



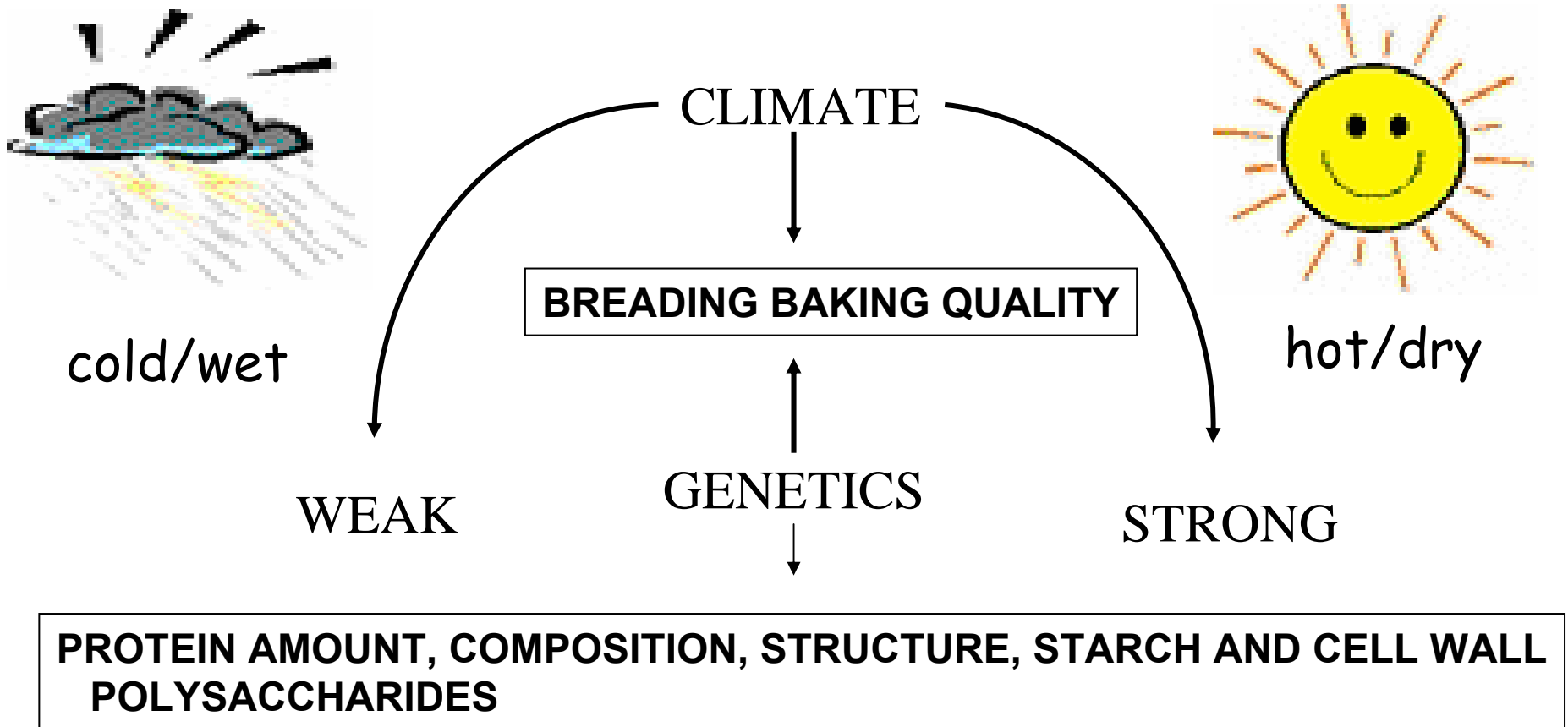
Transcriptome profiling of wheat genotypes differing in grain quality under different environments



Yongfang Wan, Rowan Mitchell, Michelle Leverington, Simon Griffiths, John Snape, Tim Wheeler, Mike Gooding, Rebecca Poole, Keith Edwards, Clare Mills, Peter Skeggs, Salvador Gezan, Sue Welham, Chrstina Shenton, Tong Zhu, Peter Shewry



THE BALANCE OF GLUTEN VISCOELASTICITY (“STRENGTH”) DETERMINES END USE QUALITY



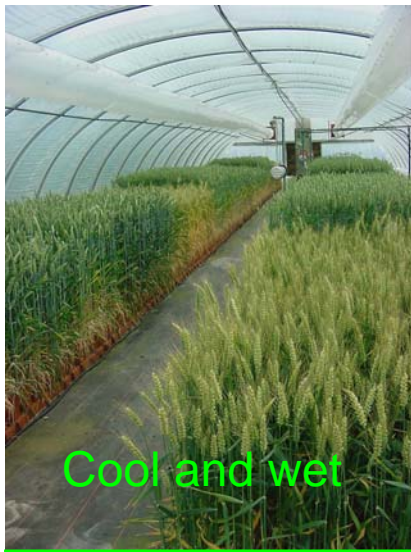
Overall Objective:

To identify alleles which confer stable high bread-making quality

- ▶ **Identification of novel transcripts where expression during grain development is consistently correlated to genetic variation in quality parameters**
- ▶ **Mapping of these transcripts to chromosomal locations and comparison with known QTLs**

Deliverables:

- 1. Molecular markers for selecting grain end-use qualities at an early stage in the breeding process**
- 2. Identification of candidate genes for further improvement**



Cool and wet

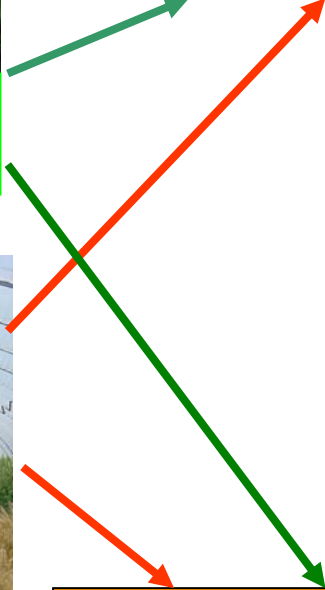
15-23°C, 100% field water capacity



Hot and dry

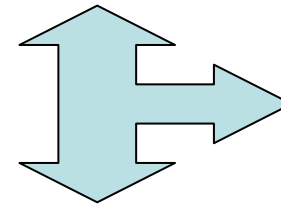
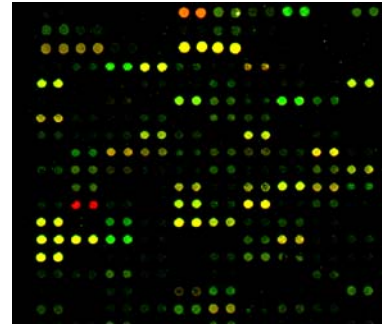
20-28°C, 44% field water capacity

Developing grain
14DAA and 23DAA



Mature grain

Transcriptome analysis



candidate genes



Functional analysis

Design

**7 DHLs from Spark-Rialto mapping population,
matched for glutenin composition, flowering time,
varying in bread-making quality**

