

Table S1. PCR primers and extension primers of the 25 SNPs.

SNP	PCR primers	Extension primers
rs2043211	F: 5'-TGAGACACAGCGTCCAATAGT-3' F: 5'-TCCAAGAAGATGATGAGACAGAGG-3'	5'-ctgactgactgactgactgactgactGACACTCAGGAACAGCACGGA-3'
rs10754558	F: 5'-GTGGAGTGTCTGGAGAAGAGA-3' F: 5'-GCTAATTACATGAGGTCACCAAGA-3'	5'-ctgactgactgactgactgactgactgCAATGACAGCATCGGGTGTGTGTT-3'
rs12185396	F: 5'-GGATGTGCCTGTGAGATTATCTT-3' F: 5'-CACTTCCTGAACCAACAATGC-3'	5'-ctgCCTGTCAGACCCTGAAACCCA-3'
rs8299	F: 5'-AGAGACTGACCGTTGAGAAGG-3' F: 5'-ATCTTTGCCGATGAAACTGTAGT-3'	5'-ctgacCAATACAGTCATCAGTGGAGTC-3'
rs580253	F: 5'-GAGCACAAGACCTCTGACAG-3' F: 5'-AATATCTACCAACCAGCCATTCAA-3'	5'-ctgactgaCTCTGAGCAAGTCCCAGATATA-3'
rs501192	F: 5'-GAGCACAAGACCTCTGACAG-3' F: 5'-AATATCTACCAACCAGCCATTCAA-3'	5'-ctgactgactgCAGGCCTGCCGTGGTGGTGAGT-3'
rs4796793	F: 5'-AGTCTCTTGTAACACGCTATCC-3' F: 5'-GCCTCTCCTATCTGCTATTTCAT-3'	5'-ctgactgactgactgactgactgGGAGTGTATAAGGTGTGTAAGT-3'
rs2293152	F: 5'-CAACAACGGCAGCCTCTC-3' F: 5'-TCCCCAACAAAACCTTACATCACAA-3'	5'-ctgactgactgactgactgactgactgacTCACAAAGGGCCTCTGGCTGC-3'
rs7525979	F: 5'-CCATCGGCAAGACCAAGAC-3' F: 5'-CCAGGCTCCTCTGTGTCA-3'	5'-ctgactgactgactgactgactgactgactgactgactgactgactgTTCTGAGCCTGTGCACA C-3'
rs35829419	F: 5'-CTGTCATCGGGTGGAGTCA-3'	5'-ctgactgactgactgactgAGAGGAGCTTGGGAGGACACACT-3'

	F: 5'-GCGAGGAAGCAGGAGGAA-3'	
rs1785929	F: 5'-TTCAGCATCATGGCAGGAAT-3'	5'-ctgactgaAGGAGTTCAATGTTCAATGGAA-3'
	F: 5'-ACACATATCCCTTACTCCAGTTAA-3'	
rs1785928	F: 5'-TTCTAGCCAAACTCCTGACTCTT-3'	5'-ctgactgactgactgactgacAGATGGTGTCTACAGCAGCCA-3'
	F: 5'-CAGTGAACATCCTTGCAGTACC-3'	
rs1026916	F: 5'-AACTGGAGTCTAGAACTGAATGA-3'	5'-cAAGTTTAACCCAAAGACTGT-3'
	F: 5'-CCACGGACGTTTACCCTAA-3'	
rs744166	F: 5'-GAGTACAAACCCTGAACCCTTT-3'	5'-ctgaATGTCTTGAGGGAATCGAGC-3'
	F: 5'-GGAGTGCCAACATTGAGAGG-3'	
rs696	F: 5'-GTACTTATATCCACACTGCACACT-3'	5'-ctgactgATCCACACTGCACACTGCCT-3'
	F: 5'-CAATGATCTTTCTCGTCCCCTAC-3'	
rs4648068	F: 5'-GGCTCATTGAACGTCTCTGT-3'	5'-ctgactgacTCTTGGTGAAATAATCCTTCA-3'
	F: 5'-TTTAAGGGAACGACCATTATCTGT-3'	
rs530537	F: 5'-TGCCAATCCCAACCACATC-3'	5'-ctgactgactCTTAATTTACAAAAACATTTGCA-3'
	F: 5'-ATGAAGCCTTTAACTGAGACTTGT-3'	
rs681757	F: 5'-AATCACAAGTAGGTCAACCCAAAT-3'	5'-ctgactgactgactgaGTCAAGTCTTCCTCAGTTATCCA-3'
	F: 5'-GGATACAATCTCACCTGAGTTCG-3'	
rs559289	F: 5'-TGGGACACTGGTGGGAAG-3'	5'-ctgactgactgactgactgactgacTCATTTGAAAGGTACTTGGAAC-3'
	F: 5'-AAGAAGATAGGGAGTTTGGCAAA-3'	
rs556205	F: 5'-TGTGCTTATTTCTTATCTACTCC-3'	5'-ctgactgactgactgactgactgactgCCATGTAGACTGAGTATTGC-3'
	F: 5'-ACAAGAGGTATCTGAGGTCAC-3'	

