Implementation of single-step genomic BLUP in the Nordic evaluation for beef cattle

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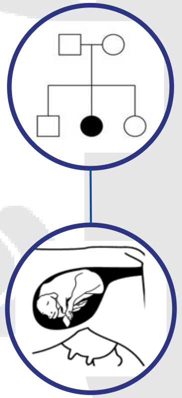
Nordic purebred beef genetic evaluation

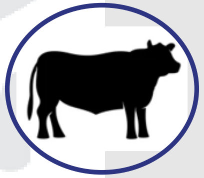


Pedigree - Breeding values

6 Calving traits and 12 EBVs

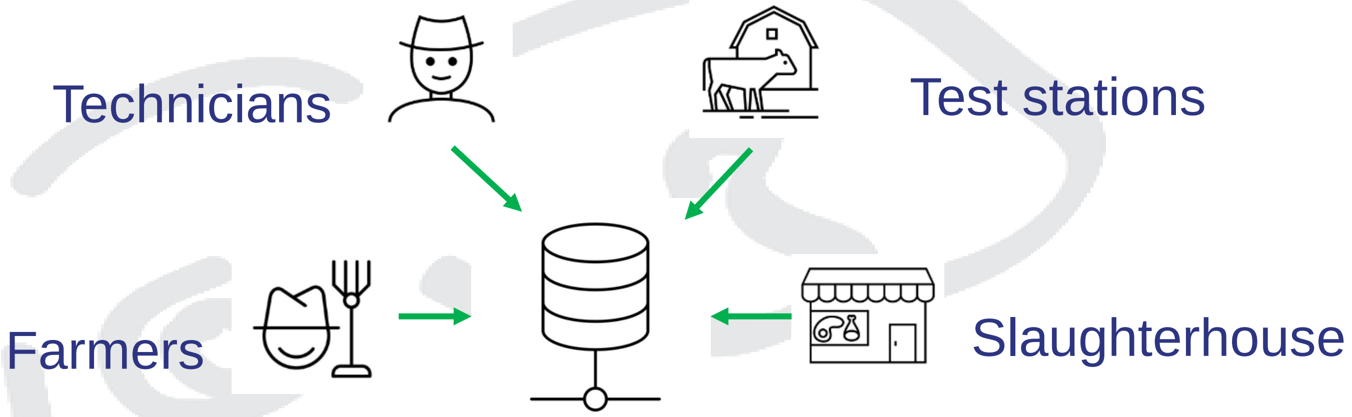
Genomic - Breeding values

7 Weight/Growth and carcass traits and 10 GEBVs



Breeds: Aberdeen Angus (AAN), Simmental (SIM), Charolais (CHA), Hereford (HER), Limousine (LIM) Blonde d'Aquitaine, Highland Cattle + Other smaller breeds

