveau NT :

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq	ATGACGCCCCAGGGCATCTTGARGGCATTTCACAGCGAAGAGAAATTCATGCAGATCCATATCAACGCACTTGCARAGATTCCCAAGAGGGAGGACAGGAGTCTAGAGGATGGCTGAGCTCCCTGA													
cds	ATGACGCCCCAGGGCATCTTGARGGCATTTCACAGCGAAGAGAAATTCATGCAGATCCATATCAACGCACTTGCARAGATTCCCAAGAGGGAGGACAGGAGTCTAGAGGATGGCTGAGCTCCCTGA													
Consensus	ATGACGCCCCAGGGCATCTTGARGGCATTTCACAGCGAAGAGAAATTCATGCAGATCCATATCAACGCACTTGCARAGATTCCCAAGAGGGAGGACAGGAGTCTAGAGGATGGCTGAGCTCCCTGA													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq	GGGCCCACATTATGCCACTGGCATTTGGGCGAGGCCGGGCTGACCTCTTTGAGAGCGAGATTATCCAGCATGGTGGCCAGGTGTGCTCTGCCAGGCCCCAGGAGTCACTACATTGTGGTGGATGAGG													
cds	GGGCCCACATTATGCCACTGGCATTTGGGCGAGGCCGGGCTGACCTCTTTGAGAGCGAGATTATCCAGCATGGTGGCCAGGTGTGCTCTGCCAGGCCCCAGGAGTCACTACATTGTGGTGGATGAGG													
Consensus	GGGCCCACATTATGCCACTGGCATTTGGGCGAGGCCGGGCTGACCTCTTTGAGAGCGAGATTATCCAGCATGGTGGCCAGGTGTGCTCTGCCAGGCCCCAGGAGTCACTACATTGTGGTGGATGAGG													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq	CATGGACTTGAACGGGCTCTCCGGCTCTCAGACTGCCCCAGCTGCCCTTGCTGCTAGCTGGTGAAGTCAGCTGGCTGAGCTTGCTGTACAGGAGAAAGAGCTGACAGACAGGAGCGATTCAAC													
cds	CATGGACTTGAACGGGCTCTCCGGCTCTCAGACTGCCCCAGCTGCCCTTGCTGCTAGCTGGTGAAGTCAGCTGGCTGAGCTTGCTGTACAGGAGAAAGAGCTGACAGACAGGAGCGATTCAAC													
Consensus	CATGGACTTGAACGGGCTCTCCGGCTCTCAGACTGCCCCAGCTGCCCTTGCTGCTAGCTGGTGAAGTCAGCTGGCTGAGCTTGCTGTACAGGAGAAAGAGCTGACAGACAGGAGCGATTCAAC													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
seq	CTTTTCAGCCCTAGAGGCTCTTGATGAGCACACAGCCAGCAGTCAGGCGAGATGCTTCTGCTCTGGCACTCAGGGGGTCTTACCCAGGACACAGCTCTCTCTTCCCTCTCTGTACCCAGAGCTG													
cds	CTTTTCAGCCCTAGAGGCTCTTGATGAGCACACAGCCAGCAGTCAGGCGAGATGCTTCTGCTCTGGCACTCAGGGGGTCTTACCCAGGACACAGCTCTCTCTTCCCTCTCTGTACCCAGAGCTG													
Consensus	CTTTTCAGCCCTAGAGGCTCTTGATGAGCACACAGCCAGCAGTCAGGCGAGATGCTTCTGCTCTGGCACTCAGGGGGTCTTACCCAGGACACAGCTCTCTCTTCCCTCTCTGTACCCAGAGCTG													
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
seq	TATCTCTCTCCCAAGGCGAAGAGCCACCAAAACCCAAACAGCTCAGCTCAGAGGATGAGCAGAGTATGGGAGAGGCGCCAGGTATGCTCAGAGCTCTGACAGCTCTGATCAGTGGGACACTA													
cds	TATCTCTCTCCCAAGGCGAAGAGCCACCAAAACCCAAACAGCTCAGCTCAGAGGATGAGCAGAGTATGGGAGAGGCGCCAGGTATGCTCAGAGCTCTGACAGCTCTGATCAGTGGGACACTA													
Consensus	TATCTCTCTCCCAAGGCGAAGAGCCACCAAAACCCAAACAGCTCAGCTCAGAGGATGAGCAGAGTATGGGAGAGGCGCCAGGTATGCTCAGAGCTCTGACAGCTCTGATCAGTGGGACACTA													
	651	660	670	680	690	700	710	720	730	740	750	760	770	780
seq	CCCACTCTCCCTCGGGAGAGATGGTGGGCTGACCCAGCCCGCAGAGCTCTGGTAGTGGGCTGTGCAACGCCCTCAGCCAGAGGCACTATTAACACCTGCACATCACAGAGAGCTCGAGTGT													
cds	CCCACTCTCCCTCGGGAGAGATGGTGGGCTGACCCAGCCCGCAGAGCTCTGGTAGTGGGCTGTGCAACGCCCTCAGCCAGAGGCACTATTAACACCTGCACATCACAGAGAGCTCGAGTGT													
Consensus	CCCACTCTCCCTCGGGAGAGATGGTGGGCTGACCCAGCCCGCAGAGCTCTGGTAGTGGGCTGTGCAACGCCCTCAGCCAGAGGCACTATTAACACCTGCACATCACAGAGAGCTCGAGTGT													
	781	790	800	810	820	830	840	850	860	870	880	890	900	910
seq	CTGGCTAAGGCTACATGTCTCAGGAGGACAGTGTGAGGGGCTCTGGGCTATGCCAGGCGCATCAGCGCCCTCAGAGGCTTCCACAGGCTGTACGTTCTTCCAGAGGGGCTGTAGCATCCCAAGGAGTTG													
cds	CTGGCTAAGGCTACATGTCTCAGGAGGACAGTGTGAGGGGCTCTGGGCTATGCCAGGCGCATCAGCGCCCTCAGAGGCTTCCACAGGCTGTACGTTCTTCCAGAGGGGCTGTAGCATCCCAAGGAGTTG													
Consensus	CTGGCTAAGGCTACATGTCTCAGGAGGACAGTGTGAGGGGCTCTGGGCTATGCCAGGCGCATCAGCGCCCTCAGAGGCTTCCACAGGCTGTACGTTCTTCCAGAGGGGCTGTAGCATCCCAAGGAGTTG													
	911	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040
seq	CAGGCGGATGTGCAGAGAGGTATGAGATCTCTGAGAGTGGGATCTGCGGAGCTGAGCCACATCAGCGACAGGCTGCGCTGTCTTAGAGCTCTCTCCACATCTGGGAGCCGGGACAGAGCTGC													
cds	CAGGCGGATGTGCAGAGAGGTATGAGATCTCTGAGAGTGGGATCTGCGGAGCTGAGCCACATCAGCGACAGGCTGCGCTGTCTTAGAGCTCTCTCCACATCTGGGAGCCGGGACAGAGCTGC													
Consensus	CAGGCGGATGTGCAGAGAGGTATGAGATCTCTGAGAGTGGGATCTGCGGAGCTGAGCCACATCAGCGACAGGCTGCGCTGTCTTAGAGCTCTCTCCACATCTGGGAGCCGGGACAGAGCTGC													
	1041	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170
seq	CAGAGTGTGGTACCATCAGGGCTCCAGAGCTAGAGATATCCAGAGGCTGGGCTCTGACCGCTCAGCAGGCGATTTGGCTTGAGCACTATGATGACTCTTGGACCGATGCCCAAGGAGGAGGCT													
cds	CAGAGTGTGGTACCATCAGGGCTCCAGAGCTAGAGATATCCAGAGGCTGGGCTCTGACCGCTCAGCAGGCGATTTGGCTTGAGCACTATGATGACTCTTGGACCGATGCCCAAGGAGGAGGCT													
Consensus	CAGAGTGTGGTACCATCAGGGCTCCAGAGCTAGAGATATCCAGAGGCTGGGCTCTGACCGCTCAGCAGGCGATTTGGCTTGAGCACTATGATGACTCTTGGACCGATGCCCAAGGAGGAGGCT													
	1171	1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
seq	GCAGAAATTGACAGATGTGTCAGATATCAGCCAGGCTCTCAACCTGGGCTGCTGTGTGGCTGTGGCTCTTTCCGTCAGGAGAGGATGACCTGAGGAGTATGATGACTTATCTACCCCG													
cds	GCAGAAATTGACAGATGTGTCAGATATCAGCCAGGCTCTCAACCTGGGCTGCTGTGTGGCTGTGGCTCTTTCCGTCAGGAGAGGATGACCTGAGGAGTATGATGACTTATCTACCCCG													
Consensus	GCAGAAATTGACAGATGTGTCAGATATCAGCCAGGCTCTCAACCTGGGCTGCTGTGTGGCTGTGGCTCTTTCCGTCAGGAGAGGATGACCTGAGGAGTATGATGACTTATCTACCCCG													
	1301	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430
seq	ACGGCCGGTCCCAACAGGCGATCTTACGCCACTCTTCACAGCTCTCGCGACAG													

