

Table S1. Genome data information used for TEs analysis.

| Species Name | Collection site | BioProject Number | SRR Number | Genome Sizes (pg) | NGS Data used in Repeatexplorer2 (reads) | Individual Clustering (coverage) | Comparative Clustering (coverage) | No. of clusters* | No. of Super Clusters* |
|-----------------------|--|-------------------|-------------|-------------------|--|----------------------------------|-----------------------------------|------------------|------------------------|
| <i>C. abbreviatus</i> | Changchun, Jilin, China | PRJNA638780 | SRR14826315 | 9.99 | 16,283,700 | 0.5x | 0.03x | 345 | 292 |
| <i>C. barbarus</i> | Alxa Zuoqi, Alxa League, Inner Mongolia, China | PRJNA638780 | SRR14826314 | 10.37 | 16,903,100 | 0.5x | 0.03x | 355 | 320 |
| <i>C. italicus</i> | Zhangye City, Gansu Province, China | PRJNA638780 | SRR14826313 | 10.1 | 16,463,000 | 0.5x | 0.03x | 479 | 453 |

*Clusters and Super Cluster above the threshold of 0.01%.

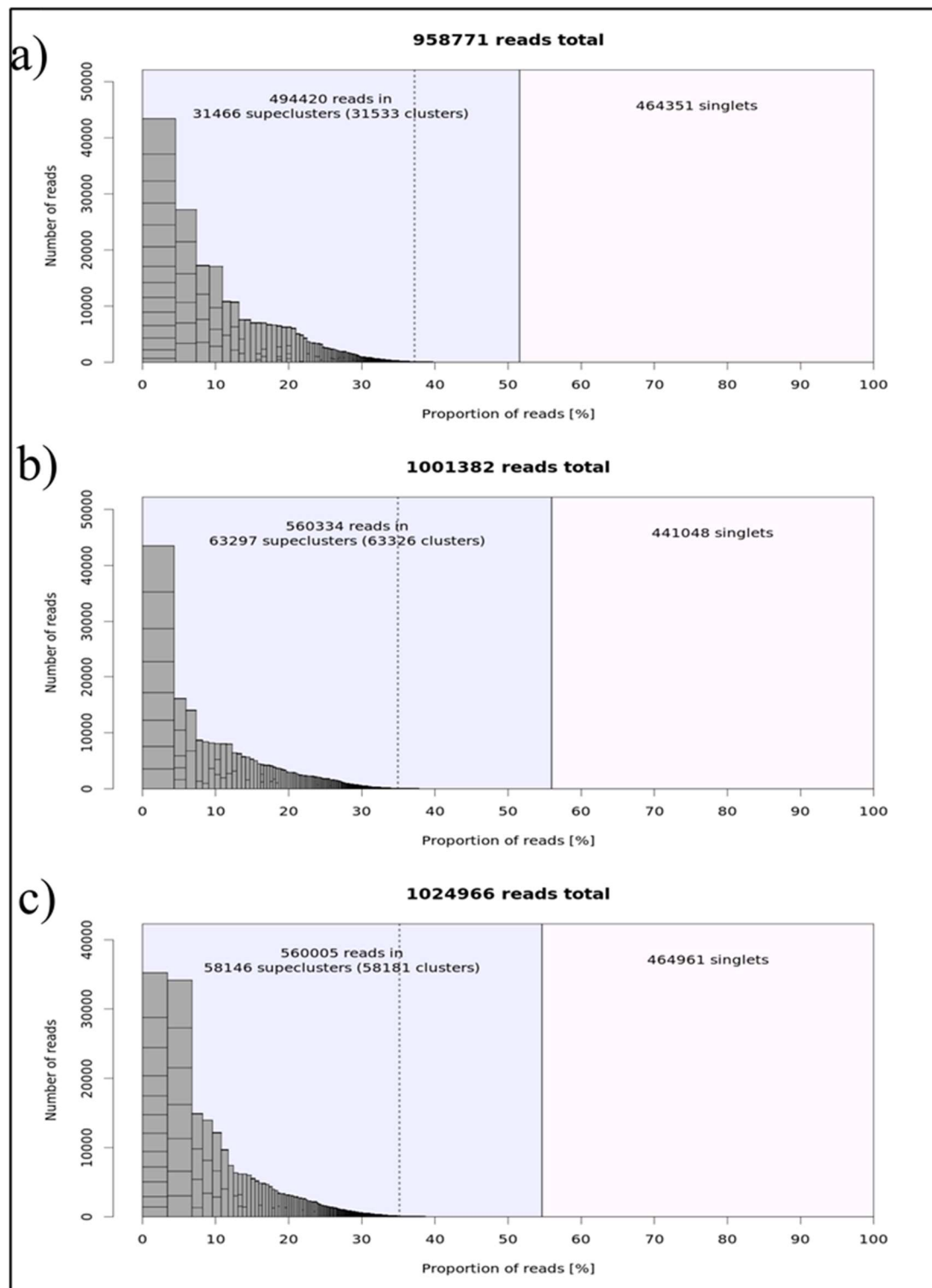


Figure S1. The graphical summary of individual clustering analysis of the genus *Calliptamus* species. The heights and widths of the bars denote superclusters, corresponding to the number of reads in the superclusters on y-axis and their proportions in all examined reads on x-axis. Individual clusters are represented by rectangles inside the supercluster bars. The proportions of clustered and single reads are shown in the blue and pink background panels, respectively. On the left of the dotted line are the top clusters. **a)** *C. abbreviatus*, **b)** *C. italicus*, **c)** *C. barbarus*.

