

Supplementary Material

Molecular Authentication and Phytochemical Evaluation of Indigenous Germplasm of Genus *Physalis* for Sustainable Utilization

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Supplementary Tables

Supplementary Table S1: BLASTn analysis results for *Physalis* accessions based on ITS2 and *rbcL* barcode regions

| Sample ID | <i>rbcL</i> | | | | | ITS2 | | | | |
|-----------|-----------------------------|--|---------|----------------------|--------------------------|------------------------------------|--|---------|----------------------|--------------------------|
| | Species of Best BLAST match | GenBank accession number (of database) | E value | Percent identity (%) | GenBank accession number | Species of Best BLAST match | GenBank accession number (of database) | E value | Percent identity (%) | GenBank accession number |
| L1 | <i>Physalis minima</i> | NC_048515.1 | 0.0 | 100 | OQ507152.1 | - | - | - | - | - |
| L2 | <i>Physalis mimima</i> | NC_048515.1 | 0.0 | 100 | OQ507153.1 | <i>Physalis purpurea</i> | MH763740.1 | 0.0 | 92.98 | OQ372021.1 |
| L3 | <i>Physalis minima</i> | NC_048515.1 | 0.0 | 99.59 | OQ507154.1 | <i>Physalis purpurea</i> | MH763740.1 | 0.0 | 94.06 | OQ372022.1 |
| L4 | <i>Physalis minima</i> | NC_048515.1 | 0.0 | 100 | OQ507155.1 | <i>Physalis peruviana</i> | AY665914.1 | 0.0 | 97.41 | OQ372023.1 |
| L5 | <i>Physalis minima</i> | NC_048515.1 | 0.0 | 99.86 | OQ507156.1 | <i>Physalis purpurea</i> | MH763740.1 | 0.0 | 94.45 | OQ372024.1 |
| L6 | <i>Physalis minima</i> | NC_048515.1 | 0.0 | 100 | OQ507157.1 | <i>Physalis aff. philadelphica</i> | AY665868.1 | 2e-144 | 91.35 | OQ372025.1 |
| L7 | <i>Physalis minima</i> | NC_048515.1 | 0.0 | 100 | OQ507158.1 | <i>Physalis purpurea</i> | MH763740.1 | 1e-148 | 86.00 | OQ372026.1 |
| L8 | <i>Physalis minima</i> | NC_048515.1 | 0.0 | 100 | OQ507159.1 | <i>Physalis purpurea</i> | MH763740.1 | 0.0 | 93.07 | OQ372027.1 |
| L9 | <i>Physalis minima</i> | NC_048515.1 | 0.0 | 100 | OQ507160.1 | <i>Physalis purpurea</i> | MH763740.1 | 0.0 | 88.96 | OQ372028.1 |
| L10 | <i>Physalis</i> | NC_048515.1 | 0.0 | 100 | OQ507161.1 | <i>Physalis</i> | MH763740. | 0.0 | 90.16 | OQ372029.1 |

| | | | | | | | | | | | |
|--|---------------|--|--|--|--|-----------------|---|--|--|--|--|
| | <i>minima</i> | | | | | <i>purpurea</i> | 1 | | | | |
|--|---------------|--|--|--|--|-----------------|---|--|--|--|--|

Supplementary Figures

Supplementary Figure S1: Multiple sequence alignment for *Physalis* accessions ITS2 and *rbcL* gene sequences as well as their reference sequences based on BLASTn analysis (<https://escript.ibcp.fr/ESPrift/temp/1818399141/0-0-1680464456-esp.pdf>)

| | 80 | 90 | 100 | 110 | 120 | 130 | 140 | 150 |
|---------------|---------------|-------------|-------------|--------------------|-------------|--------------------|-------------|-----|
| KT178121.1* | CTGAGTACCAACC | AAGGATACGT | ATATTGCGCAG | CATTCCGAG | TAACCTCTC | CACATTGGAGTC | CACACTGAA | |
| NC_026570.1* | CTGAGTACCAACC | AAGGATACGT | ATATTGCGCAG | CATTCCGAG | TAACCTCTC | CACATTGGAGTC | CACACTGAA | |
| KT178120.1* | CTGAGTACCAACC | AAGGATACGT | ATATTGCGCAG | CATTCCGAG | TAACCTCTC | CACATTGGAGTC | CACACTGAA | |
| NC_048515.1* | CTGAGTACCAACC | AAGGATACGT | ATATTGCGCAG | CATTCCGAG | TAACCTCTC | CACATTGGAGTC | CACACTGAA | |
| NC_048514.1* | CTGAGTACCAACC | AAGGATACGT | ATATTGCGCAG | CATTCCGAG | TAACCTCTC | CACATTGGAGTC | CACACTGAA | |
| NC_037634.1* | CTGAGTACCAACC | AAGGATACGT | ATATTGCGCAG | CATTCCGAG | TAACCTCTC | CACATTGGAGTC | CACACTGAA | |
| NC_037633.1* | CTGAGTACCAACC | AAGGATACGT | ATATTGCGCAG | CATTCCGAG | TAACCTCTC | CACATTGGAGTC | CACACTGAA | |
| NC_039445.1* | CTGAGTACCAACC | AAGGATACGT | ATATTGCGCAG | CATTCCGAG | TAACCTCTC | CACATTGGAGTC | CACACTGAA | |
| NC_0507152.1* | CTGAGTACCAACC | AAGGATACGT | ATATTGCGCAG | CATTCCGAG | TAACCTCTC | CACATTGGAGTC | CACACTGAA | |
| NC_0507153.1* | CTGAGTACCAACC | AAGGATACGT | ATATTGCGCAG | CATTCCGAG | TAACCTCTC | CACATTGGAGTC | CACACTGAA | |
| NC_0507154.1* | CTGAGTACCAACC | AAGGATACGT | ATATTGCGCAG | CATTCCGAG | TAACCTCTC | CACATTGGAGTC | CACACTGAA | |
| NC_0507155.1* | CTGAGTACCAACC | AAGGATACGT | ATATTGCGCAG | CATTCCGAG | TAACCTCTC | CACATTGGAGTC | CACACTGAA | |
| NC_0507156.1* | CTGAGTACCAACC | AAGGATACGT | ATATTGCGCAG | CATTCCGAG | TAACCTCTC | CACATTGGAGTC | CACACTGAA | |
| NC_0507157.1* | CTGAGTACCAACC | AAGGATACGT | ATATTGCGCAG | CATTCCGAG | TAACCTCTC | CACATTGGAGTC | CACACTGAA | |
| NC_0507158.1* | CTGAGTACCAACC | AAGGATACGT | ATATTGCGCAG | CATTCCGAG | TAACCTCTC | CACATTGGAGTC | CACACTGAA | |
| NC_0507159.1 | CTGAGTACCAACC | AAGGATACGT | ATATTGCGCAG | CATTCCGAG | TAACCTCTC | CACATTGGAGTC | CACACTGAA | |
| NC_0507160.1 | CTGAGTACCAACC | AAGGATACGT | ATATTGCGCAG | CATTCCGAG | TAACCTCTC | CACATTGGAGTC | CACACTGAA | |
| NC_0507161.1 | CTGAGTACCAACC | AAGGATACGT | ATATTGCGCAG | CATTCCGAG | TAACCTCTC | CACATTGGAGTC | CACACTGAA | |
| AY665903.1* | | CTCGGAAGGAT | | CTTGACCTGTAAG | | CAGACGCCGGAAACCTGT | TGAAAC..... | |
| AY665986.1* | | CTCGGAAGGAT | | CTTGACCTGTAAG | | CAGACGCCGGAAACCTGT | TGAAAC..... | |
| AY665910.1* | | CTCGGAAGGAT | | CTTGACCTGTAAG | | CAGACGCCGGAAACCTGT | TGAAAC..... | |
| AY665914.1* | | CTCGGAAGGAT | | CTTGACCTGTAAG | | CAGACGCCGGAAACCTGT | TGAAAC..... | |
| AY665879.1* | | CTCGGAAGGAT | | CTTGACCTGTAAG | | CAGACGCCGGAAACCTGT | TGAAAC..... | |
| AY665905.1* | | CTCGGAAGGAT | | CTTGACCTGTAAG | | CAGACGCCGGAAACCTGT | TGAAAC..... | |
| AY665886.1* | | CTCGGAAGGAT | | CTTGACCTGTAAG | | CAGACGCCGGAAACCTGT | TGAAAC..... | |
| MH76128.1* | | CTCGGAAGGAT | | CTTGACCTGTAAG | | CAGACGCCGGAAACCTGT | TGAAAC..... | |
| NC_037201.1* | | CTCGGAAGGAT | | CTTGACCTGTAAG | | CAGACGCCGGAAACCTGT | TGAAAC..... | |
| NC_037202.1 | | | | | | | | |
| NC_037202.1 | | | | | | | | |
| NC_037202.3 | | | GGGT | CGGGCTGAGACCGCTAAC | | | | |
| NC_037204.1 | | CTCGGAAGGAT | | ATTTGCGTAAG | | CAGACGCCGGAAACCTGT | TGAAAC..... | |
| NC_037205.1 | | | | ATTTGCGTAAG | | CAGACGCCGGAAACCTGT | TGAAAC..... | |
| NC_037206.1 | | | | CTGGGGT | | | | |
| NC_037207.1 | | | | | CGGGCTGAGAC | | | |
| NC_037208.1 | | | | | ATTTGCGTAAG | | | |
| NC_037209.1 | | | | | CGGGCTGAGAC | | | |

