Transcripts are subject to several steps of processing and degradation in order to become fully functional. The exosome is a highly conserved enzymatic complex with 3'-5' exoribonucleolytic activity that plays a key role in both processes, modulating the abundance of coding and non-coding RNAs. It participates in the maturation of snoRNAs, snRNAs and 5.8S rRNA precursors (constituent of the large ribosomal subunit), being also implicated in the degradation of RNA cleavage fragments and of defective RNA precursors. In the cytoplasm, it takes part in several mRNA decay pathways. In Saccharomyces cerevisiae, organism in which it was first identified, cytoplasmic exosome consists of 10 subunits, while the nuclear is formed by 11 (nine of which constitute the non-catalytic core). Six proteins (Rrp41, Rrp42, Rrp43, Rrp45, Rrp46 and Mtr3) form a structurally conserved central hexameric channel that directs single-stranded RNAs to the catalytic subunits Rrp44 and Rrp6. However, despite recent advances in its structural description, little is known about the regulatory mechanisms of the exosome activity. Recent studies showed that Nop53, an essential nucleolar protein in S. cerevisiae involved in ribosome biogenesis and rRNA processing, directly interacts with Rrp6 and modulates the exosome function. The aim of this study was to further evaluate the effect of Nop53 on the Rrp6 activity. Using a conditional mutant strain for Nop53, the effect of Nop53 on the expression of Rrp6 was assessed through quantitative western blotting and relative quantification in real-time qRT-PCR. Further analyses were performed to characterize the underlying mechanisms of those effects suggesting a transcriptional and post-transcriptional modulation. Altogether, we show that the nucleolar protein Nop53 affects the expression of the exosome nuclear catalytic subunit Rrp6, illustrating the complex interplay between ribogenesis and RNA metabolism.