

**Comparison of methods:  
Genotyping-by-sequencing and exome capture  
applied in genomic selection of Norway spruce  
(*Picea abies*)**

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# Outline

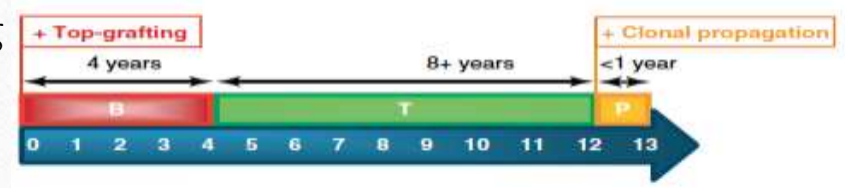
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- Background
- Project aims
- Materials and Methods
- Results
- Summary

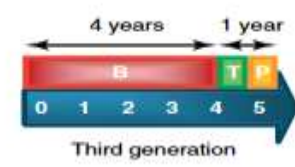
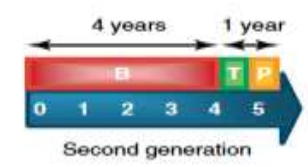
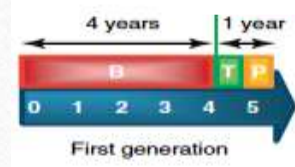


# Molecular breeding

Traditional breeding



Molecular breeding

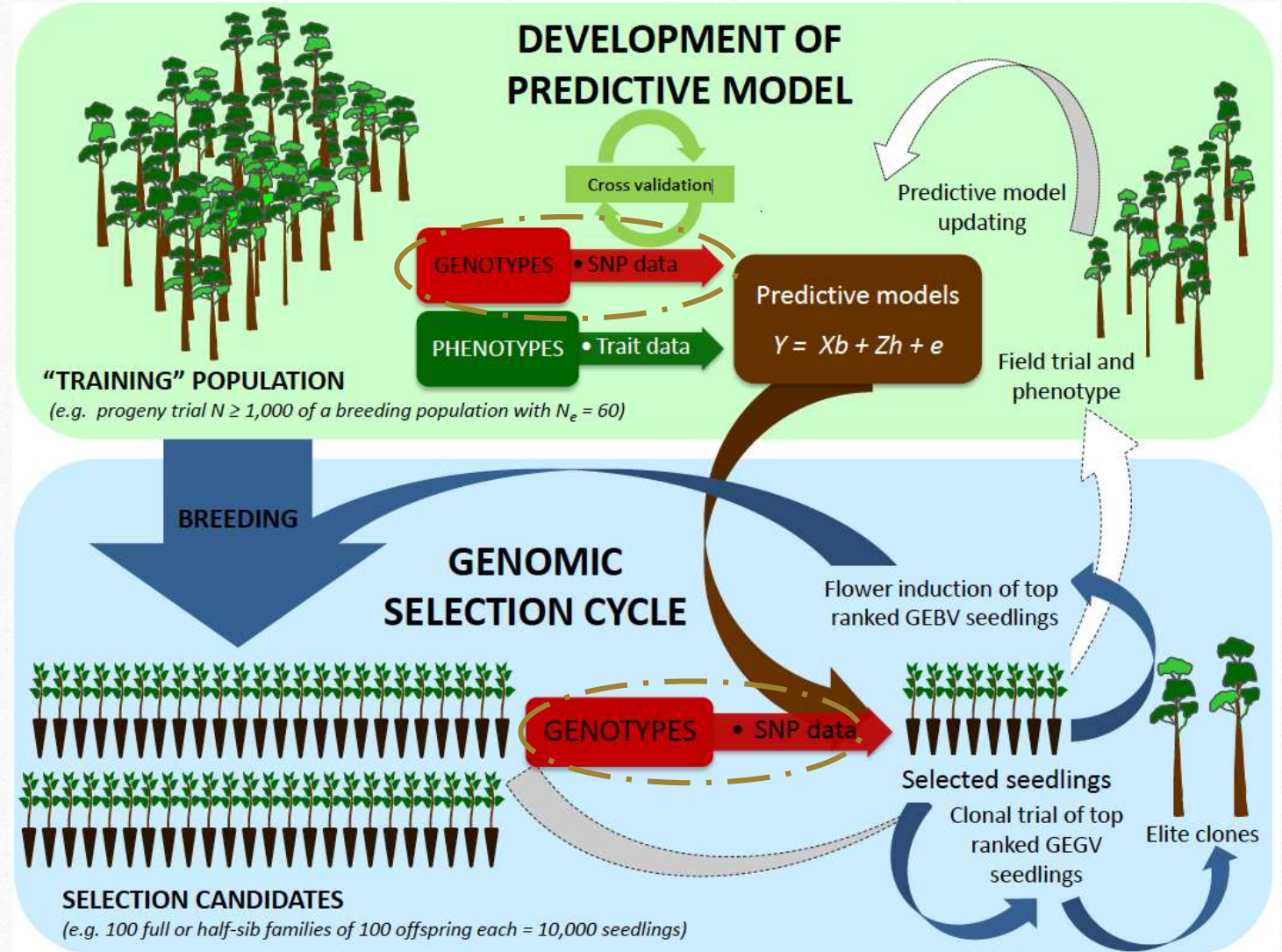


...

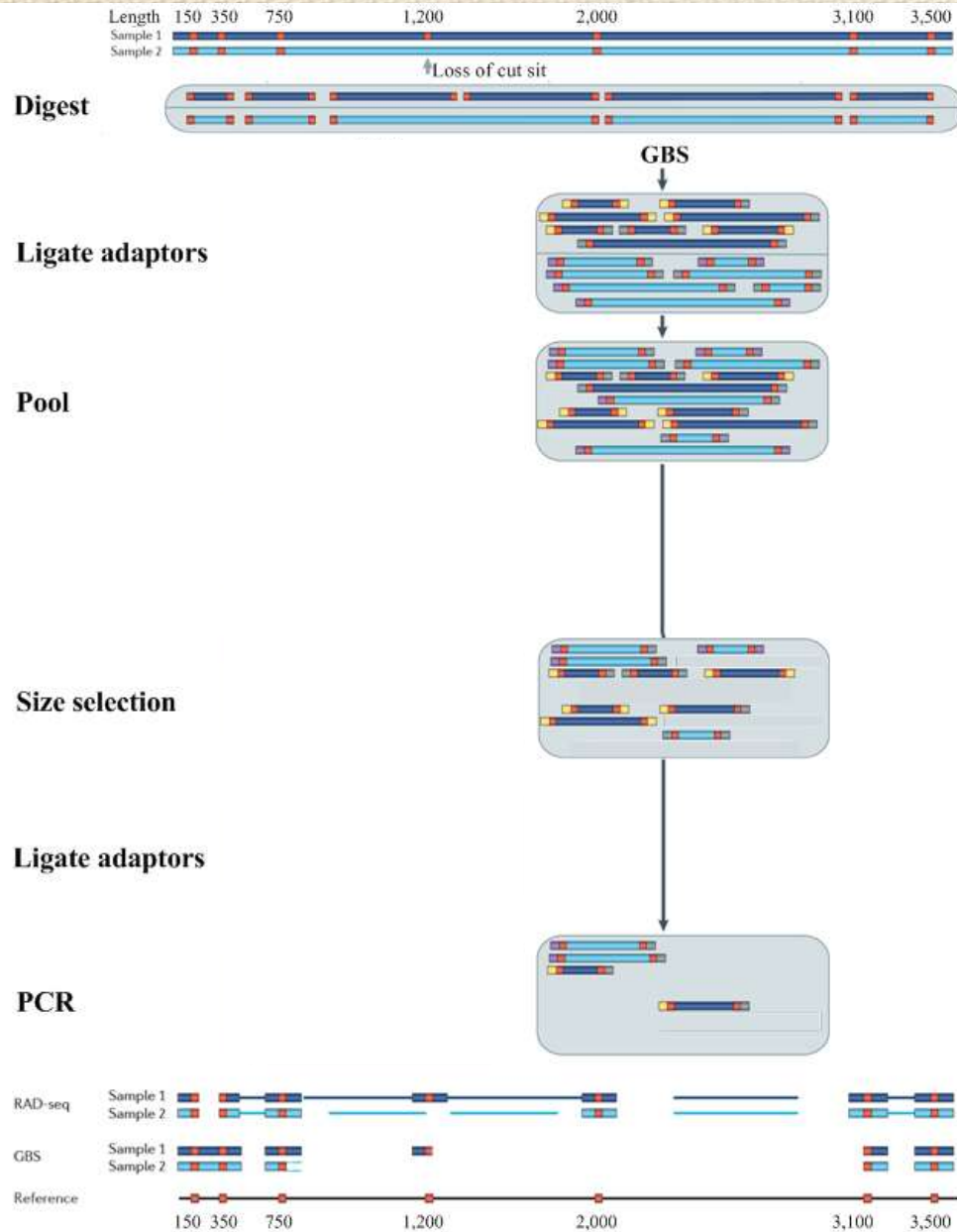
B: **B**reeding  
T: **T**esting  
P: **P**ropagate



