Supplemental Figures



Figure S1 Linkage disequilibrium test for SNPs of *VDR* gene between the controls and cases infected Beijing lineage of *M. tuberculosis* after PS. Figure S1A showed the D' values between each two loci, and Figure S1B showed the r^2 values between each two loci.



Figure S2 Linkage disequilibrium test for SNPs of *VDR* gene between the controls and cases infected non-Beijing lineage of *M. tuberculosis* after PS. Figure S2A showed the D' values between each two loci, and Figure S2B showed the r^2 values between each two loci.



Figure S3 Linkage disequilibrium test for SNPs of *VDR* gene among the cases infected different lineages of *M. tuberculosis*. Figure S3A showed the D' values between each two loci, and Figure S3B showed the r^2 values between each two loci.

Supplemental tables

Table S1 The associations between haplotype distributions of VDR gene and Beijing

lineage of <i>M</i> .	tuberculosis	in the	population	after PS
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Haplotype	Beijing	Controls (n/%)	χ^2	Р	OR (95%CI)
	lineage				
	(n/%)				
CC	41.6(68.9)	56.4(58.3)	1.759	0.185	1.579(0.802-3.107)
TG	14.6(24.2)	25.3(26.1)	0.028	0.868	0.939(0.448-1.967)
TC	4.2(6.9)	15.1(15.6)	2.697	0.101	0.390(0.123-1.238)

Haplotype	Non-Beijing	Controls	χ^2	Р	OR (95%CI)
	lineage(n/%)	(n/%)			
CC	36.1(61.2)	60.4(62.6)	0.034	0.854	0.939(0.482-1.829)
TG	14.7(24.9)	26.3(27.3)	0.052	0.820	0.918(0.438-1.922)
TC	8.2(13.9)	9.7(10.1)	0.380	0.538	1.365(0.506-3.680)

 Table S2 The associations between haplotype distributions of VDR gene and

 Non-Beijing lineage of *M. tuberculosis* in the population after PS

Table S3 The associations between haplotype distributions of VDR gene and lineages

 of *M. tuberculosis*

Haplotype	Beijing lineage (n/%)	Non-Beijing lineage (n/%)	χ ²	Р	OR (95%CI)
CC	34.6(58.6)	36.5(62.4)	0.143	0.706	0.867(0.414-1.818)
TG	18.4(31.2)	14.6(25.0)	0.379	0.538	1.288(0.575-2.885)
TC	6.0(10.2)	7.4(12.6)	0.107	0.744	0.825(0.260-2.621)