| | 160 | 170 | 180 | 190 | 200 | 210 |
|--------------|-------------|--|---------------------------|-------------|-----|-----|
| KT178121.1* | A GGGCC CCG | . GTAC C CGAA T TT TG G . | T CA G CAAC G TAT G | G AC CGA GG | | |
| NC_026570.1* | A GGGCC CCG | . GTAC C CGAA T TT TG G . | T CA G CAAC G TAT G | G AC CGA GG | | |
| KT178120.1 | A GGGCC CCG | . GTAC C CGAA T TT TG G . | T CA G CAAC G TAT G | G AC CGA GG | | |
| NC_048515.1* | A GGGCC CCG | . GTAC C CGAA T TT TG G . | T CA G CAAC G TAT G | G AC CGA GG | | |
| NC_048514.1 | A GGGCC CCG | . GTAC C CGAA T TT TG G . | T CA G CAAC G TAT G | G AC CGA GG | | |
| NC_070364.1 | A GGGCC CCG | . GTAC C CGAA T TT TG G . | T CA G CAAC G TAT G | G AC CGA GG | | |
| NC_039458.1 | A GGGCC CCG | . GTAC C CGAA T TT TG G . | T CA G CAAC G TAT G | G AC CGA GG | | |
| NC_039457.1* | A GGGCC CCG | . GTAC C CGAA T TT TG G . | T CA G CAAC G TAT G | G AC CGA GG | | |
| Q507152.1 | A GGGCC CCG | . GTAC C CGAA T TT TG G . | T CA G CAAC G TAT G | G AC CGA GG | | |
| Q507153.1 | A GGGCC CCG | . GTAC C CGAA T TT TG G . | T CA G CAAC G TAT G | G AC CGA GG | | |
| Q507154.1 | A GGGCC CCG | . GTAC C CGAA T TT TG G . | T CA G CAAC G TAT G | G AC CGA GG | | |
| Q507155.1 | A GGGCC CCG | . GTAC C CGAA T TT TG G . | T CA G CAAC G TAT G | G AC CGA GG | | |
| Q507156.1 | A GGGCC CCG | . GTAC C CGAA T TT TG G . | T CA G CAAC G TAT G | G AC CGA GG | | |
| Q507157.1 | A GGGCC CCG | . GTAC C CGAA T TT TG G . | T CA G CAAC G TAT G | G AC CGA GG | | |
| Q507158.1 | A GGGCC CCG | . GTAC C CGAA T TT TG G . | T CA G CAAC G TAT G | G AC CGA GG | | |
| Q507159.1 | A GGGCC CCG | . GTAC C CGAA T TT TG G . | T CA G CAAC G TAT G | G AC CGA GG | | |
| Q507160.1 | A GGGCC CCG | . GTAC C CGAA T TT TG G . | T CA G CAAC G TAT G | G AC CGA GG | | |
| Q507161.1 | A GGGCC CCG | . GTAC C CGAA T TT TG G . | T CA G CAAC G TAT G | G AC CGA GG | | |
| AY665903.1* | CGGG AGAC | ITCG CTCG G CG CC G GG GG GTCG GG | C CG GT G CC G G AC TAT G | G AC CGA GG | | |
| AY665868.1* | TGGGG AGAC | ITCG CTCG G CG CC G GG GG GTCG GG | C CG GT G CC G G AC TAT G | G AC CGA GG | | |
| AY665911.1* | CGGG AGAC | ITCG CTCG G CG CC G GG GG GTCG GG | C CG GT G CC G G AC TAT G | G AC CGA GG | | |
| AY665914.1* | CGGG AGAC | ITCG CTCG G CG CC G GG GG GTCG GG | C CG GT G CC G G AC TAT G | G AC CGA GG | | |
| AY665879.1* | GGGG AGAC | CGCT CTGG TC CG CC G GG GG GTCG GG | C CG GT G CC G G AC TAT G | G AC CGA GG | | |
| AY665905.1* | GGGG AGAC | ITCG CTCG G CG CC G GG GG GTCG GG | C CG GT G CC G G AC TAT G | G AC CGA GG | | |
| AY665886.1* | CGGG AGAC | CGCT CTGG TC CG CC G GG GG GTCG GG | C CG GT G CC G G AC TAT G | G AC CGA GG | | |
| MH763728.1* | CGGG AGAC | CGCT CTGG TC CG CC G GG GG GTCG GG | C CG GT G CC G G AC TAT G | G AC CGA GG | | |
| MH763740.1 | CGGG AGAC | ITCG CTCG G CG CC G GG GG GTCG GG | C CG GT G CC G G AC TAT G | G AC CGA GG | | |
| Q372021.1 | . | . | . | . | . | . |
| Q372022.1 | C GGGA AGCG | ITCG CTCG G CG CC G GG GG GTCG GG | C CG GT G CC G G AC TAT G | G AC CGA GG | | |
| Q372023.1 | C GGGA AGCG | ITCG CTCG G CG CC G GG GG GTCG GG | C CG GT G CC G G AC TAT G | G AC CGA GG | | |
| Q372024.1 | C GGGA AGCG | ITCG CTCG G CG CC G GG GG GTCG GG | C CG GT G CC G G AC TAT G | G AC CGA GG | | |
| Q372025.1 | C GGGA AGCG | ITCG CTCG G CG CC G GG GG GTCG GG | C CG GT G CC G G AC TAT G | G AC CGA GG | | |
| Q372026.1 | CAAA GGCTG | CGCA CG AC AACAA TG GAG T CA AC CAC CA | C CG GT G CC G G AC TAT G | G AC CGA GG | | |
| Q372027.1 | GGGG CACGG | ITCG GCC CAC G CA CAC A TG GAG T CA AC CAC CA | C CG GT G CC G G AC TAT G | G AC CGA GG | | |
| Q372028.1 | TGGGG AGAC | ITCG CTCG G CG CC G GG GG GTCG GG | C CG GT G CC G G AC TAT G | G AC CGA GG | | |
| Q372029.1 | GGGG CACGG | ITCG GCC CAC G CA CAC A TG GAG T CA AC CAC CA | C CG GT G CC G G AC TAT G | G AC CGA GG | | |

