

16) Pol M

D'après les amorces d'Alice : pas séquence complète

NM_001011912

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GATGA

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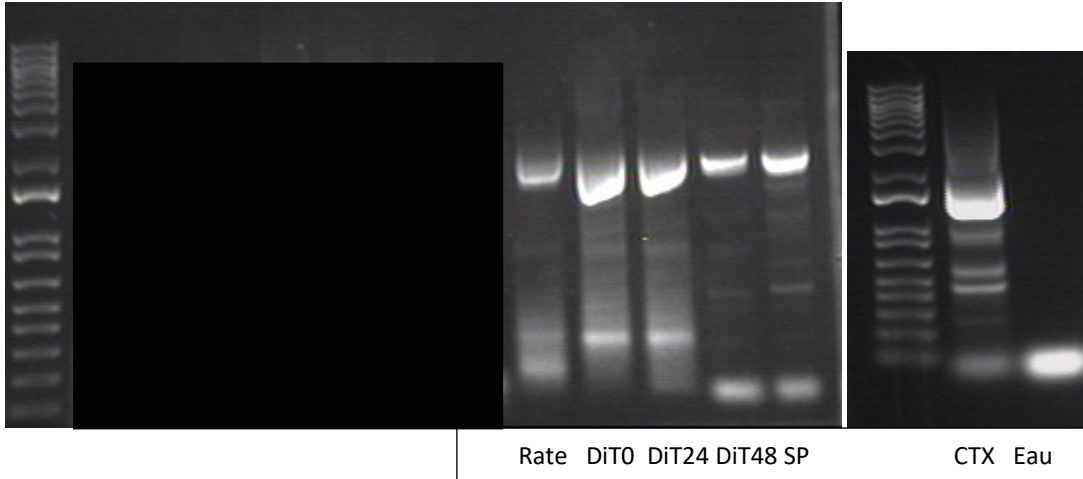
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GGAGGCTCACACCGGTGTGACTGTAACCAGAGCTGCTACAGGCGTGTGT

MLPKRRRRVRAGSPHSALASSTPPAARFPGVAIYLAEP RMGRSRRFLTRLARSKGFRILDVYSSEVTHVVMEE TSAKEAICWQK
DMNALLPDCPQPALDISWFTESMAAGQPVPPEVRRHLEVAEPRKEPPISVTIPAYACQRPSPLTPHNTLLSEALETLAEAGFEG
KEGRFLT FYRAASMLKSLPYPVTSLSQLHGLPYFGEHSFRVIQELLEHGTCEEVEQIRCSERHQTMLKLFTHIFGVGVKTASRWYQE
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QFPFALLGWTGSQFFERELRRFSRQEKGLCLNSHGLFDPERKTFHFATSEEDVFRFLGLKYLPEQRNA-

- Taille 1747 NT

- Expériences :

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



Bande pour RATE, DiT0, DiT24h, DiT48h, SP et CTX

o pCR4Blunt PolM rate

➤ Fwd rate 795NT

TGAGNNAGAGCANCCCCANNGANTGNCCAGCAGCAGAAAGCNGGGNTGCAGTNNTNCCNNNNNNGAGCN
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➤ Rev 693NT

ATGCTTCCGAAGCGACGGCGGGGTGCGAGCAGGGTCCCCACACAGCGCTTTAGCCTCTTCCACGCCCCCAG
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CGCCTGGCGCGGTCCAAAGGCTTCCGCATCCTAGATGTTTACAGCTCAGAGGTGACACATGTGGTGATGGAGGA
GACCTCAGCCAAGGAGGCCATCTGCTGGCAGAAGGACATGAATGCTCTTCTCCAGACTGCCCCGAGCCGGCTC
TGCTAGATATTAGCTGGTTTACAGAGAGCATGGCAGCAGGACAGCCTGTCCCTGAGGAGGTCCGGCACCGCCTG
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AGGGCCGTTTTCTACCTTCTACAGAGCAGCCTCCATGCTCAAGTCCCTACCCTACCCTGTCACATCTTTGAGCCA
GCTGCATGGACTGCCTTACTTTGGGGAACATTCTTTAGAGTAATCCAGGAGCTGCTAGAACATGGAACGTGTGA
GGAGGTGGAACAAATCCGTTGCTCagAAANGCACCAGACCATGAAGCTCTTCACCCACATCTTCGGGGTTGGGG
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TGACCCAGCAGCAGAAAGCAGGGCTGCAGTATTACCANNACCTGANACCCCCAGTTAGCCGGGCANAGGCCG
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➤ Synthèse séquençage rate : 1587NT

ATGCTTCCGAAGCGACGGCGGGGTGCGAGCAGGGTCCCCACACAGCGCTTTAGCCTCT	60
TCCACGCCCCCAGCGCGCGCTTCCCGGGTGTAGCCATCTACCTTGCGGAGCCGCGAATG	120
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GATGTTTACAGCTCAGAGGTGACACATGTGGTGATGGAGGAGACCTCAGCCAAGGAGGCC	240
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GAGACACTGGCGGAGGCAGCGGGCTTCGAAGGCAAAGAGGGCCGTTTTCTCACCTTCTAC	540
AGAGCAGCCTCCATGCTCAAGTCCCTACCCTACCCTGTCACATCTTTGAGCCAGCTGCAT	600
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ACGTGTGAGGAGGTGGAACAAATCCGTTGCTCagAAANGCACCAGACCATGAAGCTCTC	720
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ACCCTNNATGANCTCANAGAGCANCCCCAGANACTGACCCAGCAGCAGAAAGCAGGGCTG	840

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Séquence en trop par rapport au CDS

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 TVTLTGGF XRGLQGH D VDFLITHXEEGQEVGLLPRVMRXXRAR-
 GPPVPCPGVTTEWPSALPEPWHTRPHLPFSQGLVLYHQYHRSHLADSAHILRQRSTMDAFERSFCILRLPQSQQA
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 VFRFLGLKYL PPEQRNA-

➤ **Blast contre banque rat :**

Description	Score	Score	Cover	value	Ident	Accession
Rattus norvegicus DNA polymerase mu (Polm). mRNA	1914	2692	94%	0.0	98.41%	NM_001011912.1
PREDICTED: Rattus norvegicus polymerase (DNA) mu (Polm). transcript variant X3. mRNA	1858	2637	94%	0.0	97.32%	XM_006251213.3
PREDICTED: Rattus norvegicus polymerase (DNA) mu (Polm). transcript variant X4. mRNA	1639	2417	87%	0.0	96.54%	XM_006251214.3
PREDICTED: Rattus norvegicus polymerase (DNA) mu (Polm). transcript variant X2. mRNA	1563	2341	82%	0.0	98.07%	XM_006251212.3
PREDICTED: Rattus norvegicus polymerase (DNA) mu (Polm). transcript variant X1. mRNA	1507	2286	82%	0.0	96.76%	XM_006251211.3

➤ Différence Séquençage/CDS au niveau NT :

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq	ATGCTTCCGAGAGCAGCGGGCGGGTGCAGCAGGGTCCCAACACAGCGCTTTAGCTCTTCCAGCGCCCCAGCGGGCGGCTTCCGGGTGTAGCCATCTACCTTGCAGAGCCGCAATGGCCGCGAGCC													
refprot	ATGCTTCCGAGAGCAGCGGGCGGGTGCAGCAGGGTCCCAACACAGCGCTTTAGCTCTTCCAGCGCCCCAGCGGGCGGCTTCCGGGTGTAGCCATCTACCTTGCAGAGCCGCAATGGCCGCGAGCC													
Consensus	ATGCTTCCGAGAGCAGCGGGCGGGTGCAGCAGGGTCCCAACACAGCGCTTTAGCTCTTCCAGCGCCCCAGCGGGCGGCTTCCGGGTGTAGCCATCTACCTTGCAGAGCCGCAATGGCCGCGAGCC													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq	GCCGGGCTTCTCAGCTCGCTTGGCGGGTCCAAAGGCTTCCGCATCTAGATGTTTACAGCTCAGAGGTGACACATGTGGTGTATGAGGAGAGCTCAGCCAGGAGGGCCATCTGCTGGCAGAGGACAT													
refprot	GCCGGGCTTCTCAGCTCGCTTGGCGGGTCCAAAGGCTTCCGCATCTAGATGTTTACAGCTCAGAGGTGACACATGTGGTGTATGAGGAGAGCTCAGCCAGGAGGGCCATCTGCTGGCAGAGGACAT													
Consensus	GCCGGGCTTCTCAGCTCGCTTGGCGGGTCCAAAGGCTTCCGCATCTAGATGTTTACAGCTCAGAGGTGACACATGTGGTGTATGAGGAGAGCTCAGCCAGGAGGGCCATCTGCTGGCAGAGGACAT													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq	GAATGCTCTTCTCCAGACTGCCCGAGCGGGCTGCTAGATATTAGCTGGTTTACAGAGAGCATGGCAGCAGGACAGCCTGTCCCTGAGGAGGTCGGGACCCGCTGGAGGTAGCTGAGCCAGGAG													
refprot	GAATGCTCTTCTCCAGACTGCCCGAGCGGGCTGCTAGATATTAGCTGGTTTACAGAGAGCATGGCAGCAGGACAGCCTGTCCCTGAGGAGGTCGGGACCCGCTGGAGGTAGCTGAGCCAGGAG													
Consensus	GAATGCTCTTCTCCAGACTGCCCGAGCGGGCTGCTAGATATTAGCTGGTTTACAGAGAGCATGGCAGCAGGACAGCCTGTCCCTGAGGAGGTCGGGACCCGCTGGAGGTAGCTGAGCCAGGAG													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
seq	GAACCCCCATCTCAGTGACGATACAGCTTATGCTGTGACGCGCCCTCGCTCTCACACCCATACACACTTCCTCTCAGAGGCTCTGGAGACACTGGCGAGGACGCGGGCTTCGAGGCAAGAGAG													
refprot	GAACCCCCATCTCAGTGACGATACAGCTTATGCTGTGACGCGCCCTCGCTCTCACACCCATACACACTTCCTCTCAGAGGCTCTGGAGACACTGGCGAGGACGCGGGCTTCGAGGCAAGAGAG													
Consensus	GAACCCCCATCTCAGTGACGATACAGCTTATGCTGTGACGCGCCCTCGCTCTCACACCCATACACACTTCCTCTCAGAGGCTCTGGAGACACTGGCGAGGACGCGGGCTTCGAGGCAAGAGAG													
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
seq	GCCGTTTTCTACCTTCTACAGAGCAGCCTCCATGCTCAAGTCCCTACCTACCTGTGCACATCTTTGAGCCAGCTGCATGGACTGCCTTACTTTGGGGACATTCCTTTAGAGTATCCAGGAGCTGCT													
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Consensus	GCCGTTTTCTACCTTCTACAGAGCAGCCTCCATGCTCAAGTCCCTACCTACCTGTGCACATCTTTGAGCCAGCTGCATGGACTGCCTTACTTTGGGGACATTCCTTTAGAGTATCCAGGAGCTGCT													
	651	660	670	680	690	700	710	720	730	740	750	760	770	780
seq	AGAACATGGAGCGTGTAGGAGGTGGACAAATCCGTTGCTCAGAAAGCACCAGACCATGAGGCTCTTACCCACATCTTCGGGGTTGGGGTGAAGACTGCTAGCCGGTGGTACCAAGAGGGCTACGA													
refprot	AGAACATGGAGCGTGTAGGAGGTGGACAAATCCGTTGCTCAGAAAGCACCAGACCATGAGGCTCTTACCCACATCTTCGGGGTTGGGGTGAAGACTGCTAGCCGGTGGTACCAAGAGGGCTACGA													
Consensus	AGAACATGGAGCGTGTAGGAGGTGGACAAATCCGTTGCTCAGAAAGCACCAGACCATGAGGCTCTTACCCACATCTTCGGGGTTGGGGTGAAGACTGCTAGCCGGTGGTACCAAGAGGGCTACGA													
	781	790	800	810	820	830	840	850	860	870	880	890	900	910
seq	ACCTCTNNATGANTCANAGAGCANCACAGANACTGACCCAGCAGCAGAGAGCGGGTGCAGTATTACCANACCTGANACCCAGGTAGCCGGGAGAGGCCGAGGCTCTGCAGCAGTTGGTAGAGG													
refprot	ACCTCTGGATGAGCTCAGAGAGCAGCCCGAGAGACTGACCCAGCAGCAGAGAGCGGGTGCAGTATTACCAAGGACCTGAGACCCAGTTAGCCGGGAGAGGCCGAGGCTCTGCAGCAGTTGGTAGAGG													
Consensus	ACCTCTNNATGANTCANAGAGCANCACAGANACTGACCCAGCAGCAGAGAGCGGGTGCAGTATTACCANACCTGANACCCAGGTAGCCGGGAGAGGCCGAGGCTCTGCAGCAGTTGGTAGAGG													
	911	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040
seq	CAGCCATGAGGGAGATCTCGCCGGAGCCACTGTACACTGACTGGCGGTTTCGAGGGGGAGTTACAGGTCATGACGTGGACTTCCTTATCACCACCTTAGGAGGGGCCAGAGATAGGGCTGCT													
refprot	CAGCCATGAGGGAGATCTCGCCGGAGCCACTGTACACTGACTGGCGGTTTCGAGGGGGAGTTACAGGTCATGACGTGGACTTCCTTATCACCACCTTAGGAGGGGCCAGAGATAGGGCTGCT													
Consensus	CAGCCATGAGGGAGATCTCGCCGGAGCCACTGTACACTGACTGGCGGTTTCGAGGGGGAGTTACAGGTCATGACGTGGACTTCCTTATCACCACCTTAGGAGGGGCCAGAGATAGGGCTGCT													
	1041	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170
seq	GCCAGAGTGATGAGGTNNNTCAGAGCCAGGTGAGGGGCTTCAGTGCCCTGCCAGGAGTGACCACTGAGTGGCCCTCCGCTTCCAGAGCCGTGGCAGACAGGCCACACTGCTCCCTTCTCCAG													
refprot	GCCAGAGTGATGAGGTNNNTCAGAGCCAGGTGAGGGGCTTCAGTGCCCTGCCAGGAGTGACCACTGAGTGGCCCTCCGCTTCCAGAGCCGTGGCAGACAGGCCACACTGCTCCCTTCTCCAG													
Consensus	GCCAGAGTGATGAGGTNNNTCAGAGCCAGGTGAGGGGCTTCAGTGCCCTGCCAGGAGTGACCACTGAGTGGCCCTCCGCTTCCAGAGCCGTGGCAGACAGGCCACACTGCTCCCTTCTCCAGAG													
	1171	1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
seq	GGACTTGTGCTGTACACAGTACCATCGAGCCACTTAGCGGACTTGCCACATCTTGGCGGAGAGGTCACCATGGATGCTTTTGAAGAGGAGTTTCTGCATCTTGGCTTGCACAGTCCACAGG													
refprot	GGACTTGTGCTGTACACAGTACCATCGAGCCACTTAGCGGACTTGCCACATCTTGGCGGAGAGGTCACCATGGATGCTTTTGAAGAGGAGTTTCTGCATCTTGGCTTGCACAGTCCACAGG													
Consensus	GGACTTGTGCTGTACACAGTACCATCGAGCCACTTAGCGGACTTGCCACATCTTGGCGGAGAGGTCACCATGGATGCTTTTGAAGAGGAGTTTCTGCATCTTGGCTTGCACAGTCCACAGG													
	1301	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430
seq	CAGCTTAGAGGGGGCCCTGCATCCCTGCCARCTGGAAGCTGTGAGGGTAGATCTTGTGGTCACTCCACAGCCAGTTCCCTTTGCTCTTCTTGGCTGGACTGGCTCCAGTTTTTTGAGAGGGA													
refprot	CAGCTTAGAGGGGGCCCTGCATCCCTGCCARCTGGAAGCTGTGAGGGTAGATCTTGTGGTCACTCCACAGCCAGTTCCCTTTGCTCTTCTTGGCTGGACTGGCTCCAGTTTTTTGAGAGGGA													
Consensus	CAGCTTAGAGGGGGCCCTGCATCCCTGCCARCTGGAAGCTGTGAGGGTAGATCTTGTGGTCACTCCACAGCCAGTTCCCTTTGCTCTTCTTGGCTGGACTGGCTCCAGTTTTTTGAGAGGGA													
	1431	1440	1450	1460	1470	1480	1490	1500	1510	1520	1530	1540	1550	1560
seq	GCTACGGCGATTACGCGGGCAGAGAGAGGGGCTGTGCTTATAGCCACGGGCTGTTTGTATCTGAGCGGAGACATTTTCCACGCACTTCTGAGGAGAGATGTTTTCAGGTTCTGGGCTCAGATAT													
refprot	GCTACGGCGATTACGCGGGCAGAGAGAGGGGCTGTGCTTATAGCCACGGGCTGTTTGTATCTGAGCGGAGACATTTTCCACGCACTTCTGAGGAGAGATGTTTTCAGGTTCTGGGCTCAGATAT													
Consensus	GCTACGGCGATTACGCGGGCAGAGAGAGGGGCTGTGCTTATAGCCACGGGCTGTTTGTATCTGAGCGGAGACATTTTCCACGCACTTCTGAGGAGAGATGTTTTCAGGTTCTGGGCTCAGATAT													
	1561	1570	1580	1587										
seq	CTTCTCCAGAGCAGAGAAATGCTTGA													
refprot	CTTCTCCAGAGCAGAGAAATGCTTGA													
Consensus	CTTCTCCAGAGCAGAGAAATGCTTGA													

Intron 8-9 présent

➤ Différence au niveau PROT :

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seq      |-----|
refprot  |-----|
Consensus
MLPKRRRRVRAGSPHSALASSTPPAARFPGVAIYLAEPRHGRSRRRAFLRLARSKGFRILDVYSSEYTHVYMEETSAKEAICHQKDMNALLPDCPQPALLDISWFTESMAAGQVPVEEVHRLEVAEPRK
MLPKRRRRVRAGSPHSALASSTPPAARFPGVAIYLAEPRHGRSRRRAFLRLARSKGFRILDVYSSEYTHVYMEETSAKEAICHQKDMNALLPDCPQPALLDISWFTESMAAGQVPVEEVHRLEVAEPRK
MLPKRRRRVRAGSPHSALASSTPPAARFPGVAIYLAEPRHGRSRRRAFLRLARSKGFRILDVYSSEYTHVYMEETSAKEAICHQKDMNALLPDCPQPALLDISWFTESMAAGQVPVEEVHRLEVAEPRK

131      140      150      160      170      180      190      200      210      220      230      240      250      260
|-----|
seq      |-----|
refprot  |-----|
Consensus
EPPISVTIPAYACQRPSP LTPHNTLLSEALETLAEAGFEGKEGRFLT FYRAASHMLKSLPYPTSLSQLHGLPYFGEHSFRVIQELLEHGTCCEEVEQIRCSEHQHTMKLFTHIFGVGYKTASRHYQXGLR
EPPISVTIPAYACQRPSP LTPHNTLLSEALETLAEAGFEGKEGRFLT FYRAASHMLKSLPYPTSLSQLHGLPYFGEHSFRVIQELLEHGTCCEEVEQIRCSEHQHTMKLFTHIFGVGYKTASRHYQXGLR
EPPISVTIPAYACQRPSP LTPHNTLLSEALETLAEAGFEGKEGRFLT FYRAASHMLKSLPYPTSLSQLHGLPYFGEHSFRVIQELLEHGTCCEEVEQIRCSEHQHTMKLFTHIFGVGYKTASRHYQXGLR

261      270      280      290      300      310      320      330      340      350      360      370      380      390
|-----|
seq      |-----|
refprot  |-----|
Consensus
TXXXLXEXPQXL TQQKAGLQYYXXLXTPVSRAREALQQL YEAMREILPGATVTL TGGFXRGKLGQHDVDFLITHXEEGQEVGLLPRVHRXXRARGPPVPYPCGVTTENPSALPEPHHTRPHLPFSQ6
TLDLREQPQL TQQKAGLQYYQDLSTPVSRAREALQQL YEAMREILPGATVTL TGGFRRGKLGQHDVDFLITHPEEGQEVGLLPRVHRCLQ.....SQ6
TIdLrEqPQL TQQKAGLQYYqDLsTPVSRAREALQQL YEAMREILPGATVTL TGGFRRGKLGQHDVDFLITHPEEGQEVGLLPRVHRcLr.....SQ6

