

**PRIMER INFORMATION (for “Sarcoidosis is associated with a truncation splice site mutation in the BTNL2 gene” by Valentonyte R, Hampe J, et al.)**

**Genotyping:** Primers and probes for all Taqman SNP assays used. “Assay on Demand”

assays (starting with hCV, <https://store.appliedbiosystems.com>).

Marker	hCV number	Gene	Position (NCBI) MB	Primers: Forward 5’-3’ Reverse 5’-3’	Probes	Cohort used
rs2073528	hCV11255445	<i>BTNL2A2</i>	26,44			Basic/extension
rs2072803	hCV2474923	<i>BTNL2A2</i>	26,46			Basic/extension
	hCV2474907	<i>BTNL3A1</i>	26,48			Basic/extension
	hCV2474883		26,50			Basic/extension
	hCV9804528		26,54			Basic/extension
rs3736781	hCV9804725	<i>BTNL1A1</i>	26,57			Basic/extension
rs126007			27,80	TCCTTAACCAACCTCATCTGG TGGTAACCTGACAGCTGATCTTG	FAM-AGAAGAGCAGCAACCAAGGCTAACGTGA TET-AGAAGAGCAGCAACCAAGGCTAACGTGAGA	Basic-screen
rs929042		<i>RFP</i>	28,95	CGGACGTGTGGTTCACAGC CTCCGTGTACAATGTGTCCTG	FAM-CTGTAGCTGGCAGGAAAGCAGGAGT TET-CTGTAGCTGGCAGGAAAGCAGGAGT	Basic-screen
rs53161			29,56	GGGCTGTCCACGTGCAC GCAGAGTTGAACAGTATATAACCTTTC	FAM-AAGGGGCAACATACACAATGTGTTACCAAAATT TET-AAGGGGCAACATACACAATGTGTTACCAAAATT	Basic-screen
rs404240		<i>UBD</i>	29,59	CCACAGAAACAAGGGCAGC GAACATGTCCGGTCTAAGACCAA	FAM-TCTTGGAGCCAGCGAAAGAACCCTG TET-ATCTTGGAGCCAGCAAAGAACCCTGG	Basic-screen
rs362536		<i>UBD</i>	29,59	TGGAGAGAACCTGGAATTAAGGC GGACTATATCTAAGTCTTACTTCAATAGCTGGA	FAM-ATTGGGAGAATATTTCTGAATGAGATGAGGGAG TET-TATCTAGATTGGGAAAATATTTCTGAATGAGATGAGGGG	Basic-screen
rs1805057		<i>GABBR1</i>	29,64	CCATCTGGCCCTTGGCA GGTAATGGTCTGGTGTGTAGTTGAA	FAM-AGGAGGCGCCGCTTCTGGTGTG TET-TGGAGGAGCAGCCGCTTCTGGTGTG	Basic-screen
rs3130253		<i>MOG</i>	29,73	GTTCCTCCTCGCGGTGCTG CCCACCCCTGCCCCGTAC	FAM-CACTCTTGGCCTCGTCTCCTCTGCC TET-TCACTCTTGGCCTCATCTTCTCTGCCCT	Basic-screen
rs1569315		<i>HLA-G</i>	29,85	CGCAGGTCCTCGTTCAGG AGTGGATGATTGGCTGCGA	FAM-AGGAGGCGCTCGTTCGGACCC TET-AGGAGGCGCACCCTGCGGACCC	Basic-screen
rs8347		<i>HCG-V</i>	30,10	AGGAGACCTCAGAGCTCCAG AAGTGACCAATCTCAAGCCAGC	FAM-AAATGGAAATAAGAAATAATCATATCCTTTCTTCCCACC TET-AAATGGAAATAAGAAATAATCATATCCTTTCTTCCCACC	Basic-screen
rs1264457		<i>HLA-E</i>	30,52	CTCACCCCTGCAGTGGATG AGGGTGAGATAATCTTGGCCG	FAM-CCGACAGGCGCTTCTCCCG TET-CCGACAGGCGCTTCTCCCG	Basic-screen
rs2074510		<i>GTP2H4</i>	30,94	GAGTGCAGCTCTTATTCTCATCC TTGGCTCCTGGAGATTGAGG	FAM-CATTCTGGCTCTTGCCTGTGAAATCTTTC TET-CCATTCTGGCTCTTCTCTGAAATCTTTC	Basic-screen/extension
rs3095318		<i>CDSN</i>	31,15	CGTCTCGGGCACCCCTG AGACACACACAGACTAGAGGTAGGTGTCA	FAM-CACGGGATGATGGCACTGCTGCT TET-CACGGGATGATGGCACTGCTGCT	Basic-screen
rs2073721		<i>SC1</i>	31,19	GGTGGACCAAGAGCCCTGC CATCCAGTTCGCCCAACAC	FAM-ACCTGGGAAATGGGACCCAGC TET-ACCTGGGAAATGGGACCCAGC	Basic-screen
rs1050393		<i>HLA-C</i>	31,30	GGAGTATTGGACCCGGGAG CGCTCTGGTTGTAGTAGCCG	FAM-CCAGGCACAGGCTGACCGAGTG TET-CGCAAGGCACAGACTGACCGAGT	Basic-screen
rs1051488		<i>HLA-B</i>	31,38	CTGGCTTGCCTGTCTAGC CTTCCCAGTAATGAGGCAGGG	FAM-AGCTGTGGCTGCTGTGTGATGTGA TET-AGCTGTGGCTGCTGTGTGATGTGA	Basic-screen
rs1063630		<i>MICA</i>	31,44	CCCAGAGCCCAAGTCTT AGAAACCTGACTGCACAGATC	FAM-ATCCCCGACAGCA VIC-CATCCCAGGACAGCA	Basic/extension
rs1063635		<i>MICA</i>	31,44	CTTTGAGCCACGACCCCA GGCTCACCAGAGGGCACA	FAM-ACCAGGATTTGCCAAGGAGAGGAGCA VIC-ACCAGGATTTGCCAAGGAGAGGAGC	Basic-screen/extension
rs3828916	hCV3273671		31,53			Basic/extension
rs3131639		<i>MICB</i>	31,53	GCAGAAACGCAGGGCAA TGTCAGTCTCCGGTCTCTGTGT	FAM-CAGGACATTTTCTG TET-AGGACATCTTCTGCC	Basic/extension
rs3134900		<i>MICB</i>	31,53	CTTGGGTGAAAGGTGATGG GGTTTTGGGAGAGGAAGGCTC	FAM-TCTGTGAGATCCATGAAGACAGCAGCACC TET-CTGTGAGATGCATGAAGACAGCAGCACC	Basic-screen/extension
AC006046_G 30156A		<i>MICB</i>	31,53	CTGGCTTGCCTTTCTTCTC CGGTGATGTTGCCCTCTGA	FAM-TGCAGATGACATTCA TET-TGCAGATGACATTTC	Basic/extension
rs3130062		<i>IkBL</i>	31,59	CGGAAACATGCCCAAGT GGCTGGAGCCCTCAGCA	FAM-TGCAGGATCCCTCTGCTTCTCG TET-TGCAGGATCCCTCTGCTTCTC	Basic-screen/extension
rs1800683	hCV7514065	<i>LTA</i>	31,60			Basic/extension
rs1041981		<i>LTA</i>	31,60	CCCGTCAGCACCCCAAGATG TGGGAGTTCAGGTGATGTTTACC	FAM-TGCCACAGCAACCTCAAACCTGC TET-TTGCCACAGCACCCCTCAAACCTGC	Basic/extension
rs1799964		<i>TNPa</i>	31,60	GATGGACTCACAGGTGAGG CCAGAGTCTCTGTAACCCA	FAM-AGCAAAGGAGAAGCTGAGAAGATGAAGGAAAAGTC TET-AGCAAAGGAGAAGCTGAGAAGATGAAGGAAAAG	Basic-screen/extension
rs1799742		<i>TNPa</i>	31,60	TCCAGGGCTATGAAAGTCGA TGCTGGTTTCAGTCTTGGGT	FAM-AGTATGGGGACCCCTTAAATGAAGA TET-TATGGGGACCCCTTAAACGAAG	Basic-screen

