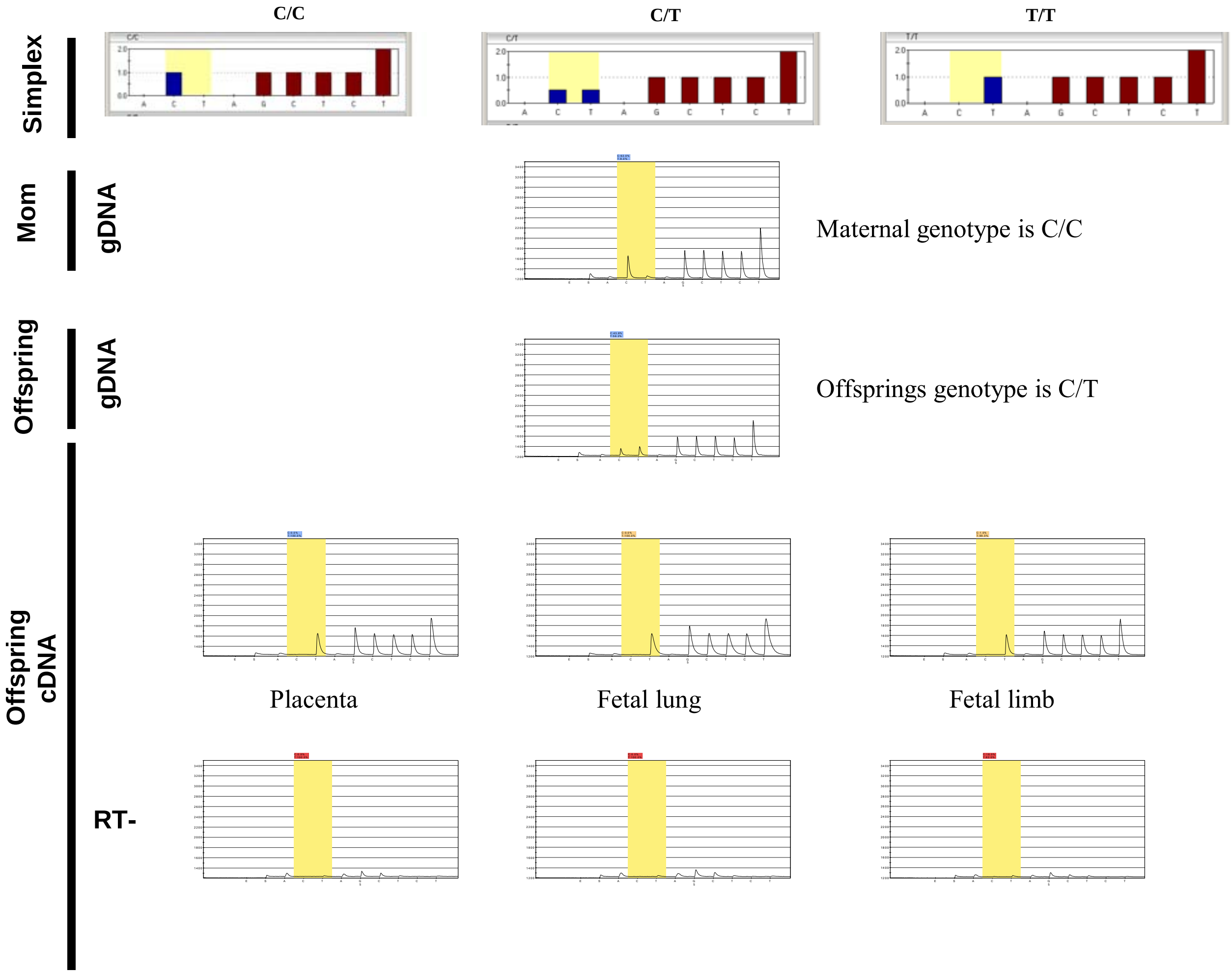
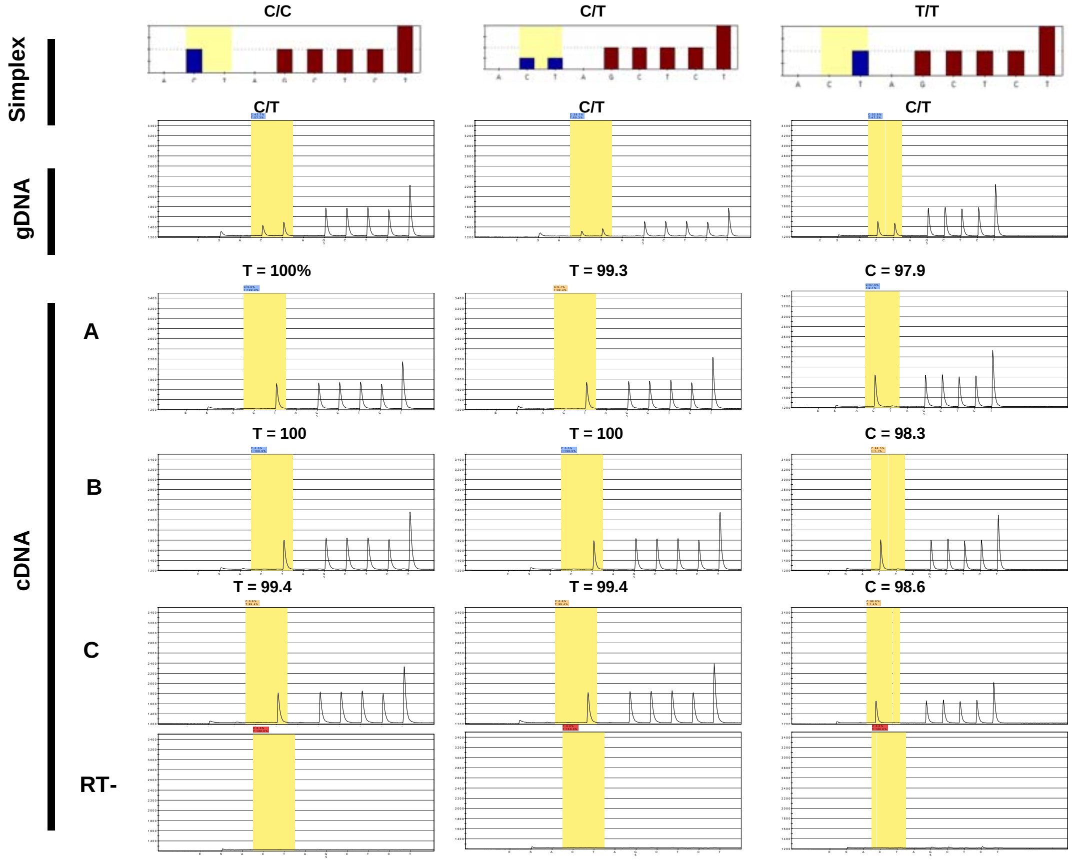
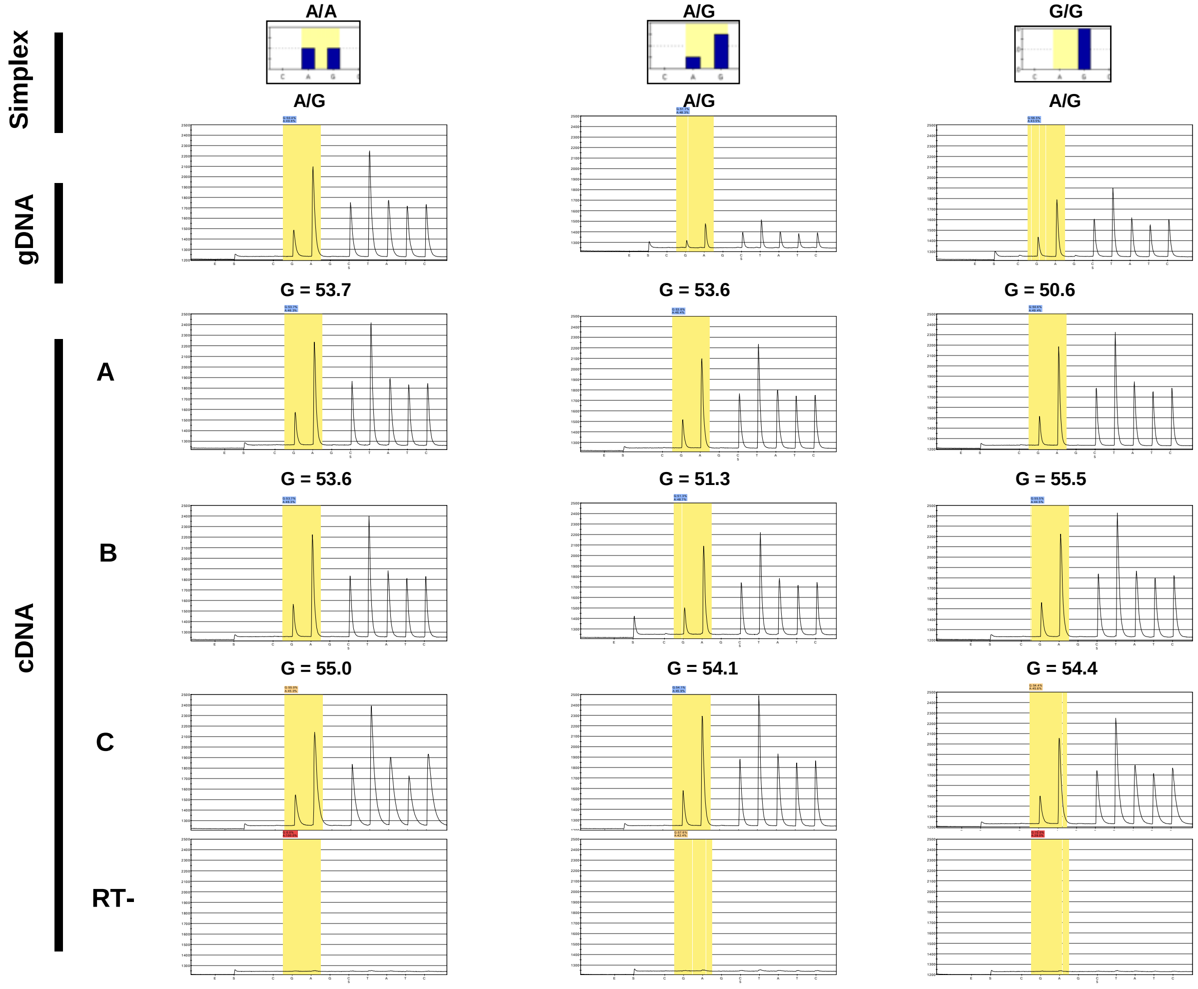
Supplemental Figure 1. Parent of origin analysis of PEG10 demonstrating that there is preferential expression of the paternal allele in a variety of fetal tissues. The first row demonstrates the simplex files for the three possible genotypes of the pyrosequencing assay. The next two rows demonstrate the pyrosequencing raw data files for the gDNA of the mother (homozygous, C/C) and the offspring (heterozygous C/T), respectively. The final rows demonstrate the ASE from cDNA of from three different tissues (Placenta, fetal lung and fetal limb) and the corresponding RT(−) control for each assay. All tissues demonstrate preferential expression from the paternal allele.