X

**2 environments: cool&wet
hot&dry applied after 14daa**

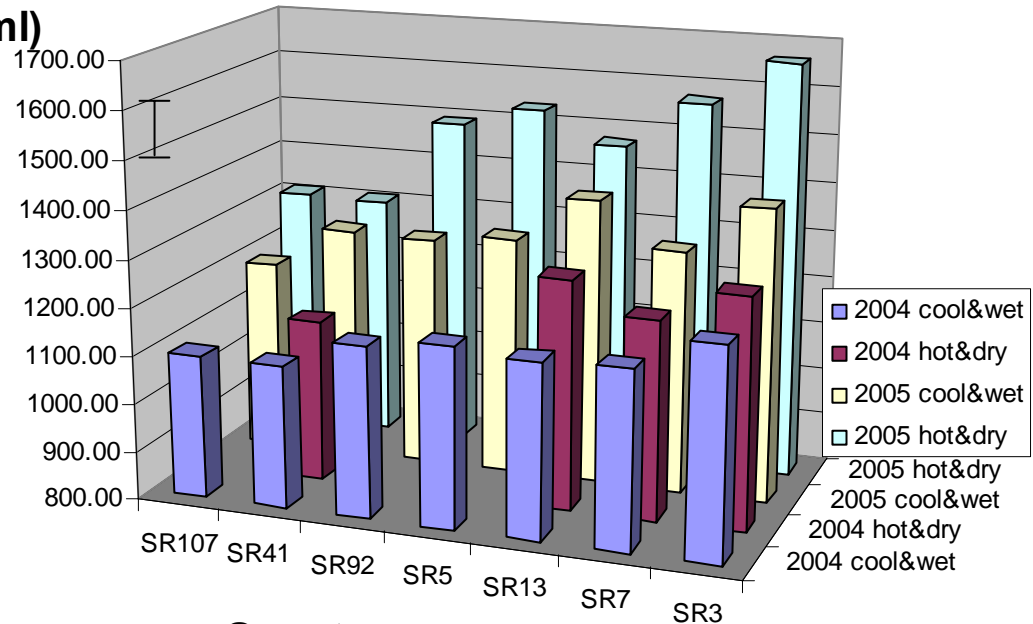
X

2 years (2004 and 2005)

**=28 transcriptome at 14daa, transcriptome at
23 daa, harvest and quality parameters.**

There are highly significant differences in quality traits between DHLs which are consistent across years

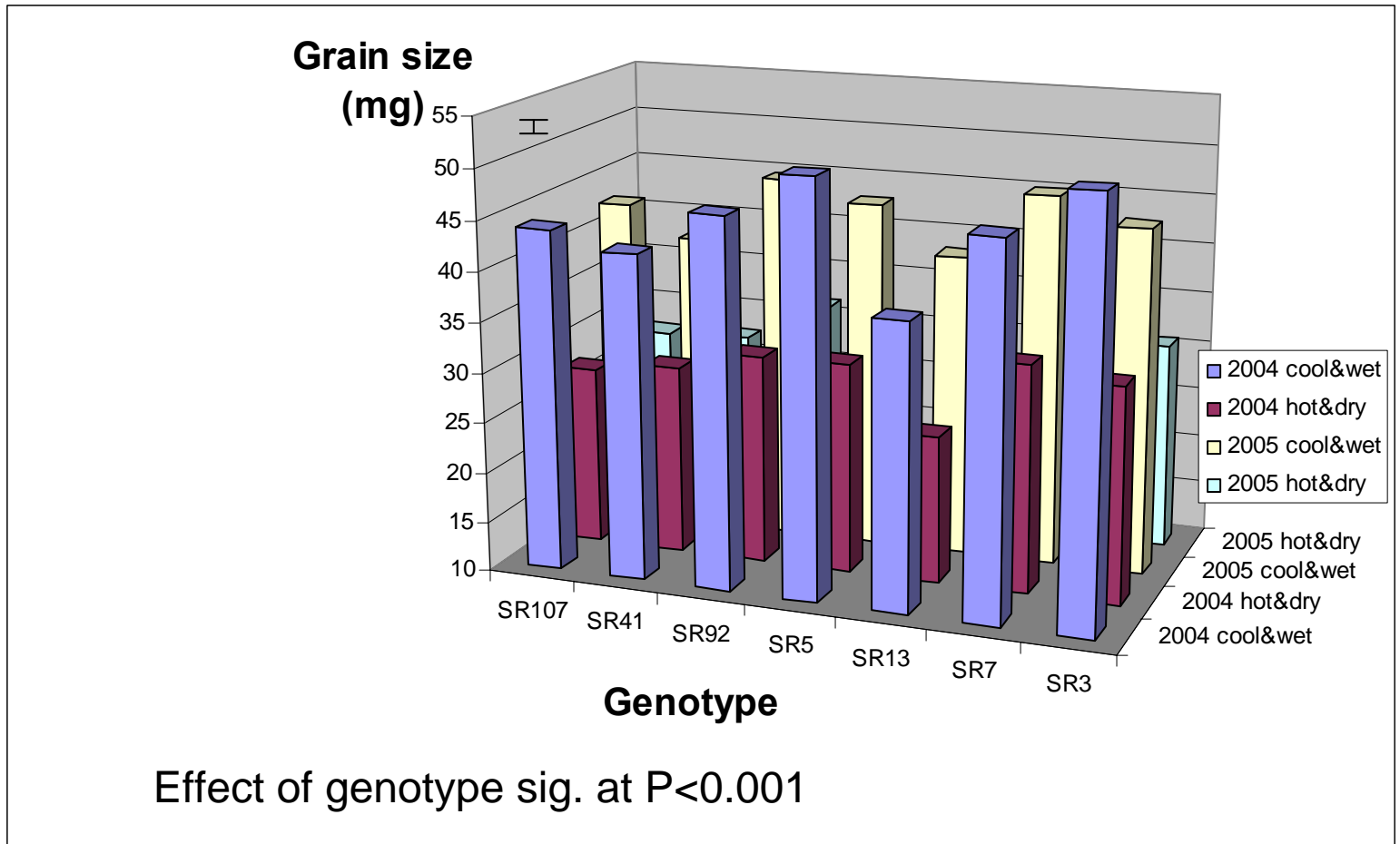
loaf volume
(ml)