391      400      410      420      430      440      450      460      470      480      490      500      510      520
|-----|
seq      |-----|
refprot  |-----|
Consensus
LVLYHQYHRSHLADSAHILRQRSTHDAFERSFCILRLPQSQQAAL EGPLHPCPTAKAVRYDLVYTPNSQFPFALLGWTGSOFFERELRRFSRQEKGLCLNSHGLFDPERKTFHFATSEEDVFRFLGLKYL
LVLYHQYHRSHLADSAHILRQRSTHDAFERSFCILRLPQSQQAAL EGPLHPCPTAKAVRYDLVYTPNSQFPFALLGWTGSOFFERELRRFSRQEKGLCLNSHGLFDPERKTFHFATSEEDVFRFLGLKYL
LVLYHQYHRSHLADSAHILRQRSTHDAFERSFCILRLPQSQQAAL EGPLHPCPTAKAVRYDLVYTPNSQFPFALLGWTGSOFFERELRRFSRQEKGLCLNSHGLFDPERKTFHFATSEEDVFRFLGLKYL

521 527
|-----|
seq      |-----|
refprot  |-----|
Consensus
PPEQRNA
PPEQRNA
PPEQRNA

```

	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
✓	DNA-directed DNA/RNA polymerase mu [Rattus norvegicus]	954	954	100%	0.0	90.89%	NP_001011912.1
✓	PREDICTED: DNA-directed DNA/RNA polymerase mu isoform X3 [Rattus norvegicus]	948	948	100%	0.0	90.21%	XP_006251275.1
✓	PREDICTED: DNA-directed DNA/RNA polymerase mu isoform X2 [Rattus norvegicus]	828	1656	89%	0.0	88.40%	XP_006251274.1
✓	PREDICTED: DNA-directed DNA/RNA polymerase mu isoform X1 [Rattus norvegicus]	822	1644	89%	0.0	87.66%	XP_006251273.1

pCR4Blunt Pol M rate (clone E) un seul intron (8-9) dans le milieu de séquence (?) voir si autre clone à séquencer sinon refaire PCR

o **pCR4Blunt PolM rate : NOUVEAU CLONAGE**

➤ **Fwd rate 962NTNT**

ATGCTTCCGAAGCGACGGCGGGGTGCGAGCAGGGTCCCCACACAGCGCTTTAGCCTCTTCCACGCCCCCAG
CGGCGCGCTTCCCGGGTGTAGCCATCTACCTTGCGGAGCCGCGAATGGGCCGAGCCGCCGGGCCTTCCTCACT
CGCCTGGCGCGGTCCAAAGGCTTCCGCATCCTAGATGTTTACAGCTCAGAGGTGACACATGTGGTGATGGAGGA
GACCTCAGCCAAGGAGGCCATCTGCTGGCAGAAGGACATGAATGCTCTTCTCCAGACTGCCCCGAGCCGGCTC
TGCTAGATATTAGCTGGTTTACAGAGAGCATGGCAGCAGGACAGCCTGTCCCTGAGGAGGTCCGGCACC GCCTG
GAGGTAGCTGAGCCCAGGAAGGAACCCCCATCTCAGTGACGATACCAGCTTATGCCTGTCAGCGCCCCCTCGCCT
CTCACACCCCATAACTCTCCTCTCAGAGGCTCTGGAGACACTGGCGGAGGCAGCGGGCTTCGAAGGCAAAG
AGGGCCGTTTTCTACCTTCTACAGAGCAGCCTCCATGCTCAAGTCCCTACCCTACCCTGTACATCTTTGAGCCA
GCTGCATGGACTGCCTTACTTTGGGGAACATTCTTTAGAGTAATCCAGGAGCTGCTAGAACATGGAACGTGTGA
GGAGGTGGAACAAATCCGTTGCTCAGAAAGGCACCAGACCATGAAGCTCTTCACcCACATCTTCGGGGTTGGGG
TGAAGACTGCTAGCCGGTGGTACCAGGAAGGGCTACGAACCCTGNATGAGCTCANANAGCAGCCCCAGAGACT
GACCCAGCAGCAGAAAGCNGNCTGCAGTATTACCAGGNNCTGAGCACCCCAGTTAGCCGGGCAGANGCCGAG
GNTCTGCANCACTTGGTAGAGGCAGCCATGANGGANATCCTGCCCGGANCNNCTGNCNNACTGACTGNNGG
NTTNCGANGGGGNAGTTNNNAGNTCATGA

➤ **Rev 962NT**

AAGCTCTTCACCCACNNNTCGGGNTNGGGTGAAGACTGCTAGCCGGNNGTACCAGGAAGGGCTACGAACCC
NGGATGAGNTCAGAGAGCAGCCCCAGAGACTGACCCAGCAGCAGAAAGCAGGGCTGCAGTATTANCAGGAC
NTGAGCACCCCAGTTAGCCGGGCAGAGGCCGAGGCTcTGCAGCAGTTGGTAGAGGCAGCCATGAGGGAGAT
CcTGCCcGGAGCCACTGTCACACTGACTGGCGGTTTCCGAAGGGGGAAGTTACAAGGTCATGACGTGGACTTC
CTTATCACCCACCcTGAGGAGGGCCAAGAAGTAGGGCTGCTGCCAGAGTGATGAGGTGCCTTCAGAGCCAG
GGACTTGTGCTGTACCACAGTACCATCGCAGCCACTTAGCGGACTCTGCCACATCCTGCGGCAGAGGTCCA
CCATGGATGCTTTTGAGAGGAGTTTCTGCATCTTGCCTTGCCACAGTCCCAACAGGCAGCTTTAGAGGGGCC
CCTGCATCCCTGCCAACCTGGAAAGCTGTGAGGGTAGATCTTGTGGTCACTCCCAACAGCCAGTTCCCTTTG
CTCTTCTTGGCTGGACTGGCTCCAGTTTTTTGAGAGGGAGCTACGGCGATTAGCCGGCAAGAGAAGGGGCT
GTGCCTTAATAGCCACGGGCTGTTTGATCCTGAGCGGAAGACATTTTTCCACGCAACTTCTGAGGAAGATGTTT
TCAGGTTCTGGGTCTCAAGTATCTTCTCCAGAGCAGAGAAATGCCTGA

ATGCTTCCGAAGCGACGGCGGGGTGCGAGCAGGGTCCCCACACAGCGCTTTAGCCTCT 60
TCCACGCCCCCAGCGGCGCGCTTCCCGGGTGTAGCCATCTACCTTGCGGAGCCGCGAATG 120
GGCCGCAGCCGCCGGGCCTTCCTCACTCGCCTGGCGCGGTCCAAAGGCTTCCGCATCCTA 180
GATGTTTACAGCTCAGAGGTGACACATGTGGTGATGGAGGAGACCTCAGCCAAGGAGGCC 240
ATCTGCTGGCAGAAGGACATGAATGCTCTTCTCCAGACTGCCCCGAGCCGGCTCTGCTA 300
GATATTAGCTGGTTTACAGAGAGCATGGCAGGACAGCCTGTCCCTGAGGAGGTCCGG 360
CACCGCCTGGAGGTAGCTGAGCCCAGGAAGGAACCCCCATCTCAGTGACGATACCAGCT 420
TATGCCTGTCAGCGCCCCCTCGCCTCTCACACCCCATAACTCTCCTCTCAGAGGCTCTG 480
GAGACACTGGCGGAGGCAGCGGGCTTCGAAGGCAAAGAGGGCCGTTTTCTCACCTTCTAC 540
AGAGCAGCCTCCATGCTCAAGTCCCTACCCTACCCTGTACATCTTTGAGCCAGCTGCAT 600
GGACTGCCTTACTTTGGGGAACATTCTTTAGAGTAATCCAGGAGCTGCTAGAACATGGA 660
ACGTGTGAGGAGGTGGAACAAATCCGTTGCTCAGAAAGGCACCAGACCATGAAGCTCTTC 720
ACcCACATCTTCGGGGTTGGGGTGAAGACTGCTAGCCGGTGGTACCAGGAAGGGCTACGA 780
ACCCTGGATGAGCTCAGAGAGCAGCCCCAGAGACTGACCCAGCAGCAGAAAGCAGGGCTG 839
CAGTATTACCAGGACCTGAGCACCCCAGTTAGCCGGGCAGAGGCCGAGGCTCTGCAGCAG 187

TTGGTAGAGGCAGCCATGAGGGAGATCCTGCCCCGAGCCACTGTCACACTGACTGGCGGT 247
 TTCCGAAGGGGGAAGTTACAAGGTCATGACGTGGACTTCCTTATCACCCACCcTGAGGAG 307
 GGCCAAGAAGTAGGGCTGCTGCCCAGAGTGATGAGGTGCCTTCAGAGCCAGGGACTTGTG 367
 CTGTACCACCAAGTACCATCGCAGCCACTTAGCGGACTCTGCCCACATCCTGCGGCAGAGG 427
 TCCACCATGGATGCTTTTGTAGAGGAGTTTCTGCATCTTGCGCTTGCCACAGTCCCAACAG 487
 GCAGCTTTAGAGGGGCCCCCTGCATCCCTGCCCAACCTGGAAAGCTGTGAGGGTAGATCTT 547
 GTGGTCACTCCCAACAGCCAGTTCCCCTTTGCTCTTCTTGCTGGACTGGCTCCCAGTTT 607
 TTTGAGAGGGAGCTACGGCGATTTCAGCCGGCAAGAGAAGGGGCTGTGCCTTAATAGCCAC 667
 GGGCTGTTTGATCCTGAGCGGAAGACATTTTCCACGCAACTTCTGAGGAAGATGTTTC 727
 AGGTTCTGGGTCTCAAGTATCTTCCTCCAGAGCAGAGAAATGCCTGA

MLPKRRRRVRAGSPHSALASSTPPAARFPGVAIYLAERPMGRSRRRAFLTRLARSKGFRILDVYSSEVTHVVMETS
 KEAICWQKDMNALLPDCPQALLDISWFTESMAAGQPVEEVRHRLEVAEPRKEPPISVTIPAYACQRPSP⁺PLPHN
 TLLSEALETLAEAAGFEGKEGRFLTFYRAASMLKSLPYPTLSQLHGLPYFGEHSFRVIQELLEHGTCEEVEQIRCSER
 HQTMLKLFTHIFGVGVKTASRWYQEGRLTDELREQPQRLTQQQKAGLQYYQDLSTPVSRAEAEALQQLVEAAMR
 EILPGATVTLTGGFRRGKLQGHDFLITHPEEGQEVGLLPRVMRCLQSQGLVLYHQYHRSHLADSAHILRQRSTM
 DAFERSFCILRLPQSQAALGGLHPCPTWKAVRVDLVVTPNSQFPFALLGWTGSQFFERELRRFSRQEKGLCLNSH
 GLFDPERKTFHFATSEEDVFRFLGLKYLPEQRNA-

➤ Blast contre banque rat

		Score	Score	Cover	value	ident	Len	
✓ Rattus norvegicus DNA polymerase mu (Polm) mRNA	Norway rat	2748	2748	100%	0.0	100.00%	2896	NM_001011912
✓ PREDICTED: Rattus norvegicus polymerase (DNA) mu (Polm) transcript variant X3 mRNA	Norway rat	2693	2693	100%	0.0	99.20%	3252	XM_006251213
✓ PREDICTED: Rattus norvegicus polymerase (DNA) mu (Polm) transcript variant X4 mRNA	Norway rat	2471	2471	93%	0.0	98.78%	2525	XM_006251214
✓ PREDICTED: Rattus norvegicus polymerase (DNA) mu (Polm) transcript variant X2 mRNA	Norway rat	2398	2398	87%	0.0	100.00%	3070	XM_006251212
✓ PREDICTED: Rattus norvegicus polymerase (DNA) mu (Polm) transcript variant X1 mRNA	Norway rat	2342	2342	87%	0.0	99.08%	3084	XM_006251211

➤ Différence Séquençage/CDS au niveau NT :

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

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

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

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

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

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

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

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

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

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

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

1431 1440 1450 1460 1470 1480 1488
 seq AGATGTTTTACAGTTCTCGGCTCTCAGTATCTTCTCCAGAGCAGAGAAATGCTGA
 cds AGATGTTTTACAGTTCTCGGCTCTCAGTATCTTCTCCAGAGCAGAGAAATGCTGA
 Consensus AGATGTTTTACAGTTCTCGGCTCTCAGTATCTTCTCCAGAGCAGAGAAATGCTGA

Clone parfait

☒	DNA-directed DNA/RNA polymerase mu [Rattus norvegicus]	Norway rat	1014	1014	100%	0.0	100.00%	495	NP_001011912.1
☒	PREDICTED: DNA-directed DNA/RNA polymerase mu isoform X3 [Rattus norvegicus]	Norway rat	1008	1008	100%	0.0	99.20%	499	XP_006251275.1
☒	PREDICTED: DNA-directed DNA/RNA polymerase mu isoform X2 [Rattus norvegicus]	Norway rat	886	886	89%	0.0	98.42%	515	XP_006251274.1

○ pCR4Blunt DiT0 clone E

➤ Fwd DiT0 976NT SEQUENCAGE AOUT

GCCTTCCTTCGTTCTGCGGCCTCCCGTGCTTCCTGAGTCGGTGTCCAG

ATGCTTCCGAAGCGACGGCGGGTGTGCGAGCAGGGTCCCCACACAGCGCTTTAGCCTCTTCCACGCCCCCAG
CGGCGCGCTTCCCGGGTGTAGCCATCTACCTTGCGGAGCCGCGAATGGGCCGAGCCGCCGGGCCTTCCTCACT
CGCCTGGCGCGGTCCAAAGGCTTCCGCATCCTAGATGTTTACAGCTCAGAGGTGACACATGTGGTGATGGAGGA
GACCTCAGCCAAGGAGGCCATCTGCTGGCAGAAGGACATGAATGCTCTTCTCCAGACTGCCCCGAGCCGGCTC
TGCTAGATATTAGCTGGTTTACAGAGAGCATGGCAGCAGGACAGCCTGTCCCTGAGGAGGTCCGGCACCGCCTG
GAGGTAGCTGAGCCCAGGAAGGAACCCCCCATCTCAGTGACGATACCAGCTTATGCCTGTCAGCGCCCCCTGCCT
CTCACACCCCATAACTCTCCTCTCAGAGGCTCTGGAGACACTGGCGGAGGCAGCGGGCTTCGAAGGCAAAG
AGGGCCGTTTTCTACCTTCTACAGAGCAGCCTCCATGCTCAAGTCCCTACCCTACCCTGTCACATCTTTGAGCCA
GCTGCATGGACTGCCTTACTTTGGGGAACATTCTTTAGAGTAATCCAGGAGCTGCTAGAACATGGAACGTGTGA
GGAGGTGGAACAAATCCGTTGCTCAgAAAGGCACCAGACCATGAAGCTTTCACCCACATCTTCNGGGTTGGGG
TGAAGACTGCTAGCCGGTGGTNCCAGNAAGGGCTACGAACCCTGNATGANCTCANANNNCANCCCCANANAC
TGACCCAGCANCANAAAGCNNNNTGCAGTATTACCAGGACCTGANACCCCCAGTTAGCCGGGNANAGGCCGA
GGCTCTGCANCAGTNNGTANAGGCAGCCATGNGGNANNTNCTGCCNGGANNCNCTGNACACNCTGACTGGNN
NNTTNCNANGGGGNAG

➤ Rev DiT0 928NT SEQUENCAGE AOUT

NGGGNGNANANTGCTAGNNNGTGGTNCCAGGAAGGGCTACGANNNTGGATGAGCTCAGAGAGCAGCCCC
AGAGACTGACCCAGCAGCAGAAAGCAGGGCTGCAGTATTACCAGGNNNGAGCACCCAGTTAGCCGGGCAG
AGGCCGAGGNTCTGCAGCAGTTNGTAGAGGCAGCCATGAGGGAGATCNTGCCCGGAGCCACTGTCACACTG
ACTGGCGGTTTTCCGAAGGGGGAAGTTACAAGGTCATGACGTGGACTTCCTTATCACCCACNTGAGGAGGGC
CAAGAAGTAGGGCTGCTGCCAGAGTGATGAGGTGCCTTCAGAGCCAGGGACTTGTGCTGTACCACAGTAC
CATCGCAGCCACTTAGCGGACTCTGCCACATCCTGCGGCAGAGGTCCACCATGGATGCTTTTGAGAGGAGTT
TCTGCATCTTGCGCTTGCCACAGTCCCAACAGGCAGCTTTAGAGGGGGCCCCCTGCATCCCTGCCAACCTGAAAA
GCTGTGAGGGTAGATCTTGTTGCTCACTCCCAACAGCCAGTTCCCTTTGCTCTTCTTGCTGGACTGGCTCCCA
GTTTTTTGAGAGGGAGCTACGGCGATTAGCCGGCAAGAGAAGGGGCTGTGCCTTAATAGCCACGGGCTGTT
TGATCCTGAGCGGAAGACATTTTTCCACGCAACTTCTGAGGAAGATGTTTTAGGTTCTGGGTCTCAAGTATC
TTCCTCCAGAGCAGAGAAATGCCTGA
GATGAAAAATGCCTGTTGGCTGCCATACCTGTCCACGAGAAGATGAGGGGCTGTCTCTTTCTTGACCAGGAAT
GTTTCTAGACAGGAGCACCGCCACCCACGGCCTCACCTGTGCAAATGGGATTTTTTATTTTTACCTCATCGGT
TGAGTGTGACCCCGAGTCAGCTCAGTTTTTCAGCCTCCATTCTCCTCACAGTCAGGTGCTCTTAAGGGCGAATTC
GTTTAAACCTGCAGGACTAG

➤ Int Fwd Dec 2020 :

CTTTGAGCNGCTGCNNGGACTGCCTTACTTTGGGGAACATTCTTTAGAGTAATCCAGGAGCTGCTAGAACAT
GGAACGTGTGAGGAGGTGGAACAAATCCGTTGCTCAGAAAGGCACCAGACCATGAAGCTCTTCACCCACATCT
TCGGGGTTGGGGTGAAGACTGCTAGCCGGTGGTACCAGGAAGGGCTACGAACCCTGGATGAGCTCAGAGAG
CAGCCCCAGAGACTGACCCAGCAGCAGAAAGCAGGGCTGCAGTATTACCAGGACCTGAGCACCCAGTTAGC
CGGGCAGAGGCCGAGGCTCTGCAGCAGTTGGTAGAGGCAGCCATGAGGGAGATCCTGCCCGGAGCCACTGT
CACTGACTGGCGGTTTTCCGAAGGGGGAAGTTACAAGGTCATGACGTGGACTTCCTTATCACCCACCTGAG
GAGGGCCAAGAAGTAGGGCTGCTGCCAGAGTGATGAGGTGCCTTCAGAGCCAGGGACTTGTGCTGTACCAC
CAGTACCATCGCAGCCACTTAGCGGACTCTGCCACATCCTGCGGCAGAGGTCCACCATGGATGCTTTTGAGA

GGAGTTTCTGCATCTTGCGCTTGCCACAGTCCCAACAGGCAGCTTTAGAGGGGGCCCCTGCATCCCTGCCCCAACC
TGGAAAGCTGTGAGGGTAGATCTTGTGGTCACTCCCAACAGCCAGTTCCCCTTTGCTCTTCTGGCTGGACTGG
CTCCCAGTTTTTTGAGAGGGAGCTACGGCGATTAGCCGGCAAGAGAAGGGGCTGTGCCTTAATAGCCACGG
GCTGTTTGATCCTGANCGGAAGANNTTTTTCCACGCAACTTCTGANGAAGANGTTTTAGNNTCCTGGGTCTC
AAGTATCTTCTCCANAGCANANAAATGCCTGANANGAAAAATGNCTGNTGGCTGCCATACCTGTCCACGAN
AAGATGAGGGGCTGTCTCTTTCTTGANNANNAATGTTTCTAGANAGGANCANCGCCNCCCNCCNGCCTCNCC
TGTGCAATGGGNNTTTTTANTTTTTA

➤ Synthèse séquençage DiT0 :

ATGCTTCCGAAGCGACGGCGGGGTGCGAGCAGGGTCCCCACACAGCGCTTTAGCCTCT	60
TCCACGCCCCCAGCGCGCGCTTCCCGGGTGTAGCCATCTACCTTGCAGGAGCCGCGAATG	120
GGCCGCGAGCCGCGGGGCTTCTCACTCGCTGGCGGGTCCAAAGGCTTCCGCATCCTA	180
GATGTTTACAGCTCAGAGGTGACACATGTGGTGATGGAGGAGACCTCAGCCAAGGAGGCC	240
ATCTGCTGGCAGAAAGACATGAATGCTCTTCTCCCAGACTGCCCGCAGCCGGCTCTGCTA	300
GATATTAGCTGGTTTACAGAGAGCATGGCAGCAGGACAGCCTGTCCCTGAGGAGGTCCGG	360
CACCGCTGGAGGTAGCTGAGCCCAGGAAGGAACCCCCATCTCAGTGACGATACCAGCT	420
TATGCCTGTGAGCGCCCCCTCGCCTCTCACACCCCATAACTCTCCTCTCAGAGGCTCTG	480
GAGACACTGGCGGAGGCGAGCGGGCTTCAAGGCAAAGAGGGCGTCTTCTCACCTTCTAC	540
AGAGCAGCCTCCATGCTCAAGTCCCTACCTACCTGTACATCTTTGAGCCAGCTGCAT	600
GGACTGCCTTACTTTGGGGAACATTCTTTAGAGTAATCCAGGAGCTGCTAGAACATGGA	660
ACGTGTGAGGAGGTGGAACAAATCCGTTGCTCAgAAAGGCACCAGACCATGAAGCTCTTC	720
ACCCACATCTTCGGGGTGGGGTGAAGACTGCTAGCCGGTGGTACCAGGAAGGGCTACGAA	
CCCTGGATGAGCTCAGAGAGCAGCCCCAGAGACTGACCCAGCAGCAGAAAGCAGGGCTGCA	
GTATTACCAGGACCTGAGCACCCAGTTAGCCGGGCGAGGCGGAGGCTCTGCAGCAGTTGG	
TAGAGGCAGCCATGAGGGAGATCCTGCCCGGAGCCACTGTACACTGACTGGCGGTTTCCGA	
AGGGGGAAGTTACAAGGTCATGACGTGACTTCCCTTATCACCCACCCTGAGGAGGGCCAAG	
AAGTAGGGCTGCTGCCAGAGTGATGAGGTGCCTTCAGAGCCAGGGACTTGTGCTGTACCAC	
CAGTACCATCGCAGCCACTTAGCGGACTCTGCCACATCCTGCGGCAGAGGTCCACCATGGAT	
GCTTTTGAGAGGAGTTTCTGCATCTTGCGCTTGCCACAGTCCCAACAGGCAGCTTTAGAGGGG	
CCCTGCATCCCTGCCAACCTGGAAAGCTGTGAGGGTAGATCTTGTGTCACCTCCCAACAG	
CCAGTTCCCCTTTGCTCTTCTTGGCTGGACTGGCTCCAGTTTTTTTGAGAGGGAGCTACGGCG	
ATTACGCCGGCAAGAGAAGGGGCTGTGCCTTAATAGCCACGGGCTGTTTGATCCTGA	
GCGGAAGACATTTTTCCACGCAACTTCTGAGGAAGATGTTTTT	1440
AGGTTCTCGGGTCTCAAGTATCTTCTCCAGAGCAGAGAAATGCCTGA	1488

MLPKRRRRVRAGSPHSALASSTPPAARFPGVAIYLAEPMRGRSRRFLTRLARSKGFRILDVYSSEVTHVMEET
SAKEAICWQKDMNALLPDCPQPALLDISWFTESMAAGQVPVEEVRRHRLEVAEPRKEPPISVTIPAYACQRPSPLT
PHNTLLSEALETLAEAAGFEGKEGRFLTIFYRAASMLKSLPYPVTSLSQLHGLPYFGEHSFRVIQELLEHGTCCEV
EQIRCSEHQTMKLFTHIFGVGVKTASRWYQEGRLTLDLREQPQRLTQQQKAGLQYYQDLSTPVSRAEAEALQQ
LVEAAMREILPGATVTLTGFRGKLQGHVDVFLITHPEEGQEVGLLPRVMRCLQSQGLVLYHQYHRSHLADSAH
ILRQRSTMDAFERSFCILRLPQSQAALLEGPLHPCPTWKAVRVDLVVTPNSQFPFALLGWTGSQFFERELRRFSR
QEKGLCLNSHGLFDPERKTFHATSEEDVFRFLGLKYLPEQRNA-

➤ Blast contre banque rat :

	Description	Commentaire	Score	Score	Cover	value	Ident	Len	Accession
✓	Rattus norvegicus DNA polymerase mu (Polm) mRNA	Norway rat	2748	2748	100%	0.0	100.00%	2896	NM_001011912.1
✓	PREDICTED: Rattus norvegicus polymerase (DNA) mu (Polm) transcript variant X3 mRNA	Norway rat	2693	2693	100%	0.0	99.20%	3252	XM_006251213.3
✓	PREDICTED: Rattus norvegicus polymerase (DNA) mu (Polm) transcript variant X4 mRNA	Norway rat	2471	2471	93%	0.0	98.78%	2525	XM_006251214.3

