SUPPLEMENTARY FIGURE LEGENDS

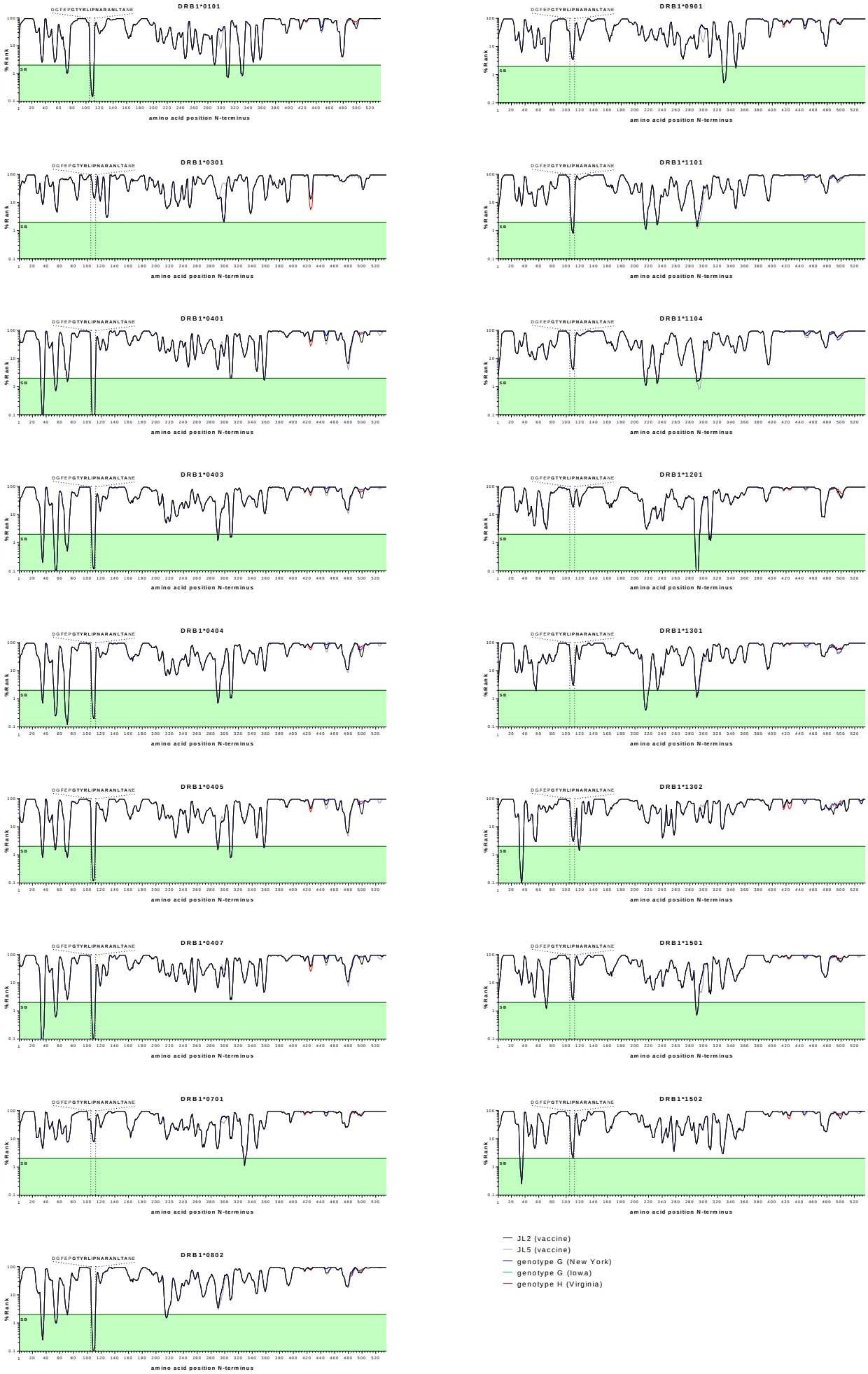
Figure S1. *In silico* prediction of peptide binding to most abundant HLA-DR alleles.

The pan-specific prediction method NETMHCIIpan3.2 was used to *in silico* determine binding sites within MuV-N for HLA-DR alleles that are most abundant among the Caucasian population. Shown is per HLA-DR allele the % Rank per tested 15-mer. Positions of peptide sequences considered strong binders, with a % Rank < 2, are recognized as intersecting the green cut-off zone.

Figure S2. Alignment of MuV-N amino acid sequences of various mumps strains.

