GN	rs#_nuc	pept	Allele count EUR (n = 379)	Allele count AFR (n = 246)	Subject EA2														
					1	3	4	5	6	7	8	12	13	14	15	16	17	18	19
BLMH	rs1050565_C	HVPEEVLAVLEQEPIvLPAWDPMGALA-	213	93															
BLMH	rs1050565_T	HVPEEVLAVLEQEPIILPAWDPMGALA-	335	228	1	1	1			1		1	1	1		1		1	
BLMH	rs1050565_C_T	HVPEEVLAVLEQEPIvLPAWDPMGALA-/HVPEEVLAVLEQEPIILPAWDPMGALA-	169	75				1	1								1		
DSP	rs6929069_A	GqSEADSDKNATILELR	102	158										1					
DSP	rs6929069_G	GR/SEADSDKNATILELR	373	211				1											
ECHS1	rs1049951_A	iFEEDPAVGAIVLTGGDK	377	185						1				1		1	1	1	
GSDMA	rs3894194_A	QLNPqGDLTPLDSLIDFK	264	109															
GSDMA	rs3894194_G	/GDLTPLDSLIDFK	308	225	1		1	1				1				1		1	
GSDMA	rs56030650_A	GHEVnLEALPK	297	220															
GSDMA	rs56030650_C	GHEVTLEALPK	265	117															
GSDMA	rs7212938_G	ALETVQER	277	56															
GSDMA	rs7212938_T	ALETIQER	296	241															
GSDMA	rs3894194_A/rs56030650_A	QLNPqGDLTPLDSLIDFK/GHEVnLEALPK	242	102						1									
GSTP1	rs1695_G	YvSLIYTNYEAGKDDYVK	206	175				1		1				1		1			
GSTP1	rs1695_A	YISLIYTNYEAGKDDYVK	343	203	1													1	
GSTP1	rs1695_A_G	YISLIYTNYEAGKDDYVK /YvSLIYTNYEAGKDDYVK	170	132			1												
HEXB	rs10805890_G	GILVDTSR	100	7															
HEXB	rs10805890_A	GILIDTSR	368	243				1									1		
JUP	rs143043662_T	NEGTATYAAAiLFR	5	0															
JUP	rs143043662_C	NEGTATYAAAVLFR	379	246															1
JUP	rs41283425_T	SAIVHLINYQDDAELAThALPELTK	46	0															
JUP	rs41283425_C	SAIVHLINYQDDAELATR	379	246	1	1				1		1	1	1	1				
JUP	rs143043662_T/rs41283425_T_C	NEGTATYAAAVLFR / SAIVHLINYQDDAELAThALPELTK / SAIVHLINYQDDAELATR	46	0			1												
JUP	rs143043662_C / rs41283425_C	NEGTATYAAAVLFR / SAIVHLINYQDDAELATR	379	246				1									1	1	
JUP	rs143043662_T/ rs41283425_C	NEGTATYAAAiLFR / SAIVHLINYQDDAELATR	5	0					1										
JUP	rs41283425_T_C	SAIVHLINYQDDAELAThALPELTK / SAIVHLINYQDDAELATR	5	0												1			
KRT1	rs17678945_A	NKLNDLEDALQQsKEDLAR	16	0															
KRT1	rs17678945_C	NKLNDLEDALQQAKEDLAR	379	246										1		1	1		1
KRT1	rs17678945_A_C	NKLNDLEDALQQsKEDLAR / NKLNDLEDALQQAKEDLAR				1													
KRT31	rs112544857_A	SQYEvLVETNR	19	1													1		
KRT31	rs6503627_A	DNvELENLIR or QLERDNvELENLIR	64	16				1				1							
KRT32	rs72830046_T	CQYEAMVEANhR	174	24															
KRT32	rs72830046_C	CQYEAMVEANRR	356	246															
KRT32	rs2071563_A	LEGEINmYR	259	163									1						
KRT32	rs2071563_G	LEGEINTYR	315	196				1			1	1					1		
KRT32	rs2071561_T	ADLEAQVEyLK	276	104															
KRT32	rs2071563_G / rs2071561_T	LEGEINTYR / ADLEAQVEyLK	276	101	1		1			1				1	1	1		1	1
