Impact of multiple ovulation and embryo transfer on genetic gain and diversity in dairy cattle

Anna-Charlotte Doublet[1,2], Gwendal Restoux[1], Sébastien Fritz[1,2],
Alexis Michenet[3], Chris Hozé[1,2], Denis Laloë[1], Pascal Croiseau[1]

[1] GABI, INRA, AgroParisTech, Université Paris-Saclay, 78350 Jouy-en-Josas, France
[2] ALLICE, Paris, France
[3] Interbull, Uppsala, Sweden

Consequences of a loss of genetic diversity

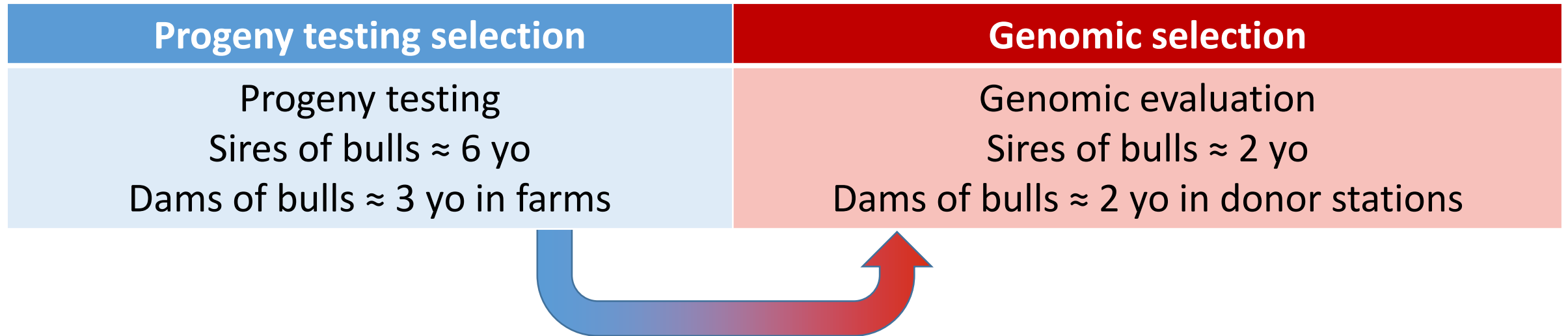Loss of additive genetic variance → **Loss of potential genetic gain**

Loss of overall genetic diversity → **Loss of adaptive potential**

Inbreeding depression → **Detrimental effects on fitness traits**

➔ **Economic impact**

Dairy cattle selection

Genomic selection in dairy cattle breeds ⇒ **New breeding schemes**

Progeny testing selection	Genomic selection
Progeny testing Sires of bulls ≈ 6 yo Dams of bulls ≈ 3 yo in farms	Genomic evaluation Sires of bulls ≈ 2 yo Dams of bulls ≈ 2 yo in donor stations

Dairy cattle selection

Genomic selection in dairy cattle breeds ⇒ **New breeding schemes**

Progeny testing selection	Genomic selection
Progeny testing Sires of bulls ≈ 6 yo Dams of bulls ≈ 3 yo in farms	Genomic evaluation Sires of bulls ≈ 2 yo Dams of bulls ≈ 2 yo in donor stations

- ↘ generation interval and more cost effective = more male candidates for selection
  - ↗ annual genetic gain

⚠ Genetic diversity
  - ↗ inbreeding rate (ΔF) in some breeds (both per year and per generation)
  - ↗ kinship within bulls in some breeds

Doublet *et al*, under review

3

New technologies?

- Change in breeding scheme → impact on genetic diversity
- Need to **predict** the impact of these changes before implementing them

New technologies?

- Change in breeding scheme → impact on genetic diversity

- Need to **predict** the impact of these changes before implementing them

- For example, **Multiple Ovulation Embryo Transfer (MOET)**

- 1 calve per female → best females have more calves (≈ 3 per flushing)
  - Intensification of the female side of breeding schemes
  - Major risk of a decrease in the diversity of dams of bulls (and maternal grand dams and grand sires of bulls)
  - Increased genetic gain BUT risk for genetic diversity

- **What about genetic diversity?**

Aim of this study

Simulate dairy cattle breeding schemes
to predict the impact of embryo donor stations
on genetic diversity and genetic gain
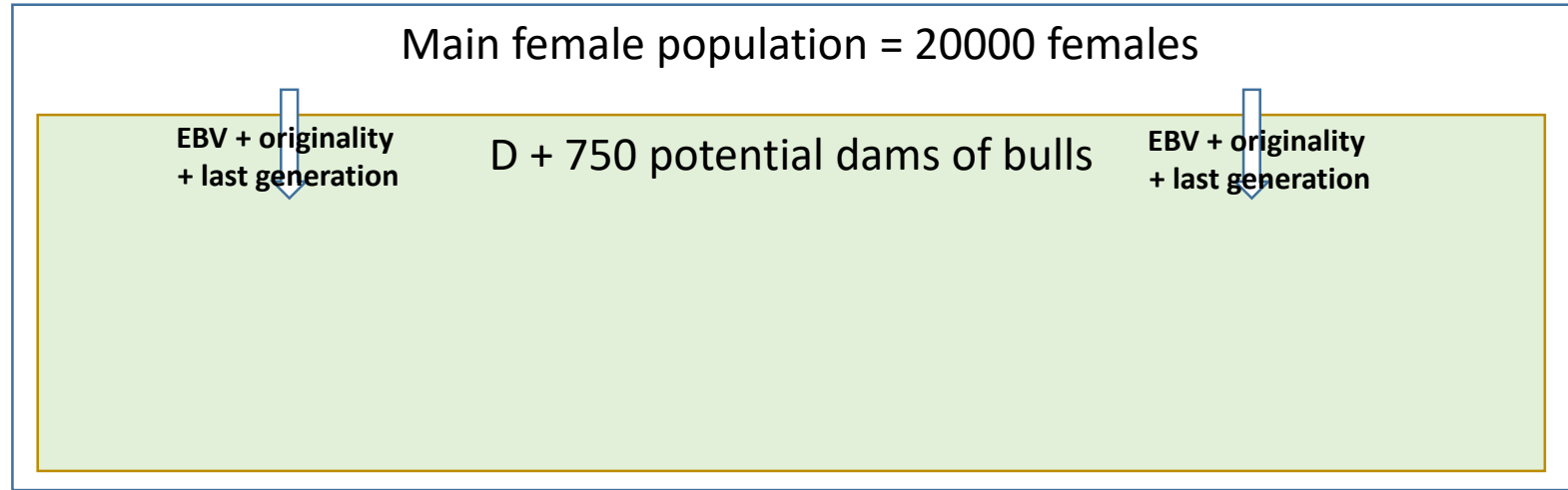
Simulated breeding scheme
≈ large French dairy cattle breed with reduced size for simulations

Main female population = 20000 females

Simulated breeding scheme

≈ large French dairy cattle breed with reduced size for simulations

Main female population = 20000 females

EBV + originality
+ last generation

D + 750 potential dams of bulls

EBV + originality
+ last generation

Simulated breeding scheme

≈ large French dairy cattle breed with reduced size for simulations
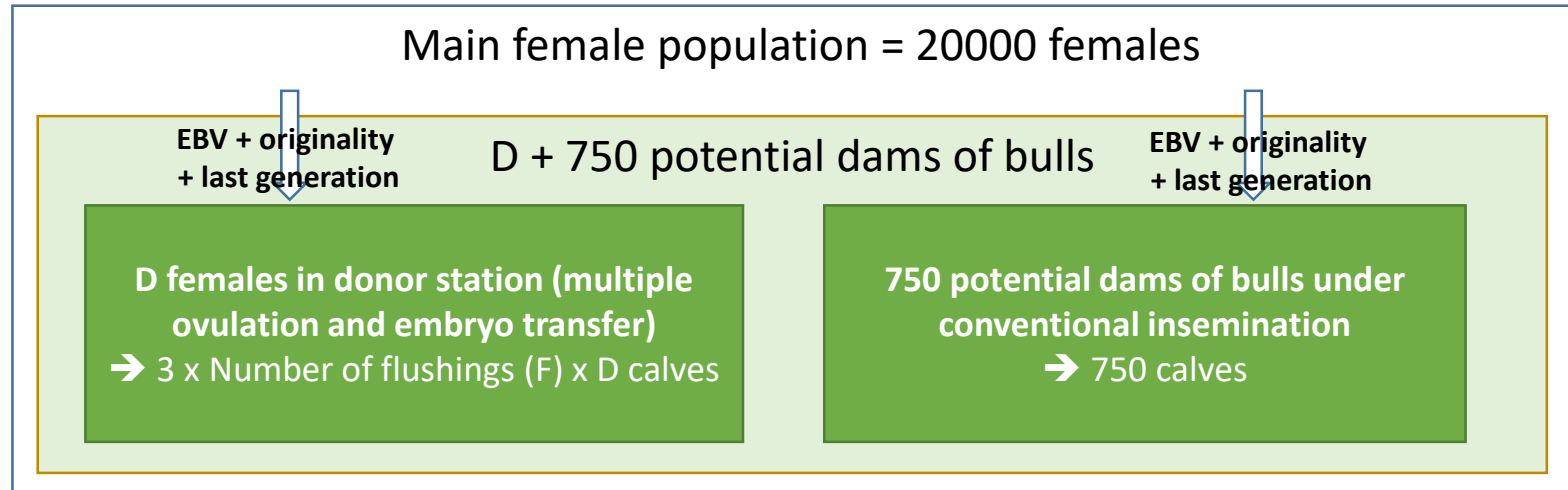

Main female population = 20000 females

D + 750 potential dams of bulls

EBV + originality + last generation

D females in donor station (multiple ovulation and embryo transfer)
➔ 3 x Number of flushings (F) x D calves