rs1800629		TNFA	31, 60	CCTGCATCCTGTCTGGAAAGTTAGAAG TGGGCCACTGACTGATTGTGTGT	FAM-AACCCCGTCTCATGCCCTC TET-AACCCCGTCCCATGCCCTC	Basic-screen
rs361525		TNFA	31, 60	CAGTGGCCCAAGACCC AGCATCAAGGATACCCCTCAC	FAM-AATCAGAGCAGGAGGATGGGA TET-AATCGAGCAGGAGGATGGG	Basic-screen
rs707916		DDAH2	31, 76	CTGGAGCCGGGAGTAGTGC CGAGCCTAAGGAGTTAAGCATCC	FAM-TTTATACTAGTCTGTCTAGGGCAGCGT TET-TTTATACTAGTCTGTCTAGGGCAGC	Basic-screen
rs707926		VARS2	31, 81	GGTGGAGTGGGAGCAGTCAG TCACGGCCGGAAGATGAG	FAM-CCATAGATGACGTCACGGGATCGAT TET-CCATAGATGACATCCAGGGATCGATG	Basic-screen
rs2075800		HSP70-HOM	31, 84	AACGAGCTCCTTTCGTGGCT CACATACCCTGTTCGCGCAGG	FAM-CATAAGAGAAAGGAATTGGAGCAGATGTGTAACCC TET-TCATAAGAGAAAGGAATTGAAGCAGATGTGTAACCC	Basic-screen
rs539689		HSPA1B	31, 86	CAAAGTCTTGAAGTCCCAACAGT AACCCCATCATCAGCGGA	FAM-CCCGAAGCCGCGCAGGCC TET-CCCGAAGCCCGCAGGCC	Basic-screen
AF019413_C 89532G		C2	31, 96	TGAGCGTGCCTATTATCACC TCCTCTCTCATCACATCACGT	FAM-TCCCGGGATATGACTGAGGTGATCAGC TET-CCCGGGATATGACTGACGTGATCAGC	Basic-screen
rs1035798		AGER	32, 18	CCAGGGTCTTCTCCAAAGGC GCCGTGAGTTCAGAGGCAG	FAM-TGGCCTCATTTCCACATACAGATTTGAGAAC TET-TGGCCTCATTTCCACACACAGAGTTGA	Basic-screen
rs2070600		AGER	32, 18	AGGCCCTGGGACAGTGT CCGACAGCCGGAAGGAA	FAM-CCACCGCTCCCT TET-CCAACAGCTCCCTC	Basic/extension
rs1800624	hCV3293837	AGER	32, 18			Basic/extension
rs2071287	hCV3293818	NOTCH4	32, 20			Basic/extension
rs384247	hCV2412441	NOTCH4	32, 21			Basic/extension
rs915894	hCV3293780	NOTCH4	32, 22			Basic/extension
rs436845	hCV2412414		32, 22			Basic/extension
rs560505	hCV2495657	TSBP	32, 29			Basic/extension
rs485774	hCV2495577	TSBP	32, 32			Basic/extension
rs552339	hCV2495574	TSBP	32, 32			Basic/extension
rs761187	hCV2234065	TSBP	32, 34			Basic/extension
rs2073044	hCV2488525	TSBP	32, 37			Basic/extension
rs2050190	hCV2488524	TSBP	32, 37			Basic/extension
rs2073045	hCV2488523	TSBP	32, 37			Basic/extension
AL034394_T 26355G			32, 37	AGAACTTCTTAGATGAGAGTGCAACTTC GGGAAAGAAAATGTCTATGGCAAAGG	FAM-TGAGCGTAGTCGATTC TET-TGAGCGTAGTAGATTC	Basic/extension
AL034394_A 26270C			32, 37	CCATAGACATTTCTTTCCTGATGATTTTTC CTTGAGACACAGATTCTGGAACCT	FAM-CAAAACACATTTTCTTTC TET-CAAAACACATGTTTCTTTC	Basic/extension
AL034394_C 20283T			32, 38	GTAGGAGCTTAAGACACTGTGTACTG GCCAAGGCATCTGAACAAAGAGA	FAM-AGGGCTATTGCTTATT TET-CAGGGCTATTACTTATT	Basic/extension
AL034394_C 16965T			32, 38	GCAGCTCATCCCAACCTCATC GCAGCTCATCCCAACCTCATC	FAM-TTCTTCAACGGAGAATG TET-TTCTTCAACAGAGAATG	Basic/extension
	hCV2488476		32, 38			Basic/extension
AL034394_C 12339T			32, 39	GTTCAGAGTGCTGTTTCATGAGTGAT CAGGATGGCAGACGTCAGA	FAM-CGCATGGGACCGC TET-CCGCATAGGACCGC	Basic/extension
AL034394_T 10552C			32, 39	ACTGTAAGAAAGAGAATCCATTCTGATAAATA TCAATAT GCTGTTTGTGTGCTCTAGAAGGTG	FAM-TTCCACTTTAAATTTCTTACGTC TET-CTTCCACTTTAAATTTCTTATGTC	Basic/extension
BTNL2_E360 Amb		BTNL2	32, 39	GCGAGGAGAAATCGCAACTT TTTCCAAACCTGGAAGACATAAGGAA	FAM-TTCTCTCTCATGTTGGTG TET-TTCTCTCTCAGGTTGGTG	Basic/extension
BTNL2_P299 Q		BTNL2	32, 39	GAGTCAGGGCCTGGGAAGA GGAGGGGCAAGAAGATGGA	FAM-TGTCCTCCACTGCA TET-ATGTCCTCCATGGC	Basic/extension/r eplication
BTNL2_M286 I		BTNL2	32, 39	ACCCTTAGCAATGCTGCACGT GGTCTTCCCCACTGATCACTG	FAM-ATCCGAAGAGCATATC FAM-CATCTGAAGAGCATATC VIC-CATCTGAAGAGCATATC VIC-ATCCGAAGAGCATATC	Basic/extension/r eplication
BTNL2_P285 L		BTNL2	32, 39	GTCTTCCCCACTGATCACTGT TGAGTCAGGGCCTGGGA	FAM-TGGAGAAATGCAGCTGA TET-ATGGAGAAATGCAGCCGA	Basic/extension/r eplication
rs2076530		BTNL2	32, 39	AGTACCGCTGCCCTTTTGAATA GTGGCAGGAGCAGGATTTGAATA	FAM-AAGGTGGTAGGTAAGAA TET-AGGTGGTAAGTAAGAA	Basic/extension/r eplication
BTNL2_S240 L		BTNL2	32, 39	AGACTGACCCCTGCAGATACTCA TTTTCAAAGGCGAGGACTG	FAM-TGCTCCAAAGGTCT TET-TGCTCCAAAGGTCT	Basic/extension
rs2076529		BTNL2	32, 39	GGAGAGCAGATGGCAGAGTACAG CCTCGTCAATGGCGTCACT	FAM-ACCAGCACAGTCT TET-ACCAGTACAGTCTC	Basic/extension
rs2294878	hCV2488463	BTNL2	32, 39			Basic/extension
BTNL2_i4_A 239T		BTNL2	32, 40	TGCGAGCTGTGTTACCTGACA CAGAGATGATGCCATGCTTCCT	FAM-ATCAGATGGTCACTAT TET-CATCAGATGGACACTAT	Basic/extension
rs2076524	hCV2488453	BTNL2	32, 40			Basic/extension
- BTNL2_i3_C 1900T		BTNL2	32, 40	TCTGAGACTCGCATCCAAGAT AGACTCTGCAGAGGCGTTCCT	FAM-TGGCTTCCACATAGA TET-CTTCCGATAGAAC	Basic/extension
rs2076523		BTNL2	32, 40	CCAGAGCCCAAGGTGATTTG TGGACCAAGCAGGACACAGA	FAM-CATCGCATCCAAGATAAAGATGGCCTGTT TET-CATCGCATCCAAGATAAAGATGGCCT	Basic- screen/extension
BTNL2_i3_A 1837G		BTNL2	32, 40	CAGAGCCCAAGGTGATTTGG	FAM-CTCCCCGATGTC	Basic/extension

