



Figure S1 Trees generated by the tree comparison tool of ClonalFrame. This tool attributes a colored circle to each node of the first consensus tree according to the level of confidence found between both trees of replicate runs (ranging from white, which indicates no confidence, to black, which indicates total confidence). For ranking purposes, a score was given to each node of the resultant tree, ranging from 0 (white nodes) to 3 (black nodes) in order to calculate the average concordance score for each data set. Strains A/Har13, B/Jali20, Ba/Apache2, C/TW3, D/UW3, E/Bour, F/IC-Cal3, G/UW57, H/UW43, I/UW12, J/UW36, K/UW31, L1/440, L2/434 and L3/404 are numbered 1 to 15, respectively.

Table S1 Oligonucleotide primers used for PCR and sequencing.

ORF ^a	Primer ^a	Primer sequence (5' to 3') ^a	Primer location ^a	Amplicon size (bp) ^a
CT048 (<i>yraL</i>)	CT048-1 ^b	GAGCCGGCTCTTTTAAATGGTTT	53104 - 53126	1059
	CT048-2 ^b	GTCGACGGAAACAGACGAAGAAA	54141 - 54162	
CT050/CT051	CT050/51-1A ^{c, d}	TGGGCGCTGTTATTAACATTTG	377806 - 377829	3704
	CT050/51-2A ^{b, d}	GACCCCATCCCCTTTGGAGT	381490 - 381509	
	CT050/51-1D ^b	ACAAAGCGCTTTCAGAACATACAT	55452 - 55475	
	CT050/51-2D ^b	AGGGCGTCTTTTCATGATTCTAT	59017 - 59040	
	CT050/51-1 ^e	CTAAGAGTTATGTAGCTATC	55542 - 55561	
	CT050/51-1S ^e	AGTTAAGGGAGAGAATCTC	55593 - 55611	
	CT050/51-3 ^e	TTGTAGTGTGCAAGATTGTC	55857 - 55876	
	CT050/51-4 ^e	TTGTGCCACTACAATACCTT	58726 - 58745	
	CT050/51-5 ^e	AACCTTTCCAATATCACCGT	56566 - 56585	
	CT050/51-6 ^e	GCACAGATCGCCAATATCAA	58076 - 58095	
	CT050/51-7 ^e	AGTCACTCCAGACAATTCTA	57699 - 57718	
	CT050/51-8 ^e	TTAGTGAGACAGGCATTGA	57160 - 57178	
	CT058/CT059 (<i>fer</i>)	CT058/9-1 ^b	AGTACCGGCCGAATCTCTTTCTCC	67315 - 67338
CT058/9-2 ^b		GTCGGGGGTTTCAATCCCTCTA	68927 - 68948	
CT058/9-3 ^e		TCTCATTACTTCTTTCGCT	68432 - 68451	
CT147 ^f	CT147-1 ^b	GGGGAAAGTGAGCTCTTCGGTATC	165430 - 165453	2819
	CT147-2 ^b	CGCCGCTACAACAGCTTTAGTGA	168226 - 168248	
	CT147-3 ^b	ATTGCGTCCAAGATATACGACAG	167928 - 167951	2294
	CT147-4 ^b	CACGCCAACCCAGAATCCTT	170202 - 170221	
	CT147-5 ^e	TAATCATCCACTAGAAGCG	166229 - 166247	
	CT147-6 ^e	TGTTCTAGCTGCTTTGAAT	167649 - 167668	
	CT147-7 ^e	TGGATGGTGTGAGAATTA	168511 - 168530	
	CT147-8 ^e	TACCTCTAGATGTTTTGCGT	169786 - 169805	
CT192	CT192-1 ^b	ATATGCGCAAGCACACCTTCC	215717 - 215737	1016
	CT192-2 ^b	CTGGGCGTCCATTCACAACA	216713 - 216732	
	CT192-3 ^e	CGTATCGATTCTTCTTCTA	215998 - 216017	
	CT192-4 ^e	CTCCTCTTATTGAAGAAGCT	2156196 - 216215	
CT195	CT195-1 ^b	CCTCCGCTAATCCTCGACTACAT	219655 - 216678	1320
	CT195-2 ^b	CCAGCGTTGATATTTCTTGATTA	220951 - 220974	
CT214	CT214-1 ^b	AGGGCTTCTATTCTCAAACAGTA	241463 - 241486	1797
	CT214-2 ^b	TTCCCGTTCTAAAGATCAGTTAT	243236 - 243259	
	CT214-3 ^e	AACAGCTGGATCTATATCA	242027 - 242046	
CT223	CT223-1 ^b	GCAACGCATATCGCTCCTCA	251102 - 251121	1308
	CT223-2 ^b	GTGCGCCCTTCTCGTAAAG	252390 - 252409	
CT228/CT229	CT228/9-1 ^b	CGGTCCCGGATTATCAAACAAGT	254667 - 254690	1816
	CT228/9-2 ^b	ATGCGGCCATCCCAGAAGC	256464 - 256482	
	CT228/9-3 ^e	AGATTACGCAAACGTTGCTC	255033 - 255052	

