**Supplementary Table 1: Chromosomes analyzed in Figure 3.** For each chromosome we show the overall strand bias of the genome, the median separation between adjacent pairs of genes on both strands, and the proportion of conserved pairs on both strands. $p$ is from the Kolmogorov-Smirnov test and is not corrected for multiple testing.

|  |  | Median Distance |  |  | % Conserved |  |
|---|---|---|---|---|---|---|
| Chromosome | %Leading | Leading | Lagging | $p$ | Leading | Lagging |
| *Acinetobacter sp. ADP1* | 61% | 42 | 73 | 2e-06 | 35.7% | 30.9% |
| *Agrobacterium tumefaciens str. C58 (Cereon)* | 56% | 43 | 48 | 0.40 | 33.1% | 27.7% |
| *Bacillus anthracis str. 'Ames Ancestor'* | 75% | 72 | 102 | 0.001 | 25.8% | 11.5% |
| *Bacillus anthracis str. Ames* | 75% | 71 | 101 | 6e-04 | 25.0% | 11.2% |
| *Bacillus anthracis str. Sterne* | 76% | 70 | 80 | 0.43 | 26.2% | 12.0% |
| *Bacillus cereus ATCC 10987* | 74% | 66 | 82 | 0.04 | 26.8% | 11.4% |
| *Bacillus cereus ATCC 14579* | 76% | 82 | 101 | 0.01 | 25.8% | 11.1% |
| *Bacillus cereus ZK* | 75% | 74 | 83 | 0.29 | 28.3% | 13.7% |
| *Bacillus halodurans* | 78% | 62 | 58 | 0.03 | 31.7% | 24.0% |
| *Bacillus licheniformis ATCC 14580* | 75% | 53 | 61 | 0.32 | 32.5% | 20.6% |
| *Bacillus licheniformis DSM 13* | 75% | 50 | 58 | 0.17 | 33.8% | 19.6% |
| *Bacillus subtilis* | 75% | 56 | 61 | 0.85 | 32.2% | 17.6% |
| *Bacillus thuringiensis serovar konkukian str. 97-27* | 75% | 77 | 82 | 0.38 | 28.2% | 12.0% |
| *Bacteroides fragilis* | 57% | 35 | 32 | 0.30 | 16.6% | 15.9% |
| *Bacteroides thetaiotaomicron VPI-5482* | 59% | 42 | 49 | 0.16 | 15.9% | 15.5% |
| *Bartonella henselae str. Houston-1* | 57% | 68 | 67 | 0.58 | 39.0% | 29.5% |
| *Bartonella quintana* | 55% | 81 | 77 | 0.21 | 46.3% | 32.0% |
| *Bdellovibrio bacteriovorus HD100* | 56% | 19 | 26 | 0.34 | 24.0% | 12.9% |
| *Bordetella bronchiseptica RB50* | 56% | 27 | 26 | 0.24 | 37.6% | 35.2% |
| *Bordetella parapertussis 12822* | 57% | 29 | 28 | 0.18 | 38.8% | 35.3% |
| *Brucella melitensis chromosome I* | 60% | 66 | 67 | 0.41 | 37.4% | 26.8% |
| *Brucella melitensis chromosome II* | 56% | 34 | 50 | 0.09 | 26.4% | 31.7% |
| *Brucella suis 1330 chromosome I* | 59% | 62 | 64 | 0.72 | 37.9% | 27.3% |
| *Brucella suis 1330 chromosome II* | 56% | 26 | 40 | 0.19 | 30.7% | 34.2% |
| *Buchnera aphidicola (Baizongia pistaciae)* | 57% | 74 | 83 | 0.89 | 64.3% | 61.3% |
| *Burkholderia mallei ATCC 23344 chromosome 1* | 57% | 73 | 74 | 0.99 | 49.8% | 38.8% |
| *Burkholderia mallei ATCC 23344 chromosome 2* | 56% | 74 | 86 | 0.12 | 30.4% | 22.7% |
| *Burkholderia pseudomallei K96243 chromosome 1* | 58% | 63 | 66 | 0.02 | 50.7% | 40.6% |
| *Burkholderia pseudomallei K96243 chromosome 2* | 59% | 53 | 79 | 0.002 | 32.2% | 27.2% |
| *Campylobacter jejuni* | 61% | 4 | 2 | 0.43 | 44.7% | 45.3% |
| *Candidatus Blochmannia floridanus* | 66% | 84 | 77 | 0.13 | 66.0% | 63.0% |
| *Caulobacter crescentus CB15* | 55% | 49 | 51 | 0.99 | 35.1% | 27.5% |
