

Estas seqüências foram empregadas para se gerar uma árvore filogenética, com vistas a verificar o agrupamento das amostras

brasileiras entre si e com as seqüências compatíveis depositadas no GenBank, e estão apresentadas nas figuras 18 e 19.

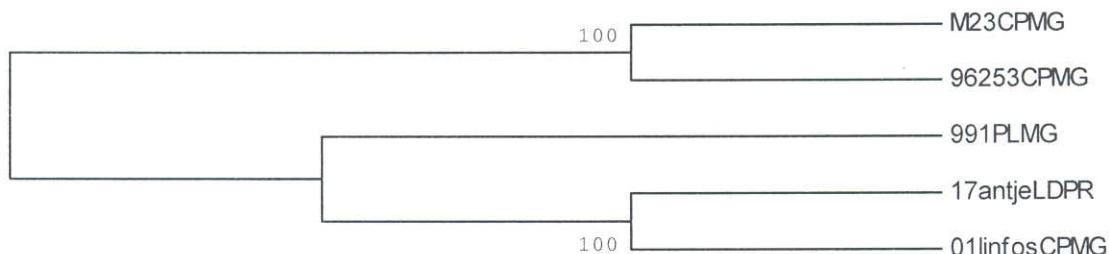


Figura 18: Relações filogenéticas de seqüências de 694pb, de parte da região *pol* do vírus BLV, obtidas entre DNAs extraídos de bovinos naturalmente infectados em três regiões brasileiras distintas: Pedro Leopoldo-MG, Coronel Pacheco-MG e Londrina-PR. Os valores dos "nós" representam a confiabilidade, em porcentagem, dos ramos à direita, resultados de bootstrap em 1000 replicatas.

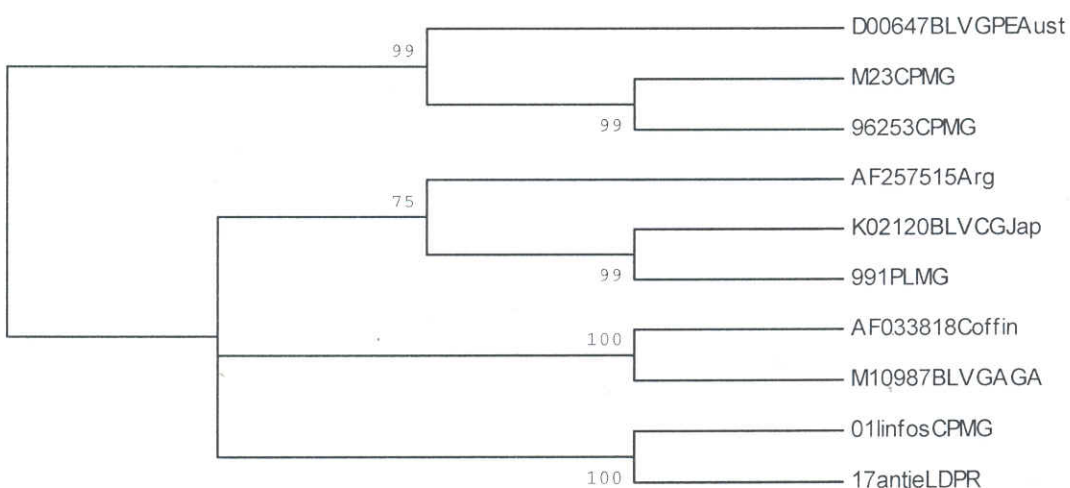


Figura 19: Relações filogenéticas de seqüências com 694pb, de parte da região *pol* do vírus BLV, obtidas entre DNAs extraídos de bovinos naturalmente infectados em três regiões brasileiras distintas: Pedro Leopoldo-MG, Coronel Pacheco-MG e Londrina-PR, e seqüências obtidas no GenBank. Os valores dos "nós" representam a confiabilidade, em porcentagem, dos ramos à direita, resultados de bootstrap em 1000 replicatas.

A observação da figura 18 mostra que as cinco amostras de *pol* formam dois agrupamentos entre si, havendo maior afinidade entre as amostras 23MCPMG e 96253CPMG, agrupadas em um ramo, e entre as amostras 17antjeLDPR, 01linfoCPMG e 991PLMG, agrupadas em

outro ramo. Os valores de bootstrap observados permitem afirmar que os dois agrupamentos são bem distintos entre si.

A figura 19 oferece a possibilidade do confronto das amostras brasileiras com as amostras disponíveis no GenBank. Pode se

observar, novamente, a formação de dois agrupamentos, onde a amostra D00647BLVGPEAust se aproximou das amostras brasileiras 23MCPMG e 96.253CPMG, constituindo o agrupamento Brasil – Austrália. Diferente do observado na árvore de 5'LTR, não houve proximidade da amostra 23MCPMG com a amostra AF257515Arg. Por outro lado, a amostra 991PLMG, que se apresentava próxima à amostra australiana, na análise filogenética de 5'LTR, agora aproximou-se das amostras japonesa K02120BLVCG e Argentina AF257515. Em relação à origem geográfica das amostras e a composição dos agrupamentos, a análise da árvore da figura 19 sugere a formação de dois agrupamentos, o primeiro Brasil – Austrália e o segundo Brasil – Argentina – América do Norte – Bélgica. Entretanto, mais uma vez a quantidade de seqüências disponíveis

para a geração da árvore é pequena, sugerindo que, com o advento de mais depósitos de seqüências, estas relações de afinidade podem ser alteradas, gerando novos agrupamentos.

De forma a tentar minimizar este problema, foi gerada uma árvore filogenética das seqüências de 230pb com todas as amostras brasileiras, totalizando 10, o que está ilustrado na figura 20. Mais uma vez formou-se dois agrupamentos, sendo o primeiro composto pelas amostras 20blesje, 97blesje e rochedo, todas de Londrina – PR, pelas amostras 991 e 922, ambas de Pedro Leopoldo – MG e pela amostra de Coronel Pacheco – MG, 96253. O segundo agrupamento foi composto pelas amostras de Londrina – PR, 195vera e 17antje, e pelas amostras de Coronel Pacheco – MG, 01linfo e 23M.

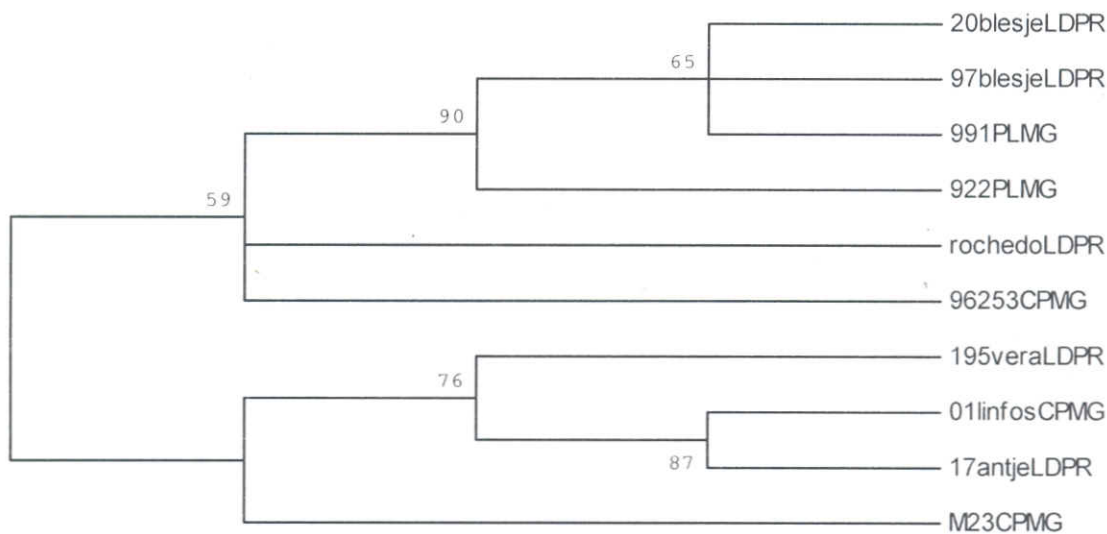


Figura 20: Relações filogenéticas de seqüências com 230pb, de parte da região *pol* do vírus BLV, obtidas entre DNAs extraídos de bovinos naturalmente infectados em três regiões brasileiras distintas: Pedro Leopoldo-MG, Coronel Pacheco-MG e Londrina-PR. Os valores dos "nós" representam a confiabilidade, em porcentagem, dos ramos à direita, resultados de bootstrap em 1000 replicatas.

A figura 21 ilustra a árvore gerada com as 10 amostras brasileiras com 230pb, mais sete seqüências disponíveis no GenBank

para esta região, o que permitiu o acréscimo de mais duas seqüências do banco em relação à árvore da figura 19.

