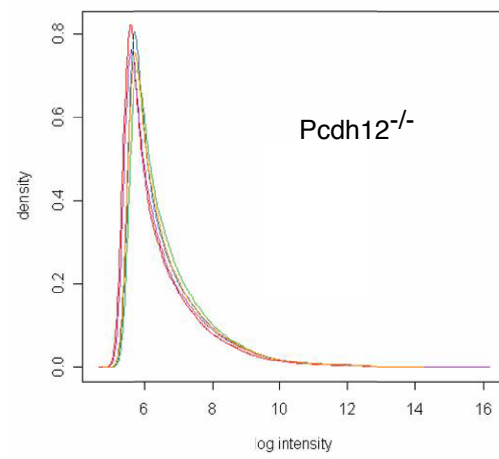
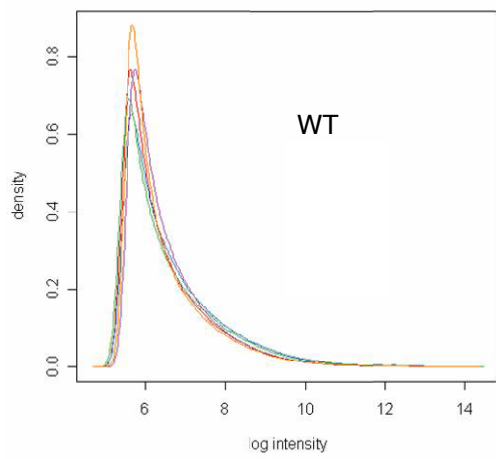
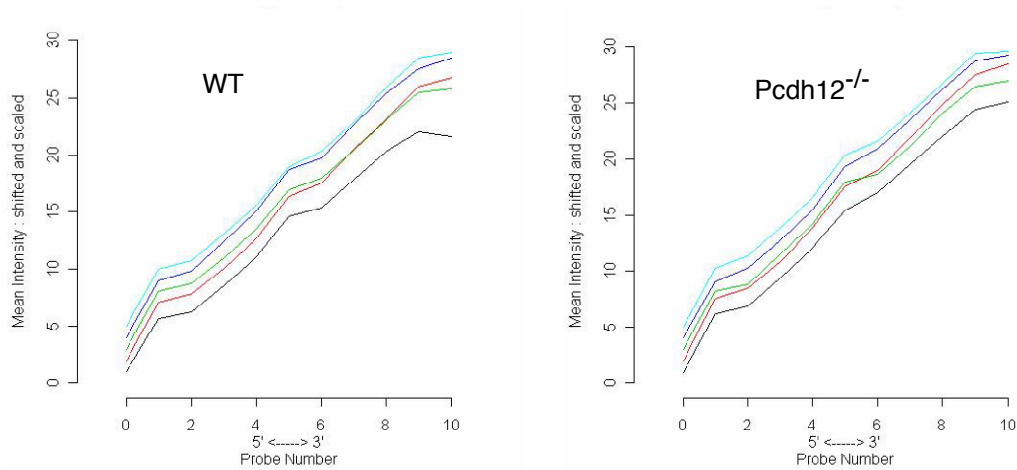