EBV + originality + last generation

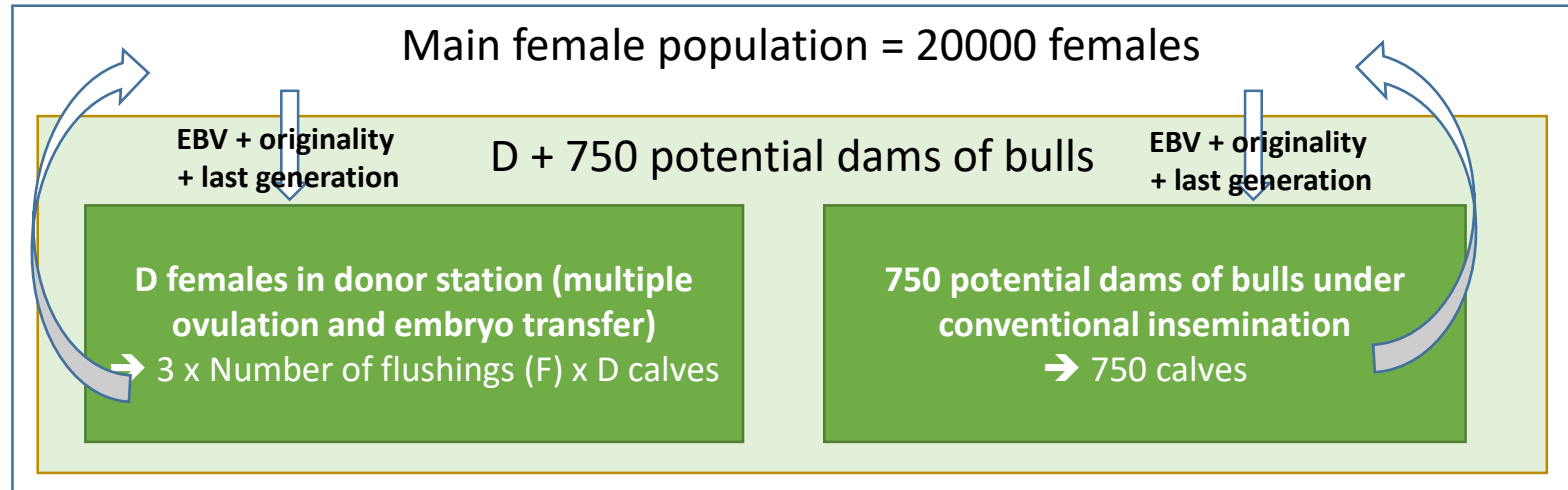**750 potential dams of bulls under conventional insemination**
➔ 750 calves

Simulated breeding scheme
≈ large French dairy cattle breed with reduced size for simulations

Culling + renewal of the population (25%)

Main female population = 20000 females

D + 750 potential dams of bulls

EBV + originality + last generation

EBV + originality + last generation

D females in donor station (multiple ovulation and embryo transfer)
➜ 3 x Number of flushings (F) x D calves

750 potential dams of bulls under conventional insemination
➜ 750 calves

Simulated breeding scheme

≈ large French dairy cattle breed with reduced size for simulations
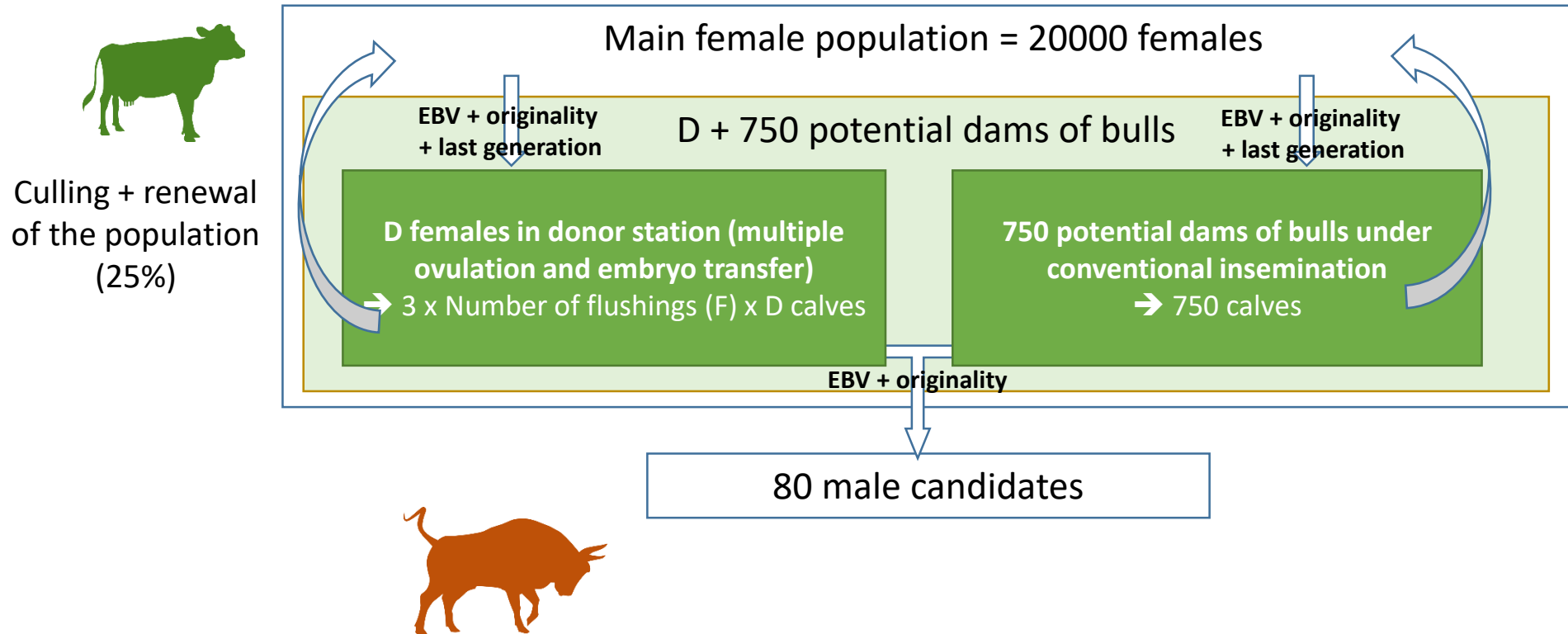
Culling + renewal
of the population
(25%)

Main female population = 20000 females

D + 750 potential dams of bulls

**EBV + originality
+ last generation**

**EBV + originality
+ last generation**

**D females in donor station (multiple
ovulation and embryo transfer)**
➔ 3 x Number of flushings (F) x D calves

**750 potential dams of bulls under
conventional insemination**
➔ 750 calves

EBV + originality

Based on MoBPS R package
Torsten Pook (2018). MoBPS: Simulation of breeding programs. R package version 1.0.2

Simulated breeding scheme
≈ large French dairy cattle breed with reduced size for simulations

Culling + renewal of the population (25%)

Main female population = 20000 females

EBV + originality + last generation

D + 750 potential dams of bulls

EBV + originality + last generation

D females in donor station (multiple ovulation and embryo transfer)
→ 3 x Number of flushings (F) x D calves

750 potential dams of bulls under conventional insemination
→ 750 calves

EBV + originality

80 male candidates

Simulated breeding scheme

≈ large French dairy cattle breed with reduced size for simulations

Culling + renewal of the population (25%)

Main female population = 20000 females

D + 750 potential dams of bulls

EBV + originality + last generation

EBV + originality + last generation

D females in donor station (multiple ovulation and embryo transfer)
➔ 3 x Number of flushings (F) x D calves

750 potential dams of bulls under conventional insemination
➔ 750 calves

EBV + originality

80 male candidates

Random choice

40 sires of bulls

All used on potential dams of bulls

Simulated breeding scheme
≈ large French dairy cattle breed with reduced size for simulations

Main female population = 20000 females

D + 750 potential dams of bulls

EBV + originality + last generation

EBV + originality + last generation

Culling + renewal of the population (25%)

D females in donor station (multiple ovulation and embryo transfer)
➔ 3 x Number of flushings (F) x D calves

750 potential dams of bulls under conventional insemination
➔ 750 calves

EBV + originality

80 male candidates

Random choice

All used on potential dams of bulls

40 sires of bulls

EBV + originality
30 marketed bulls

Used on all females

Based on MoBPS R package
Torsten Pook (2018). MoBPS: Simulation of breeding programs. R package version 1.0.2

Scenarios

		Number of heifers in donor station (D)		
		0	80	160
Number of flushings per heifer in donor station (F)	1	REF (no multiple ovulation nor embryo transfer)	D80_F1	D160_F1
	5		D80_F5	D160_F5

Scenarios

Number of flushings per heifer in donor station (F)		Number of heifers in donor station (D)		
		0	80	160
	1	REF (no multiple ovulation nor embryo transfer)	D80_F1	D160_F1
	5		D80_F5	D160_F5

G1

G9 → 50K genotypes

G19 → 50K genotypes

Burning (**8 generations**)