Mutation C<T en 625

- **Différence au niveau PROT :**

	Description	Common Name	Max Score	Total Score	Coverage	E-value	Perc. Ident.	AAC Len	Accession
☒	DNA polymerase lambda [Rattus norvegicus]	Norway rat	1179	1179	100%	0.0	100.00%	573	NP_001014190.1
☒	PREDICTED: DNA polymerase lambda isoform X1 [Rattus norvegicus]	Norway rat	1084	1084	91%	0.0	100.00%	526	XP_006231607.1
☒	PREDICTED: DNA polymerase lambda isoform X2 [Rattus norvegicus]	Norway rat	580	580	48%	0.0	99.64%	300	XP_017444945.1

Consensus
 LSSPKRLMEPQPSKSGDASAPGTGVLPTRTLSLSPCTRVRSPPPKKRAEKPPTQTQLSSSEDAESDGEGPVQSADLQALISGHYTPPGEDGGDPAPERALGKYVCPSSSQKATNYNLHITEXLEV

seq ref
 LAKAYNVQGQKRALGYAKRAINALKSFHKPYSSYOERCSIPGVGRRAAEKVMEITESGLHRKLHDHSIVSVPVLEFSNIWAGTGTAQMHWYHQGFSLSDIRGLASTAQQRIGLGKHYYDFLDNRPREEA
 LAKAYNVQGQKRALGYAKRAINALKSFHKPYSSYOERCSIPGVGRRAAEKVMEITESGLHRKLHDHSIVSVPVLEFSNIWAGTGTAQMHWYHQGFSLSDIRGLASTAQQRIGLGKHYYDFLDNRPREEA
 Consensus
 LAKAYNVQGQKRALGYAKRAINALKSFHKPYSSYOERCSIPGVGRRAAEKVMEITESGLHRKLHDHSIVSVPVLEFSNIWAGTGTAQMHWYHQGFSLSDIRGLASTAQQRIGLGKHYYDFLDNRPREEA

seq ref
 AETEQMVRYSQAQFNPGLLCVACGSFRRGKYTCGDVDYLITHPDGRSHQGISPLLDLRQQGFLTDDLVSQEENGQQQKYLGYCRLPGAGQRHRRLLDIIVYPSEFACALLYFTGSAHRNRSRALAKT
 AETEQMVRYSQAQFNPGLLCVACGSFRRGKYTCGDVDYLITHPDGRSHQGISPLLDLRQQGFLTDDLVSQEENGQQQKYLGYCRLPGAGQRHRRLLDIIVYPSEFACALLYFTGSAHRNRSRALAKT
 Consensus
 AETEQMVRYSQAQFNPGLLCVACGSFRRGKYTCGDVDYLITHPDGRSHQGISPLLDLRQQGFLTDDLVSQEENGQQQKYLGYCRLPGAGQRHRRLLDIIVYPSEFACALLYFTGSAHRNRSRALAKT

seq ref
 KGNSLSEHALSARVYRNSOGVKYGAGQVLPITPEKDVFKLLGLPYREPAERDW
 KGNSLSEHALSARVYRNSOGVKYGAGQVLPITPEKDVFKLLGLPYREPAERDW
 Consensus
 KGNSLSEHALSARVYRNSOGVKYGAGQVLPITPEKDVFKLLGLPYREPAERDW

pCR4Blunt PolL DiT0 clone D parfait

○ pCR4Blunt PolL DiT24hLPS

➤ Fwd DiT24h 1024NT SEQUENCAGE AOUT

TCATTGGCTCCCATGAAAGGTCCAGATCCAGCGCACTTCA

ATGGACCCCCAGGGCATCCTGAAGGCATTTCCCAAGCGAAAGAAAATTCATGCAGATCCATCATCAAACGCACTT
GCAAAGATTCCCAAAAGGGAGGCAGGAGATGCTAGAGGATGGCTGAGCTCCCTGAGGGCCCACATTATGCCCCA
CTGGCATTGGGCGAGCCCCGGGCTGAACCTTTTGAGAAGCAGATTATCCAGCATGGTGGCCAGGTGTGCTCTGCC
CAGGCCCCAGGAGTCACTCACATTGTGGTGGATGAAGGCATGGACTATGAACGGGGCTCTCCGGCTCCTCAGACT
GCCCCAGCTGCCCCCTGGTGCTCAGCTGGTGAAGTCAGCCTGGCTGAGCTTGTGTCTACAGGAGAAAAAGCTGA
CAGACACGGACGGATTACAGCCTTTCCAGCCCTAAGAGGTCCTTGAATGAACCACAGCCCAGCAAGTCAGGCCAA
GATGCTTCTGCTCCTGGCACTCAGGGGGTTCTACCCAGGACAACGCTCTCTCTTTCCCCTCCTTGTACCAGAGCTG
TATCTCTCCCCCAAAGGCAGAAAAGCCACCAAAACCCAAACCCAGCTCAGCTCAGAGGATGAAGCCAGTGAT
GGGGAAGGGCCCCAGAGAAGCTCGAAGTGCTGGCTAAAGCCTACAATGTCCAGGAGACAAGTGGAGGGGCTC
TGGGCTATGCCAAGGCCATCAACGCCCTCAAGAGCTTCCACAAGCCTGTCAAGTTCCTACCAGGGCTTCCGAAGCC
TANAANATATCCNAGNCTGGCCTCCCTGACCGCTCANCNNNCATTGGCTTGAANCACTATGATGACTTCTGG
ACCGCANGCCCAGGGAGGAGNNTGCANAAATTGAGCANANGGTCCNAGTATCAGCCCNGGCCTTCAACCCTG
GGCTGCTGTGTGTGGCCTGTGGCTCTTCCGTCNAGGGAANNNACCTGTGGGGNNGTANATGTAATTATTACTC
NCCNNANGNCCGGNCCCACCAGGGNANNNNCANNNNNNNNNNNCAGCNTNCNNCANCNAGGG

➤ Rev DiT24h 943NT SEQUENCAGE AOUT

GACNACGNTCTNTNTTTCCTCCTTGTACCAGAGCTNNNTCTCCTCCCCAAAGGCAGAAAAGCCACCAAAAAC
CCAAACCCAGNTCAGCTCAGAGGATGAAGCCAGTGATGGGGAAGGGCCCCAGAGAAGCTNGAAGTGCTGGNT
AAAGCNTACAATGTCCAGGGAGACAAGTGAGGGGNTNTGGGCTATGCCAAGGCCATCAACGCCCTCAAGAGCT
TCCACAAGCCTGTCAAGTTCCTANCAGGGCTTCCGAAGCCTAGAAAGATATCCGAGGCCTGGCCTCCCTGACCGCTC
AGCAGGCCATTGGCTTGAAGCACTATGATGACTTCTGGACCGCATGCCAGGGAGGAGGCTGCAGAAATTGA
GCAGATGGTCCGAGTATCAGCCCAGGCCTTCAACCCTGGGCTGCTGTGTGTGGCCTGTGGCTCTTCCGTCGAG
GGAAGGTGACCTGTGGGGATGTAGATGTACTTATTACTCACCCCGACGGCCGGTCCCACCAGGGCATCTTCAGCC
CACTCCTCGACAGCCTTCGGCAGCAAGGGTTCCTCACAGATGACTTGGTGAGCCAGGAGGAGAATGGCCAGCA
GCAGAAATACCTGGGTGTGTGCCGGCTCCAGGGGGCCGGGCAGCGCCACCGGCGACTGGACATCATCGTGGTG
CCCTACAGTGAGTTTGCCTGTGCCCTGCTCTACTTCACCGGCTCTGCCCACTTCAACCGGTCCATGAGAGCTCTGG
CCAAGACCAAGGGCATGAGCCTGTGAGAGCATGCCCTTAGTGCTGCTGTGGTCCGGAACAGCCAAGGTGTCAA
GGTCCGGGGCTGGACAAGTGCTGCCCCACCCCAACAGAGAAGGACGTCTTCAAGCTCTTAGGCCTGCCCTACCGA
GAACCGGCTGAACGGGACTGGTGACGTAGGGTTTGGGCAAGGGAAGCCACGTTGGATGA

