

Table S1 - Allele frequencies for 12 X-STRs in northern Croatia population, N=202

	LG1				LG2				LG3				LG4			
Allele	DXS10148	DXS10135	DXS8378	DXS7132	DXS10079	DXS10074	DXS10103	HPRTB	DXS10101	DXS10146	DXS10134	DXS7423	Allele			
25	0.0033	0.1026								0.0695	0.0033			25		
25.1	0.1728													25.1		
25.2									0.0166					25.2		
26	0.0066	0.0861								0.1656				26		
26.1	0.1429	0.0033												26.1		
26.2									0.0132					26.2		
27		0.0464							0.0132	0.0993				27		
27.1	0.1395								0.0530					27.1		
27.2														27.2		
28	0.0033	0.0530							0.0199	0.1589				28		
28.1	0.0698													28.1		
28.2	0.0033								0.1192					28.2		
29		0.0662							0.0166	0.1589				29		
29.1	0.0199	0.0033								0.0033				29.1		
29.2									0.1325					29.2		
30		0.0596							0.0464	0.0629				30		
30.2									0.1457					30.2		
31		0.0298							0.0497	0.0397	0.0199			31		
31.1	0.0066													31.1		
31.2									0.1556					31.2		
32		0.0033							0.1225	0.0066	0.0066			32		
32.2									0.0464					32.2		
33		0.0066							0.0232		0.0662			33		
33.2									0.0033	0.0033				33.2		
34		0.0033							0.0166		0.1788			34		
34.2									0.0033					34.2		
35									0.0033		0.1391			35		

	LG1				LG2				LG3				LG4			
Allele	DXS10148	DXS10135	DXS8378	DXS7132	DXS10079	DXS10074	DXS10103	HPRTB	DXS10101	DXS10146	DXS10134	DXS7423	Allele			
36											0.2384		36			
36.2											0.0033		36.2			
36.3											0.0033		36.3			
37											0.1788		37			
37.2										0.0066	0.0099		37.2			
38											0.0397		38			
38.3											0.0066		38.3			
39											0.0298		39			
39.2										0.0397			39.2			
39.3											0.0132		39.3			
40											0.0033		40			
40.2										0.0232			40.2			
40.3											0.0166		40.3			
41.1											0.0033		41.1			
41.2										0.0099			41.2			
41.3											0.0232		41.3			
42.2										0.0166			42.2			
42.3											0.0099		42.3			
43.2										0.0364			43.2			
43.3											0.0033		43.3			
44.2										0.0364	0.0033		44.2			
44.3													44.3			
45.2										0.0066			45.2			
46											0.0033		46			
46.2											0.0364		46.2			
Ho	0.8600	0.9500	0.6800	0.7600	0.8300	0.7900	0.7200	0.7900	0.8800	0.8800	0.8500	0.7000	Ho			
He	0.8913	0.9269	0.6884	0.7484	0.8257	0.8174	0.7355	0.7567	0.8955	0.8927	0.8358	0.7186	He			

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Allele	DXS10148	DXS10135	DXS8378	DXS7132	DXS10079	DXS10074	DXS10103	HPRTB	DXS10101	DXS10146	DXS10134	DXS7423	Allele			
P	0.3332	0.1579	0.8521	0.8068	0.4302	0.8783	0.2821	0.4568	0.4931	0.6272	0.2585	0.2865	P			
SD	0.0003	0.0001	0.0003	0.0004	0.0004	0.0003	0.0005	0.0004	0.0004	0.0003	0.0002	0.0004	SD			

Abbreviations: Ho - observed heterozygosity; He - expected heterozygosity; P-value - result of Hardy-Weinberg equilibrium test with a significance level 0.004; SD - standard deviation

No statistically significant deviation from HWE was observed in any locus.