11 generations
Scenario REF
or scenario D80_F1
or scenario D80_F5
or scenario D160_F1
or scenario D160_F5
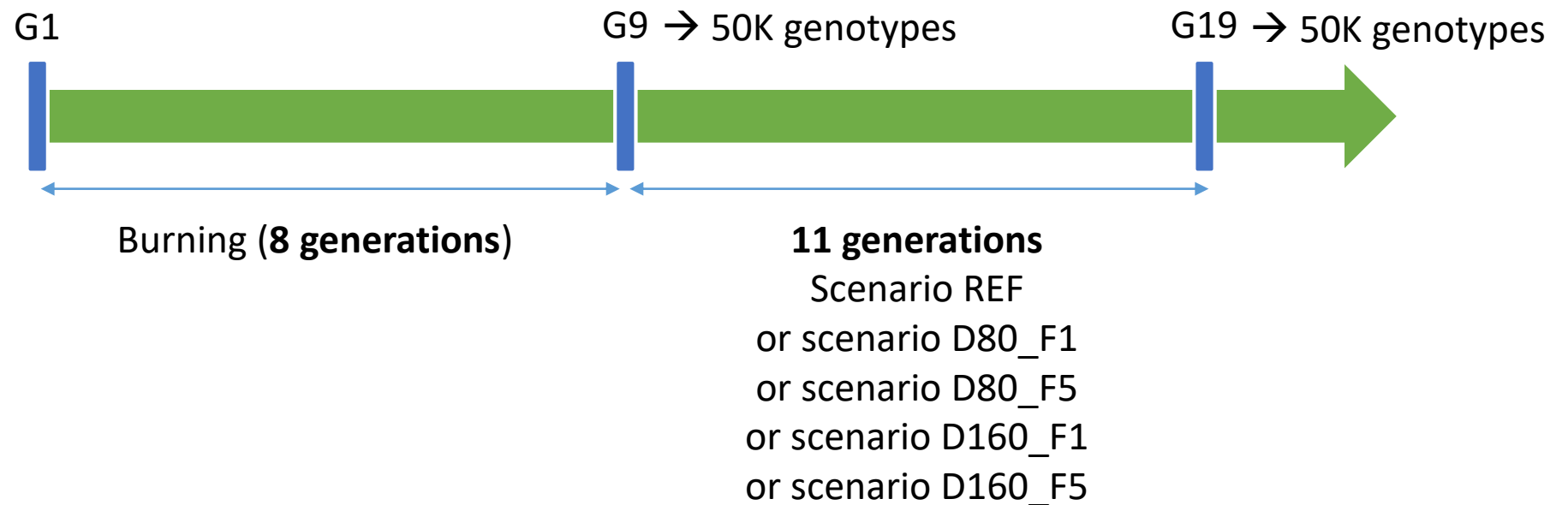
Evaluation of genetic diversity and gain

- Evolution of **True Breeding Values (TBV)**

Evaluation of genetic diversity and gain

- Evolution of **True Breeding Values (TBV)**
- Evolution of genetic diversity from **runs of homozygosity (ROH)**
≈ inbred segments of the genome (IBD)
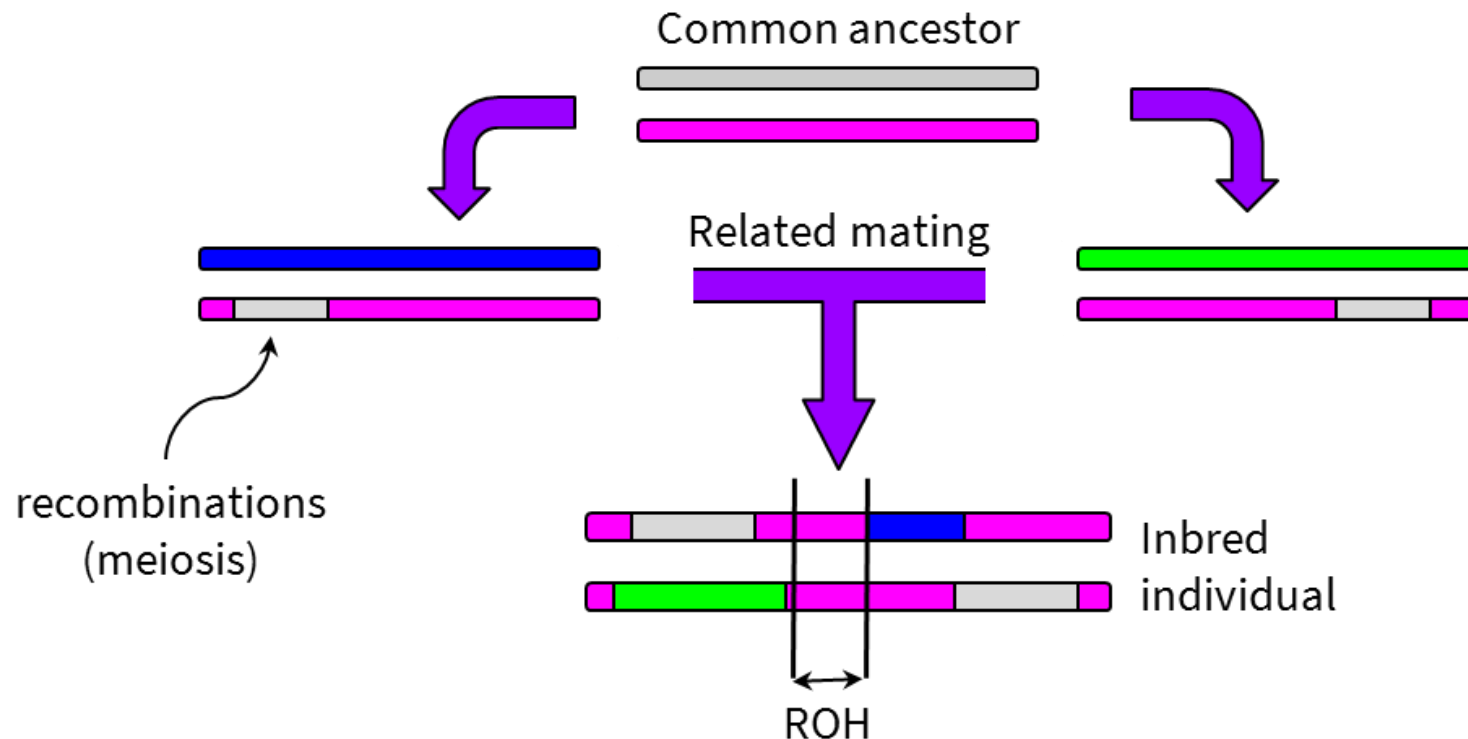
Detected with PLINK (with 50K genotyping data)
- Minimal length = 1Mb
- Minimal number of SNPs per ROH = 15 SNPs
- Sliding window = 15 SNPs
- Minimal SNP density: 1 SNP / 1000 kb
- Maximum gap: 1000 kb

Evaluation of genetic diversity and gain

- Evolution of **True Breeding Values (TBV)**
- Evolution of genetic diversity from **runs of homozygosity (ROH)**
  - Inbreeding (realized)

$$F_{\text{ROH}} = \frac{\textcolor{red}{\text{Total length of the ROH of an individual}}}{\textcolor{orange}{\text{Total length of the genome covered by SNPs}}}$$

McQuillan *et al*, 2008, adjusted as done by Doekes *et al*, 2018

Evaluation of genetic diversity and gain

- Evolution of **True Breeding Values (TBV)**
- Evolution of genetic diversity from **runs of homozygosity (ROH)**
  - Inbreeding (realized)
  - Dated inbreeding → mean ROH length
    - Shorter ROH ⇔ older inbreeding
    - Longer ROH ⇔ more recent inbreeding

Evaluation of genetic diversity and gain

- Evolution of **True Breeding Values (TBV)**
- Evolution of genetic diversity from **runs of homozygosity (ROH)**
  - Inbreeding (realized)
  - Dated inbreeding → mean ROH length
  - Number of ROH

