

Supplementary Methods

Protein expression and purification of zebrafish Rad54

Insect cells were harvested 48h postinfection and lysed in 50mM Tris pH 8.0, 5 mM DTT, 300 mM NaCl, 1ug/mL Aprotinin, Leupeptin, Pepetistatin, 45 units/L micrococcal nuclease. The GST fusion proteins were purified first by glutathione affinity chromatography, followed by cleavage with 5-10% thrombin at 4°C degrees overnight. An internal thrombin site in zebrafish Rad54 resulted in a fragment spanning residues 91 to 738 (dnRad54Δ). All Rad54 proteins were subsequently purified by hydroxyapatite (Biorad) and size exclusion SD200 chromatography (Amersham/Pharmacia), and finally concentrated to 14 mg/ml in 50 mM Tris pH8.0, 300 mM NaCl, 5 mM dithiothreitol (DTT).

Construction of the Snf2 hmm.

We constructed a SWI/SNF hmm starting with a seed alignment of 11 representative human SWI2/SNF2 proteins. The alignment encompassed the Rad54 sequence starting at the beginning of the helicase lobe 1 and ending with HD2, thus excluding the NTD and CTD. Only a single member of protein groups with over 90% pair-wise identity was included to avoid bias. This alignment was used to construct an initial HMM, which was used to search the reference sequence of the human proteome. This yielded 39 proteins, which after weeding those with over 90% identity, gave the final set of 17 proteins used to derive the final HMM. These human proteins are: Rad54, Rad54B, CSB, Kish2, Brg1, Chd2, Mi-2, Btaf1, CHD5, CHDIL, SMARCA6, ETL, HARP, ATRX, Lodestar and Ino80.