➤ Int Fwd Nov26

GGCCCCAGAGAAGCTCGAAGTGCTGGCTAAAGCCTACAATGTCCAGGGAGACAAGTGAGGGGCTCTGGGCTAT
GCCAAGGCCATCAACGCCCTCAAGAGCTTCCACAAGCCTGTCAAGTTCCTACCAGGGCTTCCGAAGCCTAGAAGA
TATCCGAGGCCTGGCCTCCCTGACCGCTCAGCAGGCCATTGGCTTGAAGCACTATGATGACTTCTGGACCGCAT
GCCCAGGGAGGAGGCTGCAGAAATTGAGCAGATGGTCCGAGTATCAGCCCAGGCCTTCAACCCTGGGCTGCTG
TGTGTGGCCTGTGGCTCTTCCGTCGAGGGAAGGTGACCTGTGGGGATGTAGATGTACTTATTACTCACCCCGAC
GGCCGGTCCCACCAGGGCATCTTCAGCCCACTCCTCGACAGCCTTCGGCAGCAAGGGTTCCTCACAGATGACTT
GGTGAGCCAGGAGGAGAATGGCCAGCAGCAGAAATACCTGGGTGTGTGCCGGCTCCAGGGGCCGGGCAGCG
CCACCGGCGACTGGACATCATCGTGGTGCCCTACAGTGAGTTTGCCTGTGCCCTGCTCTACTTCACCGGCTCTGC
CACTTCAACCGGTCCATGAGAGCTCTGGCCAAGACCAAGGGCATGAGCCTGTGAGAGCATGCCCTTAGTGCTG
CTGTGGTCCGGAACAGCCAAGGTGTCAAGGTCGGGGCTGGACAAGTGCTGCCCCACCCCAACAGAGAAGGACGT
CTTCAAGCTCTTAgGCCTGCCCTACCGAGAACCGGCTGAACGGGACTGGTGACGTANGGTTTGGGCAANGGAA
GCCACGTTGGANGAATACTGCCTCATCGCCACCCTCTAAGGGNGAATTCTNTTAAACCTGCAGGACTAGTCC

CTTTAGTGAGGGNTAATTNTGAGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCNCTCA
CAATTCCACACAANNTACNAGCNNNNAGCATAANNTGNAAAGCCNNGGNNGNCTAANGAGTGANCTANNTN
NNNTNNNTNGCGTT

➤ **Int Rev Nov26**

CTGAGCGGNCAGGGAGGCCNNGCCTCNGNTATNTNCNNNGCTTNNNNNNNCCTGGTAGGAACNGNNNNNGN
NNNNNNAGNNNCTNGAGGGNGTNNATGGNCTTGNNNGGGGNNNNAGCCNNGNNNNNGGCTCCCTGGAC
ATTGTAGGNTTTNNNNNGNNCTTCNAGCTTCTCTGNNGNCNTTNNNNNNCACTGGCTTCATCCNCGGNNCNG
AGCNGGGNTTGGGNNNNNGGTGGGTNNNGGGNNTTGGNNNNNNANNNNNNNNNNNNNNNNNNCNNGGA
GGGGANNGNNNGANNGNNNGGGGGGNNNNNNNCCTGAGGGCCANNAGCGNAANNNNNNNNGNCCT
GNNNNNNNGGNTGTGGNNNNNGGNNNNGACNNNNNNNGGNTGGAAAGGGGGANNGNGNCCGTGTCNG
GCNNCTNNGNCNCCTGNANACACNANCTCAGCCNNGNTGNNNNNNCNNNTGANNGNNNGGGGGCNGC
TGNNCCATGCCTTNNTCNACCACAATGTGAGTGA
CTCCTGGGGCCTGGGCAGAGCACACCTGGCCACCATGCTGGATAATCTGCTTCTCAAAGAGTTCAGCCCCGGCT
CGCCAATGCCAGTGGGCATAATGTGGGCCCTCAGGGAGCTCANCCATCCTCTAGCATCTCCTGCCTCCCTTTTG
GGAATCTTTGCAAGTGCCTTGTGATGATGGATCTGCATGAATTTCTTTCNCTTGGGAAATGCCTTCNNGATGCCCT
GGGGGTCCATTGAAGTGCCTGGATCTGGACCTTTCATGGNAGCCAATGAAANGGCNAATTCNCGGCCGCTAA
ATTCANNNCNCCCTNTANTGAGTCGTATTACAATCACTGGCCGTCNNTTTACAACNTCNTGACTGGGAAAACCCT
GGNNTTACCNAACNTAATCNNNTTGCANCANATCCCCTTTCNNNGCTGNNNNANTNNNNANNNNNCCNNAN
CNATCNCCNNNCNAACNNTNCNCNNNNNNNTACGTANGNANTTNA

○ **Synthèse séquençage DiT24hLPS :**

ATGGACCCCCAGGGCATCTCTGAAGGCATTTCCCAAGCGAAAGAAAATTCATGCAGATCCA
TCATCAAACGCACTTGCAAAGATTCCCAAAAGGGAGGCAGGAGATGCTAGAGGATGGCTG
AGCTCCCTGAGGGCCACATTATGCCCACTGGCATTGGGCGAGCCCGGGCTGAACCTTT
GAGAAGCAGATTATCCAGCATGGTGGCCAGGTGTGCTCTGCCAGGCCCCAGGAGTCACT
CACATTGTGGTGGATGAAGGCATGGACTATGAACGGGCTCTCCGGCTCCTCAGACTGCCC
CAGCTGCCCCCTGGTCTCAGCTGGTGAAGTCAGCCTGGCTGAGCTTGTGTCTACAGGAG
AAAAAGCTGACAGACACGGACGGATTACAGCCTTTCCAGCCCTAAGAGGTCTTGAATGAA
CCACAGCCCAGCAAGTCAGGCCAAGATGCTTCTGCTCCTGGCACTCAGGGGGTTCTACCC
AGGACAACGCTCTCTCTTTCCCTCCTTGTAACAGAGCTGTATCTCCTCCCCAAAGGCA
GAAAAGCCACCAAAACCCAAACCCAGCTCAGCTCAGAGGATGAAGCCAGTGATGGGGAA
GGGCCCCAGAGAAGCTCGAAGTGTGGCTAAAGCCTACAATGTCCAGGGAGACAAGTGGA
GGGCTCTGGGCTATGCCAAGGCCATCAACGCCCTCAAGAGCTTCCACAAGCCTGTCAAGT
CCTACCAGGGCTTCCGAAGCCTAGAAGATATCCGAGGCCTGGCCTCCCTGACCGCTCAGC
AGGCCATTGGCTTGAAGCACTATGATGACTTCTGGACCGCATGCCAGGGAGGAGGCTG
CAGAAATTGAGCAGATGGTCCGAGTATCAGCCCAGGCCTTCAACCTGGGCTGCTGTGTG
TGGCCTGTGGCTCTTTCCGTCGAGGGAAGGTGACCTGTGGGGATGTAGATGTACTTATTA
CTCACCCCAGGCGCGTCCACAGGGCATCTTCAGCCCACTCCTCGACAGCCTTCGGC
AGCAAGGGTTCTCTACAGATGACTTGGTGAGCCAGGAGGAGAATGGCCAGCAGCAGAAAT
ACCTGGGTGTGTGCCGGCTCCCAGGGGCCGGGCAGCGCCACCGGCGACTGGACATCATCG
TGGTGCCCTACAGTGAGTTTGCCTGTGCCCTGCTCTACTTCACCGGCTCTGCCACTTCA
ACCGGTCCATGAGAGCTCTGGCCAAGACCAAGGGCATGAGCCTGTGAGAGCATGCCCTTA
GTGCTGCTGTGGTCCGAACAGCCAAGGTGTCAAGGTGGGGCTGGACAAGTGTGCTGCCCA
CCCCACAGAGAAgGACGTCTTCAAGCTCTTAAGCCTGCCCTACCGAGAACCGGCTGAAC
GGGACTGGTGA

MDPQGILKAFPKRKKIHADPSSNALAKIPKREAGDARGWLSSLRAHIMPTGIGRARAELFEKQIIQHGGQVCSAQAPGVTHIVV
DEGMDYERALLRLPQLPPGAQLVKSALSLCLQEKKLTDTDGFSLSPPKRSLENPQPSKSGQDASAPGTQGVLPRTTSLSP
CTRAVSPPPKAEKPKTQTQLSSEDEASDGEQPQRSSKWLKPTMSRETSGGLWAMPRPSTPSRASTSLVPTRASEA-
KISEAWPP-PLSRPLA-STMMTSWTACPGRRQLKLSRWSEYQPRPSTLGCCVWPVALSVEGR-PVGM-
MYLLLTPTAGPTRASSAHSSTAFSGKSSQMTW-

ARRRMASSRNTWVCAGSQGPSATGDWTSSWCPTVSLPVCSTSPALPTSTGP-ELWPRPRA-
ACQSMPLVLLWSGTAKVSRSGLDKCCPPQRRSSSS-ACPTENRLNGTG

o Blast contre banque rat :

	Description	Common Name	Score	Score	Cover	value	Ident	Len	Accession
1	PREDICTED: Rattus norvegicus polymerase (DNA) lambda (Poll)_transcript variant X2_mRNA	Norway rat	1230	1348	52%	0.0	100.00%	1433	XM_017589456.1
2	PREDICTED: Rattus norvegicus polymerase (DNA) lambda (Poll)_transcript variant X1_mRNA	Norway rat	1230	2379	92%	0.0	100.00%	2210	XM_006231545.3
3	Rattus norvegicus DNA polymerase lambda (Poll)_mRNA	Norway rat	1230	2584	100%	0.0	100.00%	2320	NM_001014168.1

o Différence Séquencage/CDS au niveau NT :