Results
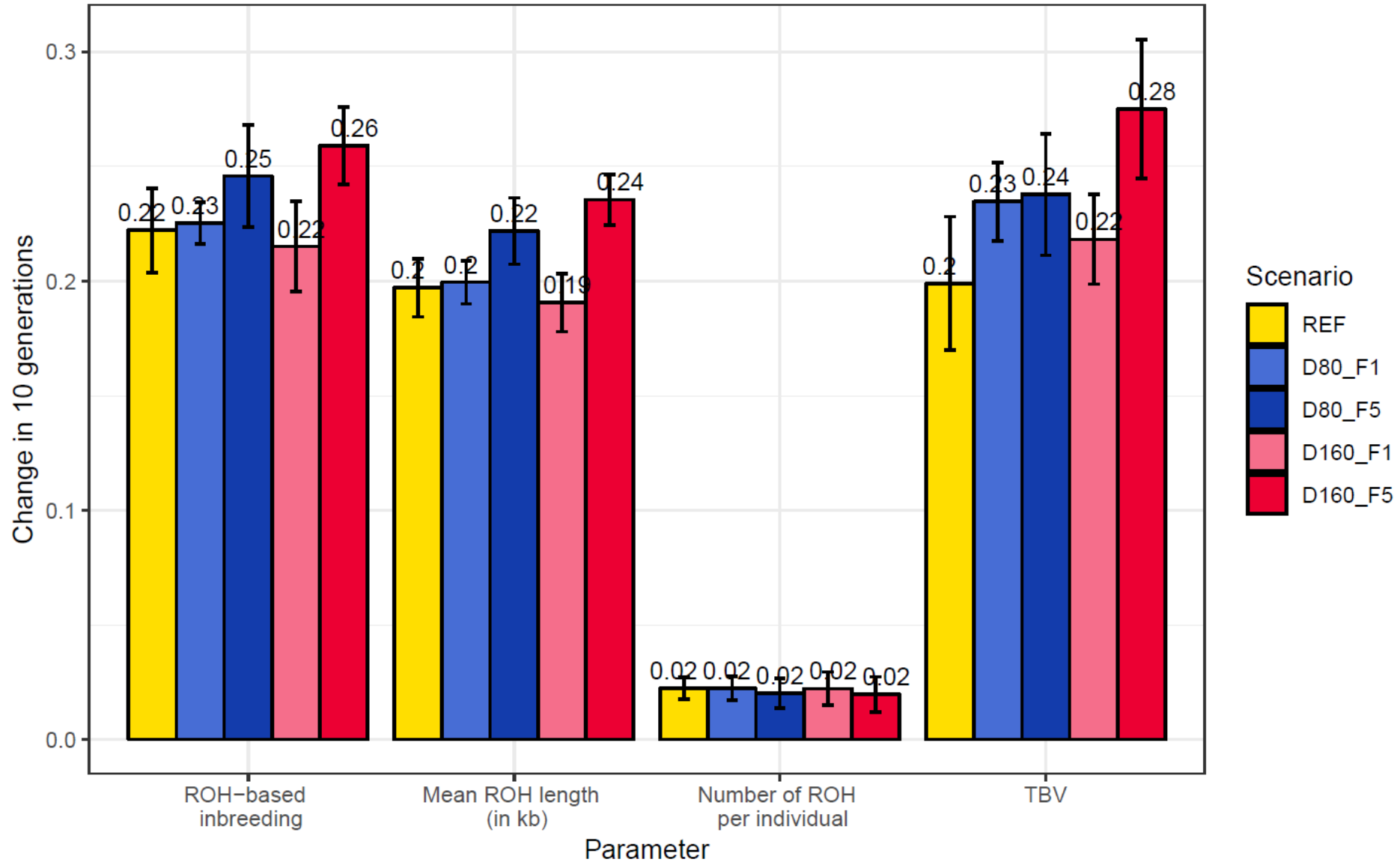
Results
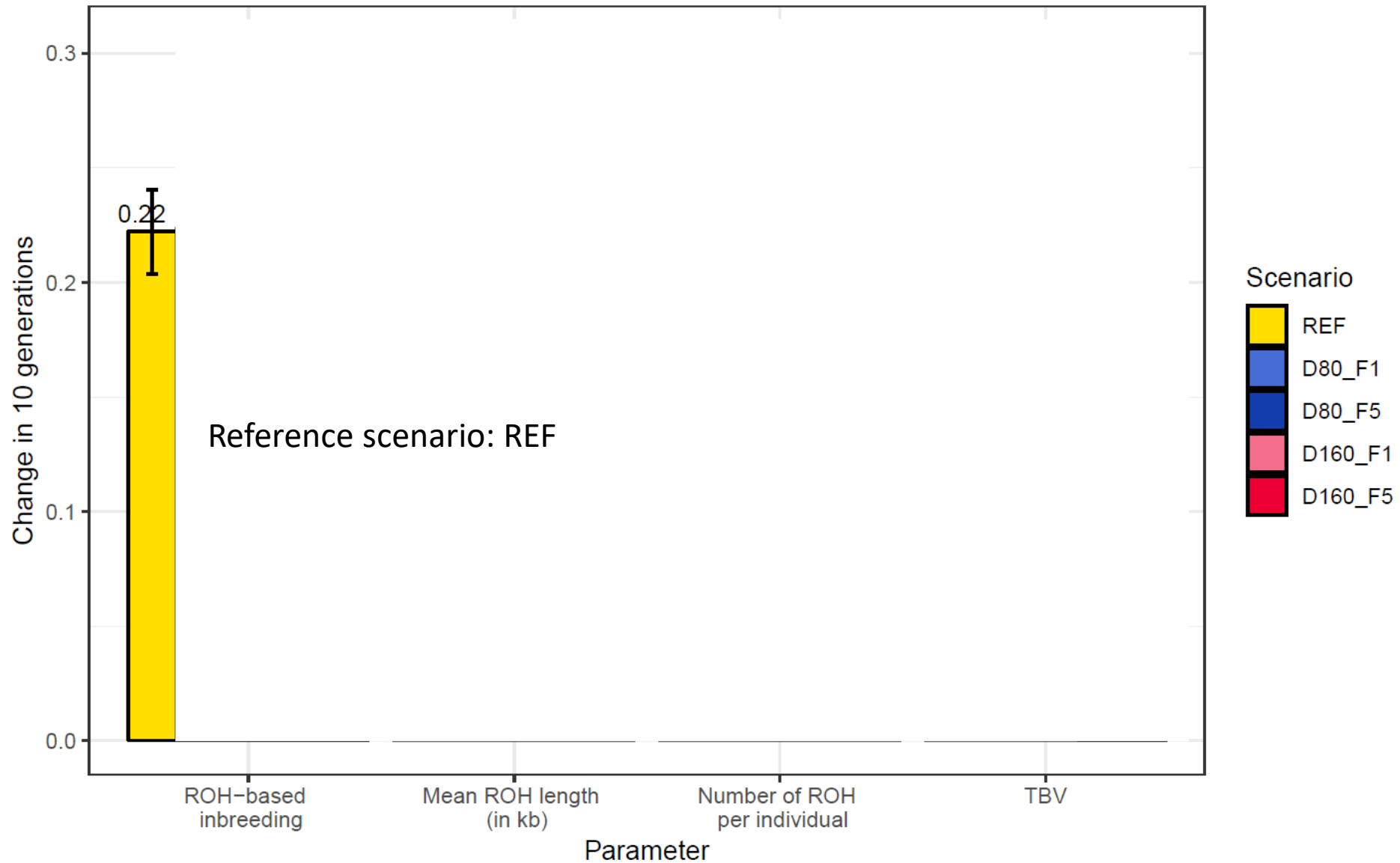
Results