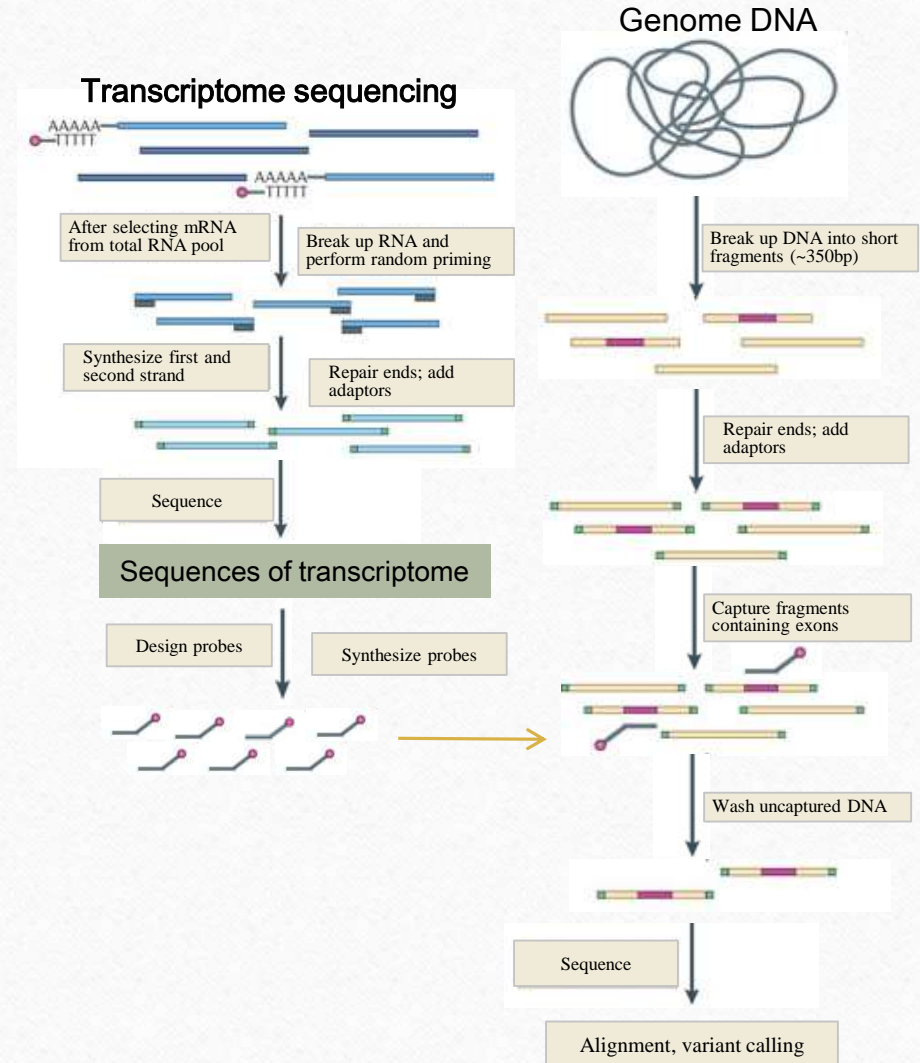
# Genomic selection







## Target enrichment Exome capture



# Disadvantage

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## GBS

- A large percentage of uncalled genotypes (missing)
- Under-calling of heterozygous genotypes (false homozygous genotypes)



# Project aims

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- Optimize SNP-calling
  - Estimate the rate of false genotypes and the rate of discordant genotypes in replicated samples
- Evaluate the potential of GBS and EC in genomic selection of Norway spruce

# Materials

## I Genotyping

- 376 samples from 24 full-sib families (31 parental individuals)
- ~100 endospurms and 5 mother trees
- 5 (GBS) or 21 (EC) individuals sequenced repeatedly (2-8×)

## II Phenotyping

4 growth and wood quality traits:

- Tree height
- Wood density (Pilodyn and Hitman)
- Wood stiffness (Modulus of elasticity - MOE)





# Methods

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## ➤ Genotyping-by-sequencing (GBS)

- *Pst*I & 230 - 430bp restriction fragments
- ~ 20,000 restriction fragments

## ➤ Exome capture (EC)

- 40,019 probes located in 24,919 scaffolds

# Results

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1. Optimization of SNP-calling
2. Comparison of GBS- and EC-SNP data

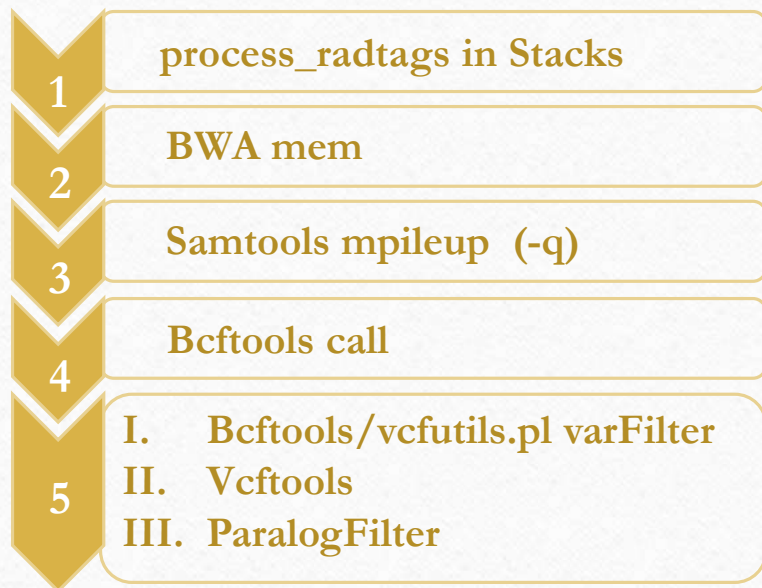


# Results

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1. Optimization of SNP-calling
2. Comparison of GBS and EC data

# GBS-SNP-calling pipeline



- Barcode identification and quality trimming of raw illumina reads

- Align sample reads to reference genome

- Align all samples together

- Call SNPs and indels

- Filter SNPs

## bcftools/vcutils.pl varFilter

```
-Q INT    minimum RMS mapping quality for SNPs [10]
-d INT    minimum read depth [2]
-D INT    maximum read depth [10000000]
-a INT    minimum number of alternate bases [2]
-w INT    SNP within INT bp around a gap to be filtered [3]
-W INT    window size for filtering adjacent gaps [10]
-1 FLOAT  min P-value for strand bias (given PV4) [0.0001]
-2 FLOAT  min P-value for baseQ bias [1e-100]
-3 FLOAT  min P-value for mapQ bias [0]
-4 FLOAT  min P-value for end distance bias [0.0001]
-e FLOAT  min P-value for HWE (plus F<0) [0.0001]
```

## vcftools

```
SNP-site-filtering options
--max-missing  FLOAT  Minimum calling rate
--max-meanDP  INT     Maximum mean read depth
--maf          FLOAT  Minimum allele frequency
Genotype-filtering options
--minQ        INT     Minimum base quality
--minGQ       INT     Minimum genotype quality
--minDP       INT     Minimum read depth
```

## ParalogFilter

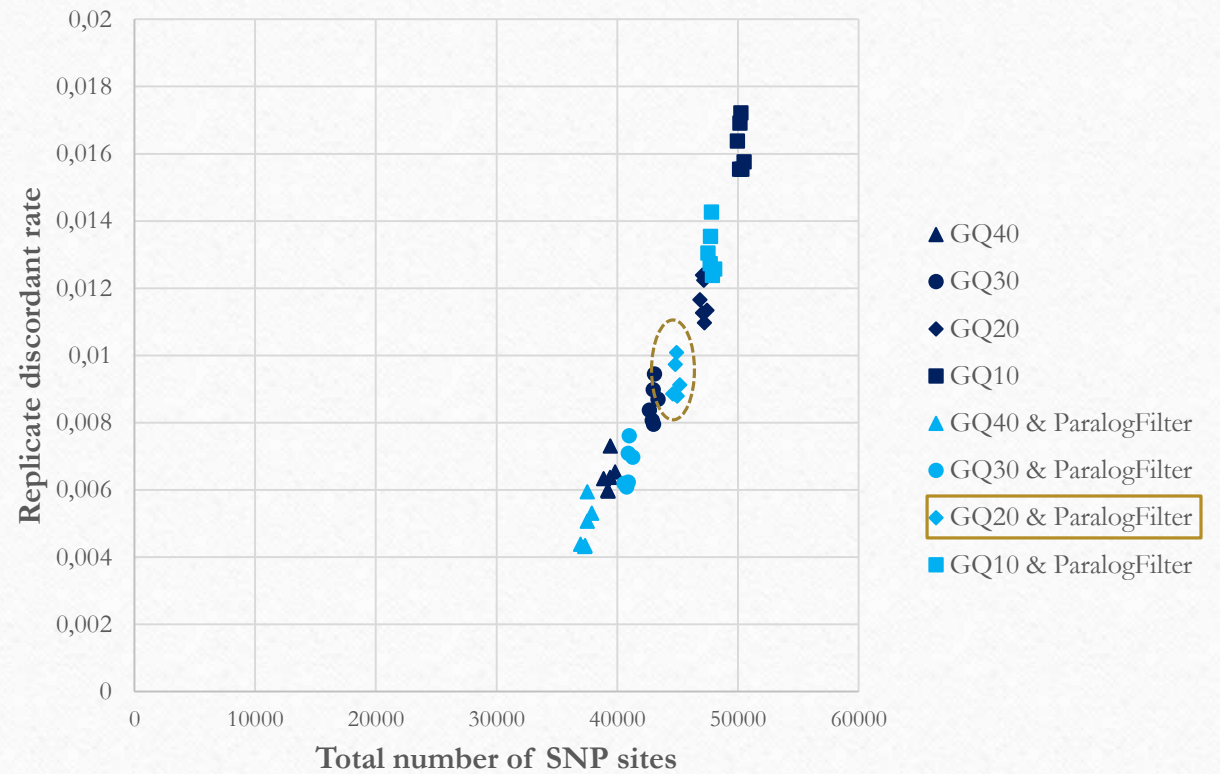
```
options
-F FLOAT      Minimum heterozygous rate based on genotypes of haplotypes
```



