	Frequency					SAP-containing Peptides in the Hair Proteome	
SIMH	0.562	AFR 0.378	nuc rs# T rs1050565	Chr 17	SAP I443V	peptide HVPFFVI AVI FOFPIN PAWDPMGAI A-	Comment on thiastn analysis
LIVIH	0.562	0.378	A rs1050565	17	1443V	HVPEEVLAVLEQEPIILPAWDPMGALA-	Only one significant this in the human genome reference assembly to BUMH on chromosome 17. The indicated polymorphism is present in the transcript database, and is therefore a reliable SAP. No evidence of false polymorphism due to paralogy.  Only one significant this in the human genome reference assembly to BUMH on chromosome 17. The indicated polymorphism is present in the transcript database, and is therefore a reliable SAP. No evidence of false polymorphism due to paralogy.
OL4A4	0.691	0.87	G rs3752895	2	S1403P	GPoGPGCKGEPGLDGR	One match to COL4A4 transcript variant X5, no significant similarly in genome search (possibly intron disruption)
	0.821	0.581	A rs3752895	2	S1403P	GPSGPGCKGEPGLDGR	One match to COL4A4 transcript variant X5, no significant similarity in genome search (possibly intron disruption)
SP	0.269	0.642	A rs6929069	6	R1738Q	GqSEADSDKNATILELR	Only one significant hit in the human genome reference assembly: to DSP on chromosome 6. The indicated polymorphism is not present in the transcript database but the SAP is likely to be reliable. No evidence of false polymorphism due to paralogy.
SDMA	0.984	0.858	G rs6929069 C rs3894194	6	R1738Q R18Q	GRSEADSDKNATILELR GDLTPLDSLIDFK	Only one significant hit in the human genome reference assembly: to DSP on chromosome 6. The indicated polymorphism is not present in the transcript database but the SAP is likely to be reliable. No evidence of false polymorphism due to paralogy.
SDMA	0.491	0.642	C rs3894194 T rs3894194	17 17	R18Q R18Q	GDLTPLDSLIDFK OLNPAGDLTPLDSLIDFK	Only one splinfact hit in the human genome reference assembly to GSDMA on chromosome 17. Also detected in mRNAs but with no variants detected. No evidence of false polymorphism due to paralogy.
SDMA	0.699	0.476	A rs56030650	17	T314N	GHEVNLEALPK	Only one significant hit in the human genome reference assembly: to GSDMA on chromosome 17. Also detected in mRNAs but with no variants detected. No evidence of false polymorphism due to paralogy.  No significant inhirity detected with a blastis reservice, sequence too short.
	0.784		C rs56030650	17	T314N	GHEVTLEALPK	No significant similarity detected with a tblastn search; sequence too short.
SDMA	0.731		G rs7212938	17	V128L	ALETVQER	No significant similarity detected with a tblastn search; sequence too short.
	0.781	0.979	T rs7212938	17	V128L	ALETIQER	No significant similarity detected with a tblastn search; sequence too short.
STP1	0.544	0.712	G rs1695 A rs1695	11	1105V	YvSLIYTNYEAGKDDYVK YISI IYTNYEAGKDDYVK	One match to GSTP mRNAs, including the indicated polymorphism, no significant similarity is genome search (possibly intron disruption)  One match to GSTP mRNAs, including the indicated polymorphism, no significant similarity is genome search (possibly intron disruption)  One match to GSTP mRNAs, including the indicated polymorphism, no significant similarity is genome search (possibly intron disruption)
IFX R	0.264	0.028	G rs10805890	- 11	1207V	GILVDTSR	No significant similarity detected with a blasty search; sequence too spirit.
	0.971	1	A rs10805890	5	1207V	GILIDTSR	No significant similarity detected with a tblastn search; sequence too short.
IIST1H1T	0.712	0.899	C rs198844	6	V14L	MSETVPAASASAGVAAMEKLPTK	Histone H1t, other significant matches had several amino acid diffrences. No evidence of false polymoprhism due to paralogy.
