# Supplementary Tables

**Table S1:** Description of five populations (Pop I – Pop V) used as a training set (n = 517 half-sib families).

|  |  |  |  |
| --- | --- | --- | --- |
| **Population1**  | **No of maternal parents**  | **Genetic relatedness2**  | **Description of genetic background** |
| Pop I | 96 | 0.33 | Cross between two New Zealand cultivars (late flowering)  |
| Pop II | 110 | 0.32 | Cross between two inter-mediate flowering cultivars (New Zealand x Spanish ecotype) |
| Pop III | 115 | 0.27 | Crosses among five New Zealand cultivars (late flowering) |
| Pop IV | 90 | 0.43 | Cross between New Zealand and European cultivar (late flowering) |
| Pop V | 106 | 0.34 | Cross between two New Zealand cultivars and Spanish ecotype |

1Population description was previously mentioned in Faville et al. (2018) and Gagic et al. (2018). 2Mean genetic relatedness within each population was calculated using genomic relationship matrix (KGD) estimated using 1.02M SNPs.

**Table S2:** Trait description, mean, minimum and maximum value for all 18 nutritive traits measured among 517 half-sib families of perennial ryegrass across the two locations and within individual location (Lincoln and Aorangi).

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|   |   | **Across Locations**  |   | **Lincoln**  |   |   | **Aorangi**  |   |   |
|  **Trait** | **Abbreviation** |  **Mean** | **Min**  |  **Max** |  **Mean** | **Min**  |  **Max** |  **Mean** | **Min**  |  **Max** |
| Acid detergent fibre | ADF | 24.03 | 23.15 | 25.08 | 26.88 | 25.71 | 28.41 | 23.44 | 22.13 | 26.01 |
| Neutral detergent fibre | NDF | 43.58 | 42.01 | 45.79 | 44.52 | 43.28 | 46.05 | 41.87 | 40.21 | 44.03 |
| Digestible organic matter in dry-matter  | DOMD | 72.54 | 70.56 | 73.94 | 72.38 | 70.97 | 73.44 | 73.64 | 70.36 | 75.02 |
| Crude fat | CFAT | 3.69 | 3.45 | 4.18 | 3.94 | 3.6 | 4.61 | 3.57 | 3.39 | 3.8 |
| Metabolisable energy  | ME | 11.61 | 11.28 | 11.83 | 11.58 | 11.36 | 11.74 | 11.78 | 11.25 | 12.02 |
| Crude protein  | CP | 23.49 | 22.57 | 24.33 | 21.45 | 20.81 | 22.05 | 25.98 | 24.42 | 27.23 |
| Calcium | Ca | 0.44 | 0.39 | 0.53 | 0.49 | 0.44 | 0.62 | 0.43 | 0.38 | 0.51 |
| Potassium | K | 3.51 | 3.26 | 3.76 | 3.35 | 3.16 | 3.55 | 3.55 | 3.32 | 3.79 |
| Magnesium | Mg | 0.23 | 0.2 | 0.26 | 0.21 | 0.19 | 0.24 | 0.23 | 0.21 | 0.27 |
| Manganese (mg/kg) | Mn  | 132.26 | 116 | 163.9 | 149.41 | 135.5 | 177.8 | 116.44 | 102.1 | 137.8 |
| Sodium | Na | 0.26 | 0.15 | 0.41 | 0.36 | 0.25 | 0.53 | 0.2 | 0.14 | 0.28 |
| Phosphorus | P | 0.3 | 0.29 | 0.32 | 0.34 | 0.32 | 0.35 | 0.28 | 0.26 | 0.3 |
| Sulphur | S | 0.4 | 0.35 | 0.46 | 0.39 | 0.35 | 0.44 | 0.42 | 0.36 | 0.48 |
| Nitrogen  | N | 3.57 | 3.44 | 3.69 | 3.29 | 3.2 | 3.39 | 3.91 | 3.66 | 4.1 |
| Tetany ratio (K/Ca+Mg) | Tetany ratio | 2.15 | 1.87 | 2.48 | 2.05 | 1.8 | 2.35 | 2.25 | 1.96 | 2.67 |
| Total water-soluble carbohydrates  | Total WSC | 119.6 | 103.7 | 138.5 | 134.57 | 117.2 | 154.4 | 112.97 | 95 | 138 |
| Low molecular weight carbohydrates  | LMW | 92.76 | 81.99 | 105.4 | 98.38 | 91.74 | 106.11 | 93.83 | 80.29 | 114.23 |
| High molecular weight carbohydrates | HMW | 26.65 | 20.5 | 37.75 | 36.51 | 27.79 | 53.22 | 19.17 | 9.12 | 37.75 |