Registrations



Technicians

Test stations

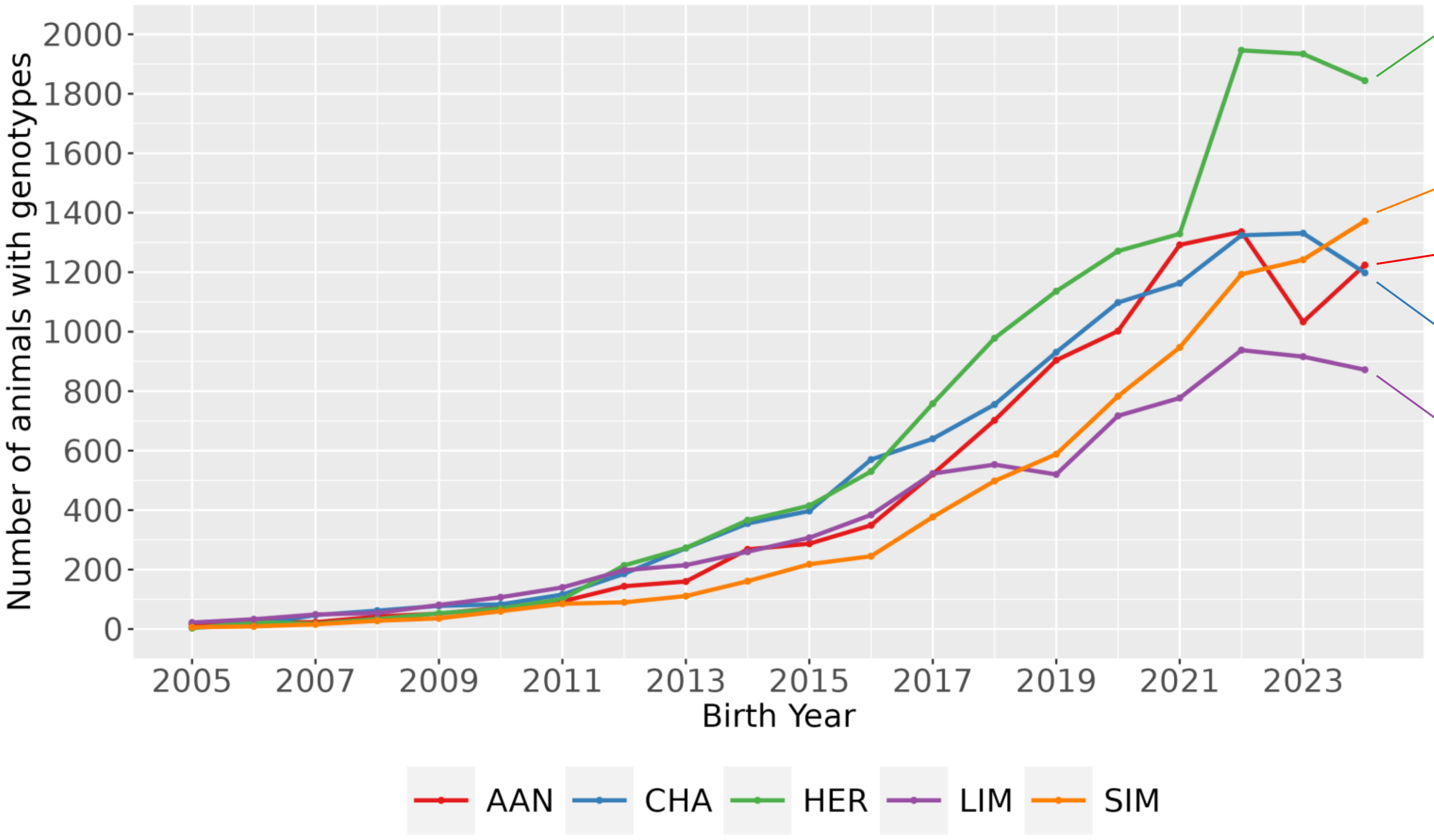
Farmers

Slaughterhouse

Nordic Cattle Genetic Evaluation (NAV)

- Calving ease and calf survival scores (> 1998)
- Birth, weaning and post-weaning weights and carcass records since the 80’s for Denmark, Sweden and 90’s for Finland