	0.792	0.582	G rs198844	6	V14L	MSETVPAASASAGIAAMEKLPTK	Histone H1t, other significant matches had several amino acid diffrences. No evidence of false polymoprhism due to paralogy.
UP	0.121	0.02	T rs41283425 C rs41283425	17 17	R142H R142H	SAIVHLINYQDDAELAThALPELTK SAIVHLINYQDDAELATR	Two matches, to JUP on chromosome 17 and CTNN81 on chromosome 3. There are several fixed variants that confirm the peptide undoubtedly belongs to JUP. Therefore there is no evidence of false polymorphism due to paralogy.
IP	0.013	0	T rs143043662	17	K142H V648I	SAIVHLINYQDDAELATR NEGTATYAAAII ER	Two matches, to LIP on chromosome 17 and CTNNB1 on chromosome 3. There are several fixed variants that confirm the peptide understedy belongs to IUP. Therefore there is no evidence of false polymorphism due to paralogy.  One match to LIP in mRNSA, No similificant similarity in exeme search, cossibly due to intron disturbiscon, No evidence of false polymorphism to be caralogy.
	1	1	C rs143043662	17	V648I	NEGTATYAAAVLFR	On ematch to JUP in mRNAS. No ginificiant similarity in genome search, possibly due to intron disruption. No evidence of lades polymorphism due to paralogy.
RT1	0.042	0	A rs17678945	12	A454S	NKLNDLEDALQQ:KEDLAR	Two matches to tandem copies of KRT1 and KRT2. KRT2, however, contains a variant amino acid residue within this peptide that confirms the peptide belongs to KRT1. Therefore, there is no evidence of a false polymorphism due to paralogy. All mRNA sequences contain the ancestral variant.
RT31	0.169	0.065	A rs6503627	17	A82V	DNvELENLIR	No significant similarity detected with a tblastn search; sequence too short.
RT31	0.05		A rs112544857	17	A234V	SQYEVLVETNR ONOFYOMLOVR	No significant similarity detected with a tblastn search; sequence too short.
RT31	0.748	0.004	T rs146247884	17	V341M S222Y	QNQEYQMLLDVR ADI FAOVEVI K	No significant similarity detected with a tibiast rosearch. No significant similarity detected with a tibiast rosearch. No significant similarity detected with a tibiast rosearch sequence too short.
RT32	0.748		T rs2071561 A rs2071563	17 17	T395M	LEGEINmYR	No significant similarity detected with a talastra search; sequence too short.  No significant similarity detected with a talastra search; sequence too short.
	0.832		G rs2071563	17	T395M	LEGEINTYR	To significant similarity detected with a thists search sequence too short.  No significant similarity detected with a thists search sequence too short.
RT32	0.459	0.098	T rs72830046	17	R280H	CQYEAMVEANhR	One match to KRT32 with no detection of polymorphism in mRNAs. No evidence of false polymorprhism due to paralogy.
	0.939	1	c rs72830046	17	R280H	CQYEAMVEANRR	One match to KRT32 with no detection of polymorphism in mRNAs. No evidence of false polymorprhism due to paralogy.
RT33A RT33R	0.446	0.597	A rs12937519 G rs114488848	17	A270V V279L	QVVSSSEQLQSYQvEIIELR TINALFIELQAQHINLR	Multiple matches in genome search, all withing the KRT gene family on chromosome 17, including pseudogenes, with no distinguishing variants elsewhere in the sequence. The mRNA search, however, revealed two mRNAs with the derived AZ70V variant, both from KRT33A, so the polymorphism is probably in thi
RT33B RT34	0.575	0.02	G rs114488848	17	V279L 1238T	SOYFALVEINR	Multiple matches in genome and mRNA search to SRT gene family on chromosome 17, including pseudogenes. None of the mRNAs contained the I238T variant, so the gene to which this variant belongs cannot be conclusively identified by this method. There is a possibility of a false polymophism due to paralogy. No self-match similarly detected with a blastin search: secure-nece too short.