rs2569190	F: 5'-CCTCCTCTGTGAACCCTGAT-3'	5'-ctgaGCAGAATCCTTCCTGTTACGG-3'
	F: 5'-GCTTAGGCTCCCGAGTCA-3'	
rs4612666	F: 5'-GGTTGCACAACAATGTGAAGT-3'	5'-TTCTCCAAGCTCCCACCAATACTAC-3'
	F: 5'-ATAACAAGTAAGCATTCTCCAAGC-3'	
rs1789547	F: 5'-GAAGAAGAGATAAATGGGTTGTGGTAT-3'	5'-ctgactgactAGCTCTAGTTATTTGTTTTTATTGCA-3'
	F: 5'-TGGAATTATAGATATTACAGCTTGCCTTT-3'	
rs2032206	F: 5'-TGGGACACTGGTGGGAAG-3'	5'-ctgactgactgactgacTTGGTCATTATGGTGACTTAGG-3'
	F: 5'-AAGAAGATAGGGAGTTTGGCAAA-3'	
rs1053004	F: 5'-GGTTTTGAGTTGCCAAATCCG-3'	5'-CTGACTGATGTTCCCATACGCACAGGAGAGGC-3'
	F: 5'-TCGTATGAGGGTGTATACCTG-3'	

SNP: Single Nucleotide Polymorphism; PCR: Polymerase Chain Reaction; F: Forward; R: Reverse.

Table S2. HWE test outcomes of the 25 gene polymorphisms for healthy controls.

SNP	χ^2 value	<i>P</i> value
rs2043211	0.095	0.758
rs10754558	0.779	0.377
rs12185396	0.647	0.421
rs8299	0.647	0.421
rs580253	0.003	0.958
rs501192	0.003	0.958
rs4796793	0.008	0.927
rs2293152	0.686	0.407
rs7525979	0.752	0.386
rs35829419	0.001	0.979
rs1785929	1.253	0.263
rs1785928	1.253	0.263
rs1026916	0.034	0.853
rs744166	0.004	0.950
rs696	3.122	0.077
rs4648068	0.002	0.967
rs530537	0.304	0.582
rs681757	0.511	0.475
rs559289	0.511	0.475
rs556205	0.003	0.958

rs2569190	1.057	0.304
rs4612666	0.265	0.607
rs1789547	0.151	0.697
rs2032206	1.490	0.222

IL: Interleukin; HWE: Hardy-Weinber Equilibrium

Table S3. Comparisons of genotype distribution, allele frequency, and genetic models of the remaining 21 SNPs between PTOM patients and healthy controls.