| | 280 | 290 | 300 | 310 | 320 | 330 | 340 | 350 |
|--------------|-----------|-----|-----|-----|------|-----|-----|-----|
| KT178121_1* | GAGAAAAAA | GAT | TCA | ATA | TGT | CTT | TGA | C |
| NC_026570_1* | GAGAAAAAA | GAT | TCA | ATA | TGT | CTT | TGA | C |
| KT178120_1* | GAGAAAAAA | GAT | TCA | ATA | TGT | CTT | TGA | C |
| NC_048515_1* | GAGAAAAAA | GAT | TCA | ATA | TGT | CTT | TGA | C |
| NC_048514_1* | GAGAAAAAA | GAT | TCA | ATA | TGT | CTT | TGA | C |
| NC_070364_1* | GAGAAAAAA | GAT | TCA | ATA | TGT | CTT | TGA | C |
| NC_039458_1* | GAGAAAAAA | GAT | TCA | ATA | TGT | CTT | TGA | C |
| NC_039457_1* | GAGAAAAAA | GAT | TCA | ATA | TGT | CTT | TGA | C |
| Q507152_1 | GAGAAAAAA | GAT | TCA | ATA | TGT | CTT | TGA | C |
| Q507153_1 | GAGAAAAAA | GAT | TCA | ATA | TGT | CTT | TGA | C |
| Q507154_1 | GAGAAAAAA | GAT | TCA | ATA | TGT | CTT | TGA | C |
| Q507155_1 | GAGAAAAAA | GAT | TCA | ATA | TGT | CTT | TGA | C |
| Q507156_1 | GAGAAAAAA | GAT | TCA | ATA | TGT | CTT | TGA | C |
| Q507157_1 | GAGAAAAAA | GAT | TCA | ATA | TGT | CTT | TGA | C |
| Q507158_1 | GAGAAAAAA | GAT | TCA | ATA | TGT | CTT | TGA | C |
| Q507159_1 | GAGAAAAAA | GAT | TCA | ATA | TGT | CTT | TGA | C |
| Q507160_1 | GAGAAAAAA | GAT | TCA | ATA | TGT | CTT | TGA | C |
| Q507161_1 | GAGAAAAAA | GAT | TCA | ATA | TGT | CTT | TGA | C |
| AE665903_1* | CGC | GGG | TGC | GCT | GTC | G | .. | A |
| AY665868_1* | CGC | GGG | TGT | GCT | GTC | G | .. | A |
| AY665869_1* | CGC | GGG | TGT | GCT | GTC | G | .. | A |
| AY665870_1* | CGC | GGG | TGC | GCT | GTC | G | .. | A |
| AY665879_1* | CGC | GGG | TGC | GCT | GTC | G | .. | A |
| AY665905_1* | CGC | GGG | TGC | GCT | GTC | G | .. | A |
| AY665886_1* | CGC | GGG | TGC | GCT | GTC | G | .. | A |
| MH763728_1* | CGC | GGG | TGC | GCT | GTC | G | .. | A |
| MH763740_1* | CGC | GGG | TGC | GCT | GTC | G | .. | A |
| Q372021_1 | CGC | GGG | TGT | TCT | GCT | G | .. | A |
| Q372022_1 | CGC | GGG | TGT | TCT | GCT | G | .. | A |
| Q372023_1 | CGC | GGG | TGT | TCT | GCT | G | .. | A |
| Q372024_1 | CGC | GGG | TGT | TCT | GCT | G | .. | A |
| Q372025_1 | CGC | GGG | TGT | TCT | GCT | G | .. | A |
| Q372026_1 | GGC | AGG | GCG | GAT | CCCA | CGT | .. | .. |
| Q372027_1 | GGC | AGG | GCG | GAT | CCCA | CGT | .. | .. |
| Q372028_1 | GGC | AGG | GCG | GAT | CCCA | CGT | .. | .. |
| Q372029_1 | GGC | AGG | GCG | GAT | CCCA | CGT | .. | .. |

