Table S3. Results of regression analysis of the estimates of *β*0’s (intercepts) and *β*1’s  (linear regression coefficients – slope) for the variables plant height, branch length, number of nodes and stem diameter in 14 genotypes of *C. arabica* with 95% confidence interval.

|  |
| --- |
| **Branch length**  |
| **Intercepts** |
| **Genotypes** | **Estimate** | **Standard Error** | **p-value** | **R2** | **Lower Limit** | **Upper Limit** |
| 1 | 0.631 | 0.011 | 0 | 0.7093 | 0.608 | 0.653 |
| 2 | 0.720 | 0.008 | 0 | 0.8485 | 0.703 | 0.737 |
| 3 | 0.510 | 0.011 | 0 | 0.7734 | 0.487 | 0.534 |
| 4 | 0.391 | 0.009 | 0 | 0.8362 | 0.371 | 0.411 |
| 5 | 0.442 | 0.007 | 0 | 0.8197 | 0.427 | 0.456 |
| 6 | 0.532 | 0.010 | 0 | 0.7774 | 0.510 | 0.554 |
| 7 | 0.778 | 0.005 | 0 | 0.6624 | 0.767 | 0.788 |
| 8 | 0.567 | 0.004 | 0 | 0.8669 | 0.557 | 0.577 |
| 9 | 0.699 | 0.006 | 0 | 0.8568 | 0.685 | 0.712 |
| 10 | 0.594 | 0.005 | 0 | 0.9204 | 0.582 | 0.606 |
| 11 | 0.406 | 0.012 | 0 | 0.7332 | 0.381 | 0.431 |
| 12 | 0.523 | 0.009 | 0 | 0.7312 | 0.504 | 0.541 |
| 13 | 0.488 | 0.011 | 0 | 0.7580 | 0.464 | 0.512 |
| 14 | 0.438 | 0.009 | 0 | 0.8411 | 0.419 | 0.456 |
| **Slope** |
| **Genotypes** | **Estimate** | **Standard Error** | **p-value** | **R2** | **Lower Limit** | **Upper Limit** |
| 1 | 0.017 | 0.001 | 0 | 0.709 | 0.013 | 0.020 |
| 2 | 0.018 | 0.001 | 0 | 0.848 | 0.015 | 0.020 |
| 3 | 0.019 | 0.001 | 0 | 0.773 | 0.016 | 0.023 |
| 4 | 0.020 | 0.001 | 0 | 0.836 | 0.017 | 0.023 |
| 5 | 0.013 | 0.001 | 0 | 0.819 | 0.011 | 0.015 |
| 6 | 0.018 | 0.001 | 0 | 0.777 | 0.015 | 0.021 |
| 7 | 0.006 | 0 | 0 | 0.662 | 0.005 | 0.008 |
| 8 | 0.013 | 0.001 | 0 | 0.866 | 0.011 | 0.016 |
| 9 | 0.015 | 0.001 | 0 | 0.856 | 0.013 | 0.018 |
| 10 | 0.018 | 0 | 0 | 0.920 | 0.016 | 0.020 |
| 11 | 0.019 | 0 | 0 | 0.733 | 0.015 | 0.022 |
| 12 | 0.014 | 0.001 | 0 | 0.731 | 0.011 | 0.018 |
| 13 | 0.020 | 0.002 | 0 | 0.758 | 0.016 | 0.025 |
| 14 | 0.019 | 0.001 | 0 | 0.841 | 0.017 | 0.022 |
| **Number of nodes** |
| **Intercepts** |
| **Genotypes** | **Estimate** | **Standard Error** | **p-value** | **R2** | **Lower Limit** | **Upper Limit** |
| 1 | 20.646 | 0.432 | 0 | 0.706 | 19.768 | 21.524 |
| 2 | 20.028 | 0.294 | 0 | 0.868 | 19.433 | 20.623 |
| 3 | 17.066 | 0.309 | 0 | 0.851 | 16.441 | 17.692 |
| 4 | 12.960 | 0.355 | 0 | 0.834 | 12.243 | 13.677 |
