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Animal Production Science

Supplementary Material

Identification of six genomic regions associated with pigment intensity in alpacas

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Supplementary material

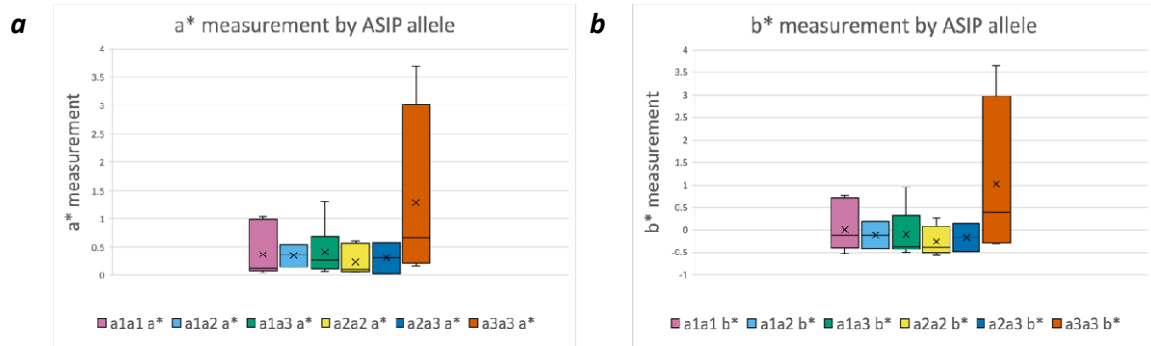


Figure S1. Average a^* and b^* values categorised by *ASIP* genotype (a) Box-and-whisker plot

of averaged a^* values of eumelanin samples categorised by *ASIP* genotype. Average a^*

measurement for each sample on the Y axis and the *ASIP* genotype on the X axis. One-way

ANOVA of the a^* values for the different *ASIP* genotypes resulted in $p = 0.23$ (b) Box-and-

whisker plot of averaged b^* values of eumelanin samples categorised by *ASIP* genotype.

Average b^* measurement for each sample on the Y axis and the *ASIP* genotype on the X axis.

One-way ANOVA of the b^* values for the different *ASIP* genotypes resulted in $p = 0.19$

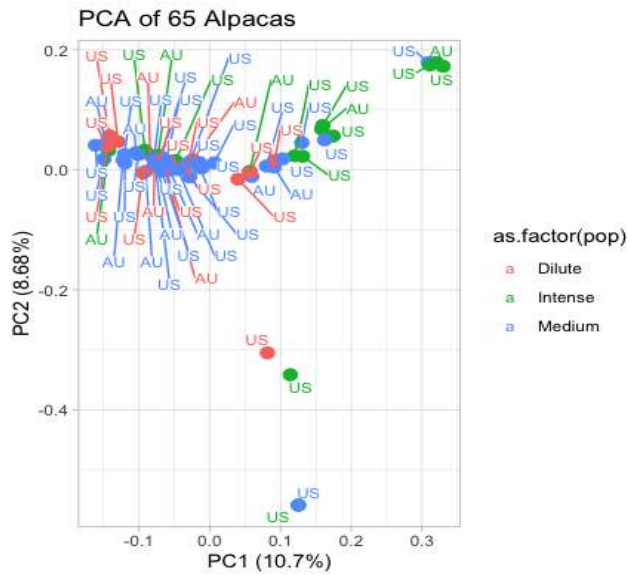


Figure S2. PCA plot of samples used in GWAS. Four samples deviated from the main cluster, and were removed from the GWAS.

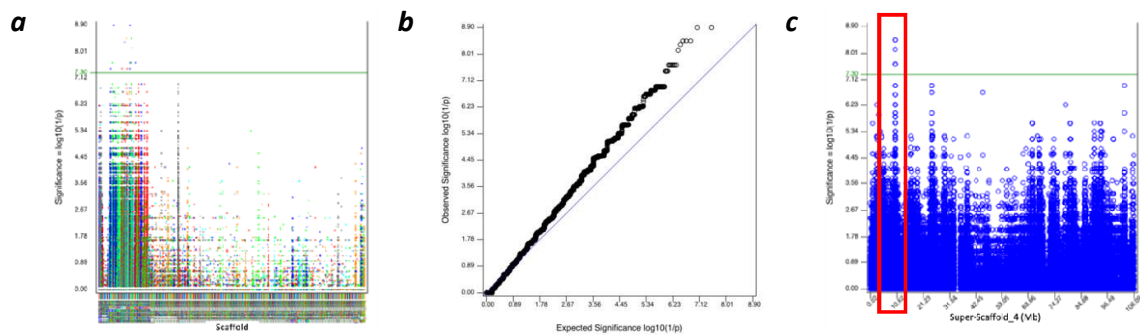


Figure S3. Pheomelanistic GWAS (**a**) Manhattan plot of GWAS using the 12 most intense and 12 most dilute pheomelanistic alpacas (**b**) Q-Q plot showing a genomic inflation factor, λ , of 1 (**c**) Super-Scaffold 4 genome-wide significant region 9.84 - 10.05 Mb highlighted in red.