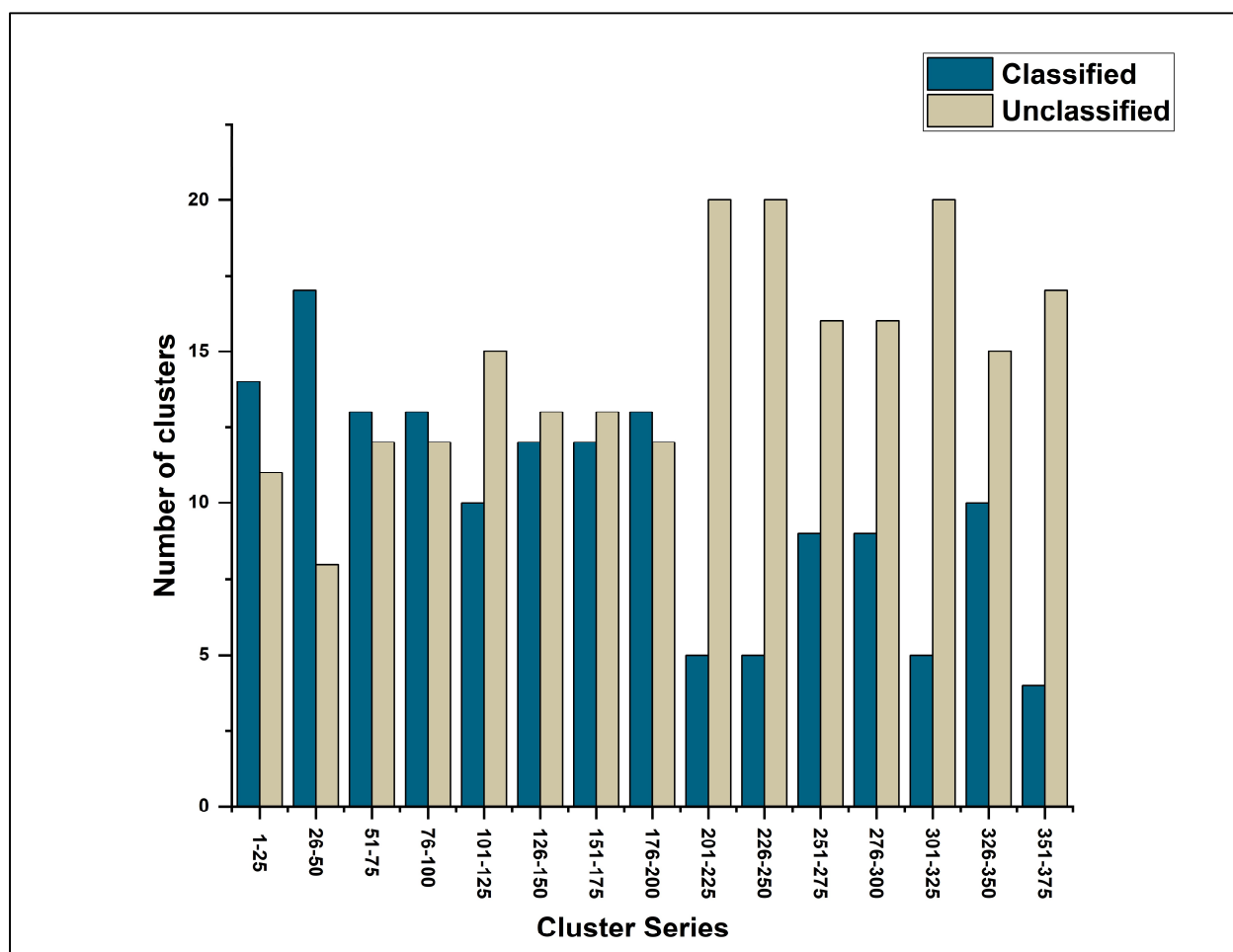


Figure S2. The proportion of annotation of classified and unclassified clusters by RepeatExplorer2. Clusters are arranged in ascending order.

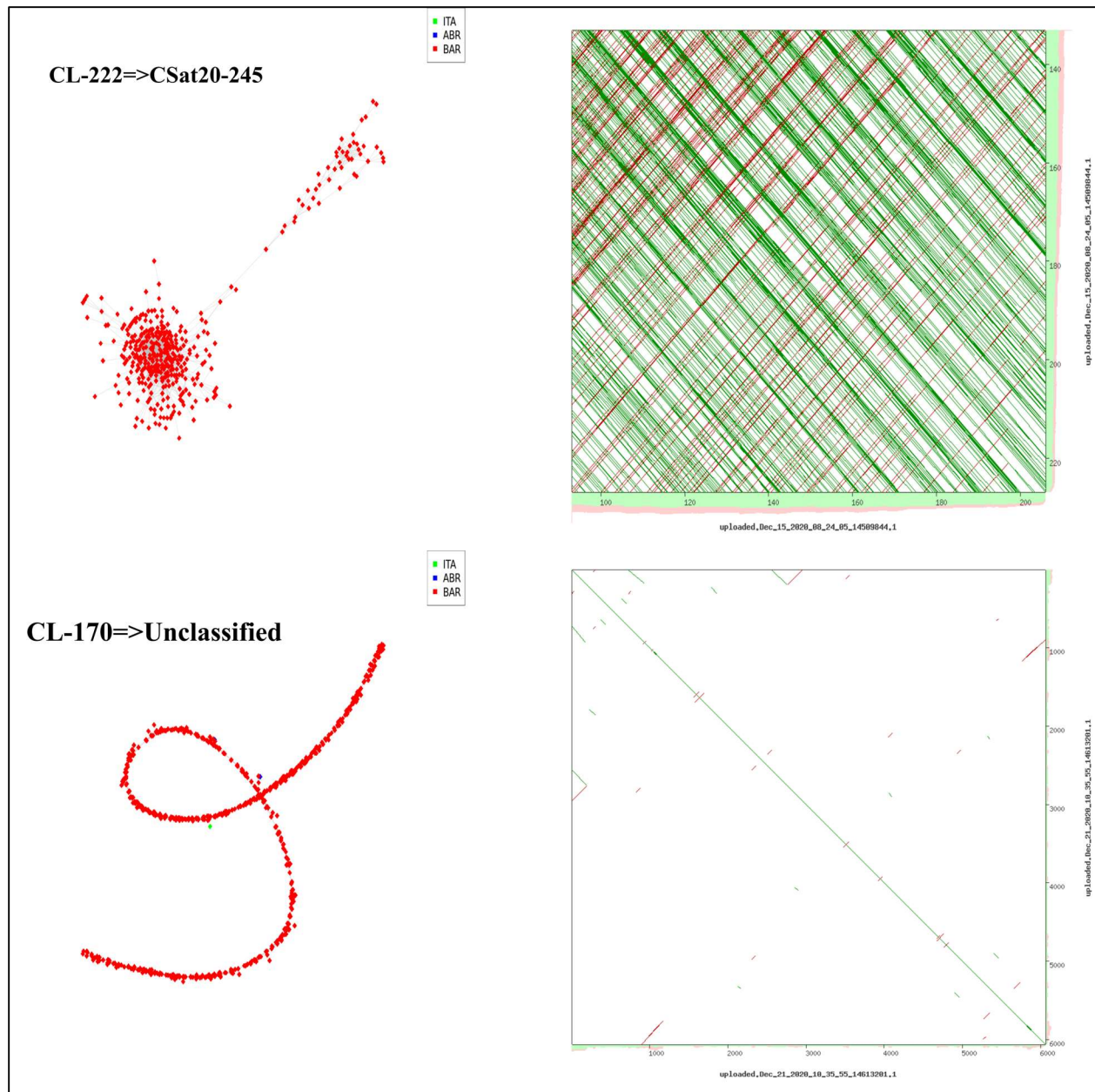


Figure S3. The classification of *C. barbarus* species-specific unclassified cluster CL-222 and CL-170 using the YASS tool. The CL-222 graph depicts a typical layout of tandem repeats, and the contigs in this cluster were compared to one another (Self-comparison). The diagonal lines (green lines) in the graph represent the tandem repeat, which allows us to characterize it as satellite DNA repeat CSat20-245. The other cluster CL-170 has not shown any evidence of tandem repeat and left it as unclassified.

| <i>C. italicus</i> | | Correlations | | | |
|--------------------|--------|-------------------------|--------|-----------|-------|
| Spearman's rho | Length | | Length | Abundance | K2P |
| | | Correlation Coefficient | 1.000 | -.100 | -.267 |
| | | Sig. (2-tailed) | . | .684 | .270 |
| | N | | 19 | 19 | 19 |
| Abundance | | Correlation Coefficient | -.100 | 1.000 | -.067 |
| | | Sig. (2-tailed) | .684 | . | .786 |
| | | N | 19 | 19 | 19 |
| K2P | | Correlation Coefficient | -.267 | -.067 | 1.000 |
| | | Sig. (2-tailed) | .270 | .786 | . |
| | | N | 19 | 19 | 19 |

