Supplementary Information for

Single-cell transcriptomes identify patient-tailored therapies for selective co-inhibition of cancer clones

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Supplementary Information

● Supplementary Tables 1-4 Pages 1-4

● Supplementary Figures 1-11 Pages 5-14

● Supplementary References Pages 14-16

Supplementary Table 1 | AML patient samples used in the study.

Pt	Disease stage	scRNA- based blast (%)	Clinical morphological blast (%)	FAB type	ELN22 risk class	Potential driver mutations	Chromosomal abnormalities	No. cells after QC ^a
1	Diagnosis	79.3	80	NA	Favorable	NPM1, DNMT3A, NRAS, IDH1, EML4	Normal karyotype	2483
2	Diagnosis ^b	38.1	70	M1	Favorable	NPM1, TET2, USP8	Normal karyotype	2874
3	Refractory ^b	56.7	42	M1	Favorable	NPM1, TET2, HDAC 1,2,7	Normal karyotype	2421
4	Diagnosis	80.3	91	M1	Favorable	RANBP2, NPM1, IDH1, FLT3	Normal karyotype	2140
5	Relapse	54.4	26	M5	Intermediate	LZTR1, AR, ICOSLG	Normal karyotype	2365
6	Relapse	40	14	M1	Intermediate	FLT3, PTPN11, TP53BP1	Polyploidy	5677
7	Diagnosis	40.8	36	NA	Adverse	RUNX1, BCORL1, PTPN11	Monosomy 7 + intra- chromosomal translocation Chrom 3	9340
8	Refractory	22.8	40	NA	Adverse	DNMT3A, ERG, U2AF1, BCOR	Normal karyotype	4461
9	Diagnosis	50	70	M1	Adverse	BCOR, IDH2	Normal karyotype	3921
10	Diagnosis	65.5	65	M2	Adverse	WT1, CCND2, CEBPA	del(5q)	3111
11	Diagnosis	42.1	32	M2	Intermediate	VAV1	Normal karyotype	5697

12	Refractory	65.3	65	M2	Adverse	MN1, MAP2K2, ETV6, FOXP1	del(5q)	3610
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Age range: 21-75 years; female/male ratio: 7/5.

Boldfacing indicates patient samples with enough cells for experimental validation.

Supplementary Table 2 | Clinical and predicted treatment responses for patients with AML.

Pt	Disease stage	Treatment before sampling (response)	Treatment after sampling (response)	Predicted response to treatment after sampling
1	Diagnosis	-	Hydroxyurea (no)	-
2	Diagnosis	-	Azacitidine (no)	-
3	Refractory	Azacitidine (no) Venetoclax (no)	-	-
4	Diagnosis	-	Hydroxyurea (yes), Cytarabine/Idarubicin (yes), Cytarabine/Daunorubicin (yes), busulfan/cyclophosphamide (yes)	Daunorubicin (HM)
5	Relapse	Hydroxyurea (yes), Cytarabine (yes), Cytarabine/Idarubicin (yes), Research drug treatment (no)	Investigational immunotherapy	-
6	Relapse	Cytarabine/Idarubicin (yes), Mitoxantrone/Cytarabine (yes), Amsacrine/Cytarabine/Etopo side (yes), Idarubicin/Cytarabine/Etopo side (yes), Clofarabine/Cytarabine/Etop oside (yes), Azacitidine (no), Azacitidine/Lenalidomide (no)	Mitoxantrone/Etoposide/Cytarabi ne (yes), Clofarabine/Cytarabine (no)	Mitoxantrone (HM), Etoposide (M)
7	Diagnosis	-	Azacitidine (no)	-
8	Refractory	Cytarabine/Idarubicin (no)	Cytarabine/Mitoxantrone (no), Azacitidine (no)	Mitoxantrone (HM), cyt:clofarabine (M-LC)
9	Diagnosis	-	Cytarabine/Idarubicin/GF (yes), Cytarabine/Mitoxantrone (yes), Cytarabine (yes)	-
10	Diagnosis	-	Cytarabine/Idarubicin (yes) Cytarabine/Idarubicin/Lenalidomi de, Cytarabine/Daunorubicin (yes), Etoposide/Mitoxantrone (yes), Lenalidomide (yes)	Etoposide (M), Lenalidomide (M-LC)
11	Diagnosis	-	NA	-
12	Refractory	NA	NA	-
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The columns include treatments before and after taking the sample, as well as the clinical response (yes/no), based on the percentage of blasts in the bone marrow of the patient. Predicted response with scTherapy to the treatments after sampling or drugs with similar mechanisms of action. Drug names in red font represent those that were

^aQuality control: filtering out low-quality cells (see Step 2 in the Methods section).