➤ Différence Séquençage/CDS au niveau NT :

	1	10	20	30	40	50	60	70	80	90	100	110	120	130	
seq	ATGCTTCCGAGCGACGGGCGCGGGTGCAGCAGGGTCCCCACACAGCGCTTAGCCTCTTCCAGCGCCCCAGCGGGCGGCTTCCCGGGTGTAGCCATCTACCTTGCGGAGCCGCGAATGGGCGGAGCC														
cds	ATGCTTCCGAGCGACGGGCGCGGGTGCAGCAGGGTCCCCACACAGCGCTTAGCCTCTTCCAGCGCCCCAGCGGGCGGCTTCCCGGGTGTAGCCATCTACCTTGCGGAGCCGCGAATGGGCGGAGCC														
Consensus	ATGCTTCCGAGCGACGGGCGCGGGTGCAGCAGGGTCCCCACACAGCGCTTAGCCTCTTCCAGCGCCCCAGCGGGCGGCTTCCCGGGTGTAGCCATCTACCTTGCGGAGCCGCGAATGGGCGGAGCC														
	131	140	150	160	170	180	190	200	210	220	230	240	250	260	
seq	GCCGGGCTTCTCAGCTGCGCTGGCGGGTCCAAAGGCTTCCGATCTCAGATGTTTACAGCTCAGAGGTGACACATGTGGTGATGGAGGAGACCTCAGCCAGGAGGCGCATCTGCTGGCAGAGGACAT														
cds	GCCGGGCTTCTCAGCTGCGCTGGCGGGTCCAAAGGCTTCCGATCTCAGATGTTTACAGCTCAGAGGTGACACATGTGGTGATGGAGGAGACCTCAGCCAGGAGGCGCATCTGCTGGCAGAGGACAT														
Consensus	GCCGGGCTTCTCAGCTGCGCTGGCGGGTCCAAAGGCTTCCGATCTCAGATGTTTACAGCTCAGAGGTGACACATGTGGTGATGGAGGAGACCTCAGCCAGGAGGCGCATCTGCTGGCAGAGGACAT														
	261	270	280	290	300	310	320	330	340	350	360	370	380	390	
seq	GAATGCTCTTCCGAGACTGCCCGAGCGCGGCTCTGCTAGATATTAGCTGGTTTACAGAGAGCATGGCAGCAGGACAGGCTGTCCCTGAGGAGGTCGGCACCCTGGAGGTAGCTGAGGCCAGGAGG														
cds	GAATGCTCTTCCGAGACTGCCCGAGCGCGGCTCTGCTAGATATTAGCTGGTTTACAGAGAGCATGGCAGCAGGACAGGCTGTCCCTGAGGAGGTCGGCACCCTGGAGGTAGCTGAGGCCAGGAGG														
Consensus	GAATGCTCTTCCGAGACTGCCCGAGCGCGGCTCTGCTAGATATTAGCTGGTTTACAGAGAGCATGGCAGCAGGACAGGCTGTCCCTGAGGAGGTCGGCACCCTGGAGGTAGCTGAGGCCAGGAGG														
	391	400	410	420	430	440	450	460	470	480	490	500	510	520	
seq	GAAACCCCATCTCAGTGACGATACCACTTATGCTGTGACGCGCCCTCGCTCTCAGACCCCATACACTCTCCTCTCAGAGGCTCTGGAGACACTGGCGAGGCGAGCGGGCTTCGAGGCGAAGAGG														
cds	GAAACCCCATCTCAGTGACGATACCACTTATGCTGTGACGCGCCCTCGCTCTCAGACCCCATACACTCTCCTCTCAGAGGCTCTGGAGACACTGGCGAGGCGAGCGGGCTTCGAGGCGAAGAGG														
Consensus	GAAACCCCATCTCAGTGACGATACCACTTATGCTGTGACGCGCCCTCGCTCTCAGACCCCATACACTCTCCTCTCAGAGGCTCTGGAGACACTGGCGAGGCGAGCGGGCTTCGAGGCGAAGAGG														
	521	530	540	550	560	570	580	590	600	610	620	630	640	650	
seq	GCCGTTTCTCAGCTTCTACAGAGAGCGCTCCATGCTCAGTCCCTACCTACCTGTGACATCTTTGAGCCAGCTGCATGGACTGCTTACTTTGGGGAGCATTCCTTTAGAGTAATCCAGAGGCTGCT														
cds	GCCGTTTCTCAGCTTCTACAGAGAGCGCTCCATGCTCAGTCCCTACCTACCTGTGACATCTTTGAGCCAGCTGCATGGACTGCTTACTTTGGGGAGCATTCCTTTAGAGTAATCCAGAGGCTGCT														
Consensus	GCCGTTTCTCAGCTTCTACAGAGAGCGCTCCATGCTCAGTCCCTACCTACCTGTGACATCTTTGAGCCAGCTGCATGGACTGCTTACTTTGGGGAGCATTCCTTTAGAGTAATCCAGAGGCTGCT														
	651	660	670	680	690	700	710	720	730	740	750	760	770	780	
seq	AGACATGGAGCTGTGAGGAGGTGGAGCAATCCGTGCTCAGAAAGGCACAGGACATGAGCTCTTCACCCACATCTTCGGGGTGGGGTGAAGACTGCTAGCCGGTGGTACCGAGAGGGGTACGA														
cds	AGACATGGAGCTGTGAGGAGGTGGAGCAATCCGTGCTCAGAAAGGCACAGGACATGAGCTCTTCACCCACATCTTCGGGGTGGGGTGAAGACTGCTAGCCGGTGGTACCGAGAGGGGTACGA														
Consensus	AGACATGGAGCTGTGAGGAGGTGGAGCAATCCGTGCTCAGAAAGGCACAGGACATGAGCTCTTCACCCACATCTTCGGGGTGGGGTGAAGACTGCTAGCCGGTGGTACCGAGAGGGGTACGA														
	781	790	800	810	820	830	840	850	860	870	880	890	900	910	
seq	ACCCTGGATGAGCTCAGAGAGCAGCCCCAGAGACTGACCCAGCAGCAGAAAGCAGGGGCTGCAGTATTACAGGACCTGAGCACCCTCAGTAGCCGGGAGAGGCCAGGGCTCTGCAGCAGTTGGTAGAGG														
cds	ACCCTGGATGAGCTCAGAGAGCAGCCCCAGAGACTGACCCAGCAGCAGAAAGCAGGGGCTGCAGTATTACAGGACCTGAGCACCCTCAGTAGCCGGGAGAGGCCAGGGCTCTGCAGCAGTTGGTAGAGG														
Consensus	ACCCTGGATGAGCTCAGAGAGCAGCCCCAGAGACTGACCCAGCAGCAGAAAGCAGGGGCTGCAGTATTACAGGACCTGAGCACCCTCAGTAGCCGGGAGAGGCCAGGGCTCTGCAGCAGTTGGTAGAGG														
	911	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040	
seq	CAGCCATGAGGGAGATCTGCCCCGGAGCCATGTCACTGACTGGCGGTTTCCGAGGGGGAGATTACAGGTCATGACGTGGACTTCCTTATCACCACCTTGGAGGGGCCAGAGATAGGGCTGCT														
cds	CAGCCATGAGGGAGATCTGCCCCGGAGCCATGTCACTGACTGGCGGTTTCCGAGGGGGAGATTACAGGTCATGACGTGGACTTCCTTATCACCACCTTGGAGGGGCCAGAGATAGGGCTGCT														
Consensus	CAGCCATGAGGGAGATCTGCCCCGGAGCCATGTCACTGACTGGCGGTTTCCGAGGGGGAGATTACAGGTCATGACGTGGACTTCCTTATCACCACCTTGGAGGGGCCAGAGATAGGGCTGCT														
	1041	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170	
seq	GCCCAGAGTGATGAGGTGCTTCAGAGCCAGGGACTTGTGCTGTACACCACTAGCATCGAGCCACTTAGCGGACTCTGCCACATCTCGCGCAGAGGTCACCATGGATGCTTTTGAAGGAGGTTTC														
cds	GCCCAGAGTGATGAGGTGCTTCAGAGCCAGGGACTTGTGCTGTACACCACTAGCATCGAGCCACTTAGCGGACTCTGCCACATCTCGCGCAGAGGTCACCATGGATGCTTTTGAAGGAGGTTTC														
Consensus	GCCCAGAGTGATGAGGTGCTTCAGAGCCAGGGACTTGTGCTGTACACCACTAGCATCGAGCCACTTAGCGGACTCTGCCACATCTCGCGCAGAGGTCACCATGGATGCTTTTGAAGGAGGTTTC														
	1171	1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300	
seq	TGATCTTTGCGCTTGCCACAGTCCCAACAGGAGCTTTAGAGGGGGCCCTGCATCCTGCCACACCTGGAAGCTGTGAGGGTAGATCTTGTTGCTACTCCACACAGCAGTTCCCTTTGCTCTTCTTG														
cds	TGATCTTTGCGCTTGCCACAGTCCCAACAGGAGCTTTAGAGGGGGCCCTGCATCCTGCCACACCTGGAAGCTGTGAGGGTAGATCTTGTTGCTACTCCACACAGCAGTTCCCTTTGCTCTTCTTG														
Consensus	TGATCTTTGCGCTTGCCACAGTCCCAACAGGAGCTTTAGAGGGGGCCCTGCATCCTGCCACACCTGGAAGCTGTGAGGGTAGATCTTGTTGCTACTCCACACAGCAGTTCCCTTTGCTCTTCTTG														
	1301	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430	
seq	GCTGGACTGGCTCCAGTTTTTTGAGAGGGAGCTACGGCGATTACGCGGCAAGAGAGGGGCTGTGCCTTATAGCCACGGGCTGTTGATCCTGAGCGGAGAGCATTTTTCCACGCACTTCTGAGGA														
cds	GCTGGACTGGCTCCAGTTTTTTGAGAGGGAGCTACGGCGATTACGCGGCAAGAGAGGGGCTGTGCCTTATAGCCACGGGCTGTTGATCCTGAGCGGAGAGCATTTTTCCACGCACTTCTGAGGA														
Consensus	GCTGGACTGGCTCCAGTTTTTTGAGAGGGAGCTACGGCGATTACGCGGCAAGAGAGGGGCTGTGCCTTATAGCCACGGGCTGTTGATCCTGAGCGGAGAGCATTTTTCCACGCACTTCTGAGGA														
	1431	1440	1450	1460	1470	1480	1488								
seq	AGATGTTTTCAAGTTCTCGGGTCTCAGATATCTTCTCCAGAGCAGAGAAATGCCTGA														
cds	AGATGTTTTCAAGTTCTCGGGTCTCAGATATCTTCTCCAGAGCAGAGAAATGCCTGA														
Consensus	AGATGTTTTCAAGTTCTCGGGTCTCAGATATCTTCTCCAGAGCAGAGAAATGCCTGA														

➤ Différence au niveau PROT :

pCR4Blunt PolM DiT0 clone D

o pCR4Blunt PolM DiT24hLPS clone A sequençage 28/10

➤ Fwd DiT24h 1024NT

GANGNNTGNTANCNGGTGGTNCNGNAAGGGNTACGAACCTGGATGAGNTCAGAGAGCAGCCCCAGAGA
NTGACCCAGCAGCAGAAAGCAGTATTACCCACAGGGCTGCAGTATTNNCAGGACNTGAGCACCCCAGTTAGCC
GGGCAGAGGCNGAGGNTNTGCAGCAGTTGGTAGAGGCAGCCATGAGGGAGANCNTGCCCCGAGCCACTGTC
ACACTGACTGGCGGTTTCCGAAGGGGGAAGTTACAAGGTCATGACGTGGACTTCCTTATCACCCACCcTGAGGA
GGGCCAAGAAGTAGGGCTGCTGCCCAGAGTGATGAGGTGCCTTCAGAGCCAGGGACTTGTGCTGTACCACCAG
TACCATCGCAGCCACTTAGCGGACTCTGCCACATCCTGCGGCAGAGGTCCACCATGGATGCTTTTTGAGAGGAGT
TTCTGCATCTTGCGCTTGCCACAGTCCCAACAGGCAGCTTTAGAGGGGGCCCCTGCATCCCTGCCAACCTGGAAA
GCTGTGAGGGTAGATCTTGTGGTCACTCCCAACAGCCAGTTCCTCTTCTTGGCTGGACTGGCTCCAG
TTTTTTGAGAGGGAGCTACGGCGATTACGCCGGCAAGAGAAGGGGCTGTGCCTTAATAGCCACGGGCTGTTTG
ATCCTGAGCGGAAGACATTTTTCCACGCAACTTCTGAGGAAGATGTTTTCAGGTTCTGGGTCTCAAGTATCTTCC
TCCAGAGCAGAGAAATGCCTGA

GATGAAAAATGCCTGTTGGCTGCCATACCTGTCCACGAGAAGATGAGGGGCTGTCTCTTTCTTGACCAGGAATGT
TTCTAGACAGGAGCACCGCCACCCACGGCCTCACCTGTGCAAATGGGATTTTTTATTTTTTACCTCATCGGTTGA
GTGTGACCCCGAGTCAGCTCAGTTTTCAGCCTCCATTCTCCTCACAGTCAGGTGCTCTT

➤ Rev DiT24h 943NT : commence trop tard : pas le début

TGCCTTCCTTCGTTCTGCGGCCTCCCGTGCTTCCTGAGTCGGTGTCCAG

ATGCTTCCGAAGCGACGGCGGGCGGCTCAGAGGTGACACATGTGGTGATGGAGGAGACCTCAGCCAAGGAGGC
CATCTGCTGGCAGAAGGACATGAATGCTCTTCTCCCAGACTGCCCCGAGCCGGCTCTGCTAGATATTAGCTGGTTT
ACAGAGAGCATGGCAGCAGGACAGCCTGTCCCTGAGGAGGTCCGGCACCGCCTGGAGGTAGCTGAGCCCAGG
AAGGAACCCCCCATCTCAGTGACGATACCAGCTTATGCCTGTGAGCGCCCCCTCGCCTCTCACACCCATAACACTC
TCCTCTCAGAGGCTCTGGAGACACTGGCGGAGGCAGCGGGCTTCGAAGGCAAAGAGGGCCGTTTTCTCACCTT
CTACAGAGCAGCCTCCATGCTCAAGTCCCTACCCTACCCTGTACATCTTTGAGCCAGCTGCATGGACTGCCTTAC
TTTGGGGAACATTCTTTAGAGTAATCCAGGAGCTGCTAGAACATGGAACGTGTGAGGAGGTGGAACAAATCCG
TTGCTCAGAAAGGCACCAGACCATGAAGCTCTTCACCCACATCTTCGGGGTTGGGGTGAAGACTGCTAGCCGGT
GGTACCAGGAAGGGCTACGAACCCTGGATGAGCTCAGAGAGCAGCCCCAGAGACTGACCCAGCAGCAGAAAG
CAGTATTACCCACAGGGCTGCAGTATTACCAGGACCTGAGCACCCAGTTAGCCgGGCAGANGCCGAGGCTCTG
CAGCAGTTGGTAGAGGCAGCCATGANGGAGATCCTGCCCCGANCCACTGNCACACTGACTGGCGGTTTCCNNA
NNGGGAAGTTACAAGGTCATGACGTGGNCTTCTTATCACNACCNTGAGNAGGGNCAAGAAGTAGGCTGCTG
CCC

➤ Synthèse séquençage DiT24hLPS :

-----ATGCTTCCGAAGC	180
GACGGCGGGCGGCTCAGAGGTGACACATGTGGTGATGGAGGAGACCTCAGCCAAGGAGGCC	240
ATCTGCTGGCAGAAGGACATGAATGCTCTTCTCCCAGACTGCCCCGAGCCGGCTCTGCTA	300
GATATTAGCTGGTTTACAGAGAGCATGGCAGCAGGACAGCCTGTCCCTGAGGAGGTCCGG	360
CACCGCCTGGAGGTAGCTGAGCCCAGGAAGGAACCCCCCATCTCAGTGACGATACCAGCT	420
TATGCCTGTGAGCGCCCCCTCGCCTCTCACACCCATAACACTCTCCTCTCAGAGGCTCTG	480
GAGACACTGGCGGAGGCAGCGGGCTTCGAAGGCAAAGAGGGCCGTTTTCTCACCTTCTAC	540
AGAGCAGCCTCCATGCTCAAGTCCCTACCCTACCCTGTACATCTTTGAGCCAGCTGCAT	600
GGACTGCCTTACTTTGGGGAACATTCTTTAGAGTAATCCAGGAGCTGCTAGAACATGGA	660
ACGTGTGAGGAGGTGGAACAAATCCGTTGCTCAGAAAGGCACCAGACCATGAAGCTCTTC	720
ACCCACATCTTCGGGGTTGGGGTGAAGACTGCTAGCCGGTGGTACCAGGAAGGGCTACGA	780
ACCTTGATGAGCTCAGAGAGCAGCCCCAGAGACTGACCCAGCAGCAGAAAGCAGTATTA	832
CCCACAGGGCTGCAGTATTACCAGGACCTGAGCACCCAGTTAGCCGGGCAGAGGCCGAG	888

GCTCTGCAGCAGTTGGTAGAGGCAGCCATGAGGGAGATCCTGCCCCGAGCCACTGTCACA	948
CTGACTGGCGGTTTCCGAAGGGGGAAGTTACAAGGTCATGACGTGGACTTCCTTATCACC	1008
CACCCtGAGGAGGGCCAAGAAGTAGGGCTGCTGCCCAGAGTGATGAGGTGCCTTCAGAGC	1068
CAGGGACTTGTGCTGTACCACCAGTACCATCGCAGCCACTTAGCGGACTCTGCCCACATC	1128
CTGCGGCAGAGGTCCACCATGGATGCTTTTGAGAGGAGTTTCTGCATCTTGCGCTTGCCA	1188
CAGTCCCAACAGGCAGCTTTAGAGGGGCCCCTGCATCCCTGCCCAACCTGGAAAGCTGTG	1248
AGGGTAGATCTTGTGGTCACTCCCAACAGCCAGTTCCTTTGCTCTTCTTGGCTGGACT	1308
GGCTCCCAGTTTTTTGAGAGGGAGCTACGGCGATTAGCCGGCAAGAGAAGGGGCTGTGC	1368
CTTAATAGCCACGGGCTGTTTGATCCTGAGCGGAAGACATTTTCCACGCAACTTCTGAG	1428
GAAGATGTTTTTCAGGTTCTTGGGTCTCAAGTATCTTCTCCAGAGCAGAGAAATGCCTGA	1488

CFRSDGGGSEVTHVMEETSACEAICWQKDMNALLPDCPQPALLDISWFTESMAAGQPVPEEVRHRLEVAEPRKE
 PPISVTIPAYACQRPSPPLTPHNTLLSEALETLAEAAGFEGKEGRFLTFYRAASMLKSLPYPVTSLSQLHGLPYFG
 EHSFRVIQELLEHGTCCEEVEQIRCSERHQTMKLFTHIFGVGVKTASRWYQEGRLTLDELREQPQRLTQQQKAVLP
 TGLQYYQDLSTPVSRAEAEALQQLVEAAMREILPGATVTLTGFFRRGKLQGHVDVDFLI THPEEGQEVGLLPVVMR
 CLQSQGLVLYHQYHRSHLADSAHILRQRSTMDAFERSFCILRLPQSQQAALEGPLHPCPTWKAVRVDLVVTPNSQ
 FPFALLGWTGSQFFERELRRFSRQEKGLCLNSHGLFDPERKTFHFATSEEDVFRFLGLKYLPPPEQRNA-

➤ **Blast contre banque rat :**

☒	PREDICTED: Rattus norvegicus polymerase (DNA) mu (Polm) .transcript variant X1 .mRNA	2462	2462	100%	0.0	100.00%	XM_006251211.3
☒	PREDICTED: Rattus norvegicus polymerase (DNA) mu (Polm) .transcript variant X3 .mRNA	2420	2420	98%	0.0	100.00%	XM_006251213.3
☒	PREDICTED: Rattus norvegicus polymerase (DNA) mu (Polm) .transcript variant X4 .mRNA	2414	2414	98%	0.0	100.00%	XM_006251214.3
☒	PREDICTED: Rattus norvegicus polymerase (DNA) mu (Polm) .transcript variant X2 .mRNA	2385	2385	100%	0.0	99.10%	XM_006251212.3
☒	Rattus norvegicus DNA polymerase mu (Polm) .mRNA	2342	2342	98%	0.0	99.08%	NM_001011912.1

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

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

seq
CDS
Consensus

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

seq
CDS
Consensus

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

seq
CDS
Consensus

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

seq
CDS
Consensus

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

seq
CDS
Consensus

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

seq
CDS
Consensus

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

seq
CDS
Consensus

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

seq
CDS
Consensus

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

seq
CDS
Consensus

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

seq
CDS
Consensus

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

seq
CDS
Consensus

1431 1440 1450 1460 1470 1480 1490 1500

seq
CDS
Consensus

➤ Différence au niveau PROT :

☒	PREDICTED: DNA-directed DNA/RNA polymerase mu isoform X1 [Rattus norvegicus]	909	909	100%	0.0	100.00%	XP_006251273.1
☒	PREDICTED: DNA-directed DNA/RNA polymerase mu isoform X2 [Rattus norvegicus]	896	896	100%	0.0	99.10%	XP_006251274.1
☒	PREDICTED: DNA-directed DNA/RNA polymerase mu isoform X3 [Rattus norvegicus]	895	895	99%	0.0	99.32%	XP_006251275.1
☒	PREDICTED: DNA-directed DNA/RNA polymerase mu isoform X4 [Rattus norvegicus]	891	891	98%	0.0	99.77%	XP_006251276.1
☒	DNA-directed DNA/RNA polymerase mu [Rattus norvegicus]	880	880	99%	0.0	98.41%	NP_001011912.1
☒	DNA nucleotidylexotransferase [Rattus norvegicus]	339	339	97%	9e-112	41.93%	NP_001012479.1

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----													
refprot	MLPKRRRRYRAGSPHSALASSTPPAARFPGVAIYLAEPHMGSRRAFLTRLARSKGFRILDVYSSSEVTHVYMEETSAKEAICWQKDMNALLPDCPQALLDISWFTESMAAGQPVPEEVHRLEVAEPRK													
Consensus	cFri.DgggSEVTHVYMEETSAKEAICWQKDMNALLPDCPQALLDISWFTESMAAGQPVPEEVHRLEVAEPRK													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----													
refprot	EPPISVTIPAYACQRPSP LTPHNTLLSEALETLAEAGFEGKEGRFLT FYRAASHMLKSLPPYVTSLSQLHGLPYFGEHSFRVTIQELLEHGTCCEEVQIRCSERHQTKMLFTHIFGVGYKTASRYQEGLR													
Consensus	EPPISVTIPAYACQRPSP LTPHNTLLSEALETLAEAGFEGKEGRFLT FYRAASHMLKSLPPYVTSLSQLHGLPYFGEHSFRVTIQELLEHGTCCEEVQIRCSERHQTKMLFTHIFGVGYKTASRYQEGLR													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----													
refprot	TLDELREQPQLTQQQKAVLPTGLQYYQDLSTPYSRAEAEALQQLVEAAMREILPGATVTLTGGFRRGKLQGHVDVFLITHPEEGQEVGLLPRVHRCQLSQGLVLYHQYHRSHLADSAHILRQRSTMDHF													
