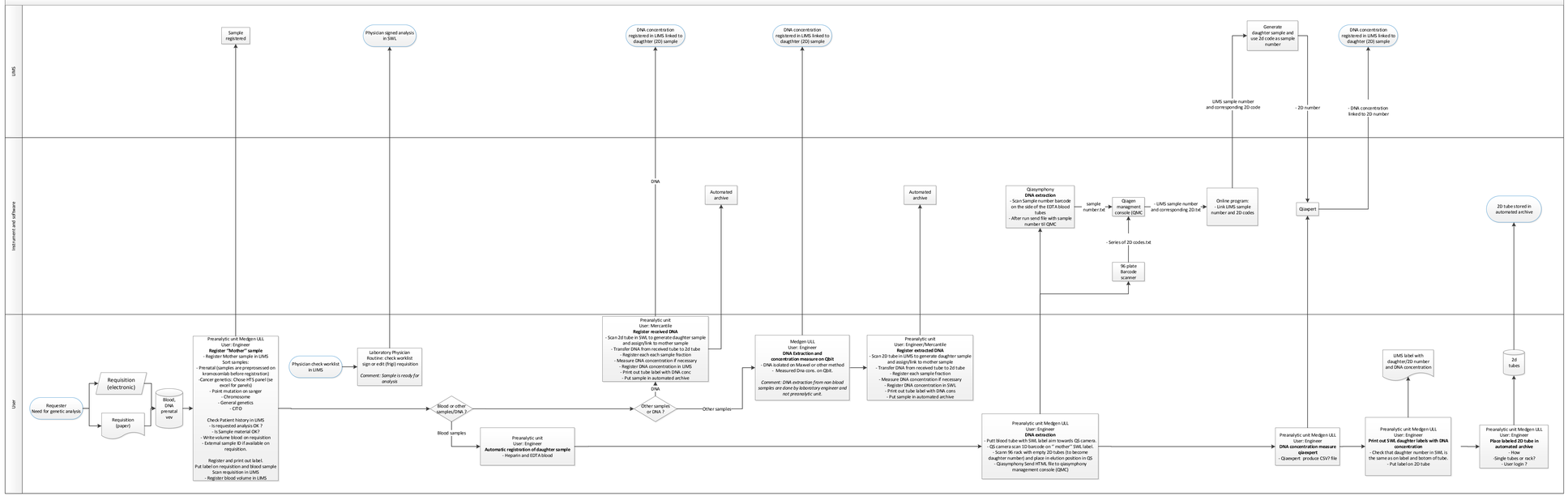
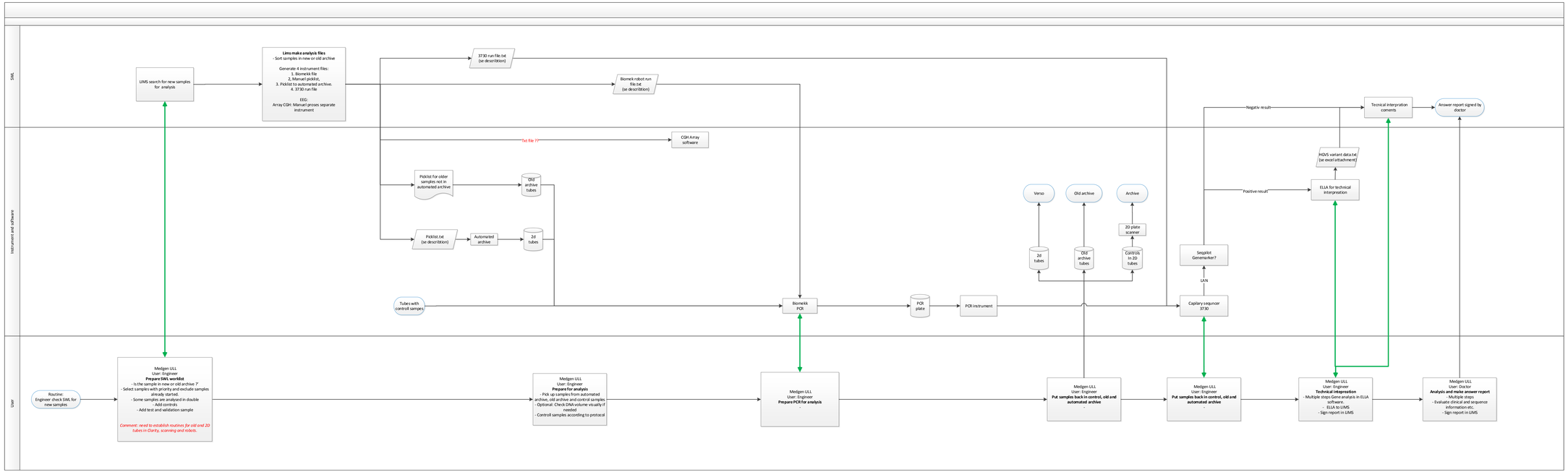
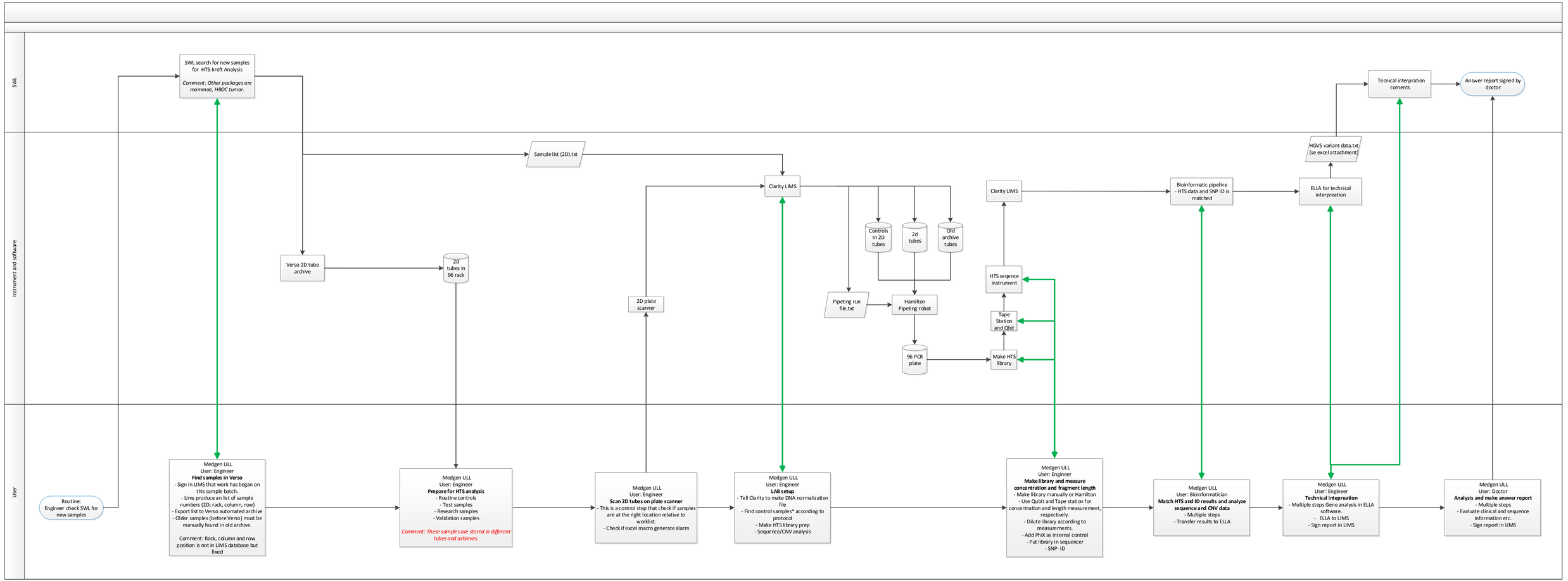
From sample received to answer report is signed and DNA is Archived




SWL
Instrument and software
User
LIMS search for new samples for analysis
Lims make analysis files
- Sort samples in new or old archive
Generate 4 instrument files:
1. Biomek file
2. Manuel picklist,
3. Picklist to automated archive.
4. 3730 run file
EEG:
Array CGH: Manuel proses separate instrument
3730 run file.txt
(se describition)
Biomek robot run file.txt
(se describition)
Txt file ??