Effect of genotype sig. at $P < 0.001$

Effect of genotype.year NS

There are highly significant differences in quality traits between DHLs



Transcriptome data are consistent with design

dev stage=14 daa

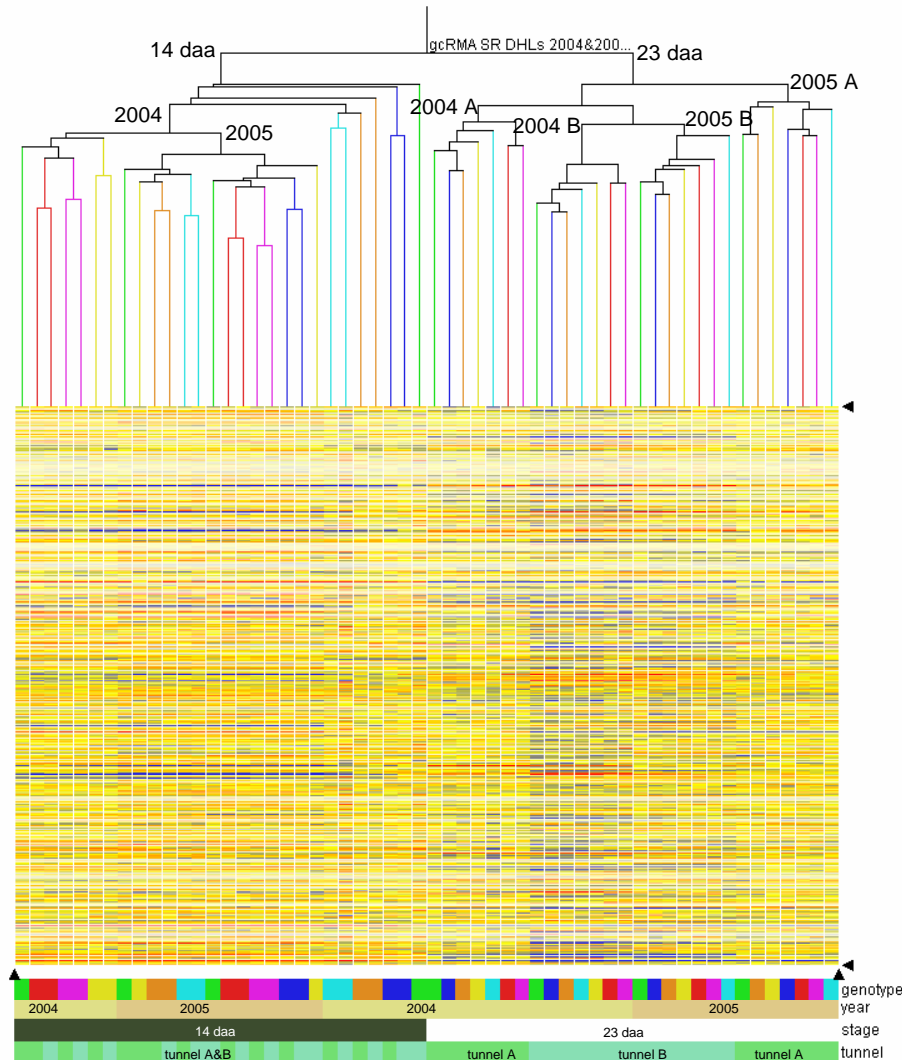
dev stage=23 daa

year

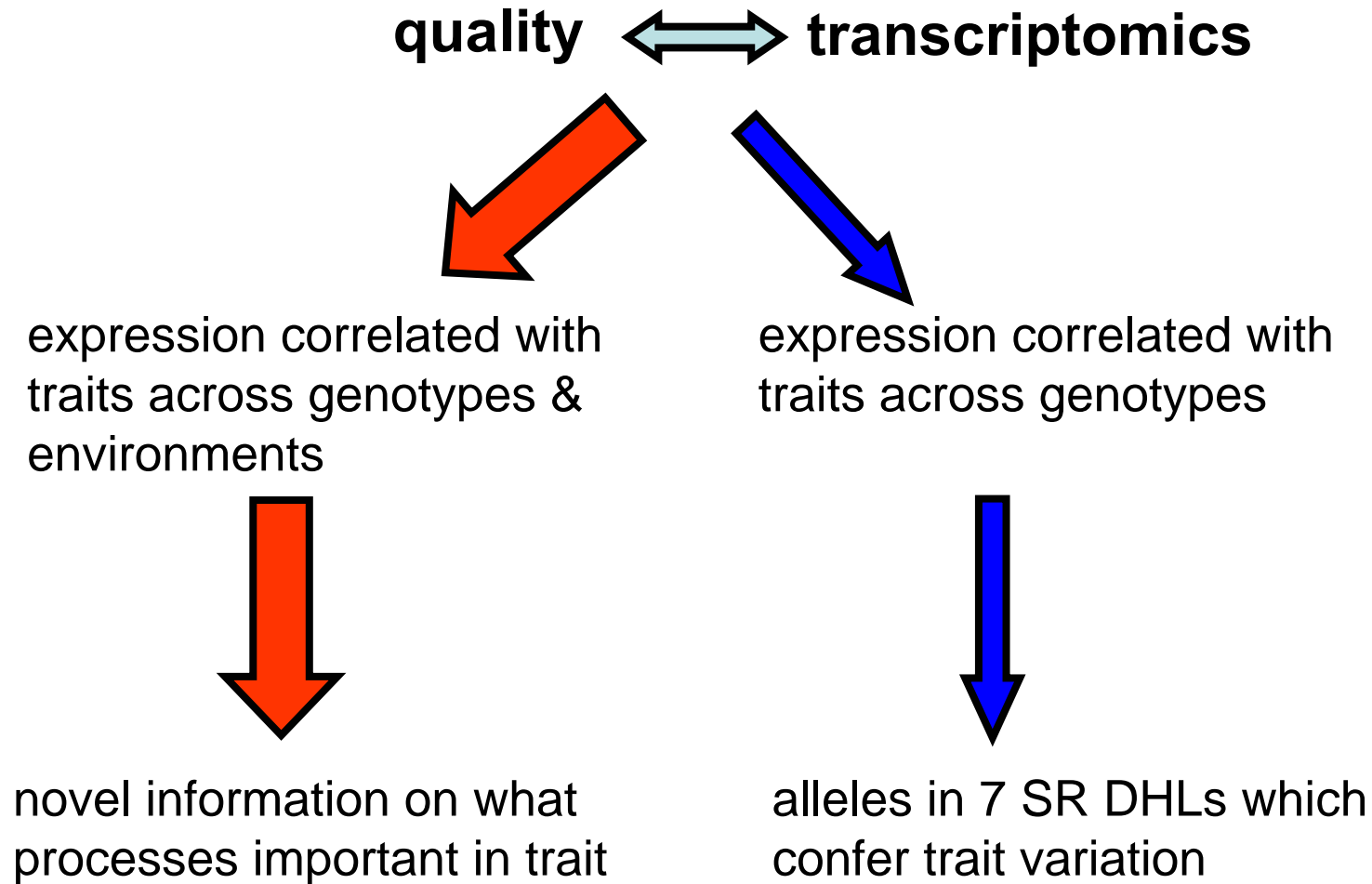
year

genotype

tunnel
(environment)



