Thin hair with small size is the first *Pld4* mutant mouse

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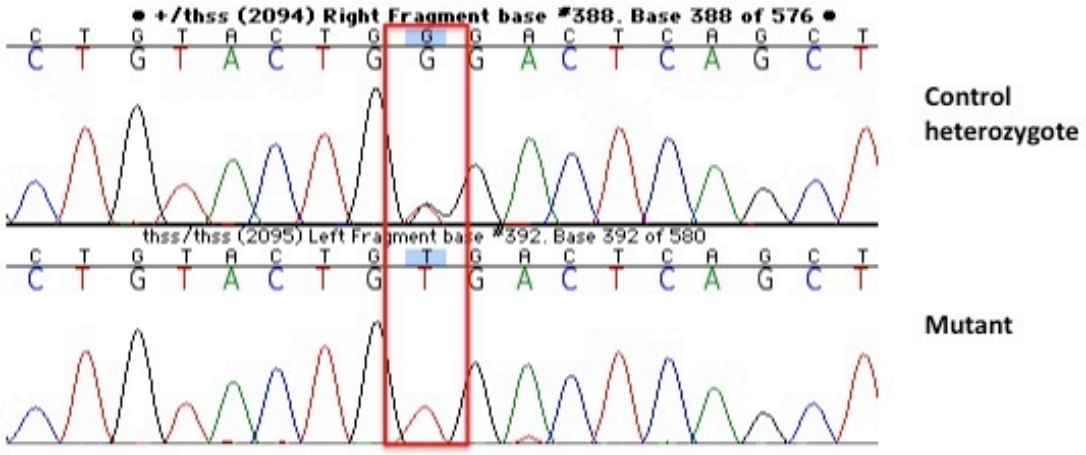
Mutation (allele) symbol: updated to *Pld4*^{thss}
Mutation (allele) name: thin hair with small size
Gene symbol: *Pld4*
Stock #012624 (jaxmice.jax.org)

Mapping data for the thin hair with small size mutation (*thss*) demonstrated linkage to Chromosome 12 (previous work). Whole exome sequencing[1] was then used to identify candidate coding mutations in the mapped region. A single nucleotide polymorphism was found on Chromosome 12 in phospholipase D family member 4 (*Pld4*). Primers were generated that produce a 586 base pair product spanning the predicted mutation: *Pld4* forward (AGGATCTCTGGAAGAGCAGTTG) and *Pld4* reverse (CACATAGCCTACAACCCTGTGA). Sequence analysis of genomic DNA samples from three homozygotes and three heterozygotes confirmed a single nucleotide transition from G to T at position 114,001,632 (NCBI build 37) which is in exon 3 of *Pld4*. This is a nonsense mutation, resulting in the introduction of a premature stop at residue 46 of the 503 amino acid protein. This is the first reported mouse model bearing a *Pld4* mutation.



Comparison of sequence chromatograms of *thss* homozygous and *thss* control heterozygous sequence

[1]The exome sequencing data were analyzed using tools and workflows provided by Genome Quest including processes for mapping (HS3), SNP calling and annotation of variants. Our analysis focused on novel variants, which were not positioned in repetitive sequence, had expected allele ratios (>0.95 for homozygous variants and >0.2 for heterozygous variants), and displayed sufficient locus coverage (at least 5X for homozygous variants and 10X for heterozygous variants) for effective mutation discovery. High priority was given to protein coding or splice variants within mapped regions, as well as unique variants that were not found in other exome data sets or in the Sanger Mouse Genomes Database. Following these analyses, re-sequencing of additional mutant and unaffected samples was performed to validate and determine the most likely causative mutation.