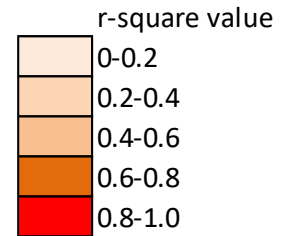


TBX15-WARS2 locus



		Sex-combined	Female	Male	Index & Trans-ethnic	AA discovery
		rs12096179	rs6701378	rs7412918	rs984222	rs10923714
Sex-combined	rs12096179		1.00 (1.00)	0.27 (1.00)	0.33 (0.92)	0.67 (0.91)
Female	rs6701378	1.00 (1.00)		0.27 (1.00)	0.33 (0.92)	0.67 (0.91)
Male	rs7412918	0.27 (1.00)	0.27 (1.00)		0.24 (0.58)	0.15 (0.66)
Index & Trans-ethnic	rs984222	0.33 (0.92)	0.33 (0.92)	0.24 (0.58)		0.48 (1.00)
AA discovery	rs10923714	0.67 (0.91)	0.67 (0.91)	0.15 (0.66)	0.48 (1.00)	

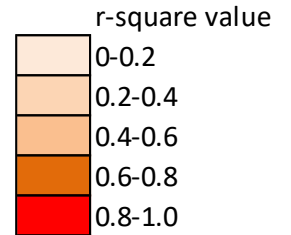
r² (D') using 1000G CEU as reference sample

		Sex-combined	Female	Male	Index & Trans-ethnic	AA discovery
		rs12096179	rs6701378	rs7412918	rs984222	rs10923714
Sex-combined	rs12096179		1.00 (1.00)	0.21 (0.88)	0.37 (0.77)	0.23 (0.89)
Female	rs6701378	1.00 (1.00)		0.21 (0.88)	0.37 (0.77)	0.23 (0.89)
Male	rs7412918	0.21 (0.88)	0.21 (0.88)		0.10 (0.85)	0.08 (1.00)
Index & Trans-ethnic	rs984222	0.37 (0.77)	0.37 (0.77)	0.10 (0.85)		0.49 (1.00)
AA discovery	rs10923714	0.23 (0.89)	0.23 (0.89)	0.08 (1.00)	0.49 (1.00)	

r² (D') using 1000G YRI or ARIC AA as reference sample

Supplementary Figure 8a. LD heat plot of lead SNPs identified from the sex-combined, female-only, male-only meta-analyses in the current study in addition to all previous SNPs identified also from the *TBX15-WARS2* locus from other studies. Top plot shows r²(D') between each SNP pair using the 1000G CEU reference population, and the bottom plot shows r²(D') between each SNP pair using 1000G YRI as reference.

GRB14 locus



		Sex-combined & Index	Female & Dimorphism	AA discovery & Extremes	Trans-ethnic
		rs10195252	rs6717858	rs13389219	rs1128249
Sex-combined & Index	rs10195252				
Female & Dimorphism	rs6717858	0.87 (0.93)			
AA discovery & Extremes	rs13389219	0.93 (1.00)	0.93 (1.00)		
Trans-ethnic	rs1128249	0.93 (1.00)	0.93 (1.00)	1.00 (1.00)	

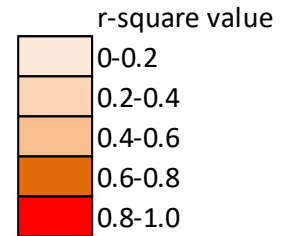
r² (D') using 1000G CEU as reference sample

		Sex-combined & Index	Female & Dimorphism	AA discovery & Extremes	Trans-ethnic
		rs10195252	rs6717858	rs13389219	rs1128249
Sex-combined & Index	rs10195252				
Female & Dimorphism	rs6717858	1.00 (1.00)			
AA discovery & Extremes	rs13389219	1.00 (1.00)	1.00 (1.00)		
Trans-ethnic	rs1128249	1.00 (1.00)	1.00 (1.00)	1.00 (1.00)	

r² (D') using 1000G YRI or ARIC AA as reference sample

Supplementary Figure 8b. LD heat plot of lead SNPs identified from the sex-combined, female-only, male-only meta-analyses in the current study in addition to all previous SNPs identified also from the *GRB14* locus from other studies. Top plot shows r²(D') between each SNP pair using the 1000G CEU reference population, and the bottom plot shows r²(D') between each SNP pair using 1000G YRI as reference.

