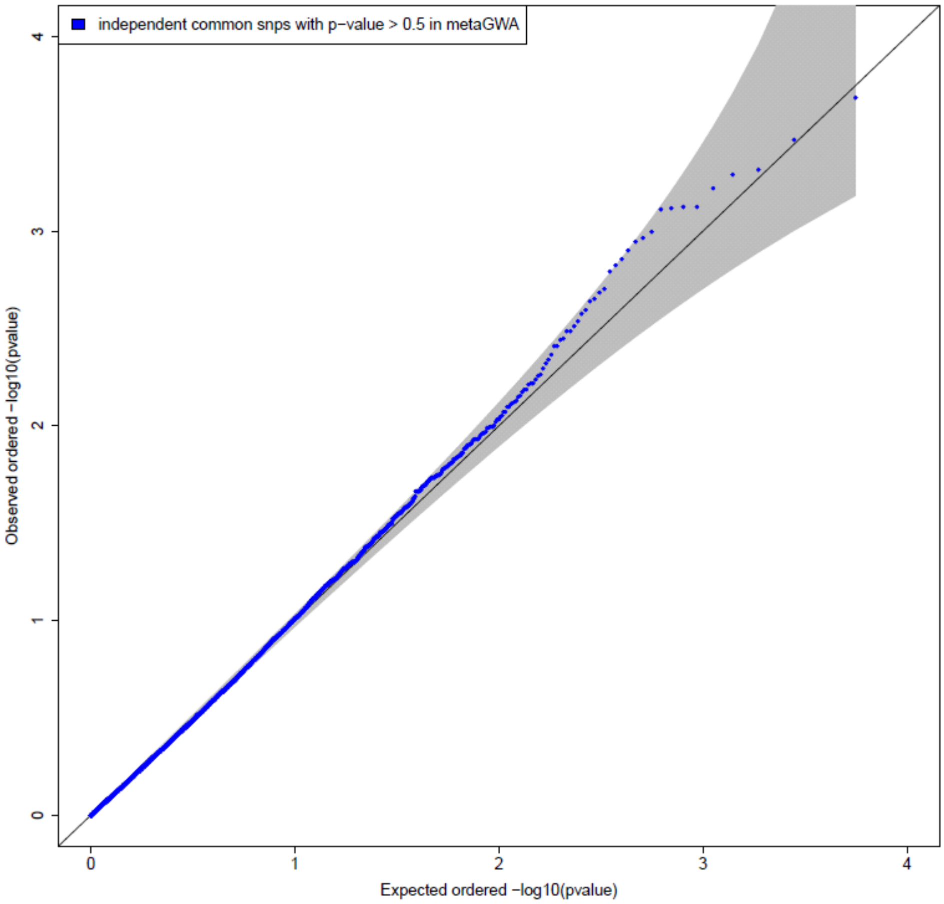
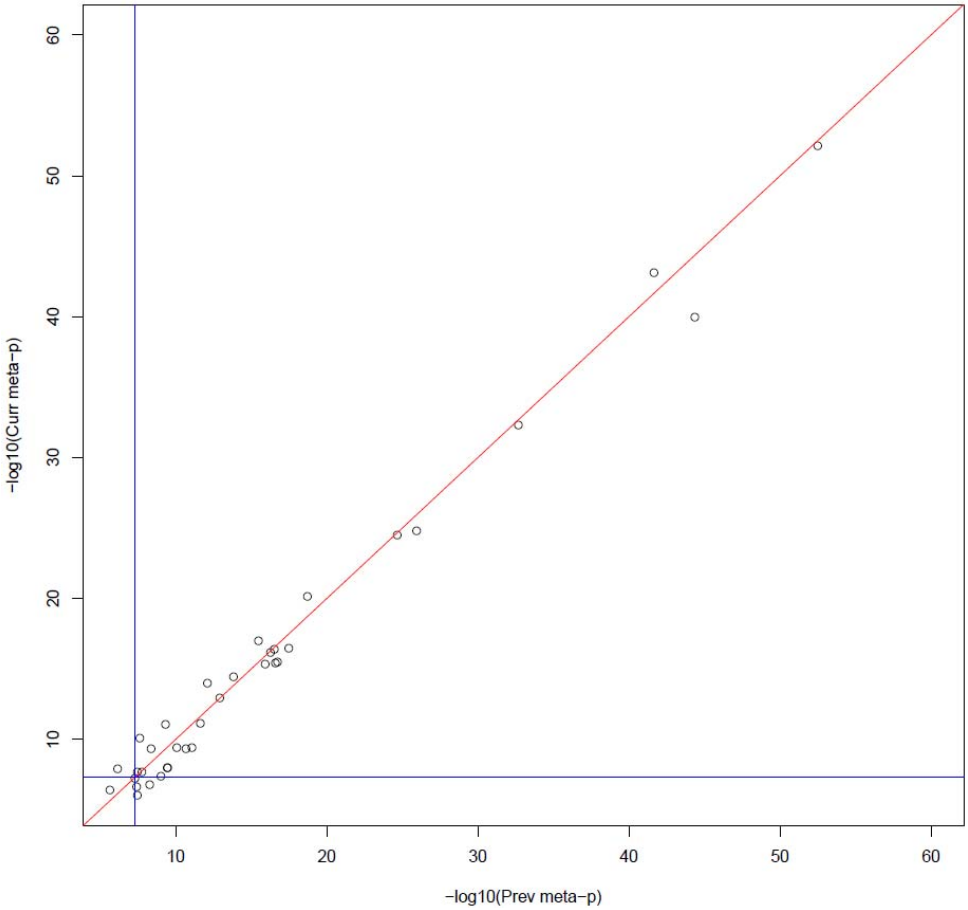