| 5 | 16.521 | 0.326 | 0 | 0.777 | 15.862 | 17.180 |
| 6 | 13.931 | 0.324 | 0 | 0.775 | 13.276 | 14.585 |
| 7 | 27.638 | 0.289 | 0 | 0.626 | 27.051 | 28.226 |
| 8 | 20.239 | 0.261 | 0 | 0.740 | 19.706 | 20.773 |
| 9 | 17.675 | 0.243 | 0 | 0.875 | 17.180 | 18.170 |
| 10 | 13.614 | 0.175 | 0 | 0.945 | 13.261 | 13.968 |
| 11 | 15.870 | 0.167 | 0 | 0.954 | 15.531 | 16.208 |
| 12 | 14.860 | 0.286 | 0 | 0.765 | 14.276 | 15.445 |
| 13 | 16.085 | 0.403 | 0 | 0.710 | 15.263 | 16.908 |
| 14 | 13.371 | 0.347 | 0 | 0.805 | 12.671 | 14.070 |
| **Slope** |
| **Genotypes** | **Estimate** | **Standard Error** | **p-value** | **R2** | **Lower Limit** | **Upper Limit** |
| 1 | 0.660 | 0.072 | 0 | 0.706 | 0.512 | 0.808 |
| 2 | 0.712 | 0.042 | 0 | 0.868 | 0.626 | 0.798 |
| 3 | 0.673 | 0.044 | 0 | 0.851 | 0.583 | 0.763 |
| 4 | 0.739 | 0.050 | 0 | 0.834 | 0.637 | 0.842 |
| 5 | 0.558 | 0.046 | 0 | 0.777 | 0.464 | 0.653 |
| 6 | 0.560 | 0.044 | 0 | 0.775 | 0.469 | 0.650 |
| 7 | 0.367 | 0.047 | 0 | 0.626 | 0.271 | 0.463 |
| 8 | 0.471 | 0.050 | 0 | 0.740 | 0.369 | 0.574 |
| 9 | 0.643 | 0.041 | 0 | 0.875 | 0.560 | 0.727 |
| 10 | 0.672 | 0.023 | 0 | 0.945 | 0.624 | 0.720 |
| 11 | 0.712 | 0.023 | 0 | 0.954 | 0.666 | 0.759 |
| 12 | 0.506 | 0.050 | 0 | 0.765 | 0.403 | 0.608 |
| 13 | 0.642 | 0.073 | 0 | 0.710 | 0.492 | 0.792 |
| 14 | 0.651 | 0.047 | 0 | 0.805 | 0.556 | 0.746 |
| **Stem diameter** |
| **Intercepts** |
| **Genotypes** | **Estimate** | **Standard Error** | **p-value** | **R2** | **Lower Limit** | **Upper Limit** |
| 1 | 0.430 | 0.001 | 0 | 0.978 | 0.427 | 0.434 |
| 2 | 0.419 | 0.003 | 0 | 0.827 | 0.412 | 0.426 |
| 3 | 0.343 | 0.002 | 0 | 0.944 | 0.338 | 0.348 |
| 4 | 0.574 | 0.006 | 0 | 0.885 | 0.560 | 0.588 |
| 5 | 0.308 | 0.008 | 0 | 0.917 | 0.289 | 0.328 |
| 6 | 0.379 | 0.004 | 0 | 0.874 | 0.369 | 0.390 |
| 7 | 0.408 | 0.003 | 0 | 0.887 | 0.401 | 0.415 |
| 8 | 0.439 | 0.002 | 0 | 0.955 | 0.434 | 0.445 |
| 9 | 0.256 | 0.003 | 0 | 0.835 | 0.249 | 0.263 |
| 10 | 0.393 | 0.001 | 0 | 0.944 | 0.389 | 0.396 |
| 11 | 0.317 | 0.002 | 0 | 0.901 | 0.311 | 0.324 |
| 12 | 0.433 | 0.002 | 0 | 0.920 | 0.426 | 0.439 |
| 13 | 0.381 | 0 | 0 | 0.967 | 0.379 | 0.383 |
| 14 | 0.262 | 0.001 | 0 | 0.969 | 0.258 | 0.266 |
| **Slope** |
| **Genotypes** | **Estimate** | **Standard Error** | **p-value** | **R2** | **Lower Limit** | **Upper Limit** |
