

Supplementary MHC data

MHC sequences from reindeer and other species used in this study, alignment of MHC sequences, primers used for amplification and MHC sequences for each animal

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1. Sampling sites on Norwegian mainland and Svalbard

Red circles show sampling areas. 1) Semi-domestic reindeer were collected from two herds located in Northern Norway. 2). Wild reindeer were sampled in Langfjella (Hardangervidda and Setesdal Ryfylke) in Southern Norway and 3) Wild reindeer sampled in high Arctic archipelago Svalbard.



2. MHC sequences from other species used in this study

Cattle MHC class II sequences from genome assembly GCA_002263795.1

>Bola-DQA2 BAA08765.1 chr.23 NC_037350: 25.583.525-25.589.147 [Bos taurus]
MVLNRLALILGALATTTMMSSGGEDIVADHVGSGYGTIYQSHGPSGQYTQEFDGDEMFYVDLGKKETVWRLPMFSQFAGFDPQAALSEIATA
KHNLVDLTKRSNFTVPINEVEPTVFSKSPVMLGQPNTLICHVDNIFPPVINITWLKNGHAVTEGVSETSFLLPKDDHSFLKIGYLTFLPSDNDIYDC
KVEHWGLDEPLLKHWEPVPAPMSELTETVVCALGLTVGLVGIVVGTIFIIQGLRSGGASRHQGPL

>Bola-DQB1 NP_001012694.2 chr.23 NC_037350:25.607.585-25.620.339[B.taurus]
MSGMVALWIPRGLWTAAMVMTLAVLSTPGAEGRDSPQDTVVHFMCCQCYFTNGTERVRYVTRYIYNQEETAYYSDVGEYRAVTQLGRTLAE
YWNSQKDILEQTRAELDTVCRHNYQLEVITSLQRQVEPTVTISLSTEALNHHNLLVCSVTDYFPGQIKVRWFQNGKEETAGIVSTPLIRNGDW
TFQILVMLEMTPKRGDVYTCRVEHPSLQSPISVEWRAQSESAQSKMMSGVGGFVLGLIFLGLGLIVRRRSQKGLMH

>Bola-DQA5 XP_005223622.1 NC_037350:25.631.994-25.643.887 [Bos taurus]
MVLNRLALILGTLATTTMMSPSGGEDIVADHVGIVGNVYQSYGPSGQFTEFDGDEQFYVDLEKKETVWKLPLFSRMLSFDPPQFALRNIAIMKL
HVDFTLTKFSNSTAATNKVPEPTVFSKSPVMLGQPNTLICHVDNIFPPVINITWLRNGHSVTEGVSETSFLLKSDYSFLKIKYLTFLPSDDDIYDCKVE
HWGLDEPLLKHWGLTRTMPLML

>Bola-DQB2 NP_001029840.2 chr.23 NC_037350:25.672.738-25.680.159 [Bos taurus]
MSGMVALWIPRGLWTAAMVMTLVMLSTPGAEGRDSPKDFVVFQKGLCYFTNGTERVRYVTRYIYNQEYVRFDSWDWLYRALTPLRPDAAE
YWNSQKDFLEQTRAEDTVCRHNYQAEITSLQRVEPTVTISPSRTEALNHHNLLVCSVTDYFSPSQIKVRWFRNDREETAGVSTPLIRNGD
WTFQILVMLEMTMPQRGDVYTCHVEHPSLQSPIMVEWRAQSESAQSKMMSGVGGFVLGLIFLGLGLIIHRSQKGLMR

>Bola-DQA1 NP_001306818.1 NC_037350.1: 25.691.259-25.695.296 [Bos taurus]
MILNRLIWGALATTTMMGPSGEDIVADHIGAYGINVYHSYGPSGYTTEFDGDEEFYVDLEKRETVWNLPLFSKFRFRDPQAGALRNIAATK
HNLEVLQRSNSTATNKVPEPTVFSKSPMMLGQPNTLICHVDNIFPPVINITWLKNGQLVIEGISETSFLLSKDDHSFSKISYLTFLPSDDDVYDCK
VEHWGLDKPLLKHWEPDIPAPMSELTETVVCALGLTVGLVGIVVGTVLIIRGLRSGGSPSRHQGPL

>Bola-DRB3 XP_024839864.1 NC_037350.1: 25.723.691-25.734.819 [Bos taurus]
MVCLYFSGGSWMAALIVMLMVLCPPLAWAREIQPHFLEYKRECHFFNGTERVRFLDRYFHNGEYVRFDSWDWGEYRAVTELQQRVAEYCN
SQKDFLERARAADTYCRHNYGVGESFTVQRRVEPIVTPAKTQPLQHNNLLVCSVNGFYFPGHIEVRWFRNGHEEEAGVISTGLIQNGDWT
FQTMVMLETVPQSGEVYTCQVEHPSRTSPITVEWRARSDSAQSKMMSGVGGFVLGLLFLAVGLFIYFRNQKGHPTLQPTGLLS

>Bola-DRB2 XP_024839853.1 NC_037350.1: 25.796.016-25.828.791 [Bos taurus]
MAALAVLLMVLSPFSWARETQPHFIHQFGECRFSNGLERMRFARYIYNTQEDVHFDSVGEFTALTELGRDLAEYWNQKQDFMEQMRA
KVDTLCRSNYQIGSFLRQRRVEPTVTPAKTQPLQHNNLLVCSVNGFYFPGHIEVRWFRNWSHEEEAGVISTGLIQNGDWTFTQTMVMLETVP
QSGEVYTCQVEHPSRTSPLTVEWRAQSDSAQRKLMMSGIGGFVLGLLFLGVGLFIHLRSKKGHPALQP

>Bola-DRA NP_001012695.1 NC_037350.1: 25.838.391-25.843.092 [Bos taurus]
 MAITRVPILGLFITVLIGLQESWAIKENHVIIQAEFYLKPEESAEMFDFDGDDEIFHVDMGKKETVWRLPEFGHFASFEAQGALANMAV/MKANL
 DIMIKRSNNTPTNPVPEVTLNPNKVELGEPNTLICFDKFSPPVISVTLRNGKPVTDGVSQTVFLPRNDHLFRKFHYLPFLPTTEDVDYCKVE
 HLGLNEPLLKHWEYEAPAPLPETTENAVCALGLIVALVGIIAGTIFIIGVRKANTVERRGPL

>Bola-DSB XP_024839519.1 NC_037350.1: 7.035.608-7.052.599 [Bos taurus]
 MVCLWFPPGSWTIVLPVILMVLSPLAWAGNTRNRYIYNREEQVQFDSLVEYRARTEMGRPAERWNRWPQALQRRARAAYHAYCASNYE
 FFASRTVQRRVQPTVTVPVKSRPLWHHNLVCSVNGFYPGHIEVRWFRNGQEEAGVSTGLIPNGDWTQIMV/MLEIVPQGGEVYACHV
 EHPSTSPVTVEWRAQDESSQEKMLSGIGACVLGLLLFGLMGLLFYIRRGRLGGPQEEGKKQREAVVWKQPSPLSPAGLLSWSRDRDTWTRTF
 CPSFFAA

>Bola-DYA NP_001012696.1 NC_037350.1: 7.072.088-7.077.975 [Bos taurus]
 MKKALILRALTLATMMSPYGGEDIVADHVGTGTNNVQTYGASGQTFEFDGDELFIYVDLGGKKETVWRLPEFSNITKFEVQSALRNIVMSKRN
 LDILIKNSSFTPATSEIPEVAVFPKSSVVLGIPNTLICQVDNIFPPVINITWFFYNGHFVAEGIAETTFYPKSDHSFLKFSYLTFLPTNEDFYDCRVEHW
 GLEELVKHWEPEIPTPTSELTETVVCALGLAMGLMGIVVGTVLILRVRLGAASRRRRAM

>Bola-DYB XP_024839162.1 NC_037350.1: 7.096.988-7.113.266 [Bos taurus]
 MRVTIPRNPPTVAGMVMMAVFLVLRPEAHCRDAPKNFVYQFKGMCYFTNGTEHVRLVARQYINKEIILHFDSDLGFEVAVTELGRVCAEIWN
 TQKDLAEFRAYVDTLCRHNKYETAGFTVQRRVEPTVTVSPASTEALNHNHLLVCSVTDYFPRQVKVWFRNQEQTAGVGFTPLTQNGDW
 TYQIHVMLETVPQLGDVYVCHVDHPSLQSPITVEWRAQSESAQSKMQSGIGGFLGLIFLGVGLFVHFWDKRASRS

>Bola-DOB BAD83671.1 NC_037350.1: 7.114.328-7.122.816 [Bos taurus]
 MSPSWVPWVVTFLSTALRLDASVTQGRDSPEDFVTQAKADCYFTNGTEKVRFFVRFIFNLEEYARFSDLGFMFVALTELGPDAERWNNRPD
 ILARSASVDMLCRRNYLGAPFTVGRRVQPEVTYYPEKTPALQHRNLLCLVTGFYPGDIKVTWFRNGQEQREGIMSTGLIRNGDWTQMT
 VMLAMTPELGEVYTCVLDHPSLLSPVSEWRAQSEYSWRKILSGAAFLVGLVFFLVGIVVHIRAWKGRVETPLPGNEVPRAVLPPP

>Bola-DMB NP_001035571.1 NC_037350.1: 7.246.590-7.253.434 [Bos taurus]
 MTVLLSLLGFSGLGCTAAGGFVAHVSTCVLDDGDGPKDFSYCISFNKDLCTWDPQLQASMIPREFGVNLGLARYLSQFLNNNSYLIQRLSGL
 QNCAHTQPFWSLTHTRPPTVQVAKTTPFNTRESVMLACYVWGFYPAADVAITWRRNGQEVLPHGRAWRIIQPNGDWTYQTVSHLATT
 SFGDTYTCVHEHGAPELILQDWTGGLPAQTVKVSVALVTLVGLIIFVGLHSWRRATSSGYIFLPGSTYPEGQHN

>Bola-DMA NP_001012692.2 NC_037350.1: 7.263.693-7.269.361 [Bos taurus]
 MDHLSQEAALLRLSLFVLLPLSWTAPEAPAGWRDELQNHTFLHTMYCQDWSPNVALSESYDEDEDQLFSDFSQIRVPRLPEFADWAHQ
 HGDTSDIMFDKGFCRAMIEIGPELEGQIPVSRGFPIVQVFTLKPLEFGKPNLTVCFISNLPPTLTNVNQHQSAPVEGAGPTFVSAVDGLTFQA
 FSYLNVTPAPSDLFSCIVTHEIDGYTAIAFWVPQNALPSDLLENVLCGVAFLGLVGLIIVGLVLFYCRKPCLG

>Bola-DOA AAY34704.1 NC_037350.1: 7.314.757-7.323.452 [Bos taurus]
 MVLGRVLVGLHTLMTLLSLQEVGAIKADHMGSYGPAFYQSYDGAGQTYDFDGEQLFSVDLKKREAVWRLPEFGNFAYFDPQSGLVSIAMI
 KAHLEDLVKRSNGTRAPNVSPRVAVLPKSRVQLGEPNVLCIVDKIFPPVINITWLRNGHPVTQGVTSQSSFYAQPDLHFRKFHYLTFVPLADDFY
 DCKVEHWGLDQPLFQHWEPQVPTALPDTTGTLCALGLVLGLGGFLGGITLIITGTCLSSTPR

Hereford Cattle MHC class I sequences from assembly GCA_002263795.1, IPD-MHC database and main text reference Schwartz et al.2021:

>Bola-2*070:01 chr.23 NC_037350.1: 28.720.808-28.724.273
 MRPRTLIIIIISGLVLTETLAGSHSLRYFYTGVSRLGEPFRIAVGVYDDTQFVRFDSDAADPRTEPRVPWMEQEGPEYWDRETRNLKDAAQ
 TFRVNLNTLLGYNNQSEAGSHTLQWMYGCDVEPDGRFLRGYRQDAYDGRDYALNQDLRSWTAADTAAQITKRKWEAAGEAERRRNYLEG
 RCVEWLRRYLENGKDTLLRADPPKAHVTRHPSSDREVTLRWALGFYPEEISLTWQHNGEDQTDQDMELVETRPSGDGTQKWAALVVPVSGE
 EQRYTCRVQHEGLREPLTLRWEPPTQTSFLTGMGIIVGLVLLVAVVAVAGAVIWRKKHSGEKGRIYTAASSDSAQGSDVSLTPKV

>Bola-5*072:01 NC_037350.1: 28.664.034-28.667.349
 MGPRTLIIIIISGLVLTETLAGSHSLRYFYTAVSRPGLGEPFRIIVGVYDDTQFVRFDSADGDPREPRARWVEQEGPEYWDQETRAKADHAQ
 FFRLGLNTLLGYNNQSEAGSHTLQWMYGCDVGPDRGRLRGFWQFQYEGRDYALNEDLRSWTAADTAAQISKRWEEAADVAERQRNYLEG
 TCVEWLPRYLENGKDTLLRADPPKAHVTHHPISGREVTLRWALGFYPEEISLTWQRNGEDQTDQDMELVETRPSGDGTQKWWALVVPVSGEE
 QRYTCSVQHEGLQEPLTLRWEPPTQTSFLTGMGIIVGLVLLVTGAVVAGFVIWMKKRSGEKGGNYIQASRSDSAQGSDVSLTPKV

>Bola-NC6:001:01 NC_037350.1: 28.614.174-28.667.358
 PPKAHVTHHPISDYEVTLRCWALGFYPEEISLTWQHNGEDQTDQDMELVETRPSGDGTQKWAALVVPVSGEEQRYMCRVQHEGLQEPLTLR
 WEPPQPSFLTGMGIIVGLVLLVAVVAVAGAVIWMKTCGKGRPTRRLQAVTVPRALMCLSRFLKC

>Bola-NC7:001:01 NC_037350.1: 28.592.553-28.590.775
 VDSPDAVPIITPACSVLQKPISLTVVDTYQFLQFSDDPNLRMEARALWMEQEGPEYWDWNMQGIKDTAQTFRVNLNSLWGYNNQSKDG
 GRHGSSDHQAQVRGLW

>Bola-NC8*001:01 NC_037350.1: 28.572.076- 28.571.567
 PPKAHVTHHPISDREVTLRWALGFYPEEISLTWQREGEDQTDQDMELVETRPSGDGTQKWAALVVPVSGEEQRYTCRVQHEGLQEPLTLRW
 EPPQPFVPIIMGIILVQVLFVAVVAVAGAVIWRKKRSGEKGQTYTAASSDSQGSDVSLTPKV

>Bola-NC1*005:02 NC_037350.1: 28.548.020-28.551.910
 MGPRTLIIIIISGLVLPDRTRAGPHSMRYFLTAVSRPGLGEPFRIIVGVYDDTQFVRFDSDRPDPRMEPRARWVEDEGPEYWDQETRIQKENT
 QTFRANLNTLLGYNNQSEAGSHTIQWMHGCVGVSDDGRLRGYNQLAYDGKDYALNEDLRSWTAADTAAQITKRKWEAAGEAERFRNYLE
 GECVKLLRRHLENGKDTLLRADPPKAHVHHPSSEREVTLRWALGFYPEEISLTWQRNGEDQIQDMELVETRPSGDGTQKWAALAVPSGE
 EQRYTCRVQHEGLQGPLTLRWEPPTQSPVPIIMGIILVLLVAVVARAVIWSKKR

>Bola-NC9*001:01 NC_037350.1: 28.527.600- 28.526.856
 MRVMGPRTLQLLSGILVLIETLAAFHSLRYFYTAVSRLPGLGEPRFIIVGYVDDTEFVRFDSDAPDPRMEPRARWVEQEGPEYWDQETRKAKD
 AAQTFRANLNSLRGYNNQSEAGSHTLQLMYGCDVGPDGSLRGYEQYGYDGRDYIALNEDLRSWTAADTAAQISKRKVEAAGDAARVRIYLG
 GPVRGVAPQIPGDREGNATARRPSKGTCDPSPHLWS
 >Bola-NC10*001:01 NC_037350.1: 28.493.422-28.501.006
 MLWGPVLLYFFLAYLPETQTRSHSLQYFYSVSEPGPVPSFMAFGFVDNQPFIRYDSEEMKAKSCVHWLREEPSYFDDTKIFTSRMKIFHLN
 LRNVQQYYNQTKEDGLNRLAQAQKQTSPTLQFTYGCLEDDGRTTWHWQYGYDGEDYLSLHMDPLQYTAATFVAQYTKQKWEAGGNFIER
 DKNYLEKECILWLWRYLTFGGESLNRTEPPKTHMTHHRISDREVTLRCWALGFYPAKISLTWQRNGEDQTDMDLVETRPSGDGTFQKWA
 LVVPSGEEQKYTCRVQHEGLQEPLTLRWEPLKTSVPITGIIVLVLLVTVRAVIWIKKLSGYYHSTNGKNRTYFQTASSNSALGSDALTDPKI

Human MHC sequences

>HLA-A2 AAA76608.2 [Homo sapiens]
 MAVMAPRTLVLSSGALALTQTWAGSHSMRYFFTSVSRPGRGEPRIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQEGPEYWDGETRK
 VKAHSQTHRVDLGTLRGYYNQSEAGSHTVQRMYGCDVGSWDRFLRGYHQYAYDGDYIALKEDLRSWTAADMAAQTTHKWEAAHVAE
 QLRAYLEGTCVEWLRRLYENGKTLQRTDAPKTHMTHHVSDEHATLRWALSFPYAEITLWQRDGEDQTDMDLVETRPSGDGTFQKWA
 AVVVPSSGQEQRYTCHVQHEGLPKPLTLRWEPSQPTPIVGIAGLVLFQAVITGAVVAAMWRRKSSDRKGGYSQAASSDSAQGSQSDVSLTA
 CKV
 >Human-CD1 NP_001307581.1 T-cell surface glycoprotein CD1a isoform 2 [Homo sapiens]
 MFAFGGATGLKEPLSFHVTWIASFYNHWSKQNLVSGWLSDLQTHTWDSNSSTIVFLCPWSRGNFSNEEWKELETFRIRTIRSFEGIRRYAHEL
 QFEYFPEIQVTGGCELHSGKVSFSLQLAYQGSDFVSFQNNSWLPYPVAGNMAKHFCVNLNQNHENDITHNLLSDTCPRFILGLLDAGKAHL
 QRQVKPEAWLSHGSPSPGPHLQLVCHVSGFYPKPVVWMMWRGEQEQQGTQRGDILPSADGTWYLRATLEVAAGEAADLSCRVKHSSLEG
 QDIVLYWEHSSVGFILAVIVPLLLIGLALWFRKRCFC