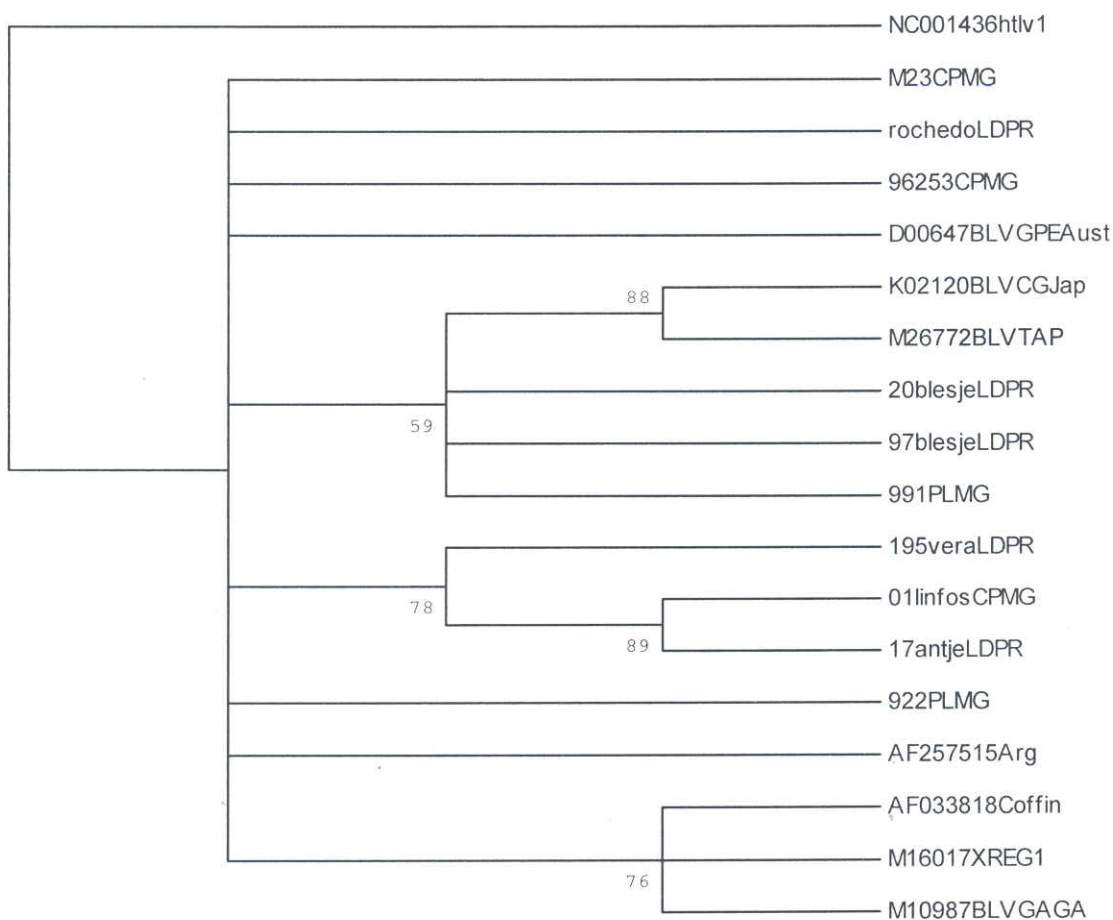


Figura 21: Relações filogenéticas de seqüências com 230pb, de parte da região *pol* do vírus BLV, obtidas entre DNAs extraídos de bovinos naturalmente infectados em três regiões brasileiras distintas: Pedro Leopoldo-MG, Coronel Pacheco-MG e Londrina-PR, e sete seqüências disponíveis no GenBank. Utilizou-se a seqüência do HTLV-1 NC001436 (acesso GenBank) como grupo externo. Os valores dos "nós" representam a confiabilidade, em porcentagem, dos ramos à direita, resultados de bootstrap em 1000 replicatas.

Ao se analisar esta figura é possível verificar que houve uma grande homogeneidade entre os DNAs seqüenciados neste trabalho e destes para aqueles já depositados no GenBank, demonstrando que a região é bastante conservada, o que é compatível

com o esperado, já que se trata de região codificadora da proteína Integrase. Todas as seqüências formaram um único macroagrupamento, ocorrendo pequenas diferenças que não foram suficientes para a formação de "clusters" ou agrupamentos

definidos. Desta forma, conclui-se que esta região não é apropriada para estudos de inferência filogenética, dada a dificuldade de caracterização de agrupamentos, ao menos ao se utilizar uma pequena seqüência de 230pb.

Esta conservação também pode ser observada quando se alinha as seqüências de aminoácidos geradas a partir dos

produtos dos seqüenciamentos. A figura 22 apresenta o resultado do alinhamento das cinco amostras com 694pb, convertidas em seqüências com 231 aminoácidos. Basicamente, todas as variações ocorridas nos nucleotídeos desta região se traduziram em apenas nove mutações nos aminoácidos, as demais permanecendo silenciosas.

```

[           1 1111111112 2222222223 3333333334 ]
[           1234567890 1234567890 1234567890 1234567890 ]
#AF033818Coffin  MRTIQRGWAP NHIWQADITH YKYKQFTYAL HVFVDITYSGA
#AF257515Arg     .....
#D00647BLVGPEAust .....
#K02120BLVCGJap .....
#M10987BLVGAGA  .....
#17antjeLDPR    .....
#991PLMG        .....
#M23CPMG        .....
#96253CPMG      .....
#011infosCPMG   .....

[           4444444445 5555555556 6666666667 7777777778 ]
[           1234567890 1234567890 1234567890 1234567890 ]
#AF033818Coffin  THASAKRGLT TQMTIEGLLE AIVHLGRPKK LNTDQGANYT
#AF257515Arg     .....
#D00647BLVGPEAust ..... ..T.....
#K02120BLVCGJap ..... ..T.....
#M10987BLVGAGA  .....
#17antjeLDPR    .....
#991PLMG        .....
#M23CPMG        ..... ..M.....
#96253CPMG      ..... ..M.....
#011infosCPMG   .....

[           8888888889 9999999990 0000000001 1111111112 ]
[           1234567890 1234567890 1234567890 1234567890 ]
#AF033818Coffin  SKTFVRFCCQ FGISLSHHVP YNPTSSGLVE RTNGLLKLKLL
#AF257515Arg     .R..A..... ..V.....I.....
#D00647BLVGPEAust .....
#K02120BLVCGJap ..... ..V..... ..D.....
#M10987BLVGAGA  .....
#17antjeLDPR    ..... ..V.....
#991PLMG        ..... ..V.....
#M23CPMG        .....
#96253CPMG      .....
#011infosCPMG   ..... ..V.....

```

```

[          1111111111 1111111111 1111111111 1111111111 ]
[          2222222223 3333333334 4444444445 5555555556 ]
[          1234567890 1234567890 1234567890 1234567890 ]
#AF033818Coffin SKYHLDEPHL PMTQALSRAL WTHNQINLLP ILKTRWELHH
#AF257515Arg      .....
#D00647BLVGPEAust .....
#K02120BLVCGJap  .....
#M10987BLVGAGA   .....
#17antjeLDPR     ..S.....
#991PLMG         .....
#M23CPMG         .....
#96253CPMG       .....
#011infosCPMG   ..S.....

[          1111111111 1111111111 1111111111 1111111112 ]
[          6666666667 7777777778 8888888889 9999999990 ]
[          1234567890 1234567890 1234567890 1234567890 ]
#AF033818Coffin SPPLAVISEG GETPKGSDKL FLYKLPQMN RRWLGPLPAL
#AF257515Arg      .....
#D00647BLVGPEAust .....
#K02120BLVCGJap  .....L.....
#M10987BLVGAGA   .....
#17antjeLDPR     .....
#991PLMG         .....
#M23CPMG         .....
#96253CPMG       .....
#011infosCPMG   .....

[          2222222222 2222222222 2222222222 2]
[          0000000001 1111111112 2222222223 3]
[          1234567890 1234567890 1234567890 1]
#AF033818Coffin VEASGGALLA TNPPVWVWVR LLKAFKCPKN D
#AF257515Arg      I......D.....
#D00647BLVGPEAust .....L..
#K02120BLVCGJap  .....D.....L..
#M10987BLVGAGA   .....
#17antjeLDPR     .....
#991PLMG         .....D.....L..
#M23CPMG         .....H..P.....
#96253CPMG       .....
#011infosCPMG   .....VQM..E R

```

Figura 22: Alinhamento de 231 aminoácidos de parte da região *pol* do BLV das cinco seqüências obtidas de amostras brasileiras, mais cinco seqüências disponíveis no GenBank. Alinhamento com programa ClustalW. Apenas os nucleotídeos diferentes da seqüência consenso estão apresentados. Os números dispostos verticalmente indicam a posição de cada nucleotídeo na seqüência.

O destaque destas mutações está no fato de sete delas terem ocorrido em uma pequena região com 20 aminoácidos, da posição 212 a posição 231 na figura 22, na porção terminal do gene que codifica a Integrase. Como esta região também é coberta pelo consenso de 230pb (76 aminoácidos) obtido para 10

amostras brasileiras, e estas puderam ser alinhadas com sete amostras disponíveis no GenBank, perfazendo um universo de 17 amostras, torna-se mais visível as alterações ocorridas na figura gerada a partir deste alinhamento (figura 23).

```

[           1 1111111112 2222222223 3333333334 ]
[           1234567890 1234567890 1234567890 1234567890 ]
#D00647BLVGPEAust WELHHSPLA VISEGGETPK GSDKLFLYKL PGQNNRRWLG
#AF257515Arg      .....
#AF033818Coffin  .....
#M10987BLVGAGA   .....
#K02120BLVCGJap .....L.
#M16017XREG1     .....
#M26772BLVTAP    .....L.
#195veraLDPR     .....
#20blesjeLDPR    .....
#922PLMG         .....
#97blesjeLDPR    .....
#rochedoLDPR     .....
#01infosCPMG     .....
#17antjeLDPR     .....
#96253CPMG       .....
#991PLMG         .....
#M23CPMG         .....

[           4444444445 5555555556 6666666667 777777]
[           1234567890 1234567890 1234567890 123456]
#D00647BLVGPEAust PLPALVEASG GALLATNPPV WVPWRLKAF KCLKND
#AF257515Arg      .....I.....D.....P...
#AF033818Coffin  .....D.....P...
#M10987BLVGAGA   .....D.....P...
#K02120BLVCGJap .....D.....
#M16017XREG1     .....P...
#M26772BLVTAP    .....D.....
#195veraLDPR     .....D...LAF AESL QMP.ER
#20blesjeLDPR    .....D.....
#922PLMG         .....D...*...S...
#97blesjeLDPR    .....D...TFAESL QMP.ER
#rochedoLDPR     .....P...
#01infosCPMG     .....V QMP.ER
#17antjeLDPR     .....P...
#96253CPMG       .....P...
#991PLMG         .....D.....
#M23CPMG         .....H...P...P...