| | 360 | 370 | 380 | 390 | 400 | 410 | 420 | 430 |
|--------------|-----|-----|----------|-----|------|-----------|-----|-----|
| KT178121.1* | TTC | CAT | TGTAGGTA | A | GTA | TTGGGTTTA | AGC | CCT |
| NC_017200.1* | TTC | CAT | TGTAGGTA | A | GTA | TTGGGTTTA | AGC | CCT |
| NC_017212.1* | TTC | CAT | TGTAGGTA | A | GTA | TTGGGTTTA | AGC | CCT |
| NC_040515.1* | TTC | CAT | TGTAGGTA | A | GTA | TTGGGTTTA | AGC | CCT |
| NC_048514.1* | TTC | CAT | TGTAGGTA | A | GTA | TTGGGTTTA | AGC | CCT |
| NC_070364.1* | TTC | CAT | TGTAGGTA | A | GTA | TTGGGTTTA | AGC | CCT |
| NC_039458.1* | TTC | CAT | TGTAGGTA | A | GTA | TTGGGTTTA | AGC | CCT |
| NC_039457.1* | TTC | CAT | TGTAGGTA | A | GTA | TTGGGTTTA | AGC | CCT |
| Q507152.1 | TTC | CAT | TGTAGGTA | A | GTA | TTGGGTTTA | AGC | CCT |
| Q507153.1 | TTC | CAT | TGTAGGTA | A | GTA | TTGGGTTTA | AGC | CCT |
| Q507154.1 | TTC | CAT | TGTAGGTA | A | GTA | TTGGGTTTA | AGC | CCT |
| Q507155.1 | TTC | CAT | TGTAGGTA | A | GTA | TTGGGTTTA | AGC | CCT |
| Q507156.1 | TTC | CAT | TGTAGGTA | A | GTA | TTGGGTTTA | AGC | CCT |
| Q507157.1 | TTC | CAT | TGTAGGTA | A | GTA | TTGGGTTTA | AGC | CCT |
| Q507158.1 | TTC | CAT | TGTAGGTA | A | GTA | TTGGGTTTA | AGC | CCT |
| Q507159.1 | TTC | CAT | TGTAGGTA | A | GTA | TTGGGTTTA | AGC | CCT |
| Q507160.1 | TTC | CAT | TGTAGGTA | A | GTA | TTGGGTTTA | AGC | CCT |
| Q507161.1 | TTC | CAT | TGTAGGTA | A | GTA | TTGGGTTTA | AGC | CCT |
| AY665903.1* | ATC | GA | AGAGA | ... | ACCA | CGAACRAAA | AGC | ATC |
| AY665986.1* | ATC | GA | AGAGA | ... | ACCA | TCCAA | AGC | ATC |
| AY665987.1* | ATC | GA | AGAGA | ... | ACCA | TCCAA | AGC | ATC |
| AY665914.1* | ATC | GA | AGAGA | ... | ACCA | TCCAA | AGC | ATC |
| AY665979.1* | ATC | GA | AGAGA | ... | ACCA | TCCAA | AGC | ATC |
| AY665905.1* | ATC | GA | AGAGA | ... | ACCA | TCCAA | AGC | ATC |
| AY665886.1* | ATC | GA | AGAGA | ... | ACCA | TCCAA | AGC | ATC |
| MH763728.1* | ATC | GA | AGAGA | ... | ACCA | TCCAA | AGC | ATC |
| MH763740.1* | ATC | GA | AGAGA | ... | ACCA | TCCAA | AGC | ATC |
| Q372021.1 | ATC | GA | AGAGA | ... | ACCA | TCCAA | AGC | ATC |
| Q372022.1 | ATC | GA | AGAGA | ... | ACCA | TCCAA | AGC | ATC |
| Q372023.1 | ATC | GA | AGAGA | ... | ACCA | TCCAA | AGC | ATC |
| Q372024.1 | ATC | GA | AGAGA | ... | ACCA | TCCAA | AGC | ATC |
| Q372025.1 | ATC | GA | AGAGA | ... | ACCA | TCCAA | AGC | ATC |
| Q372026.1 | ATC | GA | AGAGA | ... | ACCA | TCCAA | AGC | ATC |
| Q372027.1 | ATC | GA | AGAGA | ... | ACCA | TCCAA | AGC | ATC |
| Q372028.1 | ATC | GA | AGAGA | ... | ACCA | TCCAA | AGC | ATC |
| Q372029.1 | ATC | GA | AGAGA | ... | ACCA | TCCAA | AGC | ATC |

| | 440 | 450 | 460 | 470 | 480 | 490 |
|--------------|---------------|----------------|------------|------------|----------|--------------|
| NC_171821.1* | G TAAACATTTC | ...CAAAGTCCGGC | TGGCGATCCG | GGGAACTTCA | TGAAGAAG | ...AGATAAAAT |
| NC_026570.1* | G TAAACATTTC | ...CAAAGTCCGGC | TGGCGATCCG | GGGAACTTCA | TGAAGAAG | ...AGATAAAAT |
| NC_171820.1* | A TAAACATTTC | ...CAAAGTCCGGC | TGGCGATCCG | GGGAACTTCA | TGAAGAAG | ...AGATAAAAT |
| NC_048515.1* | A TAAACATTTC | ...CAAAGTCCGGC | TGGCGATCCG | GGGAACTTCA | TGAAGAAG | ...AGATAAAAT |
| NC_048514.1* | N TAAACATTTC | ...CAAAGTCCGGC | TGGCGATCCG | GGGAACTTCA | TGAAGAAG | ...AGATAAAAT |
| NC_070364.1* | A TAAACATTTC | ...CAAAGTCCGGC | TGGCGATCCG | GGGAACTTCA | TGAAGAAG | ...AGATAAAAT |
| NC_039458.1* | A TAAACATTTC | ...CAAAGTCCGGC | TGGCGATCCG | GGGAACTTCA | TGAAGAAG | ...AGATAAAAT |
| NC_039457.1* | A TAAACATTTC | ...CAAAGTCCGGC | TGGCGATCCG | GGGAACTTCA | TGAAGAAG | ...AGATAAAAT |
| NC_050715.1 | A TAAACATTTC | ...CAAAGTCCGGC | TGGCGATCCG | GGGAACTTCA | TGAAGAAG | ...AGATAAAAT |
| NC_050715.13 | A TAAACATTTC | ...CAAAGTCCGGC | TGGCGATCCG | GGGAACTTCA | TGAAGAAG | ...AGATAAAAT |
| NC_050715.14 | A TAAACATTTC | ...CAAAGTCCGGC | TGGCGATCCG | GGGAACTTCA | TGAAGAAG | ...AGATAAAAT |
| NC_050715.15 | A TAAACATTTC | ...CAAAGTCCGGC | TGGCGATCCG | GGGAACTTCA | TGAAGAAG | ...AGATAAAAT |
| NC_050715.16 | A TAAACATTTC | ...CAAAGTCCGGC | TGGCGATCCG | GGGAACTTCA | TGAAGAAG | ...AGATAAAAT |
| NC_050715.17 | A TAAACATTTC | ...CAAAGTCCGGC | TGGCGATCCG | GGGAACTTCA | TGAAGAAG | ...AGATAAAAT |
| NC_050715.18 | A TAAACATTTC | ...CAAAGTCCGGC | TGGCGATCCG | GGGAACTTCA | TGAAGAAG | ...AGATAAAAT |
| NC_050715.19 | A TAAACATTTC | ...CAAAGTCCGGC | TGGCGATCCG | GGGAACTTCA | TGAAGAAG | ...AGATAAAAT |
| NC_050716.0 | A TAAACATTTC | ...CAAAGTCCGGC | TGGCGATCCG | GGGAACTTCA | TGAAGAAG | ...AGATAAAAT |
| NC_050716.1 | A TAAACATTTC | ...CAAAGTCCGGC | TGGCGATCCG | GGGAACTTCA | TGAAGAAG | ...AGATAAAAT |
| AY665903.1* | ...TCCGATCTTT | GAACGCAAT | TGGCGATCCG | GGGAACTTCA | TGAAGAAG | ...AGATAAAAT |
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| AY665914.1* | ...TCCGATCTTT | GAACGCAAT | TGGCGATCCG | GGGAACTTCA | TGAAGAAG | ...AGATAAAAT |
| AY665879.1* | ...TCCGATCTTT | GAACGCAAT | TGGCGATCCG | GGGAACTTCA | TGAAGAAG | ...AGATAAAAT |
| AY665905.1* | ...TCCGATCTTT | GAACGCAAT | TGGCGATCCG | GGGAACTTCA | TGAAGAAG | ...AGATAAAAT |
| AY665886.1* | ...TCCGATCTTT | GAACGCAAT | TGGCGATCCG | GGGAACTTCA | TGAAGAAG | ...AGATAAAAT |
| MH763728.1* | C TGCCTTTG | GAACGCAAT | TGGCGATCCG | GGGAACTTCA | TGAAGAAG | ...AGATAAAAT |
| MH763740.1* | T CGCATCTT | GAACGCAAT | TGGCGATCCG | GGGAACTTCA | TGAAGAAG | ...AGATAAAAT |
| Q372021.21 | T CGCATCTT | GAACGCAAT | TGGCGATCCG | GGGAACTTCA | TGAAGAAG | ...AGATAAAAT |
| Q372022.1 | T CGCATCTT | GAACGCAAT | TGGCGATCCG | GGGAACTTCA | TGAAGAAG | ...AGATAAAAT |
| Q372023.1 | T CGCATCTT | GAACGCAAT | TGGCGATCCG | GGGAACTTCA | TGAAGAAG | ...AGATAAAAT |
| Q372024.1 | T CGCATCTT | GAACGCAAT | TGGCGATCCG | GGGAACTTCA | TGAAGAAG | ...AGATAAAAT |
| Q372025.1 | T CGCATCTT | GAACGCAAT | TGGCGATCCG | GGGAACTTCA | TGAAGAAG | ...AGATAAAAT |
| Q372026.1 | T CGCATCTT | GAACGCAAT | TGGCGATCCG | GGGAACTTCA | TGAAGAAG | ...AGATAAAAT |
| Q372027.1 | T CGCATCTT | GAACGCAAT | TGGCGATCCG | GGGAACTTCA | TGAAGAAG | ...AGATAAAAT |
| Q372028.1 | T CGCATCTT | GAACGCAAT | TGGCGATCCG | GGGAACTTCA | TGAAGAAG | ...AGATAAAAT |
| Q372029.1 | T CGCATCTT | GAACGCAAT | TGGCGATCCG | GGGAACTTCA | TGAAGAAG | ...AGATAAAAT |