Integrating quality and transcriptomics data



Candidate gene selection

transcripts represented on Affy chip

55,000

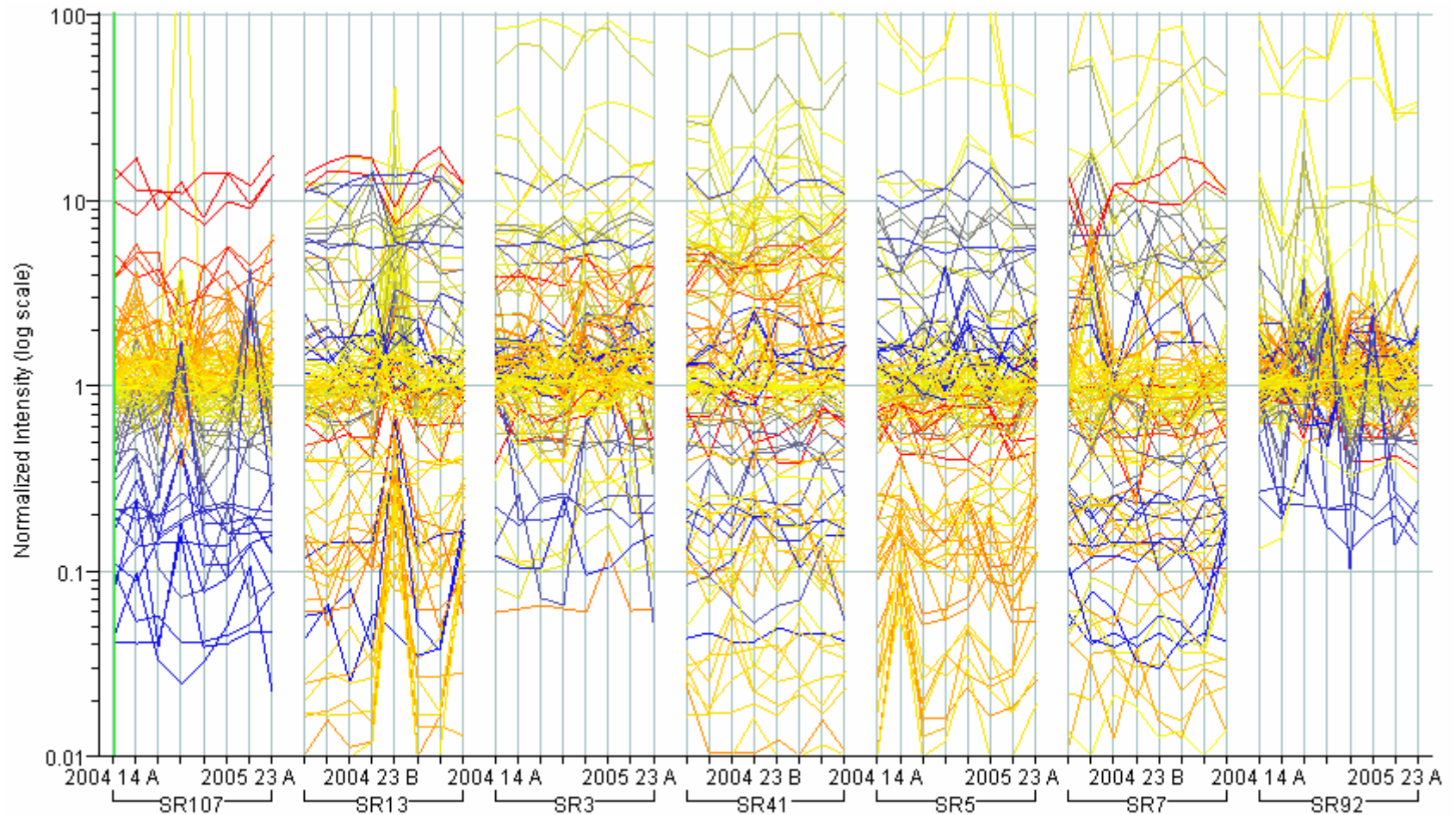


significantly different between
genotypes

1,905

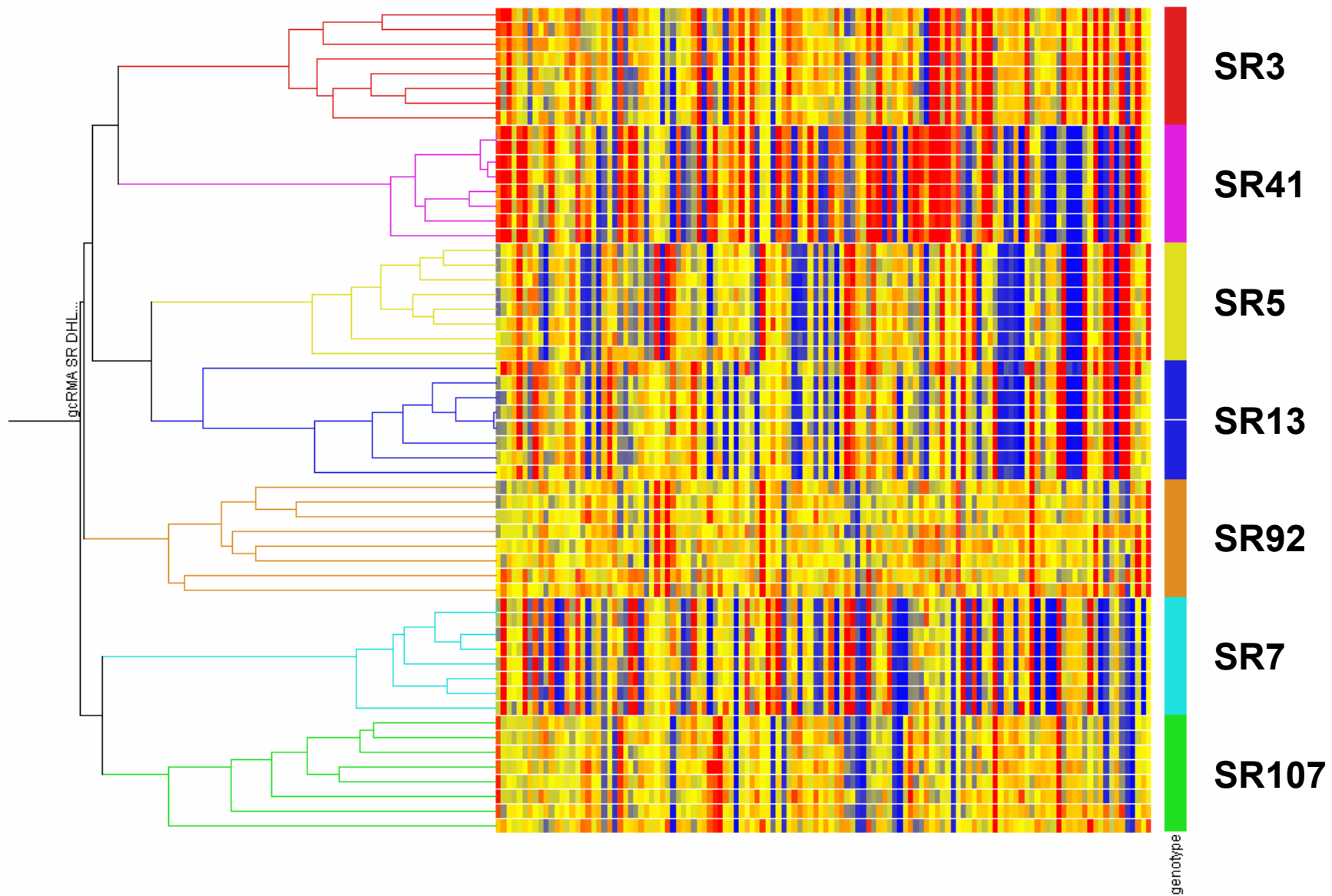
effect $P < 0.05$, MTC

Many genes are significantly different in expression between genotypes



Y-axis: gcRMA SR DHLs 2004&2005, Default Interpretation
Colored by: 2004 14 A SR107
Gene List: geno $P < 1.e-10$ (124)