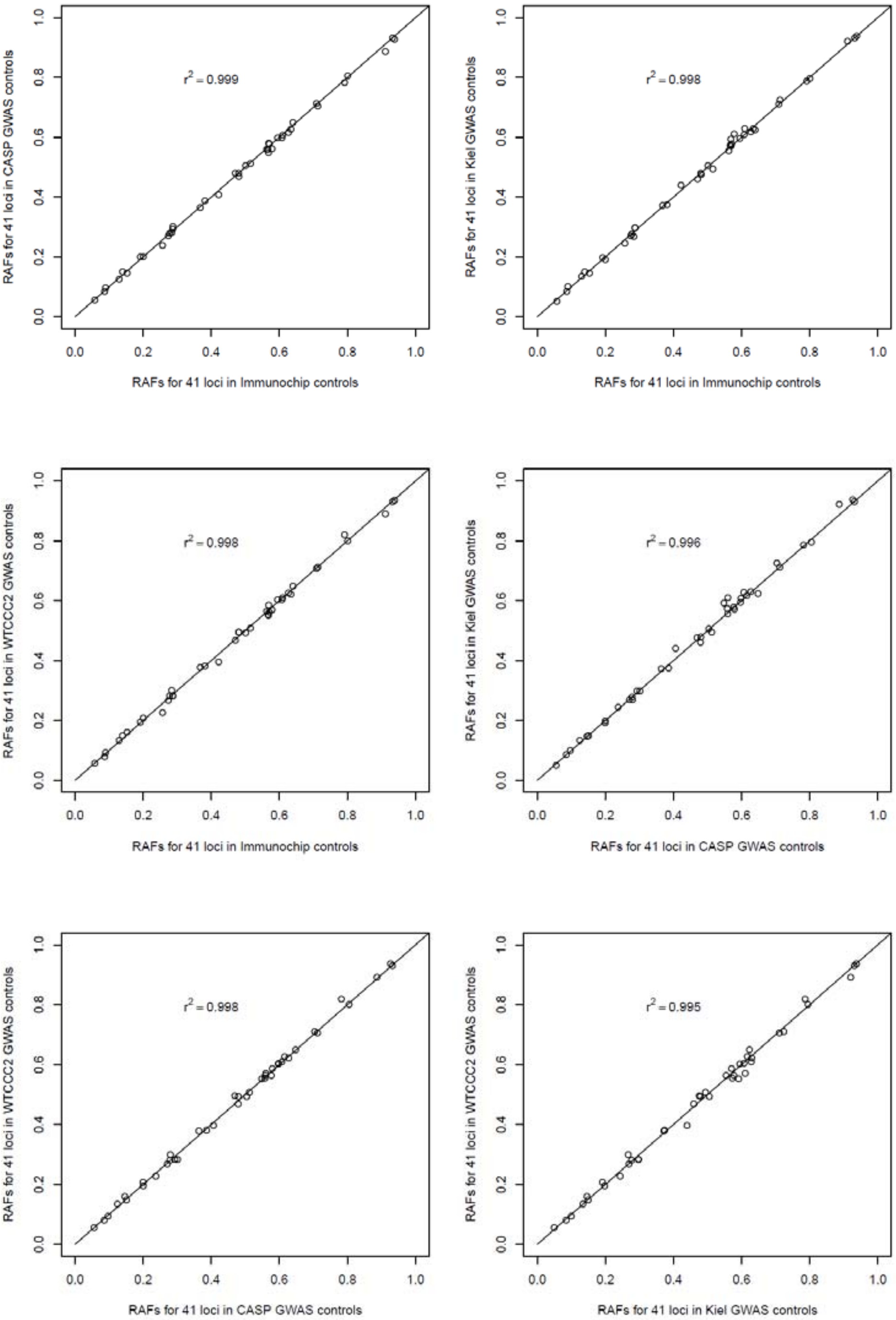
Supplementary Figures



