

Supplementary File

Association of *ANO6* gene polymorphism and expression with ankylosing spondylitis in a Chinese Han population

Suppl. Table I. Amplification primers for the *ANO6* gene exon sequences

Primer number	Primer sequence
E1	F:GCATTTCCTCCTCTCCAGT R:CGTCAGGAGCCTGTCCTC
E2	F:TACGAGGTCAGGTCCTTGTTGTT R:CTACTTGGGAAGCAGAGGTTGCA
E3	F:CCTGGCATCGTCTGGTAGAT R:TTCCCAAGAGACACCAGAGC
E4	F:TAGTGGCCATGACTGTTTGG R:CAGCTGTGAAACCAAATGAGG
E5	F:TTCTCTTGGGGATCCAACAC R:TGATTGACTCCTCTCCCAGTC
E6	F:TGATTCAAACCAAGAAATCGTCT R:TCTGCTGGCATATTTCTTTTCTT
E7	F:TGGTTTGGTTGGTTTGGTTT R:CCTGTCCATTCATTCATTCG
E8	F:GGTGGGTTATCACGTGTTCC R:CAACGAAGCTCAGCACTCTG
E9	F:ACCAGGCAAACCAGCAATAG R:CATGTCAGACACTGGGTTGG
E10	F:TGACATACAATGCTGGCAGAG R:GATTCCACTATTATCTCACTGACACTC
E11	F:TGGGATATGCAGAGTTTCACTG R:CAACCCATGCCTGAAGAACT
E12	F:TGTTTTGCTTTCCCTTCACC

	R:AAGCTCCCCCAAGTGATTCT
E13	F:CCATCAGACACCCAGATTCC
	R:GCCTTCCATTTGGTCTTCAC
E14	F:CCACCGCTGGTATCACTTATG
	R:TGTCTTTGCTTTGTCCCTTTT
E1516	F:GGGAACATGTGGGCTATTGT
	R:GTGGACATGCAGCTATGTGG
E17	F:AGCTTTGGTAAACCCTGGTG
	R:ATTCCATTTCATTGCCCAGT
E18	F:CCAGCGAATAATTCTGGTTGA
	R:GGATGACAGACTTAGCATCTTCC
E19	F:GTGGGCAGATCACCTGAGAC
	R:CCAAAGCACCTGATTGATCC
E20	F:TGCCTCAGCCACCAAATAG
	R:GCAGAGATCACATCATCGTACC
E21-1	F:CATTAGCGGTTGGTTGTGTG
	R:GACCCTGGAACAGATCTAGCC
E21-2	F: TGAGCGGATGATAGAAGCAGTAG
	R: AGCAGTCAACATTGATTAGGCAC
E21-3	F:CCTCCAGAAAGGAAACCTCA
	R:GCCTGATTGGCTCTAGAGGAG
E21-4	F:CTTGCATCCTCCATCCTGTT
	R:CCGCTTCCAGAAGCAGTATC
E21-5	F:CCAGCAGCAAAGGAAAACCTC
	R:ACTGCCACACCCATCAATTT
E21-6	F: GTGGACCTGTGAAGAGGGAGAAT
	R: AAGGGAAGACTTTGGTGACAGTTTAT

Suppl. Table II. Amplification primers for the *ANO6* gene transcription regulatory region sequences

Primer number	Primer sequence
T1-0	L: ATGAGGGTTGAATGACTGGATG R: AGTTGTTTGAACGGCAGGTTTT
T1-1	L:AGCCTGGGCAACATAGTGA R: AGGAGGATTTCCGCATACA
T1-2	L:GCTTCAGCGATTATCTTCCG R:GAGCATTGATCCCAAACAGG
T1-3	L: TTAGCTCCACGTCGCCTTTA R: TCGCTGCGGAATGATTGA
T1-4	L: TCCACTCCCGCACTCAC R: GGGCAACCCTAGCACTCT
T1-5	L: CGACTCGCAGAGTGCTAGGGT R: CCACAACAGACTGGCTTGGTAAT
T1-6	L: CAAGACGAACGGAGGGAGA R: TGTGAGAAGCTGGGCAGAC
T1-7	L: CAGGGACAAATCGAATAGAGG R: CACAGGAATAGTGGGAAATGC
T2-1	L: TGGATTTCAGGCTGTACTCTATT R: CTGTTGGTATGTTTGTCTTCCCT
T2-2	L: TGTTCAGCACCTTCTGTATGTCA R: TTCCAACCCAGGGCTATTATTTC
T2-3	L: CAGGCTCACAAGTCCAGTCGTAC R: CTAGGGTGCTTTGGCTATTACACA
T2-4	L: ACAATCTGTGAGGGTGGAAAATA R: GAAGGTTGACATGAAAGGGGTAC
T2-5	L: TGTGCTCTTGTCTGAACCCTCTA R: ATTGGCAAGGCATTATGTGAACT
T2-6	L: CCTGGCTTCACTTAGCACAATCT