				ACACGGCCAGCAGCTTCT	TET-CTCCCTGGATGTCT	
BTNL2_W94R		<i>BTNL2</i>	32, 40	GACTGAGATGCAGATGGAGGAGTAC CTTTGCCAATGCCATTCTCTATCC	FAM-AGAGGCTGGGTAGAGT TET-AGAGGCAAGGGTAGAGT	Basic/extension
BTNL2_H60H		<i>BTNL2</i>	32, 40	TGCCAGCTACTCCCAAGAG GGGCTCTGAGCGGTACCA	FAM-AATGCATGTGGAGGTG TET-AATGCACGTGGAGGT	Basic/extension
BTNL2_il_G 1717T		<i>BTNL2</i>	32, 40	GGAGCCAAAGCCCAATTCAC CAGTCTTAGCAGAGAATCCACATCA	FAM-ACCCTGGAACAGTCT TET-CCCTGCACAGTCT	Basic/extension
	hCV2455668		32, 43			Basic/extension
06DRAp_231		<i>HLA-DRA</i>	32, 43	AATGTGCTTCAGGTATATCCCTGTCT AGTAAAGTTCTTAAACAACAGGACAACAA	FAM-TGTCCGTGATTGAC TET-TGTCCGTATTGAC	Basic/extension
06DRAp_224		<i>HLA-DRA</i>	32, 43	AATGTGCTTCAGGTATATCCCTGTCT AGTAAAGTTCTTAAACAACAGGACAACAA	FAM-ATTTAAGACTGTTAGTCAAT TET-TTAAAGACTGTTAGTCAAT	Basic/extension
06DRAp_196		<i>HLA-DRA</i>	32, 43	AATGTGCTTCAGGTATATCCCTGTCT CCGTTTATTGGATAAAGTAAAGTT	FAM-CAACAACAACAACAAA TET-ACAACGACACAACAAT	Basic/extension
06DRAp_127		<i>HLA-DRA</i>	32, 43	TTATCCAATGAACGGAGTATCTTGTG ATGACGCATCTGTGTAGGG	FAM-CCTGGACTCTTTG TET-CTGGACCTTTGCA	Basic/extension
rs14004		<i>HLA-DRA</i>	32, 43	CCTCACTCCCGAGCTCTACTGA CCACTTATGGCCATTTCTTCTTG	FAM-CTCCCAACAGAGCG TET-TCCCAAAAGAGCCG	Basic/extension
	hCV2455646	<i>HLA-DRA</i>	32, 44			Basic/extension
rs8084	hCV2455637	<i>HLA-DRA</i>	32, 44			Basic/extension
rs7192		<i>HLA-DRA</i>	32, 44	TGGCCTGACTGTGGGTC ACCACACCTTAACCTCCATG	FAM-TCATCATCAAGGGATTGCGAAAAGC TET-TCATCATCAAGGGAGTGCGAAAAGC	Basic- screen/extension
rs2213584		<i>HLA-DRA</i>	32, 44	AATGGTAAAGCCAGCTTTCAG TGCAGGATTTACATATCAACATCGT	FAM-TGTCCAATCTCTTTCG TET-TGTCCAACCTCTTTG	Basic/extension
rs2395182		<i>HLA-DRA</i>	32, 44	GGTGGTTTCAAGAATCAGTCAAGCT GGCCTTACCATTCTGTAGACATA	FAM-CGGTAATAACAATAGGC TET-CTCGTAATAAATAGG	Basic/extension
rs707952		<i>HLA-DQA1</i>	32, 62	CATAGAGGTTCTGAGGTCAACA TGGTCTCAGAAACACCTTCTGT	FAM-CTGGGTCAGCCCAACACCCTC TET-CTGGGTCAGCCCAACATCCTCA	Basic- screen/extension
X66401_G48 629A		<i>TAP2</i>	32, 80	GGTGGTTTTCAGTTGGGCGAG CTCCATTCTCGGTGAAGTCA	FAM-TGTGAGGAACAACATTACTTATGGGCTGAG TET-TGAGGAACAACAATTGCTTATGGGCTGC	Basic-screen
rs1042337		<i>HLA-DMB</i>	32, 91	GCCAGCCCAATGGAGAC CCTAATTCATCCATCTGCCATAC	FAM-TGTGTGTTAGAGCACATTGGGCTCC TET-TGTGTGTTAGAGCACATTGGGCTCC	Basic-screen
rs1063478		<i>HLA-DMA</i>	32, 92	AAAAGGCTTGAAGTGTGAGTC GAGTTGGCAAGCCCAACAC	FAM-CTTCCACAGGGATGGAATGATGCTG TET-CTTCCACAGGGACGGAATGATGCT	Basic-screen
rs3918143		<i>RING3</i>	32, 95	GATGCCAGATGAACCACTAGAACCC CCTCAGAGGAGCTCTCACTGCTAC	FAM-CTTGGCTTGGCCAAATCGTCTCAG TET-CCCTGGCTTGGTCAAATCGTCTCAGA	Basic-screen
rs2581		<i>HLA-DNA</i>	32, 98	TGTGCTGACTTGTAGTGGGATC AACACCACCAAGCAATTTAGTGC	FAM-CCTTCCCAATCAACACACACACATTC TET-CCTTCCCAATCAACACACACATCTTT	Basic-screen
