

# Frequent Recombination Events in Leishmania donovani: Mining Population Data

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## Supplementary Tables and Figures

**Table S1: L. donovani DNA-seq samples (statistics of B-type reads).**

CDS+ = B-type reads overlap with protein-coding genes

CDS- = B-type reads do not overlap with protein-coding genes

STUDIED SAMPLES (28):

| Sample name  | CDS+ | CDS- |
|--------------|------|------|
| 18830        | 8    | 148  |
| 18831        | 0    | 38   |
| 18833        | 0    | 14   |
| 18850        | 138  | 1597 |
| 18851        | 56   | 546  |
| 18852        | 50   | 552  |
| 18856        | 154  | 1207 |
| 18858        | 137  | 1280 |
| 18860        | 53   | 723  |
| 18861        | 29   | 743  |
| 18862        | 0    | 103  |
| 206260       | 115  | 1071 |
| 206261       | 2    | 1067 |
| 206263       | 9    | 471  |
| 206270       | 0    | 687  |
| 206271       | 67   | 936  |
| 206273       | 45   | 564  |
| 206275       | 3    | 708  |
| 206282       | 14   | 625  |
| 206284       | 92   | 947  |
| 206285       | 0    | 15   |
| 206286       | 11   | 679  |
| 206287       | 0    | 35   |
| 206288       | 0    | 42   |
| 206289       | 0    | 43   |
| 206290       | 8    | 109  |
| 206291       | 2    | 59   |
| 206292       | 0    | 15   |
| Merged reads | 166  | 1236 |

OUTLIERS (2):

| Sample name  | CDS+ | CDS- |
|--------------|------|------|
| 206271       | 4531 | 9662 |
| 206283       | 4336 | 9968 |
| Merged reads | 2572 | 3588 |

**Supplementary Table S2. 137 L. donovani protein-coding genes that overlap with merged B-type reads.**

ChromosomeID = the last three digits of the LOCUS number (NC\_018\*\*\*)

Number of merged reads = number of merged overlapping B-type reads

Match = number of matches in the longest merged read

L = the length of the the longest merged read

F = percent identity (Match/L)

| Positions on Chromosome | ChromosomeID | #merged reads | Match | L  | F    | CDS positions       | Locus_tag    | protein product                  | status    | protein_id     |
|-------------------------|--------------|---------------|-------|----|------|---------------------|--------------|----------------------------------|-----------|----------------|
| 61398                   | 61538        | 253           | 16    | 75 | 1    | C(61468..64851)     | LDBPK_260240 | hypothetical protein             | conserved | XP_003861613.1 |
| 690030                  | 690154       | 258           | 13    | 72 | 0.96 | C(689721..692840)   | LDBPK_311500 | hypothetical protein             | unknown   | XP_003863241.1 |
| 202748                  | 202906       | 242           | 12    | 72 | 0.96 | 198985..204321      | LDBPK_150550 | hypothetical protein             | conserved | XP_003859580.1 |
| 336257                  | 336417       | 252           | 12    | 72 | 0.96 | 335255..336277      | LDBPK_250930 | hypothetical protein             | unknown   | XP_003861423.1 |
| 200249                  | 200408       | 242           | 11    | 72 | 0.96 | 198985..204321      | LDBPK_150550 | hypothetical protein             | conserved | XP_003859580.1 |
| 644053                  | 644210       | 259           | 9     | 72 | 0.96 | C(642591..644894)   | LDBPK_321700 | hypothetical protein             | conserved | XP_003863586.1 |
| 727625                  | 727736       | 247           | 9     | 72 | 0.96 | C(726932..727834)   | LDBPK_201710 | hypothetical protein             | conserved | XP_003860511.1 |
| 189492                  | 189636       | 242           | 8     | 72 | 0.96 | 188745..191753      | LDBPK_150520 | katanin-like protein             | conserved | XP_003859577.1 |
| 116492                  | 116615       | 241           | 7     | 75 | 1    | 115139..116629      | LDBPK_140370 | hypothetical protein             | conserved | XP_003859409.1 |
| 118037                  | 118148       | 249           | 7     | 72 | 0.96 | C(117509..120778)   | LDBPK_220210 | hypothetical protein             | unknown   | XP_003860771.1 |
| 1243529                 | 1243609      | 258           | 7     | 72 | 0.96 | C(1242582..1244072) | LDBPK_312550 | hypothetical protein             | conserved | XP_003863342.1 |
| 625518                  | 625683       | 255           | 6     | 72 | 0.96 | C(625597..627465)   | LDBPK_281760 | hypothetical protein             | conserved | XP_003862275.1 |
| 496911                  | 497046       | 242           | 6     | 75 | 1    | C(496744..497028)   | LDBPK_151240 | nucleoside transporter 1         | conserved | XP_003859646.1 |
| 639581                  | 639676       | 258           | 6     | 72 | 0.96 | C(639114..646298)   | LDBPK_311440 | hypothetical protein             | conserved | XP_003863235.1 |
| 438125                  | 438260       | 260           | 6     | 75 | 1    | 435816..439961      | LDBPK_331230 | hypothetical protein             | conserved | XP_003863949.1 |
| 498646                  | 498747       | 257           | 6     | 72 | 0.96 | 498149..498673      | LDBPK_301480 | amal protein                     | putative  | XP_003862861.1 |
| 273558                  | 273662       | 230           | 5     | 72 | 0.96 | C(269424..278087)   | LDBPK_030680 | hypothetical protein             | conserved | XP_003858033.1 |
| 491237                  | 491455       | 253           | 5     | 72 | 0.96 | 490443..493889      | LDBPK_261410 | hypothetical protein             | conserved | XP_003861728.1 |
| 521516                  | 521607       | 237           | 5     | 72 | 0.96 | 520477..521577      | LDBPK_101360 | hypothetical protein             | conserved | XP_003858969.1 |
| 301833                  | 301966       | 231           | 5     | 71 | 1    | C(301826..303757)   | LDBPK_040740 | hypothetical protein             | conserved | XP_003858136.1 |
| 1101774                 | 1101864      | 258           | 4     | 72 | 0.96 | C(1100850..1102613) | LDBPK_312260 | hypothetical protein             |           | XP_003863314.1 |
| 1101930                 | 1102005      | 258           | 4     | 72 | 0.96 | C(1100850..1102613) | LDBPK_312260 | hypothetical protein             |           | XP_003863314.1 |
| 1285971                 | 1286062      | 258           | 4     | 72 | 0.96 | C(1285526..1286704) | LDBPK_312690 | hypothetical protein             | conserved | XP_003863356.1 |
| 144751                  | 144850       | 262           | 4     | 72 | 0.96 | 140177..145222      | LDBPK_350480 | hypothetical protein             | conserved | XP_003864641.1 |
| 230883                  | 230980       | 252           | 4     | 75 | 1    | C(228767..233809)   | LDBPK_250690 | myosin heavy chain kinase c-like | conserved | XP_003861399.1 |
| 152349                  | 152485       | 239           | 4     | 72 | 0.96 | 150681..152351      | LDBPK_120300 | hypothetical protein             | conserved | XP_003859147.1 |
| 666719                  | 666873       | 255           | 4     | 73 | 1    | C(666186..673556)   | LDBPK_281830 | hypothetical protein             | conserved | XP_003862282.1 |
| 331661                  | 331772       | 244           | 4     | 74 | 1    | C(331662..333083)   | LDBPK_170770 | protein kinase                   | putative  | XP_003859931.1 |
| 1102345                 | 1102422      | 258           | 3     | 72 | 0.96 | C(1100850..1102613) | LDBPK_312260 | hypothetical protein             |           | XP_003863314.1 |
| 327745                  | 327869       | 239           | 3     | 72 | 0.96 | 322694..328441      | LDBPK_120540 | hypothetical protein             | conserved | XP_003859171.1 |
| 1231460                 | 1231547      | 257           | 3     | 75 | 1    | 1231356..1232528    | LDBPK_303380 | hypothetical protein             | conserved | XP_003863049.1 |
| 1090454                 | 1090613      | 256           | 3     | 72 | 0.96 | 1088835..1091009    | LDBPK_292550 | hypothetical protein             | conserved | XP_003862673.1 |
| 496777                  | 496867       | 242           | 3     | 75 | 1    | C(496744..497028)   | LDBPK_151240 | nucleoside transporter           | putative  | XP_003859646.1 |
| 265863                  | 265967       | 232           | 3     | 75 | 1    | 262729..266835      | LDBPK_050720 | phosphatase-like protein         |           | XP_003858259.1 |
| 908961                  | 909042       | 259           | 3     | 72 | 0.96 | C(908678..910600)   | LDBPK_322440 | hypothetical protein             | conserved | XP_003863657.1 |
| 194100                  | 194197       | 244           | 3     | 72 | 0.96 | C(193248..198839)   | LDBPK_170490 | hypothetical protein             | conserved | XP_003859903.1 |
| 269649                  | 269799       | 235           | 3     | 72 | 1    | 263876..270697      | LDBPK_080640 | hypothetical protein             | unknown   | XP_003858629.1 |
| 436419                  | 436512       | 237           | 3     | 72 | 1    | C(436480..436947)   | LDBPK_101050 | histone H3                       |           | XP_003858939.1 |
| 124134                  | 124217       | 243           | 3     | 72 | 0.96 | C(123927..125372)   | LDBPK_160380 | hypothetical protein             | conserved | XP_003859726.1 |
| 225374                  | 225467       | 239           | 3     | 75 | 1    | C(224123..225952)   | LDBPK_120440 | hypothetical protein             | unknown   | XP_003859161.1 |
| 85510                   | 85605        | 238           | 3     | 72 | 0.96 | 83318..88723        | LDBPK_110310 | hypothetical protein             | conserved | XP_003859008.1 |
| 689202                  | 689287       | 263           | 2     | 72 | 0.96 | C(679469..692572)   | LDBPK_361800 | hypothetical protein             | conserved | XP_003865295.1 |
| 1560393                 | 1560471      | 261           | 2     | 72 | 1    | 1560458..1562953    | LDBPK_343800 | adaptor gamma-1 chain            | putative  | XP_003864539.1 |
| 323359                  | 323433       | 239           | 2     | 72 | 0.96 | 322694..328441      | LDBPK_120540 | hypothetical protein             | conserved | XP_003859171.1 |
| 703969                  | 704061       | 256           | 2     | 72 | 0.96 | C(702923..704941)   | LDBPK_291600 | hypothetical protein             | conserved | XP_003862579.1 |
| 1455467                 | 1455541      | 261           | 2     | 75 | 1    | 1455165..1455716    | LDBPK_343500 | hypothetical protein             | conserved | XP_003864509.1 |
| 742017                  | 742098       | 255           | 2     | 72 | 0.96 | C(740223..744005)   | LDBPK_282000 | hypothetical protein             | conserved | XP_003862299.1 |
| 742492                  | 742578       | 254           | 2     | 72 | 1    | C(742346..744922)   | LDBPK_271790 | endo/exonuclease Mre11           | putative  | XP_003862030.1 |
| 2007744                 | 2007824      | 262           | 2     | 72 | 0.96 | 2006915..2007775    | LDBPK_355110 | hypothetical protein             | unknown   | XP_003865088.1 |
| 2013376                 | 2013451      | 262           | 2     | 72 | 0.96 | 2012852..2013772    | LDBPK_355130 | hypothetical protein             | conserved | XP_003865090.1 |