3. Primers used for MHC amplification

First Gene specific Illumina PCR primer sets	
DRB1.F1	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGGTGCCTGTATTCTCT
DRB1.R1	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCCGAAACCACTGACTCAA
DQB.F2	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTTGGACGGCAGCTGTGAT
DQB.R2	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCGGAACCACTGACTGAT
A1.F1	ACACTCTTTCCCTACACGACGCTCTTCCGATCTAACCTTCTCCTGCTCCTTC
A1.R1	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCCTACCGCCTTGCTCAA
A5.F2	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGAGGTATTTCTACACCGCG
A5.R2	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGCGTGTCTTCTGTCTCT
Second Dual Illumina index PCR primers	
PCR2-D-F1	AATGATACGGCGACCAACCGAGATCTACACTTGACTACACTCTTTCCCTACACGAC
PCR2-D-F2	AATGATACGGCGACCAACCGAGATCTACACGGAACACTACTCTTTCCCTACACGAC
PCR2-D-F3	AATGATACGGCGACCAACCGAGATCTACACTGACATACACTCTTTCCCTACACGAC
PCR2-D-F4	AATGATACGGCGACCAACCGAGATCTACACGGACGGACACTCTTTCCCTACACGAC
PCR2-D-F5	AATGATACGGCGACCAACCGAGATCTACACCTCTACACTCTTTCCCTACACGAC
PCR2-D-F6	AATGATACGGCGACCAACCGAGATCTACACGGGACACACTCTTTCCCTACACGAC
PCR2-D-F7	AATGATACGGCGACCAACCGAGATCTACACTTTCACACTCTTTCCCTACACGAC
PCR2-D-F8	AATGATACGGCGACCAACCGAGATCTACACGGCCACACTCTTTCCCTACACGAC
PCR2-D-R1	CAAGCAGAAGACGGCATACGAGATCGTGTGACTGGAGTTCAGACGTG
PCR2-D-R2	CAAGCAGAAGACGGCATACGAGATACATCGGTGACTGGAGTTCAGACGTG
PCR2-D-R3	CAAGCAGAAGACGGCATACGAGATGCTAAGTACTGGAGTTCAGACGTG
PCR2-D-R4	CAAGCAGAAGACGGCATACGAGATTGGTCAGTACTGGAGTTCAGACGTG
PCR2-D-R5	CAAGCAGAAGACGGCATACGAGATCACTGTGTGACTGGAGTTCAGACGTG
PCR2-D-R6	CAAGCAGAAGACGGCATACGAGATATTGGCGTACTGGAGTTCAGACGTG
PCR2-D-R7	CAAGCAGAAGACGGCATACGAGATGATCTGGTACTGGAGTTCAGACGTG
PCR2-D-R8	CAAGCAGAAGACGGCATACGAGATTCAAGTGTGACTGGAGTTCAGACGTG
PCR2-D-R9	CAAGCAGAAGACGGCATACGAGATCTGATCTGACTGGAGTTCAGACGTG
PCR2-D-R10	CAAGCAGAAGACGGCATACGAGATAAGCTAGTACTGGAGTTCAGACGTG
PCR2-D-R11	CAAGCAGAAGACGGCATACGAGATGATAGCGTACTGGAGTTCAGACGTG
PCR2-D-R12	CAAGCAGAAGACGGCATACGAGATTACAAGGTACTGGAGTTCAGACGTG

4.1 Reindeer MHC sequences identified in NCBI genomes

MHC sequences in *Rangifer tarandus tarandus* genome GCA_902712895.1:

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>Tarandus_DRA CACTHY010000040.1:101.298-104.851
MAITRIPILGLFIPLISLQESGAIKEDHVIIQAEFSKPEESSEFMDFDGDGEIFHVDMEKKETVWRLPEFGHFASFEAQGALANMAVANKANLDI
MMKRSNYTPNTNVPPEVTLLPNKPVELGEPNTLICFVDKFSPPVISVTWLRNGRPVTDGKSETVFLPRDDHLFRKFHYLPFLPTTEDVYDCKVEH
WGLDEPLLKHWEYEAPAPLPETTENAVCALGLIVALVGIIAGTIFIIGIRKANTVERQGPL
>Tarandus_DRB3 CACTHY010000040.1: 124.717-137.852
MVCWYFSRGSWMAALLVMGLSPLLAWARETQFMHQKCECRFSNGLERMRFARYYINTTEEDVHFSDSDVGEFTAVTELGRPDAEYWNQQ
KDFMEQMRKAKVDMVCRSNYLGIGSFMQRQRRVEPTVTVPYPAKTQPLQYHNLVCSVNGFYPGHIEVRWFRNGHEEEAGVISTGLIPNGDWTF
QTMVMLETVPQSGEVYTCQVEHPSQKSSITVEW
>Tarandus_DRB2 CACTHY010000040.1: 162.561-178.303
MGCSSPGSSVHRILQHDVTVPFRRLLDGSDDSDTDGDEPISRPKGIPHISAYLAGGYFYNQKELAHFHSDDVGEFRAVTELGRLFTESWNHQK
DFVEGTWAVVDTCFRHNYWLGESVTVQHQQVEPTVTVPYPAKTQPLQHNNLLVCSVNGFYPGHIEVRWFRNGHEEEAGVIFTGLIQNGDWTF
QTVVMLETVPQSGEVYTCQVAHPIQMSSVTVE
>Tarandus_DRB1 CACTHY010000040.1: 208.047-205.175
MVRLYFSGSRMAALTVMMLVLSPLAWAREIRSHFLEYFKGECHFSNGTERVQFLKRYIHNGEESVRFSDSDVGEFRAVTELGRPDAEYVWNS
RKEILEESRAEVDTCRHNYGLDSFIVQRRVEPTVTVPYPAKTQPLQHNNLLVCSVNGFYPGHIEVRWFRNGHEEEAGVISTGLIQNGDWTFQ
TMVMLETVPQSGEVYTCQVDHPSQTSPTITVEWSELSLISS
>Tarandus_DQA CACTHY010000040.1: 240.335-245.063
MVLNRLALILGALALTTMMSPSGGEDIVADHVAAYGINVYQSYGPTGYYSHEFDGDEEFYVDLEKKETVWQLPLFSQFRSFDPPQALRNIAVAK
PNLNIMIKRSNSTAATNKVPEVTVFSKSPVMLGQPNLTICHVDNIFPPVINITWLRNGHVSVEGVSETSFSLKDDHSFSKIGYLTFLPSDDDVYDC
KVEHWGLDEPLLKHWEPEIPSPMSELTETVVCALGLTVGLVGVGTILIRGLRSGGSPSRHQGPLCSAAYESKRVNMLDDLELFSGQVHHIPSL
LCSFSYFFSGT
>Tarandus_DQB DQB1CACTHY010000040.1: 251.030-264.781
MSGMVALRIPRGLWTAAMVTLAVLSTPGAEGRDSPEFVYQFKGLCYFTNGTERVRLVTRHIYNQEEYVRFSDSDVGEYRAVTPGRPDAEY
FNSQEGELERVRAEADTCRHNYQSEVRTTFQRLVEPTVTISLRTALNHHNLLVCSVTDYFPGQIKVRWFRNDQEETAGVYSTPLIRNGDW
TFQILVMLEMTQQRGDVYTCRVEHPSLQSPISVEWRAQSESAQSKMLSGVGGFVLGLIFLGLGLIVHHRSQK
>Tarandus_DOA CACTHY010000040.1: 17.511.567-17.519.310
MVLRLGRLVLGLHTLMTLLSPGEVGAIKADHMGSGYGAFAFYQSYDGAGQFTYDFDGEQLFSVDLKKREAVWRLPEFGNFAYFDPQNGLSIAMI
KAHLEDLVERSNTAPNGPSWRPVPVGFKACFLVPPRVAVLPKSRVQLGQPNVLICVDNIFPPVINVSWLRNGQPVQTQGTQTFYAQPD
HSFRKFHYLTFVPLADDFYDCKVEHWGLDQPLFQHWEPQVPTPLPDTTGLVLCALGLALGLGGLVGLITITGTCLSSPTPRCTRGLGGGRLQM
ALTKLFWPQTGVWERRLAGAIGGRQKGNP
>Tarandus_DMA CACTHY010000040.1: 17.565.591-17.567.622
MDPELSQEAALLRLLSFLWLLPLSRTAPEAPAGWRDELQNHFTLHTMYCQDWSPNVGLSEAYDDDQLFSFDFSQIRVPRLPFADWAHQH
GDTSDIMFDKGFCRAMIEEIGPKLEGQIPVSRGFPIVEFTLKPLEFGKPNLTVCFSINLFPPTLTVNWQYQSAPVEGAGPTFVSAVDGLTFQAFS
YLNFTPAPSDLFSCIVTHEIDGLTAIGFWVPQNSLPSDLLENVLCGVAFLGLLGIIVGLALIIYFRKPC
>Tarandus_DMB CACTHY010000040.1: 17.580.304-17.582.883
FVAHVSTCLDDDGNPKDFSYCISFNKDLTCDWDLQASMPVPREFGVNLASQYLSQFLNSNDALIQRLSNGLQKCAHTQPFWSSLTHRTR
PIVQVAKTTPFNTRESVMLACVWGFYPADVIITWRRNEQEVLPHGKRAQKIVQPNGDWYQTVSHLATTSPFGDTYTCVVEHIGAPELILQD
WGPGLTPTCCSVANNNEKSRELLQVGCCKKNTNTLAEGRRCREVHGTG
>Tarandus_DOB CACTHY010000040.1: 17.678.557 -17.686.475
MSPSWVPWVVAFLSTVLTLDASVTQGRNSPEDFVTQAKADCYFTNGTEKVRVVRVIFNLEEARFDSDLGMFVALTELGPDAELWNSRPDI
LARSASVDMLCRRNYKLGAPFTVGRRVQPEAVYPEKTPALQHSLLLCLVTGFYPGDIEVTWFRNGQEQREGVMSTGLIRNGDWTFQTTV
MLAVMPELGEVYTCRVNHPSPVSEVSENLVFSGPNSSRSDSERGVCYLRIHLGHSTSSSL
>Tarandus_DYB CACTHY010000040.1: 17.693.285 - 17.704.464
MRVTVPRNPGTVAGVVMMAVFLVLRIPGAHCRDAPENFVYQFKGMCYFTNGTERVRLVARQIYNKEEILHFDSDLGKFVAVTELQVCAENW
NTQKDPLEEFRAVETLCRHNYKETASFTVQRRVEPTVTVPASTEDPNHHNLLVCSVTNIFYPRQVKVWFRNQEQEETAGVGFTPLTQNGDW
TYQIHVMLETQPKQLGDVYVCRVDHPSLQSPITVEWGAQSESAQSKTRSGIGGFVLGLIFLGVSQKWDKRGVNPALPTSSIRT
>Tarandus_DYA CACTHY010000040.1:17.705.726 - 17.727.504
MKKALILRALAAVMSPCGGEDIVADHVGTYGTNVYQSYGQFTFEFDGDELFFVDLKKETVWRLPEFNITMFEIQSALRNIIIMSKRNL
DILIKNANFTPATNEIPEVAVFPKSSVVLGIPNTLICQVDNIFPPVINITSFYNGHFVAEGISSETTFYPQSDHSFLKFSYLTFLPSGDDFYDCRVEHW
GLEEPLVKHWEPIKLTPTSELTETVVCALGLAMGLVGVAGTVLILRVWCLGTASRRRRAMRKQETETGTSRTQETYETEHEPEKARNLYPRREVE
TERSSSEMSNIKRERTQRDNGQGE
>Tarandus_DSB CACTHY010000040.1: 17.759.350-17.746.831
DRYIYNREEQVRFDSLVGEYRARTEMGRPAAERWNRWPHALQARAARVTFCASNYRFFASYPAKTQPLQQHSLVCSVNGFYPGHVEVRW
FRNGREEEAGVSTGLIMLEVVPQGGEVYTCVHEHPSLTNPITVEWSAQDKSSQEKMLSGIGACVLGLLFLGMGLLFYIRRRERGKKQREEVGVE
TALSSAPAGLLSWSRDRTRARTFCPSFFAA
```

>Tarandus_NC-A5 CACTHY010001196.1: 6.417-11.190
 MRVVGRLRAVLLLSGALVLTETWAGSHSLRYFYTAWSRPLGEPFIVGYVDDTQFVRFDSDAPDPRVEPRALWVEQEGPEYWDQETQRTRD
 TAQFFRMSLNLTRGYNQSEAESHTLQEMYGCDVGPDRLLRGYDQFAYDGRDYISLNLRSWTAETAQAQISKHNAEAAGDAARVRYNL
 EGKCVWLLRYLETGNDTLRADPPKAHVNHHPISDREVLTRCWALGFYDEISLTWQRDGEDQTDQDMELVETRPSGDGSGFQKWAALVVP
 GEEQRYTCHVQHEGLQEPLTLRWEPQPSPVLMGIIVGLVLMVNGAVVIGAVIWRKKRSGEKGRYTYQAASSDSQSSSEVSLTPVK

>Tarandus_A4 CACTHY010000626.1: 7.609-10.798
 MLAMGLRTLGLLSGALVLTETWAGSHSLRYFLTSVSRPLGEPFIVGYVDDTQFVWFSDAPNPRMEPRARWVEQEGPEYWDQETKRAK
 NTAQTFFQVNLNLTLSYNNQSEAGSHTFQWVYGCNVGPDGRLLRGFEQFGYDGRDYIALNEDLRSWTAADTAAQITKRKWEAAGLAEHRNY
 LEGGCMEWLRRYLENGKDTLLRADPPKAHVNHHPISDREAILRCWALGFYDEISLTWQRDGEDQTDQDMELVETRPSGDGTFQKWAALVVP
 SGEEQKYTCHVQHEGLPEPLTLRWEPSPIMGIITSLGLLVGGAVVGGAVMWRKKHNEKEGRSAQVASSYSPLVSDVSLMGPL

>Tarandus_A3 CACTHY010000281.1: 469.656-476.056 internal stop, pseudogene
 MRIEGKRTLGLLPGALAVTETWAGSHSLRYFYTAWSRPLGEPFIVGYVDDTQFVRFDSDAPNPRMEPRARW*EQERPEYWDDEETQRARD
 TAQTFRVNLNLTLSYNNQSEAGSHTLQEMYGCDVGPDRLLRGFDQLAYDGRDYIALNEDLSSWTAADTAAQITKRKIEQRGVADDYRNYLN
 ECAEWLDPMTHTVTHHHIPGRGVTLCWALGFYDEISLTWQRDGEDQTDQDMELVETRPSGDETQKWAALVVPSSGEEQKHTCHVQHEGL
 QEPLTLRWEPQPSPITGIIVGLVGLAVVAGAVIWWKKRSGEQGGSYTQAASSDSVQSSGATGEV

>Tarandus_NC10_like CACTHY010000281.1: 40.843-48.910
 MPWAPVLLHFFLAFLPETQTRSHSLQYFYSVSEPGGVPSPMAFGFVDNQPFIRYDSEEMKAKSCVHWLREEPSYFDDDETIFTSRMKIFHLS
 LRNVQRYNNQTAQSPHTLQFTYGCLELLEDGRTTWHWQYGYDGEDYLTLMHMDPLQYTAATFIAQYTKQKWEAGGNYVERDKNYLEKECILWL
 WRYLTFGGETLNRTEPPKTYMTHHRISDREVLTRCWALGFYPAEISLTWQRNGEDQTDQDMELVETRPSGDGTFQKWAALMLPSGEEQKYTC
 HVQHEGLQEPLTLRWETLKISVPITGILVGLVLLVIRDIVWRKMRSGRKNRIYSQTASSNSALGSDVLTDPKSET

>Tarandus_A2 CACTHY010000281.1: 13.147-15.079 internal stop, pseudogene
 MRVMGPRTLGLLSSGALVLTETWAGSHSLRYFYTAWSRPLGEPFIVGYVDDTQFVRFDSDAPDPRMEPRARW*EQEGPEYWDDEETQKAKD
 AAQTLRVKLNNLTLSYNNQSEAGSHTLQWMYGCDVGPDRLLRGYVQYAYDGRDYIALNEDLRSWTAADSAAQITKRKFEQGGQADHNRNY
 LEGRCVKWLRYLENGKDTLLRADPPKAHVIRHPISDCEVTLRCWALGFYDEISLTWQCNGEDQTDQDMELVETRPSGDGTFQKWAALVVP
 GEEQKYTCHVQHEGLQEPLTLRWGEKGRIYTAASSDSAQGSDISLTPVK

MHC sequences identified in *Rangifer tarandus granti* genome GCA_014898785.1:

>Granti_DQB1 JACGUM010000255.1:8.080.006-8.094.787
 MVALRIPRGLWTAALMVTLAVLSTPGAESRDSPQDTVLYMAQCYFTNGTERVRYVTRYIYNQEETVYVDSNVGEYRAVTPLGWYLAEWNS
 QKDILEQTRAELDTVCRHNYQLEVITSLQHVEPTVTISPSTALNHNHLLVCSVDFYPGQIKVRWFRNDQEETAGVVSTPLIRNGDWTFQIL
 VMLEMTQPRGDVYTCHEHPSLQSPILVEWRVQSESAQSKMLSGVGGFVLGLIFLGLGLIIRRSQKGVKDVIT

>Granti_DQB2 JACGUM010004406.1: 5.235-23.611
 MVALWIPRGLWTAAMVTLVVLSTPGAEGRDSSQNFIQFLCLCYFTNGTERVRYVTRYIYNREEYVRFSDVNEYRAVTPLRPDAAEFWNS
 QKDILEQTRAELDTVCRHNYELELITSLQRRVEPTVTISPSTALNHNHLLVCSVDFYPGQIKVRWFRNDQEETAGIVSTPLIRNGDWTFQILV
 MLEMTQPRGDVYTCRVEHPSLQSPIMVEWRAQSESAQSKMLSGVGGFVLGLIFLGLGLIIRRS

>Granti_DQB3 JACGUM010009741.1: 37.669-43.515
 DFVYQFKGLCYFINGTERVRGVTRHIYNQEEYVRFSDVGEHWAVTPLGRRPAEYFNSQKDYLEQMRAAVDTVCRHNYQVELTSLQRRVEP
 TVTISLSRTEALNHNHLLVCSVDFYPGQIKVRWFRNDQEETARVATPLIRNGDWTFEILVMLEMTQPRGDVYTCHEHPSLQSPISVEWRAQ
 SESARSKMLSGVGGFVLGLIFLGLGLIIRRSQKGLMR

>Granti_DRB3 JACGUM010000366.1: 715.883-722.966
 MELEESTCLSDYTTKQSSSRQYAFFMHQFKCECRFSNGLRMRFFARYIYNTEEDVHFDSDVGEFTAVTELGRPDAAEYWNQKDFMEQMR
 AKVDMVCRSNYLGIGSFMRQRRVEPTVTYPAKTQPLQYHNHLLVCSVNGFYPGHIEVRWFRNGHEEEAGVISTGLIPNGDWTFQTMVMLET
 VPQSGEVYTCQVEHPSQKSSITVEWRAQSDSAQRKLMCGIGGFALGLFLVGLSIHFRSKKGHSALQAPGRS

>Granti_DRB2 JACGUM010000366.1: 743.255-758.996
 MGCSSPGSSVHRILQHDVTFPRRLDGSDDSDTDGDEPISRPKGIPHISAYLAGGYFYNNQKELAHFHSDDVGEFRAVTELGRLFTESWNHQK
 DFVEGTWAVVDTFCRHNWYLGESFTVQHVEPTVTYPAKTRPLQHNNHLLVCSVKGFFLGHVEVQWFRNGHEEEAGVIFTGLIQNGDWTF
 QTVVMLETVPQSGEVYTCQVAHPIQMSSVTVE

>Granti_DRB1 JACGUM010011381.1: 3.698-14.316
 MVRLYFSGGSRMAALTVMLMVLSPPLAWAREIRPHFLEYFKCECHFSNGTQGVQFLQRYIYNREEYVRFSDVGEFRAVTELGRKSAEGWNS
 RKEILEESRAAVDTYCRHNWYGLDSFIVQRRVEPTVTYPAKTQPLQHNNHLLVCSVNGFYPGHIEVRWFRNGHEEEAGVISTGLIQNGDWTFQ
 TMVMLETVPQSGEVYTCQVDHPSQTSPTVEWRARSDSAQRKLMCGIGGFALGLFLVGLSIHFRSKKGHSALQAPGRS

>Granti_A6 JACGUM010000065.1:233.416 - 237.942
 MQVTEPRTLGLLSSGALVLTETWAVAQIIRKWEAEGAERYREYLETCEVKWIPKYLEKGEMGLRAVPPKTHVTRHPISDHEVTLRCWALGF
 YWAEISLIWQRDGEDQTDQDMELVETRPSGDGTFQKWAALVVPSSGEEQRYTCHVQHEGLQEPLTLRWEPQPSPIMGIIVSLVLLVAVVAG
 AVSWRKKHSDGDDGGSYTTASKYGQEKTVSEALMYLSWLLKISSR

>Granti_NC-A5 JACGUM010000065.1: 281.383-284.306
 MRVVGRLRAVLLLSGALVLTETWAGSHSLRYFYTAWSRPLGEPFIVGYVDDTQFVRFDSDAPDPRVEPRALWVEQEGPEYWDQETQRTRD
 TAQFFRMSLNLTRGYNQSEAESHTLQEMYGCDVGPDRLLRGYDQFAYDGRDYISLNLRSWTAETAQAQISKHNAEAAGDAARVRYNL

EGKCVWLLRYLETGNDTLLRADPPKAHVNHHPISDREVTLCRWALGFYPDEISLTWQRDGEDQTQDMELVETRPSSGDSFQKWAALVPL
GEEQRYTCHVQHEGLQEPLTLRWEPQPQSVLIMGIIVGLVLMVNGAVVIGAVIWRKKRSGEKGRTYTAASSSDSQSSEVSLTPK
>Granti_A4 JACGUM010000065.1:370.170-372.776
MLAMGLRLLLLSGALVLTETRAGSHSLRYFLTSSRPLGEPRIIVGYVDDTQFVWFSDAPNPRMEPRARWVEQEGPEYWDQETKRAK
NTAQTFQVNLNLTLSYNNQSEAGSHTFQWVYGCNVGPDGRLLRGFEQFGYDGRDYIALNEDLSWTAADTAAQITKRKWEAAGLAEHRNY
LEGGCMEWLLRRYLENGKDTLLRADPPKAHVNHHPISDREAILRCWALGFYPDEISLTWQRDGEDQTQDMELVETRPSSGDTFQKWAALVPL
SGEEQKYTCHVQHEGLQEPLTLRWEPSPIMGIITSLGILLVGGAVVGGAVMWRKKH
>Granti_A3 JACGUM010000065.1: 499.979-502.192 internal stop, pseudogene
MRIEGKRTLLLLPGALAVTETWAGSHSLRYFYTAVSRLGEPRIIVGYVDDKQFVRFDSDAPNPRMEPRARWVEQERPEYWDQETQRARD
TAQTFRVNLNLTLSYNNQSEAGSHTLQEMYGCDVGPDPGRLLRGFDQLAYDGRDYIALNEDLSWTAADTAAQITKRKTE*AARWADDYRNYL
NRECAEWLDPPTTHVTHHHIPGRGVTLCRWALGFYPDEISLTWQRDGEDQTQDMELVETRPSSGDTFQKWAALVPLSGEEQKHTCHVQHE
GLQEPLTLRWEPQPSPITGIIVGLVGLAVVAGAVIWWKKRSGEQGGSYTAASSDSVQSSGAT
>Granti_NC10_like JACGUM010000065.1:927.474-934.548
MPWAPVLLHFFLAFLPETQTRSHSLQYFYSVSEPSPGVPFMAFGFVDNQPFIRYDSEEMKAKSCVHWLREEPSYFDDKFTSRMKIFHLS
LRNVQRYNNQTPHPTLQFTYGCLELDRGTTWHWQYGYDGEDYLLHMDPLQYTAATFIAQYTKQKWEAGGNYVERDKNYLEKECILWLW
RYLTFGGETLNRTEPPKTYMTHHRISDREVTLCRWALGFYPAEISLTWQRNGEDQTQDMELVETRPSSGDTFQKWAALMLPSGEEQKYTCH
VQHEGLQEPLTLRW
>Granti_A2 JACGUM010000065.1: 963.154-961.222 internal stop, pseudogene
MRVMGPRTLLLLSGALVKTESLAGSHSLRYFYTAVSRLGEPRIIVGYVDDTQFVRFDSDAPNPRMEPRARW*EQEGPEYWDQETQKAKD
AAQTLRVKLNLTLSYNNQSEAGSHTLQEMYGCDVGPDPGRLLRGYVQYAYDGRDYIALNEDLSWTAADTAAQITKRKFEQGGQADHNRNY
LEGRCVKWLRKYLENGKDTLLRADPPKAHVIRHPISDCEVTLCRWALGFYPDEISLTWQCNQEDQTQDMELVETRPSSGDTFQKWAALVPL
GEEQKYTCHVQHEGLQEPLTLRWEPQPSTFLTVGIIVGLVLLVAMVAGAVIGEGRIYTAASSDSAQSSDISLT
>Granti_A1 JACGUM010000065.1: 995.914-992.806
MCPRTLLLLSGVLTETRAGSHSLRYFYTAVSRLGEPRIIVGYVDDTQFVRFDSDAPNPREPRAPWMEKEGPEYWDNRTRICKDTAQ
VFRESLNNLTLSYNNQSEAGSHTLQEMYGCDVGPDPGRLLRGYVQYAYDGRDYIALNEDLSWTAADTAAQISKRKFEQGGQADHNRNYLEG
RCVEGLHRYLENGKDALRAGPPKAHVIRHPISDCEVTLCRWALGFYPDEISLTWQHSQEDQTQDMELVETRPSSGDTFQKWAALVPLSGEE
QKYTCHVQHEGLQEPLTLRWEPQPSTFLTVGIIVGLVLLMVALVAGAVIWRKKHSGEKGRIYTAASSDSAQSSDVSLTPK

MHC sequences in *Rangifer tarandus caribou* genome GCA_019903745.1:

>Caribou_DQB JAHWTM010000040.1: 177.351-192.126
MVALRIPRGLWTAALMVLAVLSTPGAESRSPQDVTVLYMAQCYFTNGTERVRYVTRYIYNQEETVYYSNVGEYRAVTLPLGWYLAEYWN
QKDILEQTRAELDTVCRHNYQLEVITSLQHQQVEPTVTISPSRTEALNHNLLVCSVTDYFPGQIKVRWFRNDQEETAGVSTPLIRNGDWTFQIL
VMLEMTQRGDVYTCHEHPSLQSPILVEWRVQSESAQSKMLSGVGGFVLGLIFLGLLIIRRRSQKGVKDVIT
>Caribou_DRB1 JAHWTM010000040.1:256.250-287.400
MVRLYFSGGSRMAALTVMLMVLSPPLAWAREIRPHFLEYFKCECHFSNGTERVQFLKRYIYNGEFVRFDSVDFRAVTELGRPDAGWNS
RKEILEESRAEVDTVCRHNYGVGESFTVQRRVEPTVTVPYAKTQPLQHNLVCSVNGFYPGHIEVRWFRNGHEEEAGVISTGLIQNGDWTFQ
TMVMLETVPQSGEVYTCQVDHPSQSPITVEWRARSDSAQSKMMSGVGGFVLGLLFLAVGLFIYFRNQKGRPTLQPTGLLS
>Caribou_DRB2 JAHWTM010000040.1: 312.585-328.325
MGCSSPGSSVHRILQHDVTVPRLLDGSSDSDTDGDEPISRPKGIPHISAYLAGGYFYNNQKELAHFHSDDVGEFRAVTELGRLFESWNHQB
DFVEGTWAVVDTCRHNHYWLGESVTVQHQQVEPTVTVPYAKTRPLQHNLVCSVKGFLGHVEVQWFRYGHHEEAGVIFTGLIQNGDWTF
QTVVMLETVPQSGEVYTCQVAHPQIMSSVTVE
>Caribou_DRB3 JAHWTM010000040.1:348.606-355.691
MELEESTCLTSDYTTKQSSRQYAFFMHQFKCECRFSNGLERMFRFARYIYNTEEDVHFDSDVGEFTAVTELGRPDAGYWNQKDFMEQMR
AKVDMVCRSNYLGIGSFMRQRRVEPTVTVPYAKTQPLQYHNLVCSVNGFYPGHIEVRWFRNGHEEEAGVISTGLIPNGDWTFQTMVMLET
VPQSGEVYTCQVEHPSQKSSITVEWRAQSDSAQRKLMCGIGGFALGLLFLGVGLSIHFRSKKGHSALQAPAGPLS
>Caribou_A6 JAHWTM010000040.1:19.062.576-19.064.607 internal stop, pseudogene
GVHSLRYFHILVSRPVLGRDLYQSVGYLEDQFVRYNSDAANPRVEPRAPWIEQEGPEY*DRHTSIATEHLQASRSNLQVIVGNHNHSEAESHS
FLWMSGCDVGPDPGRLLRGYKHFADGEDYITLNDMHSWSAAGTVAQIIRKWEAEGVAERYREYTECVKWIPKYLEKGKEMGLRAPPK
THVTRHPISDHEVTLCRWALGFYRAEISLIWQRDGEDQTQDMELVETRPSSGDTFQKWAALVPLSGEEQRYTCHVQHEGLQEPLTLRWKDE
QGGV
>Caribou_NC-A5 JAHWTM010000040.1: 19.103.730-19.106.653
MRVVGLRAVLLSGALVLTETWAGSHSLRYFYTAVSRLGEPRIIVGYVDDTQFVRFDSDAPNPRVEPRALWVEQEGPEYWDQETQRTRD
TAQFFRMSLNTLSYNNQSEAGSHTLQEMYGCDVGPDPGRLLRGYDQFAYDGRDYIALNEDLSWTAADTAAQISKHNAAAGDAARVRNYL
EGKCVWLLRYLETGNDTLLRADPPKAHVNHHPISDREVTLCRWALGFYPDEISLTWQRDGEDQTQDMELVETRPSSGDSFQKWAALVPL
GEEQRYTCHVQHEGLQEPLTLRWEPQPQSVLIMGIIVGLVLMVNGAVVIGAVIWRKKR
>Caribou_A3 JAHWTM010000040.1: 19.278.994-19.280.980 internal stop, pseudogene
MRIEGKRTLLLLPGALAVTETWAGSHSLRYFYTAVSRLGEPRIIVGYVDDKQFVRFDSDAPNPRMEPRARWVEQERPEYWDQETQRARD
TAQTFRVNLNLTLSYNNQSEAGSHTLQEMYGCDVGPDPGRLLRGFDQLAYDGRDYIALNEDLSWTAADTAAQITKRKTEQR*DPPTTHVTHH
HIPGRGVTLCRWALGFYPDEISLTWQRDGEDQTQDMELVETRPSSGDTFQKWAALVPLSGEEQKHTCHVQHEGLQEPLTLRWEPQPSPIT
GIIVGLVGLAVVAGAVIWWKKRSGEQGGSYTAASSDSVQSS

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>Caribou_NC10_like JAHWTM010000040.1: 19.718.388-19.722.045
GSHSLQYFYFVSVSEPGVPFMAFGFVDNQPFIRYDSEEMKAKSCVHWLREEPSYFDDTKIFTSRMKIFHLSLRNVQRYYNQTAGPHTLQFT
YGCELLEDGRTTWHWQYGYDGEDYLTLMHMDPLQYTAATFIAQYTKQKWEAGGNYVERDKKYLEKECILWLWRYLTFGGGETLNRTEPPKTYM
THHRISDREVLTRCWALGFYPAEISLTWQRNGEDQTDQDMELVETRPSGDGTFQKWAALMLPSGEEQKYTCHVQHEGLQEPLTLRWKDEK
>Caribou_A2 JAHWTM010000040.1: 19.750.653-19.748.496 internal stop, pseudogene
MRVMGPRTRLTLLLSGALVKTESLAGSHSLRYFYTAVSRPGLGEPRIIVGYVDDTQFVRFDRDAPDPRMEPRARW*EQEGPEYWDEEMQKAK
DAAQTLRVNLNNLRGYNNQSEAGSHTLQWMYGCDVGPDPGRLLRGYVQYAYDGRDYMALNEDLRSWTAADSAAQITKRKFEQGGQADHD
RNYLEGRCVKWLRLKYLENGKDTLLRSDPPKAHVIRHPISDREVLTRCWALGFYPEEISLTWQCNGEDQTDQDMELVETRPSGDGTFQKWVALV
VPSGEEQKYTCHVQHEGLQEPLTLRWGEGKRIYTQAASSDSAQGSISLTVPK
>Caribou_A1 JAHWTM010000040.1: 19.783.274-19.767.342
GSHSLRYFYTAVSRPGLGEPRIISVGIVDDTQFVRFDSADPNPREEPAPWMEKEGPEYWDNRNTRICKDTAQVFRESLNNLRGYNNQSEAGS
HTLQEMYGCDVGPDPGRLLRGYVQYAYDGRDYMALNEDLRSWTAADSAAQISKRFQEGGEADHSRNYLEGRCVEGLHRYLENGKDALLRAE
ITQDMELVETRPSGDGTFQKWVALVVPGEISLTWQHSGEDQTDQDMELVETRPSGDGTFQKWVALVVPSEGEQRYTCRVQHEGLPEPLTEPP
QTSFLTGIIVGLVLLMVALVAGAVIWRKKHS
```