**Table S3:** Trait family (σ2g) and residual error (σ2ε) variance components, standard errors (SE), repeatability (*R*) and genomic heritability (*h2g*) and predictive ability (rp) estimated for 18 nutritive traits, amongst 485 half-sib families of perennial ryegrass evaluated at Lincoln.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Trait** |  **σ2g ± SE** | **σ2ε ± SE** |  ***R*** |  ***h2g*** |  **rp** |
| ADF | 0.49 ± 0.126 | 3.27 ± 0.162 | 0.31 | 0.31 | -0.06 |
| NDF | 0.57 ± 0.142 | 3.64 ± 0.179 | 0.31 | 0.39 | 0.02 |
| DOMD | 0.55 ± 0.168 | 4.63 ± 0.229 | 0.25 | 0.22 | -0.02 |
| CFAT | 0.02 ± 0.003 | 0.05 ± 0.003 | 0.51 | 0.56 | 0.25 |
| ME | 0.01 ± 0.004 | 0.12 ± 0.005 | 0.25 | 0.23 | -0.02 |
| CP | 0.23 ± 0.098 | 2.94 ± 0.144 | 0.19 | 0.33 | 0.14 |
| Ca | 0.96 ± 0.119† | 1.85 ± 0.094† | 0.6 | 0.69 | 0.34 |
| K | 0.01 ± 0.003 | 0.07 ± 0.003 | 0.37 | 0.45 | 0.17 |
| Mg | 0.11 ± 0.015† | 0.27 ± 0.014† | 0.53 | 0.65 | 0.33 |
| Mn  | 100.3 ± 20 | 454.3 ± 22.8 | 0.39 | 0.49 | 0.22 |
| Na | 3.92 ± 0.460† | 6.64 ± 0.340† | 0.63 | 0.7 | 0.35 |
| P | 0.11 ±0.039† | 1.11 ± 0.055† | 0.23 | 0.31 | 0.02 |
| S | 0.41 ± 0.074† | 1.58 ± 0.080† | 0.43 | 0.53 | 0.20 |
| N | 5.56 ± 2.40† | 72.3 ± 3.50† | 0.18 | 0.31 | 0.14 |
| Tetany ratio | 0.02 ± 0.002 | 0.03 ± 0.001 | 0.59 | 0.61 | 0.29 |
| Total WSC | 142.8 ± 33.1 | 806.8 ± 40.3 | 0.33 | 0.39 | 0.08 |
| LMW | 34.2 ± 13.3 | 406 ± 19.6 | 0.2 | 0.12 | -0.03 |
| HMW | 52.2 ± 13.1 | 329.3 ± 16.4 | 0.31 | 0.43 | 0.13 |
| † x10-3 |  |  |  |  |  |  |

**Table S4:** Trait family (σ2g) and residual error (σ2ε) variance components and their associated standard errors (SE), repeatability (*R*) and genomic heritability (*h2g*) and predictive ability (rp) estimated for 18 nutritive traits, amongst 501 half-sib families of perennial ryegrass evaluated at Aorangi.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Trait** | **σ2g ± SE** | **σ2ε ± SE** |  ***R***  |  ***h2g*** |  **rp** |
| ADF | 0.60 ± 0.075 | 1.29 ± 0.061 | 0.56 | 0.65 | 0.29 |
| NDF | 0.86 ± 0.112 | 2.06 ± 0.097 | 0.54 | 0.64 | 0.35 |
| DOMD | 0.83 ± 0.130 | 2.80 ± 0.131 | 0.46 | 0.53 | 0.25 |
| CFAT | 0.01 ± 0.001 | 0.02 ± 0.001 | 0.59 | 0.69 | 0.33 |
| ME | 0.02 ± 0.003 | 0.07 ± 0.003 | 0.46 | 0.54 | 0.25 |
| CP | 0.37 ± 0.064 | 1.48 ± 0.069 | 0.42 | 0.59 | 0.21 |
| Ca | 0.60 ± 0.082† | 1.58 ± 0.074† | 0.52 | 0.6 | 0.16 |
| K | 0.01 ± 0.002 | 0.04 ± 0.002 | 0.46 | 0.6 | 0.28 |
| Mg | 0.18 ± 0.021† | 0.36 ± 0.017† | 0.59 | 0.69 | 0.34 |
| Mn  | 53.6 ± 9.1 | 206.8 ± 9.7 | 0.41 | 0.57 | 0.24 |
| Na | 1.28 ± 0.018† | 3.44 ± 0.160† | 0.5 | 0.62 | 0.26 |
| P | 0.09 ± 0.014† | 0.03 ± 0.014† | 0.49 | 0.58 | 0.24 |
| S | 0.05 ± 0.064† | 1.03 ± 0.049† | 0.61 | 0.67 | 0.47 |
| N | 0.01 ± 0.001 | 0.03 ± 0.002 | 0.43 | 0.6 | 0.20 |
| Tetany ratio | 0.02 ± 0.002 | 0.04 ± 0.002 | 0.5 | 0.59 | 0.18 |
| Total WSC | 103.7 ± 12.9 | 226.5 ± 10.7 | 0.57 | 0.65 | 0.46 |
| LMW WSC | 49 ± 7.5 | 157.8 ± 7.3 | 0.48 | 0.59 | 0.33 |
| HMW WSC | 21.71 ± 2.3 | 33.11 ± 1.57 | 0.66 | 0.68 | 0.56 |
| † x10-3 |  |  |  |  |  |

