## <u>Data Dictionary – GRS and Ancestry TGD Lab Pipeline</u>

- IID Sample identifier TGD
- RRID Sample identifier from original study
- SuperPopulationClass classified primary super population ancestry
- PopulationClass classified primary subpopulation ancestry
- 1\_AFR probability of super population ancestry (AFR=African)
- 1\_AMR probability of super population ancestry (AMR=Admixed Americans)
- 1\_EAS probability of super population ancestry (EAS=East Asians)
- 1\_EUR probability of super population ancestry (EUR=Europeans)
- 1\_SAS probability of super population ancestry (SAS=South Asians)
- 2\_ACB probability of population ancestry (ACB=African Carribean)
- 2\_ASW probability of population ancestry (ASW=African Ancestry Southwest US)
- 2\_BEB probability of population ancestry (BEB=Bengali)
- 2\_CDX probability of population ancestry (CDX=Dai Chinese)
- 2\_CEU probability of population ancestry (CEU=Utah European)
- 2 CHB probability of population ancestry (CHB=Han Chinese)
- 2 CHS probability of population ancestry (CHS=Southern Han Chinese)
- 2\_CLM probability of population ancestry (CLM=Colombian)
- 2 ESN probability of population ancestry (ESN=Esan Nigerian)
- 2 FIN probability of population ancestry (FIN=Finnish)
- 2 GBR probability of population ancestry (GBR=British)
- 2 GIH probability of population ancestry (GIH=Gujurati Indian)
- 2\_GWD probability of population ancestry (GWD=Gambian Mandinka)
- 2\_IBS probability of population ancestry (IBS=Iberian Spanish)
- 2\_ITU probability of population ancestry (ITU=Telugu Indian)
- 2 JPT probability of population ancestry (JPT=Japanese)
- 2 KHV probability of population ancestry (KHV=Kinh Vietnamese)
- 2\_LWK probability of population ancestry (LWK=Luhya Kenyan)
- 2\_MSL probability of population ancestry (MSL=Mende Sierra Leone)
- 2 MXL probability of population ancestry (MXL=Mexican American)

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2_PEL – probability of population ancestry (PEL=Peruvian)
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- 2\_PJL probability of population ancestry (PJB=Punjabi)
- 2\_PUR probability of population ancestry (PUR=Puerto Rican)
- 2\_STU probability of population ancestry (STU=Tamil Sri Lankan)
- 2 TSI probability of population ancestry (TSI=Toscani Italian)
- 2\_YRI probability of population ancestry (YRI=Yoruba Nigerian)

HLA\_DR/DQ - Sum of T1D risk at at HLA-DR/DQ haplotypes with interaction model

HLA\_Class\_1 – Sum of T1D risk at HLA class 1 alleles

HLA\_Class\_2 - Sum of T1D risk at HLA class 2 excluding DR/DQ haplotypes

Non-HLA – Sum of T1D risk at from variants outside the HLA region, genome-wide

T1D-GRS – Complete T1D genetic risk score (67 variants, Sharp et al)

T2D-GRS – Complete T2D genetic risk score (338 variants, Mahajan et al)

BETA\_CELL – Partitioned risk score cluster encoding beta cell variants (DiCorpo et al)

PROINSULIN – Cluster encoding proinsulin action variants (DiCorpo et al)

OBESITY – Cluster encoding obesity related variants (DiCorpo et al)

LIPODYSTROPHY - Cluster encoding lipodystrophy related variants (DiCorpo et al)

LIVER\_LIPID – Cluster encoding liver / lipid related variants (DiCorpo et al)

T1D-GRS% – Centile of risk T1D-GRS, derived relative to all samples in the file

T2D-GRS% – Centile of risk T2D-GRS, derived relative to all samples in the file

T1D-GRS\_norm – T1D-GRS min-max scaled relative to all samples in the file

T2D-GRS\_norm - T2D-GRS min-max scaled relative to all samples in the file