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

fud
cds
Consensus
ATGGACCCCGAGGCGATCTTGAGGCGATTCCCAAGCGAAGAGAAATTCATGCAGATCCATCATCAACGCACCTTGCAAGATTCCCAAAAGGGAGCGAGGATGCTAGAGGATGGCTGAGCTCCCTGA
ATGGACCCCGAGGCGATCTTGAGGCGATTCCCAAGCGAAGAGAAATTCATGCAGATCCATCATCAACGCACCTTGCAAGATTCCCAAAAGGGAGCGAGGATGCTAGAGGATGGCTGAGCTCCCTGA
ATGGACCCCGAGGCGATCTTGAGGCGATTCCCAAGCGAAGAGAAATTCATGCAGATCCATCATCAACGCACCTTGCAAGATTCCCAAAAGGGAGCGAGGATGCTAGAGGATGGCTGAGCTCCCTGA

131 140 150 160 170 180 190 200 210 220 230 240 250 260

fud
cds
Consensus
GGGCCCCACATTATGCCCATGGCATTTGGGCGAGCCGGGCTGAACCTTTTGAGAGCAGATTATCCAGCATGGTGGCCAGGTGTGCTCTGCCAGGCCAGAGAGTCACTACATTTGGTGGATGAAGG
GGGCCCCACATTATGCCCATGGCATTTGGGCGAGCCGGGCTGAACCTTTTGAGAGCAGATTATCCAGCATGGTGGCCAGGTGTGCTCTGCCAGGCCAGAGAGTCACTACATTTGGTGGATGAAGG
GGGCCCCACATTATGCCCATGGCATTTGGGCGAGCCGGGCTGAACCTTTTGAGAGCAGATTATCCAGCATGGTGGCCAGGTGTGCTCTGCCAGGCCAGAGAGTCACTACATTTGGTGGATGAAGG

261 270 280 290 300 310 320 330 340 350 360 370 380 390

fud
cds
Consensus
CATGGACTATGAGCGGGCTCTCCGGCTCTCAGACTGCCAGCTGCCCTGGTGTCTGAGTGGTGAAGTCAGCCTGGCTGAGCTTGTGTCTACAGGAGAAAGCTGACAGACCGGACGGATTACAG
CATGGACTATGAGCGGGCTCTCCGGCTCTCAGACTGCCAGCTGCCCTGGTGTCTGAGTGGTGAAGTCAGCCTGGCTGAGCTTGTGTCTACAGGAGAAAGCTGACAGACCGGACGGATTACAG
CATGGACTATGAGCGGGCTCTCCGGCTCTCAGACTGCCAGCTGCCCTGGTGTCTGAGTGGTGAAGTCAGCCTGGCTGAGCTTGTGTCTACAGGAGAAAGCTGACAGACCGGACGGATTACAG

391 400 410 420 430 440 450 460 470 480 490 500 510 520

fud
cds
Consensus
CTTTCCAGCCCTAGAGGCTCTTGATGAGCCACAGCCAGCAGTCAGGCCAGATGCTTGTGCTCTGGCACTCAGGGGGTTCTACCCAGGACACGCTCTCTCTTTCCCTCTTGTACAGAGCTG
CTTTCCAGCCCTAGAGGCTCTTGATGAGCCACAGCCAGCAGTCAGGCCAGATGCTTGTGCTCTGGCACTCAGGGGGTTCTACCCAGGACACGCTCTCTCTTTCCCTCTTGTACAGAGCTG
CTTTCCAGCCCTAGAGGCTCTTGATGAGCCACAGCCAGCAGTCAGGCCAGATGCTTGTGCTCTGGCACTCAGGGGGTTCTACCCAGGACACGCTCTCTCTTTCCCTCTTGTACAGAGCTG

521 530 540 550 560 570 580 590 600 610 620 630 640 650

fud
cds
Consensus
TATCTCTCTCCCAAGGCGAGAAAGCCACAAAGCCAAAGCCAGCTCAGCTCAGAGGATGAGCGAGTGATGGGAGGGGCCCCAG
TATCTCTCTCCCAAGGCGAGAAAGCCACAAAGCCAAAGCCAGCTCAGCTCAGAGGATGAGCGAGTGATGGGAGGGGCCCCAGGTTAGCTCAGCAGATTGACAGCCTTGATCAGTGGGACCTA
TATCTCTCTCCCAAGGCGAGAAAGCCACAAAGCCAAAGCCAGCTCAGCTCAGAGGATGAGCGAGTGATGGGAGGGGCCCCAG

651 660 670 680 690 700 710 720 730 740 750 760 770 780

fud
cds
Consensus
CCCCACTCCCCCTGGGAGAGTGGTGGGCTGACCCAGCCCAAGAGCTCTGGGTAGTGGGTCTGTGCACAGCCCTCAGGCCAGAGGCACTATTTACACCTGCACATCAGAGAGGCTCGAAGTG
CCCCACTCCCCCTGGGAGAGTGGTGGGCTGACCCAGCCCAAGAGCTCTGGGTAGTGGGTCTGTGCACAGCCCTCAGGCCAGAGGCACTATTTACACCTGCACATCAGAGAGGCTCGAAGTG
CCCCACTCCCCCTGGGAGAGTGGTGGGCTGACCCAGCCCAAGAGCTCTGGGTAGTGGGTCTGTGCACAGCCCTCAGGCCAGAGGCACTATTTACACCTGCACATCAGAGAGGCTCGAAGTG

781 790 800 810 820 830 840 850 860 870 880 890 900 910

fud
cds
Consensus
CTGGCTAAGGCTACATGCTCCAGGGAGCAGTGGAGGGCTCTGGGCTATGCCAGGGCCATCAGCGCCCTCAGAGGCTTCACAGGCTGTCAAGTCTCTACAGG
CTGGCTAAGGCTACATGCTCCAGGGAGCAGTGGAGGGCTCTGGGCTATGCCAGGGCCATCAGCGCCCTCAGAGGCTTCACAGGCTGTCAAGTCTCTACAGGAGGCTGTAGCATCCAGAGGTTG
CTGGCTAAGGCTACATGCTCCAGGGAGCAGTGGAGGGCTCTGGGCTATGCCAGGGCCATCAGCGCCCTCAGAGGCTTCACAGGCTGTCAAGTCTCTACAGG

911 920 930 940 950 960 970 980 990 1000 1010 1020 1030 1040

fud
cds
Consensus
GCAGGCGAATGCGAGAGAGGCTATGGAGATCTGGAGAGTGGGCTCTGCGAGGCTGACACCATCAGCGACAGCGTGCCGTCTTAGAGCTCTTCTCCACATCTGGGAGCCGGGACGAGACTGC
GCAGGCGAATGCGAGAGAGGCTATGGAGATCTGGAGAGTGGGCTCTGCGAGGCTGACACCATCAGCGACAGCGTGCCGTCTTAGAGCTCTTCTCCACATCTGGGAGCCGGGACGAGACTGC
GCAGGCGAATGCGAGAGAGGCTATGGAGATCTGGAGAGTGGGCTCTGCGAGGCTGACACCATCAGCGACAGCGTGCCGTCTTAGAGCTCTTCTCCACATCTGGGAGCCGGGACGAGACTGC

1041 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170

fud
cds
Consensus
GCTTCCAGGCTAGAGATATCCAGGGCTGGCTCCCTGACCGCTCAGCAGGCGATTGGCTTGAGCACTATGATGACTCTCTGGACCGCATGCCAGGGAGGAGGCT
CCAGATGTGGTACCATCAGG
GCTTCCAGGCTAGAGATATCCAGGGCTGGCTCCCTGACCGCTCAGCAGGCGATTGGCTTGAGCACTATGATGACTCTCTGGACCGCATGCCAGGGAGGAGGCT

1171 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300

fud
cds
Consensus
GCAGAAATGAGCAGATGGCTCGAGTATCAGCCAGGCTTCARCCCTGGGCTGCTGTGTGTGGCTGTGGCTCTTCCGTCAGGGAGAGGTGACCTGTGGGGATGATGATGACTATTACTACCCCG
GCAGAAATGAGCAGATGGCTCGAGTATCAGCCAGGCTTCARCCCTGGGCTGCTGTGTGTGGCTGTGGCTCTTCCGTCAGGGAGAGGTGACCTGTGGGGATGATGATGACTATTACTACCCCG
GCAGAAATGAGCAGATGGCTCGAGTATCAGCCAGGCTTCARCCCTGGGCTGCTGTGTGTGGCTGTGGCTCTTCCGTCAGGGAGAGGTGACCTGTGGGGATGATGATGACTATTACTACCCCG

