The National Marine Biological Analytical Quality Control Scheme

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Particle Size Results – PS52

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PARTICLE SIZE EXERCISE DETAILS

Particle Size (PS) #52

Type/Contents/Origin/Pre-treatments: **~520g Muddy Sand (Poole) <0.5 mm pre-sieve**

Circulated: **16/09/2014**

Completion Date: **31/10/2014**

Number of Subscribing Laboratories: **15**

Number of Participating Laboratories: **13**

Number of Results Received: **13***

***multiple data entries per laboratory permitted**

Table 1. Summary of the methodology and sieve metadata information received from participating laboratories and replicate analysis laboratory for the fifty-second particle size distribution - PS52.

Benchmark	Method	Sieves used	Phi; sieve mesh		Total Weight (g)
			Weight (g) < 0.00; >1 mm	Weight (g) > 0.00; <1 mm	
REPLICATE 1	NMBAQC	☑	0.03	297.80	297.83
REPLICATE 2	NMBAQC	☑	0.03	301.80	301.83
REPLICATE 3	NMBAQC	☑	0.03	295.60	295.63
REPLICATE 4	NMBAQC	☑	0.03	299.60	299.63
REPLICATE 5	NMBAQC	☑	0.03	297.20	297.23
BM AVERAGE	NMBAQC	☑	0.03	298.40	298.43

Participant	Method	Sieves used	Phi; sieve mesh		Total Weight (g)
			Weight (g) < 0.00; >1 mm	Weight (g) > 0.00; <1 mm	
PSA_2101	NMBAQC	☑	0.08	284.04	284.12
PSA_2102	NMBAQC	☒	-	-	-
PSA_2103	NMBAQC	☑	0.00	321.15	321.15
PSA_2105	NMBAQC	☑	0.03	297.80	297.83
PSA_2106	NMBAQC	☒	-	-	-
PSA_2107	NMBAQC	☑	0.13	887.06	887.19
PSA_2108_A	NMBAQC[1]	☑	0.02	293.24	293.26
PSA_2108_B	NMBAQC[1]	☑	0.01	294.04	294.06
PSA_2109	NMBAQC[2]	☑	0.03	321.37	321.39
PSA_2110	NMBAQC	☒	-	-	-
PSA_2111	NMBAQC	☒	-	-	-
PSA_2112	NMBAQC	☒	-	-	-
PSA_2113	NMBAQC	☒	-	-	-
PSA_2114	NMBAQC	☑	0.00	269.82	269.82

Key to methods

NMBAQC - NMBAQC PSA SOP for supporting biological data

NMBAQC[1] - NMBAQC PSA SOP for supporting biological data - incorporating BS1377: 1990 Parts 1-2 (sieving) and BS13320: 2009 (laser diffraction)

NMBAQC[2] - NMBAQC PSA SOP for supporting biological data and internal SOP for pipette/sieve analysis

Table 2. Summary of the <1mm; >0.00 phi metadata received from participating laboratories and replicate analysis laboratory for the fifty-second particle size distribution - PS52.

		% Sand				% Silt				% Clay
Benchmark	Laser Used	Coarse 0 - 1 phi	Medium 1 - 2 phi	Fine 2 - 3 phi	Very Fine 3 - 4 phi	Coarse 4 - 5 phi	Medium 5 - 6 phi	Fine 6 - 7 phi	Very Fine 7 - 8 phi	8 - 13 phi
REPLICATE 1	☑	1.86	19.14	44.23	10.00	4.48	4.25	5.26	4.97	5.82
REPLICATE 2	☑	1.61	18.41	44.93	11.22	4.55	3.97	4.81	4.69	5.81
REPLICATE 3	☑	1.01	21.04	46.11	9.91	3.75	3.37	4.76	4.72	5.32
REPLICATE 4	☑	1.96	19.75	46.87	10.32	3.91	3.43	4.21	4.20	5.34
REPLICATE 5	☑	2.94	18.69	43.94	10.16	4.22	3.93	4.93	5.07	6.12
BM AVERAGE	☑	1.88	19.41	45.22	10.32	4.18	3.79	4.79	4.73	5.68

		% Sand				% Silt				% Clay
Participant	Laser Used	Coarse 0 - 1 phi	Medium 1 - 2 phi	Fine 2 - 3 phi	Very Fine 3 - 4 phi	Coarse 4 - 5 phi	Medium 5 - 6 phi	Fine 6 - 7 phi	Very Fine 7 - 8 phi	8 - 13 phi
PSA_2101	☑	2.35	22.01	50.53	8.66	3.10	2.40	3.20	3.13	4.62
PSA_2102	☑	1.81	28.49	42.42	11.29	1.66	3.68	3.87	4.05	2.73
PSA_2103	☑	0.22	33.05	49.91	10.87	1.57	2.11	0.92	0.87	0.48
PSA_2105	☑	1.86	19.14	44.23	10.00	4.48	4.25	5.26	4.97	5.82
PSA_2106	☑	0.67	19.34	52.85	12.80	3.31	2.01	2.00	1.98	5.04
PSA_2107	☑	7.01	59.16	33.23	0.60	0.00	0.00	0.00	0.00	0.00
PSA_2108_A	☑	1.06	32.18	49.10	8.10	0.97	2.21	1.79	2.34	2.25
PSA_2108_B	☑	0.95	31.85	49.59	8.16	0.89	2.12	1.63	2.27	2.52
PSA_2109	☒	0.09	9.38	71.57	10.70	0.00	3.06	0.00	3.30	1.90
PSA_2110	☑	0.21	23.98	45.23	12.64	2.90	4.27	4.82	4.28	1.67
PSA_2111	☑	0.99	27.31	44.53	11.15	1.81	3.24	3.35	3.87	3.75
PSA_2112	☑	0.28	23.39	39.27	11.25	4.04	5.43	7.10	6.87	2.36
PSA_2113	☑	0.04	24.18	54.04	9.73	1.27	2.93	2.85	2.86	2.11
PSA_2114	☑	0.45	27.58	45.52	10.28	2.37	3.09	3.73	3.98	3.01

Percentages taken from the final laser data

Where there was no laser data. Percentages are calculated from re-proportioned sieve data.

Table 3. Summary of the particle size information received from participating laboratories and replicate analysis laboratory for the fifty-second particle size distribution - PS52.

Benchmark Data

					Summary Data APEM verification			
Sample	**% Gravel**	**% Sand**	**% Silt/Clay**	**Sediment Description (Post analysis)**	**% Gravel**	**% Sand**	**% Silt/Clay**	Sediment Description (Post analysis)
REPLICATE 1	0.00	75.00	25.00	Muddy sand	☑	☑	☑	☑ muddy sand
REPLICATE 2	0.00	76.00	24.00	Muddy sand	☑	☑	☑	☑ muddy sand
REPLICATE 3	0.00	78.00	22.00	Muddy sand	☑	☑	☑	☑ muddy sand
REPLICATE 4	0.00	79.00	21.00	Muddy sand	☑	☑	☑	☑ muddy sand
REPLICATE 5	0.00	76.00	24.00	Muddy sand	☑	☑	☑	☑ muddy sand
REP AVERAGE	0.00	76.80	23.20	Muddy sand	☑	☑	☑	☑ muddy sand

Participant Data

					Summary Data APEM verification			
Lab	**% Gravel**	**% Sand**	**% Silt/Clay**	**Sediment Description (Post analysis)**	**% Gravel**	**% Sand**	**% Silt/Clay**	Sediment Description (Post analysis)
PSA_2101	0.01	83.54	16.44	Muddy Sand	☑	☑	☑	muddy sand
PSA_2102	0.00	84.01	15.99	Muddy Sand	☑	☑	☑	muddy sand
PSA_2103	0.00	94.00	6.00	S	☑	☑	☑	sand
PSA_2105	0.00	75.00	25.00	Muddy Sand	☑	☑	☑	muddy sand
PSA_2106	0.00	85.80	14.00	Muddy Sand	☑	☑	☑	muddy sand
PSA_2107	0.00	100.00	0.00	Medium Sand	☑	☑	☑	sand
PSA_2108_A	0.00	90.44	9.56	Sand	☑	☑	☑	muddy sand
PSA_2108_B	0.00	90.56	9.44	Sand	☑	☑	☑	muddy sand
PSA_2109	0.00	91.80	8.20	Sand	☑	☑	☑	muddy sand
PSA_2110	0.00	82.06	17.94	slightly muddy sand	☒N/A	☒N/A	☒N/A	-
PSA_2111	0.00	83.98	16.02	slightly muddy sand	☒N/A	☒N/A	☒N/A	-
PSA_2112	0.00	75.20	24.80	Muddy Sand	☑	☒74.2	☒25.8	muddy sand
PSA_2113	0.00	87.99	12.01	Muddy Sand	☑	☑	☑	muddy sand
PSA_2114	0.00	83.80	16.20	Muddy Sand	☑	☑	☑	muddy sand

Red text - Not provided, calculated by APEM

☑ - Participant calculations of % Gravel, % Sand and % Silt/Clay are correct based on the final data submitted

Figure 1. Particle size distribution curves resulting from analysis of 5 replicate samples of sediment distibuted as PS52 (Benchmark Data).

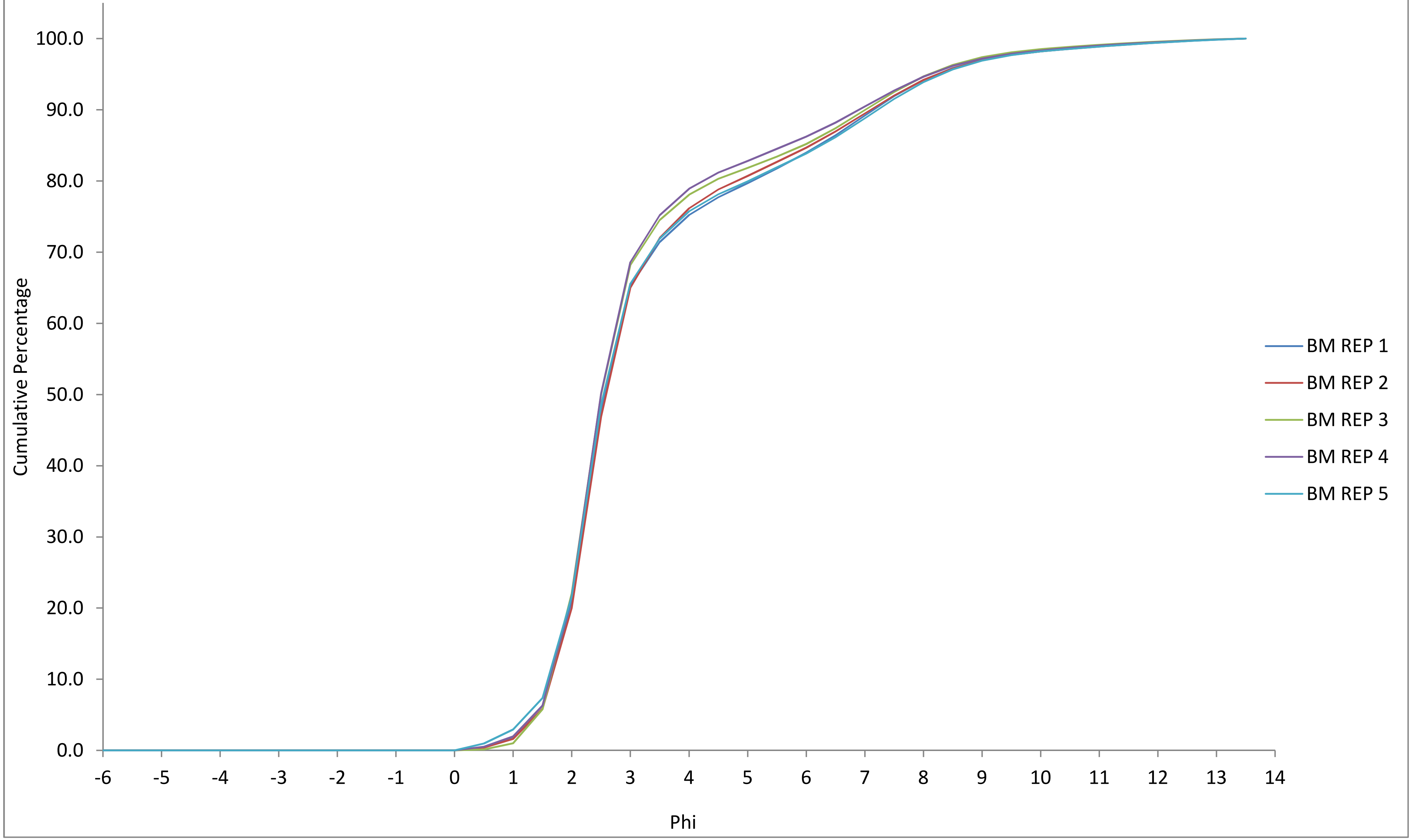


Figure 2. Particle size distribution curves from all participating laboratories for sediment distributed as PS52.

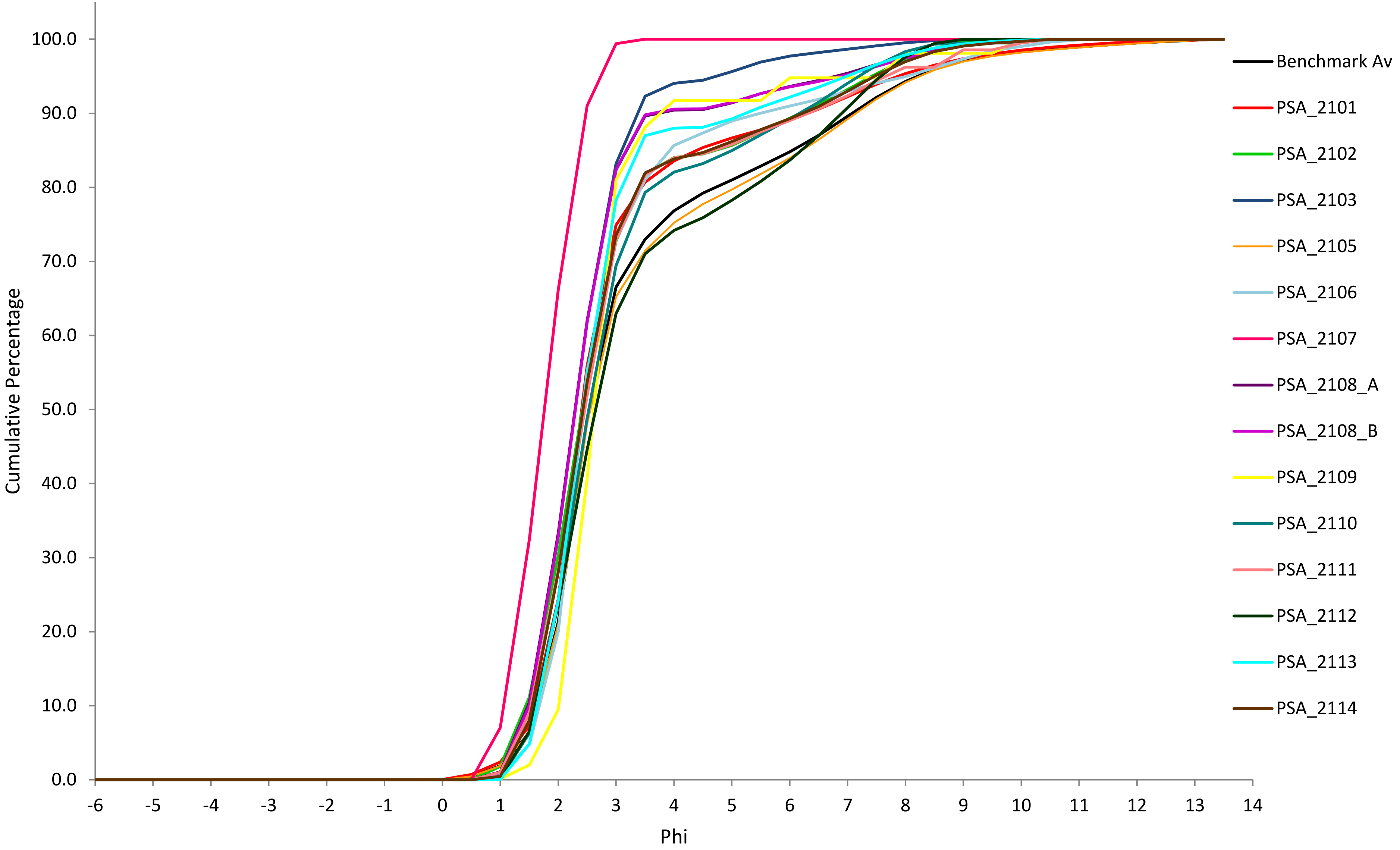


Figure 3. PSA Particle size ternary diagrams for PS52 including the Benchmark replicates and all participating laboratories for (a) Gravel, Sand and Mud and (b) Sand, Silt and Clay.