^bPaired samples from the same patient at disease diagnosis and refractory stages.

predicted by scTherapy as effective but filtered out due to low confidence of the predictions. Response prediction: HM, High-to-Moderate; M, Moderate; LC, Low confidence. - scTherapy prediction not possible for the non-targeted patient treatment or clinical response data not available (NA) at the time of the study from unpublished clinical trials.

Supplementary Table 3 | HGSC patient samples used in the study.

Patient ID	Treatment	Stage ^a (FIGO)	Anatomical location of scRNA-seq	Cell types	No. cells before QC	No. cells after QC
Patient 1	Treatment naïve	IIIC	Omentum	PAX8+	1921	1743
Patient 2	Treatment naïve	IVB	Ascites	PAX8+ PAX8-	2954	1483
Patient 3	Treatment naïve	IVA	Ascites	PAX8+ PAX8-	2178	1934
Patient 4	Treatment naïve	IIIC	Peritoneum	PAX8-	711	564
Patient 5	Treatment naïve	IIIC	Ascites	PAX8-	3666	2399

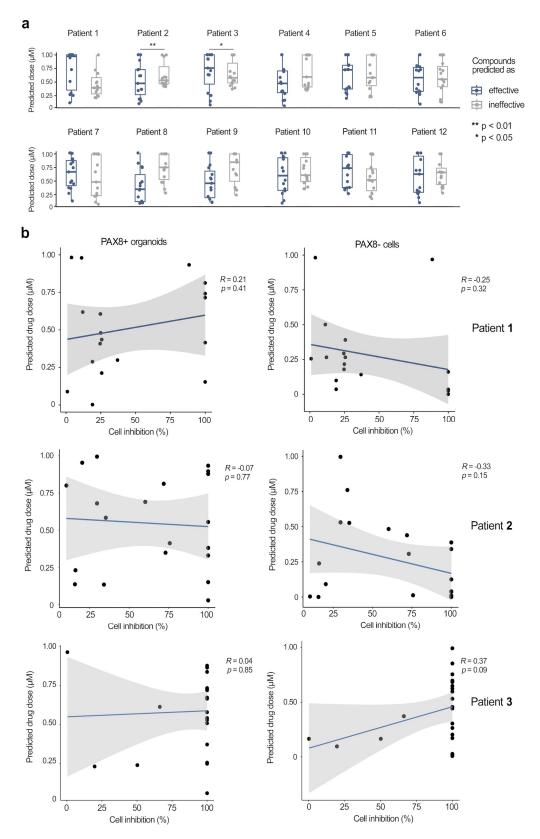
^aStage IIIC (FIGO staging): The cancer is in one or both ovaries or fallopian tubes, or there is primary peritoneal cancer, and it has spread or grown into organs outside the pelvis. The deposits of cancer are larger than 2 cm (about 3/4 inch) across and may be on the outside (the capsule) of the liver or spleen (T3c). Stage IVA: Cancer cells are found in the fluid around the lungs with no other areas of cancer spread such as the liver, spleen, intestine, or lymph nodes outside the abdomen (M1a). Stage IVB: The cancer has spread to the inside of the spleen or liver, to lymph nodes other than the retroperitoneal lymph nodes, and/or to other organs or tissues outside the peritoneal cavity such as the lungs and bones (M1b).

Supplementary Table 4 | Clinical development stages of scTherapy-predicted treatments across 5 cancer types (http://clinicaltrials.gov/).