KRT32	rs72830046_C / rs2071563_A	CQYEAMVEANRR / LEGEINmYR	155	163		1													
KRT32	rs2071563_A_G/rs2071561_T	LEGEINTYR / ADLEAQVEyLK							1										
KRT33A	rs12937519_A	QVVSSSEQLQSYQvEIIELR	169	147				1		1	1	1		1		1			1
KRT34	rs2239710_T	SQYEALVEINR	218	22		1			1	1	1	1	1	1	1	1		1	1
KRT35	rs743686_A	VSAMYSSSSCKLPSLSPVAR	266	111															
KRT35	rs743686_G	VSAMYSSSpCKLPSLSPVAR	295	228													1		
KRT35	rs12451652_T	TNySPRPICVPCPGGRF	116	33															
KRT35	rs12451652_C	TNCSPRPICVPCPGGRF	363	243															
KRT35	rs2071601_C	TNCSaRPICVPCPGGRF	295	220															
KRT35	rs2071601_G	TNCSPRPICVPCPGGRF	250	136															
KRT35	rs743686_A_G / rs12451652_C / rs2071601_G	VSAMYSSSSCKLPSLSPVAR / VSAMYSSSpCKLPSLSPVAR/TNCSPRPICVPCPGGRF	182	92		1													
KRT37	rs9910204_A	TSFYSTSSCPLcCTMAPGAR	180	73															
KRT37	rs9910204_C	TSFYSTSSCPLGCTMAPGAR	354	237															
KRT40	rs150812789_G	TASALEIELQAQQSLTESLECTVAETEAQYSSQLAQIQr / LIDNLENQLAEIR	164	27		1	1	1									1	1	
KRT40	rs150812789_A	TASALEIELQAQQSLTESLECTVAETEAQYSSQLAQIQCLIDNLENQLAEIR	353	244															
KRT81	rs6580873_A	LYEEEILILQSHISDTSVVVK	107	11	1											1			
KRT81	rs2071588_G	GLTGGFGSHSVCr	212	30		1	1				1				1				
KRT81	rs6580873_A/rs2071588_G	LYEEEILIIQSHISDTSVVVK / GLTGGFGSHSVCr	33	1				1											
KRT83	rs2852464_C	DLNMDCmVAEIK	235	179															
KRT83	rs2852464_G	DLNMDCIVAEIK	327	189	1	1	1	1		1	1	1	1		1	1	1		
KRT85	rs61630004_T	IAVGGFRAGSCGhSFGYR / AGSCGhSFGY	35	10															
KRT85	rs61630004_C	IAVGGFRAGSCGR / AGSCGR	379	246				1											
LRRC15	rs13070515_A	ELSlGIFGPMPNLR	150	38															
LRRC15	rs13070515_G	ELSPGIFGPMPNLR	358	242			1						1	1		1			1
LRRC15	rs13060627_T	LYLSNNHISQLPPSIFMQLPQLNR	168	92															
LRRC15	rs13060627_C	LYLSNNHISQLPPSVFMQLPQLNR	355	235													1		
LRRC15	rs13070515_A_G / rs13060627_T	ELSlGIFGPMPNLR / ELSPGIFGPMPNLR / LYLSNNHISQLPPSiFMQLPQLNR	128	34				1											
LRRC15	rs13070515_G/rs13060627_C	ELSPGIFGPMPNLR / LYLSNNHISQLPPSVFMQLPQLNR	355	235					1	1								1	
S100A3	rs36022742_T	AkPLEQAVAAIVCTFQEYAGR	32	145															
S100A3	rs36022742_C	ARPLEQAVAAIVCTFQEYAGR	378	211			1	1	1	1	1	1	1	1	1	1	1	1	1
S100A3	rs36022742_T_C	AkPLEQAVAAIVCTFQEYAGR / ARPLEQAVAAIVCTFQEYAGR	31	110		1													
SERPINB5	rs1455555_A	GVALSNVIHK	284	237															
SERPINB5	rs1455555_G	GVALSNVvHK	277	73						1				1					
TGM3	rs214803_C	AALGVQSINWQTAFNR	120	206															
TGM3	rs214803_A	AALGVQSINWQkAFNR	372	171		1		1	1	1							1		
TGM3	rs214803_C_A	AALGVQSINWQTAFNR / AALGVQSINWQkAFNR	114	131			1								1	1		1	