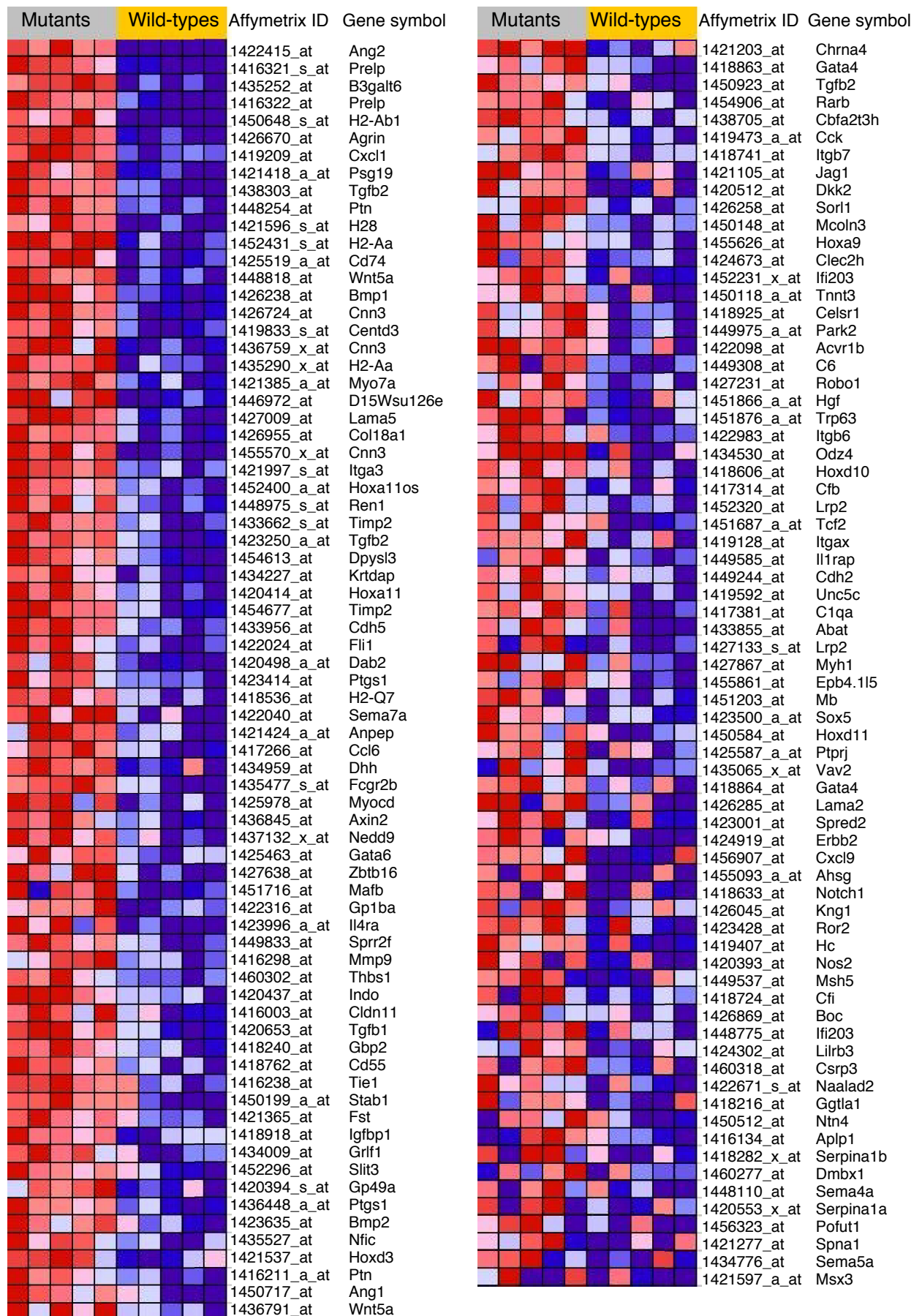
Supplemental Fig.1: Boxplots in log scale for probe level data for each sample, represented by different colors, of wild type (WT) and *Pcdh12*^{-/-} genotypes. Data show no significant difference between the samples, indicating similar signal intensities for each chip.



Supplemental Fig. 2: Densities of log signal intensities of the different wild type and Pcdh12^{-/-} samples. Data obtained for each chip is represented by a different color. Samples exhibit same profiles.