**Table S5:**  Trait mean, standard deviation, variance of family (σ2g), family-by-location interaction (σ2gl) and residual error (σ2ε), along with their associated standard errors (SE), and narrow-sense heritability (*h2*) estimated for a range of nutritive quality traits in Pop I (96 half-sib families), using data from across locations (Lincoln and Aorangi).

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Trait** |  **Mean** |  **σ** |  **σ2g ± SE** |  **σ2gl ± SE** |  **σ2ε ± SE** |  ***h2*** |
| ADF | 26.07 | 0.12 | 0.06±0.122 ‡ | 0.32±0.141 | 1.10±0.101 | 0.15 |
| NDF | 44.99 | 0.35 | 0.26±0.144 ‡ | 0.11±0.141 ‡ | 1.62±0.157 | 0.44 |
| DOMD | 72.11 | 0.48 | 0.17±0.156 ‡ | - | 2.72±0.228 | 0.27 |
| CFAT | 3.82 | 0.04 | 0.47±0.30† ‡ | 0.51±0.34 †‡ | 3.09±0.290† | 0.38 |
| ME | 11.54 | 0.08 | 0.53±0.4† ‡ | - | 7.01±0.590 | 0.31 |
| CP | 23.63 | 0.57 | 0.08±0.118 ‡ | 0.09±0.093 ‡ | 1.65±0.153 | 0.19 |
| Ca | 0.44 | 0.02 | 0.07±0.02† | 0.01±0.01 †‡ | 0.16±0.010† | 0.69 |
| K | 3.71 | 0.03 | 0.48±0.37† ‡ | 0.35±0.32 †‡ | 5.67±0.490† | 0.30 |
| Mg | 0.23 | 0.01 | - | - | - | 0.67 |
| Mn  | 138.00 | 6.25 | 78.28±22.557 | 23.02±13.171 ‡ | 174.30±16.002 | 0.66 |
| Na | 0.27 | 0.02 | 0.11±0.03† | - | 0.33±0.030† | 0.67 |
| P | 0.30 | 0.01 | - | - | - | 0.55 |
| S | 0.38 | 0.01 | 0.04±0.01† | - | 0.09±0.010† | 0.73 |
| N | 3.59 | 0.09 | 0.02±0.22† ‡ | 0.39±0.28 †‡ | 4.2±0.390† | 0.02 |
| Tetany ratio | 5.62 | 0.24 | 0.10±0.0276 | - | 0.27±0.023 | 0.68 |
| Total WSC | 114.51 | 7.46 | 12.66±37.235 ‡ | 63.53±39.089 ‡ | 439.98±42.302 | 0.11 |
| LMW WSC | 87.16 | 4.21 | 11.66±7.641 ‡ | 14.21±6.772 | 84.71±7.705 | 0.35 |
| HMW WSC | 27.32 | 3.75 | 12.49±18.829‡ | - | 263.20±23.515 | 0.22 |

 † x10-2

‡ non-significant at the 0.05 probability level

**Table S6:** Trait variance of family (σ2g), family-by-location interaction (σ2gl) and residual error (σ2ε), along with their associated standard errors (SE) and narrow-sense heritability (*h2*) estimated for a range of nutritive quality traits in Pop II (110 half-sib families), using data from across locations (Lincoln and Aorangi).