```

Figura 23: Alinhamento de 76 aminoácidos de parte da região *pol* do BLV das 10 seqüências obtidas de amostras brasileiras, mais sete seqüências disponíveis no GenBank. Alinhamento com programa ClustalW. Apenas os nucleotídeos diferentes da seqüência consenso estão apresentados. Os números dispostos verticalmente indicam a posição de cada nucleotídeo na seqüência.

Este alinhamento destaca algumas alterações que, por ocorrerem em um número expressivo de amostras, serão aqui discutidos. A primeira, situada na posição 57 da figura 23, mostra que em oito seqüências ocorre o aminoácido Ácido Aspártico (D), enquanto que em nove ocorre a Asparagina (N). Estes aminoácidos possuem

características bioquímicas muito próximas, sendo ambas do grupo ácido, o que sugere que seu intercambiamento não produza sérias mudanças na proteína. Este tipo de alteração ocorreu tanto nas amostras brasileiras quanto nas amostras disponíveis no GenBank, sugerindo se tratar de alteração comum, o que também corrobora

sua tolerabilidade por parte das variantes virais emergentes.

O segundo ponto de alteração comum a várias seqüências foi a posição 73, onde 11 amostras apresentaram o aminoácido Prolina (P), uma amostra o aminoácido Serina (S) e cinco amostras o aminoácido Leucina (L). Neste caso, este tipo de mutação aponta uma provável alteração significativa na estrutura das diferentes proteínas geradas, pois Prolina é um pequeno aminoácido polar que está relacionado com propriedades estruturais especiais, enquanto que Leucina é um aminoácido hidrofóbico alifático não polar. A ocorrência do aminoácido Serina na amostra 922PLMG, diferente de todas as demais amostras, também precedido, de forma única, de um códon de parada (stop codon) na posição 66, sugere que esta amostra expresse proteína truncada e possivelmente não ativa.

Um terceiro ponto de destaque diz respeito a amostra 23MCPMG, que apresentou uma mutação P→H63 (Prolina polar para Histidina, molécula básica, aromática não polar) e uma A→P67 (Alanina, hidrofóbica alifática para Prolina), destacando esta amostra das demais e demonstrando ser ela atípica, conforme as análises de 5'LTR já haviam sugerido. Outro aspecto importante é o perfil das variações ocorridas na porção terminal das amostras 145veraLDPR, 97blesjeLDPR e 01linfossarcomaCPMG, com as substituições de aminoácidos K→Q71, C→M72, N→E75 e D→R76, segundo a figura 23. Estes achados podem estar relacionados com animais em estágio neoplásico, como é o caso da amostra 01linfossarcoma, e justificam investigações futuras desta região em animais nesta situação.

5. CONCLUSÕES

Conclui-se no presente trabalho:

- a PCR de β -actina bovina constitui-se em uma ferramenta útil na prospecção da qualidade de DNA de origem bovina, sendo indicada em trabalhos que serão

desenvolvidos utilizando bancos de amostras;

- a PCR 5'LTR se mostrou específica, atendendo a demanda dela esperada na produção de amplificadas para seqüenciamento da região promotora 5'LTR do BLV;
- as amostras brasileiras do vírus BLV se mostraram bastante conservadas em suas regiões 5'LTR e *pol/IN*, confirmando achados anteriores que relatavam a mesma estabilidade em outras regiões do genoma do BLV;
- no alinhamento da região 5'LTR observou-se uma região de 88pb mais variável, coincidente com o motivo DAS - seqüência ativadora a jusante, enquanto que uma seqüência do tipo motivo E Box, dentro de DAS, permaneceu totalmente conservado. Estes achados sugerem que as amostras brasileiras do BLV utilizam um duplo sistema de regulação negativa da transcrição, variabilidade em DAS e conservação em E box, como escape do sistema imune;
- a PCR para *pol* BLV se mostrou menos sensível que a PCR para a região promotora viral, apresentando também o fenômeno de ampliações inespecíficas. Entretanto, atingiu o propósito do experimento de produzir DNA molde da porção terminal do gene *pol* para posterior seqüenciamento;
- o processo de seqüenciamento direto de produto de PCR se mostrou prático e menos oneroso, entretanto o sucesso de seqüenciamento foi inferior a 30% e parte das bandas seqüenciadas são perdidas no processo de edição e obtenção de consenso;
- as árvores filogenéticas geradas para a região 5'LTR do BLV demonstraram uma grande homogeneidade entre as amostras brasileiras e mesmo em relação a algumas seqüências do

GenBank, apresentando baixos valores de bootstrap

- a análise filogenética apontou a circulação de amostras de diferentes agrupamentos nos rebanhos analisados, e o perfil de restrição enzimática da região 5'LTR diferenciou amostras sul-americanas das demais amostras mundiais.

6. REFERÊNCIAS BIBLIOGRÁFICAS

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ANEXO 1

RELAÇÃO DAS AMOSTRAS DE DNA UTILIZADAS NA TESE “Vírus da Leucose
Enzoótica Bovina: filogenia e regulação gênica de LTR e *pol* em amostras
brasileiras.”, DISTRIBUÍDAS EM FUNÇÃO DO LOCAL DE ORIGEM.

PLMG	LDPR	CPMG	CRMS	OUTROS
05	01-aneti	01-linfos	03	FLK ^(*)
141	16-conta	23-M	07	MDBK ^(**)
304	17-antje	2480	115PMO4	
383	19-retje	3563	117PMO4	
387	19-silvia	7504	138	
440	20-blesje	8824	150	
485	28-pietje	9104	154	
499	30-irene	96.253	155	
617	33-herm		156	
676	40-afile		157	
678	54-vilma		160	
701	74-gessy			
733-6.4.1	92-touro			
733-4.4.1	97-blesje			
739	rochedo			
747	147-antje			
768	172			
792	195-vera			
813				
842				
857				
871				
872				
896				
898				
917				
920				
922				
926				
961				
977				
982				
989				
991				
1676				
1749				
36	18	08	11	02

Total de amostras de DNA: 73 extraídos de animais, dois extraídos de cultura de células.

PLMG: animais doadores localizados no município de Pedro Leopoldo – MG.

LDPR: animais doadores localizados no município de Londrina – PR.

CPMG: animais doadores localizados no município de Coronel Pacheco – MG

CRMS: animais doadores localizados no município de Corumbá – MS

^(*) DNA extraído de cultura de células de linhagem, persistentemente infectadas pelo BLV, Fetal Lamb Kidney

^(**) DNA extraído de cultura de células de linhagem não infectada pelo BLV, Madin-Darby Bovine Kidney.

ANEXO 2

RELAÇÃO DAS SEQÜÊNCIAS BRUTAS, OBTIDAS A PARTIR DO PRODUTO DE AMPLIFICAÇÃO DA PCR 5'LTR/BLV, ALINHADAS COM O PROGRAMA MULTALIN

Multalin version 5.4.1
 Copyright I.N.R.A. France 1989, 1991, 1994, 1996
 Published research using this software should cite
 Multiple sequence alignment with hierarchical clustering
 F. CORPET, 1988, Nucl. Acids Res., 16 (22), 10881-10890
 Symbol comparison table: blosum62
 Gap weight: 12
 Gap length weight: 2
 Consensus levels: high=90% low=50%
 Consensus symbols:
 ! is anyone of IV
 \$ is anyone of LM
 % is anyone of FY
 # is anyone of NDQEBZ

MSF:	591	Check:	0	..	Check:	2039	Weight:	1.72
Name:	40afileLDPR	Len:	591	..	Check:	2039	Weight:	1.21
Name:	54vilmaLDPR	Len:	591	..	Check:	12	Weight:	1.21
Name:	74gessyLDPR	Len:	591	..	Check:	391	Weight:	1.21
Name:	97blesjeLDPR	Len:	591	..	Check:	6437	Weight:	1.21
Name:	3563CPMG	Len:	591	..	Check:	8086	Weight:	1.21
Name:	9104CPMG	Len:	591	..	Check:	3318	Weight:	0.57
Name:	23MCPMG	Len:	591	..	Check:	4134	Weight:	0.26
Name:	16contaLDPR	Len:	591	..	Check:	4999	Weight:	0.10
Name:	485PLMG	Len:	591	..	Check:	6029	Weight:	0.10
Name:	387PLMG	Len:	591	..	Check:	4047	Weight:	0.10
Name:	195veraLDPR	Len:	591	..	Check:	5092	Weight:	0.18
Name:	676PLMG	Len:	591	..	Check:	5092	Weight:	0.18
Name:	701PLMG	Len:	591	..	Check:	5092	Weight:	0.18
Name:	440PLMG	Len:	591	..	Check:	3266	Weight:	0.18
Name:	rochedoLDPR	Len:	591	..	Check:	4327	Weight:	0.36
Name:	160S06CRMS	Len:	591	..	Check:	4909	Weight:	1.52