rs926424		<i>RXRB</i>	33, 16	CTCCTCTCTCTTCCACTGATGTGC GCACGTGAAGACCTGTGGC	FAM-ATGTGCTCTCTTTCACACCCGATCC TET-CATTGCCTCTTCTCACACCCGATCC	Basic-screen
rs1547387		<i>HKE4</i>	33, 17	AGTGGGGAGGTGAGGAATAG CCCCAATACACACTCATTTGTGC	FAM-CCTCACCACTGTGGGAGTGTCCATGT TET-CTCACCACTGTGGGAGTGTCCATGT	Basic-screen
rs466384		<i>BING4</i>	33, 26	CCTCAGGCTTAGGTGTATTAGCA TCGTGCCTGTAGAATCTACTGCC	FAM-CTTCCAGGTACTGTGCTTTATGGATCCAG TET-TCCAGGTACTGTGCTTTATGGATCCCA	Basic-screen
rs2071888		<i>TAPBP</i>	33, 27	GCAATTTGCTGTGGGATG AGCAAGCTCCAGGGTGACC	FAM-CTTCTGGCTGCCTAGAGTTCAACCTTTCA TET-TCTGGCTGCCACAGTTCAACCTTTCA	Basic-screen
rs999942		<i>ITPR3</i>	33, 63	CCCTCCATCAGACTGGCCTC CGGTCCACAGCCACATGC	FAM-CAGCAGGAGAGGCTTGCATGG TET-CAGCAGGAGAGCCTTGCATGG	Basic-screen
rs943461		<i>MLN</i>	33, 77	CCCCAAGACCCAGAGAGACC AGGGATACAGCTCCATGCTGAA	FAM-CAAGCCAGATGACAGGGCTCTG TET-CAAGCCAGATGACAGGGCTCTG	Basic-screen
rs755658		<i>FKBP5</i>	35, 55	TTGAAGTCTGTATCACAGGCATG ACCAACAGGTTTAAAGCCATGTTACTAGG	FAM-ACTCGACAGTGAAGTGAAGGCTGC TET-TCGGCAAGTGAAGTGAAGGCTGC	Basic-screen
rs992105		<i>FKBP5</i>	35, 56	TTCCATCATGACCAAGCTGTAGC CAGAGGGAGATAAGCATGGC	FAM-ACTCTGTGAAGCACTGTACAAAGTGCATCTTTAGAA TET-CGTACTCTGTGAAGCACTGTACAAAGTGAATCTTTAGA	Basic-screen
rs1320991		<i>FKBP5</i>	35, 56	TGTGGTATGTGGAGAAATATGTGAA AAACAAGTAAATTCATGCCGTGCAC	FAM-TAGAAAACCCCTACGTCTATATATGTGTGCGT TET-TAGAAAACCCCTACATGCTATATATGTGTGCGTATG	Basic-screen
rs1326752		<i>SRPK1</i>	35, 83	AAAAAGCCTGTTGCTTAGGTATGC AGAGGTTAATGCTAGGTTGGCG	FAM-CTGCAGCCAGGTCAGCCCGAA TET-CTGCAGCCAGGTCAGCCCGAA	Basic-screen
Z95152_G57 723A			36, 03	CAGGTGATTTGGTCTGTTGGAGC CCCCAAAAGAGGTCATGATAGG	FAM-TGAGTAAATTTTTTGCATTGCTCTCTGGTCTA TET-TGAGTAAATTTTTTGCATTGCTCTCTGG	Basic-screen
Z95152_T58 784G			36, 08	GGAGAAGAGGGCTAATATATCTTAGAGTAG GGCCGCTGTAATTTCTTATCTG	FAM-TTCTTCTCTGTCTAGTACTGACTGTGACTG TET-TCTTCTCTGTCTGCTACTGATGACTGTGCGAC	Basic-screen
Z95152_T10 6861C			36, 08	GAAGTCATCAGCTTTGTGCCAC ACCATGGAGAAATCTCTGCA	FAM-AAGGCTTTTTCACGGAACTCTCCAAA TET-AAGGCTTTTTCACGGAACTCTCCAAATATTC	Basic-screen
rs763096		<i>MAPK13</i>	36, 10	CTGTGAGACTGGCAGATGTG GCCTTGGCTGTCAAGTGTG	FAM-CCAGGCAAGCACTCCACAAGCTCTT TET-CAGGCAAGCAACCCCAAGTCTCT	Basic-screen
rs2007683		<i>MAPK13</i>	36, 10	CAGCTTCTTCCATCTGTCTCA ACAGTCGATATTGGTAGCCA	FAM-ATGTTGATATCTGAATCAATGCTATCTTACCACATT TET-TGTTGATATCTGAATCAATGCTATCTTACCACATTCA	Basic-screen
rs881648		<i>TEL2</i>	36, 35	CTAGGCTCCAAACCCAGGAC CCCATGGCTTATTACAGCTAGGA	FAM-CTCACTTTGGATCGAGGAAAATGAGACTTC TET-CTCACTTTGGATCGAAGAAAATGAGACTTC	Basic-screen
rs881647		<i>TEL2</i>	36, 35	TTCAGAACTGGGCTGATATCACAG AATGAGGCAATGGTGGTAC	FAM-CAAGGGACAACCTGGGAGAAATTTGAGAGT TET-AAGGGACAACCTGGGAGAAATTTGAGAGG	Basic-screen
rs916287		<i>TEL2</i>	36, 35	AGAAGAAGAGACGCAAGGACCG CCATTTTCAGAACTGGGATGATA	FAM-CTCTGAACCTGCTCTCTCAAATTTCCCCAA TET-CTCTGAACCTGCTCTCTCAAATTTCCCCA	Basic-screen

