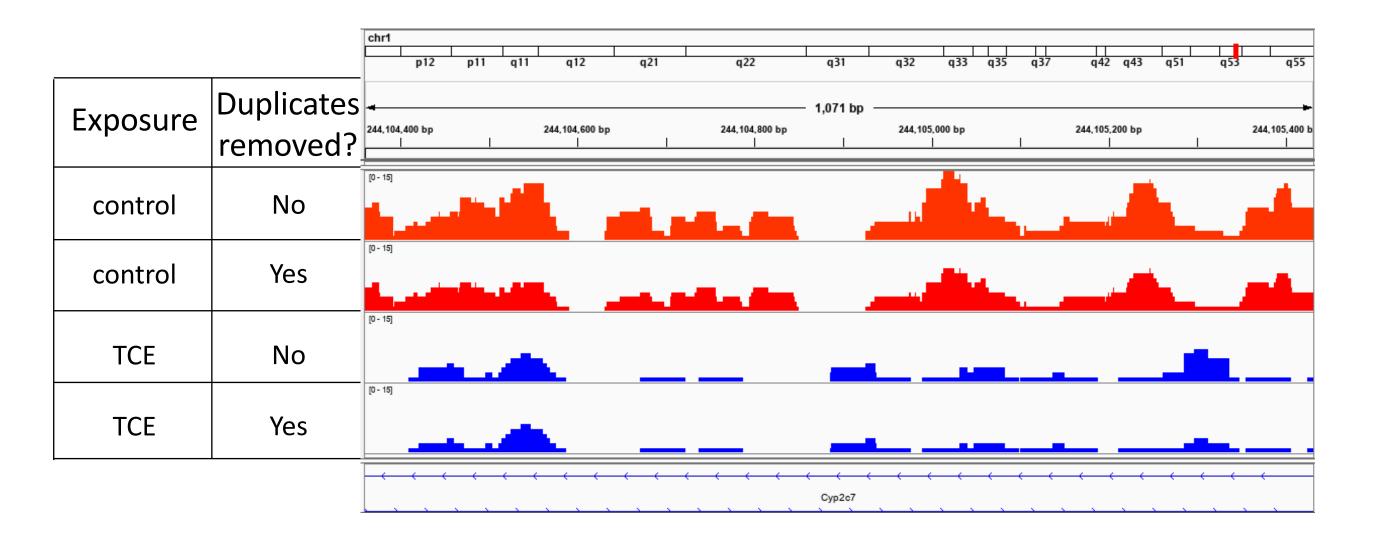
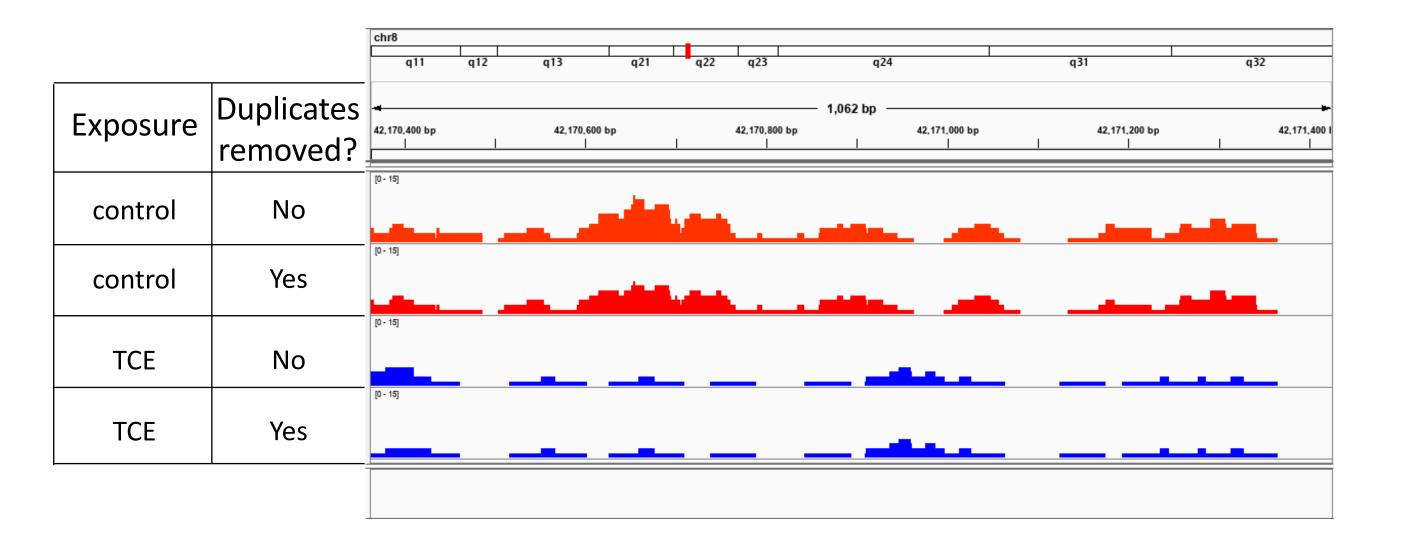
Trichloroethylene exposure alters dimethylated histone three lysine four in protein kinase A signaling pathway chromatin of rat sperm.