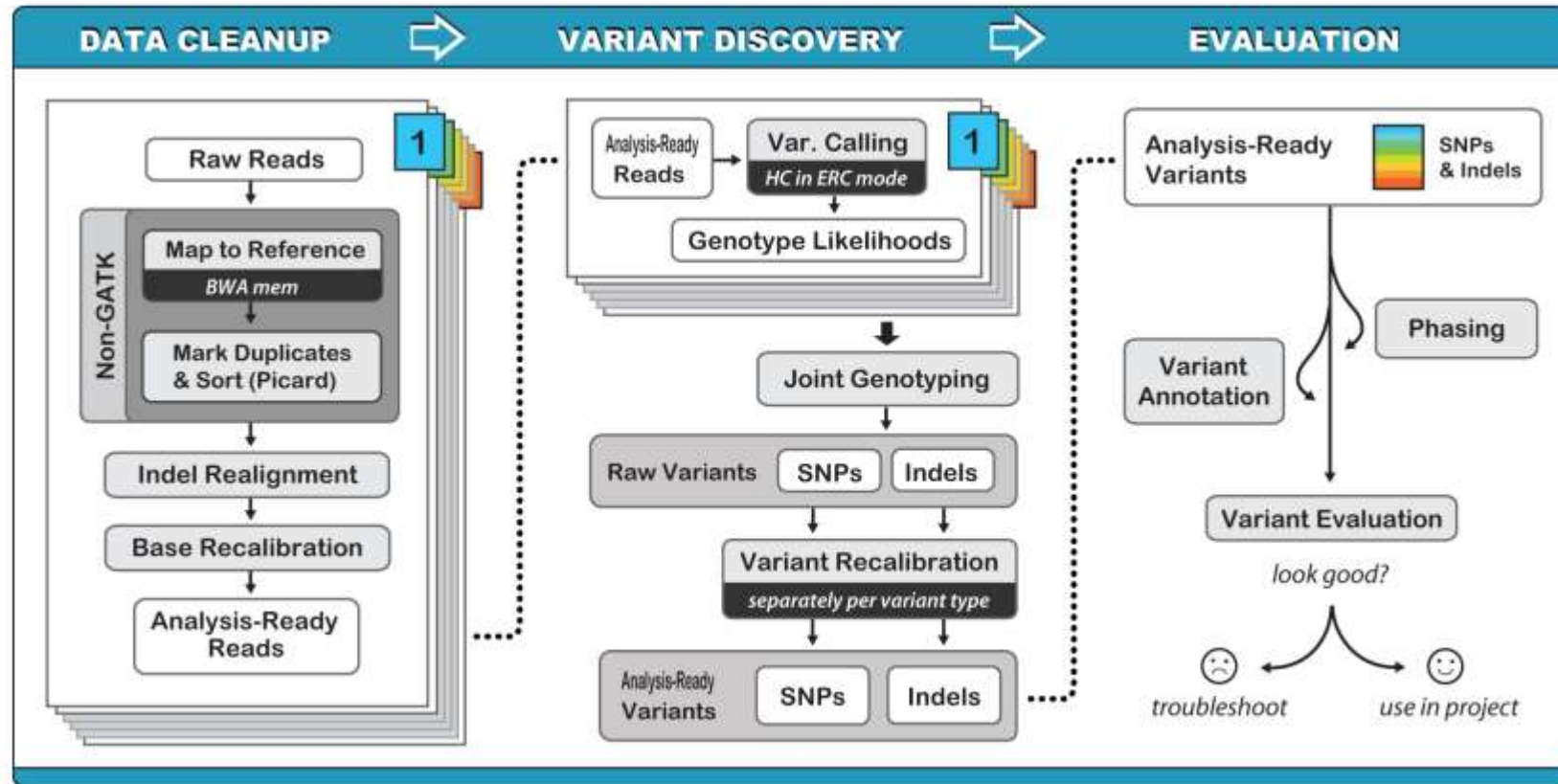
## Optimization of GBS-SNP calling

- GQ (genotype quality)
- ParalogFilter

9.2‰ replicate discordance rate



# EC-SNP-calling pipeline

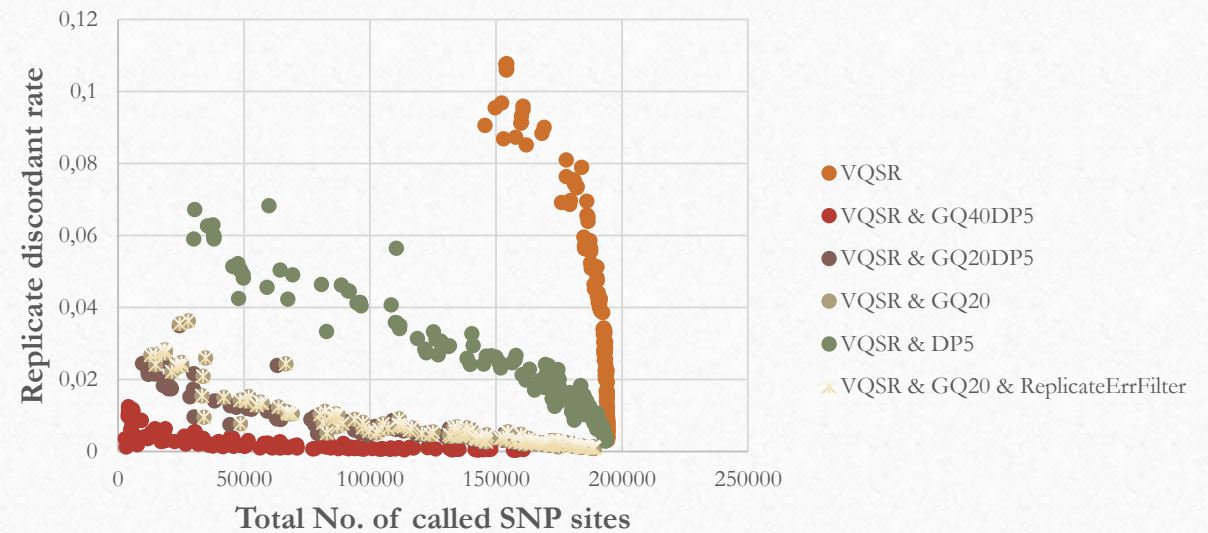


- BWA mem
- Picard
- samtools
- GATK



## Optimization of EC-SNP calling

- GQ (genotype quality)
- minDP (minimum read depth)
- ReplicateErrFilter



Filtering stratgy	Mean replicate discordance rate	No. of SNPs with <0.5 missing rate
VQSR	4%	204726
VQSR & minDP=5	2.5%	204265
VQSR & minGQ=20	0.95%	194886
VQSR & minDP=5 & minGQ=20	0.85%	192635
VQSR & minDP=5 & minGQ=40	0.28%	106714
VQSR & minGQ=20 & ReplicateErrFilter	0.80%	187496

# Results

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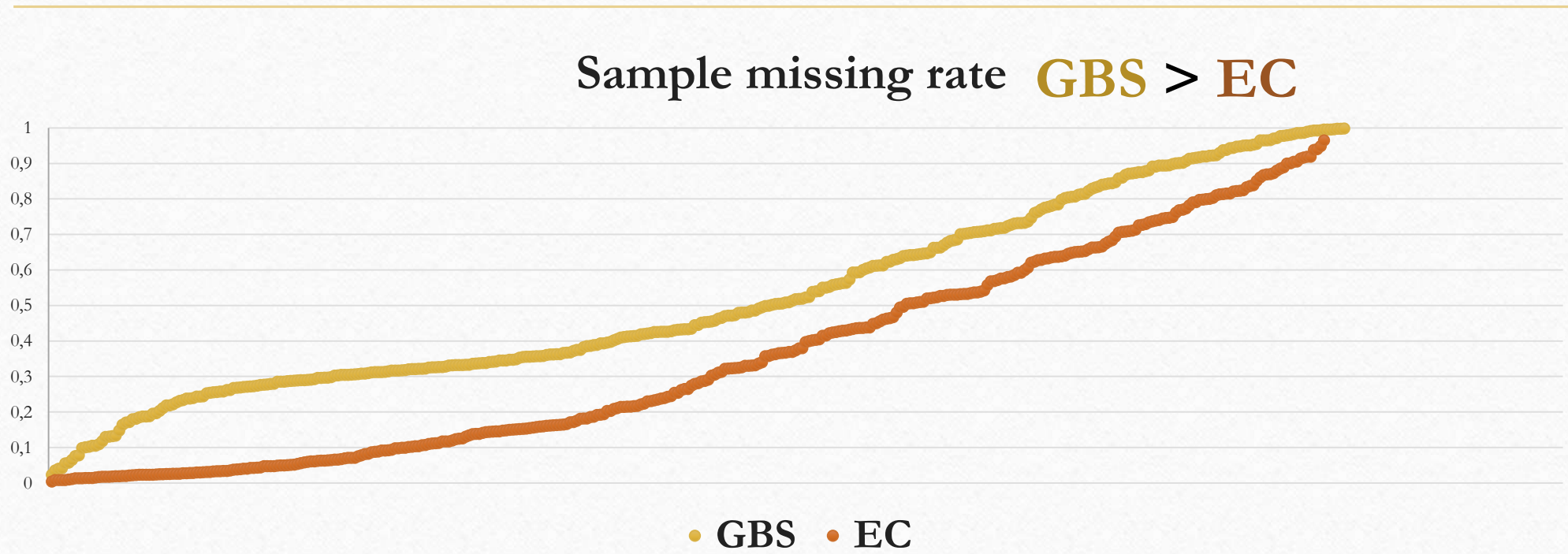
1. Optimization of GBS-SNP-calling
2. Comparison of GBS and EC data