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Name: 96253CPMG          Len: 591  Check: 7017  Weight: 1.62
Name: 92touroLDPR       Len: 591  Check: 4956  Weight: 1.67
Name: 01anetiLDPR       Len: 591  Check: 1467  Weight: 1.88
Name: 1751PLMG          Len: 591  Check: 5547  Weight: 1.93
Name: 922PLMG           Len: 591  Check: 1269  Weight: 2.06
Name: 991PLMG           Len: 591  Check: 4424  Weight: 2.57
Name: Consensus         Len: 591  Check: 8734  Weight: 0.00
//

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1 50
40afilleLDPR          . . . . . GTCAG.TGCC AGAAAA.GCT
54vilmaLDPR           . . . . . GTCAT.CGCC AGAAAA.GCT
74gessyLDPR           . . . . . GTCAG.TGCC AGAAAA.GCT
97blesjeLDPR         . . . . .
3563CPMG              . . . . .
9104CPMG              TGCCACCGCC CCGTAAACCA GACAGAA.AC GTCAGCTGCC AGAAAA.GCT
23MCPMG               TGCCACCGCC CCGTAAACCA GACAGAA.AC GTCAGCTGCC AGAAAA.GCT
16contalDPR          TGCCACCGCC CCGTAAACCA GACAGAG.AC GTCAGCTGCC AGAAAA.GCT
485PLMG               TGCCACCGCC CCGTAAACCA GACAGAGGAC GTCAGCTGCC AGAAAA.GCT
387PLMG               TGCCACCGCC CCGTAAACCA GACAGAG.AC GTCAGCTGCC AGAAAA.GCT
195veralDPR          TGCCACCGCC CCGTAAACCA GACAGAG.AC GTCAGCTGCC AGAAAA.GCT
676PLMG               TGCCACCGCC CCGTAAACCA GACAGAG.AC GTCAGCTGCC AGAAAA.GCT
701PLMG               TGCCACCGCC CCGTAAACCA GACAGAG.AC GTCAGCTGCC AGAAAA.GCT
440PLMG               TGCCACCGCC CCCTAAACCA GACAGAG.AC GTCAGCTGCC AGAAAA.GCT
rochedoLDPR          TGCCACCGCC CCGTAAACCA GACAGAG.AC GTCAGCTGCC CGAAAA.GCT
160S06CRMS           . . . . .
96253CPMG             . . . . . ..CAGCTGCC AAAAAAAGCT
92touroLDPR          . . . . .
01anetiLDPR           . . . . .
1751PLMG              . . . . .
922PLMG               . . . . .
991PLMG               . . . . .
Consensus             . . . . .

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40afilleLDPRGCA	G. CTGGTGGC	TAGAAATCCCC	G. TACCTCCC	CAACTTCCCC
54vilmaLDPR	GGCGACGGCA	G. CTGGTGGC	TAGAAATCCCC	GATACCTCCC	CAACTTCCCC
74gessyLDPR	GGTGACGGCA	G. CTGGTGGC	TAGAAATCCCC	G. TACCTCCC	CAACTTCCCC
97blesjeLDPR	GGTGACGGCA	G. CTGGTGGC	TAGTAATCCC	CGTACCTCCC	CAACTTCCCC
3563CPMGACGGCA	G. CTGGTGGC	TAGAAATCCCC	G. TACCTCCC	CAACTTCCCC
9104CPMG	GGTGACGGCA	G. CTGGTGGC	TAGAAATCCCC	G. CACCTCCC	CAACTTCCCC
23MCPMG	GGTGACGGCA	G. CTGGTGGC	TAGAAATCCCC	G. TACCTCCC	CAACTTCCCC
16contaLDPR	GGTGACGGCA	GA CTGGTGGC	TAGAAATCCCC	G. TACCTCCC	CAACTTCCCC
485PLMG	GGTGACGGCA	G. CTGGTGGC	TAGAAATCCCC	G. TACCTCCC	CAACTTCCCC
387PLMG	GGTGACGGCA	G. CTGGTGGC	TAGAAATCCCC	G. TACCTCCC	CAACTTCCCC
195veraLDPR	GGTGACGGCA	G. CTGGTGGC	TAGAAATCCCC	G. TACCTCCC	CAACTTCCCC
676PLMG	GGTGACGGCA	G. CTGGTGGC	TAGAAATCCCC	G. TACCTCCC	CAACTTCCCC
701PLMG	GGTGACGGCA	G. CTGGTGGC	TAGAAATCCCC	G. TACCTCCC	CAACTTCCCC
440PLMG	GGTGACGGCA	G. CTGGTGGC	TAGAAATCCCC	G. TACCTCCC	CAACTTCCCC
rochedoLDPR	GGTGACGGCA	G. CTGGTGGC	TAGAAATCCCC	G. CACCTCCC	CAACTTCCCC
160S06CRMSGCA	G. CTGGAGGC	TAGAAATCCCC	G. TACCTCCC	CAACTTCCCC
96253CPMG	GGTGACGGCA	G. TTGGTGGC	TAGAAATCCCC	G. TACCTCCC	CAACTTCCCC
92touroLDPRTGGTGGC	TATAATCCCC	G. TACCTCCC	CAACTTCCCC
01anetiLDPR	AGAAATCCCC	G. CACCTCCC	CAACTTCCCC
1751PLMGACCTCCC	CAACTTCCCC
922PLMGTGGTGCC	TAGAAATCCCC	G. TACCTCCC	CAACTTCCCC
991PLMG
Consensusgca	g..tgggtggc	tagaatcccc	g.tacctccc	caacttcccc

101
40afileLDPR TTTTCCCGAAA AATCC.CACC CTA.AGCTGC TG.ACCTCAC CTGCTGATAA 150
54vilmaLDPR TTTCCCGAAA AATCCACACC CTA.AGCTGC TG.ACCTCAC CTGCTGATAA
74gessylDPR TTTCCCGAGA AATCCACACC CTG.AGCTGC TG.ACCTCAC CTGCTGATAA
97blesjeLDPR TTTCCCGAAA AATCCACACC CTA.AGCTGC TG.ACCTCAC CTGCTGATAA
3563CPMG TTTCCCGAAA AATCCACACC CTA.AGCTGC TG.ACCTCAC CTGCTGATAA
9104CPMG TTTCCCGAGA AATCCACACC CTG.AGCTGC TG.ACCTCAC CTGCTGAGAA
23MCPMG TTTCCCGAAA AATCCACACC CTG.AGCTGC TG.ACCTCAC CTGCTGATAA
16contaLDPR TTTCCCGAAA AATCCACACC CTA.AGCTGC TG.ACCTCAC CTGCTGATAA
485PLMG TTTCCCGAAA AATCCACACC CTA.AGCTGC TG.ACCTCAC CTGCTGATAA
387PLMG TTTCCCGAAA AATCCACACC CTA.AGCTGC TG.ACCTCAC CTGCTGATAA
195veraLDPR TTTCCCGAGA AATCCACACC CTG.AGCTGC TG.ACCTCAC CTGCTGATAA
676PLMG TTTCCCGAGA AATCCACACC CTG.AGCTGC TG.ACCTCAC CTGCTGATAA
701PLMG TTTCCCGAGA AATCCACACC CTG.AGCTGC TG.ACCTCAC CTGCTGATAA
440PLMG TTTCCCGAAA AATCCACACC CTG.AGCTGC TG.ACCTCAC CTGCCGATAA
rochedoLDPR TTTCCCGAGA AATCCACACC CTG.AGCTGC TG.ACCTCAC CTGCTGATAA
160S06CRMS TTTCCCGAAA AATCCACACC CTG.AGCTGC TGCACCTCAC CTGCTGATAA
96253CPMG TTTCCCGAAA AATCCACATC CTG.AGCTGC TG.ACCTCAC CTGCTGATAA
92touroLDPR TTTCCCGAGA AATCCACACC CTG.AGCTGC TG.ACCTCAC CTGCTGATAA
01anetilDPR TTTCCCGAGA AATCCACACT CTGTAGCTGC TG.ACCTCAC CTGCTGATAA
1751PLMG TTTCCCGAGA AATCCACACC CTG.AGCTGC TG.ACCTCAC CTGCTGATAA
922PLMG TTTCCCGAAA AATCCACACC CTG.AGCTGC TG.ACCTCAC CTGCTGATAA
991PLMG .TTTCCCGAGA AATCCACACC CTG.AGCTGC TG.ACCTCAC CTGCTGATAA
Consensus tTTTCCCGaaa AATCCACACC CTg.AGCTGC TG.ACCTCAC CTGCTGATAA