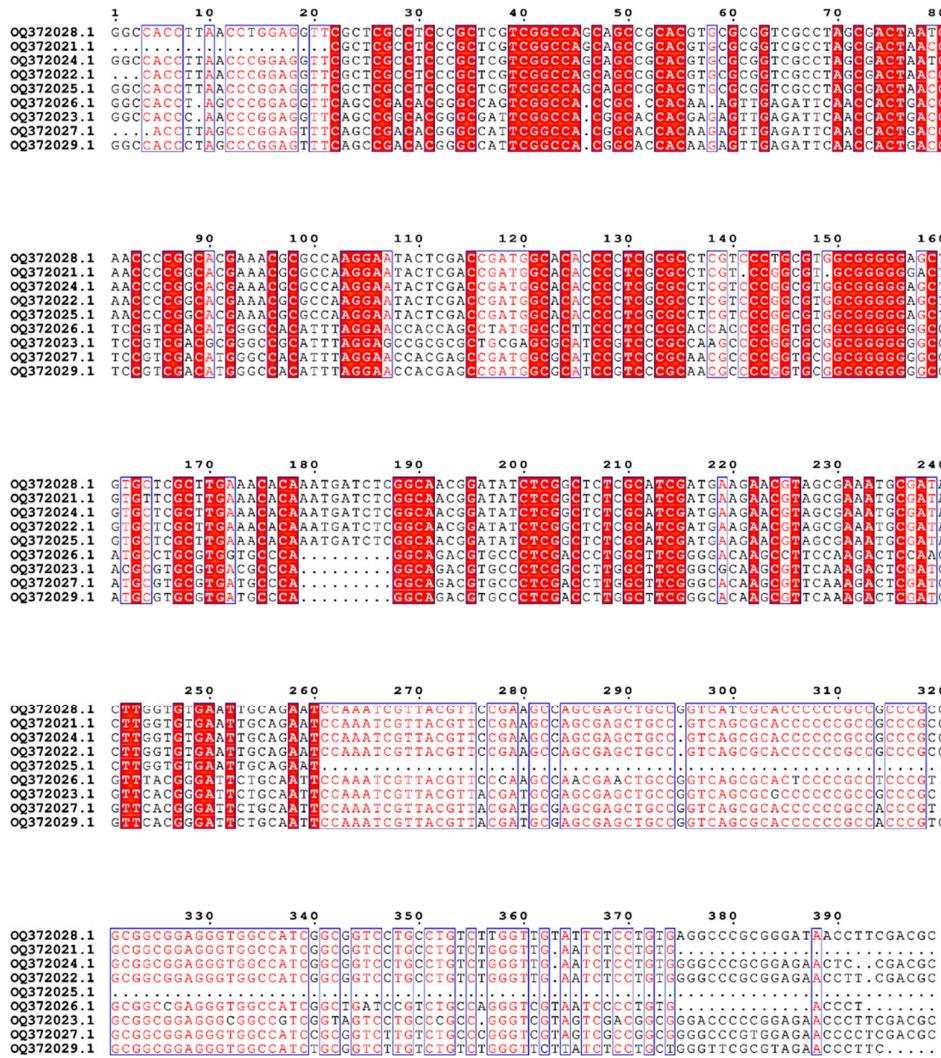
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|--------------|-------------------------|-------------------------------|-------------------------------|------|
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| NC_026270.1* | GTA . TGG . [TCG] CCCC | TGT GAT AAC TAA CTTAAAGTGCG | | |
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| NC_040515.1* | GTA . TGG . [TCG] CCCC | TGT GAT AAC TAA CTTAAAGTGCG | | |
| NC_048514.1* | GTA . TGG . [TCG] CCCC | TGT GAT AAC TAA CTTAAAGTGCG | | |
| NC_070364.1* | GTA . TGG . [TCG] CCCC | TGT GAT AAC TAA CTTAAAGTGCG | | |
| NC_039458.1* | GTA . TGG . [TCG] CCCC | TGT GAT AAC TAA CTTAAAGTGCG | | |
| NC_039457.1* | GTA . TGG . [TCG] CCCC | TGT GAT AAC TAA CTTAAAGTGCG | | |
| Q507152.1 | GTA . TGG . [TCG] CCCC | TGT GAT AAC TAA CTTAAAGTGCG | | |
| Q507153.1 | GTA . TGG . [TCG] CCCC | TGT GAT AAC TAA CTTAAAGTGCG | | |
| Q507154.1 | GTA . TGG . [TCG] CCCC | TGT GAT AAC TAA CTTAAAGTGCG | | |
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| Q507156.1 | GTA . TGG . [TCG] CCCC | TGT GAT AAC TAA CTTAAAGTGCG | | |
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| Q507158.1 | GTA . TGG . [TCG] CCCC | TGT GAT AAC TAA CTTAAAGTGCG | | |
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| Q507160.1 | GTA . TGG . [TCG] CCCC | TGT GAT AAC TAA CTTAAAGTGCG | | |
| Q507161.1 | GTA . TGG . [TCG] CCCC | TGT GAT AAC TAA CTTAAAGTGCG | | |
| AY665903.* | GCA . TCCG GTC CCCC | CTGGCCCCGCACCGCG . GGGCG CCGG | GAG . ATAC GGC CTC CGGT . ECG | |
| AY665868.* | GCA . TCCG GTC CCCC | CTGGCCCCGCACCGCG . GGGCG CCGG | GAG . ATAC GGC CTC CGGT . ECG | |
| AY665870.* | GCA . TCCG GTC CCCC | CTGGCCCCGCACCGCG . GGGCG CCGG | GAG . ATAC GGC CTC CGGT . ECG | |
| AY665874.* | GCA . TCCG GTC CCCC | CTGGCCCCGCACCGCG . GGGCG CCGG | GAG . ATAC GGC CTC CGGT . ECG | |
| AY665879.* | GCA . TCCG GTC CCCC | CTGGCCCCGCACCGCG . GGGCG CCGG | GAG . ATAC GGC CTC CGGT . ECG | |
| AY665895.0* | GCA . TCCG GTC CCCC | CTGGCCCCGCACCGCG . GGGCG CCGG | GAG . ATAC GGC CTC CGGT . ECG | |
| AY665886.1* | GCA . TCCG GTC CCCC | CTGGCCCCGCACCGCG . GGGCG CCGG | GAG . ATAC GGC CTC CGGT . ECG | |
| MH763728.1* | TCC GCG CCCC | TCC GCG CACGGG . GGCGC TGCG | GAG . ATAC GGC CTC CGGT . ECG | |
| MH763740.1* | TCC GCG CCCC | TCC GCG CACGGG . GGCGC TGCG | GAG . ATAC GGC CTC CGGT . ECG | |
| Q372021.21 | GCA . TCC CAI TCG CCCC | TCC GCG CACGGG . GGCGC TGCG | GAG . ATAC GGC CTC CGGT . ECG | |
| Q372022.1 | GCA . TCC CAI TCG CCCC | TCC GCG CACGGG . GGCGC TGCG | GAG . ATAC GGC CTC CGGT . ECG | |
| Q372023.1 | GCA . TCC CAI TCG CCCC | TCC GCG CACGGG . GGCGC TGCG | GAG . ATAC GGC CTC CGGT . ECG | |
| Q372024.1 | GCA . TCC CAI TCG CCCC | TCC GCG CACGGG . GGCGC TGCG | GAG . ATAC GGC CTC CGGT . ECG | |
| Q372025.1 | GCA . TCC CAI TCG CCCC | TCC GCG CACGGG . GGCGC TGCG | GAG . ATAC GGC CTC CGGT . ECG | |
| Q372026.1 | GCG . AAC CAC CAG TCCC | GGCGC CGGCC GAGGGGT . TGC | | |
| Q372027.1 | GCG . AAC CAC CAG TCCC | GGCGC CGGCC GAGGGGT . TGC | | |
| Q372028.1 | TCA . TTCC CAA GCG CCCC | GGCGC CGGCC GAGGGGT . TGC | | |
| Q372029.1 | TCA . TTCC CAA GCG CCCC | GGCGC CGGCC GAGGGGT . TGC | | |

