**SM Doris et al. 2015**

# SUPPLEMENTARY MATERIALS

**Figure S1. Evolutionary distribution of eukaryotic (yellow), archaeal (green), and bacterial (red) organisms.** The phylogenetic relationships of organisms whose 23S-28S rRNA sequences were included in FLORA. The cladogram was derived from the ARB/SILVA LSU Ref guide tree using the interactive tree of life (iTOL) software platform (hdp://itol.embl.de/). The number of species included for each group is indicated by the number in parentheses.

| **EUKARYA** | **ARCHAEA** | **BACTERIA** |
|---|---|---|
| A Diplomonads (2) | A Methanobacteria (3) | A Aquificae (4) |
| B Parabasalids (2) | B Methanococci (5) | B Thermotogae (10) |
| C Amoebozoa (2) | C Korarchaeota (1) | C Deinococcus - Thermus (3) |
| D Rhizaria (1) | D Thermoprotei (14) | D Chloroflexi (4) |
| E Rhodophyta (3) | E Methanopyri (1) | E Dictyoglomi (1) |
| F Embryophyta (100) | F Thermococci (5) | F Fusobacteria (5) |
| G Porifera (12) | G Archaeoglobi (1) | G Firmicutes (145) |
| H Fungi (70) | H Thermoplasmata (3) | H Tenericutes (22) |
| I Alveolata (34) | I Thermoprotei (15) | I Cyanobacteria (186) |
| J Stramenophiles (26) | J Halobacteria (11) | J Actinobacteria (64) |
| K Mollusca (11) | K Methanomicrobia (34) | K Epsilonbacteria (18) |
| L Platyhelminthes (24) | | L PVC – Planctobacteria (18) |
| M Chordata (6) | | M Spirochaetes (43) |
| N Arthropoda(5) | | N Acidobacteria (3) |
| O Nematoda (40) | | O Synergistetes (2) |
| | | P Deltaproteobacteria (23) |
| | | Q Mitochondria (36) |
| | | R Alphaproteobacteria (89) |
| | | S Betaproteobacteria (56) |
| | | T Gammaproteobacteria (179) |