1301 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430

fud
cds
Consensus
ACGGCCGGTCCACAGGGGATCTTCAGCCACTCTCGACAGCTTCGGCAGCAGGGTTCTCAGAGTGACTTGGTGAGCCAGGAGAGATGGCCAGCAGCAGAAATACCTGGGTGTGTGCCGCT
ACGGCCGGTCCACAGGGGATCTTCAGCCACTCTCGACAGCTTCGGCAGCAGGGTTCTCAGAGTGACTTGGTGAGCCAGGAGAGATGGCCAGCAGCAGAAATACCTGGGTGTGTGCCGCT
ACGGCCGGTCCACAGGGGATCTTCAGCCACTCTCGACAGCTTCGGCAGCAGGGTTCTCAGAGTGACTTGGTGAGCCAGGAGAGATGGCCAGCAGCAGAAATACCTGGGTGTGTGCCGCT

1431 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560

fud
cds
Consensus
CCAGGGGGCGGGCAGCGCCACCGGCGACTGGACATCATCTGGTGGCTTACAGTGAGTTGGCTGTGGCTTGTCTTACTTACCCGGCTCTGCCACTTCAACCGGTCATGAGAGCTCTGGCCAGAGCC
CCAGGGGGCGGGCAGCGCCACCGGCGACTGGACATCATCTGGTGGCTTACAGTGAGTTGGCTGTGGCTTGTCTTACTTACCCGGCTCTGCCACTTCAACCGGTCATGAGAGCTCTGGCCAGAGCC
CCAGGGGGCGGGCAGCGCCACCGGCGACTGGACATCATCTGGTGGCTTACAGTGAGTTGGCTGTGGCTTGTCTTACTTACCCGGCTCTGCCACTTCAACCGGTCATGAGAGCTCTGGCCAGAGCC

1561 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690

fud
cds
Consensus
AAGGGCATGAGGCTGTGAGAGCATGCCCTTAGTGCTGTGTGGTCCGAGACGCCAGGTTGTCAAGGTCGGGGCTGGACAGTGCTGCCACCCCAACAGAGAGGAGGCTCTTCAAGCTCTTAGGCTTGC
AAGGGCATGAGGCTGTGAGAGCATGCCCTTAGTGCTGTGTGGTCCGAGACGCCAGGTTGTCAAGGTCGGGGCTGGACAGTGCTGCCACCCCAACAGAGAGGAGGCTCTTCAAGCTCTTAGGCTTGC
AAGGGCATGAGGCTGTGAGAGCATGCCCTTAGTGCTGTGTGGTCCGAGACGCCAGGTTGTCAAGGTCGGGGCTGGACAGTGCTGCCACCCCAACAGAGAGGAGGCTCTTCAAGCTCTTAGGCTTGC

1691 1700 1710 1722

fud
cds
Consensus
CCTACCGAGACCGGCTGAACGGGACTGGTGA
CCTACCGAGACCGGCTGAACGGGACTGGTGA
CCTACCGAGACCGGCTGAACGGGACTGGTGA

Séquence tronquée

○ Différence au niveau PROT :

	Description	Common name	Score	Score	Cover	value	Ident	Len	Accession
✓	DNA polymerase lambda [Rattus norvegicus]	Norway rat	360	360	45%	4e-119	99.51%	573	NP_001014190.1
✓	PREDICTED: DNA polymerase lambda isoform X1 [Rattus norvegicus]	Norway rat	264	264	35%	3e-82	99.37%	526	XP_006231607.1

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq	MDPQGILKAFPKKKIADPSSNALAKIPKREAGDARGLSSLRAHIMPTGIGRARRAELEKQIIQHGGQVCSAQAPGVTHIVYDEGMDYERALLRLPQLPPGAQLYKSAMLSLCLQEKKLTDTDGFS													
ref	MDPQGILKAFPKKKIADPSSNALAKIPKREAGDARGLSSLRAHIMPTGIGRARRAELEKQIIQHGGQVCSAQAPGVTHIVYDEGMDYERALLRLPQLPPGAQLYKSAMLSLCLQEKKLTDTDGFS													
Consensus	MDPQGILKAFPKKKIADPSSNALAKIPKREAGDARGLSSLRAHIMPTGIGRARRAELEKQIIQHGGQVCSAQAPGVTHIVYDEGMDYERALLRLPQLPPGAQLYKSAMLSLCLQEKKLTDTDGFS													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq	LSSPKRSLNEPQPSKSGQDASAPGTQGVLPRTTLLSPPCTRAYSPPPKAEKPKKTQTLSSSEDEASDGGEPQSSKCHLKPTMSR-ETSGGLWHPPTSTPSRASTLSVPTBASEAKISEAWPPPLSR													
ref	LSSPKRSLNEPQPSKSGQDASAPGTQGVLPRTTLLSPPCTRAYSPPPKAEKPKKTQTLSSSEDEASDGGEPQSSADLQALISGHYPTTPGEDGGDPAPERALKWVCAQPSQKATNYNLHTEKLE-													
Consensus	LSSPKRSLNEPQPSKSGQDASAPGTQGVLPRTTLLSPPCTRAYSPPPKAEKPKKTQTLSSSEDEASDGGEPQSSadlqalingr.eTpgGedagPrPapearaktscaqPrakaaneiaipekLe.													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq	PLASTMTSHTACPGRRLOKLSRWSEYQPPSTLGCCVNPVALSVEGRPYGMHYLLLTPTAGPTRASSAHSSTAFGSKGSSQHTWARRRMASRNTHVCASQGPGSATGOWTSSMCPTYSLPYPCTSTSP													
ref	VLAKRYNVQGDKMRALGYAKAINALKSFHKPYSS---YDEACSTIPGVGRMAEKVMEILESGLRLKLOHISDSVPVLELFSTNIHGAG--TKTROMHYHQGFRLSDIRGLASLTAQQAIGLKHYDDFLD													
Consensus	pLakamntqgdacrarrlaKairalesqhrPssl.....wqeAcS!eGrgrrrMaeIl!\$eilagghraklaHiSdafgslelfqniWaar..aksa#nMycaGfrgledarGdaslsacqa!gLkhpddfld													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
seq	ALPTSTGPELWPRPRACQSMPLVLLWSGTA---KYSRSGLDKCCPPQRRTSSSSACPTEENRLNGTG													
ref	RMPREERAEIEQHVRVSAQAFNPGLLCVACGSFRGKYTCGDVVLITHPDGRSHQGIFFSPLLOSLRQQGFLTDDLYSQEENGQQQKYLGYCRLPGAGQRHRRLOIIVVPYSEFACALLYFTGSAHFNR													
Consensus	a\$PreeaaEieqrprAaaaQannlgLLcsaca.....KYsrgdLDkccphP#rRshqgiacPIe#rLrqgG.....													
	521	530	540	550	560	570	580							
seq	MRALAKTKGMSLSEHALSRAVVRNSQGVKYGAGQVLPTEKDYFKLLGLPYREPAERDM													
ref														
Consensus														

Pol L DiT24h mauvais

○ PolL DiT48hMix

Pas de clone, n'a jamais poussé

○ Pol L SP clone

Idem

o pCR4Blunt Pol L CTX clone D

➤ Fwd CTX 884NT

CCNTCAACGNCCTCAAGAGNTTCCACAANCCTGTCAGTTNCTNCCAGGAGGCCNGTAGCNTCCCAGGAGTTGG
CAGGNGAATGGCAGAGAAGGTCATGGAGATNCTGGAGAGTGGGCATNTGCGGAAGCTGGACCACATCAGCGA
CAGCGTGCCTGTCTTAGAGNTCTTCTCCAACATCTGGGGAGCCGGGACGAAGACTGCCCAGATGTGGTACCATC
AGGGCTTCCGAAGCcTAGAAGATATCCGAGGCCTGGCCTCCCTGACCGCTCAGCAGGCCATTGGCTTGAAGCAC
TATGATGACTTCCTGGACCGCATGCCCAGGGAGGAGGCTGCAGAAATTGAGCAGATGGTCCGAGTATCAGCCCCA
GGCCTTCAACCCTGGGCTGCTGTGTGTGGCCTGTGGCTCTTCCGTCGAGGGAAGGTGACCTGTGGGGATGTAG
ATGTACTTATTACTACCCCGACGGCCGGTCCCACCAGGGCATCTTCAGCCCACTCCTCGACAGCCTTCGGCAGC
AAGGGTTCTCACAGATGACTTGGTGAGCCAGGAGGAGAATGGCCAGCAGCAGAAATACCTGGGTGTGTGCCG
GCTCCCAGGGGCCGGGCAGCGCCACCGGCGACTGGACATCATCTGGTGCCCTACAGTGAGTTTGCCTGTGCC
TGCTCTACTTCACCGGCTCTGCCCACTTCAACCGTCCATGAGAGCTCTGGCCAAGACCAAGGGCATGAGCCTGT
CAGAGCATGCCCTTAGTGCTGCTGTGGTCCGGAACAGCCAAGGTGTCAAGGTCGGGGCTGGACAAGTGCTGCC
CACCCCCACAGAGAAGGACGTCTTCAAGCTCTTAGGCCTGCCCTACCGAGAACCGGCTGAACGGGACTGGTGA
CGTAGGGTTTGGGCAAGGGAAGCCACGTTGGATGAACTAACTGCCTCATCTGCCACCCTCTT