Stermer, AR, Wilson, SK, Klein, D, Hall, SJ, and Boekelheide, K.

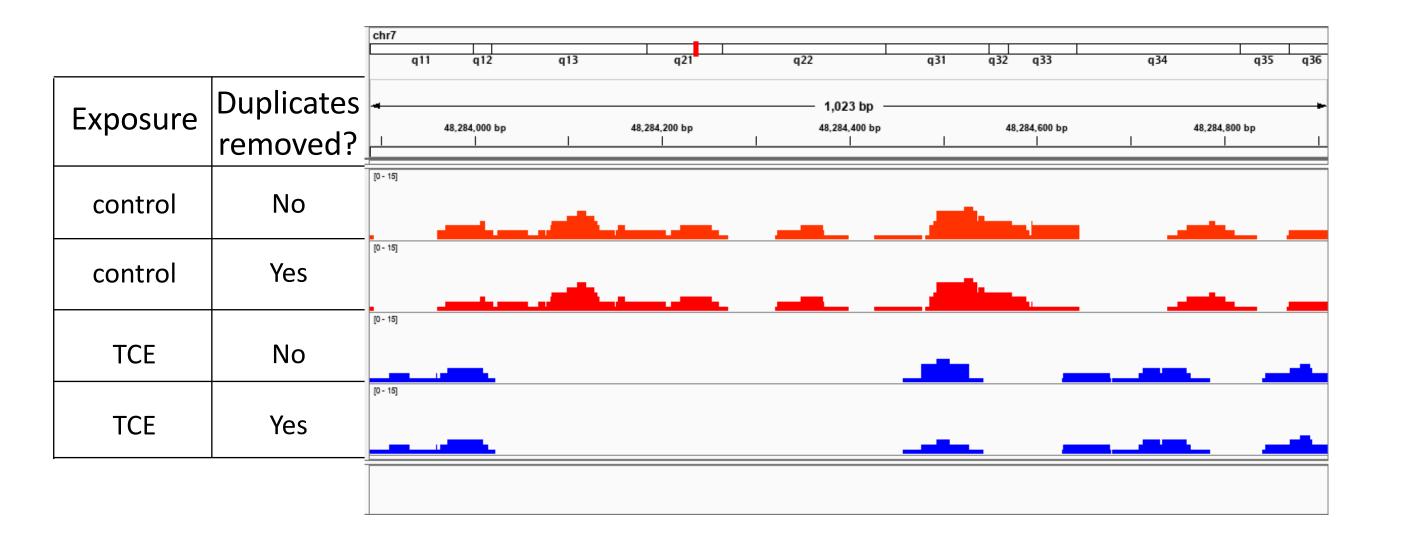
11 pages, 10 figures



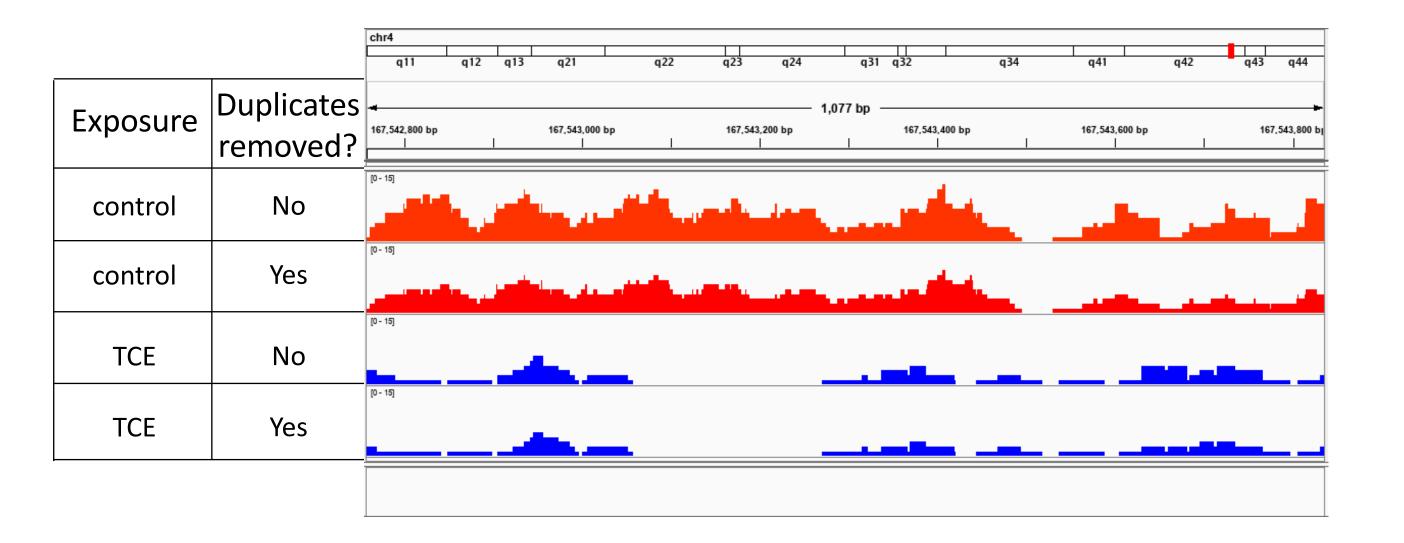
**Figure S1.** Browser tracks of read coverage for differential region of H3K4me2 binding within the gene body of Cyp2c7a. Tracks are as follows-Top- combined control samples without duplicates removed, 2<sup>nd</sup>- combined control samples with duplicates removed, 3<sup>rd</sup>- combined TCE exposed samples without duplicates removed, Bottom- combined TCE exposed samples with duplicates removed. Diffreps fold change -2.24 (TCE exposed compared to control), p adjusted value = 6.2e-04



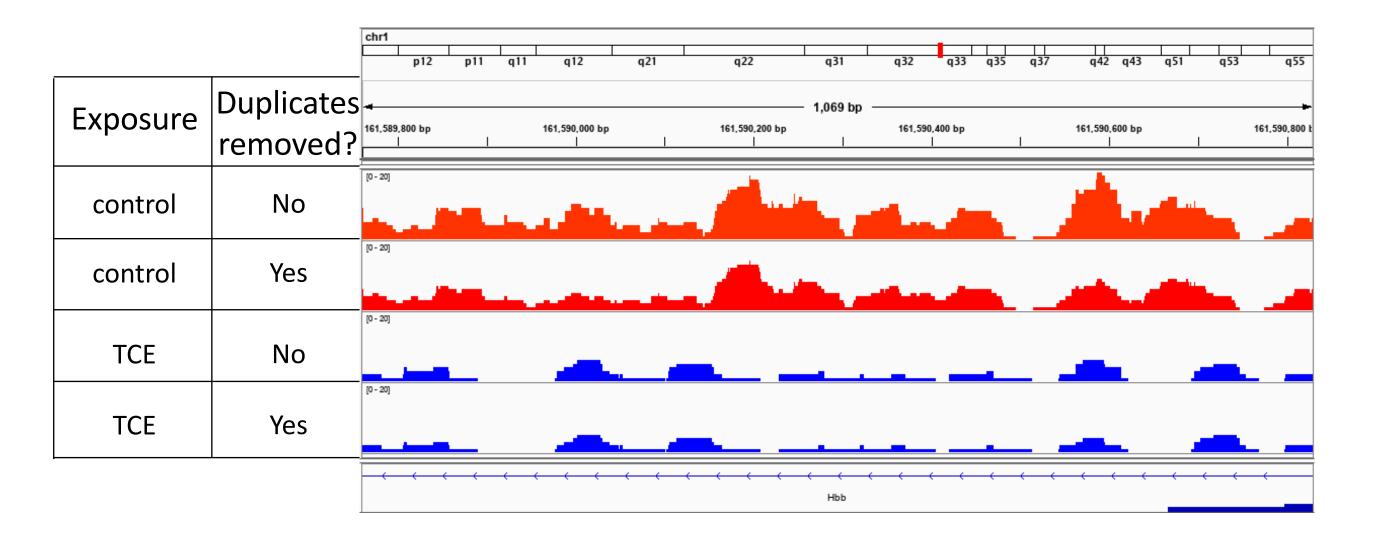
**Figure S2.** Browser tracks of read coverage for differential region of H3K4me2 binding within an intergenic region on chromosome 8. Tracks are as follows- Top- combined control samples