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Trait** |  **Mean** |  **σ** |  **σ2g ± SE** |  **σ2gl ± SE** |  **σ2ε ± SE** |  ***h2*** |
| ADF | 25.35 | 0.40 | 0.18±0.105 ‡ | 0.27±0.106 | 1.36±0.101 | 0.34 |
| NDF | 43.40 | 0.39 | - | - | - | - |
| DOMD | 72.36 | 0.30 | 0.24±0.190‡ | 0.23±0.181‡ | 3.74±0.274 | 0.25 |
| CFAT | 3.63 | 0.04 | 0.39±0.16† | 0.07±0.15†‡ | 2.0±0.20† | 0.45 |
| ME | 11.58 | 0.05 | 0.61±0.49 †‡ | 0.62±0.480† ‡ | 9.6±0.710† | 0.24 |
| CP | 24.22 | 0.39 | 0.22±0.105 | 1.06±0.103‡ | 1.72±0.129 | 0.39 |
| Ca | 0.46 | 0.02 | 0.06±0.01† | 0.01±0.01 †‡ | 0.17±0.01† | 0.66 |
| K | 3.34 | 0.07 | 1.0±0.37† | 0.44±0.35† ‡ | 4.7±0.37† | 0.50 |
| Mg | 0.23 | 0.01 | - | - | - | 0.68 |
| Mn  | 145.79 | 4.82 | 55.77±26.139† | 36.76±25.98†‡ | 356.94±27.602† | 0.42 |
| Na | 0.25 | 0.05 | 0.28±0.05† | 0.04±0.03† ‡ | 0.35±0.03† | 0.78 |
| P |  - |  - |  - |  - |  - |  - |
| S | 0.42 | 0.00 | 0.01±0.01† | 0.02±0.01†‡ | 0.13±0.01† | 0.16 |
| N | 3.65 | 0.06 | 0.51±0.24† | 0.2±0.24†‡ | 4.23±0.31† | 0.39 |
| Tetany ratio | 4.87 | 0.27 | 0.10±0.02 | 0.021±0.01‡ | 0.24±0.01 | 0.68 |
| Total WSC | 113.67 | 3.58 | 38.58±17.13 | 49.5±15.8 | 188.85±14.1 | 0.41 |
| LMW WSC | 86.71 | 2.19 | 11.52±5.6 | 18.6±6.01 | 60.02±4.6 | 0.37 |
| HMW WSC | 26.85 | 1.94 | 10.2±6.18 ‡ | 14.66±5.42 | 94.94±6.9 | 0.31 |

 † x10-2

‡ non-significant at the 0.05 probability level

**Table S7:** Trait variance of family (σ2g), family-by-location interaction (σ2gl) and residual error (σ2ε), along with their associated standard errors (SE), and narrow-sense heritability (*h2*) estimated for a range of nutritive quality traits in Pop III (115 half-sib families), using data from across locations (Lincoln and Aorangi).

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Trait** |  **Mean** |  **σ** |  **σ2g ± SE** |  **σ2gl ± SE** |  **σ2ε ± SE** |  ***h2*** |
| ADF | 24.93 | 0.57 | 0.31±0.114 | 0.20±0.115‡ | 1.55±0.112 | 0.46 |
| NDF | 42.17 | 0.71 | 0.6±0.145 | 0.21±0.102 | 1.25±0.090 | 0.68 |
| DOMD | 73.52 | 0.50 | 0.47±0.172 | 0.48±0.168 | 1.83±0.134 | 0.46 |
| CFAT | 3.75 | 0.04 | 0.31±0.37†‡ | 1.9±0.46† | 3.57±0.26† | 0.17 |
| ME | 11.76 | 0.08 | 1.2±0.45† | 1.19±0.43† | 4.86±0.35† | 0.48 |
| CP | 23.07 | 0.55 | 0.13±0.109 ‡ | 0.26±0.133‡ | 1.67±0.119‡ | 0.25 |
| Ca | 0.45 | 0.02 | 0.05±0.01† | 0.04±0.01† | 0.12±0.01† | 0.56 |
| K | 3.52 | 0.07 | 0.94±0.36† | 1.13±0.37† | 3.97±0.28† | 0.43 |
| Mg | 0.21 | 0.01 | - | - | - | 0.45 |
| Mn  | 125.26 | 7.52 | 63.15±17.524 | 17.78±14.215‡ | 225.42±16.181 | 0.58 |
| Na | 0.26 | 0.05 | 0.24±0.04† | - | 0.4±0.03† | 0.78 |
| P | 0.30 | 0.01 | - | - | - | 0.17 |
| S | 0.40 | 0.02 | 0.05±0.01† | 0.03±0.01† | 0.09±0.01† | 0.62 |
| N | 3.51 | 0.07 | 0.3±0.27 †‡ | 0.7±0.34† | 0.04±0.3† | 0.20 |
| Tetany ratio | 5.34 | 0.23 | 0.07±0.021 | 0.0581±0.019 | 2.1±1.59 | 0.55 |
| Total WSC | 129.92 | 3.93 | 43.3±23.526 ‡ | 66.62±26.461 | 306.46±22.197 | 0.34 |
| LMW WSC | 102.23 | 2.09 | 14.7±8.168 ‡ | 28.01±9.337 | 93.07±6.838 | 0.33 |
| HMW WSC | 27.67 | 2.68 | 13.39±8.539‡ | 16.74±10.170‡ | 135.39±9.845 | 0.30 |

