Analysis of protein–protein interactions in complex environment: capture of analyte–receptor complex with standard additions of receptor (CARSAR) approach

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Supplementary Figures

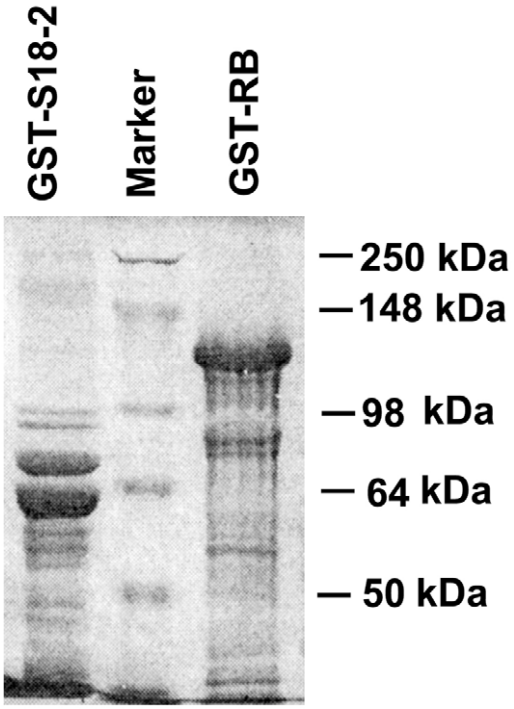

Figure S1

Western blotting and coomassie brilliant blue staining of the MRPS18-2 (S18-2) and retinoblastoma (RB) proteins as fusions with the glutathione-S-transferase (GST2TK, GST). They were isolated from bacterial cultures (BL21 DE3 strain, Invitrogen, Carlsbad, CA, USA), using GST-sephacryl beads (GE Healthcare Bio-Sciences AB, Uppsala, Sweden) according to the manufacturer's protocol. These constructs contained 266 amino acids (full length) of MRS18-2 and the residues 379-928 of RB. GST proteins were eluted from beads, using a buffer that contained a reduced form of glutathione (5 mM), 10 mM Tris-HCl (pH 8.0), and 150 mM NaCl.

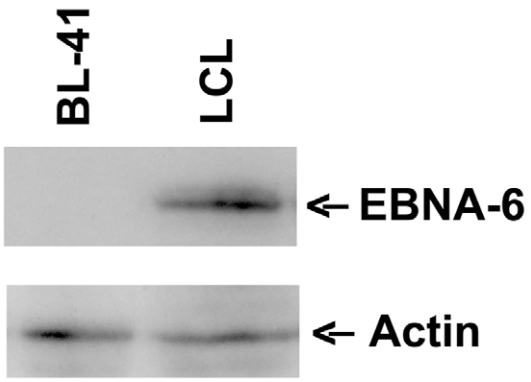

Figure S2
Western-blotting of the cell lysates of BL41 (EBV-negative Burkitt's lymphoma cell line) and LCL (070531, lymphoblastoid cell line). The membrane was probed with mouse monoclonal antibodies against EBNA-6 (kind gift of Martin Rowe, University of Wales, College of Medicine, Cardiff) and actin (Sigma-Aldrich, St Louis, MO, USA). To each well the lysate of $0{,}5x10^6$ cells was loaded.