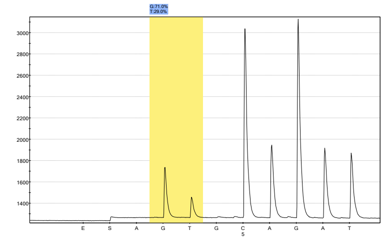
Supplemental Figure 2. Allele specific expression of PEG10 in CEPH cell lines. The first row demonstrates the simplex files for the three possible genotypes of the pyrosequencing assay. The next two rows demonstrate the pyrosequencing raw data files for the gDNA of the individual cell line (heterozygous C/T). The final rows demonstrate the ASE from cDNA of from different individuals (in triplicate) and the corresponding RT(−) control for each assay.



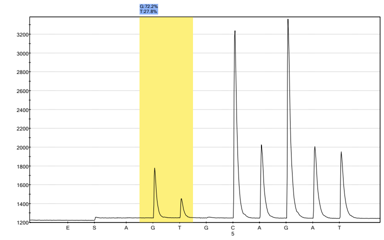
Supplemental Figure 3. ***TUBGCP6*** **is a non-imprinted gene that did not demonstrate allelic skewing.** The first row demonstrates the simplex files for the three possible genotypes of the pyrosequencing assay. The next two rows demonstrate the pyrosequencing raw data files for the gDNA of the individual cell line (heterozygous A/G). The final rows demonstrate the ASE from cDNA of from different individuals (in triplicate) and the corresponding RT(−) control for each assay.



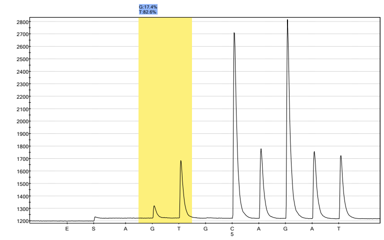
Supplemental Figure 4. ***NLRP2* demonstrates preferential expression from the maternal allele in primary fetal tissues.** Pyrosequencing analysis of cDNA from individuals 8 (top 2 panels) and 7 (bottom 2 panels) in fetal heart and kidney. Simplexes, genomic DNA tracings and RT- controls are as in Figure 4A.