rs1885205		TEL2	36, 35	CTCCTGACTCACTCTGGCCTTG TCCACTCTGAGGACAACCCTG	FAM-ACCCTCATGGCCATGGACCGG TET-CATGGCCATGGACCAGGGATGG	Basic-screen
rs2055272		FLJ20337	37, 29	CATGTTGGTAATGAATTGTGATTATG ATGCTTAAGATTATATGTCATGATCCA	FAM-AGGTAGGTTCCGGCGCTTTACATTGTCT TET-AGGTTCCGAGCGCTCTTACATTGTCTCCAC	Basic-screen
rs1004279		GLP1R	39, 03	AGGAGGCTGAGGTCAGGC GCCATCATGAACTTATCACTACTGAC	FAM-TGAGTGGTCCGCTGCCTTTCC TET-AGTGAATGGTCCACCTGCCTTTCCCTG	Basic-screen
rs1541816		KCNK5	39, 16	AGGCCTTAGGAATTGGACCA GAGCAGGAGGCCAAGTCAGA	FAM-CCCTCCGGGTTAGGCTGGGTAC TET-CCTCCCGGGTCAGGCTGGG	Basic-screen
rs1014737		APOBEC2	41, 02	AACACAGAGGGAGGGTAGGTCA GTTGTGATTATAAAGCCCTGGACA	FAM-AGCAATGGATCCTGAAGGGTTAAGTCCACT TET-AGCAATGGATCCTGAAGGGATAAGTCCACT	Basic-screen
rs2234246		TREM1	41, 25	AAAAGGCAGGGAGTTAATAACATGA TAGAGGAAACGAGGGCAGTGG	FAM-ATCTGTAATCACCGGCTATTCTAAAGTCAGCGTCT TET-ATCTGTAATCACCGCTATTCTAAAGTCAGCGTCTCA	Basic-screen
rs1817538		TREM1	41, 25	CTGCTGCATGCTGCTGATG CGAGAAGAATCCACCCCTAGTG	FAM-CCCAGAAACCTTAGAATCATTTTGCCCCAAATCT TET-CCCAGAAACCTTAGAATCATTTCGCCAAAAT	Basic-screen
rs1351835		TREM1	41, 25	ATGTTCTGCATAGCACTGGC AGGAGTGAGGGCACTGGC	FAM-CTCTCATCTGCTTGGTGTCTGCTGATGAA TET-TCTCATCTGCTGCTGCTGCTGATGA	Basic-screen
rs2234237		TREM1	41, 25	GAACCCATTCTCTTTCCCTGCT AGCGTGTAGTCAATTTACATCC	FAM-CTCCGAGCTGCAACTAAATATCTGAGGAAAAGTATGA TET-CTCCGAGCTGCAACTAAATTAAGTGAAGAAAAGTATGA	Basic-screen
AL391903_C 88694T		TREM1	41, 26	ATTACATTCAGTATCATTCTCCCTTAGAT GACATCAACACAATAATACAGAGACCAA	FAM-AGGTAATTTGTCATTATTACCACAAAAGGAAAAGTGGAG TET-AGGTAATTTGTCATTATTACCACAAAAGGAAAAGTGGAG	Basic-screen
rs742735		MDPI	41, 62	TCAATTGATGGCTGATGAGGAG AGCAGAATAAAATGGTGCCAGG	FAM-CACATCGGCTGGTGGGTGTCTG TET-CACATCGGCTGGTGGGTGTCT	Basic-screen
rs1410492		CCND3	41, 91	GGGCATTGTGTGTGATGG GCAAAGTACTAGTGTGATGATGCA	FAM-AGGGGATGCCACTCCTTGCTGGTCT TET-AGGGGATGCCACTCCTTGCTGGTCT	Basic-screen
rs1160867		TNRC5	42, 90	CCCTAACGAGGCTCTGG TTCCCCACATCTTCCAGCAC	FAM-ACCAAGACCCGAGGAGAAGAAGCCT TET-CAAGACCCGAGGAGAAGCCTGCG	Basic-screen
rs9395		SRF	43, 15	CCCAGTGAGTGAATCAGGCA ACCCAGAGCCACCGAG	FAM-ATGCGTGTGTCAGGGATGAGTTGAGGT TET-CGTGTGTGTCAGCGATGAGTTGAGGTGA	Basic-screen
rs1418488		CAPN11	44, 14	GAAGGACAGTGTGAGGCCACTG AAAGAGCCACAAATTGCTAACAACTA	FAM-CCCACCAAGAAATCATGTAAGGTAATTTTTAAGTCCC TET-CCCACCAAGAAATCATGTAAGCTAATTTTTAAGTCCC	Basic-screen

