Status as of: 2016-08-03

**Form GENO**

**DESCRIPTION OF NATIONAL GENOMIC EVALUATION SYSTEMS**

|  |  |
| --- | --- |
| Country (or countries) | Switzerland |
| Main trait groupa.  NOTE. Only one trait group per form! | Female Fertility |
| Breed(s) | Brown Swiss |
| Trait definition(s) and unit(s) of measurement Attach an appendix if needed | see GE form for conventional genetic evaluation |
| Source of genotypes (chips used) | Illumina BovineSNP50 BeadChip (v1 and v2) and various low density chips |
| Imputation method for missing genotypes | Missing genotypes are imputed using FImpute |
| Propagation of genomic information to non-genotyped descendants and ancestors | PA of non-genotyped descendants calculated with GEBVs of parents |
| Animals included in reference population (males, females, countries included, total number) | BSW males; 2800 - 4700 males (July 2016) |
| Source of phenotypic data (DYD, de-regressed proofs, national EBVs and/or MACE evaluations) | Deregressed proofs (DRP) from national and MACE evaluations. Removal of parent average effects. |
| Other criteria (data edits) for inclusion of records | A minimum reliability of 55% is required for national and MACE EBVs.  Genotypes need a minimum callrate of 0.95 and more than 88% of the genotype calls need a GC Score that is above 0.4. |
| Criteria for extension of records (if applicable) | - |
| Sire categories | - |
| Genomic model (linear, Bayesian, polygenic effect, genotypes or haplotypes) | Bayesian model (BayesC) using genotypes, without polygenic effect |
| Blending of direct genomic value (DGV) with traditional EBV | According to Sullivan's (2009) method. |
| Environmental effects in the genetic evaluation model | - |
| Adjustment for heterogeneous variance in evaluation model | - |
| Computation of genomic reliability | DGV reliability is identical for all animals and is calculated according to the following formula applied to validation bulls:  rel(DGV) = r2(DGV, EBV)  Reliability of GEBV is computed and is at least the highest of DGV and EBV reliabilities |
| Blending of foreign/Interbull information in evaluation | For some bulls MACE EBVs from previous evaluation are used as target variable in the SNP-effect estimation models |
| Genetic parameters in the evaluation | Use Appendix GENO for heritability/genetic variance estimates; for multiple-trait genetic evaluations, provide genetic correlation estimates between traits separately.Use also appendices PR, CO, BCO, SM, LO, CA, as applicable, if you participate in the international genetic evaluations of Interbull |
| Expression of genetic evaluations If standardized (e.g. RBV), give standardization formula in the appendix | DGV standardization is based on reference bulls so that their mean DGV is equal to their mean deregressed proof and the regression of DGV on deregressed proof is forced to 1. |
| Definition of genetic reference base | see GE form for conventional genetic evaluation |
| Labeling of genomic evaluations | G for animals with domestic proof  GA for animals with parent average  GI for animals with international proof |
| Criteria for official publication of evaluations | All GEBVs are published |
| Number of evaluations / publications per year | 3 full releases (April, August, December)  Immediate releases for newly genotyped animals |
| Use in total merit index | see GE form for conventional genetic evaluation |
| Anticipated changes in the near future |  |
| Key reference on methodology applied | Garrick D.J. et al. (2009): Deregressing estimated breeding values and weighting information for genomic regression analyses. Genetics Selection Evolution 41:55  Fernando R.L. and Garrick D.J. (2009): GenSel – User Manual |
| Key organization: name, address, phone, fax, e-mail, web site | Qualitas AG  Chamerstrasse 56  6300 Zug  Switzerland  phone: +41 41 768 9292  email: info@qualitasag.ch |

aEither: Production (e.g. milk, fat, protein), Conformation, Health (e.g. mastitis resistance, milk somatic cell, resistance to diseases other than mastitis), Longevity, Calving (e.g. stillbirth, calving ease), Female fertility (e.g. non-return rate, interval between reproductive events, number of AI’s, heat strength), Workability (e.g. milking speed, temperament), Beef production, Efficiency (e.g. body weight, energy balance, body conditioning score), or Other traits.

## System Validation

|  |  |
| --- | --- |
| Approximate number of test bulls for this trait group: | 60 for hco, 130 for other female fertility traits |
| If including foreign reference bulls:  4-yr old de-regressed MACE EBVs, OR  Current de-regressed MACE EBVs  If including foreign test bulls (type of proof 21 or 22), provide the reason. | Due to a model change in 2014 current de-regressed MACE EBVs have been used in the reduced dataset |
| If using a truncation ≠ 4 years, provide the reason. |  |
| If applying an age cutoff for test bulls ≠ (YYYY-8), provide the reason |  |

# Appendix GENO

## Parameters used in genetic/genomic evaluation

see GE form for conventional genetic evaluation