| *Chlamydia muridarum* | 55% | 28 | 26 | 0.12 | 25.1% | 17.9% |
| *Chlamydia trachomatis* | 56% | 31 | 28 | 0.26 | 26.0% | 17.7% |
| *Chlamydophila pneumoniae AR39* | 54% | 34 | 35 | 0.16 | 21.8% | 14.1% |
| *Chlamydophila pneumoniae CWL029* | 55% | 37 | 34 | 0.38 | 22.9% | 14.9% |
| *Chlamydophila pneumoniae J138* | 55% | 35 | 33 | 0.46 | 22.5% | 14.9% |
| *Chlamydophila pneumoniae TW-183* | 55% | 37 | 33 | 0.05 | 21.2% | 14.3% |
| *Chlorobium tepidum TLS* | 57% | 41 | 38 | 0.25 | 24.9% | 23.0% |
| *Chromobacterium violaceum ATCC 12472* | 57% | 52 | 52 | 0.65 | 39.0% | 33.2% |
| *Clostridium acetobutylicum ATCC824* | 79% | 57 | 61 | 0.40 | 30.6% | 21.8% |
| *Clostridium perfringens* | 83% | 94 | 94 | 0.47 | 35.0% | 27.6% |
| *Clostridium tetani E88* | 82% | 58 | 30 | 0.01 | 37.4% | 27.3% |
| *Corynebacterium diphtheriae* | 63% | 42 | 38 | 0.34 | 36.2% | 23.8% |
| *Corynebacterium glutamicum ATCC 13032* | 59% | 53 | 57 | 0.49 | 32.7% | 19.9% |

| | | Median Distance | | | % Conserved | |
|---|---|---|---|---|---|---|
| Chromosome | %Leading | Leading | Lagging | $p$ | Leading | Lagging |
| *Coxiella burnetii RSA 493* | 59% | 29 | 29 | 0.73 | 33.9% | 27.6% |
| *Desulfotalea psychrophila LSv54* | 54% | 63 | 52 | 0.01 | 27.7% | 31.3% |
| *Enterococcus faecalis V583* | 81% | 33 | 42 | 0.88 | 38.1% | 30.6% |
| *Erwinia carotovora subsp. atroseptica SCRI1043* | 57% | 54 | 58 | 0.41 | 41.8% | 37.1% |
| *Escherichia coli CFT073* | 55% | 28 | 30 | 0.97 | 33.1% | 31.2% |
| *Escherichia coli K12* | 56% | 37 | 40 | 0.57 | 40.7% | 34.3% |
| *Escherichia coli O157:H7* | 59% | 32 | 38 | 0.15 | 30.0% | 29.8% |
| *Escherichia coli O157:H7 EDL933* | 58% | 36 | 41 | 0.62 | 29.9% | 29.7% |
| *Fusobacterium nucleatum subsp. nucleatum ATCC 25586* | 65% | 26 | 24 | 0.16 | 25.6% | 26.0% |
| *Haemophilus ducreyi 35000HP* | 58% | 43 | 48 | 0.39 | 43.1% | 38.1% |
| *Haemophilus influenzae Rd* | 56% | 50 | 30 | 0.007 | 56.5% | 61.8% |
| *Helicobacter hepaticus ATCC 51449* | 57% | 17 | 15 | 0.32 | 44.2% | 43.3% |
| *Helicobacter pylori J99 Helicobacter pylori, strain J99* | 57% | 14 | 13 | 0.23 | 46.0% | 41.7% |
| *Lactobacillus johnsonii NCC 533* | 79% | 27 | 38 | 0.30 | 41.7% | 22.5% |
| *Lactobacillus plantarum WCFS1* | 74% | 56 | 54 | 0.75 | 38.6% | 23.5% |
| *Lactococcus lactis subsp. lactis* | 81% | 85 | 71 | 0.23 | 31.9% | 30.0% |
| *Legionella pneumophila str. Lens* | 57% | 38 | 63 | 0.03 | 39.4% | 25.8% |
| *Legionella pneumophila str. Paris* | 58% | 41 | 59 | 0.32 | 37.7% | 26.1% |
| *Legionella pneumophila str. Philadelphia 1* | 57% | 35 | 63 | 0.03 | 39.3% | 26.3% |
| *L. interrogans sv. Copenhageni str. Fiocruz L1-130 chr. I* | 57% | 33 | 59 | 0.001 | 17.7% | 10.1% |
| *L. interrogans sv. lai str. 56601 chr. I* | 57% | 42 | 48 | 0.32 | 14.2% | 7.7% |
| *Listeria innocua Clip11262* | 81% | 30 | 34 | 0.56 | 36.9% | 31.1% |
| *Listeria monocytogenes EGD-e* | 79% | 37 | 28 | 0.35 | 38.3% | 33.3% |
