

Workflow: TapeStation – Genomic center

1. Random
2. samples preparation
3. TapeStation
4. Software

Random: preparation before start



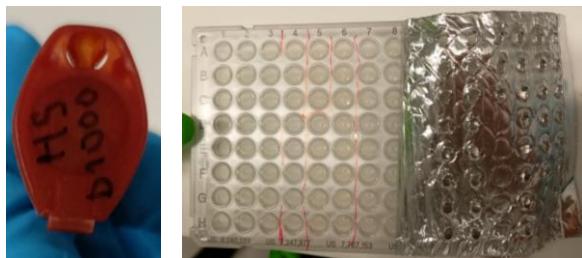
Quibit + Q. Eppendorf on the shelf

Workflow: sample preparation



High sensitivity Sample Buffer and High Sensitivity D1000 screenTape

Plate



vortex
for while



spin – don't forget balance



just random, I did (30s; 1000 rcf)

Strips



vortex on bench next to PC
sometimes already set to 1 min

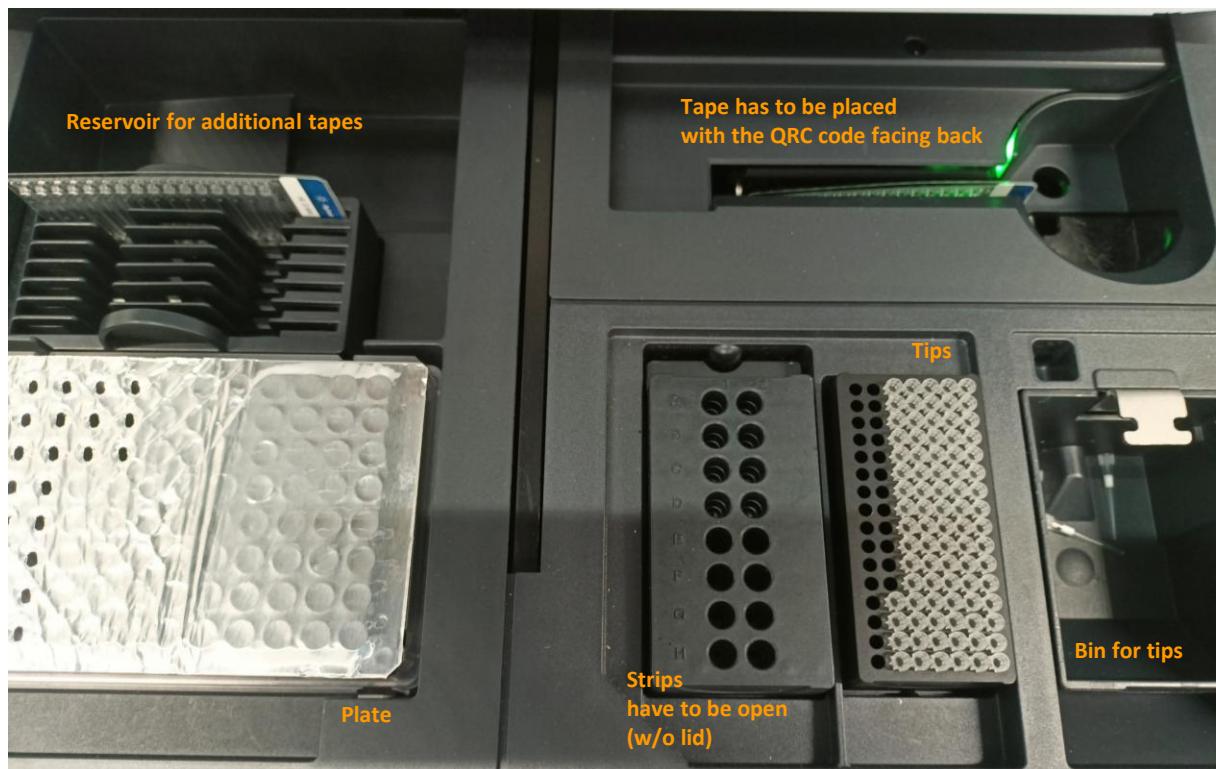
spin down
on the desk centrifuge

Workflow: TapeStation



High Sensitivity D1000 screenTape

- has to be placed with the QRC code facing back
- can be partially use (it is visible) – TapeStation will automatically read
- if needed more Tapes – place in reservoir – will be automatically replaced



Tips

- not necessary to use full box
just find some around with sufficient amount

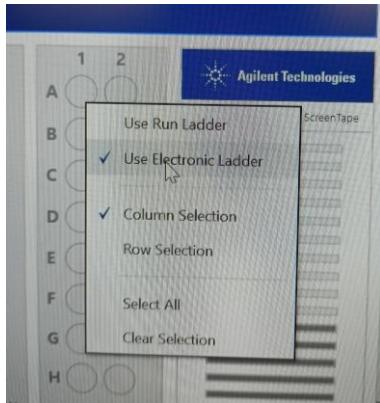
After measurement

- empty bin with tips and keep/trash tape



Workflow: Software

Warning before run!