|         |         |     |   |    |    |       |                     |              |                                                   |           |                |
|---------|---------|-----|---|----|----|-------|---------------------|--------------|---------------------------------------------------|-----------|----------------|
| 243894  | 243997  | 261 | 2 | 72 | 75 | 0.96  | 243991..247728      | LDBPK_340610 | hypothetical protein                              | conserved | XP_003864226.1 |
| 191796  | 191872  | 258 | 2 | 72 | 75 | 0.96  | C(190499..192532)   | LDBPK_310550 | hypothetical protein                              | unknown   | XP_003863145.1 |
| 143706  | 143789  | 232 | 2 | 72 | 75 | 0.96  | 141177..143738      | LDBPK_050440 | hypothetical protein                              | conserved | XP_003858231.1 |
| 242630  | 242712  | 230 | 2 | 72 | 75 | 0.96  | 242690..245086      | LDBPK_030640 | hypothetical protein                              | conserved | XP_003858029.1 |
| 910217  | 910294  | 259 | 2 | 72 | 75 | 0.96  | C(908678..910600)   | LDBPK_322440 | hypothetical protein                              | conserved | XP_003863657.1 |
| 460821  | 460899  | 244 | 2 | 72 | 75 | 0.96  | 458563..479592      | LDBPK_171090 | hypothetical protein                              | conserved | XP_003859963.1 |
| 625713  | 625789  | 255 | 2 | 72 | 75 | 0.96  | C(625597..627465)   | LDBPK_281760 | hypothetical protein                              | conserved | XP_003862275.1 |
| 2008999 | 2009075 | 262 | 2 | 72 | 75 | 0.96  | 2008138..2010021    | LDBPK_355120 | biopterin transporter                             | putative  | XP_003865089.1 |
| 181610  | 181684  | 228 | 2 | 75 | 75 | 1     | 180454..182241      | LDBPK_010640 | hypothetical protein                              | conserved | XP_003857877.1 |
| 981481  | 981569  | 253 | 2 | 72 | 75 | 0.96  | 980998..982443      | LDBPK_262540 | protein kinase                                    | putative  | XP_003861838.1 |
| 239126  | 239234  | 240 | 2 | 72 | 75 | 0.96  | C(238081..240228)   | LDBPK_130670 | protein kinase                                    | putative  | XP_003859278.1 |
| 974465  | 974540  | 258 | 2 | 72 | 75 | 0.96  | C(974451..974765)   | LDBPK_312010 | tryparedoxin-like protein                         |           | XP_003863290.1 |
| 1163191 | 1163269 | 258 | 2 | 72 | 75 | 0.96  | C(1162333..1163382) | LDBPK_312400 | 3,2-trans-enoyl-CoA isomerase, mt                 |           | XP_003863328.1 |
| 878073  | 878154  | 257 | 2 | 72 | 75 | 0.96  | C(877746..881210)   | LDBPK_302350 | zinc-finger protein                               | conserved | XP_003862947.1 |
| 189708  | 189784  | 242 | 2 | 73 | 75 | 1     | 188745..191753      | LDBPK_150520 | katanin-like protein                              |           | XP_003859577.1 |
| 22522   | 22597   | 254 | 2 | 72 | 75 | 0.96  | C(20913..22691)     | LDBPK_270090 | cytochrome p450-like protein                      |           | XP_003861867.1 |
| 204904  | 204972  | 252 | 2 | 69 | 69 | 1     | C(204904..206916)   | LDBPK_250620 | hypothetical protein                              | conserved | XP_003861392.1 |
| 610376  | 610446  | 245 | 1 | 68 | 71 | 0.958 | 608633..611323      | LDBPK_181400 | pumilio protein                                   | putative  | XP_003860154.1 |
| 509853  | 509927  | 256 | 1 | 72 | 75 | 0.96  | 504828..510272      | LDBPK_291340 | hypothetical protein                              | unknown   | XP_003862551.1 |
| 160501  | 160575  | 261 | 1 | 72 | 75 | 0.96  | 159562..161775      | LDBPK_340480 | hypothetical protein                              | unknown   | XP_003864213.1 |
| 1681477 | 1681551 | 261 | 1 | 72 | 75 | 0.96  | 1680767..1681939    | LDBPK_344190 | RNA-binding protein-like protein                  |           | XP_003864579.1 |
| 486553  | 486627  | 236 | 1 | 72 | 75 | 0.96  | C(486555..487817)   | LDBPK_091270 | hypothetical protein                              | unknown   | XP_003858805.1 |
| 285076  | 285150  | 230 | 1 | 72 | 75 | 0.96  | C(284993..286207)   | LDBPK_030710 | hypothetical protein                              | conserved | XP_003858036.1 |
| 1493124 | 1493198 | 259 | 1 | 72 | 75 | 0.96  | 1492688..1493563    | LDBPK_324000 | hypothetical protein                              | unknown   | XP_003863811.1 |
| 887542  | 887616  | 256 | 1 | 72 | 75 | 0.96  | C(885595..891426)   | LDBPK_292100 | hypothetical protein                              | conserved | XP_003862628.1 |
| 158357  | 158431  | 231 | 1 | 72 | 75 | 0.96  | C(147591..159950)   | LDBPK_040410 | hypothetical protein                              | conserved | XP_003858104.1 |
| 1664079 | 1664153 | 261 | 1 | 75 | 75 | 1     | 1664014..1664160    | LDBPK_344150 | hypothetical protein                              | conserved | XP_003864574.1 |
| 1456356 | 1456418 | 263 | 1 | 63 | 63 | 1     | 1456117..1456377    | LDBPK_363940 | 40S ribosomalS 27-1                               | putative  | XP_003865508.1 |
| 692288  | 692362  | 263 | 1 | 75 | 75 | 1     | C(679469..692572)   | LDBPK_361800 | hypothetical protein                              | conserved | XP_003865295.1 |
| 186830  | 186895  | 252 | 1 | 66 | 66 | 1     | C(186420..187313)   | LDBPK_250550 | hypothetical protein                              | conserved | XP_003861385.1 |
| 940102  | 940176  | 256 | 1 | 72 | 75 | 0.96  | C(936801..941609)   | LDBPK_292210 | hypothetical protein                              | conserved | XP_003862639.1 |
| 401489  | 401563  | 234 | 1 | 72 | 75 | 0.96  | 399386..401572      | LDBPK_070970 | hypothetical protein                              | conserved | XP_003858533.1 |
| 339534  | 339604  | 230 | 1 | 71 | 71 | 1     | C(337892..340801)   | LDBPK_013360 | uncharacterized protein                           |           | XP_003858049.1 |
| 682825  | 682899  | 255 | 1 | 72 | 75 | 0.96  | C(682700..684466)   | LDBPK_281860 | hypothetical protein                              | conserved | XP_003862285.1 |
| 487149  | 487223  | 234 | 1 | 72 | 75 | 0.96  | 481591..489309      | LDBPK_071070 | hypothetical protein                              | conserved | XP_003858543.1 |
| 440749  | 440823  | 244 | 1 | 72 | 75 | 0.96  | 438971..443749      | LDBPK_171060 | hypothetical protein                              | conserved | XP_003859960.1 |
| 211403  | 211477  | 242 | 1 | 72 | 75 | 0.96  | 209289..214544      | LDBPK_150570 | hypothetical protein                              | unknown   | XP_003859582.1 |
| 268424  | 268498  | 246 | 1 | 72 | 75 | 0.96  | 268110..270443      | LDBPK_190600 | hypothetical protein                              | unknown   | XP_003860238.1 |
| 1291806 | 1291880 | 263 | 1 | 72 | 75 | 0.96  | C(1291880..1294723) | LDBPK_363350 | DNA topoisomerase III                             | putative  | XP_003865450.1 |
| 533670  | 533732  | 259 | 1 | 63 | 63 | 1     | 533220..536534      | LDBPK_321420 | RNA guanylyltransferase                           | putative  | XP_003863558.1 |
| 308957  | 309017  | 229 | 1 | 61 | 61 | 1     | 308978..309556      | LDBPK_020650 | hypothetical protein                              | conserved | XP_003857960.1 |
| 147359  | 147433  | 241 | 1 | 72 | 75 | 0.96  | 146129..148582      | LDBPK_140430 | hypothetical protein                              | conserved | XP_003859415.1 |
| 280616  | 280690  | 252 | 1 | 72 | 75 | 0.96  | 280399..281319      | LDBPK_250810 | hypothetical protein                              | unknown   | XP_003861411.1 |
| 934506  | 934580  | 253 | 1 | 72 | 75 | 0.96  | 926370..941693      | LDBPK_262400 | hypothetical protein                              | conserved | XP_003861825.1 |
| 124863  | 124937  | 237 | 1 | 72 | 75 | 0.96  | 122945..125242      | LDBPK_100320 | hypothetical protein                              | conserved | XP_003858871.1 |
| 886959  | 887033  | 261 | 1 | 72 | 75 | 0.96  | C(885143..890974)   | LDBPK_342010 | hypothetical protein                              | conserved | XP_003864361.1 |
| 460543  | 460617  | 244 | 1 | 72 | 75 | 0.96  | 458563..479592      | LDBPK_171090 | hypothetical protein                              | conserved | XP_003859963.1 |
| 473883  | 473957  | 239 | 1 | 72 | 75 | 0.96  | 470751..474983      | LDBPK_120065 | uncharacterized protein                           |           | XP_003859191.1 |
| 151544  | 151618  | 229 | 1 | 72 | 75 | 0.96  | C(147597..152216)   | LDBPK_020300 | glycosyl transferase,                             | putative  | XP_003857926.1 |
| 227167  | 227241  | 235 | 1 | 72 | 75 | 0.96  | 226751..227788      | LDBPK_080570 | translation initiation factor-like                |           | XP_003858622.1 |
| 302757  | 302831  | 263 | 1 | 72 | 75 | 0.96  | 299919..305729      | LDBPK_070760 | hypothetical protein                              | conserved | XP_024329263.1 |
| 536222  | 536296  | 242 | 1 | 72 | 75 | 0.96  | C(534562..537066)   | LDBPK_151330 | MGT1 magnesium transporter                        |           | XP_003859656.1 |
| 467129  | 467203  | 257 | 1 | 72 | 75 | 0.96  | 466158..468299      | LDBPK_301410 | GTPase activating                                 | putative  | XP_003862854.1 |
| 939991  | 940065  | 256 | 1 | 72 | 75 | 0.96  | C(936801..941609)   | LDBPK_292210 | hypothetical protein                              | conserved | XP_003862639.1 |
| 151255  | 151327  | 239 | 1 | 73 | 73 | 1     | 150681..152351      | LDBPK_120300 | hypothetical protein                              | conserved | XP_003859147.1 |
| 778765  | 778839  | 254 | 1 | 72 | 75 | 0.96  | C(777632..778924)   | LDBPK_271880 | hypothetical protein                              | conserved | XP_003862039.1 |
| 251689  | 251763  | 262 | 1 | 72 | 75 | 0.96  | 251096..254491      | LDBPK_350560 | phosphatidylinositol-4-phosphate<br>5-kinase-like |           | XP_003864644.1 |
| 703840  | 703914  | 256 | 1 | 72 | 75 | 0.96  | C(702923..704941)   | LDBPK_291600 | hypothetical protein                              | conserved | XP_003862579.1 |

