Table S1 Primer sequence of the single nucleotide polymorphisms used in the study

SNP	Allele change	Primer sequence
rs10983755	G>A	F,5'-ATTGGAAGTGCTTGGAGGA-3' R,5'-TTGTAAAGCTTTTAGGACAGTGTCT-3'
rs11536879	A>G	F,5'-CATGTTCTCTGCAATGGTTTG-3' R,5'-GCAGCAAGGGTTGAAAAACT-3'
rs4986790	A>G	F,5'-AGCATACTTAGACTACTACCTCCATG-3' R,5'-GAGAGATTTGAGTTTCAATGTGGG-3'
rs4986791	C>T	F,5'-GGTTGCTGTTCTCAAAGTGATTTTGGGAGAA-3' R,5'-GGAAATCCAGATGTTCTAGTTGTTCTAAGCC-3'
rs1927907	G>A	F,5'-TTCAACCCTTGCTGCTTTCT-3' R,5'-CGAAAAGGCAAAGGATGTCT-3'
rs7873784	G>C	F,5'-ACGTTGGATGATGAGAGGTACCCTCTTAAC-3' R,5'-ACGTTGGATGGCTCTAAAGATCAGCTGTAT-3'
rs115336889	G>C	F,5'-GTCATTCCAAAGTTATTGCCTA-3' R,5'-CTGTGGTCATATTTCCAGTTTT-3'

Table S2 Association of haplotypes composed of rs10983755, rs4986791, rs1927907 and rs115336889 with susceptibility to benign prostatic hyperplasia.

Haplotype	Case		Control		Odds ratio	Lower limit	Upper limit	*P*-value
	Frequency	Number	Frequency	Number				
GCGG	0.032	16	0.111	107	**0.26**	**0.15**	**0.45**	**<0.001**
GCGC	0.138	69	0.190	183	**0.68**	**0.50**	**0.92**	**0.012**
GTGG	0.108	54	0.126	121	0.84	0.60	1.18	0.321
GTGC	0.461	231	0.214	206	**3.15**	**2.49**	**3.98**	**<0.001**
GTAC	0.069	35	0.053	52	1.32	0.85	2.05	0.221
ATGC	0.081	41	0.053	52	**1.56**	**1.02**	**2.39**	**0.038**

Table S3 Comparison of haplotypes composed of rs10983755, rs4986791 and rs1927907 between aggressive and non-aggressive benign prostatic hyperplasia populations

Haplotype	Aggressive		Non-aggressive		Odds ratio	Lower limit	Upper limit	*P*-value
	Frequency	Number	Frequency	Number				
GCG	0.119	26	0.202	58	**0.54**	**0.32**	**0.88**	**0.014**
GTG	0.673	145	0.495	141	**2.09**	**1.45**	**3.01**	**<0.001**
GTA	0.075	16	0.087	25	0.83	0.43	1.6	0.581
ATG	0.092	20	0.109	31	0.84	0.46	1.51	0.553