

**The National Marine Biological Analytical Quality Control Scheme**

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**Particle Size Results – PS53**

Lydia Finbow and David Hall  
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Email: [nmbaqc@apemltd.com](mailto:nmbaqc@apemltd.com)



## **Contents**

### **Tables**

- Table 1. Summary of the methodology and sieve metadata information received from participating laboratories and replicate analysis laboratory for the fifty-third particle size distribution - PS53.
- Table 2. Summary of the methodology and <1mm; >0.00 phi metadata received from participating laboratories and replicate analysis laboratory for the fifty-third particle size distribution - PS53.
- Table 3. Summary of the particle size information received from participating laboratories and replicate analysis for the fifty-third particle size distribution – PS53.
- Table 4. Summary of the z-scores for each half phi-interval for PS53.

### **Figures**

- Figure 1. Particle size distribution curves resulting from analysis of five replicate samples of sediment distributed as PS53 (Benchmark Data).
- Figure 2. Particle size distribution curves from all participating laboratories and the benchmark average for sediment sample from PS53.
- Figure 3. PSA Particle size ternary diagrams for PS53, including the Benchmark replicates and all participating laboratories for Gravel, Sand and Mud.
- Figure 4. Bar chart for PS53 showing the percentage gravel, sand and silt/ clay recorded by each participating laboratory and the benchmark average.
- Figure 5. Summary of z-scores at each half phi-interval for the benchmark data.
- Figures 6 - 9. Summary of z-scores at each half phi-interval for participating laboratories.
- Figure 10. Cluster dendrogram from a Euclidean distance matrix for all participating laboratories with the benchmark replicates averaged.
- Figure 11. Non-metric Multi-Dimensional Scaling plots from a Euclidean distance matrix for (a) all participating laboratories and the benchmark average, (b) a subset of figure 11a and (c) a subset of figure 11b.

## **Appendices**

- Appendix 1. Final Merged Data sheets as supplied by participating laboratories (arranged by Lab Code) and the benchmark replicates.
- Appendix 2. Z-score calculations when data from all participating laboratories are included in the mean and standard deviation calculations.

## **PARTICLE SIZE EXERCISE DETAILS**

### **Particle Size (PS) #53**

**Type/Contents/Origin/Pre-treatments:** ~920g Sand (Swanage) <0.5 mm pre-sieve + 1kg Gravel (aggregate source) @ various prescribed ½ phi categories

**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-third particle size distribution - PS53.**

Benchmark	Method	Sieves used	Phi; sieve mesh		Total Weight (g)
			Weight (g)	Weight (g)	
			< 0.00; >1 mm	> 0.00; <1 mm	
REPLICATE 1	NMBAQC	<input checked="" type="checkbox"/>	957.6	872.9	1830.5
REPLICATE 2	NMBAQC	<input checked="" type="checkbox"/>	954.2	878.8	1833.0
REPLICATE 3	NMBAQC	<input checked="" type="checkbox"/>	942.1	879.7	1821.8
REPLICATE 4	NMBAQC	<input checked="" type="checkbox"/>	942.7	880.0	1822.7
REPLICATE 5	NMBAQC	<input checked="" type="checkbox"/>	967.4	881.5	1848.9
BM AVERAGE	NMBAQC	<input checked="" type="checkbox"/>	952.80	878.58	1831.38

Participant	Method	Sieves used	Phi; sieve mesh		Total Weight (g)
			Weight (g)	Weight (g)	
			< 0.00; >1 mm	> 0.00; <1 mm	
PSA_2101	NMBAQC	<input checked="" type="checkbox"/>	956.7	891.8	1848.5
PSA_2102	NMBAQC	<input checked="" type="checkbox"/>	990.5	911.9	1902.4
PSA_2103	NMBAQC	<input checked="" type="checkbox"/>	992.6	902.8	1895.5
PSA_2105	NMBAQC	<input checked="" type="checkbox"/>	957.6	872.9	1830.5
PSA_2106	NMBAQC	<input checked="" type="checkbox"/>	52.2	0.0	52.2
PSA_2107	NMBAQC	<input checked="" type="checkbox"/>	992.9	322.0	1314.9
PSA_2108_A	NMBAQC <sup>1</sup>	<input checked="" type="checkbox"/>	991.2	882.3	1873.5
PSA_2108_B	NMBAQC <sup>1</sup>	<input checked="" type="checkbox"/>	991.7	883.0	1874.7
PSA_2109	NMBAQC	<input checked="" type="checkbox"/>	993.1	914.5	1907.6
PSA_2110	NMBAQC	<input checked="" type="checkbox"/>	992.3	913.8	1906.1
PSA_2111	NMBAQC	<input checked="" type="checkbox"/>	985.5	903.4	1888.9
PSA_2112	NMBAQC	<input checked="" type="checkbox"/>	968.7	1.2	969.9
PSA_2113	NMBAQC	<input checked="" type="checkbox"/>	989.8	893.2	1882.9
PSA_2114	NMBAQC	<input checked="" type="checkbox"/>	941.4	866.2	1807.6

**Key to methods**

NMBAQC - NMBAQC PSA SOP for supporting biological data

NMBAQC<sup>1</sup> - NMBAQC PSA SOP for supporting biological data - incorporating BS1377: 1990 Parts 1-2 (sieving) and BS13320: 2009 (laser diffraction)

**Table 2. Summary of the <1mm; >0.00 phi laser metadata received from participating laboratories and replicate analysis laboratory for the fifty-third particle size distribution - PS53.**

Benchmark	Laser Used	% Sand				% Silt				% Clay 8 - 13 phi
		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	
REPLICATE 1	<input checked="" type="checkbox"/>	2.98	56.63	35.99	2.33	0.41	0.24	0.20	0.22	0.99
REPLICATE 2	<input checked="" type="checkbox"/>	3.29	57.47	35.41	2.17	0.34	0.19	0.14	0.15	0.83
REPLICATE 3	<input checked="" type="checkbox"/>	4.27	61.82	30.85	1.61	0.27	0.16	0.12	0.13	0.77
REPLICATE 4	<input checked="" type="checkbox"/>	4.53	61.76	30.70	1.63	0.25	0.15	0.11	0.12	0.75
REPLICATE 5	<input checked="" type="checkbox"/>	3.48	57.48	34.84	2.29	0.42	0.28	0.18	0.17	0.87
BM AVERAGE	<input checked="" type="checkbox"/>	3.71	59.03	33.56	2.01	0.34	0.21	0.15	0.16	0.84

Participant	Laser Used	% Sand				% Silt				% Clay 8 - 13 phi
		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	
PSA_2101	<input checked="" type="checkbox"/>	5.66	59.73	31.62	1.48	0.23	0.10	0.11	0.12	0.95
PSA_2102	<input checked="" type="checkbox"/>	5.32	56.98	37.00	0.69	0.00	0.00	0.00	0.00	0.00
PSA_2103	<input checked="" type="checkbox"/>	5.68	59.93	34.04	0.35	0.00	0.00	0.00	0.00	0.00
PSA_2105	<input checked="" type="checkbox"/>	2.98	56.63	35.99	2.33	0.41	0.24	0.20	0.22	0.99
PSA_2106	<input checked="" type="checkbox"/>	-	-	-	-	-	-	-	-	-
PSA_2107	<input checked="" type="checkbox"/>	0.58	34.04	49.85	7.68	0.73	2.26	1.98	1.94	0.95
PSA_2108_A	<input checked="" type="checkbox"/>	6.51	60.20	32.97	0.33	0.00	0.00	0.00	0.00	0.00
PSA_2108_B	<input checked="" type="checkbox"/>	6.46	60.33	32.91	0.31	0.00	0.00	0.00	0.00	0.00
PSA_2109	<input checked="" type="checkbox"/>	0.05	45.94	51.87	2.07	0.06	0.00	0.00	0.00	0.00
PSA_2110	<input checked="" type="checkbox"/>	3.49	52.40	42.54	1.57	0.00	0.00	0.00	0.00	0.00
PSA_2111	<input checked="" type="checkbox"/>	5.34	56.03	37.75	0.88	0.00	0.00	0.00	0.00	0.00
PSA_2112	<input checked="" type="checkbox"/>	4.25	58.34	36.63	0.78	0.00	0.00	0.00	0.00	0.00
PSA_2113	<input checked="" type="checkbox"/>	0.04	24.18	54.04	9.73	1.27	2.93	2.85	2.86	2.11
PSA_2114	<input checked="" type="checkbox"/>	5.41	58.33	35.52	0.74	0.00	0.00	0.00	0.00	0.00

Percentages taken from the final laser data.

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

- Did not record any material <1mm; > 0 phi in the laser tab

**Table 3. Summary of the particle size information received from participating laboratories and replicate analysis laboratory for the fifty-third particle size distribution - PS53.**

**Benchmark Data**

Lab	% Gravel	% Sand	% Silt/ Clay	Sediment Description (Post analysis)	Summary Data APEM verification			
					% Gravel	% Sand	% Silt/Clay	Sediment Description (Post analysis)
REPLICATE 1	52.06	47.03	0.92	Sandy Gravel	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> Sandy Gravel
REPLICATE 2	51.71	47.49	0.80	Sandy Gravel	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> Sandy Gravel
REPLICATE 3	51.72	47.58	0.70	Sandy Gravel	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> Sandy Gravel
REPLICATE 4	52.32	47.02	0.66	Sandy Gravel	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> Sandy Gravel
REPLICATE 5	52.31	46.70	0.98	Sandy Gravel	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> Sandy Gravel
REP AVERAGE	52.03	47.16	0.81	Sandy Gravel	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> Sandy Gravel

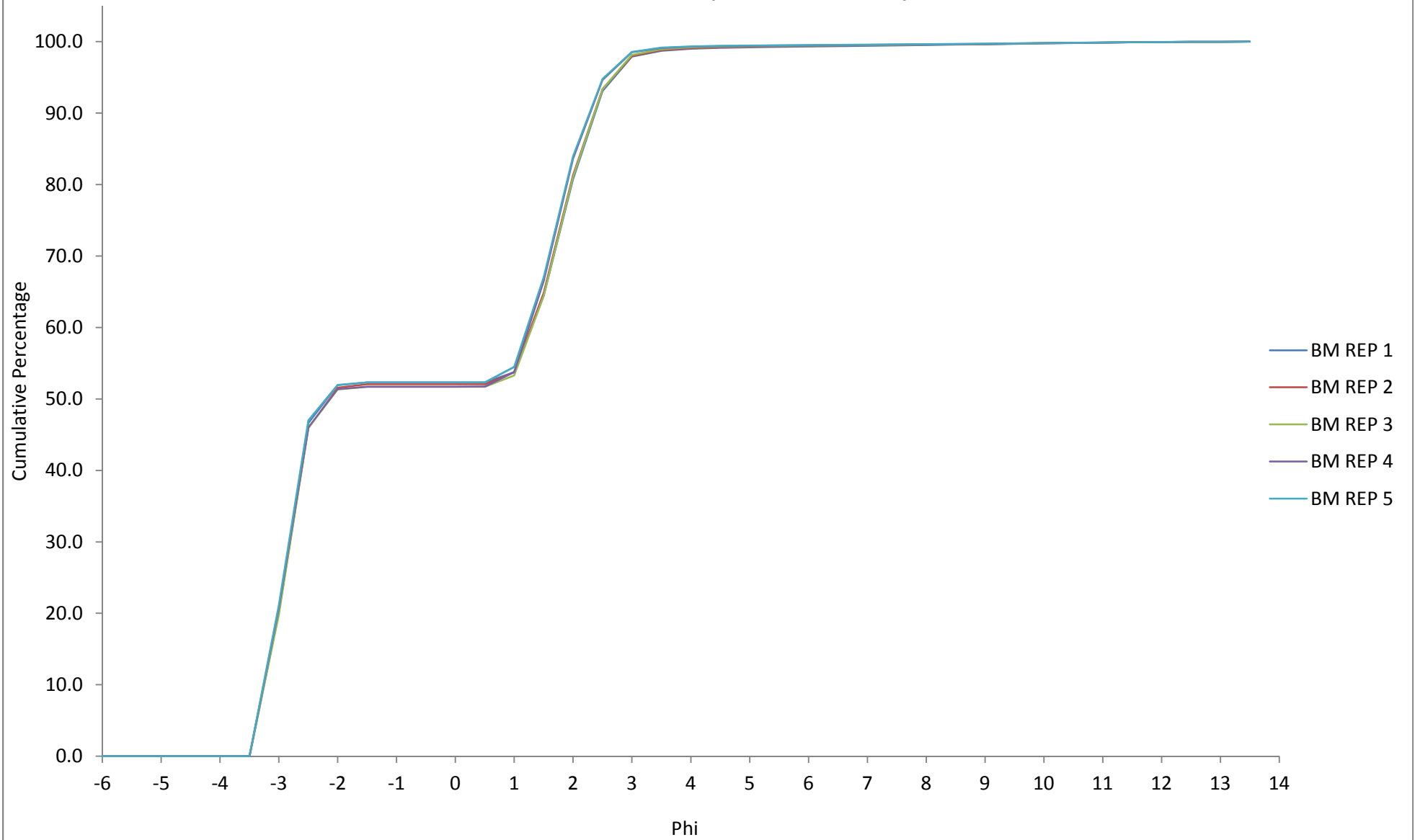
**Participant Data**

Lab	% Gravel	% Sand	% Silt/ Clay	Sediment Description (Post analysis)	Summary Data APEM verification			
					% Gravel	% Sand	% Silt/Clay	Sediment Description (Post analysis)
PSA_2101	51.75	47.52	0.73	Sandy gravel	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	sandy gravel
PSA_2102	52.06	47.94	0.00	Sandy gravel	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	sandy gravel
PSA_2103	52.37	47.63	0.00	Sandy gravel	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	sandy gravel
PSA_2105	52.06	47.03	0.92	Sandy gravel	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	sandy gravel
PSA_2106	52.00	48.00	0.00	Sandy gravel	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	sandy gravel
PSA_2107	75.50	22.60	1.90	Sandy gravel	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	very slightly muddy sandy gravel
PSA_2108_A	52.90	47.10	0.00	Sandy gravel	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	sandy gravel
PSA_2108_B	52.90	47.10	0.00	Sandy gravel	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	sandy gravel
PSA_2109	52.10	47.90	0.00	Sandy gravel	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	sandy gravel
PSA_2110	52.06	47.94	0.00	Sandy Gravel	<input checked="" type="checkbox"/> N/A	<input checked="" type="checkbox"/> N/A	<input checked="" type="checkbox"/> N/A	sandy gravel
PSA_2111	90.79	9.21	0.00	Gravel	<input checked="" type="checkbox"/> N/A	<input checked="" type="checkbox"/> N/A	<input checked="" type="checkbox"/> N/A	slightly sandy gravel
PSA_2112	53.50	46.50	0.00	Sandy gravel	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	sandy gravel
PSA_2113	52.57	41.74	5.70	Muddy sandy gravel	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	slightly muddy sandy gravel
PSA_2114	52.30	47.70	0.00	Sandy gravel	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	sandy gravel