Consensus	TLDELREQPQLTQQQKA...GLQYYQDLSTPYSRAEAEALQQLVEAAMREILPGATVTLTGGFRRGKLQGHVDVFLITHPEEGQEVGLLPRVHRCQLSQGLVLYHQYHRSHLADSAHILRQRSTMDHF													
	391	400	410	420	430	440	450	460	470	480	490	499		
seq	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----													
refprot	ERSFCILRLPQSQAALGGLHPCPTWKAVRYDLVYTPNSQFPFALLGWTGSQFFERELRRFSRQEKGLCLNSHGLFDPERKTFHATSEEDVFRFLGLKYLPPQQRNA													
Consensus	ERSFCILRLPQSQAALGGLHPCPTWKAVRYDLVYTPNSQFPFALLGWTGSQFFERELRRFSRQEKGLCLNSHGLFDPERKTFHATSEEDVFRFLGLKYLPPQQRNA													

pCR4Blunt Pol M DiT24h (clone A) le primer Fwd a du s'hybrider plus loin : il manque le début de la séquence

o **pCR4Blunt PolM DiT24hLPS clone B NOUVEAU CLONAGE**

➤ **Fwd DiT24h 934NT**

CAGACNATGAAGNTNTNNCCACATNTTCGGGTNNGGGTGAAGANTGNTAGCNGNTGGTACCAGGAAGGGNT
ACGAACCCTGGATGAGNTCAGAGAGCAGCCCCAGAGACTGACCCAGCAGCAGAAAGCAGGGCTGCAGTATTA
NCAGGactGAGCACCCAGTTAGCCGGGCAGAGGcGAGGCTCTGCAGCAGTTGGTAGAGGCAGCCATGAGGG
AGAtCCTGCCCCGAGCCACTGTCACACTGACTGGCGGTTTCCGAAGGGGGAAGTTACAAGGTCATGACGTGGA
CTTCCTTATCACCCACCcTGAGGAGGGCCAAGAAGTAGGGCTGCTGCCCAGAGTGATGAGGTGCCTTCAGAGCC
AGGGACTTGTGCTGTACCACCAGTACCATCGCAGCCACTTAGCGGACTCTGCCACATCCTGCGGCAGAGGTCCA
CCATGGATGCTTTTGAGAGGAGTTTCTGCATCTTGCGCTTGCCACAGTCCCAACAGGCAGCTTTAGAGGGGCCC
CTGCATCCCTGCCAACCTGGAAAGCTGTGAGGGTAGATCTTGTTGGTCACTCCCAACAGCCAGTTCCCTTTGCT
CTTCTTGGCTGGACTGGCTCCCAGTTTTTTGAGAGGGAGCTACGGCGATTACGCCGGCAAGAGAAGGGGCTGT
GCCTTAATAGCCACGGGCTGTTTGATCCTGAGCGGAAGACATTTTTCCACGCAACTTCTGAGGAAGATGTTTTCA
GGTTCCTGGGTCTCAAGTATCTTCCTCCAGAGCAGAGAAATGCCTGAGATGAAAAATGCCTGTTGGCTGCCATAC
CTGTCCACGAGAAGATGAGGGGCTGTCTTTTCTTGACCAGGAATGTTTCTAGACAGGAGCACCGCCACCCAC
GGCCTCACCTGTGCAAATGGGATTTTTTATTTTTTACCTCATCGGTTGAG

➤ **Rev DiT24h 953NT :**

ATGCTTCCGAAGCGACGGCGGGGTGCGAGCAGGGTCCCCACACAGCGCTTTAGCCTCTTCCACGCCCCCAG
CGGCGCGCTTCCCGGGTGTAGCCATCTACCTTGCAGGAGCCGGAATGGGCCGAGCCGCCGGGCTTCTCAC
TCGCCTGGCGCGGTCCAAAGGCTTCCGCATCCTAGATGTTTACAGCTCAGAGGTGACACATGTGGTGATGGAG
GAGACCTCAGCCAAGGAGGCCATCTGCTGGCAGAAGGACATGAATGCTCTTCTCCAGACTGCCCGCAGCCG
GCTCTGCTAGATATTAGCTGGTTTACAGAGAGCATGGCAGCAGGACAGCCTGTCCCTGAGGAGGTCCGGCACC
GCCTGGAGGTAGCTGAGCCCAGGAAGGAACCCCCATCTCAGTGACGATACCAGCTTATGCCTGTCAGCGCCC
CTCGCCTCTCACACCCATAACACTCTCCTCTCAGAGGCTCTGGAGACACTGGCGGAGGCAGCGGGCTTCGAA
GGCAAAGAGGGGCCGTTTTCTACCTTCTACAGAGCAGCCTCCATGCTCAAGTCCCTACCCTACCCTGTCACATCT
TTGAGCCAGCTGCATGGACTGCCTTACTTTGGGGAACATTCTTTAGAGTAATCCAGGAGCTGCTAGAACATG
GAACGTGTGAGGAGGTGGAACAAATCCGTTGCTCAgAAAGGCACCAGACCATGAAGCTCTTCACCCACATCTT
CgGGGTTGGGGTGAAGACTGCTAGCCGGTGGTACCagGAAGGGCTACGAACCCTGGATGAgCTCANAGAGNA
NCCCCAGAGACTGACCCAGCAGCAGAAAGCNNNNNTGCAGTATTACCAGGNNCTGAGCACCCANTTAGCCG
GGCAGAGGCCGANNTCTGCANCAAGTTGGTAGANGCAGCCNTGAGGGAGANNCTGCCNNGNCCNCCNCCNCA
CACTGACTG

➤ **Synthèse séquençage**

ATGCTTCCGAAGCGACGGCGGGGTGCGAGCAGGGTCCCCACACAGCGCTTTAGCCTCT	60
TCCACGCCCCCAGCGCGCGCTTCCCGGGTGTAGCCATCTACCTTGCAGGAGCCGGAATG	120
GGCCGAGCCGCCGGGCTTCTCACTCGCCTGGCGGGTCCAAAGGCTTCCGCATCCTA	180
GATGTTTACAGCTCAGAGGTGACACATGTGGTGATGGAGGAGACCTCAGCCAAGGAGGCC	240
ATCTGCTGGCAGAAGGACATGAATGCTCTTCTCCAGACTGCCCGCAGCCGGCTCTGCTA	300
GATATTAGCTGGTTTACAGAGAGCATGGCAGCAGGACAGCCTGTCCCTGAGGAGGTCCGG	360
CACCGCTGGAGGTAGCTGAGCCCAGGAAGGAACCCCATCTCAGTGACGATACCAGCT	420
TATGCCTGTGACGCGCCCTCGCCTCTCACACCCATAACACTCTCCTCTCAGAGGCTCTG	480
GAGACACTGGCGGAGGCAGCGGGCTTCGAAGGCAAAGAGGGCGTTTTCTCACCTTCTAC	540
AGAGCAGCCTCCATGCTCAAGTCCCTACCCTACCCTGTCACATCTTTGAGCCAGCTGCAT	600
GGACTGCCTTACTTTGGGGAACATTCTTTAGAGTAATCCAGGAGCTGCTAGAACATGGA	660
ACGTGTGAGGAGGTGGAACAAATCCGTTGCTCAgAAAGGCACCAGACCATGAAGCTCTTC	720
ACCCACATCTTCgGGGTTGGGGTGAAGACTGCTAGCCGGTGGTACCagGAAGGGCTACGA	780
ACCTGGATGAGCTCAGAGAGCAGCCCCAGAGACTGACCCAGCAGCAGAAAGCAGGGCTG	135
CAGTATTACCAGGANCTGAGCACCCAGTTAGCCGGGCAGAGGCCGAGGCTCTGCAGCAG	898
TTGGTAGAGGCAGCCATGAGGGAGAtCCTGCCCGGAGCCACTGTCACTGACTGGCGGT	254

TTCCGAAGGGGGAAGTTACAAGGTCATGACGTGGACTTCCTTATCACCACCcTGAGGAG	314
GGCCAAGAAGTAGGGCTGCTGCCCAGAGTGATGAGGTGCCTTCAGAGCCAGGGACTTGTG	374
CTGTACCACCAGTACCATCGCAGCCACTTAGCGGACTCTGCCCACATCCTGCGGCAGAGG	434
TCCACCATGGATGCTTTTGAGAGGAGTTTCTGCATCTTGCGCTTGCCACAGTCCCAACAG	494
GCAGCTTTAGAGGGGGCCCTGCATCCCTGCCCAACCTGGAAAGCTGTGAGGGTAGATCTT	554
GTGGTCACTCCCAACAGCCAGTTCCCCTTTGCTCTTCTTGGCTGGACTGGCTCCCAGTTT	614
TTTGAGAGGGAGCTACGGCGATTACGCCGGAAGAGAAGGGGCTGTGCCTTAATAGCCAC	674
GGGCTGTTTGATCCTGAGCGGAAGACATTTTCCACGCAACTTCTGAGGAAGATGTTTTC	734
AGGTTCCTGGGTCTCAAGTATCTTCCTCCAGAGCAGAGAAATGCCTGA	

MLPKRRRRVRAGSPHSALASSTPPAARFPGVAIYLAEPRMGRSRRFLTRLARSKGFRILDVYSSEVTHVVMETS
 KEAICWQKDMNALLPDCPQALLDISWFTESMAAGQVPVEEVRHRLEVAEPRKEPPISVTIPAYACQRPSP
 LTPHN
 TLLSEALETLAEAGFEGKEGRFLT FYRAASMLKSLPYPVTSLSQLHGLPYFGEHSFRVIQELLEHGT
 CEEVEQIRCSER
 HQTMLKLFTHIFGVGVKTASRWYQEGLRTLDELREQPQRLTQQQKAGLQYYQXLSTPVSRAEAEAL
 QQLVEAAMRE
 ILPGATVTLTGGFRRGKLQGHVDVFLITHPEEGQEVGLLPRVMRCLQSQGLVLYHQYHRSHLADS
 AHILRQRSTMD
 AFERSFCILRLPQSQQAALLEGPLHPCPTWKAVRVDLVVTPNSQFPFALLGWTGSQFFERELRR
 FSRQEKGLCLNSHG
 LFDPERKTFFHATSEEDVFRFLGLKYLPEQRNA-

➤ **Blast contre banque rat :**

✓	Rattus norvegicus DNA polymerase mu (Polm) mRNA	Norway rat	2745	2745	100%	0.0	99.93%	2896	NM_001011912.1	
✓	PREDICTED: Rattus norvegicus polymerase (DNA) mu (Polm) transcript variant X3 mRNA	Norway rat	2689	2689	100%	0.0	99.13%	3252	XM_006251213.3	
✓	PREDICTED: Rattus norvegicus polymerase (DNA) mu (Polm) transcript variant X4 mRNA	Norway rat	2468	2468	93%	0.0	98.71%	2525	XM_006251214.3	
✓	PREDICTED: Rattus norvegicus polymerase (DNA) mu (Polm) transcript variant X2 mRNA	Norway rat	2394	2394	87%	0.0	99.92%	3070	XM_006251212.3	

➤ **Différence au niveau protéique**

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

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq cds	ATGCTTCCGAGGCGACGGCGGGGGTGGCAGCAGGGTCCCCACACAGCGCTTTAGCCTCTTCCACGCCCCAGCGGCGCTTCCGGGGTATGACCATCTACCTTGCGGAGCCGCGAATGGGCCGAGCC													
Consensus	ATGCTTCCGAGGCGACGGCGGGTGGCAGCAGGGTCCCCACACAGCGCTTTAGCCTCTTCCACGCCCCAGCGGCGCTTCCGGGGTATGACCATCTACCTTGCGGAGCCGCGAATGGGCCGAGCC													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq cds	GCGGGGCTTCTCTACTCGCTGGCGCGGTCARAGGCTTCCGATCTAGATGTTTACAGCTCAGAGGTGACACATGTGGTGATGGAGGAGACCTCAGCCAGGAGGCGCATCTGCTGGCAGAGAGCAT													
Consensus	GCGGGGCTTCTCTACTCGCTGGCGCGGTCARAGGCTTCCGATCTAGATGTTTACAGCTCAGAGGTGACACATGTGGTGATGGAGGAGACCTCAGCCAGGAGGCGCATCTGCTGGCAGAGAGCAT													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq cds	GARTGCTCTTCCACAGACTGCCCGAGGCCGGCTGTGCTAGATATTAGCTGGTTTACAGAGAGCATGGCAGCAGGACAGCCTGCTCCAGAGAGGTCCGGACCGCTGGAGGTAGCTGAGCCAGAGAG													
Consensus	GARTGCTCTTCCACAGACTGCCCGAGGCCGGCTGTGCTAGATATTAGCTGGTTTACAGAGAGCATGGCAGCAGGACAGCCTGCTCCAGAGAGGTCCGGACCGCTGGAGGTAGCTGAGCCAGAGAG													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
seq cds	GARCCCCCATCTCAGTGACGATACAGCTTATGCTGTGAGCGCCCTCGCCTCTCACACCCCATACACTCTCTCTCAGAGGCTCTGGAGACACTTGGCGAGGCGAGCGGGCTTCAGAGGCCAAGAGG													
Consensus	GARCCCCCATCTCAGTGACGATACAGCTTATGCTGTGAGCGCCCTCGCCTCTCACACCCCATACACTCTCTCTCAGAGGCTCTGGAGACACTTGGCGAGGCGAGCGGGCTTCAGAGGCCAAGAGG													
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
seq cds	GCGCTTTTCTCACCTTCTACAGAGCAGCCTCCATGCTACAGTCCCTACCCATCCCTGTACATCTTTGAGCCAGCTGCATGGAGTGCCTTACTTTGGGAGACATTCCTTAGAGTATTCAGAGAGCTGCT													
Consensus	GCGCTTTTCTCACCTTCTACAGAGCAGCCTCCATGCTACAGTCCCTACCCATCCCTGTACATCTTTGAGCCAGCTGCATGGAGTGCCTTACTTTGGGAGACATTCCTTAGAGTATTCAGAGAGCTGCT													
	651	660	670	680	690	700	710	720	730	740	750	760	770	780
seq cds	AGAACATGGAGCGTGTAGGAGGTGGAGCAAAATCCGTGCTCAGAAAGGCCACAGACCATGAGCTCTTACCCACATCTTCCGGGTTGGGTTGAGAGCTGCTAGCCGTTGATCCAGAGAGGGCTACGA													
Consensus	AGAACATGGAGCGTGTAGGAGGTGGAGCAAAATCCGTGCTCAGAAAGGCCACAGACCATGAGCTCTTACCCACATCTTCCGGGTTGGGTTGAGAGCTGCTAGCCGTTGATCCAGAGAGGGCTACGA													
	781	790	800	810	820	830	840	850	860	870	880	890	900	910
seq cds	ACCTTGGATGAGCTCAGAGAGCAGCCCGAGAGCTGACCCAGCAGCAGAGAGCAGGGCTGCAGTATTACAGGAGCTGAGACCCCGAGTTAGCCGGGCGAGAGGCCAGAGCTCTGCAGCAGTTGGTAGAGG													
Consensus	ACCTTGGATGAGCTCAGAGAGCAGCCCGAGAGCTGACCCAGCAGCAGAGAGCAGGGCTGCAGTATTACAGGAGCTGAGACCCCGAGTTAGCCGGGCGAGAGGCCAGAGCTCTGCAGCAGTTGGTAGAGG													
	911	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040
seq cds	CAGCCATGAGGGAGATCTCGCCGGAGGCACCTGTACACTGACTGGCGGTTTCCAGAGGGGGAGTTACAGGTCATGACGTGGACCTCTTATACCCACCTCAGGAGGGGCCAGAGGTAGGGCTGCT													
Consensus	CAGCCATGAGGGAGATCTCGCCGGAGGCACCTGTACACTGACTGGCGGTTTCCAGAGGGGGAGTTACAGGTCATGACGTGGACCTCTTATACCCACCTCAGGAGGGGCCAGAGGTAGGGCTGCT													
	1041	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170
seq cds	GCCCAGAGTATGAGGTGCCCTCAGAGCCAGGGACTTGTGCTGATCCACCACTAGCTATGCGAGCCACTTACGCGACTCTGCCCATCTCTGCGGAGAGGTCACCATGGATGCTTTTGAAGGAGTTTC													
Consensus	GCCCAGAGTATGAGGTGCCCTCAGAGCCAGGGACTTGTGCTGATCCACCACTAGCTATGCGAGCCACTTACGCGACTCTGCCCATCTCTGCGGAGAGGTCACCATGGATGCTTTTGAAGGAGTTTC													
	1171	1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
seq cds	TGATCTTTCGCTTGCCACAGTCCCAACAGGCAGCTTTAGAGGGGCCCCGTGATCCTGCCACCTGCCACCTCTGAGAGCTGTAGGGTAGATCTTGTGGTCACTCCCAACAGGCAGTTCCCTTTGCTCTTTTG													
Consensus	TGATCTTTCGCTTGCCACAGTCCCAACAGGCAGCTTTAGAGGGGCCCCGTGATCCTGCCACCTGCCACCTCTGAGAGCTGTAGGGTAGATCTTGTGGTCACTCCCAACAGGCAGTTCCCTTTGCTCTTTTG													
	1301	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430
seq cds	GCTGGACTGCTCCAGTTTTTGAAGGGAGACTACGGCGATTACGCGCGCAGAGAGAGGGGCTGTGCTTATAGCCACGGGCTGTTGATCTTGAGCGGAGAGACATTTTCCACGCACTCTTGAGGA													
Consensus	GCTGGACTGCTCCAGTTTTTGAAGGGAGACTACGGCGATTACGCGCGCAGAGAGAGGGGCTGTGCTTATAGCCACGGGCTGTTGATCTTGAGCGGAGAGACATTTTCCACGCACTCTTGAGGA													
	1431	1440	1450	1460	1470	1480	1488							
seq cds	AGATGTTTTCAAGTTCTTGGGCTCAGATATCTTCTCCAGAGCAGAGAAATGCTCTGA													
Consensus	AGATGTTTTCAAGTTCTTGGGCTCAGATATCTTCTCCAGAGCAGAGAAATGCTCTGA													



Différence au niveau protéique

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq	MLPKRRRRVRAGSPHSALASSTPPAARFPGVAIYLAEPRHGRSRRRAFLTLARSKGFRILDVYSSEVTHVYMEETSAKEAICHQKDMALLPDCPQPALLDISWFTESHAAGQPYPEEVRHRLEVAEPRK													
cds	MLPKRRRRVRAGSPHSALASSTPPAARFPGVAIYLAEPRHGRSRRRAFLTLARSKGFRILDVYSSEVTHVYMEETSAKEAICHQKDMALLPDCPQPALLDISWFTESHAAGQPYPEEVRHRLEVAEPRK													
Consensus	MLPKRRRRVRAGSPHSALASSTPPAARFPGVAIYLAEPRHGRSRRRAFLTLARSKGFRILDVYSSEVTHVYMEETSAKEAICHQKDMALLPDCPQPALLDISWFTESHAAGQPYPEEVRHRLEVAEPRK													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq	EPPISVTIPAYACQRPSP LTPHNTLLSEALETLAEAGFEGKEGRFLTFYRAASHLKS LPPYVTSLSQLHGLPYFGEHSFRVIQELLEHGTCEEVEQIRCSERHQTHKLFTHIFGVGVKTASRYQEGLR													
cds	EPPISVTIPAYACQRPSP LTPHNTLLSEALETLAEAGFEGKEGRFLTFYRAASHLKS LPPYVTSLSQLHGLPYFGEHSFRVIQELLEHGTCEEVEQIRCSERHQTHKLFTHIFGVGVKTASRYQEGLR													
Consensus	EPPISVTIPAYACQRPSP LTPHNTLLSEALETLAEAGFEGKEGRFLTFYRAASHLKS LPPYVTSLSQLHGLPYFGEHSFRVIQELLEHGTCEEVEQIRCSERHQTHKLFTHIFGVGVKTASRYQEGLR													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq	TLDELREQPQRLTQQQKAGLQYYQQLSTPYSRAEAEALQQLVEAAHREILPGATVTLTGGFRRGKLQGHVDVFLITHPEEGQEVGLLPVYMRCLQSQGLVLYHQYHRSHLADSAILRQRSTHDAFERSF													
cds	TLDELREQPQRLTQQQKAGLQYYQQLSTPYSRAEAEALQQLVEAAHREILPGATVTLTGGFRRGKLQGHVDVFLITHPEEGQEVGLLPVYMRCLQSQGLVLYHQYHRSHLADSAILRQRSTHDAFERSF													
Consensus	TLDELREQPQRLTQQQKAGLQYYQQLSTPYSRAEAEALQQLVEAAHREILPGATVTLTGGFRRGKLQGHVDVFLITHPEEGQEVGLLPVYMRCLQSQGLVLYHQYHRSHLADSAILRQRSTHDAFERSF													
	391	400	410	420	430	440	450	460	470	480	490	495		
seq	CILRLPQSQAALLEGPLHPCPTHKAVRYDLVYTPNSQFFPALLGATGSQFFERELRRFSRQEKGLCLNSHGLFQPERKTFHFATSEEDVFRFLGLKYLPPQQRNA													
cds	CILRLPQSQAALLEGPLHPCPTHKAVRYDLVYTPNSQFFPALLGATGSQFFERELRRFSRQEKGLCLNSHGLFQPERKTFHFATSEEDVFRFLGLKYLPPQQRNA													
Consensus	CILRLPQSQAALLEGPLHPCPTHKAVRYDLVYTPNSQFFPALLGATGSQFFERELRRFSRQEKGLCLNSHGLFQPERKTFHFATSEEDVFRFLGLKYLPPQQRNA													

		NAME	GENE	CDNA	CDNA	CDNA	CDNA	CDNA	CDNA	CDNA
✓	DNA-directed DNA/RNA polymerase mu [Rattus norvegicus]	Norway rat	1012	1012	100%	0.0	99.80%	495	NP_001011912.1	
✓	PREDICTED: DNA-directed DNA/RNA polymerase mu isoform X3 [Rattus norvegicus]	Norway rat	1005	1005	100%	0.0	99.00%	499	XP_006251275.1	
✓	PREDICTED: DNA-directed DNA/RNA polymerase mu isoform X2 [Rattus norvegicus]	Norway rat	883	883	89%	0.0	98.19%	515	XP_006251274.1	
✓	PREDICTED: DNA-directed DNA/RNA polymerase mu isoform X1 [Rattus norvegicus]	Norway rat	879	879	89%	0.0	97.31%	519	XP_006251273.1	

○ PolM DiT48hMix clone E

➤ Fwd DiT48hMix 973NT

GCCTTCCTTCGTTCTGCGGCCTCCCGTGCTTCTGAGTCGGTGTCCAG
ATGCTTCCGAAGCGACGGCGGGCGGCTCAGAGGTGACACATGTGGTGATGGAGGAGACCTCAGCCAAGGAGGC
CATCTGCTGGCAGAAGGACATGAATGCTCTTCTCCAGACTGCCCGCAGCCGGCTCTGCTAGATATTAGCTGGTTT
ACAGAGAGCATGGCAGCAGGACAGCCTGTCCCTGAGGAGGTCCGGCACCAGCCTGGAGGTAGCTGAGCCCAGG
AAGGAACCCCCATCTCAGTGACGATACCAGCTTATGCCTGTCAGCGCCCCTCGCCTCTCACACCCATAAACTC
TCCTCTCAGAGGCTCTGGAGACACTGGCGGAGGCAGCGGGCTTCAAGGCAAAGAGGGCCGTTTTCTCACCTT
CTACAGAGCAGCCTCCATGCTCAAGTCCCTACCCTACCCTGTCACATCTTTGAGCCAGCTGCATGGACTGCCTTAC
TTTGGGGAACATTCTTTAGAGTAATCCAGGAGCTGCTAGAACATGGAACGTGTGAGGAGGTGGAACAAATCCG
TTGCTCAGAAAGGCACCAGACCATGAAGCTCTTACCCACATCTTCGGGGTTGGGGTGAAGACTGCTAGCCGGT
GGTACCAGGAAGGGCTACGAACCCTGGATGAGCTCAGAGAGCAGCCCAGAGACTGACCCAGCAGCAGAAAG
CAGTATTACCCACAGGGCTGCAGTATTACCAGGACCTGAGCACCCAGTTAGCCGGGCAGANGCCGAGGCTCTG
CAGCAGTTGGTAGAGGCAGCCATGAGGGAGNTCCTGCCCGGAGCCACTGTCACACTGACTGGCGGTTTCCGAA
