



- Putative spermidine binding site
- Putative spermine binding site
- Putative spermidine and spermine binding site
- Activity-related site
- Donor substrate binding site
- Acceptor substrate binding site
- Catalysis related loop (V31-P37)

**Additional file 1: Figure S1.** Sequence alignment of BAHD like proteins. Identical and similar amino acids were shaded in black and grey, respectively. The conserved domains (HXXXD and DFGWG) in BAHD family proteins were underlined with red solid lines. The catalytically important residues were marked with different symbols. Organism resource and accession numbers of included genes are shown in figure 4.