Red text - Not provided, calculated by APEM

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

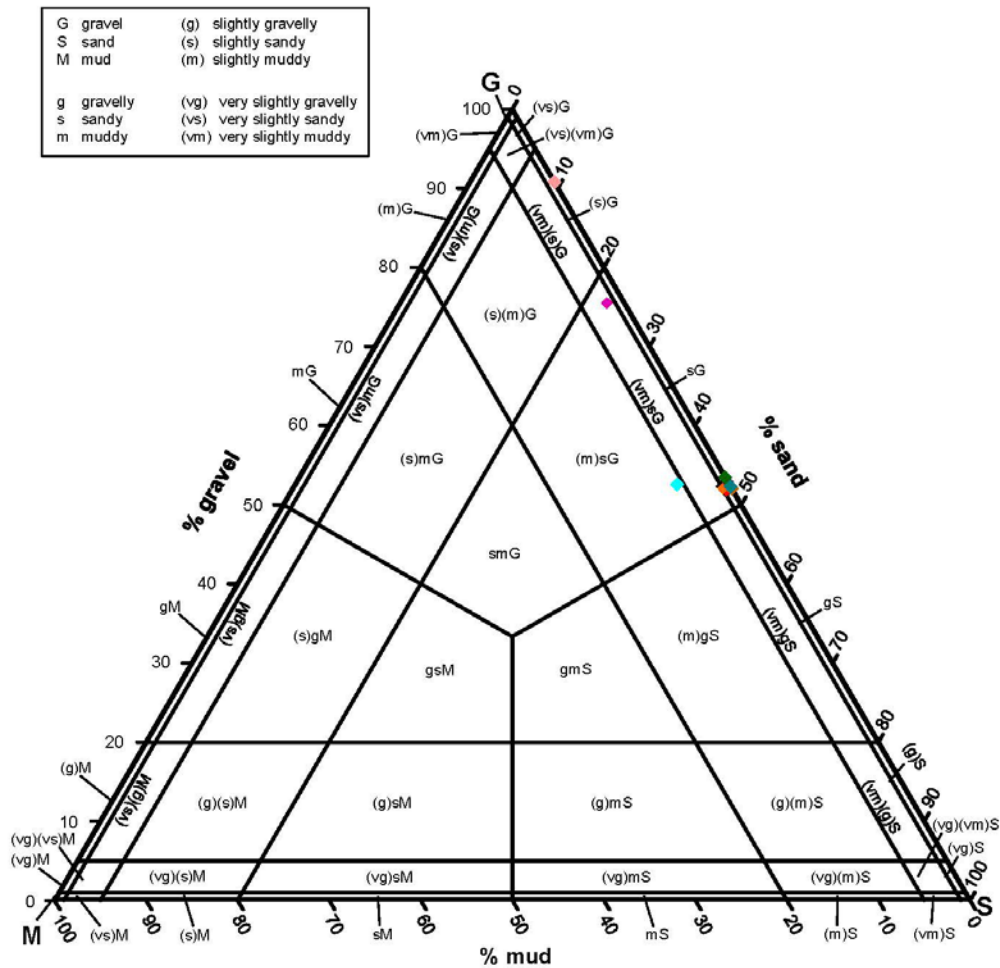
**Figure 1. Particle size distribution curves resulting from analysis of 5 replicate samples of sediment distributed as PS53 (Benchmark Data).**





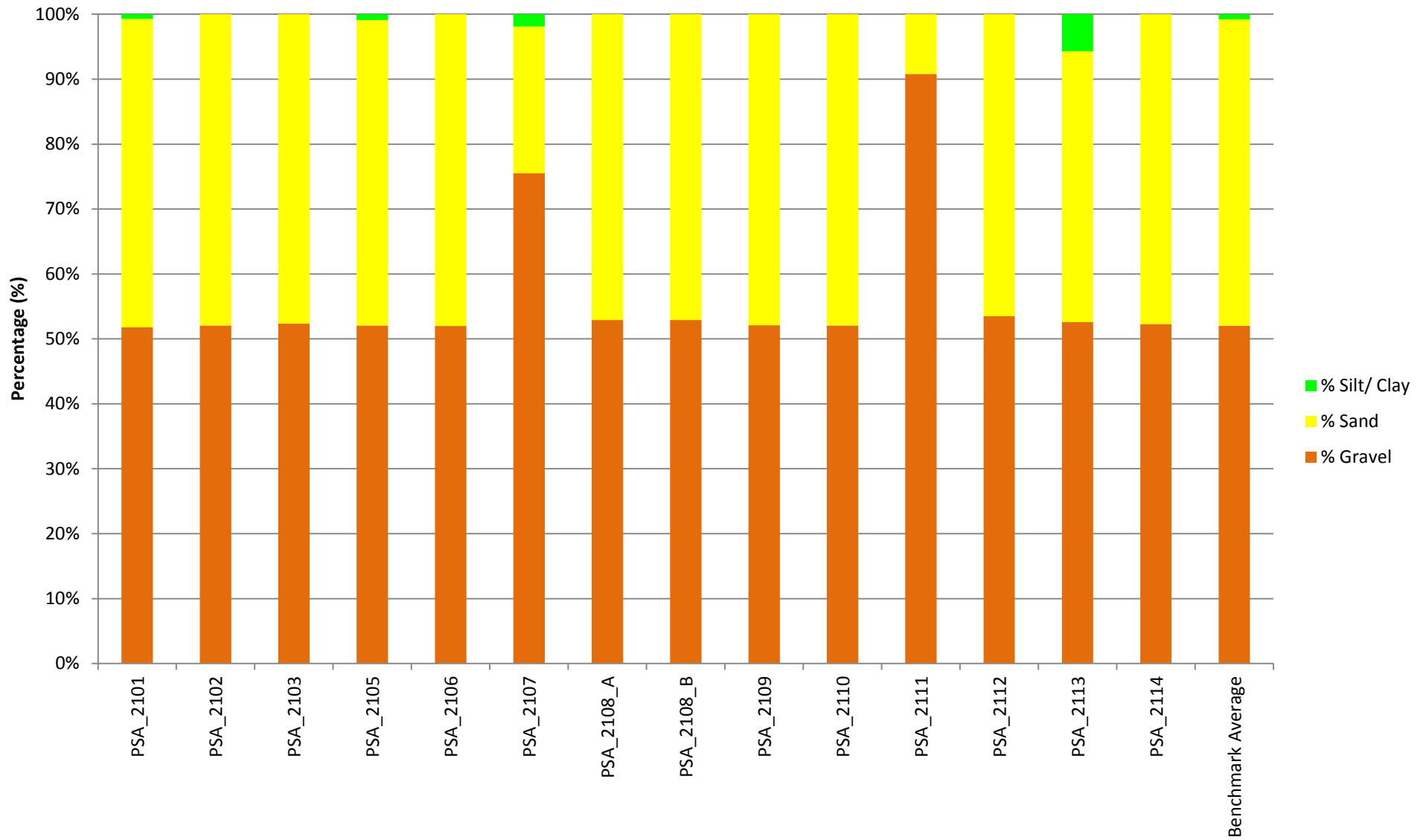


**Figure 3. PSA Particle size ternary diagrams for PS53 including the Benchmark replicates and all participating laboratories for Gravel, Sand and Mud.**



Laboratory		
◆ PS21 Benchmark Data	◆ PSA_2106	◆ PSA_2110
◆ PSA_2101	◆ PSA_2107	◆ PSA_2111
◆ PSA_2102	◆ PSA_2108A	◆ PSA_2112
◆ PSA_2103	◆ PSA_2108B	◆ PSA_2113
◆ PSA_2105	◆ PSA_2109	◆ PSA_2114

**Figure 4. Bar chart for PS53 showing the percentage gravel, sand and silt recorded by each participating laboratory and the benchmark average.**



**Table 4. Summary of z-scores for each phi-interval for PS53.**

	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	-0.26	-0.32	-0.14	-0.22	0.01	-0.17	-1.08	-0.58	-0.44	-0.41	0.16	0.85	0.34	-0.08	-0.30	-0.04
PSA_2101	0.00	0.00	0.00	0.00	-0.26	-0.32	-1.03	-0.03	0.58	-0.23	1.06	-0.64	0.11	3.33	0.77	0.89	0.41	-0.15	-0.55	-0.21
PSA_2102	0.00	0.00	0.00	0.00	-0.26	-0.30	-0.64	-0.26	1.07	0.11	0.41	1.60	0.82	0.24	0.79	0.55	0.38	0.34	-0.20	-0.43
PSA_2103	0.00	0.00	0.00	0.00	-0.26	-0.17	-0.68	0.00	-0.35	-0.46	1.17	-0.64	-0.50	-0.46	0.96	0.76	0.46	0.13	-0.54	-0.59
PSA_2105	0.00	0.00	0.00	0.00	-0.26	-0.32	-0.15	-0.19	0.01	-0.22	-1.42	-0.64	-0.50	-0.44	-0.15	0.62	0.26	0.11	-0.12	0.05
PSA_2106	0.00	0.00	0.00	0.00	-0.26	-0.17	-0.64	-0.09	-0.10	-0.01	-0.59	1.55	3.33	-0.45	-1.37	-1.02	1.22	1.17	0.43	-0.38
PSA_2107	0.00	0.00	0.00	0.00	-0.26	-0.14	1.37	1.33	0.93	1.12	1.35	1.34	0.35	-0.46	-1.25	-1.42	-1.89	-1.43	-0.03	0.94
PSA_2108_A	0.00	0.00	0.00	0.00	-0.26	-0.32	-0.40	-0.02	-0.10	-0.01	1.29	-0.42	-0.26	0.66	1.21	0.79	0.40	-0.01	-0.64	-0.60
PSA_2108_B	0.00	0.00	0.00	0.00	-0.26	-0.32	-0.32	-0.04	-0.16	0.09	0.51	-0.31	-0.26	0.56	1.19	0.80	0.41	-0.01	-0.65	-0.61
PSA_2109	0.00	0.00	0.00	0.00	-0.26	-0.24	-0.28	-0.13	-0.41	-0.40	-0.01	-0.56	-0.47	-0.42	-1.35	-1.14	0.67	1.20	1.58	0.04
PSA_2110	0.00	0.00	0.00	0.00	-0.26	-0.32	-0.53	-0.02	-0.32	0.06	0.16	-0.64	-0.50	-0.46	0.07	0.16	0.25	0.66	0.47	-0.02
PSA_2111	0.00	0.00	0.00	0.00	-0.26	-0.27	2.39	2.35	2.03	2.79	0.04	-0.64	-0.50	-0.30	-0.96	-1.59	-2.40	-2.83	-1.70	-0.67
PSA_2112	0.00	0.00	0.00	0.00	-0.26	-0.24	-0.19	-0.08	-0.10	-0.25	-1.42	-0.64	-0.19	-0.46	0.44	0.55	0.31	0.04	-0.05	-0.37
PSA_2113	0.00	0.00	0.00	0.00	3.61	3.61	1.77	-2.56	-2.62	-2.07	-0.07	1.85	-0.50	-0.46	-1.36	-1.51	-1.18	0.73	2.56	3.30
PSA_2114	0.00	0.00	0.00	0.00	-0.26	-0.15	-0.52	-0.05	-0.46	-0.34	-1.42	-0.64	-0.50	-0.46	0.85	0.70	0.36	0.14	-0.26	-0.41
$\bar{x}$	0.00	0.00	0.00	0.00	0.09	1.66	20.95	28.02	5.32	0.43	0.01	0.00	0.00	0.03	1.59	8.27	14.99	11.99	5.09	0.77
s	0.00	0.00	0.00	0.00	0.36	5.15	3.62	9.72	1.87	0.20	0.01	0.00	0.00	0.06	1.16	3.98	4.90	3.37	2.39	1.02



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 PS53.**

	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	0.89	1.75	0.01	-0.11	-0.15	-0.17	-0.19	-0.19	-0.16	-0.06	0.19	0.71	1.12	1.47	1.66	1.64	1.60	1.59	1.57	1.10
PSA_2101	0.38	1.11	-0.15	-0.27	-0.26	-0.24	-0.23	-0.23	-0.21	-0.14	0.08	0.62	1.27	1.83	2.15	2.24	2.34	2.40	2.44	3.02
PSA_2102	-0.76	-0.68	-0.42	-0.40	-0.39	-0.39	-0.38	-0.38	-0.39	-0.41	-0.46	-0.53	-0.56	-0.58	-0.51	-0.48	-0.48	-0.48	-0.48	-0.44
PSA_2103	-0.76	-0.68	-0.42	-0.40	-0.39	-0.39	-0.38	-0.38	-0.39	-0.41	-0.46	-0.53	-0.56	-0.58	-0.51	-0.48	-0.48	-0.48	-0.48	-0.44
PSA_2105	1.28	2.25	0.10	-0.08	-0.10	-0.11	-0.12	-0.11	-0.06	0.07	0.37	0.98	1.42	1.79	1.94	1.87	1.79	1.73	1.70	1.17
PSA_2106	0.22	0.11	-0.42	-0.40	-0.39	-0.39	-0.38	-0.38	-0.39	-0.41	-0.46	-0.53	-0.56	-0.58	-0.51	-0.48	-0.48	-0.48	-0.48	-0.44
PSA_2107	0.28	-0.60	0.83	1.09	1.09	1.00	0.95	0.97	0.91	0.78	0.62	-0.06	-0.56	-0.58	-0.51	-0.48	-0.48	-0.48	-0.48	-0.44
PSA_2108_A	-0.76	-0.68	-0.42	-0.40	-0.39	-0.39	-0.38	-0.38	-0.39	-0.41	-0.46	-0.53	-0.56	-0.58	-0.51	-0.48	-0.48	-0.48	-0.48	-0.44
PSA_2108_B	-0.76	-0.68	-0.42	-0.40	-0.39	-0.39	-0.38	-0.38	-0.39	-0.41	-0.46	-0.53	-0.56	-0.58	-0.51	-0.48	-0.48	-0.48	-0.48	-0.44
PSA_2109	0.54	0.00	-0.42	-0.40	-0.39	-0.39	-0.38	-0.38	-0.39	-0.41	-0.46	-0.53	-0.56	-0.58	-0.51	-0.48	-0.48	-0.48	-0.48	-0.44
PSA_2110	-0.76	-0.68	-0.42	-0.40	-0.39	-0.39	-0.38	-0.38	-0.39	-0.41	-0.46	-0.53	-0.56	-0.58	-0.51	-0.48	-0.48	-0.48	-0.48	-0.44
PSA_2111	-0.76	-0.68	-0.42	-0.40	-0.39	-0.39	-0.38	-0.38	-0.39	-0.41	-0.46	-0.53	-0.56	-0.58	-0.51	-0.48	-0.48	-0.48	-0.48	-0.44
PSA_2112	-0.76	-0.68	-0.42	-0.40	-0.39	-0.39	-0.38	-0.38	-0.39	-0.41	-0.46	-0.53	-0.56	-0.58	-0.51	-0.48	-0.48	-0.48	-0.48	-0.44
PSA_2113	2.52	0.78	3.40	3.34	3.34	3.38	3.40	3.39	3.41	3.42	3.36	3.06	2.37	1.27	-0.18	-0.48	-0.48	-0.48	-0.48	-0.44
PSA_2114	-0.76	-0.68	-0.42	-0.40	-0.39	-0.39	-0.38	-0.38	-0.39	-0.41	-0.46	-0.53	-0.56	-0.58	-0.51	-0.48	-0.48	-0.48	-0.48	-0.44

$\bar{x}$	0.11	0.03	0.06	0.08	0.07	0.07	0.07	0.07	0.06	0.05	0.03	0.02	0.02	0.01	0.01	0.01	0.01	0.01	0.00	0.00
s	0.14	0.04	0.14	0.20	0.17	0.17	0.19	0.19	0.16	0.11	0.07	0.04	0.03	0.02	0.02	0.02	0.01	0.01	0.01	0.01

z < -1.96 or z > 1.96

All laboratories recorded zero therefore mean and standard deviation equal zero.