**Figure S1.**

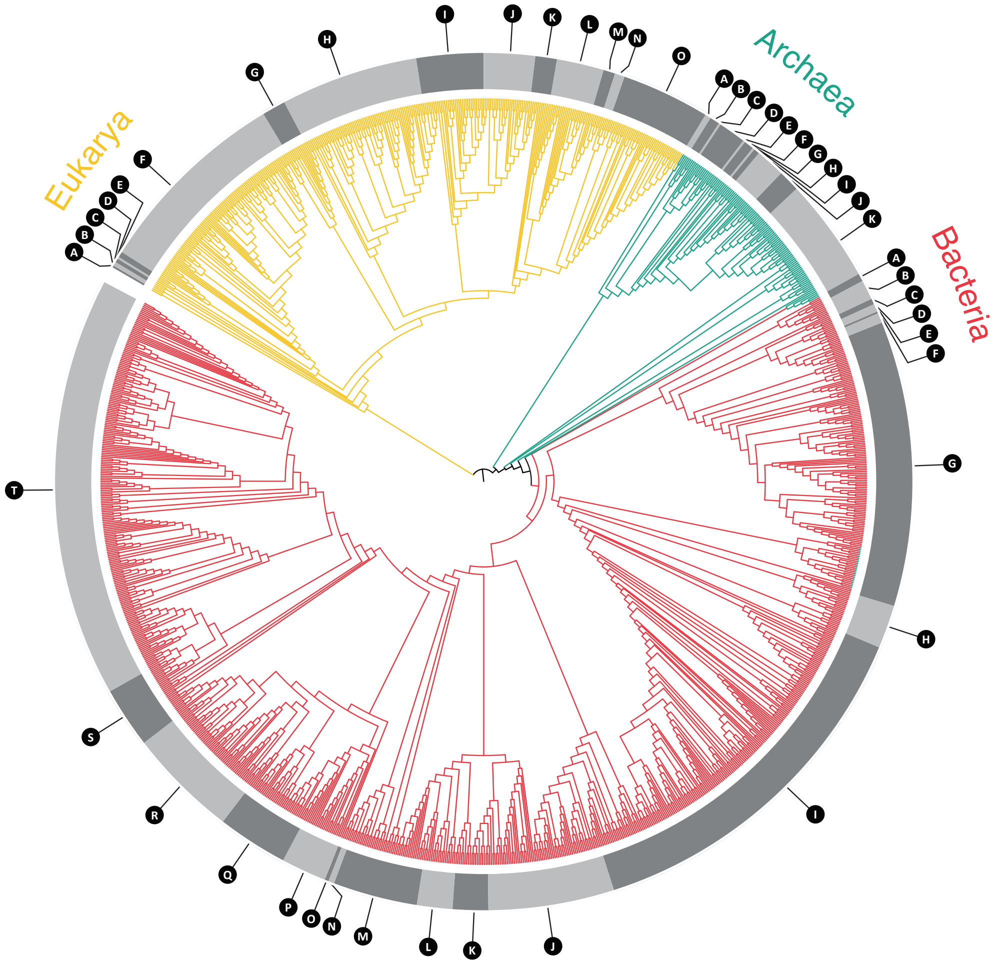

**Figure S2. Schematic of universal conserved nucleotide element (uCNE) identification.** Using the ARB aligner, the intradomain CNEs are aligned by homologous position to measure the length of overlapping nucleotides (nt) in all three domains. Homologous sequences whose overlap is equal to 6 or more nucleotides are defined as uCNEs and their consensus sequence and conservation is measured. In the first scenario eCNE1, aCNE2, and bCNE2 share a 5 nt core sequence (coordinates on right) and thus are not considered to form a uCNE. In scenario two eCNE2, aCNE3, and bCNE3 share a 7 nt core element and after deriving its consensus sequence is classified as a uCNE greater than 90% conserved in all three domains.

## Figure S2.

**uCNE1**
**conservation for consensus sequence CCGAUAG**

- **97.7% conserved Eukarya**
- **98.8% conserved Archaea**
- **97.8% conserved Bacteria**

