Table 1 Phenotypic traits of the domestic cat conferred by DNA variants

Locus (Alleles) OMIA entry link	MOI*	Phenotype	Gene	Gene name	Mutation
Agouti (A^+, *a*)[5] 000201-9685	AR	Banded fur to solid	*ASIP*	*Agouti-signaling protein*	c.122_123delCA
Brown (B^+, *b*, b^l)[6,7] 001249-9685	AR	Brown, light brown color variants	*TYRP1*	*Tyrosinase-related protein*	b = -5IVS6 b^l = c.298C>T
Color (C^+, C^b, C^s, *c*)[7–9] 000202-9685	AR	Burmese, Siamese color pattern, full albino	*TYR*	*Tyrosinase*	c^b = c.715G>T c^s = c.940G>A c = c.975delC
Dilution (D^+, *d*)[10] 000206-9685	AR	Black to grey/blue, orange to cream	*MLPH*	*Melanophilin*	c.83delT
Dwarfism 000299-9685	AD	Shortening of long bones	unknown	unknown	unknown
Extension (E^+, *e*) – *Amber*[11] 001199-9685	AR	Brown/red color variant	*MC1R*	*Melanocortin receptor 1*	c.250G>A
Fold (Fd, fd^+) 000319-9685	AD	Ventral ear fold	unpublished	unpublished	unpublished
Gloves (G^+, *g*)[12] 001580-9685	AR	White feet	*KIT*	*KIT*	c.1035_1036delinsCA
Hairless (Hr^+, *hr*)[13]	AR	Atrichia	*KRT71*	*Keratin 71*	c.816+1G>A
Inhibitor (I, i^+) 001584-9685	AD	Absence of pheomelanin	unknown	unknown	unknown
Japanese Bobtail (J, j^+)	AD	Kinked tail	unknown	unknown	unknown
Kurl (K, k^+) 000244-9685	AD	Rostral curled pinnae	unknown	unknown	unknown
LaPerm 000245-9685	AD	Curly hair coat	unknown	unknown	unknown
Longhair (L^+, *l*)[14,15] 000439-9685	AR	Long fur	*FGF5*	*Fibroblast growth factor 5*	c.356_367insT c.406C>T c.474delT c.475A>C
Tailless (Manx) (M, m^+)[16] 000975-9685	AD	Absent/short tail	*TBOX*	*T-box*	c.998delT c.1169delC c.1199delC c.998_1014dup17delGCC
Orange (O, o^+) 001201-9685	X-linked	Change in pigment hue	unknown	unknown	unknown
Peterbald 001866-9685	AD	Hairless, brush coat	unknown	unknown	unknown
Polydactyla (Pd, pd^+)[17] 000810-9685	AD	Extra toes	*SHH*	*Sonic hedgehog*	c.479A>G c.257G>C c.481A>T
Rexing (R^+, *r*)[18] 001684-9685	AR	Curly hair coat	*LPAR6*	*Lysophosphatidic acid receptor 6*	c.250_253delTTTG
Rexing (Re^+, *re*)[13] 001581-9685	AR	Curly hair coat	*KRT71*	*Keratin 71*	c.1108-4_1184del, c.1184_1185insAGTTGGAG c.1196insT
Rexing (R^S, r^{s+})[19] 001712-9685	AD	Curly hair coat	*KRT71*	*Keratin 71*	c.445-1G>C
Spotting (S, s^+)[20] 000214-9685	Co-D	Bicolor/Van white	*KIT*	*KIT*	7125ins FERV1 element
Tabby (T^M, t^b)[21] 001429-9685	AR	Blotched/classic pattern	*TAQPEP*	*Transmembrane aminopeptidase Q*	c.176C>A c.416C>A c.682C>A c.2522G>A
Ticked (Ti^a, *ti*) 001484-9685	AD	No tabby pattern	unknown	unknown	unknown
White (W, w^+)[20] 000209-9685	AD	Loss of pigmentation	*KIT*	*KIT*	FERV1 LTR ins
Wide-band	AR?	Length of pheomelanin band in hair	unknown	unknown	unknown

*Mode of inheritance of the non-wild type variant. '+' implies the wild type allele when known. In reference to the mutant allele, AD = autosomal dominant, AR = autosomal recessive, co-D = co-dominant.
OMIA: Online Mendelian Inheritance in Animals (omia.angis.org.au) entries provide links to citations and clinical descriptions of the phenotypes and the diseases. Listed citations are for the causative variant discovery