

SUPPLEMENTARY DATA

## **ONLINE\_SUPPLEMENTAL\_MATERIAL-**

### **AFAM\_V3\_CX01.DOCX**

#### **ONLINE SUPPLEMENTAL MATERIAL**

##### **Type 1 diabetes risk in African-ancestry participants and utility of an ancestry-specific genetic risk score**

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## SUPPLEMENTARY DATA

### INDEX:

### SUPPLEMENTARY TABLES:

**Supplementary Table 1.** Sample summary

**Supplementary Table 2.** Association results of type 1 diabetes-associated 99% credible SNPs in African-ancestry dataset (Uploaded as separate excel table)

**Supplementary Table 3.** HLA imputation accuracy

**Supplementary Table 4.** Quartiles for the sum of dosages across alleles by HLA locus

**Supplementary Table 5.** Associations of type 1 diabetes in African-ancestry populations with classical HLA alleles (Uploaded as separate excel table)

**Supplementary Table 6.** Fourteen HLA class II haplotypes independently associated with type 1 diabetes risk in African-ancestry populations

**Supplementary Table 7.** Type 1 diabetes-associated SNPs included in the African-ancestry genetic risk score (GRS) with weights; the “effect allele” is the risk increasing allele on the positive strand.

### SUPPLEMENTARY FIGURE:

**Supplementary Figure 1.** Principal component analysis (PCA) in African-ancestry type 1 diabetes cases and controls projected on HapMap 3 coordinates.

**Supplementary Figure 2.** Performance of different type 1 diabetes prediction models

### **Complete list of the members of the Type 1 Diabetes Genetics Consortium and SEARCH for Diabetes in Youth Study**

List of members of the Type 1 Diabetes Genetics Consortium (T1DGC)

List of members of the SEARCH for Diabetes in Youth Study

SUPPLEMENTARY DATA

SUPPLEMENTARY TABLES:

**Supplementary Table 1.** Sample summary

Cohort*	Total	Case			Control	
	Number of participants (n)	n	Male n (%)	Age at diagnosis†	n	Male n (%)
BDC	101	59	24 (40.7)	10 (2-22) ‡	42	17 (40.5)
CLEAR	368	-	-	-	368	105 (28.5)
GoKinD	41	41	17 (41.5)	13 (5-30)	-	-
NYCP	801	-	-	-	801	173 (21.6)
SEARCH	255	255	112 (43.9)	9 (0-19)	-	-
T1DGC	1262	666	290 (43.5)	9 (1-40) §	596	160 (26.9)
UAB	659	-	-	-	659	176 (26.7)
UCSF	462	-	-	-	462	160 (34.6)
<b>Overall</b>	3949	1021	449	9 (0-40)	2928	785

\* Description of cohort abbreviations: BDC = Barbara Davis Center (18); CLEAR = Consortium for the Longitudinal Evaluation of African Americans with Early Rheumatoid Arthritis (19); GoKinD = Genetics of Kidneys in Diabetes (17); NYCP = New York Control Population (20); SEARCH = SEARCH for Diabetes in Youth study (16); T1DGC = Type 1 Diabetes Genetics Consortium (15); UAB = University of Alabama at Birmingham (21); UCSF = University of California, San Francisco (22).

† Age at diagnosis, data are presented as median age in years (range).

‡ Age at diagnosis is missing for 17 participants

§ Age at diagnosis is missing for 1 participant

## SUPPLEMENTARY DATA

**Supplementary Table 2.** Association results of type 1 diabetes associated 99% credible SNPs in African-ancestry dataset (Uploaded as separate excel table,

<https://virginia.box.com/s/fqqig93jwkuj946hs44u8hqjinivp389>)

**Supplementary Table 3.** HLA imputation accuracy

<b>HLA</b>	<b>2-digit</b>	<b>4-digit</b>
<b>Locus</b>	<b>accuracy</b>	<b>accuracy</b>
A	0.964	0.916
B	0.944	0.855
C	0.998	0.946
DPA1	0.996	0.959
DPB1	0.934	0.933
DQA1	0.991	0.99
DQB1	0.996	0.973
DRB1	0.945	0.882

(indicate that 2-digit = 1 field; 4-digit = 2 fields)

SUPPLEMENTARY DATA

**Supplementary Table 4.** Quartiles for the sum of dosages across alleles by HLA locus

Locus	q2.5	q50	q97.5.
A	2	2	2.39
B	1.89	2	2.17
C	2	2	2.18
DQA1	2	2	2
DQB1	2	2	2
DRB1	1.91	2	2.06
DPA1	2	2	2.01
DPB1	1.94	2	2.06
Combined	1.98	2	2.06

**Supplementary Table 5.** Associations of type 1 diabetes in African-ancestry populations with classical HLA alleles (Uploaded as separate excel table, <https://virginia.box.com/s/9nmreisywe8pfrhlfr5v533xjfzzph08>)

