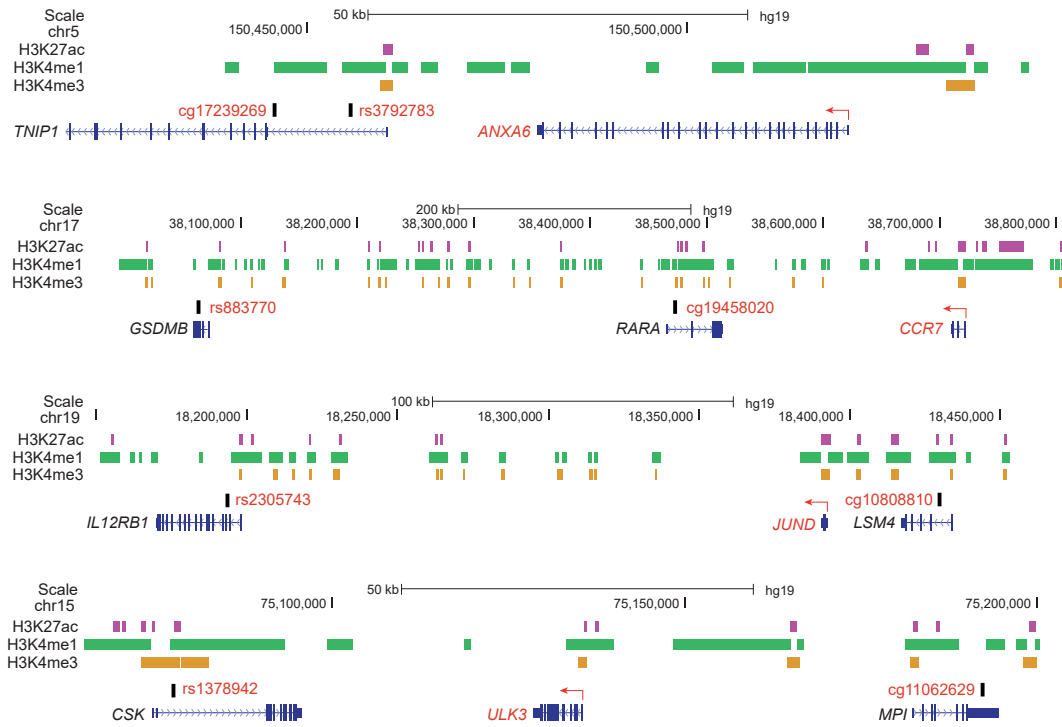


Figure S3

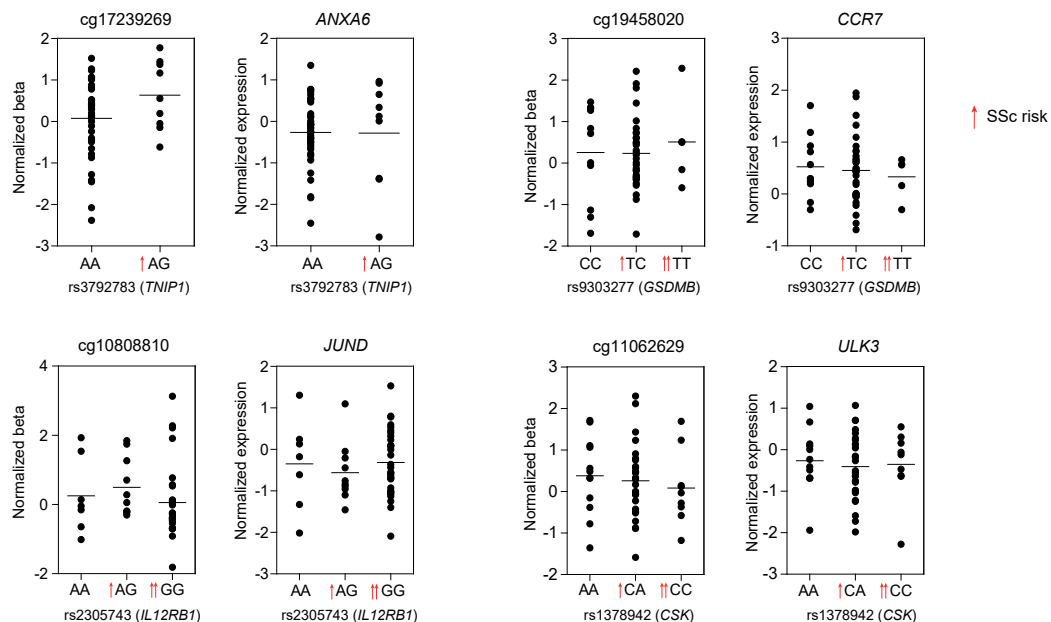
A

Chr	Locus	Independent variant	Effect allele	OR	p-value
5	<i>TNIP1</i>	rs3792783	G	1.20	2.42E-12
15	<i>CSK</i>	rs1378942	C	1.18	1.84E-14
17	<i>GSDMB</i>	rs9303277	C	0.89	9.88E-08
19	<i>IL12RB1</i>	rs2305743	A	0.83	4.64E-10

B



C



Additional file 10: Figure S3. (A) Table summarizing odds ratios and p-values of SSc risk variants identified by López-Isac et al. [15]. (B) ChIP-seq datasets obtained from total CD4⁺ T cells of H3K27ac, H3K4me1 and H3K4me3 downloaded from the BLUEPRINT database. UCSC genome browser representations of significant signals within the vicinity of interactomes rs3792783-cg17239269-ANXA6, rs883770-cg19458020-CCR7, rs2305743-cg10808810-JUND and rs1378942-cg1162629-ULK3. (C) DNA methylation of DMPs and gene expression of interacting DEGs of SSc patients separated by the presence of previously identified risk alleles annotated in (A).