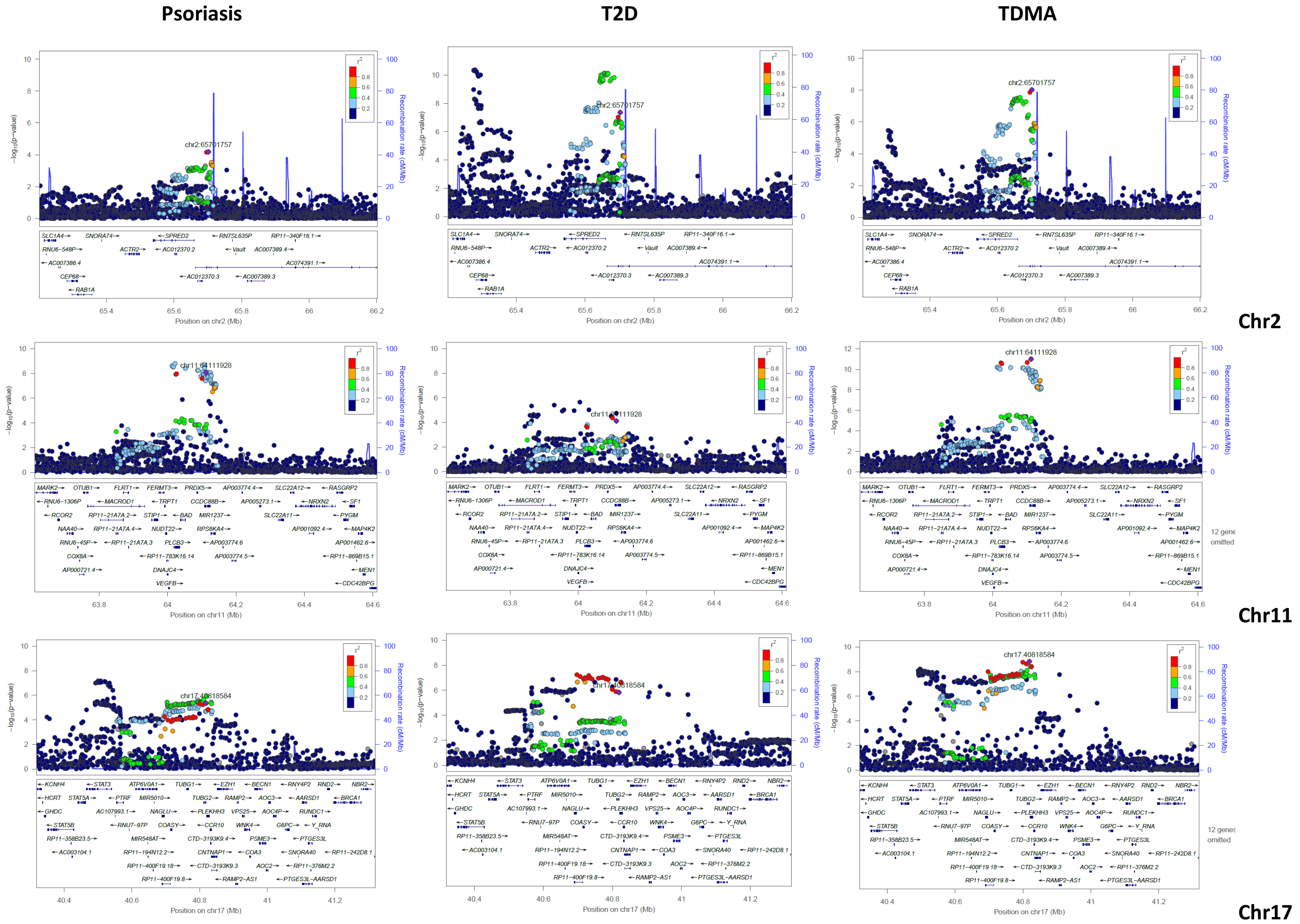
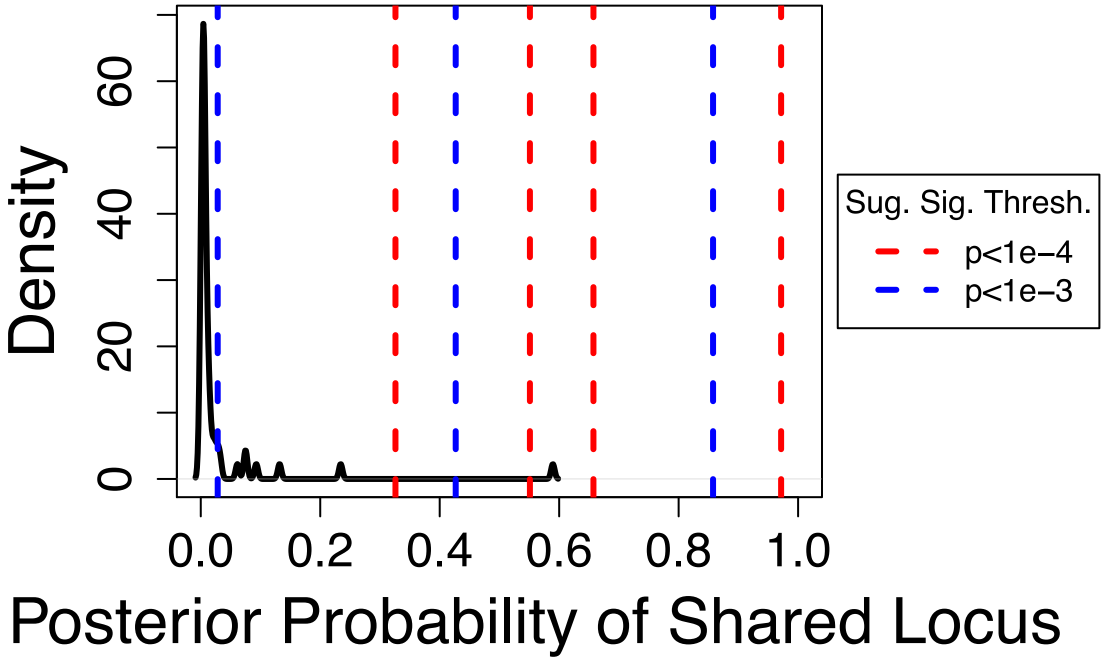
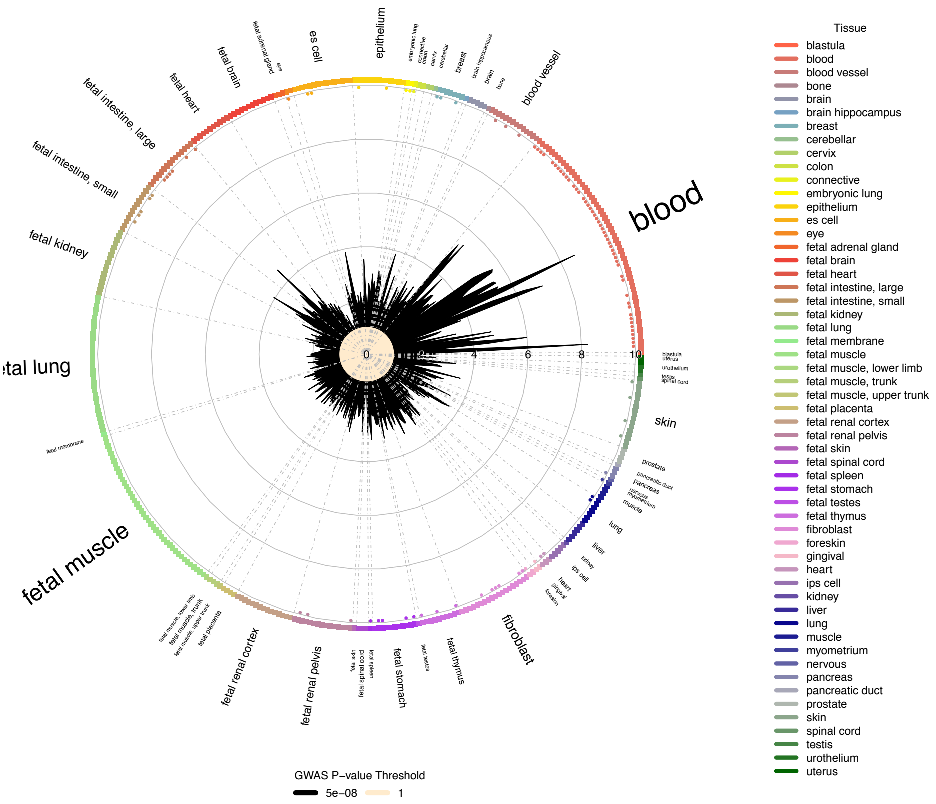