| *Listeria monocytogenes str. 4b F2365* | 79% | 42 | 31 | 0.23 | 38.0% | 31.5% |
| *Mannheimia succiniciproducens MBEL55E* | 57% | 36 | 30 | 0.22 | 51.1% | 46.0% |
| *Mesoplasma florum L1* | 89% | 23 | 59 | 0.46 | 48.6% | 34.8% |
| *Methylococcus capsulatus str. Bath* | 56% | 26 | 23 | 0.03 | 42.3% | 41.8% |
| *Mycobacterium bovis subsp. bovis AF2122/97* | 60% | 25 | 34 | 0.02 | 27.4% | 16.2% |
| *Mycobacterium leprae strain TN* | 65% | 79 | 90 | 0.71 | 41.7% | 18.5% |
| *Mycobacterium tuberculosis CDC1551* | 59% | 25 | 31 | 0.13 | 24.6% | 15.2% |
| *Mycobacterium tuberculosis H37Rv* | 59% | 24 | 36 | 0.002 | 26.1% | 15.7% |
| *Mycoplasma gallisepticum R* | 79% | 13 | 19 | 0.25 | 35.2% | 25.3% |
| *Mycoplasma genitalium* | 80% | 5 | 3 | 0.31 | 39.6% | 33.3% |
| *Mycoplasma penetrans* | 82% | 76 | 66 | 0.40 | 27.2% | 25.0% |
| *Neisseria meningitidis MC58* | 55% | 66 | 65 | 0.35 | 25.9% | 23.1% |
| *Neisseria meningitidis Z2491* | 56% | 62 | 65 | 0.02 | 27.2% | 24.5% |
| *Nitrosomonas europaea ATCC 19718* | 57% | 48 | 53 | 0.75 | 46.1% | 40.6% |
| *Oceanobacillus iheyensis HTE831* | 76% | 64 | 53 | 0.003 | 35.4% | 25.2% |
| *Pasteurella multocida* | 58% | 40 | 38 | 0.54 | 60.2% | 61.7% |
| *Photobacterium profundum SS9 chromosome 1* | 58% | 81 | 98 | 0.04 | 42.8% | 30.9% |
| *Photobacterium profundum SS9 chromosome 2* | 54% | 112 | 100 | 0.03 | 17.2% | 20.7% |
| *Photorhabdus luminescens subsp. laumondii TTO1* | 58% | 53 | 48 | 0.17 | 30.8% | 28.7% |
| *Propionibacterium acnes KPA171202* | 61% | 33 | 44 | 0.32 | 40.7% | 29.7% |
| *Pseudomonas aeruginosa PA01* | 56% | 48 | 56 | 0.25 | 41.1% | 34.1% |
| *Pseudomonas putida KT2440* | 55% | 41 | 52 | 0.03 | 37.6% | 31.9% |

| | | Median Distance | | | % Conserved | |
|---|---|---|---|---|---|---|
| Chromosome | %Leading | Leading | Lagging | $p$ | Leading | Lagging |
| *Pseudomonas syringae pv. tomato str. DC3000* | 53% | 50 | 57 | 0.004 | 39.3% | 32.2% |
| *Ralstonia solanacearum* | 60% | 44 | 48 | 0.86 | 45.5% | 37.8% |
| *Rhodopseudomonas palustris* | 57% | 62 | 75 | 0.14 | 32.7% | 26.2% |
| *Rickettsia conorii Malish 7* | 61% | 102 | 74 | 0.06 | 18.2% | 12.4% |
| *Rickettsia prowazekii strain Madrid E* | 62% | 94 | 88 | 0.75 | 28.2% | 23.0% |
| *Salmonella enterica subsp. enterica serovar Typhi* | 58% | 44 | 44 | 0.99 | 36.8% | 32.7% |
| *Salmonella enterica subsp. enterica serovar Typhi Ty2* | 58% | 47 | 45 | 0.98 | 37.8% | 32.9% |
| *Salmonella typhimurium LT2* | 59% | 42 | 46 | 0.27 | 40.3% | 35.8% |
| *Shewanella oneidensis MR-1* | 56% | 71 | 74 | 0.86 | 34.5% | 27.6% |
| *Shigella flexneri 2a str. 2457T* | 55% | 42 | 44 | 0.14 | 34.0% | 25.9% |
| *Shigella flexneri 2a str. 301* | 55% | 34 | 36 | 0.21 | 33.7% | 25.8% |
| *Sinorhizobium meliloti 1021* | 56% | 73 | 71 | 0.66 | 34.0% | 27.6% |
| *Staphylococcus aureus subsp. aureus MRSA252* | 75% | 39 | 66 | 0.22 | 35.7% | 22.3% |
| *Staphylococcus aureus subsp. aureus MSSA476* | 76% | 47 | 64 | 0.65 | 37.1% | 25.6% |