|         |         |     |   |    |    |       |                     |              |                                     |           |                |
|---------|---------|-----|---|----|----|-------|---------------------|--------------|-------------------------------------|-----------|----------------|
| 471185  | 471259  | 244 | 1 | 72 | 75 | 0.96  | 458563..479592      | LDBPK_171090 | hypothetical protein                | conserved | XP_003859963.1 |
| 395888  | 395962  | 259 | 1 | 72 | 75 | 0.96  | 395690..396919      | LDBPK_321040 | hypothetical protein                | conserved | XP_003863520.1 |
| 366716  | 366790  | 241 | 1 | 75 | 75 | 1     | C(366044..369307)   | LDBPK_140940 | hypothetical protein                | conserved | XP_003859461.1 |
| 289708  | 289782  | 246 | 1 | 72 | 75 | 0.96  | 287482..293280      | LDBPK_190650 | hypothetical protein                | conserved | XP_003860243.1 |
| 122258  | 122318  | 244 | 1 | 61 | 61 | 1     | C(121144..123501)   | LDBPK_170310 | hypothetical protein                | conserved | XP_003859885.1 |
| 279785  | 279859  | 237 | 1 | 72 | 75 | 0.96  | C(277712..280978)   | LDBPK_100590 | hypothetical protein                | unknown   | XP_003858895.1 |
| 231039  | 231113  | 252 | 1 | 72 | 75 | 0.96  | C(228767..233809)   | LDBPK_250690 | myosin heavy chain kinase c-like    |           | XP_003861399.1 |
| 313180  | 313251  | 232 | 1 | 72 | 72 | 1     | 311613..313616      | LDBPK_050850 | hypothetical protein                | conserved | XP_003858272.1 |
| 170521  | 170595  | 232 | 1 | 72 | 75 | 0.96  | 169396..175689      | LDBPK_050530 | kinetoplast-associated protein like |           | XP_003858240.1 |
| 267648  | 267712  | 242 | 1 | 65 | 65 | 1     | 265998..268094      | LDBPK_150680 | hypothetical protein                | unknown   | XP_003859593.1 |
| 534778  | 534852  | 257 | 1 | 72 | 75 | 0.96  | 533581..536754      | LDBPK_301540 | hypothetical protein                | conserved | XP_003862867.1 |
| 339626  | 339700  | 232 | 1 | 72 | 75 | 0.96  | 339118..342384      | LDBPK_050920 | paraflagellar rod                   | putative  | XP_003858279.1 |
| 738240  | 738314  | 258 | 1 | 72 | 75 | 0.96  | C(735944..738772)   | LDBPK_311550 | hypothetical protein                | conserved | XP_003863246.1 |
| 467887  | 467961  | 241 | 1 | 72 | 75 | 0.96  | 467861..469057      | LDBPK_141150 | hypothetical protein                | conserved | XP_003859482.1 |
| 1163338 | 1163412 | 258 | 1 | 72 | 75 | 0.96  | C(1162333..1163382) | LDBPK_312400 | 3,2-trans-enoyl-CoA isomerase       |           | XP_003863328.1 |
| 216852  | 216926  | 236 | 1 | 72 | 75 | 0.96  | 213108..217625      | LDBPK_090550 | hypothetical protein                | conserved | XP_003858735.1 |
| 123089  | 123163  | 228 | 1 | 72 | 75 | 0.96  | 119408..123727      | LDBPK_010480 | hypothetical                        | conserved | XP_003857861.1 |
| 664004  | 664078  | 245 | 1 | 72 | 75 | 0.96  | 663947..664093      | LDBPK_181490 | P-type H <sup>+</sup> -ATPase,      | putative  | XP_003860163.1 |
| 152401  | 152475  | 261 | 1 | 72 | 75 | 0.96  | 152165..152527      | LDBPK_340460 | ribosomal protein S25               |           | XP_003864211.1 |
| 372921  | 372995  | 258 | 1 | 72 | 75 | 0.96  | C(372754..374013)   | LDBPK_310990 | hypothetical protein                | unknown   | XP_003863191.1 |
| 103073  | 103147  | 236 | 1 | 72 | 75 | 0.96  | 101296..103848      | LDBPK_090290 | hypothetical protein                | conserved | XP_003858708.1 |
| 1285944 | 1286010 | 262 | 1 | 64 | 67 | 0.955 | C(1283936..1286689) | LDBPK_353150 | ATP-dependent RNA helicase          | putative  | XP_003864894.1 |
| 920399  | 920474  | 255 | 1 | 76 | 76 | 1     | 919135..921849      | LDBPK_282490 | hypothetical protein                | conserved | XP_003862347.1 |
| 984756  | 984830  | 254 | 1 | 75 | 75 | 1     | 983617..984900      | LDBPK_020730 | hypothetical protein                | conserved | XP_003862098.1 |
| 108379  | 108444  | 251 | 1 | 66 | 66 | 1     | 107900..108451      | LDBPK_240350 | CMP-sialic acid transporter         | putative  | XP_003861125.1 |
| 94925   | 94998   | 239 | 1 | 74 | 74 | 1     | 91189..99972        | LDBPK_120260 | hypothetical protein                | conserved | XP_003859138.1 |
| 97601   | 97663   | 236 | 1 | 63 | 63 | 1     | 95989..98748        | LDBPK_090280 | hypothetical protein                | conserved | XP_003858707.1 |
| 1092351 | 1092426 | 259 | 1 | 76 | 76 | 1     | C(1090269..1092914) | LDBPK_322900 | hypothetical protein                | conserved | XP_003863703.1 |
| 71243   | 71306   | 236 | 1 | 61 | 64 | 0.953 | 71060..71464        | LDBPK_090180 | hypothetical protein                | putative  | XP_003858697.1 |