without duplicates removed, 2<sup>nd</sup>- combined control samples with duplicates removed, 3<sup>rd</sup>- combined TCE exposed samples without duplicates removed, Bottom- combined TCE exposed samples with duplicates removed. Diffreps fold change -2.1 (TCE exposed compared to control), p adjusted value = 9.6e-05



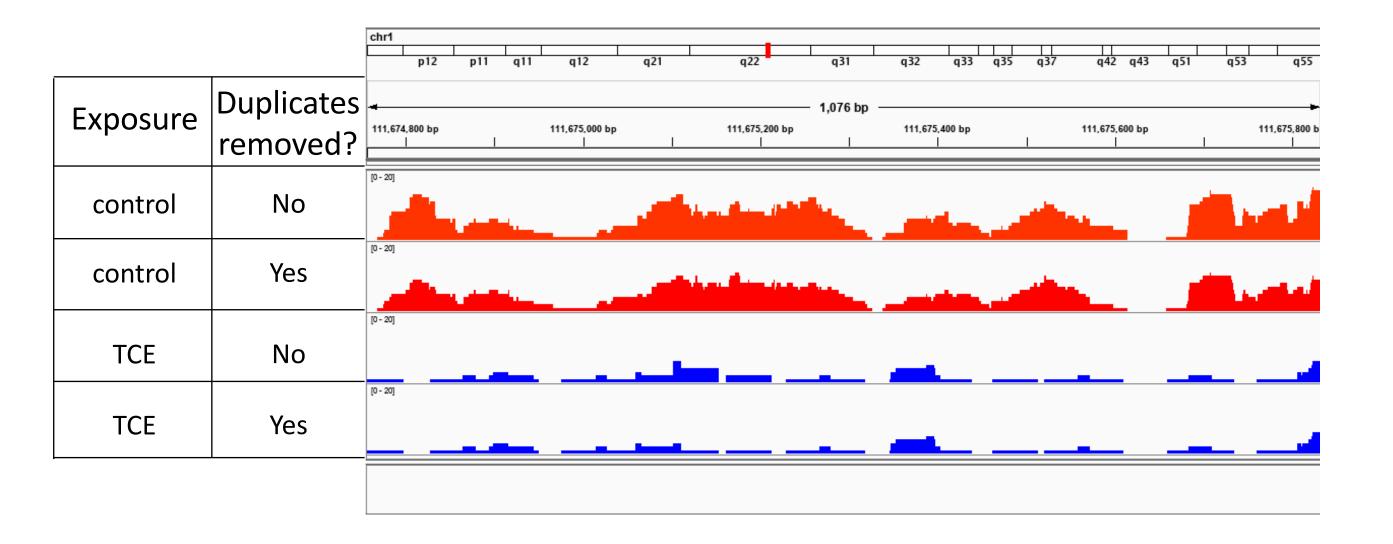
**Figure S3.** Browser tracks of read coverage for differential region of H3K4me2 binding within an intergenic region on chromosome 7. Tracks are as follows- Top- combined control samples without duplicates removed, 2<sup>nd</sup>- combined control samples with duplicates removed, 3<sup>rd</sup>- combined TCE exposed samples without duplicates removed, Bottom- combined TCE exposed samples with duplicates removed. Diffreps fold change -2.02 (TCE exposed compared to control), p adjusted value = 0.0017



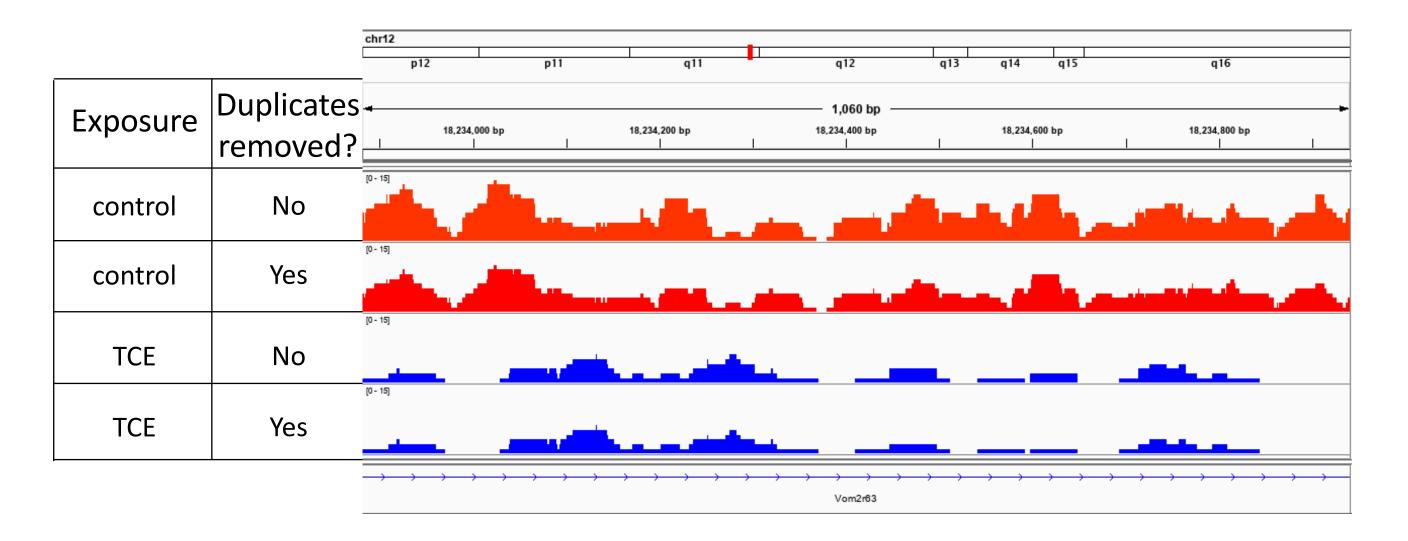
