

## Supplementary tables:

Table S1:

	Nomenclature	Chr	Allele	Gene	AA	AA position
1	c.542G>A	1	G/A	ENSG00000132681 (ATP1A4)	R/Q	181
2	c.1150A>G	1	T/C	ENSG00000137992 (DBT)	S/G	384
3	c.125G>A	1	G/A	ENSG00000213088 (DARC)	G/D	42
4	c.1693T>C	1	A/G	ENSG00000134242 (PTPN22)	W/R	565
5	c.2009G>A	1	G/A	ENSG00000169174 (PCSK9)	G/E	670
6	c.344G>A	1	C/T	ENSG00000143278 (F13B)	R/H	115
7	c.1601A>G	1	T/C	ENSG00000198734 (F5)	Q/R	534
8	c.7480T>C	1	A/G	ENSG00000066279 (ASPM)	Y/H	2494
9	c.49A>G	2	A/G	ENSG00000163599 (CTLA4)	T/A	17
10	c.380T>C	2	A/G	ENSG00000135899 (SP110)	L/S	127
11	c.733G>A	2	C/T	ENSG00000170820 (FSHR)	A/T	245
12	c.1853G>A	2	C/T	ENSG00000170820 (FSHR)	S/N	618
13	c.3448T>C	2	A/G	ENSG00000169432 (SCN9A)	W/R	1150
14	c.41C>G	3	C/G	ENSG00000173402 (DAG1)	S/W	14
15	c.743T>C	3	T/C	ENSG00000145192 (AHSG)	M/T	248
16	c.767G>C	3	G/C	ENSG00000145192 (AHSG)	S/T	256
17	c.163A>G	4	T/C	ENSG00000145384 (FABP2)	T/A	55
18	c.53C>A	4	C/A	ENSG00000154277 (UCHL1)	S/Y	18
19	c.1805G>T	4	C/A	ENSG00000174125 (TLR1)	S/I	602
20	c.3568G>A	5	G/A	ENSG00000095015 (MAP3K1)	A/T	1190
21	c.46G>A	5	G/A	ENSG00000169252 (ADRB2)	G/R	16
22	c.79G>C	5	G/C	ENSG00000169252 (ADRB2)	E/Q	27
23	c.412G>A	5	G/A	ENSG00000168685 (IL7R)	V/I	138
24	c.197T>C	5	T/C	ENSG00000168685 (IL7R)	I/T	66

25	c.2893G>A	5	C/T	ENSG00000138829 (FBN2)	V/I	965
26	c.10411G>A	5	G/A	ENSG00000164199 (GPR98)	E/K	3471
27	c.122C>A	5	G/A	ENSG00000258864 (CTC-554D6.1)	A/E	41
28	c.5465T>A	5	T/A	ENSG00000134982 (APC)	V/D	1822
29	c.1630A>C	5	A/C	ENSG00000112964 (GHR)	I/L	544
30	c.989C>T	6	G/A	ENSG00000204525 (HLA-C)	A/V	330
31	c.982G>A	6	C/T	ENSG00000204525 (HLA-C)	V/I	328
32	c.925A>G	6	T/C	ENSG00000204525 (HLA-C)	M/V	309
33	c.302G>A	6	C/T	ENSG00000234745 (HLA-B)	S/N	101
34	c.47G>C	6	C/G	ENSG00000204525 (HLA-C)	G/A	16
35	c.11T>C	6	A/G	ENSG00000234745 (HLA-B)	M/T	4
36	c.1136T>C	6	A/G	ENSG00000146070 (PLA2G7)	V/A	379
37	c.1105A>G	6	T/C	ENSG00000204525 (HLA-C)	T/A	369
38	c.991A>G	6	T/C	ENSG00000204525 (HLA-C)	M/V	331
39	c.872A>C	6	T/G	ENSG00000204525 (HLA-C)	Q/P	291
40	c.41C>G	6	G/C	ENSG00000234745 (HLA-B)	S/W	14
41	c.44C>G	6	G/C	ENSG00000234745 (HLA-B)	A/G	15
42	c.49C>G	6	G/C	ENSG00000234745 (HLA-B)	L/V	17
43	c.292G>T	6	C/A	ENSG00000234745 (HLA-B)	D/Y	98
44	c.610G>C	6	C/G	ENSG00000234745 (HLA-B)	E/Q	204
45	c.363C>G	6	G/C	ENSG00000234745 (HLA-B)	S/R	121
46	c.355C>T	6	G/A	ENSG00000234745 (HLA-B)	L/F	119
47	c.5T>G	6	A/C	ENSG00000234745 (HLA-B)	L/R	2
48	c.560A>T	6	T/A	ENSG00000234745 (HLA-B)	E/V	187
49	c.22G>A	6	C/T	ENSG00000204525 (HLA-C)	A/T	8
50	c.559G>C	6	C/G	ENSG00000234745 (HLA-B)	E/Q	187
51	c.910C>G	6	G/C	ENSG00000112619 (PRPH2)	Q/E	304
52	c.206A>C	6	T/G	ENSG00000234745 (HLA-B)	E/A	69
53	c.929G>A	6	C/T	ENSG00000112619 (PRPH2)	R/K	310