Supplementary Figure 1: Regional association plots for the chromosome 2, 11 and 17 loci in psoriasis and T2D (with the lead marker in the trans-disease meta-analysis in purple).



Supplementary Figure 2: Colocalization posterior probabilities of being a shared locus. Calculated using COLOC for loci which meet the $p<1x10^{-4}$ (red) and $p<1x10^{-3}$ (blue) criteria, compared with the 59 other previously reported loci for psoriasis (black).



Supplementary Figure 3: Cell Type Enrichment for Identified Trans-Disease Meta-Analysis (Including the MHC). Calculated using DNAse hotspots in GARFIELD. The strong enrichment of blood tissue illustrates immune-cell involvement.

Supplementary Table 1: Shared Loci from Trans-Disease Meta-Analysis

Marker ID	Chr	Position (hg19)	Alleles (risk/non-risk)	Meta-analysis P-values			Meta-analysis Odds Ratios		
				P(Psoriasis)	P(T2D)	P(TDMA)	OR(Psoriasis)	OR(T2D)	OR(TDMA)
rs438650	1	8290082	C/T	1.9x10^{-8}	3.4x10^{-1}	2.4x10^{-8}	1.14	1.01	1.07
rs78312791	1	24513613	C/A	1.3x10^{-13}	2.7x10^{-1}	2.3x10^{-13}	1.25	1.01	1.12
rs11249215	1	25297184	A/G	1.9x10^{-14}	2.9x10^{-1}	6.6x10^{-14}	1.16	1.01	1.08
rs113935720	1	67713346	T/C	7.5x10^{-16}	3.1x10^{-1}	3.8x10^{-13}	1.41	0.99	1.18
rs6677595	1	152590187	T/C	7.4x10^{-16}	8.1x10^{-1}	1.0x10^{-13}	1.18	1.00	1.08
rs35741374	2	61072567	T/C	1.2x10^{-15}	9.3x10^{-1}	1.1x10^{-13}	1.17	1.00	1.08
rs840967	**2**	**65701757**	**C/A**	**6.6x10^{-5}**	**4.4x10^{-8}**	**9.6x10^{-9}**	**1.08**	**1.04**	**1.06**
rs2111485	2	163110536	A/G	4.1x10^{-15}	9.9x10^{-1}	2.8x10^{-13}	1.16	1.00	1.08
rs7607980	2	165551201	T/C	6.7x10^{-3}	8.3x10^{-22}	2.1x10^{-8}	1.10	1.12	1.11
rs3906814	3	17011474	C/G	2.4x10^{-10}	3.8x10^{-1}	2.7x10^{-8}	1.13	0.99	1.06
rs771576	3	101616982	C/T	6.9x10^{-10}	7.6x10^{-1}	4.9x10^{-9}	1.13	1.00	1.06
rs4686392	3	185524081	G/A	4.7x10^{-2}	9.4x10^{-40}	1.3x10^{-11}	1.04	1.12	1.08
rs39841	**5**	**96120170**	**G/A**	**1.3x10^{-10}**	**3.8x10^{-2}**	**1.7x10^{-11}**	**1.14**	**1.02**	**1.08**
rs1295685	5	131996445	A/G	1.5x10^{-15}	5.9x10^{-1}	4.5x10^{-13}	1.21	1.01	1.10
rs75851973	5	150464579	G/A	2.6x10^{-39}	2.1x10^{-1}	3.0x10^{-35}	1.61	1.02	1.28
rs12188300	5	158829527	T/A	5.9x10^{-62}	2.3x10^{-1}	2.4x10^{-56}	1.69	1.02	1.31
rs7756992	6	20679709	G/A	5.4x10^{-3}	1.4x10^{-73}	2.0x10^{-20}	1.06	1.16	1.11
rs13214872	6	31255008	G/C	6.2x10^{-359}	9.4x10^{-1}	1.9x10^{-302}	2.78	1.00	1.67
rs9481169	6	111929862	T/G	4.5x10^{-27}	7.3x10^{-1}	1.3x10^{-22}	1.39	1.00	1.18
rs582757	6	138197824	C/T	6.4x10^{-16}	5.6x10^{-1}	3.3x10^{-13}	1.18	1.00	1.08
rs849135	7	28196413	G/A	1.8x10^{-1}	7.2x10^{-41}	5.0x10^{-10}	1.03	1.11	1.06
rs9650069	8	118204020	C/T	6.6x10^{-1}	1.5x10^{-50}	1.1x10^{-8}	1.01	1.13	1.07
rs10811660	9	22134068	G/A	2.2x10^{-1}	5.9x10^{-69}	9.6x10^{-12}	1.04	1.20	1.11
rs11795343	**9**	**32523737**	**T/C**	**5.2x10^{-8}**	**1.9x10^{-4}**	**1.5x10^{-10}**	**1.11**	**1.03**	**1.07**
rs10761661	**10**	**64525135**	**C/T**	**4.9x10^{-6}**	**4.1x10^{-4}**	**3.4x10^{-8}**	**1.09**	**1.03**	**1.06**
rs2459446	**10**	**75601596**	**C/T**	**1.5x10^{-10}**	**3.8x10^{-3}**	**1.8x10^{-12}**	**1.13**	**1.02**	**1.08**
rs12265333	**10**	**102011211**	**A/G**	**1.6x10^{-6}**	**7.1x10^{-7}**	**1.0x10^{-9}**	**1.12**	**1.04**	**1.08**
rs35198068	10	114754784	C/T	1.8x10^{-1}	1.8x10^{-421}	9.1x10^{-48}	0.97	1.43	1.18
rs5215	11	17408630	C/T	1.2x10^{-3}	9.4x10^{-25}	1.4x10^{-11}	1.07	1.08	1.07
rs685870	**11**	**64111928**	**T/C**	**8.5x10^{-9}**	**7.8x10^{-5}**	**1.0x10^{-11}**	**1.13**	**1.03**	**1.08**
rs4561177	11	109962432	A/G	1.5x10^{-11}	9.4x10^{-1}	4.1x10^{-10}	1.14	1.00	1.07
rs10893884	**11**	**128410264**	**T/C**	**1.7x10^{-9}**	**8.1x10^{-2}**	**4.4x10^{-10}**	**1.12**	**1.01**	**1.07**
rs76895963	12	4384844	T/G	1.8x10^{-1}	1.3x10^{-64}	3.7x10^{-9}	1.15	1.68	1.39
rs57137641	12	56741228	G/A	9.0x10^{-16}	3.7x10^{-1}	4.6x10^{-15}	1.38	1.01	1.18
rs653178	**12**	**112007756**	**C/T**	**1.7x10^{-4}**	**9.0x10^{-8}**	**4.9x10^{-8}**	**1.07**	**1.04**	**1.06**
rs9591325	**13**	**50811220**	**T/C**	**6.6x10^{-9}**	**8.1x10^{-3}**	**2.1x10^{-10}**	**1.24**	**1.04**	**1.14**
rs12884468	14	35852486	C/T	7.3x10^{-15}	6.2x10^{-1}	1.8x10^{-12}	1.16	1.00	1.08
rs2199036	16	31006972	T/C	1.0x10^{-11}	8.2x10^{-1}	4.7x10^{-10}	1.14	1.00	1.07
rs17817712	16	53821125	G/A	2.2x10^{-4}	1.9x10^{-12}	1.9x10^{-9}	1.07	1.05	1.06
rs28998802	17	26124908	A/G	2.0x10^{-16}	7.5x10^{-1}	1.3x10^{-14}	1.24	1.00	1.12
rs2292749	**17**	**40818584**	**T/C**	**4.4x10^{-6}**	**1.5x10^{-6}**	**1.5x10^{-9}**	**1.10**	**1.04**	**1.07**
rs34536443	19	10463118	G/C	9.4x10^{-30}	2.6x10^{-1}	8.0x10^{-29}	1.95	1.02	1.41
rs6063454	20	48590791	G/T	3.1x10^{-16}	8.0x10^{-1}	1.2x10^{-14}	1.17	1.00	1.08