**Figure 5. Summary of z-scores for the Benchmark Average; when data from all participating laboratories are included in the mean and standard deviation calculations.**

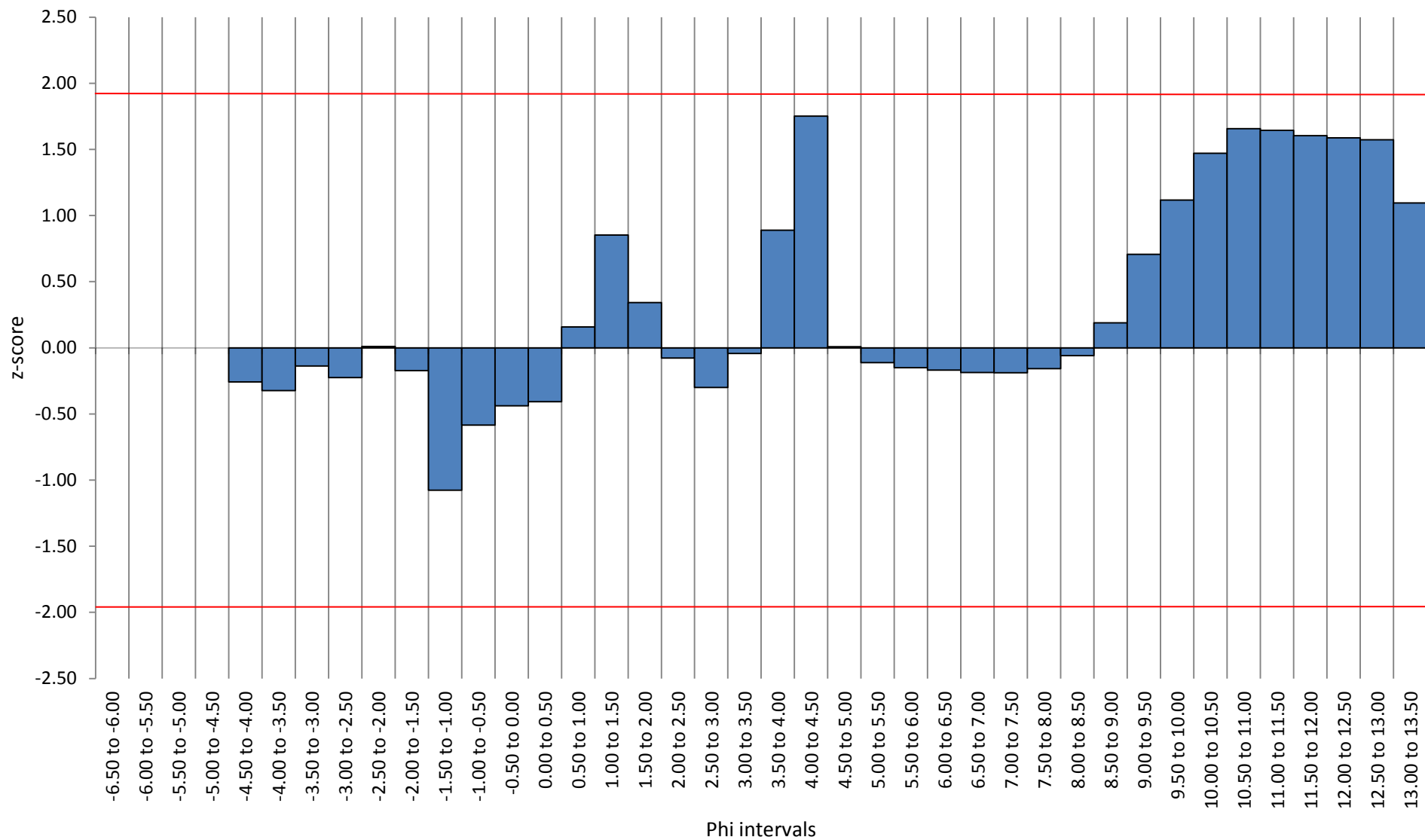
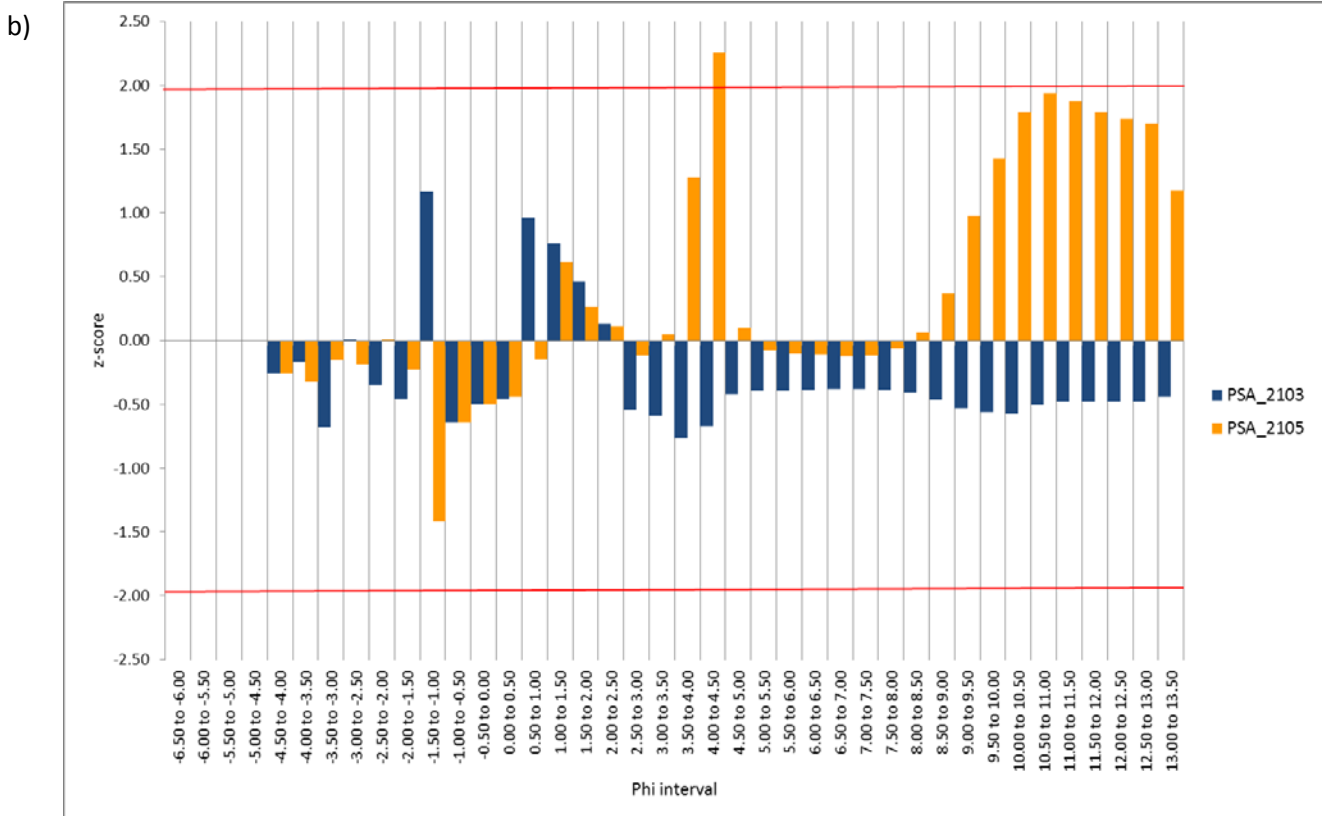
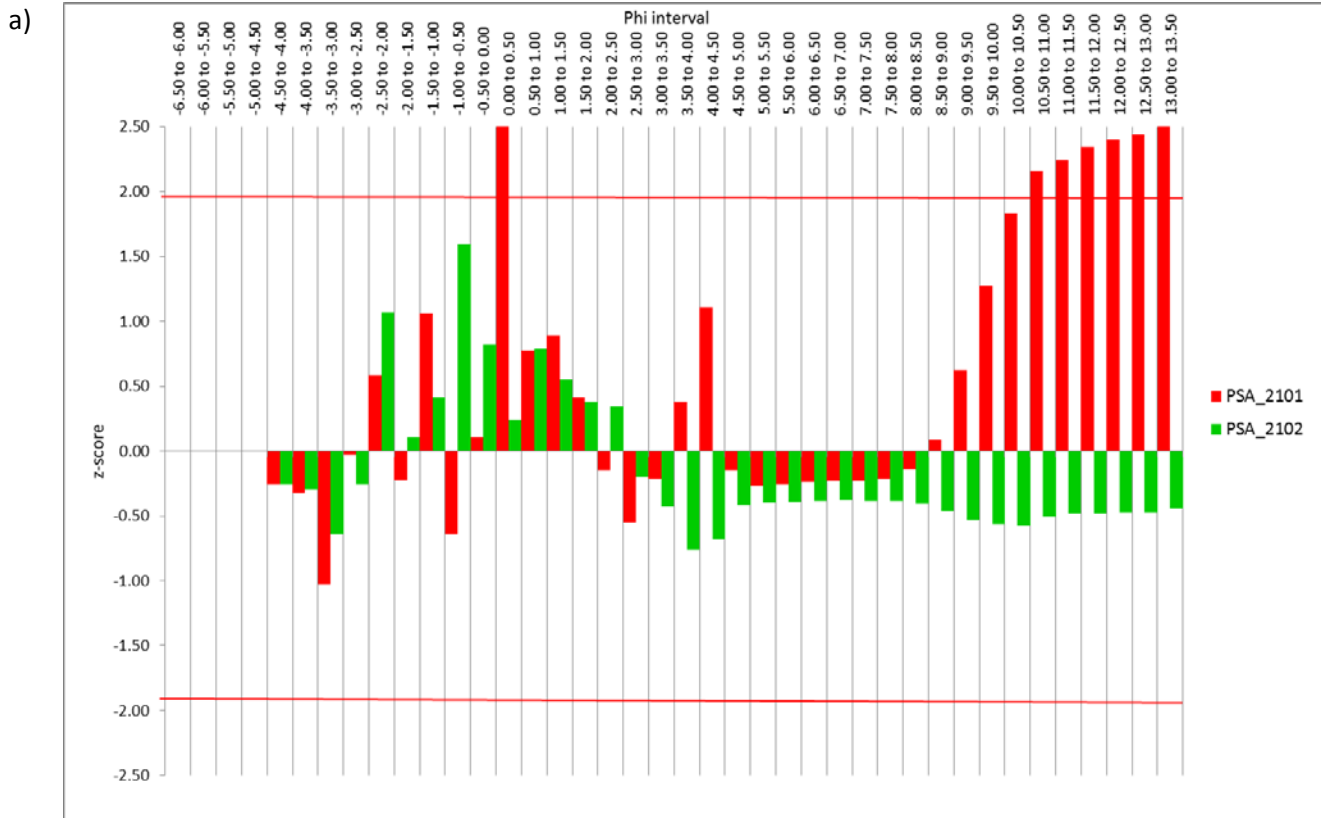
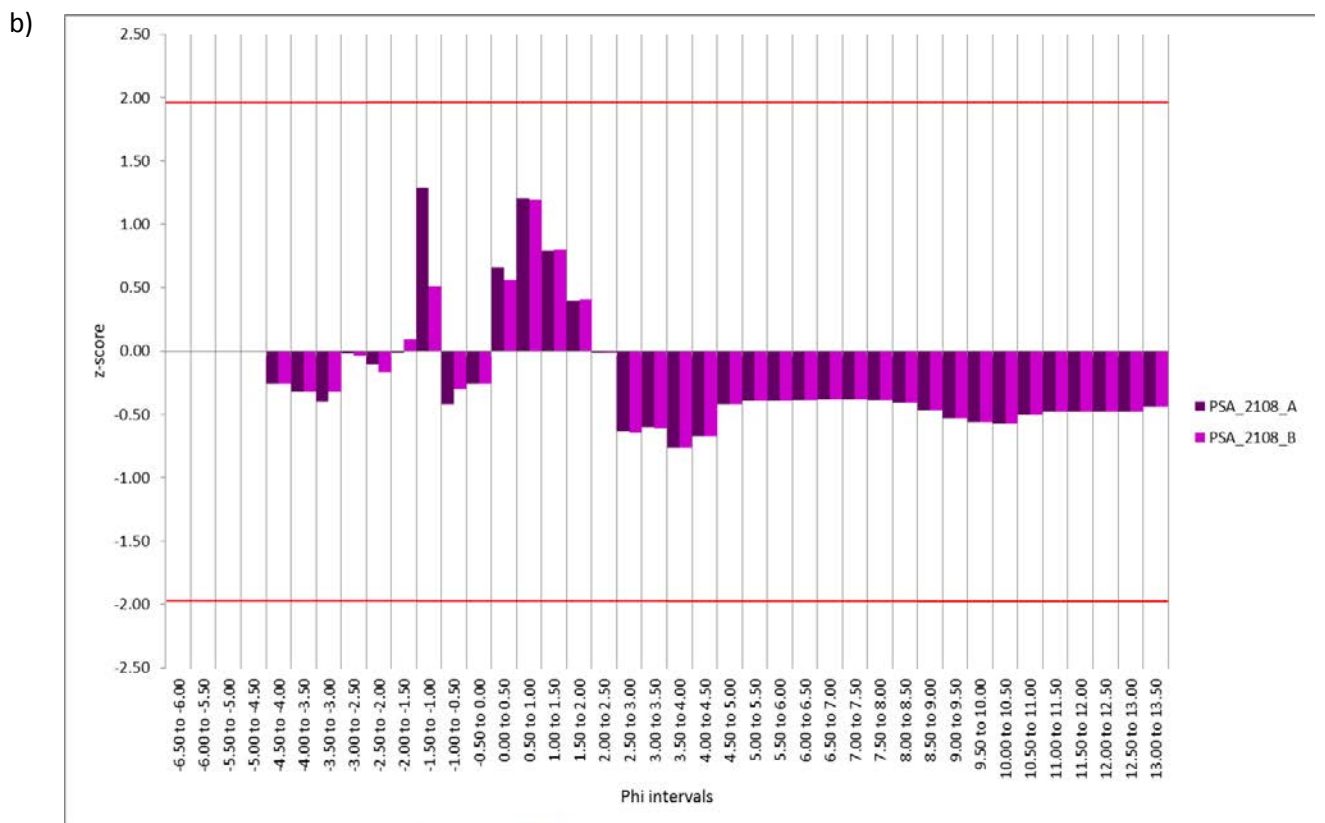
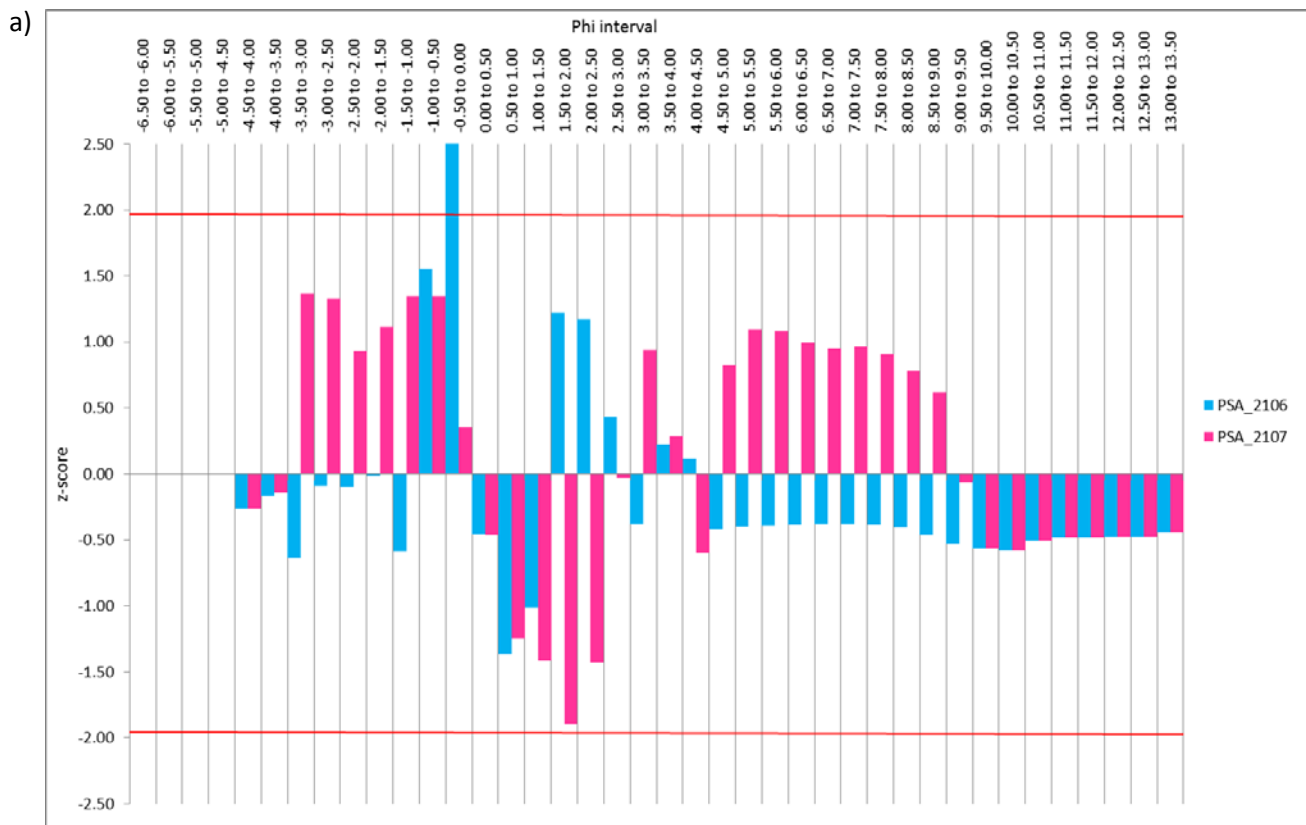