ADAMTS9 locus



		Sex-combined & Female	Index	AA discovery	Trans-ethnic
		rs2059092	rs6795735	rs13060013	rs4132228
Sex-combined & Female	rs2059092		0.06 (1.00)	0.01 (1.00)	0.06 (1.00)
Index	rs6795735	0.06 (1.00)		0.33 (1.00)	0.39 (1.00)
AA discovery	rs13060013	0.01 (1.00)	0.33 (1.00)		0.01 (0.23)
Trans-ethnic	rs4132228	0.06 (1.00)	0.39 (1.00)	0.01 (0.23)	

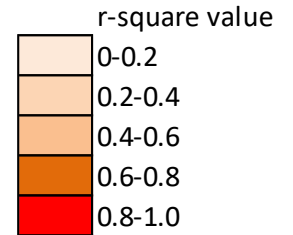
r2 (D') using 1000G CEU as reference sample

		Sex-combined & Female	Index	AA discovery	Trans-ethnic
		rs2059092	rs6795735	rs13060013	rs4132228
Sex-combined & Female	rs2059092		0.09 (1.00)	0.28 (1.00)	0.26 (0.90)
Index	rs6795735	0.09 (1.00)		0.01 (0.45)	0.11 (1.00)
AA discovery	rs13060013	0.28 (1.00)	0.01 (0.45)		0.68 (0.87)
Trans-ethnic	rs4132228	0.26 (0.90)	0.11 (1.00)	0.68 (0.87)	

r2 (D') using 1000G YRI or ARIC AA as reference sample

Supplementary Figure 8c. LD heat plot of lead SNPs identified from the sex-combined, female-only, male-only meta-analyses in the current study in addition to all previous SNPs identified also from the *ADAMTS9* locus from other studies. Top plot shows $r^2(D')$ between each SNP pair using the 1000G CEU reference population, and the bottom plot shows $r^2(D')$ between each SNP pair using 1000G YRI as reference.