NGGGGAAGTTACAAGGTCATGACGTNGNCTTCTTATCACCCACCCTGAGNAGGGCCAAGAAGTNGGGCTGCT
GCCANAGTGATGAGGTGCCTTCANAGNNAGGGNCTNNNGCTGNACNNCCAGNACCATCNNAGCCNCTTANC
GNANTCTNNCCNCTNC

➤ Rev DiT48hMix 764NT

GGGNNGGNNGAAGANTGNTAGCCGGTGGTNCCAGGAAGGGCTACGANNTTGGATGAGNTCAGAGAGCAGC
CCCAGAGACTGACCCAGCAGCAGAAAGCAGTATTACCCACAGGGCTGCAGTATTACCAGGNNGAGCACCCCA
GTTAGCCGGGCAGAGGCCGAGGNTCTGCAGCAGTTGGTAGAGGCAGCCATGAGGGAGATCNTGCCNNGAGCC
ACTGTCACACTGACTGGCGGTTTCNGAAGGGGGAAGTTACAAGGTCATGACGTGGACTTCcTTATCACCCACCcT
GAGGAGGGCCAAGAAGTAGGGCTGCTGCCAGAGTGATGAGGTGCCTTCAGAGCCAGGGACTTGTGCTGTACC
ACCAGTACCATCGCAGCCACTTAGCGGACTCTGCCACATCCTGCGGCAGAGGTCCACCATGGATGCTTTTGAGA
GGAGTTTCTGCATCTTGCGCTTGCCACAGTCCCAACAGGCAGCTTTAGAGGGGGCCCTGCATCCCTGCCAACCT
GGAAAGCTGTGAGGGTAGATCTTGTTGCTACTCCCAACAGCCAGTTCCCCTTTGCTCTTCTTGCTGGACTGGCT
CCCAGTTTTTTGAGAGGGAGCTACGGCGATTAGCCGGCAAGAGAAGGGGCTGTGCCTTAATAGCCACGGGCT
GTTTGATCCTGAGCGGAAGACATTTTTCCACGCAACTTCTGAGGAAGATGTTTTTCAGGTTCTGGGTCTCAAGTA
TCTTCTCCAGAGCAGAGAAATGCCTGA

GATGAAAAATGCCTGTTGGCTGCCATACCTGTCCACGAGAAGATGAGGGGCTGTCTCTTTCTTGACCAGGAATGT
TTCTAGACAGGAGCACCGCCACCCACGGCCTCACCTGTGCAAATGGGATTTTTTATTTTTTACCTCATCGGTTGA
GTGTGACCCCGAGTCAGCTCAGTTTTTCAGCCTCCATTCTCCTCACAGTCAGGTGCTCTT

➤ Synthèse séquençage DiT48hMix :

-----ATGCTTCCGAAGC	180
GACGGCGGGCGGCTCAGAGGTGACACATGTGGTGATGGAGGAGACCTCAGCCAAGGAGGCC	240
ATCTGCTGGCAGAAGGACATGAATGCTCTTCTCCAGACTGCCCGCAGCCGGCTCTGCTA	300
GATATTAGCTGGTTTACAGAGAGCATGGCAGCAGGACAGCCTGTCCCTGAGGAGGTCCGG	360
CACCGCCTGGAGGTAGCTGAGCCCAGGAAGGAACCCCCATCTCAGTGACGATACCAGCT	420
TATGCCTGTGTCAGCGCCCCCTCGCCTCTCACACCCATAAACTCTCCTCTCAGAGGCTCTG	480
GAGACACTGGCGGAGGCAGCGGGCTTCAAGGCAAAGAGGGCCGTTTTCTCACCTTCTAC	540
AGAGCAGCCTCCATGCTCAAGTCCCTACCCTACCCTGTCACATCTTTGAGCCAGCTGCAT	600
GGACTGCCTTACTTTGGGGAACATTCTTTAGAGTAATCCAGGAGCTGCTAGAACATGGA	660
ACGTGTGAGGAGGTGGAACAAATCCGTTGCTCAGAAAGGCACCAGACCATGAAGCTCTTC	720
ACCCACATCTTCGGGGTTGGGGTGAAGACTGCTAGCCGGTGGTACCAGGAAGGGCTACGA	780
ACCTTGGATGAGCTCAGAGAGCAGCCCAGAGACTGACCCAGCAGCAGAAAGCAGTATTA	840

CCCACAGGGCTGCAGTATTACCAGGACCTGAGCACCCAGTTAGCCGGGCAGAGGCCGAG	888
GCTCTGCAGCAGTTGGTAGAGGCAGCCATGAGGGAGATCCTGCCCGGAGCCACTGTCACA	948
CTGACTGGCGGTTTCCGAAGGGGGAAGTTACAAGGTCATGACGTGGACTTCCTTATCACC	1008
CACCCCTGAGGAGGGCCAAGAAGTAGGGCTGCTGCCCAGAGTGATGAGGTGCCTTCAGAGC	1068
CAGGGACTTGCTGCTGTACCACAGTACCATCGCAGCCACTTAGCGGACTCTGCCACATC	1128
CTGCGGCAGAGGTCCACCATGGATGCTTTTGAGAGGAGTTTCTGCATCTTGCCTTGCCA	1188
CAGTCCCAACAGGCAGCTTTAGAGGGGCCCTGCATCCCTGCCCAACCTGGAAAGCTGTG	1248
AGGGTAGATCTTGTGGTCACTCCCAACAGCCAGTTCCTTTGCTCTTCTGGCTGGACT	1308
GGCTCCCAAGTTTTTTGAGAGGGAGCTACGGCGATTAGCCGGCAAGAGAAGGGGCTGTGC	1368
CTTAATAGCCACGGGCTGTTTGATCCTGAGCGGAAGACATTTTCCACGCAACTTCTGAG	1428
GAAGATGTTTTTCAGGTTCTGGGTCTCAAGTATCTTCTCCAGAGCAGAGAAATGCCTGA	1488

CFRSDGGGSEVTHVVMEEETSAKEAICWQKDMNALLPDCPQPALDISWFTESMAAGQPVPVEVRHRLEVAEPRK
EPPISVTIPAYACQRPSLTPHNTLLSEALETLAEAGFEGKEGRFLTIFYRAASMLKSLPYPVTSLSQLHGLPYFGEHSF
RVIQELLEHGTCEEVEQIRCSERHQTMKLFTHIFGVGVKTASRWYQEGRLTDELREQPRLTQQQKAVLPTGLQYY
QDLSTPVSRAEAEALQQLVEAMREILPGATVTLTGGFRRGKLQGHVDVFLITHPEEGQEVGLLPRVMRCLQSQGL
VLYHQYHRSHLADSAILRQRSTMDAFERSFCILRLPQSQQAALEGPLHPCPTWKAVRVDLVVTPNSQFPFALLGW
TGSQFFERELRRFSRQEKGLCLNSHGLFDPERKTFHATSEEDVFRFLGLKYLPEQRNA-

➤ **Blast contre banque rat :**

	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
2	PREDICTED: Rattus norvegicus polymerase (DNA) mu (Polm) transcript variant X1 mRNA	2462	2462	100%	0.0	100.00%	XM_006251211.3
2	PREDICTED: Rattus norvegicus polymerase (DNA) mu (Polm) transcript variant X3 mRNA	2420	2420	98%	0.0	100.00%	XM_006251213.3
2	PREDICTED: Rattus norvegicus polymerase (DNA) mu (Polm) transcript variant X4 mRNA	2414	2414	98%	0.0	100.00%	XM_006251214.3
2	PREDICTED: Rattus norvegicus polymerase (DNA) mu (Polm) transcript variant X2 mRNA	2385	2385	100%	0.0	99.10%	XM_006251212.3
2	Rattus norvegicus DNA polymerase mu (Polm) mRNA	2342	2342	98%	0.0	99.08%	NM_001011912.1

Comme pour DiT24h

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

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

seq
CDS
Consensus
ATGCTTCCGAGCGACGGCGGGTGCAGACAGGGTCCACACAGCGCTTTAGCTCTTCCACGCCCCAGCGGGCGCTTCCGGGTGAGCATCTACCTTGCAGGAGCGCGAATGGGCCGACGCC

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

seq
CDS
Consensus
GCGGGGCTTCTCACTCGCTGGCGGGTCCAAAGGCTTCCGATCTAGATGTTTACAGCTCAGAGGTGACACATGTGGTATGAGGAGACCTCAGCCAGGAGGCGCATCTGCTGGCAGAGGACAT
.....AgGCTTCCGAGC.....GAcGgggaCaGCTCAGAGGTGACACATGTGGTATGAGGAGACCTCAGCCAGGAGGCGCATCTGCTGGCAGAGGACAT

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

seq
CDS
Consensus
GAATGCTCTTCTCCAGACTGCCCGAGCGGGCTGTGTAGATATTAGCTGGTTTACAGAGACATGGCAGCAGGACAGCTGTCCCTGAGGAGGTCCGCGACCGCTGGAGGTAGCTAGGCCAGGAG
GAATGCTCTTCTCCAGACTGCCCGAGCGGGCTGTGTAGATATTAGCTGGTTTACAGAGACATGGCAGCAGGACAGCTGTCCCTGAGGAGGTCCGCGACCGCTGGAGGTAGCTAGGCCAGGAG
GAATGCTCTTCTCCAGACTGCCCGAGCGGGCTGTGTAGATATTAGCTGGTTTACAGAGACATGGCAGCAGGACAGCTGTCCCTGAGGAGGTCCGCGACCGCTGGAGGTAGCTAGGCCAGGAG

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

seq
CDS
Consensus
GARCCCCCATCTCAGTGACGATACAGCTTATGCTGTACGGGCCCTCGCCTCTCACACCCCATACACATCTCCTCTCAGAGGCTCTGGAGACATGGCGAGGAGCGGGCTTCGAGGCAAGAGAG
GARCCCCCATCTCAGTGACGATACAGCTTATGCTGTACGGGCCCTCGCCTCTCACACCCCATACACATCTCCTCTCAGAGGCTCTGGAGACATGGCGAGGAGCGGGCTTCGAGGCAAGAGAG
GARCCCCCATCTCAGTGACGATACAGCTTATGCTGTACGGGCCCTCGCCTCTCACACCCCATACACATCTCCTCTCAGAGGCTCTGGAGACATGGCGAGGAGCGGGCTTCGAGGCAAGAGAG

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

seq
CDS
Consensus
GCCGTTTTCTACCTTCTACAGAGCAGCTCCATGCTCAGTCCCTACCTACCTGTACATCTTTGAGGCAGCTGCATGGACTGCCTTACTTTGGGAGACATTCCTTTAGAGTATCTCAGAGCTGCT
GCCGTTTTCTACCTTCTACAGAGCAGCTCCATGCTCAGTCCCTACCTACCTGTACATCTTTGAGGCAGCTGCATGGACTGCCTTACTTTGGGAGACATTCCTTTAGAGTATCTCAGAGCTGCT
GCCGTTTTCTACCTTCTACAGAGCAGCTCCATGCTCAGTCCCTACCTACCTGTACATCTTTGAGGCAGCTGCATGGACTGCCTTACTTTGGGAGACATTCCTTTAGAGTATCTCAGAGCTGCT

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

seq
CDS
Consensus
AGACATGGAGCTGTGAGGAGGTGGACAAATCCGTTGCTCAGAGAGGACACAGCCATGAGCTCTTACCCACATCTTCGCGGTTGGGGTGAAGAGTGTAGCCGCTGCTACAGGAGGGCTACGA
AGACATGGAGCTGTGAGGAGGTGGACAAATCCGTTGCTCAGAGAGGACACAGCCATGAGCTCTTACCCACATCTTCGCGGTTGGGGTGAAGAGTGTAGCCGCTGCTACAGGAGGGCTACGA
AGACATGGAGCTGTGAGGAGGTGGACAAATCCGTTGCTCAGAGAGGACACAGCCATGAGCTCTTACCCACATCTTCGCGGTTGGGGTGAAGAGTGTAGCCGCTGCTACAGGAGGGCTACGA

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

seq
CDS
Consensus
ACCCTGGATGAGCTCAGAGAGCAGCCCCAGAGACTGACCCAGCAGCAGAGAGCAGTATTACCCACAGCGCTGCAGTATTACAGGACCTGAGCACCACAGTATAGCCGGGAGAGGCGAGGCTCTGAGC
ACCCTGGATGAGCTCAGAGAGCAGCCCCAGAGACTGACCCAGCAGCAGAGAGCAG.....GGCTCGAGTATTACAGGACCTGAGCACCACAGTATAGCCGGGAGAGGCGAGGCTCTGAGC
ACCCTGGATGAGCTCAGAGAGCAGCCCCAGAGACTGACCCAGCAGCAGAGAGCAG.....GGCTCGAGTATTACAGGACCTGAGCACCACAGTATAGCCGGGAGAGGCGAGGCTCTGAGC

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

seq
CDS
Consensus
AGTTGGTAGAGCAGCCATGAGGAGATCTGCCCGAGGACCTGTACACTGACTGGCGGTTCCGAGGGGGAGGTTACAGGTCATGACGTGGACTTCCTTATACCCACCTTGAGGAGGGCCAGGA
AGTTGGTAGAGCAGCCATGAGGAGATCTGCCCGAGGACCTGTACACTGACTGGCGGTTCCGAGGGGGAGGTTACAGGTCATGACGTGGACTTCCTTATACCCACCTTGAGGAGGGCCAGGA
AGTTGGTAGAGCAGCCATGAGGAGATCTGCCCGAGGACCTGTACACTGACTGGCGGTTCCGAGGGGGAGGTTACAGGTCATGACGTGGACTTCCTTATACCCACCTTGAGGAGGGCCAGGA

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

seq
CDS
Consensus
AGTAGGGCTGCTGCCCHAGTGATGAGGTGCTTCAGAGCCAGGGACTTGTGCTGTACACCACTGATACCTGCGAGCCTTAGCGGACTCTGCCACATCTTCGCGGAGAGGTCCACCATGGATGCTTT
AGTAGGGCTGCTGCCCHAGTGATGAGGTGCTTCAGAGCCAGGGACTTGTGCTGTACACCACTGATACCTGCGAGCCTTAGCGGACTCTGCCACATCTTCGCGGAGAGGTCCACCATGGATGCTTT
AGTAGGGCTGCTGCCCHAGTGATGAGGTGCTTCAGAGCCAGGGACTTGTGCTGTACACCACTGATACCTGCGAGCCTTAGCGGACTCTGCCACATCTTCGCGGAGAGGTCCACCATGGATGCTTT

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

seq
CDS
Consensus
GAGAGGAGTTTCTGATCTTTCGCTTGGCAGAGTCCACACAGGACGCTTTAGAGGGGCCCTGATCCCTGCCACACCTGGAGAGCTGTGAGGGTAGATCTTGTGGTCACTCCACACAGGTTCCCT
GAGAGGAGTTTCTGATCTTTCGCTTGGCAGAGTCCACACAGGACGCTTTAGAGGGGCCCTGATCCCTGCCACACCTGGAGAGCTGTGAGGGTAGATCTTGTGGTCACTCCACACAGGTTCCCT
GAGAGGAGTTTCTGATCTTTCGCTTGGCAGAGTCCACACAGGACGCTTTAGAGGGGCCCTGATCCCTGCCACACCTGGAGAGCTGTGAGGGTAGATCTTGTGGTCACTCCACACAGGTTCCCT

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

seq
CDS
Consensus
TTGCTCTTCTTGGCTGAGCTGGCTCCAGTTTTTTGAGAGGGAGCTACGGCGATTACGCCGAGAGAGAGGGGCTGTGCTTATAGCCACGGGCTGTTGATCTTGGCTGAGCGAGAGCATTTTTCCACGC
TTGCTCTTCTTGGCTGAGCTGGCTCCAGTTTTTTGAGAGGGAGCTACGGCGATTACGCCGAGAGAGAGGGGCTGTGCTTATAGCCACGGGCTGTTGATCTTGGCTGAGCGAGAGCATTTTTCCACGC
TTGCTCTTCTTGGCTGAGCTGGCTCCAGTTTTTTGAGAGGGAGCTACGGCGATTACGCCGAGAGAGAGGGGCTGTGCTTATAGCCACGGGCTGTTGATCTTGGCTGAGCGAGAGCATTTTTCCACGC

1431 1440 1450 1460 1470 1480 1490 1500

seq
CDS
Consensus
AACTTCTGAGGAGATGTTTTTCAGGTTCTTGGGCTCAGATATCTTCTCCAGAGCAGAGAAATGCTGA
AACTTCTGAGGAGATGTTTTTCAGGTTCTTGGGCTCAGATATCTTCTCCAGAGCAGAGAAATGCTGA
AACTTCTGAGGAGATGTTTTTCAGGTTCTTGGGCTCAGATATCTTCTCCAGAGCAGAGAAATGCTGA

➤ Différence au niveau PROT :

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

seq
refprot
Consensus
MLPKRRRRYRAGSPHSLASSTPPAARFPVAVIYLAERPMGRSRRAFLLRLARSKGFRILDVYSEVTHVYMEETSAKEAICQKQDMNALLPDCQPALLDISMFTESHAAGQVPYEEVHRHLEVAEPRK
.....cFri..DgggSEVTHVYMEETSAKEAICQKQDMNALLPDCQPALLDISMFTESHAAGQVPYEEVHRHLEVAEPRK

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

seq
refprot
Consensus
EPPISVTIPAYACQRPSPPLTPHNTLLSEALETLAERAGFEGKEGRFLTFRARASHLKSLLPYPTSLSQLHGLPYFGEHSFRVIQELLEHGTCCEEVEQIRCSERHQTHKLFTHIFGVGVKTASRYQEGLR
EPPISVTIPAYACQRPSPPLTPHNTLLSEALETLAERAGFEGKEGRFLTFRARASHLKSLLPYPTSLSQLHGLPYFGEHSFRVIQELLEHGTCCEEVEQIRCSERHQTHKLFTHIFGVGVKTASRYQEGLR
EPPISVTIPAYACQRPSPPLTPHNTLLSEALETLAERAGFEGKEGRFLTFRARASHLKSLLPYPTSLSQLHGLPYFGEHSFRVIQELLEHGTCCEEVEQIRCSERHQTHKLFTHIFGVGVKTASRYQEGLR

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

seq
refprot
Consensus
TLDELREQPRLTQQQKAVLPTGLQYYQDLSTPYSRAEAREALQQLVEAHREILPGATVTLTGFFRRGKLQGHQVDFLITHPEEGQEVGLLPRVMRCLQSQGLVLYHQYHRSHLADSAILRQRSTHDAF
TLDELREQPRLTQQQK.....GLQYYQDLSTPYSRAEAREALQQLVEAHREILPGATVTLTGFFRRGKLQGHQVDFLITHPEEGQEVGLLPRVMRCLQSQGLVLYHQYHRSHLADSAILRQRSTHDAF
TLDELREQPRLTQQQK.....GLQYYQDLSTPYSRAEAREALQQLVEAHREILPGATVTLTGFFRRGKLQGHQVDFLITHPEEGQEVGLLPRVMRCLQSQGLVLYHQYHRSHLADSAILRQRSTHDAF

391 400 410 420 430 440 450 460 470 480 490 499

seq
refprot
Consensus
ERSFCILRLPQSQQRAALEGLPHCPCTWAKAVRYDLVYTPNSQFPFALLGATGSOFFERELRRFSRQEKGLCLNSHGLFDPERKTFHFATSEEDVFRFLGLKYLPPPEQRNA
ERSFCILRLPQSQQRAALEGLPHCPCTWAKAVRYDLVYTPNSQFPFALLGATGSOFFERELRRFSRQEKGLCLNSHGLFDPERKTFHFATSEEDVFRFLGLKYLPPPEQRNA
ERSFCILRLPQSQQRAALEGLPHCPCTWAKAVRYDLVYTPNSQFPFALLGATGSOFFERELRRFSRQEKGLCLNSHGLFDPERKTFHFATSEEDVFRFLGLKYLPPPEQRNA

	Score	Score	Cover	value	Ident	Accession
✓ PREDICTED: DNA-directed DNA/RNA polymerase mu isoform X1 [Rattus norvegicus]	909	909	100%	0.0	100.00%	XP_006251273.1
✓ PREDICTED: DNA-directed DNA/RNA polymerase mu isoform X2 [Rattus norvegicus]	896	896	100%	0.0	99.10%	XP_006251274.1
✓ PREDICTED: DNA-directed DNA/RNA polymerase mu isoform X3 [Rattus norvegicus]	895	895	99%	0.0	99.32%	XP_006251275.1
✓ PREDICTED: DNA-directed DNA/RNA polymerase mu isoform X4 [Rattus norvegicus]	891	891	98%	0.0	99.77%	XP_006251276.1
✓ DNA-directed DNA/RNA polymerase mu [Rattus norvegicus]	880	880	99%	0.0	98.41%	NP_001011912.1

pCR4Blunt Pol M DiT48h (clone E) comme pour DiT24h :
le primer Fwd a du s'hybrider plus loin : il manque le
début de la séquence

○ **PolM DiT48hMix NOUVEAU CLONAGE**

➤ **Fwd DiT48hMix 948NT**

AAGGCACCAGNCNATGAAGCTNTNACCNACNTNTTNNGGNNNGGGTGAAGANTGCTANNNGGNG
GTACCAGGAAGGGNTACGANCCNGGATGAGCTCAGAGAGCANCCCCAGAGACTGACCCAGCAGC
AGAAAGCAGGGCTGCAGTATTACCAGGACNTGAGCANCCCAGTTAGCCGGGCAGAGGCCGAGGCTC
TGCAGCAGTTGGTAGAGGCAGCCATGAGGGAGATCCTGCCNNGAGCCACTGTCACACTGACTGGCG
GTTTCcGAAGGGGGAAGTTACAAGGTCATGACGTGGACTTCCTTATCACCCACCcTGAGGAGGGCCA
AGAAGTAGGGCTGCTGCCCAGAGTGATGAGGTGCCTTCAGAGCCAGGGACTTGTGCTGTACCACCA
GTACCATCGCAGCCACTTAGCGGACTCTGCCACATCCTGCGGCAGAGGTCCACCATGGATGCTTTTG
AGAGGAGTTTCTGCATCTTGCGCTTGCCACAGTCCCAACAGGCAGCTTTAGAGGGGCCCTGCATCCC
TGCCCAACCTGGAAAGCTGTGAGGGTAGATCTTGTGGTCACTCCCAACAGCCAGTTCCCTTTGCTCT
TCTTGGCTGGACTGGCTCCAGTTTTTTGAGAGGGAGCTACGGCGATTACGCCGGAAGAGAAGGG
GCTGTGCCTTAATAGCCACGGGCTGTTTGATCCTGAGCGGAAGACATTTTTCCACGCAACTTCTGAGG
AAGATGTTTTTCAGGTTCTGGGTCTCAAGTATCTTCTCCAGAGCAGAGAAATGCCTGAGATGAAAAA
TGCCTGTTGGCTGCCATACCTGTCCACGAGAAGATGAGGGGCTGTCTCTTTCTTGACCAGGAATGTTT
CTAGACAGGAGCACCGCCACCCACGGCCTCACCTGTGCAAATGGGATTTTTTATTTTTTACCTCATCG
GTTGAGTGTGA

➤ **Rev DiT48hMix 924NT**

ATGCTTCCGAAGCGACGGCGGGCGGCTCAGAGGTGACACATGTGGTGATGGAGGAGACCTCAGCCAA
GGAGGCCATCTGCTGGCAGAAGGACATGAATGCTCTTCTCCCAGACTGCCCCGAGCCGGCTCTGCTA
GATATTAGCTGGTTTACAGAGAGCATGGCAGCAGGACAGCCTGTCCCTGAGGAGGTCCGGCACCGCC
TGGAGGTAGCTGAGCCCAGGAAGGAACCCCCATCTCAGTGACGATACCAGCTTATGCCTGTCAGCG
CCCCTCGCCTCTCACACCCATAAACACTCTCCTCTCAGAGGCTCTGGAGACACTGGCGGAGGCAGCGG
GCTTCGAAGGCAAAGAGGGCCGTTTTCTACCTTCTACAGAGCAGCCTCCATGCTCAAGTCCCTACCC
TACCCTGTCACATCTTTGAGCCAGCTGCATGGACTGCCTTACTTTGGGGAACATTCTTTAGAGTAATC
CAGGAGCTGCTAGAACATGGAACGTGTGAGGAGGTGGAACAAATCCGTTGCTCAGAAAGGCACCAG
ACCATGAAGCTCTTACCCACATCTTCGGGGTTGGGGTGAAGACTGCTAGCCGGTGGTACCAGGAAG
GGCTACGAACCCTGGATGAGCTCAGAGAGCAGCCCCAGAGACTGACCCAGCNGCAGAAAGCagGGC
TGCNGTATTACCAGgACCTGAGCACCCAGTTAGCCgGGCAGAGGCCGAGGcTCTGCANCAAGTTGGT
AGAGGCAGCNNTGNNGGAGATCCTGNCCGGANCCNCTGTCACACTGACTGGNGGNTTCCGAANGG
GGNAGTTACNNNNCATGACGTGNACTTNCTTATCACCCACCCTGAGNNGGNCANNAGTNNGNNNN
TGCCNGAGTGATGAGGTGCCTTCANNGCCNNGGACTTGTGCTGTACNNNCAGTACC

➤ **Synthèse séquençage DiT48hMix :**