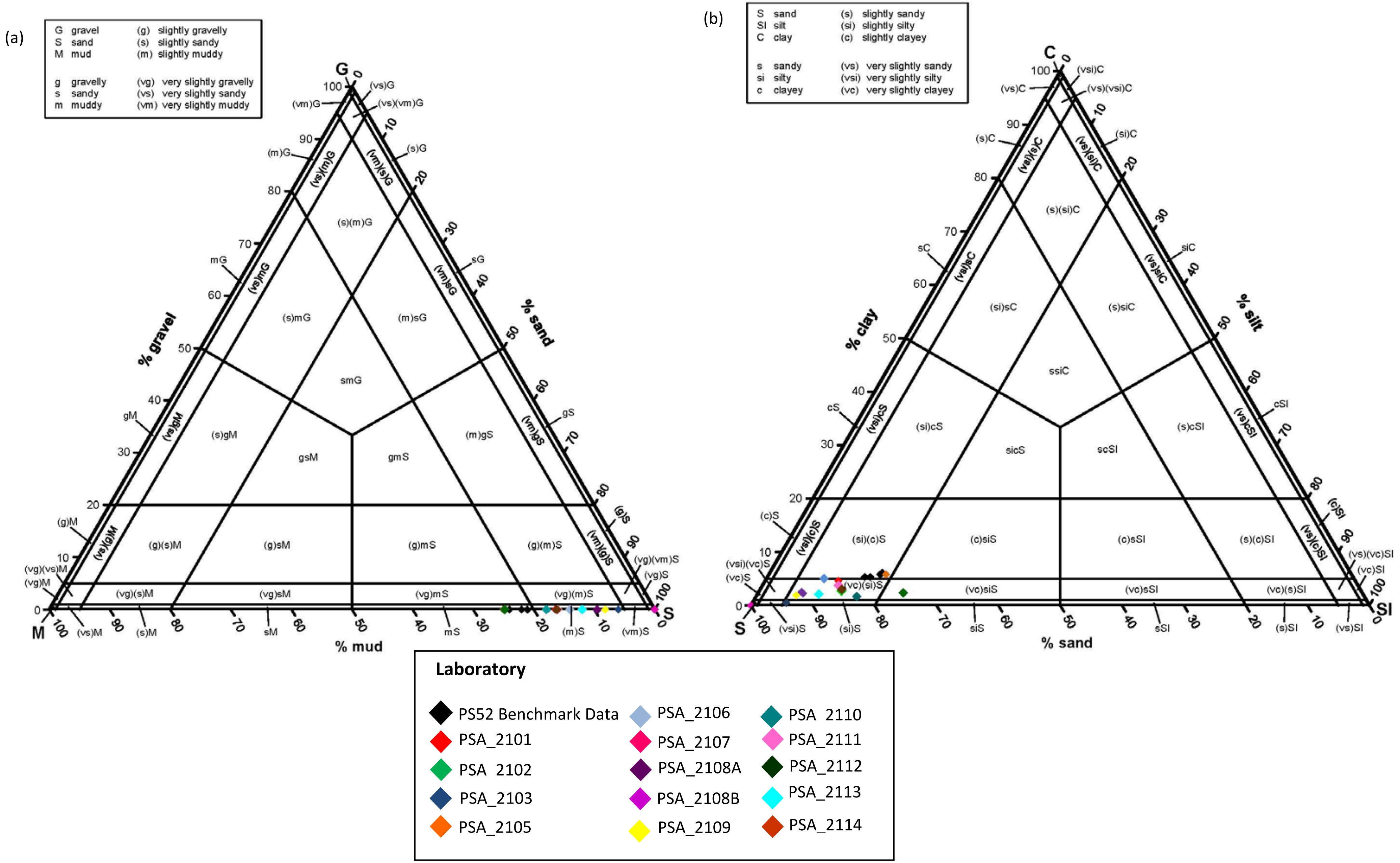


Figure 4. Bar chart for PS52 showing the percentage gravel, sand, silt and mud recorded by each participating laboratory and the benchmark average.

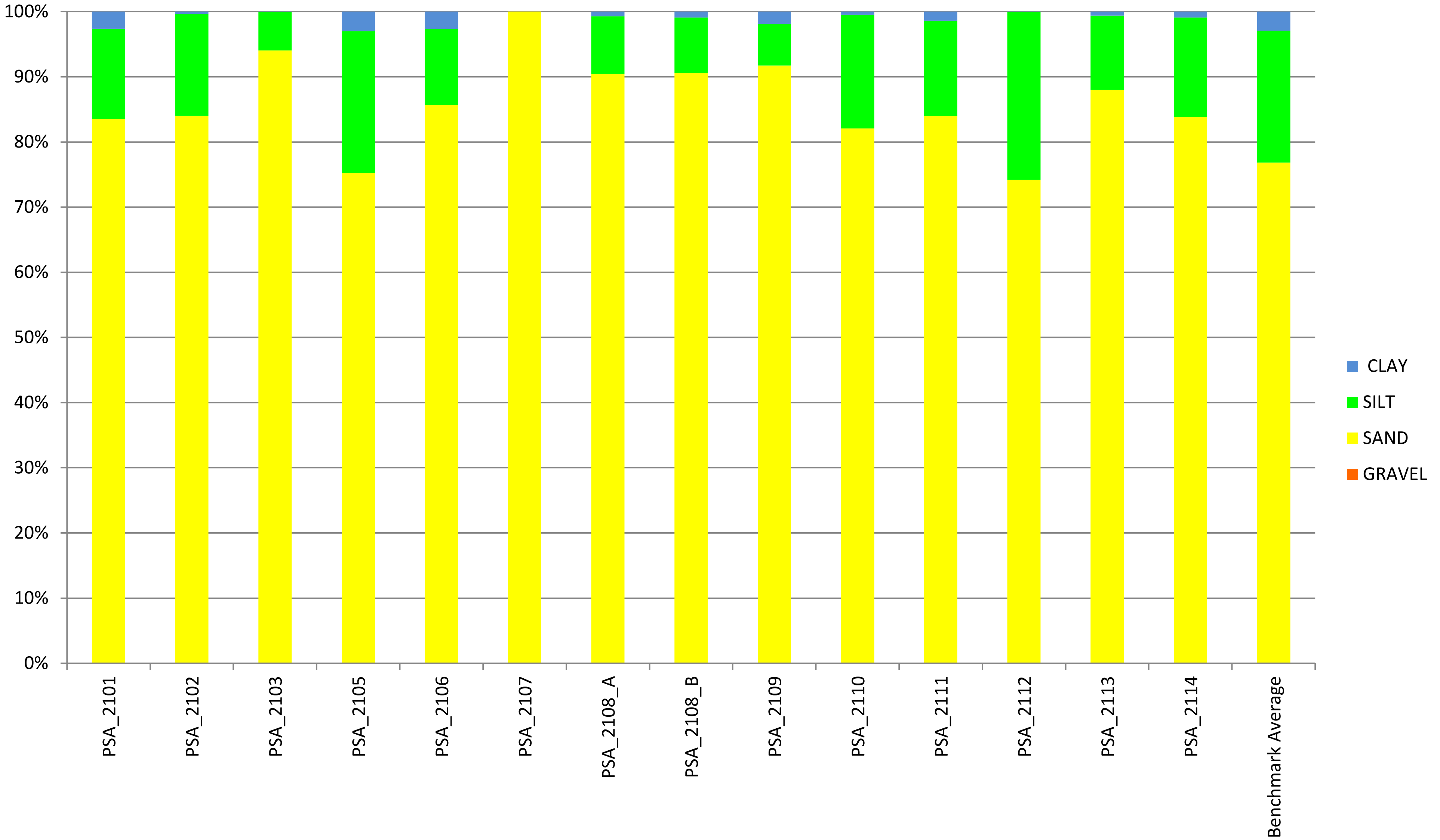


Table 4. Summary of z-scores for each phi-interval for PS52; data from all participating laboratories included in mean and standard deviation calculations.

	Phi-interval																			
	-6.50 to -6.00	-6.00 to -5.50	-5.50 to -5.00	-5.00 to -4.50	-4.50 to -4.00	-4.00 to -3.50	-3.50 to -3.00	-3.00 to -2.50	-2.50 to -2.00	-2.00 to -1.50	-1.50 to -1.00	-1.00 to -0.50	-0.50 to 0.00	0.00 to 0.50	0.50 to 1.00	1.00 to 1.50	1.50 to 2.00	2.00 to 2.50	2.50 to 3.00	3.00 to 3.50
Benchmark Average	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.36	-0.36	-0.56	1.70	1.64	0.10	-0.60	-0.70	-0.01	-0.39	-0.41
PSA_2101	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.16	1.48	2.35	1.67	2.54	0.26	-0.53	-0.32	1.08	-0.20	-0.73
PSA_2102	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.36	-0.36	-0.56	-0.67	-0.48	0.35	0.30	0.03	-1.03	-0.24	0.74
PSA_2103	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.36	-0.36	-0.56	-0.67	-0.48	-0.58	0.44	0.70	0.28	0.16	0.77
PSA_2105	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.36	-0.36	-0.56	1.76	1.47	0.12	-0.60	-0.75	-0.13	-0.48	-0.55
PSA_2106	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.36	-0.36	-0.56	-0.67	-0.48	-0.32	-0.66	-0.66	2.07	-0.41	0.36
PSA_2107	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.52	3.18	1.30	-0.67	-0.48	3.39	3.24	2.60	-0.71	-1.84	-3.07
PSA_2108_A	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.36	-0.36	1.41	-0.07	-0.48	-0.09	0.30	0.68	0.35	0.00	-0.05
PSA_2108_B	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.36	-0.36	1.13	-0.07	-0.48	-0.15	0.25	0.66	0.41	0.04	-0.01
PSA_2109	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.36	-0.36	-0.56	1.06	-0.39	-0.67	-1.07	-2.02	0.98	3.09	-0.15
PSA_2110	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.36	-0.36	-0.56	-0.67	-0.48	-0.59	-0.30	-0.19	-0.77	0.04	1.11
PSA_2111	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.36	-0.36	-0.56	-0.67	-0.48	-0.13	0.05	0.06	-1.04	0.09	0.65
PSA_2112	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.36	-0.36	-0.56	-0.67	-0.48	-0.55	-0.27	-0.33	-1.76	-0.30	0.30
PSA_2113	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.36	-0.36	-0.56	-0.67	-0.48	-0.69	-0.54	0.07	0.79	0.51	0.59
PSA_2114	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.36	-0.36	-0.56	-0.67	-0.48	-0.45	-0.02	0.17	-0.50	-0.07	0.45

$\bar{x}$	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.001	0.001	0.001	0.003	0.110	1.214	7.729	18.965	27.495	20.319	7.415
s	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.003	0.002	0.001	0.004	0.230	1.707	5.456	5.681	3.722	6.501	2.222

🟨	$z<-1.96$ or $z>1.96$
🟦	All laboratories recorded zero therefore mean and standard deviation equal zero.

Table 3. Summary of z-scores for each phi-interval for PS52; data from all participating laboratories included in mean and standard deviation calculations.

	Phi-interval																			
	3.50 to 4.00	4.00 to 4.50	4.50 to 5.00	5.00 to 5.50	5.50 to 6.00	6.00 to 6.50	6.50 to 7.00	7.00 to 7.50	7.50 to 8.00	8.00 to 8.50	8.50 to 9.00	9.00 to 9.50	9.50 to 10.00	10.00 to 10.50	10.50 to 11.00	11.00 to 11.50	11.50 to 12.00	12.00 to 12.50	12.50 to 13.00	13.00 to 13.50
Benchmark Average	1.10	1.66	0.82	0.63	0.46	0.87	0.89	0.85	0.60	1.11	0.66	1.15	0.18	0.64	1.57	1.96	2.04	2.09	2.12	1.94
PSA_2101	0.38	0.99	0.06	-0.43	-0.33	0.11	0.06	0.02	-0.21	0.27	0.19	0.92	0.23	0.79	1.59	1.66	1.47	1.24	1.09	1.59
PSA_2102	-0.09	-0.50	-0.11	0.55	0.39	0.48	0.37	0.44	0.33	0.85	0.26	0.04	-0.78	-1.05	-0.60	-0.53	-0.48	-0.47	-0.47	-0.48
PSA_2103	-0.45	-0.55	-0.16	-0.18	-0.91	-0.98	-1.09	-1.14	-1.38	-1.07	-0.93	-0.96	-0.78	-1.05	-0.60	-0.53	-0.48	-0.47	-0.47	-0.48
PSA_2105	1.08	1.77	1.12	0.93	0.77	1.13	1.09	1.00	0.70	1.15	0.67	1.15	0.19	0.66	1.63	2.08	2.22	2.33	2.39	2.23
PSA_2106	1.68	0.85	0.59	-0.51	-0.74	-0.52	-0.50	-0.52	-0.87	0.35	0.81	2.17	0.48	1.60	1.61	0.13	-0.48	-0.47	-0.47	-0.48
PSA_2107	-1.77	-1.03	-1.93	-1.99	-1.93	-1.50	-1.50	-1.58	-1.84	-1.54	-1.24	-0.99	-0.78	-1.05	-0.60	-0.53	-0.48	-0.47	-0.47	-0.48
PSA_2108_A	-1.17	-0.97	-0.51	-0.24	-0.74	-0.64	-0.59	-0.45	-0.54	-0.05	-0.20	0.08	-0.33	-0.51	-0.60	-0.53	-0.48	-0.47	-0.47	-0.48
PSA_2108_B	-1.19	-1.00	-0.58	-0.29	-0.80	-0.72	-0.66	-0.51	-0.55	0.01	-0.10	0.23	-0.25	-0.17	-0.48	-0.53	-0.48	-0.47	-0.47	-0.48
PSA_2109	0.95	-1.03	-1.93	-1.99	1.86	-1.50	-1.50	-1.58	1.85	-1.54	-1.24	-0.99	3.02	-1.05	-0.60	-0.53	-0.48	-0.47	-0.47	-0.48
PSA_2110	0.30	0.27	0.76	0.99	0.73	0.90	0.89	0.73	0.24	0.05	-0.95	-0.99	-0.78	1.36	-0.60	-0.53	-0.48	-0.47	-0.47	-0.48
PSA_2111	-0.05	-0.39	-0.02	0.43	-0.05	0.15	0.17	0.35	0.23	-1.54	2.69	-0.99	1.04	1.40	-0.60	-0.53	-0.48	-0.47	-0.47	-0.48
PSA_2112	0.61	0.87	1.69	1.63	1.61	2.04	2.02	2.03	1.62	1.35	-0.35	-0.90	-0.78	-1.05	-0.60	-0.53	-0.48	-0.47	-0.47	-0.48
PSA_2113	-1.02	-0.89	-0.17	0.20	-0.23	-0.08	-0.10	-0.10	-0.37	-0.06	-0.28	-0.07	-0.39	-0.61	-0.50	-0.53	-0.48	-0.47	-0.47	-0.48
PSA_2114	-0.37	-0.05	0.37	0.27	-0.10	0.24	0.45	0.48	0.19	0.66	0.01	0.15	-0.26	0.08	-0.60	-0.53	-0.48	-0.47	-0.47	-0.48

$\bar{x}$	2.356	0.919	1.249	1.415	1.557	1.410	1.611	1.653	1.647	0.959	0.732	0.339	0.391	0.222	0.083	0.058	0.047	0.040	0.032	0.024
s	1.332	0.893	0.647	0.712	0.807	0.940	1.071	1.044	0.895	0.623	0.590	0.341	0.500	0.212	0.139	0.110	0.099	0.085	0.069	0.050

🟨	z<-1.96 or z >1.96
🟦	All laboratories recorded zero therefore mean and standard deviation equal zero.

Figure 5. Summary of z-scores at each half phi-interval for the Benchmark Average.