Length vs abundance ($r_s = -0.1$, $t = 0.684$, $p = 0.68$), Length Vs K2P ($r_s = -0.267$, $t = 0.270$, $p = 0.26$)
K2P vs abundance ($r_s = -0.067$, $t = 0.786$, $p = 0.78$), Length vs A+T ($r_s = -0.322$, $t = 1.40$, $p = 0.17$)

| <i>C. barbarus</i> | | Correlations | | | |
|--------------------|--------|-------------------------|-------|-------|-------|
| Spearman's rho | Length | Correlation Coefficient | 1.000 | -.233 | .477* |
| | | Sig. (2-tailed) | . | .336 | .039 |
| | | N | 19 | 19 | 19 |
| Abundance | | Correlation Coefficient | -.233 | 1.000 | -.086 |
| | | Sig. (2-tailed) | .336 | . | .726 |
| | | N | 19 | 19 | 19 |
| K2P | | Correlation Coefficient | .477* | -.086 | 1.000 |
| | | Sig. (2-tailed) | .039 | .726 | . |
| | | N | 19 | 19 | 19 |

*. Correlation is significant at the 0.05 level (2-tailed).
Length vs abundance ($r_s = 0.233$, $t = 0.336$, $p = .31$), Length Vs K2P ($r_s = 0.477$, $t = 0.03$, $p = 0.03$)
K2P vs abundance ($r_s = -0.086$, $t = 0.726$, $p = 0.70$), Length vs A+T ($r_s = -0.322$, $t = 1.40$, $p = 0.17$)

| <i>C. abbreviatus</i> | | Correlations | | | |
|-----------------------|--------|-------------------------|--------|-------|--------|
| Spearman's rho | Length | Correlation Coefficient | 1.000 | .311 | -.531* |
| | | Sig. (2-tailed) | . | .196 | .023 |
| | | N | 19 | 19 | 18 |
| Abundance | | Correlation Coefficient | .311 | 1.000 | -.294 |
| | | Sig. (2-tailed) | .196 | . | .236 |
| | | N | 19 | 19 | 18 |
| K2P | | Correlation Coefficient | -.531* | -.294 | 1.000 |
| | | Sig. (2-tailed) | .023 | .236 | . |
| | | N | 18 | 18 | 18 |

*. Correlation is significant at the 0.05 level (2-tailed).
Length vs abundance ($r_s = -0.311$, $t = 0.196$, $p = .44$), Length Vs K2P ($r_s = 0.531$, $t = 0.023$, $p = 0.023$)
K2P vs abundance ($r_s = -0.294$, $t = 0.236$, $p = 0.23$), Length vs A+T ($r_s = -0.322$, $t = 1.40$, $p = 0.17$)

Figure S4. The Spearsman rank-order correlation test. There was no significant correlation observed between K2P divergence against monomer length ($r_s = -0.267$, $t = 0.270$, $p = 0.26$) and A+T content ($r_s = 0.02$, $t = 0.09$, $p = 0.92$) in *Calliptamus italicus* species. the K2P divergence has shown a positive correlation with monomer length ($r_s = 0.477$, $t = 0.03$, $p = 0.03$) in *Calliptamus barbarus* and in *Calliptamus abbreviatus* ($r_s = 0.531$, $t = 0.023$, $p = 0.023$).

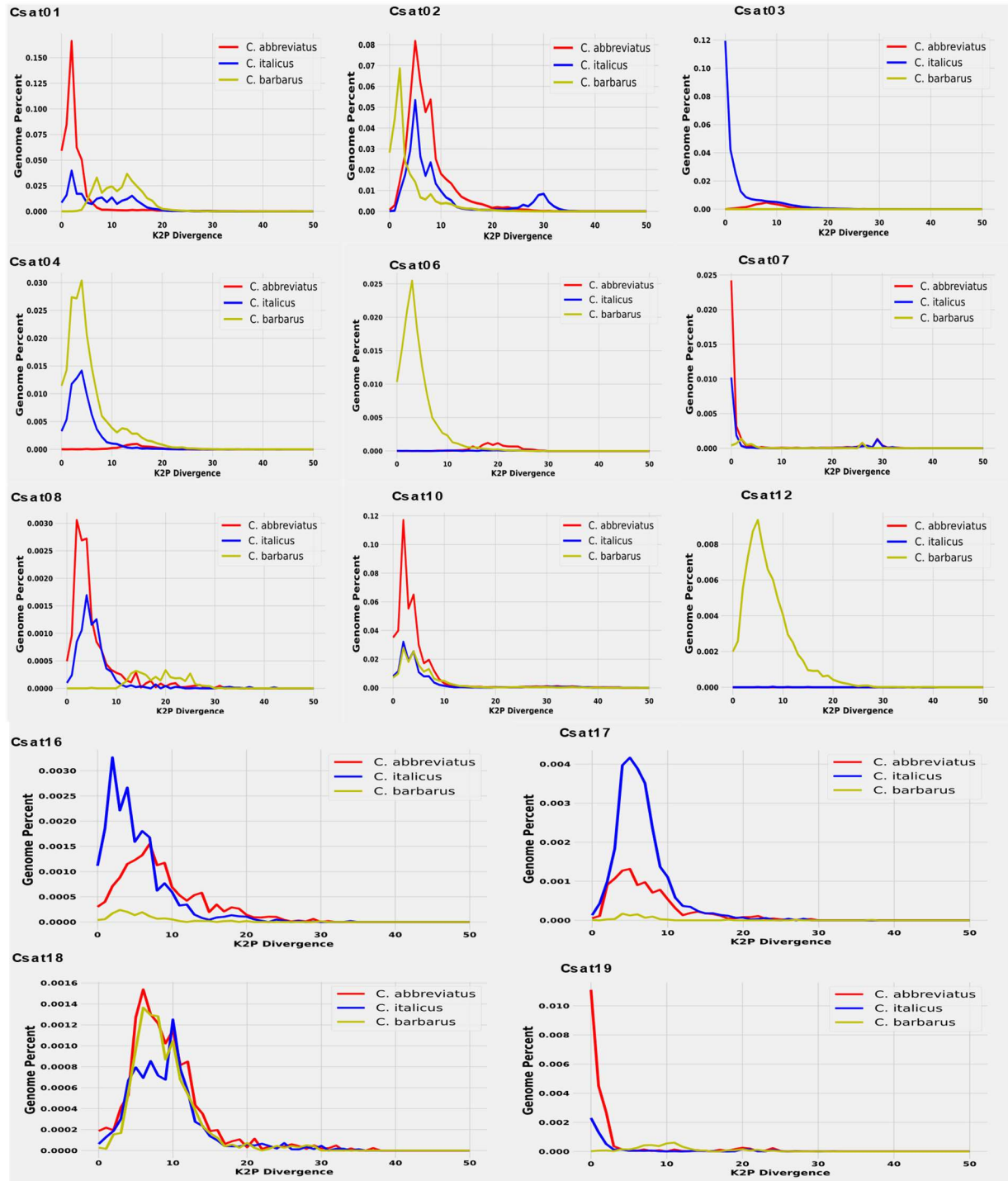


Figure S5. Satellitome comparative line graphs with single-peak and flattened distribution of abundance against the divergence.

