The Gleason Grading System is the system used by pathologists to assess prognosis of prostate cancer (PCa), and is based upon the composite score of major and minor architectural regions (with corresponding grades) of PCa tumors. Following prostatectomy and preparation of a histological section, a pathologist will assign a Gleason score. The higher the Gleason score, the greater the degree of cellular de-differentiation, and the poorer the prognosis. Our hypothesis is that the translational regulator Threonyl-tRNA Synthetase (TARS) is upregulated at the transcriptional level in high-grade Prostate Cancer (PCa). TARS is proposed to be pro-angiogenic, by specifically binding to the Von Hippel–Lindau factor and activating transcription of Vascular Endothelial Growth Factor by Hypoxia-Inducible Factor (HIF-1). If our hypothesis is correct, increased TARS protein expression should be associated with high Gleason Score, because this indicates poor prognosis and high metastatic potential. We assembled a collection of prostatectomy specimens from 56 high-grade cases from Fletcher Allen Health Care (FAHC) and slides were examined to find appropriate sections. Immunohistochemistry (IHC) for TARS was performed on these samples and two blind scorers graded stain intensity, Gleason score, percent tumor, high-grade Prostatic Intraepithelial Neoplasia, and several benign controls, including normal tissue, atrophy, and Benign Prostatic Hyperplasia. Using a non-parametric ANOVA, we looked at correlations between TARS intensity and Gleason grade, and percent tumor and Gleason grade, both within individual patient samples and across a sample population. We also performed a meta-analysis of TARS expression in PCa using the Oncomine database.