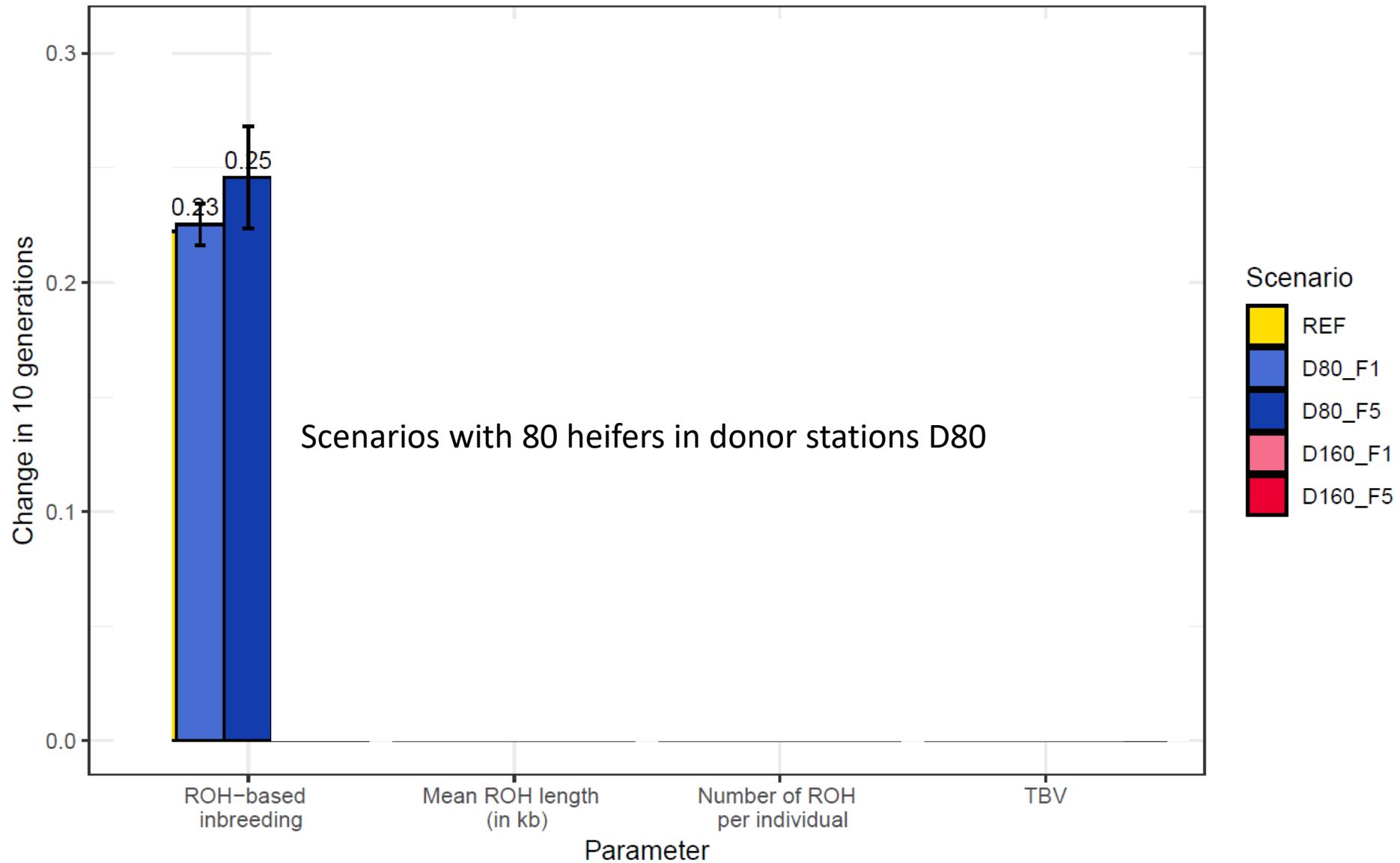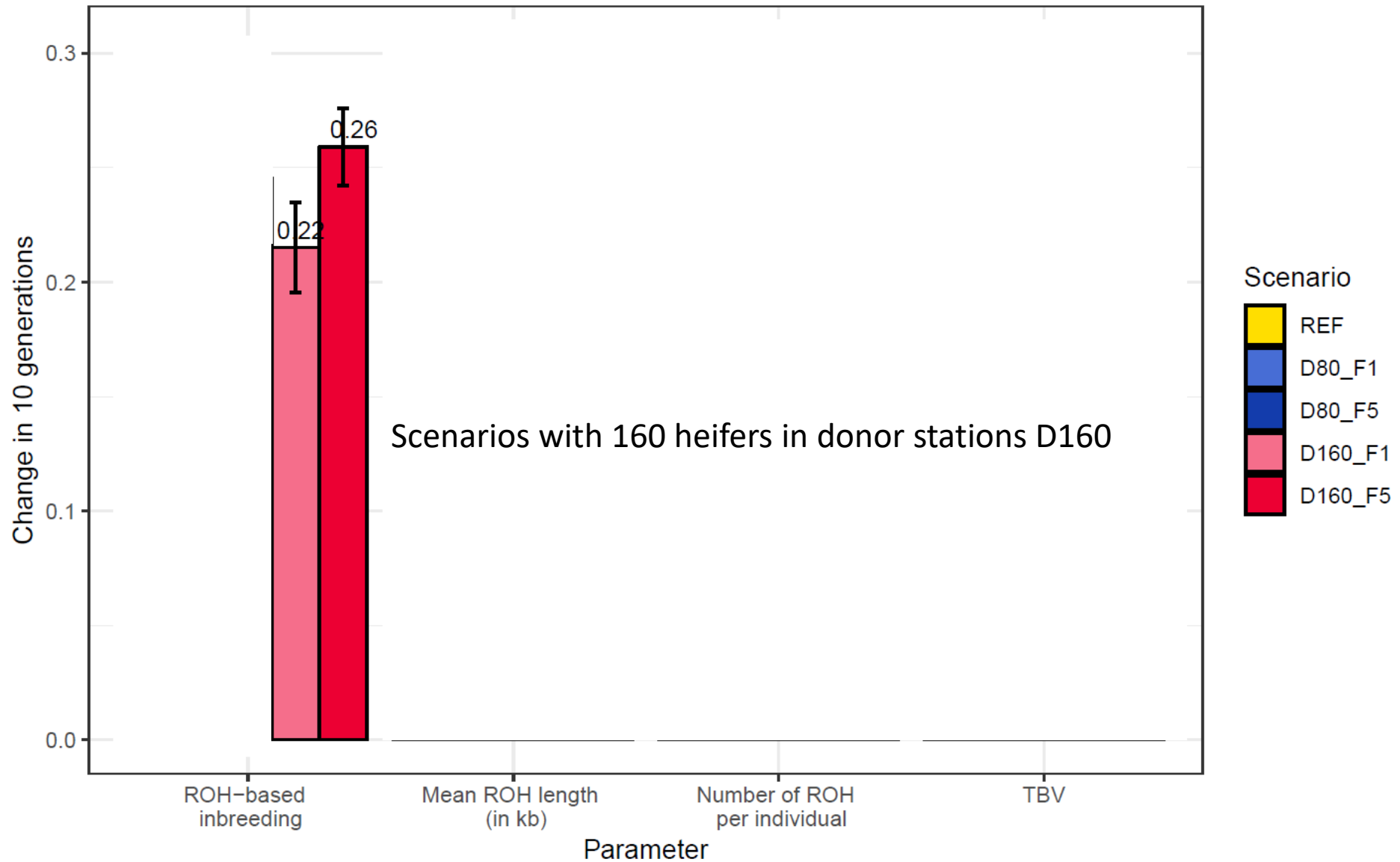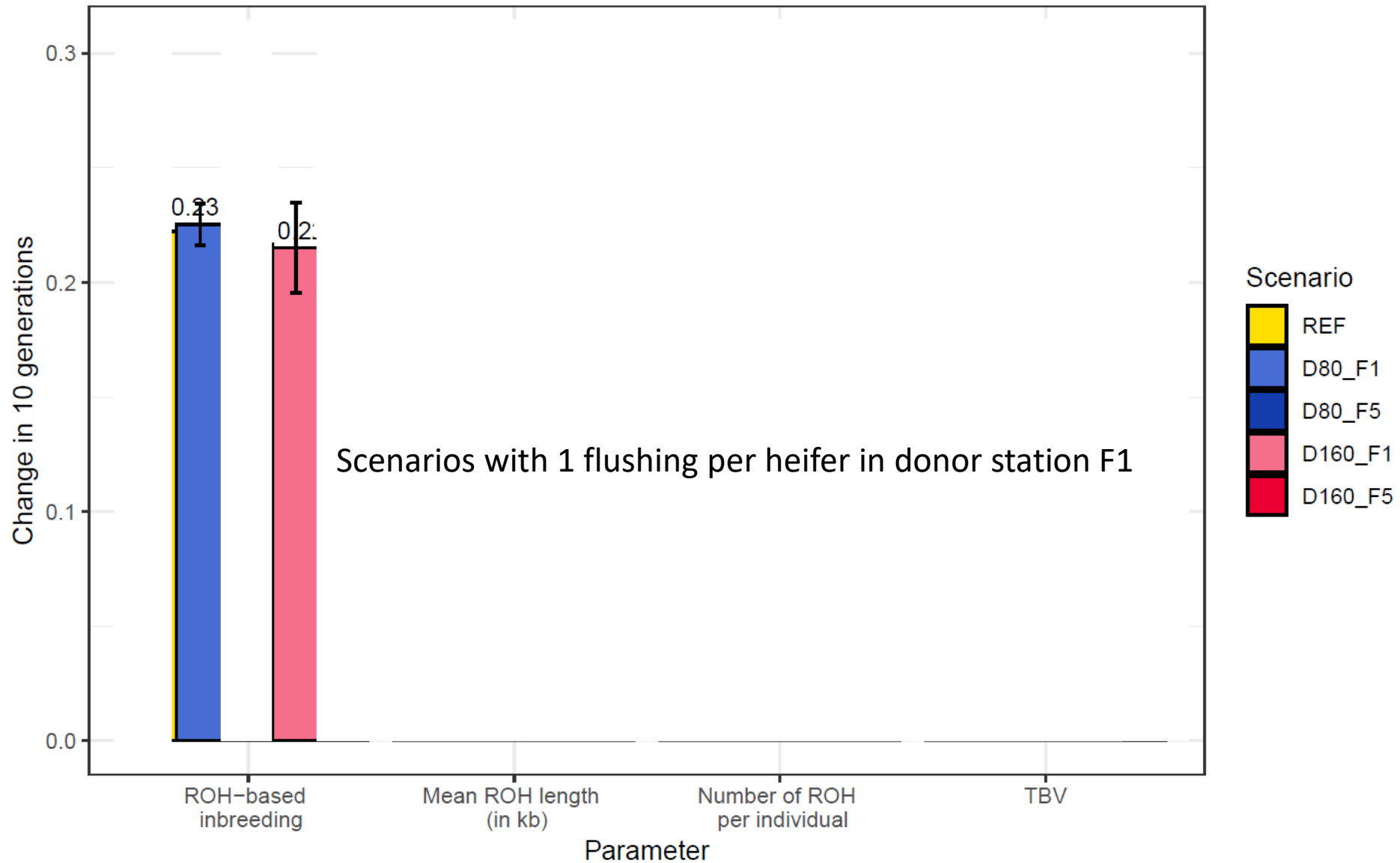