Abbreviations are as follows: Chr, chromosome; OR, odds ratio; p, p-value; TDMA, trans-disease meta-analysis. Loci with lower p-value in trans-disease meta-analysis than either trait are marked in **bold**, of which those suggestive significant ($p<1x10^{-4}$) in both traits are marked in **red**.

Supplementary Table 2: Opposing Loci from Trans-Disease Meta-Analysis

Marker ID	**Chr**	**Position (hg19)**	**Alleles (risk/non-risk)**	**Meta-analysis P-values**			**Meta-analysis Odds Ratios**		
				P(Psoriasis)	P(T2D)	P(TDMA)	OR(Psoriasis)	OR(T2D)	OR(TDMA)
rs4649201	1	24509435	G/A	2.1x10^{-13}	5.0x10^{-1}	2.8x10^{-11}	1.25	1.01	1.11
rs6672420	1	25291010	T/A	8.8x10^{-15}	4.8x10^{-1}	3.4x10^{-12}	1.16	1.01	1.07
rs113935720	1	67713346	T/C	7.5x10^{-16}	3.1x10^{-1}	2.2x10^{-15}	1.41	0.99	1.19
rs11205044	1	152593437	C/T	6.3x10^{-16}	7.4x10^{-1}	1.8x10^{-14}	1.18	1.00	1.09
rs340874	1	214159256	C/T	3.0x10^{-2}	4.8x10^{-21}	3.2x10^{-8}	0.96	1.07	1.06
rs6544662	2	43712093	C/A	4.6x10^{-1}	5.1x10^{-22}	2.6x10^{-8}	0.98	1.19	1.10
rs35741374	2	61072567	T/C	1.2x10^{-15}	9.3x10^{-1}	6.6x10^{-14}	1.17	1.00	1.08
rs4672505	**2**	**62560332**	**A/G**	**1.9x10^{-8}**	**3.1x10^{-2}**	**1.6x10^{-9}**	**1.12**	**0.98**	**1.07**
rs1990760	2	163124051	T/C	5.7x10^{-15}	8.8x10^{-1}	2.2x10^{-13}	1.16	1.00	1.08
rs3906814	3	17011474	C/G	2.4x10^{-10}	3.8x10^{-1}	5.4x10^{-10}	1.13	0.99	1.07
rs771576	3	101616982	C/T	6.9x10^{-10}	7.6x10^{-1}	1.9x10^{-8}	1.13	1.00	1.06
rs1295685	5	131996445	G/A	1.5x10^{-15}	5.9x10^{-1}	2.2x10^{-14}	1.21	0.99	1.10
rs2233278	5	150467189	C/G	2.3x10^{-39}	2.2x10^{-1}	5.0x10^{-30}	1.61	1.02	1.26
rs62377586	5	158766022	G/A	3.5x10^{-54}	2.3x10^{-1}	3.1x10^{-50}	1.38	0.99	1.18
rs6928012	6	20728513	C/T	1.7x10^{-5}	8.6x10^{-20}	2.4x10^{-13}	0.92	1.07	1.08
rs10484554	6	31274555	T/C	7.5x10^{-358}	9.1x10^{-1}	1.9x10^{-302}	2.78	1.00	1.67
rs9481169	6	111929862	T/G	4.5x10^{-27}	7.3x10^{-1}	7.9x10^{-24}	1.39	1.00	1.18
rs610604	6	138199417	G/T	8.5x10^{-16}	4.6x10^{-1}	8.6x10^{-15}	1.17	0.99	1.09
rs1838488	**9**	**75332795**	**C/T**	**2.0x10^{-6}**	**1.8x10^{-3}**	**4.4x10^{-8}**	**1.12**	**0.98**	**1.07**
rs1108617	**10**	**81043573**	**A/G**	**2.8x10^{-10}**	**3.0x10^{-2}**	**3.1x10^{-11}**	**1.13**	**0.98**	**1.07**
rs10882102	10	94466495	G/C	1.7x10^{-4}	2.4x10^{-57}	1.6x10^{-20}	0.93	1.13	1.10
rs35198068	10	114754784	C/T	1.8x10^{-1}	1.8x10^{-421}	5.3x10^{-65}	0.97	1.43	1.21
rs1648153	11	109959638	G/A	1.6x10^{-11}	9.3x10^{-1}	2.7x10^{-10}	1.14	1.00	1.07
rs7108992	**11**	**128381867**	**A/C**	**6.9x10^{-8}**	**4.7x10^{-2}**	**7.8x10^{-9}**	**1.11**	**0.98**	**1.06**
rs111885088	12	56657216	A/C	1.1x10^{-15}	4.1x10^{-1}	4.4x10^{-13}	1.38	1.01	1.17
rs74899623	13	50794228	G/A	1.7x10^{-8}	3.9x10^{-1}	2.5x10^{-8}	1.34	0.98	1.17
rs8016947	14	35832666	G/T	3.8x10^{-14}	2.6x10^{-1}	9.3x10^{-14}	1.15	0.99	1.08
rs413024	16	11354091	A/G	1.2x10^{-8}	6.4x10^{-1}	4.2x10^{-8}	1.13	1.00	1.06
rs4889526	16	31030344	A/C	8.5x10^{-12}	6.1x10^{-1}	6.0x10^{-11}	1.14	1.00	1.07
rs28998802	17	26124908	A/G	2.0x10^{-16}	7.5x10^{-1}	7.9x10^{-14}	1.24	1.00	1.11
rs34536443	19	10463118	G/C	9.4x10^{-30}	2.6x10^{-1}	1.8x10^{-25}	1.95	1.02	1.38
rs6063454	20	48590791	G/T	3.1x10^{-16}	8.0x10^{-1}	5.1x10^{-14}	1.17	1.00	1.08

Abbreviations are as follows: Chr, chromosome; OR, odds ratio; p, p-value; TDMA, trans-disease meta-analysis. Risk alleles and effect sizes are given with respect to the trait with more significant p-value for each marker. Loci with lower p-value in trans-disease meta-analysis than either trait are indicated in **bold**, of which none are suggestive significant (p<1x10^{-4}) in both traits.