**Figure S4.** Browser tracks of read coverage for differential region of H3K4me2 binding within an intergenic region on chromosome 4. Tracks are as follows- Top- combined control samples without duplicates removed, 2<sup>nd</sup>- combined control samples with duplicates removed, 3<sup>rd</sup>- combined TCE exposed samples without duplicates removed, Bottom- combined TCE exposed samples with duplicates removed. Diffreps fold change -1.99 (TCE exposed compared to control), p adjusted value = 8.5e-05



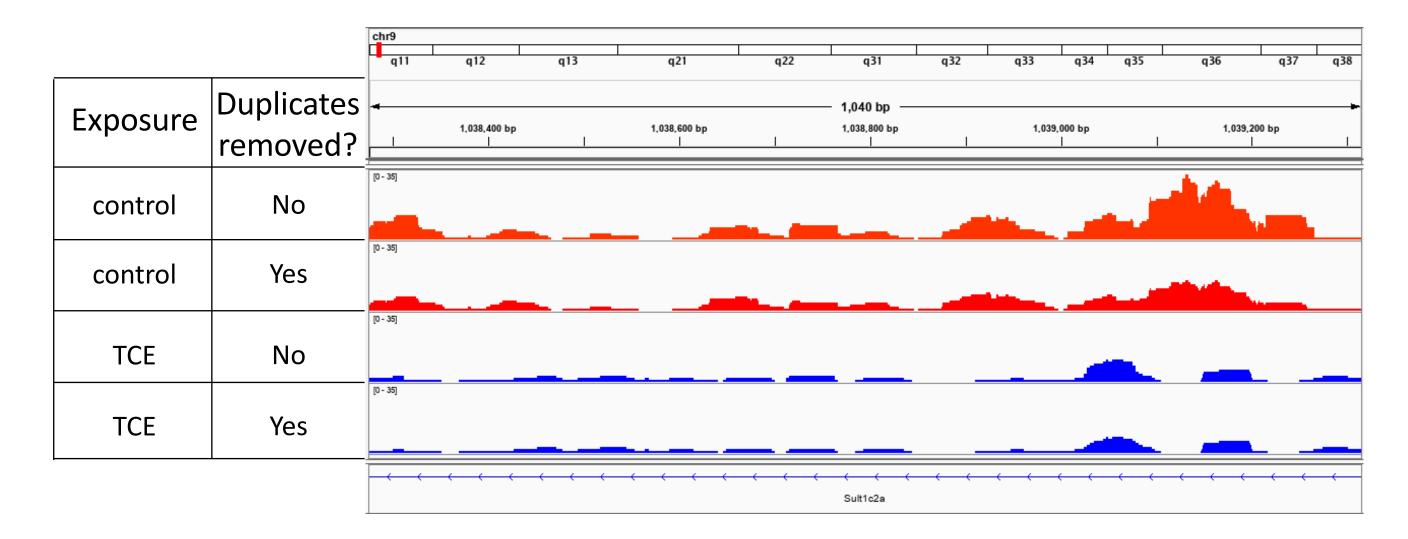
**Figure S5.** Browser tracks of read coverage for differential region of H3K4me2 binding within the gene body of Hbb. Tracks are as follows- Top-combined control samples without duplicates removed, 2<sup>nd</sup>- combined control samples with duplicates removed, 3<sup>rd</sup>- combined TCE exposed samples without duplicates removed, Bottom- combined