```

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

131    140     150     160     170     180     190     200     210     220     230     240     250     260
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
seq
cds
Consensus
ATGCTTCCGAGCG---GACGCGGGCGCTCAGAGGTGACACATGTGGTATGGAGAGACCTCAGCCAGAGGGCCATCTGCTGGCAGAGGACAT
GCGGGGCTTCTCCTACTCGCTGGCGGGTCCAAAGGCTTCCGATCTCTAGTGTTCAGCTCAGAGGTGACACATGTGGTATGGAGAGACCTCAGCCAGAGGGCCATCTGCTGGCAGAGGACAT
AgGCTTCCGaAgC...GAcGgcgaCaGCTCAGAGGTGACACATGTGGTATGGAGAGACCTCAGCCAGAGGGCCATCTGCTGGCAGAGGACAT

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

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

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

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

781    790     800     810     820     830     840     850     860     870     880     890     900     910
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
seq
cds
Consensus
ACCTTGGATGAGCTCAGAGAGCAGCCCCAGAGCTGACCCAGCAGCAGAGAGCAGGGCTGCAGCTATTACAGGACCTGAGCACCCTAGTTAGCCGGGCGAGAGGCCAGGCTCTGCAGCAGTTGGTAGAGG
ACCTTGGATGAGCTCAGAGAGCAGCCCCAGAGCTGACCCAGCAGCAGAGAGCAGGGCTGCAGCTATTACAGGACCTGAGCACCCTAGTTAGCCGGGCGAGAGGCCAGGCTCTGCAGCAGTTGGTAGAGG
ACCTTGGATGAGCTCAGAGAGCAGCCCCAGAGCTGACCCAGCaGCAGAGAGCAGGGCTGCAGTATTACAGGACCTGAGCACCCTAGTTAGCCGGGCGAGAGGCCAGGCTCTGCAGCAGTTGGTAGAGG

911    920     930     940     950     960     970     980     990     1000    1010    1020    1030    1040
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
seq
cds
Consensus
CAGCnNTGNNGGAGATCCTGnCCGGANCCnCTGTCACTGACTGnGGnTTCCGARNGGGGnAGTTACn--nNNCATGACGTnACTnCTTATCACCACCCTGAGnGGnC--nNNAGTnGGNNn-T
CAGCnCATGAGGAGATCCTGCCCCGAGCCnCTGTCACTGACTGnGGnTTCCGARNGGGGnAGTTACnAGGTCATGACGTGnACTnCTTATCACCACCCTGAGnGGnCCnAGAGnAGTnAGGCTGCT
CAGCnATGnGGAGATCCTGnCCGGAnCCnCTGTCACTGACTGnGGnTTCCGARNGGGGnAGTTACn--nNNCATGACGTnACTnCTTATCACCACCCTGAGnGGnC..nAnAGTnAGnNNn-T

1041   1050     1060     1070     1080     1090     1100     1110     1120     1130     1140     1150     1160     1170
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
seq
cds
Consensus
GCC-nGAGTGATGAGGTGCTTCAnNGCCnNGGACTTGtGTACnNnAGTACC
GCCnAGAGTGATGAGGTGCTTCAGAGCCnAGGGACTTGtGTGTACnCCAGTACC
GCC..aGAGTGATGAGGTGCTTCAnGCCnAGGACTTGtGTGTACnAnAGTACC.....