SUPPLEMENTARY DATA

**Supplementary Table 6.** Fifteen HLA class II haplotypes are independently associated with T1D in African Americans

DRB1	DQA1	DQB1	OR	P
03:01	05:01	02:01	3.74	4.7x10 <sup>-49</sup>
09:01	03:01	02:01	5.75	2.5x10 <sup>-34</sup>
04:05	03:01	03:02	7.66	9.6x10 <sup>-32</sup>
04:01	03:01	03:02	6.66	4.1x10 <sup>-26</sup>
07:01	03:01	02:01	4.69	6.4x10 <sup>-15</sup>
04:04	03:01	03:02	3.73	4.5x10 <sup>-09</sup>
15:03	01:02	06:02	0.21	5.6x10 <sup>-15</sup>
03:02	04:01	04:02	0.2	6.5x10 <sup>-10</sup>
15:01	01:02	06:02	0.08	1.5x10 <sup>-06</sup>
11:01	01:02	06:02	0.14	6.0x10 <sup>-07</sup>
11:01	05:01	03:01	0.25	3.1x10 <sup>-08</sup>
08:04	04:01	03:01	0.35	1.0x10 <sup>-04</sup>
10:01	01:01	05:01	0.34	8.3x10 <sup>-04</sup>
13:01	01:03	06:03	0.48	9.9x10 <sup>-04</sup>
14:01	01:01	05:03	0.17	4.8x10 <sup>-03</sup>

Odds ratios (OR) and *P*-values generated by multivariable logistic regression of T1D risk, including 2 principal components, sex, and all 15 alleles as independent variables. Significance evaluated at a  $P < 1.5 \times 10^{-3}$  threshold (Bonferroni correction at family-wise error rate of 0.05 given  $\leq 33$  haplotypes tested at each round of conditional analysis).

SUPPLEMENTARY DATA

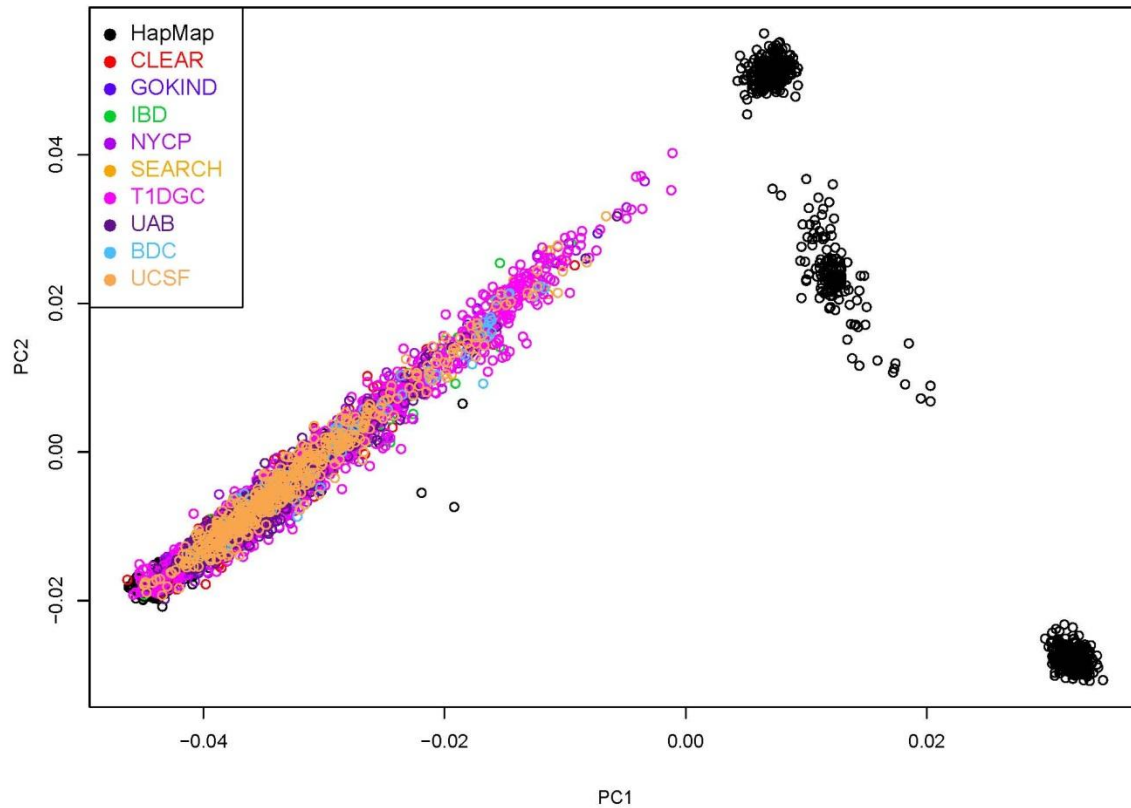
**Supplementary Table 7** – Type 1 diabetes-associated SNPs included in the African-ancestry genetic risk score

(GRS) with weights; the “effect allele” is the risk increasing allele on the positive strand