Number of genotyped animals –
breed and birth year



13 898, HER

8 450, SIM

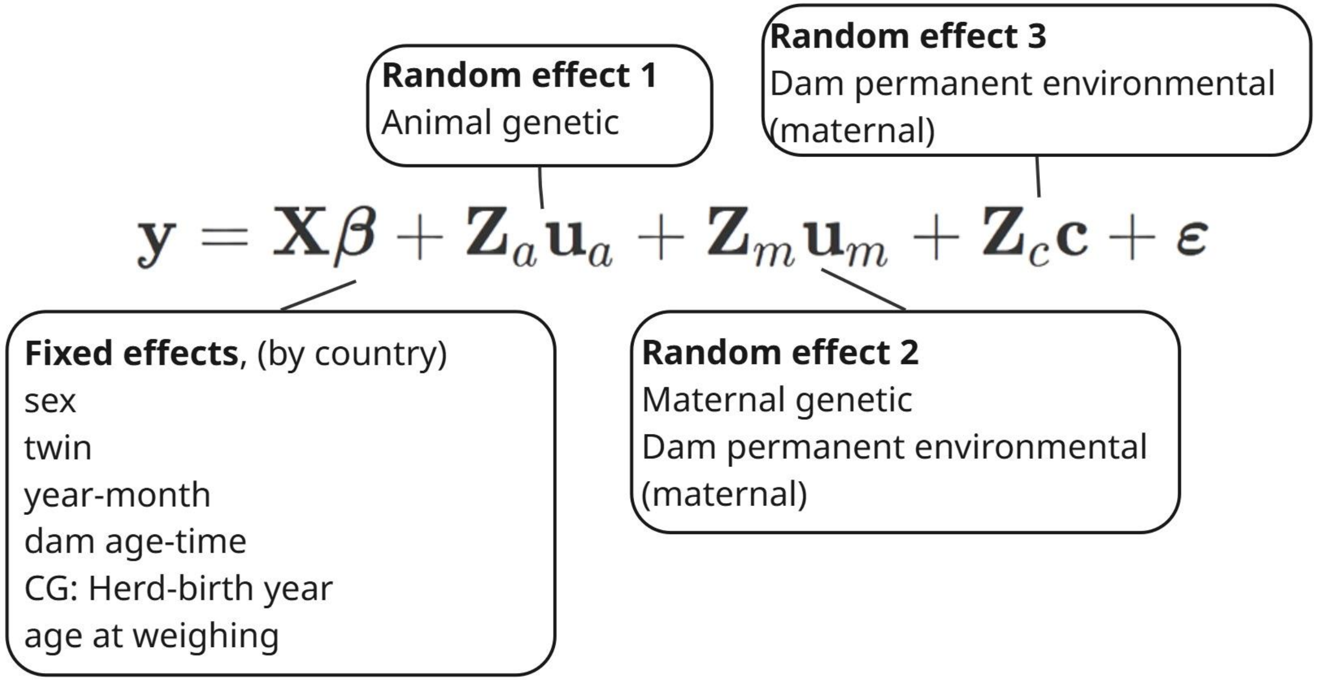
9 787, AAN

11 051, CHA

7 940, LIM

Single-step GBLUP
Breed-wise multi-trait animal model

Statistical mode



Random effect 1
Animal genetic

Random effect 3
Dam permanent environmental (maternal)

$$\mathbf{y} = \mathbf{X}\beta + \mathbf{Z}_a\mathbf{u}_a + \mathbf{Z}_m\mathbf{u}_m + \mathbf{Z}_c\mathbf{c} + \varepsilon$$

Fixed effects, (by country)
sex
twin
year-month
dam age-time
CG: Herd-birth year
age at weighing

Random effect 2
Maternal genetic
Dam permanent environmental (maternal)

Solver - MiX99 family of programs

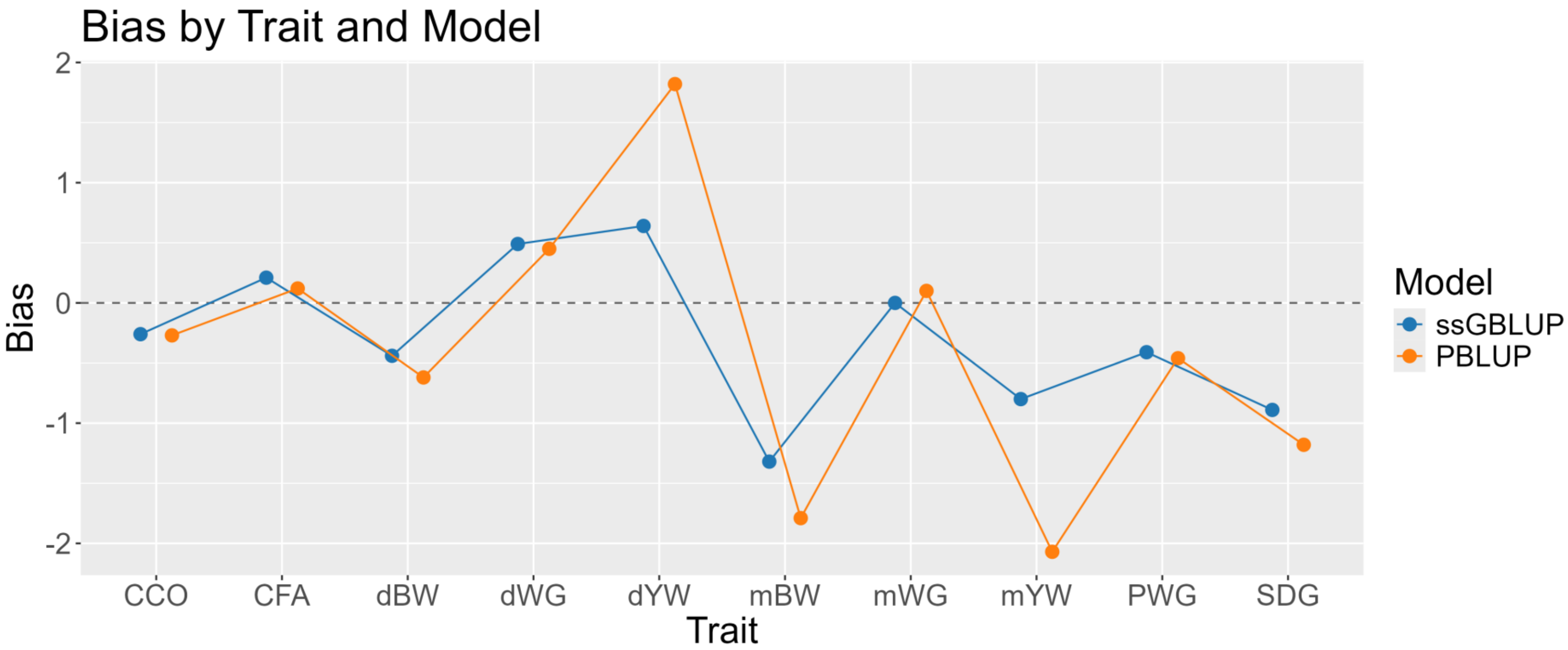
- **Polygenic effect: 30%**
- **Genetic groups**