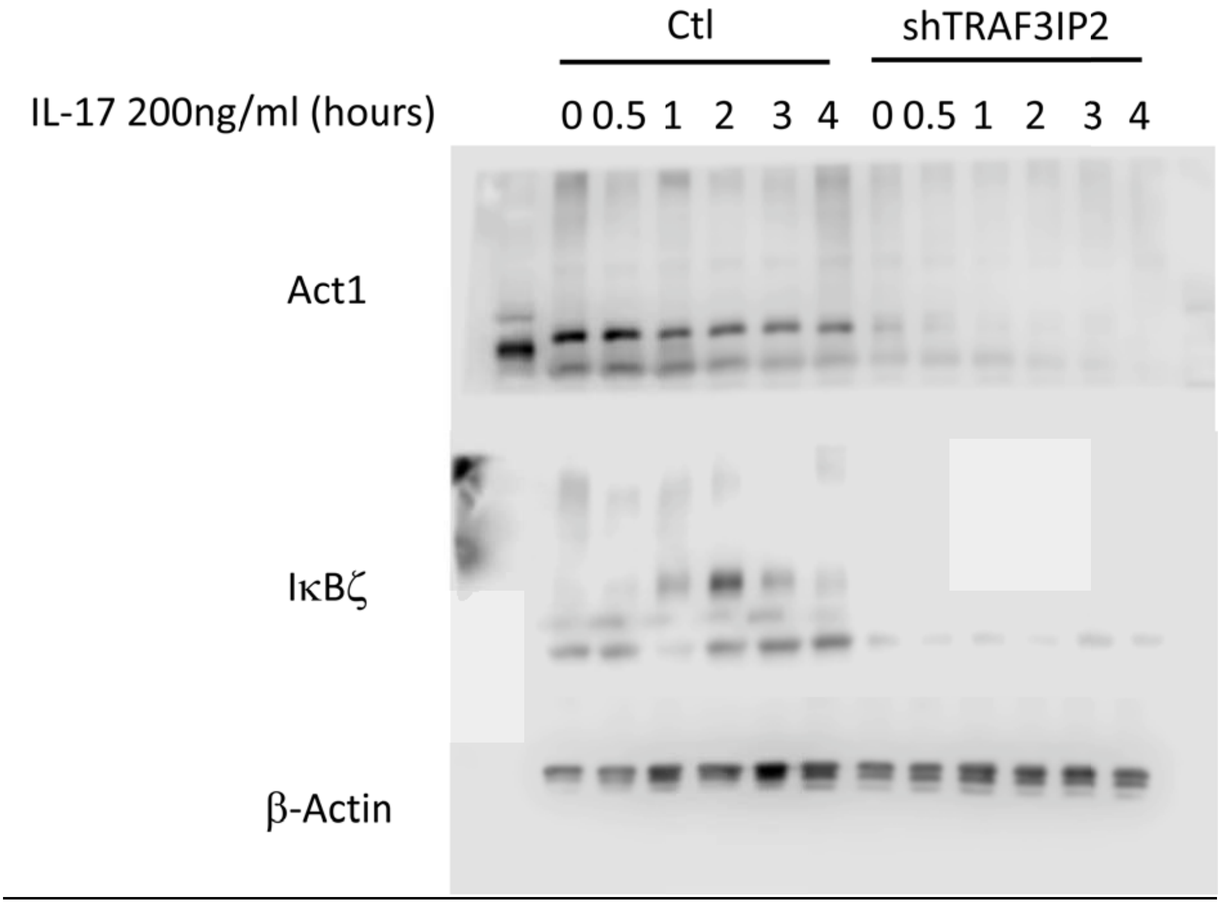
Supplementary Figure 1. Quantile-Quantile (Q-Q) plot for the association result of the combined Immunochip dataset (GAPC+PAGE). Only common (MAF≥1%) independent markers with $p^{\mathrm{GWA}} \geq 0.5$ were used. The genomic inflation factor was estimated to be 0.96, indicating the population stratification was well-adjusted.