Samples are consistent within genotypes



Candidate gene selection

transcripts represented on Affy chip

55,000



effect $P < 0.05$, MTC

significantly different between
genotypes

1,905

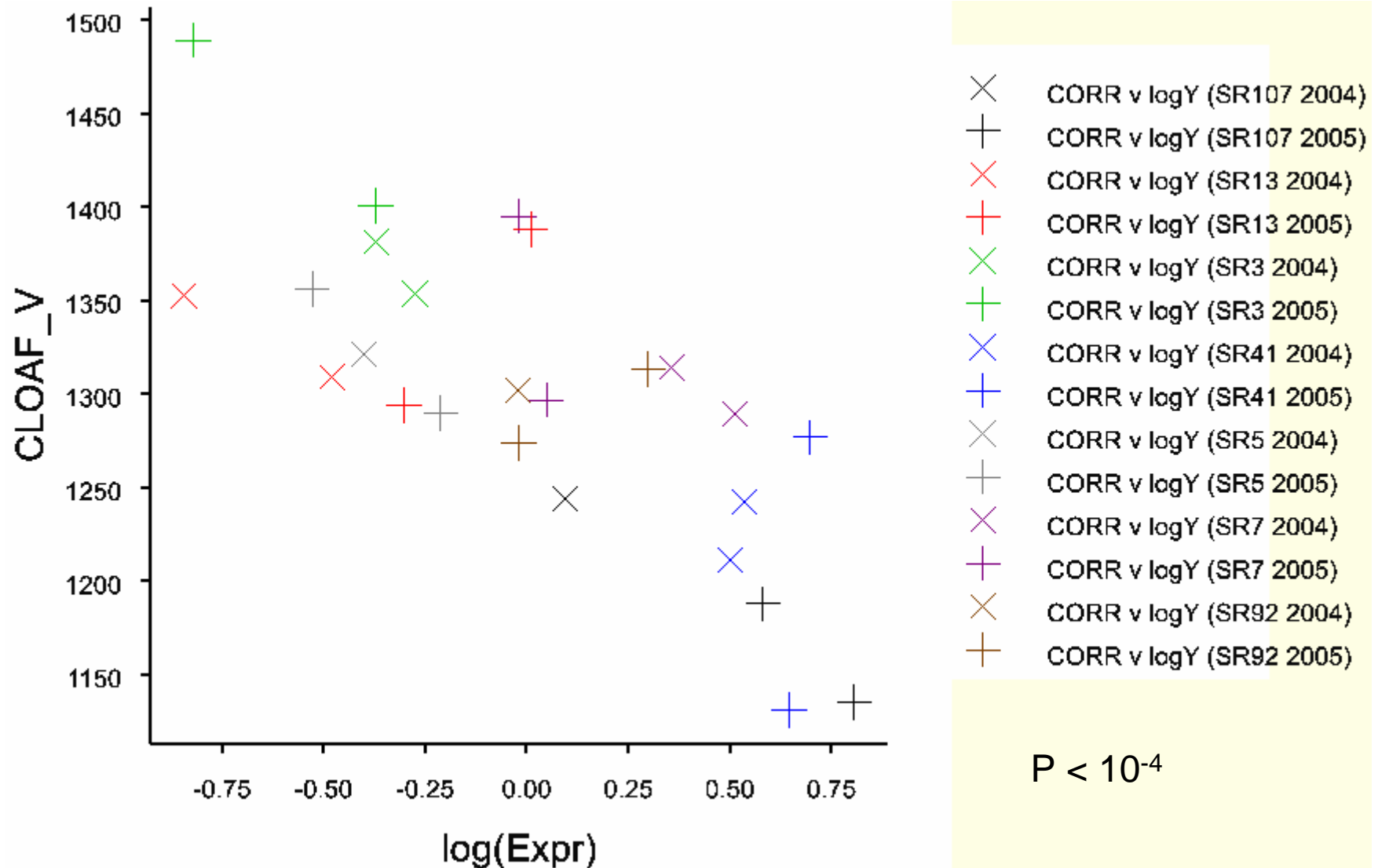


correlation $P < 0.01$

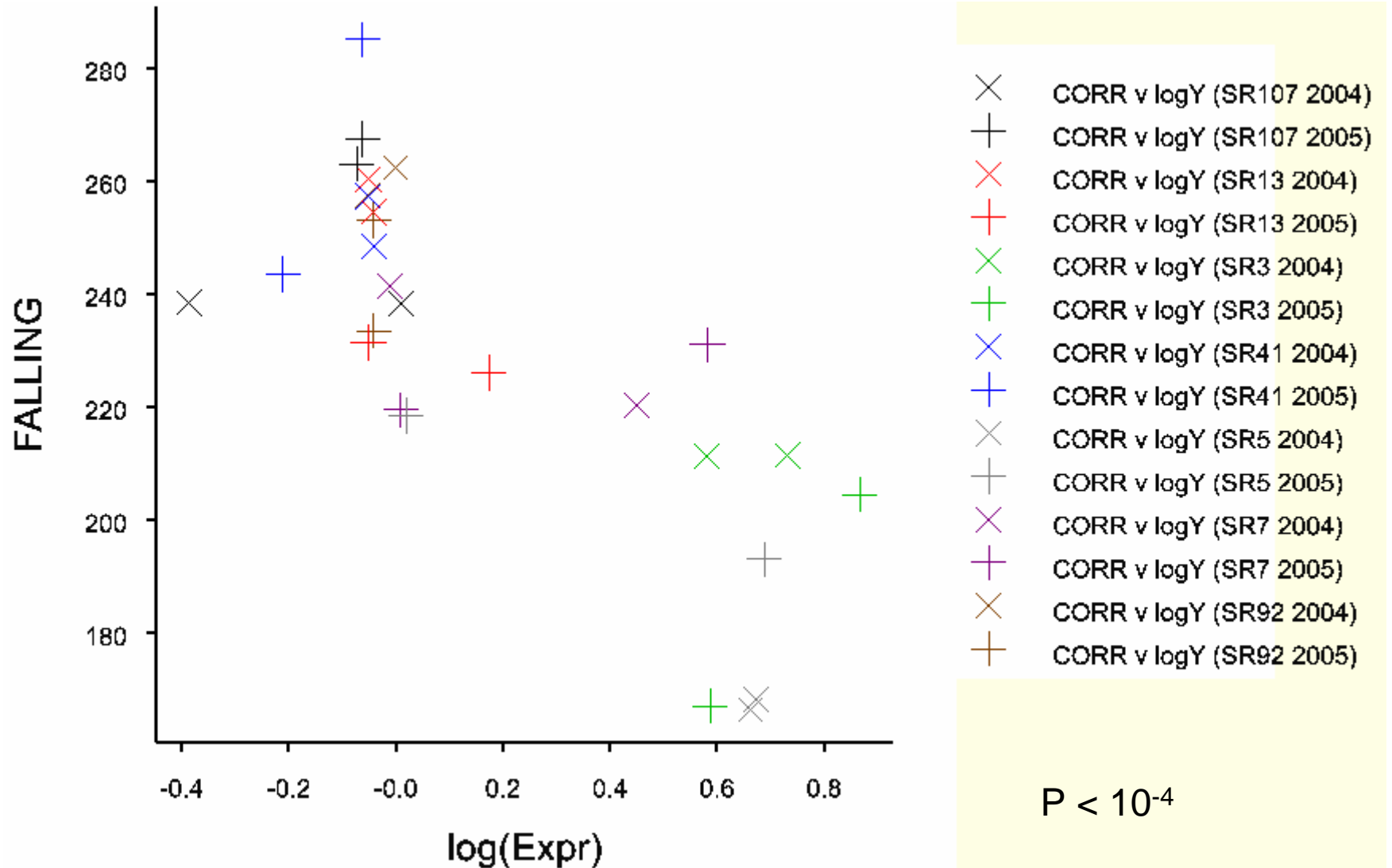
expression significantly
correlated with quality trait