	CT228/9-4 ^e	GTTGTGATTGCAGCAGTAG	255972 - 255990	
CT232/CT233	CT232/3-1 ^b	GATTAGGCGGAGGGGTTCTCTT	259223 - 259244	1262
(<i>incB/incC</i>)	CT232/3-2 ^b	CTCTCCGCGACGCAAATAAG	260464 - 260484	
CT249	CT249-1 ^b	ACCACCCCTTAGCCATCCATCC	279170 - 279192	704
	CT249-2 ^b	AATTGCGCCGCCTCCTTGTA	279854 - 279873	
CT288	CT288-1 ^b	TTTTACGCACAATGAACCCAGAAA	321582 - 321605	2063
	CT288-2 ^b	CGGGCTCCTCGGGAACAG	323627 - 323644	
	CT288-3 ^e	TTACCTGACCTCAGACACC	322164 - 322182	
	CT288-4 ^e	GTCAGCTCGTCGTTTATTG	323121 - 323139	
CT293 (<i>accD</i>)	CT293-1 ^b	TGCGCCAGAAGCTCCAGAAGTAGC	326322 - 326345	1350
	CT293-2 ^b	AGGATCTGGCTGGGGATGGTTAGC	327648 - 327671	
CT365	CT365-1 ^b	AAATTCGCAAATTGCTCTTTTTTC	416102 - 416125	2213
	CT365-2 ^b	GATCGGGATTCCCCTGGATA	418295 - 418314	
	CT365-3 ^e	CTAACTCCAAGTTTCTCT	416572 - 416591	
	CT365-4 ^e	CTCATTGCAGGTATTGTTGT	417720 - 417739	
CT442 (<i>crpA</i>)	CT442-1 ^b	CTCCTCCCTTCCATACATCATCT	511256 - 511279	783
	CT442-2 ^b	AAGCGATTCTTCTCCGATACAT	512015 - 512038	
CT456 (<i>tarp</i>)	CT456-1 ^b	ACAAACGTTACCCGGTATGCTGTT	530723 - 530746	3362
	CT456-2 ^b	TTGCGCCTTGTCGATTGTGAT	534064 - 534084	
	CT456-3 ^e	TACCTCATCAAGCGATCATA	531252 - 531271	
	CT456-4 ^e	CCACCAGTTGTTATTATGTC	533470 - 533489	
	CT456-5 ^e	AGACATGTCTCTTCTTCAT	531867 - 531886	
	CT456-6 ^e	TACATCAGAGATTACGTCTC	532889 - 532908	
	CT456-7 ^e	GAGTTTCATTGGAGAAGGAA	532413 - 532432	
	CT456-8 ^e	CGTTACCCGGTATGCTGTT	530728 - 530746	
	CT456-9 ^e	TACAAACACTACTGCCTTCA	533363 - 533382	
	CT456-10 ^e	TTGTTACTACCTACGTCATC	531328 - 531347	
	CT456-11 ^e	CTAATTAATCGGCTGTTG	530869 - 530887	
CT529	CT529-1 ^b	ACGCGGCTCCTTAAAGCAAACAA	596464 - 596486	1659
	CT529-2 ^b	CGCGCATATCCGGGGAGTCT	598103 - 598122	
	CT529-3 ^e	TCTCGCAAGCATTTCCTCT	596984 - 597003	
CT618	CT618-1 ^b	TCCCGATATGCCTCCTTTGAGTC	698080 - 698103	1360
	CT618-2 ^b	ATGCGCACGCAAGCCAATC	699421 - 699439	
CT622	CT622-1 ^b	GGCTCCCCCTCAATTCACAAACTT	707046 - 707069	2319
	CT622-2 ^b	GGTCGCGGAAACCAATGAAATA	709342 - 709364	
	CT622-3 ^e	TGATTGCTTGTATTTGCGCT	707784 - 707803	
	CT622-4 ^e	TTCAGCATCGTCTCTGTAA	708885 - 708904	
	CT622-5 ^e	AGAAGAGATTATGCAGAAGC	707298 - 707317	
CT623	CT623-1 ^b	TTTGCCCATTAATAATTGGATTCA	708957 - 708980	1516
	CT623-2 ^b	CATGGGTGCGTTGTATGAGATGT	710450 - 710472	
CT653 (<i>yhbG</i>)	CT653-1 ^b	AGCCGCGATAGCTAACGAAGTG	750194 - 750215	922
	CT653-2 ^b	GAAGGCGGAATGAAAGTCCTCTC	751093 - 751115	