Supplementary Figure 2. Comparison of p-values computed from the previous meta-analysis (x-axis) versus the current discovery meta-analysis (y-axis). Circles indicate the best markers from the known psoriasis loci identified in Tsoi et al., 2012. Blue lines represent genomewide significance level (5 x 10^{-8}).



Supplementary Figure 3. Pairwise comparisons of risk allele frequencies for the 41 known psoriasis loci between the controls of different studies.



Supplementary Figure 4. The uncropped scans for the Western blot analysis of time courses of IκB-zeta and Act1 expressions.

Supplementary Tables

Supplementary Table 1. The best signals from the novel loci identified in the current discovery meta-analysis and the original meta-analysis.

	Current best signal			Original best signal in the novel loci				
Region	**Current Best signal**	**Original meta p-value**	**Current meta P-value (effective sample size weighted)**	**Original best signal**	**Original meta P-value (effective sample size weighted)**	**Current meta p-value (effective sample size weighted)**	**Original Imm p-value (EMMAX)**	**Current Imm p-value (EMMAX)**
Intergenic	chr1:69788482	NA	1.43E-08	chr1:69779437	3.67E-07	1.73E-08	7.74E-05	9.69E-06
PLCL2 (intronic)	chr3:16996035	NA	8.58E-09	chr3:17019857	3.51E-07	5.09E-08	4.43E-04	3.51E-05
NFKBIZ (intronic)	chr3:101663555	NA	2.07E-09	chr3:10163564	8.02E-08	2.82E-09	8.02E-08	1.89E-09
Intergenic	chr5:40370724	NA	1.27E-08	chr5:40398923	5.14E-07	2.55E-08	7.30E-05	1.25E-05
CAMK2G (intronic)	chr10:75599127	NA	7.35E-09	chr10:75658349	1.25E-06	3.03E-07	7.29E-05	1.94E-05
AKAP13 (intronic)	chr15:86079115	NA	3.10E-08	chr15:86075417	1.28E-06	3.65E-08	1.08E-02	1.54E-03

Supplementary Table 2. Imputation quality, summary statistics, and heterogeneity p-values for the best signals identified in the loci reaching genomewide significance in the discovery meta-analysis.

	Immunochip (PAGE+GAPC): 6,268 cases and 14,172 controls					CASP GWAS: 1,352 cases and 1,389 controls					Kiel GWAS: 464 cases and 1,135 controls					WTCCC2: 2,178 cases and 5,175 controls					Meta	
	RAF					RAF					RAF					RAF						
	Case	Cont	r2	ORs	p (EMMAX)	Case	Cont	r2	ORs	p (logistic)	Case	Cont	r2	ORs	p (logistic)	Case	Cont	r2	ORs	p (logistic)	p (effective sample size weighted)	Het-p
chr1:69788482	0.295	0.257	0.82	1.11	9.30E-06	0.25	0.24	0.98	1.12	7.51E-02	0.26	0.24	0.99	1.12	2.18E-01	0.24	0.23	0.99	1.14	4.08E-03	1.43E-08	9.99E-01
chr3:16996035	0.493	0.481	0.88	1.12	2.16E-05	0.51	0.47	0.97	1.16	6.13E-03	0.50	0.48	0.96	1.09	2.91E-01	0.52	0.49	0.97	1.11	5.01E-03	8.58E-09	8.04E-01
chr3:101663555	0.829	0.801	0.77	1.17	2.34E-09	0.83	0.80	1.00	1.16	3.69E-02	0.80	0.80	0.99	1.05	6.21E-01	0.82	0.80	0.99	1.05	2.90E-01	2.07E-09	1.46E-01
chr5:40370724	0.929	0.911	0.91	1.16	5.83E-06	0.91	0.89	0.94	1.39	5.23E-04	0.94	0.92	0.90	1.45	2.35E-02	0.89	0.89	0.93	1.07	2.63E-01	1.27E-08	1.01E-01
chr10:75599127	0.575	0.563	0.70	1.12	1.83E-05	0.60	0.56	0.91	1.20	1.43E-03	0.60	0.55	0.99	1.20	2.45E-02	0.58	0.56	0.98	1.08	5.20E-02	7.35E-09	3.24E-01
chr15:86079115	0.370	0.349	0.93	1.06	1.23E-03	0.36	0.33	0.97	1.18	4.87E-03	0.38	0.36	0.99	1.17	7.23E-02	0.35	0.32	0.98	1.16	2.34E-04	3.10E-08	2.87E-01