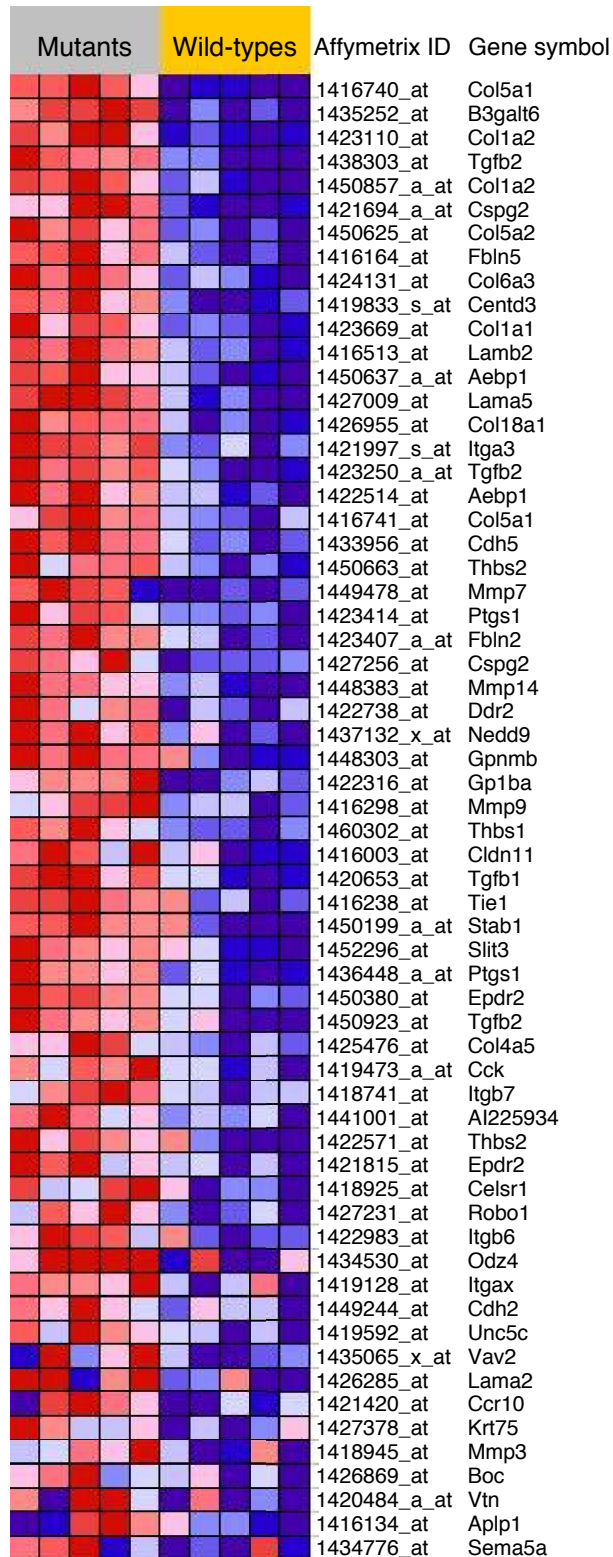


Supplemental Fig. 3: Assessment of RNA degradation by “RNA digestion plots” method available in the Bioconductor affy package. The RNA digestion plot represents the average intensity of 11 probes for each chip from 5' to 3'. Each line represents one chip. The mean intensity by probe set position is plotted on the Y axis. Data show similar slopes between all samples indicating normal 5' to 3' patterns.



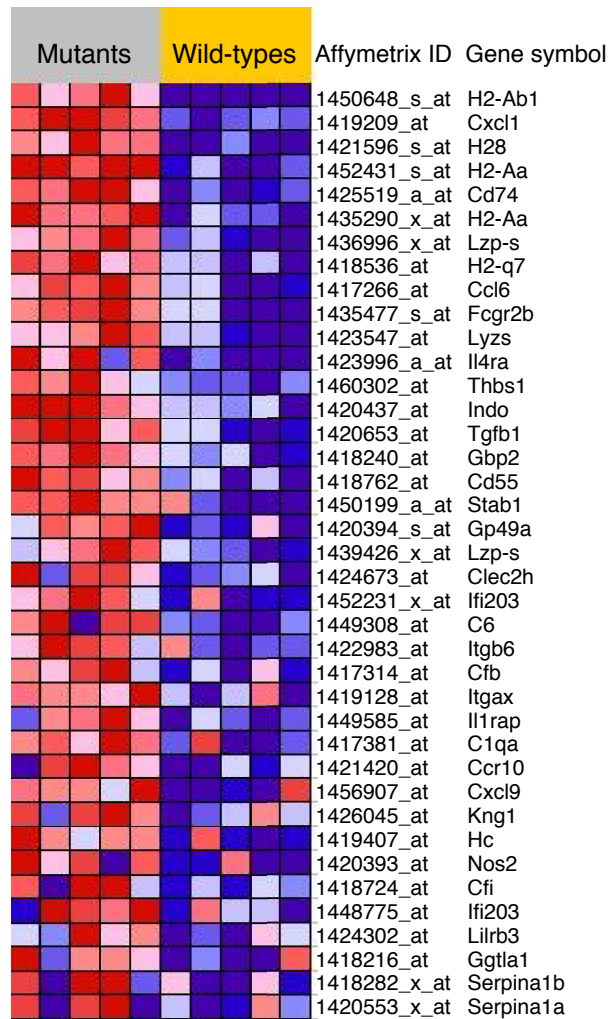
Supplemental Fig. 4: Heat map of differentially expressed genes related to development and tissue morphogenesis