CT674 (<i>yscC</i>)	CT674-1 ^b	TTTCAAGCGGAATCGCAAGGAAT	770234 - 770256	3229	
	CT674-2 ^b	CCGGGATCGAACCGACGAC	773444 - 773462		
	CT674-3 ^e	AGAGCCATCAGATTTTCTCT	770846 - 770865		
	CT674-4 ^e	AGAGGAAGAGAACTGAGTAA	772996 - 773015		
	CT674-5 ^e	ATGACTTGAAAGTCGTTGAA	771470 - 771489		
	CT674-6 ^e	TCCGTACATCATATCACTGA	772505 - 775524		
	CT674-7 ^e	GATATCGGAGTCAATCTTGTT	772771 - 772791		
CT675 (<i>karG</i>)/	CT675/6-1 ^b	CCCGGCTTTGGGCATTCC	773458 - 773475	1933	
CT676	CT675/6-2 ^b	TCATTCCGGTAACAGGGGTTCG	775369 - 775390		
	CT675/6-3 ^e	CGTGATCAGATTAATCAGCT	774669 - 774688		
CT677/CT678/	CT677/9-1 ^b	ATGGGGCCAGGACGGGTCTA	775420 - 775439	2393	
CT679 (<i>frr</i> , <i>pyrH</i> , <i>tsf</i>)	CT677/9-2 ^b	AAATTTTATCTCCGGTGCCTCTG	777789 - 777812		
	CT677/9-4 ^e	GAAGATATCACTGTACCAAC	776088 - 776107		
CT682 (<i>pbpB</i>) [†]	CT677/9-5 ^e	TGGCTAAAGACATTGCTATG	777107 - 777126	3149	
	CT682-1 ^b	GCATTGTGATCGCGCAGGAGTA	780841 - 780862		
	CT682-2 ^b	TTCCGCCTCTCCATAGTCGTTC	783966 - 783989		
	CT682-3 ^e	TTGATAGGCAAGCGATCTAT	781484 - 781503		
	CT682-4 ^e	ATATTCTCCAGGAAGTCCTA	783318 - 783337		
CT683 (<i>TPR-</i> <i>motif protein</i>)	CT682-5 ^e	TGGAAATGTTTGAGTGTGAA	782079 - 782098	1702	
	CT683-1 ^b	TCGCTGCGGTAGGATATGAAGATG	783756 - 783779		
	CT683-2 ^b	TCGCCGCGTAAATGAACCAAT	785437 - 785457		
CT684 [†]	CT683-3 ^e	GACTGTCAAACAGCCCTTAA	785108 - 785127	1471	
	CT684-A1 ^b	TGGGCATTACAATCTTGGGTTATG	784615 - 784638		
	CT684-A2 ^b	AACAGCGGCATGCAGTTGATG	786065 - 786085		
	CT684-B1 ^b	ATTCGGGAGGCAATCCACAAT	785785 - 785806		1398
	CT684-B2 ^b	TCCCGGGAATCCATATACCTCTTC	787159 - 787182		
	CT684-A3 ^e	TCATCAATAGGGATGCCTAA	785651 - 785670		
	CT685/CT686	CT684-A4 ^e	TCTGGATCTGCGTCTTCTAA		785609 - 785628
CT685/6-1 ^b		GCTCGGGAAGCAACCAAGTTATTA	786722 - 786745		
CT685/6-2 ^b		AAGCGAGTCCCATGATACGAGAT	789084 - 789107		
CT685/6-3 ^e		TCTTGATGTCGATGCTTTGA	787308 - 787327		
CT694	CT685/6-4 ^e	ATGCAGAAGCTCGATTACTT	788502 - 788521	1541	
	CT694-1 ^b	TACAGGGGGAGGCGCTTCCTTA	796071 - 796092		
	CT694-2 ^b	CGCGCTCTTCTAGCTCTCCCTCTT	796528 - 797551		
CT760 (<i>ftsW</i>)	CT694-3 ^e	GATAACTCTTAACCCCATG	796267 - 796286	1417	
	CT760-1 ^b	CTTGGGCCATTGCATTGAGTAAT	892695 - 892717		
	CT760-2 ^b	CCCCAGAGAACATCCGATTGAC	894090 - 894111		
CT783	CT760-3 ^e	AGGATGTAGGTAAACTTGCA	893445 - 893464	1427	
	CT783-1 ^b	AGCGGGGATTCAGCATTCTCT	919328 - 919347		
	CT783-2 ^b	TGCCCTCGCCTCTTCATC	920676 - 920694		
CT813	CT783-3 ^e	TGTCAATACCTTCCCTAGTT	919913 - 919932	1460	
	CT813-1 ^b	CTGCGTGTGCTCTGGAAAATAAT	954988 - 955011		

