



# Cancer Genomics: Chapter 16. Thyroid Cancer

*Angela Greco, Claudia Miranda, Maria Grazia Borrello, Marco A. Pierotti*

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Thyroid cancer represents the most common endocrine malignancy and its incidence is increasing. The majority of thyroid tumours (90–95%) originate from the follicular epithelial cells; it includes several histotypes and related variants characterized by different biological and clinical behavior, such as differentiated papillary and follicular carcinoma (PTC and FTC), and poorly differentiated and anaplastic carcinoma (PDTC and ATC). Medullary thyroid carcinoma (MTC) represents a small fraction of thyroid tumors and originates from the parafollicular C cells. PTCs feature a frequent deregulation of the MAPK pathway, as RET/PTC, TRK, RAS or BRAF oncogenes have been found in about 70% of cases. FTCs are associated with RAS mutations and PAX8/PPAR $\gamma$  oncogenic chromosome rearrangements. PDTCs and ATCs display some alterations occurring in differentiated tumors, as well as other alterations specific of late tumor stages. MTC carry RET or RAS mutations. Here we summarize the molecular alterations detected in each thyroid tumor type, their role in the process of thyroid carcinogenesis, as well as how high-throughput gene expression analyses have contributed to the study of this malignancy.

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