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

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

1431   1440     1450     1460     1470     1480     1488
|-----|-----|-----|-----|-----|-----|
seq
cds
Consensus
AGATGTTTTAGGTTCTCGAGTATCTTCTCCAGAGCAGAGAAATGCCTGA

```

Comme autre clone 48h

Pol M SP clone E

➤ Fwd SP 990NT

GCCTTCCTTCGTTCTGCGGCCTCCCGTGCTTCCTGAGTCGGTGTCCAG
ATGCTTCCGAAGCGACGGCGGGGTGCGAGCAGGGTCCCCACACAGCGCTTTAGCCTCTTCACGCCCCCAG
CGGCGCGCTTCCCGGGTGTAGCCATCTACCTTGCGGAGCCGCGAATGGGCCGAGCCGCCGGGCCTTCCTCACT
CGCCTGGCGCGGTCCAAAGGCTTCCGCATCCTAGATGTTTACAGCTCAGAGGTGACACATGTGGTGATGGAGGA
GACCTCAGCCAAGGAGGCCATCTGCTGGCAGAAGGACATGAATGCTCTTCTCCAGACTGCCCCGAGCCGGCTC
TGCTAGATATTAGCTGGTTTACAGAGAGCATGGCAGCAGGACAGCCTGTCCCTGAGGAGGTCCGGCACC GCCTG
GAGGTAGCTGAGCCCAGGAAGGAACCCCCCATCTCAGTGACGATACCAGCTTATGCCTGTCAGCGCCCCCTGCCT
CTCACACCCCATAAACTCTCCTCTCAGAGGCTCTGGAGACACTGGCGGAGGCAGCGGGCTTCGAAGGCAAAG
AGGGCCGTTTTCTACCTTCTACAGAGCAGCCTCCATGCTCAAGTCCCTACCCTACCCTGTACATCTTTGAGCCA
GCTGCATGGACTGCCTTACTTTGGGGAACATTCTTTAGAGTAATCCAGGAGCTGCTAGAACATGGAACGTGTGA
GGAGGTGGAACAAATCCGTTGCTCAGAAAGGCACCAGACCATGAAGCTCTTACCCACATCTTCGGGGTTGGG
GTGAAGACTGCTAGCCGGTGGTANCAGGAAGGGCTACGAACCCTGNNTGAGCTCANANAGCAGCCCCAGANA
CTGACCCANCAGCANAAAGCNNGGCTGCAGTATTACCAGGACCTGAGCACCCAGTTAGCCGGGCAGAGGCC
GAGGCTCTGCANCAAGTTGGTANAGGCAGCCATGNNGGANATCCTGCCNGGAGCANNCTGNACNCTGACTGGN
NGNTTNCNANNGGNNNGNTANNAGNTCNTGACG

➤ Rev SP 796NT

AGAAAGNNNCCAGNCNNTGAAGCTNNTCACCCACNTNTTCGGGGTNGGGGTGAAGANTGNTAGCNGGTGG
TNCCAGGAANGGCTACGAACCCTGGATGAGNTCAGAGAGCAGCCCCAGAGACTGACCCAGCAGCAGAAAGC
AGGGCTGCAGTATTANCAGGACNTGAGCACCCAGTNAGCCGGGCAGAGGCNGAGGCTCTGCAGCAGTTGG
TAGAGGCAGCCATGAGGGAGATCNTGCCNGGAGCCACTGTCACTGACTGGCGGTTTCCGAAGGGGGAAG
TTACAAGGTCATGACGTGGACTTCCTTATCACCCACCcTGAGGAGGGCCAAGAAGTAGGGCTGCTGCCAGAG
TGATGAGGTGCCTTCAGAGCCAGGGACTTGTGCTGTACCACCACTACCATCGCAGCCACTTAGCGGACTCTGC
CCACATCTGCGGCAGAGGTCCACCATGGATGCTTTTGAAGAGGATTTCTGCATCTTGCGCTTGCCACAGTCCC
AACAGGCAGCTTTAGAGGGGGCCCCTGCATCCCTGCCAACCTGGAAAGCTGTGAGGGTAGATCTTGTGGTCAC
TCCCAACAGCCAGTTCCCCTTTGCTCTTCTTGCTGGACTGGCTCCCAGTTTTTTGAGAGGGAGCTACGGCGAT
TCAGCCGGCAAGAGAAGGGGCTGTGCCTAATAGCCACGGGCTGTTTGATCCTGAGCGGAAGACATTTTTTCCA
CGCAACTTCTGAGGAAGATGTTTTAGGTTCTGGGTCTCAAGTATCTTCTCCAGAGCAGAGAAATGCCTGA

GATGAAAAATGCCTGTTGGCTGCCATACCTGTCCACGAGAAGATGAGGGGCTGTCTCTTTCTTGACCAGGAAT
GTTTCTAGACAGGAGCACCGCCACCCACGGCCTACCTGTGCAAATGGGATTTTTTATTTTTTACCTCATCGGT
TGAGTGTGACCCCGAGTCAGCTCAGTTTTCAGCCTCCATTCTCCTCACAGTCAGGTGCTCTT

➤ Synthèse séquençage SP: 1488NT

ATGCTTCCGAAGCGACGGCGGGGTGCGAGCAGGGTCCCCACACAGCGCTTTAGCCTCT	60
TCCACGCCCCCAGCGCGCGCTTCCCGGGTGTAGCCATCTACCTTGCGGAGCCGCGAATG	120
GGCCGAGCCGCCGGGCCTTCCTCACTCGCCTGGCGCGGTCCAAAGGCTTCCGCATCCTA	180
GATGTTTACAGCTCAGAGGTGACACATGTGGTGATGGAGGAGACCTCAGCCAAGGAGGCC	240
ATCTGCTGGCAGAAGGACATGAATGCTCTTCTCCAGACTGCCCCGAGCCGGCTCTGCTA	300
GATATTAGCTGGTTTACAGAGAGCATGGCAGCAGGACAGCCTGTCCCTGAGGAGGTCCGG	360

CACCGCCTGGAGGTAGCTGAGCCCAGGAAGGAACCCCCCATCTCAGTGACGATACCAGCT	420
TATGCCTGTTCAGCGCCCTCGCCTCTCACACCCATAACACTCTCCTCTCAGAGGCTCTG	480
GAGACACTGGCGGAGGCAGCGGGCTTCGAAGGCAAAGAGGGCCGTTTTCTCACCTTCTAC	540
AGAGCAGCCTCCATGCTCAAGTCCCTACCCTACCCTGTCACATCTTTGAGCCAGCTGCAT	600
GGACTGCCTTACTTTGGGGAACATTCCCTTTAGAGTAATCCAGGAGCTGCTAGAACATGGA	660
ACGTGTGAGGAGGTGGAACAAATCCGTTGCTCAGAAAGGCACCAGACCATGAAGCTCTTC	720
ACCCACATCTTCGGGGTTGGGGTGAAGACTGCTAGCCGGTGGTACCAGGAAGGGCTACGA	780
ACCTTGGATGAGCTCAGAGAGCAGCCCCAGAGACTGACCCAGCAGCAGAAAGCAGGGCTG	840
CAGTATTACCAGGACCTGAGCACCCAGTTAGCCGGGCAGAGGCCGAGGCTCTGCAGCAG	900
TTGGTAGAGGCAGCCATGAGGGAGATCCTGCCCCGAGCCACTGTCACACTGACTGGCGGT	268
TTCCGAAGGGGGAAGTTACAAGGTCATGACGTGGACTTCCTTATCACCACCcTGAGGAG	1020
GGCCAAGAAGTAGGGCTGCTGCCCAGAGTGATGAGGTGCCTTCAGAGCCAGGGACTTGTG	1080
CTGTACCACCAGTACCATCGCAGCCACTTAGCGGACTCTGCCACATCCTGCGGCAGAGG	1140
TCCACCATGGATGCTTTTGAGAGGAGTTTCTGCATCTTGCGCTTGCCACAGTCCCAACAG	1200
GCAGCTTTAGAGGGGGCCCTGCATCCCTGCCCAACCTGGAAAGCTGTGAGGGTAGATCTT	1260
GTGGTCACTCCCAACAGCCAGTTCCCTTTGCTCTTCTTGGCTGGACTGGCTCCCAGTTT	1320
TTTGAGAGGGAGCTACGGCGATTACGCCGGCAAGAGAAGGGGCTGTGCCTTAATAGCCAC	1380
GGGCTGTTTGATCCTGAGCGGAAGACATTTTCCACGCAACTCTGAGGAAGATGTTTTC	1440
AGGTTCTCTGGGTCTCAAGTATCTTCCTCCAGAGCAGAGAAATGCCTGA	1488

MLPKRRRRVRAGSPHSALASSTPPAARFPGVAIYLAERPMGRSRRFLTRLARSKGRILDVYSSEVTHVVMETS
 KEAICWQKDMNALLPDCPQALLDISWFTESMAAGQPVPVEVRHRLEVAEPRKEPPISVTIPAYACQRPSP
 LTPHN
 TLLSEALETLAEAAGFEGKEGRFLTFYRAASMLKSLPYPVTSLSQLHGLPYFGEHSFRVIQELLEHGT
 CEEVEQIRCSER
 HQTMKLFTHIFGVGVKTASRWYQEGLRTLDELREQPQRLTQQQKAGLQYYQDLSTPVSRAEAEALQ
 QLVEAAMR
 EILPGATVTLTGGFRRGKLQGHDFLITHPEEGQEVGLLPRVMRCLQSQGLVLYHQYHRSHLADSAH
 ILRQRSTM
 DAFERSFCILRLPQSQQAALGPLHPCPTWKAVRVDLVVTPNSQFPFALLGWTGSQFFERELRRFSR
 QEKGLCLNSH
 GLFDPERKTFHFATSEEDVFRFLGLKYLPEQRNA-

➤ **Blast contre banque rat :**

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Rattus norvegicus DNA polymerase mu (Polm) .mRNA	2748	2748	100%	0.0	100.00%	NM_001011912.1
PREDICTED: Rattus norvegicus polymerase (DNA) mu (Polm) .transcript variant X3 .mRNA	2693	2693	100%	0.0	99.20%	XM_006251213.3
PREDICTED: Rattus norvegicus polymerase (DNA) mu (Polm) .transcript variant X4 .mRNA	2471	2471	93%	0.0	98.78%	XM_006251214.3
PREDICTED: Rattus norvegicus polymerase (DNA) mu (Polm) .transcript variant X2 .mRNA	2398	2398	87%	0.0	100.00%	XM_006251212.3
PREDICTED: Rattus norvegicus polymerase (DNA) mu (Polm) .transcript variant X1 .mRNA	2342	2342	87%	0.0	99.08%	XM_006251211.3

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

1 10 20 30 40 50 60 70 80 90 100 110 120 130
seq
CDS
Consensus
ATGCTTCCGAGAGCGAGCGGCGGTCGAGCAGGGTCCCCACACAGCGCTTTAGCCTCTTCCAGCGCCCCAGCGCGCGCTTCCGCGGTGAGCCATCTACCTTGC6GAGCCGCGARTGGGCCGAGCC
ATGCTTCCGAGAGCGAGCGGCGGTCGAGCAGGGTCCCCACACAGCGCTTTAGCCTCTTCCAGCGCCCCAGCGCGCGCTTCCGCGGTGAGCCATCTACCTTGC6GAGCCGCGARTGGGCCGAGCC
ATGCTTCCGAGAGCGAGCGGCGGTCGAGCAGGGTCCCCACACAGCGCTTTAGCCTCTTCCAGCGCCCCAGCGCGCGCTTCCGCGGTGAGCCATCTACCTTGC6GAGCCGCGARTGGGCCGAGCC

131 140 150 160 170 180 190 200 210 220 230 240 250 260
seq
CDS
Consensus
GCCG6GCTTCTCACTCGCCTGGCGCGGTCGAGAGGCTTCCGATCTAGATGTTTACAGCTCAGAGGTGACACATGTGGTATGAGGAGAGCCCTAGCCAGGAGGCGCATCTGCTGGCAGAGGACAT
GCCG6GCTTCTCACTCGCCTGGCGCGGTCGAGAGGCTTCCGATCTAGATGTTTACAGCTCAGAGGTGACACATGTGGTATGAGGAGAGCCCTAGCCAGGAGGCGCATCTGCTGGCAGAGGACAT
GCCG6GCTTCTCACTCGCCTGGCGCGGTCGAGAGGCTTCCGATCTAGATGTTTACAGCTCAGAGGTGACACATGTGGTATGAGGAGAGCCCTAGCCAGGAGGCGCATCTGCTGGCAGAGGACAT

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

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

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

651 660 670 680 690 700 710 720 730 740 750 760 770 780
seq
CDS
Consensus
AGAACATGGAGCTGTGAGGAGGTGAGCAATCCGTTGCTCAGAAAGGCCAGAGCATGAGGCTCTTACCCACATCTTCG6G6TTGGGTTGAGGATGCTAGCCG6TTGATCAGGAGG6GCTACGA
AGAACATGGAGCTGTGAGGAGGTGAGCAATCCGTTGCTCAGAAAGGCCAGAGCATGAGGCTCTTACCCACATCTTCG6G6TTGGGTTGAGGATGCTAGCCG6TTGATCAGGAGG6GCTACGA
AGAACATGGAGCTGTGAGGAGGTGAGCAATCCGTTGCTCAGAAAGGCCAGAGCATGAGGCTCTTACCCACATCTTCG6G6TTGGGTTGAGGATGCTAGCCG6TTGATCAGGAGG6GCTACGA

781 790 800 810 820 830 840 850 860 870 880 890 900 910
seq
CDS
Consensus
ACCTGGATGAGCTCAGAGAGCAGCCAGAGACTGACCCAGCAGCAGAAAGCAGGGCTGCACTATTACAGGACCTGAGCACCACAGTTAGCCG6GAGAGG6GCTGCTGAGCAGTTGATAGAG
ACCTGGATGAGCTCAGAGAGCAGCCAGAGACTGACCCAGCAGCAGAAAGCAGGGCTGCACTATTACAGGACCTGAGCACCACAGTTAGCCG6GAGAGG6GCTGCTGAGCAGTTGATAGAG
ACCTGGATGAGCTCAGAGAGCAGCCAGAGACTGACCCAGCAGCAGAAAGCAGGGCTGCACTATTACAGGACCTGAGCACCACAGTTAGCCG6GAGAGG6GCTGCTGAGCAGTTGATAGAG

911 920 930 940 950 960 970 980 990 1000 1010 1020 1030 1040
seq
CDS
Consensus
CAGCCATGAGGAGATCTGCCCGGAGCCTGTACACTGACTG6GCGTTTCCGAGG6G6GAGTTACAGGTCATGACGTGACTTCTTATCACCACCCCTGAGGAGG6GCAAGAGTAGGGCTGCT
CAGCCATGAGGAGATCTGCCCGGAGCCTGTACACTGACTG6GCGTTTCCGAGG6G6GAGTTACAGGTCATGACGTGACTTCTTATCACCACCCCTGAGGAGG6GCAAGAGTAGGGCTGCT
CAGCCATGAGGAGATCTGCCCGGAGCCTGTACACTGACTG6GCGTTTCCGAGG6G6GAGTTACAGGTCATGACGTGACTTCTTATCACCACCCCTGAGGAGG6GCAAGAGTAGGGCTGCT

1041 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170
seq
CDS
Consensus
GCCAGAGTGATGAGGTGCTTCCAGAGCCAGGAGCTTGTGCTGATCACCAGTACCATCGCAGGACCTTAGCGGACTCTGCCACATCTTGC6GAGAGGTCACCATGGATGCTTTTGAAGGAGTTTC
GCCAGAGTGATGAGGTGCTTCCAGAGCCAGGAGCTTGTGCTGATCACCAGTACCATCGCAGGACCTTAGCGGACTCTGCCACATCTTGC6GAGAGGTCACCATGGATGCTTTTGAAGGAGTTTC
GCCAGAGTGATGAGGTGCTTCCAGAGCCAGGAGCTTGTGCTGATCACCAGTACCATCGCAGGACCTTAGCGGACTCTGCCACATCTTGC6GAGAGGTCACCATGGATGCTTTTGAAGGAGTTTC

1171 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
seq
CDS
Consensus
TGATCTTGGCTTGGCAGCTCCACAGGCGCTTTAGAGG6G6GCTTGCATCCCTGCCACACTGGAAGGCTGTGAGG6TAGATCTGTG6TCACTCCACAGCAGGCTCCCTTGTCTCTCTTG
TGATCTTGGCTTGGCAGCTCCACAGGCGCTTTAGAGG6G6GCTTGCATCCCTGCCACACTGGAAGGCTGTGAGG6TAGATCTGTG6TCACTCCACAGCAGGCTCCCTTGTCTCTCTTG
TGATCTTGGCTTGGCAGCTCCACAGGCGCTTTAGAGG6G6GCTTGCATCCCTGCCACACTGGAAGGCTGTGAGG6TAGATCTGTG6TCACTCCACAGCAGGCTCCCTTGTCTCTCTTG

1301 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430
seq
CDS
Consensus
GCTGGATGCTCCAGTTTGTGAGG6GAGCTACGGCGATTGAGCCGCGAGAGAGG6GCTGCTTATAGCCACG6GCTGTTGATCTTGAAGGAGAGCATTTTTCACGCACTCTTGAAGA
GCTGGATGCTCCAGTTTGTGAGG6GAGCTACGGCGATTGAGCCGCGAGAGAGG6GCTGCTTATAGCCACG6GCTGTTGATCTTGAAGGAGAGCATTTTTCACGCACTCTTGAAGA
GCTGGATGCTCCAGTTTGTGAGG6GAGCTACGGCGATTGAGCCGCGAGAGAGG6GCTGCTTATAGCCACG6GCTGTTGATCTTGAAGGAGAGCATTTTTCACGCACTCTTGAAGA

1431 1440 1450 1460 1470 1480 1488
seq
CDS
Consensus
AGATGTTTTCAGGTTCTG6GCTCAGATATCTTCTCCAGAGCAGAGAAATGCTGGA
AGATGTTTTCAGGTTCTG6GCTCAGATATCTTCTCCAGAGCAGAGAAATGCTGGA
AGATGTTTTCAGGTTCTG6GCTCAGATATCTTCTCCAGAGCAGAGAAATGCTGGA

➤ Différence au niveau PROT :

	seq refprot	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
		DNA-directed DNA/RNA polymerase mu [Rattus norvegicus]	1014	1014	100%	0.0	100.00%	NP_001011912.1
		PREDICTED: DNA-directed DNA/RNA polymerase mu isoform X3 [Rattus norvegicus]	1008	1008	100%	0.0	99.20%	XP_006251275.1
		PREDICTED: DNA-directed DNA/RNA polymerase mu isoform X2 [Rattus norvegicus]	1008	1008	100%	0.0	99.20%	XP_006251274.1
	seq refprot Consensus	TLDELREQPQRLTQQQKAGLQYYQDLSTPYSRAEAEALQQLVEAMREILPGATVYLTGGFRRGKLQGHVDVFLITHPEEGQEVGLLPRYMRCLQSQGLVLYHQYHRSHLADSAHILRQRSTHDAFERSF TLDELREQPQRLTQQQKAGLQYYQDLSTPYSRAEAEALQQLVEAMREILPGATVYLTGGFRRGKLQGHVDVFLITHPEEGQEVGLLPRYMRCLQSQGLVLYHQYHRSHLADSAHILRQRSTHDAFERSF TLDELREQPQRLTQQQKAGLQYYQDLSTPYSRAEAEALQQLVEAMREILPGATVYLTGGFRRGKLQGHVDVFLITHPEEGQEVGLLPRYMRCLQSQGLVLYHQYHRSHLADSAHILRQRSTHDAFERSF						
	seq refprot Consensus	CILRLPQSQAALLEGPLHPCPTAKAVRYDLVYTPNSQFPFALLGWTGSQFFERELRRFSRQEKGLCLNSHGLFQPERKTFHFATSEEDVFRFLGLKYLPPQQRNA CILRLPQSQAALLEGPLHPCPTAKAVRYDLVYTPNSQFPFALLGWTGSQFFERELRRFSRQEKGLCLNSHGLFQPERKTFHFATSEEDVFRFLGLKYLPPQQRNA CILRLPQSQAALLEGPLHPCPTAKAVRYDLVYTPNSQFPFALLGWTGSQFFERELRRFSRQEKGLCLNSHGLFQPERKTFHFATSEEDVFRFLGLKYLPPQQRNA						

pCR4Blunt Pol M SP (clone E) parfait

pCR4Blunt Pol M CTX clone E

➤ Fwd CTX 859NT

CNTNAGAGTNNNNANNAGNTGNTNNNNATNNNANGNGNGANGAGNNGNNNCAANNNGTTGNTNAGAA
AGNCNNCAGNCCATGAAGCTCTTCACCCACNNNTTCGGGGTNGGGGTGAAGANTGCTAGCCGGTGGNNCCA
GGAAGGGNTACGAACNTGGATGAGCTCAGAGAGCAGCCCCAGAGACTGACCCAGCAGCAGAAAGCAGGGN
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AGCCATGAGGGAGATCCTGCCNGGAGCCACTGTCACACTGACTGGCGGTTTCCGAAGGGGGAAGTTACAAGGT
CATGACGTGGACTTCCTTATCACCCACNTGAGGAGGGCCAAGAAGTAGGGCTGCTGCCCAGAGTGATGAGGT
GCcTTCAGAGCCAGGGACTTGTGCTGTACCACCAGTACCATCGCAGCCACTTAGCGGACTCTGCCACATCCTGC
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GTTCCCCTTTGCTCTTCTTGCTGGACTGGCTCCAGTTTTTTTGAGAGGGAGCTACGGCGATTACAGCCGGCAAG
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GAAGATGTTTTAGGTTCTGGGTCTCAAGTATCTTCTCCAGAGCAGAGAAATGCCTGA
GATGAAAAATGCCTGTTGGCTGCCATACCTGTCCACGAGAAGATGAGGGGCTGTCTCTTTCTTGACCAGGAATGT
TTCTAGACAGGAGCACCGCCACCCACGGCCTCACCTGTGCAAATGGGATTTTTTATTTTTTACCTCATCGGTTGA
GTGTGACCCCGAGTCAGCTCAGTTTTTCAGCCTCCATTCTCCTCACAGTCAGGTGCTCTT

TCAGNAAGGCACCAGACCANGAAGNTNNTCACCCACNTNTCGGGGTGGGGTGAAGANTGNTAGCCGGTGG
TNCCAGGAAGGGNTNCGAACCTGGATGAGNTCAGAGAGCAGCCCCAGAGACTGACCCAGCAGCAGAAAGC
AGGGCTGCAGTATTACCAGGACNNGAGCACCCAGTTAGCCGGGCAGAGGCCGAGGCTNTGCAGCAGTTGGT
AGAGGCAGCCATGAGGGAGATCCTGCCNGGAGCCACTGTCACACTGACTGGCGGTTTCCGAAGGGGGAAGTT
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TGAGGTGCCTTCAGAGCCAGGGACTTGTGCTGTACCACCAGTACCATCGCAGCCACTTAGCGGACTCTGCCACA
TCCTGCGGCAGAGGTCCACCATGGATGCTTTTGAGAGGAGTTTCTGCATCTTGCCTTGCCACAGTCCCAACAG
GCAGCTTTAGAGGGGCCCCCTGCATCCCTGCCAACCTGGAAAGCTGTGAGGGTAGATCTTGTGGTCACTCCAA
CAGCCAGTTCCCCTTTGCTCTTCTTGCTGGACTGGCTCCAGTTTTTTGAGAGGGAGCTACGGCGATTACAGCCG
GCAAGAGAAGGGGCTGTGCCTTAATAGCCACGGGCTGTTTGATCCTGAGCGGAAGACATTTTTCCACGCAACTT
CTGAGGAAGATGTTTTAGGTTCTGGGTCTCAAGTATCTTCTCCAGAGCAGAGAAATGCCTGA
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TTCTAGACAGGAGCACCGCCACCCACGGCCTCACCTGTGCAAATGGGATTTTTTATTTTTTACCTCATCGGTTGA
GTGTGACCCCGAGTCAGCTCAGTTTTTCAGCCTCCaTTCTCCTCACAGTCAGGTGCTCTTAAGGGC

➤ BGHRev CTX 894NT

GCCTTCCTTCGTTCTGCGGCCTCCCGTGCTTCTGAGTCGGTGTCCAG

ATGCTTCCGAAGCGACGGCGGGCTCAGAGGTGACACATGTGGTGATGGAGGAGACCTCAGCCAAGGAGGC
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ACAGAGAGCATGGCAGCAGGACAGCCTGTCCCTGAGGAGGTCCGGCACCGCCTGGAGGTAGCTGAGCCCAGG
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TCCTCTCAGAGGCTCTGGAGAACTGGCGGAGGCAGCGGGCTTGAAGGCAAAGAGGGCCGTTTTCTCACCTT
CTACAGAGCAGCCTCCATGCTCAAGTCCCTACCCTACCCTGTCACATCTTTGAGCCAGCTGCATGGACTGCCTTAC
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TTGCTCAGAAAGGCACCAGACCATGAAGCTCTTCACCCACATCTTCGGGGTGGGGTGAAGACTGCTAGCCGGT
GGTACCAGGAAGGGCTACGAACCTGGATGAGCTCAGAGAGCAGCCCCAGAGACTGACCCAGCAGCAGAAAG
CAGGGCTGCAGTATTACCAGgACCTGAGCACCCAGTTAGCCGGGCAGAGGCCGAGGNTCTGCAGCAGTTGGT

AGAGGCAGCCATGANGGANATCCTGCCCCGAGCCNCTGTCACACTGACTGGCGGNTTCNNNGGGGAAGTTA
CANGGNCATGACGTGGACTTCCTTATCACCCACCCTGAGGAGGGNCAANAAGTAGGGCTGCTGCCCAGANTGA
TGAGGNGNCTT

Int

CTTTNAGCCNGCTGCNTGGACTGCCTTACTTTGGGGAACATTCCTTTAGAGTAATCCAGGAGCTGCTAGAACATG
GAACGTGTGAGGAGGTGGAACAAATCCGTTGCTCAGAAAGGCACCAGACCATGAAGCTCTTCACCCACATCTTC
GGGGTTGGGGTGAAGACTGCTAGCCGGTGGTACCAGGAAGGGCTACGAACCCTGGATGAGCTCAGAGAGCAG
CCCCAGAGACTGACCCAGCAGCAGAAAGCAGGGCTGCAGTATTACCAGGACCTGAGCACCCCAAGTTAGCCGGG
CAGAGGCCGAGGCTCTGCAGCAGTTGGTAGAGGCAGCCATGAGGGAGATCCTGCCCCGAGCCACTGTCACACT
GACTGGCGGTTTCCGAAGGGGGGAAGTTACAAGGTCATGACGTGGACTTCCTTATCACCCACCCTGAGGAGGGC
CAAGAAGTAGGGCTGCTGCCCAGAGTGATGAGGTGCCTTCAGAGCCAGGGACTTGTGCTGTACCACCAGTACCA
TCGCAGCCACTTAGCGGACTCTGCCCACATCCTGCGGCAGAGGTCCACCATGGATGCTTTTGAGAGGAGTTTCT
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GTGAGGGTAGATCTTGTGGTCACTCCCAACAGCCAGTTCCCTTTGCTCTTCTGGCTGGACTGGCTCCCAGTTT
TTTGAGAGGGAGCTACGGCGATTACGCCGGAAGAGAAGGGGCTGTGCCTTAATAGCCACGGGCTGTTTGATC
CTGAGCGGAAGANATTTTTCCACGCAACTTCTGANGAANATGTTTTCNNTCCTGGGTCTCAAGTATCTTCCTCC
ANAGCANANAAATGNCTGANANGAAAAATGNCTGTTGGCTGNCNTACCTGTCCACGAGAANANGAGGGGCT
GTCTCTTTCTTNACCNNNAATGTTTCTAGACAGGANCNNGCNCNCCCCACGGCNCNNGTGAATGGNNT
TTTTNNTTTTAC

➤ Synthèse séquençage CTX: **NT**

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-----ATGCTTCCGAAGC 180
GACGGCGGCGGCTCAGAGGTGACACATGTGGTGATGGAGGAGACCTCAGCCAAGGAGGCC 240
ATCTGCTGGCAGAAGGACATGAATGCTCTTCTCCCAGACTGCCCCGAGCCGGCTCTGCTA 300
GATATTAGCTGGTTTACAGAGAGCATGGCAGCAGGACAGCCTGTCCCTGAGGAGGTCCGG 360
CACCGCCTGGAGGTAGCTGAGCCCAGGAAGGAACCCCCATCTCAGTGACGATACCAGCT 420
TATGCCTGTGACGCCCCCTCGCCTCTCACACCCATAACACTCTCCTCTCAGAGGCTCTG 480
GAGACACTGGCGGAGGCAGCGGGCTTCGAAGGCAAAGAGGGCCGTTTTCTCACCTTCTAC 540
AGAGCAGCCTCCATGCTCAAGTCCCTACCCTACCCTGTCACATCTTTGAGCCAGCTGCAT 600
GGACTGCCTTACTTTGGGGAACATTCCTTTAGAGTAATCCAGGAGCTGCTAGAACATGGA 660
ACGTGTGAGGAGGTGGAACAAATCCGTTGCTCAGAAAGGCACCAGACCATGAAGCTCTTC 720
ACCCACATCTTCGGGGTTGGGGTGAAGACTGCTAGCCGGTGGTACCAGGAAGGGCTACGA 780
ACCCTGGATGAGCTCAGAGAGCAGCCCCAGAGACTGACCCAGCAGCAGAAAGCAgGGCTG 840
CAGTATTACCAGgACCTGAGCACCACAGTTAGCCGGGAGAGGCCGAGGCTCTGCAGCAG 900
TTGGTAGAGGCAGCCATGAGGGAGATCCTGCCCCGAGCCACTGTCACACTGACTGGCGGT 960
TTCCGAAGGGGGAAGTTACAAGGTCATGACGTGGACTTCCTTATCACCCACCCTGAGGAG 1020
GGCCAAGAAGTAGGGCTGCTGCCCAGAGTGATGAGGTGCcTTCAGAGCCAGGGACTTGTG 1080
CTGTACCACCAGTACCATCGCAGCCACTTAGCGGACTCTGCCACATCCTGCGGCAGAGG 1140
TCCACCATGGATGCTTTTGAGAGGAGTTTCTGCATCTTGCGCTTGCCACAGTCCCAACAG 1200
GCAGCTTTAGAGGGGGCCCCTGCATCCCTGCCAACCTGGAAAGCTGTGAGGGTAGATCTT 1260
GTGGTCACTCCCAACAGCCAGTTCCCCTTTGCTCTTCTTGGCTGGACTGGCTCCCAGTTT 1320
TTTGAGAGGGAGCTACGGCGATTACGCCGGAAGAGAAGGGGCTGTGCCTTAATAGCCAC 1380
GGGCTGTTTGATCCTGAGCGGAAGACATTTTTCCACGCAACTTCTGAGGAAGATGTTTTC 1440
AGGTTCTGCGGTCTCAAGTATCTTCTCCAGAGCAGAGAAATGCCTGA 1488
```