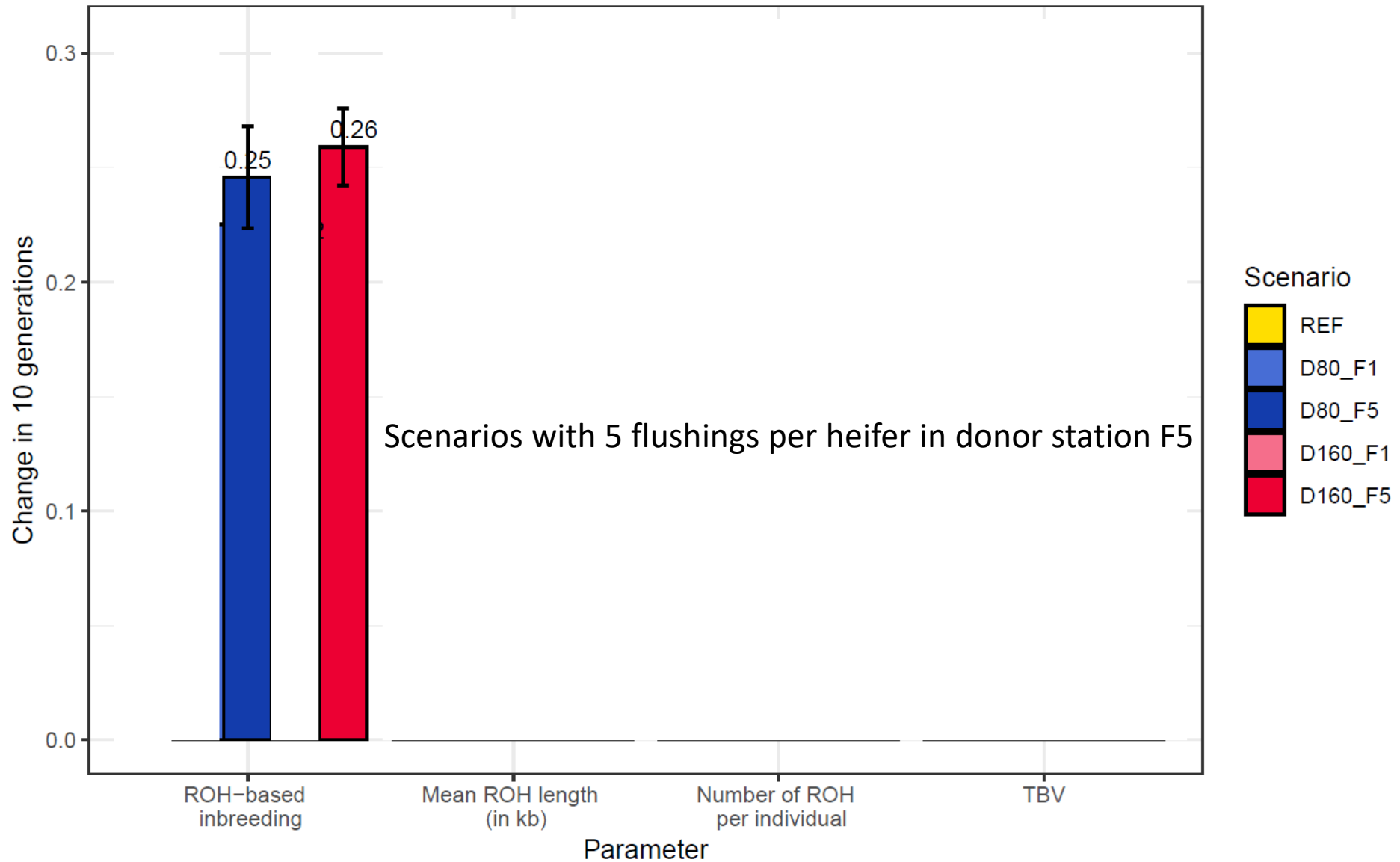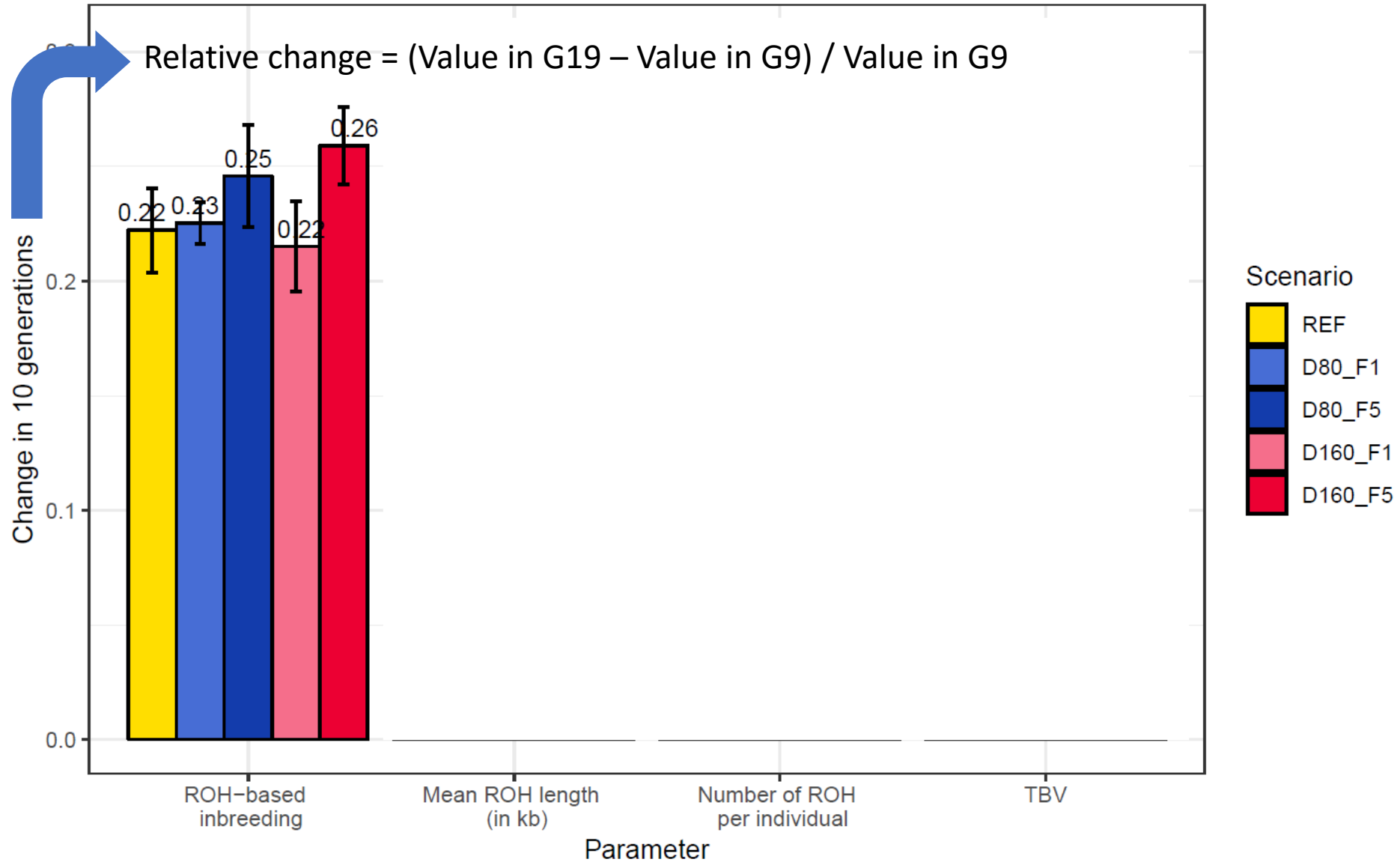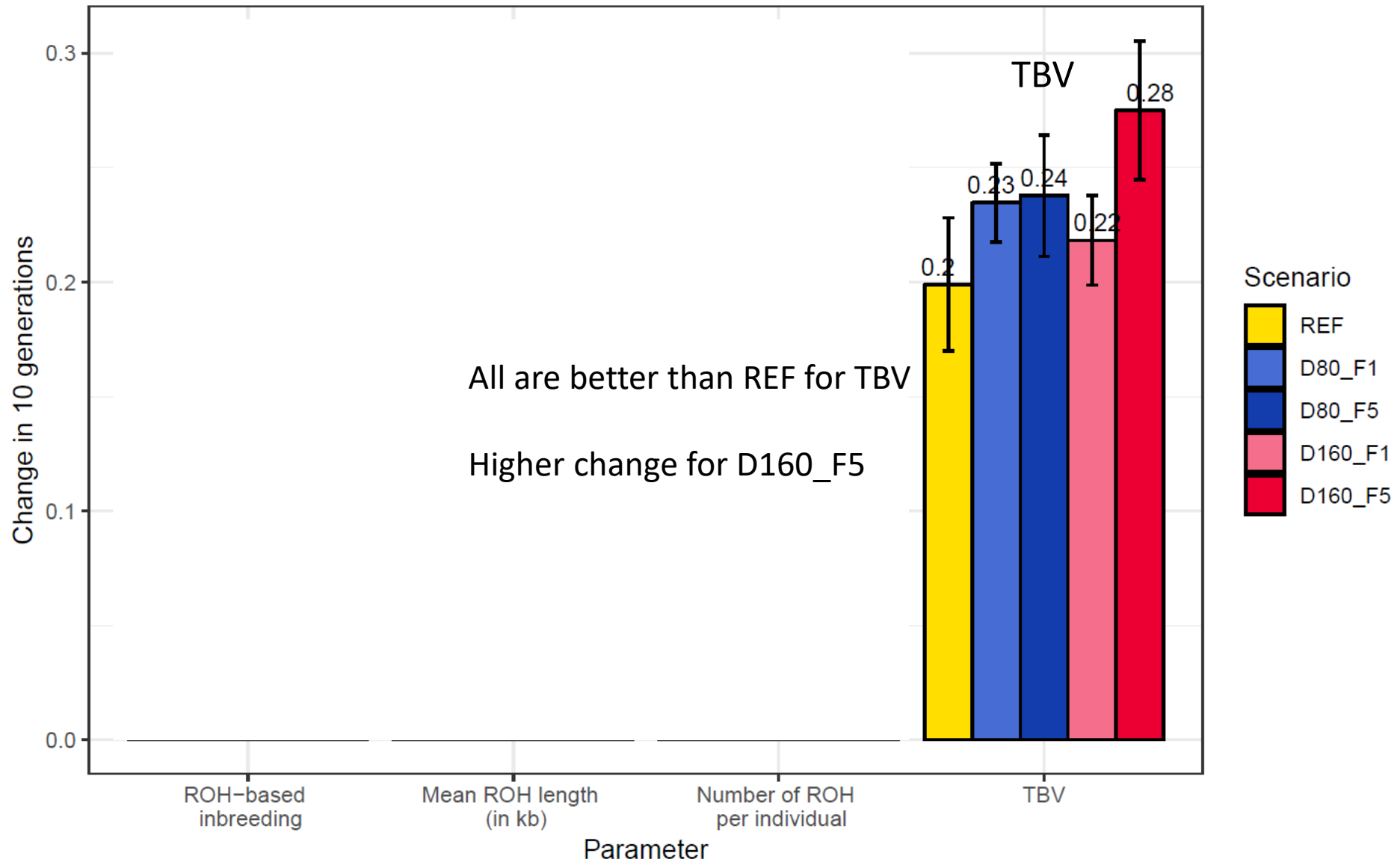
Results