SNP	Item	Allele or genotype	Patients	Controls	<i>P</i> values	OR (95% CI)
rs2043211	Genotype (n, %)	TT	85 (27.78)	108 (29.35)	0.731	NA
		AT	159 (51.96)	180 (48.91)		
		AA	62 (20.26)	80 (21.74)		
	Allele frequency	T vs. A	329/283	396/340	0.987	0.998 (0.805, 1.238)
	Dominant model	TT+AT vs. AA	244/62	288/80	0.640	1.093 (0.753, 1.587)
	Recessive model	TT vs. AT+AA	85/221	108/260	0.654	0.926 (0.662, 1.296)
	Homozygous model	TT vs. AA	85/62	108/80	0.945	1.016 (0.656, 1.572)
	Heterzygous model	AT vs. AA	159/62	180/80	0.515	1.140 (0.768, 1.691)
rs2569190	Genotype (n, %)	GG	57 (18.63)	58 (15.76)	0.521	NA
		AG	145 (47.39)	188 (51.09)		
		AA	104 (33.99)	122 (33.15)		
	Allele frequency	G vs. A	259/353	304/432	0.707	1.043 (0.839, 1.296)
	Dominant model	GG+AG vs. AA	202/104	246/122	0.819	0.963 (0.699, 1.328)
	Recessive model	GG vs. AG+AA	57/249	58/310	0.325	1.224 (0.819, 1.829)
	Homozygous model	GG vs. AA	57/104	58/122	0.535	1.153 (0.735, 1.807)
	Heterzygous model	AG vs. AA	145/104	188/122	0.564	0.905 (0.644, 1.271)
rs1785929	Genotype (n, %)	AA	9 (2.94)	9 (2.45)	0.444	NA
		AG	83 (27.12)	116 (31.52)		
		GG	214 (69.93)	243 (66.03)		
	Allele frequency	A vs. G	101/511	134/602	0.412	0.888 (0.668, 1.179)

rs1789547	Dominant model	AA+AG vs. GG	92/214	125/243	0.280	0.836 (0.603, 1.158)
	Recessive model	AA vs. AG+GG	9/297	9/359	0.691	1.209 (0.474, 3.084)
	Homozygous model	AA vs. GG	9/214	9/243	0.791	1.136 (0.443, 2.913)
	Heterzygous model	AG vs. GG	83/214	116/243	0.226	0.812 (0.580, 1.137)
	Genotype (n, %)	TT	7 (2.29)	8 (2.17)	0.830	NA
		CT	76 (24.84)	99 (26.90)		
		CC	223 (72.88)	261 (70.92)		
	Allele frequency	T vs. C	90/522	115/621	0.640	0.931 (0.690, 1.256)
	Dominant model	TT+CT vs. CC	83/223	107/261	0.575	0.908 (0.648, 1.273)
	Recessive model	TT vs. CT+CC	7/299	8/360	0.921	1.054 (0.378, 2.939)
rs1785928	Homozygous model	TT vs. CC	7/223	8/261	0.964	1.024 (0.366, 2.869)
	Heterzygous model	CT vs. CC	76/223	99/261	0.547	0.898 (0.634, 1.273)
	Genotype (n, %)	AA	9 (2.94)	9 (2.45)	0.444	NA
		AG	83 (27.12)	116 (31.52)		
		GG	214 (69.93)	243 (66.03)		
	Allele frequency	A vs. G	101/511	134/602	0.412	0.888 (0.668, 1.179)
	Dominant model	AA+AG vs. GG	92/214	125/243	0.280	0.836 (0.603, 1.158)
	Recessive model	AA vs. AG+GG	9/297	9/359	0.691	1.209 (0.474, 3.084)
	Homozygous model	AA vs. GG	9/214	9/243	0.791	1.136 (0.443, 2.913)
	Heterzygous model	AG vs. GG	83/214	116/243	0,226	0.812 (0.580, 1.137)
rs12185396	Genotype (n, %)	CC	212 (69.28)	246 (66.85)	0.761	NA
		CT	85 (27.78)	110 (29.89)		
		TT	9 (2.94)	9 (2.45)		