Validation

1. **Semi-parametric LR method (Legarra & Reverter, 2018) (70/30 training/test, cut-off 2 year of data)**
2. Comparison of two consecutive evaluation using informative statistics (regression, slope, adjusted correlations (adjusted by changes in reliability), genetic trends and SD of breeding values)
3. Mendelian sampling deviations

LR method – BIAS results for Charolais

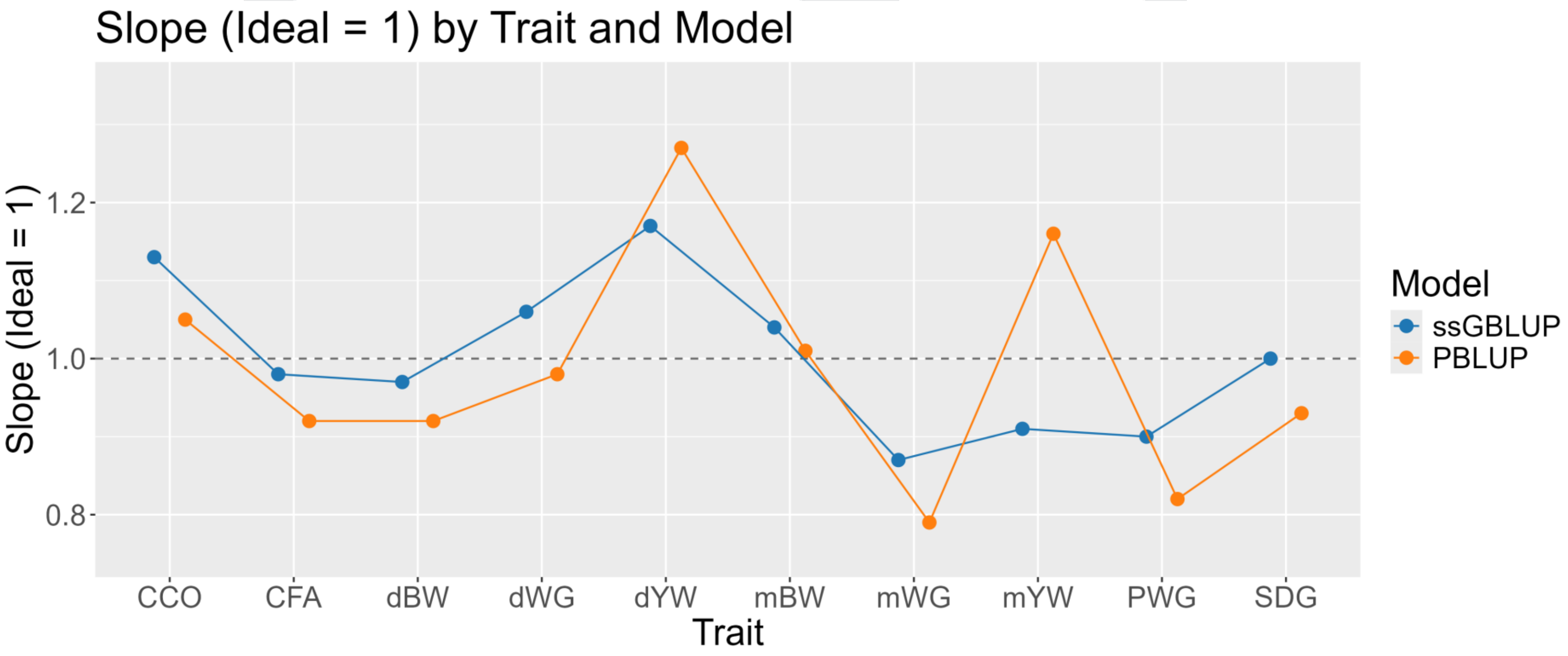
(large reference population)



CCO=carcass conformation, **CFA**=carcass fat, DIRECT and MATERNAL: **BW**=birth weight, **WG**=weaning weight gain, **YW**=yearling weight, **PWG**=post weaning weight gain and **SDG**=slaughter daily gain