➤ BGHRev CTX 985NT

TCATTGGCTCCCATGAAAGGTCCAGATCCAGCGCACTTCA

ATGGACCCCCAGGGCATCCTGAAGGCATTTCCTCAAGCGAAAGAAAATTCATGCAGATCCATCATCAAACGCACTT
GCAAAGATTCCCAAAAGGGAGGCAGGAGATGCTAGAGGATGGCTGAGCTCCCTGAGGGGCCACATTATGCCCA
CTGGCATTGGGCGAGCCCGGGCTGAAGTCTTTGAGAAGCAGATTATCCAGCATGGTGGCCAGGTGTGCTCTGCC
CAGGCCCCAGGAGTCACTCACATTGTGGTGGATGAAGGCATGGACTATGAACGGGCTCTCCGGCTCTCAGACT
GCCCCAGCTGCCCCCTGGTGCTCAGCTGGTGAAGTCAGCCTGGCTGAGCTTGTGTCTACAGGAGAAAAAGCTGA
CAGACACGGACGGATTACGCCTTTCAGCCCTAAGAGGTCTTGAATGAACCACAGCCCAGCAAGTCAGGCCAA
GATGCTTCTGCTCCTGGCACTCAGGGGGTTCTACCCAGGACAACGCTCTCTCTTCCCCTCCTTGTACCAGAGCTG
TATCTCTCCCCCAAAGGCAGAAAAGCCACCAAAAACCCAAACCCAGCTCAGCTCAGAGGATGAAGCCAGTGAT
GGGGAAGGGCCCCAGGTTAGCTCAGCAGATCTGCAAGCCTTGATCAGTGGGCACTACCCCACTCCCCCTGGGG
AAGAtGGTGGCCTGACCCAGCCCCAGAAGCTCTGGGTAAGTGGGTCTGTGCACAGCCCTCAAGCCAGAANN
AACTAATTACNACCTGCACATCACAGANAANCTCGAAGTGCTGGCTAAAGCCTACAATGTCCANGGAGACAAGT
GGAGGGNTCTGGGCTATGCCAAGGCCATCAACGCCCTCAANAGCTTCCACAAGCCTGTCAAGTCTTACCANGAG
GCCTGTANCATCCCAGNANTTGGCAGGNNAATGGNANANAAGGNCATGG

➤ Int Fwd Nov 25 (erreur : désigné DiT48 dans fichier séquençage)

GTGNNGGGGNNNGGCCCCAGGTTAGCTCAGCAGATCTGCAAGCCTTGATCAGTGGGCACTACCCCACTCCCC
TGGGGAAGATGGTGGGCCTGACCCAGCCCCAGAAGCTCTGGGTAAGTGGGTCTGTGCACAGCCCTCAAGCCAG
AAGGCAACTAATTACAACCTGCACATCACAGAGAAGCTCGAAGTGCTGGCTAAAGCCTACAATGTCCAGGGAGA
CAAGTGGAGGGCTCTGGGCTATGCCAAGGCCATCAACGCCCTCAAGAGCTTCCACAAGCCTGTCAAGTCTTACC
AGGAGGCCTGTAGCATCCCAGGAGTTGGCAGGCGAATGGCAGAGAAGGTCATGGAGATCCTGGAGAGTGGGC
ATCTGCGGAAGCTGGACCACATCAGCGACAGCGTGCCTGTCTTAGAGCTCTTCTCCAACATCTGGGGAGCCGGG
ACGAAGACTGCCCAGATGTGGTACCATCAGGGCTTCCGAAGCCTAGAAGATATCCGAGGCCTGGCCTCCCTGAC
CGCTCAGCAGGCCATTGGCTTGAAGCACTATGATGACTTCTGGACCGCATGCCAGGGAGGAGGCTGCAGAAA
TTGAGCAGATGGTCCGAGTATCAGCCAGGCCTTCAACCTGGGCTGCTGTGTGTGGCCTGTGGCTCTTCCGTC
GAGGGAAGGTGACCTGTGGGGATGTAGATGTACTTATTACTACCCCGACGGCCGGTCCCACCAGGGCATCTTC
AGCCCACTCCTCGACAGCCTTCGGCAGCAAGGGTTCCTCACAGATGACTTGGTGAGCCAGGAGGANAATGGNC

AGCAGCAGAAATACCTGGGTGTGTGCCGGCTCCCAGGGGCCGGGCAGCGCCACCGGCGACTGNACATCATCGT
GGTGCCCTACAGTGAGTTTGCTGTGCCCTGCTCTACTTCACCGGCTCTGCCACTTCAACCGGTCCATGANAGC
TCTGGCCAANACCAAGGGCATGAGCCTGTCANANCATGCCCTTANTGCTGCTGTGGTCCGGAACANCCAANN
TCANGNTNNGGNTNGANNAGTGCTGCCNACCCCNNNNAGAAAGNNGTNTCANNTNNTNGNNTNCCNTA
CC

➤ **Int rev Nov 25 (erreur : désigné DiT48 dans fichier séquençage)**

ATCCANCANCAANNCTNNNNNNNTNNCAAANNNGCANNNGATGNNAGNGNANGNNGNGNTCCTGN
NNNNNACANTNNGNNCCNNCANNNNGNCGNNCNCGNNTGAACTCTTTGAGNAGCANATNATCCNNCANG
GTGNCCAGNTGTGNTCTNCCNAGGCCCNAGNNNNNNCTCACNNTGTGNTGGANGANNNCNNNNNNNNNN
NNNNGGCTNTCNGNNTCCTNNNNNNNNCNNNNNNNTGCCCCNNGGTGNTCAGNNNNNNNNNNTCANNNNNN
NNGNNNNNTGTGTNTNNNNNNGANNNNNNNNNNCANNNNNNNNNNNGNNNNNNNCNNNNNNNANCCNTAAG
AGGTCNTTGAATGNNNCACAGCCCAGCAAGTCAGGNNANNNNNNTTCTGCTNNTGGCANTCAGGGGGTTCT
ACNCNNGACAACGNTNNNNCTTTCCCNCTTGNACNANNNTGTNNNNCNTCCCCANNNNNNGAAAAG
CCACCAAANNCCAAACCCAGNTCAGCNCANAGGNGAAGCCANTGANGGGGAAGGGCCCCAGGTTAGCTC
AGCAGATCTGCNAGCCTTGATCAGNGGGCNCNTNCCCCACTCCCCNNGGGAAGATGGTGGGCCTGACCCANC
NCCAGAAGNTNNGGNAAGNGGGTNTGTGCACAGCCCTCAANNCAGNNNNNAACTAATTACNACNTGCACA
TCACAGAGAAGCTNGAAGTGCTGGCTAAAGCCTNCAATGTCCNNGGAGACNAGTGAGGGCTNTGGGNTNN
GCCAAGGCCATCAACGCCCTCAAGNGCNTCCACNNGCCNGTCAGTTCCTNCCAGGAGGCCTGTAGCATCCAG
GAGTTGGCAGGCGAATGGCAGAGAAGGTCATGNAGATCCTGGAGNGTGGGCANNTGCGGAAGCNGGNCCAC
ATCAGCNACAGCGTGCTGTCTTAGAGCTCTTCTCAACATCNGGGNAGCCGGGNCGAAGNCTGCCAGATGT
GGTACCATCAGNGCTCNGAAGCNGAA

