**Supplementary Tables**

**Supplementary Table 1.  HBV, HCV, and HIV Assays Used by Facility A, Facility B, and PHRL.**

|  |  |  |  |
| --- | --- | --- | --- |
|  | Facility A | Facility B | PHRL |
| HBsAg HBsAbHBcAb | Pre 4/1/2014 – Abbott ArchitectPost 4/1/ 2014 – Advia Centaur XP | Immunochemiluminometric Siemens Centaur XP | Not Applicable |
| HCV Ab | Same as above | Not Applicable | Not Applicable |
| HBV viral load | Not Applicable | Not Applicable | ARUP Laboratories;PHRL in-house real time PCR |
| HCV viral load | Not Applicable | COBAS AmpliPrepCOBAS Taqman | Quest Diagnostics;ARUP Laboratories |
| HIV AbHIV viral load | BioRad GS HIV1/HIV2+ EIA | Immunochemiluminometric Siemens Centaur XPCOBAS AmpliPrepCOBAS Taqman | Not Applicable |

**Supplementary Table 2. Demographic Breakdown of Facility A and B as well as Total Cohort in Total as well as Newly Identified Infections.**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | **Facility A** | **Facility A Newly Identified Positives\*****(N=22)** | **Facility B** | **Facility B Newly Identified Positives\*** **(N=47)** | **Total Cohort** | **Total Cohort Newly Identified Positives\*****(N=68)** |
| **Unique Patients** | **718** | **21\*\*** | **1073** | **47** | **1791** | **67** |
| **Male (%): Female (%)** | **695 (97%):23 (3%)** | **20 (95%):1(5%)** | **1039 (97%):34 (3%)** | **46 (98%):1(2%)** | **1734 (97%): 57 (3%)** | **65 (97%):2(3%)** |
| **Median Age (Range)** | **66 (23-95)** | **70 (50-94)** | **66 (22-96)** | **64 (39-83)** | **66(22-96)** | **66 (39-94)** |

\*Newly identified positive result for one or more viral infections

\*\*One patient was positive for HBV and HCV

**Supplementary Table 3. Percent Nucleotide Difference between HCV Sequences in Genotype 1a Patients from Site A.**

|  |  |
| --- | --- |
|  | Median Percent Nucleotide Difference Between HCV Sequences |
| Pt. | B1 | B2 | B3 | B4 | B5 | B6\* | B7 | B8 | B9 | B10 | B15 | ENR1a | ENR2a |
| B1 | 3.3 |  |  |  |  |  |  |  |  |  |  |  |  |
| B2 | 14.3 | 1.7 |  |  |  |  |  |  |  |  |  |  |  |
| B3 | 14.6 | 14.0 | 2.7 |  |  |  |  |  |  |  |  |  |  |
| B4 | 20.6 | 19.3 | 19.3 | 2.0 |  |  |  |  |  |  |  |  |  |
| B5 | 13.5 | 15.3 | 15.3 | 22.6 | 0.9 |  |  |  |  |  |  |  |  |
| B6\* | 20.9 | 20.6 | 17.9 | 14.3 | 21.3 | 3.0 |  |  |  |  |  |  |  |
| B7 | 20.6 | 17.6 | 19.6 | 13.3 | 19.6 | 14.6 | 0.7 |  |  |  |  |  |  |
| B8 | 13.6 | 12.6 | 13.6 | 20.3 | 13.2 | 19.6 | 17.3 | 3.6 |  |  |  |  |  |
| B9 | 20.3 | 18.9 | 18.3 | 14.3 | 20.9 | 16.3 | 18.3 | 19.3 | 2.0 |  |  |  |  |
| B10 | 14.6 | 12.0 | 14.0 | 19.3 | 15.0 | 17.9 | 19.3 | 10.6 | 17.6 | 3.0 |  |  |  |
| B15 | 13.3 | 12.3 | 14.0 | 19.3 | 15.0 | 19.6 | 20.6 | 14.0 | 17.6 | 12.0 | 1.0 |  |  |
| ENR1a | 15.2 | 14.5 | 16.2 | 18.8 | 19.1 | 20.1 | 20.5 | 13.9 | 17.5 | 13.2 | 12.2 | 0.7 |  |
| ENR2 a | 15.5 | 13.2 | 14.9 | 17.2 | 14.9 | 19.1 | 18.2 | 13.2 | 17.5 | 12.2 | 13.2 | 12.8 | 2.0 |