# 1 - Mapping results

	GBS (Median $\pm$ SD)	EC (Median $\pm$ SD)
Total No.	1,879,903 $\pm$ 5,104,604 reads	4,897,552 $\pm$ 2,597,783 reads
Mapped reads	1,313,744 $\pm$ 4,064,215 reads	4,821,132 $\pm$ 2,584,842 reads
properly_paired	1,156,043 $\pm$ 3,569,836 reads	NA
MQ0 reads	94,272 $\pm$ 249,546 reads	504,494 $\pm$ 253,716 reads
Mean covered bases (5 $\times$ )	2,037,017 $\pm$ 1,104,354 bp	19,249,840 $\pm$ 6,473,049 bp
Mean coverage depth (5 $\times$ )	$\times$ 58 $\pm$ 72	$\times$ 16 $\pm$ 5

## 2 – Coverage bias





## 3 - Replicate discordance

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After optimization of SNP-calling

- GBS ~9.2‰ replicate discordance rate
- EC ~ 8 ‰ replicate discordance rate

## 4 - SNP data

### Individual Filter

- Maximum missing rate: 90%

### SNP site Filter

- Minimum calling rate: 50%
- Minimum allele frequency: 0.05

### Genotype Filter

- Minimum read depth: 5
- Minimum genotype quality: 20

	GBS	EC
Sample No.	334	367
SNP No.	19,603	105,209
Overlapped SNP No.	572	
Scaffold No.	6,002	21,547
Overlapped scaffold No.	2,279	
Mean SNP No. per scaffold	$3 \pm 3$	$5 \pm 4$
SNP density (per 1000bp)	~10	~5
Proportion of missing	27.3%	26.5%



# 5 – SNP annotation

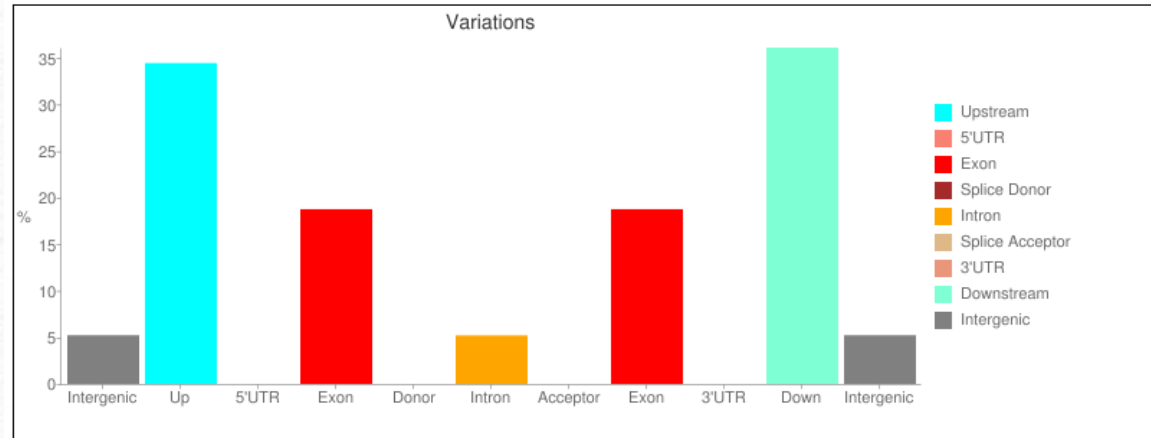
## Comparison of GBS and EC SNP data

### GBS

Number of effects by functional class

Type (alphabetical order)	Count	Percent
MISSENSE	1,683	34.014%
NONSENSE	48	0.97%
SILENT	3,217	65.016%

Missense / Silent ratio: **0.5232**

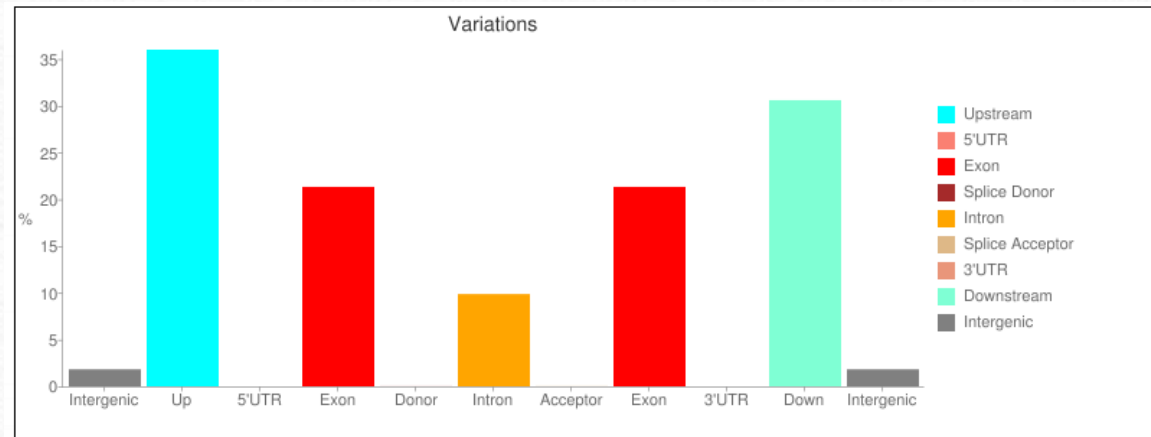


### EC

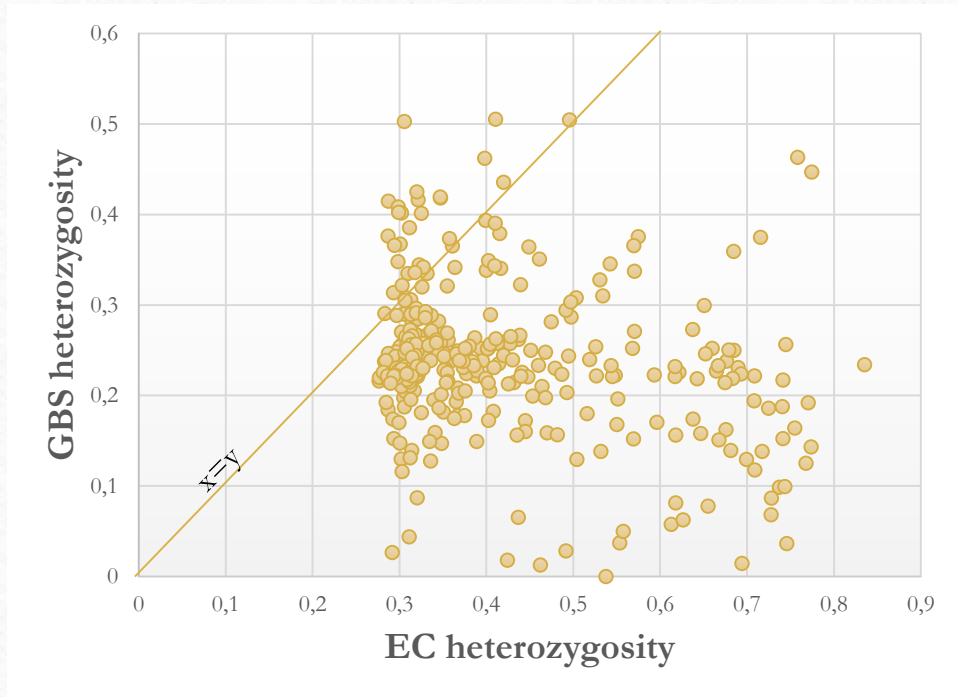
Number of effects by functional class

Type (alphabetical order)	Count	Percent
MISSENSE	29,835	60.793%
NONSENSE	968	1.972%
SILENT	18,273	37.234%