RT35	0.373	0.089	A rs743686	17	\$36P	VSAMYSSSCKI PSI SPVAR	no significant similarity detected with a fusion security. Sequence, S169 variant not detected in any sequence. No evidence of false polymorphism due to paralogous sequences.  On enatch to K1785 in genomic assembly and in miRNA sequences, S169 variant not detected in any sequence. No evidence of false polymorphism due to paralogous sequences.
	0.778	0.927	G rs743686	17	S36P	VSAMYSSSoCKLPSLSPVAR	One match to KRT35 in genomic assembly and in mRNA sequences. S36P variant not detected in any sequence. No evidence of false polymorphism due to paralogous sequences.
RT35	0.708	0.623	C rs2071601	17	P443A	TNCSaRPICVPCPGGRF	One match to KRT35 in genomic assembly and in mRNA sequences. P443A variant detected in mRNA sequences. No evidence of false polymorphism due to paralogous sequences.
	0.798	0.859	G rs2071601	17	P443A	TNCSPRPICVPCPGGRF	One match to KRT35 in genomic assembly and in mRNA sequences. P443A variant detected in mRNA sequences. No evidence of false polymorphism due to paralogous sequences.
RT35	0.306	0.134	T rs12451652 C rs12451652	17 17	C441Y	TNySPRPICVPCPGGRF TNCSPRPICVPCPGGRF	One match to KRTS's in genomic assembly and in mRMA sequences. C441 variant not detected in mRMA sequences. The residence of false polymorphism due to paradiagous sequences. There is a common variant at MM407 present in several of the mRMA sequences. Determine the mRMA sequences for several or the mRMA sequences. There is a common variant at MM407 present in several of the mRMA sequences.
RT35	0.958	0.988	rs12451652 rs138303882	17	C441Y R163W	YETEVSLWOLVESDINGLR	One match to KR12s in genome: assembly and in mRNAs sequence far valuation of the control of the
	1	1	rs138303882	17	R163W	YETEVSLRQLVESDINGLR	Multiple matches in genome search, all withing the Kit gene family on chromosome 17, including pseudogenes, but with at least one distinguishing warrant. Best match is KRT3S. No evidence of R163W variant in mRNA. No evidence of raise polymorphism due to paralogy.
RT37	0.475	0.297	A rs9910204	17	G13C	TSFYSTSSCPLcCTMAPGAR	One match to KRT37 in both genomic and mRNA databases. No evidence of G13C variant in mRNAs. No evidence of false polymorphism due to paralogy.
	0.934	0.963	C rs9910204	17	G13C	TSFYSTSSCPLGCTMAPGAR	One match to KRT37 in both genomic and mRNA databases. No evidence of G13C variant in mRNAs. No evidence of false polymorphism due to paralogy.
RT39	0	0.02	T rs142154718		\$86N \$86N	FSLDDCnWYGEGINSNEK FSLDDCSWYGEGINSNEK	One match to KRT39 in both genomic and mRNA databases. No evidence of \$86N variant in mRNAs. No evidence of false polymorphism due to paralogy.
RT40	0.433	0.11	C rs142154718 G rs150812789	17	586N C349R	TASALEIELQAQOSLTESLECTVAETEAQYSSQLAQIQILIDNLENQLAEIR	One match to KRT39 in both genomic and mRNA databases. No evidence of S86N variant in mRNAs. No evidence of faste polymorphism due to paralogy.  One match to KRT40 in both genomic and mRNA databases. No evidence of S86N variant in mRNAs. No evidence of faste polymorphism due to paralogy.  One match to KRT40 in both genomic and mRNA databases. No evidence of s86N polymorphism due to paralogy.
1140	0.931	0.992	A rs150812789	17	C349R		One match to KRT40 in both genome, and and RMA databases. C3499 variant detected in mines, are independent of false polymorphism due to paralogy.  One match to KRT40 in both genome, and mRMA databases. C3499 variant detected in mRMA. No evidence of false polymorphism due to paralogy.
RT40	0.647	0.925	C rs2010027	17	R235H	NHEEEVNLLREQLGDR	One match to KRT40 in both genomic and mRNA databases, albeit with two variants in the genomic database. The protein database, however, shows a complete 100% match. No evidence of false polymorphism due to paralogy.
