Supplementary Table 1: Allele, genotype and homo- or heterozygote frequencies of VNTR polymorphism in our study groups and Chan *et al*..

VNTR polymorphism	Beijing populations, No. (%)				Tianjin populations, No. (%)			Hong Kong populations, No. (%)[b]			
	Community patients (*n* = 339)	Random controls (*n* = 227)	HCW SARS (*n* = 42)	HCW controls (*n* = 40)	Community patients (*n* = 60)	Random controls (*n* = 85)	HCW controls (*n* = 44)	Community patients (*n* = 218)	Outpatient controls (*n* = 290)	HCW SARS (*n* = 67)	HCW controls (*n* = 172)
Genotypes[a]											
5/5	18 (5.3)	6 (2.6)	3 (7.1)	3 (7.5)	2 (3.3)	5 (5.9)	1 (2.3)	8 (3.7)	14 (4.8)	1 (1.5)	19 (11.0)
5/9	14 (4.1)	10 (4.4)	0 (0.0)	4 (10.0)	1 (1.7)	5 (5.9)	1 (2.3)	7 (3.2)	8 (2.8)	2 (3.0)	3 (1.7)
6/5	7 (2.1)	1 (0.4)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	2 (4.5)	3 (1.4)	2 (0.7)	0 (0.0)	7 (4.1)
6/6	1 (0.3)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	1 (0.5)	0 (0.0)	0 (0.0)	0 (0.0)
6/9	1 (0.3)	2 (0.9)	0 (0.0)	0 (0.0)	2 (3.3)	0 (0.0)	0 (0.0)	3 (1.4)	3 (1.0)	1 (1.5)	1 (0.6)
7/4	1 (0.3)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
7/5	48 (14.2)	42 (18.5)	5 (11.9)	10 (25.0)	15 (25.0)	19 (22.3)	11 (25.0)	49 (22.5)	50 (17.2)	16 (23.9)	25 (14.5)
7/6	15 (4.4)	13 (5.7)	1 (2.4)	1 (2.5)	3 (5.0)	0 (0.0)	3 (6.8)	12 (5.5)	25 (8.6)	7 (10.4)	6 (3.5)
7/7	175 (51.6)	107 (47.1)	24 (57.1)	18 (45.0)	25 (41.7)	34 (40.0)	14 (31.8)	86 (39.4)	145 (50.0)	27 (40.3)	76 (44.2)
7/8	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	1 (0.6)
7/9	53 (15.6)	42 (18.5)	8 (19.0)	3 (7.5)	12 (20.0)	21 (24.7)	10 (22.7)	41 (18.8)	39 (13.4)	12 (17.9)	28 (16.3)
9/9	6 (1.8)	4 (1.8)	1 (2.4)	1 (2.5)	0 (0.0)	1 (1.2)	2 (4.6)	8 (3.7)	4 (1.4)	1 (1.5)	6 (3.5)
Alleles[a]											
4	1 (0.1)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
5	105 (15.5)	65 (14.3)	11 (13.1)	20 (25.0)	20 (16.7)	34 (20.0)	16 (18.2)	75 (17.2)	88 (15.2)	20 (14.9)	73 (21.2)
6	25 (3.7)	16 (3.5)	1 (1.2)	1 (1.3)	5 (4.2)	0 (0.0)	5 (5.7)	20 (4.6)	30 (5.2)	8 (6.0)	14 (4.1)
7	467 (68.9)	311 (68.5)	62 (73.8)	50 (62.5)	80 (66.6)	108 (63.5)	52 (59.1)	274 (62.8)	404 (69.6)	89 (66.4)	212 (61.6)
8	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	1 (0.3)
9	80 (11.8)	62 (13.7)	10 (11.9)	9 (11.3)	15 (12.5)	28 (16.5)	15 (17.0)	67 (15.4)	58 (10.0)	17 (12.7)	44 (12.8)
Homo- or heterozygosity											
Heterozygotes	139 (41.0)	110 (48.5)	14 (33.3)	18 (45.0)	33 (55.0)	45 (52.9)	27 (61.4)	115 (52.8)	127 (43.8)	38 (56.7)	71 (41.3)
Homozygotes	200 (59.0)	117 (51.5)	28 (66.7)	22 (55.0)	27 (45.0)	40 (47.1)	17 (38.6)	103 (47.2)	163 (56.2)	29 (43.3)	101 (58.7)

All groups except the community patients in our Beijing populations were in Hardy-Weinberg equilibrium. Hardy-Weinberg Exact Test for our Beijing community patients, random controls, HCW SARS, HCW controls, and Tianjin community patients, HCW controls and random controls gave $P = 0.0006$, P

= 0.922, P = 0.055, P = 0.257, P = 0.397, P = 0.610 and P = 0.518, respectively.

The comparison between groups within Beijing populations: Between community patients and HCW patients, the differences in allele (CLUMP T1 = 2.033, P = 0.729 by CLUMP), genotype (CLUMP T1 = 4.275, P = 0.934 by CLUMP) and homo- or heterozygote (χ^2 =0.915, P = 0.339 by SPSS) frequencies are not significant. Similarly, between random controls and our HCW controls, the differences in allele (CLUMP T1 = 6.640, P = 0.0844 by CLUMP), genotype (CLUMP T1 = 8.926, P = 0.629 by CLUMP) and homo- or heterozygote (χ^2 = 0.163, P = 0.686 by SPSS) frequencies are also not significant. Between community patients and random controls, the allele (CLUMP T1 = 1.690, P = 0.792 by CLUMP) and genotype (CLUMP T1 = 10.357, P = 0.410 by CLUMP) frequencies are similar. Similarly, the differences in allele (CLUMP T1 = 3.856, P = 0.278 by CLUMP) and genotype (CLUMP T1 = 8.753, P = 0.188 by CLUMP) frequencies between HCW patients and HCW controls are also not significant.