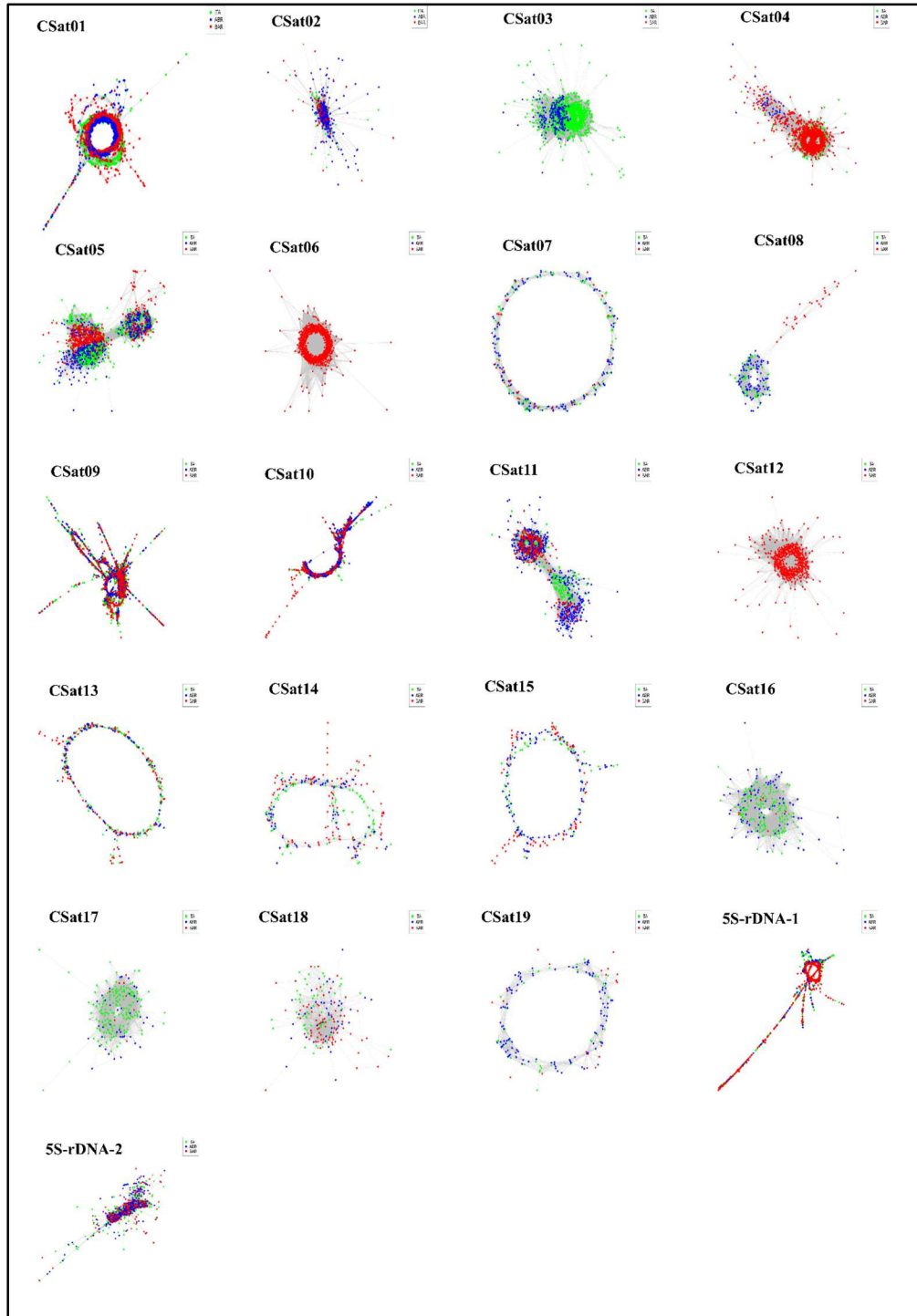


Figure S6. Satellitome graphical-structures for each family of satDNAs. The comparative graphical structures of satellite DNAs and rDNA-repeats reported in the Repeatexplorer2 output. Colors in the graph represent the species-specific reads (green-for-*italicus*, blue-for-*abbreviatus*, and red-for-*barbarus*) where the node denotes a specific read and the edges as a bridge (connecting lines) between the similar reads.

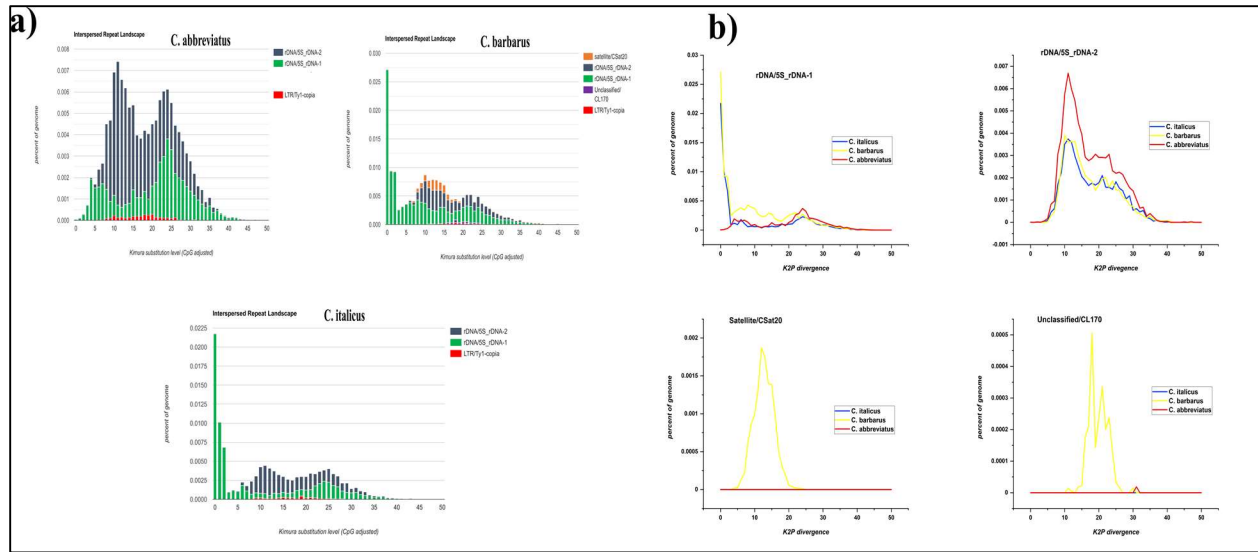
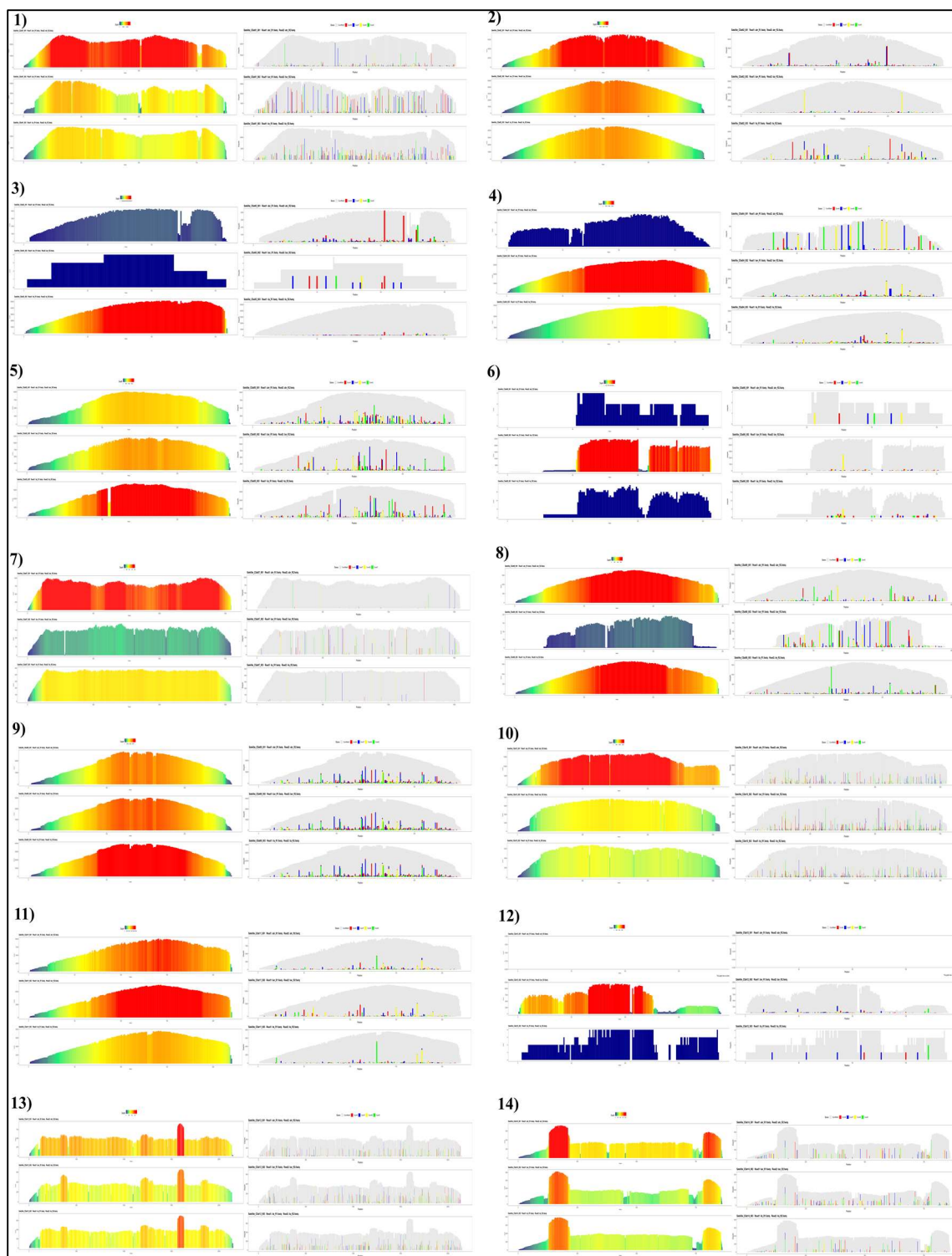