151	ATTAATAAAA	TGCCGGCCCT	GTCG. GTTAG	CGGCACCAGA	AGCG. TTCCTT	200
40afilleLDPR	ATTAATAAAA	TGCCGGCCCT	GTCGAGTTAG	CGGCACCAGA	AGCG. TTCCTT	
54vilmaLDPR	ATTAATAAAA	TGCCGGCCCT	GTCGAGTTAG	CGGCACCAGA	AGCG. TTCCTT	
74gessyLDPR	ATTAATAAAA	TGCCGGCCCT	GTCGAGTTAG	CGGCACCAGA	AGCG. TTCCTT	
97blesjeLDPR	ATTAATAAAA	TGCCGGCCCT	GTCGAGTTAG	CGGCACCAGA	AGCG. TTCCTT	
3563CPMG	ATTAATAAAA	TGCCGGCCCT	GTCGAGTTAA	CGGCACCAGA	AGCG. TTCCTT	
9104CPMG	ATTAATACAA	TGCCGGCCCT	GTCGAGTTAG	CGGCACCAGA	AGCG. TTCCTT	
23MCPMG	ATTAATAAAA	TGCCGGCCCT	GTCGAGTTAG	CGGCACCAGA	AGCG. TTCCTT	
16contalLDPR	ATTAATAAAA	TGCCGGCCCT	GTCGAGTTAG	CGGCACCAGA	AGCG. TTCCTT	
485PLMG	ATTAATAAAA	TGCCGGCCCT	GTCGAGTTAG	CGGCACCAGA	AGCG. TTCCTT	
387PLMG	ATTAATAAAA	TGCCGGCCCT	GTCGAGTTAG	CGGCACCAGA	AGCG. TTCCTT	
195veraLDPR	ATTAATAAAA	TGCCGGCCCT	GTCGAGTTAG	CGGCACCAGA	AGCG. TTCCTT	
676PLMG	ATTAATAAAA	TGCCGGCCCT	GTCGAGTTAG	CGGCACCAGA	AGCG. TTCCTT	
701PLMG	ATTAATAAAA	TGCCGGCCCT	GTCGAGTTAG	CGGCACCAGA	AGCG. TTCCTT	
440PLMG	ATTAATAAAA	TGCCGGCCCT	GTCGAGTTAG	CGGCACCAGA	AGCG. TTCCTT	
rochedoLDPR	ATTAATAAAA	TGCCGGCCCT	GTCGAGTTAG	CGGCACCAGA	AGCG. TTCCTT	
160S06CRMS	ATTAATAAAA	TGCCGGCCCT	GTCGAGTTAG	CGGCACCAGA	AGCG. TTCCTT	
96253CPMG	ATTAATAAAA	TGCCGGCCCT	GTCGAGTTAA	CGGCACCAGA	AGCG. TTCCTT	
92touroLDPR	ATTAATAAAA	TGCCGGCCCT	GTCGAGTTAG	CGGCACCAGA	AGCG. TTCCTT	
01anetiLDPR	ATTAATAAAA	TGCCGGCCCT	GTCGAGTTAG	CGGCACCAGA	AGCG. TTCCTT	
1751PLMG	ATTAATAAAA	TGCCGGCCCT	GTCGAGTTAG	CGGCACCAGA	AGCG. TTCCTT	
922PLMG	ATTAATAAAA	TGCCGGCCCT	GTCGAGTTAG	CGGCACCAGA	AGCG. TTCCTT	
991PLMG	ATTAATAAAA	TGCCGGCCCT	GTCGAGTTAG	CGGCACCAGA	AGCG. TTCCTT	
Consensus	ATTAATAAAA	TGCCGGCCCT	GTCGAGTTAG	CGGCACCAGA	AGCG. TTCCTT	

40afileLDPR	CTCCTGAGAC	CCTCGTG.CT	CAGCTCTCGG	TCC.GAGCTC	TCTTGCTCCC
54vilmaLDPR	CTCCTGAGAC	CCTCGTG.CT	CAGCTCTCGG	TCCTGAGCTC	TCTTGCTCCC
74gessyLDPR	CTCCTGAGAC	CCTCGTG.CT	CAGCTCTCGG	TCCTGAGCTC	TCTTGCTCCC
97blesjeLDPR	CTCCTGAGAC	CCTCGTG.CT	CAGCTCTCGG	TCCTGAGCTC	TCTTGCTCCC
3563CPMG	CTCCTGAGAC	CCTCGTG.CT	CAGCTCTCGG	TCCTGAGCTC	TCTTGCTCCC
9104CPMG	CTCCTGAGAC	CCTCGTG.CT	CAGCTCTCGG	TCCTGAGCTC	TCTTGCTCCC
23MCPMG	CTCCTGAGAC	CCTCGTG.CT	CAGCTCTCGG	TCCTGAGCTT	TCTTGCTCCC
16contaLDPR	CTCCTGAGAC	CCTCGTG.CT	CAGCTCTCGG	TCCTGAGCTC	TCTTGCTCCC
485PLMG	CTCCTGAGAC	CCTCGTG.CT	CAGCTCTCGG	TCCTGAGCTC	TCTTGCTCCC
387PLMG	CTCCTGAGAC	CCTCGTG.CT	CAGCTCTCGG	TCCTGAGCTC	TCTTGCTCCC
195veraLDPR	CTCCTGAGAC	CCTCGTG.CT	CAGCTCTCGG	TCCTGAGCTC	TCTTGCTCCC
676PLMG	CTCCTGAGAC	CCTCGTG.CT	CAGCTCTCGG	TCCTGAGCTC	TCTTGCTCCC
701PLMG	CTCCTGAGAC	CCTCGTG.CT	CAGCTCTCGG	TCCTGAGCTC	TCTTGCTCCC
440PLMG	CTCCTGAGAC	CCTCGTG.CT	CAGCTCTCGG	TCCTGAGCTC	TCTTGCTCCC
rochedoLDPR	CTCCTGAGAC	CCTCGTG.CT	CAGCTCTCGG	TCCTGAGCTC	TCTTGCTCCC
160S06CRMS	CTCCTGAGAC	CCTCGTGACT	CAGCTCTCGG	TCCTGAGCTC	TCTTGCTCCC
96253CPMG	CTCCTGAGAC	CCTCGTG.CT	CAGCTCTCGG	TCCTGAGCTC	TCTTGCTCCC
92touroLDPR	CTCCTGAGAC	CCTCGTG.CT	CAGCTCTCGG	TCCTGAGCTC	TCTTGCTCCC
01anetiLDPR	CTCCTGAGAC	CCTCGTG.CT	CAGCTCTCGG	TCCTGAGCTC	TCTTGCTCCC
1751PLMG	CTCCTGAGAC	CCTCGTG.CT	CAGCTCTCGG	TCCTGAGCTC	TCTTGCTCCC
922PLMG	CTCCTGAGAC	CCTCGTG.CT	CAGCTCTCGG	TCCTGAGCTC	TCTTGCTCCC
991PLMG	CTCCTGAGAC	CCTCGTG.CT	CAGCTCTCGG	TCCTGAGCTC	TCTTGCTCCC
Consensus	CTCCTGAGAC	CCTCGTG.CT	CAGCTCTCGG	TCCTGAGCTC	TCTTGCTCCC

201

250

40afilleLDPR	CCTCTGACCG	TCTCCACAGTG	G.ACTCTCTC	CTTTGCCCTCC	TGACCCCGCG
54vilmaLDPR	CCTTTGACCG	TCTCCACAGTG	G.ACTCTCTC	CTTTGCCCTCC	TGACCCCGCG
74gessyLDPR	CCTCTGACCG	TCTCCACAGTG	G.ACTCTCTC	CCTTGCCCTCC	TGACCCCGCG
97blesjeLDPR	CCTCTGACCG	TCTCCACAGTG	G.ACTCTCTC	CTTTGCCCTCC	TGACCCCGCG
3563CPMG	CCTCTGACCG	TCTCCACAGTG	G.ACTCTCTC	CTTTGCCCTCC	TGACCCCGCG
9104CPMG	CCT.TGACCG	TCTCCACAGTG	G.ACTCTCTC	TCTCGCCCTCC	TGACCCCGCG
23MCPMG	CCTCGGACCG	TCTCCACAGTG	G.ACTCTCTC	TCTTGCCCTCC	TGACCCCGCG
16contaLDPR	CCTCTGACCG	TCTCCACAGTG	G.ACTCTCTC	CTTTGCCCTCC	TGACCCCGCG
485PLMG	CCTCTGACCG	TCTCCACAGTG	G.ACTCTCTC	CTTTGCCCTCC	TGACCCCGCG
387PLMG	CCTCTGACCG	TCTCCACAGTG	G.ACTCTCTC	CTTTGCCCTCC	TGACCCCGCG
195veraLDPR	CCTCTGACCG	TCTCCACAGTG	G.ACTCTCTC	CCTTGCCCTCC	TGACCCCGCG
676PLMG	CCTCTGACCG	TCTCCACAGTG	G.ACTCTCTC	CCTTGCCCTCC	TGACCCCGCG
701PLMG	CCTCTGACCG	TCTCCACAGTG	G.ACTCTCTC	CCTTGCCCTCC	TGACCCCGCG
440PLMG	CCTCTGACCG	TCTCCACAGTG	G.ACTCTCTC	CCTTGCCCTCC	TGACCCCGCG
rochedoLDPR	CCT.TGACCG	TCTCCACAGTG	G.ACTCTCTC	TCTTGCCCTCC	TGACCCCGCG
160S06CRMS	CCTCTGACCG	TCTCCACAGTG	G.ACTCTCTC	CCTTGCCCTCC	TGACCCCGCG
96253CPMG	CCTCTGACCG	TCTCCACAGTG	G.ACTCTCTC	CCTTGCCCTCC	TGACCCCGCG
92touroLDPR	CCTCTGACCG	TCTCCACAGTG	G.ACTCTCTC	CCTTGCCCTCC	TGACCCCGCG
01anetiLDPR	CCT.TGACCG	TCTCCACAGTG	GGACCCCTCTC	TCTTGCCCTCC	TGACCCCGCG
1751PLMG	CCTCTGACCG	TCTCCACAGTG	G.ACTCTCTC	CCTTGCCCTCC	TGACCCCGCG
922PLMG	CCTCTGACCG	TCTCCACAGTG	G.ACTCTCTC	CCTTGCCCTCC	TGAGCCCGCG
991PLMG	CCT.TGACCG	TCTCCACAGTG	G.ACTCTCTC	TCTTGCCCTCC	TGACCCCGCG
Consensus	CCTcTGACCG	TCTCCACAGTG	G.AcTcTCTC	ctTTTGCCCTCC	TGACCCCGCG