CFRSDGGGSEVTHVMEETSACEAICWQKDMNALLPDCPQPALLDISWFTESMAAGQVPPEEVRHRLEVAEPRKE
PPISVTIPAYACQRPSPPLTPHNLLSEALETLAAAGFEGKEGRFLTIFYRAASMLKSLPYPVTSLSQLHGLPYFG
EHSFRVIQELLEHGTCCEEVEQIRCSERHQTMKLFTHIFGVGVKTASRWYQEGRLTLDELREQPQRLTQQQKAGLQ
YYQDLSTPVSRAEAEALQQLVEAAMREILPGATVTLTGFFRRGKLQGHVDVFLITHPEEGQEVGLLPRVMRCLQS
QGLVLYHQYHRSHLADSAHILRQRSTMDAFERSFCILRLPQSQQALEGPLHPCPTWKAVRVDLVVTPNSQFPFA
LLGWTGSQFFERELRRFSRQEKGLCLNSHGLFDPERKTFHATSEEDVFRFLGLKYLPEQRNA-

➤ **Blast contre banque rat :**

	Gene	Score	Length	Score	Length	Score	Length	Score	Length
	PREDICTED: Rattus norvegicus polymerase (DNA) mu (Polm) transcript variant X2 mRNA	2440	2440	100%	0.0	100.00%		XM_006251212.3	
	Rattus norvegicus DNA polymerase mu (Polm) mRNA	2398	2398	98%	0.0	100.00%		NM_001011912.1	
	PREDICTED: Rattus norvegicus polymerase (DNA) mu (Polm) transcript variant X1 mRNA	2385	2385	100%	0.0	99.10%		XM_006251211.3	
	PREDICTED: Rattus norvegicus polymerase (DNA) mu (Polm) transcript variant X3 mRNA	2342	2342	98%	0.0	99.08%		XM_006251213.3	
	PREDICTED: Rattus norvegicus polymerase (DNA) mu (Polm) transcript variant X4 mRNA	2337	2337	98%	0.0	99.08%		XM_006251214.3	

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

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

➤ Différence au niveau PROT :

pCR4Blunt poM CTX (clone E) comme DiT0 et T24h

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
seq	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----													
refprot	MLPKRRRRYRAGSPHSALASSTPPAARFPGVAYILAEPMRGRSRAFLTRLARSKGFRILDVYSSSEVTHVYMEETSACEAICQKQDMNALLPDCPQPALLDISNFTESMAAGQPVPEEYRHRLEVAEPRK													
Consensus	cFRi.DgggSEVTHVYMEETSACEAICQKQDMNALLPDCPQPALLDISNFTESMAAGQPVPEEYRHRLEVAEPRK													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
seq	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----													
refprot	EPPISVTIPAYACQRPSP LTPHNTLLSEALETLAEAGFEGKEGRFLT FYRAASHMLKSLPYPTSLSQLHGLPYFGEHSFRVIQELLEHGTCEEVEQIRCSEHQTHMLFTHIFGVGVKTASRWYQEGLR													
Consensus	EPPISVTIPAYACQRPSP LTPHNTLLSEALETLAEAGFEGKEGRFLT FYRAASHMLKSLPYPTSLSQLHGLPYFGEHSFRVIQELLEHGTCEEVEQIRCSEHQTHMLFTHIFGVGVKTASRWYQEGLR													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
seq	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----													
refprot	TLDELREQPRLTQQKAGLQYYQDLSTPVSRAEAEALQQLVEAAMREILPGATVTLTGGFRRGKLQGHQVDFLITHPEEGQEVGLLPRVNRCLQSQGLVLYHQYHRSHLADSAHILRQRSTHDAFERSF													
Consensus	TLDELREQPRLTQQKAGLQYYQDLSTPVSRAEAEALQQLVEAAMREILPGATVTLTGGFRRGKLQGHQVDFLITHPEEGQEVGLLPRVNRCLQSQGLVLYHQYHRSHLADSAHILRQRSTHDAFERSF													
	391	400	410	420	430	440	450	460	470	480	490	495		
seq	----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- ----- -----													
refprot	CILRLPQSQAALLEGPLHPCPTAKAVRYDLVYTPNSQFPFALLGATGSQFFERELRRFSRQEKGLCLNSHGLFDPERKTFHFATSEEDVFRFLGLKYLPPPEQRNA													
Consensus	CILRLPQSQAALLEGPLHPCPTAKAVRYDLVYTPNSQFPFALLGATGSQFFERELRRFSRQEKGLCLNSHGLFDPERKTFHFATSEEDVFRFLGLKYLPPPEQRNA													

	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
✓	PREDICTED: DNA-directed DNA/RNA polymerase mu isoform X2 [Rattus norvegicus]	901	901	100%	0.0	100.00%	XP_006251274.1
✓	PREDICTED: DNA-directed DNA/RNA polymerase mu isoform X1 [Rattus norvegicus]	897	897	100%	0.0	99.10%	XP_006251273.1
✓	DNA-directed DNA/RNA polymerase mu [Rattus norvegicus]	887	887	99%	0.0	99.31%	NP_001011912.1
✓	PREDICTED: DNA-directed DNA/RNA polymerase mu isoform X3 [Rattus norvegicus]	881	881	99%	0.0	98.41%	XP_006251275.1

- **pCR4Blunt Pol M CTX NOUVEAU CLONAGE**

- **Fwd CTX 938NT**

ATGCTTCCGAAGCGACGGCGGCGGCTCAGAGGTGACACATGTGGTGATGGAGGAGACCTCAGCCAAGGAGG
CCATCTGCTGGCAGAAGGACATGAATGCTCTTCTCCCAGACTGCCCCGAGCCGGCTCTGCTAGATATTAGCTGG
TTTACAGAGAGCATGGCAGCAGGACAGCCTGTCCCTGAGGAGGTCCGGCACCGCCTGGAGGTAGCTGAGCCC
AGGAAGGAACCCCCCATCTCAGTGACGATAACCAGCTTATGCCTGTCAGCGCCCCCTCGCCTCTCACACCCATAA
CACTCTCCTCTCAGAGGCTCTGGAGACACTGGCGGAGGCAGCGGGCTTCTGAAGGCAAAGAGGGCCGTTTTCT
CACCTTCTACAGAGCAGCCTCCATGCTCAAGTCCCTACCCTACCCTGTACATCTTTGAGCCAGCTGCATGGACT
GCCTTACTTTGGGGAACATTCTTTAGAGTAATCCAGGAGCTGCTAGAACATGGAACGTGTGAGGAGGTGGA
ACAAATCCGTTGCTCAGAAAGGCACCAGACCATGAAGCTCTTCACCCACATCTTCGGGGTTGGGGTGAAGACT
GCTAGCCGGTGGTACCAGGAAGGGCTACGAACCCTGGATGAGCTCAGAGAGCAGCCCCAGAGACTGACCCA
GCAGCAGAAAGCAgGGCTGCAGTATTACCAGGACCTGAGCACCCAGTTAGCCGGGCAGAGGCCGAGGCTCT
GCAGCAGTTGGTAGAgGCAGCCATGAgGGAGATCCTGCCGGAgCCACTGTCACACTGACTGGCGGTTTCCGA
ANGGGAAGTTACNNNNCATGACGTGGNCTTCCTTATCACCCACCCTGAGGAGGGNCNAGAAGTANGGCTGC
TGCCAGAGNGATGAGGTGNCTTCAGAGCCAGGGNNTTNGNGCTGTACNANCAGTACCATCINNAGCCAC

- **BGHRev CTX 805NT**

AAATNNNTNCTCANAAAGNCANNAGNCNNNGAAGNTCNTCACCCACNTNTTCGGGNTGGGGTGAAGANTG
NTANNCGGTGGTACCAGGAAGGGNTACGANNTGGATGAGNTCAGAGAGCAGCCCCAGAGACTGACCCAG
CAGCAGAAAGCAGGGCTGCAGTATTACCAGNNNGAGCACCCAGTTAGCCGGGCAGAGGCCGAGGCTCTG
CAGCAGTTGGTAGAGGCAGCCATGAGGGAGATCCTGCCcGGAGCCACTGTACACTGACTGGCGGTTTCCGA
AGGGGGAAGTTACAAGGTCATGACGTGGACTTCCTTATCACCCACCcTGAGGAGGGCCAAGAAGTAGGGCTG
CTGCCAGAGTGATGAGGTGCCTTCAGAGCCAGGGACTTGTGCTGTACCACAGTACCATCGCAGCCACTTAG
CGGACTCTGCCACATCCTGCGGCAGAGGTCCACCATGGATGCTTTTGAGAGGAGTTTCTGCATCTTGCGCTTG
CCACAGTCCCAACAGGCAGCTTTAGAGGGGCCCTGCATCCCTGCCAACCTGGAAAGCTGTGAGGGTAGATC
TTGTGGTCACTCCCAACAGCCAGTTCCCCTTTGCTCTTCTTGGCTGGACTGGCTCCAGTTTTTTGAGAGGGAGC
TACGGCGATTGAGCCGGCAAGAGAAGGGGCTGTGCCTTAATAGCCACGGGCTGTTTGATCCTGAGCGGAAGA
CATTTTTCCACGCAACTTCTGAGGAAGATGTTTTAGGTTCTGGGTCTCAAGTATCTTCTCCAGAGCAGAGA
AATGCCTGA

- **Synthèse séquençage CTX: NT**

idem

PolM_SeqInt_Fwd_1

540 pour 690

AGAGCAGCCTCCATGCTCAAG

PolM_SeqInt_Rev_1

1330 pour 1180

CCCTCTCAAAAAACTGGGAG