Corrigendum

Corrigendum to “Polymorphisms within human cytomegalovirus chemokine (UL146/UL147) and cytokine receptor genes (UL144) are not predictive of sequelae in congenitally infected children” [Virology 378 (2008) 86–96]

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The reference strain for Merlin UL146 sequence was input incorrectly. This does not change the conclusions of the paper but does alter slightly the percentage similarity and identity and their subsequent phylogenetic groupings. The authors apologize for this oversight.

The corrected text appears below, and Fig. 1, Fig. 2 and Fig. 3 are published in their corrected forms:

Results, p. 89, 2nd column:

“The mature forms without the signal sequence and the reference sequences contain between 93 and 103 residues that show 5% identity (6 residues) and 8% similarity (9 residues) (Fig. 1). All sequences were assigned to 11 distinct vCXCL-1 clades (Fig. 2). The intravariability within each clade was less than 6%. The designated genotypic group numbers were assigned according to the 14 UL146 groups described by Dolan et al. (2004). No vCXCL-1 sequences were found in groups 3, 4, and 5.”

“If the most distant reference group is removed (NT from Group 4, for which we did not assign any samples), the number of 100% consensus residues increases from 6 to 11. This includes the CXC chemokine motif and the four cysteine residues. This implies that this isolate is a very distant cousin of other vCXCL-1s.”

Discussion, p. 92, 2nd column:

“Our results demonstrate that out of the 14 groups, 11 of the clades did not exhibit a definitive association between UL146 genotypes and symptoms.”
Fig. 1. Amino acid alignments of the mature forms of vCXCL-1s from clinical isolates. vCXCL-1 amino acid sequences from 51 clinical isolates were analyzed. Eighteen symptomatic clinical isolates are indicated in bold. The vCXCL-1 sequences from reference strains Toledo, Towne, C952, C954, C956, E760, ML1, TB40/E, FS, AL, 6397, KM, RK, Davis, NT, Merlin, and KSG (GenBank accession numbers AY681092, AY681095, DQ115733, DQ115734, DQ115735, DQ115754, AY446880, AY446866, AY446877, AY446887, AY446893, AY446870, AY446893, AY446868, AY446890, AY446894, and AY446889, respectively) plus strain [F] from Prichard et al. (2001) are boxed. The ELR motif and N-loop region, which are important in receptor binding and activation, are indicated at the top. Residues that are 100% conserved are shaded black and residues that are conserved in greater than 80% of the sequences are shaded in gray. Consensus sequences with 100%, 90%, and 80% conservations are shown at the bottom.
Fig. 2. vCXCL-1 phylogenetic analysis. The mature forms of vCXCL-1 from 51 clinical isolates with the reference sequences (shaded gray) were assembled into a phylogenetic tree using ClustalW. Eighteen symptomatic clinical isolates are indicated in bold. Bootstrap numbers are shown. Group designations correspond to those used by Dolan et al. (2004).
Fig. 3. Phylogenetic analysis for the N-loop region of vCXCL-1. The N-loop regions of vCXCL-1 from 51 clinical isolates with the reference sequences (in gray box) were analyzed using ClustalX. Eighteen symptomatic clinical isolates are indicated in bold. Bootstrap numbers are shown. Group designations correspond to those of the mature forms of UL146 amino acid (Fig. 2).