**Supporting information**

**Materials and methods**

**Phylogenetic analysis of HAdV species isolated from the present cohort**

The nucleotide sequences obtained from HAdV nested PCR amplicons, were aligned using the MAFFT algorithm [1] implemented in Geneious R7 (Biomatters, New Zealand). The nucleotide substitution model was determined in MEGA 6.0 [2] and maximum likelihood tree was constructed using PhyML [3] and bootstrapped 1000 times in SeaView [4]. Trees were projected using FigTree v1.4.2 [5]. Bootstrap values greater than 80% were considered significant.

**Purification of the tonsillar B and T lymphocytes by Fluorescence Activated Cell Sorting (FACS)**

Cryopreserved MNCs were thawed in a 37 °C water bath and immediately dispersed into 10 ml of pre-warmed Hanks balanced salt solution (HBSS, Gibco) supplemented with 5% fetal bovine serum (FBS, PAA), 10 mM Glutamine, 0.05 mg/ml Gentamicin and 1% Antibiotic-Antimycotic mix (Penicillin, Streptomycin and Amphotericin B, Gibco). The cells were spun down at 300 × g for 5 min and the resulting cell pellet was re-suspended in HBSS. Prior to the immunostaining, MNCs rested for 2 hours in supplemented HBSS medium at 37 °C and 5% CO2.

To obtain a single cell suspension for FACS staining, approximately 2-3 × 107 MNCs were filtered through a 40 μM plastic cell strainer. The cells were washed and re-suspended in ice-cold PBSA (PBS containing 0.2% BSA) to reach the density of 107 cells/ml. In order to block the Fc receptors, cells were incubated with 1 ml of PBS containing 10% heat inactivated human serum (Rockland Immunochemicals) for 1 min at room temperature. After washing in ice-cold PBSA, B and T lymphocyte surface antigens were stained with anti-CD20 and anti-CD2 monoclonal antibodies (BD Biosciences), respectively, as previously described [6]. The stained cells were sorted using BD FACSaria III  cell sorter (BD Biosciences). Subsequent FACS data analysis was performed using BD FACSDiva 8.0.1 software (BD Biosciences). An 85-m ceramic nozzle (BD Biosciences), a sheath pressure of 35-40 pounds per square inch (PSI) and an acquisition rate of 1000-2000 events per second were used as parameters for the cell sorting. The sorting speed was adjusted to ensure that the sorting efficiency was above 90%. The purity of the sorted fractions was checked after acquisition of at least 5 × 106 cells. DNA was extracted from immunosorted tonsillar B and T lymphocyte fractions and the presence of HAdV DNA in these samples was detected by qPCR as previously described [6].

**References**

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