**Mutation detection:** Primers for mutation detection in the *BTNL2* gene and extra-genic regions of disease association. For: forward primer; Rev: reverse primer.

Primer	Sequence	Amplicon length	SNP marker*
1_For	5'-CCTCACACATGCCAATTCCC-3'	463bp	06orf_001
1_Rev	5'-TTTTGCCTCCCATCGAC-3'		06orf_002
2_For	5'-CCTCACACATGCCAATTCCC-3'	359bp.	06orf_004
2_Rev	5'-TTTTGCCTCCCATCGAC-3'		
3_For	5'-CAAACCACCACTCTCTTTCATTG-3'	384bp.	06orf_005
3_Rev	5'-CTCCCTCTTGTITTTCTCCATTCT-3'		
4_For	5'-TAAACATTTGTGGAAGAATAATGTGTAGTT-3'	271bp.	06orf_007
4_Rev	5'-TCAAGAAGATAAACTATATGTGGAAGACAG-3'		
5_For	5'-GAGCTGTGTTTGAAGCCAATGTC-3'	540bp.	06orf_009
5_Rev	5'-GAGCCTCCCTTTTACAAGTCA-3'		
<i>BTNL2</i> _e8_For	5'-CTTGTCTTCCTGTTTGGCTGTTAA-3'	497bp.	
<i>BTNL2</i> _e8_Rev	5'-GGGAAGGTGTAGATAGGGCACTT-3'		
<i>BTNL2</i> _e7_For	5'-AGCAGGCCAACTGCTTCCT-3'	402bp.	
<i>BTNL2</i> _e7_Rev	5'-ACTGAGCCTGGATTGCATGAT-3'		
<i>BTNL2</i> _e6_For	5'-CCTGGCCGAAGTTATTTTGT-3'	738bp.	<i>BTNL2</i> _e6_E360Amb <i>BTNL2</i> _e6_P299Q <i>BTNL2</i> _e6_M286I <i>BTNL2</i> _e6_P285L
<i>BTNL2</i> _e6_Rev	5'-TAGAATCCCTGGGTGTCCTG-3'		
<i>BTNL2</i> _e5_For	5'-GGTTTCTAAACTCCAATGGAGCTGTT-3'	528bp.	<i>BTNL2</i> _e5_S240L
<i>BTNL2</i> _e5_Rev	5'-CAAATGTCAGAGAAATTGTCCAGGA-3'		
<i>BTNL2</i> _i4_For	5'-GGTAAGTACGAGGTGCTGGCA-3'	541bp.	<i>BTNL2</i> _i4_A239T
<i>BTNL2</i> _i4_Rev	5'-TTGCTACACTCACAGTATCCCAGG-3'		
<i>BTNL2</i> _e4_For	5'-GTGACAGCATTTTTGTTGTGCAG-3'	474bp.	
<i>BTNL2</i> _e4_Rev	5'-GGTGTCCATCTGATGCTCACTG-3'		
<i>BTNL2</i> _i3_For	5'-CCTCAGACTCCTGAACTCCG-3'	469bp.	<i>BTNL2</i> _i3_C1900T <i>BTNL2</i> _i3_A1837G
<i>BTNL2</i> _i3_Rev	5'-GGTGCTATGGTGCAGTCCC-3'		
<i>BTNL2</i> _e3_For	5'-CATTTTGACAGGCTGGACACC-3'	511bp.	<i>BTNL2</i> _e3_W94R <i>BTNL2</i> _e3_H60H
<i>BTNL2</i> _e3_Rev	5'-CCTCAACTGTCACAAAGCTTACCA-3'		
<i>BTNL2</i> _e2_For	5'-CAATGGAAGCCATGGAGTGTG-3'	489bp.	
<i>BTNL2</i> _e2_Rev	5'-AACGTGGTGCAACCACTGATT-3'		
<i>BTNL2</i> _i1_For	5'-AAGCCGAACACTACATCAACGTTT-3'	528bp.	<i>BTNL2</i> _i1_G1717T
<i>BTNL2</i> _i1_Rev	5'-CTGCACCAGACAGATTGTAGCC-3'		
<i>BTNL2</i> _e1_For	5'-TGTCTCTAAGGGCAAAACAGC-3'	693bp.	
<i>BTNL2</i> _e1_Rev	5'-GTTTCCCCCTTTCCAAGAACTA-3'		
DRAp_For	5'-TAGGTGTTTCCATTGATCTATTCTCAC-3'	462bp.	06DRAp_231 06DRAp_224 06DRAp_196 06DRAp_127
DRAp_Rev	5'-TGATAGCCCATGATTCCTGAGC-3'		