 † x10-2

‡ non-significant at the 0.05 probability level

**Table S8:** Trait variance of family (σ2g), family-by-location interaction (σ2gl) and residual error (σ2ε), along with their associated standard errors (SE) and narrow-sense heritability (*h2*) estimated for a range of nutritive quality traits in Pop IV (90 half-sib families), using the data from across locations (Lincoln and Aorangi).

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Trait** |  **Mean** |  **σ** |  **σ2g ± SE** |  **σ2gl ± SE** |  **σ2ε ± SE** |  ***h2*** |
| ADF | 23.41 | 1.32 | 0.70±0.216 | - | 0.99±0.142 | 0.81 |
| NDF | 42.41 | 1.18 | 0.69±0.225 | - | 1.24±0.167 | 0.77 |
| DOMD | 74.42 | 1.16 | 1.59±0.683 | - | 1.53±0.244 | 0.86 |
| CFAT |  - |  - | - | - | - |  - |
| ME | 11.91 | 0.17 | 3.60±1.62† | 0.72±0.82† | 3.68±0.62†‡ | 0.79 |
| CP | 24.19 | 1.04 | 0.34±0.229‡ | 0.056±0.151 | 1.24±0.227 ‡ | 0.60 |
| Ca | 0.44 | 0.01 | 0.03±0.02† ‡ | 0.03±0.02† | 0.1±0.01† ‡ | 0.49 |
| K | 3.53 | 0.08 | 1.31±0.65† | 0.78±0.55† | 2.22±0.38†‡ | 0.63 |
| Mg | 0.23 | 0.01 | - | - | - | 0.66 |
| Mn  | 128.86 | 7.08 | 39.9±45.340†‡ | 93.06±46.412† | 175.98±28.674 †‡ | 0.35 |
| Na | 0.20 | 0.04 | 0.07±0.03† | 0.06±0.0† | 0.18±0.03†‡ | 0.52 |
| P | 0.31 | 0.01 | 0.01±0.01†  | 0.01±0.01† | 0.03±0.01†‡ | 0.36 |
| S | 0.44 | 0.01 | 0.04±0.02†  | 0.04±0.02† | 0.05±0.01† ‡ | 0.62 |
| N | 3.68 | 0.14 | 0.81±0.52†‡ | 0.1±0.31† | 2.95±0.51†‡ | 0.60 |
| Tetany ratio | 5.31 | 0.25 | 0.10±0.034 | - | 0.17±0.023 ‡ | 0.79 |
| Total WSC | 124.13 | 6.42 | 50.3±26.384 ‡ | 13.16±21.149 | 208.64±27.998‡ | 0.55 |
| LMW WSC | 103.19 | 2.83 | 18.62±16.381 ‡ | 19.63±14.479 | 135.25±18.456‡ | 0.37 |
| HMW WSC | 20.56 | 6.68 | 7.09±9.480‡ | 41.74±13.329 | 24.35±5.692 | 0.22 |

† x10-2

‡ non-significant at the 0.05 probability level

**Table S9:** Trait variance of family (σ2g), family-by-location interaction (σ2gl) and residual error (σ2ε), along with their associated standard errors (SE) and narrow-sense heritability (*h2*) estimated for a range of nutritive quality traits in Pop V (106 half-sib families), using data from across locations (Lincoln and Aorangi).