54	c.594G>T	6	G/T	ENSG00000078401 (EDN1)	K/N	198
55	c.829C>G	6	G/C	ENSG000000204525 (HLA-C)	Q/E	277
56	c.142T>G	6	A/C	ENSG000000234745 (HLA-B)	S/A	48
57	c.205G>A	6	C/T	ENSG000000234745 (HLA-B)	E/K	69
58	c.71C>T	7	C/T	ENSG000000184408 (KCND2)	S/L	24
59	c.553A>C	7	T/G	ENSG000000188050 (RNF133)	I/L	185
60	c.1642G>A	7	G/A	ENSG000000257743 (RP11-1220K2.2)	E/K	548
61	c.236T>C	7	T/C	ENSG000000211746 (TRBV19)	I/T	79
62	c.785C>T	7	G/A	ENSG000000257138 (TAS2R38)	A/V	262
63	c.894T>G	7	T/G	ENSG000000164867 (NOS3)	D/E	298
64	c.1388T>C	7	A/G	ENSG00000004948 (CALCR)	L/P	463
65	c.1408C>T	7	G/A	ENSG000000122512 (PMS2)	P/S	470
66	c.1739T>C	7	A/G	ENSG000000105929 (ATP6V0A4)	M/T	580
67	c.2200T>G	8	T/G	ENSG00000042832 (TG)	S/A	734
68	c.5995C>T	8	C/T	ENSG00000042832 (TG)	R/W	1999
69	c.2564C>G	9	G/C	ENSG000000165271 (NOL6)	A/G	855
70	c.494G>T	9	G/T	ENSG000000137124 (ALDH1B1)	G/V	165
71	c.1091G>A	9	C/T	ENSG000000095397 (DFNB31)	R/H	364
72	c.6011C>G	10	C/G	ENSG000000107736 (CDH23)	T/S	2004
73	c.244G>C	10	G/C	ENSG000000107736 (CDH23)	G/R	82
74	c.457T>C	10	T/C	ENSG000000165730 (STOX1)	Y/H	153
75	c.145A>G	10	A/G	ENSG00000043591 (ADRB1)	S/G	49
76	c.1165G>C	10	G/C	ENSG00000043591 (ADRB1)	G/R	389
77	c.361C>T	11	C/T	ENSG000000150455 (TIRAP)	R/W	121
78	c.328A>C	11	A/G	ENSG000000109861 (CTSC)	I/L	110
79	c.775A>G	11	T/C	ENSG000000172638 (EFEMP2)	I/V	259
80	c.388C>T	12	G/A	ENSG000000121318 (TAS2R10)	P/S	130
81	c.242C>G	12	G/C	ENSG000000197870 (PRB3)	P/R	81