**Supplementary Table 1A. |Eukarya conserved nucleotide elements**

|  |  |  | **Structural filter** |  |  |  |
|---|---|---|---|---|---|---|
|  |  |  | ***S. cerevisiae*** |  | ***A. thaliana*** |  |
| **eCNE No.** | **eCNE sequence** | **Position** | **Length** | **IC Score** | **Length** | **IC Score** |
| 1 | GCUAAAUA | 319 | 8 | 15.0 | 8 | 15.1 |
| 2 | CCGAUAGC | 338 | 8 | 15.2 | 8 | 15.3 |
| 3 | AACAAGUAC | 347 | 9 | 17.1 | 9 | 17.2 |
| 4 | CCCGUCUUGAAACACGGACCAAG | 635 | 23 | 44.3 | 23 | 44.5 |
| 5 | ACCCGAA | 800 | 7 | 12.8 | 7 | 12.9 |
| 6 | AACUAUGC | 815 | 8 | 14.5 | 8 | 14.6 |
| 7 | GAAACUCUG | 844 | 9 | 16.9 | 9 | 17.0 |
| 8 | CUGACGUGCAAAUCG | 872 | 15 | 29.0 | 15 | 29.2 |
| 9 | GGGCGAAAGACUAAUCGAACCAUCUAGUAGCUGGUUCCC | 907 | 39 | 72.2 | 39 | 74.2 |
| 10 | AAGUUUCCCUCAGGAUAGC | 950 | 19 | 36.1 | 19 | 36.3 |
| 11 | GGUAAAGC | 992 | 8 | 14.9 | 8 | 14.9 |
| 12 | AAUGAUUAG | 1001 | 9 | 15.1 | 9 | 16.8 |
| 13 | CCUAUUCUCAAACUUUAA | 1036 | 18 | 34.5 | 18 | 34.7 |
| 14 | GUGGGCCA | 1112 | 8 | 15.0 | 8 | 15.0 |
| 15 | UGGUAAGCA | 1124 | 9 | 16.7 | 9 | 16.7 |
| 16 | ACUGGCG | 1135 | 7 | 12.8 | 7 | 12.8 |
| 17 | UGAACC | 1150 | 6 | 11.2 | 6 | 11.2 |
| 18 | GACAGCA | 1221 | 7 | 12.8 | 7 | 12.8 |
| 19 | GACGGUGG | 1229 | 8 | 14.5 | 8 | 14.5 |
| 20 | CAUGGAAGUCG | 1238 | 11 | 20.5 | 11 | 20.5 |
| 21 | AUCCGCUAAGGAGUGUGUAACAACUCACCUGCCGAAU | 1251 | 37 | 71.8 | 37 | 71.7 |
| 22 | CUAGCCCUGAAAAUGGAUGGCGCU | 1291 | 24 | 42.7 | 24 | 44.4 |
| 23 | GCAGAUCUUGGU | 1430 | 12 | 22.3 | 12 | 22.4 |
| 24 | GGUAGUAGCAAAUAUUCA | 1442 | 18 | 33.2 | 18 | 33.2 |
| 25 | GGUUCCAU | 1491 | 8 | 14.5 | 8 | 14.5 |
| 26 | UCCUAAG | 1529 | 7 | 13.3 | 7 | 13.3 |
| 27 | UCUUUUCU | 1682 | 8 | 15.6 | 8 | 15.5 |
| 28 | CCUUGAAAA | 1790 | 9 | 16.8 | 9 | 16.8 |
| 29 | UCGUACU | 1829 | 7 | 12.5 | 7 | 12.5 |
| 30 | AACCGCAUCAGGUCUCCAAGGU | 1839 | 22 | 41.5 | 22 | 41.5 |
| 31 | CAGCCUCUG | 1864 | 9 | 16.3 | 9 | 16.4 |
| 32 | AGGGAAGUCGGCAA | 1894 | 14 | 26.2 | 14 | 26.2 |
| 33 | GAUCCGUAACUUCG | 1912 | 14 | 26.4 | 14 | 26.4 |
| 34 | AGGAUUGGCUCU | 1931 | 12 | 22.6 | 12 | 22.6 |
| 35 | AUCCGACUGUUUAAUUAAAACA | 2125 | 22 | 42.0 | 22 | 42.0 |
| 36 | GUGAUUUCUGCCCAGUGCUCUGAAUGUCAA | 2184 | 30 | 58.5 | 30 | 58.4 |
| 37 | AAUUCAA | 2222 | 7 | 13.1 | 7 | 13.0 |
| 38 | CAAGCGCGGGUAAACGGCGGGAGUAACUAUGACUCUCUUAAGGUAGCCAAAUGCCUCGUCAUCUAAUUA | 2230 | 69 | 133.2 | 69 | 133.1 |
| 39 | UGACGCGCAUGAAUGGAUUAACGAGAUUCCCACUGUCCCUA | 2300 | 41 | 79.0 | 41 | 78.9 |
| 40 | UCUACUAUCUAGCGAAACCACAGCCAAGGGAACGG | 2341 | 35 | 63.0 | 35 | 64.4 |
| 41 | AGCGGGGAAAGAAGACCCUGUUGAGCUUGACUCUAGU | 2389 | 37 | 71.9 | 37 | 71.9 |
| 42 | AAAUACCACUAC | 2483 | 12 | 22.1 | 12 | 22.1 |
| 43 | UUUACUUAUU | 2507 | 10 | 18.5 | 10 | 18.4 |
| 44 | GAGUUUG | 2607 | 7 | 13.0 | 7 | 12.9 |
| 45 | CUGGGGC | 2615 | 7 | 13.2 | 7 | 13.2 |
| 46 | ACAUCUGU | 2625 | 8 | 15.2 | 8 | 15.2 |
| 47 | GUGUCCUAAG | 2648 | 10 | 18.3 | 10 | 18.3 |
| 48 | ACAGAAAUCU | 2673 | 10 | 18.4 | 9 | 16.6 |
| 49 | UUGAUU | 2709 | 6 | 11.2 | 6 | 11.2 |
| 50 | AUUUUCAGU | 2717 | 8 | 14.7 | 6 | 11.0 |
| 51 | UGGCCUAUCGAUCCUUUA | 2748 | 18 | 33.6 | 18 | 33.6 |
| 52 | CAGAAAAGUUACCACAGGGAUAACUGGCUUGUGGC | 2794 | 35 | 68.4 | 35 | 68.3 |
| 53 | GCCAAGCGUUCAUAGCGACGUUGCUUUUUGAUCCUUCGAUGUCGGCUCUUCCUAUCAUU | 2830 | 59 | 115.5 | 59 | 115.4 |
| 54 | GGAUUGUUCACCCAC | 2913 | 15 | 29.3 | 15 | 29.3 |
| 55 | AGGGAACGUGAGCUGGGUUUAGACCGUCGUGAGACAGGUUAGUUUUACCCUACUGA | 2932 | 56 | 109.5 | 56 | 109.4 |
| 56 | UAGUACGAGAGGAAC | 3017 | 15 | 28.3 | 15 | 28.2 |
| 57 | CGCCUCUA | 3111 | 8 | 14.7 | 8 | 14.7 |