Supplementary Table 3. Detailed results for the replication and combined association analysis of the novel loci.

Discovery meta-analysis				Replication																Combined	
3GWAS+Imm: 10,262 case+21,871controls				Exomechip 1: 913 cases+1,494 controls				Exomechip 2: 3,168 cases + 2,864 controls				PsA GWAS: 191 cases+356 controls				Genizon GWAS: 761 cases+993 controls				15,295 cases + 27,578 controls	
Marker	RA	ORs	P (effective sample size weighted)	Marker	RA	ORs	P (logistic)	Marker	RA	ORs	P (logistic)	Marker	RA	ORs	P (logistic)	Marker	RA	ORs	P (logistic)	MetaP (effective sample size weighted)	MetaDir
chr1:69788482	G	1.12	1.43E-08	NA	NA	NA	NA	NA	NA	NA	NA	chr1:69779437	T	1.16	3.01E-01	chr1:69779437	T	1.13	1.37E-01	2.76E-09	+??++
chr3:16996035	G	1.12	8.58E-09	chr3:17080974	A	1.24	3.63E-04	chr3:17080974	A	1.12	1.78E-03	chr3:17016794	A	1.10	4.39E-01	chr3:17019857	C	1.13	6.82E-02	7.23E-14	+++++
chr3:101663555	A	1.14	2.07E-09	chr3:101663555	A	1.20	2.14E-02	chr3:101663555	A	1.02	6.72E-01	chr3:101635645	G	1.38	5.47E-02	chr3:101635645	G	1.15	1.12E-01	1.66E-10	+++++
chr5:40370724	C	1.17	1.27E-08	chr5:40385142	T	1.08	5.08E-01	chr5:40385142	T	1.10	1.62E-01	chr5:40373134	T	1.02	9.25E-01	chr5:40379350	C	1.16	2.36E-01	5.68E-09	+++++
chr10:75599127	A	1.12	7.35E-09	chr10:75632760	T	1.12	6.03E-02	chr10:75632760	T	1.21	2.46E-07	chr10:75620757	T	1.18	2.01E-01	chr10:75632760	T	1.08	2.33E-01	1.58E-14	+++-+
chr15:86079115	G	1.10	3.10E-08	chr15:86075417	A	1.00	9.87E-01	chr15:86075417	G	1.01	8.69E-01	chr15:86054490	T	1.55	1.25E-03	chr15:86075417	A	1.01	8.61E-01	1.71E-06	+-+--
								Michigan Genotyping: 3,030 cases + 2,859 controls												14,996 cases + 27,217 controls	
								Marker	RA	ORs	P (logistic)										
chr3:16996035	G	1.12	8.58E-09	chr3:17080974	A	1.24	3.63E-04	chr3:16996035	G	1.12	9.20E-05					chr3:17019857	C	1.13	6.82E-02	8.95E-15	++++

Supplementary Table 4. Psoriasis susceptibility loci identified in European-origin (EUR), Chinese-origin (CHN), or both populations. The five novel loci identified in this study are marked with an asterisk(*).