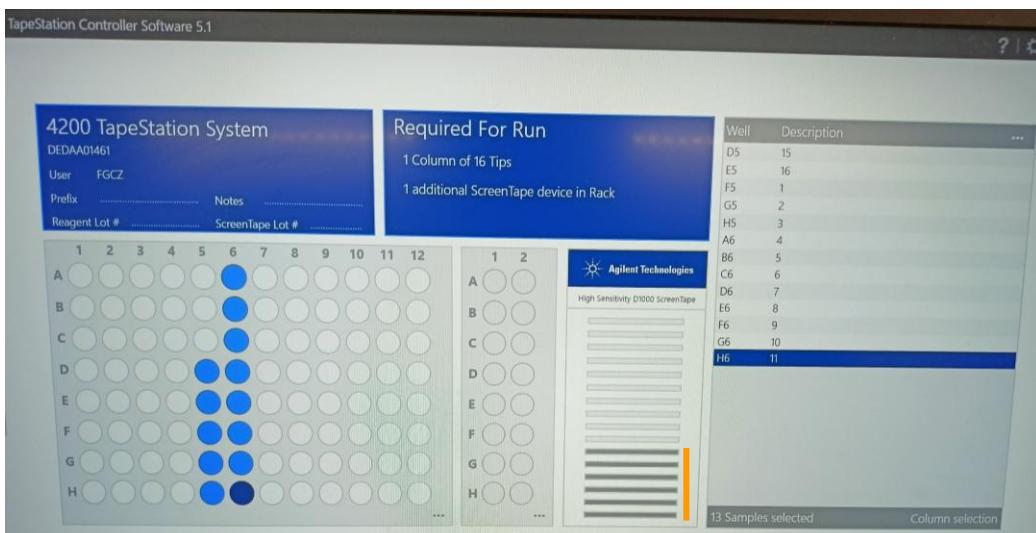
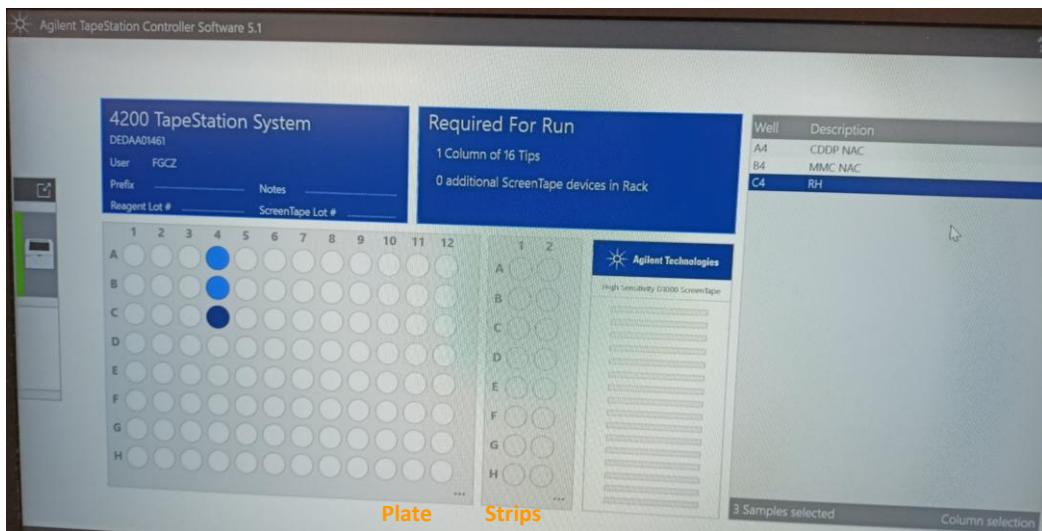
Position A1 is always for ladder

- right click A1
- select "Use Electronic Ladder!"
- the analysis software requires the Ladder

Select position of samples

and

name the samples (Well and Description)



These columns were already used

Workflow: Software

Genomic center UZH

- create your folder on the descope



Comparison (bar up; the last option)

- select samples (only click)
- save comparison file (upper bar, last icon)

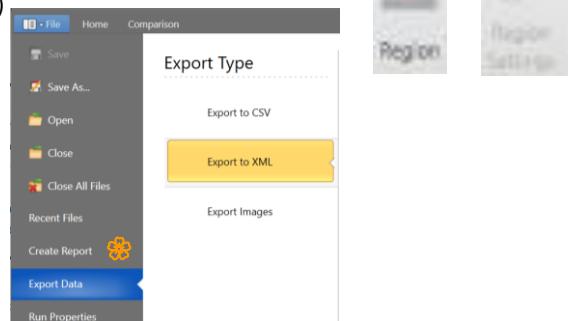
Home

- to see the runs
- select Regions
 - Click Region
 - Region Settings
 - Select region: define range (100 – 1000)
 - Note: for R-loop Cut & Tag should be 180 – 600 bp, up to 800 bp