Supplementary Table 3: Top 5 Histone Modifications and DNAse Hotspots with Most Enrichment

Enrichment p-Value	Cell type	Enrichment Mark
1.3×10^{-7}	HeLa S3	H3K4me2
1.5×10^{-7}	GM12878	H3K9ac
6.4×10^{-7}	GM12878	H3K4me3
9.7×10^{-7}	GM12878	H3K4me1
1.6×10^{-6}	GM12878	H3K79me2

Supplementary Table 4: Bayesian Credible Set Sizes (95% Confidence Interval)

Lead Marker ID	**Chr**	**Position (hg19)**	**Alleles (risk/non-risk)**	**Credible Set Sizes**			
				Psoriasis	T2D	TDMA	Intersect
rs840967	2	65701757	C/A	2,195	33	27	24
rs12265333	10	102011211	A/G	46	62	20	20
rs685870	11	64111928	T/C	31	37	27	4
rs2292749	17	40818584	T/C	60	104	184	2

Abbreviations are as follows: Chr, chromosome; T2D, type 2 diabetes; TDMA, trans-disease meta-analysis.

Supplementary Table 5: Bayesian Credible Sets intersected in the TDMA and individual trait meta-analysis (95% Confidence Interval)

Marker ID	Chr	Position (hg19)	Alleles (risk/non-risk)	P-value (TDMA)	OR (TDMA)	Raw CADD score	PHRED-Scaled CADD score	GM12878 Overlap annotation[a]
rs6731993	2	65642097	A/T	8.3×10^{-8}	1.06	-0.059	1.84	000000
rs7557569	2	65644561	T/C	6.3×10^{-8}	1.06	-0.029	2.20	001010
rs62141075	2	65644616	C/T	7.1×10^{-8}	1.06	0.224	6.18	001010
rs13383320	2	65645137	C/A	5.8×10^{-8}	1.06	0.161	5.25	101010
rs10166100	2	65645750	C/T	6.3×10^{-8}	1.06	-0.281	0.42	001010
rs10166362	2	65645774	G/A	6.0×10^{-8}	1.06	-0.234	0.57	001000
rs7565437	2	65646966	T/C	5.8×10^{-8}	1.06	0.177	5.49	000000
rs10153675	2	65649580	G/A	3.8×10^{-8}	1.06	0.380	8.17	000000
rs55792977	2	65650864	G/T	4.7×10^{-8}	1.06	-0.142	1.05	000000
rs12470883	2	65651851	G/A	4.6×10^{-8}	1.06	0.119	4.58	000000
rs7572922	2	65652156	C/T	4.1×10^{-8}	1.06	-0.013	2.43	000000
rs2028150	2	65655012	C/G	4.0×10^{-8}	1.06	0.291	7.09	000000
rs2028151	2	65655613	A/T	4.8×10^{-8}	1.06	1.702	16.80	000100
rs7569257	2	65656976	G/A	3.3×10^{-8}	1.06	0.186	5.63	101111
rs7569113	2	65657041	C/T	4.1×10^{-8}	1.06	0.372	8.08	101111
rs12185577	2	65659488	A/G	4.7×10^{-8}	1.06	0.363	7.98	111101
rs12185610	2	65661468	A/C	3.2×10^{-8}	1.06	-0.075	1.66	000000
rs1807337	2	65663167	G/C	3.5×10^{-8}	1.06	1.282	14.84	111101
rs1437466	2	65664350	C/T	3.7×10^{-8}	1.06	0.576	10.07	111101
rs2860773	2	65665641	G/T	3.0×10^{-8}	1.06	0.062	3.63	000000
rs6752053	2	65666674	T/C	2.9×10^{-8}	1.06	0.288	7.06	000000
rs62141115	2	65672192	A/G	5.0×10^{-8}	1.06	0.314	7.40	000000
rs6546151	2	65676583	G/A	7.2×10^{-8}	1.06	-0.477	0.10	000000
rs10184881	2	65684152	A/G	5.4×10^{-8}	1.06	-0.036	2.11	000000
rs10786583	10	101946014	C/G	1.2×10^{-8}	1.07	0.382	8.19	111111
rs7923726	10	101963299	G/T	1.2×10^{-9}	1.08	-0.450	0.13	000000
rs7909855	10	101967212	C/G	1.4×10^{-8}	1.07	0.191	5.71	000000
rs12269373	10	101972378	T/C	1.5×10^{-9}	1.08	-0.182	0.81	000000
rs7898075	10	101973097	T/C	1.5×10^{-9}	1.08	-0.303	0.36	000000
rs34136767	10	101973388	T/C	1.5×10^{-9}	1.08	0.339	7.70	000000
rs2230804	10	101977883	C/T	1.4×10^{-8}	1.07	2.206	21.40	000000
rs7905395	10	101996286	C/T	2.5×10^{-9}	1.07	0.210	5.99	000000
rs7905302	10	101996295	A/G	2.3×10^{-9}	1.07	0.087	4.05	000000
rs4917889	10	101999394	A/G	8.1×10^{-9}	1.07	-0.316	0.33	000000
rs4919438	10	102006429	T/C	8.1×10^{-9}	1.07	0.084	3.99	000000
rs6584354	10	102007714	A/C	1.2×10^{-9}	1.08	0.024	3.01	000000
rs7079072	10	102008169	C/G	1.1×10^{-9}	1.08	0.409	8.49	000000
rs12265333	10	102011211	A/G	1.0×10^{-9}	1.08	0.873	12.40	000000
rs2270961	10	102016268	G/A	1.1×10^{-8}	1.07	0.786	11.76	000000
rs7922807	10	102023006	C/T	1.2×10^{-9}	1.08	0.059	3.59	000010
rs7922807	10	102028467	T/C	1.4×10^{-9}	1.08	0.017	2.89	001000
rs12254005	10	102038685	T/A	1.6×10^{-9}	1.08	0.043	3.31	000000
rs4919446	10	102039458	G/A	1.7×10^{-9}	1.08	0.246	6.50	000000
rs4917896	10	102039463	T/C	1.5×10^{-9}	1.08	0.317	7.44	000000

Supplementary Table 5: Bayesian Credible Sets (95% Confidence Interval) *continued*

Marker ID	Chr	Position (hg19)	Alleles (risk/non-risk)	P-value (TDMA)	OR (TDMA)	Raw CADD score	PHRED-Scaled CADD score	GM12878 Overlap annotation[a]
rs588177	11	64024056	C/A	2.4×10^{-11}	1.08	0.091	4.12	000000
rs2244625	11	64026144	G/A	2.9×10^{-11}	1.08	0.250	6.55	000000
rs1662185	11	64100776	A/G	2.2×10^{-11}	1.08	0.188	5.66	000000
rs685870	11	64111928	T/C	1.0×10^{-11}	1.08	-0.223	0.61	000000
rs66918837	17	40799633	A/G	1.8×10^{-9}	1.07	-0.262	0.47	000000
rs2292749	17	40818584	T/C	1.5×10^{-9}	1.07	0.559	9.91	000000

Abbreviations are as follows: Chr, chromosome; TDMA, trans-disease meta-analysis; CADD, Combined Annotation Dependent Depletion. [a]Indicates whether marker overlaps (1) or does not overlap (0) GM12878 (lymphoblastoid) cell type annotations using the following 6 marks: DNAse-seq, H3K27ac, H3K4me2, H3K4me3, H3K79me2, H3K9ac.