rs681757	Allele frequency	C vs. T	509/103	602/128	0.734	1.051 (0.790, 1.397)
	Dominant model	CC+CT vs. TT	297/9	356/9	0.704	0.834 (0.327, 2.129)
	Recessive model	CC vs. CT+TT	212/94	246/119	0.602	1.091 (0.787, 1.531)
	Homozygous model	CC vs. TT	212/9	246/9	0.757	0.862 (0.336, 2.211)
	Heterzygous model	CT vs. TT	85/9	110/9	0.600	0.773 (0.294, 2.031)
	Genotype (n, %)	GG	9 (2.94)	9 (2.45)	0.634	NA
		GT	81 (26.47)	109 (29.62)		
		TT	216 (70.59)	250 (67.93)		
	Allele frequency	G vs. T	99/513	127/609	0.598	0.925 (0.694, 1.234)
	Dominant model	GG+GT vs. TT	90/216	118/250	0.458	0.883 (0.635, 1.227)
rs8299	Recessive model	GG vs. GT+TT	9/297	9/359	0.691	1.209 (0.474, 3.084)
	Homozygous model	GG vs. TT	9/216	9/250	0.761	1.157 (0.451, 2.968)
	Heterzygous model	GT vs. TT	81/216	109/250	0.385	0.860 (0.612, 1.209)
	Genotype (n, %)	TT	9 (2.94)	9 (2.45)	0.761	NA
		CT	85 (27.78)	110 (29.89)		
		CC	212 (69.28)	246 (66.85)		
	Allele frequency	T vs. C	103/509	128/602	0.734	0.952 (0.716, 1.266)
	Dominant model	TT+CT vs. CC	94/212	119/246	0.602	0.917 (0.661, 1.271)
	Recessive model	TT vs. CT+CC	9/297	9/356	0.704	1.199 (0.470, 3.058)
	Homozygous model	TT vs. CC	9/212	9/246	0.757	1.160 (0.452, 2.977)
rs2032206	Heterzygous model	CT vs. CC	85/212	110/246	0.526	0.897 (0.640, 1.257)
	Genotype (n, %)	GG	150 (49.02)	181 (49.18)	0.636	NA
		AG	129 (42.16)	147 (39.95)		

		AA	27 (8.82)	40 (10.87)		
	Allele frequency	G vs. A	429/183	509/227	0.709	1.045 (0.828, 1.320)
	Dominant model	GG+AG vs. AA	279/27	328/40	0.377	1.260 (0.754, 2.106)
	Recessive model	GG vs. AG+AA	150/156	181/187	0.966	0.993 (0.734, 1.345)
	Homozygous model	GG vs. AA	150/27	181/40	0.451	1.228 (0.720, 2.094)
	Heterzygous model	AG vs. AA	129/27	147/40	0.342	1.300 (0.756, 2.236)
rs559289	Genotype (n, %)	CC	9 (2.94)	9 (2.45)	0.634	NA
		AC	81 (26.47)	109 (29.62)		
		AA	216 (70.59)	250 (67.93)		
	Allele frequency	C vs. A	99/513	127/609	0.598	0.925 (0.694, 1.234)
	Dominant model	CC+AC vs. AA	90/216	118/250	0.458	0.883 (0.635, 1.227)
	Recessive model	CC vs. AC+AA	9/297	9/359	0.691	1.209 (0.474, 3.084)
	Homozygous model	CC vs. AA	9/216	9/250	0.761	1.157 (0.451, 2.968)
	Heterzygous model	AC vs. AA	81/216	109/250	0.385	0.860 (0.612, 1.209)
rs4796793	Genotype (n, %)	CC	113 (36.93)	134 (36.41)	0.405	NA
		CG	135 (44.12)	175 (47.55)		
		GG	58 (18.95)	56 (15.22)		
	Allele frequency	C vs. G	361/251	443/287	0.527	0.932 (0.748, 1.160)
	Dominant model	CC+CG vs. GG	248/58	309/56	0.215	0.775 (0.518, 1.160)
	Recessive model	CC vs. CG+GG	113/193	134/231	0.954	1.009 (0.737, 1.383)
	Homozygous model	CC vs. GG	113/58	134/56	0.364	0.814 (0.522, 1.270)
	Heterzygous model	CG vs. GG	135/58	175/56	0.179	0.745 (0.484, 1.145)
rs744166	Genotype (n, %)	GG	63 (20.59)	66 (17.93)	0.680	NA