RSPO3 locus



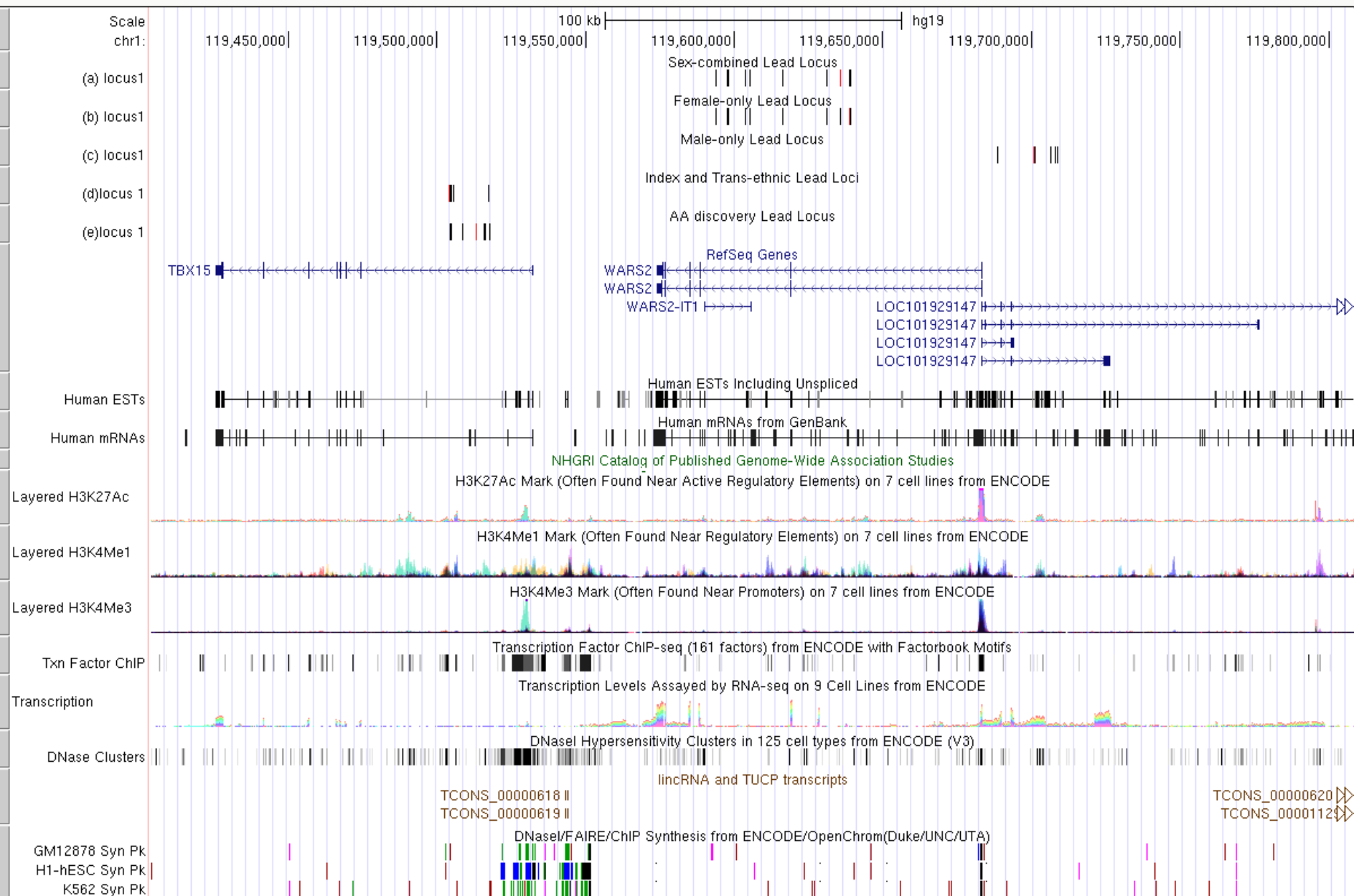
		Sex-combined	Female & Index	AA discovery	Trans-ethnic	Dimorphism	Extremes
		rs9321069	rs9491696	rs1936806	rs7766106	rs1936805	rs7745274
Sex-combined	rs9321069						
Female & Index	rs9491696	0.37 (0.74)					
AA discovery	rs1936806	0.30 (0.71)	0.88 (1.00)				
Trans-ethnic	rs7766106	0.39 (0.75)	0.97 (1.00)	0.85 (1.00)			
Dimorphism	rs1936805	0.39 (0.75)	0.97 (1.00)	0.85 (1.00)	1.00 (1.00)		
Extremes	rs7745274	0.41 (0.70)	0.79 (1.00)	0.69 (1.00)	0.82 (1.00)	0.82 (1.00)	