Supplementary Table S3: TriTryp.DB names of the putative adenylate cyclase proteins (Figures 4 and 5).

| Refseq ID    | TriTrypDB ID        |
|--------------|---------------------|
| XP_003858708 | LdBPK_090290.1      |
| XP_001463486 | LINF_090008900      |
| XP_001681205 | LmjF.09.0330        |
| XP_003872713 | LmxM.09.0330        |
| GET86282     | LtaP19.0800         |
| XP_001562648 | LbrM.09.0320        |
| XP_010704270 | LPMP_090320         |
| XP_015655949 | LpyrH10_16_0770     |
| XP_015655950 | LpyrH10_16_0780     |
| KPI86299     | Lsey_0138_0140      |
| XP_001463485 | LINF_090008800      |
| XP_003858707 | LdBPK_090280.1      |
| VDZ42437     | LdBPK.09.2.000280.1 |
| XP_003872712 | LmxM.09.0320        |
| XP_001681204 | LmjF.09.0320        |
| GET86281     | LtaP30.0010         |
| XP_001562647 | LbrM.09.0310        |
| XP_010704269 | LPMP_090310         |
| XP_001681206 | LmjF.09.0340        |
| XP_003872714 | LmxM.09.0340        |
| AYU76476     | LdCL_090008700      |
| XP_001463487 | LINF_090009000      |
| XP_003858709 | LdBPK_090300.1      |
| KPI86300     | Lsey_0138_0150      |
| XP_001562649 | LbrM.09.0330        |
| GET86283     | LtaP09.0330         |
| XP_010704271 | LPMP_090330         |
| XP_015655951 | LpyrH10_16_0790     |

Supplementary Figure S1. A BLASTP output for the XP\_003861613.1 protein sequence. The blue arrow at the end of the protein-coding region shows the merged B-type read (Supplementary Table S2).