	CT813-2 ^b	AGGCCGAGCCCTACTCAAAAAC	956365 - 956387	
CT818 (<i>tyrP_2</i>)	CT818-1 ^b	CCTGGCGGGAAAGGGACTCT	961600 - 961619	1531
	CT818-2 ^b	GCGCATAATCGCGATCATAAATC	963107 - 963130	
	CT818-3 ^e	GAATAGCACGTTTAACTCA	962512 - 962531	
CT852 (<i>yhgN</i>)	CT852-1 ^b	CTGCCGACCAGCAAGGAT	1001213 - 1001231	768
	CT852-2 ^b	TAGGCGCTCAACTTCTGGTATCTG	1001957 - 1001980	
CT859 (<i>ispH</i>)/	CT856/60-1 ^b	GAGGGGGCTTTGCGGATTAT	1011689 - 1011709	2779
CT860	CT856/60-2 ^b	CCGGAATGCTTGGCTTGACA	1014448 - 1014467	
	CT856/60-3 ^e	ACGACATTGAGTATGGATGA	1012253 - 1012272	
	CT856/60-4 ^e	ACCCCGATATCTCATAAATC	1013829 - 1013848	
	CT856/60-5 ^e	GTATTCAGTTGCTAAGGA	1012658 - 1012677	
CT861/CT862	CT861/2-1 ^c	GAGGGCAGAGGCTTCTCACAAG	1014122 - 1014144	2400
(<i>lcrH_2</i>)	CT861/2-2 ^b	CTAGGCGTCCCAATTGGAGACTC	1016499 - 1016521	
	CT861/2-3 ^e	AATAGCTCTCCAACCATCAA	1014640 - 1014659	
	CT861/2-4 ^e	GACTATGAGGAAAGTTCTAC	1016071 - 1016090	
	CT861/2-5 ^e	TCTCTGTTGCTATTGTTTG	1014159 - 1014178	
	CT861/2-6 ^e	TTGACTTTCTCTGATGCTT	1015102 - 1015121	
CT867/CT868	CT867/8-1 ^c	TCCCAGCTGCTGGGGCTTAGA	1022902 - 1022922	2889
	CT867/8-2 ^c	CATCGCGTCATGCCATGTCCTAT	1025768 - 1025790	
	CT867/8-3 ^e	TCCTTCAGCTACTCTGATT	1022935 - 1022953	
	CT867/8-4 ^e	TGGTAAGCGGATTACAGAT	1023641 - 1023659	
	CT867/8-5 ^e	TTCATGGCGTTCTACAGAAT	1024302 - 1024321	
	CT867/8-6 ^e	AATGTCAGAATCCCAAGCA	1024923 - 1024941	
	CT867/8-7 ^e	AGAGGGAAGTCTTAATTTCC	1025542 - 1025561	

