**Table S1. Posterior means of variance components explained by genome wide markers for RFI and its related traits using RFI selection lines by a Bayesian approach.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Trait** | **No. of animals** | **Genetic variance** | **Residual variance** | **Estimated total variance** | **Proportion of phenotypic variance explained by markers** |
| RFI | 1410 | 0.014 | 0.013 | 0.027 | 0.523 |
| ADFI | 1417 | 0.021 | 0.023 | 0.044 | 0.475 |
| ADG | 1418 | 0.002 | 0.004 | 0.006 | 0.341 |
| BF | 1412 | 6.097 | 6.322 | 12.419 | 0.490 |
| LMA | 1410 | 7.733 | 12.345 | 20.078 | 0.385 |