|                |     |                                                                                    |     |
|----------------|-----|------------------------------------------------------------------------------------|-----|
| XP_003861613.1 | 1   | MDTSSSARYADQLSVVHLSHIHEGVQLQREHLRSALLDDSPQTEMIVYTRLYQLYRDFYLPFFVAKLHIPSQ LPPGAGSA  | 80  |
| AYU79624.1     | 1   | MDTSSSARYADQLSVVHLSHIHEGVQLQREHLRSALLDDSPQTEMIVYTRLYQLYRDFYLPFFVAKLHIPSQ LPPGAGSA  | 80  |
| VDZ45478.1     | 1   | MDTSSSARYADQLSVVHLSHIHEGVQLQREHLRSALLDDSPQTEMIVYTRLYQLYRDFYLPFFVAKLHIPSQ LPPGAGSA  | 80  |
| TPP41076.1     | 1   | MDTSSSARYADQLSVVHLSHIHEGVQLQREHLRSALLDDSPQTEMIVYTRLYQLYRDFYLPFFVAKLHIPSQ LPPGAGSA  | 80  |
| TPP51924.1     | 1   | MDTSSSARYADQLSVVHLSHIHEGVQLQREHLRSALLDDSPQTEMIVYTRLYQLYRDFYLPFFVAKLHIPSQ LPPGAGSA  | 80  |
|                |     |                                                                                    |     |
| XP_003861613.1 | 81  | PSPDARPAASAEARFVMTTYYTQDVLAAACVYLLDPASLPATYIVTSTPPACEEAQNEANASSVYISAEQRRFCGRVFLYMC | 160 |
| AYU79624.1     | 81  | PSPDARPAASAEARFVMTTYYTQDVLAAACVYLLDPASLPATYIVTSTPPACEEAQNEANASSVYISAEQRRFCGRVFLYMC | 160 |
| VDZ45478.1     | 81  | PSLDARPAASAEARFVMTTYYTQDVLAAACVYLLDPASLPATYIVTSTPPACEEAQNEANASSVYISAEQRRFCGRVFLYMC | 160 |
| TPP41076.1     | 81  | PSPDARPAASAEARFVMTTYYTQDVLAAACVYLLDPASLPATYIVTSTPPACEEAQNEANASSVYISAEQRRFCGRVFLYMC | 160 |
| TPP51924.1     | 81  | PSLDARPAASAEARFVMTTYYTQDVLAAACVYLLDPASLPATYIVTSTPPACEEAQNEANASSVYISAEQRRFCGRVFLYMC | 160 |
|                |     |                                                                                    |     |
| XP_003861613.1 | 161 | WASAALPLHIVLQALYPLLDPGVSGAPRATTTTLSTTADPPRERQGPSLTENHIAADLFSQERFACQKRLRLDTLNLGLVL  | 240 |
| AYU79624.1     | 161 | WASAALPLHIVLQALYPLLDPGVSGAPRATTTTLSTTADPPRERQGPSLTENHIAADLFSQERFACQKRLRLDTLNLGLVL  | 240 |
| VDZ45478.1     | 161 | WASAALPLHIVLQALYPLLDPGVSGAPRATTTTLSTTADPPRERQGPSLTENHIAADLFSQERFACQKRLRLDTLNLGLVL  | 240 |
| TPP41076.1     | 161 | WASAALPLHIVLQALYPLLDPGVSGAPRATTTTLSTTADPPRERQGPSLTENHIAADLFSQERFACQKRLRLDTLNLGLVL  | 240 |
| TPP51924.1     | 161 | WASAALPLHIVLQALYPLLDPGVSGAPRATTTTLSTTADPPRERQGPSLTENHIAADLFSQERFACQKRLRLDTLNLGLVL  | 240 |
|                |     |                                                                                    |     |
| XP_003861613.1 | 241 | TRANGVRALLRVLLNDRVTTEMTGEAAQLLVQLLTSPVFTLWQQQQPQQLGESLGYRSPFSAAGEEECAAEVVVTHVTT    | 320 |
| AYU79624.1     | 241 | TRANGVRALLRVLLNDRVTTEMTGEAAQLLVQLLTSPVFTLWQQQQPQQLGESLGYRSPFSAAGEEECAAEVVVTHVTT    | 320 |
| VDZ45478.1     | 241 | TRANGVRALLRVLLNDRVTTEMTGEAAQLLVQLLTSPVFTLWQQQQPQQLGESLGYRSPFSAAGEEECAAEVVVTHVTT    | 320 |
| TPP41076.1     | 241 | TRANGVRALLRVLLNDRVTTEMTGEAAQLLVQLLTSPVFT-----PFSAGEEECAAEVVVTHVTT                  | 302 |
| TPP51924.1     | 241 | TRANGVRALLRVLLNDRVTTEMTGEAAQLLVQLLTSPVFT-----PFSAGEEECAAEVVVTHVTT                  | 302 |
|                |     |                                                                                    |     |
| XP_003861613.1 | 321 | ALSVEDQVRLAPQLLALLEEHADATLAVSSASRTAARPRFLARLDAARLRLPAETLEQRLHLALTMLLNALVRLPPRDK    | 400 |
| AYU79624.1     | 321 | ALSVEDQVRLAPQLLALLEEHADATLAVSSASRTAARPRFLARLDAARLRLPAETLEQRLHLALTMLLNALVRLPPRDK    | 400 |
| VDZ45478.1     | 321 | ALSVEDQVRLAPQLLALLEEHADATLAVSSASRTAARPRFLARLDAARLRLPAETLEQRLHLALTMLLNALVRLPPRDK    | 400 |
| TPP41076.1     | 303 | ALSVEDQVRLAPQLLALLEEHADATLAVSSASRTAARPRFLARLDAARLRLPAETLEQRLHLALTMLLNALVRLPPRDK    | 382 |
| TPP51924.1     | 303 | ALSVEDQVRLAPQLLALLEEHADATLAVSSASRTAARPRFLARLDAARLRLPAETLEQRLHLALTMLLNALVRLPPRDK    | 382 |
|                |     |                                                                                    |     |
| XP_003861613.1 | 401 | HDFARSYRQLFYTNKFVLSPGFGCLSLRSDTDVVEDDAIAALLRLGSLIKGVSSGAGSGVMHVLPATAAGLLNICAVLA    | 480 |
| AYU79624.1     | 401 | HDFARSYRQLFYTNKFVLSPGFGCLSLRSDTDVVEDDAIAALLRLGSLIKGVSSGAGSGVMHVLPATAAGLLNICAVLA    | 480 |
| VDZ45478.1     | 401 | HDFARSYRQLFYTNKFVLSPGFGCLSLRSDTDVVEDDAIAALLRLGSLIKGVSSGAGSGVMHVLPATAAGLLNICAVLA    | 480 |
| TPP41076.1     | 383 | HDFARSYRQLFYTNKFVLSPGFGCLSLRSDTDVVEDDAIAALLRLGSLIKGVSSGAGSGVMHVLPATAAGLLNICAVLA    | 462 |
| TPP51924.1     | 383 | HDFARSYRQLFYTNKFVLSPGFGCLSLRSDTDVVEDDAIAALLRLGSLIKGVSSGAGSGVMHVLPATAAGLLNICAVLA    | 462 |
|                |     |                                                                                    |     |
| XP_003861613.1 | 481 | RSCDGDGNAAQFVSPSLPATLRLSLFSELLSSPSLYDLCCARALVNACGEARAHCYLPGNAAQPRLYTRDVCGRERLVTGL  | 560 |
| AYU79624.1     | 481 | RSCDGDGNAAQFVSPSLPATLRLSLFSELLSSPSLYDLCCARALVNACGEARAHCYLPGNAAQPRLYTRDVCGRERLVTGL  | 560 |
| VDZ45478.1     | 481 | RSCDGDGNAAQFVSPSLPATLRLSLFSELLSSPSLYDLCCARALVNACGEARAHCYLPGNAAQPRLYTRDVCGRERLVTGL  | 560 |
| TPP41076.1     | 463 | RSCDGDGNAAQFVSPSLPATLRLSLFSELLSSPSLYDLCCARALVNACGEARAHCYLPGNAAQPRLYTRDVCGRERLVTGL  | 542 |
| TPP51924.1     | 463 | RSCDGDGNAAQFVSPSLPATLRLSLFSELLSSPSLYDLCCARALVNACGEARAHCYLPGNAAQPRLYTRDVCGRERLVTGL  | 542 |
|                |     |                                                                                    |     |
| XP_003861613.1 | 561 | QWLLLDVAATTDFVHTCVDVMVEACHLELFAAGVENLTVSPAPRLTETKLLVSAPTENDTSPLIALLERLSLEATPEA     | 640 |
| AYU79624.1     | 561 | QWLLLDVAATTDFVHTCVDVMVEACHLELFAAGVENLTVSPAPRLTETKLLVSAPTENDTSPLIALLERLSLEATPEA     | 640 |
| VDZ45478.1     | 561 | QWLLLDVAATTDFVHTCVDVMVEACHLELFAAGVENLTVSPAPRLTETKLLVSAPTENDTSPLIALLERLSLEATPEA     | 640 |
| TPP41076.1     | 543 | QWLLLDVAATTDFVHTCVDVMVEACHLELFAAGVENLTVSPAPRLTETKLLVSAPTENDTSPLIALLERLSLEATPEA     | 622 |
| TPP51924.1     | 543 | QWLLLDVAATTDFVHTCVDVMVEACHLELFAAGVENLTVSPAPRLTETKLLVSAPTENDTSPLIALLERLSLEATPEA     | 622 |
|                |     |                                                                                    |     |
| XP_003861613.1 | 641 | LFGSRGASLASTLELLGRMLALSGALYRWALGLVEHLLAASSVEVHLGGGDTRAERWQNLRLQRCRSLKILASLTQLNTP   | 720 |
| AYU79624.1     | 641 | LFGSRGASLASTLELLGRMLALSGALYRWALGLVEHLLAASSVEVHLGGGDTRAERWQNLRLQRCRSLKILASLTQLNTP   | 720 |
| VDZ45478.1     | 641 | LFGSRGASLASTLELLGRMLALSGALYRWALGLVEHLLAASSVEVHLGGGDTRAERWQNLRLQRCRSLKILASLTQLNTP   | 720 |
| TPP41076.1     | 623 | LFGSRGASLASTLELLGRMLALSGALYRWALGLVEHLLAASSVEVHLGGGDTRAERWQNLRLQRCRSLKILASLTQLNTP   | 702 |
| TPP51924.1     | 623 | LFGSRGASLASTLELLGRMLALSGALYRWALGLVEHLLAASSVEVHLGGGDTRAERWQNLRLQRCRSLKILASLTQLNTP   | 702 |
|                |     |                                                                                    |     |
| XP_003861613.1 | 721 | TPRGGAWHSVSTDGAQLSLTARVQQALGAFLERIEEHLASCEAVEQLSYDKQHRQGEAITAVRAEWEQLAEKLRALDS     | 800 |
| AYU79624.1     | 721 | TPRGGAWHSVSTDGAQLSLTARVQQALGAFLERIEEHLASCEAVEQLSYDKQHRQGEAITAVRAEWEQLAEKLRALDS     | 800 |
| VDZ45478.1     | 721 | TPRGGAWHSVSTDGAQLSLTARVQQALGAFLERIEEHLASCEAVEQLSYDKQHRQGEAITAVRAEWEQLAEKLRALDS     | 800 |
| TPP41076.1     | 703 | TPRGGAWHSVSTDGAQLSLTARVQQALGAFLERIEEHLASCEAVEQLSYDKQHRQGEAITAVRAEWEQLAEKLRALDS     | 782 |
| TPP51924.1     | 703 | TPRGGAWHSVSTDGAQLSLTARVQQALGAFLERIEEHLASCEAVEQLSYDKQHRQGEAITAVRAEWEQLAEKLRALDS     | 782 |

