Supplementary Table 1: Sequencing Quality Metrics and Coverage Summary

Sample	Sample Type	Sequencing Method	Average Depth (×)	Coverage ≥10× (%)	Coverage ≥20× (%)	Key Genetic Findings
Proband (Lesion FFPE)	FFPE tissue	Whole-exome sequencing (WES)	333.85	99.71	99.58	No pathogenic variants in known nevus/fat-related genes
Proband (Blood)	Peripheral blood	WES	149.63	99.61	99.03	Consistent with FFPE results
Proband (Fresh tissue)	Fresh tissue	Whole-genome sequencing (WGS)	55.13	98.90	98.26	No pathogenic SVs, CNVs, or mitochondrial variants
Father (Blood)	Peripheral blood	WES	146.72	99.86	99.61	Carrier of CYP2C19, PLEC, ABCA1, COL5A1 variants
Mother (Blood)	Peripheral blood	WES	134.66	99.56	98.73	Carrier of PRKCSH variant

Abbreviations:

FFPE = formalin-fixed paraffin-embedded; SV = structural variant; CNV = copy number variation.

Supplementary Table 2: Summary of Key Genetic Variants Detected in the Proband and Parents

Gene	Chromosome (hg19)	Nucleotide Change	Protein Change	Zygosity in Proband	Parental Origin	ACMG Classification	Associated Phenotypes (OMIM/ ClinVar)	Potential Relevance to Current Phenotype
CYP2C19	chr2:219679132	c.1214G>A	p.Arg405Gln	Heterozygous	Paternal	Likely pathogenic	Cerebrotendinous xanthomatosis (AR)	Lipid metabolism disorder; may involve skin/subcutaneous tissue
UGT1A1	chr2:234669144	c.211G>A	p.Gly71Arg	Homozygous	Both parents (Mother: het, Father: hom)	Likely pathogenic	Gilbert syndrome (AR)	Bilirubin metabolism; possible indirect link to skin pigmentation
PLEC	chr8:145003337	c.3194C>T	p.Ser1065Leu	Heterozygous	Paternal	Uncertain significance	Epidermolysis bullosa simplex with muscular dystrophy (AR/AD)	Encodes plectin, involved in skin structural integrity
PRKCSH	chr19:11559797	c.1355G>A	p.Ser452Asn	Heterozygous	Maternal	Uncertain significance	Polycystic liver disease 1 (AD)	Cyst formation-related gene
ABCA1	chr9:107558399	c.5317G>C	p.Val1773Leu	Heterozygous	Paternal	Uncertain significance	Tangier disease (AR) / HDL deficiency	Lipid transporter; possible link to

							(AD)	fat metabolism
COL5A1	chr9:137708930	c.4176+5A>G	Splice site variant	Heterozygous	Paternal	Uncertain significance	Ehlers-Danlos syndrome (AD)	Collagen gene; associated with skin elasticity

Abbreviations:

AR = autosomal recessive; AD = autosomal dominant; het = heterozygous; hom = homozygous.

Note:

No pathogenic or likely pathogenic variants were identified in genes known to be associated with superficial lipomatous nevus or related dermatological conditions.

Supplementary Table 3: Summary of Genetic Findings and Conclusions

Category	Finding	Interpretation
Pathogenic Variants	No pathogenic or likely pathogenic variants were identified in genes known to be associated with superficial lipomatous nevus or related dermatologic conditions.	The patient's phenotype is unlikely to be caused by a monogenic germline mutation in currently known genes.
Variants of Uncertain Significance (VUS)	VUS were detected in genes involved in lipid metabolism (CYP2C19, ABCA1), skin structure (PLEC, COL5A1), and liver function (PRKCSH, UGT1A1).	None are established causes of the reported phenotype; clinical relevance remains unclear.
Structural/Copy Number Variants	Whole-genome sequencing revealed no pathogenic SVs, CNVs, or mitochondrial mutations.	Large genomic rearrangements are not likely contributing to the disease.
Overall Genetic Conclusion	The genetic etiology of the patient's superficial lipomatous nevus remains undetermined.	Suggests a possible non-Mendelian, mosaic, epigenetic, or yet-undiscovered genetic mechanism.