Supplementary Table 6: Significant eQTLs for Markers in Intersection of Bayesian Credible Sets

Gene	Chr	pcHi-C	eQTLGen			NESDA/NTR			GeneNetwork	
			Marker	P-value	OR	Marker	P-value	OR	Marker	P-value
ACTR2	2	+++++++				rs7557569-T	1.1x10^{-19}	1.18		
CEP68	2	+++++++	rs6752053-C	1.5x10^{-5}	1.04					
SPRED2	2	+++++++	rs10153675-G	3.3x10^{-5}	1.14				rs7557569-T	2.4x10^{-3}
BLOC1S2	10	++++++-	rs10786583-G	4.4x10^{-23}	1.08	rs7922807-T	1.3x10^{-21}	1.20		
CHUK	10	++-+++-	rs10786583-G	4.3x10^{-19}	1.07				rs12254005-A	2.3x10^{-6}
CWF19L1	10	++++++-	rs10786583-G	3.3x10^{-310}	1.63	rs6584354-C	6.2x10^{-9}	1.12	rs7922807-T	2.2x10^{-152}
DNMBP	10	++-++++	rs10786583-G	2.90x10^{-6}	1.04					
ERLIN1	10	++++++-	rs10786583-C	6.3x10^{-21}	1.08	rs4919438-T	2.3x10^{-9}	1.12		
PHBP9	10	-------	rs10786583-G	2.0x10^{-26}	1.09					
PKD2L1	10	++-+++-	rs10786583-G	2.3x10^{-27}	1.09					
RP11-316M21.6	10	++-+++-	rs10786583-G	3.1x10^{-13}	1.06					
AP003774.1	11	-------	rs1662185-G	3.3x10^{-310}	1.41					
AP003774.4	11	++-+++-	rs1662185-G	5.2x10^{-6}	1.04					
AP003774.6	11	-------	rs1662185-G	3.5x10^{-45}	1.13					
CCDC88B	11	+----+-	rs1662185-A	1.8x10^{-219}	1.31					
FERMT3	11	++++++-	rs1662185-G	1.5x10^{-8}	1.05					
GPR137	11	++++-+-	rs1662185-A	3.2x10^{-40}	1.12				rs2244625-G	4.8x10^{-25}
PLA2G16	11	----+--	rs1662185-G	4.2x10^{-14}	1.07					
PLCB3	11	++-+-+-	rs1662185-A	2.9x10^{-7}	1.05					
PPP1R14B	11	++-+-+-	rs1662185-A	5.3x10^{-9}	1.05					
PRDX5	11	++++++-	rs1662185-A	3.3x10^{-297}	1.37				rs685870-T	5.2x10^{-109}
RPS6KA4	11	++++-+-	rs1662185-G	3.0x10^{-23}	1.09				rs685870-C	2.3x10^{-4}
TRMT112	11	++++++-	rs1662185-G	1.3x10^{-62}	1.15	rs685870-C	9.8x10^{-6}	1.10		
TRPT1	11	++-+-+-	rs685870-C	6.5x10^{-6}	1.04	rs588177-A	5.9x10^{-19}	1.20	rs2244625-G	1.2x10^{-4}
BECN1	17	++++-+-	rs2292749-T	3.9x10^{-44}	1.13	rs2292749-C	1.3x10^{-24}	1.12	rs2292749-T	4.8x10^{-19}
FAM134C	17	+++++++	rs2292749-C	1.8x10^{-15}	1.07	rs66918837-G	7.1x10^{-26}	1.21		
HSD17B1	17	+--+++-	rs2292749-C	1.3x10^{-38}	1.12					
HSD17B1P1	17	+--+++-	rs2292749-C	1.3x10^{-11}	1.06					
JUP	17	++-----	rs2292749-T	5.7x10^{-14}	1.07					
MLX	17	++++-+-	rs2292749-T	3.8x10^{-51}	1.14					
NAGLU	17	++-+---	rs2292749-C	9.0x10^{-24}	1.09					
NT5C3B	17	+------	rs2292749-C	4.7x10^{-11}	1.06					
PSMC3IP	17	++++-++	rs2292749-T	8.1x10^{-22}	1.09					
STAT3	17	+---+--	rs2292749-C	1.9x10^{-11}	1.06					

Abbreviations are as follows: Chr, chromosome; NESDA, Netherlands Study of Depression and Anxiety; NTR, Netherlands Tweelingen Register. Markers are presented using their reference SNP ID along with the risk allele. pcHi-C indicates whether promoter capture Hi-C contacts were identified between regions surrounding at least one of the markers in the Bayesian credible set intersection and a promoter for each gene in 7 different tissues (+: present; -: not present): lymphoblastoid, pancreas, adipose, liver, psoas, thymus, keratinocyte.

Supplementary Table 7: Comparing PHRED-Scaled CADD Scores for eQTLs Between the Intersection of the Bayesian Credible Set and All the eQTLs for Each Gene

Gene	Credible Set Intersection			All eQTLs for Gene		
	N	Mean	SD	N	Mean	SD
AP003774.1	4	4.24	2.61	1271	4.17	4.51
AP003774.4	1	5.66	NA	148	3.13	3.35
AP003774.6	4	4.24	2.61	909	4.08	4.57
BECN1	2	5.19	6.67	900	4.13	4.39
BLOC1S2	20	5.9	5.09	469	3.67	3.76
CCDC88B	4	4.24	2.61	1492	4.07	4.41
CEP68	1	7.06	NA	627	3.95	3.93
CHUK	20	5.90	5.09	617	3.62	3.66
CWF19L1	20	5.90	5.09	2137	3.78	3.93
DNMBP	20	5.90	5.09	520	3.59	3.62
ERLIN1	20	5.90	5.09	472	3.81	4.11
FAM134C	2	5.19	6.67	369	4.46	4.34
FERMT3	4	4.24	2.61	444	4.03	4.42
GPR137	*4*	*4.24*	*2.61*	*405*	*4.74*	*4.75*
HSD17B1	2	5.19	6.67	536	4.45	4.33
HSD17B1P1	2	5.19	6.67	551	4.23	4.35
JUP	2	5.19	6.67	1840	3.88	4.42
MLX	2	5.19	6.67	499	4.14	4.09
NAGLU	2	5.19	6.67	517	4.33	4.11
NT5C3B	2	5.19	6.67	1961	3.99	4.30
PHBP9	20	5.90	5.09	329	3.78	3.80
PKD2L1	20	5.90	5.09	661	3.60	3.75
PLA2G16	4	4.24	2.61	2213	3.42	4.14
PLCB3	4	4.24	2.61	286	4.30	4.37
PPP1R14B	4	4.24	2.61	233	4.82	4.77
PRDX5	4	4.24	2.61	1369	3.97	4.33
PSMC3IP	2	5.19	6.67	302	4.67	4.28
RP11-316M21.6	20	5.90	5.09	184	3.79	3.87
RPS6KA4	4	4.24	2.61	1136	3.92	4.37
SPRED2	24	5.44	4.31	535	3.95	3.98
STAT3	2	5.19	6.67	1141	3.95	3.95
TRMT112	4	4.24	2.61	930	3.98	4.36
TRPT1	*1*	*0.61*	*NA*	*534*	*3.99*	*4.42*

Abbreviations are as follows: N, number of eQTLs for gene; Mean, mean PHRED-Scaled CADD score of eQTLs for gene; SD, standard deviation of PHRED-Scaled CADD score of eQTLs for gene.