The comparison between groups withinTianjin populations: Between community patients and controls (containing the HCW controls and Random controls), the differences in allele (CLUMP T1 = 3.069, P = 0.689 by CLUMP), genotype (CLUMP T1 = 9.257, P = 0.598 by CLUMP) and homo- or heterozygote (χ^2 =0.011, P = 0.916 by SPSS) frequencies are not significant. Between random controls and HCW controls, the differences in allele (CLUMP T1 = 9.954, P = 0.0768 by CLUMP), genotype (CLUMP T1 = 13.355, P = 0.271 by CLUMP) and homo- or heterozygote (χ^2 = 0.834, P = 0.361 by SPSS) frequencies are also not significant. Between community patients and random controls, the allele (CLUMP T1 = 8.358, P = 0.138 by CLUMP) and genotype (CLUMP T1 = 10.245, P = 0.509 by CLUMP) frequencies are similar. Similarly, the differences in allele (CLUMP T1 = 1.496, P = 0.913 by CLUMP) and genotype (CLUMP T1 = 7.960, P = 0.717 by CLUMP) frequencies between community patients and HCW controls are also not significant.

The comparison between Beijing and Tianjin populations: Between Beijing community patients and Tianjin community patients, there are no significant differences in allele (CLUMP T1 = 0.445, P = 0.994 by CLUMP), genotype (CLUMP T1 = 15.570, P = 0.158 by CLUMP) and homo- or heterozygote (χ^2 = 3.261, P = 0.071 by SPSS) frequencies. Similarly, the comparison between Beijing HCW controls and Tianjin HCW controls is not significant for allele (CLUMP T1 = 4.279, P = 0.510 by CLUMP), genotype (CLUMP T1 = 10.283, P = 0.505 by CLUMP) and homo- or heterozygote (χ^2 = 2.256, P = 0.133 by SPSS) frequencies. Between Beijing random controls and Tianjin random controls, the differences in allele (CLUMP T1 = 9.644, P = 0.086 by CLUMP) and genotype (CLUMP T1 = 10.589, P = 0.478 by CLUMP) and homo- or heterozygote (χ^2 = 0.497, P = 0.481 by SPSS) frequencies were also not significant.

The comparison between Hong Kong and Beijing populations: Between Hong Kong outpatient controls and Beijing random controls, there are no

significant differences in allele (CLUMP T1 = 4.664, P = 0.198 by CLUMP), genotype (CLUMP T1 = 6.705, P = 0.822 by CLUMP) and homo- or heterozygote (χ^2 = 1.116, P = 0.291 by SPSS) frequencies. Similarly, the comparison between Hong Kong HCW controls and Beijing HCW controls is not significant for allele (CLUMP T1 = 2.245, P = 0.691 by CLUMP), genotype (CLUMP T1 = 13.246, P = 0.278 by CLUMP) and homo- or heterozygote (χ^2 = 0.184, P = 0.668 by SPSS) frequencies. Between Hong Kong community patients and Beijing community patients, the differences in allele (CLUMP T1 = 5.670, P = 0.225 by CLUMP) and genotype (CLUMP T1 = 16.797, P = 0.114 by CLUMP) frequencies were not significant; however, the differences in homo- or heterozygote (χ^2 = 7.384, P = 0.0066 by SPSS) frequencies differed significantly. Between Hong Kong HCW patients and Beijing HCW patients, the differences in allele (CLUMP T1 = 3.412, P = 0.333 by CLUMP) and genotype (CLUMP T1 = 10.032, P = 0.528 by CLUMP) frequencies were not significant; however, the differences in homo- or heterozygote (χ^2 = 5.658, P = 0.017 by SPSS) frequencies differed significantly.

The comparison between Hong Kong and Tianjin populations: Between Hong Kong outpatient controls and Tianjin random controls, there are no significant differences in genotype (CLUMP T1 = 18.325, P = 0.0747 by CLUMP) and homo- or heterozygote (χ^2 = 2.216, P = 0.137 by SPSS) frequencies; however, the difference in allele (CLUMP T1 = 16.199, P = 0.00635 by CLUMP) frequency differed significantly. The comparison between Hong Kong HCW controls and Tianjin HCW controls is not significant for allele (CLUMP T1 = 1.987, P = 0.851 by CLUMP) and genotype (CLUMP T1 = 8.951, P = 0.626 by CLUMP) frequencies; however, the differences in homo- or heterozygote (χ^2 = 5.702, P = 0.0169 by SPSS) frequencies differed significantly. Between Hong Kong community patients and Tianjin community patients, the differences in allele (CLUMP T1 = 0.793, P = 0.977 by CLUMP), genotype (CLUMP T1 = 4.955, P = 0.933 by CLUMP) and homo- or heterozygote (χ^2 = 0.095, P = 0.757 by SPSS) frequencies were not significant. Similarly, between Hong Kong HCW patients and Tianjin community patients, the differences in allele (CLUMP T1 = 0.527, P = 0.991 by CLUMP), genotype (CLUMP T1 = 3.333, P = 0.986 by CLUMP) and homo- or heterozygote (χ^2 = 0.038, P = 0.846 by SPSS) frequencies were not significant.

[a]Numbers of the tandem repeats at exon 4.

[b]The data of Hong Kong populations are derived from Chan *et al.*[1].

Reference

1. Chan, V.S. *et al*. *Nat*. *Genet*. **38**, 38-46 (2006).