40afilleLDP	CTCCAAGG.C	GTCTGGCTTG	CACCCGCGTT	TGT.TTCCTG	TC.TTACTTT	450
54vilmaLDP	CTCCAAGGC	GTCTGGCTTG	CACCCGCGTT	TGT.TTCCTG	TC.TTACTTT	
74gessyLDP	CTCCAAGGC	GTCTGGCTTG	CACCCGCGTT	TGT.TTCCTG	TC.TTACTTT	
97blesjeLDP	CTCCAAGGC	GTCTGGCTTG	CACCCGCGTT	TGT.TTCCTG	TC.TTACTTT	
3563CPMG	CTCCAAGGC	GTCTGGCTTG	CACCCGCGTT	TGT.TTCCTG	TC.TTACTTT	
9104CPMG	CTCCAAGGC	GTCTGGCTTG	CACCCGCGTT	TGT.TTCCTG	TC.TTACTTT	
23MCPMG	CTCCAAGGC	GTCTGGCTTG	CACCCGCGTT	TGT.TTCCTG	TC.TTACTTT	
16contaLDP	CTCCAAGGC	GTCTGGCTTG	CACCCGCGTT	TGT.TTCCTG	TC.TTACTTT	
485PLMG	CTCCAAGGC	GTCTGGCTTG	CACCCGCGTT	TGT.TTCCTG	TC.TTACTTT	
387PLMG	CTCCAAGGC	GTCTGGCTTG	CACCCGCGTT	TGT.TTCCTG	TC.TTACTTT	
195veraLDP	CTCCAAGGC	GTCTGGCTTG	CACCCGCGTT	TGT.TTCCTG	TC.TTACTTT	
676PLMG	CTCCAAGGC	GTCTGGCTTG	CACCCGCGTT	TGT.TTCCTG	TC.TTACTTT	
701PLMG	CTCCAAGGC	GTCTGGCTTG	CACCCGCGTT	TGT.TTCCTG	TC.TTACTTT	
440PLMG	CTCCAAGGC	GTCTGGCTTG	CACCCGCGTT	TGT.TTCCTG	TC.TTACTTT	
rochedoLDP	CTCCAAGGC	GTCTGGCTTG	CACCCGCGTT	TGT.TTCCTG	TC.TTACTTT	
160S06CRMS	CTCCAAGGC	GTCTGGCTTG	CACCCGCGTT	TGT.TTCCTG	TC.TTACTTT	
96253CPMG	CTCCAAGGC	GTCTGGCTTG	CACCCGCGTT	TGT.TTCCTG	TC.TTACTTT	
92touroLDP	CTCCAAGGC	GTCTGGCTTG	CACCCGCGTT	TGT.TTCCTG	TC.TTACTTT	
01anetiLDP	CTCCAAGGC	GTCTGGCTTG	CACCCGCGTT	TGT.TTCCTG	TC.TTACTTT	
1751PLMG	CTCCAAGGC	GTCTGGCTTG	CACCCGCGTT	TGT.TTCCTG	TC.TTACTTT	
922PLMG	CTCCAAGGC	GTCTGGCTTG	CACCCGCGTT	TGT.TTCCTG	TC.TTACTTT	
991PLMG	CTCCAAGGC	GTCTGGCTTG	CACCCGCGTT	TGT.TTCCTG	TC.TTACTTT	
Consensus	CTCCAAGGC	GTCTGGCTTG	CACCCGCGTT	TGT.TTCCTG	TC.TTACTTT	

40afilleLDPR	CTGTTT.CTC	GCGGCC.CG	CTCTCTCCCTT	C	CGGGCCCCTC	500	TAGGGCCAG
54vilmaLDPR	CTGTTT.CTC	GCGGCCCGCG	CTCTCTCCCTT	C	CGGGCCCCTC		TAGGGCCAG
74gessyLDPR	CTGTTT.CTC	GCGGCCCGCG	CTCTCTCCCTT	C	CGGGCCCCTC		TAGGGCCAG
97blesjeLDPR	CTGTTT.CTC	GCGGCCCGCG	CTCTCTCCCTT	C	CGGGCCCCTC		TAGGGCCAG
3563CPMG	CTGTTT.CTC	GCGGCCCGCG	CTCTCTCCCTT	C	CGGGCCCCTC		TAGGGCCAG
9104CPMG	CAGTTTCTC	GCGGCCCCCG	CTCTCTCCCTT	C	CGGGCCCCTC		TAGGGCCAG
23MCPMG	CTGTTT.CTC	GCGGCCCGCG	CTCTCTCCCTT	C	CGGGCCCCTC		CAGGGCCAG
16contaLDPR	CTGTTT.CTC	GCGGCCCGCG	CTCTCTCCCTT	C	CGGGCCCCTC		TAGGGCCAG
485PLMG	CTGTTT.CTC	GCGGCCCGCG	CTCTCTCCCTT	C	CGGGCCCCTC		TAGGGCCAG
387PLMG	CTGTTT.CTC	GCGGCCCGCG	CTCTCTCCCTT	C	CGGGCCCCTC		TAGGGCCAG
195veraLDPR	CTGTTT.CTC	GCGGCCCGCG	CTCTCTCCCTT	C	CGGGCCCCTC		TAGGGCCAG
676PLMG	CTGTTT.CTC	GCGGCCCGCG	CTCTCTCCCTT	C	CGGGCCCCTC		TAGGGCCAG
701PLMG	CTGTTT.CTC	GCGGCCCGCG	CTCTCTCCCTT	C	CGGGCCCCTC		TAGGGCCAG
440PLMG	CTGTTT.CTC	GCGGCCCGCG	CTCTCTCCCTT	C	CGGGCCCCTC		TAGGGCCAG
rochedoLDPR	CTGTTT.CTC	GCGGCCCGCG	TTCCCTCCCTT	C	CGGGCCCCTC		TAGGGCCAG
160S06CRMS	CTGTTT.CTC	GCGGCCCGCG	CTCTCTCCCTT	C	CGGGCCCCTC		TAGGGCCAG
96253CPMG	CTGTTT.CTC	GCGGCCCGCG	CTCTCTCCCTT	C	CGGGCCCCTC		TAGGGCCAG
92touroLDPR	CTGTTT.CTC	GCGGCCCGCG	CTCTCTCCCTT	C	CGGGCCCCTC		TAGGGCCAG
01anetiLDPR	CTGTTT.CTC	GCGGCCCGCG	TTCCCTCCCTT	C	CGGGCCCCTC		TAGGGCCAG
1751PLMG	CTGTTT.CTC	GCGGCCGGGG	CTCTCTCCCTT	C	CGGGCCCCTC		TATCGGCCAG
922PLMG	CTGTTT.CGC	GCGGCCCGCG	CTCTCTCCCTT	C	CGGGCCCCTC		TATCG.CCAG
991PLMG	CTGTTT.CTC	GCGGNCCCGG	NTCCCTCCCTT	C	CGGGCCCCTC		TAGGGCCAG
Consensus	CTGTTT.CTC	GCGGCCCGCG	cTctCTCCCTT	C	CGGGCCCCTC		TAGGGCCAG

501
40afilleLDPG GAGA.GACCG GCAAACAATT GGGGGTCC.. TTCCGGGA.T TGATCACCCC
54vilmaLDPG GAGA.GACCG GCAAACAATT GGGGGTCCG TACCGGGAAT TGATCACCCC
74gessyLDPG GAGA.GACCG GCAAACAATT GGGGGTCC.G TACCGGGA.T TGATCACCCC
97blesjeLDPG GAGA.GACCG GCAAACAATT GGGGGTCC.G T.CCGGGA.T TGATCACCCC
3563CPMG GAGA.GACCG GCAAACAATT GGGGGTCC.G T.CCGGGA.T TGATCACCCC
9104CPMG GAGA.GAGAC ACAACAATT GGGGGTCC.G T.CCGGG.A AAATCACCCC
23MCPMG GAGA.GACCG GCAAACAATT GGGGGTCC.G T.CCGGGA.T TGATCACCCC
16contaLDPG GAGA.GACCG GCAAACAATT GGGGGTCC.G T.CCGGGA.T TGATCACCCC
485PLMG GAGA.GACCG GCAAACAATT GGGGGTCC.G T.CCGGGA.T TGATCACCCC
387PLMG GAGA.GACCG GCAAACAATT GGGGGTCC.G T.CCGGGA.T TGATCACCCC
195veraLDPG GAGA.GACCG GCAAACAATT GGGGGTCC.G T.CCGGGA.T TGATCACCCC
676PLMG GAGA.GACCG GCAAACAATT GGGGGTCC.G T.CCGGGA.T TGATCACCCC
701PLMG GAGA.GACCG GCAAACAATT GGGGGTCC.G T.CCGGGA.T TGATCACCCC
440PLMG GAGA.GACCG GCAAACAATT GGGGGTCC.G T.CCGGGA.T TGATCACCCC
rochedoLDPG GAGA.GACCG GCAAACAATT GGGGGTCC.G T.CCGGGA.T TGATCACCCC
160S06CRMS AAGC.GCACG GCAAA.ATTT GGGGGTCC.G T.CCGGGA.T TGATCACCCC
96253CPMG GAGA.GACCG GCAAACAATT GGGGGTCC.. GACCGGA.T TGAACACC..
92touroLDPG GAGA.GACCG GCAAACAATT GGGGGTCC.G TACCGGGA.T TGATCACCCC
01anetiLDPG GAAAAGACCG GCAAACAATT GGGGGTCC.. GTCCGGGA.T TGATCACCCC
1751PLMG GAGA.GACCG GCAAACAATT GGGGGTCC.. GTCCGGGA.T TGATCACCCC
922PLMG GAGA.GACCG CAGTACAATT GAGGGTCC.G TTCTGCA..T TGATCTCCC.
991PLMG GAGA.GACCG GCAAACAATT GGGGGTCC.. .GTCGGGGAT TGATCA....
Consensus GAGA.GACcG gCAAACAATT GGGGGcTC.g t.cCGGGa.T TGATCacccc