➤ **Synthèse séquençage CTX: NT**

ATGGACCCCCAGGGCATCCTGAAGGCATTTCCCAAGCGAAAGAAAATTCATGCAGATCCA	60
TCATCAAACGCACTTGCAAAGATTCCCAAAAGGGAGGCAGGAGATGCTAGAGGATGGCTG	120
AGTCCCTGAGGGCCACATTATGCCCACTGGCATTGGGCGAGCCCGGGCTGAACTCTTT	180
GAGAAGCAGATTATCCAGCATGGTGGCCAGGTGTGCTCTGCCAGGCCCCAGGAGTCACT	240
CACATTGTGGTGGATGAAGGCATGGACTATGAACGGGCTCTCCGGCTCCTCAGACTGCCC	300
CAGCTGCCCCCTGGTGCTCAGCTGGTGAAGTCAGCCTGGCTGAGCTTGTGTCTACAGGAG	360
AAAAAGCTGACAGACACGGACGGATTACGCCTTTCCAGCCCTAAGAGGTCTTGAATGAA	420
CCACAGCCCAGCAAGTCAGGCCAAGATGCTTCTGCTCCTGGCACTCAGGGGGTTCTACCC	480
AGGACAACGCTCTCTCTTTCCCTCCTTGTAACAGAGCTGTATCTCCTCCCCAAAGGCA	540
GAAAAGCCACCAAAACCCAAACCCAGCTCAGCTCAGAGGATGAAGCCAGTGATGGGGAA	600
GGGCCCCAGGTTAGCTCAGCAGATCTGCAAGCCTTGATCAGTGGGCACTACCCACTCCC	660
CCTGGGGAAGATGGTGGGCTGACCCAGCCCCAGAAGCTCTGGGTAAAGTGGGTCTGTGCA	720
CAGCCCTCAAGCCAGAAGGCAACTAATTACAACCTGCACATCACAGAGAAGCTCGAAGTG	
CTGGCTAAAGCCTACAATGTCCAGGGAGACAAGTGGAGGGCTCTGGGCTATGCCAAGGCC	
ATCAACGCCCTCAAGAGCTTCCACAAGCCTGTCAAGTTCCTACCAGGAGGCCTGTAGCATC	
CCAGGAGTTGGCAGGCGAATGGCAGAGCATGGAGATCCTGGAGAGTGGGCATCTG	
CGGAAGCTGGACCACATCAGCAGCAGCGTGCCTGTCTTAGAGCTCTTCTCCAACATCTGG	
GGAGCCGGGACGAAGACTGCCAGATGTGGTACCATCAGGGCTTCCGAAGCCTAGAAGAT	
ATCCGAGGCCTGGCCTCCCTGACCGCTCAGCAGGCCATTGGCTTGAAGCACTATGATGAC	
TTCTTGACCGCATGCCAGGGAGGAGGCTGCAGAAATTGAGCAGATGGTCCGAGTATCA	
GCCAGGCCTTCAACCCTGGGCTGCTGTGTGTGGCTGTGGCTCTTTCCGTCGAGGGAAG	
GTGACCTGTGGGGATGTAGATGTACTTATTACTACCCCGACGGCCGGTCCCACCAGGGC	
ATCTTCAGCCCACTCCTCGACAGCCTTCGGCAGCAAGGGTTCTCAGATGACTTGGTG	
AGCCAGGAGGAGAAATGGCCAGCAGCAGAAATACCTGGTGTGTGCCGGCTCCCAGGGGCC	1440
GGGCAGCGCCACCGGCGACTGGACATCATCGTGGTGCCTACAGTGAGTTTGCCTGTGCC	1500
CTGCTCTACTTCACCGGCTCTGCCCACTTCAACCGGTCCATGAGAGCTCTGGCCAAGACC	1560
AAGGCATGAGCCTGTAGAGCATGCCCTTAGTGCTGTGGTCCGGAACAGCCAAGGT	1620
GTCAAGGTCGGGGCTGGACAAGTGCTGCCACCCCCACAGAGAAGGACGTCTTCAAGCTC	1680
TTAGGCTGCCCTACCAGAACCGGTGAACGGGACTGGTGA	1722

MDPQILKAFPKRKIIHADPSSNALAKIPKREAGDARGWLSLRAHIMPTGIGRARAELFEKQIIQHGGQVCSAQAPGVTHIVV
DEGMDYERALLRLPQLPPGAQLVKSAWLSLCLQEKLTDTDGFSLSSPKRSLNEPQPSKSGQDASAPGTQGVLPRTTSLSP

CTRAVSPPPKAEKPKKTQTQLSSEDEASDGEQPVSSADLQALISGHYPTPPGEDGGPDPAPEALGKVVCAQPSSQKATNYNL
HITEKLEVLAKAYNVQGDKWRALGYAKAINALKSFHKPVSSYQEA CSIPGVGRRMAEKVMEILESGLRLKLDHISDVPVLELFS
NIWGAGTKTQMWHYHQGFRSLEDIRGLASLTAQQAIGLKHYYDDFLDRMPREEAAIEQMVRVSAQAFNPGLLCVACGSFRRG
KVTCGDVDVLITHPDGRSHQGI FSPLLDSL RQQGFLTDDLVSQEENGQQQKYLGVCR LPGAQQRHRLDIIVVPYSEFACALLYF
TGS AHFNRS MRALAKTKGMSLSEHALSAAVVRNSQGVKV GAGQVLPTPEKDFV KLLGLPYREPAERDW-

- **Blast contre banque rat :**

	Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☒	Rattus norvegicus DNA polymerase lambda (Poll)_mRNA	Norway rat	3175	3175	100%	0.0	99.94%	2320	NM_001014168.1
☒	PREDICTED: Rattus norvegicus polymerase (DNA) lambda (Poll)_transcript variant X1_mRNA	Norway rat	2970	2970	93%	0.0	99.94%	2210	XM_006231545.3
☒	PREDICTED: Rattus norvegicus polymerase (DNA) lambda (Poll)_transcript variant X2_mRNA	Norway rat	1546	1664	52%	0.0	100.00%	1433	XM_017589456.1

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

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq cds	ATGGACCCCCAGGGCATCTCGAGGCATTTCCTCCAGCGAAGAGAAATCATGCAGATCCATCATCAAGCGACATTCGAAGATTCCCAAGAGGGAGGCGAGAGATGCTAGAGGATGGCTGAGCTCCCTGA													
Consensus	ATGGACCCCCAGGGCATCTCGAGGCATTTCCTCCAGCGAAGAGAAATCATGCAGATCCATCATCAAGCGACATTCGAAGATTCCCAAGAGGGAGGCGAGAGATGCTAGAGGATGGCTGAGCTCCCTGA													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq cds	GGGCCACCATATATGCCACTGGCATTTGGGCGAGCCGGGCTGACCTCTTTGAGAGCAGATTATCCAGCATGGTGCCACAGGTGTGCTCTGCCAGGCCCCAGGAGTCACTACATTGTGGTGGATGAGG													
Consensus	GGGCCACCATATATGCCACTGGCATTTGGGCGAGCCGGGCTGACCTCTTTGAGAGCAGATTATCCAGCATGGTGCCACAGGTGTGCTCTGCCAGGCCCCAGGAGTCACTACATTGTGGTGGATGAGG													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq cds	CATGGACTATGACGGGGTCTTCGGGCTCTCAGACTGCCCGAGCTGCCCTGGTGCTGAGCTGGTGAGTCAAGCTGGCTGAGCTGTGTCTACAGGAGAAAGCTGACAGACAGCGAGGATTCAG													
Consensus	CATGGACTATGACGGGGTCTTCGGGCTCTCAGACTGCCCGAGCTGCCCTGGTGCTGAGCTGGTGAGTCAAGCTGGCTGAGCTGTGTCTACAGGAGAAAGCTGACAGACAGCGAGGATTCAG													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
seq cds	CTTTCCAGGCTTAGAGGTTCTTGATGAAACACAGCCAGCAGCTCAGGCGAGGATGCTTCTGCTCTGGCCTCAGGGGGTTCTACCCAGGACAGCGCTCTCTCTTCCCTCTCTGTACAGAGCTG													
Consensus	CTTTCCAGGCTTAGAGGTTCTTGATGAAACACAGCCAGCAGCTCAGGCGAGGATGCTTCTGCTCTGGCCTCAGGGGGTTCTACCCAGGACAGCGCTCTCTCTTCCCTCTCTGTACAGAGCTG													
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
seq cds	TATCTCTCCCCCAAGGCGAAGAAAGCCACCAAAAGCCAAAGCCAGCTCAGCTCAGAGGATGAGCAGTGATGGGGAAGGGGCCAGGTTAGCTCAGCAGATCTGCAGGCTTGATCAGTGGGCACTA													
Consensus	TATCTCTCCCCCAAGGCGAAGAAAGCCACCAAAAGCCAAAGCCAGCTCAGCTCAGAGGATGAGCAGTGATGGGGAAGGGGCCAGGTTAGCTCAGCAGATCTGCAGGCTTGATCAGTGGGCACTA													
	651	660	670	680	690	700	710	720	730	740	750	760	770	780
seq cds	CCCCACTCCCCCTGGGAGAGATGGTGGGCTTGACCCAGGCCCCAGAGGCTCTGGGTAGTGGGTCTGTGCACAGCCCTCAGGCCAGAGGGCACTAATTACACCTGACATCACAGAGAGCTCGAGTG													
Consensus	CCCCACTCCCCCTGGGAGAGATGGTGGGCTTGACCCAGGCCCCAGAGGCTCTGGGTAGTGGGTCTGTGCACAGCCCTCAGGCCAGAGGGCACTAATTACACCTGACATCACAGAGAGCTCGAGTG													
	781	790	800	810	820	830	840	850	860	870	880	890	900	910
seq cds	CTGGCTAAGGCTTACATATGCTCCAGGGAGCAGTGGAGGGCTCTGGGCTATGCCAGGCCATCAGCGCCCTCAGAGGCTCCACAGGCTGTGAGTCTTCCACAGGGGCTTGAGCATCCAGAGGTTG													
Consensus	CTGGCTAAGGCTTACATATGCTCCAGGGAGCAGTGGAGGGCTCTGGGCTATGCCAGGGCATTACGCGCCCTCAGAGGCTCCACAGGCTGTGAGTCTTCCACAGGGGCTTGAGCATCCAGAGGTTG													
	911	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040
seq cds	GCGGCGAATGGCAGAGAGGCTCATGGAGATCTGGAGAGTGGGCATCTGCGGAAGCTGGACCATCATGCGACAGCGCTGCCTGTCTTAGAGCTCTTCTCCACATCTGGGGAGCCGGGACGAGAGCTGC													
Consensus	GCGGCGAATGGCAGAGAGGCTCATGGAGATCTGGAGAGTGGGCATCTGCGGAAGCTGGACCATCATGCGACAGCGCTGCCTGTCTTAGAGCTCTTCTCCACATCTGGGGAGCCGGGACGAGAGCTGC													
	1041	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170
seq cds	CCGAGTGTGGTACCATCAGGGCTCTCCAGAGCTAGAGATATCCGAGGCTTGCCCTCCCTGACCGCTCAGCAGGCGCATTTGGCTTGAGGACATATGATGACTTCTGGAGCCGATGCCAGGGAGGAGGCT													
Consensus	CCGAGTGTGGTACCATCAGGGCTCTCCAGAGCTAGAGATATCCGAGGCTTGCCCTCCCTGACCGCTCAGCAGGCGCATTTGGCTTGAGGACATATGATGACTTCTGGAGCCGATGCCAGGGAGGAGGCT													
	1171	1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
seq cds	GCAGAAATTGAGCAGATGGTCCGAGTATCAGCCAGGCTCTCAACCTGGGCTGCTGTGTGTGGCTGTGGCTCTTCCGTCAGGGAGAGGTGACCTGTGGGGATGTAGATGTACTTATTACTACCCCG													
Consensus	GCAGAAATTGAGCAGATGGTCCGAGTATCAGCCAGGCTCTCAACCTGGGCTGCTGTGTGTGGCTGTGGCTCTTCCGTCAGGGAGAGGTGACCTGTGGGGATGTAGATGTACTTATTACTACCCCG													
	1301	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430
seq cds	ACGGCCGGTCCACAGGAGCATCTTCAGCCACTCTTCAGAGGCTTCGGCAGCAGGGTTCCTCAGATGACTTGGTAGCCAGGAGGAGATGGCCAGCAGCAGAAATACCTGGGTGTGTGCCGGCT													
Consensus	ACGGCCGGTCCACAGGAGCATCTTCAGCCACTCTTCAGAGGCTTCGGCAGCAGGGTTCCTCAGATGACTTGGTAGCCAGGAGGAGATGGCCAGCAGCAGAAATACCTGGGTGTGTGCCGGCT													
	1431	1440	1450	1460	1470	1480	1490	1500	1510	1520	1530	1540	1550	1560
seq cds	CCAGGGGGCGGGCAGGCCACCGGCGATGGACATCATGTTGTCCTACAGTGAATTTGCTGTGCTGCTTACTTCTACCGGCTTGCCCACTTACCCGGTCCATGAGAGCTCTGGCCAGAGCC													
Consensus	CCAGGGGGCGGGCAGGCCACCGGCGATGGACATCATGTTGTCCTACAGTGAATTTGCTGTGCTGCTTACTTCTACCGGCTTGCCCACTTACCCGGTCCATGAGAGCTCTGGCCAGAGCC													
	1561	1570	1580	1590	1600	1610	1620	1630	1640	1650	1660	1670	1680	1690
seq cds	AAGGGCATGAGCTGTGAGGATGCTTCTAGTGTGCTGTGGTCCGGAACAGCCAGGTTGAGGCTCGGGCTGGACAGTGTGCTCCACCCCAAGAGAGAGGAGCTTTCAGGCTCTTAGGCTGTC													
Consensus	AAGGGCATGAGCTGTGAGGATGCTTCTAGTGTGCTGTGGTCCGGAACAGCCAGGTTGAGGCTCGGGCTGGACAGTGTGCTCCACCCCAAGAGAGAGGAGCTTTCAGGCTCTTAGGCTGTC													
	1691	1700	1710	1720	1730	1740	1750	1760	1770	1780	1790	1800	1810	1820