	R: TGGAATCTAATATCCTGCACCAA
T2-7	L: GACCTATCCAAATGAAGGAGCAG
	R: TACAGGAAGGAGGAGAAGTAGCA
T2-8	L: GTGTTTCCTAATCACCCCTCTTGCCC
	R:GAGCCACAGGTGCTGGAGTTAAAAG
T2-9	L: CCTCCTGGGCATAATAGAAATCC
	R: TAACAACCTGACAGTGGCACATAC
T3	L: AATAACTGGGCTCTGATCTTGG
	R:TAGGCAATGGTGAAC TAAACAAAC
T4-1	L: GTGCCTTAGTTTCCTCATTGGTA
	R:TAAGTGAAGAAGTAAAGCCGACA
T4-2	L: CTCACTTGTTCTTTCCCAATCTC
	R: TAGGTGGTATCACTGCATAGGTT

Suppl. Table III. Genotype frequency of 9 SNPs of *ANO6*
in 29 AS and 30 healthy controls

	Genotype frequency	AS patients	Healthy controls	<i>p</i>
rs17095830	AA	0	26	< 0.0001
	AG	0	4	
	GG	29	0	
rs146601792	GG	8	29	< 0.0001
	G-	13	1	
	--	8	0	
rs11612233	CC	4	15	< 0.0001
	CA	2	12	
	CG	13	0	
rs3759080	AA	1	3	0.0009
	GG	9	0	
	AA	4	15	
rs3759079	AG	14	11	0.0167
	GG	11	4	
	CC	7	15	
rs79662606	CT	13	11	< 0.0001
	TT	9	4	
	AA	8	30	
rs75712006	AG	12	0	< 0.0001
	GG	9	0	
	AA	7	29	
rs79010229	AG	13	1	< 0.0001
	GG	9	0	
	TT	7	30	
rs80224086	TC	13	0	< 0.0001
	CC	9	0	
	TT	7	30	
rs76186361	TC	11	0	< 0.0001
	CC	11	0	
	CC	6	28	
rs76186361	CT	13	2	< 0.0001
	TT	10	0	

‘--’ indicates missing genotype data due to amplification failure

Suppl. Table IV. Relative expression level of *ANO6* mRNA
in AS patients and healthy controls

	Relative expression level	<i>p</i>
AS patients	0.49 ± 0.21	< 0.001
Healthy controls	0.86 ± 0.38	

Suppl. Table V. Histoscore of IHC of ANO6 protein in tendon tissue
of AS patients and controls

Groups	Case number	Histoscore	<i>p</i>
AS patients	9	182.22 ± 30.732	0.001
Controls	5	62.00 ± 35.637	

Suppl. Fig. 1. Linkage disequilibrium (LD) analysis of 5 SNPs in *ANO6*. D' values are represented by color gradients (red = strong LD, white = weak LD)

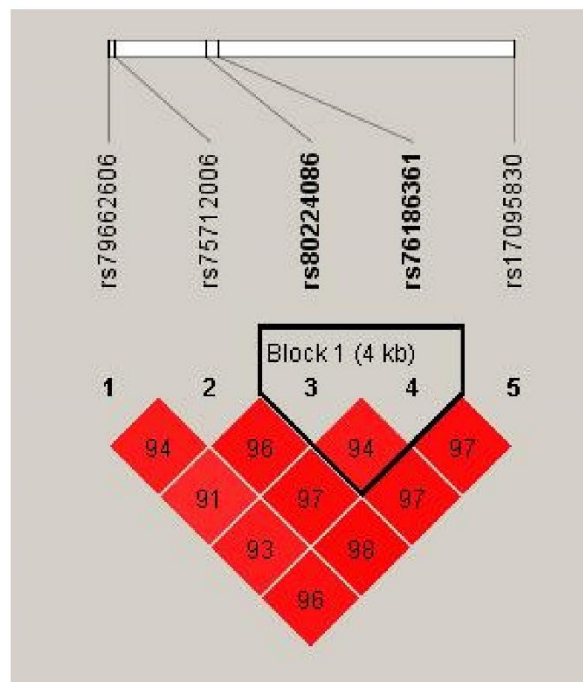


Figure S1 Linkage disequilibrium (LD) analysis of 5 SNPs in *ANO6*. D' values are represented by color gradients (red: strong LD, white: weak LD)

