

WIF1 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~WIF1^#gephebase-summary-title)	Gephebase Gene	GP00002255	GepheID
Published	Entry Status	Martin	Main curator

Morphology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Morphology~#gephebase-summary-title)		Trait Category	
Ear size (https://www.gephebase.org/search-criteria?/and+Trait=~Ear+size~#gephebase-summary-title)		Trait	
WT ear size		Trait State in Taxon A	
Large ears in Large White and Minzhu breeds		Trait State in Taxon B	
Taxon A		Ancestral State	
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Domesticated~#gephebase-summary-title)		Taxonomic Status	
Taxon A		Taxon B	
Latin Name		Latin Name	
Sus scrofa (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Sus+scrofa~#gephebase-summary-title)		Sus scrofa (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Sus+scrofa~#gephebase-summary-title)	
Common Name		Common Name	
pig		pig	
Synonyms		Synonyms	
pig; pigs; swine; wild boar; Sus scrofa Linnaeus, 1758; Sus scrofus		pig; pigs; swine; wild boar; Sus scrofa Linnaeus, 1758; Sus scrofus	
Rank		Rank	
species		species	
Lineage		Lineage	
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus		cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus	
Parent		Parent	
Sus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9822)		Sus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9822)	
NCBI Taxonomy ID		NCBI Taxonomy ID	
9823 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9823)		9823 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9823)	
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
No		No	

WIF1	Generic Gene Name	Q9Y5W5 (http://www.uniprot.org/uniprot/Q9Y5W5)	UniProtKB Homo sapiens
WIF-1; UNQ191/PRO217	Synonyms	Q86YH6 (https://www.ncbi.nlm.nih.gov/nuccore/Q86YH6)	GenebankID or UniProtKB
9606.ENSPP00000286574 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9606.ENSPP00000286574)	String		
	Sequence Similarities		
-			
GO:0005102 : signaling receptor binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005102)	GO - Molecular Function		
GO:0017147 : Wnt-protein binding (https://www.ebi.ac.uk/QuickGO/term/GO:0017147)			
GO:0007275 : multicellular organism development (https://www.ebi.ac.uk/QuickGO/term/GO:0007275)	GO - Biological Process		
GO:0007165 : signal transduction (https://www.ebi.ac.uk/QuickGO/term/GO:0007165)			

GO:0045600 : positive regulation of fat cell differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045600>)
GO:0016055 : Wnt signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016055>)
GO:0048856 : anatomical structure development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048856>)
GO:0030178 : negative regulation of Wnt signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030178>)

GO - Cellular Component

GO:0005576 : extracellular region (<https://www.ebi.ac.uk/QuickGO/term/GO:0005576>)
GO:0009986 : cell surface (<https://www.ebi.ac.uk/QuickGO/term/GO:0009986>)

Presumptive Null

No ([https://www.gephebase.org/search-criteria?/and+Presumptive Null="+No^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive Null=))

Molecular Type

Coding ([https://www.gephebase.org/search-criteria?/and+Molecular Type="+Coding^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular Type=))

Aberration Type

SNP ([https://www.gephebase.org/search-criteria?/and+Aberration Type="+SNP^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration Type=))

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

p.Phe236Leu

Experimental Evidence

Candidate Gene ([https://www.gephebase.org/search-criteria?/and+Experimental Evidence="+Candidate Gene^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental Evidence=))

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Phe	Leu	236

Main Reference

Molecular cloning of WIF1 and HMGA2 reveals ear-preferential expression while uncovering a missense mutation associated with porcine ear size in WIF1. (2019)
(<https://pubmed.ncbi.nlm.nih.gov/30815903>)

Authors

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Abstract

Considerable diversity exists in porcine ear size, which is an important morphological feature of pig breeds. Previously, we localized four crucial candidate genes-high mobility group AT-hook 2 (HMGA2), LEM domain-containing 3 (LEMD3), methionine sulfoxide reductase B3 (MSRB3) and Wnt inhibitory factor 1 (WIF1)-on Sus Scrofa chromosome 5 affecting porcine ear size, then cloned LEMD3 and MSBR3. In this study, we performed rapid amplification of cDNA ends to obtain full-length cDNA sequences of 2338-bp WIF1 and 2998-bp HMGA2. Using quantitative real-time PCR, we revealed that WIF1 expression was highest in ear cartilage of 60-day-old pigs and that this is therefore a better candidate gene for ear size than HMGA2. We further screened coding sequence variants in both genes and identified only one missense mutation (WIF1:c.1167C>G) in a conserved epidermal growth factor-like domain from the mammalian WIF1 protein. The protein-altering mutation was significantly associated with ear size across the Large White×Minzhu hybrid and Beijing Black pig populations. When WIF1:c.1167C>G was included as fixed effect in the model to re-run a genome-wide association study in the Large White×Minzhu intercross population the P-value of the peak SNP on SSC5 from re-running the genome-wide association study dropped from 2.45E-12 to 7.33E-05. Taken together, the WIF1:c.1167C>G could be an important mutation associated with ear size. Our findings provide helpful information for further studies of the molecular mechanisms controlling porcine ear size.

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Additional References

RELATED GEPHE

Related Genes

2 (HMGA2, PPAR-delta) ([https://www.gephebase.org/search-criteria?/or+Taxon ID="+9823^/and+Trait=Ear size/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon ID=))

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

<https://omia.org/OMIA001579/9823/>