|                |      |                                                |                                    |                                    |
|----------------|------|------------------------------------------------|------------------------------------|------------------------------------|
| XP_003861613.1 | 801  | RAAIDVAVTLAKLAHGVDDVVFVETDPQPLYDTTQRLLQLLVRVLC | EADDVGAAVRAVHCVAWLGMYRFDSKDSTYMADV | 880                                |
| AYU79624.1     | 801  | RAAIDVAVTLAKLAHGVDDVVFVETDPQPLYDTTQRLLQLLVRVLC | EADDVGAAVRAVHCVAWLGMYRFDSKDSTYMADV | 880                                |
| VDZ45478.1     | 801  | RAAIDVAVTLAKLAHGVDDVVFVETDPQPLYDTTQRLLQLLVRVLC | EADDVGAAVRAVHCVAWLGMYRFDSKDSTYMADV | 880                                |
| TPP41076.1     | 783  | RAAIDVAVTLAKLAHGVDDVVFVETDPQPLYDTTQRLLQLLVRVLC | EADDVGAAVRAVHCVAWLGMYRFDSKDSTYMADV | 862                                |
| TPP51924.1     | 783  | RAAIDVAVTLAKLAHGVDDVVFVETDPQPLYDTTQRLLQLLVRVLC | EADDVGAAVRAVHCVAWLGMYRFDSKDSTYMADV | 862                                |
|                |      |                                                |                                    |                                    |
| XP_003861613.1 | 881  | MWSVLAEDHLPWLSASA                              | EYTVATQAAAA                        | SRICRLRVRVLDVLLSWTDYDEDDLT         |
| AYU79624.1     | 881  | MWSVLAEDHLPWLSASA                              | EYTVATQAAAA                        | SRICRLRVRVLDVLLSWTDYDEDDLT         |
| VDZ45478.1     | 881  | MWSVLAEDHLPWLSASA                              | EYTVATQAAAA                        | SRICRLRVRVLDVLLSWTDYDEDDLT         |
| TPP41076.1     | 863  | MWSVLAEDHLPWLSASA                              | EYTVATQAAAA                        | SRICRLRVRVLDVLLSWTDYDEDDLT         |
| TPP51924.1     | 863  | MWSVLAEDHLPWLSASA                              | EYTVATQAAAA                        | SRICRLRVRVLDVLLSWTDYDEDDLT         |
|                |      |                                                |                                    |                                    |
| XP_003861613.1 | 961  | STEDAFVQVAALHFIGTYALAMQPRVPVSAICDL             | CRDVFRLSRHEMAKAA                   | CAALGKIVASLCHPSDATLLVLSELDINN      |
| AYU79624.1     | 961  | STEDAFVQVAALHFIGTYALAMQPRVPVSAICDL             | CRDVFRLSRHEMAKAA                   | CAALGKIVASLCHPSDATLLVLSELDINN      |
| VDZ45478.1     | 961  | STEDAFVQVAALHFIGTYALAMQPRVPVSAICDL             | CRDVFRLSRHEMAKAA                   | CAALGKIVASLCHPSDATLLVLSELDINN      |
| TPP41076.1     | 943  | STEDAFVQVAALHFIGTYALAMQPRVPVSAICDL             | CRDVFRLSRHEMAKAA                   | CAALGKIVASLCHPSDATLLVLSELDINN      |
| TPP51924.1     | 943  | STEDAFVQVAALHFIGTYALAMQPRVPVSAICDL             | CRDVFRLSRHEMAKAA                   | CAALGKIVASLCHPSDATLLVLSELDINN      |
|                |      |                                                |                                    |                                    |
| XP_003861613.1 | 1041 | LQTLASAMSSYRGRPHVEGNTSVTAPAMSA                 | AAETDLHDEVIRLHG                    | REMLAILRRTSLGFGGARAGAAPAAADLRVSSLR |
| AYU79624.1     | 1041 | LQTLASAMSSYRGRPHVEGNTSVTAPAMSA                 | AAETDLHDEVIRLHG                    | REMLAILRRTSLGFGGARAGAAPAAADLRVSSLR |
| VDZ45478.1     | 1041 | LQTLASAMSSYRGRPHVEGNTSVTAPAMSA                 | AAETDLHDEVIRLHG                    | REMLAILRRTSLGFGGARAGAAPAAADLRVSSLR |
| TPP41076.1     | 1023 | LQTLASAMSSYRGRPHVEGNTSVTAPAMSA                 | AAETDLHDEVIRLHG                    | REMLAILRRTSLGFGGARAGAAPAAADLRVSSLR |
| TPP51924.1     | 1023 | LQTLASAMSSYRGRPHVEGNTSVTAPAMSA                 | AAETDLHDEVIRLHG                    | REMLAILRRTSLGFGGARAGAAPAAADLRVSSLR |
|                |      |                                                |                                    |                                    |
| XP_003861613.1 | 1121 | VSEL                                           | RRA                                | 1127                               |
| AYU79624.1     | 1121 | VSEL                                           | RRA                                | 1127                               |
| VDZ45478.1     | 1121 | VSEL                                           | RRA                                | 1127                               |
| TPP41076.1     | 1103 | VSEL                                           | RRA                                | 1109                               |
| TPP51924.1     | 1103 | VSEL                                           | RRA                                | 1109                               |

3' flanking region



Supplementary Figure S2. Schematic representation of an insertion in the 3' flanking region near the end of the gene encoding the XP\_003861613.1 protein. The gene is located in the complementary strand.





**Supplementary Figure S3. A BLASTP output showing 2 conserved regions in the XP\_003858708.1 protein sequence.**

BLASTP 2.2.6 [Apr-09-2003]

Query= "XP\_003858708.1"  
(850 letters)

Database: ldon.fa  
8014 sequences; 4,920,192 total letters

| Sequences producing significant alignments:                         | Score<br>(bits) | E<br>Value |
|---------------------------------------------------------------------|-----------------|------------|
| XP_003858707.1 hypothetical protein, conserved [Leishmania donov... | 675             | 0.0        |
| XP_003858709.1 hypothetical protein, conserved [Leishmania donov... | 342             | 3e-094     |

>XP\_003858707.1 hypothetical protein, conserved [Leishmania donovani]  
Length = 919

Score = 675 bits (1741), Expect = 0.0  
Identities = 412/814 (50%), Positives = 496/814 (60%), Gaps = 59/814 (7%)

Query: 26 YIGIVAFVACLLLIFVGIFSPILVLRNMDKSYEAEYIEYTLANKAVAPYRVVMVEAFA 85  
          YI    + C L IF+GI P++V+R    + A +R EY    +    + R VM+E FA  
Sbjct: 99 YIITACVLGCALTIFIGILVPMPLVIRRSANIHNAVVRakeYDAVASAWASVLRDVMIEGFA 158

Query: 86 ISQALEGYVMSRMLVMPNLSAP-----PLERIQQQNFTNFDDIGATLRNTTMIAMTA 138  
          ++AL GY +S    P L P    P ++I    F    +    +    +A+ A  
Sbjct: 159 ATRALAGYSIS---TFPPLQTPTNASDSIPSDKITAY-LKRFPRFASLIASKKPAVAIQ 214

Query: 139 LQPGGVYAFFSPRNATKYGRDTLDPNDNAQNFKPTPFETILSGRAVYVGPFRSTSDVLRG 198  
          + PGGV A   P +   GRD + P+D   +KP+ ET   SGR   VGP R+T   L+  
Sbjct: 215 ICPGGVIAMTHPHDPDTVGRDLMSPSDPTNRYKPKSTRETAQSGRYAIVGPRTTIASLKQ 274

Query: 199 HWGLAIRRPIYNRTSYESADIR-TFWGFAFTLVNISGLIDKNPFAFTSLSKKRDVDYLLS 257  
          W +   R P+Y TS    + TFWGF   +VN++G +D    L+K   ++DY+L  
Sbjct: 275 IWVIFTRAPLYRNTSKGVIPSQETFWGFLVNVNVTGALDV--MDLDKLAKDHNLDYVLY 332

Query: 258 VHNETSGVITVLATSLKQPTATQLADFVRLGTSVGIT----PNHPFLLTIRGRDYGSNLS 313  
          + SG   V+A+SL P+    D+    +T    P+    + +R R+   +L+  
Sbjct: 333 DTSTESGDTHVIASSL--PSGAMQPDYEEFVAESTVTDVLAPHSSLYIAVRSRETYVSLT 390

Query: 314 PANIIIVVSTVLSGLLAIFAAVIAAVLWCTATYDAAAHAPKMAPFAMLTIGPCRGEELWD 373   Conserved  
          P NII++V   L G L +   IAAVLWCTATYDAAAHAPKMAPFAMLTIGPCRGEELWD  
Sbjct: 391 PTNIIIVVWTLFGSLLLLGISIAAVLWCTATYDAAAHAPKMAPFAMLTIGPCRGEELWD 450