Figure S7. Interspersed repeat landscapes and line graphs of rDNAs and CSat20-45 family. The interspersed repeat landscape of rDNA-repeat, CSat20, and unclassified cluster has been shown here (a). In *C. barbarus*, a distinct individual repeat landscape demonstrates the existence of a single abundant peak of CSat20-245 satellite DNA. Similarly, the recent abundant copy of 5S-rDNA-01 in *C. italicus* and *C. barbarus* revealed one peak and multi-variant flat distribution in *C. abbreviatus*. There are two peaks of 5S-rDNA-02, the recent one and another ancient/degenerated highly divergent copy (b).



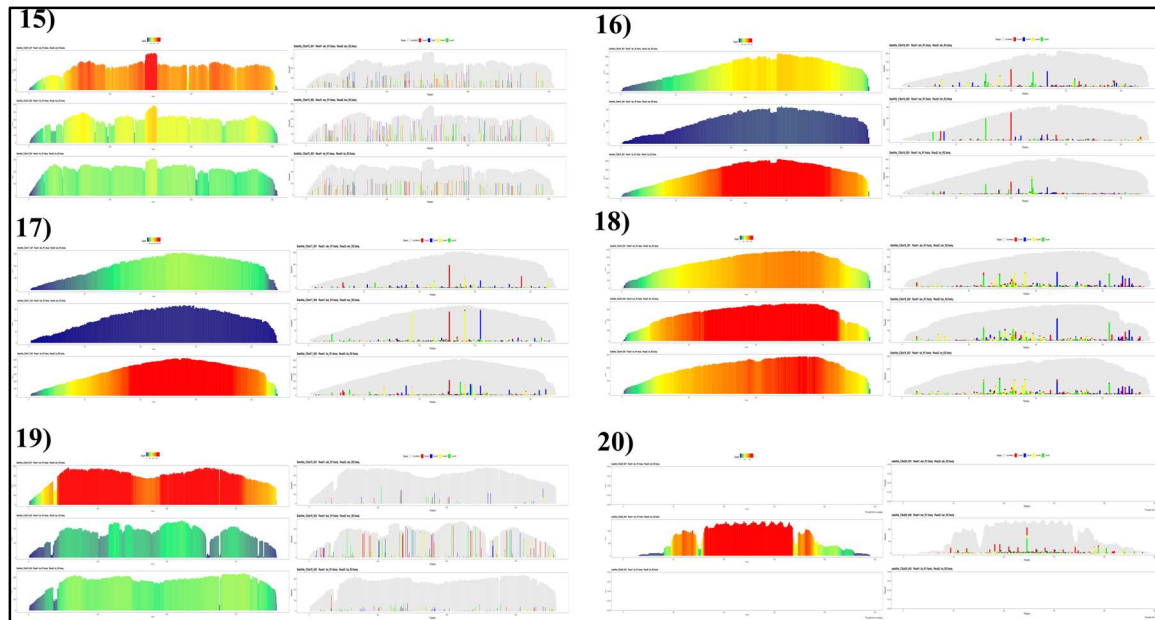


Figure S8. The individual satellite DNAs repeat and variant profiles demonstrate the strong species-specific signatures. Species profiles arranged in a sequence of *C. abbreviatus* => *C. barbarus* => *C. italicus*. Most of the satDNAs profiles have shown reasonable read depth coverage with the decrease of variation in the variant profiles, which are represented in dark red color. The CSat12 profile uneven coverage of repeats with sharp boundaries shows the differential amplification of fragmented copies of this repeat, implying the novel spread of satellite DNA sequence. Additionally, some profiles suggest the residual existence of some of the satDNAs degenerated copies such as CSat12 profile in *C. italicus*.

The detail of consensus sequences of the satDNAs and 5S-rDNAs identified in the current experiment.