**Supplementary Table 1B. | Archaea conserved nucleotide elements**

| | | | Structural filter | | | |
|---|---|---|---|---|---|---|
| | | | H. marismortui | | S. solfataricus | |
| aCNE No. | aCNE sequence | Position | Length | IC Score | Length | IC Score |
| 1 | AAACAUCUUA | 165 | 10 | 18.1 | 10 | 18.1 |
| 2 | UAAAUA | 434 | 6 | 11.1 | 6 | 11.1 |
| 3 | ACCGAUAG | 449 | 8 | 15.2 | 8 | 15.2 |
| 4 | CUGAAAAG | 480 | 8 | 15.4 | 8 | 15.4 |
| 5 | UGAAAC | 517 | 6 | 11.4 | 6 | 11.4 |
| 6 | CGAUCUA | 773 | 7 | 13.4 | 7 | 13.4 |
| 7 | CCAAUC | 878 | 6 | 11.2 | 6 | 11.2 |
| 8 | CUGGUUCCC | 898 | 9 | 16.1 | 9 | 16.1 |
| 9 | UCAAACUCCGAA | 1002 | 12 | 22.8 | 12 | 22.8 |
| 10 | GGUUAAGG | 1092 | 8 | 14.3 | 8 | 14.3 |
| 11 | CUAAGUG | 1114 | 7 | 13.0 | 7 | 13.0 |
| 12 | AGCAGCUA | 1173 | 8 | 14.7 | 8 | 14.7 |
| 13 | CGUAACAG | 1195 | 8 | 14.5 | 9 | 15.9 |
| 14 | UGGACC | 1336 | 6 | 11.2 | 6 | 11.2 |
| 15 | AUCCUG | 1356 | 6 | 11.0 | 6 | 11.0 |
| 16 | GGUCCUAAG | 1450 | 9 | 16.1 | 9 | 16.1 |
| 17 | GGUUAAUAUUCC | 1495 | 12 | 24.5 | 12 | 24.5 |
| 18 | CGUAAU | 1592 | 6 | 11.1 | 6 | 11.1 |
| 19 | UGAAAA | 1651 | 6 | 11.1 | 6 | 11.1 |
| 20 | CCGUACC | 1671 | 7 | 13.1 | 7 | 13.1 |
| 21 | AGGGAA | 1739 | 6 | 11.0 | 6 | 11.0 |
| 22 | UCGGCAAAUU | 1746 | 10 | 18.9 | 10 | 18.9 |
| 23 | UAACUU | 1763 | 6 | 11.2 | 6 | 11.2 |
| 24 | GUCGCA | 1803 | 6 | 11.1 | 6 | 11.1 |
| 25 | GACUGUUUAAU | 1825 | 11 | 20.1 | 11 | 20.1 |
| 26 | AACAUA | 1839 | 6 | 11.1 | 6 | 11.1 |
| 27 | GGUAACUAU | 1947 | 9 | 16.8 | 9 | 16.8 |
| 28 | ACCCUCUUAAGGUAGC | 1957 | 16 | 31.6 | 16 | 31.6 |
| 29 | UACCUUGCC | 1977 | 9 | 16.2 | 9 | 16.1 |
| 30 | GCAUGAAU | 2002 | 8 | 15.2 | 8 | 15.2 |
| 31 | CACUGUCCC | 2026 | 9 | 17.2 | 9 | 17.2 |
| 32 | AAGACCC | 2097 | 7 | 13.4 | 7 | 13.4 |
| 33 | GAGCUUUACUGCA | 2108 | 13 | 24.4 | 13 | 24.4 |
| 34 | GCAGUU | 2269 | 6 | 11.2 | 6 | 11.2 |
| 35 | UGGGGC | 2279 | 6 | 11.0 | 6 | 11.0 |
| 36 | AGAAAA | 2461 | 6 | 11.1 | 6 | 11.1 |
| 37 | CUACCCC | 2468 | 7 | 12.4 | 7 | 12.4 |
| 38 | GGAUAAC | 2477 | 7 | 12.8 | 7 | 12.8 |
| 39 | UUGCUACCUC | 2523 | 10 | 18.6 | 10 | 18.6 |
| 40 | GAUGUCG | 2533 | 7 | 13.0 | 7 | 13.0 |
| 41 | CCAUCCUG | 2547 | 8 | 15.2 | 9 | 16.8 |
| 42 | CAAGGGU | 2570 | 7 | 13.4 | 7 | 13.4 |
| 43 | CCUAUUAAAGG | 2588 | 11 | 20.3 | 11 | 20.3 |
| 44 | UGAGCUGGGUUUAGACCGUCGUGAGACAGGU | 2605 | 31 | 58.3 | 31 | 58.3 |
| 45 | UAGUACGAGAGGAAC | 2685 | 15 | 28.0 | 15 | 28.0 |
| 46 | GUUGUC | 2726 | 6 | 11.2 | 6 | 11.1 |
| 47 | GCUGAA | 2774 | 6 | 11.4 | 6 | 11.4 |
| 48 | GCAUCUAAGC | 2781 | 10 | 19.7 | 10 | 19.7 |