Locus	Population	Notable nearby genes
1p36.23	EUR	*SLC45A1, TNFRSF9*
1p36	BOTH	*IL28RA*
1p36.11	EUR	*RUNX3*
1p31.3	BOTH	*IL23R*
1q31.1*	EUR	*LRRC7*
1q21.3	BOTH	*LCE3B, LCE3D*
2p16.1	EUR	*FLJ16341, REL*
2p15	EUR	*B3GNT2*
2q24	BOTH	*KCNH7, IFIH1*
3p24.3*	EUR	*PLCL2*
3q12.3*	EUR	*NFKBIZ*
4q24	CHN	*NFKB1*
5p13.1*	EUR	*PTGER4, CARD6*
5q15	BOTH	*ERAP1, LNPEP*
5q31.1	EUR	*IL13, IL4*
5q33.1	BOTH	*TNIP1*
5q33.3	BOTH	*IL12B*
5q33.3	CHN	*PTTG1*
6p25.3	EUR	*EXOC2, IRF4*
6p21	BOTH	*HLA-B, HLA-C*
6q21	EUR	*TRAF3IP2*
6q23.3	EUR	*TNFAIP3*
6q25.3	EUR	*TAGAP*
7p14.1	EUR	*ELMO1*
8p23.2	CHN	*CSMD1*
9p21.1	EUR	*DDX58*
9q31.2	EUR	*KLF4*
10q22.2*	EUR	*CAMK2G, FUT11*
10q22.3	EUR	*ZMIZ1*
11q13.1	EUR	*RPS6KA4, PRDX5*
11q22.3	EUR	*ZC3H12C*
11q24.3	EUR	*ETS1*
12p13.3	CHN	*CD27-LAG3*
12q13.3	EUR	*STAT2, IL23A*
13q12.11	CHN	*GJB2*
14q13	BOTH	*NFKBIA*
16p13.13	EUR	*PRM3, SOCS1*
16p11.2	EUR	*PRSS53, FBXL19*
17q11.2	EUR	*NOS2*
17q12	CHN	*IKZF3*
17q21.2	EUR	*PTRF, STAT3, STAT5A/B*
17q25.3	EUR	*CARD14*
18q21.2	EUR	*POL1, STARD6, MBD2*
18q22.1	CHN	*SERPINB8*
19p13.2	EUR	*TYK2*
19p13.2	EUR	*ILF3,CARM1*
19q13.41	CHN	*ZNF816A*
20q13.13	EUR	*RNF114*
22q11.21	EUR	*UBE2L3*

Supplementary Table 5. Genomic features from lymphoblastoids and keratinocytes overlapping with the identified novel loci.

Cell	Genomic Features		3p24.3	3q12.3	5p13.1	10q22.2
GM12878	Histone Modifications	H3K27ac	X	X		X
		H3K36me3	X			X
		H3K4me1	X	X	X	X
		H3K4me2	X	X	X	X
		H3K79me2	X			X
		H3K9me3	X	X	X	
		H4K20me1	X			X
		H3K4me3		X		X
		H3K9ac				X
	Transcription factor binding sites	BATF	X	X		X
		BCL11A	X	X		
		BCL3	X			
		IRF4	X	X		
		JunD	X			
		MEF2A	X			
		NFKB	X	X		
		RXRA	X			
		PU.1		X		
		EBF			X	
		EBF1			X	
NHEK	Histone Modifications	H3K36me3				X
		H3K4me3				X
		H3K27ac	X	X	X	X
		H3K4me1	X	X	X	X
		H3K4me2	X	X	X	X
		H3K9ac		X	X	X

Supplementary Table 6. Quality measurements for each dataset in the discovery meta-analysis.

	Sample call rate		Marker call rate				
	Avg	**Min**	**Avg**	**Min**	**Min MAF**	**# of markers**	**well-imputed and non-rare markers**
Immunochip	1.00	0.99	1.00	0.97	2.45E-05	170,637	759,972
CASP GWAS	0.99	0.96	0.99	0.95	9.50E-03	438,609	7,268,506
Kiel GWAS	1.00	0.95	1.00	0.95	1.94E-02	504,637	7,521,945
WTCCC2 GWAS	1.00	0.97	1.00	0.98	1.00E-02	528,089	7,597,164

Supplementary Note 1: Membership of Contributing Consortia

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