S1 Table. Peptide mass finger print analysis of host cell proteins coeluting with YopM-SBP-CBP

<table>
<thead>
<tr>
<th>protein</th>
<th>Mascot score</th>
<th>Expectation value</th>
<th>Peptide</th>
</tr>
</thead>
<tbody>
<tr>
<td>DDX3X</td>
<td>99</td>
<td>1.7e-6</td>
<td>YIPPHLR; SDEDDWSKPLPPSER; LEQELFSGGNTGINFE; YTRPTPVQK; QYPISLVLAPTR; ELAVQHYEEAR; VRPCVVYYGAEIGQQI; GCHLLVATPGR; MLDMGFEPQIR; HTMMFSATFPK; EEALHQFR; SPILVATAVAAR; VGNLGLATSFFNER</td>
</tr>
<tr>
<td>DDX3Y</td>
<td>119</td>
<td>1.6e-8</td>
<td>YIPPHLR; GKPNFYFSDR; SDEDDWSKPLPPSER; LEQELFSGGNTGINFE; YTRPTPVQK; QYPISLVLAPTR; ELAVQHYEEAR; VRPCVVYYGADTVQQI; GCHLLVATPGR; MLDMGFEPQIR; HTMMFSATFPK; YACTSIHGDR; EEALHQFR; KPILVATAVAAR</td>
</tr>
</tbody>
</table>

S1 Table: The final elution fraction of YopM-SBP-CBP tandem affinity purified from infected murine J774A.1 macrophages [1] was subjected to SDS-PAGE. Visible Coomassie-stained bands were excised, enzymatically digested and masses of the resulting peptides were subsequently determined on MALDI-TOF mass spectrometer. Data analysis of the obtained peptide mass fingerprints was performed with Mascot (http://www.matrixscience.com) obtaining indicated scores. The peptide-mass-fingerprint analysis significantly identified DDX3X or DDX3Y (p < 0.05 at a score threshold of 55).

Using this methodology, RSK 1, 2 and PKN 1, 2 were confirmed as binding partners of YopM-SBP-CBP in previous work [1]. In the same experiments peptides matching the protein sequence of DEAD box RNA helicase 3 (DDX3) were identified. DDX3X and DDX3Y are encoded by the X- and Y-chromosome, respectively [2]. The peptide mass fingerprint analysis revealed indicated expectation values matching the DDX3X- or DDX3Y protein sequence. The lower the expectation value, the more significant the score.

References Supporting Information