Supplementary Table 8: Differential Expression for eQTL Gene Targets

Gene	**Chr**	**Psoriasis (Gudjonsson)**		**Psoriasis (Tsoi)**		**T2D Pancreas**		**T2D Skeletal Muscle**		**T2D Liver**		**T2D Adipose**	
		P-value	*Log2(FC)*	*P-value*	*Log2(FC)*	*P-value*	*Log2(FC)*	*P-value*	*Log2(FC)*	*P-value*	*Log2(FC)*	*P-value*	*Log2(FC)*
ACTR2	2	**$5.0x10^{-18}$**	**0.884**	$1.7x10^{-14}$	0.566	**$1.6x10^{-2}$**	**-1.71**	**$8.7x10^{-12}$**	**0.817**	$1.0x10^{-2}$	0.821	**$2.4x10^{-2}$**	**0.656**
CEP68	2	**$8.7x10^{-31}$**	**-1.05**	**$6.0x10^{-27}$**	**-0.867**	$4.8x10^{-2}$	0.326	**$1.3x10^{-5}$**	**0.591**	**$1.4x10^{-3}$**	**-1.05**	$8.1x10^{-2}$	0.258
SPRED2	2	$1.8x10^{-16}$	-0.541	$9.0x10^{-4}$	-0.221	**$5.4x10^{-4}$**	**-1.19**	$7.7x10^{-2}$	-0.092	**$5.9x10^{-3}$**	**-1.48**	$1.7x10^{-1}$	-0.064
BLOC1S2	10	$5.1x10^{-25}$	0.400	**$1.5x10^{-15}$**	**0.788**							$5.5x10^{-1}$	0.080
CHUK	10	$8.7x10^{-8}$	0.334	$3.7x10^{-12}$	0.480	**$3.1x10^{-4}$**	**-1.74**	$1.6x10^{-6}$	0.528	**$2.0x10^{-2}$**	**-0.975**	$5.4x10^{-1}$	0.120
CWF19L1	10	$6.5x10^{-11}$	0.297	$1.8x10^{-11}$	0.443	$3.9x10^{-1}$	0.199			$5.5x10^{-1}$	-0.398	$8.9x10^{-2}$	0.476
DNMBP	10	**$1.4x10^{-28}$**	**-0.638**	**$1.6x10^{-21}$**	**-0.828**	$2.7x10^{-1}$	0.238	$2.0x10^{-1}$	0.057	**$1.5x10^{-2}$**	**-0.815**	**$2.5x10^{-2}$**	**1.12**
ERLIN1	10	$8.0x10^{-14}$	0.457	$5.6x10^{-2}$	0.114	**$2.7x10^{-3}$**	**-0.817**	$1.8x10^{-6}$	-0.257	1.3x10-^{1}	0.802	$4.5x10^{-2}$	0.850
PHBP9	10			$2.4x10^{-1}$	0.210								
PKD2L1	10	$6.3x10^{-1}$	0.022			$5.3x10^{-1}$	0.113			$7.1x10^{-1}$	-0.197	$5.7x10^{-1}$	0.112
AP003774.1	11			**$1.0x10^{-2}$**	**0.706**								
CCDC88B	11	$5.0x10^{-9}$	0.281	**$7.9x10^{-16}$**	**1.49**							$2.8x10^{-1}$	-0.046
FERMT3	11	$4.9x10^{-20}$	0.512	**$4.7x10^{-10}$**	**0.773**							**$6.6x10^{-3}$**	**0.960**
GPR137	11	$3.8x10^{-3}$	0.126	$2.5x10^{-10}$	0.516	$7.6x10^{-3}$	0.403			$1.8x10^{-1}$	0.656	$1.9x10^{-1}$	-0.190
PLA2G16	11	**$5.5x10^{-13}$**	**-0.672**	$1.5x10^{-2}$	-0.526	**$2.8x10^{-2}$**	**-0.725**	$7.9x10^{-2}$	0.146	$8.7x10^{-1}$	0.046	$7.6x10^{-2}$	1.35
PLCB3	11	$7.4x10^{-6}$	0.217	**$2.5x10^{-17}$**	**0.696**	**$1.2x10^{-5}$**	**0.730**	$7.1x10^{-8}$	-0.505	$2.7x10^{-1}$	0.479	$3.4x10^{-1}$	0.222
PPP1R14B	11	$2.0x10^{-15}$	0.296	$8.0x10^{-9}$	0.397	$4.9x10^{-1}$	-0.183			$3.5x10^{-1}$	0.315	**$1.4x10^{-2}$**	**0.668**
PRDX5	11	$2.2x10^{-9}$	0.204	**$1.1x10^{-14}$**	**0.746**							$8.7x10^{-2}$	0.670
RPS6KA4	11	$3.7x10^{-17}$	0.421	**$3.0x10^{-27}$**	**1.42**	**$8.0x10^{-3}$**	**0.664**	$4.5x10^{-9}$	-0.317	$8.4x10^{-1}$	0.056	$1.9x10^{-1}$	-0.066
TRMT112	11	$2.8x10^{-22}$	0.290	**$5.4x10^{-13}$**	**0.649**	**$4.8x10^{-3}$**	**-0.677**			$5.1x10^{-1}$	0.155	$7.3x10^{-1}$	-0.094
TRPT1	11	$4.5x10^{-8}$	0.171	$1.2x10^{-9}$	0.487							$2.6x10^{-1}$	0.310
BECN1	17	$6.3x10^{-7}$	0.195	$1.6x10^{-13}$	0.449	**$3.3x10^{-2}$**	**-1.05**	**$5.4x10^{-7}$**	**0.768**	$6.9x10^{-2}$	-0.523	$2.9x10^{-2}$	0.438
FAM134C	17	$5.0x10^{-2}$	-0.058	$4.5x10^{-6}$	0.207	$4.3x10^{-1}$	0.178	$2.5x10^{-2}$	0.212	$1.8x10^{-1}$	-0.343	$7.6x10^{-2}$	0.380
HSD17B1	17	**$4.0x10^{-43}$**	**1.43**	$1.7x10^{-9}$	0.564	$2.1x10^{-1}$	0.154	**$7.6x10^{-7}$**	**-0.622**	$7.3x10^{-1}$	-0.255	$1.8x10^{-1}$	0.144
HSD17B1P1	17			**$2.6x10^{-5}$**	**-0.731**								
JUP	17	$4.0x10^{-11}$	0.392	$2.7x10^{-8}$	0.419	$1.2x10^{-1}$	0.378	$1.0x10^{-2}$	0.186	$2.2x10^{-1}$	0.457	$3.5x10^{-1}$	0.204
MLX	17	$1.8x10^{-31}$	0.502	$1.7x10^{-12}$	0.495	**$6.4x10^{-4}$**	**-0.804**	$6.3x10^{-1}$	0.033	$6.5x10^{-2}$	0.691	**$2.7x10^{-2}$**	**-0.598**
NAGLU	17	$4.5x10^{-2}$	0.073	$1.1x10^{-3}$	0.294	$1.6x10^{-1}$	-0.211	$2.9x10^{-6}$	-0.279	$4.8x10^{-1}$	0.223	$8.1x10^{-3}$	0.396
NT5C3B	17	$4.7x10^{-1}$	0.028	$1.8x10^{-7}$	0.560							$2.6x10^{-2}$	0.546
PSMC3IP	17	$1.3x10^{-7}$	0.207	**$1.7x10^{-8}$**	**0.589**	$1.2x10^{-2}$	0.329	$1.1x10^{-4}$	-0.212	$7.2x10^{-1}$	-0.371	$7.7x10^{-2}$	0.444
STAT3	17	**$3.0x10^{-35}$**	**1.09**	**$4.6x10^{-28}$**	**1.74**	$4.8x10^{-2}$	-0.699	$8.3x10^{-2}$	0.201	**$1.0x10^{-2}$**	**1.37**	**$3.3x10^{-4}$**	**0.796**

