Supplementary Table S7. *Differentially methylated CpG sites (DMCs) associated with SLE disease manifestations in the discovery cohort*.

ACR criterion	Manifestation	positive cases, n	negative cases, n	DMCs, n*	Genes annotated to DMCs
1	Malar rash	169	131	0	n.a.
2	Discoid rash	65	235	3	*ELOVL2*, *OTUD7A*
3	Photosensitivity	183	117	0	n.a.
4	Oral ulcers	62	238	14	*AP3S1*, *C9orf131*, *FAM120B*, *FCAR*, *GJB6*, *IFFO1*, *PTEN*, *TFDP1*, *WDFY1*
5	Non-erosive arthritis	220	80	0	n.a.
6	Serositis	124	176	0	n.a.
7	Renal disorder	81	219	1	*FADD*
8	Neurological disorder	16	284	0	n.a.
9	Hematological disorder	180	120	1	*IFITM1*†
10	Immunological disorder	174	126	0	n.a.
11	Antinuclear antibody positive	293	7	30	*C1orf21*, *CCT5*, *CDK5R2*, *DMRTA2*, *DYNLT1*, *EPG5*, *EYA1*, *FAM217B*, *FAM46B*, *FAM47E, GCFC1-AS1*, *HNRNPR*, *KLHDC4*, *NKX2-5*, *RASGEF1C*, *RNF213*, *SHANK2*, *WDR17*, *ZFAND3*

*Discovery cohort SLE case-case logistic regression association analysis, $p < 1.3 \times 10^{-7}$, $|\Delta\beta| > 0.05$

† The DMC at cg23570810 in *IFITM1* was nominally significant in the replication cohort ($p\text{-value}_{replicationl} = 0.00103$, $\Delta\beta_{replication} = -0.082$).

n.a., not applicable