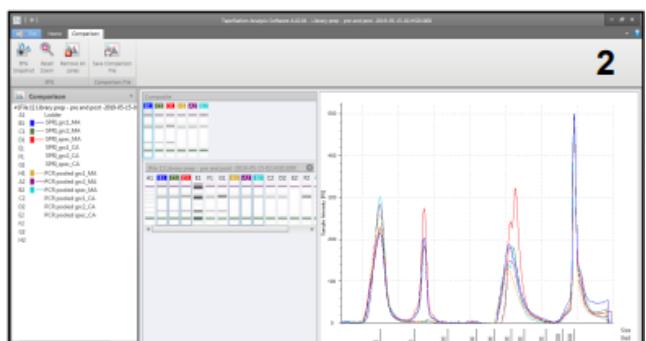
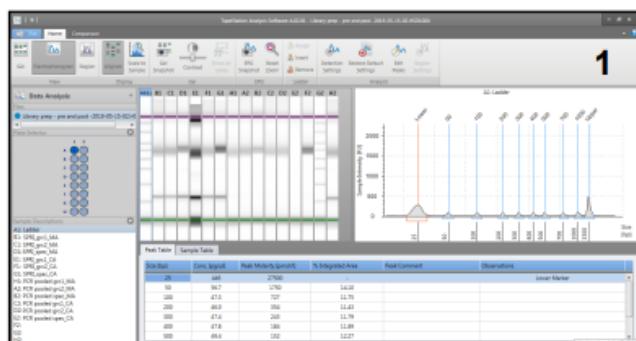


File

- Export data
 - CSV (excel)
 - Sample table: concentrations
 - Peak table: all peaks
 - Region table
- Create Report

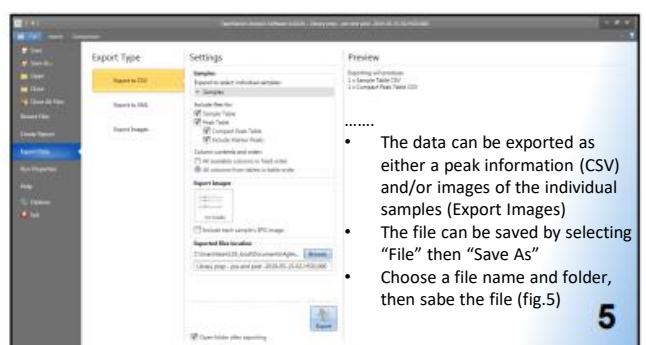
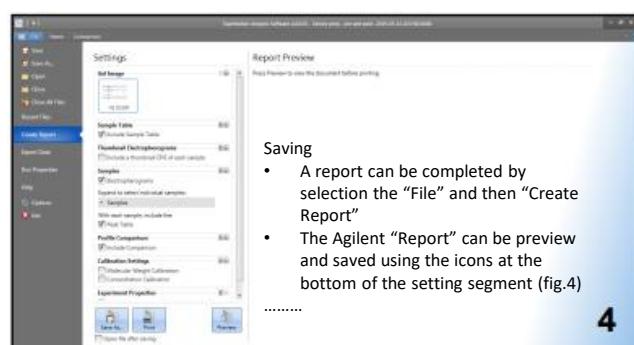
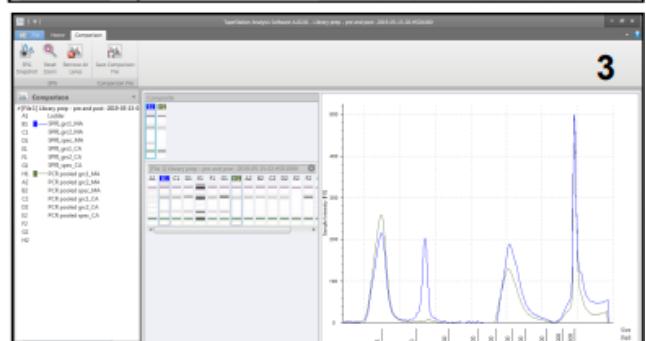


Source (link on the website, below): Agilent TapeStation; https://www.malariaigen.net/wp-content/uploads/2023/10/GbS04_Agilent_TapeStation.pdf



Comparison software

- will open once the run is complete (fig.1)
- for comparison select the comparison tab (fig.2)
- specific samples can be compared by selecting and de-selecting sample within the comparison window (fig.2&3)
- save: by selecting “Save Comparison File”



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