468

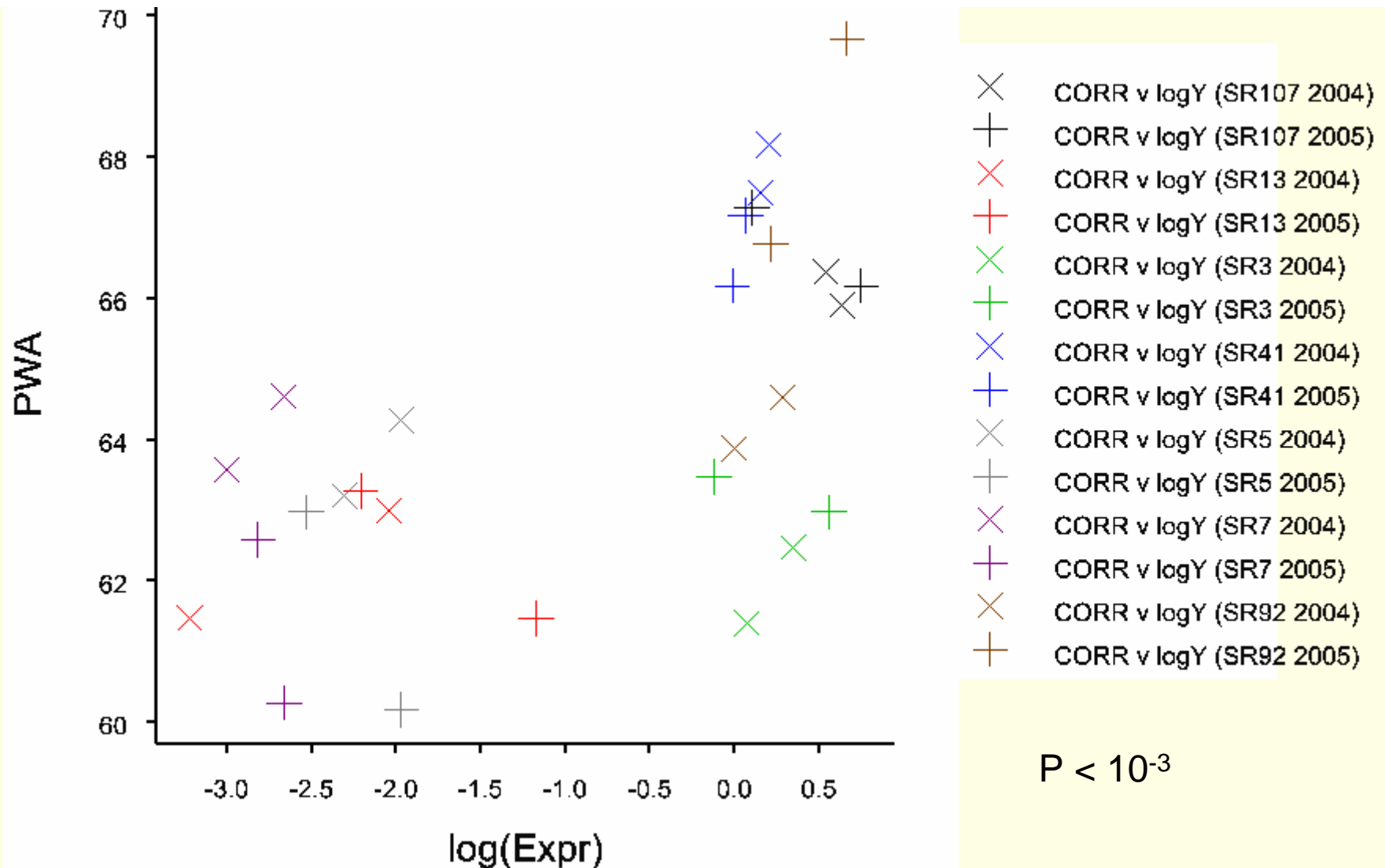
Negative correlation of expression (14 daa) of unknown function transcript with corrected loaf volume