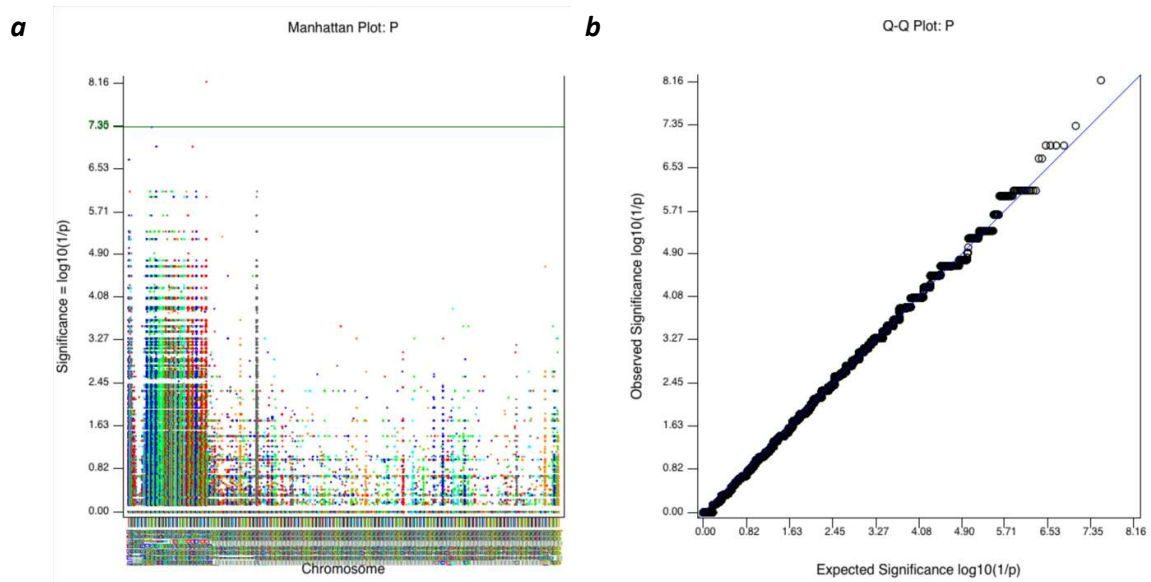


Figure S4. Eumelanic GWAS (**a**) Manhattan plot of GWAS using 8 most intense and 8 most dilute eumelanic alpacas (**b**) Q-Q plot showing a genomic inflation factor, λ , of 1.

Table S1. Genes located in regions of genome-wide significance

GWAS	Scaffold	Genes located within 500 kb
Combined	Super-Scaffold 15	<i>KITLG</i> , <i>POC1B</i> , <i>CEP290</i> , <i>DUSP6</i> , <i>TMTC3</i> , <i>C12H12orf50</i> , <i>C12H12orf29</i>
Combined	Super-Scaffold 19	<i>KNOP1</i> , <i>VPS35L</i> , <i>CCP110</i> , <i>GDE1</i> , <i>TMC5</i> , <i>TMC7</i> , <i>COQ7</i> , <i>ITRIPL2</i> , <i>SYT17</i> , <i>CLEC19A</i> , <i>SMG1</i> , <i>ARL6IP1</i> , <i>RPS15A</i>
Combined	Super-Scaffold 100005	<i>COL9A1</i> , <i>FAM135A</i> , <i>SDHAF4</i> , <i>B3GAT2</i> , <i>SMAP1</i> , <i>OGFRL1</i> , <i>RIMS1</i> , <i>KCNQ5</i>
Combined	Super-Scaffold 4	<i>BEND5</i> , <i>AGBL4</i>
Combined	Super-Scaffold 10	No known genes
Combined	Super-Scaffold 31	<i>SYT4</i>
Pheomelanic only	Super-Scaffold 4	<i>GEMIN8</i>