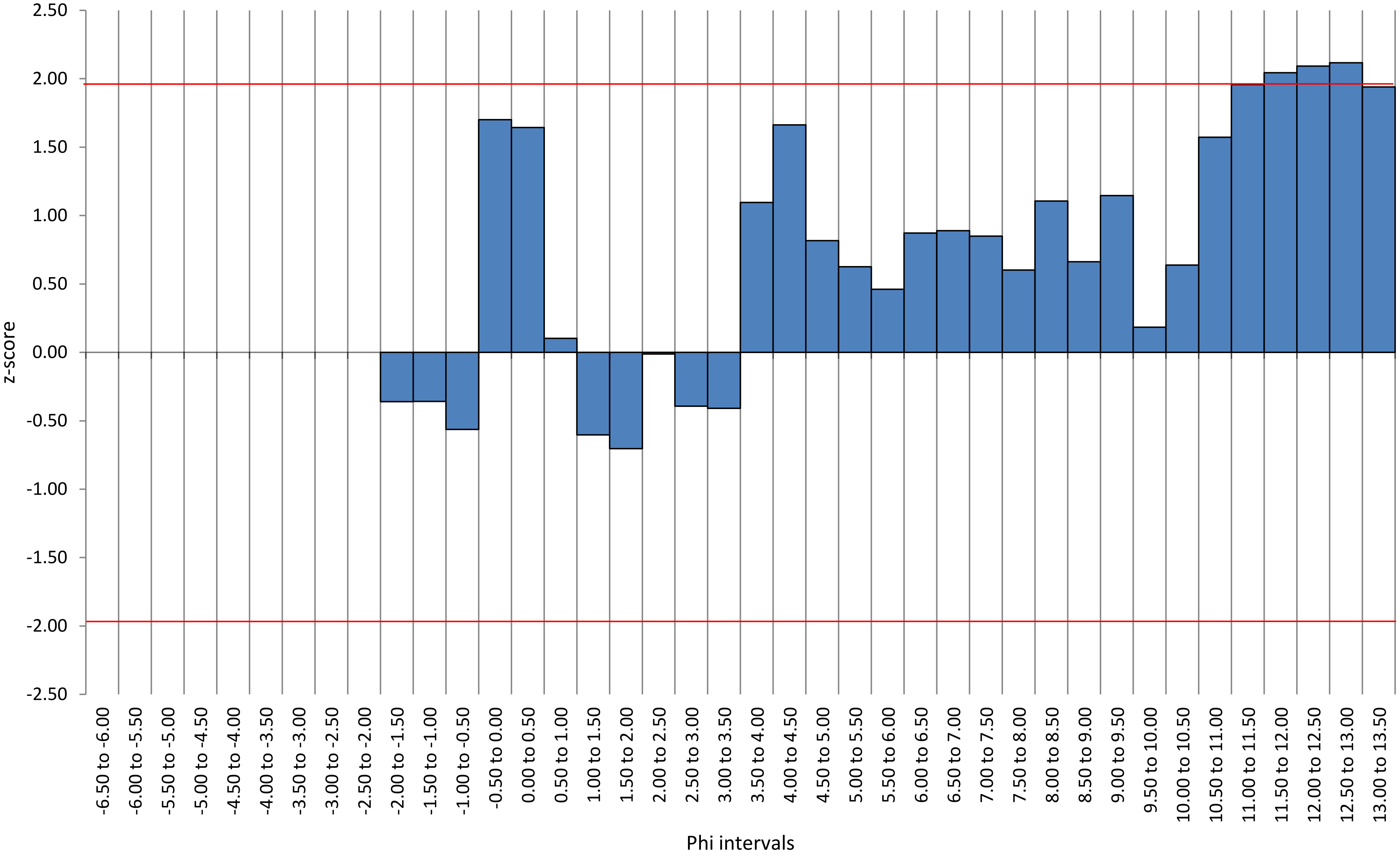
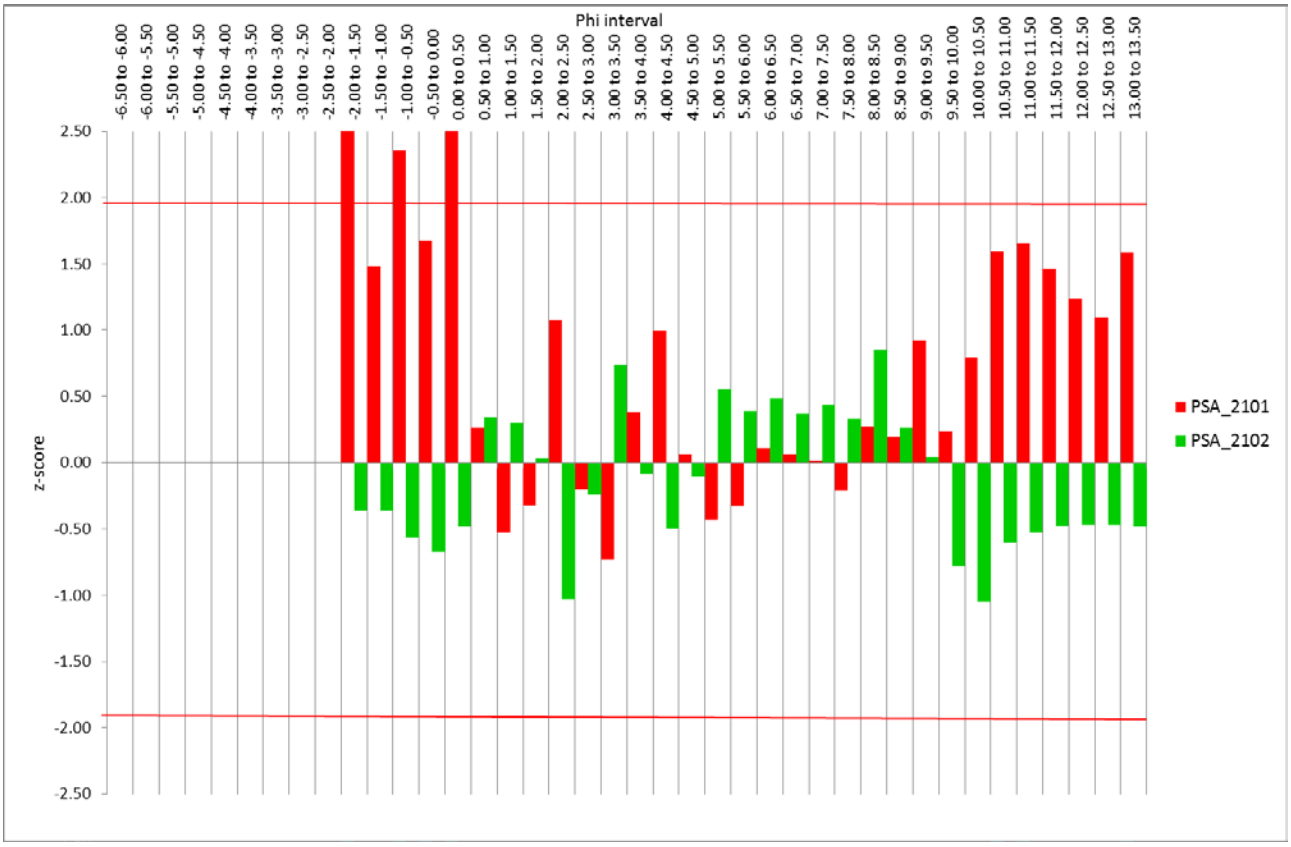


Figure 6. Summary of z-scores at each half phi-interval for a) PSA_2101 and PSA_2102 and b) PSA_2103 and PSA_2105

a)



b)

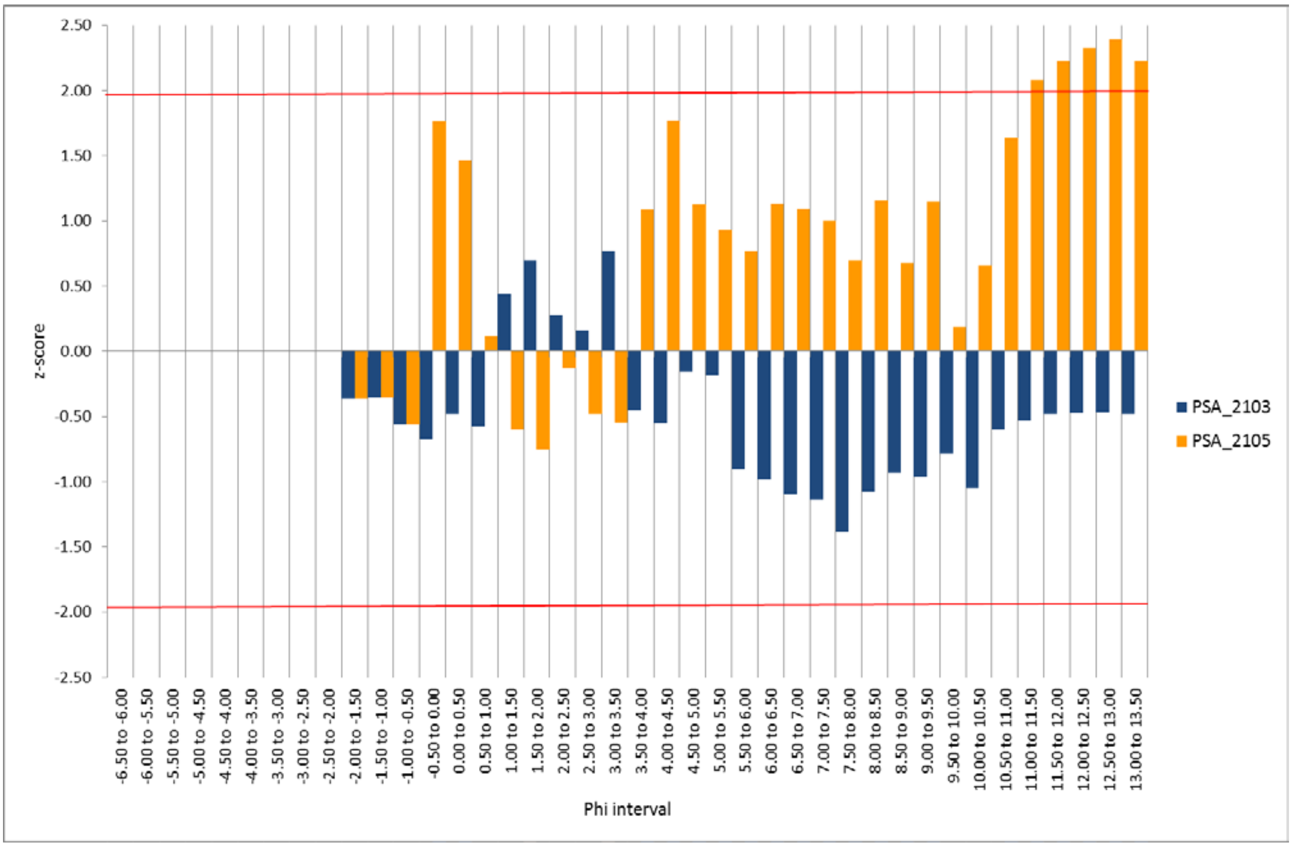


Figure 7 Summary of z-scores at each half phi-interval for a) PSA_2106 and PSA_2107 and b) PSA_2108A and PSA_2108B

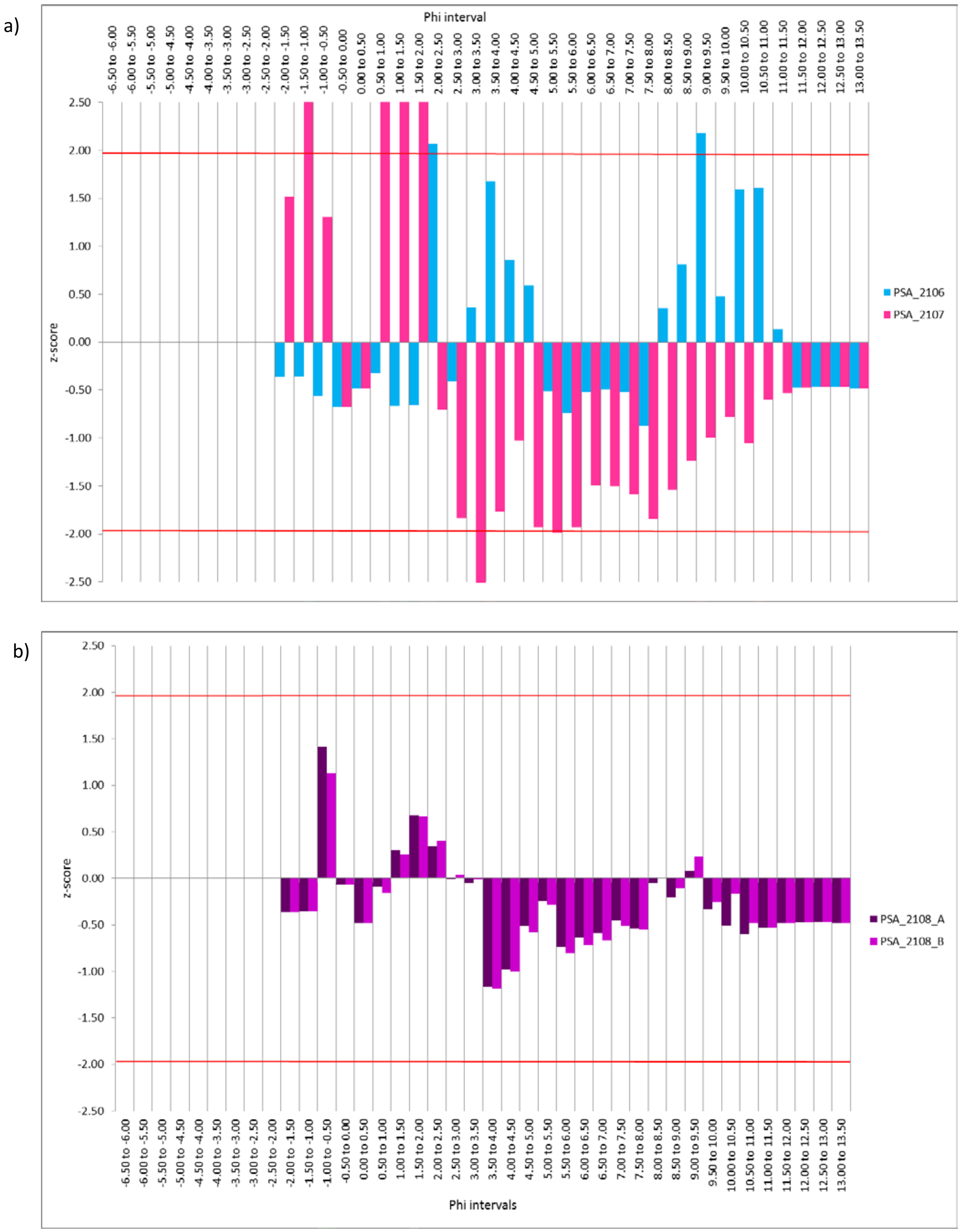


Figure 8. Summary of z-scores at each half phi-interval for a) PSA_2109 and PSA_2110 and b) PSA_2111 and PSA_2112

