**Table S1.** Primers used for genotyping the *NOD2* gene with high resolution melting analysis (HRMA) and Sanger sequencing and pyrosequencing (PyroSeq). Primers marked with * were biotinylated. F – forward primer, R – reverse primer, S – sequencing primer, Tm – primers annealing temperature.

SNP	Method	Primer Sequence (5'-3')	PCR product (bp)	Tm (°C)
rs2066842 c.802C>T p.P268S	HRMA	F: GGAGGTCTGGGCAGATGTG R: ACAGTGTCCGCATCGTCA	114	56
	PyroSeq	F: GGAGGTCTGGGCAGATGTG* R: ACAGTGTCCGCATCGTCA S: GGGCTCTCTGCGGG	144	60
rs2066844 c.2104C>T p.R702W	HRMA	F: GAGCCGCACAACCTTCAGAT R: GCGGGATGGAGTGGAAGT	172	64
	PyroSeq	F: GAGCCGCACAACCTTCAGAT* R: GCGGGATGGAGTGGAAGT S:GGCACAGGCCTGGCG	172	60
rs2066845 c.2722G>C p.G908R	HRMA	F: GACTCTTTGGCCTTTTCAGATT R: CCAATGGTCTTTTTTCCTTACTCC	242	58
	PyroSeq	F: GACTCTTTTGGCCTTTTCAGATT* R: CCAATGGTCTTTTTTCCTTACTCC S: TCGTCACCCACTCTGT	242	60
rs5743289 c.2798+158C>T IVS8+158	HRMA	F: TGCAGTTTTCTTGGGGAGA R: TGTACCTGATCCAGCCCAA	231	58
rs5743293 c.3020insC p.1007fs	HRMA	F: GGGACAGGTGGGCTTCAGTA R: CCATTCCTCTCTCCCGTCAC	279	55
	PyroSeq	F: ACCTACCTAGGGGCAGAAGC R: CAGACTTCCAGGATGGTGTCA* S: CCCTCCTGCAGGCCC	65	60
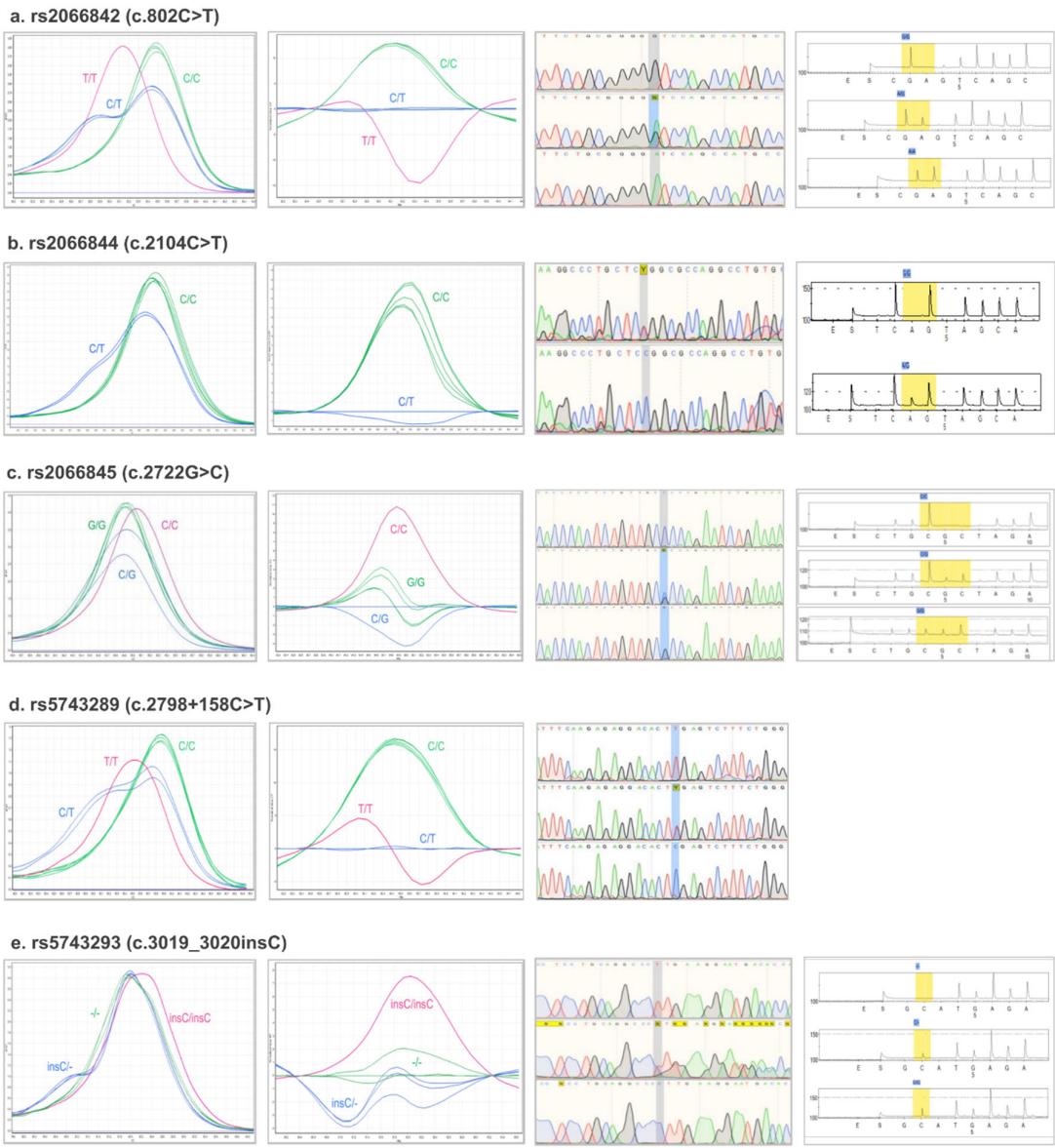
Supplementary Figure S1. Genotyping results for *NOD2* gene variants: a.) c.802C>T (p.P268S, rs2066842), b.) c.2104C>T (p.R702W, rs2066844), c.) c.2722G>C (p.G908R, rs2066845), d.) c.2798+158C>T, rs5743289, e.) c.3020insC (p.1007fs rs5743293) obtained using HRMA (melting curves and differential graphs), pyrosequencing and Sanger sequencing. Rs5743289 *locus* was genotyped only with HRMA and Sanger sequencing. In the case of a.) c.802C>T variant, sequencing primers (Sanger and pyrosequencing) were reverse; in case of b.) c.2104C>T variant Sanger sequencing primer was forward and pyrosequencing primer was reverse, c.), d.) and e.) – sequencing primers were forward.