Supplementary Fig. S4. *In silico* subtraction strategy identifies genes involved in tooth development and craniofacial defects. (A) The 200 most highly ranked genes with WB subtraction (with WB) and without WB subtraction (without WB) at E13.5 are obtained, and they are tested against several functional biological gene categories to identify statistically significantly enriched gene sets (Fisher's Exact Test, Bonferroni corrected $p<0.01$, odds ratio of gene set overlap > 20). Significantly enriched genes sets are visualized in the heat map. (B) Heat maps showing the expression levels, and the tooth enrichment $p$-values, of all human tooth agenesis and orofacial clefting genes. (C) A rank list showing the distribution of known genes related to tooth specific genes based on the tooth enrichment $t$-statistics (with WB) or the microarray expression alone (without WB).