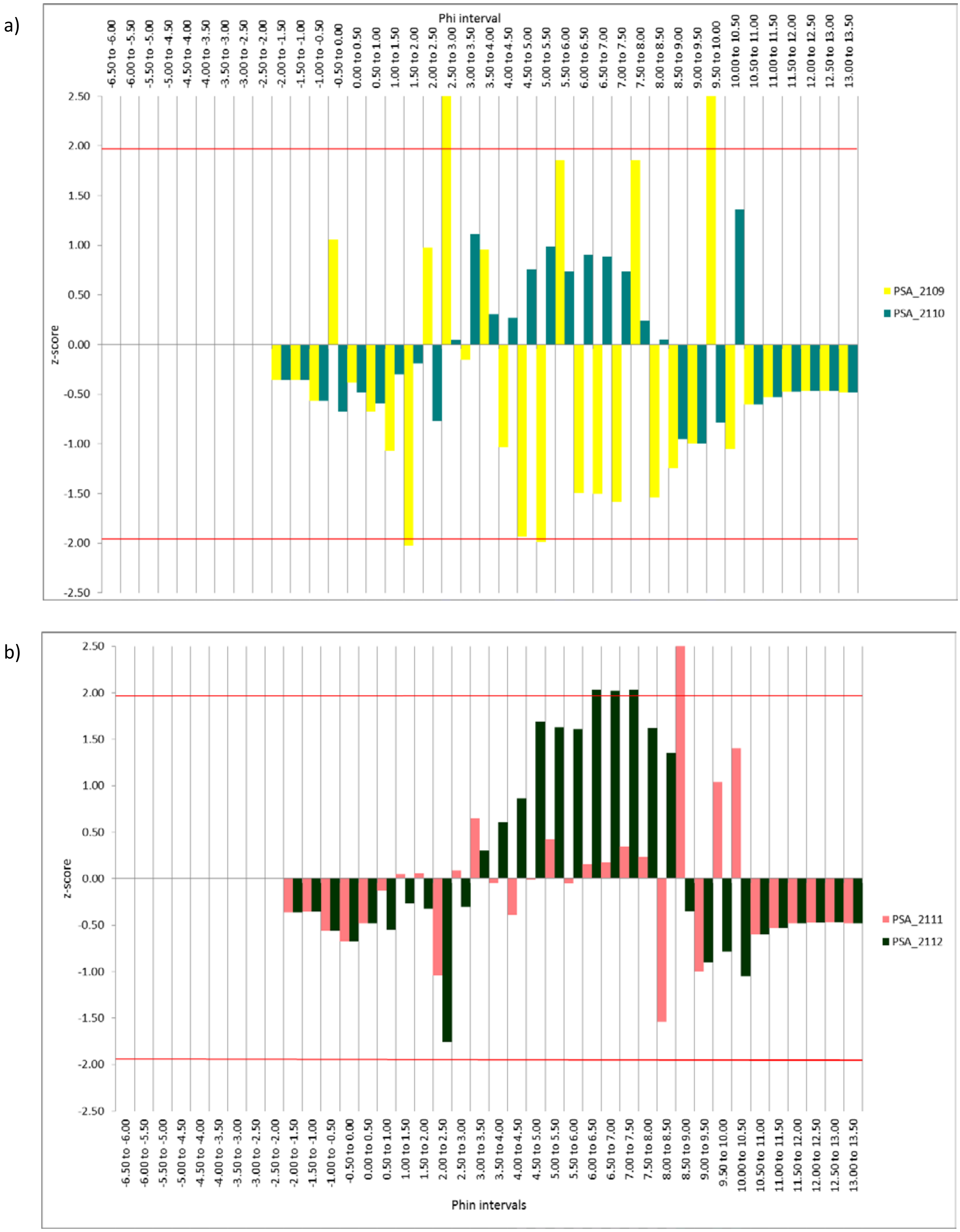
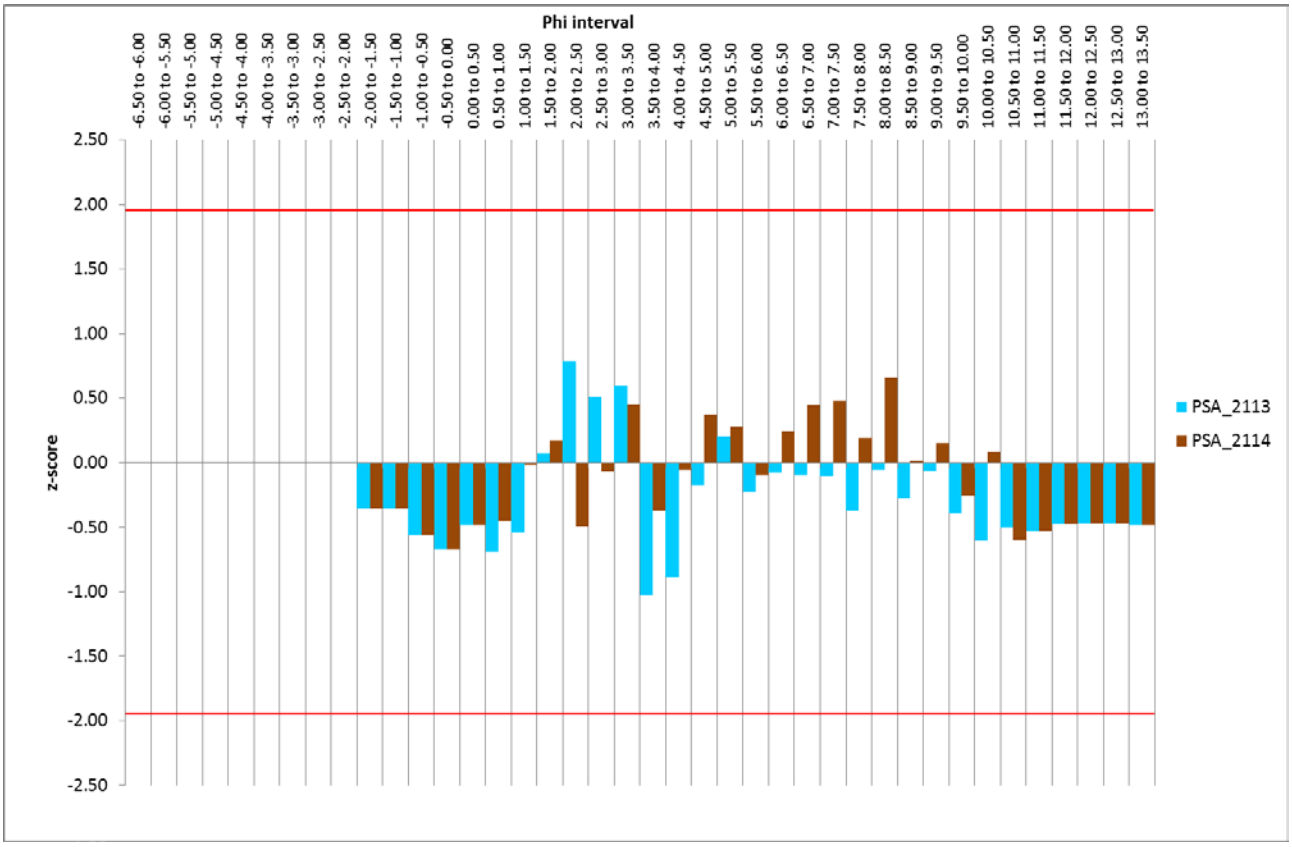


Figure 9 Summary of z-scores at each half phi-interval for PSA_2113 and PSA_2114



Results of SIMPROF testing on PSA Ring test PS52 data

Data was entered into PRIMER v.6.1.13 in half-phi intervals; any missing data was entered as zero. The data did not need to be transformed as all data was on a similar percentage scale. A Euclidean distance matrix was created from the data. The Euclidian distance between two samples is (labs) j and k, is defined algebraically as;

$$\boldsymbol{d_{jk}} = \sqrt{\sum\nolimits_{\boldsymbol{i=1}}^{\boldsymbol{p}} (\boldsymbol{y_{ij}} - \boldsymbol{y_{ik}})^{\boldsymbol{2}}}$$

From this distance matrix cluster analysis was carried out. The most commonly used clustering methods are hierarchical agglomerative methods. These use a similarity or distance matrix as their starting point and successively fuse the samples into groups and the groups into larger clusters, starting with the highest mutual similarities then gradually lowering the similarity level at which groups are formed. The result of hierarchical clustering are represented by a dendrogram (Figure 10), with the X axis representing the full set of samples (labs) and the y axis defining the similarity at which two samples or groups are considered to have fused (Clarke &Warwick, 2001)[1].

A similarity profile routine, SIMPROF was run on the data in conjunction with the cluster analysis. Similarity profile analysis examines whether the similarities observed in the data are smaller and/or larger than those expected by chance. The red SIMPROF lines on the dendrogram (Figure 10) indicate that labs cannot be distinguished from each other at the 5% significance level; black lines indicate labs that can be distinguished from each other.

Non-metric Multi-Dimensional Scaling (MDS) was run on the similarity matrix, results of which can be seen in Figure 11a and 11b. MDS constructs a “map” or configuration of the samples, in a specified number of dimensions, which attempts to satisfy all the conditions imposed by the similarity matrix. For example if sample 1 has higher similarity to sample 2 than it does to sample 3, then sample 1 will be placed closer on the map to sample 2 than it will be to sample 3 (Clarke &Warwick, 2001)[1]. It is important to note that although the MDS plot is bounded by a box, the box does not represent either axes or scale. The correct configuration of sample points will be multi-dimensional and the plot represents the best 2-dimensional solution to the problem. The technique should be viewed as complementary to cluster analysis, offering a different perspective of the same information.

Each MDS plot (figure 11a and 11b) has a stress value. This is the extent to which the samples deviate from the line measuring the rank order dissimilarities and can be measured by:

$$Stress = \sqrt{\sum_j \sum_k (d_{jk} - \hat{d}_{jk})^2 / \sum_j \sum_k {d^2}_{jk}}$$

Where $\hat{d}_{jk}$ is the distance predicted from the fitted regression line corresponding to dissimilarity, δ_{jk} . Large scatter leads to large stress. Stress can increase when compressing sample relationships into two dimensions. A stress value less than 0.2 is a good representation of the data and is fairly reliable. Whereas, a stress value of greater than 0.3 indicates random data.

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[1] Clarke, K.R. & Warwick,R.M. (2001). Changes in Marine Communities; an approach to statistical analysis and interpretation. 2nd Ed. PRIMER-E Ltd. Plymouth.

The MDS plots in figure 11a and 11b have stress values of 0.01 and 0.04 respectively. Indicating that the plots are a good representation of the data.

The cluster analysis separates the labs into 9 SIMPROF cluster groups, 5 of these groups compromise a single lab.

Cluster group A (PSA_2109) and cluster group B (PSA_2107) can found situated far away from each other and from the other laboratories. Table 3 shows that PSA_2107 recorded the PS52 sample as 100% sand, displacing their cumulative percentage curve in Figure 2. LB_2109 were the only lab not to use a laser, as a result of this they are missing data for a number of half phi-intervals.

There are three other single laboratory cluster groups; cluster E (PSA_2112), cluster G (PSA_2113) and cluster H (PSA_2103).

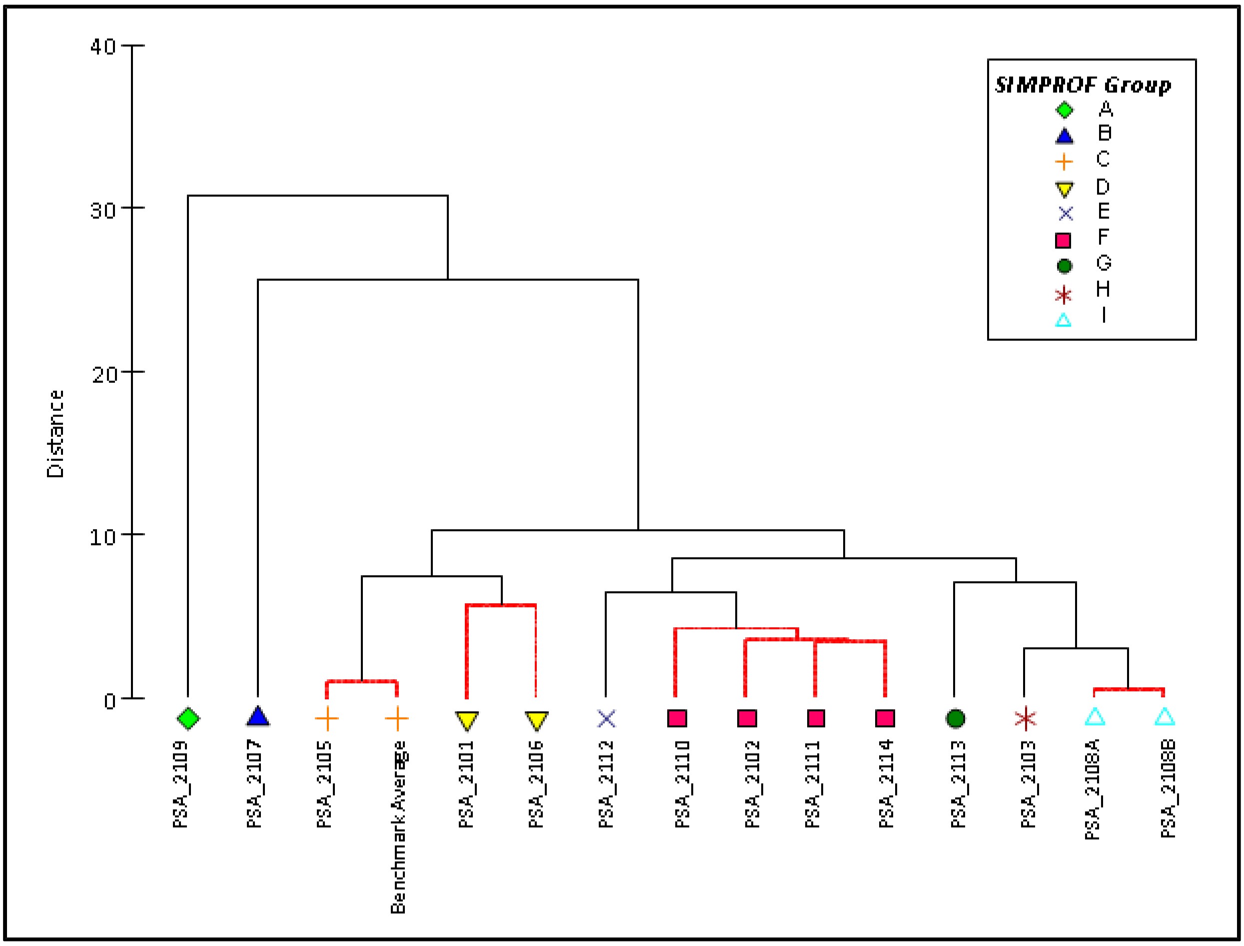
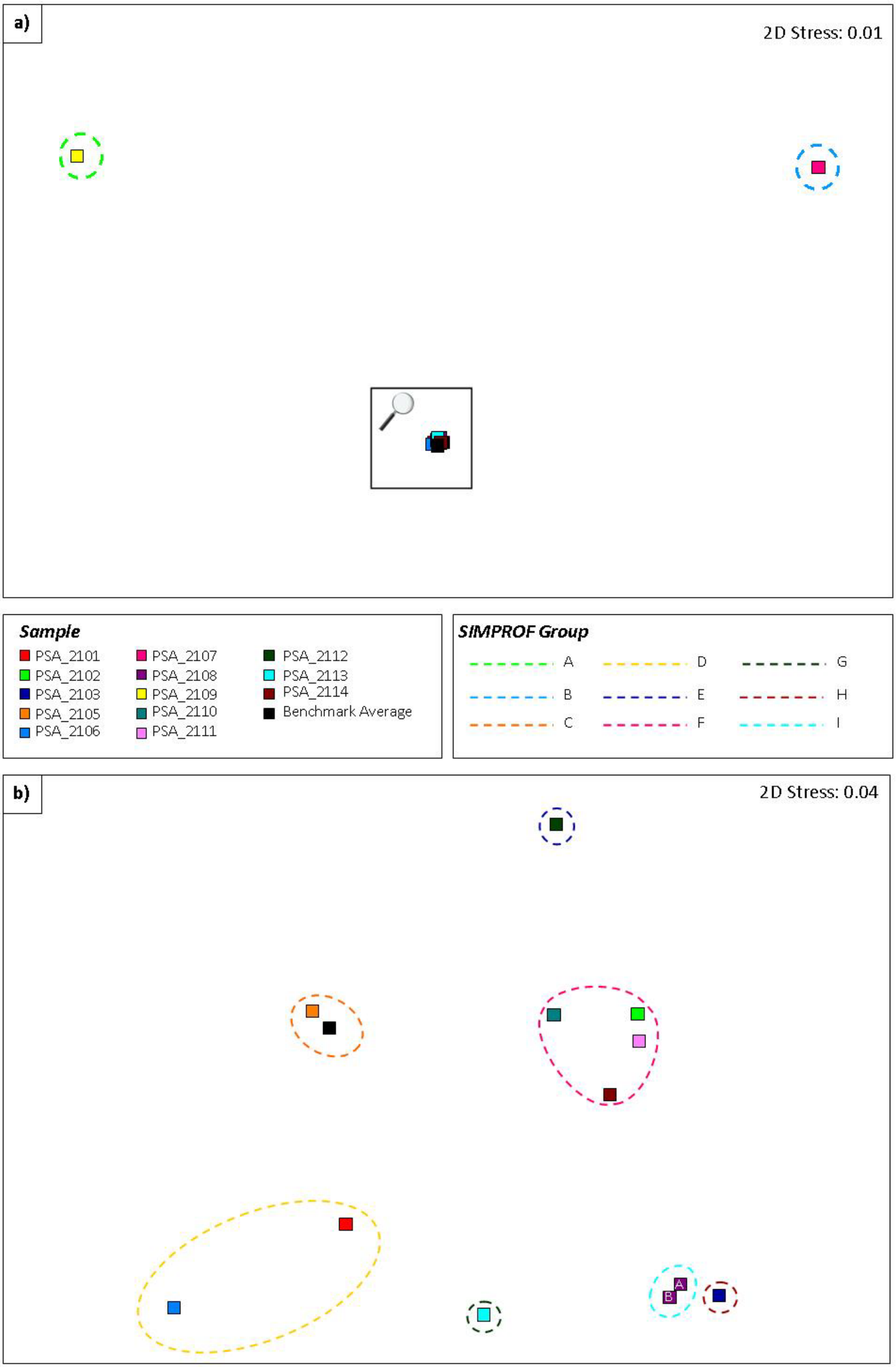


Figure 10. Cluster dendrogram of PS52 including all labs, with the benchmark replicates averaged.

Figure 11. MDS plots of PS52 with the benchmark replicates averaged showing SIMPROF group overlays including a) all laboratories and b) a sub-set of figure 11a.