| | 540 | 550 | 560 | 570 | 580 |
|--------------|------------------------|--------|--|--|-----|
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| NC_026570.1* | TTA TCT GC | T..... | AAAAA CTA CGTA GAGC ..TGT TTA ATG | ATG CTTC GCG | |
| KT178120.1* | TTA TCT GC | T..... | AAAAA CTA CGTA GAGC ..TGT TTA ATG | ATG CTTC GCG | |
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| NC_048514.1* | TTA TCT GC | T..... | AAAAA CTA CGGT AAGC ..TGT TTA ATG | ATG CTTC GCG | |
| NC_039458.1* | TTA TCT GC | T..... | AAAAA CTA CGGT AAGC ..TGT TTA ATG | ATG CTTC GCG | |
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| Q957153.1 | TTA TCT GC | T..... | AAAAA CTA CGGT AAGC ..TGT TTA ATG | ATG CTTC GCG | |
| Q957154.1 | TTA TCT GC | T..... | AAAAA CTA CGGT AAGC ..TGT TTA ATG | ATG CTTC GCG | |
| Q957155.1 | TTA TCT GC | T..... | AAAAA CTA CGGT AAGC ..TGT TTA ATG | ATG CTTC GCG | |
| Q957156.1 | TTA TCT GC | T..... | AAAAA CTA CGGT AAGC ..TGT TTA ATG | ATG CTTC GCG | |
| Q957157.1 | TTA TCT GC | T..... | AAAAA CTA CGGT AAGC ..TGT TTA ATG | ATG CTTC GCG | |
| Q957158.1 | TTA TCT GC | T..... | AAAAA CTA CGGT AAGC ..TGT TTA ATG | ATG CTTC GCG | |
| Q957159.1 | TTA TCT GC | T..... | AAAAA CTA CGGT AAGC ..TGT TTA ATG | ATG CTTC GCG | |
| Q957160.1 | TTA TCT GC | T..... | AAAAA CTA CGGT AAGC ..TGT TTA ATG | ATG CTTC GCG | |
| Q957161.1 | TTA TCT GC | T..... | AAAAA CTA CGGT AAGC ..TGT TTA ATG | ATG CTTC GCG | |
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| AY665910.1* | CTGCA | G.CCGG | .GCTGGC CTA ATGAGC GAGC CGGCGT CGACCG | ACGTCACGG..CAAGTG | |
| AY665914.1* | CTGCG | AGCG | .GCTGGC CTA ATGAGC GAGC CGGCGT CGACCG | ACGTCACGG..CAAGTG | |
| AY665879.1* | CTGCG | AGCG | .GCTGGC CTA ATGAGC GAGC CGGCGT CGACCG | ACGTCACGG..CAAGTG | |
| AY665905.1* | CTGCG | AGCG | .GCTGGC CTA ATGAGC GAGC CGGCGT CGACCG | ACGTCACGG..CAAGTG | |
| AY665886.1* | CTC | TCAGG | .GCTGGC CTA ATGAGC GAGC CGGCGT CGACCG | ACGTCACGG..CAAGTG | |
| MH763728.1* | CTC | TCAGG | .GCTGGC CTA ATGAGC GAGC CGGCGT CGACCG | ACGTCACGG..CAAGTG | |
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| Q9372023.1 | CCATCGGT | CGGGGT | .GTTGGC CTA ATGAGC GAGC CGGCGT CGACCG | ACGTCACGG..CAAGTG | |
| Q9372024.1 | CCATCGGT | T.CCGT | .GTTGGC CTA ATGAGC GAGC CGGCGT CGACCG | ACGTCACGG..CAAGTG | |
| Q9372025.1 | CCATCGGT | T.CCGT | .GTTGGC CTA ATGAGC GAGC CGGCGT CGACCG | ACGTCACGG..CAAGTG | |
| Q9372026.1 | CCATCGGT | T.CAGT | .GTTGGC CTA ATGAGC GAGC CGGCGT CGACCG | ATTTCCTGG.. | |
| Q9372027.1 | CCATCGGT | .CGAG | .TATTCT CTA GGCG GAGC CGGCGT CGACCG | TTTCCTGG..GTTCGTTAGTCGCTAGGGCGACCG..CGCACGCG | |
| Q9372028.1 | CCATCGGT | .CGTG | .GAATGC GAGC CGGCGT CGACCG | ACGTCATT..TTTAGTIT | |
| Q9372029.1 | CCATCGGT | .CGAG | .TATTCT CTT GGCG GTT CTGG GTT TCATTATCTC TAGCG CTACCG..CTCAATI | | |