>CSat01#Satellite/CSat01

gtaataggcagccactaagcagagtgtcgcagtgggaagcttactgggaccataactcacaggtccgtggatcgaaaccaagcctataagt
atcgtgcgcaatccagttgtgccactggggctacagcacagccttccaaacagccatattcacattaaatccgtcgtgtagcgaccagaaat
acgtcatctatcgtcatttacggctgtactgagacttcggcaactgcctacgaatgattcacactactctactttggtacaacgattacttgcaa
atggacagcttttagtcacggaatacgtgcagaaaaccgcgccttgcgtttgctaactgacacacagcgaaacaaggtaggtggcgtg
ttctaagttctgaaggagcacagcgaatgcgcatctccagcagaggcgctttccttgggtgctgccagtagggcgagaaggccagagg
gaagatgctatcgttgccaatggacaaaaggaaaaacaaaagcagaaaaaatccttccttgtgtagcaacacttttctgcgagactgagg
agaaagcagtggcctgtgacgcaacggataacgcctctgaccacgggcagaagattccagggtcaaactctggcaggggtcgtaattttgt
taattgggtggagcgttgctaggcaacggacctggccatcttactgctcttattcccacgggtatttcgagttgcaagccttgctgacacgata
aataccgcctcccgaagcgtcagcgtagcgtcagtcgagcaagtcgagccaagtcaagctgagagctgtaggaaatgctgcacatcttaa
attagatataaaaaacatcgcaggggaagacttctcatgagttccgtgtcagag

>CSat02#Satellite/CSat02

gaatatagtataaacagcattggcgattcagtgaaatttccgaactttcgtcgtgtctaaacgacttgcaagcgtttggcgctcatggcgca
cctcagcagccactgggcagtgctgggacaaccaaagaatcgatttagtataaacagcattggcgattcagtgaaatttccgaactttcgtc
gtgtctaaacgacttgcaagcgtttggcgctcatggcgcacctcagcagccactgggcagtgctgggacaaccaaagaatcgattgaata

>CSat03#Satellite/CSat03

gttagttgattcaatcgagatgcgaagagcaggattatgatgggaagcgttttgcgggcatggggcaactcagtaggcccgggatagt
tggggacaaccgtagaatcgatcgaatgcaggtaacaggagcactggcgatgggtctgaaatttctaaat

>CSat04#Satellite/CSat04

gcttctaagggaacgtccttctgtgtgtgctgactggctcgtgaacaattgcacatattgtcgttgaatacagtgctaaattaatgtaaag
ccactgagctacaccgggattttcatacatatccagacctgtatcgacaaaatcaactgtttcggagagtctcgtaatttgcgttc

>CSat05#Satellite/CSat05

ccttccaaaagtatttcacgatacaaaaagtaggtgtttcataatcagcatccatccagtagcgacagtgtagcgttgcagagttaatttc
gtttcgtattagttttacaagcaatcgacgactgagaaataacattgtaagcctttgtgtaacttctgtccaaaatctatttgtgtgttaacgcct
atggcattaaacataggttgaaaattcccccttaagggggaaatggggcctcctcctcccttacagcccgccttt

>CSat06#Satellite/CSat06

gtcgaggatttggctacctaagagacttaagagagtcgaggatttggctacgatttggctacctaagagagtcgatgatttggctaccta
agagagtcgagcgaggatttggctacctaagagagtggaatttggctacctaagagagtcga

>CSat07#Satellite/CSat07

actctgtcacacaccagaaagttttcataacgcaggcgttgactacaacagcttcccttcacagacgacttatccgactttgcacgacgt
cacgcagcgtcacgctagcgacatcctctcttaaaacttcagtcgagcctaaaaatatgagcacgtatctcctaggacacagggccacctc

ctaccgttggtgcacgatgtgtggagtcagcgcagggccgcaggctttcactgttcacgcctacaaaacctctgctcgttgtaaagagctg
aaaaaatcgcgagactccatgtcgtacacgatttcattggcacgacatctgccgtcaggtgtctcaacctcaacatcagcagctccccga
atggacgtgaaaaaagaaagctgtactggagatttcattgcttcggcacaaggcagttcttttcgacgcagcttgagtatcttatggaagt
gcttgtagctcctaagcaaattttggggaacaatggagggctgtgtgcacataataatgcatttactcggagttcagatccattgcage
cgtaagccttcgcaactgcctttctggtcaccagcacgctcctcactggaccttattgacagctcattgttctacatgctcgccagtcctatgtg
tttaaaacgttggagacgcgggtatcgatccccggtaacctctcgatgctaagcgagcgtctaccatctgagctacgtccccacactgcg
atgtgtagcctcgggaaggtaattcagtgacaaagatacaactactgccttcattccgcagacagccactaatctcaacaagcctcgtgaag
acggcgacaagtgttgactgcacttttagaccagtcccagatggacgtatgcagagtagcactcactatgtcgaaaatgattctaaggccgt
tcgctgaataaagctacaaccttgctgctgatgtaagctgttacacctagagacgtttcaccttgaggcagctcgagtgctgaaaatcct
ttcatcacagctcacatcacctcgctcagtgctccatcctgtgtgattctgacgctgctttggacatttcgctgattacgagaaggctcgacaa
cttacgcttaccaccaagggagtacaaaatttggaggcgccggggtgaacccgggacctttcacatgcaaagcgaacgctctaccagct
gagctacgccccacgtgctagtaaacgctctgggtgacctcctctgttcttactctgcactaacagacgttcacacagacagtatgtctcg
ttgctcacataaaataagtaacaacttttgccagctgttacgtcttacagtgaaaggtaacttggcataatcgctcctttctcgctccctgtcgacaatca
cacagcaagaaagtaaacacaagccaatctcaagtcggctgctgcactgactgtgcataatcaactagctgcctcacagggttttactgcgtac
cacgcgggtcttggaaactacatatgggagagcttctccattttcacg

>CSat08#Satellite/CSat08

tatacagctcacgtggtgtagtgcggtccgccaccatttacctgaaatgcaagctccagacatgacctggcgtaagaaggaaacgtgc
ttatttgagcaggcaatacgtctccaccattcgacttaaacgttccctccagtcataactgatgaactcgtgtaataatgtgggcacaca
tattggctcatatgcagagctgtgtttccaatgtgtgttttcatggcggaaccaatacgtgctgtcttcaaatctaccacattctgccac
ctaccattc

>CSat09#Satellite/CSat09

tacggatttcgacagaatccacagttttattccgatcttgatgaaattttgcacacttgaccttcaaaacaagaggaaggctactgtctacataa
aatttcgtatggtgcatggcggagggtactttacttacggacttcgacagaatccacagttttattccgatcttgatgaaattttgcacactga
ccttcaaaacaagaggaaggctactgtctacataaaattcgtaggtgcatggcgagggtactttact

>CSat10#Satellite/CSat10

taaccgtttaaatagtattttaccctgttcatttgaactcttgaataacattgtattagatcgccacacctaattcagggatatacacgtctcacag
tattggagccaacattttgagtgaatgctaaaatatgtgtcagattctgtttctgcgttctcgttgataatgctaggactggcagggaaagta
agagcctccttaagtactaggaagatctttctgcgcctcattccagtaaaacttggcatctccctgcagaagttcttgaatggacgtgcctt
gttacagaaatctttatgaagcgtcggttagtacgagcacatcccagggaagcttctcacatcacgaatgtgtcggttagttggcaattctgt
gactgcccttattttctgtatcaggacggactccatctccgttaactagggtgccccaggattttatctcttgggcgacaaataggcgcttct
cggattcagacggagacatgcagttgaacacacttcaacacagctgacaggcgactcagatgttcttcaaatgttttcgagaaaacgacaa
atcatctagatagcaaagacacgtcgtccacttaagggtgtcgaagcaagtagtccatcatgcgtttgaatgtggccggagcattacatagtc
caaatagcattactttgaattcatagaggccgtcaggtgaataaaagccgtcttttcctgtcagcttcgtcaacctcgatttgccaataacct
gtttgcatgtccatggttgagaaatacttagcacattcaagcagctaaagggtgtcgtcaatacgcggcagtggttagacgtctttcttgtga
ctttgttcagccgagataatcgacacagaaacgccagtgccatatttcttcttacgaggaccactggagaagaccaaggactctctgag
gggtgaataatgtctcgtgcagcatcttccacttctcccggtcattcgtcttcagctgggtgacatcctatacgaatgctagctaattgtag
gatgatccccagtggtgatacggctctttaccgtgggctgttttgcatggctcttctcctgctgggctttgaatgcacccgaaaattggcgtagt

atagctaacacctgctggcggtgttcttgggtcaggctgggcccatttgaattccacagttgtccctccagcggtgtgtctgtattaacaac
agagcatgggtcttcgtgaa