Figure 6. Summary of z-scores in each half phi-interval a) PSA\_2101 and PSA\_2102 and b) PSA\_2103 and PSA\_2105



**Figure 7. Summary of z-scores in each half phi-interval a) PSA\_2106 and PSA\_2107 and b) PSA\_2108A and PSA\_2108B**





**Figure 8. Summary of z-scores in each half phi-interval a) PSA\_2109 and PSA\_2110 and b) PSA\_2111 and PSA\_2112**

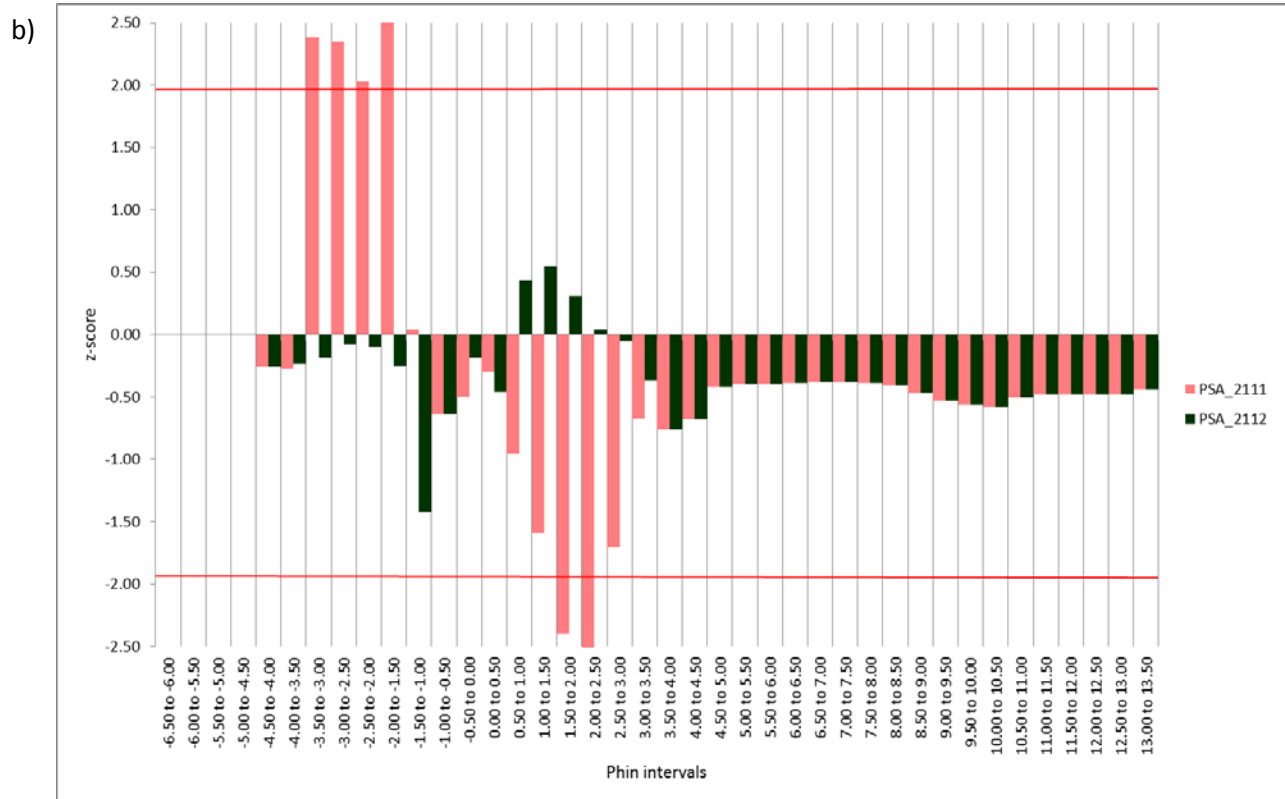
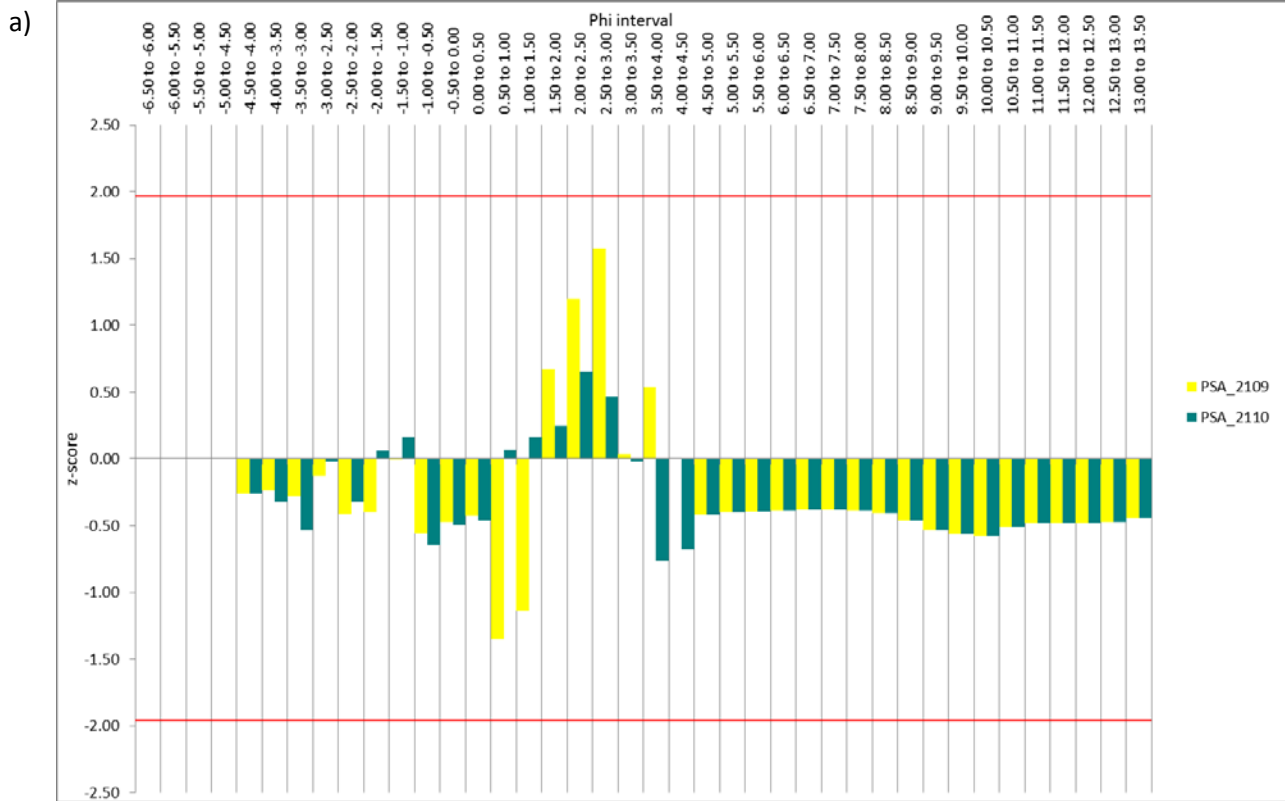
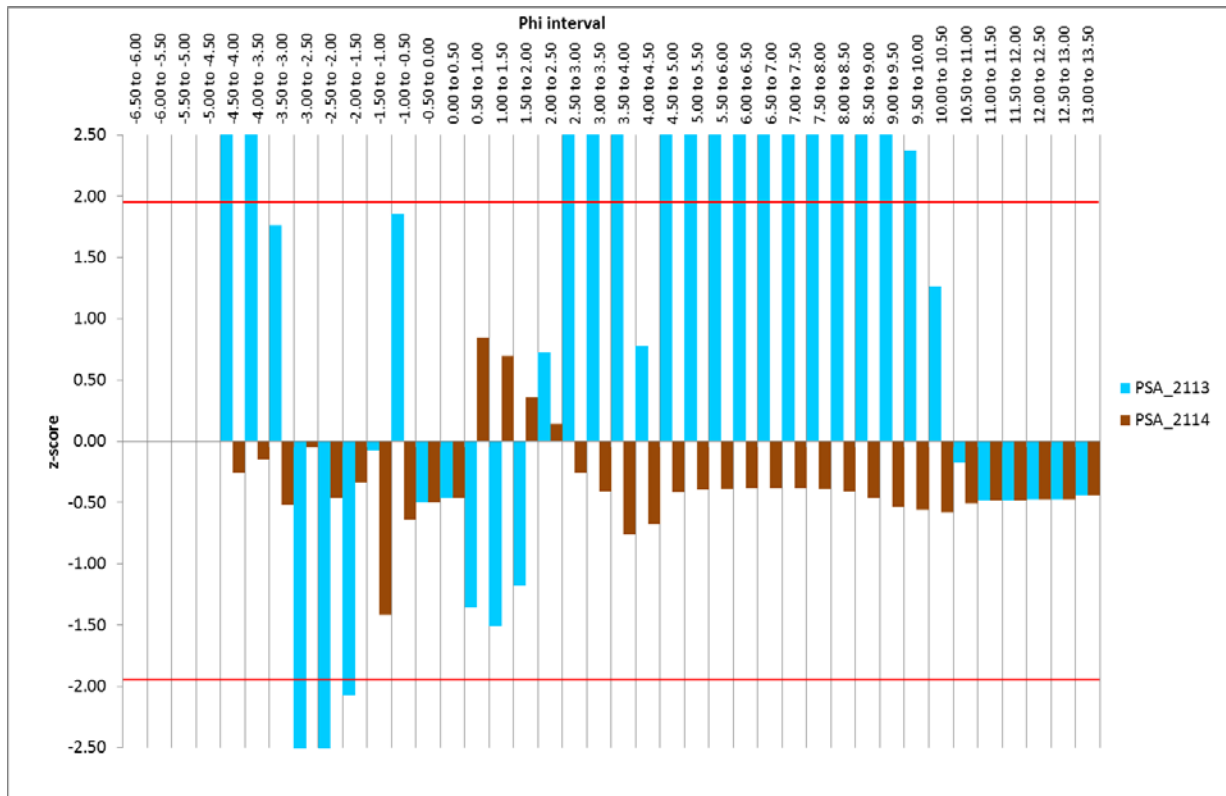


Figure 9. Summary of z-scores in each half phi-interval for PSA\_2113 and PSA\_2114



## Results of SIMPROF testing on PSA Ring test PS53 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 Euclidean distance between two samples  $j$  and  $k$ , is defined algebraically as;

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

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 a hierarchical clustering is 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)<sup>1</sup>.