^a Open reading frame (ORF) numbers, primer location (genome coordinates), primer sequences and amplicon size are based on the D/UW3 strain genome annotation (GenBank accession number NC_000117).

^b Amplification primers also used for automated sequencing.

^c Primers exclusively used for PCR amplification.

^d Primer sequences, location and amplicon size refers to the L2/434 strain genome annotation (GenBank accession number NC_010287) as these primers were designed for amplification and automated sequencing in LGV and ocular strains, and they have no homology in the D/UW3 genome sequence.

^e Primers exclusively used for automated sequencing.

^f Due to the large gene size (for CT147 and CT682) or for PCR optimization (for CT684), two PCR primer pairs were designed to generate two overlapping amplicons for the entire gene. The primer pair for the amplification of the first region of the CT682 gene was previously described in Gomes et al. 2007 (data not shown).

Table S2 List of the studied loci.

Loci ^a	Alleles Number ^b	$d_N/d_S > 1$ (Z-test; $p < 0,05$) ^c
IGR (CT044/CT045)	-	
IGR (CT047/CT048)	-	
CT048 (<i>yraL</i>)	6	
IGR (CT048/CT049)	-	
CT049	13	
CT050	11	
CT051	11	
CT058	11	
IGR (CT058/CT059)	-	
CT059 (<i>fer</i>)	5	
CT115	6	
IGR (CT115/CT116)	-	
CT116	8	+
CT117	7	
IGR (CT117/CT118)	-	
CT118	5	+
IGR (CT118/CT119)	-	
CT121 (<i>araD</i>) ^d	3	
CT144	9	
IGR (CT144/CT145)	-	
CT147 (<i>EEA1</i>)	12	
IGR (CT191/CT192)	-	
CT192	8	
IGR (CT192/CT193)	-	
CT195	8	
CT209 (<i>leuS</i>) ^{d,e}	5	
CT214	8	
IGR (CT222/CT223)	-	
CT223	11	+
IGR (CT223/CT224)	-	
CT228	6	+
IGR (CT228/CT229)	-	
CT229	7	+
IGR (CT229/CT230)	-	
IGR (CT231/CT232)	-	
CT232 (<i>IncB</i>)	5	
IGR (CT232/CT233)	-	
CT233 (<i>IncC</i>)	7	
IGR (CT233/CT234)	-	
CT245 (<i>pdhA</i>) ^{d,e}	2	

