Dataset: SNP\_ALLCAPs\_3528\_Cleaned.txt, map.txt

Downloaded from THT. 3,781 lines, 2,726 SNPs (2,482 SNPs on chromosome 1-7, 244 SNPs not mapped).

After removing 253 lines, 3,528 lines left. Remove other three lines: **MAJA**, no growth habit specified; **ORCA**, the only spring barley in OR; **MT090001**, the only 6-row barley in MT. Finally, 3,525 lines left.

Hierarchical structure:

Fst analysis

MAF > 0, missing data < 10%. 2,391 SNPs left. Populations: whole, spring, winter, spring2, spring6, winter6. Fst was calculated based on the method below:

<http://www.uwyo.edu/dbmcd/popecol/maylects/fst.html>

Figures:

1. Manhattan plot of Fst in different populations.
2. Boxplot of Fst different populations.
3. MAF-Fst plot (6 figures).

Tables:

1. Calculated Fst in different populations.
2. List of interested SNPs in different populations.