Appendices

Appendix 1. Final Merged Data sheets as supplied by participating laboratories (arranged by Lab Code) and benchmark replicates. Where the Final Merged Data sheet was not filled in the Final Laser Data sheet has been shown.

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Return to APEM Ltd. by 31-10-14

Exercise Code:	PS52
LabCode:	PSA_2101
Sample Code:	PS522101

Phi interval (explicit) + sieve mesh (theoretical sieves shown in brackets)	Volume/Weight (mark as "0" for not analysed or no material)
-6.50 to -6.00; 63 mm	**0.0000**
-6.00 to -5.50; 45 mm	**0.0000**
-5.50 to -5.00; 31.5 mm	**0.0000**
-5.00 to -4.50; 22.4 mm	**0.0000**
-4.50 to -4.00; 16 mm	**0.0000**
-4.00 to -3.50; 11.2 mm	**0.0000**
-3.50 to -3.00; 8 mm	**0.0000**
-3.00 to -2.50; 5.6 mm	**0.0000**
-2.50 to -2.00; 4 mm	**0.0000**
-2.00 to -1.50; 2.8 mm	**0.0106**
-1.50 to -1.00; 2 mm	**0.0035**
-1.00 to -0.50; 1.4 mm	**0.0035**
-0.50 to 0.00; 1 mm	**0.0106**
0.00 to 0.50; (707 µm)	0.6942
0.50 to 1.00; (500 µm)	1.6586
1.00 to 1.50; (353.6 µm)	4.8616
1.50 to 2.00; (250 µm)	17.1409
2.00 to 2.50; (176.8 µm)	31.5090
2.50 to 3.00; (125 µm)	19.0062
3.00 to 3.50; (88.39 µm)	5.7909
3.50 to 4.00; (62.5 µm)	2.8669
4.00 to 4.50; (44.19 µm)	1.8048
4.50 to 5.00; (31.25 µm)	1.2906
5.00 to 5.50; (22.097 µm)	1.1091
5.50 to 6.00; (15.625 µm)	1.2923
6.00 to 6.50; (11.049 µm)	1.5158
6.50 to 7.00; (7.813 µm)	1.6805
7.00 to 7.50; (5.524 µm)	1.6704
7.50 to 8.00; (3.906 µm)	1.4620
8.00 to 8.50; (2.762 µm)	1.1276
8.50 to 9.00; (1.953 µm)	0.8453
9.00 to 9.50; (1.381 µm)	0.6537
9.50 to 10.00; (0.977 µm)	0.5075
10.00 to 10.50; (0.691 µm)	0.3899
10.50 to 11.00; (0.488 µm)	0.3042
11.00 to 11.50; (0.345 µm)	0.2403
11.50 to 12.00; (0.244 µm)	0.1933
12.00 to 12.50; (0.173 µm)	0.1445
12.50 to 13.00; (0.122 µm)	0.1079
13.00 to 13.50; (0.086 µm)	0.1038

Appendix 1. Final Merged Data sheets as supplied by participating laboratories (arranged by Lab Code) and benchmark replicates. Where the Final Merged Data sheet was not filled in the Final Laser Data sheet has been shown.

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Exercise Code:	**PS52**
LabCode:	**PSA_2102**
Sample Code:	**PS522102**

Phi interval (explicit) + sieve mesh (theoretical sieves shown in brackets)	Volume/Weight (mark as "0" for not analysed or no material)
-6.50 to -6.00; 63 mm	
-6.00 to -5.50; 45 mm	
-5.50 to -5.00; 31.5 mm	
-5.00 to -4.50; 22.4 mm	
-4.50 to -4.00; 16 mm	
-4.00 to -3.50; 11.2 mm	
-3.50 to -3.00; 8 mm	
-3.00 to -2.50; 5.6 mm	
-2.50 to -2.00; 4 mm	
-2.00 to -1.50; 2.8 mm	
-1.50 to -1.00; 2 mm	
-1.00 to -0.50; 1.4 mm	
-0.50 to 0.00; 1 mm	
0.00 to 0.50; (707 µm)	*0.0000*
0.50 to 1.00; (500 µm)	*1.8061*
1.00 to 1.50; (353.6 µm)	*9.3513*
1.50 to 2.00; (250 µm)	*19.1433*
2.00 to 2.50; (176.8 µm)	*23.6721*
2.50 to 3.00; (125 µm)	*18.7490*
3.00 to 3.50; (88.39 µm)	*9.0553*
3.50 to 4.00; (62.5 µm)	*2.2376*
4.00 to 4.50; (44.19 µm)	*0.4763*
4.50 to 5.00; (31.25 µm)	*1.1809*
5.00 to 5.50; (22.097 µm)	*1.8080*
5.50 to 6.00; (15.625 µm)	*1.8721*
6.00 to 6.50; (11.049 µm)	*1.8632*
6.50 to 7.00; (7.813 µm)	*2.0053*
7.00 to 7.50; (5.524 µm)	*2.1083*
7.50 to 8.00; (3.906 µm)	*1.9440*
8.00 to 8.50; (2.762 µm)	*1.4868*
8.50 to 9.00; (1.953 µm)	*0.8866*
9.00 to 9.50; (1.381 µm)	*0.3540*
9.50 to 10.00; (0.977 µm)	*0.0000*
10.00 to 10.50; (0.691 µm)	*0.0000*
10.50 to 11.00; (0.488 µm)	*0.0000*
11.00 to 11.50; (0.345 µm)	*0.0000*
11.50 to 12.00; (0.244 µm)	*0.0000*
12.00 to 12.50; (0.173 µm)	*0.0000*
12.50 to 13.00; (0.122 µm)	*0.0000*
13.00 to 13.50; (0.086 µm)	*0.0000*

Appendix 1. Final Merged Data sheets as supplied by participating laboratories (arranged by Lab Code) and benchmark replicates. Where the Final Merged Data sheet was not filled in the Final Laser Data sheet has been shown.

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Exercise Code:	**PS52**
LabCode:	**PSA_2103**
Sample Code:	**PS522103**

Phi interval (explicit) + sieve mesh (theoretical sieves shown in brackets)	**Volume/Weight (mark as "0" for not analysed or no material)**
-6.50 to -6.00; 63 mm	**0.0000**
-6.00 to -5.50; 45 mm	**0.0000**
-5.50 to -5.00; 31.5 mm	**0.0000**
-5.00 to -4.50; 22.4 mm	**0.0000**
-4.50 to -4.00; 16 mm	**0.0000**
-4.00 to -3.50; 11.2 mm	**0.0000**
-3.50 to -3.00; 8 mm	**0.0000**
-3.00 to -2.50; 5.6 mm	**0.0000**
-2.50 to -2.00; 4 mm	**0.0000**
-2.00 to -1.50; 2.8 mm	**0.0000**
-1.50 to -1.00; 2 mm	**0.0000**
-1.00 to -0.50; 1.4 mm	**0.0000**
-0.50 to 0.00; 1 mm	**0.0000**
0.00 to 0.50; (707 µm)	0.0000
0.50 to 1.00; (500 µm)	0.2244
1.00 to 1.50; (353.6 µm)	10.1211
1.50 to 2.00; (250 µm)	22.9267
2.00 to 2.50; (176.8 µm)	28.5300
2.50 to 3.00; (125 µm)	21.3778
3.00 to 3.50; (88.39 µm)	9.1156
3.50 to 4.00; (62.5 µm)	1.7544
4.00 to 4.50; (44.19 µm)	0.4244
4.50 to 5.00; (31.25 µm)	1.1467
5.00 to 5.50; (22.097 µm)	1.2833
5.50 to 6.00; (15.625 µm)	0.8233
6.00 to 6.50; (11.049 µm)	0.4844
6.50 to 7.00; (7.813 µm)	0.4400
7.00 to 7.50; (5.524 µm)	0.4633
7.50 to 8.00; (3.906 µm)	0.4078
8.00 to 8.50; (2.762 µm)	0.2911
8.50 to 9.00; (1.953 µm)	0.1822
9.00 to 9.50; (1.381 µm)	0.0100
9.50 to 10.00; (0.977 µm)	0.0000
10.00 to 10.50; (0.691 µm)	0.0000
10.50 to 11.00; (0.488 µm)	0.0000
11.00 to 11.50; (0.345 µm)	0.0000
11.50 to 12.00; (0.244 µm)	0.0000
12.00 to 12.50; (0.173 µm)	0.0000
12.50 to 13.00; (0.122 µm)	0.0000
13.00 to 13.50; (0.086 µm)	0.0000

Appendix 1. Final Merged Data sheets as supplied by participating laboratories (arranged by Lab Code) and benchmark replicates. Where the Final Merged Data sheet was not filled in the Final Laser Data sheet has been shown.

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Exercise Code:	**PS52**
LabCode:	**PSA_2105**
Sample Code:	**PS522105**

Phi interval (explicit) + sieve mesh (theoretical sieves shown in brackets)	**Volume/Weight (mark as "0" for not analysed or no material)**
-6.50 to -6.00; 63 mm	**0.0000**
-6.00 to -5.50; 45 mm	**0.0000**
-5.50 to -5.00; 31.5 mm	**0.0000**
-5.00 to -4.50; 22.4 mm	**0.0000**
-4.50 to -4.00; 16 mm	**0.0000**
-4.00 to -3.50; 11.2 mm	**0.0000**
-3.50 to -3.00; 8 mm	**0.0000**
-3.00 to -2.50; 5.6 mm	**0.0000**
-2.50 to -2.00; 4 mm	**0.0000**
-2.00 to -1.50; 2.8 mm	**0.0000**
-1.50 to -1.00; 2 mm	**0.0000**
-1.00 to -0.50; 1.4 mm	**0.0000**
-0.50 to 0.00; 1 mm	**0.0109**
0.00 to 0.50; (707 µm)	0.4474
0.50 to 1.00; (500 µm)	1.4127
1.00 to 1.50; (353.6 µm)	4.4306
1.50 to 2.00; (250 µm)	14.7054
2.00 to 2.50; (176.8 µm)	27.0186
2.50 to 3.00; (125 µm)	17.2039
3.00 to 3.50; (88.39 µm)	6.2018
3.50 to 4.00; (62.5 µm)	3.7979
4.00 to 4.50; (44.19 µm)	2.5006
4.50 to 5.00; (31.25 µm)	1.9747
5.00 to 5.50; (22.097 µm)	2.0789
5.50 to 6.00; (15.625 µm)	2.1751
6.00 to 6.50; (11.049 µm)	2.4754
6.50 to 7.00; (7.813 µm)	2.7808
7.00 to 7.50; (5.524 µm)	2.6960
7.50 to 8.00; (3.906 µm)	2.2687
8.00 to 8.50; (2.762 µm)	1.6778
8.50 to 9.00; (1.953 µm)	1.1305
9.00 to 9.50; (1.381 µm)	0.7314
9.50 to 10.00; (0.977 µm)	0.4850
10.00 to 10.50; (0.691 µm)	0.3613
10.50 to 11.00; (0.488 µm)	0.3096
11.00 to 11.50; (0.345 µm)	0.2864
11.50 to 12.00; (0.244 µm)	0.2685
12.00 to 12.50; (0.173 µm)	0.2367
12.50 to 13.00; (0.122 µm)	0.1974
13.00 to 13.50; (0.086 µm)	0.1359

Appendix 1. Final Merged Data sheets as supplied by participating laboratories (arranged by Lab Code) and benchmark replicates. Where the Final Merged Data sheet was not filled in the Final Laser Data sheet has been shown.

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Exercise Code:	**PS52**
LabCode:	**PSA_2106**
Sample Code:	**PS522106**

Phi interval (explicit) + sieve mesh (theoretical sieves shown in brackets)	**Volume/Weight (mark as "0" for not analysed or no material)**
-6.50 to -6.00; 63 mm	**0.0000**
-6.00 to -5.50; 45 mm	**0.0000**
-5.50 to -5.00; 31.5 mm	**0.0000**
-5.00 to -4.50; 22.4 mm	**0.0000**
-4.50 to -4.00; 16 mm	**0.0000**
-4.00 to -3.50; 11.2 mm	**0.0000**
-3.50 to -3.00; 8 mm	**0.0000**
-3.00 to -2.50; 5.6 mm	**0.0000**
-2.50 to -2.00; 4 mm	**0.0000**
-2.00 to -1.50; 2.8 mm	**0.0000**
-1.50 to -1.00; 2 mm	**0.0000**
-1.00 to -0.50; 1.4 mm	**0.0000**
-0.50 to 0.00; 1 mm	**0.0000**
0.00 to 0.50; (707 µm)	0.0000
0.50 to 1.00; (500 µm)	0.6650
1.00 to 1.50; (353.6 µm)	4.1100
1.50 to 2.00; (250 µm)	15.2300
2.00 to 2.50; (176.8 µm)	35.2100
2.50 to 3.00; (125 µm)	17.6400
3.00 to 3.50; (88.39 µm)	8.2100
3.50 to 4.00; (62.5 µm)	4.5900
4.00 to 4.50; (44.19 µm)	1.6800
4.50 to 5.00; (31.25 µm)	1.6300
5.00 to 5.50; (22.097 µm)	1.0500
5.50 to 6.00; (15.625 µm)	0.9600
6.00 to 6.50; (11.049 µm)	0.9200
6.50 to 7.00; (7.813 µm)	1.0800
7.00 to 7.50; (5.524 µm)	1.1100
7.50 to 8.00; (3.906 µm)	0.8700
8.00 to 8.50; (2.762 µm)	1.1800
8.50 to 9.00; (1.953 µm)	1.2100
9.00 to 9.50; (1.381 µm)	1.0800
9.50 to 10.00; (0.977 µm)	0.6300
10.00 to 10.50; (0.691 µm)	0.5600
10.50 to 11.00; (0.488 µm)	0.3060
11.00 to 11.50; (0.345 µm)	0.0730
11.50 to 12.00; (0.244 µm)	0.0000
12.00 to 12.50; (0.173 µm)	0.0000
12.50 to 13.00; (0.122 µm)	0.0000
13.00 to 13.50; (0.086 µm)	0.0000

Appendix 1. Final Merged Data sheets as supplied by participating laboratories (arranged by Lab Code) and benchmark replicates. Where the Final Merged Data sheet was not filled in the Final Laser Data sheet has been shown.

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Exercise Code:	PS53[+]
LabCode:	PSA_2107
Sample Code:	PS532107

Phi interval (explicit) + sieve mesh (theoretical sieves shown in brackets)	Volume/Weight (mark as "0" for not analysed or no material)
-6.50 to -6.00; 63 mm	**0.0000**
-6.00 to -5.50; 45 mm	**0.0000**
-5.50 to -5.00; 31.5 mm	**0.0000**
-5.00 to -4.50; 22.4 mm	**0.0000**
-4.50 to -4.00; 16 mm	**0.0000**
-4.00 to -3.50; 11.2 mm	**0.0000**
-3.50 to -3.00; 8 mm	**0.0000**
-3.00 to -2.50; 5.6 mm	**0.0000**
-2.50 to -2.00; 4 mm	**0.0000**
-2.00 to -1.50; 2.8 mm	**0.0056**
-1.50 to -1.00; 2 mm	**0.0068**
-1.00 to -0.50; 1.4 mm	**0.0023**
-0.50 to 0.00; 1 mm	**0.0000**
0.00 to 0.50; (707 µm)	0.0000
0.50 to 1.00; (500 µm)	7.0080
1.00 to 1.50; (353.6 µm)	25.4311
1.50 to 2.00; (250 µm)	33.7225
2.00 to 2.50; (176.8 µm)	24.8511
2.50 to 3.00; (125 µm)	8.3759
3.00 to 3.50; (88.39 µm)	0.5965
3.50 to 4.00; (62.5 µm)	0.0000
4.00 to 4.50; (44.19 µm)	0.0000
4.50 to 5.00; (31.25 µm)	0.0000
5.00 to 5.50; (22.097 µm)	0.0000
5.50 to 6.00; (15.625 µm)	0.0000
6.00 to 6.50; (11.049 µm)	0.0000
6.50 to 7.00; (7.813 µm)	0.0000
7.00 to 7.50; (5.524 µm)	0.0000
7.50 to 8.00; (3.906 µm)	0.0000
8.00 to 8.50; (2.762 µm)	0.0000
8.50 to 9.00; (1.953 µm)	0.0000
9.00 to 9.50; (1.381 µm)	0.0000
9.50 to 10.00; (0.977 µm)	0.0000
10.00 to 10.50; (0.691 µm)	0.0000
10.50 to 11.00; (0.488 µm)	0.0000
11.00 to 11.50; (0.345 µm)	0.0000
11.50 to 12.00; (0.244 µm)	0.0000
12.00 to 12.50; (0.173 µm)	0.0000
12.50 to 13.00; (0.122 µm)	0.0000
13.00 to 13.50; (0.086 µm)	0.0000

[+] Data for PS52 submitted as PS53 and vice versa.