4.2. Alignment of genomic nucleotide sequences with primer location

Alignment of genomic DRB nucleotide sequences with primer location

Yellow or green shading show location of primers. Only regions relevant for primer design are shown.

```
DRB1.F1 TGGTGCGCCTGTATTCTCT
          *          20          *          40          *          60
DRB1_taran : atggtgcgccctgtatttctctggagagctcccgatggcagctttgacagtgatgctaagtgtgc : 64
DRB1_grant : ..... : 64
DRB1_carib : ..... : 64
DRB3_grant : ...a..-----tgga.ga.tca.cctgcc..actt : 31
DRB3_carib : ...a..-----tgga.ga.tca.cctgcc..actt : 31
DRB3_taran : ..-----ag.ga.aca..ga..ca..a : 24
DRB2_grant : ...a..t.a...g...c.c.....ta.....c.....a.g.....a : 64
DRB2_taran : ...a..t.a...g...c.c.....ta.....c.....a.g.....a : 64
DRB2_carib : ...a..t.a...g...c.c.....ta.....c.....a.g.....a : 64
          *          80          *          100          *          120
DRB1_taran : tgagccc-tcctctggcctggcgagggagatccgac---cacatttcctggagtattttaagg : 124
DRB1_grant : .....-..... : 124
DRB1_carib : .....-..... : 124
DRB3_grant : caga.ta-.a..acaaagccacagtcacga.ga.agtatg.gtt...a..c.tc.g.....t : 94
DRB3_carib : caga.ta-.a..acaaagccacagtcacga.ga.agtatg.gtt...a..c.tc.g.....t : 94
DRB3_taran : caga.tt-.at.t...ggg.ct...aaatc.ctgc.gatg.gtt...a..c.tc.g.....t : 87
DRB2_grant : ...a...a..ag.a...caa.....t.c.c...--ata.g.g...----- : 111
DRB2_taran : ...a...a..ag.a...caa.....t.c.c...--ata.g.g...----- : 111
DRB2_carib : ...a...a..ag.a...caa.....t.c.c...--ata.g.g...----- : 111
          *          140          *          160          *          180
DRB1_taran : gcgagtgatcatttctccaacgggacggagcgggtgcagttcctgaagagatacatccataacgg : 188
DRB1_grant : .....c.g.....c.....t.....c : 188
DRB1_carib : ..... : 188
DRB3_grant : .t.....g.....tt...a..a...ga...t.tgcc.....t.c...ac : 158
DRB3_carib : .t.....g.....tt...a..a...ga...t.tgcc.....t.c...ac : 158
DRB3_taran : .t.....g.....tt...a..a...ga...t.tgcc.....t.c...ac : 151
DRB2_grant : -----cc.tgcagg.g.....t.t.....ca : 139
DRB2_taran : -----cc.tgcagg.g.....t.t.....ca : 139
DRB2_carib : -----cc.tgcagg.g.....t.t.....ca : 139
          *          200          *          220          *          240
DRB1_taran : agaagagtcggtgcgcttcgacag---cgacgtgggcgagttccggcggtgaccgagctgggg : 249
DRB1_grant : g.....ac..... : 249
DRB1_carib : .....tc..... : 249
DRB3_grant : g.g...gat...a.....-...t.....g.....ac...c.....g..... : 219
DRB3_carib : g.g...gat...a.....-...t.....g.....ac...c.....g..... : 219
DRB3_taran : g.g...gat...a.....-...t.....g.....ac...c.....g..... : 212
DRB2_grant : ga.g...t.c..at..tc...tga.....t.....a...a.....c : 203
DRB2_taran : ga.g...t.c..at..tc...tga.....t.....a...a.....c : 203
DRB2_carib : ga.g...t.c..at..tc...tga.....t.....a...a.....c : 203
```



