Supplementary Figure 5 WaferGen SmartChIP QRTPCR verification of RNA-Seq and Agilent responses for the most divergent genes identified as DEG by microarray. 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 (±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 (μg/kg), number of aligned RNA-Seq reads, and number of samples with Ct values lower than background from top to bottom. Dashed lines indicate 1.5 and 2.0 |fold-change| thresholds to identify DEGs.