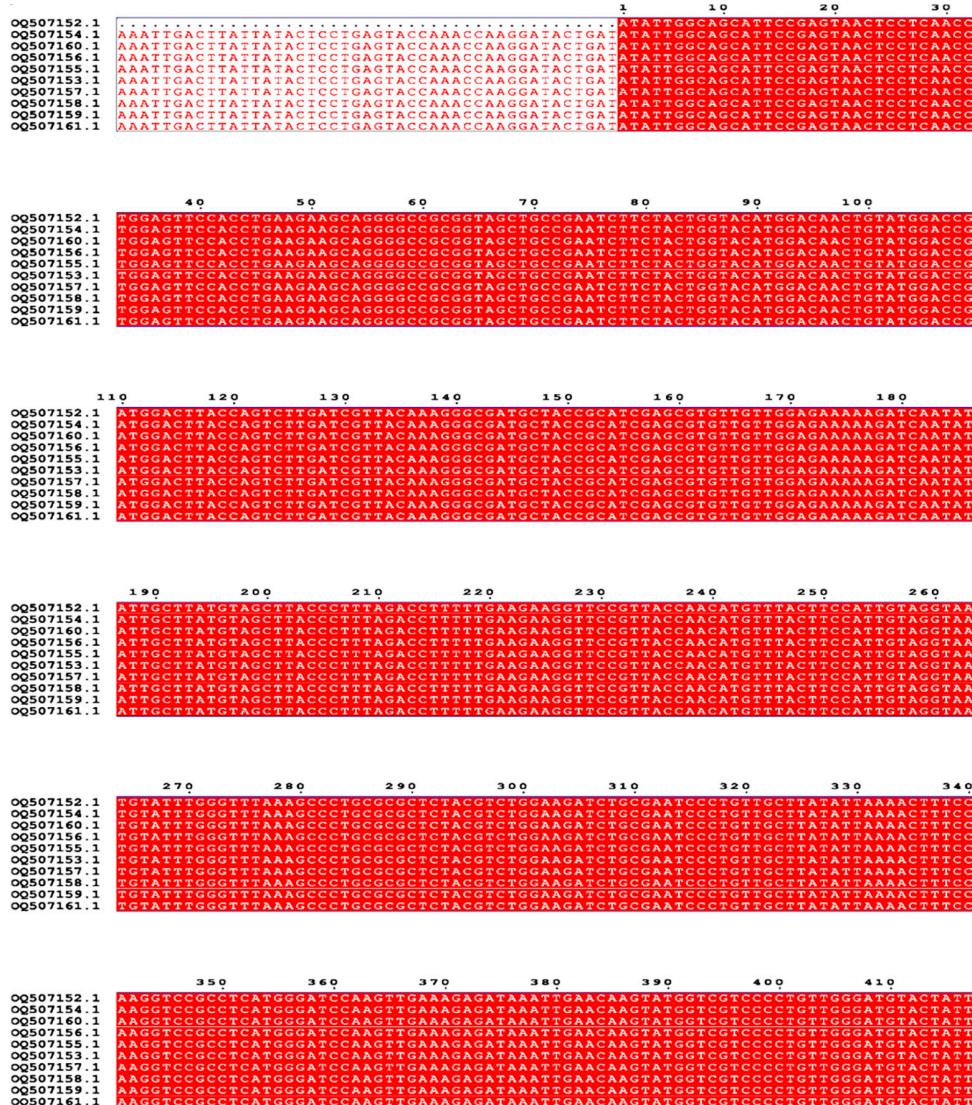
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| NC_026570.1* | GTGGACT | TGAT T AC | CAAAGA | TGAT T AGAA | CGT GAA CTC | CAA C AT T TAT | .G T TG G AGA A TC | TTT T TG C T |
| KT178120.1* | GTGGACT | TGAT T AC | CAAAGA | TGAT T AGAA | CGT GAA CTC | CAA C AT T TAT | .G T TG G AGA A TC | TTT T TG C T |
| NC_048515.1* | GTGGACT | TGAT T AC | CAAAGA | TGAT T AGAA | CGT GAA CTC | CAA C AT T TAT | .G T TG G AGA A TC | TTT T TG C T |
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| NC_039458.1* | GTGGACT | TGAT T AC | CAAAGA | TGAT T AGAA | CGT GAA CTC | CAA C AT T TAT | .G T TG G AGA A TC | TTT T TG C T |
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| Q957156.1 | GTGGACT | TGA T AT T AC | CAAAGA | TGAT T AGAA | CGT GAA CTC | CAA C AT T TAT | .G T TG G AGA A TC | TTT T TG C T |
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| Q957159.1 | GTGGACT | TGA T AT T AC | CAAAGA | TGAT T AGAA | CGT GAA CTC | CAA C AT T TAT | .G T TG G AGA A TC | TTT T TG C T |
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| AY665903.1* | GTC | TG | CG | CG | CG | CG | CG | CG |
| AY665910.1* | GTC | TG | CG | CG | CG | CG | CG | CG |
| AY665914.1* | GTC | TG | CG | CG | CG | CG | CG | CG |
| AY665879.1* | GTC | TG | CG | CG | CG | CG | CG | CG |
| AY665905.1* | GTC | TG | CG | CG | CG | CG | CG | CG |
| AY665886.1* | GTC | TG | CG | CG | CG | CG | CG | CG |
| MH763728.1* | GTC | TG | CG | CG | CG | CG | CG | CG |
| MH763728.1* | GTC | TG | CG | CG | CG | CG | CG | CG |
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| Q9372022.1 | GTC | TG | CG | CG | CG | CG | CG | CG |
| Q9372023.1 | GTC | TG | CG | CG | CG | CG | CG | CG |
| Q9372024.1 | GTC | TG | CG | CG | CG | CG | CG | CG |
| Q9372025.1 | | | | | | | | |
| Q9372026.1 | | | | | | | | |
| Q9372027.1 | | | | | | | | |
| Q9372028.1 | | | | | | | | |
| Q9372029.1 | | | | | | | | |

| | 660 | 670 | 680 | 690 | 700 | 710 | 720 | 730 |
|--------------|------|------|------|------|------|------|------|------|
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| NC_026570.1* | TTC | GT | GC | CG | AG | CA | T | TCTG |
| KT178120.1* | TTC | GT | GC | CG | AG | CA | T | TCTG |
| NC_048515.1* | TTC | GT | GC | CG | AG | CA | T | TCTG |
| NC_048514.1* | TTC | GT | GC | CG | AG | CA | T | TCTG |
| NC_039458.1* | TTC | GT | GC | CG | AG | CA | T | TCTG |
| NC_039457.1* | TTC | GT | GC | CG | AG | CA | T | TCTG |
| Q957152.1 | TTC | GT | GC | CG | AG | CA | T | TCTG |
| Q957153.1 | TTC | GT | GC | CG | AG | CA | T | TCTG |
| Q957154.1 | TTC | GT | GC | CG | AG | CA | T | TCTG |
| Q957155.1 | | | | | | | | |
| Q957156.1 | TTC | GT | GC | CG | AG | CA | T | TCTG |
| Q957157.1 | TTC | GT | GC | CG | AG | CA | T | TCTG |
| Q957158.1 | TTC | GT | GC | CG | AG | CA | T | TCTG |
| Q957159.1 | TTC | GT | GC | CG | AG | CA | T | TCTG |
| Q957160.1 | TTC | GT | GC | CG | AG | CA | T | TCTG |
| AY665903.1* | T.. | .. | .. | .. | .. | .. | .. | .. |
| AY665910.1* | G.. | .. | .. | .. | .. | .. | .. | .. |
| AY665914.1* | G.. | .. | .. | .. | .. | .. | .. | .. |
| AY665879.1* | G.. | .. | .. | .. | .. | .. | .. | .. |
| AY665905.1* | G.. | .. | .. | .. | .. | .. | .. | .. |
| AY665886.1* | G.. | .. | .. | .. | .. | .. | .. | .. |
| MH763728.1* | G.. | .. | .. | .. | .. | .. | .. | .. |
| MH763728.1* | G.. | .. | .. | .. | .. | .. | .. | .. |
| Q9372021.1 | G.. | .. | .. | .. | .. | .. | .. | .. |
| Q9372022.1 | G.. | .. | .. | .. | .. | .. | .. | .. |
| Q9372023.1 | G.. | .. | .. | .. | .. | .. | .. | .. |
| Q9372024.1 | G.. | .. | .. | .. | .. | .. | .. | .. |
| Q9372025.1 | .. | .. | .. | .. | .. | .. | .. | .. |
| Q9372026.1 | .. | .. | .. | .. | .. | .. | .. | .. |
| Q9372027.1 | GCT | CT | GT | CG | AG | CA | T | TCTG |
| Q9372028.1 | GGG | TT | TT | AG | CG | CC | T | CCCC |
| Q9372029.1 | GGG | TT | TT | AG | CG | CC | T | CCCC |