**Supplementary Table 1C. |Bacteria conserved nucleotide elements**

| | | | Structural filter | | | |
|---|---|---|---|---|---|---|
| | | | E. coli | | C. ramosum | |
| **bCNE No.** | **bCNE sequence** | **Position** | **Length** | **IC Score** | **Length** | **IC Score** |
| 1 | UGAAACAUCU | 193 | 10 | 19.3 | 10 | 19.3 |
| 2 | CUAAAU | 426 | 6 | 11.1 | 6 | 11.1 |
| 3 | ACCGAUAG | 443 | 8 | 15.0 | 8 | 15.0 |
| 4 | AGUACCGU | 457 | 8 | 15.1 | 8 | 15.1 |
| 5 | CCUUUUG | 564 | 7 | 13.4 | 7 | 13.4 |
| 6 | ACCCGAA | 670 | 7 | 13.2 | 7 | 13.2 |
| 7 | UGAUCUA | 683 | 7 | 13.2 | 7 | 13.2 |
| 8 | CCGAAC | 731 | 6 | 11.3 | 6 | 11.3 |
| 9 | AUAGCUGGUUCUCC | 802 | 14 | 26.0 | 14 | 26.0 |
| 10 | AGCACU | 863 | 6 | 11.5 | 6 | 11.5 |
| 11 | CAAACUC | 908 | 7 | 12.8 | 7 | 12.8 |
| 12 | GAAGCAGCCA | 1068 | 10 | 18.4 | 10 | 18.4 |
| 13 | GCGUAAUAGCUCACUG | 1091 | 16 | 29.9 | 16 | 29.9 |
| 14 | UGAGUA | 1263 | 6 | 11.1 | 6 | 11.1 |
| 15 | CCUAAG | 1350 | 6 | 11.5 | 6 | 11.5 |
| 16 | CGUACC | 1600 | 6 | 11.2 | 6 | 11.2 |
| 17 | ACCGACAC | 1610 | 8 | 15.2 | 8 | 15.2 |
| 18 | AGGAACUCGGC | 1665 | 11 | 20.2 | 11 | 20.2 |
| 19 | CCGUAACUUCGG | 1685 | 12 | 22.6 | 12 | 22.6 |
| 20 | GACUGUUUA | 1772 | 9 | 17.8 | 9 | 17.8 |
| 21 | AAAAACACAG | 1783 | 10 | 18.6 | 10 | 18.6 |
| 22 | ACGCCUGCCCGGU | 1829 | 13 | 24.1 | 13 | 24.1 |
| 23 | AAGCCC | 1889 | 6 | 11.2 | 6 | 11.2 |
| 24 | AACGGC | 1900 | 6 | 11.3 | 6 | 11.2 |
| 25 | CCGUAACUAUAACGGUCCUAAGGUAGCGAAAUUCCUUGUCGG | 1908 | 42 | 81.1 | 42 | 81.1 |
| 26 | GUAAGUUCCGACCUGCACGAA | 1950 | 21 | 39.1 | 21 | 39.1 |
| 27 | ACUGUCUC | 1989 | 8 | 15.9 | 8 | 15.9 |
| 28 | AAAGACCCCGU | 2058 | 11 | 20.1 | 11 | 20.1 |
| 29 | ACCUUUACU | 2071 | 9 | 17.5 | 9 | 17.5 |
| 30 | UCUAAC | 2195 | 6 | 11.3 | 6 | 11.3 |
| 31 | CAGUUUG | 2240 | 7 | 12.4 | 7 | 12.4 |
| 32 | UGGGGC | 2249 | 6 | 11.2 | 6 | 11.2 |
| 33 | GCCUCCCAA | 2259 | 9 | 16.4 | 9 | 16.4 |
| 34 | GUAACGGA | 2271 | 8 | 15.1 | 8 | 15.1 |
| 35 | UUGACUG | 2343 | 7 | 12.9 | 7 | 12.9 |
| 36 | UAGUGAUCCG | 2387 | 10 | 19.6 | 10 | 19.6 |