82	c.1751C>T	12	C/T	ENSG00000182326 (C1S)	A/V	584
83	c.603G>T	13	G/T	ENSG00000123171 (CCDC70)	E/D	201
84	c.7397T>C	13	T/C	ENSG00000139618 (BRCA2)	V/A	2466
85	c.1120T>G	13	A/C	ENSG00000123191 (ATP7B)	S/A	374
86	c.1270G>C	13	C/G	ENSG00000123191 (ATP7B)	V/L	424
87	c.2129T>C	13	A/G	ENSG00000123191 (ATP7B)	V/A	710
88	c.1565G>A	13	C/T	ENSG00000123191 (ATP7B)	R/K	522
89	c.2126G>A	14	G/A	ENSG00000100714 (MTHFD1)	R/Q	709
90	c.259G>A	15	C/T	ENSG00000159337 (PLA2G4D)	V/I	87
91	c.1061T>C	15	T/C	ENSG00000140463 (BBS4)	I/T	354
92	c.1331A>C	16	A/C	ENSG00000179588 (ZFPM1)	E/A	444
93	c.538G>A	16	C/T	ENSG00000121270 (ABCC11)	G/R	180
94	c.1066A>G	17	T/C	ENSG00000108578 (BLMH)	I/V	356
95	c.154G>T	17	G/T	ENSG00000132518 (GUCY2D)	A/S	52
96	c.188A>G	19	T/C	ENSG00000131398 (KCNC3)	D/G	63
97	c.7211G>C	20	C/G	ENSG00000130702 (LAMA5)	R/P	2404
98	c.385A>G	20	A/G	ENSG00000171867 (PRNP)	M/V	129
99	c.2339A>C	20	T/G	ENSG00000075043 (KCNQ2)	N/T	780
100	c.112A>G	21	T/C	ENSG00000180509 (KCNE1)	S/G	38
101	c.185A>G	22	A/G	ENSG00000211647 (IGLV5-48)	E/G	62
102	c.226A>G	22	A/G	ENSG00000211647 (IGLV5-48)	S/G	76
103	c.227G>A	22	G/A	ENSG00000211647 (IGLV5-48)	S/N	76
104	c.1049A>G	22	T/C	ENSG00000100299 (ARSA)	N/S	350
105	c.1172C>G	22	G/C	ENSG00000100299 (ARSA)	T/S	391
106	c.466A>G	X	A/G	ENSG00000101981 (F9)	T/A	156
107	c.97T>C	X	T/C	ENSG00000147100 (SLC16A2)	S/P	33

Table S2:

ANTIGEN	Controls (n=11)		IRAK4 <sup>-/-</sup> or MyD88 <sup>-/-</sup> (n=6)			Patient (Tirap <sup>-/-</sup> )			Healthy Tirap <sup>-/-</sup> relatives (n=6)		
	Mean	SD	Mean	SD	Difference from controls	Mean	SD	Difference from controls	Mean	SD	Difference from controls
lukS	7858	4788	10201	4213	ns	16101	1685	**	15158	4463	*
fnbpB5	1603	2194	643	387	ns	2586	1952	ns	1002	1339	ns
CHIPS	13332	7139	18752	2287	ns	15310	3108	ns	17858	2357	ns
eapH2	8513	6242	17449	4792	*	15821	5272	ns	12783	6814	ns
clfBN2,3	7252	4927	7166	4749	ns	3198	1055	ns	7484	3602	ns
fnbpA1	3719	4580	2577	2803	ns	259	219	ns	5206	3337	ns
flip-R	6752	7105	7395	2962	ns	30.8	41.3	ns	4300	2863	ns
SEM	979	1617	1827	1274	ns	128	132	ns	2606	2558	ns
ETA	928	1560	3251	4680	ns	589	919	ns	6189	6222	ns
SEH	1666	2642	4729	6702	ns	120	88.3	ns	1604	2893	ns
sdrD	993	1515	2348	2668	ns	829	270	ns	1183	623	ns
fndpA2	625	673	2850	3697	ns	2468	576	ns	4533	2618	**
SCIN	6051	5072	9487	6094	ns	14700	2490	**	10059	4400	ns
TSST-1	5464	7542	11846	9159	ns	857	1426	ns	12967	3838	ns
fnbpA3	1771	2428	3706	3870	ns	850	438	ns	4711	3087	ns
hlgB	9996	4257	12800	2716	ns	11915	2507	ns	13878	2583	ns
Nuc	4187	4733	12337	6345	ns	14860	3065	*	10325	8195	ns
fnbpA5	1095	1540	3063	3626	ns	2579	2280	ns	2592	2670	ns
SEB	2315	3328	3566	3790	ns	11940	9488	*	11248	8091	ns
SEA	2333	2946	7571	6999	ns	6581	3120	ns	12030	4061	***
lukE	11775	6025	15911	4041	ns	12915	2182	ns	17219	3311	ns
lukD	10921	5598	11314	3694	ns	9710	1359	ns	14191	3657	ns
eap	6709	3166	14967	2424	***	13178	2035	***	13154	1843	***
clfAN2,3	2260	2512	3886	5438	ns	8120	4415	*	5536	2257	ns
A-tox	8050	5053	13513	5196	ns	13210	2040	ns	13791	4941	ns
ssl-1	5833	5231	11074	8742	ns	1980	1616	ns	9521	5242	ns
sasH	406	516	415	584	ns	213	138	ns	269	338	ns
ssl-3	9652	6770	12954	3787	ns	6048	4741	ns	14085	3514	ns
ssl-5	3274	2055	4918	2768	ns	2344	1132	ns	4184	1800	ns
ssl-9	10101	5194	15332	2994	ns	9048	4923	ns	14444	5669	ns
fnbpA6	561	432	1458	2632	ns	134	47.8	ns	1024	629	ns
ssl-10	6309	4233	8170	3254	ns	2594	1361	ns	7962	1364	ns
ssl-11	1589	1999	1792	2021	ns	85.7	79.7	ns	1125	1401	ns
sec	7475	8773	14402	6989	ns	9714	7676	ns	15402	4819	ns
etb	182	246	2672	5129	ns	79	60.7	ns	454	745	ns
seo	608	720	2156	1622	*	338	266	ns	1246	536	ns
fnbpB	562	847	285	255	ns	2300	1506	**	946	948	ns
fnbpB1	699	1123	472	531	ns	158	85.2	ns	372	310	ns
isdA	14551	4645	17305	2466	ns	18029	1641	ns	13815	8321	ns