Appendix 1. Final Merged Data sheets as supplied by participating laboratories (arranged by Lab Code) and benchmark replicates. Where the Final Merged Data sheet was not filled in the Final Laser Data sheet has been shown.

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Exercise Code:	**PS52**
LabCode:	**PSA_2108A**
Sample Code:	**PS522108A**

Phi interval (explicit) + sieve mesh (theoretical sieves shown in brackets)	Volume/Weight (mark as "0" for not analysed or no material)
-6.50 to -6.00; 63 mm	**0.0000**
-6.00 to -5.50; 45 mm	**0.0000**
-5.50 to -5.00; 31.5 mm	**0.0000**
-5.00 to -4.50; 22.4 mm	**0.0000**
-4.50 to -4.00; 16 mm	**0.0000**
-4.00 to -3.50; 11.2 mm	**0.0000**
-3.50 to -3.00; 8 mm	**0.0000**
-3.00 to -2.50; 5.6 mm	**0.0000**
-2.50 to -2.00; 4 mm	**0.0000**
-2.00 to -1.50; 2.8 mm	**0.0000**
-1.50 to -1.00; 2 mm	**0.0000**
-1.00 to -0.50; 1.4 mm	**0.0024**
-0.50 to 0.00; 1 mm	**0.0027**
0.00 to 0.50; (707 µm)	0.0000
0.50 to 1.00; (500 µm)	1.0622
1.00 to 1.50; (353.6 µm)	9.3729
1.50 to 2.00; (250 µm)	22.8101
2.00 to 2.50; (176.8 µm)	28.7879
2.50 to 3.00; (125 µm)	20.3062
3.00 to 3.50; (88.39 µm)	7.2973
3.50 to 4.00; (62.5 µm)	0.8021
4.00 to 4.50; (44.19 µm)	0.0484
4.50 to 5.00; (31.25 µm)	0.9186
5.00 to 5.50; (22.097 µm)	1.2456
5.50 to 6.00; (15.625 µm)	0.9595
6.00 to 6.50; (11.049 µm)	0.8112
6.50 to 7.00; (7.813 µm)	0.9817
7.00 to 7.50; (5.524 µm)	1.1799
7.50 to 8.00; (3.906 µm)	1.1632
8.00 to 8.50; (2.762 µm)	0.9272
8.50 to 9.00; (1.953 µm)	0.6151
9.00 to 9.50; (1.381 µm)	0.3658
9.50 to 10.00; (0.977 µm)	0.2251
10.00 to 10.50; (0.691 µm)	0.1148
10.50 to 11.00; (0.488 µm)	0.0000
11.00 to 11.50; (0.345 µm)	0.0000
11.50 to 12.00; (0.244 µm)	0.0000
12.00 to 12.50; (0.173 µm)	0.0000
12.50 to 13.00; (0.122 µm)	0.0000
13.00 to 13.50; (0.086 µm)	0.0000

Appendix 1. Final Merged Data sheets as supplied by participating laboratories (arranged by Lab Code) and benchmark replicates. Where the Final Merged Data sheet was not filled in the Final Laser Data sheet has been shown.

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Exercise Code:	PS52
LabCode:	PSA_2108B
Sample Code:	PS522108B

Phi interval (explicit) + sieve mesh (theoretical sieves shown in brackets)	Volume/Weight (mark as "0" for not analysed or no material)
-6.50 to -6.00; 63 mm	**0.0000**
-6.00 to -5.50; 45 mm	**0.0000**
-5.50 to -5.00; 31.5 mm	**0.0000**
-5.00 to -4.50; 22.4 mm	**0.0000**
-4.50 to -4.00; 16 mm	**0.0000**
-4.00 to -3.50; 11.2 mm	**0.0000**
-3.50 to -3.00; 8 mm	**0.0000**
-3.00 to -2.50; 5.6 mm	**0.0000**
-2.50 to -2.00; 4 mm	**0.0000**
-2.00 to -1.50; 2.8 mm	**0.0000**
-1.50 to -1.00; 2 mm	**0.0000**
-1.00 to -0.50; 1.4 mm	**0.0020**
-0.50 to 0.00; 1 mm	**0.0027**
0.00 to 0.50; (707 µm)	0.0000
0.50 to 1.00; (500 µm)	0.9512
1.00 to 1.50; (353.6 µm)	9.1205
1.50 to 2.00; (250 µm)	22.7302
2.00 to 2.50; (176.8 µm)	29.0162
2.50 to 3.00; (125 µm)	20.5750
3.00 to 3.50; (88.39 µm)	7.3863
3.50 to 4.00; (62.5 µm)	0.7750
4.00 to 4.50; (44.19 µm)	0.0235
4.50 to 5.00; (31.25 µm)	0.8712
5.00 to 5.50; (22.097 µm)	1.2094
5.50 to 6.00; (15.625 µm)	0.9074
6.00 to 6.50; (11.049 µm)	0.7353
6.50 to 7.00; (7.813 µm)	0.8992
7.00 to 7.50; (5.524 µm)	1.1217
7.50 to 8.00; (3.906 µm)	1.1529
8.00 to 8.50; (2.762 µm)	0.9627
8.50 to 9.00; (1.953 µm)	0.6717
9.00 to 9.50; (1.381 µm)	0.4178
9.50 to 10.00; (0.977 µm)	0.2636
10.00 to 10.50; (0.691 µm)	0.1872
10.50 to 11.00; (0.488 µm)	0.0173
11.00 to 11.50; (0.345 µm)	0.0000
11.50 to 12.00; (0.244 µm)	0.0000
12.00 to 12.50; (0.173 µm)	0.0000
12.50 to 13.00; (0.122 µm)	0.0000
13.00 to 13.50; (0.086 µm)	0.0000

Appendix 1. Final Merged Data sheets as supplied by participating laboratories (arranged by Lab Code) and benchmark replicates. Where the Final Merged Data sheet was not filled in the Final Laser Data sheet has been shown.

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Exercise Code:	**PS52**
LabCode:	**PSA_2109**
Sample Code:	**PS522109**

Phi interval (explicit) + sieve mesh (theoretical sieves shown in brackets)	**Volume/Weight (mark as "0" for not analysed or no material)**
-6.50 to -6.00; 63 mm	**0.0000**
-6.00 to -5.50; 45 mm	**0.0000**
-5.50 to -5.00; 31.5 mm	**0.0000**
-5.00 to -4.50; 22.4 mm	**0.0000**
-4.50 to -4.00; 16 mm	**0.0000**
-4.00 to -3.50; 11.2 mm	**0.0000**
-3.50 to -3.00; 8 mm	**0.0000**
-3.00 to -2.50; 5.6 mm	**0.0000**
-2.50 to -2.00; 4 mm	**0.0000**
-2.00 to -1.50; 2.8 mm	**0.0000**
-1.50 to -1.00; 2 mm	**0.0000**
-1.00 to -0.50; 1.4 mm	**0.0000**
-0.50 to 0.00; 1 mm	**0.0250**
0.00 to 0.50; (707 µm)	0.0690
0.50 to 1.00; (500 µm)	0.2170
1.00 to 1.50; (353.6 µm)	6.1230
1.50 to 2.00; (250 µm)	24.0070
2.00 to 2.50; (176.8 µm)	100.0360
2.50 to 3.00; (125 µm)	129.9700
3.00 to 3.50; (88.39 µm)	22.7500
3.50 to 4.00; (62.5 µm)	11.6440
4.00 to 4.50; (44.19 µm)	0.0000
4.50 to 5.00; (31.25 µm)	0.0000
5.00 to 5.50; (22.097 µm)	0.0000
5.50 to 6.00; (15.625 µm)	9.8200
6.00 to 6.50; (11.049 µm)	0.0000
6.50 to 7.00; (7.813 µm)	0.0000
7.00 to 7.50; (5.524 µm)	0.0000
7.50 to 8.00; (3.906 µm)	10.6200
8.00 to 8.50; (2.762 µm)	0.0000
8.50 to 9.00; (1.953 µm)	0.0000
9.00 to 9.50; (1.381 µm)	0.0000
9.50 to 10.00; (0.977 µm)	6.1100
10.00 to 10.50; (0.691 µm)	0.0000
10.50 to 11.00; (0.488 µm)	0.0000
11.00 to 11.50; (0.345 µm)	0.0000
11.50 to 12.00; (0.244 µm)	0.0000
12.00 to 12.50; (0.173 µm)	0.0000
12.50 to 13.00; (0.122 µm)	0.0000
13.00 to 13.50; (0.086 µm)	0.0000

Appendix 1. Final Merged Data sheets as supplied by participating laboratories (arranged by Lab Code) and benchmark replicates. Where the Final Merged Data sheet was not filled in the Final Laser Data sheet has been shown.

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Exercise Code:	**PS52**
LabCode:	**PSA_2110**
Sample Code:	**PS522110**

Phi interval (explicit) + sieve mesh (theoretical sieves shown in brackets)	**Volume/Weight** (mark as "0" for not analysed or no material)
-6.50 to -6.00; 63 mm	**0.0000**
-6.00 to -5.50; 45 mm	**0.0000**
-5.50 to -5.00; 31.5 mm	**0.0000**
-5.00 to -4.50; 22.4 mm	**0.0000**
-4.50 to -4.00; 16 mm	**0.0000**
-4.00 to -3.50; 11.2 mm	**0.0000**
-3.50 to -3.00; 8 mm	**0.0000**
-3.00 to -2.50; 5.6 mm	**0.0000**
-2.50 to -2.00; 4 mm	**0.0000**
-2.00 to -1.50; 2.8 mm	**0.0000**
-1.50 to -1.00; 2 mm	**0.0000**
-1.00 to -0.50; 1.4 mm	**0.0000**
-0.50 to 0.00; 1 mm	**0.0000**
0.00 to 0.50; (707 µm)	*0.0000*
0.50 to 1.00; (500 µm)	*0.2100*
1.00 to 1.50; (353.6 µm)	*6.0900*
1.50 to 2.00; (250 µm)	*17.8900*
2.00 to 2.50; (176.8 µm)	*24.6300*
2.50 to 3.00; (125 µm)	*20.6000*
3.00 to 3.50; (88.39 µm)	*9.8800*
3.50 to 4.00; (62.5 µm)	*2.7600*
4.00 to 4.50; (44.19 µm)	*1.1600*
4.50 to 5.00; (31.25 µm)	*1.7400*
5.00 to 5.50; (22.097 µm)	*2.1200*
5.50 to 6.00; (15.625 µm)	*2.1500*
6.00 to 6.50; (11.049 µm)	*2.2600*
6.50 to 7.00; (7.813 µm)	*2.5600*
7.00 to 7.50; (5.524 µm)	*2.4200*
7.50 to 8.00; (3.906 µm)	*1.8600*
8.00 to 8.50; (2.762 µm)	*0.9900*
8.50 to 9.00; (1.953 µm)	*0.1700*
9.00 to 9.50; (1.381 µm)	*0.0000*
9.50 to 10.00; (0.977 µm)	*0.0000*
10.00 to 10.50; (0.691 µm)	*0.5100*
10.50 to 11.00; (0.488 µm)	
11.00 to 11.50; (0.345 µm)	
11.50 to 12.00; (0.244 µm)	
12.00 to 12.50; (0.173 µm)	
12.50 to 13.00; (0.122 µm)	
13.00 to 13.50; (0.086 µm)	

Appendix 1. Final Merged Data sheets as supplied by participating laboratories (arranged by Lab Code) and benchmark replicates. Where the Final Merged Data sheet was not filled in the Final Laser Data sheet has been shown.

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Exercise Code:	**PS52**
LabCode:	**PSA_2111**
Sample Code:	**PS522111**

Phi interval (explicit) + sieve mesh (theoretical sieves shown in brackets)	Volume/Weight (mark as "0" for not analysed or no material)
-6.50 to -6.00; 63 mm	
-6.00 to -5.50; 45 mm	
-5.50 to -5.00; 31.5 mm	
-5.00 to -4.50; 22.4 mm	
-4.50 to -4.00; 16 mm	
-4.00 to -3.50; 11.2 mm	
-3.50 to -3.00; 8 mm	
-3.00 to -2.50; 5.6 mm	
-2.50 to -2.00; 4 mm	
-2.00 to -1.50; 2.8 mm	
-1.50 to -1.00; 2 mm	
-1.00 to -0.50; 1.4 mm	
-0.50 to 0.00; 1 mm	
0.00 to 0.50; (707 µm)	0.00
0.50 to 1.00; (500 µm)	0.99
1.00 to 1.50; (353.6 µm)	8.01
1.50 to 2.00; (250 µm)	19.30
2.00 to 2.50; (176.8 µm)	23.61
2.50 to 3.00; (125 µm)	20.91
3.00 to 3.50; (88.39 µm)	8.86
3.50 to 4.00; (62.5 µm)	2.29
4.00 to 4.50; (44.19 µm)	0.57
4.50 to 5.00; (31.25 µm)	1.24
5.00 to 5.50; (22.097 µm)	1.72
5.50 to 6.00; (15.625 µm)	1.52
6.00 to 6.50; (11.049 µm)	1.55
6.50 to 7.00; (7.813 µm)	1.80
7.00 to 7.50; (5.524 µm)	2.02
7.50 to 8.00; (3.906 µm)	1.85
8.00 to 8.50; (2.762 µm)	
8.50 to 9.00; (1.953 µm)	2.32
9.00 to 9.50; (1.381 µm)	
9.50 to 10.00; (0.977 µm)	0.91
10.00 to 10.50; (0.691 µm)	0.52
10.50 to 11.00; (0.488 µm)	
11.00 to 11.50; (0.345 µm)	
11.50 to 12.00; (0.244 µm)	
12.00 to 12.50; (0.173 µm)	
12.50 to 13.00; (0.122 µm)	
13.00 to 13.50; (0.086 µm)	

Appendix 1. Final Merged Data sheets as supplied by participating laboratories (arranged by Lab Code) and benchmark replicates. Where the Final Merged Data sheet was not filled in the Final Laser Data sheet has been shown.

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Exercise Code:	PS52
LabCode:	PSA_2112
Sample Code:	PS522112

Phi interval (explicit) + sieve mesh (theoretical sieves shown in brackets)	Volume/Weight (mark as "0" for not analysed or no material)
-6.50 to -6.00; 63 mm	
-6.00 to -5.50; 45 mm	
-5.50 to -5.00; 31.5 mm	
-5.00 to -4.50; 22.4 mm	
-4.50 to -4.00; 16 mm	
-4.00 to -3.50; 11.2 mm	
-3.50 to -3.00; 8 mm	
-3.00 to -2.50; 5.6 mm	
-2.50 to -2.00; 4 mm	
-2.00 to -1.50; 2.8 mm	
-1.50 to -1.00; 2 mm	
-1.00 to -0.50; 1.4 mm	
-0.50 to 0.00; 1 mm	
0.00 to 0.50; (707 µm)	*0.0000*
0.50 to 1.00; (500 µm)	*0.2764*
1.00 to 1.50; (353.6 µm)	*6.2821*
1.50 to 2.00; (250 µm)	*17.1127*
2.00 to 2.50; (176.8 µm)	*20.9356*
2.50 to 3.00; (125 µm)	*18.3393*
3.00 to 3.50; (88.39 µm)	*8.0877*
3.50 to 4.00; (62.5 µm)	*3.1642*
4.00 to 4.50; (44.19 µm)	*1.6938*
4.50 to 5.00; (31.25 µm)	*2.3445*
5.00 to 5.50; (22.097 µm)	*2.5728*
5.50 to 6.00; (15.625 µm)	*2.8575*
6.00 to 6.50; (11.049 µm)	*3.3245*
6.50 to 7.00; (7.813 µm)	*3.7795*
7.00 to 7.50; (5.524 µm)	*3.7748*
7.50 to 8.00; (3.906 µm)	*3.0970*
8.00 to 8.50; (2.762 µm)	*1.7995*
8.50 to 9.00; (1.953 µm)	*0.5253*
9.00 to 9.50; (1.381 µm)	*0.0327*
9.50 to 10.00; (0.977 µm)	*0.0000*
10.00 to 10.50; (0.691 µm)	*0.0000*
10.50 to 11.00; (0.488 µm)	*0.0000*
11.00 to 11.50; (0.345 µm)	*0.0000*
11.50 to 12.00; (0.244 µm)	*0.0000*
12.00 to 12.50; (0.173 µm)	*0.0000*
12.50 to 13.00; (0.122 µm)	*0.0000*
13.00 to 13.50; (0.086 µm)	*0.0000*

Appendix 1. Final Merged Data sheets as supplied by participating laboratories (arranged by Lab Code) and benchmark replicates. Where the Final Merged Data sheet was not filled in the Final Laser Data sheet has been shown.

