

Molecular evolution of *HR*, a gene that regulates the postnatal cycle of the hair follicle

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Supplementary Table: DNA sequence variations in human *HR*.

SNP	dbSNP Number (build 131)	Coding exon (<i>HR</i>)	Position (GRCh37)	Nucleotide change	Validation
1	rs77620102	1	21986657-21986657	C to T	by-cluster,by-frequency,by-1000genomes
2	rs73549525	1	21986496-21986496	G (P) to C(R)	by-cluster,by-frequency,by-1000genomes
3	rs12679538	1	21986395-21986395	G (L) to T (M)	by-cluster,by-frequency,by-hapmap
4	rs79783229	2	21985226-21985226	G to A	by-1000genomes
5	rs77758962	2	21984999-21984999	G (P) to A (L)	by-cluster,by-frequency,by-1000genomes
6	rs12675375	2	21984945-21984945	C(G) to T(D)	by-cluster,by-frequency,by-hapmap,by-1000genomes
7	rs73549523	2	21984765-21984765	C (C) to T (Y)	by-cluster,by-frequency,by-1000genomes
8	rs12675745	2	21984650-21984650	A to G	by-cluster,by-frequency,by-hapmap,by-1000genomes
9	rs78489044	2	21984596-21984596	C to T	by-1000genomes
10	rs78703240	3	21983190-21983190	G to A	by-frequency,by-1000genomes
11	rs73549518	3	21983124-21983124	C to T	by-cluster,by-1000genomes
12	rs76691356	3	21983120-21983120	C (A) to G (P)	by-frequency,by-1000genomes
13	rs56140348	4	21982997-21982997	A (L) to G (P)	by-cluster,by-1000genomes
14	rs75362423	5	21981170-21981170	T (E) to C (G)	by-cluster,by-frequency,by-1000genomes
15	rs78939934	6	21980352-21980352	G to A	by-1000genomes
16	rs77689228	9	21978734-21978734	G to A	by-frequency,by-1000genomes
17	rs58080661	9	21978578-21978578	A to G	by-cluster,by-1000genomes
18	rs57903149	10	21978469-21978469	A to G	by-cluster,by-1000genomes
19	rs76547188	10	21978372-21978372	C (G) to T (S)	by-cluster,by-frequency,by-1000genomes
20	rs11990451	11	21977898-21977898	G (S) to T (R)	by-cluster,by-hapmap
21	rs11990450	11	21977897-21977897	G to A	by-hapmap
22	rs11990421	11	21977860-21977860	G (P) to A (L)	by-cluster,by-hapmap
23	rs79077385	13	21977390-21977390	C (A) to G (P)	by-frequency,by-1000genomes
24	rs7014851	14	21976710-21976710	T (T) to C (A)	by-cluster,by-frequency

Reference number, nucleotide positions within each exon, direction of change and validation source for 24 intraspecific coding polymorphisms used in neutrality tests. Direction of nucleotide changes are determined by using chimpanzee, orangutan and macaque as outgroup. The amino acid changes are given (bracket enclosed-fifth column) for non-synonymous nucleotide changes.