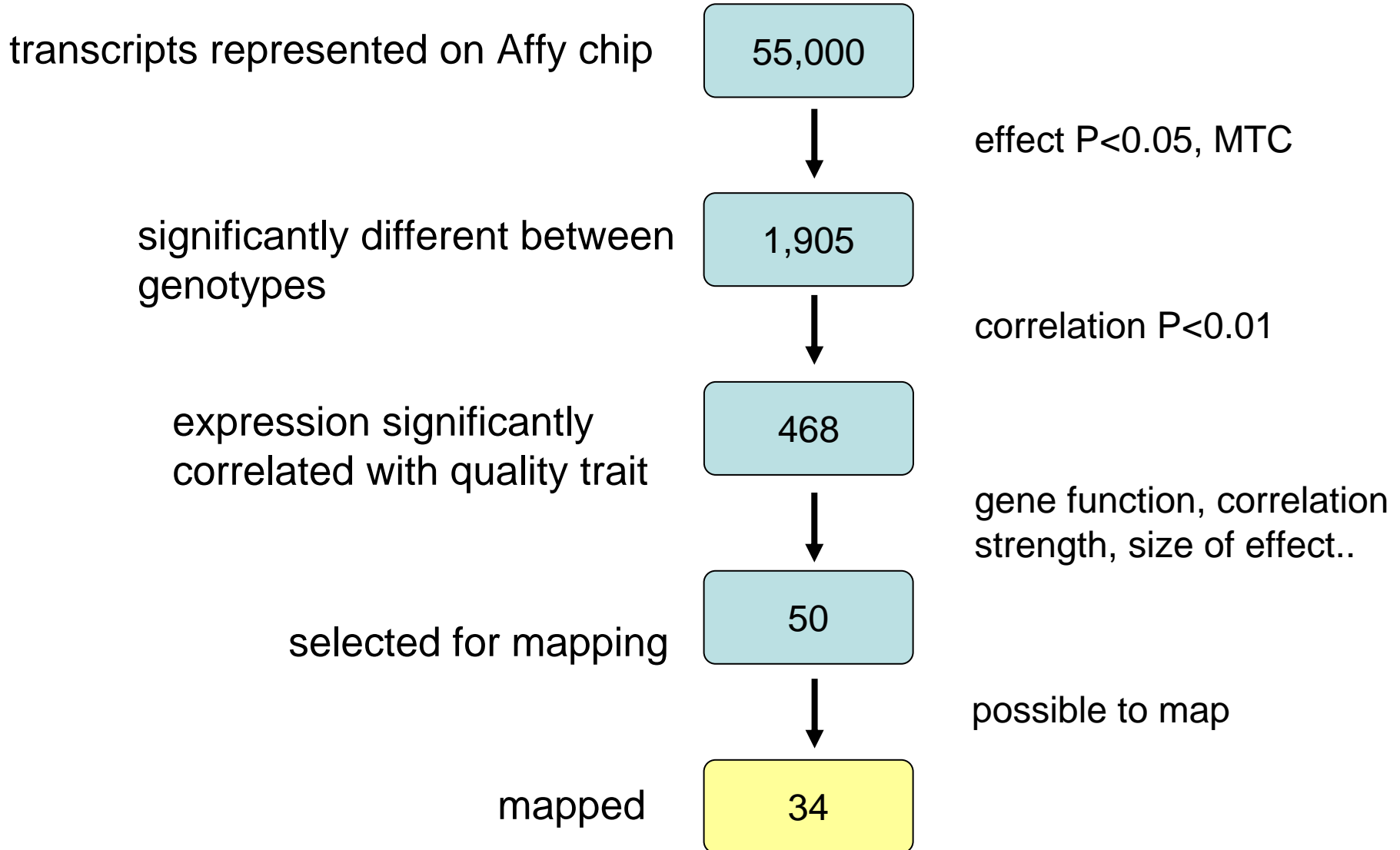
Negative correlation of expression (14 daa) of a MADS-family transcription factor with Hagberg falling number



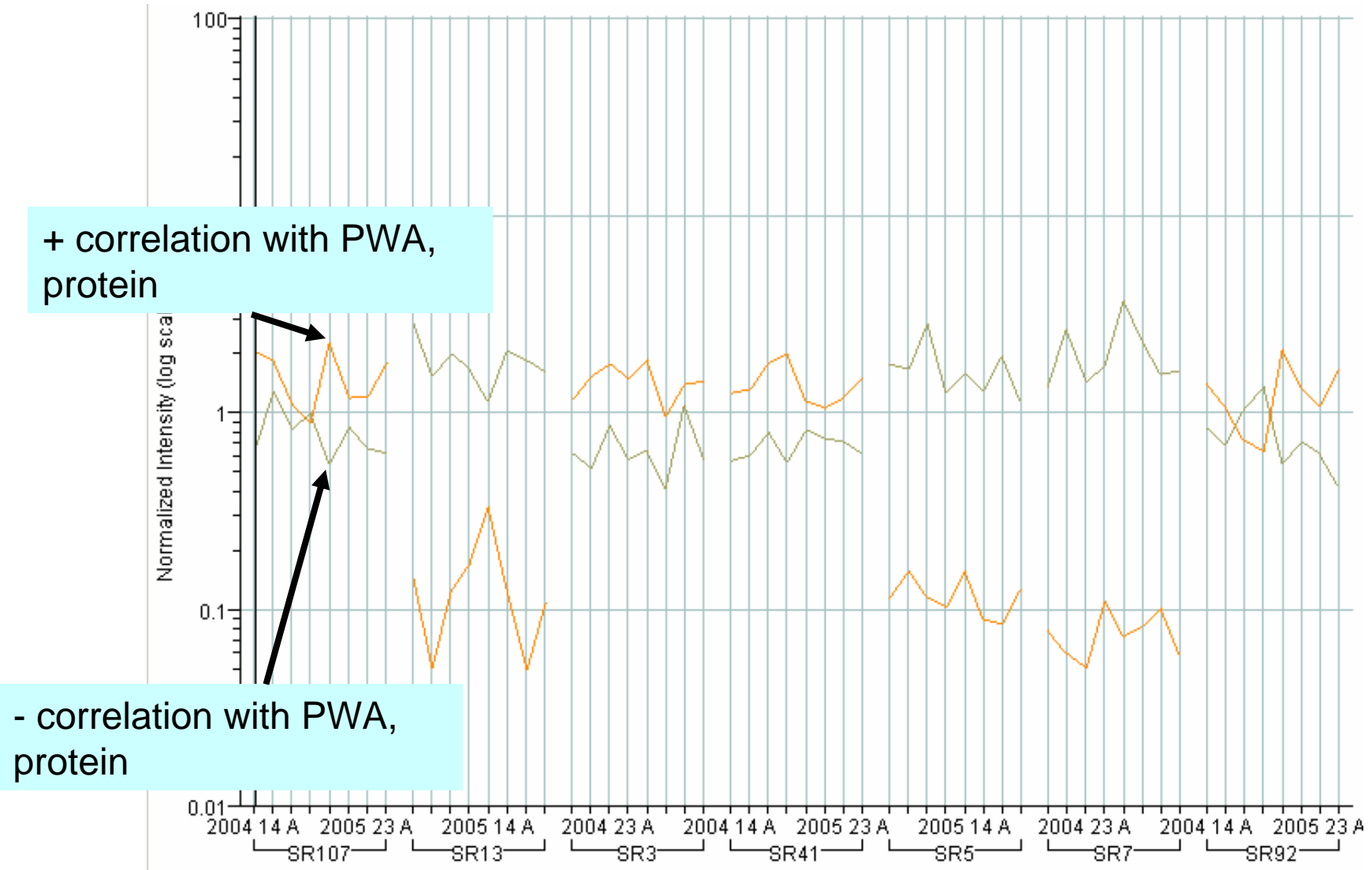
Correlation of a AP2-ERE BP-family TF (14 daa) with Water absorption in flour