Abbreviations are as follows: Chr, chromosome; FC, fold change. Values in **bold** indicate significant differential expression (FDR<0.05, |FC|>1

Supplementary Table 9: Single-Variable Mendelian Randomization

	Approach	**Psoriasis on T2D**					**T2D on Psoriasis**				
		Num. Markers	Unadjusted		BMI-adjusted		Num. Markers	Unadjusted		BMI-adjusted	
			OR	*P*	*OR*	*P*		*OR*	*P*	*OR*	*P*
Established ($p<5x10^{-8}$) loci	IVW (standard)	36/ 36	1.02	0.139	1.01	0.187	206/ 148	1.06	0.107	1.06	0.247
	MR-Egger		1.04	0.196	1.03	0.334		1.04	0.102	0.98	0.885
	Median		1.01	0.260	1.00	0.832		1.03	0.049	1.04	0.394
	Mode		1.00	0.823	0.98	0.390		0.80	0.145	1.17	0.198
	MR-RAPS		1.02	0.017	1.02	0.061		1.06	0.040	1.05	0.279
Genome-wide information	IVW (standard)	5,877/ 5,822	1.01	$1.38x10^{-3}$	1.01	$1.59x10^{-3}$	4,636/ 5,157	0.98	0.014	0.97	$3.10x10^{-4}$
	MR-Egger		1.00	$1.87x10^{-3}$	1.01	$2.16x10^{-3}$		0.95	0.014	0.94	$5.08x10^{-7}$
	Median		1.01	$2.27x10^{-3}$	1.01	$2.62x10^{-3}$		1.09	0.038	1.06	$7.18x10^{-2}$
	Mode		1.57	$1.06x10^{-3}$	3.00	$4.17x10^{-2}$		1.86	0.093	4.07	0.997
	MR-RAPS		1.01	$2.02x10^{-3}$	1.01	$2.44x10^{-3}$		1.10	0.087	0.93	$9.91x10^{-3}$

Abbreviations are as follows: IVW, inverse variance weighted; Num., number of; T2D, type 2 diabetes; OR, odds ratio; p, p-value. Number of markers are given first using the unadjusted T2D summary statistics, and then using the BMI-adjusted summary statistics.

Supplementary Table 10: Lead Marker in Each Locus (Which Meet Our Criteria) Using Different Approaches for Trans-Disease Meta-Analysis

Chr	Risk Allele Frequency				
	TDMA	IVW	CCMA	RE2	ASSET
2	rs840967				
6					rs9273366
10	rs12265333	rs7923726	rs12265333	rs12265333	rs7923726
11	rs685870	rs1662185	rs685870	rs685870	
17	rs2292749	rs684214	rs684214	rs684214	rs684214

The results are largely consistent between techniques, with the chromosome 10 and 17 loci revealed by all, and all but ASSET revealing the chromosome 11 locus. Only TDMA identifies the chromosome 2 locus as significant because the lead marker for the other techniques (rs2860773) is not suggestive significant for T2D. This suggests the differences between techniques are not so much due to large changes in p-value, but rather small changes in the ordering of most significant markers. Abbreviations are as follows: Chr, chromosome; TDMA, Unweighted Trans-Disease Meta-Analysis; IVW, Inverse-Variance Weighted; CCMA, Compare and Contrast Meta-Analysis; RE2, Buhm Han's revised random effects model for meta-analysis; ASSET, ASsociation analysis based on subSETs.

Supplementary Table 11: Additional Loci for Trans-Disease Meta-Analysis with $p<1x10^{-3}$ Suggestive Significance Threshold

Marker ID	**Chr**	**Position (hg19)**	**Alleles (risk/non-risk)**	**Meta-analysis P-values**			**Meta-analysis Odds Ratios**			**Nearby Gene**	**BMI Locus?**[a]	**New GWS Locus?**[a]
				P(Psoriasis)	P(T2D)	P(Both)	OR(Psoriasis)	OR(T2D)	OR(Both)			
rs11795343	9	32523737	T/C	$5.2x10^{-8}$	$1.9x10^{-4}$	$1.4x10^{-10}$	1.11	1.03	1.07	*DDX58*	No	T2D
rs10761661	10	64525135	C/T	$4.9x10^{-6}$	$4.1x10^{-4}$	$3.4x10^{-8}$	1.09	1.03	1.06	*ZNF365*	Yes	T2D
rs653178	12	112007756	C/T	$1.7x10^{-4}$	$9.0x10^{-8}$	$4.9x10^{-8}$	1.07	1.04	1.06	*BRAP*	Yes	No

Abbreviations are as follows: Chr, chromosome; OR, odds ratio; p, p-value; T2D, type 2 diabetes; BMI, body mass index; GWS, genome-wide significant (i.e. $p<5x10^{-8}$). [a]We determine whether a locus is previously known to be associated with BMI, psoriasis, or T2D according to data from the GIANT and DIAGRAM consortium, as well as a search of the available literature.

Supplementary Table 12: Additional Shared Loci ($p<1x10^{-3}$) in the Michigan Genomics Initiative

Marker ID	**Chr**	**Position (hg19)**	**Alleles (risk/non-risk)**	**Risk Allele Frequency**			
				Control	Psoriasis (only)	T2D (only)	Both
rs11795343	9	32523737	T/C	0.601	0.641	0.606	0.640
rs10761661	10	64525135	C/T	0.567	0.585	0.565	0.572
rs653178	12	112007756	C/T	0.491	0.523	0.501	0.536

Abbreviations are as follows: Chr, chromosome; T2D, type 2 diabetes.