	0.816	0.474	T rs2010027	17	R235H	NHEEEVNLLhEQLGDR	One match to KRT40 in both genomic and mRNA databases, albeit with two variants in the genomic database. The protein database, however, shows a complete 100% match. No evidence of false polymorphism due to paralogy.
RT81	0.282	0.045	A rs6580873	12	R248L	LYEEEILILQSHISDTSVVVK	One match to KRT81 in both genomic and mRNA databases, albeit with several variants in the genomic database. The protein and mRNA databases, however, show 100% identity across the entire sequence. No evidence of false polymorphism due to paralogy.
RT81	0.56	0.122	C rs2071588 G rs79897879	12 12	G52R S13R	GLTGGFGSHSVCr FrCISACGPRPGR	100% match to mRNA incorrectly identified as KRIF6s, according to my own analysis,it's a better match to KRIF1s, including the GS24 variant in the mRNA database (emb [V19206.1]). No evidence of faise polymorphism due to paralogy.  One match to KRIF1s in both genomic and mRNA databases. All mRNAs have the cancertar is expense. No evidence of faise polymorphism due to paralogy.
KISI	0.008		T rs79897879	12	S13R S13B	FSCISACGPRPGR FSCISACGPRPGR	Une matici to Air, lai in on genomic an impart database, air, minkan save in executar sequence, no evidence or also paragory.  One matich to XII bit in both genomic and mRNA database. All mRNAs have the executar sequence, no evidence or also paragory.  One matich to XII bit in both genomic and mRNA database. All mRNAs have the ancestral sequence. No evidence or also paragory.
RT82	0.734	0.569	G rs2658658	12	T458M	GAFLYEPCGVSTPVLSTGVLR	One match to KRI2 in both enrichment and mRNA databases. All milkes have the ancestral sequence. No evidence of false opening minimum of the ancestral sequence when the a
	0.797	0.878	A rs2658658	12	T458M	GAFLYEPCGVSmPVLSTGVLR	One match to KRT82 in both genomic and mRNA databases. All mRNAs have the ancestral sequence. No evidence of false polymorphism due to paralogy.
RT83	0.863	0.768	C rs2852464	12	1279M	DLNMDCIVAEIK	No significant similarity detected with a tblastn search.
RT83	0.62	0.728	G rs2852464 T rs140635030	12 12	1279M G362S	DLNMDCmVAEIK LEAAVAOSEOOSEAALSDAR	No significant similarity detected with a tibiastry search. Multiple matteries agreemen and mRNA search to RRT gene family on chromosome 12, including pseudogenes. None of the mRNAs contained the G8625 variant, so the gene to which this variant belongs cannot be conclusively identified by this method. There is a possibility of a false polymorphism due to paralog
RT84	0.48	0.077	A rs951773	12	G362S C446R	CEYOELMNAKLGLDIEIATYR	Multiple matches in genome and mRNA search to KRI gene barming on chromosome 12, including pseudogenes. None of the mRNAs contained the G3625 variant, so the gene to which this variant belongs cannot be conclusively identified by this method. There is a possibility or a table polymorphism due to paralog. One match to SKRI48. No evidence of laike polymorphism due to paralog.
IN 104	0.46	0.107	G rs951773	12	C446R	rEYOFI MNAKI GI DIFIATYR	One match to KH-N. We evidence of false polymorphism due to paralogy.  One match to KH-N. We evidence of false polymorphism due to paralogy.
RT85	0.092	0.041	A rs61630004	12	R78H	IAVGGFRAGSCGhSFGYR	One match to KRTSS, R78H ophymorphism not detected. No evidence of false polymorphism due to paralogy.
	1	1	G rs61630004	12	R78H	IAVGGFRAGSCGR	One match to KRT8S, R78H polymorphism not detected. No evidence of false polymorphism due to paralogy.
RT86	0	0.065	T rs139895699	12	R327C	TKEEINELNcMIQR	Best match is KRT81 and some KRT pseudogenes. Uncertain. Possible false polymorphism.