Supplementary Figure S2: Multiple sequence alignment for *Physalis* accessions based on ITS2 gene only (<https://escript.ibcp.fr/ESPrift/temp/1397454355/0-0-1688383432-esp.pdf>)



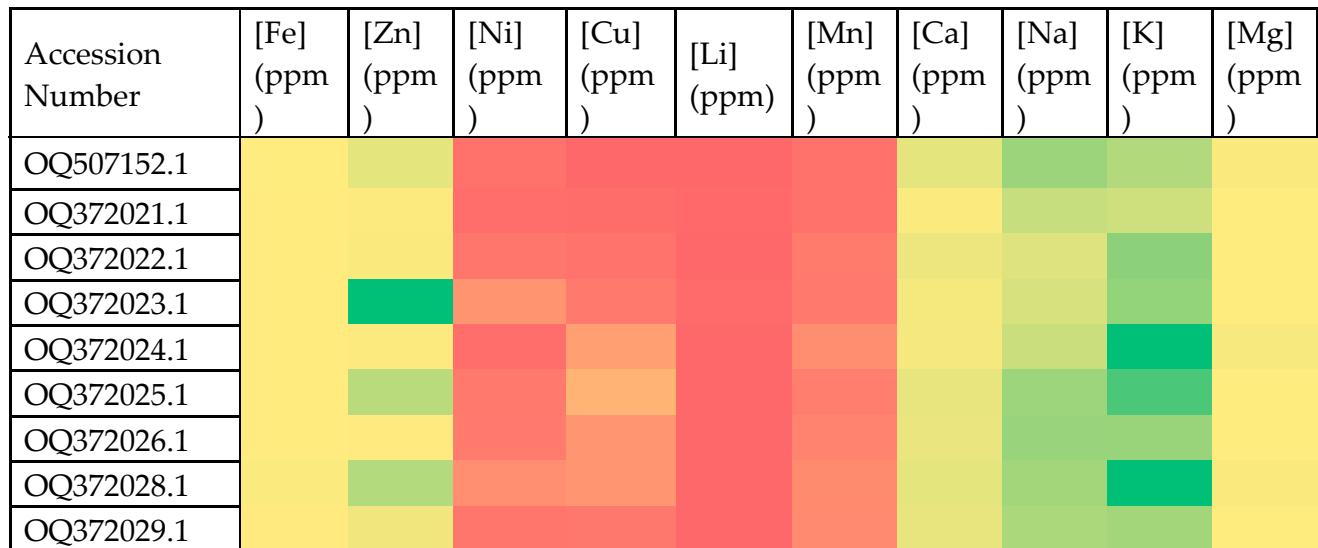
Supplementary Figure S3: Multiple sequence alignment of Physalis accessions based on *rbcL* gene only (<https://escript.ibcp.fr/EScript/temp/1129027434/0-0-1688384286-esp.pdf>)



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QQ507152.1 CAAAGATGATGACAACGTGAACCTCACACCATTATCGTTGGAGAGATCGTT CCGAAGCACT
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QQ507157.1 CAAAGATGATGAGAACGTGAACCTCACACCATTATCGTTGGAGAGATCGTT CCGAAGCACT
QQ507158.1 CAAAGATGATGAGAACGTGAACCTCACACCATTATCGTTGGAGAGATCGTT CCGAAGCACT
QQ507159.1 CAAAGATGATGAGAACGTGAACCTCACACCATTATCGTTGGAGAGATCGTT CCGAAGCACT
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Supplementary Figure S4: Heat map representation of the mineral content of *Physalis* accessions.



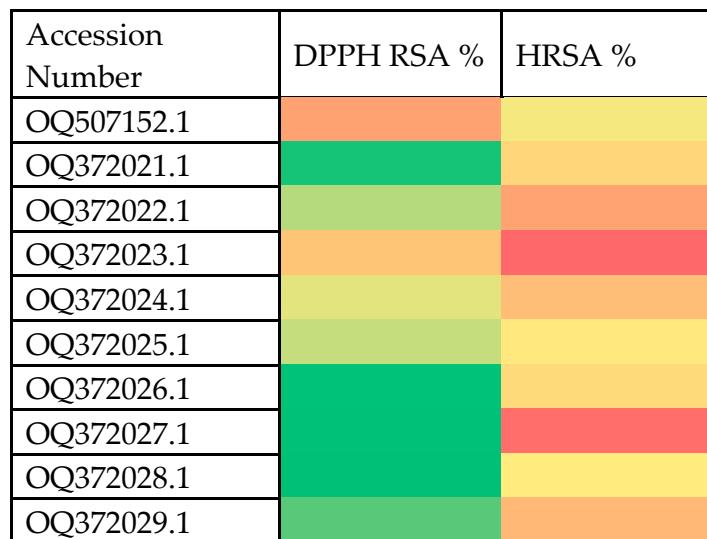
Green color represents specific high mineral concentration for the *Physalis* accession while yellow represents specific moderate mineral concentration and red represents specific low mineral concentration.

Supplementary Figure S5: Heat map for the polyphenol content distribution of *Physalis* accessions

| Accession Number | TPC (mg GAE /g DW) | TTC (mg Tannic acid/g DW) | TFC (mg Rutin/g DW) |
|------------------|--------------------|---------------------------|---------------------|
| OQ507152.1 | Yellow | Green | Green |
| OQ372021.1 | Orange | Green | Yellow |
| OQ372022.1 | Red | Yellow | Yellow |
| OQ372023.1 | Orange | Green | Orange |
| OQ372024.1 | Red | Dark Green | Yellow |
| OQ372025.1 | Yellow | Orange | Yellow |
| OQ372026.1 | Orange | Orange | Orange |
| OQ372027.1 | Yellow | Orange | Yellow |
| OQ372028.1 | Orange | Red | Green |
| OQ372029.1 | Yellow | Yellow | Green |

Green color represents specific high polyphenol concentration for the *Physalis* accession while yellow represents specific moderate polyphenol concentration and red represents specific low polyphenol concentration

Supplementary Figure S6: Heat map for the radical scavenging activity of *Physalis* accessions



Green color represents specific high radical scavenging activity for the *Physalis* accession while yellow represents specific moderate radical scavenging activity and red represents specific low radical scavenging activity.