Supplemental Data

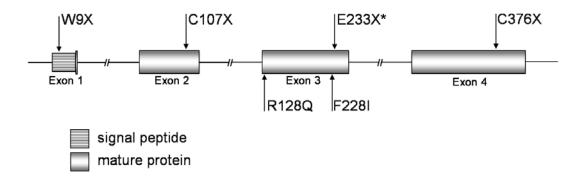
WNT10A Mutations Are a Frequent Cause

of a Broad Spectrum of Ectodermal Dysplasias

with Sex-Biased Manifestation Pattern in Heterozygotes

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Figure S1. Distribution of Previously Known and Recently Identified Mutations within the *WNT10A* Gene



Previously known mutation is marked by an asterisk (see ref. 1).

Figure S2. Evolutionary Conservation of *WNT10A* p.128R and p.228F Amino Acids

	R128Q	F228I
Homo sapiens	YESPIFSRGF R ESAFAYAIAA	.MGFGERFSKD F LDSREPHRDI
Pan troglodytes	YESPIFSRGF R ESAFAYAIAA	.MGFGERFSKD F LDSREPHRDI
Macaca mulatto	YESPIFSRGF R ESAFAYAIAA	.MGFGERFSKD F LDSREPHRDI
Rattus norvegicus	YESPIFSRGF R ESAFAYAIAA	.VGFGERFSKD F LDSREPHRDI
Mus musculus	YESPIFSRGF R ESAFAYAIAA	.VGFGERFSKD F LDSREPHRDI
Canis lupus	YESPIFSRGF R ESAFAYAIAA	.VGFGERFSKD F LDSREPHRDI
Gallus gallus	YESIIFSRGF R ESAFAYAIAA	.VDYGEKFSKD F LDSRETYRDI
Xenopus laevis	YDSAVFSRGF R ESAYVYAIAA	.VEYGERFSKE F LDSRELFRDI
D.melanogaster	HASSLLKKGY R ESAFAFAISA	.MDFGVEYSKL F LDCREKAGDI

NCBI Protein Database: http://www.ncbi.nlm.nih.gov/protein/ (for Homo sapiens [NP_079492.2], Pan troglodytes [XP_516098.2], Macaca mulatto [XP_001095740.1], Rattus norvegicus [NP_001101697.1], Mus musculus [NP_033544.1], Canis lupus [XP_545648.2], Gallus gallus [NP_001006590.1], Xenops laevis [NP_001092186.1], and D. melanogaster [NP_609109.2]).

Figure S3. Symptoms in Patients with *WNT10A* Associated Ectodermal Dysplasia



Facial phenotype in five patients (**a-h**). Note variability concerning hypotrichosis, sparse eyebrows, and facial skin erythema. Palmar hyperkeratosis (**i**) can be mild and nails may be differently affected in the same patient (**j**). Numerous cysts along eyelid margins (**k**) are a typical finding in Schöpf-Schulz-Passarge syndrome.

Figure S4. Dental and Oral Findings in Patients with *WNT10A* Associated Ectodermal Dysplasia



Dentition of patient 7 (**a-c**) at age 12 years and patient 12 (**d-f**) at age 12 years. Teeth are marked with an identity number (FDI Two-Digit Notation). In this two-digit numbering, the first number represents a tooth's quadrant (1 = upper right, 2 = upper left, 3 = lower left, and 4= lower right). The second number represents the number of the tooth from the midline of the face (1 = central incisor, 2 = lateral incisor, 3 = canine, 4 = first premolar, 5 = second premolar, 6 = first molar, 7 = second molar, 8 = wisdom tooth). For deciduous teeth, the system varies slightly, the quadrants are numbered from 5 to 8 (5 = upper right, 6 = upper left, 7 = lower left, and 8 = lower right). In patient 12, the identity of a conical permanent tooth (c) cannot be determined. The tongues (**g,h**) show reduced filiform and fungiform papillae. Panoramic radiograph (**i**) of patient 8 at age eight years shows severe oligodontia concerning the permanent teeth (upper right quadrant with 17, 55, 54, 53, 52, 11, and permanent tooth germs of the second premolar and canine, upper left quadrant with 21, 62, 63, 64, 65, 26, and permanent canine tooth germ, lower left and right quadrant with complete deciduous dentition and permanent first molars as well as tooth germs of both permanent canines).

AJHG, Volume 85

Table S1. Primer Sequences and PCR Conditions

Primer	Forward sequence	Reverse sequence	Amplified Segment	Annealing temperature
Exon 1	gagtcggagctgtgtgtcg	gagctcactgcctttggttg	385	60°C
Exon 2	ccgttgggacagagtgtgtg	cagcttgaggcagtgggttag	441	62°C
Exon 3	gggcttcagtttctccttgg	agcaacgtggtcctcagaag	570	60°C
Exon 4-1	gggagtgggtttcagaagcag	ctggcgcaggatgttgtg	493	56°C
Exon 4-2	cctggtctacttcgaaaagtctcc	acagaagtgagtggtggggttc	452	58°C

Table S2. Mutational Analysis in Control DNA Samples

			Analyzed Controls by		Chromosomes with		Frequency	
DNA Modification	Exon	Predicted Relevance	Mutation Restriction	High Resolution Melting	Sequencing	Wildtype	Substitution	-
c.27G>A	1	pathogenic	194	-	-	388	-	Unknown
c.321C>A	2	pathogenic	160	-	-	320	-	Unknown
c.383G>A	3	pathogenic	132	-	96	456	-	Unknown
c.493G>A	3	SNP [ss131007345]#	-	121	96	431	3	~0.7%
c.682T>A	3	pathogenic	-	102	96	394	2	~0.5%
c.1128C>A	4	pathogenic	-	-	103	206	-	Unknown

^{# =} refSNP ID [dbSNP Database]

Table S3. Restriction Endonucleases and HRM Primer Pairs

DNA Modification	Exon	Restriction Endonuclease /	
		HRM Primer Pairs	
c.27G>A	1	BsaXI	
c.321C>A	2	Bcll	
c.383G>A	3	Hpy188I	
c.493G>A	3	ccgtgtccaatgcgtgtg	
		gcagggctgggtgttcc	
c.682T>A	3	ccagccctgcccacag	
		tctcacctgcctcccaactc	
c.1128C>A	4	gccgacctggtctacttcg	
		cagacgctgacccactcg	

Supplemental Reference

1. Adaimy, L., Chouery, E., Mégarbané, H., Mroueh, S., Delague, V., Nicolas, E., Belguith, H., de Mazancourt, P., and Mégarbané, A. (2007). Mutation in WNT10A is associated with an autosomal recessive ectodermal dysplasia: the odonto-onycho-dermal dysplasia. Am. J. Hum. Genet. *81*, 821–828.