Supplementary Table I: GenBank Accession Numbers of human and mouse AAF-132 and AAF-44 clones

GenBank Accession No:	Species:	Description:
AAF-132: NM_025099 NM_026889 NM_001013256*	human mouse mouse	cDNA, 5036 bp, with 59 nucleotides of 5'UTR cDNA, 3980 bp, with 20 nucleotides of 5'UTR cDNA, 3964 bp, with 20 nucleotides of 5'UTR
NT_096135 NW_001030477	mouse mouse	genomic clone, chromosome 11 genomic clone, chromosome 11
BB854410 BY024588 BY024814	mouse mouse	463 bp EST, extending 5'UTR to 222 nucleotides 362 bp EST, extending 5'UTR to 208 nucleotides 373 bp EST, extending 5'UTR to 208 nucleotides
AAF-44: NM_024928 NM_175360	human mouse	cDNA, 1451 bp, with171 nucleotides of 5'UTR cDNA, 1878 bp, with 229 nucleotides of 5'UTR
NT_039687 NW_001030643	mouse mouse	genomic clone, chromosome 19 genomic clone, chromosome 19
W17593 BY104517 WI7719	mouse mouse	206 bp EST, extending 5'UTR to 349 nucleotides 341 bp EST, extending 5'UTR to 332 nucleotides 293 bp EST, extending 5'UTR to 327 nucleotides

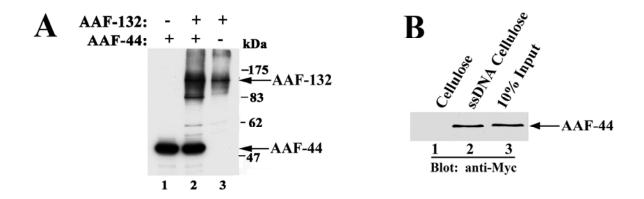
^{*} NM_001013256 contains a 16 bp deletion between nucleotides 218 and 233 of NM_026889 (nucleotide 217 represents the end of exon II).

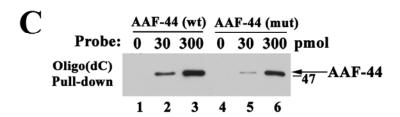
<u>Supplementary Table II:</u> Sequence Discrepancies Found in Murine AAF-132 and AAF-44 cDNA Sequences. The cDNA sequences obtained for murine AAF-132 and AAF-44 were compared with the respective cDNA clones published in GenBank. Differences are indicated by listing the nucleotides with their positions in NM_026889 (for AAF-132) or NM_175360 (for AAF-44), followed by the nucleotides found in our clones, and the amino acid change, if applicable. The corresponding amino acid in the human sequence (NM_025099) is noted under "remarks."

Nucleotide Change*	Amino Acid Change	Remarks:
AAF 132:		
C854T	No Change	
A866G	No Change	
T1061C	No Change	
T1365C	S449P	S in the human sequence
T1398C	No Change	_
C1829T	No Change	
T1922G	No Change	
A2336G	No Change	
T2469C, C2471T	S817P	P in the human sequence
G2511T	A831S	S in the human sequence
C2915T	No Change	
G3260A	No Change	
A3610G	Q1197R	R in the human sequence
A3641G	No Change	
AAF 44:		
T1249C	No Change	

^{*}GenBank *versus* our sequence

Supplemental Fig. 1

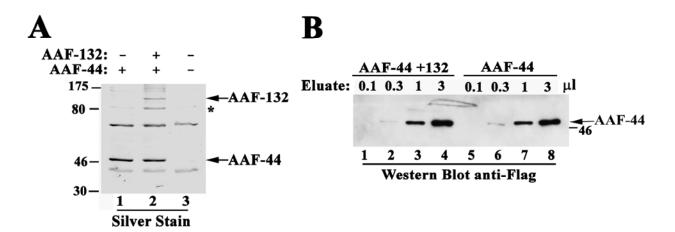




Supplemental Fig. 1:

A: 293T cells were transfected as described in Fig. 4A with equal amounts of expression vectors encoding Myc epitope-tagged AAF-44 (lane 1), Myc-tagged AAF-132 (lane 3), or both (lane 2), and equal amounts of cell lysate protein were analyzed by Western blotting with anti-Myc antibody. **B:** Cells were transfected with Myc epitope-tagged AAF-44 and ~200 μg of cell lysate protein was incubated for 1 h at 4°C with 25 μl of pre-swelled ssDNA cellulose (ssDNA from calf thymus) or plain control cellulose in a total volume of 200 μl (both types of cellulose were from Sigma). The cellulose beads were washed three times in lysis buffer, bound proteins were eluted in SDS sample buffer, and analyzed by SDS-PAGE/Western blotting using an anti-Myc antibody. **C:** Cells were transfected with equal amounts of vector expressing Flag-tagged wild type AAF-44 (lanes 1-3) or mutant AAF-44 (W96A/F151A, lanes 4-6), and binding to 30 or 300 pmol of oligo(dC)₃₀ probe was assessed by Western blotting with anti-Flag antibody as described in Fig. Fig. 4A.

Supplemental Fig. 2



Supplemental Fig. 2:

A: 293T cells were transfected with Flag-tagged AAF-44 (lanes 1 and 2), Myc-tagged AAF-132 (lane 2), or empty vector (lane 3); cell lysate proteins were passed over an anti-Flag antibody affinity matrix, and eluted with Flag peptide as described in Experimental Procedures. Equal amounts of eluates were analyzed by SDS-PAGE/silver staining. Full-length AAF-132 and -44 are indicated by arrows, and the asterisk denotes an ~80 kDa breakdown product of AAF-132, as confirmed by Western blotting with anti-Myc antibodies (not shown). **B:** Increasing amounts of the eluates described in lanes 1 and 2 of panel A were analyzed by SDS-PAGE/Western blotting with anti-Flag antibody.