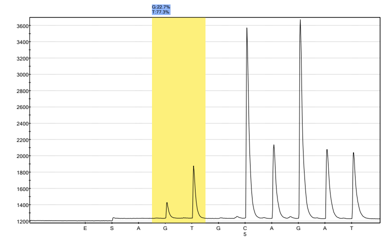
Fetal heart



Fetal kidney

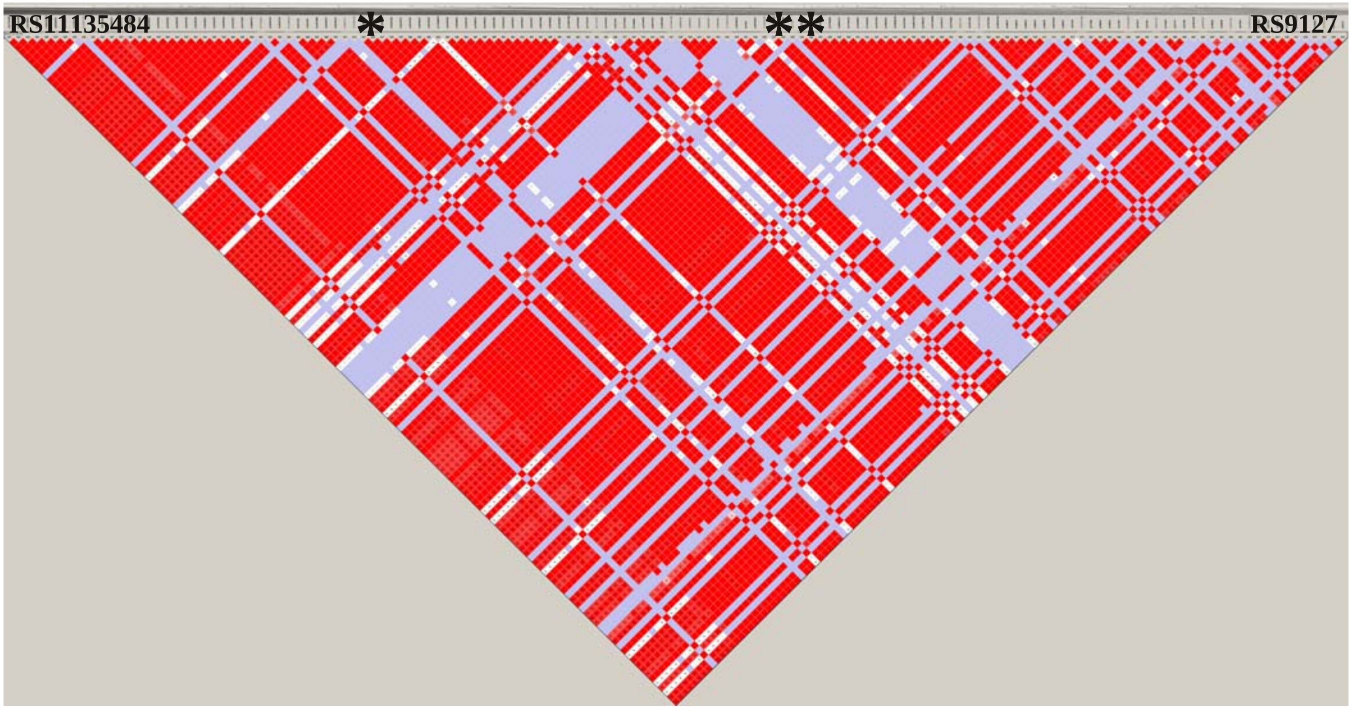


Fetal heart



Fetal kidney

Supplemental Figure 5. The expressed SNP in *LRAP* is in the same linkage disequilibrium group as two nonexonic SNPs previously shown to be associated with *LRAP* expression. The expressed SNP (rs2287988) is shown with a single star, and is part of a 150 kb haplotype block on chromosome 5 that also includes rs2762 (double star), previously found to correlate with overall expression of *LRAP*.



Supplemental Figure 6. ***SCRN1*** **demonstrated monoallelic expression.** The first row demonstrates the simplex files for the three possible genotypes of the pyrosequencing assay. The next two rows demonstrate the pyrosequencing raw data files for the gDNA of the individual cell line (heterozygous A/G). The final rows demonstrate the ASE from cDNA of from the same individuals (in triplicate) and the corresponding RT(−) control for each assay.