

A

rs12713768: C>A

<i>Homo sapiens</i>	87	GAAACCACTCAGG	CCCTGGCCAGGTTCTCCTGTC	AACAGGCCAGCCTGAGACAGTCCA
<i>Pan troglodytes</i>	87	GAAACCACTCAGG	CCCTGGCCAGGTTCTCCTGTC	AACAGGCCAGCCTGAGACAGTCCA
<i>Gorilla gorilla</i>	87	GAAACCACTCAGG	CCCTGGCCAGGTTCTCCTGTC	AACAGGCCAGCCTGAGACAGTCCA
<i>Macaca mulatta</i>	116	AGCACACTCT	CCCTCCCTCCATCTGTCTGACTAATAGTCCCTTCTGCAA	
<i>Papio anubis</i>	87	GAAACCACTCAGG	CCCTGGCCAGGTTCTCCTGTC	AACAGGCCAGCCTGAGACAGTCCA
<i>Pongo abelii</i>	116	AGCACACTCT	CCCTCCCTCCATCTGTCTGACTAATAGTCCCTTCTGCAA	
<i>Chlorocebus sabaeus</i>	116	AGCACACTCT	CCCTCCCTCCATCTGTCTGACTAATAGTCCCTTCTGCAA	
<i>Callithrix jacchus</i>	87	GAAACCACTC	GGCCCTGGCCAGGTTCTCCTGTC	AACAGGCCAGCCTGAGACAGTCCA
<i>Sus scrofa</i>	102	AGCACACTCT	CCCTCCCTCCATCTGTCTGACTAATAGTCCCTTCTGCGA	
<i>Felis catus</i>	72	GAAACCACTGAGG	CCCTGGCTAGGTTCTCCCTCAGGAATGGCCAGCCGCAAGGCTCCA	
<i>Mus musculus</i>	73	GAAACCACTCAGG	CTGGCCAGGTTCTTTTGGCAAATAGGCCAGCCG	
<i>Ovis aries</i>	88	GAAACCTCTTGGG	CCCTGGCAGGTTTCCACCAAAACAGGCCACTCTGTGAGGCTCTG	
<i>Oryctolagus cuniculus</i>	69	AGCACACTCT	CTCTCCTTCCGTCTGTCTGAC	CAGATTCCATGGCAA
<i>Rattus norvegicus</i>	90	GAAACCACTCAGG	CTGGCCAGGTTCTTTTGGGC	CACAGGCCAGC
<i>Equus caballus</i>	116	AGCACACTCT	CTCTCCCTTCATCTGCCTGACTAATGTTCCCATTTGCAA	
<i>Canis familiaris</i>	118	AGCACGTCTCT	CCCTCCC	TCTCTCTGACTAATGTTTCCATCTGTGA
<i>Bos taurus</i>	117	AGCACACTCT	CCCTCCTCTGTCTGTCTGACTAATGCTCCCATTAAGCAA	
consensus	121	gaaACcatCT	ggCcCtggc aggTttttctgaC	aAtaggcCagcctg ga

B

Organism	Chr	Identity ^a	Distance (bp) ^b	Gene ^c	Location ^d	Accession
<i>Pan troglodytes</i>	2A	100%	118532	LOC738157	Chr2A: 72,283,693-72,302,973	NC_036880.1
<i>Gorilla gorilla</i>	2A	99.50%	118598	LOC101126229	Chr2A: 88,488,277-88,506,890	NC_044603.1
<i>Macaca mulatta</i>	13	98.51%	104361	LOC704750	Chr13: 36,656,295-36,675,586	NC_041766.1
<i>Papio anubis</i>	14	98.51%	104537	CYP26B1	Chr14: 72,460,531-72,479,135	NC_044989.1
<i>Pongo abelii</i>	2A	98.01%	105239	LOC100446166	Chr2A: 36,432,062-36,452,148	NC_036904.1
<i>Chlorocebus sabaeus</i>	14	96.52%	97379	CYP26B1	Chr14: 35,030,011-35,057,164	NC_023655.1
<i>Callithrix jacchus</i>	14	94.55%	106747	CYP26B1	Chr14: 37,259,670-37,279,488	NC_048396.1
<i>Sus scrofa</i>	3	82.21%	104699	LOC100521659	Chr3: 70,573,551-70,593,416	NC_010445.4
<i>Felis catus</i>	A3	80.85%	81186	CYP26B1	ChrA3: 91,168,443-91,189,206	NC_018725.3
<i>Mus musculus</i>	6	80.83%	82692	CYP26B1	Chr6: 84,548,396-84,570,890	NC_000072.7
<i>Ovis aries</i>	3	78.43%	128627	LOC101110922	Chr3: 100,383,775-100,400,597	NC_040254.1
<i>Oryctolagus cuniculus</i>	2	78.06%	89698	LOC100341926	Chr2: 114,279,277-114,297,359	NC_013670.1
<i>Rattus norvegicus</i>	4	77.61%	94475	CYP26B1	Chr4: 116,261,796-116,278,615	NC_005103.4
<i>Equus caballus</i>	15	76.96%	97426	CYP26B1	Chr15: 31,695,380-31,715,089	NC_009158.3
<i>Canis familiaris</i>	17	74.76%	78225	CYP26B1	Chr17: 50,633,397-50,653,882	NC_006599.3
<i>Bos taurus</i>	11	74.61%	116041	CYP26B1	Chr11: 12,371,161-12,396,520	NC_037338.1

Chr, chromosome.

^asimilarity retrieved from 100bp flanking sequences up- and downstream of SNP rs12713768 compared to human

^bdistance from C allele of rs12713768 to the coding sequence of CYP26B1 gene

^cname of CYP26B1 gene in each organism retrieved from NCBI

^dposition of CYP26B1 gene in each organism

Supplementary Figure S3. The risk-conferring C allele of SNP rs12713768 is **A** conserved and **B** located within 150kb from gene CYP26B1 across 16 mammalian genomes.