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Trait** |  **Mean** |  **σ** |  **σ2g ± SE** |  **σ2gl ± SE** |  **σ2ε ± SE** |  ***h2*** |
| ADF | 25.15 | 0.37 | 0.21±0.089 | 0.17±0.072 | 1.03±0.081 | 0.46 |
| NDF | 42.29 | 0.58 | 0.52±0.125 | 0.12±0.065 ‡ | 1.14±0.089 | 0.67 |
| DOMD | 73.14 | 0.55 | 0.60±0.186 | 0.29±0.147 | 1.87±0.148 | 0.57 |
| CFAT | 3.89 | 0.07 | 0.89±0.33† | 1.03±0.32† | 2.81±0.23† | 0.48 |
| ME | 11.70 | 0.09 | 1.61±0.49† | 0.77±0.38† | 4.85±0.38† | 0.58 |
| CP | 23.72 | 0.27 | 0.03±0.099†‡ | 29.23±11.65† | 122.2±97.8† | 0.08 |
| Ca | 0.49 | 0.01 | 0.03±0.01† | 0.03±0.01† | 0.13±0.01† | 0.48 |
| K | 3.04 | 0.05 | 0.7±0.32† | 0.49±0.31† | 4.37±00.35†‡ | 0.42 |
| Mg | 0.21 | 0.01 | - | - | - | 0.72 |
| Mn  | 127.56 | 6.32 | 57.35±17.813 | 31.39±15.714 | 171.39±13.872 ‡ | 0.56 |
| Na | 0.39 | 0.04 | 0.2±0.05† | 0.13±0.04† | 0.41±0.03† | 0.60 |
| P | 0.32 | 0.01 | - | - | - | 0.31 |
| S | 0.36 | 0.01 | 0.01±0.01†  | 0.02±0.01† | 0.07±0.01†‡ | 0.36 |
| N | 3.59 | 0.04 | 0.09±0.23†‡ | 0.66±0.28† | 3.15±0.25† | 0.10 |
| Tetany ratio | 4.42 | 0.11 | 0.023±0.01 | 0.01±0.008 | 0.16±0.012‡ | 0.40 |
| Total WSC | 142.35 | 4.53 | 57.8±27.232 | 85.90±27.256 | 303.92±24.30 | 0.38 |
| LMW WSC | 103.39 | 1.84 | 12.5±9.713‡ | 29.65±11.309 | 123.6±10.040 | 0.26 |
| HMW WSC | 38.98 | 2.68 | 19.79±8.325 | 25.99±7.742 | 90.03±7.068 | 0.41 |

 † x10-2

‡ non-significant at the 0.05 probability level

**Table S10:** Phenotypic correlation for a range of nutritive quality traits among 517 half-sib families, estimated using data from across two locations (Lincoln and Aorangi).

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|   | **ADF** | **NDF** | **DOMD** | **CFAT** | **ME** | **CP** | **N** | **Ca** | **K** | **Mg** | **Mn** | **Na** | **P** | **S** | **Tetany** | **LMW WSC** | **HMW WSC** | **Total WSC** |
| ADF | 1 | 0.57 | −0.59 | −0.35 | −0.59 | −0.43 | −0.40 | 0.14 | −0.14 | 0.26 | 0.26 | 0.12 | −0.10 | 0.03† | −0.24 | −0.39 | −0.21 | −0.36 |
| NDF |  | 1 | −0.73 | −0.05† | −0.73 | −0.25 | −0.23 | 0.09 | 0.03† | 0.38 | 0.21 | 0.14 | −0.07† | 0.06† | −0.14 | −0.62 | −0.44 | −0.63 |
| DOMD |  |  | 1 | 0.06† | 1 | 0.31 | 0.28 | −0.24 | 0.13 | −0.48 | −0.38 | −0.20 | 0.07† | −0.09† | 0.34 | 0.57 | 0.36 | 0.56 |
| CFAT |  |  |  | 1 | 0.05† | 0.44 | 0.44 | −0.05† | 0.32 | −0.08† | −0.21 | 0† | 0.16 | 0.01 | 0.24 | 0.02† | −0.20 | −0.11† |
| ME |  |  |  |  | 1 | 0.3 | 0.28 | −0.23 | 0.13 | −0.49 | −0.37 | −0.21 | 0.07† | −0.09† | 0.34 | 0.56 | 0.37 | 0.55 |
| CP |  |  |  |  |  | 1 | 0.99 | 0† | 0.42 | −0.01† | −0.13 | −0.14 | 0.28 | 0.25 | 0.25 | −0.05† | −0.45 | -0.29 |
| N |  |  |  |  |  |  | 1 | 0.01† | 0.43 | 0† | −0.12 | −0.14 | 0.27 | 0.25 | 0.25 | −0.06† | −0.45 | −0.30 |
| Ca |  |  |  |  |  |  |  | 1 | −0.16 | 0.36 | 0.4 | 0.19 | 0.16 | 0.2 | −0.77 | −0.10 | −0.19 | -0.17 |
| K |  |  |  |  |  |  |  |  | 1 | 0.02† | −0.02† | −0.41 | 0.2 | 0.33 | 0.67 | −0.14 | −0.31 | −0.27 |
| Mg |  |  |  |  |  |  |  |  |  | 1 | 0.41 | 0.15 | 0.1 | 0.33 | −0.48 | −0.39 | −0.38 | -0.45 |
| Mn |  |  |  |  |  |  |  |  |  |  | 1 | −0.10 | 0.13 | 0.25 | −0.35 | −0.23 | −0.17 | −0.24 |
| Na |  |  |  |  |  |  |  |  |  |  |  | 1 | 0.03† | 0.01† | −0.40 | −0.07† | −0.10 | -0.1† |
| P |  |  |  |  |  |  |  |  |  |  |  |  | 1 | 0.39 | 0.01† | −0.01† | −0.21 | −0.13 |
| S |  |  |  |  |  |  |  |  |  |  |  |  |  | 1 | −0.01† | −0.19† | −0.31† | -0.29 |
| Tetany |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 1 | 0.08 | 0.03 | 0.06† |
| LMW WSC |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 1 | 0.43 | 0.85 |
| HMW WSC |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 1 | 0.83 |
| Total WSC |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   | 1 |

