

# Integrated landscape of copy number variation and RNA metastasis in invasive ductal breast carcinoma

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Citation Report

#	ARTICLE	IF	CITATIONS
1	DNA Methylation and Gene Expression with Clinical Covariates Explain Variation in Aggressiveness and Survival of Pancreatic Cancer Patients. <i>Cancer Investigation</i> , 2020, 38, 502-506.	0.6	2
2	Multi-omic signatures identify pan-cancer classes of tumors beyond tissue of origin. <i>Scientific Reports</i> , 2020, 10, 8341.	1.6	22
3	The genomic landscape of metastasis in treatment-naïve breast cancer models. <i>PLoS Genetics</i> , 2020, 16, e1008743.	1.5	17
4	MetaCancer: A deep learning-based pan-cancer metastasis prediction model developed using multi-omics data. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 4404-4411.	1.9	19
5	Lipidomics investigations into the tissue phospholipidomic landscape of invasive ductal carcinoma of the breast. <i>RSC Advances</i> , 2020, 11, 397-407.	1.7	1
6	Copy number variation in triple-negative breast cancer samples associated with lymph node metastasis. <i>Neoplasia</i> , 2021, 23, 743-753.	2.3	21