20161011\_NBS\_Notes

Attendees: Joshua, Riki, Heather, Ashleigh, Brendan, Rhonda, Emily, Lura, Rebecca, Suran,

1. Michigan IG and LOINC Mapping (Heather Wood)

Working on results IG also has shared the orders IG in MI as well as the LOINC code mapping is in rough form – hopefully will be cleaner before in the results IG

See ppt

MiHIN is doing validation on the received messages

Going into MI PHL LIMS (Perkin Elmer) = BOL in the diagram

Have 3 main pilot hospitals – working on use agreements and legal stuff right now

ACK comes from data hub – including validation errors – some rejections and errors

Then ORL if they can do the test will send to the hospital

ORU that specimen as received from BOL to hospital

ACK for all ORUs

Have 36 messages for testing the LIMS – accuracy against the IGs and LOINC mappings

Demographic data includes Hep test date and Hep test result – that is part of min. required elements

When specimen arrives enter the Kitnumber –> fetches demographic info is in holding table after the OML has been received

have checks for error messages, messages without specimen etc

testing for 53 disorders, includes the analystes etc – all disorder groups need to have associated group codes

have also initial test and confirmation test – if normal, report, if abnormal, repeat test 2 more times and then will need a different result code locally

sharing spreadsheet worksheet example snippet

analyte – reportable Y/N – disorder group and result answer (LA answer code, local code, description, mailer text, determination, interpretation = this worked for all, except Hemoglobin, as they have first – fifth level of Hb detected, then interpretation (had a lot of patterns that were not available as drop down

comparing final lab result format

have situations that are positive and unsatisfactory – transfusion sample if positive will be reported as positive – if abnormal anywhere – overall = abnormal; if unsat due to specimen = overall = unsat, unless positive

reports are currently mailed or faxed – we do have other ways to contact, for positive for faster result distribution, if needed

For Hb testing – initial screen with HLPC, if flagged aberrant, or if %A too high, then get the pattern – so that only comes across, if that testing has been done

For SCID don’t report numbers at all due to the different approaches on property, very low for strong positive and low for borderline, so that is a non-numeric – similar for biotinidase

Use of the repeating OBRs without OBX – seems to be hard for a lot of systems

The current guide will not support that with the use of LRI

Great presentation – cool to see same questions we have in TX, hence we all need to work together on this

For order using the high level order code

The IG we are working on – in our use case we do not address the message that goes out when the physical specimen is received – consider adding to the IG – at least as an optional element – this is a CAP requirement on the hospital, so that way they can have this – also good for education about turn-around time

For some tests MI is reporting values, for others not – in the current IG we are reviewing the requirement to send the numeric values and currently as the – also reporting some qualitative value for the analyte

There are no determination flag in the messages at this point – will be added in the next message iteration.

Also looking at many more analytes using mass spec than what we are reporting

Will be hard to validate that sites can receive ALL the individual results – in TX we are migrating the qualitative reports into text and then just report the high level result groups

More questions at the NewSteps360 related to workflow

Hemoglobinopathies – have mapped out to first to fifth – not using the LOINCs that are structured that way, because many patterns are missing; no longer = now have separate questions for first, second most predominant – use those LOINCs – can share test message screenshots of that, to confirm, that is what is being used - happy to share all the test messages with this group

Guideline says something about cases of variants from certified patterns, they also want to report all the approved hemoglobins that can be identified – first LOINC in that panel for most predominant – does anyone do that? WA does, because in order to report unknown findings would be important to know what all was looked for – not the patterns, just all the Hb that can be IDed – one for each one – hard to have the receiver system represent that – is different from results for tests – in future could use the repeating OBX-5 to get all that information as a list type; or send as NTE following the result, that way always displayed with each result, as the list will not change with every test

Possibly set up a separate call for Hemoglobin handling?

For the order guide – are there specific elements you are getting push-back on required elements – example follow up provider information – have not heard back from hospitals, as this is early in the initiation phase; will be flexible with the pilots

We are not planning to send the HL7 to multiple places, so hospital will have to forward the HL7 message – currently mailing 2 copies, for hospital to forward – for positive results there are additional ways to contact Can share any feedback to help us

1. LOINC comparisons from merged documents (Riki) – review for next call – set up for next week
2. Virginia Use Case Review