Results

Results

Scenarios with 5 flushings per heifer in donor station F5

Results

Relative change = (Value in G19 – Value in G9) / Value in G9

Results (preliminary)

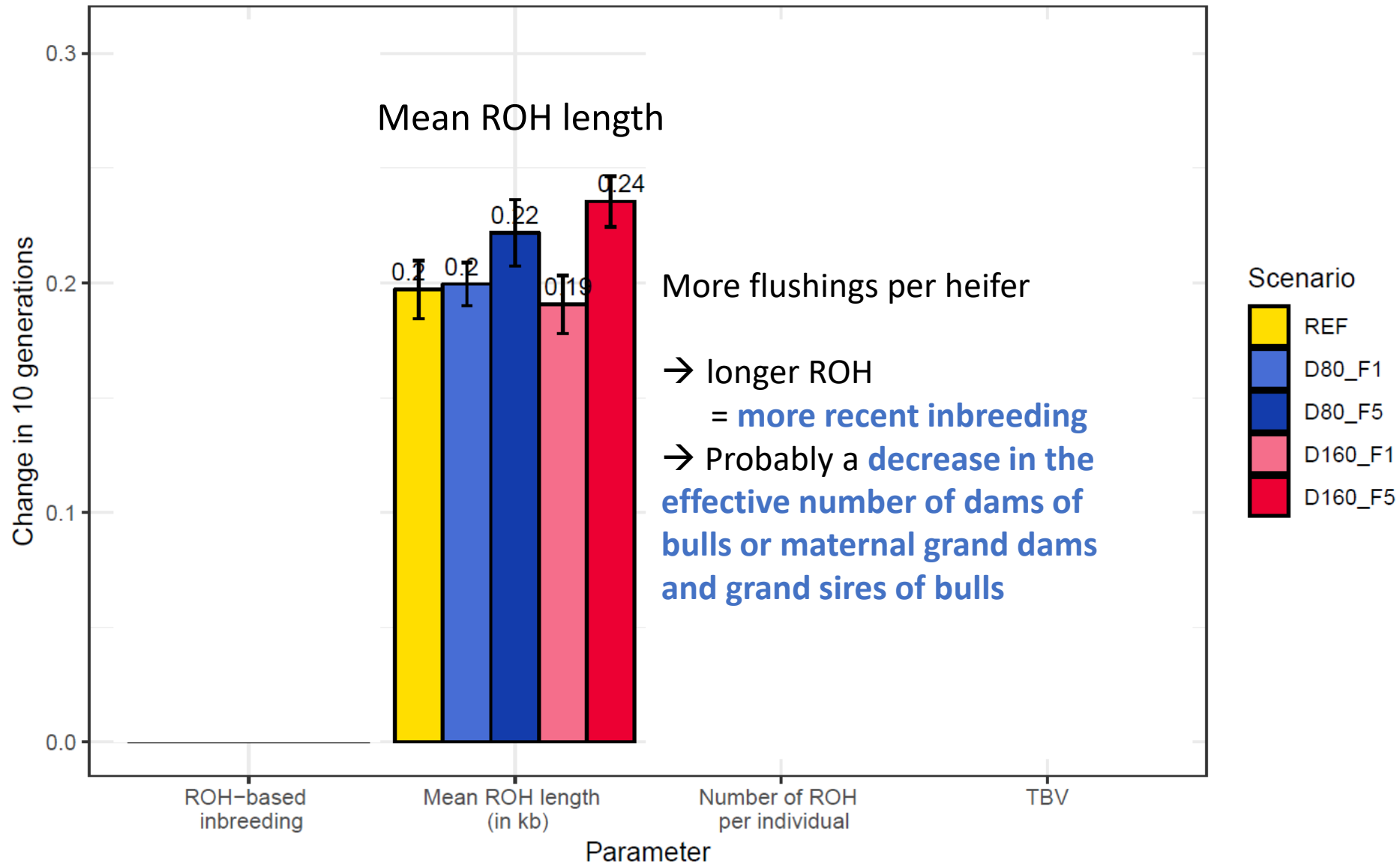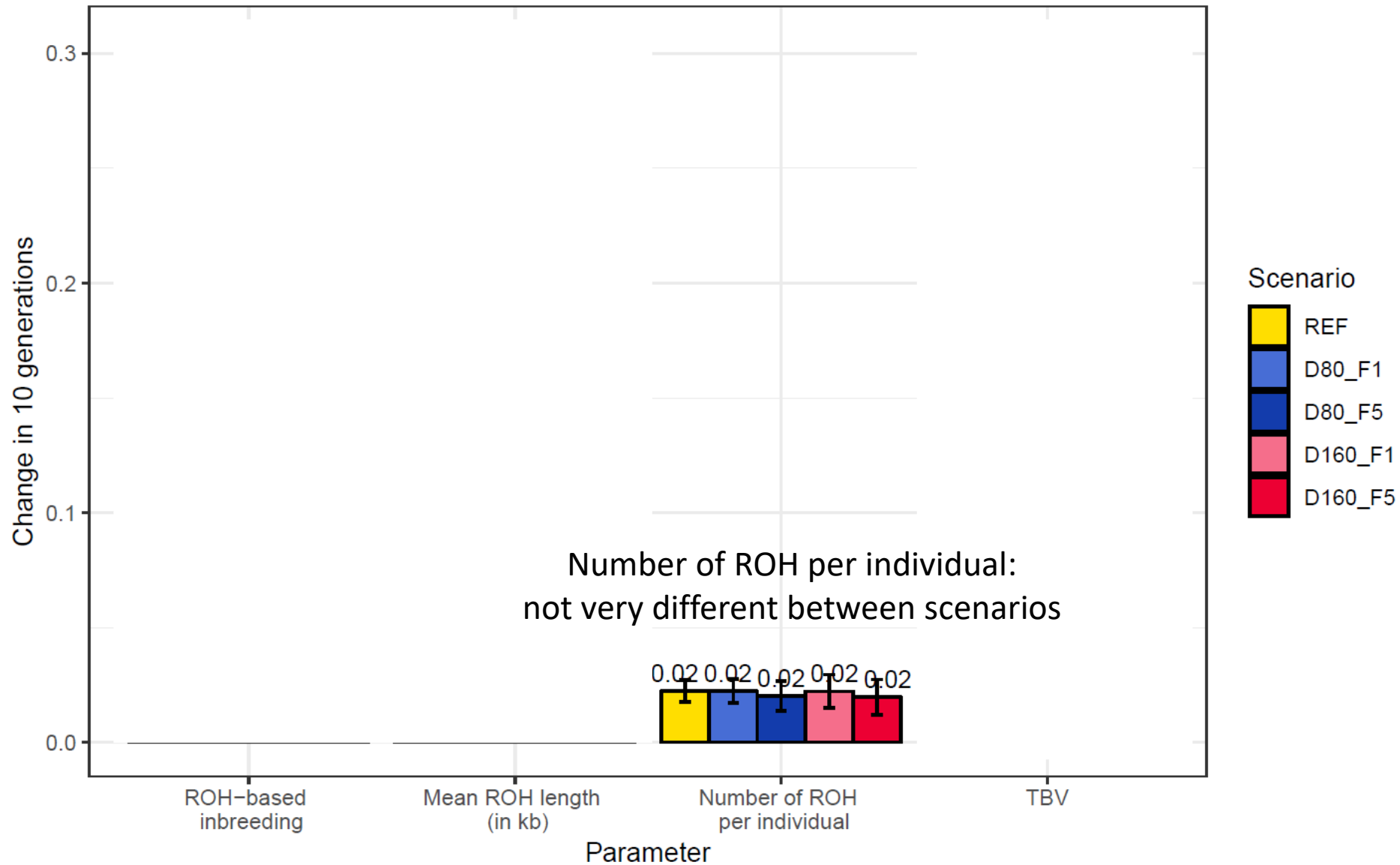# Results (preliminary)
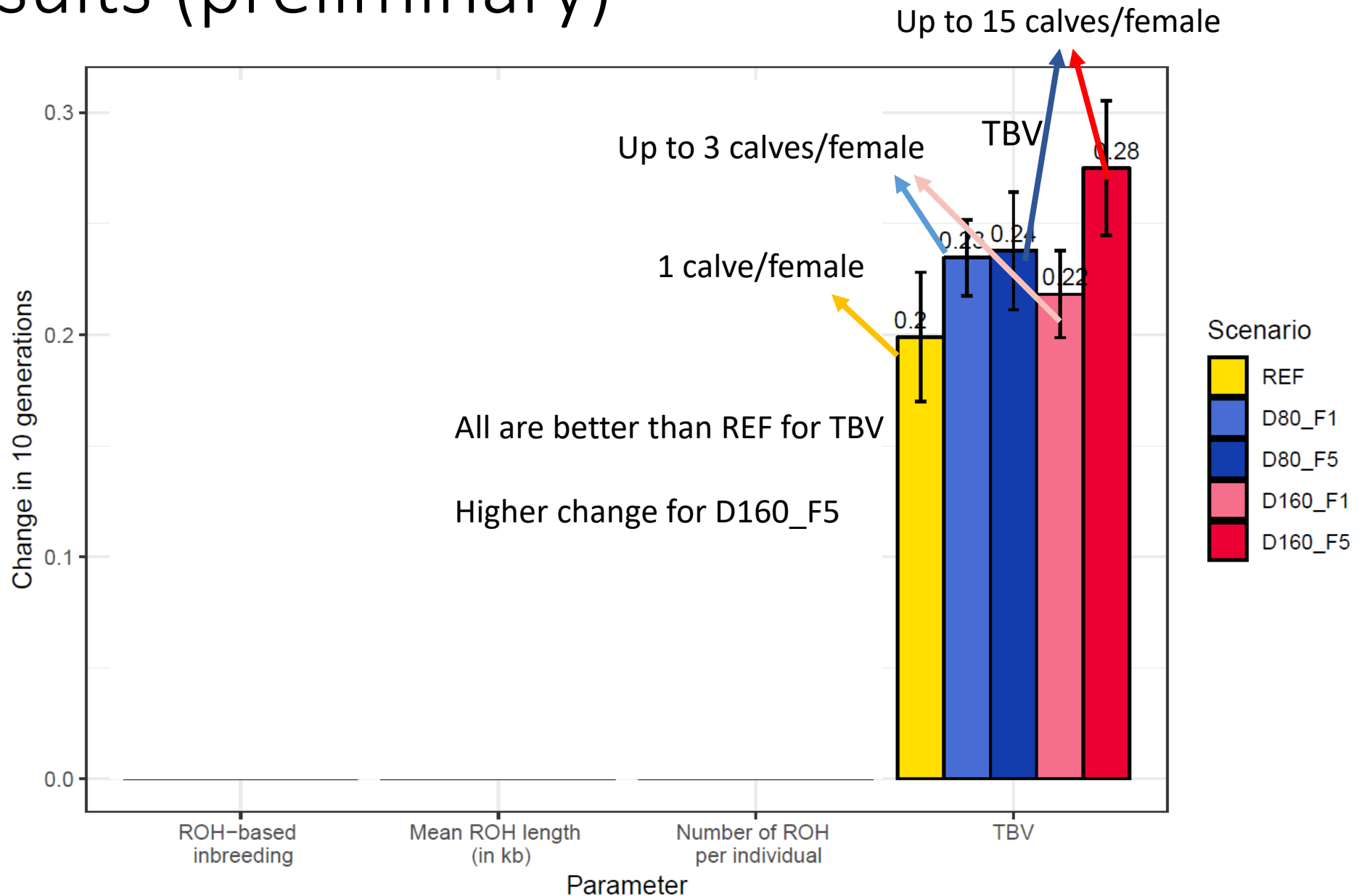
Results (preliminary)
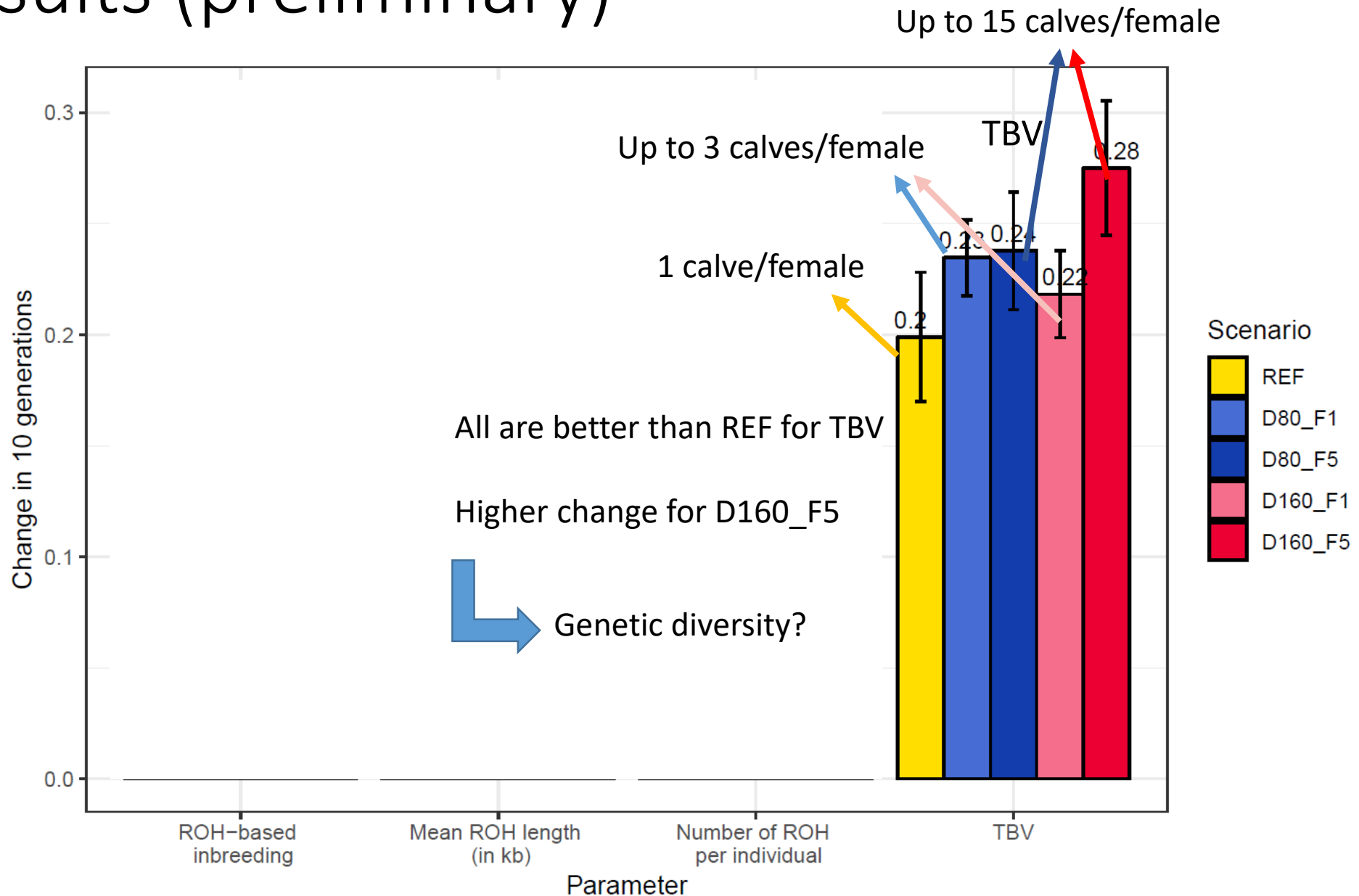
Results (preliminary)
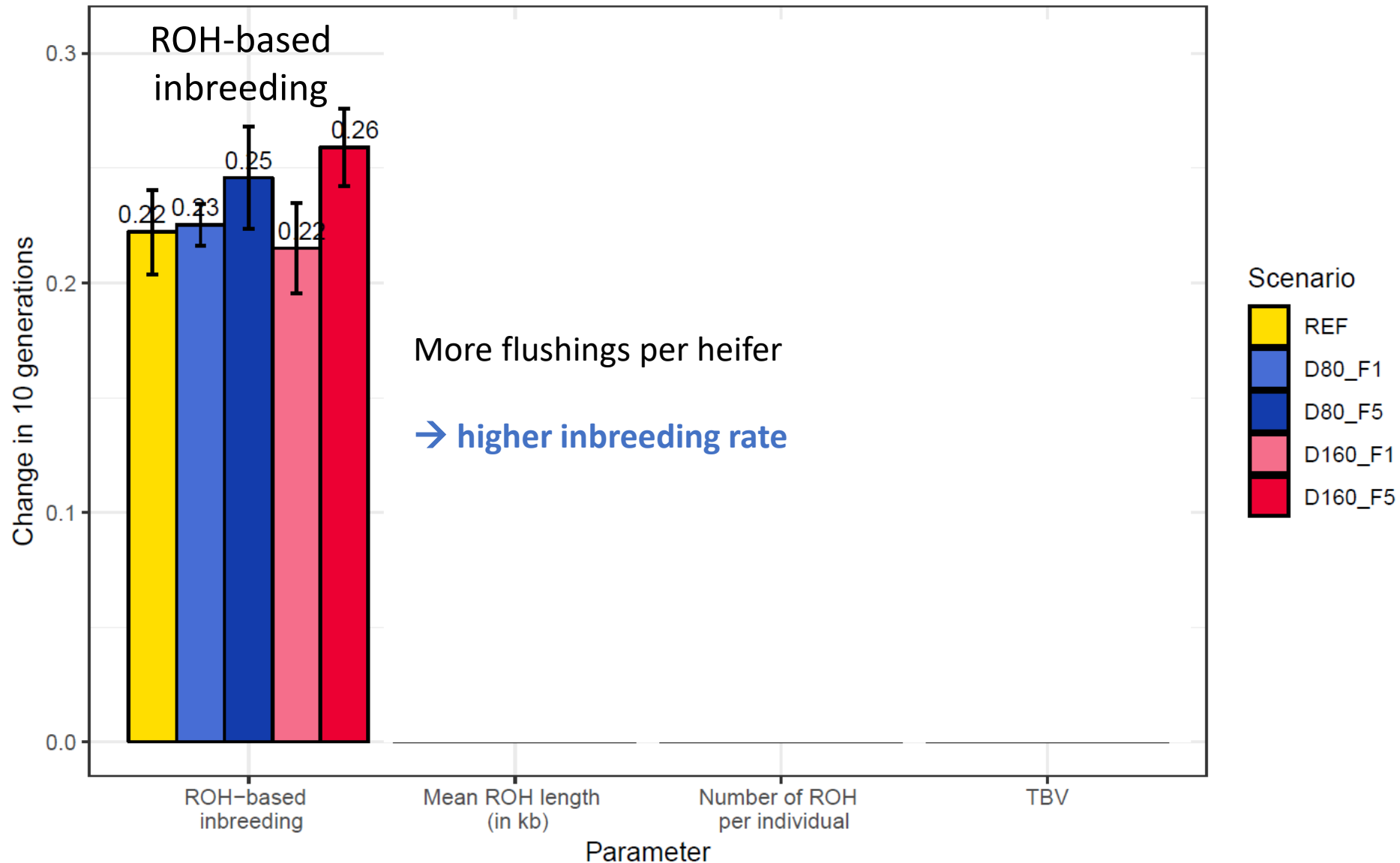
Results (preliminary)