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Exercise Code:	PS52
LabCode:	PSA_2113
Sample Code:	PS522113

Phi interval (explicit) + sieve mesh (theoretical sieves shown in brackets)	Volume/Weight (mark as "0" for not analysed or no material)
-6.50 to -6.00; 63 mm	
-6.00 to -5.50; 45 mm	
-5.50 to -5.00; 31.5 mm	
-5.00 to -4.50; 22.4 mm	
-4.50 to -4.00; 16 mm	
-4.00 to -3.50; 11.2 mm	
-3.50 to -3.00; 8 mm	
-3.00 to -2.50; 5.6 mm	
-2.50 to -2.00; 4 mm	
-2.00 to -1.50; 2.8 mm	
-1.50 to -1.00; 2 mm	
-1.00 to -0.50; 1.4 mm	
-0.50 to 0.00; 1 mm	
0.00 to 0.50; (707 µm)	*0.0000*
0.50 to 1.00; (500 µm)	*0.0360*
1.00 to 1.50; (353.6 µm)	*4.7916*
1.50 to 2.00; (250 µm)	*19.3859*
2.00 to 2.50; (176.8 µm)	*30.4212*
2.50 to 3.00; (125 µm)	*23.6203*
3.00 to 3.50; (88.39 µm)	*8.7360*
3.50 to 4.00; (62.5 µm)	*0.9952*
4.00 to 4.50; (44.19 µm)	*0.1284*
4.50 to 5.00; (31.25 µm)	*1.1373*
5.00 to 5.50; (22.097 µm)	*1.5583*
5.50 to 6.00; (15.625 µm)	*1.3750*
6.00 to 6.50; (11.049 µm)	*1.3393*
6.50 to 7.00; (7.813 µm)	*1.5090*
7.00 to 7.50; (5.524 µm)	*1.5456*
7.50 to 8.00; (3.906 µm)	*1.3119*
8.00 to 8.50; (2.762 µm)	*0.9242*
8.50 to 9.00; (1.953 µm)	*0.5657*
9.00 to 9.50; (1.381 µm)	*0.3160*
9.50 to 10.00; (0.977 µm)	*0.1954*
10.00 to 10.50; (0.691 µm)	*0.0932*
10.50 to 11.00; (0.488 µm)	*0.0139*
11.00 to 11.50; (0.345 µm)	*0.0000*
11.50 to 12.00; (0.244 µm)	*0.0000*
12.00 to 12.50; (0.173 µm)	*0.0000*
12.50 to 13.00; (0.122 µm)	*0.0000*
13.00 to 13.50; (0.086 µm)	*0.0000*

Appendix 1. Final Merged Data sheets as supplied by participating laboratories (arranged by Lab Code) and benchmark replicates. Where the Final Merged Data sheet was not filled in the Final Laser Data sheet has been shown.

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Exercise Code:	**PS52**
LabCode:	**PSA_2114**
Sample Code:	**PS522114**

Phi interval (explicit) **+ sieve mesh (theoretical sieves shown in brackets)**	**Volume/Weight** **(mark as "0" for not analysed or no material)**
-6.50 to -6.00; 63 mm	**0.0000**
-6.00 to -5.50; 45 mm	**0.0000**
-5.50 to -5.00; 31.5 mm	**0.0000**
-5.00 to -4.50; 22.4 mm	**0.0000**
-4.50 to -4.00; 16 mm	**0.0000**
-4.00 to -3.50; 11.2 mm	**0.0000**
-3.50 to -3.00; 8 mm	**0.0000**
-3.00 to -2.50; 5.6 mm	**0.0000**
-2.50 to -2.00; 4 mm	**0.0000**
-2.00 to -1.50; 2.8 mm	**0.0000**
-1.50 to -1.00; 2 mm	**0.0000**
-1.00 to -0.50; 1.4 mm	**0.0000**
-0.50 to 0.00; 1 mm	**0.0000**
0.00 to 0.50; (707 µm)	0.0000
0.50 to 1.00; (500 µm)	0.4500
1.00 to 1.50; (353.6 µm)	7.6300
1.50 to 2.00; (250 µm)	19.9400
2.00 to 2.50; (176.8 µm)	25.6500
2.50 to 3.00; (125 µm)	19.8700
3.00 to 3.50; (88.39 µm)	8.4200
3.50 to 4.00; (62.5 µm)	1.8600
4.00 to 4.50; (44.19 µm)	0.8700
4.50 to 5.00; (31.25 µm)	1.4900
5.00 to 5.50; (22.097 µm)	1.6100
5.50 to 6.00; (15.625 µm)	1.4800
6.00 to 6.50; (11.049 µm)	1.6400
6.50 to 7.00; (7.813 µm)	2.0900
7.00 to 7.50; (5.524 µm)	2.1500
7.50 to 8.00; (3.906 µm)	1.8200
8.00 to 8.50; (2.762 µm)	1.3700
8.50 to 9.00; (1.953 µm)	0.7400
9.00 to 9.50; (1.381 µm)	0.3900
9.50 to 10.00; (0.977 µm)	0.2600
10.00 to 10.50; (0.691 µm)	0.2400
10.50 to 11.00; (0.488 µm)	0.0000
11.00 to 11.50; (0.345 µm)	0.0000
11.50 to 12.00; (0.244 µm)	0.0000
12.00 to 12.50; (0.173 µm)	0.0000
12.50 to 13.00; (0.122 µm)	0.0000
13.00 to 13.50; (0.086 µm)	0.0000

Appendix 1. Final Merged Data sheets as supplied by participating laboratories (arranged by Lab Code) and benchmark replicates. Where the Final Merged Data sheet was not filled in the Final Laser Data sheet has been shown.

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Exercise Code:	**PS52**
LabCode:	**PSA_21 BENCHMARK REP 1**
Sample Code:	**PS5221BMREP1**

Phi interval (explicit) **+ sieve mesh (theoretical sieves shown in brackets)**	**Volume/Weight** **(mark as "0" for not analysed or no material)**
-6.50 to -6.00; 63 mm	**0.0000**
-6.00 to -5.50; 45 mm	**0.0000**
-5.50 to -5.00; 31.5 mm	**0.0000**
-5.00 to -4.50; 22.4 mm	**0.0000**
-4.50 to -4.00; 16 mm	**0.0000**
-4.00 to -3.50; 11.2 mm	**0.0000**
-3.50 to -3.00; 8 mm	**0.0000**
-3.00 to -2.50; 5.6 mm	**0.0000**
-2.50 to -2.00; 4 mm	**0.0000**
-2.00 to -1.50; 2.8 mm	**0.0000**
-1.50 to -1.00; 2 mm	**0.0000**
-1.00 to -0.50; 1.4 mm	**0.0000**
-0.50 to 0.00; 1 mm	**0.0109**
0.00 to 0.50; (707 µm)	0.4474
0.50 to 1.00; (500 µm)	1.4127
1.00 to 1.50; (353.6 µm)	4.4306
1.50 to 2.00; (250 µm)	14.7054
2.00 to 2.50; (176.8 µm)	27.0186
2.50 to 3.00; (125 µm)	17.2039
3.00 to 3.50; (88.39 µm)	6.2018
3.50 to 4.00; (62.5 µm)	3.7979
4.00 to 4.50; (44.19 µm)	2.5006
4.50 to 5.00; (31.25 µm)	1.9747
5.00 to 5.50; (22.097 µm)	2.0789
5.50 to 6.00; (15.625 µm)	2.1751
6.00 to 6.50; (11.049 µm)	2.4754
6.50 to 7.00; (7.813 µm)	2.7808
7.00 to 7.50; (5.524 µm)	2.6960
7.50 to 8.00; (3.906 µm)	2.2687
8.00 to 8.50; (2.762 µm)	1.6778
8.50 to 9.00; (1.953 µm)	1.1305
9.00 to 9.50; (1.381 µm)	0.7314
9.50 to 10.00; (0.977 µm)	0.4850
10.00 to 10.50; (0.691 µm)	0.3613
10.50 to 11.00; (0.488 µm)	0.3096
11.00 to 11.50; (0.345 µm)	0.2864
11.50 to 12.00; (0.244 µm)	0.2685
12.00 to 12.50; (0.173 µm)	0.2367
12.50 to 13.00; (0.122 µm)	0.1974
13.00 to 13.50; (0.086 µm)	0.1359

Appendix 1. Final Merged Data sheets as supplied by participating laboratories (arranged by Lab Code) and benchmark replicates. Where the Final Merged Data sheet was not filled in the Final Laser Data sheet has been shown.

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Exercise Code:	**PS52**
LabCode:	**PSA_21 BENCHMARK REP 2**
Sample Code:	**PS5221BMREP2**

Phi interval (explicit) + sieve mesh (theoretical sieves shown in brackets)	Volume/Weight (mark as "0" for not analysed or no material)
-6.50 to -6.00; 63 mm	**0.0000**
-6.00 to -5.50; 45 mm	**0.0000**
-5.50 to -5.00; 31.5 mm	**0.0000**
-5.00 to -4.50; 22.4 mm	**0.0000**
-4.50 to -4.00; 16 mm	**0.0000**
-4.00 to -3.50; 11.2 mm	**0.0000**
-3.50 to -3.00; 8 mm	**0.0000**
-3.00 to -2.50; 5.6 mm	**0.0000**
-2.50 to -2.00; 4 mm	**0.0000**
-2.00 to -1.50; 2.8 mm	**0.0000**
-1.50 to -1.00; 2 mm	**0.0000**
-1.00 to -0.50; 1.4 mm	**0.0000**
-0.50 to 0.00; 1 mm	**0.0102**
0.00 to 0.50; (707 µm)	0.3727
0.50 to 1.00; (500 µm)	1.2343
1.00 to 1.50; (353.6 µm)	4.2363
1.50 to 2.00; (250 µm)	14.1740
2.00 to 2.50; (176.8 µm)	26.8813
2.50 to 3.00; (125 µm)	18.0482
3.00 to 3.50; (88.39 µm)	7.0366
3.50 to 4.00; (62.5 µm)	4.1830
4.00 to 4.50; (44.19 µm)	2.6305
4.50 to 5.00; (31.25 µm)	1.9185
5.00 to 5.50; (22.097 µm)	1.9672
5.50 to 6.00; (15.625 µm)	1.9987
6.00 to 6.50; (11.049 µm)	2.2521
6.50 to 7.00; (7.813 µm)	2.5561
7.00 to 7.50; (5.524 µm)	2.5220
7.50 to 8.00; (3.906 µm)	2.1667
8.00 to 8.50; (2.762 µm)	1.6401
8.50 to 9.00; (1.953 µm)	1.1316
9.00 to 9.50; (1.381 µm)	0.7477
9.50 to 10.00; (0.977 µm)	0.5027
10.00 to 10.50; (0.691 µm)	0.3743
10.50 to 11.00; (0.488 µm)	0.3164
11.00 to 11.50; (0.345 µm)	0.2873
11.50 to 12.00; (0.244 µm)	0.2645
12.00 to 12.50; (0.173 µm)	0.2294
12.50 to 13.00; (0.122 µm)	0.1891
13.00 to 13.50; (0.086 µm)	0.1286

Appendix 1. Final Merged Data sheets as supplied by participating laboratories (arranged by Lab Code) and benchmark replicates. Where the Final Merged Data sheet was not filled in the Final Laser Data sheet has been shown.

NMBAQCS - PS Exercise Data Workbook
(Page 2 - Final Merged Data Submission)

Return to APEM Ltd. by 31-10-14

Exercise Code:	**PS52**
LabCode:	**PSA_21 BENCHMARK REP 3**
Sample Code:	**PS5221BMREP3**

Phi interval (explicit) + sieve mesh (theoretical sieves shown in brackets)	**Volume/Weight (mark as "0" for not analysed or no material)**
-6.50 to -6.00; 63 mm	**0.0000**
-6.00 to -5.50; 45 mm	**0.0000**
-5.50 to -5.00; 31.5 mm	**0.0000**
-5.00 to -4.50; 22.4 mm	**0.0000**
-4.50 to -4.00; 16 mm	**0.0000**
-4.00 to -3.50; 11.2 mm	**0.0000**
-3.50 to -3.00; 8 mm	**0.0000**
-3.00 to -2.50; 5.6 mm	**0.0000**
-2.50 to -2.00; 4 mm	**0.0000**
-2.00 to -1.50; 2.8 mm	**0.0000**
-1.50 to -1.00; 2 mm	**0.0000**
-1.00 to -0.50; 1.4 mm	**0.0000**
-0.50 to 0.00; 1 mm	**0.0108**
0.00 to 0.50; (707 µm)	0.1382
0.50 to 1.00; (500 µm)	0.8732
1.00 to 1.50; (353.6 µm)	4.7645
1.50 to 2.00; (250 µm)	16.2752
2.00 to 2.50; (176.8 µm)	27.9746
2.50 to 3.00; (125 µm)	18.1299
3.00 to 3.50; (88.39 µm)	6.3563
3.50 to 4.00; (62.5 µm)	3.5544
4.00 to 4.50; (44.19 µm)	2.2177
4.50 to 5.00; (31.25 µm)	1.5350
5.00 to 5.50; (22.097 µm)	1.6051
5.50 to 6.00; (15.625 µm)	1.7672
6.00 to 6.50; (11.049 µm)	2.1978
6.50 to 7.00; (7.813 µm)	2.5625
7.00 to 7.50; (5.524 µm)	2.5374
7.50 to 8.00; (3.906 µm)	2.1774
8.00 to 8.50; (2.762 µm)	1.6278
8.50 to 9.00; (1.953 µm)	1.0868
9.00 to 9.50; (1.381 µm)	0.6868
9.50 to 10.00; (0.977 µm)	0.4475
10.00 to 10.50; (0.691 µm)	0.3295
10.50 to 11.00; (0.488 µm)	0.2739
11.00 to 11.50; (0.345 µm)	0.2406
11.50 to 12.00; (0.244 µm)	0.2128
12.00 to 12.50; (0.173 µm)	0.1780
12.50 to 13.00; (0.122 µm)	0.1432
13.00 to 13.50; (0.086 µm)	0.0960

Appendix 1. Final Merged Data sheets as supplied by participating laboratories (arranged by Lab Code) and benchmark replicates. Where the Final Merged Data sheet was not filled in the Final Laser Data sheet has been shown.

NMBAQCS - PS Exercise Data Workbook
(Page 2 - Final Merged Data Submission)

Return to APEM Ltd. by 31-10-14

Exercise Code:	PS52
LabCode:	PSA_21 BENCHMARK REP 4
Sample Code:	PS5221BMREP4

Phi interval (explicit) + sieve mesh (theoretical sieves shown in brackets)	Volume/Weight (mark as "0" for not analysed or no material)
-6.50 to -6.00; 63 mm	**0.0000**
-6.00 to -5.50; 45 mm	**0.0000**
-5.50 to -5.00; 31.5 mm	**0.0000**
-5.00 to -4.50; 22.4 mm	**0.0000**
-4.50 to -4.00; 16 mm	**0.0000**
-4.00 to -3.50; 11.2 mm	**0.0000**
-3.50 to -3.00; 8 mm	**0.0000**
-3.00 to -2.50; 5.6 mm	**0.0000**
-2.50 to -2.00; 4 mm	**0.0000**
-2.00 to -1.50; 2.8 mm	**0.0000**
-1.50 to -1.00; 2 mm	**0.0000**
-1.00 to -0.50; 1.4 mm	**0.0000**
-0.50 to 0.00; 1 mm	**0.0104**
0.00 to 0.50; (707 µm)	0.5283
0.50 to 1.00; (500 µm)	1.4320
1.00 to 1.50; (353.6 µm)	4.3206
1.50 to 2.00; (250 µm)	15.4266
2.00 to 2.50; (176.8 µm)	28.4486
2.50 to 3.00; (125 µm)	18.4210
3.00 to 3.50; (88.39 µm)	6.5990
3.50 to 4.00; (62.5 µm)	3.7209
4.00 to 4.50; (44.19 µm)	2.2691
4.50 to 5.00; (31.25 µm)	1.6406
5.00 to 5.50; (22.097 µm)	1.7079
5.50 to 6.00; (15.625 µm)	1.7216
6.00 to 6.50; (11.049 µm)	1.9623
6.50 to 7.00; (7.813 µm)	2.2498
7.00 to 7.50; (5.524 µm)	2.2441
7.50 to 8.00; (3.906 µm)	1.9551
8.00 to 8.50; (2.762 µm)	1.5003
8.50 to 9.00; (1.953 µm)	1.0437
9.00 to 9.50; (1.381 µm)	0.6925
9.50 to 10.00; (0.977 µm)	0.4684
10.00 to 10.50; (0.691 µm)	0.3508
10.50 to 11.00; (0.488 µm)	0.2955
11.00 to 11.50; (0.345 µm)	0.2647
11.50 to 12.00; (0.244 µm)	0.2397
12.00 to 12.50; (0.173 µm)	0.2051
12.50 to 13.00; (0.122 µm)	0.1676
13.00 to 13.50; (0.086 µm)	0.1136

Appendix 1. Final Merged Data sheets as supplied by participating laboratories (arranged by Lab Code) and benchmark replicates. Where the Final Merged Data sheet was not filled in the Final Laser Data sheet has been shown.