† non-significant at the 0.05 probability level

Table S11: Random subsets of markers ranging from 0.10% (n = 1,093) to 100% (n = 1,093,464) of the full GBS SNP dataset used in a GBLUP model to estimate predictive ability (rp) and bias (β) for 18 nutritive traits.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Trait  | 100% |   | 80% |   | 60% |   | 40% |   | 20% |   |
|   |  rp |  β |  rp |  β |  rp |  β |  rp |  β |  rp |  β |
| ADF | **0.22** | 0.98 | **0.22** | 1.02 | **0.22** | 0.99 | **0.22** | 1.00 | **0.22** | 1.00 |
| NDF | **0.37** | 0.94 | **0.36** | 0.90 | **0.37** | 0.92 | **0.37** | 0.94 | **0.36** | 0.92 |
| DOMD | **0.23** | 0.95 | **0.22** | 0.93 | **0.22** | 0.90 | **0.22** | 0.88 | **0.22** | 0.90 |
| CFAT | **0.35** | 1.02 | **0.36** | 1.04 | **0.35** | 1.01 | **0.36** | 1.03 | **0.35** | 1.02 |
| ME | **0.23** | 0.86 | **0.23** | 0.91 | **0.23** | 0.89 | **0.23** | 0.91 | **0.23** | 0.87 |
| CP | **0.27** | 1.00 | **0.26** | 0.98 | **0.27** | 1.00 | **0.26** | 0.98 | **0.27** | 0.99 |
| N | **0.25** | 1.01 | **0.25** | 1.01 | **0.25** | 0.99 | **0.25** | 1.02 | **0.25** | 1.01 |
| Ca | **0.31** | 0.98 | **0.31** | 0.97 | **0.31** | 0.95 | **0.31** | 0.99 | **0.30** | 0.97 |
| K | **0.32** | 1.01 | **0.32** | 1.02 | **0.32** | 1.00 | **0.32** | 1.02 | **0.32** | 1.00 |
| Mg | **0.45** | 1.02 | **0.45** | 1.03 | **0.45** | 1.02 | **0.44** | 1.01 | **0.44** | 1.02 |
| Mn | **0.31** | 1.03 | **0.31** | 1.01 | **0.31** | 1.01 | **0.31** | 1.01 | **0.30** | 1.00 |
| Na | **0.44** | 1.00 | **0.43** | 1.00 | **0.43** | 0.98 | **0.44** | 1.00 | **0.43** | 1.00 |
| P | **0.14** | 1.46 | **0.14** | 1.04 | **0.15** | 1.08 | **0.15** | 1.33 | **0.15** | 1.05 |
| S | **0.45** | 0.97 | **0.45** | 0.97 | **0.44** | 0.96 | **0.45** | 0.98 | **0.45** | 0.98 |
| Tetany ratio | **0.34** | 1.00 | **0.34** | 0.98 | **0.34** | 1.01 | **0.34** | 1.00 | **0.34** | 0.97 |
| LMW WSC | **0.36** | 1.04 | **0.36** | 1.04 | **0.36** | 1.04 | **0.36** | 1.04 | **0.35** | 1.04 |
| HMW WSC | **0.23** | 1.07 | **0.23** | 1.07 | **0.23** | 1.05 | **0.23** | 1.12 | **0.23** | 1.05 |
| Total WSC | **0.31** | 1.03 | **0.30** | 1.02 | **0.30** | 1.00 | **0.30** | 1.03 | **0.30** | 1.02 |