rs1026916		AG	143 (46.73)	179 (48.37)		
		AA	100 (32.68)	123 (33.42)		
	Allele frequency	G vs. A	269/343	311/425	0.531	1.072 (0.863, 1.331)
	Dominant model	GG+AG vs. AA	206/100	245/123	0.838	1.034 (0.749, 1.428)
	Recessive model	GG vs. AG+AA	63/243	66/302	0.383	1.186 (0.808, 1.742)
	Homozygous model	GG vs. AA	63/100	66/123	0.469	1.174 (0.760, 1.813)
	Heterzygous model	AG vs. AA	143/100	179/123	0.920	0.983 (0.697, 1.385)
	Genotype (n, %)	GG	100 (32.68)	123 (33.42)	0.736	NA
		AG	143 (46.73)	178 (48.37)		
		AA	63 (20.59)	67 (18.21)		
	Allele frequency	G vs. A	343/269	424/312	0.564	0.938 (0.756, 1.165)
	Dominant model	GG+AG vs. AA	243/63	301/67	0.435	0.859 (0.585, 1.260)
	Recessive model	GG vs. AG+AA	100/206	123/245	0.838	0.967 (0.700, 1.335)
	Homozygous model	GG vs. AA	100/63	123/67	0.511	0.865 (0.560, 1.334)
rs2293152	Heterzygous model	AG vs. AA	143/63	178/67	0.450	0.854 (0.568, 1.285)
	Genotype (n, %)	CC	72 (23.53)	96 (26.09)	0.671	NA
		CG	162 (52.94)	190 (51.63)		
		GG	72 (23.53)	79 (21.47)		
	Allele frequency	C vs. G	306/306	382/348	0.395	0.911 (0.735, 1.129)
	Dominant model	CC+CG vs. GG	234/72	286/79	0.560	0.898 (0.624, 1.291)
	Recessive model	CC vs. CG+GG	72/234	96/269	0.409	0.862 (0.606, 1.226)
	Homozygous model	CC vs. GG	72/72	96/79	0.387	0.823 (0.529, 1.280)
	Heterzygous model	CG vs. GG	162/72	190/79	0.732	0.936 (0.639, 1.371)

rs696	Genotype (n, %)	TT	48 (15.69)	71 (19.29)	0.224	NA
		CT	154 (41.85)	162 (44.02)		
		CC	104 (33.99)	135 (36.68)		
	Allele frequency	T vs. C	250/362	304/432	0.866	0.981 (0.789, 1.220)
	Dominant model	TT+CT vs. CC	202/104	233/135	0.466	1.125 (0.819, 1.546)
	Recessive model	TT vs. CT+CC	48/258	71/297	0.221	0.778 (0.520, 1.164)
	Homozygous model	TT vs. CC	48/104	71/135	0.567	0.878 (0.561, 1.372)
	Heterzygous model	CT vs. CC	154/104	162/135	0.222	1.234 (0.880, 1.730)
rs4648068	Genotype (n, %)	GG	61 (19.93)	82 (22.28)	0.224	NA
		AG	160 (52.29)	183 (49.73)		
		AA	85 (27.78)	103 (27.99)		
	Allele frequency	G vs. A	282/330	347/389	0.696	0.968 (0.773, 1.188)
	Dominant model	GG+AG vs. AA	221/85	265/103	0.951	1.011 (0.721, 1.417)
	Recessive model	GG vs. AG+AA	61/245	82/286	0.458	0.868 (0.598, 1.261)
	Homozygous model	GG vs. AA	61/90	82/103	0.469	0.851 (0.551, 1.316)
	Heterzygous model	AG vs. AA	160/85	183/103	0.751	1.059 (0.741, 1.514)
rs501192	Genotype (n, %)	TT	0 (0.0)	0 (0.0)	NA	NA
		CT	3 (0.98)	2 (0.55)		
		CC	303 (99.02)	363 (99.45)		
	Allele frequency	T vs. C	3/609	2/728	0.843	1.793 (0.299, 10.766)
	Dominant model	TT+CT vs. CC	3/303	2/363	0.836	1.812 (0.301, 10.914)
	Recessive model	TT vs. CT+CC	0/306	0/365	NA	NA
	Homozygous model	TT vs. CC	0/306	0/363	NA	NA