>CSat11#Satellite/CSat11

tattttgattgcagcagccgctccccagcgaagaggacgccagtggactacgatcaagacacccccacacaaaggcttctttgagatgtg
ggcaagggaagaaatttcttcattttggtaagtatttttgacgtttctaagtgtatataattcactcagtgcgtacactaggagatatctaca
aaaaatggaagcttaattaacattttcatgcc

>CSat12#Satellite/CSat12

ggggcggttgcaactgcttctggggcggttgcaactgcttctcaactgcttctggggcggttggttctggggcggttgcaactgcttctgg
ggcggttgcaactgcttctggggcggttgcaacggttgcaactgcttctggggcggttgcaactgcttctggggcggttgcaactgcttctgg
actgc

>CSat13#Satellite/CSat13

cttgacgctgttgagtggacaggtgaaacgcactgccacctggttgcctctgagtagcttaaggcggtgctgtgcagccactgtgaaatga
aggagtgtgtcgtgtgcctgtgtcgtcacctcccctcgtgtctctcagtcgattttgatgcttgccttgatataggccgaactgagagcgta
gctctcgctcagctctcgaaagtcgagacaagtcgagacacatatcacactacgggccgactgcaatgagttgtcgggggaaaaac
gttaattttaaggcgctgcagacgtgttcatacgaataaagaaggcatgttgcggtggccgggaatcgaaaccggatcaactgcttg
gaaggcaactatgctgaccattacaccaccacgcacggcgcggaagagagttacgccgaggcgatcggttcccgcctgccagcagc
ggccgaagttgatcgtagctgtaggcgattacgatgtaggtgagcacatccacacacattcggacaacgcctttacgcggattttgcgtctt
ttcacgacagacgccaccgacgccgactcagaggatcgcatgtagcgtcattgtaacgagtagactgcaggactctgttcaatagcgt
gttttcgggaggataagacagcgctaggcggcagtccttctcactgcaaacgactgctgaggaagcaccaggaagctcatctccagcc
gagcatcggttggttcagtggtagaatgctcgctgccacgcggggcgcccggttcgattcccggcgatgcatcattttatagtttctgca
acaattcggccgatgcttacttatttgagctgcacgtgcttcaattatgtccaccgggactcgctgccagaaaaacaaacatgctgcacgc
acgagacgttgctggacgctggcgccgaaatgtcagcagactatggtcggctcggcgctacgagttgagtgctcgttgggtgcttggtg
atgtggcgtaacggacaagcggagctgccttcggtaggaaaaatcgagctccatttaacctgctgagcagacaatgtgcatgtagcagc
tgaagacaccattaaggaagcaaaactgccctaatttagagtacttacaaatttctagaagcgtgcaagccaggtgcctcggtagcgca
gtaggcagcgcgtaagtctcataatcttaaggctcgtgagttcgatcctcaccggggcatttaatttagtctcgatcagcgccgaattcacgg
cggtgctgttgtaggaaacgatcttatttgttgttgaaccacgagttttgcagcacaaaacgagaaaatttttgctccagctgttact
accttgcttcatctctcgcgtaggaatacacgatgcaaaaagcgatgggtcttttctgtgttctcgacatttagtatacgtaaaggttctcac
aaaccgagaggcgcgccgacgcagactgcagattggacacgaatacgcattggagtgctgtaaacgagacgttggaagtgcgtctcc
ggtgtggtctagtggttaggatacctggctttcacccaggaggcccggttcgattcccgggtaccggaacagaattttccgcacacaact
cgtagagttttagccctcgaaataccgtttctggtcctcctcgtaggattagtagtaggacctgaataacaggagaagagcgtgctatgcc
attggacagcaacatgcaacgtgcttctctgtatcgagcaagggtctgtttcacgaggccggttagctcagttggttagagcgctcgtgcta
ataacgcgaaggctggtgggttcgatccccccacgggccacgtcgatttttctattgaaaaaaccaacgccgattttcgacaggcaaatggtg
gcaaatgtcattacttttgtgtggaactgagacaggatccgatcccgatttgcgagacacgcttcagccttcatccttaacggccatatcac

tttgaataacctgtttctcgtccgatctccgctattagcaactttgggccttgtcattatttgggtgtgacagccggggaacacaaagtgtg
tcgactgcattaacttatttgcctcat

>CSat14#Satellite/CSat14

ctccttcgtagcagctagtgttagcgatgaaagcacttcggaaaataacgcaggtacatcgcttaattgtcaacataattgctctaaactgca
gcaaattgcatacgtctaaagactgttcgtcagcaagcagtcgtggccgagtggttaaggcgtctgactagaaatcagattccctctgggag
cgtaggttcgagtcctaccggctgcgttcgattttgaataaaaacaagcagatatttcgcagaaatttgaaagatgccgataacaggtgga
agcagggccactgatgcagttaccaacaagacgcggatttctgttttaggaatgtttatttagttcacgacggccgctccttctgtacagccatcg
gttcacctgcaccaagcgtacgacagcgccattggactaggacggcagagcgccagcactgagccacgaggccccagtcgtttcgtcga
gccgtctcgggtgtttgtaaacacgcaaggtgctgcatgtactagaaagtgtagtgggcagcgatcactcattactgttcttaaatttcggttc
attctttcgattacgatttccgttatcaggcagcggttccttgtcttatagatctcgagctacttggaaagtgggtccatcatttaagatcccgcaa
actagcgtcagcgtggcgctcagtgagggaagtctgtgaagtcgccagtggagccagaagccagtaattgcaatactacgcattcacacacac
atgtgagttggcatgcactccacaatcgccgtgtgtgagaccggatagctcagtcggtagagcattaggcttttaacctaagggtccagggt
tcaagtcctgtccggggaagatttaa