r² (D') using 1000G CEU as reference sample

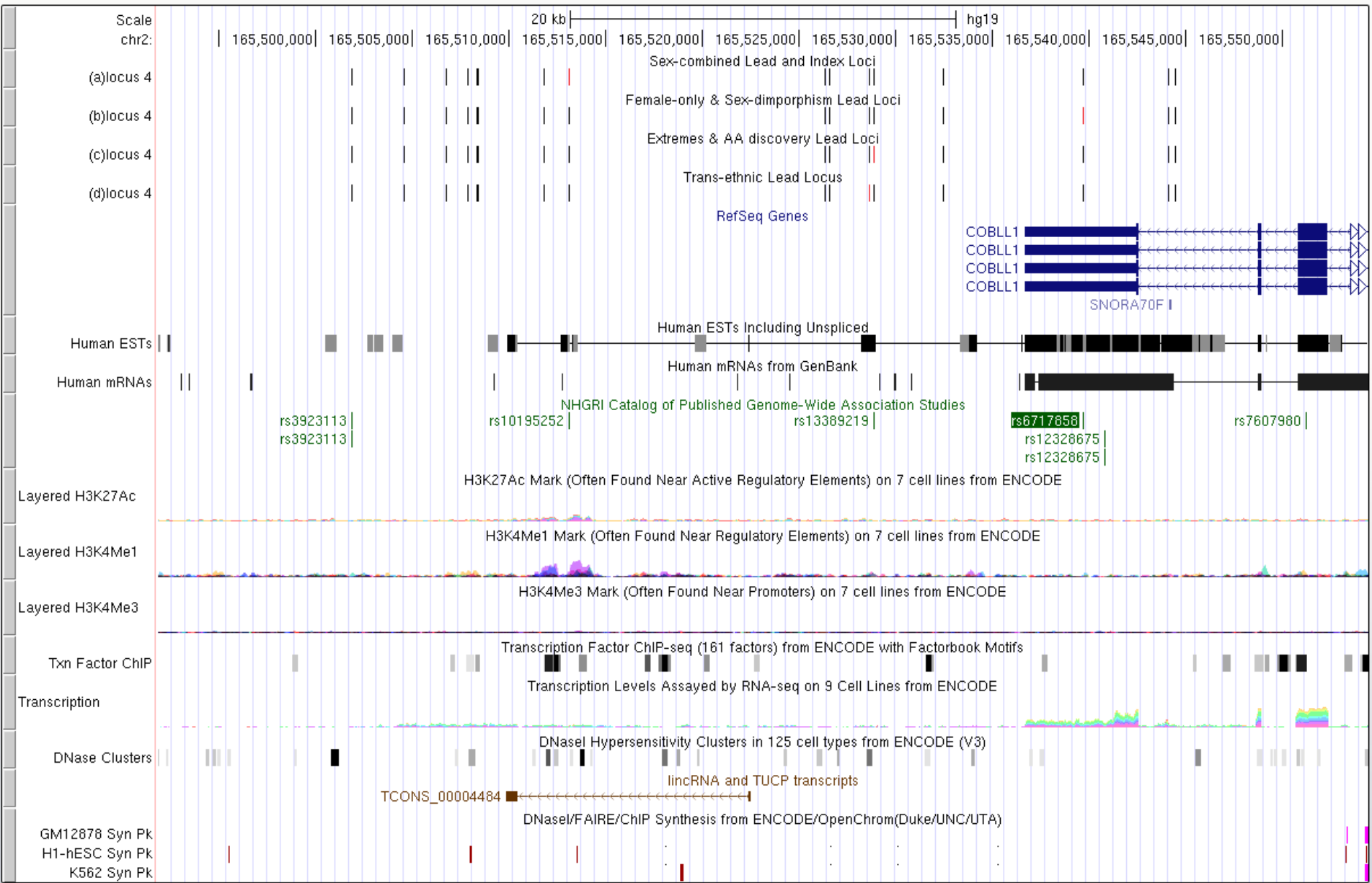
		Sex-combined	Female & Index	AA discovery	Trans-ethnic	Dimorphism	Extremes
		rs9321069	rs9491696	rs1936806	rs7766106	rs1936805	rs7745274
Sex-combined	rs9321069						
Female & Index	rs9491696	0.07 (0.43)					
AA discovery	rs1936806	0.08 (0.62)	0.52 (1.00)				
Trans-ethnic	rs7766106	0.08 (0.48)	0.77 (0.92)	0.58 (1.00)			
Dimorphism	rs1936805	0.18 (0.43)	0.42 (1.00)	0.22 (1.00)	0.58 (1.00)		
Extremes	rs7745274	0.14 (0.39)	0.32 (0.86)	0.22 (1.00)	0.33 (0.93)	0.66 (0.81)	