rs580253	Heterzygous model	CT vs. CC	3/303	2/363	0.836	1.812 (0.301, 10.914)
	Genotype (n, %)	AA	0 (0.0)	0 (0.0)	NA	NA
		AG	3 (0.98)	2 (0.55)		
		GG	303 (99.02)	363 (99.45)		
	Allele frequency	A vs. G	3/609	2/728	0.843	1.793 (0.299, 10.766)
	Dominant model	AA+AG vs. GG	3/303	2/363	0.836	1.812 (0.301, 10.914)
	Recessive model	AA vs. AG+GG	0/306	0/365	NA	NA
rs556205	Homozygous model	AA vs. GG	0/303	0/363	NA	NA
	Heterzygous model	AG vs. GG	3/303	2/363	0.836	1.812 (0.301, 10.914)
	Genotype (n, %)	GG	0 (0.0)	0 (0.0)	NA	NA
		GT	3 (0.98)	2 (0.54)		
		TT	303 (99.02)	366 (99.46)		
	Allele frequency	G vs. T	3/609	2/734	0.836	1.808 (0.301, 10.854)
	Dominant model	GG+GT vs. TT	3/303	2/366	0.836	1.812 (0.301, 10.914)
rs530537	Recessive model	GG vs. GT+TT	0/306	0/368	NA	NA
	Homozygous model	GG vs. TT	0/303	0/366	NA	NA
	Heterzygous model	GT vs. TT	3/303	2/366	0.836	1.812 (0.301, 10.914)
	Genotype (n, %)	CC	10 (3.27)	22 (5.98)	0.193	NA
		CT	132 (43.14)	144 (39.13)		
		TT	164 (53.59)	202 (54.89)		
	Allele frequency	C vs. T	152/460	188/548	0.766	0.963 (0.752, 1.233)
	Dominant model	CC+CT vs. TT	142/164	166/202	0.737	1.054 (0.777, 1.428)
	Recessive model	CC vs. CT+TT	10/296	22/346	0.099	0.531 (0.248, 1.140)

rs1053004	Homozygous model	CC vs. TT	10/164	22/202	0.138	0.560 (0.258, 1.216)
	Heterzygous model	CT vs. TT	132/164	144/202	0.448	1.129 (0.825, 1.545)
	Genotype (n, %)	AA	125 (40.98)	143 (39.61)	0.396	NA
		AG	140 (45.90)	157 (43.49)		
		GG	40 (13.11)	61 (16.90)		
	Allele frequency	A vs. G	390/220	443/279	0.333	1.116 (0.893, 1.395)
	Dominant model	AA+AG vs. GG	265/40	300/61	0.175	1.347 (0.875, 2.074)
	Recessive model	AA vs. AG+GG	125/180	143/218	0.719	1.059 (0.776, 1.444)
	Homozygous model	AA vs. GG	125/40	143/61	0.225	1.333 (0.837, 2.123)
	Heterzygous model	AG vs. GG	140/40	157/61	0.189	1.360 (0.859, 2.153)

PTOM: Posttraumatic osteomyelitis; OR: odds ratio, CI: confidence interval; NA: not available.