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      ....|....|  ....|....|  ....|....|  ....|....|  ....|....|
            10      20      30      40      50
consensus  MGARASVLSG  GKLDREWEKIR  LRPGGKKKVR  LKHIVWASRE  LERFAVNPGL

      ....|....|  ....|....|  ....|....|  ....|....|  ....|....|
            60      70      80      90     100
consensus  LETSEGCRQI  LGQLQPSLQT  GSEELRSLYN  TVAVLYCVHQ  KIEVKDTKEA

      ....|....|  ....|....|  ....|....|  ....|....|  ....|....|
            110     120     130     140     150
consensus  LDKIEEEQNK  SKQKTQAAA  DKGNSSQVSQ  NYPIVQNLQG  QMVHQAI SPR

      ....|....|  ....|....|  ....|....|  ....|....|  ....|....|
            160     170     180     190     200
consensus  TLNAWVKVVE  EKAFSPEVIP  MFSALSEGAT  PQDLNTMLNT  VGGHQAAQM

      ....|....|  ....|....|  ....|....|  ....|....|  ....|....|
            210     220     230     240     250
consensus  LKDTINEEAA  EWDRLHPVHA  GPIPPGQMRE  PRGSDIAGTT  STLQEIQWM

      ....|....|  ....|....|  ....|....|  ....|....|  ....|....|
            260     270     280     290     300
consensus  TSNPPVPVGE  IYKRWIILGL  NKIVRMYSPV  SILDIRQGPK  EPFRDYVDRF

      ....|....|  ....|....|  ....|....|  ....|....|  ....|....|
            310     320     330     340     350
consensus  FKTLRAEQAT  QEVKNWMTET  LLVQNaNPDC  KTILKALGPG  ATLEEMMTAC

      ....|....|  ....|....|  ....|....|  ....|....|  ....|....|
            360     370     380     390
consensus  QGVGGPGHKA  RVLAEAMSQV  TNSTNVMMQK  SNFKGQRKIV  KCFNCGKEG

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**Figure S1** Consensus sequence obtained for the HLA/polymorphism analysis. Highlighted are positions where potential CTL-escape mutations are located, underlined those identified through statistical analysis.