| *Staphylococcus aureus subsp. aureus Mu50* | 75% | 42 | 67 | 0.10 | 36.6% | 23.7% |
| *Staphylococcus aureus subsp. aureus MW2* | 76% | 48 | 67 | 0.47 | 37.9% | 25.3% |
| *Staphylococcus aureus subsp. aureus N315* | 75% | 48 | 76 | 0.14 | 38.3% | 23.4% |
| *Staphylococcus epidermidis ATCC 12228* | 73% | 52 | 56 | 0.99 | 38.3% | 24.9% |
| *Streptococcus agalactiae 2603V/R* | 81% | 38 | 43 | 0.34 | 42.4% | 45.4% |
| *Streptococcus agalactiae NEM316* | 82% | 41 | 51 | 0.63 | 42.6% | 48.3% |
| *Streptococcus mutans UA159* | 81% | 50 | 45 | 0.81 | 46.4% | 37.9% |
| *Streptococcus pneumoniae R6* | 79% | 33 | 22 | 0.48 | 42.4% | 39.1% |
| *Streptococcus pneumoniae TIGR4* | 80% | 35 | 51 | 0.54 | 40.5% | 40.3% |
| *Streptococcus pyogenes M1 GAS* | 80% | 43 | 51 | 0.62 | 46.7% | 45.9% |
| *Streptococcus pyogenes MGAS10394* | 79% | 32 | 48 | 0.18 | 45.7% | 41.3% |
| *Streptococcus pyogenes MGAS315* | 82% | 39 | 50 | 0.68 | 43.9% | 45.0% |
| *Streptococcus pyogenes MGAS8232* | 81% | 30 | 56 | 0.04 | 44.6% | 45.9% |
| *Streptococcus pyogenes SSI-1* | 81% | 38 | 49 | 0.52 | 43.5% | 42.6% |
| *Symbiobacterium thermophilum* | 74% | 54 | 46 | 0.53 | 33.3% | 24.4% |
| *Thermoanaerobacter tengcongensis strain MB4T* | 86% | 29 | 19 | 0.07 | 40.3% | 32.1% |
| *Treponema denticola ATCC 35405* | 61% | 25 | 23 | 0.55 | 25.3% | 23.5% |
| *Treponema pallidum* | 66% | 25 | 22 | 0.32 | 40.6% | 34.8% |
| *Ureaplasma urealyticum* | 72% | 24 | 19 | 0.24 | 38.6% | 28.0% |
| *Vibrio cholerae chromosome I* | 59% | 31 | 43 | 0.08 | 44.4% | 34.4% |
| *Vibrio cholerae chromosome II* | 59% | 88 | 56 | 0.002 | 16.2% | 22.0% |
| *Vibrio parahaemolyticus RIMD 2210633 chromosome I* | 61% | 49 | 62 | 0.18 | 41.8% | 34.3% |
| *Vibrio parahaemolyticus RIMD 2210633 chromosome II* | 56% | 50 | 68 | 0.14 | 22.6% | 23.6% |
| *Vibrio vulnificus CMCP6 chromosome I* | 62% | 57 | 67 | 0.11 | 39.5% | 34.3% |
| *Vibrio vulnificus CMCP6 chromosome II* | 54% | 60 | 85 | 0.08 | 24.7% | 22.1% |
| *Vibrio vulnificus YJ016 chromosome I* | 62% | 41 | 49 | 0.37 | 38.7% | 32.2% |
| *Vibrio vulnificus YJ016 chromosome II* | 53% | 41 | 53 | 0.20 | 23.6% | 19.1% |
| *Wolinella succinogenes* | 60% | 10 | 9 | 0.43 | 53.7% | 41.8% |
| *Xanthomonas axonopodis pv. citri str. 306* | 55% | 67 | 70 | 0.33 | 35.0% | 28.4% |
| *Xanthomonas campestris pv. campestris str. ATCC 33913* | 56% | 63 | 69 | 0.33 | 33.5% | 29.9% |
| *Xylella fastidiosa 9a5c* | 59% | 46 | 52 | 0.88 | 29.9% | 27.1% |

| Chromosome | %Leading | Median Distance Leading | Median Distance Lagging | $p$ | % Conserved Leading | % Conserved Lagging |
|---|---|---|---|---|---|---|
| *Xylella fastidiosa Temecula1* | 57% | 59 | 60 | 0.71 | 37.3% | 30.4% |
| *Yersinia pestis KIM* | 57% | 65 | 64 | 0.52 | 37.3% | 33.2% |
| *Yersinia pestis strain CO92* | 57% | 74 | 70 | 0.47 | 41.2% | 34.2% |
| *Yersinia pseudotuberculosis IP 32953* | 59% | 66 | 84 | 0.05 | 42.7% | 37.8% |