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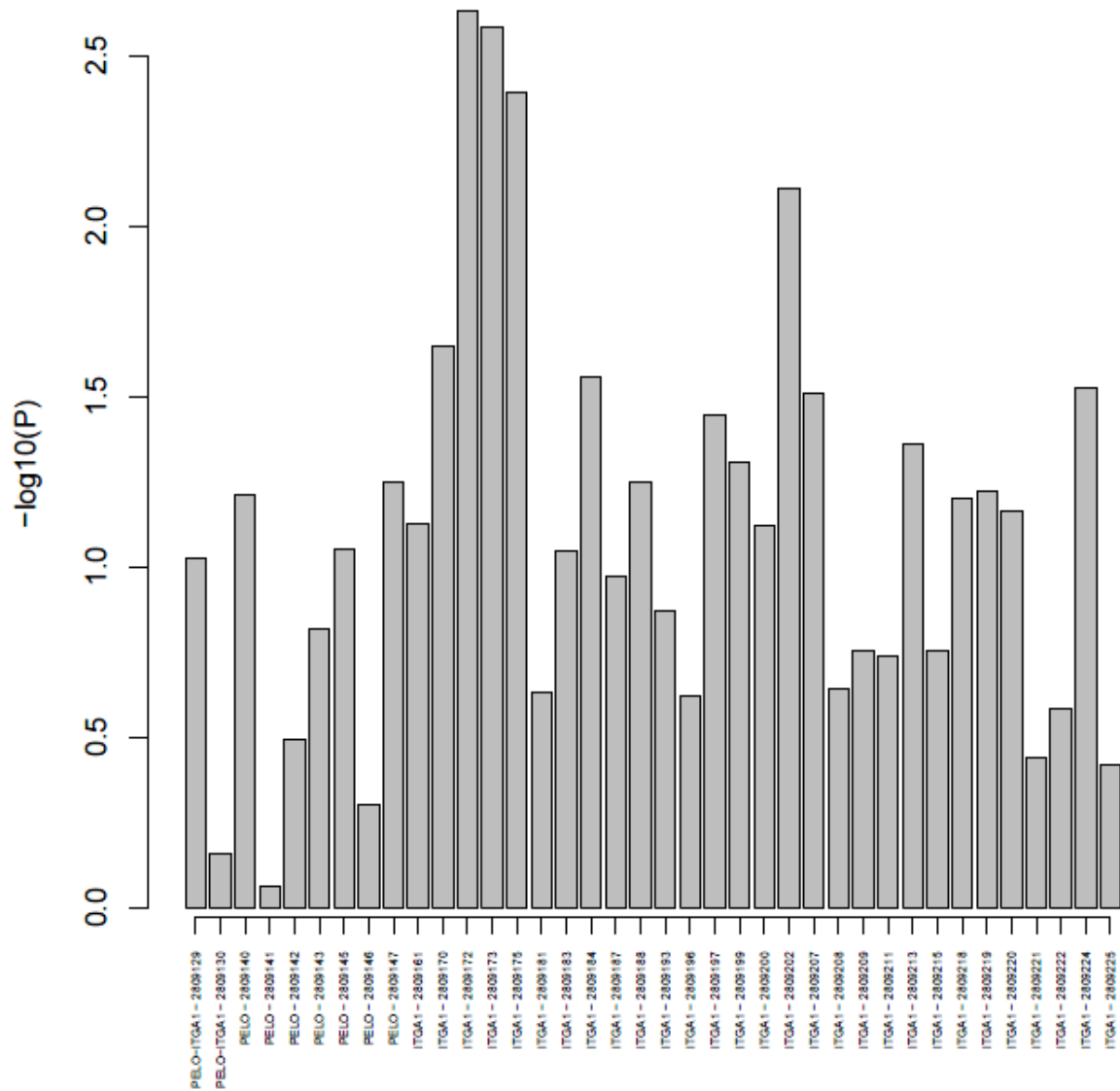
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SUPPLEMENTARY DATA

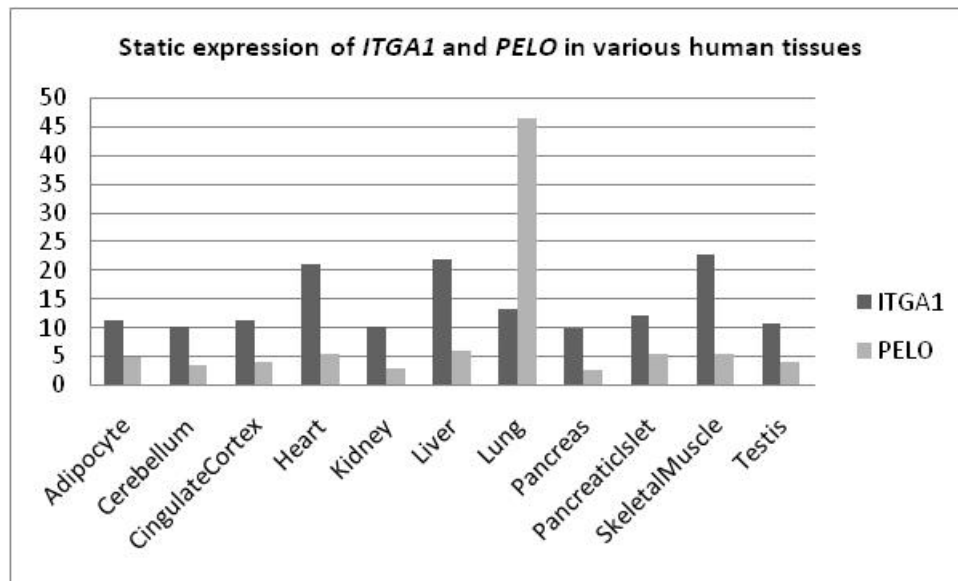
Association of SNP rs10512997 with individual regions within *ITGA1/PELO*



The x-axis indicates the Affymetrix probe set ID and for which isoform it measures expression. Each of these Affymetrix probe sets ID roughly correspond to an exon and each of them are components of the Affymetrix meta-probe set 2809128, which was used to obtain overall *ITGA1/PELO* expression. The figure illustrates that the SNP rs10512997 was associated with *ITGA1* gene expression at a greater level of significance than *PELO* gene expression. The twelve other SNPs depict similar patterns.

## SUPPLEMENTARY DATA

### Static expression of *ITGA1* and *PELO* in various human tissues



*ITGA1* appears to be more highly expressed than *PELO* in liver, adipocytes, and pancreatic islets. These expression data were obtained from the BioGPS application at [biogps.org](http://biogps.org) and the primary data sets cited here :

Wu C, Orozco C, Boyer J, Leglise M, Goodale J, Batalov S, Hodge CL, Haase J, Janes J, Huss JW 3rd, Su AI (2009) BioGPS: an extensible and customizable portal for querying and organizing gene annotation resources. *Genome Biol.* **10**(11):R130.

Su AI, Wiltshire T, Batalov S, Lapp H, Ching KA, Block D, Zhang J, Soden R, Hayakawa M, Kreiman G, Cooke MP, Walker JR, Hogenesch JB (2004) A gene atlas of the mouse and human protein-encoding transcriptomes. *Proc Natl Acad Sci U S A.* 101(16):6062-7.