Results (preliminary)

Conclusion

- Preliminary results

- **Higher genetic gain with MOET**, especially when more flushings per heifer

Conclusion

- Preliminary results

- **Higher genetic gain with MOET**, especially when more flushings per heifer

BUT

- More flushings per heifer

→ **Higher inbreeding rate**

→ Longer ROH = **more recent inbreeding**

→ Probably a **decrease in the effective number of dams of bulls or maternal grand dams and grand sires of bulls**

Conclusion

- Preliminary results

- **Higher genetic gain with MOET**, especially when more flushings per heifer

BUT

- More flushings per heifer

→ **Higher inbreeding rate**

→ Longer ROH = **more recent inbreeding**

→ Probably a **decrease in the effective number of dams of bulls or maternal grand dams and grand sires of bulls**

More flushings per heifer = higher chance of selecting two male calves from one female rather than one from a female and another one from a less good female

Conclusion

- Preliminary results

- **Higher genetic gain with MOET**, especially when more flushings per heifer

BUT

- More flushings per heifer

→ **Higher inbreeding rate**

→ Longer ROH = **more recent inbreeding**

→ Probably a **decrease in the effective number of dams of bulls or maternal grand dams and grand sires of bulls**

More flushings per heifer = higher chance of selecting two male calves from one female rather than one from a female and another one from a less good female

In these simulations, to maintain a balance between genetic gain and genetic diversity: should not increase the number of heifers in donor stations

Future work

Other ways of dealing with kinship?

Quotas of bulls per dam?

→ **Solutions to limit the loss of genetic diversity while still increasing genetic gain**

Thank you for your attention!
Any questions?

EBV + originality = ISUO

$$ISUO = ISU + 3*ORIC + 3*ORIT + 3*ORIF$$

ISU = total merit index combining production, functional and type traits

ORI = originality index

- Define a population of interest
  - ORIC: male candidates
  - ORIT: sires of bulls
  - ORIF: all females from last generation
- Compute allelic frequencies of all SNPs in population of interest
- Compute mean frequency of SNPs of the individual to evaluate
  - $f_i = [f_{SNP1}(A1)+f_{SNP1}(A2)+f_{SNP2}(A1)+f_{SNP2}(A2)+f_{SNP3}(A1)+f_{SNP3}(A2)+...]/2n$
- ORI = - $(f_i - f_{pop})/\sigma_{pop}$ → > 0 = the individual is original compared to the population of interest