| 37 | UCGCUCAACG | 2419 | 10 | 18.9 | 10 | 18.9 |
| 38 | GAUAAAAG | 2429 | 8 | 14.8 | 8 | 14.8 |
| 39 | GGGAUAACAGGCUGAU | 2445 | 16 | 30.1 | 16 | 30.1 |
| 40 | CACAUCGACG | 2475 | 10 | 18.4 | 10 | 18.4 |
| 41 | GUUUGGCACCUCGAUGUCGGCUCAUC | 2490 | 26 | 51.8 | 26 | 51.8 |
| 42 | CAUCCUGGG | 2517 | 9 | 16.1 | 9 | 16.1 |
| 43 | GUCCCAAGGGU | 2536 | 11 | 20.7 | 11 | 20.7 |
| 44 | GGCUGUUCGCC | 2549 | 11 | 22.1 | 11 | 22.1 |
| 45 | UUAAAG | 2562 | 6 | 11.5 | 6 | 11.5 |
| 46 | GAGCUGGGUUCA | 2576 | 12 | 22.4 | 12 | 22.4 |
| 47 | GAACGUCGUGAGACAGUUCGGUCCCUAUCU | 2588 | 30 | 56.7 | 30 | 56.7 |
| 48 | CUAGUACGAGAGGACC | 2652 | 16 | 29.9 | 16 | 29.9 |
| 49 | GCAUCUAA | 2751 | 8 | 14.7 | 8 | 14.7 |

Supplementary Table 2. | Summary of Conserved Nucleotide Element False Discovery Rates

| **Length** | **Euk CNE** | **Arc CNE** | **Bac CNE** | **Univ CNE** |
|---|---|---|---|---|
| 6 | 0.549517241 | 0.279764706 | 0.38428 | 0.116222222 |
| 7 | 0.288321429 | 0.197225806 | 0.229435897 | 0.053789474 |
| 8 | 0.198208333 | 0.141666667 | 0.156363636 | 0.025882353 |
| 9 | 0.158944444 | 0.097666667 | 0.110615385 | 0.0175 |
| 10 | 0.108258065 | 0.070923077 | 0.072818182 | 0.0086 |
| 11 | 0.066785714 | 0.047555556 | 0.050125 | 0.00475 |
| 12 | 0.040518519 | 0.031428571 | 0.033166667 | 0.0032 |
| 13 | 0.030666667 | 0.03 | 0.0248 | 0.002 |
| 14 | 0.020833333 | 0.023 | 0.017555556 | 0.000666667 |
| 15 | 0.015454545 | 0.0185 | 0.01225 | 0 |
| 16 | 0.013578947 | 0.02 | 0.008 | 0 |
| 17 | 0.011052632 | 0.022 | 0.0104 | 0 |
| 18 | 0.008210526 | 0.017 | 0.008 | 0 |
| 19 | 0.00775 | 0.01 | 0.0068 | 0 |
| 20 | 0.006933333 | 0.01 | 0.0064 | 0 |
| 21 | 0.006 | 0.007 | 0.0048 | 0 |
| 22 | 0.005333333 | 0.006 | 0.006 | 0 |
| 23 | 0.005846154 | 0.004 | 0.004 | 0 |
| 24 | 0.006727273 | 0.003 | 0.004 | 0 |
| 25 | 0.006363636 | 0.003 | 0.004 | 0 |
| 26 | 0.006 | 0.003 | 0.004 | 0 |
| 27 | 0.005818182 | 0.002 | 0.004 | 0 |
| 28 | 0.005454545 | 0.002 | 0.004 | 0 |
| 29 | 0.005454545 | 0.002 | 0.002 | 0 |
| 30 | 0.004727273 | 0.002 | 0.001333333 | 0 |