Supplementary Note 1: Previous reporting of shared loci

The gene targets suggested for the loci in previous research are: *CEP68* (Mahajan et al., 2018) and *SPRED2* (Xue et al., 2018) for 2p14; *CHUK* (Tsoi et al., 2017, Xue et al., 2018) for 10q24.31; *PRDX5* (Ellinghaus et al., 2012, Stuart et al., 2015) and *RPS6KA4* (Stuart et al., 2015) for 11q13.1; *MLX* (Mahajan et al., 2018), *PTRF* (Tsoi et al., 2012), *STAT3* (Tsoi et al., 2012, Xue et al., 2018), *STAT5A* (Tsoi et al., 2012) and *STAT5B* (Tsoi et al., 2012) for 17q21.2. The chromosome 2 locus has not previously been identified as genome-wide significant for psoriasis, although the surrounding D2S134 region has been suggested through linkage analysis (Trembath et al., 1997) ($p=0.0077$) and is a known locus for rheumatoid arthritis (Stahl et al., 2010) ($p=5.3x10^{-10}; OR=1.13$) and systemic lupus erythematosus (Bentham et al., 2015) ($p=2.3x10^{-8}; OR=1.20$). The chromosome 11 locus has not previously been identified as genome-wide significant for T2D, although it was previously shown to be genome-wide significant for alopecia areata (Betz et al., 2015) ($p=8.7x10^{-14}; OR=1.32$), primary biliary cirrhosis (Mells et al., 2011) ($p=2.1x10^{-10}; OR=1.23$), primary sclerosing cholangitis (Ji et al., 2017) ($p=2.2x10^{-13}; OR=1.20$), leprosy (Liu et al., 2015) ($p=8.8x10^{-14}; OR=1.24$), Crohn's disease (Franke et al., 2010) ($p=6.0x10^{-10}; OR=1.10$), multiple sclerosis (Beecham et al., 2013) ($p=2.0x10^{-9}; OR=1.07$), sarcoidosis (Fischer et al., 2012) ($p=3.2x10^{-8}; OR=1.32$), and vitiligo (Jin et al., 2016) ($p=4.81x10^{-8}; OR=1.15$).

Supplementary Note 2: Patient Identification

Patients from the Michigan Genomics Initiative (MGI) were identified as having a diagnosis of psoriasis and/or type 2 diabetes (T2D) if they had at least one of the following ICD9/10 codes, respectively:

Psoriasis: L40.0, L40.1, L40.2, L40.3, L40.4, L40.8, L40.9, L40.50, L40.52, L40.54, L40.53, L40.59, L40.51, 696.1, 696.0

T2D: E11.9, E11.22, E11.319, E11.65, E11.40, E11.42, E11.21, E11.8, E11.69, E11.621, E11.29, E11.59, E11.329, E11.359, E11.43, E11.311, E11.610, E11.49, E11.649, E11.51, E11.39, E11.351, E11.00, E11.622, E11.52, E11.331, E11.321, E11.41, E11.628, E11.339, E11.620, E11.341, E11.36, E11.01, E11.618, E11.44, E11.349, E11.638, E11.641, E11.630, E11, 250.00, 250.02, 250.60, 250.52, 250.50, 250.40, 250.80, 250.90, 250.70, 250.92, 250.62, 250.10, 250.82, 250.42, 250.72, 250.12, 250.20, 250.30, 250.22, 250.32

Supplementary Note 3: Trans-disease meta-analysis (TDMA)

$\beta_{PsV,T2D} = \frac{\beta_{PsV}+\beta_{T2D}}{2}$ $\quad V_{PsV,T2D} = \frac{V_{PsV}+V_{T2D}}{4}$ $\quad Z_{PsV,T2D} = \frac{\beta_{PsV,T2D}}{\sqrt{V_{PsV,T2D}}}$

β_{PsV} and β_{T2D} are the log odds-ratios for psoriasis vs. control and T2D vs. control meta-analyses, respectively; V_{PsV} and V_{T2D} are the corresponding variances. The meta-analysis effect size and variance equations were derived from a weighted sum with equal weight ($w = \frac{1}{2}$): $\beta_{PsV,T2D} = E(wPsV + wT2D) = wE(PsV) + wE(T2D) = \frac{\beta_{PsV}+\beta_{T2D}}{2}$; $V_{PsV,T2D} = Var(wPsV + wT2D) = Var(wPsV) + Var(wT2D) = w^2Var(PsV) + w^2Var(T2D) = \frac{V_{PsV}+V_{T2D}}{4}$.

Other approaches compared against: CCMA (Baurecht et al., 2016) (Compare and Contrast Meta-Analysis), RE2 (Han and Eskin, 2011) (random effects model), and ASSET (Bhattacharjee et al., 2012) (ASsociation analysis based on subSETs).

Colocalization: COLOC (Giambartolomei et al., 2014) tests the following hypotheses: H_0: no association with either trait; H_1: association with T2D, not with psoriasis; H_2: Association with psoriasis, not with T2D; H_3: association with both diseases, but with different causal variants; and H_4: association with both diseases with the same causal variant. We define the posterior probability of colocalization as the posterior probability of H_4. Psoriasis/T2D colocalization was compared between the loci identified by our approach and 59 other previously identified (Bowes et al., 2015, Patrick et al., 2018, Stuart et al., 2015, Tsoi et al., 2015, Tsoi et al., 2012, Tsoi et al., 2017, Yin et al., 2015) psoriasis loci more than 500kb away. The effect sizes and standard errors of markers within +-100kb of the lead marker for each locus were supplied as input to COLOC.

Supplementary Note 4: Locus interpretation

GARFIELD (Iotchkova et al., 2019) (GWAS Analysis of Regulatory or Functional Information Enrichment with LD correction) was used to perform enrichment analysis across >1,000 different chromatin marks and identify the cell types/tissues involved. As input data for the enrichment, all LD-independent markers (with and without the MHC) from the TDMA that were more significant than in both the individual meta-analyses were used. To further investigate the results illustrating enriched chromatin marks among immune cell types, we studied eQTLs from different databases to identify potential gene targets: eQTLGen (Võsa et al., 2018) (31,684 whole blood samples), the Gene Network blood eQTL browser (Westra et al., 2013) (5,311 peripheral blood samples), and the NESDA/NTR eQTL catalog (Jansen et al., 2017) (4,896 peripheral blood samples). We explored the impact our loci might have on these genes using results from two differential expression studies for psoriasis (58 lesional skin and 64 controls from Gudjonsson et al. (Gudjonsson et al., 2009); 28 lesional skin and 38 controls from Tsoi et al. (Tsoi et al., 2019)) in addition to four differential expression studies for type 2 diabetes: skeletal muscle (Wu et al., 2007) (15 T2D cases and 20 controls), pancreatic islets (Dominguez et al., 2011) (6 T2D cases and 7 controls), liver (Pihlajamaki et al., 2009) (4 T2D cases and 5 controls) and subcutaneous adipose (Soronen et al., 2012) under hyperinsulinemia (5 T2D cases and 5 controls). We investigated the physical interaction between the gene target enhancers and potential causal variants (from Bayesian credible sets with 95% confidence interval) using promoter capture Hi-C data in 7 tissues from 2 different sources (pancreas, adipose, liver, skeletal muscle, lymphoblastoid and thymus from Jung et al. (Jung et al., 2019) and keratinocytes from Rubin et al. (Rubin et al., 2017)). Finally, enrichment analysis was performed across protein-protein interaction (PPI) sets (Chen et al., 2012), to identify hub proteins connecting the gene targets from each locus.

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