TCE exposed samples with duplicates removed. Diffreps fold change -1.98 (TCE exposed compared to control), p adjusted value = 0.0071



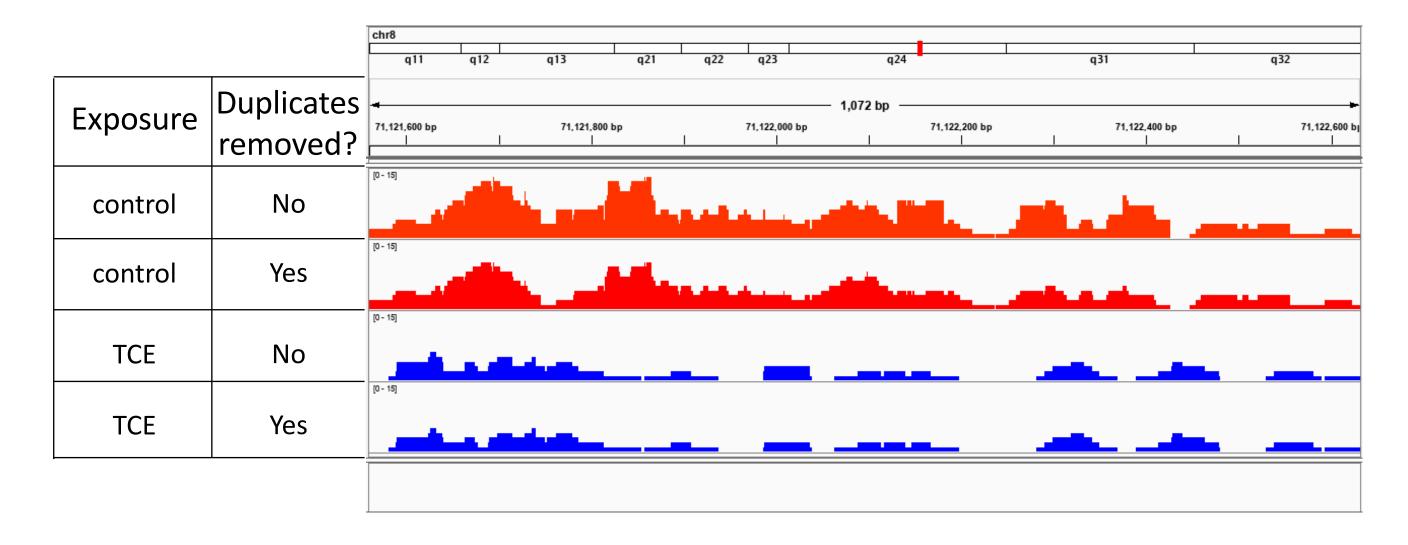
**Figure S6.** Browser tracks of read coverage for differential region of H3K4me2 binding within an intergenic region on chromosome 1. Tracks are as follows- Top- combined control samples without duplicates removed, 2<sup>nd</sup>- combined control samples with duplicates removed, 3<sup>rd</sup>- combined TCE exposed samples without duplicates removed, Bottom- combined TCE exposed samples with duplicates removed. Diffreps fold change -1.97 (TCE exposed compared to control), p adjusted value = 0.0041



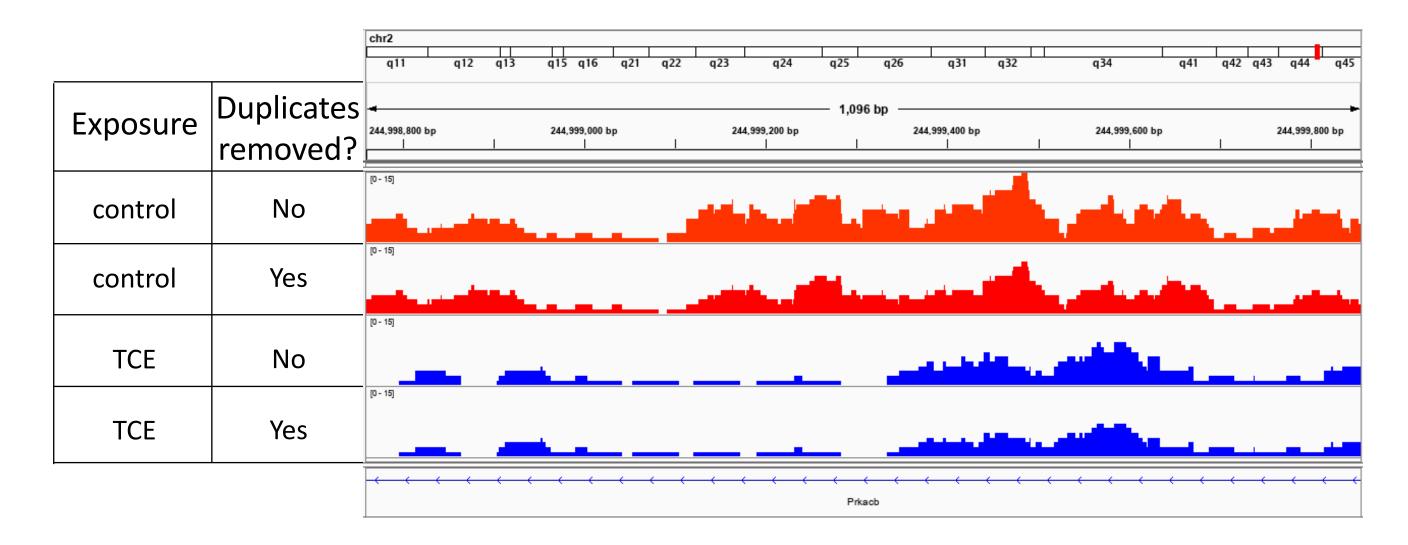
**Figure S7.** Browser tracks of read coverage for differential region of H3K4me2 binding within the gene body of Vom2r63. Tracks are as follows-Top- combined control