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      *           260           *           280           *           300           *
DRB1_taran : cggccggagccgaggtctggaacagccggaaggagatcctggaggagagccgggcccaggtgg : 313
DRB1_grant : ...aa.ag.....g.....c..... : 313
DRB1_carib : .....g..... : 313
DRB3_grant : a.....ta.....cag.aa.....ct.ta.....C...tg.....a..... : 283
DRB3_carib : a.....ta.....cag.aa.....ct.ta.....C...tg.....a..... : 283
DRB3_taran : a.....ta.....cag.aa.....ct.ta.....C...tg.....a..... : 276
DRB2_grant : a...tcctt.a.t...agt....tca..a.....ct..g.....g...cgt....t.t.... : 267
DRB2_taran : a...tcctt.a.t...agt....tca..a.....ct..g.....g...cgt....t.t.... : 267
DRB2_carib : a...tcctt.a.t...agt....tca..a.....ct..g.....g...cgt....t.t.... : 267

      320           *           340           *           360           *
DRB1_taran : acacagtgtgcagacacaaactacggggttcttgacagtttcattgtgcagcggcgagtgagcc : 377
DRB1_grant : ....gtac..... : 377
DRB1_carib : .....cgg...g.....c..... : 377
DRB3_grant : ...tg.....tc.....tt..gca..gt..c....gag.....c..... : 347
DRB3_carib : ...tg.....tc.....tt..gca..gt..c....gag.....c..... : 347
DRB3_taran : ...tg.....tc.....tt..gca..gt..c....gag.....c..... : 340
DRB2_grant : ....gt.c.....t..c..gg...g..c....cg.....at.a..... : 331
DRB2_taran : ....gt.c.....t..c..gg...g..c....cg.....at.a..... : 331
DRB2_carib : ....gt.c.....t..c..gg...g..c....cg.....at.a..... : 331

      380           *           400           *           420           *           440
DRB1_taran : tacagtgtgtgtatcctgcaaagaccagccctgcagcaccacaacctcctggtctgtctct : 441
DRB1_grant : ..... : 441
DRB1_carib : ..... : 441
DRB3_grant : .....t.....t..... : 411
DRB3_carib : .....t.....t..... : 411
DRB3_taran : .....t.....t..... : 404
DRB2_grant : .....g..... : 395
DRB2_taran : .....g..... : 395
DRB2_carib : .....g..... : 395

DRB1_R1 TTGAAGTCAGGTGGTTCCGG

      *           460           *           480           *           500
DRB1_taran : gtgaacgggtttctaccagagacacattgaagtcaggtggttccgggaatggccatgaagaggagg : 505
DRB1_grant : ..... : 505
DRB1_carib : ..... : 505
DRB3_grant : ..... : 475
DRB3_carib : .....c..... : 475
DRB3_taran : .....c..... : 468
DRB2_grant : .....a.....t.tg..c...g.....ca.....t..c....c..... : 459
DRB2_taran : .....g.....t.tg..c...g.....ca.....t..c....c..... : 459
DRB2_carib : .....g.....t.tg..c...g.....ca.....t..c....c..... : 459

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Alignment of genomic DQB nucleotide sequence with primer locations

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      DQB.F2 TTTGGACGGCAGCTGTGAT
      *           20           *           40           *           60
DQB_tarand : atggtggctctgcggatccccagagcccttggagcggcagctgtgatgggtgacactggcgggtgc : 64
DQB_caribo : .....a.....t..... : 64
DQB1_grant : .....a.....t..... : 64
DQB2_grant : .....t.....a.....t..... : 64
DQB3_grant : ----- : -

      *           80           *           100           *           120
DQB_tarand : tgagcaccccgagggtgagggcagagactctccacaggatttcgtgtaccagtttaagggcct : 128
DQB_caribo : .....a.....a...ac...gt..tc.a..t..c..a : 128
DQB1_grant : .....a.....a...ac...gt..tc.a..t..c..a : 128
DQB2_grant : .....c.....t.....a.....a.agtt....ct.t... : 128
DQB3_grant : ----- : 26

      *           140           *           160           *           180           *
DQB_tarand : gtgttactttaccaacggaacggagcgggtgcggctcgtgaccagacacatctacaaccaggaa : 192
DQB_caribo : .....c..t..t..c.....ta.....t.....g : 192
DQB1_grant : .....c..t..t..c.....ta.....t.....g : 192
DQB2_grant : .....c.....g..a.....ta.....t.....aga..g : 192
DQB3_grant : .....c..t.....g.....ggt.....a... : 90

      200           *           220           *           240           *
DQB_tarand : gagtacgtgcgggttcgacagcgacgtgggcgagtagccgggcagtgaccccgctggggcgggcgg : 256
DQB_caribo : ..ac....tac.a.....a.....a.....t.....a..a..t..tatt : 256
DQB1_grant : ..ac....tac.a.....a.....a.....t.....a..a..t..tatt : 256
DQB2_grant : .....a...t.....aa.....g..... : 256
DQB3_grant : .....c..t...g.....g..c : 154

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      260      *      280      *      300      *      320
DQB_tarand : acgccgagtacttcaacagccaggagggcggaactggagcgggtgcggggccgagggcgacacggt : 320
DQB_caribo : tg..t.....gg.....a.a.atatc.....a.acc.....g...ct..... : 320
DQB1_grant : tg..t.....gg.....a.a.atatc.....a.acc.....g...ct..... : 320
DQB2_grant : .....t..gg.....a..a.atc.....a.ac.....t.....a.. : 320
DQB3_grant : cg.....a...a..t.c.....a.a.....c..t..... : 218

      *      340      *      360      *      380
DQB_tarand : gtgcagacacaactaccagtcagaggtccgcacgacctttcagcgtctagtggaaacctacagt : 384
DQB_caribo : ...t.....t.....ctg.....at...t...g...ac.c..... : 384
DQB1_grant : ...t.....t.....ctg.....at...t...g...ac.c..... : 384
DQB2_grant : .....g.actg..ac..at...at...g....a.g..... : 384
DQB3_grant : .....gtg...c..ac..at...g....g.a.....g..... : 282

      *      400      *      420      *      440
DQB_tarand : accatctccctgtccaggactgaggtctctaaaccaccacaatctactgggttgcctcgggtgacag : 448
DQB_caribo : .....c...t.....c.g....c....a..... : 448
DQB1_grant : .....c...t.....c.g....c....a..... : 448
DQB2_grant : ....t....ca...c.....c.g....c....a..... : 448
DQB3_grant : .....gt.....c.....c.....c..... : 346

      DQB.R2 ATCAAGGTTCGGTGGTTCCG
      *      460      *      480      *      500      *
DQB_tarand : atttctatccaggccagatcaaggttcgggttcggaatgaccaggaggagacagccggcgt : 512
DQB_caribo : .....a.. : 512
DQB1_grant : .....a.. : 512
DQB2_grant : .....t...a.. : 512
DQB3_grant : .....a.g.. : 410

