

Supp. Table S1. Filtering steps of NGS

Filtering step	SNV + Indel
Dominant variants	
Heterozygous variants shared by four patients	4,545
Heterozygous variants shared by three LBP patients	587
Removal of synonymous SNVs	118
Allele frequency less than 0.01 in ExAC EAS	11
Frameshift, splice site, start-loss, stop-loss, start-gain, or stop-gain mutations	1

Supp. Figure S1.

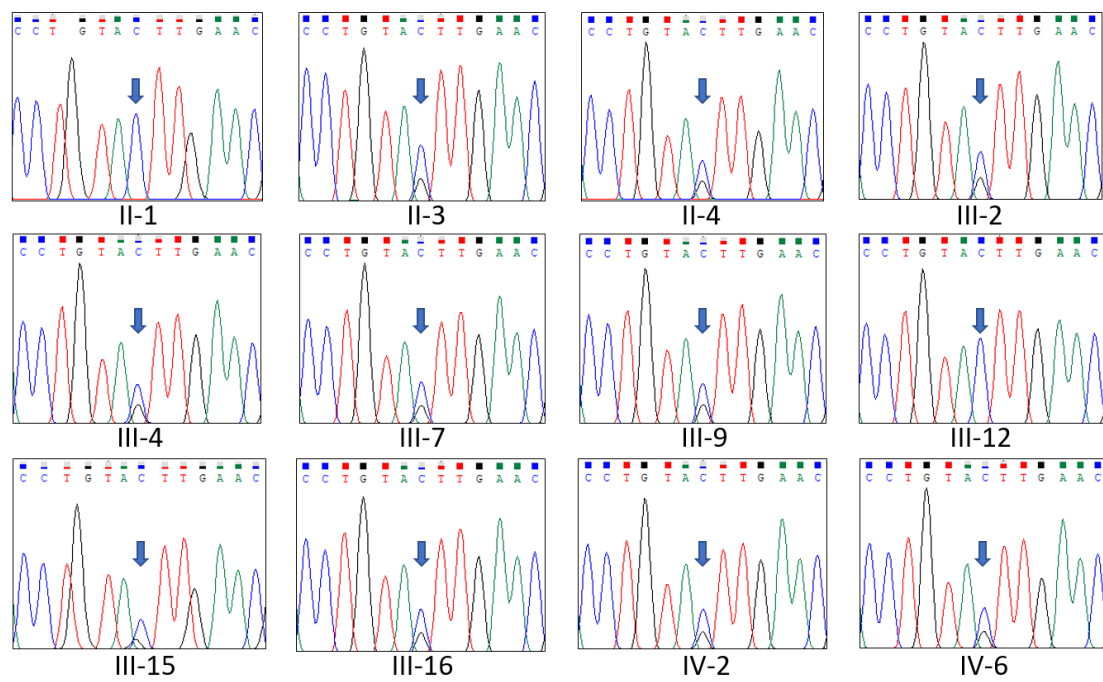


Figure S1. Sanger sequencing results of the c.417C>G mutation in *IL3Ra* in the family members with lumbar spinal stenosis. Mutation positions are indicated by arrows.

Supp. Table S2. Primers for real-time PCR

Gene		Sequence (5' to 3')	Length (bp)	Product size (bp)
<i>IL3Ra</i>	Forward	GGACGTCCAGTACGACCTGT	20	142
	Reverse	ACTTTGAGAACCGCTGGAGA	20	
<i>EsRa</i>	Forward	TGGGCTTACTGACCAACCTG	20	99
	Reverse	CCTGATCATGGAGGGTCAAA	20	
<i>EsRb</i>	Forward	AGAGTCCCTGGTGTGAAGCAA	21	143
	Reverse	GACAGCGCAGAAAGTGAGCATC	21	
<i>MMP-1</i>	Forward	AGCTAGCTCAGGATGACATTGATG	24	58
	Reverse	GCCGATGGGCTGGACAG	17	
<i>MMP-3</i>	Forward	CACTCACAGACCTGACTCGG	20	81
	Reverse	AGTCAGGGGGAGGTCCATAG	20	
<i>MMP-10</i>	Forward	GACAGAAGATGCATCAGGCAC	21	133
	Reverse	GGCGAGCTCTGTGAATGAGT	21	
<i>COL11A2</i>	Forward	GCCTCAGCCTAGCAGAT	17	145
	Reverse	ATCACTCCATGGGTGTCCAATA	22	
<i>GAPDH</i>	Forward	GACCTGCCGTCTAGAAAAAC	20	126
	Reverse	TTGAAGTCAGAGGAGACCAC	20	