

R-L47 Allele Diversity

Allele	All	UK&I	NWE	Sca	CE	NEE	SEE	SWE
393	0.1370	0.1176				0.2500		
390	0.3656	0.1176				0.6071		
19	0.1656	0.1176				0.4286		
391	0.4994	0.4853				0.4286		
385	0.4565	0.5147				0.0000		
426	0.0357	0.0000				0.0000		
388	0.0357	0.1176				0.0000		
439	0.5682	0.5809				0.4286		
389	0.5779	0.5956				0.2500		
392	0.0357	0.0000				0.0000		
458	0.7016	0.7279				0.4643		
459	0.1419	0.2279				0.2500		
455	0.0370	0.1176				0.0000		
454	0.0000	0.0000				0.0000		
447	0.3725	0.4044				0.5714		
437	0.0727	0.0000				0.0000		
448	0.1761	0.2206				0.2500		
449	0.6338	0.6985				0.2500		
464	0.9085	0.7868				0.8571		
460	0.2380	0.2206				0.2500		
GATA H4	0.2438	0.4191				0.0000		
YCA II	0.5007	0.6544				0.4643		
456	0.5965	0.4853				0.5357		
607	0.3295	0.4706				0.0000		
576	0.6509	0.6324				0.6071		
570	0.6357	0.5074				0.7500		
CDY	0.9253	0.9118				0.8929		
442	0.3556	0.4853				0.2500		
438	0.2337	0.1176				0.5357		
531	0.1246	0.2637				0.0000		
578	0.0000	0.0000				0.0000		
395S1	0.2039	0.2747				0.2857		
590	0.0000	0.0000				0.0000		
537	0.1246	0.1429				0.0000		
641	0.0000	0.0000				0.0000		
472	0.0000	0.0000				0.0000		
406S1	0.2396	0.2747				0.2857		
511	0.1623	0.2637				0.0000		
425	0.0435	0.1429				0.0000		
413	0.4097	0.2637				0.5714		
557	0.3449	0.2747				0.5238		
594	0.0435	0.0000				0.0000		
436	0.0435	0.0000				0.0000		
490	0.0000	0.0000				0.0000		
534	0.5671	0.5824				0.6667		
450	0.0000	0.0000				0.0000		
444	0.4976	0.4835				0.4762		
481	0.6541	0.6593				0.5714		
520	0.3478	0.1429				0.5714		
446	0.4338	0.4945				0.2857		
617	0.0860	0.2747				0.0000		
568	0.0435	0.1429				0.0000		
487	0.1246	0.0000				0.4762		
572	0.3082	0.3626				0.4762		
640	0.0000	0.0000				0.0000		
492	0.0000	0.0000				0.0000		
565	0.2039	0.1429				0.0000		
461	0.2500							
462	0.0000							
A10	0.4286							

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Allele	All	UK&I	NWE	Sca	CE	NEE	SEE	SWE
635	0.0000							
1B07	0.2500							
441	0.5714							
445	0.0000							
452	0.2500							
463	0.4286							

Allele	All	UK&I	NWE	Sca	CE	NEE	SEE	SWE
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Allele diversity ( $h$ ) calculated as:

$$h = \frac{n}{n-1} \left( 1 - \sum_{i=1}^M x_i^2 \right)$$

$n$  is number of haplotypes,  $M$  is the number of unique allele values and  $x_i$  is the allele frequency

Reference: *Arlequin* V3.1 Manual, Section 7.1.1.1 - Gene Diversity (from p. 180 of Nei, M., 1987 Molecular Evolutionary Genetics. Columbia University Press, New York, NY, USA.)  
[<http://cmpg.unibe.ch/software/arlequin3/arlequin31.pdf>]

<p>Region Index:  UK&amp;I - United Kingdom &amp; Ireland  NWE - North Western Europe  Sca - Scandinavia  CE - Central Europe  NEE - North Eastern Europe  SWE - South Western Europe  SEE - South Eastern Europe</p>
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