LR method – SLOPE results for Charolais

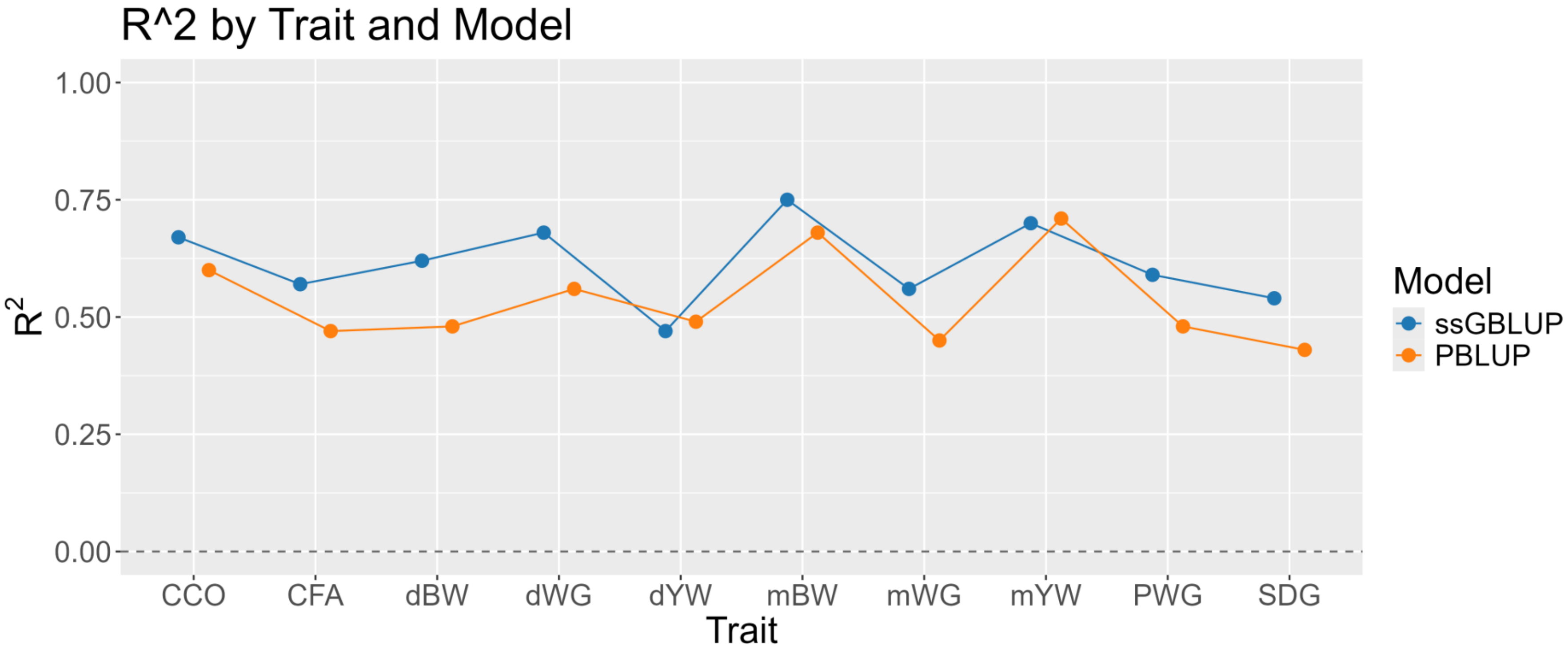
(large reference population)



CCO=carcass conformation, **CFA**=carcass fat, DIRECT and MATERNAL: **BW**=birth weight, **WG**=weaning weight gain, **YW**=yearling weight, **PWG**=post weaning weight gain and **SDG**=slaughter daily gain

LR method – R^2 results for Charolais

(large reference population)



CCO=carcass conformation, **CFA**=carcass fat, DIRECT and MATERNAL: **BW**=birth weight, **WG**=weaning weight gain, **YW**=yearling weight, **PWG**=post weaning weight gain and **SDG**=slaughter daily gain

What’s next?

Genomic breeding values for calving traits

How to handle selective genotyping?

Investigate the possibility of Genomic breeding values for small population size breeds

Ongoing reliabilities including genomic information


ACCGGCGGCAGGGGT
GCTGACGTGAGATCA
AAGCGGGGATGCGTA
CGGGCTACTACGGCA
ACGTGGGCAGCTGTA
ACGCGAGTGGAGCGT
GCTAGGTACGTGGAG
GTGCACGTGATTGGA
AAGGCCGGCTGCGTA
ACGGTAGTGAGGTAG
GCGTTCGGTATCGGA