CGH Array software
Picklist for older samples not in automated archive
Old archive tubes
Picklist.txt
(se describition)
Automated archive
2d tubes
Tubes with controll samples
Biomek PCR
PCR plate
PCR instrument
Verso
Old archive
Archive
2D plate scanner
2d tubes
Old archive tubes
Controls in 2D tubes
Seqpilot Genemarker?
LAN
Capilary sequncer 3730
Negativ result
Positive result
Tecnical interpration coments
Answer report signed by doctor
HGVS variant data.txt
(se excel attachment)
ELLA for technical interpreation
Routine:
Engineer check SWL for new samples
Medgen ULL
User: Engineer
Prepare SWL worklist
- Is the sample in new or old archive ?
- Select samples with priority and exclude samples already started.
- Some samples are analysed in double
- Add controls
- Add test and validation sample
Comment: need to establish routines for old and 2D tubes in Clarity, scanning and robots.
Medgen ULL
User: Engineer
Prepare for analysis
- Pick up samples from automated archive, old archive and control samples
- Optional: Check DNA volume visually if needed
- Controll samples according to protocol
Medgen ULL
User: Engineer
Prepare PCR for analysis
Medgen ULL
User: Engineer
Put samples back in control, old and automated archive
Medgen ULL
User: Engineer
Put samples back in control, old and automated archive
Medgen ULL
User: Engineer
Technical interpreation
- Multiple steps Gene analysis in ELLA software.
- ELLA to LIMS
- Sign report in LIMS
Medgen ULL
User: Doctor
Analysis and make answer report
- Multiple steps
- Evaluate clinical and sequence information etc.
- Sign report in LIMS


SWL
Instrument and software
User
SWL search for new samples for HTS-kreft Analysis
Comment: Other packages are mammae, HBOC tumor.
Sample list (2D).txt
Clarity LIMS
Controls In 2D tubes
2d tubes
Old archive tubes
Verso 2D tube archive
2d tubes in 96 rack
2D plate scanner
Pipeting run file.txt
Hamilton Pipeting robot
96 PCR plate
Make HTS library
Tape Station and Qbit
HTS seqence instrument
Clarity LIMS
Bioinformatic pipeline - HTS data and SNP ID is matched
ELLA for technical interpreation
HGVS variant data.txt (se excel attachment)
Tecnical interpration coments
Answer report signed by doctor
Routine: Engineer check SWL for new samples
Medgen ULL
User: Engineer
Find samples in Verso
- Sign in LIMS that work has began on this sample batch.
- Lims produce an list of sample numbers (2D; rack, column, row)
- Export list to Verso automated archive
- Older samples (before Verso) must be manually found in old archive.
Comment: Rack, column and row position is not in LIMS database but fixed
Medgen ULL
User: Engineer
Prepare for HTS analysis
- Routine controls
- Test samples
- Research samples
- Validation samples
Comment: These samples are stored in different tubes and acheves.
Medgen ULL
User: Engineer
Scan 2D tubes on plate scanner
- This is a control step that check if samples are at the right location relative to worklist.
- Check if excel macro generate alarm
Medgen ULL
User: Engineer
LAB setup
- Tell Clarity to make DNA normalization file
- Find control samples* according to protocol
- Make HTS library prep
- Sequence/CNV analysis
Medgen ULL
User: Engineer
Make library and measure concentration and fragment length
- Make library manually or Hamilton
- Use Qubit and Tape station for concentration and length measurement, respectively.
- Dilute library according to measurements.
- Add PhiX as internal control
- Put library in sequencer
- SNP- ID
Medgen ULL
User: Bioinformatician
Match HTS and ID results and analyze sequence and CNV data
- Multiple steps
- Transfer results to ELLA
Medgen ULL
User: Engineer
Technical intepreation
- Multiple steps Gene analysis in ELLA software.
- ELLA to LIMS
- Sign report in LIMS
Medgen ULL
User: Doctor
Analysis and make answer report
- Multiple steps
- Evaluate clinical and sequence information etc.
- Sign report in LIMS