Supplementary Table 3.

Variant annotation for signficant variants and their near-perfect proxies (LD $r^2 > 0.9$). Significant variants are makerd in bold letters. Associated region for each loci was defined by proxies for our significant SNPs (LD $r^2 >= 0.9$). A blue box denotes that the variant in that row has been annotated for the type of annotation in that column. The last column annotates the variants in terms of enhancers, repressors, prmotoers of NHEK cell lines. Base positions for variants are on build 37/ hg 19.

NHEK Cell Lines Abbreviations:

HL	Heterochromatin; low signal
SE	Strong Enhancer
WT	Weak Transcribed
WE	Weak Enahncer
PR	Polycomb-repressed
I	Insulator
TT	Transcriptional transition
TE	Transcriptional elongation

Loci (Associated Region)		Chr	Base Position	Rs ID	Ref	Alt	splicing, upstream, downstream	exonic	ncRNA intronic	intronic	intergenic	UTR3	UTR5	Most Conserved Element (phastCons 44-way)	Transcription Factor Binding Site	Trancribed Regions for GM12878 cell lines	Enhancer Region (based on H3K4Me1)	Enhancer Region (based on H3K4Me3)	Enhancer Region (based on H3K27Ac)	DNAse I hypersensitivity sites from ENCODE	CTCF Binding Sites	ENCODE transcription factor ChIP-Seq data	Chromatin state of ENCODE NHEK Cell Line (epidermal keratinocytes)
IL13		5	131,995,843	rs1295686	T	C																	
		5	131,995,964	rs20541	A	G				*IL13*													**HL**
	Primary Signal	**5**	**131,996,445**	**rs1295685**	**A**	**G**																	**HL**
		5	131,996,500	rs848	A	C						*IL13*											**HL**
		5	131,996,669	rs847	T	C						*IL13*											**HL**
TNIP1		5	150,464,579	rs75851973	G	A						*IL13*											**HL**
		5	150,464,641	rs76956521	C	A				*TNIP1*													**SE**
		5	150,466,690	rs8177833	C	-				*TNIP1*													**SE**
		5	150,467,189	rs2233278	C	G							*TNIP1*										**SE**
		5	150,469,973	rs74817271	A	G							*TNIP1*										**SE**
		5	150,471,878	rs146571698	T	C							*TNIP1*										**SE**
		5	150,476,675	rs71678466	T	G							*TNIP1*										**SE**
		5	150,478,223	rs76462670	A	G							*TNIP1*										**SE**
	Primary Signal	**5**	**150,478,318**	**rs17728338**	**A**	**G**							*TNIP1*										**SE**
IL12B		5	158,764,177	rs7709212	C	T																	**WT**
		5	158,764,478	rs4921482	C	T																	**WE**
	Primary Signal	**5**	**158,766,022**	**rs62377586**	**A**	**G**																	**HL**
		5	158,826,357	rs918519	A	G																	**HL**
	Secondary Signal	**5**	**158,826,493**	**rs918518**	**A**	G																	**HL**
		5	158,829,289	rs733589	A	G																	**HL**
MHC	**Tertiary Signal**	**6**	**29,924,728**	**rs892666**	**T**	**C**																	**HL**
		6	31,242,731	rs12199223	A	T																	**HL**
		6	31,251,924	rs12189871	T	C				*HLA-B*													**HL**
		6	31,266,090	rs4406273	A	G				*HLA-B*													**HL**
		6	31,269,946	rs12211087	A	T				*HLA-B*													**PR**
		6	31,289,714	rs28894993	T	G				*HLA-B*													**PR**
	Primary Signal	**6**	**31,316,699**	**rs28732138**	**A**	G				*HLA-B*										**|**		**|**	**I**
	Secondary Signal	**6**	**31,358,302**	**rs6924962**	**C**	**T**				*HLA-B*													**PR**
TNFAIP3		6	138,189,884	rs583522	C	T																	**SE**
		6	138,195,402	rs598493	T	C				*TNFAIP3*													**TT**
		6	138,195,693	rs643177	T	C				*TNFAIP3*													**SE**
		6	138,197,824	rs582757	C	T				*TNFAIP3*													**TT**
	Primary Signal	**6**	**138,206,783**	**rs642627**	**A**	**G**				*TNFAIP3*													**TE**
		6	138,212,961	rs612217	A	G																	**WT**
		6	138,236,977	rs4895498	C	T																	**WT**
		6	138,239,434	rs6933987	T	C																	**HL**
		6	138,242,487	rs6909442	G	C																	**HL**
		6	138,242,623	rs139299350	TAAAT	0																	**HL**
IL23A	**Primary Signal**	**12**	**56,653,695**	**rs61937678**	**T**	**C**			*LOC285626*														**SE**
									LOC285626														**SE**
									LOC285626														**WE**
																							HL
																							HL
																							HL
																							HL
																							PR
																							PR
																							I
																							PR
																							SE
																							TT
																							SE
																							TT
																							TE
																							WT
																							WT
																							HL
																							HL
																							HL
																							HL
																							WT