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Alignment of genomic MHC class I nucleotide sequences with primer location

```

      A1.F1 AACCCTTCTCCTGCTCCTTTG
      *      20      *      40      *      60
A5_tarand : atgcgggtcgtgggtctgagagc---cgtactgctgctctcggggccctggtctctgaccgag : 60
A5_caribou : .....g.--- : 60
A5_granti : ..... : 60
A4_tarany : ...t..c.a...gt..c..a.cct.c.c.....c.....c..... : 63
A4_granti : ...t..c.a...gt..c..a.cct.c.c.....c.....c..... : 63
A1_granti : -----a..t...c.c..a.ccttc.c.....c..t.....t..... : 54
A2_caribou : ....c..aa...g.c.c..a.cct.c.c.....a...aaa..... : 63
A2_granti : ....c..aa...g.c.c..a.cct.c.c.....a...aaa..... : 63
A2_tarand : ....c..aa...g.c.c..a.cct.c.c.....a...aaa..... : 63
A3_tarand : ...a..a...a...gaa...a.tct.c.c.....gc.t..t.g...ctg..... : 63
A3_caribou : ...a..a...a...gaa...a.tct.c.c.....gc.t..t.g...ctg..... : 63
A3_granti : ...a..a...a...gaa...a.tct.c.c.....gc.t..t.g...ctg..... : 63

      Alpha 1 domain
      A5.F2 TGAGGTATTCTACACCGCCG
      *      80      *      100      *      120
A5_tarand : acctggggcgggc tccactccc tgaggtatttctacaccgcccgtgtccggcgggcctcggg : 123
A5_caribou : ..... : 123
A5_granti : ..... : 123
A4_tarany : ...c...c... ..ct...ag.....c..... : 126
A4_granti : ...c...c... ..ct...ag.....c..... : 126
A1_granti : ...c...t..t.....c..... : 117
A2_caribou : .g.ct...t... ..a..c..... : 126
A2_granti : .g.ct...t... ..a..c..... : 126
A2_tarand : .g.ct...t... ..a..c..... : 126
A3_tarand : .g..... ..a.....c..t..... : 126
A3_caribou : .g..... ..a.....c..t..... : 126
A3_granti : .g..... ..a.....c..t..... : 126

      *      140      *      160      *      180
A5_tarand : gagccccgcttcatcaccgtcgggtacgtggacgacgcagttcgtgcggttcgacagcgac : 186
A5_caribou : ..... : 186
A5_granti : ..... : 186
A4_tarany : .....t.....t..... : 189
A4_granti : .....t.....t..... : 189
A1_granti : .....t..t..... : 180
A2_caribou : .....t.....t...a... : 189
A2_granti : .....t.....t..... : 189
A2_tarand : .....t.....t..... : 189
A3_tarand : .....t.....t.....a.....t.....t... : 189
A3_caribou : .....t.....t.....a.....t.....t... : 189
A3_granti : .....t.....t.....a.....t.....t... : 189

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		*	200	*	220	*	240	
A5_tarand	:	gccccggatccgagggtagaaccgcggcgctgtgggtggagcaggaggggccccgagtattgg	:	249				
A5_caribou	:	:	249				
A5_granti	:	:	249				
A4_tarany	:	..a...a.....a.g..g.....g.....	:	252				
A4_granti	:	..a...a.....a.g..g.....g.....	:	252				
A1_granti	:a.....a.....a...a.ca...a.....g.....	:	243				
A2_caribou	:a.g..g.....g...tt...-----	:	229				
A2_granti	:a.g..g.....g...tt...-----	:	229				
A2_tarand	:a.g..g.....g...tt...-----	:	229				
A3_tarand	:ta.....a.g..g.....g.....c.....	:	252				
A3_caribou	:ta.....a.g..g.....g.....c.....	:	252				
A3_granti	:ta.....a.g..g.....g.....c.....	:	252				
		*	260	*	280	*	300	*
A5_tarand	:	gatcaggagactcagagaaccagagataccgcacagtttttccgaatgagcctgaacaccctg	:	312				
A5_caribou	:	:	312				
A5_granti	:	:	312				
A4_tarand	:ga...gg.t.aga.c.....ac....a.g...a.....	:	315				
A4_granti	:ga...gg.t.aga.c.....ac....a.g...a.....	:	315				
A1_granti	:	..agaa.c..gaga.tctg..ag..c..g.....g.....ga.....at...	:	306				
A2_caribou	:	-----tt.a.t....gc.	:	243				
A2_granti	:	-----tt.a.t....gc.	:	243				
A2_tarand	:	-----tt.a.t....gc.	:	243				
A3_tarand	:	..g.....g.....c.....ac.....g...a.....t...	:	315				
A3_caribou	:	..g.....g.....c.....ac.....g...a.....t...	:	315				
A3_granti	:	..g.....g.....c.....ac.....g...a.....t...	:	315				
			Alpha 2 domain					
		320	*	340	*	360	*	
A5_tarand	:	cgcggtactacaaccagagcgaggcc	:	gagttctcacaccctccaggagatgtatggctgcgac	:	375		
A5_caribou	:	:	:	375		
A5_granti	:	:	:	375		
A4_tarany	:	...a.....t	:	.g.....t....tg.g...c.....a..	:	378		
A4_granti	:	...a.....t	:	.g.....t....tg.g...c.....a..	:	378		
A1_granti	:t	:	.g.....c.....	:	369		
A2_caribou	:	g.t..-----t.g.g..g.t.a	:	.g.....tg....c.....	:	297		
A2_granti	:	g.t..-----t.g.g..g.t.a	:	.g.....tg....c.....	:	297		
A2_tarand	:	g.t..-----t.g.g..g.t.a	:	.g.....tg....c.....	:	297		
A3_tarand	:t	:	.g.....c.....	:	378		
A3_caribou	:t	:	.g.....c.....	:	378		
A3_granti	:t	:	.g.....c.....	:	378		
		380	*	400	*	420	*	
A5_tarand	:	gtggggccggaacgggcgtctcctccgcgggtatgaccagttcgcctacgacggcgagagattac	:	438				
A5_caribou	:	:	:	438		
A5_granti	:	:	:	438		
A4_tarany	:t.....tc.g....t.g....t.a.....	:	441				
A4_granti	:t.....tc.g....t.g....t.a.....	:	441				
A1_granti	:c.....c.....c.tg...a.....c...	:	432				
A2_caribou	:c.....c.....c.tg...a.....c...	:	360				
A2_granti	:c.....c.....c.tg...a.....c...	:	360				
A2_tarand	:c.....c.....c.tg...a.....c...	:	360				
A3_tarand	:t.....t...t....a.....	:	438				
A3_caribou	:t.....t...t....a.....	:	438				
A3_granti	:t.....t...t....a.....	:	438				
		440	*	460	*	480	*	500
A5_tarand	:	atctccctgaatgaggacctgcgctcctggaccgcggcgagacggcggtcagatctccaag	:	501				
A5_caribou	:	:	:	501		
A5_granti	:	:	:	501		
A4_tarany	:	..g.t....c.....a.c.a.....a....	:	504				
A4_granti	:	..g.t....c.....a.c.a.....a....	:	504				
A1_granti	:	..gg.....c.....ct.....	:	495				
A2_caribou	:	..gg.....c.....ct.....a....	:	423				
A2_granti	:	..g.....c.....ct.....a....	:	423				
A2_tarand	:	..g.....c.....ct.....a....	:	423				
A3_tarand	:	..g.....c.....a.....c.....a....	:	501				
A3_caribou	:	..g.....c.....a.....c.....a....	:	501				
A3_granti	:	..g.....c.....a.....c.....a....	:	501				

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A1.R1 TTGAGCAAGCGGTGAGG
      *          520      *          540      *          560
A5_tarand : cacaatgctgaggcgccggtgatgcgcgcgtgtgaggaactatctggagggcaagtgcgtg : 564
A5_caribou : ..... : 564
A5_granti : ..... : 564
A4_tarany : .g...gtgg.....a..cct....a.gaacac.....C.....gg....a.. : 567
A4_granti : .g...gtgg.....a..cct....a.gaacac.....C.....gg....a.. : 567
A1_granti : .g...gtt....caa.g.....g.....at.acagc.....C.....cg..... : 558
A2_caribou : .g...gtt....caa.g.....c.g....at.ac.ac..a.....C.....g..... : 486
A2_granti : .g...gtt....caa.g.....c.g....at.ac.ac..a.....C.....g..... : 486
A2_tarand : .g...gtt....caa.g.....c.g....at.ac.ac..a.....C.....g..... : 486
A3_tarand : .g...gat....ca.cg....tg...atgactac.....C..aa.cc..g.....c. : 564
A3_caribou : .g...ga....ca.cg.----- : 519
A3_granti : .g...ga....ca.cg.----- : 519

      A5.R2 AGAGACAGGAACGACACGC
      *          580      *          600      *          620
A5_tarand : gagggtctcctcagatacctagagacaggaacgacacgctgctgcgcgcagaccctccaaag : 627
A5_caribou : .....g..... : 627
A5_granti : ..... : 627
A4_tarany : .....g.ga.....g....ac..g..g.....g... : 630
A4_granti : .....g.ga.....g....ac..g..g.....g... : 630
A1_granti : ...g.....a.....g....ac..g..g.....g... : 621
A2_caribou : a.....g.ga.a.....g....ac..g..g.....t..... : 549
A2_granti : a.....g.ga.a.....g....ac..g..g..... : 549
A2_tarand : a.....g.ga.a.....g....ac..g..g..... : 549
A3_tarand : .....g.....gc....ga.....t. : 627
A3_caribou : ----- : 531
A3_granti : ----- : 531

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5. Expressed reindeer MHC amplicon sequences

5.1 Expressed DRB data

Deduced amino acids of expressed MHCII DRB1 allele sequences

>Rata-DRB1*01:01 ON411554

VRLYFSGGSRMAALTVMMLVLSPLAWAREIRPHFLEYFKCECHFSNGTQGVQFLQRYIYNREEYVRFDSVDVGEFRAVTELGRKSAEGWNSRK
EILEESRAAVDTYCRHNYGVGESFTVQRRVEPTVTVPYPAKTQPLQHHNLLVCSVNGFYPGHIEVRWFR

>Rata-DRB1*01:02 ON411555

VRLYFSGGSRMAALTVMMLVLSPLAWAREIRPHFLEYFKCECHFSNGTQGVQFLQRYIYNREEYVRFDSVDVGEFRAVTELGRKSAEGWNSRK
EILEESRAAVDTYCRHNYGVLDSEFIVQRRVEPTVTVPYPAKTQPLQHHNLLVCSVNGFYPGHIEVRWFR

>Rata-DRB1*01:03 ON411556

VRLYFSGGSRMAALTVMMLVLSPLAWAREIRPHFLEYFKCECHFSNGTQGVQFLQRYIYNREEYVRFDSVDVGEFRAVTELGRKSAEGWNSQ
KEILEESRAAVDTYCRHNYGVGESFTVQRRVEPTVTVPYPAKTQPLQHHNLLVCSVNGFYPGHIEVRWFR

>Rata-DRB1*02:01 ON411557

VRLYFSGGSRMAALTVMMLVLSPLAWAREIRPHFLEYFKGECHFSNGTERVQFLKRYIHNGEESVRFDSVDVGEFRAVTELGRPDAEVWNSRK
EILEESRAEVDTVCRHNYGVLDSEFIVQRRVEPTVTVPYPAKTQPLQHHNLLVCSVNGFYPGHIEVRWFR

>Rata-DRB1*03:01 ON411558

VRLYFSGGSRMAALTVMMLVLSPLAWAREIRPHFLEYVKSECHFSNGTQGVQFLQRHIYNGEEFLRFDSVDVGEFRAVTELGRPDAEGWNSR
KDILEDKRAAVDTYCRHNYGVLDSEFIVQRRVEPTVTVPYPAKTQPLQHHNLLVCSVNGFYPGHIEVRWFR

>Rata-DRB1*04:01 ON411559

VRLYFSGGSRMAALTVMMLVLSPLAWAREIRPHFLEYVKSECHFSNGTERVQFLKRFIYNGEELVRFDSVDVGEFRAVTELGRPDAEGWNSRK
DILEDKRAAVDTYCRHNYGVGESFTVQRRVEPTVTVPYPAKTQPLQHHNLLVCSVNGFYPGHIEVRWFR

>Rata-DRB1*05:01 ON411560

VRLYFSGGSRMAALTVMMLVLSPLAWAREIRPHFLEYFKCECHFSNGTERVQFLKRFIYNGEELVRFDSVDVGEFRAVTELGRPDAEVWNSRKE
ILEESRAEVDTVCRHNYGVLDSEFIVQRRVEPTVTVPYPAKTQPLQHHNLLVCSVNGFYPGHIEVRWFR

>Rata-DRB1*05:02 ON411561

VRLYFSGGSRMAALTVMMLVLSPLAWAREIRPHFLEYFKCECHFSNGTERVQFLKRFIYNGEELVRFDSVDVGEFRAVTELGRPVAEVWNSRK
EILEESRAEVDTVCRHNYGVLDSEFIVQRRVEPTVTVPYPAKTQPLQHHNLLVCSVNGFYPGHIEVRWFR

>Rata-DRB1*05:03 ON411562

VRLYFSGGSRMAALTVMMLVLSPLAWAREIRPHFLEYFKCECHFSNGTERVQFLKRYIYNGEELVRFDSVDVGEFRAVTELGRPDAEGWNSRK
EILEESRAEVDTVCRHNYGVLDSEFIVQRRVEPTVTVPYPAKTQPLQHHNLLVCSVNGFYPGHIEVRWFR

>Rata-DRB1*05:04 ON411563

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VRLYFSGGSWMAALTVMMLVSPPLAWAREIRPHFLEYFKCECHFSNGTERVQFLKRYIYNGEEFVRFDSVDVGEFRAVTELGRPDAEVWNSR
KEILEESRAEVDTCRHNYGVLDSTFVQRRVEPTVTVPYPAKTQPLQHHNLLVCSVNGFYPGHIEVRWFR
>Rata-DRB1*05:05 ON411564
VRLYFSGGSWMAALTVMMLVSPPLAWAREIRPHFLEYFKCECHFSNGTERVQFLKRYIYNGEEFVRFDSVDVGEFRAVTELGRPDAEVWNSR
KEILEESRAEVDTCRHNYGVGESFTVQRRVEPTVTVPYPAKTQPLQHHNLLVCSVNGFYPGHIEVRWFR
>Rata-DRB1*06:01 ON411565
VRLYFSGGSMAALTVMMLVSPPLAWAREIRPHFLEYVKGECHFSNGTERVQLLQRFIYNGEEFVRFDSVDVGEFRAVTELGRPDAEVWNSQ
KEILEESRAAVDTYCRHNYGVGESFTVQRRVEPTVTVPYPAKTQPLQHHNLLVCSVNGFYPGHIEVRWFR
>Rata-DRB1*07:01 ON411566
VRLYFSGGSMAALTVMMLVSPPLAWAREIRPHFLEYVKSECHFSNGTERVQFLKRYIHNGEELVRFDSVDVGEFRAVTELGRPDAEVWNSRK
DILEDKRAAVDTYCRHNYGVLDSTFVQRRVEPTVTVPYPAKTQPLQHHNLLVCSVNGFYPGHIEVRWFR
>Rata-DRB1*15:01 ON411567
VRLYFSGGSMAALTVMMLVSPPLAWAREIRPHFLEYVKSECHFSNGTQGVQFLQRYIYNGEEYVRFDSVDVGEFRAVTELGRKSAEGWNSQ
KEILEDKRAAVDTYCRHNYGVGESFTVQRRVEPTVTVPYPAKTQPLQHHNLLVCSVNGFYPGHIEVRWFR
>Rata-DRB1*16:01 ON411568
VRLYFSGGSMAALTVMMLVSPPLAWAREIRPHFLEYVKSECHFSNGTQGVQFLQRYIYNREEYVRFDSVDVGEFRAVTELGRPDAEVWNSR
KEILEESRAEVDTCRHNYGVLDSTFVQRRVEPTVTVPYPAKTQPLQHHNLLVCSVNGFYPGHIEVRWFR

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Alignment of expressed deduced amino acid sequences of MHC class II DRB alleles

Yellow shading shows location of primers. Individual domain are shown. Abbreviations are CP= connecting peptide, TM= transmembrane domain, CYT= cytoplasmic domain. Numbering according to top sequence. Residues are colour coded according to physiochemical properties. Yellow or green shading shows location of primers.

		Leader sequence				Beta 1 domain			
		*	20	*	40	*	60		
Caribou DRB1	:	MVRLYFS	GGSRMAALTVMMLVLSPLAWARE	IR	PHFLEYFKCECHFSNGTERVQFLKRYIYNGEE	:	65		
Granti DRB1	:	G.	Q.	R.	: 65
Tarandus DRB1	:	.	.	.	S.	G.	.	H.	: 65
Rata-DRB1*01:01	:	-	.	.	.	G.	Q.	R.	: 64
Rata-DRB1*01:02	:	-	.	.	.	G.	Q.	R.	: 64
Rata-DRB1*01:03	:	-	.	.	.	G.	Q.	R.	: 64
Rata-DRB1*02:01	:	-	.	.	G.	.	.	H.	: 64
Rata-DRB1*03:01	:	-	.	.	V.S.	G.	Q.H.	.	: 64
Rata-DRB1*04:01	:	-	.	.	V.S.	.	.	.	: 64
Rata-DRB1*05:01	:	-	: 64
Rata-DRB1*05:02	:	-	: 64
Rata-DRB1*05:03	:	-	: 64
Rata-DRB1*05:04	:	-	.	W.	: 64
Rata-DRB1*05:05	:	-	.	W.	: 64
Rata-DRB1*06:01	:	-	.	.	V.G.	.	L.Q.	.	: 64
Rata-DRB1*07:01	:	-	.	.	V.S.	.	.	H.	: 64
Rata-DRB1*15:01	:	-	.	.	V.S.	G.	Q.	.	: 64
Rata-DRB1*16:01	:	-	.	.	V.S.	G.	Q.	R.	: 64
Beta 2 domain									
		*	80	*	100	*	120	*	
Caribou DRB1	:	FVRFDSVDVGEFRAVTELGRPDAEGWNSRKEILEESRAEVDTCRHNYGVGESFTVQRR	VEPTVTV	:	130				
Granti DRB1	:	.	KS.	.	A.	Y.	LD.	I.	: 130
Tarandus DRB1	:	S.	.	V.	.	.	LD.	I.	: 130
Rata-DRB1*01:01	:	.	KS.	.	A.	Y.	.	.	: 129
Rata-DRB1*01:02	:	.	KS.	.	A.	Y.	LD.	I.	: 129
Rata-DRB1*01:03	:	.	KS.	Q.	A.	Y.	.	.	: 129
Rata-DRB1*02:01	:	S.	.	V.	.	.	LD.	I.	: 129
Rata-DRB1*03:01	:	.	.	D.	DK.	A.	Y.	LD.	: 129
Rata-DRB1*04:01	:	L.	.	D.	DK.	A.	Y.	I.	: 129
Rata-DRB1*05:01	:	.	.	V.	.	.	LD.	I.	: 129
Rata-DRB1*05:02	:	.	.	V.	V.	.	LD.	I.	: 129
Rata-DRB1*05:03	:	LD.	I.	: 129
Rata-DRB1*05:04	:	.	.	V.	.	.	LD.	I.	: 129
Rata-DRB1*05:05	:	.	.	V.	.	.	LD.	I.	: 129
Rata-DRB1*06:01	:	.	.	V.	Q.	A.	Y.	.	: 129
Rata-DRB1*07:01	:	L.	.	V.	D.	DK.	A.	Y.	: 129
Rata-DRB1*15:01	:	.	KS.	Q.	DK.	A.	.	.	: 129
Rata-DRB1*16:01	:	.	.	V.	.	.	LD.	.	: 129