IGR (CT248/CT249)	-	
CT249	9	+
IGR (CT287/CT288)	-	
CT288	9	+
IGR (CT288/CT289)	-	
IGR (CT292/CT293)	-	
CT293 (<i>accD</i>)	4	
IGR (CT293/CT294)	-	
IGR (CT315/CT316)	-	
CT332 (<i>pykF</i>) ^{d,e}	5	
CT365	8	
IGR (CT365/CT366)	-	
CT376 (<i>mdhC</i>) ^{d,e}	4	
CT412 (<i>pmpA</i>)	10	
CT413 (<i>pmpB</i>)	13	+
IGR (CT413/CT414)	-	
CT414 (<i>pmpC</i>)	13	
CT432 (<i>glyA</i>) ^{d,e}	3	
IGR (CT441/CT442)	-	
CT442 (<i>crpA</i>)	8	+
IGR (CT442/CT443)	-	
CT443 (<i>omcB</i>)	7	
CT456 (<i>tarp</i>)	13	+
CT505 (<i>gapA</i>) ^d	3	
CT529	9	
IGR (CT529/CT530)	-	
CT618	8	
IGR (CT618/CT619)	-	
CT622	12	
IGR (CT622/CT623)	-	
CT623	6	
IGR (CT624/CT625)	-	
IGR (CT652.1/CT653)	-	
CT653 (<i>yhbG</i>) ^e	3	
IGR (CT653/CT654)	-	
CT674 (<i>yscC</i>)	11	
IGR (CT674/CT675)	-	
CT675 (<i>karG</i>)	10	
CT676	8	
IGR (CT676/CT677)	-	
CT677 (<i>frr</i>)	10	
CT678 (<i>pyrH</i>)	10	
IGR (CT678/CT679)	-	
CT679 (<i>tsf</i>)	12	

CT680 (<i>rs2</i> or <i>rpsB</i>)	12	
IGR (CT680/CT681)	-	
CT681 (<i>ompA</i>)	15	
IGR (CT681/CT682)	-	
CT682 (<i>pbpB</i>)	14	
IGR (CT682/CT683)	-	
CT683 (<i>TPR-motif protein</i>)	7	
IGR (CT683/CT684)	-	
CT684	6	
CT685	5	
CT686	9	
CT687 (<i>yfhO_1</i>)	5	
IGR (CT687/CT688)	-	
CT688 (<i>parB</i>)	8	
CT689 (<i>dppF</i>)	6	
CT690 (<i>dppD</i>) ^d	6	
CT694	10	+
IGR (CT698/CT699)	-	
CT713 (<i>porB</i>) ^d	4	
16SrRNA	6	
IGR (CT759/CT760)	-	
CT760 (<i>ftsW</i>)	6	
CT781 (<i>lysS</i>) ^{d,e}	4	
IGR (CT782/CT783)	-	
CT783	8	
IGR (CT783/CT784)	-	
IGR (CT796/CT797)	-	
CT812 (<i>pmpD</i>)	10	
IGR (CT812/CT813)	-	
CT813	7	+
IGR (CT813/CT814)	-	
IGR (CT817/CT818)	-	
CT818 (<i>tyrP_2</i>)	9	
IGR (CT818/CT819)	-	
IGR (CT851/CT852)	-	
CT852 (<i>yhgN</i>)	9	
IGR (CT852/CT853)	-	
CT859 (<i>ispH</i>)	6	
IGR (CT859/CT860)	-	
CT860	10	
IGR (CT860/CT861)	-	
CT861	7	
IGR (CT861/CT862)	-	
CT862 (<i>lcrH_2</i>)	3	

CT867	10	+
CT868	13	+
CT869 (<i>pmpE</i>)	11	
CT870 (<i>pmpF</i>)	9	
IGR (CT870/CT871)	-	
CT871 (<i>pmpG</i>)	12	
CT872 (<i>pmpH</i>)	10	
CT874 (<i>pmpI</i>)	12	

^a Open reading frame (ORF) numbers are based on the D/UW3 strain genome annotation (GenBank accession number NC_000117).

^b Number of alleles that each gene assigns were determined based on MEGA5 evolutionary analysis (distance matrices and phylogenetic trees) of each gene (for more details see the Materials and Methods section).

^c Genes putatively under positive selection that compose the PSG data set (Joseph et al. 2011; Borges V, Nunes A, Ferreira R, Borrego MJ, Gomes JP, unpublished data)..

