Molecular Serology Data Interpretation		
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Abbreviations

CPA - control's peak area
CV – coefficient of variation
CytoC – bovine cytochrome C standard peptide
FIS - fragment ion ratio score
RTCV - retention time concordance CV
SPA - sample's peak area
SPA-CPA – sample fold change
XIC - extracted ion chromatograms
MSDA(Molecular Serology Data Analysis)-Script

1 Result Calling Criteria

1.1 The Body Fluid Proteomics assay is a classification assay that determines whether a body fluid is present in or absent from a sample. It is not a quantitative assay and does not determine how much body fluid is present.

1.2 There are three parameters that are used to discriminate the quality of the data coming from the mass spectrometer in order to ascertain whether a sample (or item) is positive or negative for a specific body fluid: the intensities of ions of interest (peak areas), the ratio of the peak areas of fragment ions that come from the same parent ion, (fragment ion ratio scores), and the time at which targeted ions are detected after the beginning of a mass spectrometry run (retention time concordance).

1.2.1 **Peak Area** - Peak area is the area under the curve of extracted ion chromatograms (**XIC**) for fragment ions (transitions) of a peptide of interest. Peak area is log2 transformed.

1.2.2 **Fragment Ion Score** - The intensity (peak areas) of marker peptide fragments ions is compared to generate a fragment ion ratio score. Because the relative ratio of peak areas of each fragment ion (transition) for a given peptide marker are consistent regardless of the amount of marker peptide present in a sample, the ratio of a peptide's fragment ions (transitions) to each other is consistent and stable. How well the fragment ion ratios match their expected ratio pattern is assessed by calculating the normalized contrast angle of scaled fragment ion peak areas to those fragments from synthetically made standards. This score accounts for the number of fragment ions detected, e.g., if a peak area for one transition is 0 the score will suffer, and a positive ID is unlikely.

1.2.3 **Retention Time Concordance –** A marker peptide elutes from the HPLC column as a single molecule, which is fragmented in the mass spectrometer. Thus, the retention times recorded for each of the four fragment ions measured per peptide should be identical or extremely close. Larger than expected variation in fragment ion retention time is evidence of an interference signal not originating from the target peptide. Retention times concordance is measured by calculating the coefficient of variation (**CV**) of recorded retention times of fragment ions for a peptide. Retention time CV is expected to be close to

0. Acceptable ranges of retention time CVs for each target peptide were established from a set of technical and biological replicates of pure sample at optimal loading amount.

1.3 Taking all three parameters into account, a score is given to each peptide for each parameter. The scores granted to each peptide are compared to those in the tables below (see tables below).

1.3.1 To account for possible HPLC carryover from a previous sample, a blank run is performed prior to each sample run. A peptide fragment ion score (FIS) of 0.6 or greater in the blank run indicates the presence of carry-over. The low score threshold for carry-over detection in the blank runs allows for conservative detection of carry-over and more accurate identification of peaks attributable to carry-over verses true peptides present in the subsequent sample run.

- IF no carryover is detected, a sample peptide's Peak Area and Fragment Ion Score (FIS) values must be greater than the Peak Area and FIS values in table below, and Retention Time CV (RTCV) below the threshold values in the tables below for that peptide to pass (Detected).
- IF carryover is detected prior to a sample's run, the Sample's Peak Area (**SPA**) must be one or more times greater than the Control's Peak Area (**CPA**), in addition to the above criteria for Peak Area, FIS, and RTCV, for that peptide to pass (Detected). This fold change (**SPA-CPA**) is given in Column 6 in the tables below.

1.3.1.1 Cytochrome C Standard

1	2	3	4	5	6
Protein	Peptide	FIS	RTCV	Peak Area (log2)	SPA-CPA
Cyto C	EDLIAYLK	0.796	0.0042	17.52	1.00
	TGPNLHGLFGR	0.830	0.0091	12.77	1.00
	TGQAPGFSYTDANK	0.782	0.0106	14.83	1.00

1.3.1.2 Blood

1	2	3	4	5	6
Protein	Peptide	FIS	RTCV	Peak Area (log2)	SPA-CPA
B3AT	ADFLEQPVLGFVR	0.713	0.0016	15.06	3.00
	ASTPGAAAQIQEVK	0.869	0.0167	13.8	2.83
	IPPDSEATLVLVGR	0.734	0.0242	15.23	3.30
HBB	LLVVYPWTQR	0.67	0.0014	23.80	2.75
	SAVTALWGK	0.67	0.0023	23.40	3.00
	VNVDEVGGEALGR	0.688	0.0018	22.83	3.03
HBA	FLASVSTVLTSK	0.737	0.0018	17.00	2.74
	TYFPHFDLSHGSAQVK	0.814	0.0016	19.55	3.31
	VGAHAGEYGAEALER	0.688	0.0030	23.55	3.00