Supplementary Table 3. | Inter-subunit bridges involving 23S-28S rRNA CNEs

| **Bridge*** | **uCNE** | **eCNE** |
|---|---|---|
| B1a*** | X | X |
| B2a | uCNE 12, 13 | eCNE 38 |
| B2b | uCNE 13 | eCNE 36, 38 |
| B2c | X | eCNE 36 |
| B3 | uCNE 20 | eCNE 38, 39 |
| B4*** | X | eCNE 7 |
| B5** | uCNE 4, 15 | X |
| B6 | uCNE 4 | X |
| B7a | X | eCNE 36, 38 |

* Positions of bridges taken from Yusupov et al. (2001) for bacteria and Ben-Shem et al. (2010, 2011) for yeast.

** Bridge B5 has shifted from its position in bacteria upward to sites in an expansion segment region in yeast. uCNE5 is directly adjacent to nucleotides utilized for bridge B5 in bacteria (Yusupov et al 2001), but uCNE5 (within eCNE35) is directly adjacent to nucleotides utilized for bridge B3 in yeast (Ben-Shem et al. 2011).

*** Bridges B1a and B4 are not clustered with the other rRNA-containing bridges

Supplementary Table 4 | Cross-domain conservation of eCNEs

| eCNE No. | Euk Position | Euk Percent | Arc Position | Arc Percent | Bac Position | Bac Percent |
|---|---|---|---|---|---|---|
| 1 | 319 | 98.0 | 432 | 87.6 | 425 | 92.7 |
| 2 | 338 | 97.8 | 450 | 94.3 | 444 | 89.6 |
| 3 | 347 | 98.1 | 459 | 73.5 | 453 | 83.5 |
| 4 | 635 | 98.3 | 619 | 73.3 | 562 | 47.4 |
| 5 | 800 | 96.9 | 760 | 82.8 | 670 | 98.0 |
| 6 | 815 | 96.5 | 775 | 69.3 | 685 | 66.5 |
| 7 | 844 | 97.7 | 804 | 57.3 | 714 | 32.5 |
| 8 | 872 | 98.8 | 832 | 66.0 | 741 | 39.0 |
| 9 | 907 | 97.2 | 868 | 68.2 | 776 | 68.7 |
| 10 | 950 | 97.7 | 911 | 56.1 | 819 | 46.6 |
| 11 | 992 | 98.7 | 951 | 79.2 | 858 | 89.5 |
| 12 | 1001 | 97.7 | 960 | 64.5 | 866 | 62.1 |
| 13 | 1036 | 97.3 | 995 | 56.1 | 900 | 46.3 |
| 14[DS] | 1112 | 99.0 | 1040 | 33.2 | 942 | 46.4 |
| 15 | 1124 | 98.2 | 1052 | 67.4 | 954 | 47.1 |
| 16[DS] | 1135 | 98.2 | 1063 | 38.9 | 966 | 40.7 |
| 17 | 1150 | 96.9 | 1078 | 67.3 | 981 | 57.4 |
| 18 | 1221 | 97.2 | 1150 | 86.6 | 1047 | 73.9 |
| 19 | 1229 | 99.0 | 1158 | 64.5 | 1055 | 54.6 |
| 20 | 1238 | 98.7 | 1167 | 58.9 | 1064 | 63.4 |
| 21 | 1251 | 98.7 | 1180 | 74.8 | 1077 | 64.5 |
| 22 | 1291 | 96.6 | 1220 | 65.6 | 1117 | 60.5 |
| 23[DS] | 1430 | 97.8 | 1352 | 45.5 | 1250 | 48.7 |
| 24 | 1442 | 97.9 | 1364 | 53.0 | 1262 | 45.5 |