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.

Multi-dimensional scaling (MDS) was run on the similarity matrix, results of which can be seen in Figures 11a, 11b and 11c. 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)<sup>1</sup>. 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 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:

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

Where  $\hat{d}_{jk}$  is the distance predicted from the fitted regression line corresponding to dissimilarity,  $d_{jk}$ .

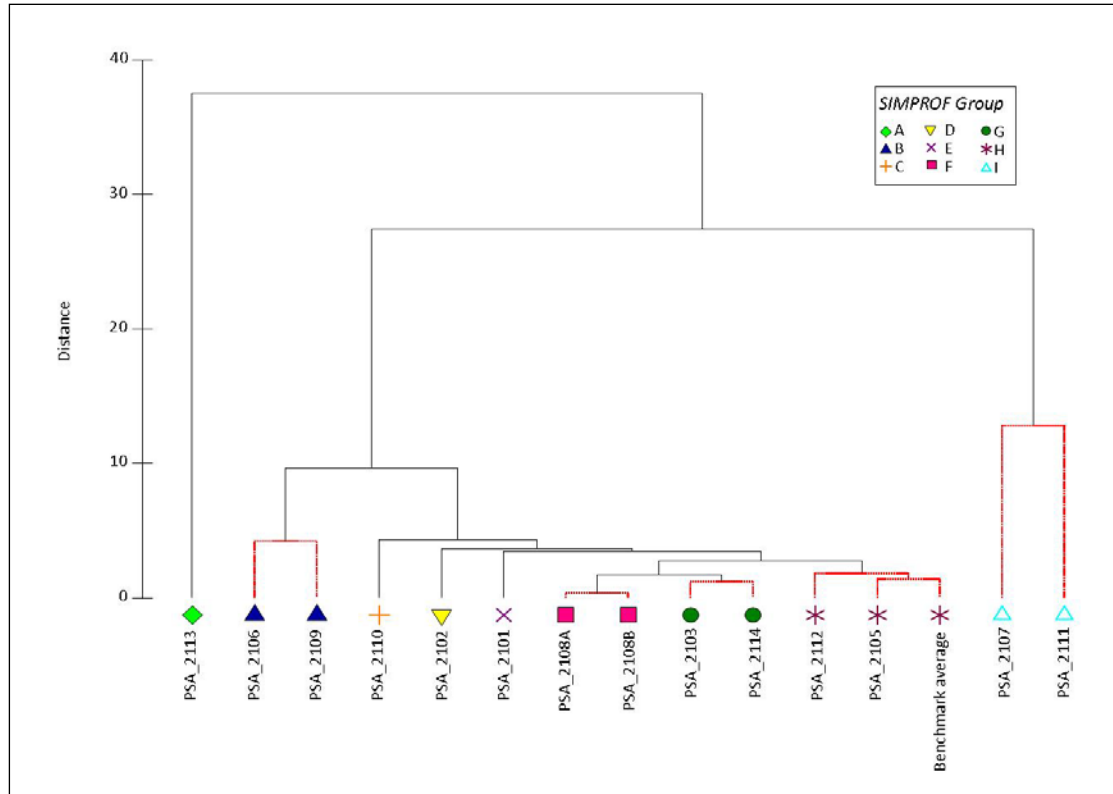
Large scatter leads to large stress. Stress can increase when compressing sample relationships into two dimensions. A stress value less than 0.2 is a good representation of the data and is fairly reliable. Whereas, a stress value of greater than 0.3 indicates random

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

data. The MDS plots in figure 11a, 11b and 11c have stress values of 0.01, 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, 4 of these groups compromise a single lab.



**Figure 10. Cluster dendrogram of PS53 including all labs, with the benchmark replicates averaged.**

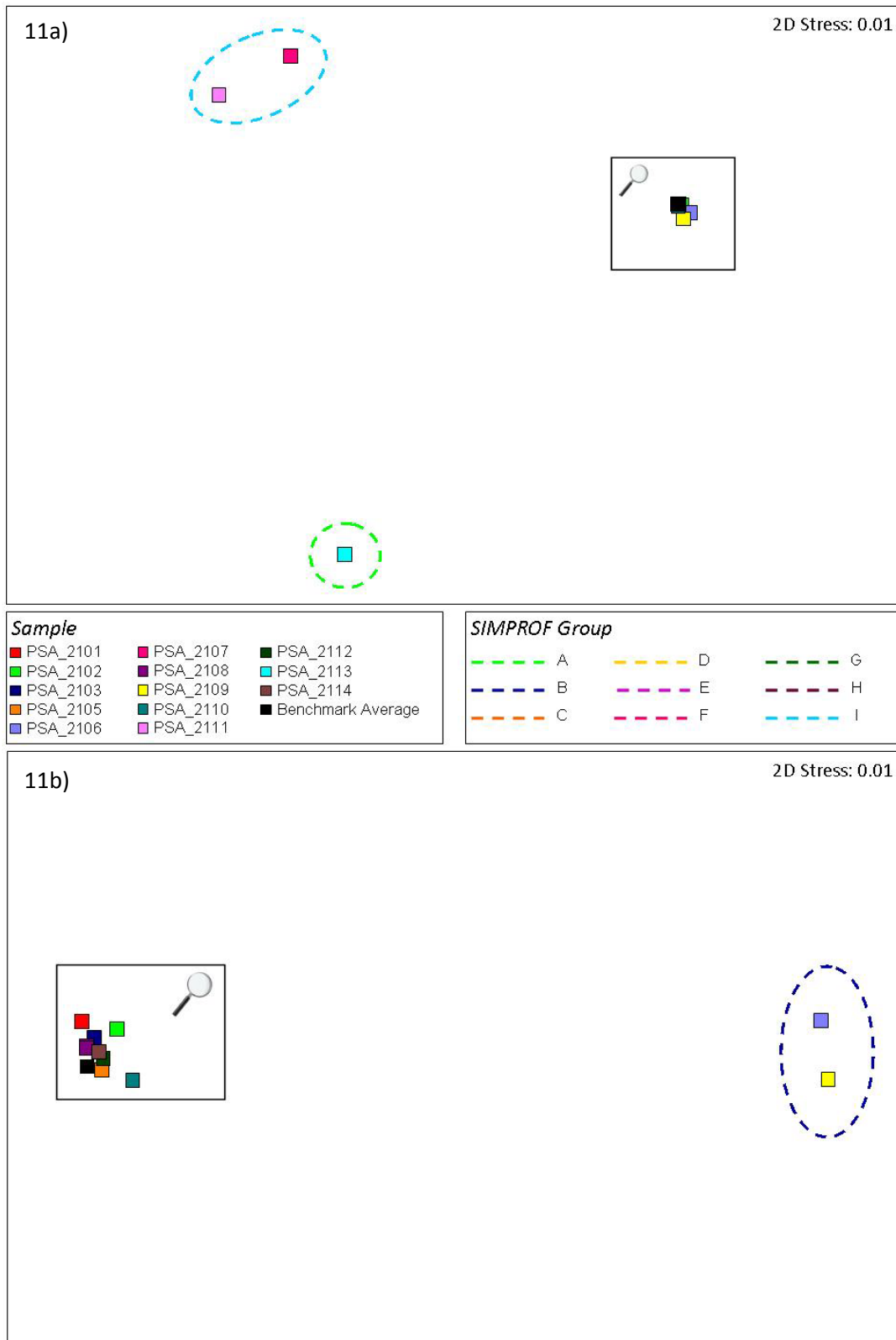
Figure 11a shows that cluster group A (PSA\_2113) and cluster group I (PSA\_2107 and PSA\_2111) can be found situated far away from each other and from the other laboratories. Table 3 shows that both samples in cluster I (PSA\_2107 and PSA\_2111) recorded a much higher percentage of sand in PS53 compared to other laboratories. PSA\_2113 recorded a higher percentage of gravel in comparison to other laboratories. The cumulative percentage curve for PSA\_2113 in Figure 2 looks as if the results have been displaced by -0.5 phi in categories less than zero phi and displaced by +0.5 phi in the categories greater than zero phi.

The MDS plot in Figure 11b shows that cluster group B (PSA\_2106 and PSA\_2109) is clustered away from the remaining laboratories. The cumulative percentage curve in Figure 2 shows that both labs in cluster B recorded less than the average recorded by the other labs in the MDS subset in Figure 11b for phi intervals 0.5 to 1.0 and 1.0 to 1.5. They recorded more than the average recorded by the other labs in the MDS subset in Figure 11c for phi intervals 1.5 to 2.0.

Figure 11c shows the remaining cluster groups; cluster H (PSA\_2105, PSA\_2112 and the benchmark average), cluster G (PSA\_2103 and PSA\_2114), cluster F (PSA\_2108A and

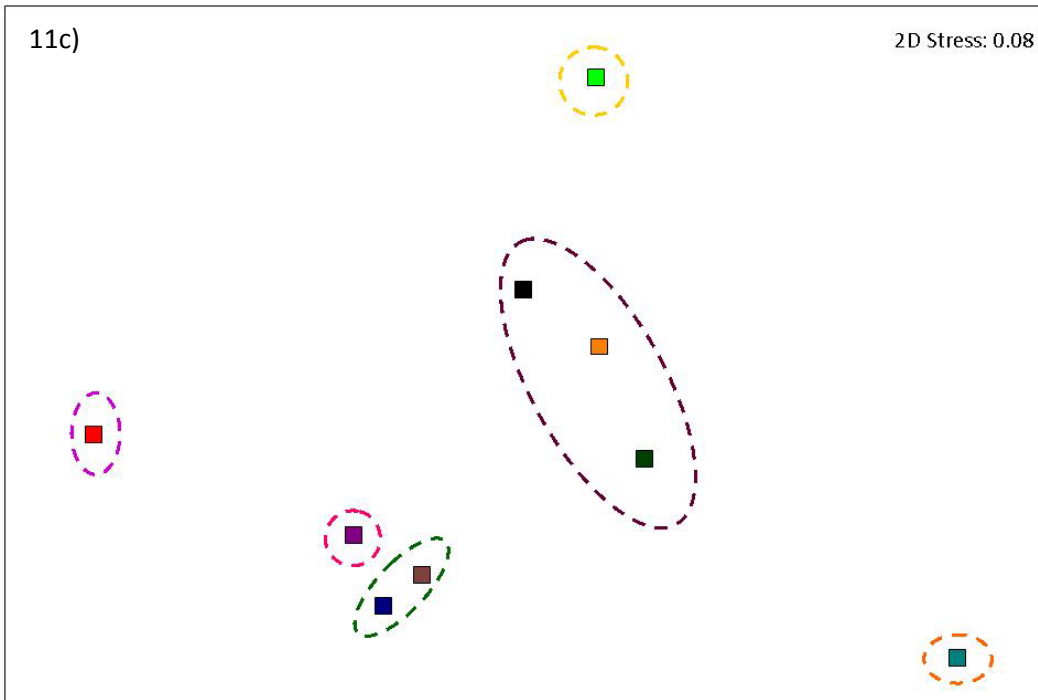
PSA\_2108B). The remaining clusters all comprise of single labs; cluster C (PSA\_2110), cluster D (PSA\_2102), and cluster E (PSA\_2101).

**Figure 11. MDS plots of PS53 with benchmark replicates averaged showing SIMPROF group overlays including a) all laboratories; b) a sub-set of figure 11a and c) a sub-set of figure 11b.**



11c)

2D Stress: 0.08



**Sample**

PSA_2101	PSA_2107	PSA_2112
PSA_2102	PSA_2108	PSA_2113
PSA_2103	PSA_2109	PSA_2114
PSA_2105	PSA_2110	Benchmark Average
PSA_2106	PSA_2111	

**SIMPROF Group**

A	D	G
B	E	H
C	F	I

## Appendices



**Appendix 1. Final Merged Data sheets as supplied by participating laboratories  
(arranged by Lab Code).**

**NMBAQCS - PS Exercise Data Workbook** Return to APEM Ltd. by 31-10-14  
(Page 2 - Final Merged Data Submission)

Exercise Code:	<b>PS53</b>
LabCode:	<b>PSA_2101</b>
Sample Code:	<b>PS532101</b>

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	17.2182
-3.00 to -2.50; 5.6 mm	27.7283
-2.50 to -2.00; 4 mm	6.4095
-2.00 to -1.50; 2.8 mm	0.3819
-1.50 to -1.00; 2 mm	0.0157
-1.00 to -0.50; 1.4 mm	0.0000
-0.50 to 0.00; 1 mm	0.0011
0.00 to 0.50; (707 µm)	0.2387
0.50 to 1.00; (500 µm)	2.4909
1.00 to 1.50; (353.6 µm)	11.8155
1.50 to 2.00; (250 µm)	16.9998
2.00 to 2.50; (176.8 µm)	11.4779
2.50 to 3.00; (125 µm)	3.7761
3.00 to 3.50; (88.39 µm)	0.5522
3.50 to 4.00; (62.5 µm)	0.1640
4.00 to 4.50; (44.19 µm)	0.0748
4.50 to 5.00; (31.25 µm)	0.0379
5.00 to 5.50; (22.097 µm)	0.0248
5.50 to 6.00; (15.625 µm)	0.0229
6.00 to 6.50; (11.049 µm)	0.0253
6.50 to 7.00; (7.813 µm)	0.0285
7.00 to 7.50; (5.524 µm)	0.0294
7.50 to 8.00; (3.906 µm)	0.0285
8.00 to 8.50; (2.762 µm)	0.0301
8.50 to 9.00; (1.953 µm)	0.0383
9.00 to 9.50; (1.381 µm)	0.0482
9.50 to 10.00; (0.977 µm)	0.0579
10.00 to 10.50; (0.691 µm)	0.0579
10.50 to 11.00; (0.488 µm)	0.0530
11.00 to 11.50; (0.345 µm)	0.0468
11.50 to 12.00; (0.244 µm)	0.0408
12.00 to 12.50; (0.173 µm)	0.0326
12.50 to 13.00; (0.122 µm)	0.0256
13.00 to 13.50; (0.086 µm)	0.0272