RTAP10-8	0.095	0.089	A rs411254	21	H26R	TYVIAASTMSVCSSDVGHVSR	One match to KRTAP10-8. H26R variant is present in the mRNA database. No evidence of false polymorphism due to paralogy.
RRC15	0.997	1	G rs411254	21	H26R	TYVIAASTMSVCSSDVGr	One match to KRTAP10-8. H26R variant is present in the mRNA database. No evidence of false polymorphism due to paralogy.
RRC15	0.395	0.154	A rs13070515 G rs13070515	3	P286L P286L	ELSIGIFGPMPNLR FLSPGIFGPMPNLR	One match to 18RCIS. 2928 (polymorphism is in the mRNA datablase. No evidence of false polymorphism.  One match to 18RCIS. 2928 (polymorphism is in the mRNA datablase. No evidence of false polymorphism.  One match to 18RCIS. 2928 (polymorphism is in the mRNA datablase. No evidence of false polymorphism.
RRC15	0.443	0.374	T rs13060627	3	V270L	LYLSNNHISQLPPSIFMQLPQLNR	Une match to LMCLLS. #2200 polymorphism is in the mixed cataciase. No evidence of take polymorphism.  One match to LMCLS. #2200 polymorphism is in the mixed cataciase. No evidence of take polymorphism.  One match to LMCLS. *2700 polymorphism and televated in the mRNA database. No evidence of false polymorphism.
	0.937	0.955	C rs13060627	3	V270L	LYLSNNHISQLPPSVFMQLPQLNR	One match to LRRC1S. V270L polymorphism not detected in the mRNA database. No evidence of false polymorphism.
	0.755	0.973	C rs2233391	2	H168N	EWSTFAVGPGHCLQLHDR	One match to NEU2. H168N polymorphism is present in the mRNA database. No evidence of false polymorphism.
IEU2	0.778	0.285	A rs2233391	2	H168N	EWSTFAVGPGHCLQLnDR	One match to NEU2. H168N polymorphism is present in the mRNA database. No evidence of false polymorphism.
	0.770		T rs61818256	1	R684W	AAEAAWLLLSDMWSSK AAEAARI I I SDMWSSK	One match to PRF1. R6SBM to phymorphism is not detected in the mRNA database. No evidence of false polymorphism.  One match to PRF1. R6SBM to phymorphism is not detected in the mRNA database. No evidence of false polymorphism.
	0.021	0					
PKP1	0.021	0 1	C rs61818256	1	R684W		One match to \$100.02 202 information in ord detected in the minute dissipation of false and more minute and the minute dissipation of the match to \$100.02 202 information in ord detected in the minute dissipation of the match to \$100.02 202 information in ord detected in the minute dissipation of the match to \$100.02 202 information or detected in the minute dissipation of the minute displacement dissipation of the minute displace
	0.770	0 1 0.589 0.858	C rs61818256 T rs36022742 C rs36022742	1 1	R684W R3K R3K	ARPLEQAVAAIVCTFQEYAGR ARPLEQAVAAIVCTFGEYAGR	One match to \$100A3. R3K polymorphism is not detected in the mRNA database. No evidence of false polymorphism.
PKP1	0.021 1 0.085		T rs36022742	1 1 1	R3K	AkPLEQAVAAIVCTFQEYAGR	One match to SIGNA, Rix polymorphisms in ot detected in the mRNA database. No evidence of false polymorphism.  One match to SIGNA, Rix polymorphism is not detected in the mRNA database. No evidence of false polymorphism.  One match to SIGNA, Rix polymorphism is not detected in the mRNA database. No evidence of false polymorphism.  No significant similarly detected with a Vallation search.
KP1 100A3	0.021 1 0.085 0.998	0.858	T rs36022742 C rs36022742	1	R3K R3K	Akpleqavaaivctfqeyagr Arpleqavaaivctfqeyagr	One match to SIOORA. R.RX polymorphism is not detected in the mRNA database. No evidence of false polymorphism.  One match to SIOORA R.RX polymorphism is not detected in the mRNA database. No evidence of false polymorphism.  One match to SIOORA R.RX polymorphism is not detected in the mRNA database. No evidence of false polymorphism.