Query: 374 LATDQMAEVTEKLDQVLVRQMERHRAYQIQVHPLTTSYVTRSVAAAVQMAFSTIEELQR 433  
          LATDQMAEVTEKLDQVLVRQMERHRAYQIQVHPLTTSYVTRSVAAAVQMAFSTIEELQR  
Sbjct: 451 LATDQMAEVTEKLDQVLVRQMERHRAYQIQVHPLTTSYVTRSVAAAVQMAFSTIEELQR 510

Query: 434 HPIDGPLRAVLGDEVRLLLCYAVHWCTDAAVRVESLEGTYRYEGCDVVFGRMWAFAPSA 493  
          HPIDGPLRAVLGDEVRLLLCYAVHWCTDAAVRVESLEGTYRYEGCDVVFGRMWAFAPSA  
Sbjct: 511 HPIDGPLRAVLGDEVRLLLCYAVHWCTDAAVRVESLEGTYRYEGCDVVFGRMWAFAPSA 570

Query: 494 VVTASEAVVQTLPCFGLRSIDTRPRCVVNVVRSRTLCGATGGKEL-----GGKSA 543   region #1  
          VVTASEAVVQTLPCFGL + TR   V+V+R+ T   T G E           GG SA  
Sbjct: 571 VVTASEAVVQTLPCFGLSGVVTRAYQTVDVMRT-TRASYTDGSEAGSSDASSTIGGGGSA 629

Query: 544 TIY-VPHSPPTTVQATAGVRRGRAVSSAAPLESSSDTEDTQSLPPQQLFTLLDTR--RP 600  
T+Y + H+ + A A A + P + P L+ L TR P  
Sbjct: 630 TLYL LVHAAKQDLVAGAEATAAAAAAGAMVPQLMVGNA-----PAPSLYCGLITRGNSP 683

Query: 601 ALMAAEAAATHDADSVSASCPSDSAAIPAMDLPAGERAVLPVSPSSAADGSSANNAEMA 660  
+L A A+ D VS+ S +S+A A A S ++ ++A+  
Sbjct: 684 SLEAGRASVPSLQD-VSARSPEIESSASSAWSSAA-----STKGSSRATNASQRRGR 734

Query: 661 TAAHTSARSDAPTENEGNELLSASSPSVAPPLSHASSSFDIGVSNGATTAVQLSSSLAFQG 720  
AA SAR+ P L ++ + A N A+T Q + +  
Sbjct: 735 AAAERSARTRNPL--SRGYLDTEQQALVRKQALAK-----HNAASTPEQHRLVLIEA 784

Query: 721 DAVTRALLQPLIPRALDVALRVAFDYQSITLDVRYAEVRVLVYFYSSYKILFRPLAAPE 780 Conserved  
DAVTRALLQPLIPRALDVALRVAFDYQSITLDVRYAEVRVLVYFYSSYKILFRPLAAPE  
Sbjct: 785 DAVTRALLQPLIPRALDVALRVAFDYQSITLDVRYAEVRVLVYFYSSYKILFRPLAAPE 844

Query: 781 RHNIFRRLVTAFGVPQQGILEHLAARCVIRHVQQ 814 region#2  
RHNIFRRLVTAFGVPQQGILEHLAAR ++ + Q  
Sbjct: 845 RHNIFRRLVTAFGVPQQGILEHLAARGAVQWLSQ 878

>XP\_003858709.1 hypothetical protein, conserved [Leishmania donovani]  
Length = 993

Score = 342 bits (877), Expect = 3e-094  
Identities = 200/456 (43%), Positives = 264/456 (57%), Gaps = 26/456 (5%)

Query: 76 YRVVMVEAFAISQALEGYVMSRMLVMPNLSAPPLERIQQNQFTNFDDIGATLRRNTTMIA 135  
+R ++ A + +EGY+M M +PNL+ P +R+ GQ F F + ++ I+  
Sbjct: 7 FRDAILGAISAVYGVGYIMGLMKSLPNLNETPAQRVAGQYFPKFGYAELVSSSSPHIS 66

Query: 136 MTALQPGGVYAFFSPRNATKYGR--DTLDPN-----DNAQNFKPTPFETILSGRAVYVGP 188  
+ A PGGV P K+ D L+ + D A ++ PF TI +G GP  
Sbjct: 67 LFATAPGGVVLQVYPSEDEKFMENWDLLNSSCENHTDPAAAYREDPFTTIKNGLLALTGP 126

Query: 189 FRSTSDVLRGH-----WGLAIRRPIYNRTSYESADIRTFWGFATLVNISGLIDK 238  
++S +RG W + +R+PIYN TS TFWGFA ++ GLI K  
Sbjct: 127 YKSPGLPIRGWDSSSGEAHNMWVDLRQPIYNATSTALITNSTFWGFAIVFFSVVDGLIRK 186

Query: 239 N--PFAFTSLSKKRDVDYLLSVHNETSGVITVLATSLKQPTATQLADFVR-----LGTSV 291  
P SL + Y S+ N + G +LA+S+ + F++ T  
Sbjct: 187 KGLPEKMNSLEMayII-YTASI-NGSDGCTVILASSMFKGETDCSKPFMKKFLDDATTRD 244

Query: 292 GITPNHPFLLTIRGRDYGSNLSPANIIIVVSTVLSGLLAIFAAVIAAVLWCTATYDAAAH 351  
+ + + + +P +V T + G+ +FA + ++ CT YD A H  
Sbjct: 245 VLKEKLSWKIALKSMKRVNRFTPRVRNAIVITSVIGVSLFLALFMYVIVRCTRVDGAKH 304

Query: 352 APKMAPFAMLTIGPCRGEELWDLATDQMAEVTEKLDQVLVRQMERHRAVYQIQVHPLTTS 411  
APKMAPFAMLTIGPCRGEELWDLA+DQM EVTE+L VL RQM R+ AYQIQVHPLTTS  
Sbjct: 305 APKMAPFAMLTIGPCRGEELWDLASDQMVEVTERLGHVLRQMVRVYHAYQIQVHPLTTS 364

Query: 412 YVTRSVAAAVQMAFSTIEELQRHPIDGPLRAVLGDEVRLLLCYAVHWCTDAAVRVESLEG 471  
YVTRSVAAAVQMAFSTIEEL PID PLR +LGDE LLLCYAVHWCTDAAVR+E++ G  
Sbjct: 365 YVTRSVAAAVQMAFSTIEELYSFPIDEPLRRLGDEGSLLL CYAVHWCTDAAVRMEAIGG 424

Query: 472 TYRYEGCDVVFGGRMWAFAPS VVTASEAVVQTLPC 507  
RYEG DVV+GGRMW FA P+VVT S+A + + C  
Sbjct: 425 GLRYEGPDVVYGGRMWVFAGPNVVTVSQAALPSTTC 460

Score = 135 bits (340), Expect = 5e-032  
Identities = 113/331 (34%), Positives = 152/331 (45%), Gaps = 55/331 (16%)

Query: 551 PPTTVQATAGVRRGRAVSSTAAPLESSSDTEDTQSLPPQQLFTLLDTRRPALMAAEAAAT 610  
PP + A A V G + SS++A S E + PP L L P + A T  
Sbjct: 648 PPRDL-AAANVVSGSSRSSSSAASVGSEKEETSPGEPPTPL--LQPVSPEVSVTAATGT 703

Query: 611 -----HDADSVSSASCPSDSAAIPAMDLPAGERA-----VLPVSPSSAAD 650  
H A +++ S +PA ++ V P+ D  
Sbjct: 704 VRPRRGQDNAHTAPGATASGSNSIGFRDSCSGIPATSSVRHHDLLLNTNPLVVVPPAVTVD 763

Query: 651 -----GSSANNAEMATAAHTSARSDAPTENEGNELLSASSPSVAPPLSHASSSFDI 701  
G SA+ ++ + S+ PT + N L ++ + A + S  
Sbjct: 764 ATAHGLCGGGGSASTTPISGESTGGRHSNFPTCGD-NPLAHGTTAAAAAKVDALSGGITG 822

Query: 702 GVSNGATTAV-----QLSSLAFQG-----DAVTRALLQPLIPRALDVALRVAFD 745  
SNG AV + A QG D + LL+P I D+ LR FD  
Sbjct: 823 LASNGGRGAVGGTPAACRPGNSEGNALQGSGPALDNFSDLLLRPAISTQSDLLLRVAFD 882

Query: 746 YQSITLDVRYAEVRVLVYYFYSSYKILFRPLAAPERHNIFRRLVTAFGVPQQGILEHLAA 805  
Q++ LD+ Y VRVLVYYFYSSYKILFRPLAAPE HNI+RRL+TAFGVPQQGILEHLAA  
Sbjct: 883 RQAVALDLSYDSVRVLVYYFYSSYKILFRPLAAPELHNIYRRLMTAFGVPQQGILEHLAA 942

Query: 806 RCVIRHVQ--QRLKSLQFAPQH--PHLRAA 831  
RC R +Q + ++L + QH H+R+A  
Sbjct: 943 RCATRFLQRHEETQTLLWDQQHRLQMHIRSA 973

Supplementary Figure S4. Multiple sequence alignment in the MEGA format. Refseq IDs are shown. The list of corresponding TriTryp.DB IDs is shown in the Supplementary Table S3.

