

Table S20. Anticancer drug candidates predicted by transcriptomic signatures of linc-genes encoding lincRNAs of human chromosome 18 in cancer cell lines.

Predicted drugs (p-value <0.1)	Drug concentration**	Cell line	Cancer type
<i>Canagliflozin</i> *	0.25 μ M	THP1	Leukemia
<i>Conivaptan</i>	0.03 μ M	YAPC	Pancreatic carcinoma
<i>Darapladib</i>	0.08 μ M	PC3	Prostate adenocarcinoma
<i>Dipraglurant</i>	0.03 μ M	PC3	Prostate adenocarcinoma
<i>Fluticasone-propionate</i>	0.08 μ M	JURKAT	Leukemia
Givinostat	0.66 μ M	HAP1	Chronic myeloid leukemia
Ibrutinib	0.66 μ M	TMD8	Lymphoma
Lapatinib	0.66 μ M	BJAB	Lymphoma
Lucitanib	0.08 μ M	PC3	Prostate adenocarcinoma
<i>Methapyrilene</i>	0.66 μ M	HEPG2	Liver carcinoma
<i>Primaquine</i>	0.37 μ M	HT29	Colon adenocarcinoma
Quizartinib	0.08 μ M	MCF10A	Breast carcinoma
Rebastinib	0.37 μ M	JURKAT	Leukemia
<i>Talinolol</i>	0.37 μ M	MDAMB231	Breast adenocarcinoma
<i>Tizanidine</i>	0.12 μ M	PC3	Prostate adenocarcinoma
Tozasertib	0.12 μ M	OCILY19	Lymphoma

* Repositioning drugs as anti-cancer agents are highlighted with italic font;

**Cell lines were exposed to drugs for 24 h.

*** SigCom-Library web-based tool (<https://maayanlab.cloud/sigcom-lincs/#/SignatureSearch/UpDown>) was used to analyze transcriptomic profiling data of cancer cell lines being exposed to various concentrations of drugs.