\*- only markers selected for genotyping are included in the table. Data of other SNPs are not shown.

**RT-PCR and cloning:** Primers for RT-PCR and cDNA cloning. The position of the primer sequences in the revised *BTNL2* transcript refers to the 5' end for forward primers and to the 3' end for reverse primers.

Designation	Sequence	Position in cDNA
BTNL2f1	ACCCTTCAGTCTAAGGGGAG	1
BTNL2f2	TGGTGGATTTTCCAGGCTAC	45
BTNL2f3	TTAGAGTCATTGGCCCTGCT	126
BTNL2r1	CTTCAGTGCCACATTTCCCT	370
BTNL2r2	CTTCTCCCACTCTGACGAGG	542
BTNL2f4	CCTGCAGATACTCAGTGCCA	733
BTNL2r3	CGAAGGTCTGGCACTGAGTA	760
BTNL2f5	AGTACCGCTGCCTTTTTGAA	771
BTNL2r4	TTCAAAAAGGCAGCGGTACT	790
BTNL2f6	TCGTCTTTCCTTCCATGTCC	958
BTNL2f7	CGGAGATGTTTGTGACCCTT	1042
BTNL2f8	ACTTGTTCCATCAGCATCCC	1073
BTNL2r5	TGGATCACACGCTTGTTCTG	1282
BTNL2r6	GCCCATAGAGCAGATAGTCAG	1337

For expression analysis, nested PCR was performed with primers

TTAGAGTCATTGGCCCTGCT and GCCCATAGAGCAGATAGTCAG for the first, and AGTACCGCTGCCTTTTTGAA and TGGATCACACGCTTGTTCTG for the second round of amplification.

Full-length allelic variants of the *BTNL2* transcript were constructed from clones generated during the gene model verification. Final full-length amplification was performed with primers GTC TCG AGA TGG TGG ATT TTC CAG GC and CAC CCG GGG CTC CTC TTC CTG, for the untruncated transcript (BTNL2-L) and GTC TCG AGA TGG TGG ATT TTC CAG GC, AAC CCG GGG TGG GGA AGA ACC for the 4pb deletion variant (BTNL2-S).

**DRB1 genotyping:** Primers used for the subcharacterization of the *HLA-DRB1* amplification groups 2 and 3 (other primers for group typing are given in reference 22 of the main manuscript). Primers were used as suggested in: *Olerup O, Zetterquist H. HLA-DR typing by PCR amplification with sequence specific primers (PCR-SSP) in 2 hours: An alternative to serological DR typing in clinical practice including donor-recipient matching in cadaveric transplantation. Tissue Antigens 1992; 39: 225-235.*

DRB1 allele groups	5' primer	3' primer
Amp3 "+" group		
DRB1*03 <sup>1)</sup>	5'TACTTCCATAACCAGGAGGAGA	5'TGCAGTAGTTGTCCACCCG
DRB1*08"	5'AGTACTCTACGGGTGAGTGTT	5'CTGCAGTAGGTGTCCACCAG
DRB1*11"	5'GTTTCTTGGAGTACTCTACGTC	5'CTGGCTGTTCCAGTACTCCT
DRB1*12"	5'AGTACTCTACGGGTGAGTGTT	5'CACTGTGAAGCTCTCCACAG
DRB1*13"	5'TACTTCCATAACCAGGAGGAGA	5'CCCGCTCGTCTTCCAGGAT
DRB1*14"	5'GTTTCTTGGAGTACTCTACGTC	5'TCTGCAATAGGTGTCCACCT
Amp2 "+" group		
DRB1*15"	5'TCCTGTGGCAGCCTAAGAG	5'CCGCGCCTGCTCCAGGAT
DRB1*16"	5'TCCTGTGGCAGCCTAAGAG	5'AGGTGTCCACCGCGGCG

<sup>1)</sup> main alleles. The full list of alleles is given in table 3a of the main manuscript.