samples without duplicates removed, 2<sup>nd</sup>- combined control samples with duplicates removed, 3<sup>rd</sup>- combined TCE exposed samples without duplicates removed, Bottom- combined TCE exposed samples with duplicates removed. Diffreps fold change -1.94 (TCE exposed compared to control), p adjusted value = 6.3e-05



**Figure S8.** Browser tracks of read coverage for differential region of H3K4me2 binding within the gene body of Sult1c2a. Tracks are as follows-Top- combined control samples without duplicates removed, 2<sup>nd</sup>- combined control samples with duplicates removed, 3<sup>rd</sup>- combined TCE exposed samples without duplicates removed, Bottom- combined TCE exposed samples with duplicates removed. Diffreps fold change -1.91 (TCE exposed compared to control), p adjusted value = 5.9e-04



**Figure S9.** Browser tracks of read coverage for differential region of H3K4me2 binding just upstream of Aph1b. Tracks are as follows- Top-combined control samples without duplicates removed, 2<sup>nd</sup>- combined control samples with duplicates removed, 3<sup>rd</sup>- combined TCE exposed samples without duplicates removed, Bottom- combined TCE exposed samples with duplicates removed. Diffreps fold change -1.89 (TCE exposed compared to control), p adjusted value = 0.0043



**Figure S10.** Browser tracks of read coverage for differential region of H3K4me2 binding within the gene body of Prkacb. Tracks are as follows-Top- combined control samples without duplicates removed, 2<sup>nd</sup>- combined control samples with duplicates removed, 3<sup>rd</sup>- combined TCE exposed samples without duplicates removed, Bottom- combined TCE exposed samples with duplicates removed. Diffreps fold change -1.4 (TCE exposed compared to control), p adjusted value = 0.0068