

Conclusions

- LD decay similar between breeds — low S2 for all chromosomes
- Magnitude / variability of LD differ between breeds — nonzero S3 for many chromosomes

Material and methods



source : <http://www.thecattlesite.com/breeds/dairy/115/fleckvieh/>

1) 985 Braunvieh & 1 999 Fleckvieh cows genotyped by Genomic Profiler HD BeadChip.

2) 76 932 SNPs after editing

3) Pairwise LD between linked SNPs expressed by R²

4) SNP preselection, removing:

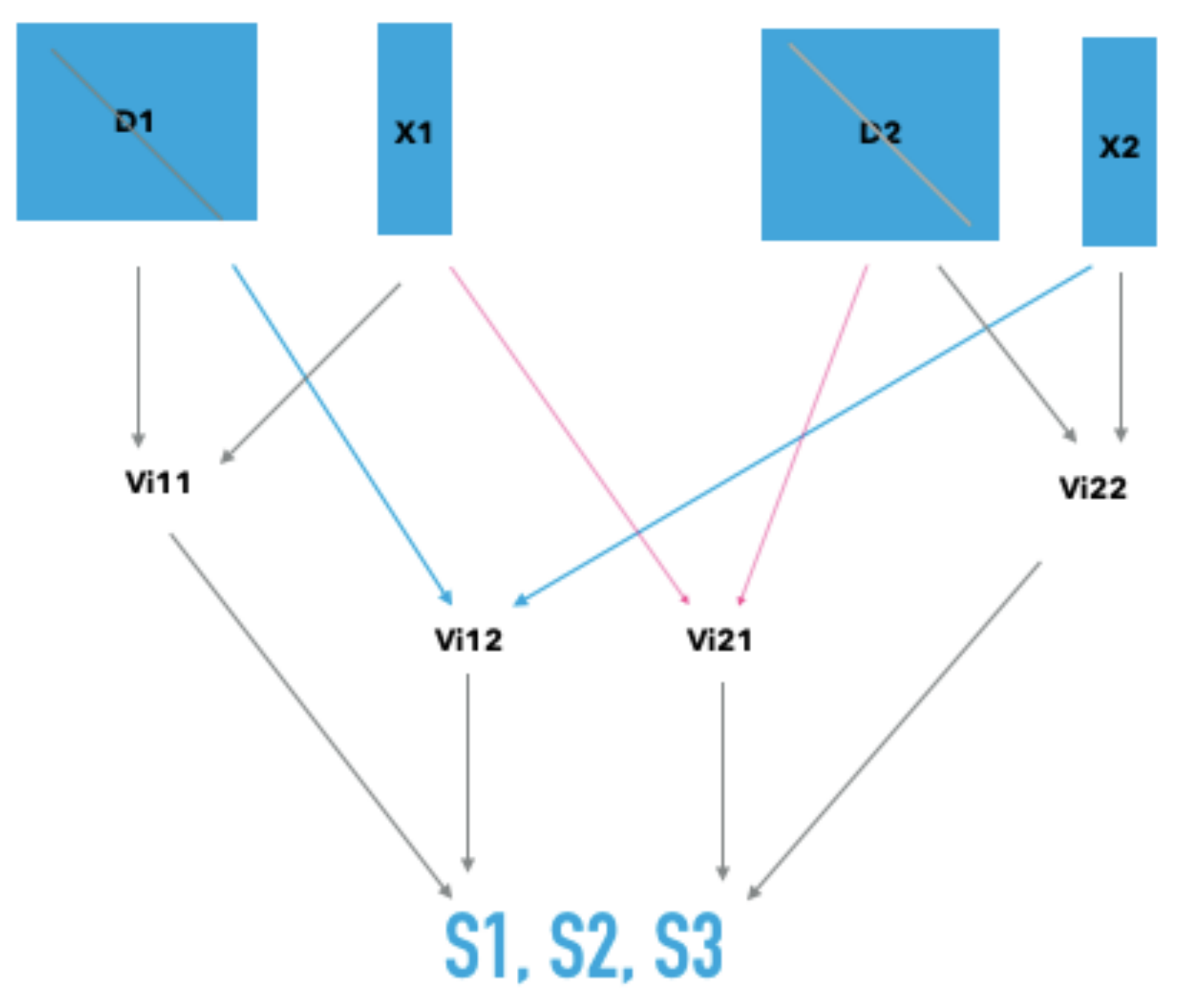
- SNPs with call rate < 95%
- SNPs with MAF < 5%.