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          140          *          160          *          180          *
Caribou_DRB1 : YPAKTQPLQHNNLLVCSVNGFYPGHIEVVRWFRNGHEEEAGVISTGLIQNGDWTFTQTMVMLETVPQ : 195
Granti_DRB1 : ..... : 195
Tarandus_DRB1 : ..... : 195
Rata-DRB1*01:01 : ..... : 161
Rata-DRB1*01:02 : ..... : 161
Rata-DRB1*01:03 : ..... : 161
Rata-DRB1*02:01 : ..... : 161
Rata-DRB1*03:01 : ..... : 161
Rata-DRB1*04:01 : ..... : 161
Rata-DRB1*05:01 : ..... : 161
Rata-DRB1*05:02 : ..... : 161
Rata-DRB1*05:03 : ..... : 161
Rata-DRB1*05:04 : ..... : 161
Rata-DRB1*05:05 : ..... : 161
Rata-DRB1*06:01 : ..... : 161
Rata-DRB1*07:01 : ..... : 161
Rata-DRB1*15:01 : ..... : 161
Rata-DRB1*16:01 : ..... : 161

          CP/  TM/  CYT
          200          *          220          *          240          *          260
Caribou_DRB1 : SGEVYTCQVDHPSQTSPITVEW RARSDSAQSKMMSGVGGFVLGLLFLAVGLFIYFRNQKGRPTLQ : 260
Granti_DRB1 : ..... : 260

Caribou_DRB1 : PTGLLS : 266
Granti_DRB1 : ..... : 266

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MHCII DRB1 allele frequencies in selected reindeer populations

DRB1 allele	SemiD N=62	Wild N=18	Svalbard	North	Norway/Svalbard
DRB1*01:01	0.02 (3)	0.14 (5)		QCU79927.1	AAB66609.1
DRB1*01:02	0.15 (18)	0.03 (1)		QCU79923.1	AAB66610.1
DRB1*01:03			0.05 (1)	QCU79926.1	AAB66611.1
DRB1*02:01	0.14 (17)	0.22 (8)		QCU79918.1	AAB66612.1
DRB1*03:01	0.04 (5)	0.19 (7)		QCU79920.1	AAB66613.1
DRB1*04:01	0.41 (51)	0.22 (8)			AAB66614.1
DRB1*05:01	0.02 (3)				AAB66615.1
DRB1*05:02	0.01 (1)	0.06 (2)			
DRB1*05:03	0.01 (1)				
DRB1*05:04		0.03 (1)			
DRB1*05:05	0.02 (2)	0.03 (1)			
DRB1*06:01			0.94 (17)	QCU79925.1	AAB66616.1
DRB1*07:01	0.07 (9)	0.08 (3)			AAB66617.1
DRB1*15:01	0.08 (10)			QCU79932.1	
DRB1*16:01	0.03 (4)				
No. alleles (15)	12	9	2		

Allele frequencies **calculated as number of given allele divided by total number of alleles** per each of the three populations are shown with number of given alleles listed in parenthesis. N refers to the number of animals sampled per population and SemiD is semi-domesticated. NCBI Accession numbers for DRB1 alleles in North American reindeer originate from Gagnon et al.2020 (see Main text reference) while those from Norway/Svalbard are from Mikko et al.1999 (see Main text reference).

5.2 Expressed DQB data

Deduced amino acids of expressed MHCII DQB sequence variants

>Rata-DQB2*02 ON411569

WTAAMVMTLVVLSTPGAEGRDSSQNFIQFLGLCYFTNGTERVRLVTRYIYNREEYVRFDSVDVNEYRAVTPLRPDADFWSQKDILEQTRAE
VDTVCRHNYELETLSLQRRVEPTVTISPSTREALNHHNLLVCSVTDFYPGQIKVRWFR


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>Rata-DQB2*03 ON411570
WTAAMVMTLVVLSTPGAEGRDSSQNFIQFLGLCYFTNGTERVRYVTRYIYNREEYVRFDSVDVNEYRAVTPPLGRPDAEFWNSQKDILEQTRAE
VDTVCRHNYEELITSLQRRVEPTVTISPSRTEALNHHNLLVCSVTDFFYPGQIKVRWFR
>Rata-DQB2*04 ON411571
WTAAMVMTLVVLSTPGAEGRDSSQNFIQFLGLCYFTNGTERVRSVTRYIYNREEYVRFDSVDVNEYRAVTPPLGRPDAEFCNSQKDILEQTRAEV
DTCVCRHNYEELITSLQRRVEPTVTISPSRTEALNHHNLLVCSVTDFFYPGQIKVRWFR
>Rata-DQB2*05 ON411572
WTAAMVMTLVVLSTPGAEGRDSSQNFIQFLGLCYFTNGTERVRYVTRYIYNREEYVRFDSVDVNEYRAVTPPLGRPDAEFCNSQKDILEQTRAEV
DTCVCRHNYEELITSLQRRVEPTVTISPSRTEALNHHNLLVCSVTDFFYPGQIKVRWFR
>Rata-DQB3*02 ON411573
WTAAMVMTLVVLSTPGAEGGESPQDFVYQFKGLCYFTNGTERVRLVTRHIYNQEEYLRFDSDVGEYRAVTPPLGRRQAEYFNSQEGKLERVRAE
ADTVCRHNYQVELTSLQRRVEPTVTISLSRTEALNHHNLLVCSVTDFFYPGKIKVRWFR
>Rata-DQB3*03 ON411574
WTAAMVMTLVVLSTPGAEGGESPQDFVYQFKGLCYFTNGTERVRLVTRHIYNQEEYLRFDSDVGEYRAVTPPLGRRQAEYFNSQEGELERVRAE
ADTVCRHNYQVELTSLQRRVEPTVTISLSRTEALNHHNLLVCSVTDFFYPGKIKVRWFR
>Rata-DQB3*04 ON411575
WTAAMVMTLVVLSTPGAEGGESPQDFVYQFKGLCYFTNGTERVRLVTRHIYNQEEHLRFDSVDVGEYRAVTPPLGRRQAEYFNSQEGQLERVRAE
ADTVCRHNYQVELTSLQRRVEPTVTISLSRTEALNHHNLLVCSVTDFFYPGKIKVRWFR
>Rata-DQB3*05 ON411576
WTAAMVMTLVVLSTPGAEGGESPQDFVYQFKGLCYFTNGTERVGVTRHIYNQEEYVRFDSVDVGEHWAVTPPLGRRPAEYFNSQKDYLEQMRA
AVDTVCRHNYQVELTSLQRRVEPTVTISLSRTEALNHHNLLVCSVTDFFYPGKIKVRWFR
>Rata-DQB4*01 ON411577 rata11-DQB1-3529
WTAAMVMTLAVLSTPGAEGRDSPQDFVCQFKGLCYFTNGTERVRLVTRHIYNQEEYVRFDSVDVGEYRAVTPPLGRPDAEYWNSQEGELERVRA
EADTVCRHNYQSEVRTTFQRLVEPTVTISLSRTEALNHHNLLVCSVTDFFYPGQIKVRWFR
>Rata-DQB4*02 ON411579
WTAAMVMTLAVLSTPGAEGRDSPQDFVYQFKGLCYFTNGTERVRLVTRHIYNQEEYVRFDSVDVGEYRAVTPPLGRPDAEYWNSQEGELERVRA
EADTVCRHNYQSEVRTTFQRLVEPTVTISLSRTEALNHHNLLVCSVTDFFYPGQIKVRWFR
>Rata-DQB4*03 ON411580
WTAAMVMTLAVLSTPGAEGRDSPQDFVYQFKGLCYFTNGTERVRLVTRHIYNQEEYVRFDSVDVGEYRAVTPPLGRPDAEYFNSQEGELERVRAE
ADTVCRHNYQSEVRTTFQRLVEPTVTISLSRTEALNHHNLLVCSVTDFFYPGQIKVRWFR

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Alignment of expressed deduced amino acid sequences of MHC class II DQB alleles

Yellow shading shows location of primers. Individual domain are shown. Abbreviations are CP= connecting peptide, TM= transmembrane domain, CYT= cytoplasmic domain. Numbering according to top sequence. Residues are colour coded according to physiochemical properties. Yellow or green shading shows location of primers.

	Leader sequence			Beta 1 domain			
		*	20	*	40	*	60
Granti DQB2	: ---MVALWIPRG	WTAAMV	TLVVLSTPGA	EGRDSS	QNFIVQFLCLCYFTNGTERVRYVTRYIYNREE	:	65
Rata-DQB2*02	: -----			G.....L.....	:	55
Rata-DQB2*03	: -----			G.....	:	55
Rata-DQB2*05	: -----				:	55
Rata-DQB2*04	: -----			G.....S.....	:	55
Granti DQB3	: -----				...Y..KG...I.....G...H...Q..	:	31
Rata-DQB3*02	: -----		I..T..GE.P		...Y..KG...L...H...Q..	:	55
Rata-DQB3*03	: -----		I..T..GE.P		...Y..KG...L...H...Q..	:	55
Rata-DQB3*04	: -----		I..T..GE.P		...F..KG...L...H...Q..	:	55
Rata-DQB3*05	: -----		I..T..GE.P		...Y..KG...I.....G...H...Q..	:	55
Rata-DQB4*01	: -----		A.....P		...C..KG...L...Q..	:	55
Rata-DQB4*02	: -----		A.....P		...Y..KG...L...Q..	:	55
Rata-DQB4*03	: -----		A.....P		...Y..KG...L...H...Q..	:	55
Granti_DQB1	: ---...R.....		A.....S...P		..T..L..AQ.....Q..	:	65
Caribou DQB	: ---...R.....		A.....S...P		..T..L..AQ.....Q..	:	65
Tarandus_DQB	: MSG...R.....		A.....P		...Y..KG...L...H...Q..	:	68

Beta 2 domain

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      *           80           *           100           *           120           *
Granti_DQB2 : YVRFDSVDVNEYRAVITPLGRPDAEFWNSQKDILEQTRADEVDTVCRHNYELELITSLQRR VEPTVTISPS : 133
Rata-DQB2*02 : ..... : 123
Rata-DQB2*03 : ..... : 123
Rata-DQB2*05 : .....C..... : 123
Rata-DQB2*04 : .....C..... : 123
Granti_DQB3 : .....G.HW.....RP.....Y...M..A.....T.....L : 99
Rata-DQB3*02 : .....G.....RQ.....EGK..RV...A.....T.....L : 123
Rata-DQB3*03 : .....G.....RQ.....EGE..RV...A.....T.....L : 123
Rata-DQB3*04 : H.....G.....RQ.....EGQ..RV...A.....T.....L : 123
Rata-DQB3*05 : .....G.HW.....RP.....Y...M..A.....T.....L : 123
Rata-DQB4*01 : .....G.....EGE..RV...A.....S..R..F..L : 123
Rata-DQB4*02 : .....G.....EGE..RV...A.....S..R..F..L : 123
Rata-DQB4*03 : .....G.....EGE..RV...A.....S..R..F..L : 123
Granti_DQB1 : T.Y.....G.....WYL..... : 133
Caribou_DQB : T.Y.....G.....WYL.....HQ : 133
Tarandus_DQB : .....G.....EGE..RV...A.....S..R..F..L : 136

      140           *           160           *           180           *           200
Granti_DQB2 : RTEALNHHNLLVCSVTDFYPGQIKVWRERNDQEETAGIVSTPLIRNGDWTFFQILVMLEMTPQRGDVYT : 201
Rata-DQB2*02 : ..... : 151
Rata-DQB2*03 : ..... : 151
Rata-DQB2*05 : ..... : 151
Rata-DQB2*04 : ..... : 151
Granti_DQB3 : .....K.....R..A.....K..... : 167
Rata-DQB3*02 : .....K..... : 151
Rata-DQB3*03 : .....K..... : 151
Rata-DQB3*04 : .....K..... : 151
Rata-DQB3*05 : .....K..... : 151
Rata-DQB4*01 : ..... : 151
Rata-DQB4*02 : ..... : 151
Rata-DQB4*03 : ..... : 151
Granti_DQB1 : ..... : 201
Caribou_DQB : ..... : 201
Tarandus_DQB : ..... : 204

      CP/ TM/ CYT
      *           220           *           240           *
Granti_DQB2 : CRVEHPSLQSPIMVEWR AQSESAQSKMLSGVGGFVLGLIFLGLGLIHRRS----- : 252
Granti_DQB3 : .H.....S.....R.....RH...QKGLMR--- : 224
Granti_DQB1 : .H.....V.....R...QKGVKDVIIT : 261
Caribou_DQB : .H.....V.....R...QKGVKDVIIT : 261
Tarandus_DQB : .....S.....H...QK----- : 257

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MHCII DQB sequence frequencies in the three reindeer populations

DQB variant	SemiD	Wild N=18	Svalbard N=8
DQB2*02	0.54 (67)	0.33 (12)	
DQB2*03	0.02 (2)	0.11 (4)	
DQB2*04	0.05 (6)	0.14 (5)	
DQB2*05	0.06 (7)		
DQB3*02			1.0 (16)
DQB3*03		0.06 (2)	
DQB3*04	0.01 (1)		
DQB3*05	0.04 (5)	0.03 (1)	
DQB4*01	0.10 (13)	0.03 (1)	
DQB4*02	0.02 (2)		
DQB4*03	0.16 (20)	0.31 (11)	
No.alleles (11)	9	7	1

N refers to the number of animals sampled per population and SemiD is semi-domesticated.
Number of alleles are shown in parenthesis.

Deduced MHCII DRB1 and DQB haplotypes

DRB1 allele	Haplotype 1	Haplotype 2	Haplotype 3	Haplotype 4
DRB1*01:01	DQB2*03 (6)	DQB2*04 (1)	DQB4*02 (1)	
DRB1*01:02	DQB2*02 (14)	DQB2*05 (5)	DQB4*03 (1)	
DRB1*01:03	DQB3*02 (1)			
DRB1*02:01	DQB4*03 (25)			
DRB1*03:01	DQB2*04 (2)	DQB3*03 (1)	DQB4*01 (4)	DQB4*03
DRB1*04:01	DQB2*02 (58)	DQB2*04 (1)		
DRB1*05:01	DQB3*05 (3)			
DRB1*05:02	DQB2*04 (2)	DQB3*04 (1)		
DRB1*05:03	DQB4*02 (1)			
DRB1*05:04	DQB3*03 (1)			
DRB1*05:05	DQB3*05 (3)			
DRB1*06:01	DQB3*02 (15)			
DRB1*07:01	DQB2*02 (10)	DQB2*05 (2)		
DRB1*15:01	DQB4*01 (10)			
DRB1*16:01	DQB2*04 (4)			

DRB1 alleles segregating with individual DQB variants present in 89 animals.

Number of animals with each haplotype is shown in parenthesis.

5.3 Expressed MHC I data

Deduced amino acids of expressed MHC I A5 allele sequences

>Rata-A5*01:01

RYFYTAVSRLGLGEPFRITVGYYDDTQFVRFSDAPDPRVEPRALWVEQEGPEYWDQETQRTDRTAQFFRMSLNTLRGYNNQSEAESHTLQE
MYGCDVGPDRLLRGYDQFAYDGRDYISLNEDLRSWTAAETAQISKHNAEAAGDAARVRNLYEGKCEWLLRYLETGNDT

>Rata-A5*01:02

RYFYTAVSRLGLGEPFRITVGYYDDTQFVRFSDAPDPRVEPRALWVEQEGPEYWDQETQRTDRTAQFFRMSLNTLRGYNNQSEAESHTLQE
MYGCDVGPDRLLRGYDQFAYDGRDYISLNEDLRSWTAAETAQISKHNAEAAGDAARVRNLYEGKCEWLLRYLETGNDT

MHC I A5 pseudogene sequence or sequences with nucleotide differences not affecting amino acid sequence:

>Rata-A5*01:01:01 ON411550

TGAGGTATTTCTACACCGCCGTGTCCCGGCCGGGCTCGGGGAGCCCCGCTTCATCACCGTCGGCTACGTGGACGACACGCAGTTCGTG
CGGTTTCGACAGCGACGCCCCGGATCCGAGGGTAGAACCGCGGGCGCTGTGGGTGGAGCAGGAGGGGCCCCGAGTATTGGGATCAGGA
GACTCAGAGAACCAGAGATACCGCACAGTTTTTCCGAATGAGCCTGAACACCTGCGCGGCTACTACAACCAGAGCGAGGCCGAGTCTC
ACACCTCCAGGAGATGTATGGCTGCGACGTGGGGCCGGACGGGCGTCTCCTCCGCGGGTATGACCAGTTCGCTACGACGGCAGAGA
TTACATCTCCCTGAATGAGGACCTGCGCTCCTGGACCGCGCGGAGACGGCGGCTCAGATCTCAAGCACAAATGCTGAGGCGGCCGGTG
ATGCGGCGCGTGTGAGGAACCTATCTGAGGGCAAGTGCGTGGAGTGGCTCCTCAGATACCTAGAGACAGGAAACGACACGC

>Rata-A5*01:01:02 ON411551

TGAGGTATTTCTACACCGCCGTGTCCCGGCCGGGCTCGGGGAGCCCCGCTTCATCACCGTCGGCTACGTGGACGACACGCAGTTCGTG
CGGTTTCGACAGCGACGCCCCGGATCCGAGGGTAGAACCGAGGGCGCTGTGGGTGGAGCAGGAGGGGCCCCGAGTATTGGGATCAGGA
GACTCAGAGAACCAGAGATACCGCACAGTTTTTCCGAATGAGCCTGAACACCTGCGCGGCTACTACAACCAGAGCGAGGCCGAGTCTC
ACACCTCCAGGAGATGTATGGCTGCGACGTGGGGCCGGACGGGCGTCTCCTCCGCGGGTATGACCAGTTCGCTACGACGGCAGAGA
TTACATCTCCCTGAATGAGGACCTGCGCTCCTGGACCGCGCGGAGACGGCGGCTCAGATCTCAAGCACAAATGCTGAGGCGGCCGGTG
ATGCGGCGCGTGTGAGGAACCTATCTGAGGGCAAGTGCGTGGAGTGGCTCCTCAGATACCTAGAGACAGGAAACGACACGC

>Rata-A5*01:02:01 ON411552

TGAGGTATTTCTACACCGCCGTGTCCCGGCCGGGCTCGGGGAGCCCCGCTTCATCACCGTCGGCTACGTGGACGACACGCAGTTCGTG
CGGTTTCGACAGCGACGCCCCGGATCCGAGGGTAGAACCGCGGGCGCTGTGGGTGGAGCAGGAGGGGCCCCGAGTATTGGGATCAGGA
GACTCAGAGAACCAGAGATACCGCACAGTTTTTCCGAATGAGCCTGAACACCTGCGCGGCTACTACAACCAGAGCGAGGCCGAGTCTC
ACACCTCCAGGAGATGTATGGCTGCGACGTGGGGCCGGACGGGCGTCTCCTCCGCGGGTATGACCAGTTCGCTACGACGGCAGAGA

TTACATCTCCCTGAATGAGGACCTGCGCTCCTGGACCGCGGCGGAGACGGCGGCTCAGATCTCCAAGCACAAATGCTGAGGCGGCCGGTG
 ATGCGGCGCGTGTGAGGAATCTGAGAGGCAAGTGCCTGGAGTGGCTCCGAGATACCTAGAGACAGGAAACGACACGC
 >Rata-A5*01:02:02 ON411553
 TGAGGTATTTCTACACCGCCGTGTCCCGGCCGGGCTCGGGGAGCCCCGCTTCATCACCGTCGGCTACGTGGACGACACGCAGTTCGTG
 CGGTTTCGACAGCGACGCCCCGGATCCGAGGGTAGAACCGCGGGCGCTGTGGGTGGAGCAGGAGGGGCCCCGAGTATTGGGATCAGGA
 GACTCAGAGAACCAGAGACACCGCACAGTTTTCCGAATGAGCCTGAACACCTGCGCGGCTACTACAACCAGAGCGAGGCCGAGTCTC
 ACACCTCCAGGAGATGTATGGCTGCGACGTGGGGCCGGACGGGCGTCTCCTCCGCGGGTATGACCAAGTTCGCTACGACGGCAGAGA
 TTACATCTCCCTGAATGAGGACCTGCGCTCCTGGACCGCGGCGGAGACGGCGGCTCAGATCTCCAAGCACAAATGCTGAGGCGGCCGGTG
 ATGCGGCGCGTGTGAGGAATCTGAGAGGCAAGTGCCTGGAGTGGCTCCGAGATACCTAGAGACAGGAAACGACACGC
 >Rata-A5-pseudogene with stop codon
 TGAGGTATTTCTACACCGCCGTGTCCCGGCCGGGCTCGGGGAGCCCCGCTTCATCACCGTCGGCTAAGTGGACGACACGCAGTTCGTG