fnbpB2	2021	1901	2132	1722	ns	3835	1315	ns	4857	2757	ns
fnbpB4	1504	2328	1809	2445	ns	543	239	ns	1235	1139	ns
fnbpB6	438	596	704	477	ns	167	54.4	ns	1089	1081	ns
fnbpB7	1448	2504	1716	2539	ns	440	177	ns	1194	1273	ns
fnbpA7	741	832	1542	2410	ns	483	721	ns	1367	1279	ns
sasC	154	124	329	416	ns	140	74.7	ns	310	181	ns
flipR-L	5760	5261	9998	4771	ns	97	72.4	ns	4849	3099	ns
esxB	259	299	247	225	ns	148	191	ns	159	147	ns
prsA	621	908	2336	2516	ns	2727	3676	ns	572	308	ns
atl2	7643	4486	14766	3511	*	17075	4651	**	14688	3973	*
lipase	11684	7289	17179	3296	ns	4671	3633	ns	10058	6773	ns
sed	1528	2142	1757	684	ns	703	276	ns	516	308	ns
fnbpA	2609	3450	3057	4941	ns	849	863	ns	2685	1722	ns
sdrE	1541	1876	2450	2785	ns	1008	507	ns	2158	1399	ns
SEE	253	620	3777	4716	ns	2646	1587	ns	5403	2913	**
SEJ	2491	3455	5448	1919	ns	1825	868	ns	2573	1698	ns
isdH	695	920	796	623	ns	911	349	ns	740	728	ns
sasG	850	1456	777	1042	ns	177	159	ns	1608	1932	ns
sdrC	1478	1642	3970	3871	ns	897	835	ns	4118	3403	ns
SEI	511	669	1499	1007	ns	298	145	ns	3369	3106	**
SEQ	745	1709	1484	1646	ns	74.7	41.6	ns	2098	1742	ns
isaA	7943	5917	17129	6758	*	2210	1136	ns	6631	4743	ns
lyt M	1678	2595	8325	6795	**	900	631	ns	2280	1613	ns
SER	312	573	725	832	ns	132	136	ns	1274	1705	ns
Aly	1391	1447	3361	1938	ns	3427	1824	ns	2198	1016	ns
pro Atl	1361	2225	4501	6461	ns	6402	3651	ns	3597	1229	ns
SEG	493	596	1733	1107	ns	303	322	ns	3606	2476	***
eapH1	827	1128	2255	2254	ns	1471	1009	ns	1204	1083	ns
SA2097	4.02	6.71	15.6	14.9	ns	25.6	18.8	*	8.42	8.23	ns

**Table S3 :**

	P1 (III.1)	II.5	I.1
Single/Paired-end	Paired-end	Paired-end	Paired-end
Bait-set	50 Mb	50 Mb	71 Mb
Total reads	164,759,220	184,566,394	132,090,076
Total reads aligned in the targeted regions	22,485,016	26,512,246	75,999,552
Mean coverage	44.97	53.02	107.04
Target bases covered by > 2X	99.4	99.6	99.7
Target bases covered by > 10X	92.3	94.6	98.5
Target bases covered by > 20X	75.8	81.5	95.2
Target bases covered by > 30X	58.4	66.1	90