Missense / Silent ratio: **1.6327**



# 6 - Proportion of heterozygous genotypes



**EC > GBS**

Under-calling of *heterozygous* genotypes  
(false homozygous genotypes):  
~8%

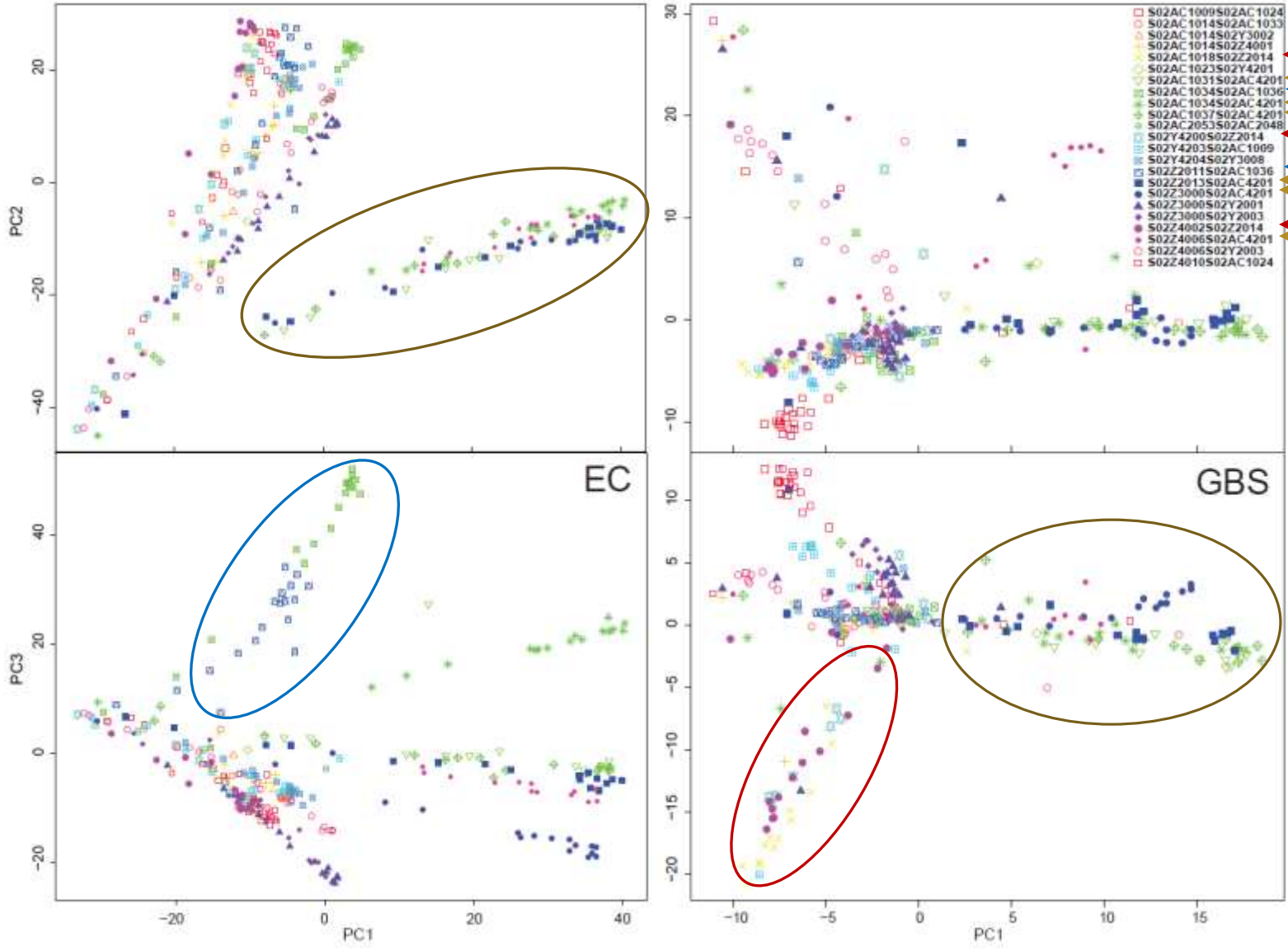


## 7 – Relatedness analyses

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- PCA
- Genetic distance
- Kinship ( under EM and LD kNNi imputation )

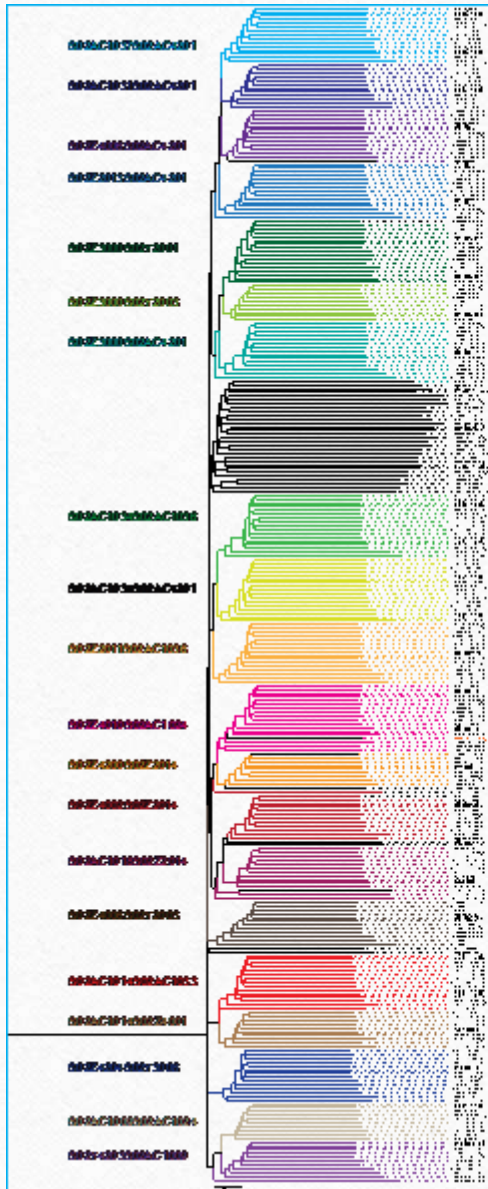
7 – Relatedness analyses



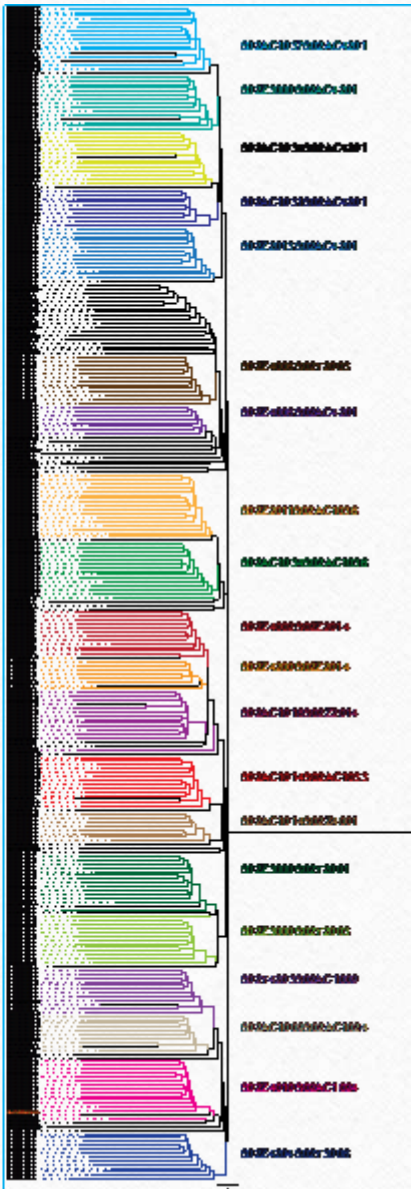
PCA analysis



EC-NJtree



GBS-NJtree



Genetic distance

## 7 – Relatedness analyses

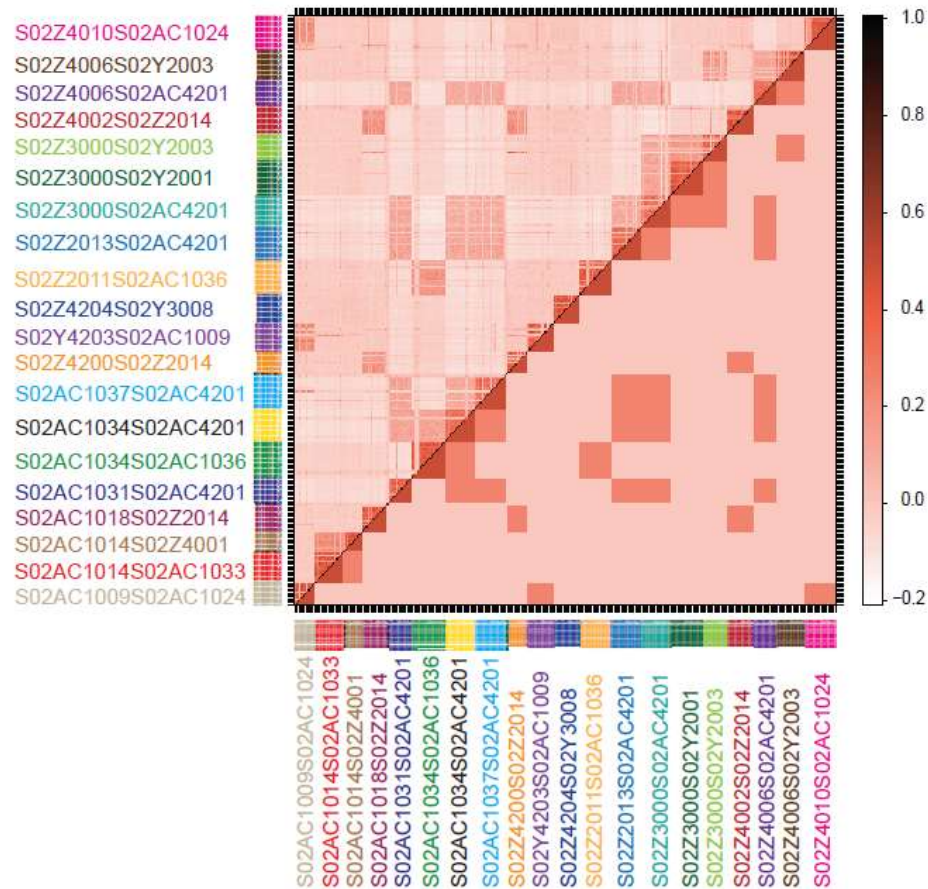
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- PCA
- Genetic distance
- Kinship ( under EM and LD kNNi imputation )