 CGGTTTCGACAGCGACGCCCCGGATCCGAGGGTAGAACCGCGGGCGCTGTGGGTGGAGCAGGAGGGGCCCCGAGTATTGGGATCAGGA
 GACTCAGAGAACCAGAGATACCGCACAGTTTTCCGAATGAGCCTGAACACCTGCGCGGCTACTACAACCAGAGCGAGGCCGAGTCTC
 ACACCTCCAGGAGATGTATGGCTGCGACGTGGGGCCGGACGGGCGTCTCCTCCGCGGGTATGACCAAGTTCGCTACGACGGCAGAGA
 TTACATCTCCCTGAATGAGGACCTGCGCTCCTGGACCGCGGCGGAGACGGCGGCTCAGATCTCCAAGCACAAATGCTGAGGCGGCCGGTG
 ATGCGGCGCGTGTGAGGAATCTGAGAGGCAAGTGCCTGGAGTGGCTCCGAGATACCTAGAGACAGGAAACGACACGC

Deduced amino acids of expressed MHC I A1 allele sequences

>Rata-A1*02:01 ON411528
 TLLLLSGVLVLTETRAGSHSMRYFSTAVSRPGLGEPQFIVGVYDDTHFVRFDNDAPNPRMEPRARWVEQEGPEYWDDEETQKQKHAQTF
 RVSLNLRGYNNQSEAGSHTFQWMYGCDDVGPDRLLRGFDQFAYDGRDYALNEDLRSWTAADSAAQITKRKWEQGGE
 >Rata-A1*02:02 ON411529
 TLLLLSGVLVLTETRAGSHSMRYFSTAVSRPGLGEPQFIVGVYDDTHFVRFDNDAPNPRMEPRARWVEQEGPEYWDDEETQKQKHAQTFR
 VSLNLRGYNNQSEAGSHTFQWMYGCDDVGPDRLLRGFDQFAYDGRDYALNEDLRSWTAADSAAQITKRKWEQGGE
 >Rata-A1*02:03 ON411530
 TLLLLSGVLVLTETRAGSHSMRYFSTAVSRPGLGEPQFIVGVYDDTHFVRFDNDAPNPRMEPRARWVEQEGPEYWDDEETQKQKHAQTFR
 VSLNLRGYNNQSEAGSHTFQWMYGCDDVGPDRLLRGYQYAYDGRDYALNEDLRSWTAADSAAQITKRKWEQGGE
 >Rata-A1*03:01 ON411531
 TLLLLSGVLVLTETRAGSHSLRYFYTAVSRPGLGEPQFISVGIVDDTHFVRFDNDAPNPRMEPRARWVEQEGPEYWDQETQTLKHAQTFRV
 SLNLRGYNNQSEAGSHTLQWMYGCDDVGPDRLLRGFDQFAYDGRDYALNEDLRSWTAADSAAQISKRKFEQGGE
 >Rata-A1*04:01 ON411532
 TLLLLSGVLVLTETRAGSHSLRYFYTAVSRAGLGEPPQFIVGVYDDTHFVRFDNDAPNPRMEPRARWVEQEGPEYWDDEETQKLKDTAQFFRV
 GLNLRGYNNQSEAGSHTLQWMYGCDDVGPDRLLRGFDQFAYDGRDYALNEDLRSWTAADSAAQISKRKWEQGGE
 >Rata-A1*05:01 ON411533
 TLLLLSGVLVLTETRAGSHSLRYFYTAVSRAGLGEPPQFIVGVYDDTHFVRFDNDAPNPRMEPRARWVEQEGPEYWDDEETQKLKDTAQVFRV
 DLNLRGYNNQSEAGSHTLQWMYGCDDVGPDRLLRGFWQFAYDGRDYALNEDLRSWTAADSAAQITKRKWEQGGE
 >Rata-A1*06:01 ON411534
 TLLLLSGVLVLTETRAGSHSLRYFSTAVSRPGLGEPQFIVGVYDDTQFVRFDNDAPNPRMEPRARWVEQEGPEYWDQETQKQKGTAAQFFR
 VNLNLRGYNNQSEAGSHTLQWMYGCDDVGPDRLLRGYMQYAYDGRDYALNEDLRSWTAADSAAQISKRKFEQGGE
 >Rata-A1*07:01 ON411535
 TLLLLSGVLVLTETRAGSHSMRYFSTAVSRPGLGEPQFIVGVYDDTHFVRFDNDAPNPRMEPRARWVEQEGPEYWDRETQKQKDAQFFR
 VSLNLRGYNNQSEAGSHTLQWMYGCDDVGPDRLLRGFWQYAYDGRDYALNEDLRSWTAADSAAQISKRKFEQGGE
 >Rata-A1*08:01 ON411536
 TLLLLSGVLVLTETRAGSHSMRYFSTAVSRPGLGEPQFIVGVYDDTHFVRFDNDAPNPRMEPRARWVEQEGPEYWDDEETQKAKDAQFFR
 VNLNLRGYNNQSEAGSHTLQWMYGCDDVGPDRLLRGFWQYAYDGRDYALNEDLRSWTAADSAAQISKRKWEQGGE
 >Rata-A1*08:02 ON411537
 TLLLLSGVLVLTETRAGSHSMRYFSTAVSRPGLGEPQFIVGVYDDTHFVRFDNDAPNPRMEPRARWVEQEGPEYWDDEETQKAKDAQFFR
 VNLNLRGYNNQSEAGSHTLQWMHGCDDVGPDRLLRGFWQYAYDGRDYALNEDLRSWTAADSAAQISKRKWEQGGE
 >Rata-A1*08:03 ON411538
 TLLLLSGVLVLTETRAGSHSMRYFSTAVSRPGLGEPQFIVGVYDDTHFVRFDNDAPNPRMEPRARWVEQEGPEYWDDEETQKAKDAQFFR
 VNLNLRGYNNQSEAGSHTLQWMHGCDDVGPDRLLRGFWQYAYDGRDYALNEDLRSWTAADSAAQISKRKWEQGGE
 >Rata-A1*09:01 ON411539
 TLLLLSGVLVLTETRAGSHSMRYFSTAVSRPGLGEPQFIVGVYDDTQFVRFDSDAPNPRMEPRARWVEQEGPEYWDQETQKAKDAQFFR
 VSLNLRGYNNQSEAGSHTLQWMHGCDDVGPDRLLRGYVQFAYDGRDYALNEDLRSWTAADSAAQISKRKFEQGGE
 >Rata-A1*10:01 ON411540
 TLLLLSGVLVLTETRAGSHSMRYFSTAVSRPGLGEPQFIVGVYDDTQFVRFDSDAPNPRMEPRARWVEQEGPEYWDQETQKVKDAQFFR
 VGLNLRGYNNQSEAGSHTLQWMHGCDDVGPDRLLRGFWQFAYDGRDYALNEDLRSWTAADSAAQITKRKWEQGGE
 >Rata-A1*10:02 ON411541
 TLLLLSGVLVLTETRAGSHSMRYFSTAVSRPGLGEPQFIVGVYDDTQFVRFDSDAPNPRMEPRARWVEQEGPEYWDQETQKVKDAQFFR
 VGLNLRGYNNQSEAGSHTLQWMHGCDDVGPDRLLRGFDQFAYDGRDYALNEDLRSWTAADSAAQITKRKWEQGGE

>Rata-A1*11:01 ON411542

TLLLLSGVLVLTETRAGSHSLRYFSTAVSRPGLGEPQFISVGYVDDTQFVRFDSDAPNPREEPRARWVEQEGPEYWDEETQKAKDAAQVFRV
DLNLRGYYNQSEAGSHTLQEMYGCDVGPDRLLRGVQSAFYDGRDYIALNEDLRSWTAADAAQITKRKWEQGGE

>Rata-A1*11:02 ON411543

TLLLLSGVLVLTETRAGSHSMRYFSTAVSRPGLGEPQFISVGYVDDTQFVRFDSDAPNPREEPRARWVEQEGPEYWDEETQKAKDAAQVFRV
SLNLRGYYNQSEAGSHTLQEMYGCDVGPDRLLRGFWQSAFYDGRDYIALNEDLRSWTAADTAAQITKRKWEQGGE

>Rata-A1*12:01 ON411544

TLLLLSGVLVLTETRAGSHSMRYFYTGVSRLPGLGEPFISVGYVDDTQFVRFDSDAPNPREEPRAPWMEKEGPEYWDEETQKAKDAAQTFRV
SLNLRGYYNQSEAGSHTLQWMYGCDVGPDRLLRGFWQSAFYDGRDYIALNEDLRSWTAADSAAQITKRKWEQGGE

>Rata-A1*13:01 ON411545

TLLLLSGVLVLTETRAGSHSLRYFYTGVSRLPGLGEPFISVGYVDDTQFVRFDSDAPNPREEPRAPWMEEGPEYWDRNTRICKDTAQFFRESL
NLRGYYNQSEAGSHTLQWMYGCDVGPDRLLRGFDQSAFYDGRDYIALNEDLRSWTAADSAAQISKRFQEGGE

>Rata-A1*14:01:01 ON411546

TLLLLSGVLVLTETRAGSHSLRYFYTGVSRLPGLGEPFISVGYVDDTQFVRFDSDAPNPREEPRAPWMEKEGPEYWDRNTRIYKDTAQFFRESL
NNLRGYYNQSEAGSHTLQWMYGCDVGPDRLLRGFWQSAFYDGRDYIALNEDLRSWTAADSAAQISKRFQEGGE

>Rata-A1*14:01:02 ON411547

TLLLLSGVLVLTETRAGSHSLRYFYTGVSRLPGLGEPFISVGYVDDTQFVRFDSDAPNPREEPRAPWMEKEGPEYWDRNTRIYKDTAQFFRESL
NNLRGYYNQSEAGSHTLQWMYGCDVGPDRLLRGFWQSAFYDGRDYIALNEDLRSWTAADSAAQITKRKWEQGGE

>Rata-A1*14:01:03 ON411548

TLLLLSGVLVLTETRAGSHSLRYFYTGVSRLPGLGEPFISVGYVDDTQFVRFDSDAPNPREEPRAPWMEKEGPEYWDRNTRIYKDTAQFFRESL
NNLRGYYNQSEAGSHTLQWMYGCDVGPDRLLRGFWQSAFYDGRDYIALNEDLRSWTAADSAAQITKRKWEQGGE

>Rata-A1*14:02 ON411549

TLLLLSGVLVLTETRAGSHSLRYFYTGVSRLPGLGEPFISVGYVDDTQFVRFDSDAPNPREEPRAPWMEKEGPEYWDRNTRIYKDTAQFFRESL
NNLRGYYNQSEAGSHTLQWMYGCDVGPDRLLRGFDQSAFYDGRDYIALNEDLRSWTAADSAAQISKRFQEGGE

Rata-A1 sequences with nucleotide variation not affecting amino acid translation:

>Rata-A1*14:01:02

AACCCCTTCCTGCTCCTTCGCGGGTCTGCTGCTGACCGAGACCGGGCTGGTTCCCACTCCCTGAGGTATTTCTACACCGGCGTGTCC
CGGCCCGGCTCGGGGAGCCCGCTTCATCTCTGTCGGCTACGTGGACGACACGAGTTCGTGCGGTTGACAGCGACGCCCCGAATCC
GAGGGAAGAACCGAGGGCACCATGGATGGAGAAGGAGGGGCCGGAGTATTGGGATAGAAACACGAGAATCTACAAGGACACGGCAC
AGTTTTTCCGAGAGAGCCTGAACAATCTGCGCGGCTACTACAACAGAGCGAGGCCGGGTCTCACACCTCCAGTGGATGTACGGCTGC
GACGTGGGGCCCGACGGGCGCTCCTCCGCGGGTCTGGCAGTTCGCCTACGACGGCAGAGACTACATGGCCCTGAACGAGGACCTGC
GCTCCTGGACCGCGGCGGACTCGGCGGCTCAGATACCAAGCGCAAGTGGGAGCAAGGCGGTGAGG

>Rata-A1*14:01:03

AACCCCTTCCTGCTCCTTCGCGGGTCTGCTGCTGACCGAGACCGGGCTGGTTCCCACTCCCTGAGGTATTTCTACACCGGCGTGTCC
CGGCCCGGCTCGGGGAGCCCGCTTCATCTCTGTCGGCTACGTGGACGACACGAGTTCGTGCGGTTGACAGCGACGCCCCGAATCC
GAGGGAAGAACCGAGGGCACCATGGATGGAGAAGGAGGGGCCGGAGTATTGGGATAGAAACACGAGAATCTACAAGGACACGGCAC
AGTTTTTCCGAGAGAGCCTGAACAATCTGCGCGGCTACTACAACAGAGCGAGGCCGGGTCTCACACCTCCAGTGGATGTACGGCTGC
GACGTGGGGCCCGACGGGCGCTCCTCCGCGGGTCTGGCAGTTCGCCTACGACGGCAGAGACTACATGGCCCTGAACGAGGACCTGC
GCTCCTGGACCGCGGCGGACTCGGCGGCTCAGATAACCAAGCGCAAGTGGGAGCAAGGCGGTGAGG

Alignment of expressed deduced MHC class I amino acid sequences of A1 and A5 alleles

Yellow shading shows location of primers. Individual domain are shown. Abbreviations are CP= connecting peptide, TM= transmembrane domain, CYT= cytoplasmic domain. Numbering according to top sequence. Residues are colour coded according to physiochemical properties. Yellow or green shading shows location of primers.

	Leader sequence	Alpha 1 domain	
	*	20	*
			40
			*
			60
Granti A1	: ---MCPRTLLLLLSGVLVLTE	TRA GSHSLRYFYTAVSRPGLGEPRFISVGYYDDTQFVRFDS	DAPNPR : 65
Caribou-A1	: -----	: 44
Rata-A1*02:01	: -----S.....Q..V.....H.....N.....	: 61
Rata-A1*02:02	: -----S.....Q..V.....H.....N.....	: 61
Rata-A1*02:03	: -----S.....Q..V.....H.....N.....	: 61
Rata-A1*03:01	: -----Q.....H.....N.....	: 61
Rata-A1*04:01	: -----A.....Q..V.....H.....N.....	: 61
Rata-A1*05:01	: -----A.....Q..V.....H.....N.....	: 61
Rata-A1*06:01	: -----S.....Q..V.....N.....	: 61
Rata-A1*07:01	: -----S.....Q..V.....H.....N.....	: 61
Rata-A1*08:01	: -----S.....Q..V.....H.....N.....	: 61
Rata-A1*08:02	: -----S.....Q..V.....H.....N.....	: 61
Rata-A1*08:03	: -----S.....Q..V.....H.....N.....	: 61
Rata-A1*09:01	: -----S.....Q..A.....	: 61
Rata-A1*10:01	: -----S.....Q..A.....	: 61
Rata-A1*10:02	: -----S.....Q..A.....	: 61
Rata-A1*11:01	: -----S.....Q.....	: 61
Rata-A1*11:02	: -----S.....Q.....	: 61
Rata-A1*12:01	: -----G.....	: 61
Rata-A1*13:01	: -----G.....	: 61
Rata-A1*14:01:1	: -----G.....	: 61
Rata-A1*14:01:2	: -----G.....	: 61
Rata-A1*14:01:3	: -----G.....	: 61
Rata-A1*14:02	: -----G.....	: 61
Granti A5	: MRV.GL-RA.....A.....W.....		: 67
Tarandus_A5	: MRV.GL-RA.....A.....W.....		: 67
Caribou A5	: MRV.GL-RA.....A.....W.....		: 67
Rata-A5*01:01:1	: -----	-----	: 39
Rata-A5*01:01:2	: -----	-----	: 39
Rata-A5*01:02:1	: -----	-----	: 39
Rata-A5*01:02:2	: -----	-----	: 39
		Alpha 2 domain	
	*	80	*
			100
			*
			120
			*
Granti A1	: EEPRAPWMEKEGPEYWDNRNTRICKDTAQVFRESLNNLRGYYNQSEA	GSHTLQEMYGCDVGPDRLLRG	: 133
Caribou-A1	:	: 112
Rata-A1*02:01	: M...R...Q.....EE.QKQ.GH..T..V.....F.W.....		: 129
Rata-A1*02:02	: M...R...Q.....EE..KQ.GN..T..V.....F.W.....		: 129
Rata-A1*02:03	: M...R...Q.....EE.QKQ.GH..T..V.....F.W.....		: 129
Rata-A1*03:01	: M...R...Q.....QE.QTL.GH..T..V.....W.V.....		: 129
Rata-A1*04:01	: M...R...Q.....EE.QKL.....F..VG..T.....W...H.....		: 129
Rata-A1*05:01	: M...R...Q.....EE.QKL.....VD..T.....W.....		: 129
Rata-A1*06:01	: M...R...Q.....QE.QKQ.G..F..VN..T.....W.....		: 129
Rata-A1*07:01	: M...R...Q.....E.QKQ..A..F..V.....W.....		: 129
Rata-A1*08:01	: M...R...Q.....EE.QKA..A..F..VN..T.....W.....		: 129
Rata-A1*08:02	: M...R...Q.....EE.QKA..A..F..VN..T.....W.H.....		: 129
Rata-A1*08:03	: M...R...Q.....EE.QKA..A..F..VN..T.....W.N.....		: 129
Rata-A1*09:01	: M...R...Q.....QE.QKA..A..F..V.....W.H.....W.....		: 129
Rata-A1*10:01	: M...R...Q.....QE.QKV..A..F..VG..T.....W.H.....		: 129
Rata-A1*10:02	: M...R...Q.....QE.QKV..A..F..VG..T.....W.H.....		: 129
Rata-A1*11:01	: ...R...Q.....EE.QKA..A.....VD..T.....		: 129
Rata-A1*11:02	: ...R...Q.....EE.QKA..A.....V..T.....		: 129
Rata-A1*12:01	:EE.QKA..A..T..V.....F.W.....		: 129
Rata-A1*13:01	:F.....T.....F.W.....		: 128
Rata-A1*14:01:1	:Y.....F.....W.....		: 129
Rata-A1*14:01:2	:Y.....F.....W.....		: 129
Rata-A1*14:01:3	:Y.....F.....W.....		: 129
Rata-A1*14:02	:Y.....F.....W.V.....		: 129
Granti A5	: V...L...Q.....QE.QRT...F..M...T.....E.....		: 135
Tarandus_A5	: V...L...Q.....QE.QRT...F..M...T.....E.....		: 135
Caribou A5	: V...L...Q.....QE.QRT...F..M...T.....E.....		: 135
Rata-A5*01:01:1	: V...L...Q.....QE.QRT...F..M...T.....E.....		: 107
Rata-A5*01:01:2	: V...L...Q.....QE.QRT...F..M...T.....E.....		: 107
Rata-A5*01:02:1	: V...L...Q.....QE.QRT...F..M...T.....E.....		: 107
Rata-A5*01:02:2	: V...L...Q.....QE.QRT...F..M...T.....E.....		: 107

	140	*	160	*	180	*	200	
Granti_A1	: YVQYAYDGRDYMALNEDLRSWTAADSAAQISKRKFEQGGGE-ADHSRNYLEGRVCVEGLHRYLENGKDAL	:	200					
Caribou-A1	:	:	179					
Rata-A1*02:01	: .D.....	:	169					
Rata-A1*02:02	: .D.....	:	169					
Rata-A1*02:03	: .G.....	:	169					
Rata-A1*03:01	: .D.....	:	169					
Rata-A1*04:01	: .D.....	:	169					
Rata-A1*05:01	: .W.....	:	169					
Rata-A1*06:01	:	:	169					
Rata-A1*07:01	: .W.....	:	169					
Rata-A1*08:01	: .W.....	:	169					
Rata-A1*08:02	: .W.....	:	169					
Rata-A1*08:03	: .W.....	:	169					
Rata-A1*09:01	:	:	169					
Rata-A1*10:01	: .W.....	:	169					
Rata-A1*10:02	: .D.....	:	169					
Rata-A1*11:01	: ...S.....A.....	:	169					
Rata-A1*11:02	: .W.S.....	:	169					
Rata-A1*12:01	: .D.....	:	169					
Rata-A1*13:01	: .D.S.....	:	168					
Rata-A1*14:01:1	: .W.....	:	169					
Rata-A1*14:01:2	: .W.....	:	169					
Rata-A1*14:01:3	: .W.....	:	169					
Rata-A1*14:02	: .D.....	:	169					
Granti_A5	: .D.....S.....E.....HNA.AA.D-ARV.....W.L...T.N...	:	202					
Tarandus_A5	: .D.....S.....E.....HNA.AA.D-ARV.....W.L...T.N.T.	:	202					
Caribou_A5	: .D.....S.....E.....HNA.AA.D-ARV.....W.R...T.N.T.	:	202					
Rata-A5*01:01:1	: .D.....S.....E.....HNA.AA.D-ARV.....W.L...T.N.T-	:	173					
Rata-A5*01:01:2	: .D.....S.....E.....HNA.AA.D-ARV.....W.L...T.N.T-	:	173					
Rata-A5*01:02:1	: .D.....S.....E.....HNA.AA.D-ARV.....W.R...T.N.T-	:	173					
Rata-A5*01:02:2	: .D.....S.....E.....HNA.AA.D-ARV.....W.R...T.N.T-	:	173					
Alpha 3 domain								
	*	220	*	240	*	260		
Granti_A1	: LRA GPPKAHVIRHPISDCEVTLRCWALGFYFEEISLTWQHSGEDQTQDMELVETRPSGDGTFFQKWVAL	:	268					
Caribou-A1	: ...EITQDME.VETRPBGDG.FQK.VALLV.G.....	:	247					
Granti_A5	: ...D.....NH.....R.....D.....RD.....A.....	:	270					
Tarandus_A5	: ...D.....NH.....R.....D.....RD.....A.....	:	270					
Caribou_A5	: ...D.....NH.....R.....D.....RD.....A.....	:	270					
CP/ TM/ CYT								
	*	280	*	300	*	320	*	
Granti_A1	: VVPSGEEQKYTCHVQHEGLQEPPLTLRW EPPQTSFLTVGIIIVGLVLLMV--ALVAGAVIWRKKHSGEKG	:	334					
Caribou-A1	:R.....P.....	:	306					
Granti_A5	: ...L.....P.V.I.....N-G...I.....R.....	:	337					
Tarandus_A5	: ...L.....P.V.I.....N-G...I.....R.....	:	337					
Caribou_A5	: ...L.....P.V.I.....N-G...I.....R.....	:	333					
	340	*						
Granti_A1	: RIYTQAASSDSAQSSDVSLTVPK-----	:	357					
Caribou-A1	: -----	:	-					
Granti_A5	: .T.....D...E.....	:	360					