Mutation en 625 C<T

o Différence au niveau PROT :

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq	MDPQGLKAFPKRKKIHADPSSNALAKIPKREAGDARGHLSSLRAHIMPTGIGRARAELFEKQITQHGQVCSAQAPGYTHIVYDEGMDYERALLRLPQLPPGAQLYKSAHLSLCLQEKKLTDTGFGS													
ref	MDPQGLKAFPKRKKIHADPSSNALAKIPKREAGDARGHLSSLRAHIMPTGIGRARAELFEKQITQHGQVCSAQAPGYTHIVYDEGMDYERALLRLPQLPPGAQLYKSAHLSLCLQEKKLTDTGFGS													
Consensus	MDPQGLKAFPKRKKIHADPSSNALAKIPKREAGDARGHLSSLRAHIMPTGIGRARAELFEKQITQHGQVCSAQAPGYTHIVYDEGMDYERALLRLPQLPPGAQLYKSAHLSLCLQEKKLTDTGFGS													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq	LSSPKRSLNEPQPSKSGQDASAPGTQGVLPRTTSLSPPTCRAYSPPPKAEKPKPTQTLSSSEDEASDGEQPVSSADLQALISGHYPTPPGEDGGDPAPERALGKMYCAQPSQKATNYNLHITKELEY													
ref	LSSPKRSLNEPQPSKSGQDASAPGTQGVLPRTTSLSPPTCRAYSPPPKAEKPKPTQTLSSSEDEASDGEQPVSSADLQALISGHYPTPPGEDGGDPAPERALGKMYCAQPSQKATNYNLHITKELEY													
Consensus	LSSPKRSLNEPQPSKSGQDASAPGTQGVLPRTTSLSPPTCRAYSPPPKAEKPKPTQTLSSSEDEASDGEQPVSSADLQALISGHYPTPPGEDGGDPAPERALGKMYCAQPSQKATNYNLHITKELEY													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq	LAKAYNVQDGKARALGYAKAINALKSFHKPYSSYQACSIPIGVGRRAEKVMEILESGHLRKLHISDSVPVLELFSNINAGGKTAKMWHYHQGFRSLEDIRGLASLTAQQAIGLKHYYDFLDRMPREER													
ref	LAKAYNVQDGKARALGYAKAINALKSFHKPYSSYQACSIPIGVGRRAEKVMEILESGHLRKLHISDSVPVLELFSNINAGGKTAKMWHYHQGFRSLEDIRGLASLTAQQAIGLKHYYDFLDRMPREER													
Consensus	LAKAYNVQDGKARALGYAKAINALKSFHKPYSSYQACSIPIGVGRRAEKVMEILESGHLRKLHISDSVPVLELFSNINAGGKTAKMWHYHQGFRSLEDIRGLASLTAQQAIGLKHYYDFLDRMPREER													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
seq	AEIEQMVRYSAQAFNPGLLCVACGSFRRGKYTCGDVDVLIITHPDGRSHQGITSPLLDSLQQGFLTDOLVSQEENGQQQKYLGVCRPGAGQRHRLDIIVVPYSEFACALLYFTGSAHFNRSRALAKT													
ref	AEIEQMVRYSAQAFNPGLLCVACGSFRRGKYTCGDVDVLIITHPDGRSHQGITSPLLDSLQQGFLTDOLVSQEENGQQQKYLGVCRPGAGQRHRLDIIVVPYSEFACALLYFTGSAHFNRSRALAKT													
Consensus	AEIEQMVRYSAQAFNPGLLCVACGSFRRGKYTCGDVDVLIITHPDGRSHQGITSPLLDSLQQGFLTDOLVSQEENGQQQKYLGVCRPGAGQRHRLDIIVVPYSEFACALLYFTGSAHFNRSRALAKT													
	521	530	540	550	560	570	573							
seq	KGMSLSEHALSAAVVRNSQGVKVGAGQVLPTEKDYFKLLGLPYREPAERDM													
ref	KGMSLSEHALSAAVVRNSQGVKVGAGQVLPTEKDYFKLLGLPYREPAERDM													
Consensus	KGMSLSEHALSAAVVRNSQGVKVGAGQVLPTEKDYFKLLGLPYREPAERDM													

	Name	Score	Score	Cover	value	Ident	Len	Accession
DNA polymerase lambda [Rattus norvegicus]	Norway rat	1179	1179	100%	0.0	100.00%	573	NP_001014190.1
PREDICTED: DNA polymerase lambda isoform X1 [Rattus norvegicus]	Norway rat	1084	1084	91%	0.0	100.00%	526	XP_006231607.1
PREDICTED: DNA polymerase lambda isoform X2 [Rattus norvegicus]	Norway rat	580	580	48%	0.0	99.64%	300	XP_017444945.1
DNA polymerase beta [Rattus norvegicus]	Norway rat	201	201	55%	3e-59	35.15%	335	NP_058837.2

pCR4Blunt poL CTX (clone D) parfait

Séquençage int

PolL_SeqInt_Fwd_1

579 pour 600

AGAAAAGCCACCAAAAACCC

Pol_SeqInt_Rev_1

1160 pour 1010

CAATGGCCTGCTGAGCGG

Pol_SeqInt_Rev_2

1200 pour 1070

CCAGGGTTGAAGGCCTGGGC