**Table S11:** continued

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Trait  | 10% |   | 5% |   | 1% |   | 0.50% |   | 0.10% |   |
|   |  rp |  β |  rp |  β |  rp |  β |  rp |  β |  rp |  β |
| ADF | **0.22** | 0.99 | **0.22** | 1.00 | **0.20** | 1.10 | **0.19** | 1.08 | **0.15** | 1.22 |
| NDF | **0.36** | 0.93 | **0.37** | 0.96 | **0.35** | 0.96 | **0.34** | 0.98 | **0.29** | 1.00 |
| DOMD | **0.22** | 0.92 | **0.22** | 0.92 | **0.21** | 0.95 | **0.20** | 0.98 | **0.15** | 1.40 |
| CFAT | **0.35** | 1.01 | **0.35** | 1.01 | **0.34** | 1.03 | **0.31** | 0.99 | **0.27** | 1.03 |
| ME | **0.23** | 0.92 | **0.23** | 0.90 | **0.22** | 1.05 | **0.20** | 0.95 | **0.16** | 1.11 |
| CP | **0.26** | 0.98 | **0.26** | 0.98 | **0.25** | 1.00 | **0.24** | 1.01 | **0.20** | 1.07 |
| N | **0.25** | 1.00 | **0.25** | 1.00 | **0.24** | 1.03 | **0.23** | 1.03 | **0.20** | 1.14 |
| Ca | **0.30** | 0.98 | **0.30** | 0.97 | **0.29** | 1.00 | **0.27** | 0.99 | **0.22** | 1.06 |
| K | **0.32** | 1.02 | **0.32** | 1.00 | **0.31** | 1.03 | **0.31** | 1.05 | **0.26** | 1.04 |
| Mg | **0.44** | 1.01 | **0.44** | 0.99 | **0.41** | 0.95 | **0.39** | 0.96 | **0.33** | 1.00 |
| Mn | **0.31** | 1.02 | **0.29** | 0.97 | **0.28** | 1.00 | **0.25** | 1.01 | **0.17** | 1.35 |
| Na | **0.44** | 1.00 | **0.43** | 0.98 | **0.41** | 0.98 | **0.40** | 0.99 | **0.34** | 1.01 |
| P | **0.14** | 0.99 | **0.14** | 1.20 | **0.14** | 1.04 | **0.13** | 1.67 | **0.09** | 1.46 |
| S | **0.45** | 0.96 | **0.45** | 0.98 | **0.43** | 0.96 | **0.42** | 0.98 | **0.37** | 0.99 |
| Tetany ratio | **0.34** | 0.98 | **0.33** | 0.99 | **0.32** | 1.00 | **0.31** | 1.00 | **0.26** | 1.02 |
| LMW WSC | **0.36** | 1.05 | **0.35** | 1.03 | **0.34** | 1.04 | **0.34** | 1.05 | **0.31** | 1.06 |
| HMW WSC  | **0.22** | 1.05 | **0.22** | 1.04 | **0.21** | 1.04 | **0.22** | 1.13 | **0.18** | 1.26 |
| Total WSC | **0.30** | 1.02 | **0.29** | 0.99 | **0.29** | 1.02 | **0.29** | 1.04 | **0.26** | 1.04 |

# Supplementary Figure

**Figure S1:** Daily rainfall, sunshine hours and minimum and maximum air temperatures recorded at stations in the NIWA National Climate network (<https://cliflo.niwa.co.nz>; Lincoln Broadfield EWS; Palmerston North EWS) closest to the two experimental sites. Data are presented for the period leading up to and including tissue harvests. Harvest periods at the two locations are indicated by coloured blocks (orange = Lincoln; blue = Aorangi).

**Figure S1:** Continued.