Blue boxes indicate differences between MuV strains. Vaccine strains: JL2, Jeryl Lynn 2; JL5, Jeryl Lynn 5 (vaccine strains). Recent outbreak strains: genG_NY, genotype G NewYork strain; genG_Iowa, genotype G Iowa strain; genH, genotype H strain. The conserved MuV-$NP_{110\text{-}124}$ MuTER.1 epitope sequence GTYRLIPNARANLTA is indicated in red.

Figure S1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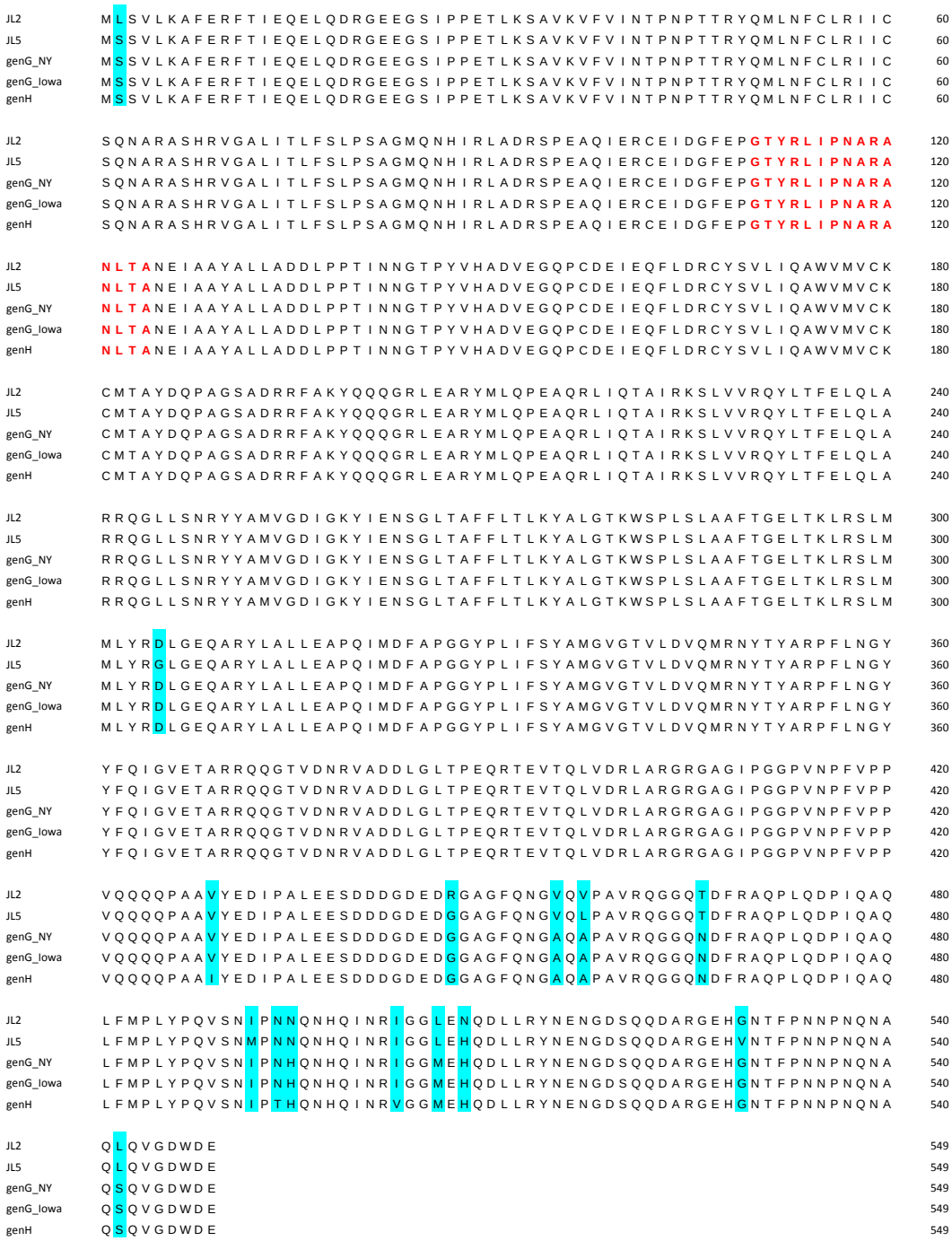
DRB1*0901
DRB1*0301
DRB1*1101
DRB1*0401
DRB1*1104
DRB1*0403
DRB1*1201
DRB1*0404
DRB1*1301
DRB1*0405
DRB1*1302
DRB1*0407
DRB1*1501
DRB1*0701
DRB1*1502
DRB1*0802
DGFEPGTYRLIPNARANLTANE
%Rank
SB
amino acid position N-terminus
JL2 (vaccine)
JL5 (vaccine)
genotype G (New York)
genotype G (Iowa)
genotype H (Virginia)