1.3.1.3 Saliva

1	2	3	4	5	6
Protein	Peptide	FIS	RTCV	Peak Area (log2)	SPA-CPA
AMY1	ALVFVDNHDNQR	0.708	0.0025	18.31	3.03
	IYVSDDGK	0.726	0.0131	15.90	2.77
	LSGLLDLALGK	0.736	0.0013	14.04	1.62
CYTT	ALHFVISEYNK	0.819	0.0073	13.60	2.72
	ATEDEYYR	0.708	0.0040	13.15	3.06
	SQPNLDTCAFHEQPELQK	0.694	0.0094	15.71	2.78
HIS1	EFPFYGDYGSNYLYDN	0.734	0.0121	11.24	1.32
LEG1H	ESPGQLSDYR	0.754	0.0149	11.15	1.83

1.3.1.4 Semen

1	2	3	4	5	6
Protein	Peptide	FIS	RTCV	Peak Area (log2)	SPA-CPA
SEMG1	EQDLLSHEQK	0.649	0.0139	11.16	1.55
	HLGGSQQLLHNK	0.706	0.0061	10.64	1.54
	SQIQAPNPK	0.714	0.0041	14.22	3.00
KLK3	IVGGWECEK	0.731	0.0097	15.85	1.85
	LSEPAELTDAVK	0.702	0.0033	16.95	2.65
	SVILLGR	0.700	0.0023	16.32	2.78
SEMG2	GQLPSGSSQFPHGQK	0.621	0.0188	12.37	1.38
	GSISIQTEEK	0.736	0.003	14.78	2.72
	LWVHGLSK	0.702	0.0028	15.44	1.00

1.3.2 At least one of three Cytochrome C Standard peptides must be detected (pass) in order for sample to be considered.

1.3.2.1 If no cytochrome C standard peptides are detected, sample failed to inject or a system error occurred, and sample must be re-injected.

1.3.2.2 Cytochrome C standard peptide must be detected before looking at other body fluid detection.

1.3.3 Detection (passing) of ALL 9 blood target peptides from ALL 3 blood protein markers are required for a sample to be **DETECTED** for blood. Detection of at least 7 out of 9 semen peptide markers, including ALL 3 target peptides for KLK3 and 2 of 3 peptides markers for each SEMG1 and SEMG2 are required for a sample to be **DETECTED** for semen. Detection of at least 7 of 8 saliva peptides markers, including ALL 6 AMY1 and CYTT peptides and EITHER 1 LEG1 OR 1 HIS1 peptide, are required for a sample to be **DETECTED** for saliva.

1.3.4 If three or less peptides of the target peptides as described above are detected (i.e., criteria stated above are not met for the specific peptide), that body fluid is **NOT DETECTED**.

1.3.4.1 If more than three peptides but LESS THAN a full marker peptide profile (as defined in 1.3.3) are detected, that sample or item is **INCONCLUSIVE** for that body fluid.

1.4 All samples within a batch will be re-injected if the Negative Control shows presence of four or more peptides.

2 Viewing Marker Peptide Spectrum on Skyline

2.1 Open the Skyline document for your batch. Each Skyline document has several files of the same name associated with it, to open the document double click on the file with type "Skyline Document".

2.2 Use the Replicate drop down menu in the top left to select the specific sample run you wish to view.

2.3 Use the targets pane on the left to select the peptide that you want to view. The peaks for all fragment ions for that peptide will be displayed.

2.4 Check that the peak area and retention times shown in the spectrum graph make sense compared to the calculated metrics in the Peptide Result pdf for this sample run.

2.5 Check that there is only one peak occurring in the instrument sampling window.

2.5.1 If additional peaks are present, in some rare cases Skyline may select a high intensity nuisance peak from the unknown sample matrix instead of the correct peptide peak. The peak selected by Skyline is indicated by a black triangle arrow at the apex of the peak. If you suspect an incorrect peak was picked, compare the additional peak to the peak of that peptide in the positive control for the run. The fragment ion pattern should be similar.

2.5.1.1 To select a different peak for integration and export, click on the retention time shown at the top of the peak. The black arrow indicator will move to the new peak.

2.5.1.2 Save the Skyline document, and re-run the R Analysis Script. The script will re-export the data from the edited Skyline document and calculate metrics from the newly selected peak.