#mega

TITLE: adenylateCyclase

#XP\_003858708\_Leishmania\_donovani

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PPLERIQQG--NFTNFDDIGATLRRNTMIAMTALQPGGVYAFFSPRNATKY--GRD
TLDPN-----DNAQNFKPTPFETILSGRAVYVGPFRSTSDVLR-----
-GHWGLAIRRPIYNRTSYESA-DIRTFWGFATLVNISGLIDKNPFAFTSLSKKRD--V
DYLLSVH--NETSGVITVLATSL---KQPTATQLADFVRLGTSVGIT-PNHPFLLTIR-
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FSTIEELQRHPIDGPLRAVLGDEVRLLLCYAVHWCTDAAVRVESLEGTYRYEGCDVVF
GGRMWAFAPSVVTASEAVVQTLPCFG-----LRSIDTR-----
-PRCVNVVRSRT-----
-----LCGATGG-----KELGGKS-----
--ATIIY-VPHS---PP-----TTVQATAGVRR-----GRAVSS
TAAPLESSTDT-----EDTQSLPPQQLFT-----LLD-TRRPALM
AAEAAA-----THDADSVSSASC---PSDSAAIPAMDLPAGER
A VL-----PVSPSSAADG
SSANNAEMATAAHTSARSDAPTENEGNELLSASSP---SVAPPLSHASSSFD-----
-----IGVSNG-ATTAVQLSSLAFAQGDAV-----TRALLQPLIPRA
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R-----
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#XP\_001463486\_Leishmania\_infantum\_JPCM5

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PPLERIQQG--NFTNFDDIGATLRRNTMIAMTALQPGGVYAFFSPRNATKY--GRD
TLDPN-----DNAQNFKPTPFETILSGRAVYVGPFRSTSDVLR-----
-GHWGLAIRRPIYNRTSYESA-DIRTFWGFATLVNISGLIDKNPFAFTSLSKKRD--V
DYLLSVH--NETSGVITVLATSL---KQPTATQLAEFVRLGTSVGIT-PNHPFLLTIR-
GRDYGSNLSPANIIIVVSTVLSGLLAIFAAVIAAVLWCTATYDAAAHAPKMAPFAMLTIG
PCRGEELWDLATDQMAEVTEKLDQVLVRQMERHRAVQIQVHPLTTSYVTRSVAAAVQMA
FSTIEELQRHPIDGPLRAVLGDEVRLLLCYAVHWCTDAAVRVESLEGTYRYEGCDVVF
GGRMWAFAPSVVTASEAVVQTLPCFG-----LGSIDTR-----
-PRCVNVVRSRT-----
-----LCGATGG-----KELGGKS-----
--ATIIY-VPHS---PP-----TTVQATAGVRR-----GRAVSS
TAAPLESSTDT-----EDTQSLPPQQLFT-----LLD-TRRPALM
AAEAAA-----PHDADSVSSASC---PSDSAAIPAMDLPAGER
A V-----LPVSPSSAAD
GSSANAEMATAAHTSARSDAPTENEGNELLSASSP---SVAPPLSHASSSFD-----
-----IGVSNG-ATTAVQLSSLAFAQGDAV-----TRALLQPLIPRA
LDVALRVAFDYQSITLDVRYAEVRVLVYFYSSYKILFRPLAAPERHNI
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#XP\_001681205\_\_Leishmania\_major\_strain\_Friedlin

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PPLERIEGQ--NFTNFDDISVTLRRNMTMIAMTALQPGGVYAFFSPCNATKY--GRD
TLDPK-----DNAQNFKPTPFETILGGRAVYVGPFRYTSGLVQ-----
-GHWGLAIRRPIYNRTSYKSA-DIHTFWGFALTLVNISGLIERNPFAFISLTTKKR--DV
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-PCCVNVVRSRT-----  
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--ATII-MPHS--LP-----TTAQATAGVQC-----GKAVSP  
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AAEAAA-----PRNVDSVSSASC---PSDSAEIPAMNLLAGECA  
VL-----PVLPSAADG  
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R-----  
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PPLERIRDQ--NFTNFDEIGITLRRNTNAIAMTALQPGGVYAFFSPSNATTY--GRD  
TLD  
PH-----DNAQNFNPWPWETIRSGRAVYVGPFRSTSDVLR-----  
-QWGLAVRRPIYNRTSYESA-DISTFWGFAFTLVNISGLMEENPFVFTNFTTKRR--SF  
DYLLSVH--NETSDAITVLATSL---KNPTATQLAEFARLGTSGIT-PNHPFLITIR-  
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IL-----PVSSSSTADG  
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D  
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VL-----PVSASTVTDG  
VSANNAETAPVARTGTSLYPPPENEGNDLLSARSP---SVALLMSHASGSSE-----  
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 PPAERIHGQ--NFFNFDSVGRITLVRNMTMISMTALQPGGVYAFISPANAASY--GRDTLD  
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 -GYWGFVARRPIFNRTDYSMA-DIHTFWGFTFTLVNISGILSTNPFDFSSSGVQQS--SF  
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 -PLRMVNVIYSWT-----  
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 --ATIIY-VPYP--LP-----ITLQNTAGGRR-----GSAISS  
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 AS-----SVPTFSAVDG  
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 AS-----SVPTFSAVDG  
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HE-----VVAGSGAVAR  
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TE-----  
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HE-----VVAGSGAVAR  
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-SEWTMVVRRPIYNRTDIHAPVDIQTFWGFAASTVNISSILANNPFPNFSVYFNGRK-PKV  
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RMWVFAAPS VVTVSEAVEQVLPRFG-----LGYVTVE-----  
-SYRRVNVVRSRS-----  
-----VCGATGD---CVINGGSRSSSSGA-----  
--ATIY-VFPF---AP-----TTVQATIGMSLDLG-----GVAAAH  
DI-----DKGD-----DREIHLPAQALMT-----LVD-TRRPVLV  
AARDAA-----P--TPRQHSLPL---SASFHVAEEMGGSTPRHV  
RD-----IVASPITASM  
RDAESQNAVGNVHSGSFFHS-SEEEAVEAASSVSP---APSLP-NFGSSSSE-----  
-----VGIS---GANVMERGVFVIQGDGV-----TRALLRPVIAHA  
LDVALHAAFDYQSITLDVSYDSVRVLVYYFYSSYKILFRPLAAPERHNIYRRLVTAFGVP  
QQGILEHLAARCAIRCLQHS AKLRQTA-TQRQRGNAGTTPV--SGPLEENTLKHS GHEA  
VD-----

#XP\_001463485\_Leishmania\_infantum\_JPCM5

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SDSIPSDKITAYLKRFPFRFASLIASKKPAVAIQAICPGGVIAMTHPHDPDTV--GRDLMS  
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-QIWVIFTRAPLYRNTSKGVIPSQETFWGFVLLVVNVGTALDV--MDLDKLAKDHN--L  
DYVLYDT--STESGDTHVIASSL--PSGAMQPDYEEFVAESTVTDVLAPHSSSLHIAVR-  
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-AYQTVDMRTTR-----  
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--ATLYLLVHA---AK-----PDLVAGAEATAAAAA-----AVAMVP  
QLMV-----GNAPAPSLYCGL-----ITR-GNSPSLE  
AGRAAV-----P-----SL----QDVSARSPEIESSASSAW  
SS-----AASTKGSSRA  
TNASQRRGAAAERSARTRNPLSRGDLDTQQALV---RKQALAKHNA-----  
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LDVALRVAFDYQSITLDVRYAEVRVLVYFYSSYKILFRPLAAPERHNI FRRLVTAFGVP  
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#XP\_003858707\_Leishmania\_donovani

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