**Appendix 1. Final Merged Data sheets as supplied by participating laboratories  
(arranged by Lab Code).**

**NMBAQCS - PS Exercise Data Workbook** Return to APEM Ltd. by 31-10-14  
(Page 2 - Final Merged Data Submission)

Exercise Code:	<b>PS53</b>
LabCode:	<b>PSA_2102</b>
Sample Code:	<b>PS532102</b>

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	0.1333
-3.50 to -3.00; 8 mm	18.6384
-3.00 to -2.50; 5.6 mm	25.5102
-2.50 to -2.00; 4 mm	7.3184
-2.00 to -1.50; 2.8 mm	0.4487
-1.50 to -1.00; 2 mm	0.0116
-1.00 to -0.50; 1.4 mm	0.0043
-0.50 to 0.00; 1 mm	0.0024
0.00 to 0.50; (707 µm)	0.0441
0.50 to 1.00; (500 µm)	2.5080
1.00 to 1.50; (353.6 µm)	10.4701
1.50 to 2.00; (250 µm)	16.8417
2.00 to 2.50; (176.8 µm)	13.1329
2.50 to 3.00; (125 µm)	4.6037
3.00 to 3.50; (88.39 µm)	0.3322
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

**Appendix 1. Final Merged Data sheets as supplied by participating laboratories  
(arranged by Lab Code).**

**NMBAQCS - PS Exercise Data Workbook** Return to APEM Ltd. by 31-10-14  
(Page 2 - Final Merged Data Submission)

Exercise Code:	<b>PS53</b>
LabCode:	<b>PSA_2103</b>
Sample Code:	<b>PS532103</b>

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	15.4300
-3.50 to -3.00; 8 mm	350.6200
-3.00 to -2.50; 5.6 mm	531.4400
-2.50 to -2.00; 4 mm	88.4900
-2.00 to -1.50; 2.8 mm	6.3500
-1.50 to -1.00; 2 mm	0.3100
-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)	51.2607
1.00 to 1.50; (353.6 µm)	214.0409
1.50 to 2.00; (250 µm)	326.9850
2.00 to 2.50; (176.8 µm)	235.4581
2.50 to 3.00; (125 µm)	71.8753
3.00 to 3.50; (88.39 µm)	3.2000
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

Appendix 1. Final Merged Data sheets as supplied by participating laboratories  
(arranged by Lab Code).

**NMBAQCS - PS Exercise Data Workbook**  
(Page 2 - Final Merged Data Submission) Return to APEM Ltd. by 31-10-14

Exercise Code:	<b>PS53</b>
LabCode:	<b>PSA_2105</b>
Sample Code:	<b>PS532105</b>

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	20.3988
-3.00 to -2.50; 5.6 mm	26.2005
-2.50 to -2.00; 4 mm	5.3319
-2.00 to -1.50; 2.8 mm	0.3824
-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)	0.0012
0.50 to 1.00; (500 µm)	1.4213
1.00 to 1.50; (353.6 µm)	10.7216
1.50 to 2.00; (250 µm)	16.2827
2.00 to 2.50; (176.8 µm)	12.3509
2.50 to 3.00; (125 µm)	4.8117
3.00 to 3.50; (88.39 µm)	0.8192
3.50 to 4.00; (62.5 µm)	0.2931
4.00 to 4.50; (44.19 µm)	0.1228
4.50 to 5.00; (31.25 µm)	0.0733
5.00 to 5.50; (22.097 µm)	0.0635
5.50 to 6.00; (15.625 µm)	0.0504
6.00 to 6.50; (11.049 µm)	0.0463
6.50 to 7.00; (7.813 µm)	0.0489
7.00 to 7.50; (5.524 µm)	0.0525
7.50 to 8.00; (3.906 µm)	0.0534
8.00 to 8.50; (2.762 µm)	0.0541
8.50 to 9.00; (1.953 µm)	0.0584
9.00 to 9.50; (1.381 µm)	0.0630
9.50 to 10.00; (0.977 µm)	0.0627
10.00 to 10.50; (0.691 µm)	0.0567
10.50 to 11.00; (0.488 µm)	0.0487
11.00 to 11.50; (0.345 µm)	0.0404
11.50 to 12.00; (0.244 µm)	0.0327
12.00 to 12.50; (0.173 µm)	0.0250
12.50 to 13.00; (0.122 µm)	0.0191
13.00 to 13.50; (0.086 µm)	0.0127

**Appendix 1. Final Merged Data sheets as supplied by participating laboratories  
(arranged by Lab Code).**

**NMBAQCS - PS Exercise Data Workbook** Return to APEM Ltd. by 31-10-14  
(Page 2 - Final Merged Data Submission)

Exercise Code:	<b>PS53</b>
LabCode:	<b>PSA_2106</b>
Sample Code:	<b>PS532106</b>

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	0.8106
-3.50 to -3.00; 8 mm	18.6386
-3.00 to -2.50; 5.6 mm	27.1646
-2.50 to -2.00; 4 mm	5.1422
-2.00 to -1.50; 2.8 mm	0.4248
-1.50 to -1.00; 2 mm	0.0053
-1.00 to -0.50; 1.4 mm	0.0042
-0.50 to 0.00; 1 mm	0.0068
0.00 to 0.50; (707 µm)	0.0005
0.50 to 1.00; (500 µm)	0.0037
1.00 to 1.50; (353.6 µm)	4.2281
1.50 to 2.00; (250 µm)	20.9663
2.00 to 2.50; (176.8 µm)	15.9266
2.50 to 3.00; (125 µm)	6.1210
3.00 to 3.50; (88.39 µm)	0.3822
3.50 to 4.00; (62.5 µm)	0.1414
4.00 to 4.50; (44.19 µm)	0.0331
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

**Appendix 1. Final Merged Data sheets as supplied by participating laboratories  
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**NMBAQCS - PS Exercise Data Workbook** Return to APEM Ltd. by 31-10-14  
(Page 2 - Final Merged Data Submission)

Exercise Code:	PS52 <sup>+</sup>
LabCode:	PSA_2107
Sample Code:	PS522107

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	0.9332
-3.50 to -3.00; 8 mm	25.9056
-3.00 to -2.50; 5.6 mm	40.9312
-2.50 to -2.00; 4 mm	7.0683
-2.00 to -1.50; 2.8 mm	0.6510
-1.50 to -1.00; 2 mm	0.0175
-1.00 to -0.50; 1.4 mm	0.0038
-0.50 to 0.00; 1 mm	0.0015
0.00 to 0.50; (707 µm)	0.0000
0.50 to 1.00; (500 µm)	0.1419
1.00 to 1.50; (353.6 µm)	2.6252
1.50 to 2.00; (250 µm)	5.7093
2.00 to 2.50; (176.8 µm)	7.1848
2.50 to 3.00; (125 µm)	5.0233
3.00 to 3.50; (88.39 µm)	1.7291
3.50 to 4.00; (62.5 µm)	0.1504
4.00 to 4.50; (44.19 µm)	0.0032
4.50 to 5.00; (31.25 µm)	0.1759
5.00 to 5.50; (22.097 µm)	0.2953
5.50 to 6.00; (15.625 µm)	0.2577
6.00 to 6.50; (11.049 µm)	0.2334
6.50 to 7.00; (7.813 µm)	0.2518
7.00 to 7.50; (5.524 µm)	0.2619
7.50 to 8.00; (3.906 µm)	0.2127
8.00 to 8.50; (2.762 µm)	0.1361
8.50 to 9.00; (1.953 µm)	0.0761
9.00 to 9.50; (1.381 µm)	0.0195
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

<sup>+</sup> Data for PS53 submitted as PS52 and vice versa.

Appendix 1. Final Merged Data sheets as supplied by participating laboratories  
(arranged by Lab Code).

**NMBAQCS - PS Exercise Data Workbook**  
(Page 2 - Final Merged Data Submission) Return to APEM Ltd. by 31-10-14

Exercise Code:	<b>PS53</b>
LabCode:	<b>PSA_2108A</b>
Sample Code:	<b>PS532108A</b>

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	19.5133
-3.00 to -2.50; 5.6 mm	27.8171
-2.50 to -2.00; 4 mm	5.1317
-2.00 to -1.50; 2.8 mm	0.4248
-1.50 to -1.00; 2 mm	0.0171
-1.00 to -0.50; 1.4 mm	0.0004
-0.50 to 0.00; 1 mm	0.0004
0.00 to 0.50; (707 µm)	0.0709
0.50 to 1.00; (500 µm)	2.9948
1.00 to 1.50; (353.6 µm)	11.4081
1.50 to 2.00; (250 µm)	16.9410
2.00 to 2.50; (176.8 µm)	11.9547
2.50 to 3.00; (125 µm)	3.5721
3.00 to 3.50; (88.39 µm)	0.1538
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

Appendix 1. Final Merged Data sheets as supplied by participating laboratories  
(arranged by Lab Code).

**NMBAQCS - PS Exercise Data Workbook**  
(Page 2 - Final Merged Data Submission) Return to APEM Ltd. by 31-10-14

Exercise Code:	PS53
LabCode:	PSA_2108B
Sample Code:	PS532108B

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	19.7842
-3.00 to -2.50; 5.6 mm	27.6455
-2.50 to -2.00; 4 mm	5.0119
-2.00 to -1.50; 2.8 mm	0.4463
-1.50 to -1.00; 2 mm	0.0122
-1.00 to -0.50; 1.4 mm	0.0006
-0.50 to 0.00; 1 mm	0.0004
0.00 to 0.50; (707 µm)	0.0645
0.50 to 1.00; (500 µm)	2.9766
1.00 to 1.50; (353.6 µm)	11.4317
1.50 to 2.00; (250 µm)	16.9823
2.00 to 2.50; (176.8 µm)	11.9547
2.50 to 3.00; (125 µm)	3.5441
3.00 to 3.50; (88.39 µm)	0.1450
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



**Appendix 1. Final Merged Data sheets as supplied by participating laboratories  
(arranged by Lab Code).**

**NMBAQCS - PS Exercise Data Workbook** Return to APEM Ltd. by 31-10-14  
(Page 2 - Final Merged Data Submission)

Exercise Code:	<b>PS53</b>
LabCode:	<b>PSA_2109</b>
Sample Code:	<b>PS532109</b>

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	8.2530
-3.50 to -3.00; 8 mm	380.3220
-3.00 to -2.50; 5.6 mm	510.8980
-2.50 to -2.00; 4 mm	86.7890
-2.00 to -1.50; 2.8 mm	6.6370
-1.50 to -1.00; 2 mm	0.1700
-1.00 to -0.50; 1.4 mm	0.0030
-0.50 to 0.00; 1 mm	0.0010
0.00 to 0.50; (707 µm)	0.0480
0.50 to 1.00; (500 µm)	0.4430
1.00 to 1.50; (353.6 µm)	71.4500
1.50 to 2.00; (250 µm)	348.6470
2.00 to 2.50; (176.8 µm)	305.5920
2.50 to 3.00; (125 µm)	168.7680
3.00 to 3.50; (88.39 µm)	15.3640
3.50 to 4.00; (62.5 µm)	3.5650
4.00 to 4.50; (44.19 µm)	0.5410
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

Appendix 1. Final Merged Data sheets as supplied by participating laboratories  
(arranged by Lab Code).

**NMBAQCS - PS Exercise Data Workbook**  
(Page 2 - Final Merged Data Submission) Return to APEM Ltd. by 31-10-14

Exercise Code:	<b>PS53</b>
LabCode:	<b>PSA_2110</b>
Sample Code:	<b>PS532110</b>

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	19.0300
-3.00 to -2.50; 5.6 mm	27.8600
-2.50 to -2.00; 4 mm	4.7200
-2.00 to -1.50; 2.8 mm	0.4400
-1.50 to -1.00; 2 mm	0.0100
-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)	1.6700
1.00 to 1.50; (353.6 µm)	8.9100
1.50 to 2.00; (250 µm)	16.2100
2.00 to 2.50; (176.8 µm)	14.2000
2.50 to 3.00; (125 µm)	6.2000
3.00 to 3.50; (88.39 µm)	0.7500
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

Appendix 1. Final Merged Data sheets as supplied by participating laboratories  
(arranged by Lab Code).

**NMBAQCS - PS Exercise Data Workbook**  
(Page 2 - Final Merged Data Submission) Return to APEM Ltd. by 31-10-14

Exercise Code:	<b>PS53</b>
LabCode:	<b>PSA_2111</b>
Sample Code:	<b>PS532111</b>

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	0.00
-6.00 to -5.50; 45 mm	0.00
-5.50 to -5.00; 31.5 mm	0.00
-5.00 to -4.50; 22.4 mm	0.00
-4.50 to -4.00; 16 mm	0.00
-4.00 to -3.50; 11.2 mm	2.80
-3.50 to -3.00; 8 mm	321.20
-3.00 to -2.50; 5.6 mm	551.60
-2.50 to -2.00; 4 mm	99.10
-2.00 to -1.50; 2.8 mm	10.70
-1.50 to -1.00; 2 mm	0.10
-1.00 to -0.50; 1.4 mm	0.00
-0.50 to 0.00; 1 mm	0.00
0.00 to 0.50; (707 µm)	0.11
0.50 to 1.00; (500 µm)	5.23
1.00 to 1.50; (353.6 µm)	21.00
1.50 to 2.00; (250 µm)	35.03
2.00 to 2.50; (176.8 µm)	26.64
2.50 to 3.00; (125 µm)	11.11
3.00 to 3.50; (88.39 µm)	0.88
3.50 to 4.00; (62.5 µm)	0.00
4.00 to 4.50; (44.19 µm)	0.00
4.50 to 5.00; (31.25 µm)	0.00
5.00 to 5.50; (22.097 µm)	0.00
5.50 to 6.00; (15.625 µm)	0.00
6.00 to 6.50; (11.049 µm)	0.00
6.50 to 7.00; (7.813 µm)	0.00
7.00 to 7.50; (5.524 µm)	0.00
7.50 to 8.00; (3.906 µm)	0.00
8.00 to 8.50; (2.762 µm)	
8.50 to 9.00; (1.953 µm)	0.00
9.00 to 9.50; (1.381 µm)	
9.50 to 10.00; (0.977 µm)	0.00
10.00 to 10.50; (0.691 µm)	0.00
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).**