<b>SNP</b>	<b>Chr</b>	<b>Position (bp)</b>	<b>Effect Allele</b>	<b>Effect Allele Frequency</b>	<b>Odds Ratio (OR)</b>	<b>Weight</b>
rs34303755	6	32450613	C	0.216	2.94	1.079
rs34850435	6	32583299	T	0.345	2.31	0.839
rs9271594	6	32591213	G	0.095	6.06	1.801
rs2187668	6	32605884	T	0.076	3.93	1.367
rs9273363	6	32626272	A	0.131	5.48	1.702
rs689	11	2182224	T	0.265	1.50	0.403
rs2290400	17	38066240	C	0.459	1.34	0.295

SUPPLEMENTARY DATA  
SUPPLEMENTARY FIGURE:

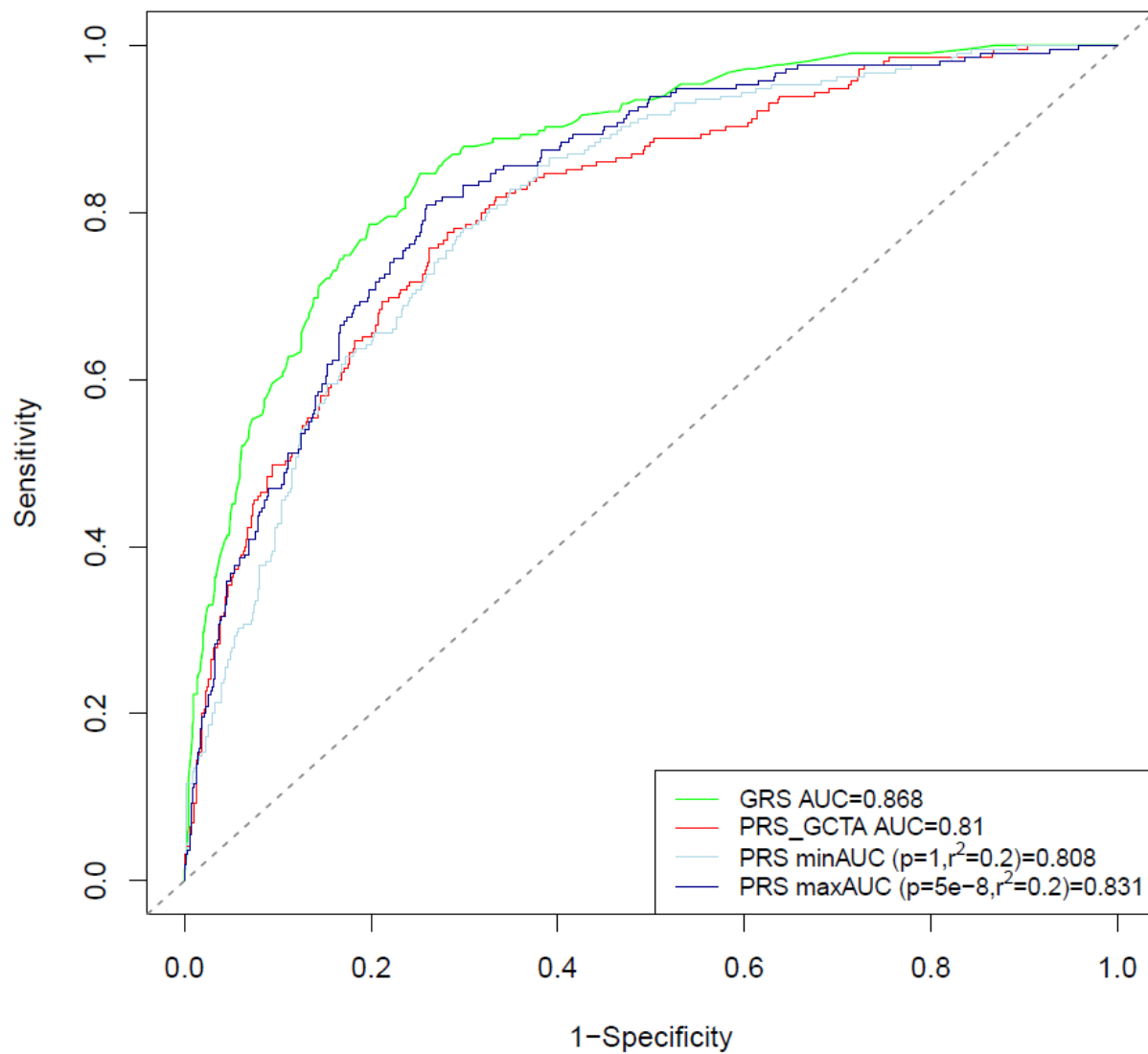
**Supplementary Figure 1.** Principal component analysis (PCA) in African-ancestry type 1 diabetes cases and controls projected on HapMap 3 coordinates.





**Supplementary Figure 2.** Performance of different type 1 diabetes prediction models

### T1D Prediction in One Cross Validation Dataset



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