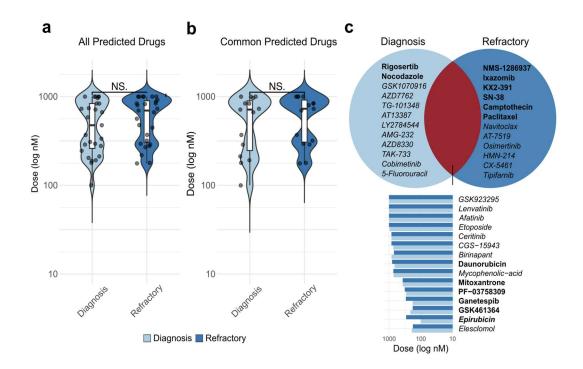
Indication	Treatment	Phase	NCT identifier number
Breast	abemaciclib	3	NCT05952557,NCT03155997 ¹
	alpelisib	3	NCT05501886,NCT04251533
	epirubicin	4	NCT01642771 ² ,NCT01216111 ³ ,NCT00630032,NCT005 40800 ⁴ , NCT01199432 ,NCT00689156 ⁵ ,NCT03498716 NCT04301739,NCT03036488, NCT04136782 ,NCT0586 2064,NCT02455141,NCT04031703,NCT03876886 NCT04296175,NCT01378533,NCT04335669,NCT0611 2379,NCT00912444
	5-fluorouracil	3	NCT00121992 ⁶ ,NCT04031703
Lung	etoposide	3	NCT00003364,NCT00717938 ⁷ ,NCT00632853 ⁸ ,NCT000 02858,NCT00003696,NCT00003606,NCT00003299,NC T00061919,NCT00011921,NCT00433498,NCT0004516 2,NCT02875457,NCT00002822,NCT00812266
	paclitaxel	3	NCT00003696,NCT000032999,NCT00011921,NCT0000 331710,NCT0000358911,NCT0247782612,NCT00054184, NCT00795340,NCT00054197,NCT00006049,NCT0005 4210,NCT0055173313
	epirubicin	3	NCT00003606 ¹⁴ ,NCT00011921

	docetaxel	3	NCT00074204,NCT00022022 ¹⁵ ,NCT00883675 ¹⁶ ,NCT00 054184,NCT02076477
	tivantinib	3	NCT01244191 ¹⁷
AML	daunorubicin	3	NCT00428558 ¹⁸ ,NCT00589082 ¹⁹ ,NCT04174612,NCT00 266136 ²⁰ ,NCT00931138 ²¹ ,NCT00715637 ²² ,NCT038971 27,NCT02013648,NCT00703820,NCT04293562,NCT00 927498 ²³ ,NCT00363025 ²⁴
	decitabine	3	NCT03941964,NCT05177731,NCT02172872 ²⁵ ,NCT055 86074,NCT02348489,NCT01633099,NCT02785900
	etoposide	3	NCT00052299 ²⁶ ,NCT02421939,NCT03504410,NCT031 82244,NCT00703820,NCT04293562
	mitoxantrone	4	NCT01828489,NCT00052299 ²⁶ ,NCT02421939 ²⁷ ,NCT03 504410,NCT03182244,NCT02461537,NCT04293562, N CT00180102
	panobinostat	3	NCT04326764
	tipifarnib	3	NCT00093990 ²⁸
HGSC	alpelisib	3	NCT04729387 ²⁹ .
	cyclophosphamide	3	NCT00003214 ³⁰ ,NCT00004921 ³¹ ,NCT00002477,NCT04 520074,NCT00002819,NCT00068601 ³²
	etoposide	3	NCT04000295,NCT04520074
	olaparib	4	NCT03737643,NCT02392676, NCT02476968 ,NCT0340 2841 ³³ ,NCT05255471 ³⁴ ,NCT03106987,NCT01874353 ³³ , NCT04729387 ²⁹ ,NCT03534453 ³⁵ ,NCT01844986 ³⁶ ,NCT0 2282020 ³⁷ ,NCT04884360,NCT04330040,NCT02477644 ³⁸ ,NCT03740165
	paclitaxel	4	NCT03737643,NCT05371301,NCT00326456 ³⁹ ,NCT047 29608,NCT00657878,NCT00660842 ⁴⁰ ,NCT00003214 ³⁰ , NCT03940196,NCT00004921 ³¹ ,NCT04000295,NCT033 98655,NCT04337632,NCT02718417,NCT01239732,NC T01802749, NCT01706120 ,NCT04729387,NCT0000289 4 ⁴¹ ,NCT00003644 ⁴² ,NCT01684878,NCT03690739,NCT 05145218,NCT00002717 ⁴³ ,NCT06072781,NCT0000281 9,NCT05009082,NCT00189553,NCT00003322 ⁴⁴ ,NCT00 003998 ⁴⁵ ,NCT03806049,NCT01654146,NCT02470585 ⁴⁶ ,NCT05281471,NCT03740165,NCT03794778,NCT0000 6454 ⁴⁷ ,NCT00028743 ⁴⁸ ,NCT00483782 ⁴⁹ ,NCT02631876, NCT00002568 ⁵⁰ ,NCT05601700,NCT04908787,NCT001 89371
Pancreas	5-fluorouracil	3	NCT00417209,NCT00602745,NCT05314998
	paclitaxel	4	NCT03721744, NCT04217096 ,NCT01836432 ⁵¹ ,NCT039 41093,NCT02506842,NCT04229004,NCT05178628,NC T04617821, NCT05035147 ,NCT05751850,NCT0483506 4,NCT05653453,NCT04674956,NCT06017284,NCT043 29949,NCT04935359,NCT02101021,NCT03943667 ⁵² ,N CT02715804, NCT04480268 ⁵³ ,NCT02993731, NCT0340 1827 ⁵⁴