**NMBAQCS - PS Exercise Data Workbook** Return to APEM Ltd. by 31-10-14  
(Page 2 - Final Merged Data Submission)

Exercise Code:	<b>PS53</b>
LabCode:	<b>PSA_2112</b>
Sample Code:	<b>PS532112</b>

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	0.00
-6.00 to -5.50; 45 mm	0.00
-5.50 to -5.00; 31.5 mm	0.00
-5.00 to -4.50; 22.4 mm	0.00
-4.50 to -4.00; 16 mm	0.00
-4.00 to -3.50; 11.2 mm	8.17
-3.50 to -3.00; 8 mm	367.25
-3.00 to -2.50; 5.6 mm	493.40
-2.50 to -2.00; 4 mm	93.03
-2.00 to -1.50; 2.8 mm	6.83
-1.50 to -1.00; 2 mm	0.00
-1.00 to -0.50; 1.4 mm	0.00
-0.50 to 0.00; 1 mm	0.01
0.00 to 0.50; (707 µm)	0.0031
0.50 to 1.00; (500 µm)	38.0898
1.00 to 1.50; (353.6 µm)	189.4129
1.50 to 2.00; (250 µm)	299.1854
2.00 to 2.50; (176.8 µm)	219.5124
2.50 to 3.00; (125 µm)	89.9038
3.00 to 3.50; (88.39 µm)	7.0749
3.50 to 4.00; (62.5 µm)	0.0076
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

**Appendix 1. Final Merged Data sheets as supplied by participating laboratories  
(arranged by Lab Code).**

**NMBAQCS - PS Exercise Data Workbook** Return to APEM Ltd. by 31-10-14  
(Page 2 - Final Merged Data Submission)

Exercise Code:	<b>PS53</b>
LabCode:	<b>PSA_2113</b>
Sample Code:	<b>PS532113</b>

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	1.3904
-4.00 to -3.50; 11.2 mm	20.2239
-3.50 to -3.00; 8 mm	27.3453
-3.00 to -2.50; 5.6 mm	3.1706
-2.50 to -2.00; 4 mm	0.4089
-2.00 to -1.50; 2.8 mm	0.0133
-1.50 to -1.00; 2 mm	0.0085
-1.00 to -0.50; 1.4 mm	0.0048
-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)	0.0171
1.00 to 1.50; (353.6 µm)	2.2728
1.50 to 2.00; (250 µm)	9.1956
2.00 to 2.50; (176.8 µm)	14.4301
2.50 to 3.00; (125 µm)	11.2041
3.00 to 3.50; (88.39 µm)	4.1439
3.50 to 4.00; (62.5 µm)	0.4721
4.00 to 4.50; (44.19 µm)	0.0609
4.50 to 5.00; (31.25 µm)	0.5395
5.00 to 5.50; (22.097 µm)	0.7392
5.50 to 6.00; (15.625 µm)	0.6522
6.00 to 6.50; (11.049 µm)	0.6353
6.50 to 7.00; (7.813 µm)	0.7158
7.00 to 7.50; (5.524 µm)	0.7331
7.50 to 8.00; (3.906 µm)	0.6223
8.00 to 8.50; (2.762 µm)	0.4384
8.50 to 9.00; (1.953 µm)	0.2683
9.00 to 9.50; (1.381 µm)	0.1499
9.50 to 10.00; (0.977 µm)	0.0927
10.00 to 10.50; (0.691 µm)	0.0442
10.50 to 11.00; (0.488 µm)	0.0066
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).**

**NMBAQCS - PS Exercise Data Workbook** Return to APEM Ltd. by 31-10-14  
(Page 2 - Final Merged Data Submission)

Exercise Code:	<b>PS53</b>
LabCode:	<b>PSA_2114</b>
Sample Code:	<b>PS532114</b>

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	0.9000
-3.50 to -3.00; 8 mm	19.0600
-3.00 to -2.50; 5.6 mm	27.5500
-2.50 to -2.00; 4 mm	4.4500
-2.00 to -1.50; 2.8 mm	0.3600
-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)	2.5800
1.00 to 1.50; (353.6 µm)	11.0500
1.50 to 2.00; (250 µm)	16.7500
2.00 to 2.50; (176.8 µm)	12.4600
2.50 to 3.00; (125 µm)	4.4700
3.00 to 3.50; (88.39 µm)	0.3500
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

Appendix 1. Final Merged Data sheets as supplied by participating laboratories  
(arranged by Lab Code).

**NMBAQCS - PS Exercise Data Workbook** Return to APEM Ltd. by 31-10-14  
(Page 2 - Final Merged Data Submission)

Exercise Code:	PS53
LabCode:	PSA_21 BENCHMARK REP 1
Sample Code:	PS5321BMREP1

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	20.3988
-3.00 to -2.50; 5.6 mm	26.2005
-2.50 to -2.00; 4 mm	5.3319
-2.00 to -1.50; 2.8 mm	0.3824
-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)	0.0012
0.50 to 1.00; (500 µm)	1.4213
1.00 to 1.50; (353.6 µm)	10.7216
1.50 to 2.00; (250 µm)	16.2827
2.00 to 2.50; (176.8 µm)	12.3509
2.50 to 3.00; (125 µm)	4.8117
3.00 to 3.50; (88.39 µm)	0.8192
3.50 to 4.00; (62.5 µm)	0.2931
4.00 to 4.50; (44.19 µm)	0.1228
4.50 to 5.00; (31.25 µm)	0.0733
5.00 to 5.50; (22.097 µm)	0.0635
5.50 to 6.00; (15.625 µm)	0.0504
6.00 to 6.50; (11.049 µm)	0.0463
6.50 to 7.00; (7.813 µm)	0.0489
7.00 to 7.50; (5.524 µm)	0.0525
7.50 to 8.00; (3.906 µm)	0.0534
8.00 to 8.50; (2.762 µm)	0.0541
8.50 to 9.00; (1.953 µm)	0.0584
9.00 to 9.50; (1.381 µm)	0.0630
9.50 to 10.00; (0.977 µm)	0.0627
10.00 to 10.50; (0.691 µm)	0.0567
10.50 to 11.00; (0.488 µm)	0.0487
11.00 to 11.50; (0.345 µm)	0.0404
11.50 to 12.00; (0.244 µm)	0.0327
12.00 to 12.50; (0.173 µm)	0.0250
12.50 to 13.00; (0.122 µm)	0.0191
13.00 to 13.50; (0.086 µm)	0.0127

Appendix 1. Final Merged Data sheets as supplied by participating laboratories  
(arranged by Lab Code).

**NMBAQCS - PS Exercise Data Workbook**  
(Page 2 - Final Merged Data Submission) Return to APEM Ltd. by 31-10-14

Exercise Code:	PS53
LabCode:	PSA_21 BENCHMARK REP 2
Sample Code:	PS5321BMREP2

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	20.1909
-3.00 to -2.50; 5.6 mm	25.7501
-2.50 to -2.00; 4 mm	5.6356
-2.00 to -1.50; 2.8 mm	0.4801
-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)	0.0030
0.50 to 1.00; (500 µm)	1.6644
1.00 to 1.50; (353.6 µm)	11.1269
1.50 to 2.00; (250 µm)	16.4327
2.00 to 2.50; (176.8 µm)	12.0908
2.50 to 3.00; (125 µm)	4.6111
3.00 to 3.50; (88.39 µm)	0.8198
3.50 to 4.00; (62.5 µm)	0.2769
4.00 to 4.50; (44.19 µm)	0.1255
4.50 to 5.00; (31.25 µm)	0.0765
5.00 to 5.50; (22.097 µm)	0.0789
5.50 to 6.00; (15.625 µm)	0.0550
6.00 to 6.50; (11.049 µm)	0.0452
6.50 to 7.00; (7.813 µm)	0.0417
7.00 to 7.50; (5.524 µm)	0.0409
7.50 to 8.00; (3.906 µm)	0.0388
8.00 to 8.50; (2.762 µm)	0.0407
8.50 to 9.00; (1.953 µm)	0.0472
9.00 to 9.50; (1.381 µm)	0.0518
9.50 to 10.00; (0.977 µm)	0.0521
10.00 to 10.50; (0.691 µm)	0.0487
10.50 to 11.00; (0.488 µm)	0.0439
11.00 to 11.50; (0.345 µm)	0.0384
11.50 to 12.00; (0.244 µm)	0.0325
12.00 to 12.50; (0.173 µm)	0.0259
12.50 to 13.00; (0.122 µm)	0.0202
13.00 to 13.50; (0.086 µm)	0.0137



**Appendix 1. Final Merged Data sheets as supplied by participating laboratories  
(arranged by Lab Code).**

**NMBAQCS - PS Exercise Data Workbook** Return to APEM Ltd. by 31-10-14  
(Page 2 - Final Merged Data Submission)

Exercise Code:	PS53
LabCode:	PSA_21 BENCHMARK REP 3
Sample Code:	PS5321BMREP3

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	19.7991
-3.00 to -2.50; 5.6 mm	26.0896
-2.50 to -2.00; 4 mm	5.4287
-2.00 to -1.50; 2.8 mm	0.3952
-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)	0.0022
0.50 to 1.00; (500 µm)	1.5859
1.00 to 1.50; (353.6 µm)	11.1658
1.50 to 2.00; (250 µm)	16.5862
2.00 to 2.50; (176.8 µm)	12.3129
2.50 to 3.00; (125 µm)	4.7840
3.00 to 3.50; (88.39 µm)	0.7913
3.50 to 4.00; (62.5 µm)	0.2579
4.00 to 4.50; (44.19 µm)	0.1057
4.50 to 5.00; (31.25 µm)	0.0607
5.00 to 5.50; (22.097 µm)	0.0528
5.50 to 6.00; (15.625 µm)	0.0405
6.00 to 6.50; (11.049 µm)	0.0350
6.50 to 7.00; (7.813 µm)	0.0350
7.00 to 7.50; (5.524 µm)	0.0359
7.50 to 8.00; (3.906 µm)	0.0362
8.00 to 8.50; (2.762 µm)	0.0386
8.50 to 9.00; (1.953 µm)	0.0454
9.00 to 9.50; (1.381 µm)	0.0523
9.50 to 10.00; (0.977 µm)	0.0541
10.00 to 10.50; (0.691 µm)	0.0498
10.50 to 11.00; (0.488 µm)	0.0432
11.00 to 11.50; (0.345 µm)	0.0360
11.50 to 12.00; (0.244 µm)	0.0292
12.00 to 12.50; (0.173 µm)	0.0224
12.50 to 13.00; (0.122 µm)	0.0171
13.00 to 13.50; (0.086 µm)	0.0114

Appendix 1. Final Merged Data sheets as supplied by participating laboratories  
(arranged by Lab Code).

**NMBAQCS - PS Exercise Data Workbook** Return to APEM Ltd. by 31-10-14  
(Page 2 - Final Merged Data Submission)

Exercise Code:	PS53
LabCode:	PSA_21 BENCHMARK REP 4
Sample Code:	PS5321BMREP4

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	20.7714
-3.00 to -2.50; 5.6 mm	25.2483
-2.50 to -2.00; 4 mm	5.3547
-2.00 to -1.50; 2.8 mm	0.3456
-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)	0.0044
0.50 to 1.00; (500 µm)	2.0596
1.00 to 1.50; (353.6 µm)	12.7171
1.50 to 2.00; (250 µm)	17.1274
2.00 to 2.50; (176.8 µm)	11.0364
2.50 to 3.00; (125 µm)	3.8596
3.00 to 3.50; (88.39 µm)	0.5954
3.50 to 4.00; (62.5 µm)	0.1800
4.00 to 4.50; (44.19 µm)	0.0804
4.50 to 5.00; (31.25 µm)	0.0482
5.00 to 5.50; (22.097 µm)	0.0454
5.50 to 6.00; (15.625 µm)	0.0336
6.00 to 6.50; (11.049 µm)	0.0293
6.50 to 7.00; (7.813 µm)	0.0303
7.00 to 7.50; (5.524 µm)	0.0316
7.50 to 8.00; (3.906 µm)	0.0320
8.00 to 8.50; (2.762 µm)	0.0344
8.50 to 9.00; (1.953 µm)	0.0407
9.00 to 9.50; (1.381 µm)	0.0476
9.50 to 10.00; (0.977 µm)	0.0497
10.00 to 10.50; (0.691 µm)	0.0462
10.50 to 11.00; (0.488 µm)	0.0404
11.00 to 11.50; (0.345 µm)	0.0339
11.50 to 12.00; (0.244 µm)	0.0277
12.00 to 12.50; (0.173 µm)	0.0214
12.50 to 13.00; (0.122 µm)	0.0164
13.00 to 13.50; (0.086 µm)	0.0110

Appendix 1. Final Merged Data sheets as supplied by participating laboratories  
(arranged by Lab Code).

**NMBAQCS - PS Exercise Data Workbook** Return to APEM Ltd. by 31-10-14  
(Page 2 - Final Merged Data Submission)

Exercise Code:	PS53
LabCode:	PSA_21 BENCHMARK REP 5
Sample Code:	PS5321BMREP5

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	21.1042
-3.00 to -2.50; 5.6 mm	25.9016
-2.50 to -2.00; 4 mm	4.9434
-2.00 to -1.50; 2.8 mm	0.3624
-1.50 to -1.00; 2 mm	0.0108
-1.00 to -0.50; 1.4 mm	0.0005
-0.50 to 0.00; 1 mm	0.0005
0.00 to 0.50; (707 µm)	0.0064
0.50 to 1.00; (500 µm)	2.1539
1.00 to 1.50; (353.6 µm)	12.5621
1.50 to 2.00; (250 µm)	16.8807
2.00 to 2.50; (176.8 µm)	10.8480
2.50 to 3.00; (125 µm)	3.7906
3.00 to 3.50; (88.39 µm)	0.5977
3.50 to 4.00; (62.5 µm)	0.1795
4.00 to 4.50; (44.19 µm)	0.0743
4.50 to 5.00; (31.25 µm)	0.0432
5.00 to 5.50; (22.097 µm)	0.0424
5.50 to 6.00; (15.625 µm)	0.0309
6.00 to 6.50; (11.049 µm)	0.0271
6.50 to 7.00; (7.813 µm)	0.0277
7.00 to 7.50; (5.524 µm)	0.0283
7.50 to 8.00; (3.906 µm)	0.0286
8.00 to 8.50; (2.762 µm)	0.0310
8.50 to 9.00; (1.953 µm)	0.0371
9.00 to 9.50; (1.381 µm)	0.0438
9.50 to 10.00; (0.977 µm)	0.0466
10.00 to 10.50; (0.691 µm)	0.0442
10.50 to 11.00; (0.488 µm)	0.0395
11.00 to 11.50; (0.345 µm)	0.0339
11.50 to 12.00; (0.244 µm)	0.0282
12.00 to 12.50; (0.173 µm)	0.0221
12.50 to 13.00; (0.122 µm)	0.0171
13.00 to 13.50; (0.086 µm)	0.0116