r² (D') using 1000G YRI or ARIC AA as reference sample

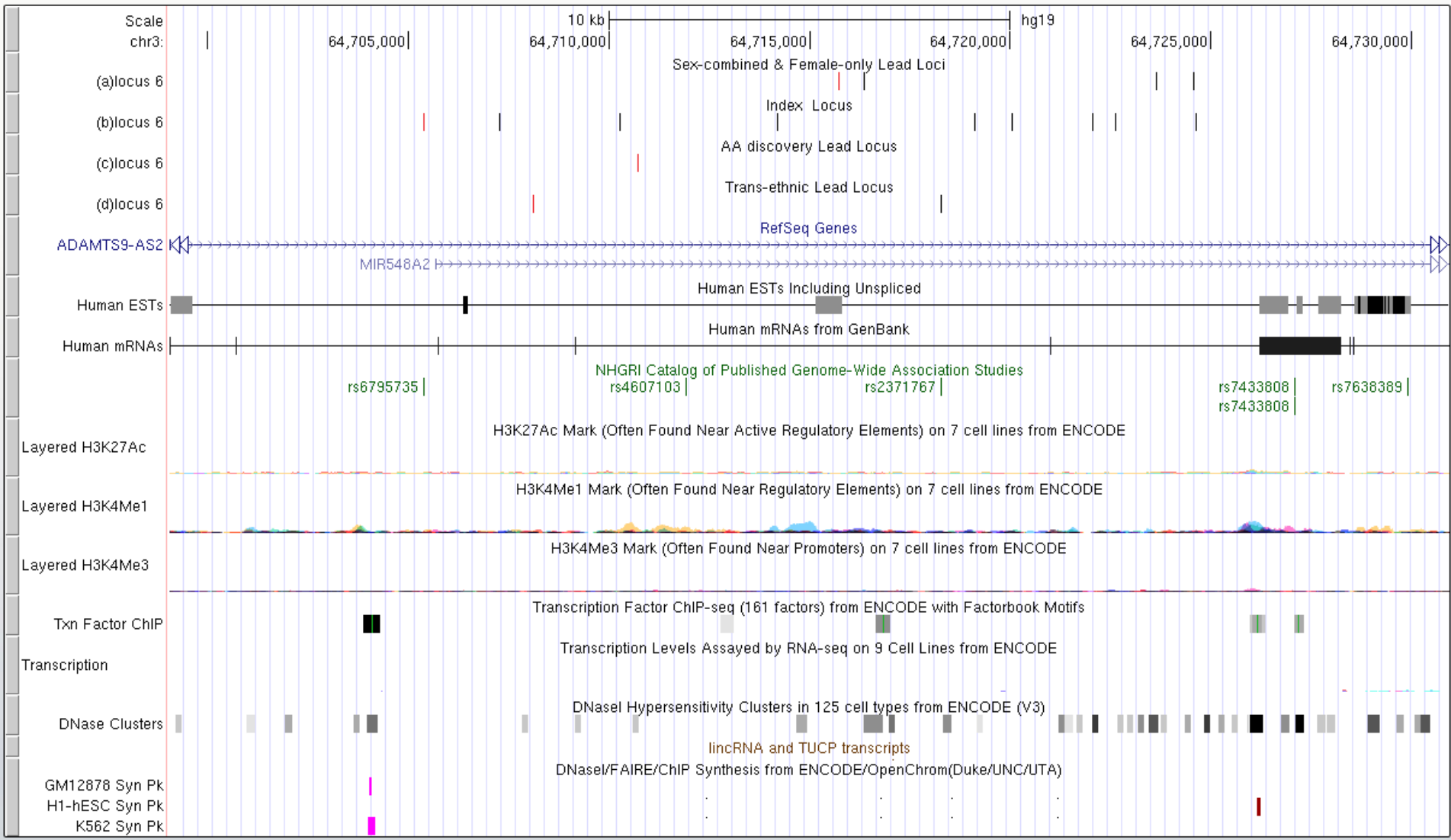
Supplementary Figure 8d. LD heat plot of lead SNPs identified from the sex-combined, female-only, male-only meta-analyses in the current study in addition to all previous SNPs identified also from the *RSPO3* locus from other studies. Top plot shows r²(D') between each SNP pair using the 1000G CEU reference population, and the bottom plot shows r²(D') between each SNP pair using 1000G YRI as reference.