ANEXO 3
RELAÇÃO DAS SEQÜÊNCIAS BRUTAS COMPLETAS, OBTIDAS A PARTIR DO PRODUTO DE AMPLIFICAÇÃO DA PCR
POI/BLV, ALINHADAS COM O PROGRAMA MULTALIN

1				50
991PLMG	GTGTGAAACC	TGTCAAAAAGC	TTAATCCAAC	TGGAGGATGA
17antjeLDPR	AAGATGCGAA
011infosCPMGAGCGGA
96253CPMGAC	AAGATGCGAA
M23CPMGATGCGGA
ConsensusAGGCAGA
				AAGATGCGGA
				...aggc.ga
				aagATGCGGaa
51				100
991PLMG	CTATTTCAGAG	AGGGTGGGCC	CCGAACCATA	TTTTGGCAGGC
17antjeLDPR	CTATTTCAGAG	AGGGTGGGCC	CCAAATCATA	TTTTGGCAGGC
011infosCPMG	CTATTTCAGAG	AGGGTGGGCC	CCAAATCATA	TTTTGGCAGGC
96253CPMG	CTATTTCAGAG	AGGGTGGGCC	CCAAACCATA	TCTGGCAGGC
M23CPMG	CTATTTCAGAG	AGGGTGGGCC	CCAAACCATA	TCTGGCAGGC
Consensus	CTATTTCAGAG	AGGGTGGGCC	CCAAAACATA	TtTTGGCAGGC
				CGATATAAACC
101				150
991PLMG	CATTATAAAT	ACAAACAGTT	CACCTACGCT	CTGCATGTGT
17antjeLDPR	CATTATAAAT	ACAAACAGTT	CACCTACGCT	TTGCACGTGT
011infosCPMG	CATTATAAAT	ACAAACAGTT	CACCTACGCT	TTGCACGTGT
96253CPMG	CATTATAAAT	ACAAACAGTT	CACCTACGCT	TTGCACGTGT
M23CPMG	CATTATAAAT	ACAAACAGTT	CACCTACGCT	TTGCACGTGT
Consensus	CATTATAAAT	ACAAACAGTT	CACCTACGCT	tTGCacGTGT
				TTGTAGATAC
151				200
991PLMG	TTACTCTGGA	GCTACTCATG	CCTCGCGAA	GCGTGGGCTC
17antjeLDPR	TTACTCTGGA	GCTACTCATG	CCTCAGCGAA	GCGAGGACTC
011infosCPMG	TTACTCTGGA	GCTACTCATG	CCTCAGCGAA	GCGAGGACTC
96253CPMG	TTACTCTGGA	GCTACTCATG	CCTCAGCAAA	GCGAGGGCTC
M23CPMG	TTACTCTGGA	GCTACTCATG	CCTCAGCAAA	GCGAGGGCTC
Consensus	TTACTCTGGA	GCTACTCATG	CCTCaGCgAA	GCGaGGgCTC
				ACCACTCAAA

201
 991PLMG TGACCAATTGA GGGCCCTTCTTT GAGGCCATAG TGCAATCTAGG TCGTCCAAAA
 17antjeLDPR TGACCAATTGA GGGCCCTTCTTT GAGGCCATAG TGCAATCTGGG TCGTCCAAAA
 011infosCPMG TGACCAATTGA GGGCCCTTCTTT GAGGCCATAG TGCAATCTGGG TCGTCCAAAA
 96253CPMG TGACCAATGGA GGGCCCTTCTTT GAGGCCATAG TGCAATCTAGG TCGTCCAAAA
 M23CPMG TGACCAATGGA GGGCCCTTCTTT GAGGCCATAG TGCAATCTAGG TCGTCCAAAA
 Consensus TGACCAATTGA GGGCCCTTCTTT GAGGCCATAG TGCAATCTAGG TCGTCCAAAA

251
 991PLMG AAGCTAAACA CTGACCAAGG TGCAAAATTAC ACCTCCAAAA CCTTTGTTCAG
 17antjeLDPR AAGCTAAACA CTGACCAAGG AGCAAACTAC ACCTCTAAAA CCTTTGTTCAG
 011infosCPMG AAGCTAAACA CTGACCAAGG AGCAAACTAC ACCTCTAAAA CCTTTGTTCAG
 96253CPMG AAGCTAAACA CCGACCAAGG TGCAAACTAC ACCTCCAAAA CCTTTGTTCAG
 M23CPMG AAGCTAAACA CCGACCAAGG TGCAAACTAC ACCTCCAAAA CCTTTGTTCAG
 Consensus AAGCTAAACA CTGACCAAGG TGCAAACTAC ACCTCCAAAA CCTTTGTTCAG

301
 991PLMG GTTTTGCCAG CAGTTCGGAG TTTCCCTTTC TCATCATGTT CCTTACAACC
 17antjeLDPR GTTTTGCCAG CAGTTCGGAG TTTCCCTTTC CCTTACAACC
 011infosCPMG GTTTTGCCAG CAGTTCGGAG TTTCCCTTTC CCTTACAACC
 96253CPMG GTTTTGCCAG CAGTTCGGAA TTTCCCTTTC TCATCATGTT CCTTACAACC
 M23CPMG GTTTTGCCAG CAGTTCGGAA TTTCCCTTTC TCATCATGTT CCTTACAACC
 Consensus GTTTTGCCAG CAGTTCGGAG TTTCCCTTTC TCATCATGTT CCTTACAACC

351
 991PLMG CCACAAAGTTC GGGGTTAGTA GAACGGACAA ATGGACTGCT CAAAACCTTCTT
 17antjeLDPR CCACAAAGTTC AGGATTGGTA GAACGGACAA ATGGGCTGCT CAAAACCTTCTT
 011infosCPMG CCACAAAGTTC AGGATTGGTA GAACGGACAA ATGGGCTGCT CAAAACCTTCTT
 96253CPMG CCACAAAGTTC AGGGTTAGTG GAACGGACAA ATGGACTGCT CAAAACCTTCTT
 M23CPMG CCACAAAGTTC AGGGTTAGTG GAACGGACAA ATGGACTGCT CAAAACCTTCTT
 Consensus CCACAAAGTTC aGGgTTaGTa GAACGGACAA ATGGaCTGCT CAAAACCTTCTT

400
 991PLMG
 17antjeLDPR
 011infosCPMG
 96253CPMG
 M23CPMG
 Consensus

401
 991PLMG CTATCTAAAT ACCACCTAGA CGAACCACCAC CTTCCCATGA CTCAGGCCCT 450
 17antjeLDPR TTGTCTAAAT ATCACCTAGA CGAACCACCAC CTTCCCATGT CTCAGGCCCT
 011infosCPMG TTGTCTAAAT ATCACCTAGA CGAACCACCAC CTTCCCATGT CTCAGGCCCT
 96253CPMG TTGTCTAAAT ATCACCTAGA CGAACCACCAC CTTCCCATGA CTCAGGCCCT
 M23CPMG TTGTCTAAAT ATCACCTAGA CGAACCACCAC CTTCCCATGA CTCAGGCCCT
 Consensus tTgTCTAAAT AtCACcTAGA CGAACCACCAC CTTCCCATGa CTCAGGCCCT

451
 991PLMG TTCTCGAGCC CTCTGGACTC ACAATCAGAT TAACCTCCTA CCAATTCTAA 500
 17antjeLDPR TTCTCGAGCC CTCTGGACTC ACAATCAGAT TAACCTCCTA CCGATTCTAA
 011infosCPMG TTCTCGAGCC CTCTGGACTC ACAATCAGAT TAACCTCCTA CCGATTCTAA
 96253CPMG TTCTCGAGCC CTCTGGACTC ATAACCAGAT TAACCTCCTA CCAATTCTAA
 M23CPMG TTCTCGAGCC CTCTGGACTC ATAACCAGAT TAATCTCCTA CCAATTCTAA
 Consensus TTCTCGAGCC CTCTGGACTC AcaAtCAGAT TAaCCTCCTA CCaATTCTAA

501
 991PLMG AGACCAGATG GGAGCTACAC CATTCAACCC CACTTGCTGT CATTTCAGAG 550
 17antjeLDPR AGACCAGATG GGAGCTACAC CATTCAACCC CACTTGCTGT CATTTCAGAG
 011infosCPMG AGACCAGATG GGAGCTACAC CATTCAACCC CACTTGCTGT CATTTCAGAG
 96253CPMG AGACCAGATG GGAGCTACAC CATTCAACCC CACTTGCTGT CATTTCAGAG
 M23CPMG AGACCAGATG GGAGCTACAC CATTCAACCC CACTTGCTGT CATTTCAGAG
 Consensus AGACCAGATG GGAGCTACAC CATTCAACCC CACTTGCTGT CATTTCAGAG