**DQB1 genotyping:** Primers used for the HLA-DQB1- SSP – typing: Primers were used as suggested in: Olerup O, Aldener A, Fogdell A. *HLA-DQB1 and -DQA1 typing by PCR amplification with sequence-specific primers (PCR-SSP) in 2 hours. Tissue Antigens. 1993 : 41 :119-34* and *The IHWG XI<sup>th</sup> Workshop protocol, Kimura A, Sasazuki T. Eleventh International Histocompatibility Workshop reference protocol for the HLA DNA-typing technique. In: Eleventh International Histocompatibility Workshop reference protocol for the HLA DNA-typing technique. Oxford: Oxford University Press, 1991: 397-419.*)

DQB1-PCR reactions	allele grouping	5' primer	3' primer
1	DQB1*02	5'GTGCGTCTTGTGAGCAGAAG	5'GCAAGGTCGTGCGGAGCT
2	DQB1*03	5'CATGTGCTACTTCACCAACGG	5'AGTACTCGGCGTCAGGCG
3	DQB1*04, *0306	5'CATGTGCTACTTCACCAACGG	5'GGTAGTTGTGTCTGCATACG
4	DQB1*0501	5'CGGAGCGCGTGCGGGG	5'GCTGTTCCAGTACTCGGCAA
5	DQB1*0502, *0504	5'TGCGGGGTGTGACCAGAC	5'TGTTCCAGTACTCGGCGCT
6	DQB1*0503	5'TGCGGGGTGTGACCAGAC	5'GCGGCGTCACCGCCCGA
7	DQB1*06 except *0601, *0602, *0610, *061101, *0613, *0615, *0616, *0619, *0620	5'GGAGCGCGTGCGTCTTGTA	5'CTCGTAGTTGTGTCTGCACAC
8	DQB1*0601 except *060102	5'GCCATGTGCTACTTCACCAAT	5'CACCGTGTCCAACCTCCGCT
9	DQB1*0602, *0610, *0611, *0613, *0615, *0616, *0620	5'CGTGCGTCTTGTGACCAGAT	5'CCTGCGGCGTCACCGCG

**DPB1 genotyping:** Primers used for HLA-DPB1 – SSP typing. The *DPB1* allele grouping was performed according to *Gilchrist FC, Bunce M, Lympny PA, Welsh KI, Du Bois RM. Comprehensive HLA-DP typing using polymerase chain reaction with sequence-specific primers and 95 sequence specific mixes. Tissue antigens 1998: 51: 51-61.*

DPB1-PCR reactions	5' primer	3' primer	positive reactions for alleles
1	5'CCCGCAGAGAATTACCTTTT	5'CTGTTCCAGTACTCCGCAG	DPB1*0401, *2301, *3101, *3301, *3401, *3901, *4001, *6201, *6301, *6501, *7101, *7201, *9501, *9601, *9901
2	5'ATCTACAACCGGGAGGAGTT	5'CAGGGTCATGGGCCCGC	DPB1*0201, *0401, *0402, *2301, *2401, *3201, *3301, *4101, *4601, *4701, *5101, *5901, *6001, *7001, *7101, *7201, *7301, *7501, *7701, *8001, *8101, *8201, *8301, *8601, *9401, *9901
3	5'CCCGCAGAGAATTACCTTTT	5'GCTGTTCCAGTAC/GTCCTCAT	DPB1*0201, *0402, *0801, *1601, *2801, *3201, *4101, *4601, *4801, *4901, *5101, *5301, *5701, *5901, *6001, *6801, *7301, *7501, *7701, *8001, *8101, *8201, *8301, *9401
4	5'CCCGCAGAGAATTACCTTTT	5'TCCGGCACTGCCCCGTC	DPB1*0201, *0202, *0801, *1601, *1901, *2201, *3201, *3301, *4101, *4601, *4701, *4801, *7101, *8101, *9501
5	5'TCTACAACCGGGAGGAGCT	5'CAGGGTCATGGGCCCGC	DPB1*0202, *4801, *9501
6	5'GAGAATTACGTGTACCAGGG	5'CTCGTAGTTGTGTCTGCATAC	DPB1*0101, *5001, *9001
7	5'GAGAATTACGTGTACCAGGG	5'CCCGCTT/CCTCCTCCAGGAT	DPB1*0101, *1801, *8901, *9001
8	5'CAGAGAATTACGTGTACCAGT	5'CCTTCTGGCTGTTCCAGTAG	DPB1*0301, *0601, *2001, *2901, *4401, *6101N, *6401N, *6901, *7801, *8801, *9201 False positive reactions: *0901, *1001, *1401, *1701, *3001, *3501, *4501, *5401, *5501, *5801, *6601, *6701, *7601, *8601, *9101, *9801
9	5'CCGCAGAGAATTACGTGTA	5'AGCTCGTAGTTGTGTCTGCA	DPB1*0101, *0301, *0601, *1101, *1301, *1501, *1801, *2001, *2101, *2501, *2601, *2701, *2901, *3601, *3701, *4401, *5001, *5201, *5601, *6101N, *6401N, *6901, *7401, *7801, *7901, *8501, *8701, *8801, *8901, *9001, *9201, *9301
10	5'ATCTACAACCGGGAGGAGTT	5'GTCCGGCAC/ATGCCCGCTT	DPB1*0301, *0401, *0402, *1401, *1801, *2001, *2301, *2401, *2501, *2801, *3101, *3501, *4501, *5001, *5101, *5201, *5601, *5701, *5901, *6001, *6101, *6601, *6701, *6801, *7001, *7201, *7301, *7501, *7601, *7701, *7801, *7901, *8001, *8201, *8301, *8401, *8701, *9001, *9101, *9201, *9801, *9901