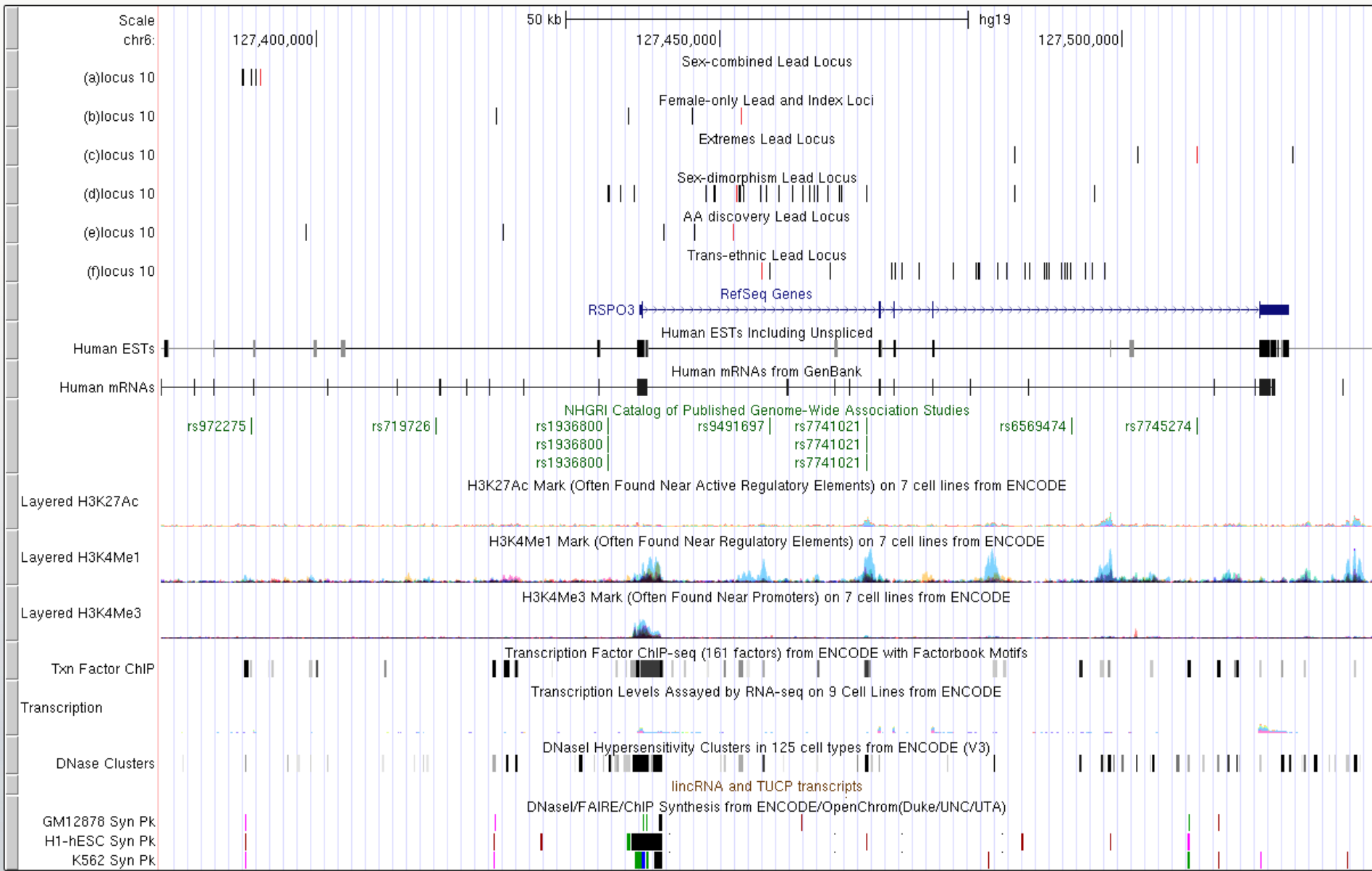
Supplementary Figure 9. Visualization of the *TBX15*-*WARS2* locus using the UCSC genome browser. Top tracks show lead SNPs from current and previous studies. The lead SNP is shown in a red vertical bar. All SNPs in r^2 of 0.8 or higher with the lead SNP using 1000G YRI is shown in black vertical bars.



Supplementary Figure 10. Visualization of the *GRB14* locus using the UCSC genome browser. Top tracks show lead SNPs from current and previous studies. The lead SNP is shown in a red vertical bar. All SNPs in r^2 of 0.8 or higher with the lead SNP using 1000G YRI is shown in black vertical bars.



Supplementary Figure 11. Visualization of the *ADAMTS9* locus using the UCSC genome browser. Top tracks show lead SNPs from current and previous studies. The lead SNP is shown in a red vertical bar. All SNPs in r^2 of 0.8 or higher with the lead SNP using 1000G YRI is shown in black vertical bars.



Supplementary Figure 12. Visualization of the *RSPO3* locus using the UCSC genome browser. Top tracks show lead SNPs from current and previous studies. The lead SNP is shown in a red vertical bar. All SNPs in r^2 of 0.8 or higher with the lead SNP using 1000G YRI is shown in black vertical bars.