Gene selection was obtained from GSEA. Columns represent a single placental array, and each row represents a single probe set. The expression values of the 144 genes are well correlated with the mutant and wild type genotype. Each colored cell in the heat map represents the gene expression value for a probe in a sample. The highest gene expression values are displayed in red, the lowest values in blue.



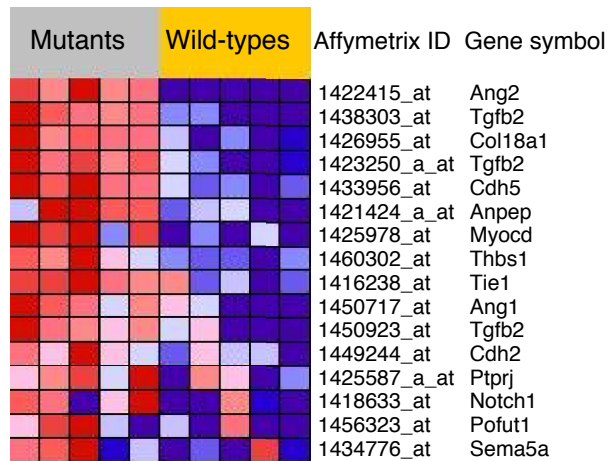
Supplemental Fig. 5: Heat map of differentially expressed genes related to cell adhesion, migration and matrix proteins

Gene selection was obtained from GSEA. Columns represent a single placental array, and each row represents a single probe set. The expression values of the 62 genes are well correlated with the mutant and wild type genotype. Each colored cell in the heat map represents the gene expression value for a probe in a sample. The highest gene expression values are displayed in red, the lowest values in blue.



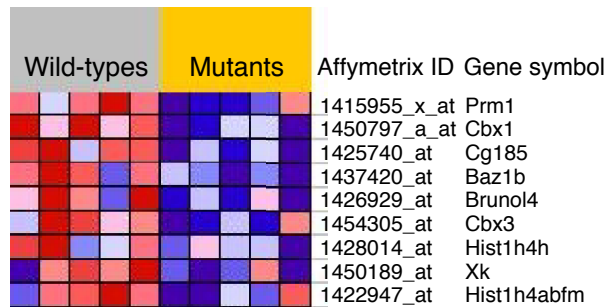
Supplemental Fig. 6: Heat map of differentially expressed genes related to immune response

Gene selection was obtained from GSEA. Columns represent a single placental array, and each row represents a single probe set. The expression values of the 39 genes are well correlated with the mutant and wild type genotype. Each colored cell in the heat map represents the gene expression value for a probe in a sample. The highest gene expression values are displayed in red, the lowest values in blue.



Supplemental Fig. 7: Heat map of differentially expressed genes related to angiogenesis

Gene selection was obtained from GSEA. Columns represent a single placental array, and each row represents a single probe set. The expression values of the 16 genes are well correlated with the mutant and wild type genotype. Each colored cell in the heat map represents the gene expression value for a probe in a sample. The highest gene expression values are displayed in red, the lowest values in blue.



Supplemental Fig. 8: Heat map of differentially expressed genes related to chromatin

Gene selection was obtained from GSEA. Columns represent a single placental array, and each row represents a single probe set. The expression values of the 9 genes are well correlated with the mutant and wild type genotype. Each colored cell in the heat map represents the gene expression value for a probe in a sample. The highest gene expression values are displayed in red, the lowest values in blue.