**Supplementary Table S1** Overview of imputation accuracies and allele imputation error rate (AIER) for imputation of 50k genotypes in dairy cattle.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Reference | Method1 | Breed2 | Population | Accuracy | AIER (%)3 |
|  |   |  | Ref. | Val. | 384 | 3k4 | 6k5 | 384 | 3k4 | 6/7k5 |
| Dassoneville *et al.* ([2012](#_ENREF_13)) | Beagle | MON | 997 | 222 | . | 0.94 | 0.97 | . | 2.6 | 1.0 |
|  | Beagle | HF | 3,071 | 966 | . | 0.93 | 0.96 | . | 2.6 | 0.9 |
| Jiménez-Montero *et al.* ([2013](#_ENREF_35)) | Beagle | HF | 1,632 | 834 | . | . | . | . | 3.1 | 1.3 |
| Chen *et al.* ([2011](#_ENREF_11))  | Findhap | HF | 3,589 | 458 | . | . | . | . | 2.6 | . |
|  | DAGPHASE | HF | 3,589 | 458 | . | . | . | . | 5.0 | . |
|  | Beagle | HF | 3,589 | 458 | . | . | . | . | 1.7 | . |
|  | Findhap | HF | 14,385 | 1,019 | . | . | . | . | 3.3 | . |
|  | DAGPHASE | HF | 14,385 | 1,019 | . | . | . | . | 2.7 | . |
|  | Beagle | HF | 14,385 | 1,019 | . | . | . | . | 1.6 | . |
|  | Findhap | HF | 32,597 | 1,881 | . | . | . | . | 2.7 | . |
| Weng *et al.* ([2013](#_ENREF_62)) | Beagle | HF | 1,098 | 1,010 | . | . | . | . | 3.6 | 1.7 |
|  | fastPHASE | HF | 1,098 | 1,010 | . | . | . | . | 12.5 | 5.4 |
|  | Findhap | HF | 1,098 | 1,010 | . | . | . | . | 5.5 | 3.1 |
| Weigel *et al.* ([2010a](#_ENREF_59)) | IMPUTE2 | JER | 1,446 | 316 | . | . | . | 13.3 | 4.4 | . |
| Berry and Kearney ([2011](#_ENREF_3)) | Beagle | HF | 4,725 | 764 | . | 0.96 | . | . | 2.6 | . |
| Berry *et al.* (2014) | Beagle | HF | 2,4246 | 31 | . | . | 0.93 | . | . | 4.6 |
| Mulder *et al.* ([2012](#_ENREF_40)) | Mult. BLUP | HF | 5,304 | 4,074 | 0.65 | 0.71 | 0.73 | 16.3 | 14.6 | 13.5 |
|  | DAGPHASE | HF | 5,304 | 4,074 | 0.58 | 0.88 | 0.92 | 13.6 | 3.8 | 2.6 |
|  | DAGPHASEgc  | HF | 5,304 | 4,074 | . | 0.92 | . | . | 4.3 | . |
|  | CHROMIBD | HF | 5,304 | 4,074 | . | 0.93 | . | . | 3.8 | . |
| Segelke *et al.* ([2012](#_ENREF_48)) | Findhap | HF | 11,670 | 388 | . | . | . | . | 3.8 | 2.2 |
|  | Findhap | HF | 14,405 | 1,019 | . | . | . | . | 3.3 | 1.7 |
|  | Findhap | HF | 31,597 | 1,881 | . | . | . | . | 2.7 | 1.2 |
|  | Beagle | HF | 14,405 | 1,019 | . | . | . | . | 1.6 | 0.6 |
| Johnston *et al.* ([2011](#_ENREF_36)) | AlphaImpute7 | BS | 1,270 | 209 | . | . | . | . | 3.3 | . |
|  | Beagle | BS | 1,270 | 209 | . | . | . | . | 2.9 | . |
|  | FImpute7 | BS | 1,270 | 209 | . | . | . | . | 2.4 | . |
|  | Findhap | BS | 1,270 | 209 | . | . | . | . | 3.1 | . |
|  | Phasebook | BS | 1,270 | 209 | . | . | . | . | 3.4 | . |
|  | Beagle | HF | 7,224 | 20,000 | . | . | . | . | 2.4 | . |
|  | FImpute7 | HF | 7,224 | 20,000 | . | . | . | . | 1.5 | . |
|  | Findhap | HF | 7,224 | 20,000 | . | . | . | . | 2.1 | . |
|  | Phasebook | HF | 7,224 | 20,000 | . | . | . | . | 1.9 | . |
| Gredler *et al.* ([2011](#_ENREF_23)) | AlphaImpute7 | BS | 3,015 | 723 | . | . | . | . | 2.9 | . |
|  | Findhap | BS | 3,015 | 723 | . | . | . | . | 3.7 | . |
|  | AlphaImpute7 | MIX | 3,817 | 936 | . | . | . | . | 5.7 | . |
|  | Findhap | MIX | 3,817 | 936 | . | . | . | . | 5.5 | . |
| Nicolazzi *et al.* ([2013](#_ENREF_41)) | PEDIMPUTE7 | HF | 15,671 | 4,233 | . | . | 0.99 | . | . | 0.9 |
|  | Findhap | HF | 15,671 | 4,233 | . | . | 0.99 | . | . | 0.8 |
|  | Beagle | HF | 15,671 | 4,233 | . | . | 0.99 | . | . | 0.4 |
| Ma *et al.* ([2013](#_ENREF_39)) | Beagle | NR | 2,931 | 977 | . | 0.87 | . | . | 3.7 | . |
|  | Findhap | NR | 2,931 | 977 | . | 0.75 | . | . | 6.3 | . |
|  | AlphaImpute | NR | 2,931 | 977 | . | 0.76 | . | . | 6.3 | . |
|  | FImpute | NR | 2,931 | 977 | . | 0.81 | . | . | 4.8 | . |
|  | IMPUTE2 | NR | 2,931 | 977 | . | 0.89 | . | . | 2.9 | . |
| Average |  |  |  |  | 0.62 | 0.86 | 0.94 | 14.4 | 3.9 | 2.6 |

1 Description and references of imputation methods are given in Table 1.

2 MON = Montbéliarde, HF = Holstein, JER=Jersey, BS = Brown Swiss, NR = Nordic Red, MIX is a combined dataset containing Simmental, Swiss Fleckvieh, and Holstein.

3 Allele imputation error rate (AIER) is computed as half the genotype imputation error rate for studies that provided the latter measure.

4 This is the Bovine3K (Illumina Inc.), or an in silico 3k panel designed within the study ([Weigel *et al.*, 2010a](#_ENREF_59), [Mulder *et al.*, 2012](#_ENREF_40)). Dassoneville *et al.* (2012) used both the Bovine3K and an silico panel.

5 This is the BovineLD with 6,909 SNPs (Illumina Inc.), or an in silico 6k panel designed within the study ([Dassonneville *et al.*, 2012](#_ENREF_13), [Mulder *et al.*, 2012](#_ENREF_40)).

6 This is a multibreed reference population (including: 195, 140, 526, 189, 688, 506, and 180 bulls for Aberdeen Angus, Belgian Blue, Charolais, Hereford, Holstein-Friesian, Limousin and Simmental, respectively).

7 Reported not imputed genotypes, are multiplied by 0.375 and then added to genotype imputation error rates, considering a MAF of 0.25 and imputation of those genotypes based on allele frequencies.