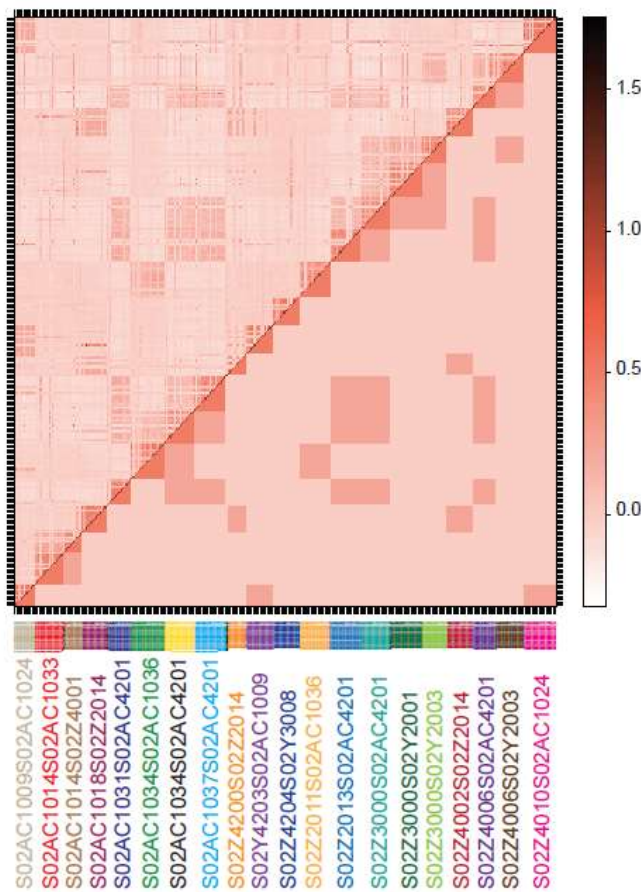


# Kinship

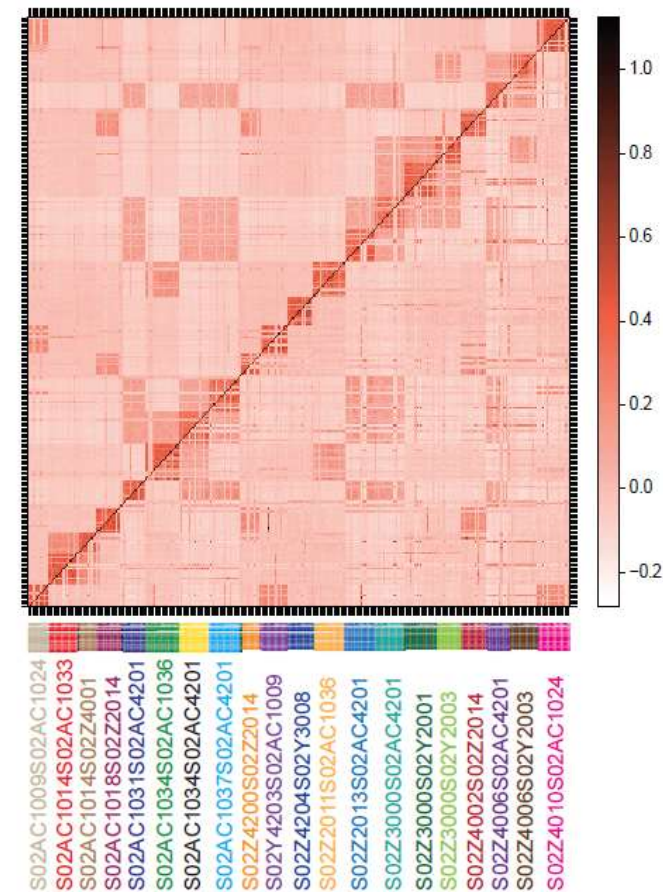
Pedigree & genomic relationship based on EC-SNPs



Pedigree & genomic relationship based on GBS-SNPs



Genomic relationship based on EC- & GBS-SNPs



Imputation method: EM (Endelman and Jannink 2012)

The RMS error < 0.01



# Mean genomic relationship within and between family based on the EC-SNP data

Imputation method: **EM** (Endelman and Jannink 2012) with RMS error < 0.01 & **LD-kNNi** (Money et al., 2015)

502AC1009	502AC1014S	502AC1014S	502AC1018S	502AC1031S	502AC1034S	502AC1034S	502AC1037S	502Y420050	502Y420350	502Y420450	502Z201150	502Z201350	502Z300050	502Z300050	502Z300050	502Z400250	502Z400650	502Z400650	502Z401050											
502AC1024	02AC1033	0224001	0222014	02AC4201	02AC1036	02AC4201	02AC4201	222014	2AC1009	2Y3008	2AC1036	2AC4201	2AC4201	2Y2001	2Y2003	222014	2AC4201	2Y2003	2AC1024											
0.296 ± 0.177	-0.015 ± 0.020	-0.015 ± 0.010	-0.008 ± 0.029	-0.068 ± 0.026	-0.029 ± 0.023	-0.079 ± 0.028	-0.039 ± 0.064	-0.005 ± 0.025	0.139 ± 0.038	-0.010 ± 0.019	-0.011 ± 0.025	-0.049 ± 0.045	-0.064 ± 0.044	-0.030 ± 0.016	-0.025 ± 0.020	-0.012 ± 0.025	-0.075 ± 0.020	-0.017 ± 0.025	0.135 ± 0.080	502AC1009	EM									
0.289 ± 0.188	-0.013 ± 0.013	-0.012 ± 0.009	-0.004 ± 0.024	-0.069 ± 0.027	-0.030 ± 0.019	-0.082 ± 0.030	-0.040 ± 0.081	-0.003 ± 0.012	0.132 ± 0.097	-0.006 ± 0.012	-0.011 ± 0.014	-0.050 ± 0.045	-0.070 ± 0.038	-0.030 ± 0.013	-0.022 ± 0.017	-0.011 ± 0.013	-0.076 ± 0.025	-0.012 ± 0.013	0.142 ± 0.086	502AC1024	LD kNNi									
		0.183 ± 0.057	-0.022 ± 0.017	-0.051 ± 0.017	-0.027 ± 0.018	-0.063 ± 0.025	-0.042 ± 0.040	-0.015 ± 0.022	0.010 ± 0.053	-0.002 ± 0.013	-0.018 ± 0.019	-0.045 ± 0.029	-0.065 ± 0.022	-0.024 ± 0.013	-0.019 ± 0.014	-0.013 ± 0.022	-0.058 ± 0.014	-0.008 ± 0.017	-0.019 ± 0.019	502AC1014S										
			0.180 ± 0.068	-0.017 ± 0.010	-0.050 ± 0.020	-0.027 ± 0.017	-0.065 ± 0.027	-0.041 ± 0.036	-0.012 ± 0.014	0.013 ± 0.049	0.001 ± 0.009	-0.016 ± 0.014	-0.045 ± 0.030	-0.085 ± 0.027	0.022 ± 0.010	-0.016 ± 0.012	-0.012 ± 0.016	-0.058 ± 0.019	-0.003 ± 0.008	-0.018 ± 0.017	502AC1033									
				-0.019 ± 0.013	-0.057 ± 0.010	-0.026 ± 0.014	-0.069 ± 0.016	-0.046 ± 0.026	-0.012 ± 0.010	-0.005 ± 0.016	0.003 ± 0.010	-0.006 ± 0.015	-0.046 ± 0.013	-0.065 ± 0.017	-0.010 ± 0.011	-0.010 ± 0.013	-0.008 ± 0.011	-0.069 ± 0.009	-0.007 ± 0.012	-0.014 ± 0.010	502AC1014									
					-0.015 ± 0.011	-0.055 ± 0.014	-0.026 ± 0.016	-0.070 ± 0.021	-0.044 ± 0.027	-0.009 ± 0.009	-0.000 ± 0.013	0.006 ± 0.008	-0.004 ± 0.012	-0.045 ± 0.018	-0.065 ± 0.022	-0.009 ± 0.007	-0.008 ± 0.011	-0.067 ± 0.013	-0.002 ± 0.008	-0.013 ± 0.009	502Z4001									
						-0.062 ± 0.021	-0.030 ± 0.021	-0.085 ± 0.036	-0.052 ± 0.029	0.138 ± 0.075	-0.003 ± 0.028	-0.010 ± 0.016	-0.020 ± 0.023	-0.055 ± 0.032	-0.077 ± 0.034	-0.036 ± 0.020	-0.020 ± 0.064	0.147 ± 0.073	-0.062 ± 0.023	-0.005 ± 0.051	0.015 ± 0.060	502AC1018								
							0.297 ± 0.136	-0.064 ± 0.020	-0.033 ± 0.019	-0.074 ± 0.033	-0.053 ± 0.028	0.139 ± 0.083	-0.002 ± 0.013	-0.006 ± 0.010	-0.020 ± 0.016	-0.059 ± 0.030	-0.082 ± 0.034	-0.036 ± 0.016	-0.015 ± 0.064	0.159 ± 0.072	-0.067 ± 0.025	-0.008 ± 0.020	0.015 ± 0.055	502Z2014						
									-0.053 ± 0.062	0.114 ± 0.037	0.097 ± 0.060	-0.053 ± 0.023	-0.055 ± 0.019	-0.051 ± 0.012	-0.050 ± 0.036	0.103 ± 0.054	0.088 ± 0.048	0.072 ± 0.012	-0.067 ± 0.024	-0.071 ± 0.017	0.105 ± 0.040	-0.064 ± 0.025	-0.066 ± 0.016	502AC1031						
											-0.049 ± 0.026	-0.051 ± 0.023	-0.049 ± 0.015	-0.050 ± 0.036	0.100 ± 0.060	0.085 ± 0.046	-0.067 ± 0.017	-0.058 ± 0.028	-0.069 ± 0.021	0.105 ± 0.041	-0.053 ± 0.031	-0.066 ± 0.021	502AC4201							
												0.105 ± 0.057	-0.055 ± 0.033	-0.025 ± 0.020	-0.016 ± 0.022	-0.024 ± 0.015	0.135 ± 0.075	-0.069 ± 0.035	-0.090 ± 0.035	-0.040 ± 0.019	-0.037 ± 0.020	-0.030 ± 0.022	-0.087 ± 0.022	-0.028 ± 0.023	-0.022 ± 0.023	502AC1034				
													0.102 ± 0.060	-0.052 ± 0.034	-0.024 ± 0.017	-0.015 ± 0.017	-0.023 ± 0.016	0.138 ± 0.080	-0.067 ± 0.035	-0.088 ± 0.039	-0.042 ± 0.023	-0.037 ± 0.024	-0.031 ± 0.018	-0.085 ± 0.030	-0.026 ± 0.021	-0.024 ± 0.019	502AC1036			
														0.076 ± 0.059	-0.069 ± 0.027	-0.065 ± 0.034	-0.066 ± 0.017	-0.068 ± 0.019	0.084 ± 0.051	0.069 ± 0.044	-0.084 ± 0.017	-0.083 ± 0.030	-0.079 ± 0.026	0.091 ± 0.032	-0.073 ± 0.031	-0.073 ± 0.021	502AC1034			
															0.076 ± 0.061	-0.067 ± 0.034	-0.063 ± 0.027	-0.065 ± 0.020	-0.063 ± 0.010	0.083 ± 0.054	0.070 ± 0.040	-0.084 ± 0.022	-0.077 ± 0.037	-0.081 ± 0.027	0.093 ± 0.033	-0.066 ± 0.039	-0.076 ± 0.026	502AC4201		
																													502AC1037	
																													502AC4201	
																													502Y42005	
																													0222014	
																													502Y42035	
																													02AC1009	
																													502Y42045	
																													02Y3008	
																													502Z20115	
																													02AC1036	
																													502Z20135	
																													02AC4201	
																													502Z30005	
																													02AC4201	
																													502Z30005	
																													02Y2001	
																													502Z30005	
																													02Y2003	
																													502Z40025	
																													502Z40065	
																													02AC4201	
																													502Z40065	
																													02Y2003	
																													502Z40105	
																													02AC1024	