Tarandus_A5	: .T.....D...E.....	:	360					

MHCI A1 allele frequencies in the three reindeer populations

A1 allele	SemiD N=62	Wild N=18	Svalbard N=9	Total number of alleles
A1*02:01:01	0.06 (7)	0.11 (4)		11
A1*02:02:01	0.04 (5)	0.03 (1)		6
A1*02:03:01	0.01 (1)	0.06 (2)		3
A1*03:01:01	0.02 (2)			2
A1*04:01:01		0.06 (2)		2
A1*05:01:01	0.07 (9)	0.11 (4)		13
A1*06:01:01	0.19 (24)	0.06 (2)		26
A1*07:01:01	0.06 (7)	0.28 (10)		17
A1*08:01:01	0.07 (9)	0.03 (1)		10
A1*08:02:01	0.06 (7)	0.03 (1)		8
A1*08:03:01		0.11 (4)		4
A1*09:01:01	0.01 (1)	0.06 (2)		3
A1*10:01:01	0.05 (6)			6
A1*10:02:01			0.94 (17)	17
A1*11:01:01			0.06 (1)	1
A1*11:02:01	0.02 (3)	0.03 (1)		4
A1*12:01:01	0.06 (8)			8
A1*13:01:01	0.06 (8)	0.06 (2)		10
A1*14:01:01	0.04 (5)			5
A1*14:01:02	0.13 (16)			16
A1*14:01:03	0.01 (1)			1
A1*14:02	0.04 (5)			5
No.alleles (22)	18	13	2	

N refers to the number of animals sampled per population and SemiD is semi-domesticated.

Number of **each given allele** is shown in parenthesis **while total number of alleles summarizes across populations.**

6. Phylogenetic tree of deduced DRB1 sequences

Phylogenetic tree of deduced reindeer DRB beta 1 domain amino acid sequences from NCBI as well as from this study. Rata sequences shown in red font originate from this study. Sequences shown with green shading originate from Mikko et al.(1999) and Taylor et al.(2012). All QCU sequences originate from Gagnon et al.(2020). Caribou, Tarandus and Granti sequences are genomic sequences from this study while the remaining sequences are unpublished. See main text for references. The evolutionary history was inferred using the Neighbor-Joining method (Saitou and Nei 1987). The optimal tree with the sum of branch length = 2.16665847 is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches (Felsenstein 1985). The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Poisson correction method (Zuckerandl and Pauling 1965) and are in the units of the number of amino acid substitutions per site. The analysis involved 73 amino acid sequences. All ambiguous positions were removed for each sequence pair. There were a total of 85 positions in the final dataset. Evolutionary analyses were conducted in MEGA7 (Kumar *et al.*, 2016).

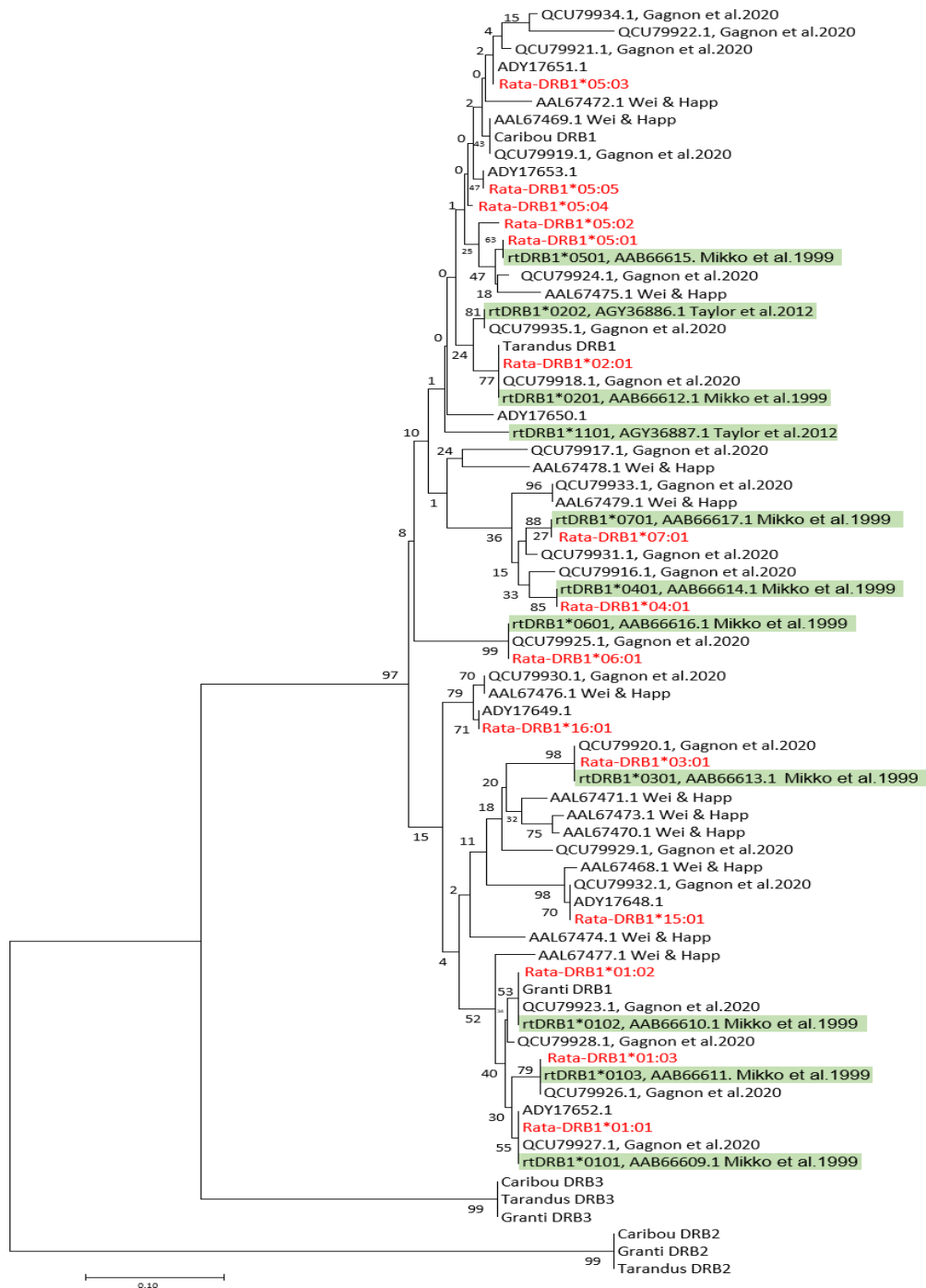
Other References:

Saitou N. and Nei M. (1987). The neighbor-joining method: A new method for reconstructing phylogenetic trees. *Molecular Biology and Evolution* 4:406-425.

Felsenstein J. (1985). Confidence limits on phylogenies: An approach using the bootstrap. *Evolution* 39:783-791.

Zuckerandl E. and Pauling L. (1965). Evolutionary divergence and convergence in proteins. Edited in *Evolving Genes and Proteins* by V. Bryson and H.J. Vogel, pp. 97-166. Academic Press, New York.

Kumar S., Stecher G., and Tamura K. (2016). MEGA7: Molecular Evolutionary Genetics Analysis version 7.0 for bigger datasets. *Molecular Biology and Evolution* 33:1870-1874.



7. MHC I and II haplotype test

Test of DRB-A1-A5 haplotypes was performed using the online tool SHEsis [[Analysis tool for random samples, by YongYong Shi. \(bio-x.cn\)](#); Shi YY, He L. SHEsis, a powerful software platform for analyses of linkage disequilibrium, haplotype construction, and genetic association at polymorphism loci. Cell Res. 2005 Feb;15(2):97-8. doi: 10.1038/sj.cr.7290272. PMID: 15740637]. Haplotype frequencies, chi-square test and Fisher exact test values for each of the significantly detected haplotypes are shown below. For the mainland animals, including both wild and semi-domesticated populations, of the folur discernible haplotypes, the *DRB1*040101* allele segregates with three different A1 alleles exemplifying the lack of stable haplotypes in our

material.

Mainland animal haplotypes:

*DRB1*010201- A1*140102- A5*010101*, frequency=0.049, chi2=5.559, Fisher test P-value=0.018428

*DRB1*040101- A1*020101- A5*010101*, frequency=0.050, chi2=5.709, Fisher test P-value=0.016911

*DRB1*040101- A1*050101- A5*010201*, frequency=0.047, chi2=5.339, Fisher test P-value=0.020898

*DRB1*040101- A1*060101- A5*010201*, frequency=0.043, chi2=4.754, Fisher test P-value=0.029280

Svalbard haplotypes:

*DRB1*010301- A1*110101- A5*010201*, frequency=0.056, chi2=1.715, Fisher test P-value=0.190351

*DRB1*060101- A1*100201- A5*010201*, frequency=0.944, chi2=44.098, Fisher test P-value=3.45e-011

8. MHC alleles per individual reindeer

Pop.	ID	DRB1 # 1	DRB1 a# 2	DQB # 1	DQB # 2	A1 # 1	A1 # 2	A5 # 1	A5 # 2
1	RaTa1	DRB1*07:01	DRB1*01:02	DQB2*02	DQB2*05	A1*12:01	A1*14:01:02	A5*01:01:01	A5*01:02:01
1	RaTa4	DRB1*04:01	Homo	DQB2*02	Homo	A1*08:01	A1*10:01	A5*01:02:01	Homo
1	RaTa5	DRB1*01:02	DRB1*05:05	DQB2*05	DQB3*05	A1*06:01	A1*07:01	A5*01:01:01	Homo
1	RaTa6	DRB1*04:01	DRB1*02:01	DQB4*03	DQB2*02	A1*06:01	Homo	A5*01:01:01	A5*01:02:01
1	RaTa7	DRB1*04:01	Homo	DQB2*02	Homo	A1*06:01	Homo	A5*01:02:01	A5*pseudo
1	RaTa8	DRB1*04:01	DRB1*01:02	DQB2*02	DQB2*05	A1*05:01	A1*14:01:02	A5*01:01:01	A5*01:02:01
1	RaTa9	DRB1*02:01	Homo	DQB4*03	Homo	A1*06:01	Homo	A5*01:01:01	Homo
1	RaTa10	DRB1*02:01	DRB1*01:02	DQB4*03	DQB2*04	A1*02:02	Homo	A5*01:01:01	Homo
1	RaTa11	DRB1*02:01	DRB1*15:01	DQB4*03	DQB4*01	A1*08:01	A1*08:02	A5*01:02:01	Homo
1	RaTa12	DRB1*04:01	DRB1*01:02	DQB2*02	Homo	A1*14:01:02	Homo	A5*01:01:01	A5*01:02:01
1	RaTa13	DRB1*02:01	DRB1*01:02	DQB4*03	DQB2*02	A1*02:02	Homo	A5*01:01:01	A5*01:02:01
1	RaTa14	DRB1*04:01	Homo	DQB2*02	Homo	A1*06:01	Homo	A5*01:01:01	A5*01:02:01
1	RaTa16	DRB1*01:01	DRB1*05:03	DQB4*02	DQB2*04	A1*06:01	Homo	A5*01:02:01	Homo
1	RaTa17	DRB1*02:01	Homo	DQB4*03	Homo	A1*02:02	A1*14:01:02	A5*01:01:01	A5*01:02:01
1	RaTa18	DRB1*04:01	Homo	DQB2*02	Homo	A1*02:01	Homo	A5*01:01:01	Homo
1	RaTa19	DRB1*04:01	Homo	DQB2*02	Homo	A1*05:01	Homo	A5*01:02:01	Homo
1	RaTa20	DRB1*04:01	DRB1*15:01	DQB4*01	DQB2*02	A1*14:01:01	Homo	A5*01:01:01	A5*01:02:01
1	RaTa21	DRB1*04:01	DRB1*01:02	DQB2*02	Homo	A1*14:01:02	A1*14:01:03	A5*01:01:01	A5*01:02:01
1	RaTa22	DRB1*04:01	DRB1*03:01	DQB4*01	DQB2*02	A1*08:01	A1*14:01:02	A5*01:01:01	A5*01:02:01
1	RaTa23	DRB1*05:05	DRB1*01:02	DQB2*02	DQB3*05	A1*03:01	Homo	A5*01:01:01	A5*01:02:01
1	RaTa24	DRB1*04:01	DRB1*03:01	DQB4*03	DQB2*02	A1*05:01	A1*10:01	A5*01:02:01	Homo
1	RaTa25	DRB1*04:01	DRB1*01:02	DQB2*02	DQB2*05	A1*14:01:01	Homo	A5*01:01:01	A5*01:02:01
1	RaTa26	DRB1*02:01	DRB1*15:01	DQB4*03	DQB4*01	A1*08:02	A1*10:01	A5*01:02:01	Homo
1	RaTa27	DRB1*02:01	DRB1*15:01	DQB4*01	DQB4*03	A1*05:01	A1*08:01	A5*01:02:01	Homo
1	RaTa29	DRB1*02:01	DRB1*04:01	DQB2*02	DQB4*03	A1*05:01	A1*08:02	A5*01:02:01	Homo
1	RaTa30	DRB1*02:01	DRB1*04:01	DQB2*02	DQB4*03	A1*05:01	A1*10:01	A5*01:02:01	Homo
1	RaTa31	DRB1*02:01	DRB1*01:02	DQB2*02	DQB4*03	A1*06:01	Homo	A5*01:02:01	Homo
1	RaTa32	DRB1*04:01	Homo	DQB2*02	Homo	A1*06:01	A1*09:01	A5*01:02:01	Homo
1	RaTa33	DRB1*04:01	DRB1*02:01	DQB2*02	DQB4*03	A1*11:02	Homo	A5*01:02:01	A5*pseudo
1	RaTa51	DRB1*15:01	DRB1*16:01	DQB4*01	DQB2*04	A1*13:01	Homo	A5*01:01:01	A5*01:02:01
1	RaTa52	DRB1*04:01	DRB1*01:01	DQB2*03	DQB2*02	A1*13:01	Homo	A5*01:01:01	A5*01:02:01
1	RaTa53	DRB1*07:01	DRB1*15:01	DQB2*02	DQB4*01	A1*05:01	A1*12:01	A5*01:01:01	A5*01:02:01
1	RaTa54	DRB1*04:01	DRB1*15:01	DQB2*02	DQB4*01	A1*08:01	A1*14:01:02	A5*01:01:01	A5*01:02:01

1	RaTa55	DRB1*04:01	Homo	DQB2*02	Homo	A1*06:01	A1*14:01:01	A5*01:01:01	Homo
1	RaTa56	DRB1*03:01	DRB1*01:02	DQB2*02	DQB4*01	A1*08:01	A1*12:01	A5*01:01:01	A5*01:02:01
1	RaTa57	DRB1*07:01	DRB1*01:02	DQB2*02	Homo	A1*14:01:02	Homo	A5*01:01:01	Homo
1	RaTa58	DRB1*04:01	Homo	DQB2*02	Homo	A1*08:02	Homo	A5*01:02:01	Homo
1	RaTa59	DRB1*04:01	DRB1*01:01	DQB2*03	DQB2*04	A1*13:01	Homo	A5*01:01:01	Homo
1	RaTa60	DRB1*01:02	Homo	DQB2*02	Homo	A1*06:01	Homo	A5*01:01:01	Homo
1	RaTa61	DRB1*04:01	DRB1*01:02	DQB2*02	DQB2*05	A1*02:01	A1*14:01:02	A5*01:01:01	Homo
1	RaTa62	DRB1*04:01	Homo	DQB2*02	Homo	A1*02:01	A1*12:01	A5*01:01:01	Homo
1	RaTa63	DRB1*04:01	DRB1*16:01	DQB2*02	DQB2*04	A1*08:01	Homo	A5*01:01:01	A5*01:02:01
1	RaTa64	DRB1*03:01	DRB1*15:01	DQB4*01	Homo	A1*12:01	A1*14:01:02	A5*01:01:01	A5*01:02:01
1	RaTa65	DRB1*04:01	DRB1*07:01	DQB2*02	Homo	A1*02:01	Homo	A5*01:01:01	Homo
1	RaTa66	DRB1*01:02	Homo	DQB2*02	DQB2*05	A1*14:01:02	Homo	A5*01:01:01	Homo
1	RaTa67	DRB1*07:01	DRB1*05:01	DQB2*02	DQB3*05	A1*14:02	Homo	A5*01:02:01	Homo
1	RaTa68	DRB1*02:01	DRB1*01:02	DQB2*02	DQB4*03	A1*06:01	Homo	A5*01:02:01	A5*pseudo
1	RaTa69	DRB1*04:01	Homo	DQB2*02	Homo	A1*02:01	A1*14:01:02	A5*01:01:01	Homo
1	RaTa70	DRB1*04:01	DRB1*07:01	DQB2*02	Homo	A1*10:01	A1*14:01:02	A5*01:02:01	Homo
1	RaTa71	DRB1*04:01	Homo	DQB2*02	Homo	A1*06:01	A1*14:02	A5*01:01:01	A5*01:02:01
1	RaTa72	DRB1*07:01	DRB1*04:01	DQB2*02	DQB2*05	A1*05:01	A1*11:02	A5*01:02:01	A5*pseudo
1	RaTa73	DRB1*05:02	DRB1*04:01	DQB2*02	DQB3*04	A1*06:01	Homo	A5*01:02:01	Homo
1	RaTa74	DRB1*04:01	Homo	DQB2*02	Homo	A1*07:01	Homo	A5*01:02:01	Homo
1	RaTa75	DRB1*07:01	DRB1*15:01	DQB2*02	DQB4*01	A1*13:01	Homo	A5*01:01:01	A5*01:02:01
1	RaTa76	DRB1*04:01	Homo	DQB2*02	Homo	A1*02:03	A1*10:01	A5*01:02:01	Homo
1	RaTa77	DRB1*04:01	DRB1*15:01	DQB2*02	DQB4*01	A1*08:01	A1*12:01	A5*01:02:01	Homo
1	RaTa78	DRB1*07:01	DRB1*04:01	DQB2*02	Homo	A1*08:02	Homo	A5*01:01:01	A5*01:02:01
1	RaTa79	DRB1*05:01	DRB1*04:01	DQB2*02	DQB3*05	A1*06:01	Homo	A5*01:02:01	Homo
1	RaTa80	DRB1*04:01	DRB1*03:01	DQB2*02	DQB4*03	A1*07:01	Homo	A5*01:01:01	A5*01:02:01
1	RaTa81	DRB1*02:01	DRB1*16:01	DQB4*03	DQB2*04	A1*14:02	Homo	A5*01:01:01	A5*01:02:01
1	RaTa82	DRB1*05:01	DRB1*02:01	DQB3*05	DQB4*03	A1*12:01	Homo	A5*01:02:01	A5*01:01:02
1	RaTa89	DRB1*04:01	DRB1*16:01	DQB2*04	DQB2*02	A1*07:01	Homo	A5*01:01:01	Homo
2	V0279	DRB1*04:01	DRB1*02:01	DQB2*02	DQB4*03	A1*05:01	A1*08:03	A5*01:01:01	A5*01:02:01
2	V0281	DRB1*04:01	DRB1*02:01	DQB2*02	DQB4*03	A1*05:01	Homo	A5*01:02:01	Homo
2	V0282	DRB1*04:01	DRB1*03:01	DQB2*02	DQB2*04	A1*07:01	Homo	A5*01:02:01	Homo
2	V0283	DRB1*04:01	Homo	DQB2*02	Homo	A1*08:01	A1*08:02	A5*01:02:01	Homo
2	V0285	DRB1*04:01	DRB1*02:01	DQB2*02	DQB4*03	A1*07:01	Homo	A5*01:01:01	A5*01:02:01
2	V0286	DRB1*02:01	DRB1*05:04	DQB3*03	DQB4*03	A1*07:01	Homo	A5*01:01:01	A5*pseudo
2	V0287	DRB1*03:01	Homo	DQB4*03	Homo	A1*07:01	Homo	A5*01:01:01	A5*01:02:01
2	V0288	DRB1*07:01	DRB1*02:01	DQB2*02	DQB4*03	A1*06:01	Homo	A5*01:01:01	Homo
2	V0290	DRB1*04:01	Homo	DQB2*02	Homo	A1*02:01	Homo	A5*01:01:01	Homo
2	V0291	DRB1*01:01	DRB1*05:05	DQB3*05	DQB2*04	A1*05:01	A1*08:03	A5*01:02:01	Homo
2	V0292	DRB1*01:01	DRB1*03:01	DQB2*03	DQB4*01	A1*04:01	A1*02:01	A5*01:02:01	A5*01:02:02
2	V0296	DRB1*02:01	Homo	DQB4*03	Homo	A1*08:03	A1*11:02	A5*01:01:01	A5*pseudo
2	V0297	DRB1*01:01	Homo	DQB2*03	Homo	A1*07:01	Homo	A5*01:02:01	A5*01:02:02
2	V0298	DRB1*01:01	DRB1*05:02	DQB2*03	DQB2*04	A1*02:01	A1*04:01	A5*01:02:01	A5*01:02:02
2	V0299	DRB1*01:02	DRB1*03:01	DQB2*02	DQB4*03	A1*02:03	Homo	A5*01:02:01	Homo
2	V0300	DRB1*07:01	DRB1*03:01	DQB2*02	DQB3*03	A1*13:01	Homo	A5*01:01:01	A5*01:02:01
2	V0301	DRB1*05:02	DRB1*03:01	DQB2*04	Homo	A1*08:03	A1*02:02	A5*01:01:01	A5*01:02:01

2	V0302	DRB1*07:01	DRB1*02:01	DQB2*02	DQB4*03	A1*09:01	Homo	A5*01:01:01	Homo
3	Svalb1	DRB1*06:01	Homo	DQB3*02	Homo	A1*10:02	Homo	A5*01:02:01	Homo
3	Svalb2	DRB1*06:01	Homo	DQB3*02	Homo	A1*10:02	Homo	A5*01:02:01	Homo
3	Svalb3	DRB1*06:01	Homo	DQB3*02	Homo	A1*10:02	Homo	A5*01:02:01	Homo
3	Svalb4	DRB1*06:01	Homo	DQB3*02	Homo	A1*10:02	Homo	A5*01:02:01	Homo
3	Svalb9	DRB1*06:01	DRB1*01:03	DQB3*02	Homo	A1*10:02	A1*11:01	A5*01:02:01	Homo
3	Svalb10	DRB1*06:01	Homo	DQB3*02	Homo	A1*10:02	Homo	A5*01:02:01	Homo
3	Svalb11	DRB1*06:01	Homo	DQB3*02	Homo	A1*10:02	Homo	A5*01:02:01	Homo
3	Svalb12	DRB1*06:01	Homo	DQB3*02	Homo	A1*10:02	Homo	A5*01:02:01	Homo
3	Svalb13	DRB1*06:01	Homo	0**	0**	A1*10:02	Homo	A5*01:02:01	Homo

*Population 1 includes semi-domesticated reindeer sampled from two herds located in close proximity in the Northern parts of Norway. Population 2 includes wild reindeer sampled on Hardangervidda in Southern parts of Norway where both Population 1 and 2 are *Rangifer tarandus tarandus*. Population 3 includes *Rangifer tarandus platyrhynchus* animals sampled on the archipelago Svalbard.

** No sequences were amplified for this primer pair in the Svalbard animal 13 (Svalb13).