The genus *Bartonella* contains over 30 species of Gram-negative arthropod-borne bacteria that are found in many small animal reservoirs and some of which are capable of causing human disease. The high molecular weight autotransporter BadA has been shown by others to be an important virulence factor in *B. henselae* associated with aggregative growth, host cell attachment, inhibition of phagocytosis and induction of a pro-angiogenic host response. However, very little is known about the regulation of the *badA* gene and gene regulation in *Bartonella* in general. The transcriptome of the Houston-1 strain of *B. henselae* was examined using RNA-seq revealing a family of nine novel, highly expressed intergenic transcripts (**B**artonella **r**egulatory **t**ranscripts, **Brts**). The Brt family of RNAs ranges from 200-205 nucleotides with a high degree of homology and stable predicted secondary structures. Northern blot analysis indicates expression of these RNAs appears to be highest under conditions mimicking those of the cat flea vector. Immediately down stream of each of the nine RNAs is a helix-turn-helix DNA binding protein (**T**ranscriptional **r**egulatory **p**rotein, **Trp**) that is poorly transcribed under the laboratory growth conditions used for RNA-Seq. This gene organization is suggestive of a potential riboswitch mechanism with the RNA secondary structure controlling transcription of the downstream DNA binding protein gene. The role of this unique regulatory system in controlling expression of *badA* and the associated phenotypic properties including the growth of *B. henselae* in aggregates and biofilms will be presented.