Brown number: p-value < 0.01 in paired t-test

Deep yellow: ful-sib family

Light yellow: half-sib family

EC

Mean relative difference: 0.147

GBS

Mean relative difference: 0.181



# Mean genomic relationship within and between family based on the EC- and GBS-SNP data

Imputation method: **EM** (Endelman and Jannink 2012) with RMS error < 0.01

502AC10095	502AC101450	502AC10145	502AC101850	502AC10315	502AC10345	502AC10345	502AC10375	502Y420050	502Y420350	502Y420450	502Z201150	502Z201350	502Z300050	502Z300050	502Z400250	502Z400650	502Z400650	502Z4010502									
02AC1024	2AC1033	02Z4001	Z2Z014	02AC4201	02AC1036	02AC4201	02AC4201	Z2Z014	ZAC1009	ZY3008	ZAC1036	ZAC4201	ZAC4201	ZY2001	ZY2003	Z2Z014	ZAC4201	ZY2003	AC1024								
0.296 ± 0.177	-0.015 ± 0.020	-0.015 ± 0.010	-0.008 ± 0.029	-0.068 ± 0.026	-0.029 ± 0.023	-0.079 ± 0.028	-0.039 ± 0.064	-0.005 ± 0.025	0.139 ± 0.098	-0.010 ± 0.019	-0.011 ± 0.025	-0.049 ± 0.045	-0.064 ± 0.044	-0.030 ± 0.016	-0.025 ± 0.020	-0.012 ± 0.025	-0.073 ± 0.020	-0.017 ± 0.025	0.135 ± 0.089	502AC1009 EC							
0.257 ± 0.212	-0.020 ± 0.045	-0.013 ± 0.057	-0.029 ± 0.019	-0.042 ± 0.075	-0.012 ± 0.057	-0.060 ± 0.061	-0.032 ± 0.098	0.007 ± 0.083	0.124 ± 0.108	-0.010 ± 0.093	-0.010 ± 0.027	-0.028 ± 0.123	-0.066 ± 0.063	-0.038 ± 0.052	-0.040 ± 0.025	-0.019 ± 0.035	-0.043 ± 0.102	-0.033 ± 0.082	0.119 ± 0.121	502AC1024 GBS							
	0.136 ± 0.116	0.183 ± 0.057	0.022 ± 0.017	-0.051 ± 0.017	-0.027 ± 0.018	-0.063 ± 0.025	-0.042 ± 0.040	-0.015 ± 0.022	0.010 ± 0.053	-0.002 ± 0.013	-0.038 ± 0.019	-0.045 ± 0.029	-0.065 ± 0.022	-0.024 ± 0.013	-0.019 ± 0.014	-0.013 ± 0.022	-0.058 ± 0.014	-0.008 ± 0.017	-0.019 ± 0.019	502AC1014							
	0.264 ± 0.204	0.119 ± 0.133	-0.013 ± 0.042	-0.029 ± 0.052	-0.018 ± 0.032	-0.028 ± 0.091	-0.027 ± 0.076	-0.034 ± 0.032	-0.000 ± 0.057	-0.008 ± 0.032	-0.017 ± 0.025	-0.032 ± 0.051	-0.043 ± 0.068	-0.021 ± 0.061	-0.033 ± 0.025	0.001 ± 0.081	-0.034 ± 0.080	-0.016 ± 0.058	-0.028 ± 0.046	502AC1033							
		0.194 ± 0.059	-0.019 ± 0.013	-0.057 ± 0.010	-0.026 ± 0.014	-0.069 ± 0.016	-0.046 ± 0.026	-0.012 ± 0.010	-0.005 ± 0.016	0.003 ± 0.010	-0.006 ± 0.015	-0.046 ± 0.013	-0.065 ± 0.017	-0.010 ± 0.011	-0.010 ± 0.013	-0.008 ± 0.011	-0.069 ± 0.009	-0.007 ± 0.012	-0.014 ± 0.010	502AC1014							
		0.214 ± 0.236	0.007 ± 0.067	-0.049 ± 0.049	-0.007 ± 0.036	-0.047 ± 0.075	-0.057 ± 0.067	-0.003 ± 0.058	-0.005 ± 0.030	0.000 ± 0.043	0.003 ± 0.034	-0.053 ± 0.058	-0.062 ± 0.068	0.004 ± 0.075	-0.008 ± 0.030	0.023 ± 0.109	-0.028 ± 0.139	0.010 ± 0.101	-0.016 ± 0.071	502Z4001							
			0.301 ± 0.181	-0.062 ± 0.021	-0.030 ± 0.021	-0.065 ± 0.036	-0.052 ± 0.029	0.138 ± 0.075	-0.003 ± 0.028	-0.010 ± 0.015	-0.020 ± 0.023	-0.055 ± 0.032	-0.077 ± 0.034	-0.036 ± 0.030	-0.020 ± 0.064	0.147 ± 0.073	-0.062 ± 0.023	-0.009 ± 0.031	0.015 ± 0.060	502AC1018							
			0.377 ± 0.175	-0.050 ± 0.030	-0.037 ± 0.026	-0.047 ± 0.078	-0.059 ± 0.026	0.107 ± 0.121	0.024 ± 0.134	-0.008 ± 0.021	-0.026 ± 0.015	-0.060 ± 0.048	-0.075 ± 0.041	-0.020 ± 0.072	-0.036 ± 0.025	0.147 ± 0.099	-0.074 ± 0.036	-0.037 ± 0.024	-0.031 ± 0.023	502Z2014							
			0.308 ± 0.087	-0.059 ± 0.062	0.114 ± 0.037	0.097 ± 0.060	-0.053 ± 0.023	-0.015 ± 0.019	-0.051 ± 0.012	-0.050 ± 0.036	0.105 ± 0.058	0.088 ± 0.046	-0.072 ± 0.012	-0.067 ± 0.024	-0.071 ± 0.017	0.105 ± 0.040	-0.064 ± 0.025	-0.066 ± 0.016	-0.064 ± 0.016	502AC1031							
			0.217 ± 0.221	-0.043 ± 0.034	0.069 ± 0.103	0.086 ± 0.106	-0.028 ± 0.044	-0.042 ± 0.044	-0.034 ± 0.048	-0.043 ± 0.036	0.081 ± 0.105	0.088 ± 0.091	-0.056 ± 0.053	-0.065 ± 0.034	-0.052 ± 0.038	0.049 ± 0.087	-0.035 ± 0.070	-0.037 ± 0.075	-0.037 ± 0.075	502AC4201							
					0.301 ± 0.167	0.103 ± 0.057	-0.055 ± 0.033	-0.025 ± 0.020	-0.016 ± 0.022	-0.074 ± 0.015	0.135 ± 0.075	-0.069 ± 0.035	-0.090 ± 0.033	-0.040 ± 0.019	-0.037 ± 0.020	-0.030 ± 0.022	0.087 ± 0.027	0.028 ± 0.023	-0.022 ± 0.023	502AC1034							
					0.216 ± 0.173	0.065 ± 0.075	-0.051 ± 0.042	-0.021 ± 0.030	-0.013 ± 0.030	0.010 ± 0.025	0.110 ± 0.078	-0.059 ± 0.036	-0.059 ± 0.049	-0.029 ± 0.033	-0.033 ± 0.024	-0.030 ± 0.026	0.048 ± 0.075	-0.025 ± 0.053	-0.012 ± 0.043	502AC1036							
						0.289 ± 0.091	0.076 ± 0.059	-0.069 ± 0.027	-0.065 ± 0.024	-0.066 ± 0.017	-0.068 ± 0.029	0.084 ± 0.051	0.069 ± 0.044	-0.084 ± 0.017	-0.082 ± 0.030	-0.079 ± 0.026	0.091 ± 0.032	0.073 ± 0.031	0.073 ± 0.021	502AC1034							
						0.171 ± 0.189	0.059 ± 0.100	-0.011 ± 0.057	-0.056 ± 0.050	-0.032 ± 0.038	-0.048 ± 0.053	0.061 ± 0.096	0.059 ± 0.100	-0.060 ± 0.071	-0.070 ± 0.041	-0.055 ± 0.063	0.049 ± 0.091	0.044 ± 0.092	-0.058 ± 0.073	502AC4201							
