***cHematology Lab Meeting.***

*8/2/2018 @ 9:00 am*

|  |  |
| --- | --- |
| *Present:* | ***Donna Fico, Parveen Bahel, Elizabeth D'Angelo, Natalie Drew, John Errico*** |

Announcement:

* If you get a request from new born ICU/ PDED for micro method tube, please process their request ASAP. Prepare micro method tube as per protocol (take out 200 ml of anticoagulant from blue top tube, label as micro method) and send it to the floor with instructions.

We are able to run any three routine coag tests (PT/PTT/FIB or DDI) on a micro method sample.

We can also run one special coag test on micro method sample like FVIII activity or anti-Xa etc along with one or two routine coag tests depending on how much plasma we have after spinning the sample.

 Just a reminder, icteric, lipemic and hemolyzed plasma should be run directly on 570 curves. DO NOT run that sample on a regular curve. Always run micro method sample in a coag cup.

If you are not sure about special coag order on micro method, please forward that question to Special coag tech or supervisor.

* On the XN if a “not measured” result is listed for the nRBCs please perform a WBC estimate and a manual differential. We recently had a patient which the WBC had to be corrected because the nRBC value was invalid and the nRBC were counted in the White count giving a false WBC result.
* Reminder that TEG Heparinase cups need to be stored properly to prevent stability issues. The box should be shut with the desiccant inside and the bag completely sealed.
* When working the XN, please check the integrity of special heme samples before putting them in the bucket. Check samples for clots and put clotted specimens in for redraw. It is better to get these in for redraw when received in the lab rather than waiting until the sample is run on a later date.
* BSINTS that come from Smilow 4 that are Y numbers are to be processed by the Main Lab. If CBC was run at Smilow 4, print the CBC Beaker report and make smears as usual.
* RL solutions should be completed for any problems with samples coming to the main lab that are not mapped for YSC and should have been processed else where. This is the only way to correct these issues.