NMBAQCS - PS Exercise Data Workbook
(Page 2 - Final Merged Data Submission)

Return to APEM Ltd. by 31-10-14

Exercise Code:	**PS52**
LabCode:	**PSA_21 BENCHMARK REP 5**
Sample Code:	**PS5221BMREP5**

Phi interval (explicit) + sieve mesh (theoretical sieves shown in brackets)	**Volume/Weight (mark as "0" for not analysed or no material)**
-6.50 to -6.00; 63 mm	**0.0000**
-6.00 to -5.50; 45 mm	**0.0000**
-5.50 to -5.00; 31.5 mm	**0.0000**
-5.00 to -4.50; 22.4 mm	**0.0000**
-4.50 to -4.00; 16 mm	**0.0000**
-4.00 to -3.50; 11.2 mm	**0.0000**
-3.50 to -3.00; 8 mm	**0.0000**
-3.00 to -2.50; 5.6 mm	**0.0000**
-2.50 to -2.00; 4 mm	**0.0000**
-2.00 to -1.50; 2.8 mm	**0.0000**
-1.50 to -1.00; 2 mm	**0.0000**
-1.00 to -0.50; 1.4 mm	**0.0000**
-0.50 to 0.00; 1 mm	**0.0110**
0.00 to 0.50; (707 µm)	0.9512
0.50 to 1.00; (500 µm)	1.9874
1.00 to 1.50; (353.6 µm)	4.4241
1.50 to 2.00; (250 µm)	14.2650
2.00 to 2.50; (176.8 µm)	26.9292
2.50 to 3.00; (125 µm)	17.0093
3.00 to 3.50; (88.39 µm)	6.3350
3.50 to 4.00; (62.5 µm)	3.8214
4.00 to 4.50; (44.19 µm)	2.4030
4.50 to 5.00; (31.25 µm)	1.8189
5.00 to 5.50; (22.097 µm)	1.9430
5.50 to 6.00; (15.625 µm)	1.9860
6.00 to 6.50; (11.049 µm)	2.2668
6.50 to 7.00; (7.813 µm)	2.6666
7.00 to 7.50; (5.524 µm)	2.7036
7.50 to 8.00; (3.906 µm)	2.3615
8.00 to 8.50; (2.762 µm)	1.7952
8.50 to 9.00; (1.953 µm)	1.2247
9.00 to 9.50; (1.381 µm)	0.7869
9.50 to 10.00; (0.977 µm)	0.5097
10.00 to 10.50; (0.691 µm)	0.3701
10.50 to 11.00; (0.488 µm)	0.3121
11.00 to 11.50; (0.345 µm)	0.2867
11.50 to 12.00; (0.244 µm)	0.2680
12.00 to 12.50; (0.173 µm)	0.2352
12.50 to 13.00; (0.122 µm)	0.1953
13.00 to 13.50; (0.086 µm)	0.1334

Appendix 2. z-score calculations at each half phi-interval for participating laboratories and the benchmark average.

	Phi - interval																				
	-6.50 to -6.00	-6.00 to -5.50	-5.50 to -5.00	-5.00 to -4.50	-4.50 to -4.00	-4.00 to -3.50	-3.50 to -3.00	-3.00 to -2.50	-2.50 to -2.00	-2.00 to -1.50	z-score	-1.50 to -1.00	z-score	-1.00 to -0.50	z-score	-0.50 to 0.00	z-score	0.00 to 0.50	z-score	0.50 to 1.00	z-score
Benchmark Average	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.36	0.00	-0.36	0.00	-0.56	0.01	1.70	0.49	1.64	1.39	0.10
PSA_2101	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	3.16	0.00	1.48	0.00	2.35	0.01	1.67	0.69	2.54	1.66	0.26
PSA_2102	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.36	0.00	-0.36	0.00	-0.56	0.00	-0.67	0.00	-0.48	1.81	0.35
PSA_2103	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.36	0.00	-0.36	0.00	-0.56	0.00	-0.67	0.00	-0.48	0.22	-0.58
PSA_2105	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.36	0.00	-0.36	0.00	-0.56	0.01	1.76	0.45	1.47	1.41	0.12
PSA_2106	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.36	0.00	-0.36	0.00	-0.56	0.00	-0.67	0.00	-0.48	0.67	-0.32
PSA_2107	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	1.52	0.01	3.18	0.00	1.30	0.00	-0.67	0.00	-0.48	7.01	3.39
PSA_2108_A	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.36	0.00	-0.36	0.00	1.41	0.00	-0.07	0.00	-0.48	1.06	-0.09
PSA_2108_B	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.36	0.00	-0.36	0.00	1.13	0.00	-0.07	0.00	-0.48	0.95	-0.15
PSA_2109	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.36	0.00	-0.36	0.00	-0.56	0.01	1.06	0.02	-0.39	0.07	-0.67
PSA_2110	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.36	0.00	-0.36	0.00	-0.56	0.00	-0.67	0.00	-0.48	0.21	-0.59
PSA_2111	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.36	0.00	-0.36	0.00	-0.56	0.00	-0.67	0.00	-0.48	0.99	-0.13
PSA_2112	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.36	0.00	-0.36	0.00	-0.56	0.00	-0.67	0.00	-0.48	0.28	-0.55
PSA_2113	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.36	0.00	-0.36	0.00	-0.56	0.00	-0.67	0.00	-0.48	0.04	-0.69
PSA_2114	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.36	0.00	-0.36	0.00	-0.56	0.00	-0.67	0.00	-0.48	0.45	-0.45

MEAN	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.001		0.001		0.001		0.003		0.110		1.214	
STANDARD DEVIATION	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.003		0.002		0.001		0.004		0.230		1.707	

🟦 All labs recorded zero therefore the mean and standard deviation were also zero.

Appendix 2. z-score calculations at each half phi-interval for participating laboratories and the benchmark average.

	Phi-interval																					
	1.00 to 1.50	z-score	1.50 to 2.00	z-score	2.00 to 2.50	z-score	2.50 to 3.00	z-score	3.00 to 3.50	z-score	3.50 to 4.00	z-score	4.00 to 4.50	z-score	4.50 to 5.00	z-score	5.00 to 5.50	z-score	5.50 to 6.00	z-score	6.00 to 6.50	z-score
Benchmark Average	4.44	-0.60	14.97	-0.70	27.45	-0.01	17.76	-0.39	6.51	-0.41	3.82	1.10	2.40	1.66	1.78	0.82	1.86	0.63	1.93	0.46	2.23	0.87
PSA_2101	4.86	-0.53	17.14	-0.32	31.51	1.08	19.01	-0.20	5.79	-0.73	2.87	0.38	1.80	0.99	1.29	0.06	1.11	-0.43	1.29	-0.33	1.52	0.11
PSA_2102	9.35	0.30	19.14	0.03	23.67	-1.03	18.75	-0.24	9.06	0.74	2.24	-0.09	0.48	-0.50	1.18	-0.11	1.81	0.55	1.87	0.39	1.86	0.48
PSA_2103	10.12	0.44	22.93	0.70	28.53	0.28	21.38	0.16	9.12	0.77	1.75	-0.45	0.42	-0.55	1.15	-0.16	1.28	-0.18	0.82	-0.91	0.48	-0.98
PSA_2105	4.43	-0.60	14.71	-0.75	27.02	-0.13	17.20	-0.48	6.20	-0.55	3.80	1.08	2.50	1.77	1.97	1.12	2.08	0.93	2.18	0.77	2.48	1.13
PSA_2106	4.11	-0.66	15.23	-0.66	35.21	2.07	17.64	-0.41	8.21	0.36	4.59	1.68	1.68	0.85	1.63	0.59	1.05	-0.51	0.96	-0.74	0.92	-0.52
PSA_2107	25.43	3.24	33.72	2.60	24.85	-0.71	8.38	-1.84	0.60	-3.07	0.00	-1.77	0.00	-1.03	0.00	-1.93	0.00	-1.99	0.00	-1.93	0.00	-1.50
PSA_2108_A	9.37	0.30	22.81	0.68	28.79	0.35	20.31	0.00	7.30	-0.05	0.80	-1.17	0.05	-0.97	0.92	-0.51	1.25	-0.24	0.96	-0.74	0.81	-0.64
PSA_2108_B	9.12	0.25	22.73	0.66	29.02	0.41	20.57	0.04	7.39	-0.01	0.78	-1.19	0.02	-1.00	0.87	-0.58	1.21	-0.29	0.91	-0.80	0.74	-0.72
PSA_2109	1.91	-1.07	7.47	-2.02	31.13	0.98	40.44	3.09	7.08	-0.15	3.62	0.95	0.00	-1.03	0.00	-1.93	0.00	-1.99	3.06	1.86	0.00	-1.50
PSA_2110	6.09	-0.30	17.89	-0.19	24.63	-0.77	20.60	0.04	9.88	1.11	2.76	0.30	1.16	0.27	1.74	0.76	2.12	0.99	2.15	0.73	2.26	0.90
PSA_2111	8.01	0.05	19.30	0.06	23.61	-1.04	20.91	0.09	8.86	0.65	2.29	-0.05	0.57	-0.39	1.24	-0.02	1.72	0.43	1.52	-0.05	1.55	0.15
PSA_2112	6.28	-0.27	17.11	-0.33	20.94	-1.76	18.34	-0.30	8.09	0.30	3.16	0.61	1.69	0.87	2.34	1.69	2.57	1.63	2.86	1.61	3.32	2.04
PSA_2113	4.79	-0.54	19.39	0.07	30.42	0.79	23.62	0.51	8.74	0.59	1.00	-1.02	0.13	-0.89	1.14	-0.17	1.56	0.20	1.38	-0.23	1.34	-0.08
PSA_2114	7.63	-0.02	19.94	0.17	25.65	-0.50	19.87	-0.07	8.42	0.45	1.86	-0.37	0.87	-0.05	1.49	0.37	1.61	0.27	1.48	-0.10	1.64	0.24

MEAN	7.729		18.965		27.495		20.319		7.415		2.356		0.919		1.249		1.415		1.557		1.410	
STANDARD DEVIATION	5.456		5.681		3.722		6.501		2.222		1.332		0.893		0.647		0.712		0.807		0.940	

Appendix 2. z-score calculations at each half phi-interval for participating laboratories and the benchmark average.

	Phi-interval																					
	6.50 to 7.00	z-score	7.00 to 7.50	z-score	7.50 to 8.00	z-score	8.00 to 8.50	z-score	8.50 to 9.00	z-score	9.00 to 9.50	z-score	9.50 to 10.00	z-score	10.00 to 10.50	z-score	10.50 to 11.00	z-score	11.00 to 11.50	z-score	11.50 to 12.00	z-score
Benchmark Average	2.56	0.89	2.54	0.85	2.19	0.60	1.65	1.11	1.12	0.66	0.73	1.15	0.48	0.18	0.36	0.64	0.30	1.57	0.27	1.96	0.25	2.04
PSA_2101	1.68	0.06	1.67	0.02	1.46	-0.21	1.13	0.27	0.85	0.19	0.65	0.92	0.51	0.23	0.39	0.79	0.30	1.59	0.24	1.66	0.19	1.47
PSA_2102	2.01	0.37	2.11	0.44	1.94	0.33	1.49	0.85	0.89	0.26	0.35	0.04	0.00	-0.78	0.00	-1.05	0.00	-0.60	0.00	-0.53	0.00	-0.48
PSA_2103	0.44	-1.09	0.46	-1.14	0.41	-1.38	0.29	-1.07	0.18	-0.93	0.01	-0.96	0.00	-0.78	0.00	-1.05	0.00	-0.60	0.00	-0.53	0.00	-0.48
PSA_2105	2.78	1.09	2.70	1.00	2.27	0.70	1.68	1.15	1.13	0.67	0.73	1.15	0.49	0.19	0.36	0.66	0.31	1.63	0.29	2.08	0.27	2.22
PSA_2106	1.08	-0.50	1.11	-0.52	0.87	-0.87	1.18	0.35	1.21	0.81	1.08	2.17	0.63	0.48	0.56	1.60	0.31	1.61	0.07	0.13	0.00	-0.48
PSA_2107	0.00	-1.50	0.00	-1.58	0.00	-1.84	0.00	-1.54	0.00	-1.24	0.00	-0.99	0.00	-0.78	0.00	-1.05	0.00	-0.60	0.00	-0.53	0.00	-0.48
PSA_2108_A	0.98	-0.59	1.18	-0.45	1.16	-0.54	0.93	-0.05	0.62	-0.20	0.37	0.08	0.23	-0.33	0.11	-0.51	0.00	-0.60	0.00	-0.53	0.00	-0.48
PSA_2108_B	0.90	-0.66	1.12	-0.51	1.15	-0.55	0.96	0.01	0.67	-0.10	0.42	0.23	0.26	-0.25	0.19	-0.17	0.02	-0.48	0.00	-0.53	0.00	-0.48
PSA_2109	0.00	-1.50	0.00	-1.58	3.30	1.85	0.00	-1.54	0.00	-1.24	0.00	-0.99	1.90	3.02	0.00	-1.05	0.00	-0.60	0.00	-0.53	0.00	-0.48
PSA_2110	2.56	0.89	2.42	0.73	1.86	0.24	0.99	0.05	0.17	-0.95	0.00	-0.99	0.00	-0.78	0.51	1.36	0.00	-0.60	0.00	-0.53	0.00	-0.48
PSA_2111	1.80	0.17	2.02	0.35	1.85	0.23	0.00	-1.54	2.32	2.69	0.00	-0.99	0.91	1.04	0.52	1.40	0.00	-0.60	0.00	-0.53	0.00	-0.48
PSA_2112	3.78	2.02	3.77	2.03	3.10	1.62	1.80	1.35	0.53	-0.35	0.03	-0.90	0.00	-0.78	0.00	-1.05	0.00	-0.60	0.00	-0.53	0.00	-0.48
PSA_2113	1.51	-0.10	1.55	-0.10	1.31	-0.37	0.92	-0.06	0.57	-0.28	0.32	-0.07	0.20	-0.39	0.09	-0.61	0.01	-0.50	0.00	-0.53	0.00	-0.48
PSA_2114	2.09	0.45	2.15	0.48	1.82	0.19	1.37	0.66	0.74	0.01	0.39	0.15	0.26	-0.26	0.24	0.08	0.00	-0.60	0.00	-0.53	0.00	-0.48

MEAN	1.611	1.653	1.647	0.959	0.732	0.339	0.391	0.222	0.083	0.058	0.047
STANDARD DEVIATION	1.071	1.044	0.895	0.623	0.590	0.341	0.500	0.212	0.139	0.110	0.099

Appendix 2. z-score calculations at each half phi-interval for participating laboratories and the benchmark average.

	Phi-interval					
	12.00 to 12.50	z-score	12.50 to 13.00	z-score	13.00 to 13.50	z-score
Benchmark Average	0.22	2.09	0.18	2.12	0.12	1.94
PSA_2101	0.14	1.24	0.11	1.09	0.10	1.59
PSA_2102	0.00	-0.47	0.00	-0.47	0.00	-0.48
PSA_2103	0.00	-0.47	0.00	-0.47	0.00	-0.48
PSA_2105	0.24	2.33	0.20	2.39	0.14	2.23
PSA_2106	0.00	-0.47	0.00	-0.47	0.00	-0.48
PSA_2107	0.00	-0.47	0.00	-0.47	0.00	-0.48
PSA_2108_A	0.00	-0.47	0.00	-0.47	0.00	-0.48
PSA_2108_B	0.00	-0.47	0.00	-0.47	0.00	-0.48
PSA_2109	0.00	-0.47	0.00	-0.47	0.00	-0.48
PSA_2110	0.00	-0.47	0.00	-0.47	0.00	-0.48
PSA_2111	0.00	-0.47	0.00	-0.47	0.00	-0.48
PSA_2112	0.00	-0.47	0.00	-0.47	0.00	-0.48
PSA_2113	0.00	-0.47	0.00	-0.47	0.00	-0.48
PSA_2114	0.00	-0.47	0.00	-0.47	0.00	-0.48

MEAN	0.040	0.032	0.024
STANDARD DEVIATION	0.085	0.069	0.050