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Insights on Gastric Cancer: applied bioinformatics approaches

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Gastric cancer (GC) remains one of the major causes of cancer-related mortality worldwide. Molecular heterogeneity is a major determinant for the clinical outcomes and an exhaustive tumor classification is currently missing. Histologically normal tissue adjacent to the tumor (NAT) is commonly used as a control in cancer studies, nevertheless shows unique characteristics in several tumor types, possibly leading to suboptimal tumor features definition. Moreover, several limitations to the success of current therapeutic GC treatments may be due to cancer drug resistance that leads to tumor recurrence and metastasis. Apoptosis evasion represents a causative factor for treatment failure in GC as in other cancers and intracellular calcium homeostasis regulation has been found to be associated with apoptosis resistance. Finally, although extensive literature was produced to better define Lauren's classification subgroups, characterizing pathways and actionable candidates in clinical practice are still missing. Here I'd like to show:

1. Our efforts to molecularly define the gastric NATs and their confounding impact on GC analyses.
2. The prognostic value for TRPV2 calcium channel expression in GC and its role as potential target for overcoming cisplatin resistance by promoting apoptosis.
3. The molecular differences, the active subnetworks, the prognostic and actionable candidates between Lauren's Diffuse and the Intestinal subtypes.

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