HAPLOTYPE SOURCE	# CLONES/ # TOTAL CLONES SEQ'D	EXON	1		2	3						4				6									
		SEQUENCE VARIANT	C/T	C/T	A/G	A/G	G/C	G/A	G/A	T/C	C/G	T/G/*	T/C	T/C	C/T	T/C	G/C	G/A	C/T	C/T	G/A	C/T	G/T	G/A	C/T
		AMINO ACID	L/F	A/V	Q/R	E/G	T	G/S	G/D	S/P	P/A	Y/D/*	P	C	V	I	D/H	P	P/S	P	A/T	N	S/I	P	A/V
		GENOMIC CO-ORD	163	209	6632	6972	7002	7003	7004	7033	7059	7276	7284	7290	7365	8003	8004	8012	8031	8033	8040	8045	8059	8108	8152
		VARIATION NO.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23
BC048328	n.a.		C	C	G	A	G	G	G	T	C	T	T	T	C	T	G	G	C	C	G	C	G	G	C
CHR 20 HYB PANEL A	n.a.		T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
CHR 20 HYB PANEL B	n.a.		T	T	-	-	-	-	-	-	-	G	C	C	-	-	-	A	-	-	-	-	T	A	-
CHR 9 ASSEMBLY	n.a.		T	-	A	G	-	-	-	C	-	G	-	C	-	C	C	A	-	-	-	-	-	A	T
GM10540.genomic.1	1/15		n.d.	n.d.	n.d.	-	C	A	-	C	-	-	-	C	-	-	-	A	T	T	-	T	T	A	T
GM10540.genomic.2*	2/15		n.d.	n.d.	n.d.	-	C	A	-	C	-	G	-	C	-	-	-	A	T	T	-	T	T	A	T
GM10540.fs9-12.1	2/4		n.d.	n.d.	n.d.	-	C	-	-	C	-	G	-	C	-	-	-	A	T	-	-	T	T	A	T
GM10540.fs20.1*	3/3		n.d.	n.d.	n.d.	-	C	A	-	C	-	G	-	C	-	-	-	A	T	T	-	T	T	A	T
GM07791.fs9-12.1	3/3		n.d.	n.d.	n.d.	-	C	-	-	C	-	G	-	C	T	-	-	A	T	-	-	T	T	A	T
GM07791.fs20.1	7/7		n.d.	n.d.	n.d.	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
GM10494.genomic.1	1/10		n.d.	n.d.	n.d.	-	C	-	-	-	-	G	-	C	-	-	C	A	-	-	A	T	T	A	T
GM10494.genomic.2	1/10		n.d.	n.d.	n.d.	-	-	-	-	C	-	G	-	C	-	-	C	A	-	-	-	-	T	A	T
GM10494.genomic.3	1/10		n.d.	n.d.	n.d.	-	C	-	A	C	G	G	-	C	-	-	-	A	-	-	-	-	T	A	T
GM10494.fs9-12.1	2/6		n.d.	n.d.	n.d.	-	C	-	-	C	-	G	-	C	-	-	-	A	T	-	-	T	T	A	T
GM10494.fs20.1	7/9		n.d.	n.d.	n.d.	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Supplementary Table 1. Locations of sequence variants identified in 14 different WASH ORFs that appear to be intact, at least in coding exons 2-10. We used the cDNA sequence BC048328 as reference; "-" indicates where a sequence is not different from BC048328. These variants were derived from chromosomes captured in a monochromosomal hybrid panel, certain chromosomes isolated by flow-sorting (20 or 9-12) from three individuals, and copies PCR amplified from genomic DNA (without chromosomal assignment) from the same individuals. Note: Two ORFs in one individual (with asterisks) were identical in coding sequence, but differed by 3% in intronic sequence implying that they derive from different chromosomal locations. n.a., not applicable; n.d., not determined. The SNP highlighted in blue is unconfirmed, as it was observed only once in this survey and is not a variant site in EST sequences in public databases. The variant sequences are provided in fasta format in Supplementary Data File.

7					8							9	10						
9nt/del	T/A	T/C	A/G	G/A	C/T	C/T	G/A	G/A	C/G	A/C	A/C	G/C	G/A	C/T	C/T	C/G/T	G/A	C/T	G/C
APP/del	P	P/S	S/G	A	V	R/W	G/S	V/M	L/V	K/Q	K/Q	D/H	G/R	A/V	R	L/V/L	V	D	S
8270	8289	8320	8377	8391	9086	9102	9144	9165	9180	9189	9192	9998	10198	10235	10239	10261	10263	10302	10314
24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43
9nt	T	T	A	G	C	C	G	G	C	A	A	G	G	C	C	C	G	C	G
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
del	A	C	-	-	-	T	-	A	-	-	-	C	-	-	-	-	-	-	C
del	A	C	-	A	-	T	-	A	-	C	C	C	-	T	-	T	-	-	-
del	A	C	-	-	-	T	A	A	-	-	C	C	-	-	-	-	-	-	n.d.
del	A	C	-	-	-	T	A	A	-	-	C	C	-	-	-	-	-	-	n.d.
del	A	-	-	-	-	T	-	A	G	-	-	C	A	-	-	-	-	-	n.d.
del	A	C	-	-	-	T	A	A	-	-	C	C	-	-	-	-	-	-	n.d.
del	A	-	G	-	-	T	-	A	G	-	-	C	A	-	-	-	-	-	n.d.
-	-	-	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	n.d.
del	A	C	-	-	-	T	-	A	G	-	-	C	A	-	-	G	-	C	n.d.
del	A	C	-	-	T	T	-	A	-	-	-	C	-	-	-	G	-	-	n.d.
del	A	C	-	A	-	-	-	A	G	C	C	C	-	-	-	-	-	-	n.d.
del	A	C	-	-	-	T	-	A	G	-	-	C	A	-	T	-	A	-	n.d.
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	n.d.

Synonymous Substitutions

Non-Synonymous Substitutions

Stop/Frameshift Mutations

SNPs without support