

## GEPHE SUMMARY

<p>Microphthalmia-associated transcription factor (<a href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase+Microphthalmia-associated+transcription+factor">#gephebase-summary-title</a>)</p> <p>Published</p>	<p>Gephebase Gene</p> <p>GP00002325</p> <p>Martin</p> <p>Entry Status</p>	<p>GepheID</p> <p>Main curator</p>
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## PHENOTYPIC CHANGE

<p>Morphology (<a href="https://www.gephebase.org/search-criteria?/and+Trait+Category+Morphology">#gephebase-summary-title</a>)</p> <p>Coloration (coat) (<a href="https://www.gephebase.org/search-criteria?/and+Trait+Coloration+coat">#gephebase-summary-title</a>)</p> <p>Equus caballus</p> <p>American Paint Horse with white spotting</p> <p>Taxon A</p> <p>Domesticated (<a href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status+Domesticated">#gephebase-summary-title</a>)</p>	<p>Trait Category</p> <p>Trait</p> <p>Trait State in Taxon A</p> <p>Trait State in Taxon B</p> <p>Ancestral State</p> <p>Taxonomic Status</p>	<p>Equus caballus</p> <p>horse</p> <p>Equus przewalskii f. caballus; Equus przewalskii forma caballus; horse; domestic horse; equine; Equus caballus Linnaeus, 1758</p> <p>species</p> <p>cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Laurasiatheria; Perissodactyla; Equidae; Equus; Equus</p> <p>Equus () - (Rank: subgenus) (<a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=35510">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=35510</a>)</p> <p>9796 (<a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9796">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9796</a>)</p> <p>No</p>	<p>Latin Name</p> <p>Common Name</p> <p>Synonyms</p> <p>Rank</p> <p>Lineage</p> <p>Parent</p> <p>NCBI Taxonomy ID</p> <p>is Taxon A an Intraspecies?</p>	<p>Equus caballus</p> <p>horse</p> <p>Equus przewalskii f. caballus; Equus przewalskii forma caballus; horse; domestic horse; equine; Equus caballus Linnaeus, 1758</p> <p>species</p> <p>cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Laurasiatheria; Perissodactyla; Equidae; Equus; Equus</p> <p>Equus () - (Rank: subgenus) (<a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=35510">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=35510</a>)</p> <p>9796 (<a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9796">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9796</a>)</p> <p>Yes</p>	<p>Latin Name</p> <p>Common Name</p> <p>Synonyms</p> <p>Rank</p> <p>Lineage</p> <p>Parent</p> <p>NCBI Taxonomy ID</p> <p>is Taxon B an Intraspecies?</p> <p>Taxon B Description</p>
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## GENOTYPIC CHANGE

<p>Mitf</p> <p>Wh; bw; mi; vit; BCC2; Bhlhe32; Gsfbcc2; Vitiligo; Bw; Mi; Vit</p> <p>10090.ENSMUSP00000044938 (<a href="http://string-db.org/newstring.cgi/show_network_section.pl?identifier=10090.ENSMUSP00000044938">http://string-db.org/newstring.cgi/show_network_section.pl?identifier=10090.ENSMUSP00000044938</a>)</p> <p>Belongs to the MiT/TFE family.</p> <p>GO:0046983 : protein dimerization activity (<a href="https://www.ebi.ac.uk/QuickGO/term/GO:0046983">https://www.ebi.ac.uk/QuickGO/term/GO:0046983</a>)</p> <p>GO:0003700 : DNA-binding transcription factor activity</p>	<p>Generic Gene Name</p> <p>Synonyms</p> <p>String</p> <p>Sequence Similarities</p> <p>GO - Molecular Function</p>	<p>Q08874 (<a href="http://www.uniprot.org/uniprot/Q08874">http://www.uniprot.org/uniprot/Q08874</a>)</p> <p>()</p>	<p>UniProtKB Mus musculus</p> <p>GenebankID or UniProtKB</p>
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(<https://www.ebi.ac.uk/QuickGO/term/GO:0003700>)  
 GO:0043565 : sequence-specific DNA binding  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0043565>)  
 GO:0003677 : DNA binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0003677>)  
 GO:0003682 : chromatin binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0003682>)  
 GO:0000981 : DNA-binding transcription factor activity, RNA polymerase II-specific  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0000981>)  
 GO:0001077 : proximal promoter DNA-binding transcription activator activity, RNA  
 polymerase II-specific (<https://www.ebi.ac.uk/QuickGO/term/GO:0001077>)  
 GO:0000978 : RNA polymerase II proximal promoter sequence-specific DNA binding  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0000978>)  
 GO:0070888 : E-box binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0070888>)  
 GO:0003705 : transcription factor activity, RNA polymerase II distal enhancer sequence-  
 specific binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0003705>)