| 1 | 0.004 | 0 | 0 | 0.978 | 0.004 | 0.005 |
| 2 | 0.003 | 0 | 0 | 0.827 | 0.002 | 0.003 |
| 3 | 0.003 | 0 | 0 | 0.944 | 0.003 | 0.004 |
| 4 | 0.006 | 0 | 0 | 0.885 | 0.004 | 0.007 |
| 5 | 0.012 | 0.001 | 0 | 0.917 | 0.009 | 0.015 |
| 6 | 0.005 | 0 | 0 | 0.874 | 0.003 | 0.006 |
| 7 | 0.003 | 0 | 0 | 0.887 | 0.002 | 0.004 |
| 8 | 0.005 | 0 | 0 | 0.955 | 0.004 | 0.005 |
| 9 | 0.003 | 0 | 0 | 0.835 | 0.002 | 0.003 |
| 10 | 0.002 | 0 | 0 | 0.944 | 0.002 | 0.003 |
| 11 | 0.003 | 0 | 0 | 0.901 | 0.002 | 0.004 |
| 12 | 0.004 | 0 | 0 | 0.920 | 0.003 | 0.004 |
| 13 | 0.001 | 0 | 0 | 0.967 | 0.001 | 0.002 |
| 14 | 0.004 | 0 | 0 | 0.969 | 0.003 | 0.004 |
| **Plant height** |
| **Intercepts** |
| **Genotypes** | **Estimate** | **Standard Error** | **p-value** | **R2** | **Lower Limit** | **Upper Limit** |
| 1 | 3.211 | 0.011 | 0 | 0.873 | 3.186 | 3.237 |
| 2 | 3.458 | 0.011 | 0 | 0.719 | 3.433 | 3.483 |
| 3 | 3.333 | 0.024 | 0 | 0.769 | 3.278 | 3.389 |
| 4 | 3.310 | 0.009 | 0 | 0.986 | 3.288 | 3.331 |
| 5 | 3.052 | 0.009 | 0 | 0.901 | 3.031 | 3.073 |
| 6 | 3.293 | 0.004 | 0 | 0.963 | 3.282 | 3.304 |
| 7 | 2.887 | 0.005 | 0 | 0.976 | 2.875 | 2.899 |
| 8 | 3.320 | 0.006 | 0 | 0.975 | 3.305 | 3.334 |
| 9 | 2.766 | 0.007 | 0 | 0.970 | 2.750 | 2.783 |
| 10 | 3.211 | 0.010 | 0 | 0.957 | 3.188 | 3.233 |
| 11 | 2.945 | 0.014 | 0 | 0.946 | 2.914 | 2.976 |
| 12 | 3.654 | 0.010 | 0 | 0.926 | 3.631 | 3.677 |
| 13 | 3.565 | 0.004 | 0 | 0.948 | 3.554 | 3.575 |
| 14 | 3.111 | 0.015 | 0 | 0.938 | 3.077 | 3.146 |
| **Slope** |
| **Genotypes** | **Estimate** | **Standard Error** | **p-value** | **R2** | **Lower Limit** | **Upper Limit** |
| 1 | 0.012 | 0.001 | 0e+00 | 0.873 | 0.009 | 0.016 |
| 2 | 0.007 | 0.001 | 5e-04 | 0.719 | 0.004 | 0.011 |
| 3 | 0.019 | 0.003 | 2e-04 | 0.769 | 0.012 | 0.027 |
| 4 | 0.035 | 0.001 | 0e+00 | 0.986 | 0.033 | 0.038 |
| 5 | 0.012 | 0.001 | 0e+00 | 0.901 | 0.009 | 0.015 |
| 6 | 0.010 | 0 | 0e+00 | 0.963 | 0.009 | 0.012 |
| 7 | 0.014 | 0 | 0e+00 | 0.976 | 0.012 | 0.016 |
| 8 | 0.017 | 0 | 0e+00 | 0.975 | 0.015 | 0.019 |
| 9 | 0.018 | 0 | 0e+00 | 0.970 | 0.016 | 0.020 |
| 10 | 0.020 | 0.001 | 0e+00 | 0.957 | 0.017 | 0.023 |
| 11 | 0.025 | 0.001 | 0e+00 | 0.946 | 0.021 | 0.029 |
| 12 | 0.015 | 0.001 | 0e+00 | 0.926 | 0.012 | 0.019 |
| 13 | 0.008 | 0 | 0e+00 | 0.948 | 0.007 | 0.010 |
| 14 | 0.025 | 0 | 0e+00 | 0.938 | 0.021 | 0.030 |