Figure S2


JL2 MLSVLKAFERFTIEQELQDRGEEGSIPPETLKSAVKVFVINTPNPTTRYQMLNFCLRIIC 60
JL5 MSSVLKAFERFTIEQELQDRGEEGSIPPETLKSAVKVFVINTPNPTTRYQMLNFCLRIIC 60
genG_NY MSSVLKAFERFTIEQELQDRGEEGSIPPETLKSAVKVFVINTPNPTTRYQMLNFCLRIIC 60
genG_Iowa MSSVLKAFERFTIEQELQDRGEEGSIPPETLKSAVKVFVINTPNPTTRYQMLNFCLRIIC 60
genH MSSVLKAFERFTIEQELQDRGEEGSIPPETLKSAVKVFVINTPNPTTRYQMLNFCLRIIC 60
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JL5 SQNARASHRVGALITLFSLPSAGMQNHIRLADRSPEAQIERCEIDGFEPGTYRLIPNARA 120
genG_NY SQNARASHRVGALITLFSLPSAGMQNHIRLADRSPEAQIERCEIDGFEPGTYRLIPNARA 120
genG_Iowa SQNARASHRVGALITLFSLPSAGMQNHIRLADRSPEAQIERCEIDGFEPGTYRLIPNARA 120
genH SQNARASHRVGALITLFSLPSAGMQNHIRLADRSPEAQIERCEIDGFEPGTYRLIPNARA 120
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JL5 NLTANEIAAYALLADDLPPTINNGTPYVHADVEGQPCDEIEQFLDRCYSVLIQAWVMVCK 180
genG_NY NLTANEIAAYALLADDLPPTINNGTPYVHADVEGQPCDEIEQFLDRCYSVLIQAWVMVCK 180
genG_Iowa NLTANEIAAYALLADDLPPTINNGTPYVHADVEGQPCDEIEQFLDRCYSVLIQAWVMVCK 180
genH NLTANEIAAYALLADDLPPTINNGTPYVHADVEGQPCDEIEQFLDRCYSVLIQAWVMVCK 180
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genG_Iowa CMTAYDQPAGSADRRFAKYQQQGRLEARYMLQPEAQRLIQTAIRKSLVVRQYLTFELQLA 240
genH CMTAYDQPAGSADRRFAKYQQQGRLEARYMLQPEAQRLIQTAIRKSLVVRQYLTFELQLA 240
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JL5 RRQGLLSNRYYAMVGDIGKYIENSGLTAFFLTLKYALGTKWSPLSLAAFTGELTKLRSLM 300
genG_NY RRQGLLSNRYYAMVGDIGKYIENSGLTAFFLTLKYALGTKWSPLSLAAFTGELTKLRSLM 300
genG_Iowa RRQGLLSNRYYAMVGDIGKYIENSGLTAFFLTLKYALGTKWSPLSLAAFTGELTKLRSLM 300
genH RRQGLLSNRYYAMVGDIGKYIENSGLTAFFLTLKYALGTKWSPLSLAAFTGELTKLRSLM 300
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JL5 MLYRGLGEQARYLALLEAPQIMDFAPGGYPLIFSYAMGVGTVLDVQMRNYTYARPFLNGY 360
genG_NY MLYRDLGEQARYLALLEAPQIMDFAPGGYPLIFSYAMGVGTVLDVQMRNYTYARPFLNGY 360
genG_Iowa MLYRDLGEQARYLALLEAPQIMDFAPGGYPLIFSYAMGVGTVLDVQMRNYTYARPFLNGY 360
genH MLYRDLGEQARYLALLEAPQIMDFAPGGYPLIFSYAMGVGTVLDVQMRNYTYARPFLNGY 360
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genG_NY YFQIGVETARRQQGTVDNRVADDLGLTPEQRTEVTQLVDRLARGRGAGIPGGPVNPFVPP 420
genG_Iowa YFQIGVETARRQQGTVDNRVADDLGLTPEQRTEVTQLVDRLARGRGAGIPGGPVNPFVPP 420
genH YFQIGVETARRQQGTVDNRVADDLGLTPEQRTEVTQLVDRLARGRGAGIPGGPVNPFVPP 420
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genH VQQQQPAAIYEDIPALEESDDDGDEDGGAGFQNGAQAPAVRQGGQNDFRAQPLQDPIQAQ 480
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genG_Iowa LFMPLYPQVSNIPNHQNHQINRIGGMEHQDLLRYNENGDSQQDARGEHGNTFPNNPNQNA 540
genH LFMPLYPQVSNIPTHQNHQINRVGGMEHQDLLRYNENGDSQQDARGEHGNTFPNNPNQNA 540
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