							0.199 ± 0.144	-0.047 ± 0.034	0.036 ± 0.035	-0.046 ± 0.024	0.041 ± 0.036	0.079 ± 0.062	0.065 ± 0.061	-0.060 ± 0.022	-0.058 ± 0.028	-0.056 ± 0.030	0.084 ± 0.059	0.050 ± 0.036	-0.041 ± 0.057	502AC1037							
							0.236 ± 0.199	-0.035 ± 0.055	-0.051 ± 0.028	-0.044 ± 0.040	-0.052 ± 0.030	0.088 ± 0.105	0.068 ± 0.091	-0.062 ± 0.067	-0.069 ± 0.032	-0.060 ± 0.045	0.057 ± 0.126	0.066 ± 0.099	-0.031 ± 0.099	502AC4201							
								0.225 ± 0.165	0.017 ± 0.049	-0.004 ± 0.016	-0.011 ± 0.020	-0.054 ± 0.035	-0.072 ± 0.037	-0.025 ± 0.023	-0.005 ± 0.098	0.143 ± 0.076	0.061 ± 0.023	0.007 ± 0.030	0.066 ± 0.034	502Y42005							
								0.341 ± 0.209	0.032 ± 0.082	-0.008 ± 0.031	-0.015 ± 0.020	-0.017 ± 0.060	-0.052 ± 0.050	-0.023 ± 0.053	-0.033 ± 0.029	0.103 ± 0.115	0.028 ± 0.081	-0.013 ± 0.064	0.008 ± 0.058	502Z2014							
									0.195 ± 0.174	0.002 ± 0.017	0.001 ± 0.024	-0.039 ± 0.042	-0.054 ± 0.037	-0.018 ± 0.016	-0.012 ± 0.027	-0.005 ± 0.025	-0.056 ± 0.018	-0.000 ± 0.028	0.008 ± 0.038	502Y42035							
									0.254 ± 0.231	-0.004 ± 0.023	-0.001 ± 0.024	-0.037 ± 0.054	-0.065 ± 0.026	-0.022 ± 0.029	-0.028 ± 0.019	0.012 ± 0.062	-0.046 ± 0.071	-0.032 ± 0.021	0.007 ± 0.028	02AC1009							
										0.164 ± 0.130	-0.010 ± 0.018	-0.042 ± 0.022	-0.061 ± 0.020	-0.000 ± 0.021	-0.008 ± 0.018	0.003 ± 0.022	-0.055 ± 0.011	-0.001 ± 0.016	0.005 ± 0.015	502Y42045							
										0.240 ± 0.211	-0.005 ± 0.021	-0.037 ± 0.032	-0.040 ± 0.050	0.007 ± 0.066	0.000 ± 0.034	0.001 ± 0.028	-0.041 ± 0.055	-0.008 ± 0.051	0.012 ± 0.056	02Y3008							
											0.295 ± 0.144	-0.050 ± 0.034	-0.074 ± 0.033	-0.034 ± 0.015	-0.027 ± 0.021	-0.015 ± 0.022	-0.068 ± 0.026	-0.016 ± 0.024	-0.018 ± 0.019	502Z20115							
												0.257 ± 0.142	-0.049 ± 0.028	-0.061 ± 0.038	-0.022 ± 0.027	-0.029 ± 0.024	-0.012 ± 0.019	-0.039 ± 0.073	-0.023 ± 0.040	-0.015 ± 0.027	02AC1036						
													0.236 ± 0.134	0.072 ± 0.056	-0.065 ± 0.020	-0.058 ± 0.026	-0.059 ± 0.031	0.097 ± 0.053	-0.044 ± 0.031	-0.054 ± 0.029	502Z20135						
														0.221 ± 0.191	0.065 ± 0.084	-0.058 ± 0.060	-0.062 ± 0.034	-0.062 ± 0.042	0.059 ± 0.100	-0.043 ± 0.082	-0.041 ± 0.089	02AC4201					
															0.217 ± 0.129	0.092 ± 0.063	0.065 ± 0.077	-0.082 ± 0.037	0.086 ± 0.060	-0.056 ± 0.044	-0.070 ± 0.029	502Z30005					
																0.187 ± 0.156	0.058 ± 0.089	0.070 ± 0.067	-0.075 ± 0.049	0.036 ± 0.092	-0.060 ± 0.093	-0.057 ± 0.086	02AC4201				
																	0.351 ± 0.082	0.124 ± 0.072	-0.022 ± 0.044	-0.086 ± 0.009	-0.022 ± 0.014	-0.025 ± 0.015	502Z30005				
																		0.234 ± 0.136	0.111 ± 0.095	-0.021 ± 0.069	-0.043 ± 0.118	-0.002 ± 0.099	-0.022 ± 0.068	02Y2001			
																			0.206 ± 0.167	-0.015 ± 0.055	-0.075 ± 0.022	0.099 ± 0.078	-0.016 ± 0.018	502Z30005			
																				0.293 ± 0.168	-0.036 ± 0.027	-0.072 ± 0.057	0.115 ± 0.066	-0.023 ± 0.031	02Y2003		
																					0.284 ± 0.148	-0.071 ± 0.019	-0.012 ± 0.026	0.017 ± 0.055	502Z40025		
																						0.255 ± 0.161	-0.048 ± 0.077	-0.017 ± 0.070	-0.015 ± 0.046	02Z2014	
																							0.321 ± 0.038	0.093 ± 0.049	-0.071 ± 0.012	502Z40065	
																								0.181 ± 0.170	0.099 ± 0.110	-0.044 ± 0.171	02AC4201
																									0.256 ± 0.146	-0.008 ± 0.019	502Z40065
																									0.261 ± 0.148	-0.020 ± 0.098	02Y2003
																										0.273 ± 0.166	502Z40105
																										0.278 ± 0.256	02AC1024

Deep yellow: ful-sib family  
Light yellow: half-sib family

ful-sib family (0.5):  
GBS 0.377 – 0.141  
EC 0.394 – 0.195  
half-sib family (0.25):  
GBS 0.147 – 0.036  
EC 0.183 – 0.072

**EM**  
Mean relative difference: 0.775

**LD KNNi**  
Mean relative difference: 0.812



# GBS Summary & Next work

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- Coverage bias
- ~ 8% underestimation of herterozygous genotypes
- Relatively high proportion of genetic variances in non-coding regions
- The number of covered bases is less than predicted
- Obvious difference between GBS- and EC- G matrixes
  
- ✓ Develop predictive model and evaluate predictive ability
- ✓ Estimate the impact of error genotypes in Genomic prediction
- ✓ ... ..



# Acknowledgement



Forest Genetic Group in UPSC



*Boosting business with science*



**SKOGFORSK**



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**Thanks for your attention!**