551
 991PLMG GGCGGAGAAA CACCCAAGGG CTCTGATAAA CTCCTTTTGT ACAAGCTCCC 600
 17antjeLDPR GGCGGAGAAA CACCCAAGGG CTCTGATAAA CTCCTTTTGT ACAAGCTCCC
 011infosCPMG GGCGGAGAAA CACCCAAGGG CTCTGATAAA CTCCTTTTGT ACAAGCTCCC
 96253CPMG GGCGGAGAAA CACCCAAGGG CTCTGATAAA CTCCTTTTGT ACAAGCTCCC
 M23CPMG GGCGGAGAAA CACCCAAGGG CTCTGATAAA CTCCTTTTGT ACAAGCTCCC
 Consensus GGCGGAGAAA CACCCAAGGG CTCTGATAAA CTCCTTTTGT ACAAGCTCCC

601
 991PLMG CGGGCAAAAC AATCGTCGGT GGCTAGGACC ACTCCCGGCC CTAGTCGAAG 650
 17antjeLDPR CGGGCAAAAC AATCGCCGGT GGCTGGGACC ACTCCCGGCC CTAGTCGAAG
 011infosCPMG CGGGCAAAAC AATCGCCGGT GGCTGGGACC ACTCCCGGCC CTAGTCGAAG
 96253CPMG CGGGCAAAAC AATCGTCGGT GGCTAGGACC ACTCCCGGCC CTAGTCGAAG
 M23CPMG CGGGCAAAAC AATCGTCGGT GGCTAGGACC ACTCCCGGCC CTAGTCGAAG
 Consensus CGGGCAAAAC AATCGtCGGT GGCTaGGACC ACTCCCGGCC CTAGTCGAAG

651
 991PLMG CCTCGGGAGG CGCTCTCCTG GCTACTGACC CCCCCTGTGTG GGTTCCTTGG 700
 17antjeLDPR CCTCGGGAGG CGCTCTCCTG GCTACTAACC CCCCCTGTGTG GGTTCCTTGG
 011infosCPMG CCTCGGGAGG CGCTCTCCTG GCTACTAACC CCCCCTGTGTG GGTTCCTTGG
 96253CPMG CCTCGGGAGG CGCTCTCCTG GCTACTAACC CCCCCTGTGTG GGTTCCTTGG
 M23CPMG CCTCGGGAGG CGCTCTCCTG GCTACTAACC CCCCCTGTGTG GGTTCCTTGG
 Consensus CCTCGGGAGG CGCTCTCCTG GCTACTaACC CCCCCTGTGTG GGTTCcctTGG

701
 991PLMG CGTTTGCTGA AAGCC.TTCA AATGCCATAA GAACGACGG. 750
 17antjeLDPR CGTTTGCTGA AAGCC.TTCA AATGCCATAA GAACGACGGT CCCGA.....
 011infosCPMG CGTTTGCTGA AAGCCGTTC AATGCCATAA GAACGACGGT CCCGAA.....
 96253CPMG CGTTTGCTGA A.GCCCTTCA AATGCCATAA GAACGACGGT CCCGAAAGACG
 M23CPMG CGTTTGCTGA A.GCCGTTC AATGCCATAA GAACGACGGT CCCGA.....
 Consensus CGTTTGCTGA AaGc.TTCA AATGCCcAAA GAACGACGgt cccga.....

751
 991PLMG
 17antjeLDPR
 011infosCPMG
 96253CPMG CCAAA
 M23CPMG
 Consensus

ANEXO 4

RELAÇÃO DAS SEQUÊNCIAS BRUTAS PARCIAIS, GRUPO “TRUNCADAS 345”, OBTIDAS A PARTIR DO PRODUTO DE AMPLIFICAÇÃO DA PCR POL/BLV, ALINHADAS COM O PROGRAMA MULTALIN

1				50
922PLMG	AAC	TCTTCT	ATCTAAATAT	CACCTAGACG AACCCACACCT TCCTATGACT
rochedoLDPR	AAC	TCTTCT	GTCTAAATAT	CACCTAGACG AACCCACACCT TCCCATGACT
Consensus	AAC	TCTTCT	aTCTAAATAT	CACcTAGACG AACCCACACCT TCCcATGACT
51				100
922PLMG	CAG	GC	TCTTTT	CTCGAGCCCT CAGGACTCAC AATCAGATTA ACCTCCTACC
rochedoLDPR	CAG	GC	CCCTTT	CTCGAGCCCT CTGGACTCAT AACAGATTA ACCTCCTACC
Consensus	CAG	Gc	CcTtTt	CTCGAGCCCT CaGGACTCAC AACAGATTA ACCTCCTACC
101				150
922PLMG	AAT	TCTAAAG	ACCAGATGGG	AGCTACACCA TTCACCCCCA CTTGCTGTCA
rochedoLDPR	AAT	TCTAAAG	ACCAGATGGG	AGCTACACCA TTCACCCCCA CTTGCTGTCA
Consensus	AAT	TCTAAAG	ACCAGATGGG	AGCTACACCA TTCACCCCCA CTTGCTGTCA
151				200
922PLMG	TTT	CAGAGGG	CGGAGAAACA	CCCAAGGGCT CTGATAAACT CTTTTTGTAC
rochedoLDPR	TTT	CAGAGGG	CGGAGAAACA	CCCAAGGGCT CTGATAAACT CTTTTTGTAC
Consensus	TTT	CAGAGGG	CGGAGAAACA	CCCAAGGGCT CTGATAAACT CTTTTTGTAC
201				250
922PLMG	AAG	TCCCCG	GGCAAAACAA	TCGTGCGTGG CTAGGACCAC TCCCGGCCCT
rochedoLDPR	AAG	TCCCCG	GGCAAAACAA	TCGTGCGTGG CTAGGACCAC TCCCGGCCCT
Consensus	AAG	TCCCCG	GGCAAAACAA	TCGTGCGTGG CTAGGACCAC TCCCGGCCCT
251				300
922PLMG	AGT	CGAAGCC	TCGGGAGGCG	CTCTCCTGGC TACTGACCCC CCCGTGTGGG
rochedoLDPR	AGT	CGAAGCC	TCGGGAGGCG	CTCTCCTGGC TACTGACCCC CCCGTGTGGG
Consensus	AGT	CGAAGCC	TCGGGAGGCG	CTCTCCTGGC TACTGACCCC CCCGTGTGGG
301				345
922PLMG	TTT	CCCTGGCG	TTAGCTGAAA	GCCTTCAAAT GCTCAAAGAA CGACG
rochedoLDPR	TTT	CCCTGGCG	TTTGTGAAG	GCCTTCAAAT GCCCAAAGAA CGACG
Consensus	TTT	CCCTGGCG	TTaGCTGAAA	GCCTTCAAAT GcCcaAAGAA CGACG

ANEXO 5
RELAÇÃO DAS SEQÜÊNCIAS BRUTAS PARCIAIS, GRUPO "TRUNCADAS 230", OBTIDAS A PARTIR DO PRODUTO DE AMPLIFICAÇÃO DA PCR POL/BLV, ALINHADAS COM O PROGRAMA MULTALIN

1	50
20blesjeLDPR	ATGGGAGCTA CACCAATTAC CCCCACTTGC TGTCATTTCA GAGGGCGGAG
195veraLDPR	ATGGGAGCTA CACCAATTAC CCCCACTTGC TGTCATTTCA GAGGGCGGAG
97blesjeLDPR	ATGGGAGCTA CACCAATTAC CCCCACTTGC TGTCATTTCA GAGGGCGGAG
Consensus	ATGGGAGCTA CACCAATTAC CCCCACTTGC TGTCATTTCA GAGGGCGGAG
51	100
20blesjeLDPR	AAACACCCAA GGGCTCTGAT AAACCTTTTT TGTACAAGCT CCCCAGGCAA
195veraLDPR	AAACACCCAA GGGCTCTGAT AAACCTTTTT TGTACAAGCT CCCCAGGCAA
97blesjeLDPR	AAACACCCAA GGGCTCTGAT AAACCTTTTT TGTACAAGCT CCCCAGGCAA
Consensus	AAACACCCAA GGGCTCTGAT AAACCTTTTT TGTACAAGCT CCCCAGGCAA
101	150
20blesjeLDPR	AACAATCGTC GGTGGCTAGG ACCACTCCCG GCCCTAGTCG AAGCCTCGGG
195veraLDPR	AACAATCGTC GGTGGCTAGG ACCACTCCCG GCCCTAGTCG AAGCCTCGGG
97blesjeLDPR	AACAATCGTC GGTGGCTAGG ACCACTCCCG GCCCTAGTCG AAGCCTCGGG
Consensus	AACAATCGTC GGTGGCTAGG ACCACTCCCG GCCCTAGTCG AAGCCTCGGG
151	200
20blesjeLDPR	AGGCGCTCTC CTGGCTACTG ACCCCCCCGT GTGGGTCCC T.GGCGTTTG
195veraLDPR	AGGCGCTCTC CTGGCTACTG ACCCCCCCGT GTGGGTCCC TGGCGTTTG
97blesjeLDPR	AGGCGCTCTC CTGGCTACTG ACCCCCCCGT GTGGGTCCC TGGCGTTTG
Consensus	AGGCGCTCTC CTGGCTACTG ACCCCCCCGT GTGGGTCCC T.GGCGTTTG
201	231
20blesjeLDPR	CTGAAAAGCCT TCAAAATGCCT AAAGAACGAC G
195veraLDPR	CTGAAAAGCCT TCAAAATGCCT AAAGAACGAC G
97blesjeLDPR	CTGAAAAGCCT TCAAAATGCCT AAAGAACGAC G
Consensus	CTGAAAAGCCT TCAAAATGCCT AAAGAACGAC