^d For these genes, the partial sequences available at the GenBank were used.

^e Genes that constitute a previously defined MLST scheme for *Chlamydia trachomatis* molecular characterization (Dean et al. 2009).

The partial sequences used for typing purposes compose the HK-MLST data set.

Table S3 Contingency table for estimating the significance of the polymorphism present in the loci studied.

	Inside Region (bp) ^a	Outside Region (bp)	
SNPs	1802	1552	3354 ^b
Without SNPs	112530	926635	1039165
	114332	928187	1042519 ^c

^a Chromosomal region evaluated in the present study (composed by the 136 genomic regions: 80 genes and 56 intergenic regions). ^b

Total number of SNPs identified between the *Chlamydia trachomatis* serovars A/Har13 (NC_007429) and D/UW3 (NC_000117)

(Carlson et al. 2005).^c Total length of the chromosome of *C. trachomatis* serovar D/UW3 (NC_000117). The polymorphism

significance ($p < 10^{-7}$) of the analyzed regions was calculated using the Fisher's exact test.

Table S4 Accuracy results and r/m and ρ/θ estimates for all loci data sets.

Loci Data Sets	Accuracy Assessments			ClonalFrame Results			
	Trees concordance score	Gelman-Rubin test		r/m (mean; [95% CI])		ρ/θ (mean; [95% CI])	
		Test statistics	Convergence	1 st run	2 nd run	1 st run	2 nd run
Wide genomic	3	1.00 (θ , ν , δ); 0.99 (R)	+	0.21; [0.18-0.25]	0.21; [0.18-0.24]	0.01; [0.01-0.01]	0.01; [0.01-0.01]
HK-MLST	2.875	1.00 (θ , ν , δ , R)	+	0.91; [0.05-3.95]	1.09; [0.07-5.02]	0.12; [0.004-0.42]	0.14; [0.01-0.58]
1 to 5 alleles	2.667	1.00 (θ , δ , R); 0.99 (ν)	+	4.77; [1.77-10.72]	5.09; [1.76-12.36]	0.91; [0.27-2.27]	1.02; [0.27-2.87]
6 and 7 alleles	2.7	1.00 (δ , R); 0.99 (θ , ν)	+	7.04; [3.45-12.67]	6.98; [3.47-12.57]	0.89; [0.42-1.71]	0.87; [0.41-1.62]
8 and 9 alleles	2.643	1.04 (θ); 1.15 (R); 1.58 (ν); 1.23 (δ)	-	2.38; [1.54-3.65]	2.44; [1.55-3.77]	0.21; [0.12-0.33]	0.21; [0.12-0.33]
10 and 11 alleles	2.786	1.13 (θ); 1.21 (R); 1(ν); 1.28 (δ)	-	3.41; [0.47-5.21]	4.12; [3.09-5.38]	0.27; [0.03-0.41]	0.35; [0.27-0.45]
12 to 15 alleles	2.714	6.51 (θ); 1(R); 16.99 (ν); 1.02 (δ)	-	0.58; [0.3-0.96]	0.29; [0.21-0.38]	0.03; [0.01-0.05]	0.01; [0.01-0.01]
PSG	2.357	2.70 (θ); 1.73 (R); 37.74 (ν); 11.45 (δ)	-	0.05; [0.02-0.1]	3.15; [1.6-5.31]	0.08; [0.05-0.13]	0.39; [0.2-0.7]
IGR	2.769	1.00 (θ , ν , δ , R)	+	1.38; [0.82-2.17]	1.38; [0.8-2.19]	0.3; [0.17-0.48]	0.29; [0.17-0.47]

CI – Confidence interval; **θ** – mutation rate; **ν** – rate of new polymorphism introduced by recombination; **δ** – average tract length of a recombination event; **R** – recombination rate; **r/m** – measure of the weight of recombination on the diversification relative to mutation; **ρ/θ** – measure of the frequency of occurrence of recombination relative to mutation events.