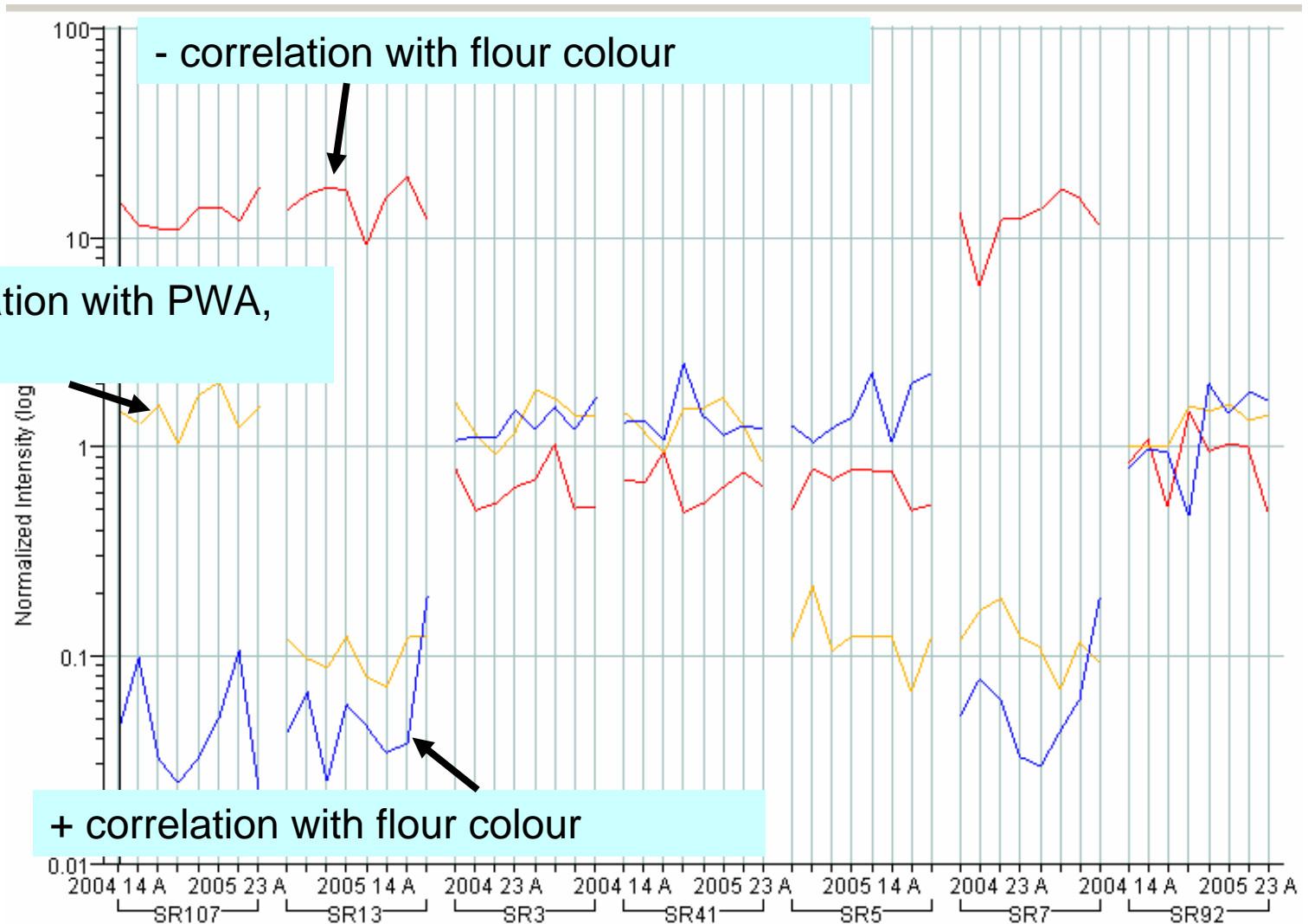
Candidate gene selection



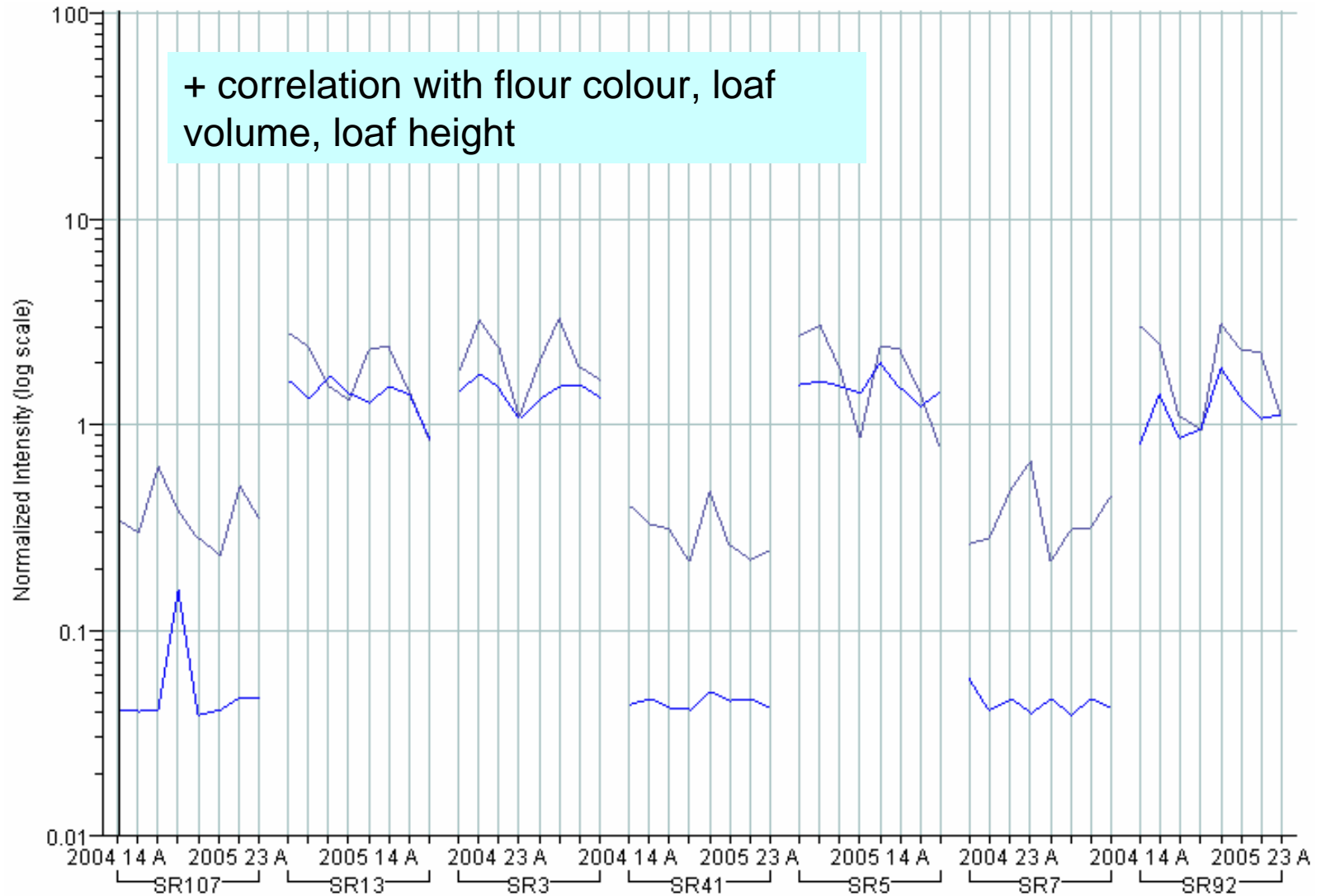
2 Transcripts which map to same SSR on 7B show opposite expression trends



2 out of 3 Transcripts which map to same SSR on 7B show opposite expression trends



2 transcripts which map to same SSR on 3D show same expression trend



Next steps

- Complete analysis
 - compare traits with field data
 - quality QTLs for whole population
 - quality QTLs of other populations
- Confirm allelic expression differences
- Final ranking of candidates for conferring beneficial traits

- Pursue promising candidates further ?



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