Values represent the median percent nucleotide difference between pairwise comparisons of HCV single genome sequences from each patient (mean = 20 sequences per patient, range 10-24 sequences). Strains with greater than 5% nucleotide difference were considered unrelated [33](#_ENREF_33).

\*Newly found to be infected patient

aENR = epidemiologically non-related patient

**Supplementary Table 4. Percent Nucleotide Difference between HCV Sequences in Genotype 1b Patients from Site A.**

|  |  |
| --- | --- |
|  | Median Percent Nucleotide Difference Between HCV Sequences |
| Pt. | B11 | B12\* | B13 | B14 | B16 | B17 | B18 | B19 | ENR3a | ENR4a |
| B11 | 3.7 |  |  |  |  |  |  |  |  |  |
| B12\* | 14.0 | 1.0 |  |  |  |  |  |  |  |  |
| B13 | 16.6 | 16.6 | 1.0 |  |  |  |  |  |  |  |
| B14 | 14.6 | 17.3 | 14.0 | 0.7 |  |  |  |  |  |  |
| B16 | 13.8 | 15.8 | 13.8 | 13.5 | 3.9 |  |  |  |  |  |
| B17 | 14.0 | 14.6 | 14.6 | 15.9 | 17.1 | 1.3 |  |  |  |  |
| B18 | 15.9 | 16.4 | 14.0 | 13.0 | 14.1 | 15.9 | 0.3 |  |  |  |
| B19 | 13.3 | 14.6 | 12.6 | 14.0 | 12.8 | 15.3 | 14.6 | 0.7 |  |  |
| ENR3 a | 15.9 | 16.9 | 15.9 | 15.6 | 16.1 | 16.9 | 16.2 | 16.9 | 8.0 |  |
| ENR4 a | 18.7 | 16.8 | 16.8 | 16.1 | 13.2 | 18.7 | 16.8 | 15.2 | 18.4 | 0.6 |

Values represent the median percent nucleotide difference between pairwise comparisons of HCV single genome sequences from each patient (mean = 21 sequences per patient, range 15-24 sequences). Strains with greater than 5% nucleotide difference were considered unrelated[33](#_ENREF_33).

\*Newly found to be infected patient

aENR = epidemiologically non-related patient

**Supplementary Table 5:** **Percent Nucleotide Difference between HCV Sequences in Genotype 2b Patients from Site B.**

|  |  |
| --- | --- |
|  | Median Percent Nucleotide Difference Between HCV Sequences |
| Pt. | Pt. D | Pt. S | Pt. H | ENR 54 | ENR 19 |
| Pt. D | 1.0 |  |  |  |  |
| Pt. S | 20.3 | 2.7 |  |  |  |
| Pt. H\* | 21.0 | 24.0 | 0.3 |  |  |
| ENR 54 a | 20.7 | 20.3 | 23.3 | 0.3 |  |
| ENR 19 a | 23.3 | 24.0 | 21.3 | 25.3 | 1.3 |

Values represent the median percent nucleotide difference between pairwise comparisons of HCV single genome sequences from each patient. Strains with greater than 5% nucleotide difference were considered unrelated[33](#_ENREF_33)

\*Newly found to be infected patient

aENR = epidemiologically non-related patient

**Supplementary Figures**

**Supplementary Figure 1: Patient Flow Diagram for HBV, HCV, and HIV for Facility A**



**Supplementary Figure 2. Patient Flow Diagram for HBV, HCV, and HIV for Facility B**