GO - Biological Process

GO:0043066 : negative regulation of apoptotic process  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0043066>)  
 GO:0045944 : positive regulation of transcription by RNA polymerase II  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0045944>)  
 GO:0006357 : regulation of transcription by RNA polymerase II  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0006357>)  
 GO:0006355 : regulation of transcription, DNA-templated  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0006355>)  
 GO:0030154 : cell differentiation (<https://www.ebi.ac.uk/QuickGO/term/GO:0030154>)  
 GO:0043473 : pigmentation (<https://www.ebi.ac.uk/QuickGO/term/GO:0043473>)  
 GO:0000122 : negative regulation of transcription by RNA polymerase II  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0000122>)  
 GO:0045893 : positive regulation of transcription, DNA-templated  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0045893>)  
 GO:0010628 : positive regulation of gene expression  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0010628>)  
 GO:0006351 : transcription, DNA-templated  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0006351>)  
 GO:0045165 : cell fate commitment (<https://www.ebi.ac.uk/QuickGO/term/GO:0045165>)  
 GO:0010468 : regulation of gene expression  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0010468>)  
 GO:0030318 : melanocyte differentiation  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0030318>)  
 GO:0043010 : camera-type eye development  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0043010>)  
 GO:0030316 : osteoclast differentiation  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0030316>)  
 GO:0042127 : regulation of cell proliferation  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0042127>)  
 GO:0046849 : bone remodeling (<https://www.ebi.ac.uk/QuickGO/term/GO:0046849>)  
 GO:0044336 : canonical Wnt signaling pathway involved in negative regulation of apoptotic  
 process (<https://www.ebi.ac.uk/QuickGO/term/GO:0044336>)  
 GO:0030336 : negative regulation of cell migration  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0030336>)  
 GO:2000144 : positive regulation of DNA-templated transcription, initiation  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:2000144>)  
 GO:0065003 : protein-containing complex assembly  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0065003>)  
 GO:0045670 : regulation of osteoclast differentiation  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0045670>)  
 GO:2001141 : regulation of RNA biosynthetic process  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:2001141>)  
 GO:0016055 : Wnt signaling pathway  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0016055>)

GO - Cellular Component

GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)  
 GO:0032991 : protein-containing complex  
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0032991>)

Yes ([#gpebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive+Null=~Yes)) Presumptive Null  
 Coding ([#gpebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular+Type=~Coding)) Molecular Type  
 Deletion ([#gpebase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration+Type=~Deletion)) Aberration Type  
 10-100 kb Deletion Size  
 8.7 kb deletion Molecular Details of the Mutation  
 Candidate Gene ([#gpebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=~Candidate+Gene)) Experimental Evidence  
 A De Novo MITF Deletion Explains a Novel Splashed White Phenotype in an American Paint Horse. (2020) (<https://pubmed.ncbi.nlm.nih.gov/32242630>) Main Reference  
 Authors

Splashed white is a coat color pattern in horses characterized by extensive white patterning on the legs, belly, and face often accompanied by blue eyes and deafness. Three mutations in microphthalmia-associated transcription factor (MITF) and two mutations in Paired Box 3 (PAX3) have been identified that explain splashed white patterns (SW1-SW5). An American Paint Horse stallion with a splashed white phenotype and blue eyes, whose parents were not white patterned, was negative for the 5 known splashed white variants and other known white spotting alleles. This novel splashed white phenotype (SW6) was hypothesized to be caused by a de novo mutation in MITF or PAX3. Analysis of whole-genome sequencing using the EquCab3.0 reference genome for comparison identified an 8.7 kb deletion in MITF on ECA16 (NC\_009159.3:g.21551060-21559770del). The deletion encompassed part of intron 7 through the 3' UTR of exon 9 of MITF, including the helix-loop-helix DNA-binding domain (ENSECAT0000006375.3). This variant is predicted to truncate protein and impair binding to DNA. Sanger sequencing confirmed the stallion was heterozygous for the MITF deletion. No single nucleotide polymorphisms (SNPs) or structural variants were identified in PAX3 or any of the other candidate genes that were unique to the stallion or predicted to affect protein function. Genotyping five of the stallion's splashed white offspring, including one all white foal, found that they were also heterozygous for the deletion. Given the role of MITF in producing white pattern phenotypes, and the predicted deleterious effect of this mutation, this 8.7 kb deletion is the likely causal variant for SW6.

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Additional References

## RELATED GEPHE

Related Genes

13 (Agouti, Endothelin receptor B, Kit (type III receptor protein-tyrosine kinase), MC1R, MFSD12, Pax3, PMEL17, SLC24A, SLC36A1, SLC45A2=MATP, syntaxin-17, T-box transcription factor (TBX3), TRPM1) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=^9796^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

5 (<https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^Microphthalmia-associated transcription factor^/and+Taxon ID=^9796^/or+Gene Gephebase=^Microphthalmia-associated transcription factor^/and+Taxon ID=^9796^#gephebase-summary-title>)

## EXTERNAL LINKS

## COMMENTS

@Parallelism @HeterozygoteAdvantage <https://omia.org/OMIA000214/9796/>