

Supplementary Figure 2 WaferGen SmartChIP QRTPCR verification of RNA-Seq and Agilent responses for typical AhR responsive genes. Official gene symbols are indicated in upper left corner with the number of RNA-Seq aligned reads in parentheses ( ) and number of samples with  $C_t$  values lower than background in brackets [ ] for vehicle control samples. Bars represent mean fold-change determined by WaferGen technology ( $\pm$ SEM), the red line represents RNA-Seq fold-change, and the green line represents Agilent fold change. Significant differences within WaferGen data were determined by one-way ANOVA followed by Dunnett's *post-hoc* test and indicated by an asterisk (\*). Red (RNA-Seq) and green (Agilent) dots represent P1(t) values with size indicating level of significance (small ~0.8, large ~1). Labels on the X-axis indicate the dose of TCDD ( $\mu$ g/kg), number of aligned RNA-Seq reads, and number of samples with  $C_t$  values lower than background. Dashed lines indicate 1.5 and 2.0 |fold-change| thresholds to identify DEGs.