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Title	Population data for 21 autosomal short tandem repeat markers in the Arabic population of the United Arab Emirates
Type	Article
URL	<a href="https://clock.uclan.ac.uk/id/eprint/17475/">https://clock.uclan.ac.uk/id/eprint/17475/</a>
DOI	<a href="https://doi.org/10.1016/j.fsigen.2017.02.015">https://doi.org/10.1016/j.fsigen.2017.02.015</a>
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Citation	Jones, Rebecca J, Al Tayaare, Wafa, Tay, Guan K, Alsafar, Habiba and Goodwin, William H (2017) Population data for 21 autosomal short tandem repeat markers in the Arabic population of the United Arab Emirates. <i>Forensic Science International: Genetics</i> , 28. e41-e42. ISSN 1872-4973
Creators	Jones, Rebecca J, Al Tayaare, Wafa, Tay, Guan K, Alsafar, Habiba and Goodwin, William H

It is advisable to refer to the publisher's version if you intend to cite from the work.  
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18	0.130	0.210				0.002		0.077		0.001
18.2										0.001
18.3										
19	0.014	0.068	0.002					0.049		
19.1										
19.2										
19.3										
20		0.009						0.019		
20.2										
20.3										
21		0.002						0.005		
21.1										
21.2								0.002		
22								0.005		
22.2										
23										
23.2										
24								0.001		
24.2										
25										
25.2										
25.3										
26							0.001			
26.2										
27							0.024			
27.2										
28							0.165			
28.2										
28.3										
29							0.219			
29.2							0.001			
30							0.239			
30.2							0.027			
31							0.044			
31.2							0.096			
31.3							0.001			
32							0.007			
32.2							0.123			
33							0.002			
33.2							0.038			
34							0.002			

34.2							0.006				
35							0.006				
35.2							0.001				
36							0.002				
36.2											
37											
<b>N</b>	996	996	996	996	995	996	996	996	996	996	996
<b>Ho</b>	0.750	0.801	0.738	0.715	0.687	0.798	0.827	0.858	0.732	0.819	0.766
<b>He</b>	0.766	0.799	0.771	0.725	0.697	0.839	0.839	0.878	0.752	0.852	0.782
<b>HWE</b>	0.399	0.537	0.383	0.196	0.195	0.202	0.020	0.012	0.056	0.000	0.031
<b>PD</b>	0.908	0.928	0.916	0.872	0.863	0.955	0.953	0.972	0.900	0.962	0.920
<b>MP</b>	0.092	0.072	0.084	0.129	0.137	0.045	0.047	0.028	0.100	0.038	0.081
<b>PE</b>	0.510	0.601	0.489	0.452	0.408	0.601	0.650	0.711	0.479	0.635	0.538
<b>TPI</b>	2.000	2.513	1.908	1.754	1.597	2.475	2.890	3.521	1.866	2.762	2.137
<b>PIC</b>	0.726	0.768	0.738	0.673	0.653	0.819	0.819	0.864	0.718	0.836	0.748
<b>CPD</b>	0.9999999999										
<b>CMP</b>	4.38x10 <sup>-27</sup>										
<b>CPE</b>	0.9999999964										

N: Number of Samples, Ho: Observed Heterozygosity, He: Expected Heterozygosity, HWE: Hardy Weinberg p-value, PD: Power of Discrimination, MP: Match Probability, PE: Power of Exclusion, TPI: Typical Paternity Index, PIC: Polymorphic Information Content, CPD: Combined Match Probability, CMP: Combined Match Probability, CPE: Combined Power of Exclusion.



17.3					0.001		0.032	0.007	
18	0.005	0.004			0.101	0.002	0.006	0.177	0.099
18.2	0.001								
18.3							0.016	0.012	
19	0.063				0.082		0.001	0.123	0.140
19.1								0.001	
19.2	0.005				0.001			0.001	
19.3							0.005	0.002	
20	0.087				0.042			0.128	0.164
20.2	0.003				0.004				
20.3								0.001	
21	0.117				0.018			0.125	0.064
21.1					0.001				
21.2	0.004				0.015				
22	0.152				0.006			0.088	0.043
22.2	0.006				0.020				
23	0.167				0.003			0.089	0.109
23.2	0.002				0.021				
24	0.217				0.002			0.049	0.076
24.2	0.002				0.030				
25	0.109	0.001						0.019	0.048
25.2	0.001				0.034				
25.3	0.001								
26	0.040							0.005	0.009
26.2					0.043				
27	0.007								0.002
27.2					0.054				
28	0.005								
28.2					0.066				
28.3					0.001				
29	0.002				0.002				
29.2					0.059				
30	0.001								
30.2					0.038				
31	0.001				0.001				
31.2	0.001				0.036				
31.3									
32					0.001				
32.2					0.022				
33					0.002				
33.2					0.006				

34						0.010				
34.2						0.004				
35						0.004				
35.2						0.001				
36						0.002				
36.2						0.001				
37						0.002				
<b>N</b>	991	996	996	996	996	991	996	996	996	996
<b>Ho</b>	0.850	0.689	0.749	0.785	0.783	0.917	0.730	0.859	0.878	0.850
<b>He</b>	0.863	0.732	0.746	0.782	0.788	0.948	0.763	0.883	0.886	0.877
<b>HWE</b>	0.294	0.024	0.629	0.648	0.230	0.000	0.009	0.305	0.376	0.000
<b>PD</b>	0.967	0.832	0.888	0.922	0.922	0.994	0.907	0.975	0.975	0.972
<b>MP</b>	0.034	0.108	0.112	0.078	0.078	0.006	0.093	0.025	0.025	0.028
<b>PE</b>	0.695	0.411	0.508	0.572	0.568	0.830	0.476	0.713	0.751	0.695
<b>TPI</b>	3.333	1.608	1.992	2.326	2.304	6.024	1.852	3.546	4.098	3.333
<b>PIC</b>	0.848	0.693	0.704	0.751	0.755	0.945	0.725	0.871	0.875	0.864
<b>CPD</b>	0.9999999999									
<b>CMP</b>	4.38x10 <sup>-27</sup>									
<b>CPE</b>	0.9999999964									

N: Number of Samples, Ho: Observed Heterozygosity, He: Expected Heterozygosity, HWE: Hardy Weinberg p-value, PD: Power of Discrimination, MP: Match Probability, PE: Power of Exclusion, TPI: Typical Paternity Index, PIC: Polymorphic Information Content, CPD: Combined Match Probability, CMP: Combined Match Probability, CPE: Combined Power of Exclusion.