**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	z-score	-4.00 to -3.50	z-score	-3.50 to -3.00	z-score	-3.00 to -2.50	z-score	-2.50 to -2.00	z-score	-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
Benchmark Average	0.00	0.00	0.00	0.00	0.00	-0.26	0.00	-0.32	20.45	-0.14	25.84	-0.22	5.34	0.01	0.39	-0.17	0.00	-1.08	0.00	-0.58	0.00	-0.44
PSA_2101	0.00	0.00	0.00	0.00	0.00	-0.26	0.00	-0.32	17.22	-1.03	27.73	-0.03	6.41	0.58	0.38	-0.23	0.02	1.06	0.00	-0.64	0.00	0.11
PSA_2102	0.00	0.00	0.00	0.00	0.00	-0.26	0.13	-0.30	18.64	-0.64	25.51	-0.26	7.32	1.07	0.45	0.11	0.01	0.41	0.00	1.60	0.00	0.82
PSA_2103	0.00	0.00	0.00	0.00	0.00	-0.26	0.81	-0.17	18.50	-0.68	28.04	0.00	4.67	-0.35	0.34	-0.46	0.02	1.17	0.00	-0.64	0.00	-0.50
PSA_2105	0.00	0.00	0.00	0.00	0.00	-0.26	0.00	-0.32	20.40	-0.15	26.20	-0.19	5.33	0.01	0.38	-0.22	0.00	-1.42	0.00	-0.64	0.00	-0.50
PSA_2106	0.00	0.00	0.00	0.00	0.00	-0.26	0.81	-0.17	18.64	-0.64	27.16	-0.09	5.14	-0.10	0.42	-0.01	0.01	-0.59	0.00	1.55	0.01	3.33
PSA_2107	0.00	0.00	0.00	0.00	0.00	-0.26	0.93	-0.14	25.91	1.37	40.93	1.33	7.07	0.93	0.65	1.12	0.02	1.35	0.00	1.34	0.00	0.35
PSA_2108_A	0.00	0.00	0.00	0.00	0.00	-0.26	0.00	-0.32	19.51	-0.40	27.82	-0.02	5.13	-0.10	0.42	-0.01	0.02	1.29	0.00	-0.42	0.00	-0.26
PSA_2108_B	0.00	0.00	0.00	0.00	0.00	-0.26	0.00	-0.32	19.78	-0.32	27.65	-0.04	5.01	-0.16	0.45	0.09	0.01	0.51	0.00	-0.31	0.00	-0.26
PSA_2109	0.00	0.00	0.00	0.00	0.00	-0.26	0.43	-0.24	19.94	-0.28	26.78	-0.13	4.55	-0.41	0.35	-0.40	0.01	-0.01	0.00	-0.56	0.00	-0.47
PSA_2110	0.00	0.00	0.00	0.00	0.00	-0.26	0.00	-0.32	19.03	-0.53	27.86	-0.02	4.72	-0.32	0.44	0.06	0.01	0.16	0.00	-0.64	0.00	-0.50
PSA_2111	0.00	0.00	0.00	0.00	0.00	-0.26	0.26	-0.27	29.59	2.39	50.82	2.35	9.13	2.03	0.99	2.79	0.01	0.04	0.00	-0.64	0.00	-0.50
PSA_2112	0.00	0.00	0.00	0.00	0.00	-0.26	0.45	-0.24	20.27	-0.19	27.23	-0.08	5.13	-0.10	0.38	-0.25	0.00	-1.42	0.00	-0.64	0.00	-0.19
PSA_2113	0.00	0.00	0.00	0.00	1.39	3.61	20.22	3.61	27.35	1.77	3.17	-2.56	0.41	-2.62	0.01	-2.07	0.01	-0.07	0.00	1.85	0.00	-0.50
PSA_2114	0.00	0.00	0.00	0.00	0.00	-0.26	0.90	-0.15	19.06	-0.52	27.55	-0.05	4.45	-0.46	0.36	-0.34	0.00	-1.42	0.00	-0.64	0.00	-0.50
MEAN	0.00	0.00	0.00	0.00	0.09	1.664	20.952	28.019	5.321	0.427	0.009	0.001	0.001									
STANDARD DEVIATION	0.00	0.00	0.00	0.00	0.36	5.148	3.620	9.716	1.875	0.200	0.006	0.002	0.002									

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																					
	0.00 to 0.50	z-score	0.50 to 1.00	z-score	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
Benchmark Average	0.00	-0.41	1.78	0.16	11.66	0.85	16.66	0.34	11.73	-0.08	4.37	-0.30	0.72	-0.04	0.24	0.89	0.10	1.75	0.06	0.01	0.06	-0.11
PSA_2101	0.24	3.33	2.49	0.77	11.82	0.89	17.00	0.41	11.48	-0.15	3.78	-0.55	0.55	-0.21	0.16	0.38	0.07	1.11	0.04	-0.15	0.02	-0.27
PSA_2102	0.04	0.24	2.51	0.79	10.47	0.55	16.84	0.38	13.13	0.34	4.60	-0.20	0.33	-0.43	0.00	-0.76	0.00	-0.68	0.00	-0.42	0.00	-0.40
PSA_2103	0.00	-0.46	2.70	0.96	11.29	0.76	17.25	0.46	12.42	0.13	3.79	-0.54	0.17	-0.59	0.00	-0.76	0.00	-0.68	0.00	-0.42	0.00	-0.40
PSA_2105	0.00	-0.44	1.42	-0.15	10.72	0.62	16.28	0.26	12.35	0.11	4.81	-0.12	0.82	0.05	0.29	1.28	0.12	2.25	0.07	0.10	0.06	-0.08
PSA_2106	0.00	-0.45	0.00	-1.37	4.23	-1.02	20.97	1.22	15.93	1.17	6.12	0.43	0.38	-0.38	0.14	0.22	0.03	0.11	0.00	-0.42	0.00	-0.40
PSA_2107	0.00	-0.46	0.14	-1.25	2.63	-1.42	5.71	-1.89	7.18	-1.43	5.02	-0.03	1.73	0.94	0.15	0.28	0.00	-0.60	0.18	0.83	0.30	1.09
PSA_2108_A	0.07	0.66	2.99	1.21	11.41	0.79	16.94	0.40	11.95	-0.01	3.57	-0.64	0.15	-0.60	0.00	-0.76	0.00	-0.68	0.00	-0.42	0.00	-0.40
PSA_2108_B	0.06	0.56	2.98	1.19	11.43	0.80	16.98	0.41	11.95	-0.01	3.54	-0.65	0.14	-0.61	0.00	-0.76	0.00	-0.68	0.00	-0.42	0.00	-0.40
PSA_2109	0.00	-0.42	0.02	-1.35	3.75	-1.14	18.28	0.67	16.02	1.20	8.85	1.58	0.81	0.04	0.19	0.54	0.03	0.00	0.00	-0.42	0.00	-0.40
PSA_2110	0.00	-0.46	1.67	0.07	8.91	0.16	16.21	0.25	14.20	0.66	6.20	0.47	0.75	-0.02	0.00	-0.76	0.00	-0.68	0.00	-0.42	0.00	-0.40
PSA_2111	0.01	-0.30	0.48	-0.96	1.94	-1.59	3.23	-2.40	2.45	-2.83	1.02	-1.70	0.08	-0.67	0.00	-0.76	0.00	-0.68	0.00	-0.42	0.00	-0.40
PSA_2112	0.00	-0.46	2.10	0.44	10.45	0.55	16.51	0.31	12.12	0.04	4.96	-0.05	0.39	-0.37	0.00	-0.76	0.00	-0.68	0.00	-0.42	0.00	-0.40
PSA_2113	0.00	-0.46	0.02	-1.36	2.27	-1.51	9.20	-1.18	14.43	0.73	11.20	2.56	4.14	3.30	0.47	2.52	0.06	0.78	0.54	3.40	0.74	3.34
PSA_2114	0.00	-0.46	2.58	0.85	11.05	0.70	16.75	0.36	12.46	0.14	4.47	-0.26	0.35	-0.41	0.00	-0.76	0.00	-0.68	0.00	-0.42	0.00	-0.40
MEAN	0.029		1.593		8.268		14.987		11.988		5.088		0.769		0.110		0.028		0.059		0.079	
STANDARD DEVIATION	0.063		1.161		3.978		4.901		3.368		2.386		1.022		0.144		0.042		0.141		0.198	

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

	Phi-interval																					
	5.50 to 6.00	z-score	6.00 to 6.50	z-score	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
Benchmark Average	0.04	-0.15	0.04	-0.17	0.04	-0.19	0.04	-0.19	0.04	-0.16	0.04	-0.06	0.05	0.19	0.05	0.71	0.05	1.12	0.05	1.47	0.04	1.66
PSA_2101	0.02	-0.26	0.03	-0.24	0.03	-0.23	0.03	-0.23	0.03	-0.21	0.03	-0.14	0.04	0.08	0.05	0.62	0.06	1.27	0.06	1.83	0.05	2.15
PSA_2102	0.00	-0.39	0.00	-0.39	0.00	-0.38	0.00	-0.38	0.00	-0.39	0.00	-0.41	0.00	-0.46	0.00	-0.53	0.00	-0.56	0.00	-0.58	0.00	-0.51
PSA_2103	0.00	-0.39	0.00	-0.39	0.00	-0.38	0.00	-0.38	0.00	-0.39	0.00	-0.41	0.00	-0.46	0.00	-0.53	0.00	-0.56	0.00	-0.58	0.00	-0.51
PSA_2105	0.05	-0.10	0.05	-0.11	0.05	-0.12	0.05	-0.11	0.05	-0.06	0.05	0.07	0.06	0.37	0.06	0.98	0.06	1.42	0.06	1.79	0.05	1.94
PSA_2106	0.00	-0.39	0.00	-0.39	0.00	-0.38	0.00	-0.38	0.00	-0.39	0.00	-0.41	0.00	-0.46	0.00	-0.53	0.00	-0.56	0.00	-0.58	0.00	-0.51
PSA_2107	0.26	1.09	0.23	1.00	0.25	0.95	0.26	0.97	0.21	0.91	0.14	0.78	0.08	0.62	0.02	-0.06	0.00	-0.56	0.00	-0.58	0.00	-0.51
PSA_2108_A	0.00	-0.39	0.00	-0.39	0.00	-0.38	0.00	-0.38	0.00	-0.39	0.00	-0.41	0.00	-0.46	0.00	-0.53	0.00	-0.56	0.00	-0.58	0.00	-0.51
PSA_2108_B	0.00	-0.39	0.00	-0.39	0.00	-0.38	0.00	-0.38	0.00	-0.39	0.00	-0.41	0.00	-0.46	0.00	-0.53	0.00	-0.56	0.00	-0.58	0.00	-0.51
PSA_2109	0.00	-0.39	0.00	-0.39	0.00	-0.38	0.00	-0.38	0.00	-0.39	0.00	-0.41	0.00	-0.46	0.00	-0.53	0.00	-0.56	0.00	-0.58	0.00	-0.51
PSA_2110	0.00	-0.39	0.00	-0.39	0.00	-0.38	0.00	-0.38	0.00	-0.39	0.00	-0.41	0.00	-0.46	0.00	-0.53	0.00	-0.56	0.00	-0.58	0.00	-0.51
PSA_2111	0.00	-0.39	0.00	-0.39	0.00	-0.38	0.00	-0.38	0.00	-0.39	0.00	-0.41	0.00	-0.46	0.00	-0.53	0.00	-0.56	0.00	-0.58	0.00	-0.51
PSA_2112	0.00	-0.39	0.00	-0.39	0.00	-0.38	0.00	-0.38	0.00	-0.39	0.00	-0.41	0.00	-0.46	0.00	-0.53	0.00	-0.56	0.00	-0.58	0.00	-0.51
PSA_2113	0.65	3.34	0.64	3.38	0.72	3.40	0.73	3.39	0.62	3.41	0.44	3.42	0.27	3.36	0.15	3.06	0.09	2.37	0.04	1.27	0.01	-0.18
PSA_2114	0.00	-0.39	0.00	-0.39	0.00	-0.38	0.00	-0.38	0.00	-0.39	0.00	-0.41	0.00	-0.46	0.00	-0.53	0.00	-0.56	0.00	-0.58	0.00	-0.51
MEAN	0.068		0.065		0.072		0.074		0.064		0.047		0.032		0.022		0.018		0.014		0.010	
STANDARD DEVIATION	0.175		0.169		0.189		0.194		0.164		0.115		0.070		0.042		0.032		0.024		0.020	

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

	Phi-interval									
	11.00 to 11.50	z-score	11.50 to 12.00	z-score	12.00 to 12.50	z-score	12.50 to 13.00	z-score	13.00 to 13.50	z-score
Benchmark Average	0.04	1.64	0.03	1.60	0.02	1.59	0.02	1.57	0.01	1.10
PSA_2101	0.05	2.24	0.04	2.34	0.03	2.40	0.03	2.44	0.03	3.02
PSA_2102	0.00	-0.48	0.00	-0.48	0.00	-0.48	0.00	-0.48	0.00	-0.44
PSA_2103	0.00	-0.48	0.00	-0.48	0.00	-0.48	0.00	-0.48	0.00	-0.44
PSA_2105	0.04	1.87	0.03	1.79	0.03	1.73	0.02	1.70	0.01	1.17
PSA_2106	0.00	-0.48	0.00	-0.48	0.00	-0.48	0.00	-0.48	0.00	-0.44
PSA_2107	0.00	-0.48	0.00	-0.48	0.00	-0.48	0.00	-0.48	0.00	-0.44
PSA_2108_A	0.00	-0.48	0.00	-0.48	0.00	-0.48	0.00	-0.48	0.00	-0.44
PSA_2108_B	0.00	-0.48	0.00	-0.48	0.00	-0.48	0.00	-0.48	0.00	-0.44
PSA_2109	0.00	-0.48	0.00	-0.48	0.00	-0.48	0.00	-0.48	0.00	-0.44
PSA_2110	0.00	-0.48	0.00	-0.48	0.00	-0.48	0.00	-0.48	0.00	-0.44
PSA_2111	0.00	-0.48	0.00	-0.48	0.00	-0.48	0.00	-0.48	0.00	-0.44
PSA_2112	0.00	-0.48	0.00	-0.48	0.00	-0.48	0.00	-0.48	0.00	-0.44
PSA_2113	0.00	-0.48	0.00	-0.48	0.00	-0.48	0.00	-0.48	0.00	-0.44
PSA_2114	0.00	-0.48	0.00	-0.48	0.00	-0.48	0.00	-0.48	0.00	-0.44
MEAN	0.008		0.007		0.005		0.004		0.003	
STANDARD DEVIATION	0.017		0.014		0.011		0.009		0.008	