>CSat15#Satellite/CSat15

gaactgtgatgtagcaaaattatcggcacagcgccgttcgagagagtttggctgacacctccacgtctaagacaggatatgactgctacac
tgtaagtattgttaaaatcgagtaaacgtgtttgttaatggcaccactacttccgtaggtctgcattcagttgtcacctctcagagacctttgc
aatgaacaaaaatcacttgcagaaaagacattagacggttaagaagagatcgtgtaaggaccacaaggccgaacagtagtgttcccat
gtgattcgttcacaagcaggcggtgtgcccggctagctcagtcggtagagcatgagactcttaatctcagggctgtgggttcgagcccca
cgctgggcgaggtagaattttgtctcctgcagattcaagatgcctttgtttatgaaatctacttaacggacgtagctgcatagcagctgc
ctggctctactacagtctcagagaaacgatactggaagctgcaggtgattcggtaaacacggtaaaatgccttgttctgaaagtacaggtg
tcgttcgttgttagtacaccggatatgtgtgagacatgatggggagcagtaatgacgcttcttagttgcaaattttagtcgtaatacatgtt
attttcaggtgaagccagacgattcacatgcttgcattggacgaagtaccagaaggcacaacgggcgccgctcttagctcagtggcaga
gcactggtctagtaaaccaggggtcgtgagttcgatctcacaggaggcaaatgcattttgaaagcagttgcgcttctggccatttcgaa
agttctttccagaaatacgaagttggcaatgggcatcaactacaatacaaatctcgcatgtgaatagggtggaatgttgttttaagtag
gtcgcaaaacggcactgtttttggcggtttaaagggtatcgatgccttctactactcgatcccttatttttacgagtaataaacactctcg
cgaatgtcgtcgtcgtcggcgccgcccgcctcttgagcagtggttggtcaaacgccattgtatgacaagcaggggagggaccacctgctgt
cgattgagaaggcagtttagtgttggctctgatttcgaaactctgtttcatcagtcacatacgttggtggaaaatgacgggtgtataggaaaca
ggaagacgaagcgtcgcatttttagcagtgaaatttgaggtcaagaatggcgccatagagggaagcaccttcgttaaggtgtacgacgtt
tagaaatgagacgtatgtaaggaggtgttgaacgtcagtgaccgtgtggcctaattggataaggcgtcggacttcggatccgaagattgca
ggttcgaatcctgtcaggtcgtgttttccactctgcaaaagagacataaccgttttactgtgatattagagcaatacaaaaccctctcaaagtt
tcagcgtccggctgcagtttgagagaccagtttgagttgactgacaagac

>CSat16#Satellite/CSat16

atacagaagcattgtggtcactcgccaagctgggggttaaataatttttagcagaagatgtgaaacaagcaggagcctgtgttcttttaggaga
gagcagtggtgtgtgtgtgtttatcctttttgacgtttacttggggggctctgccatgtaatacaaaagccttttgtagtaactgaatcacaggtt
ctcccctaacacttataaaaaagaaacagatatcccc

>CSat17#Satellite/CSat17

gcagcctgggtagcctaagtggtaacaggaggataaactgttctcaaatttctgccaggtaggtagacacaggggtgctacgccacagccta
aatattcggtatgtctctgtaatatataggggtgtggctactcgccagtcataattgttaaaagagtaatttttaattaacgaaaaatgaagctg
ggaagtatcattccaactcacctaccccaaaggagg

>CSat18#Satellite/CSat18

cggcgctccaatttcagacgtccataactaaataaataattcgtcgtcgcgaatatccactttcagcatccatagtagactacttatttagttatgtga
caaaaaatcaaatcatttctatggctctattaggatctataggccactgaataccgaaggaaatacgcgggacgcctgggtgctgctct

>CSat19#Satellite/CSat19

aaatcgaggtgaaatgcagaaaactcgactcaaatacaaaattcagaaagtcgtccattatacacatttactatgtatgacaataaaacgtcg
tcgtcgtcgccgccgacgcacgtcatatggaacacatgccgtaaaacacggaatagtgcttagaaacgcaggggtgctaccgacagtatg
aaaattcgacagggtagcaactgaccaatactggacaggtgactcgataccgctgcattcgtactgtcctaggagggtcttaacgttgtct
gctgtgagtatatggacctgaaagtgaatactgggtgtacattctgcactacatctttgcggcggtcgttgcggacgtcaaacgagggcgga
agcttatggttgcgtagtgtggcgccagatacacatcaagaaacgagctacaagtatagtaaatacatgaaatgagggtaccacacgcaa
gtgtcaggatggccgagcgggtctaaggcgccagactcaaggagcaccttggctgcaaatgcagcctgagccttctggctcctcgtctgag
ggcgtgggttcgaatccactcctgacaaagattttactctttcgtacacaagtgtgcacatcgagagaacgggtgtaatggggtaaaac
atgcagaaacgcacatcttgcgtggaacctacacctgccctatcaaaactcaactctgcaatagtgtgaagcttcaaacgcagagtactggttgca
aatgcggcggttaccctccgctgtctcactgacctccagctcacagtcgcacaaatattataatgagcactcgagatcttactgaatgtgtct
agacgcaaactgctaatacgaatgcaaggaaacactacatccttaccactttacgaggttaaccctct

>CSat20#satellite/CSat20

gacctatgagcatgaatgacccaaatgacctatgacctagacctagacctaaagacccaaaagacccaaaagacccaaaactaaaagacccaaa
atgacccaaaagacccaaaagacccaaaagacccaaaagacccaaaagacccaaaagacccaaaagacccaaaagacccaaagagccc
aaaagacccaaaacctaataaaacacaaaaggcccaaaaaaaccaaaaagaacaaaagcccaaaaa

>5S_rDNA-1#rDNA/5S_rDNA-1

tactggtgtttccataagaaataacattaccgaaatgaacatgacattccatagtgatgaaaatacagagaataatgggcggggcaaaagct
acgaaatgcactgtgagaagcacaagctgtatgattccagaggcattttgtgaaataaagtagaacctgttactcagtagcagtgtaatttc
cccatttgtaataaagtttatctcttttcacatgtcccaacgcttaatgccactgttttcgaacgtctcgccgctctcgagatgtttatcat
ccttttgcgtcatatgggccagaccccgagcggcagcgagcggcagcgagcaaaagtcgggacaagtcgggacggaaggggagggg
gcacctgcgaatgcagcttgcactcgctataaatgcctctaattttgcgagttgcgtgtcgcgagctttacctcgctagcagtggcgctctcc
agcacgacaatgcggtcgctgtgacgtgaagcatagtagcgtgcaacgtcccgcctcctcgcggaagtgactggcggtgatatagggc
agcccgctcgacgtggcgggccacctgccaattcggcagacgctcctggggcgcgaaaggcgcgccctgtggcgggagaagatg
cattccatcaaattaccgacctgtttctgccgaaaattcaactttagggtgtcaccagaggagcagaagccgattcctggcgcgccactacatt
ttactggcgccaacggccatacaacgttgaatacaccggttctcgtccgatcacggaagttaagcaacattgggcccgggttagtacttggat
gggtgaccgctgggaaccgaaataaacacgaggtacaaaattgatgaaaatgggagaacaaatgagtgaagcaaaactaccaactgt
gctttgataataacgaagctgcatgagtgagtgatattttctgaaatattacagagccattactcagtagcagtgtaattttccgaatttga
aataaagggttatctttatcgtaaaaaatgggtgctgttgagctttttgtctcctatttctacttttctccacccccctcattgttaaactaccgt
tttcttgc

>5S_rDNA-2#rDNA/5S_rDNA-2

gtctgcgggcgctgttggcaagcggggtgcactcaaccctgtgaggcaaattcaggatcaacttgattgagaagtagcggctctggtctt
gaaaactgacatacggccgagagagcgggtgtgctgaccacacaccactccataccgcagccggcgacgcatttgggccgaggatgacac
ggcggcctgtccgtaccgatgggcccttcgcggcctgttccgt

>CL170#Unclassified/CL170

tgttttcaaataatccccagcaccgacacacagtatggtactcagtgtcagatacagcaggaaaatctgattgcagtgtagggcccaagt
tataaaaaatttagtatgcagcattgtagtacttgaactcaaaaggaacaaacttcggaccctataaagtcaaaccaggaatcatatctga
cgcaataagtat