$$S2 = \sum_{i=1}^n [(V_{i11} + V_{i22}) - (V_{i12} + V_{i21})]^2$$

$$S3 = \sum_{i=1}^n [(V_{i11} + V_{i22}) - (V_{i21} + V_{i12})]^2$$

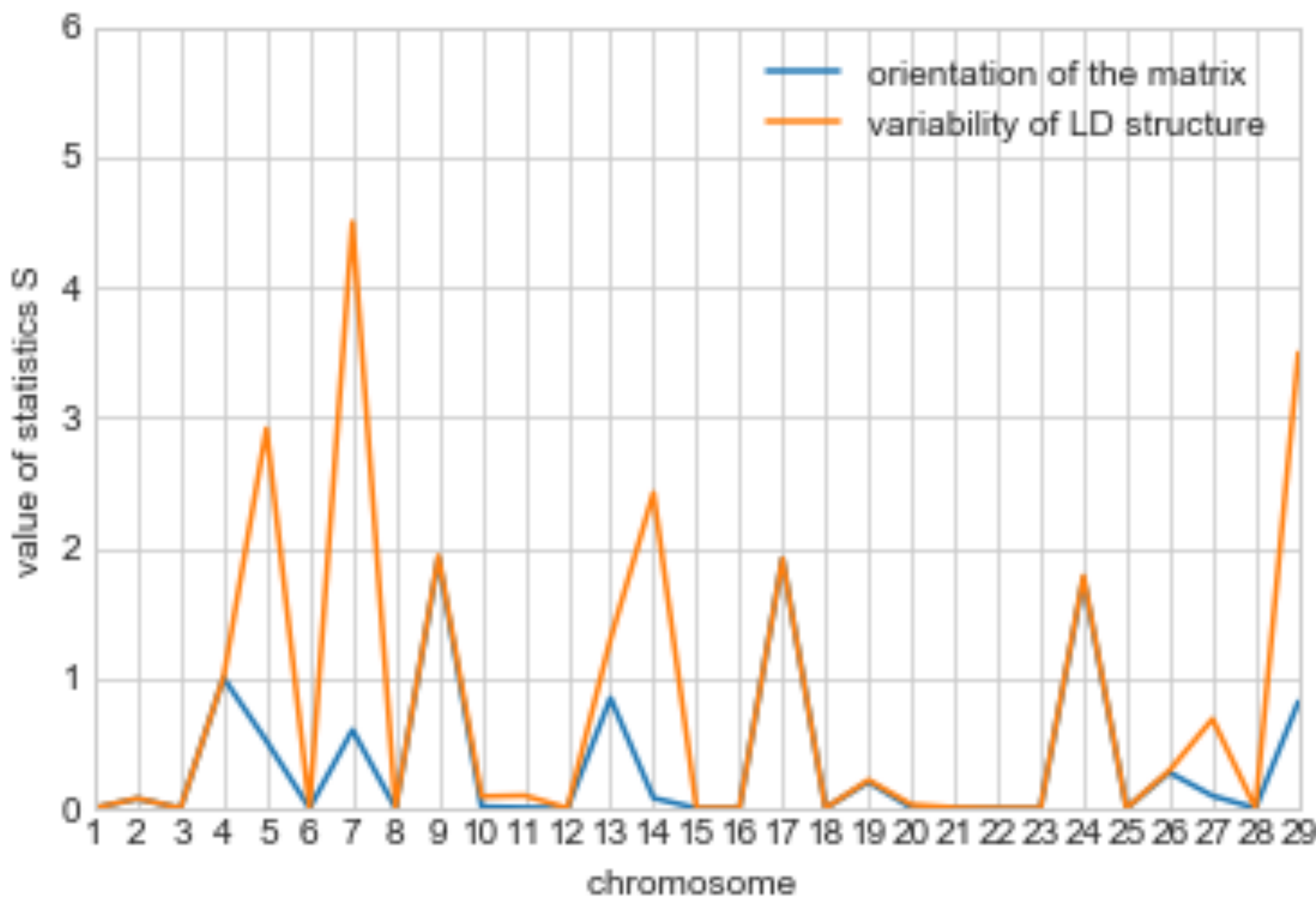
S2 — measures changes in orientation = express LD decay with distance
S3 — measures changes in variability = express LD variation

Comparing the LD matrices using S statistics



Results

Chromosome-wise LD comparison



chromosomes that show high values of statistics S	S2	S3
4	0,99	1,00
5	0,52	2,91
7	0,60	4,50
13	0,84	1,30
14	0,08	2,42
17	1,91	1,91
24	1,76	1,78
29	0,812	3,49

LD differences along chromosomes (sliding windows of 50 SNPs)