| 25 | 1491 | 96.0 | 1414 | 72.1 | 1310 | 69.3 |
| 26 | 1529 | 97.9 | 1452 | 89.1 | 1349 | 85.6 |
| 27[DS] | 1682 | 96.4 | 1558 | 4.9 | 1456 | 23.6 |
| 28 | 1790 | 97.7 | 1649 | 76.2 | 1565 | 64.7 |
| 29 | 1829 | 91.6 | 1671 | 74.4 | 1599 | 70.4 |
| 30 | 1839 | 96.8 | 1681 | 58.1 | 1609 | 57.5 |
| 31 | 1864 | 93.5 | 1707 | 53.4 | 1634 | 42.6 |
| 32 | 1894 | 99.1 | 1739 | 92.1 | 1664 | 83.3 |
| 33 | 1912 | 96.8 | 1757 | 80.6 | 1682 | 81.6 |
| 34[DS] | 1931 | 98.2 | 1776 | 33.8 | 1701 | 45.2 |
| 35 | 2125 | 96.9 | 1821 | 80.5 | 1768 | 76.5 |
| 36 | 2184 | 98.6 | 1879 | 64.9 | 1826 | 70.6 |
| 37[DS] | 2222 | 97.3 | 1917 | 11.8 | 1871 | 0.0 |
| 38 | 2230 | 98.8 | 1926 | 72.3 | 1888 | 74.1 |
| 39 | 2300 | 98.2 | 1996 | 77.8 | 1958 | 66.2 |
| 40[DS] | 2341 | 96.7 | 2037 | 43.9 | 1999 | 34.3 |
| 41 | 2389 | 99.5 | 2086 | 73.0 | 2048 | 60.5 |
| 42 | 2483 | 96.5 | 2211 | 60.8 | 2169 | 69.9 |
| 43[DS] | 2507 | 96.4 | 2234 | 46.0 | 2192 | 42.9 |
| 44 | 2607 | 98.7 | 2270 | 87.0 | 2240 | 82.2 |
| 45 | 2615 | 99.2 | 2278 | 96.8 | 2248 | 97.4 |
| 46 | 2625 | 97.8 | 2288 | 51.3 | 2258 | 34.5 |
| 47 | 2648 | 97.0 | 2311 | 71.9 | 2280 | 65.1 |
| 48 | 2673 | 95.6 | 2336 | 62.5 | 2305 | 60.6 |
| 49 | 2709 | 97.1 | 2374 | 61.6 | 2343 | 77.6 |
| 50[DS] | 2717 | 94.3 | 2383 | 0.0 | 2352 | 27.5 |
| 51 | 2748 | 96.6 | 2415 | 68.0 | 2382 | 54.7 |
| 52 | 2794 | 99.5 | 2460 | 76.5 | 2427 | 66.3 |
| 53 | 2830 | 98.1 | 2496 | 66.7 | 2465 | 68.9 |
| 54 | 2913 | 98.2 | 2578 | 65.1 | 2548 | 64.0 |
| 55 | 2932 | 99.4 | 2597 | 76.1 | 2567 | 68.4 |
| 56 | 3017 | 98.7 | 2685 | 97.8 | 2653 | 92.8 |
| 57 | 3111 | 90.2 | 2780 | 80.7 | 2750 | 70.3 |

DS = domain specific conservation

Supplementary Table 5. |Correlation of domain-specific eCNEs with ribosome functions

| **ds eCNE No.** | **Possible Function** |
|---|---|
| 14 | tunnel; contacts eukaryotic-specific ribosomal protein L29e |
| 16 | tunnel; contacts eukaryotic-specific ribosomal protein L29e |
| 23 | tunnel |
| 27 | unknown |
| 34 | abuts expansion segment 27L |
| 37 | contacts eukaryotic-specific ribosomal protein L36e |
| 40 | tunnel |
| 43 | E site tRNA ; abuts expansion segment 31L |
| 50 | contacts eukaryotic-specific ribosomal protein L29e |