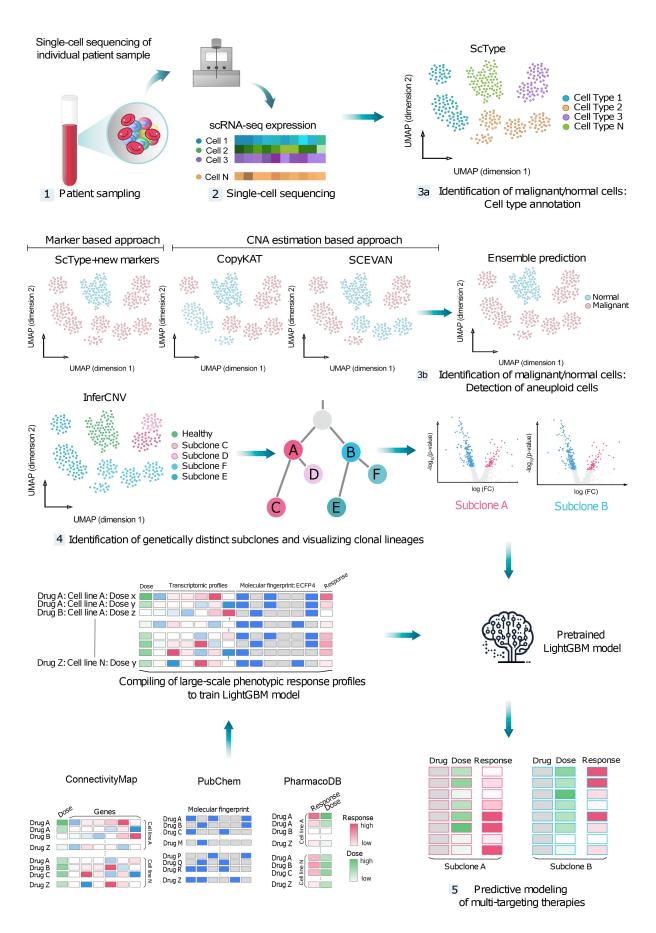
Boldfaced NCT IDs represent clinical trials that have reached phase 4.



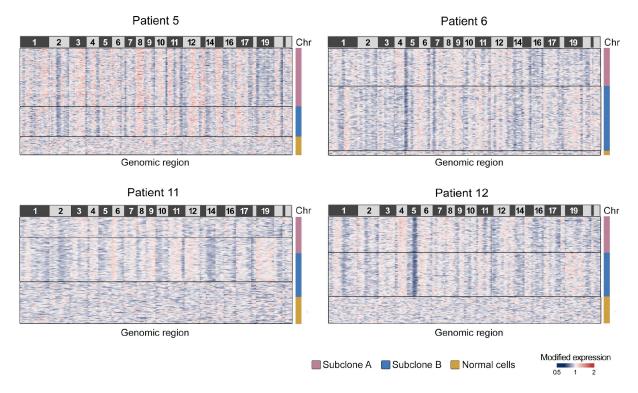
Supplementary Fig. 1 | Drug doses of the predicted single-agent treatments. (a) Drug doses (μ M) for single-agent treatments predicted by the model to be either effective or ineffective for 12 AML patients (two-sided Wilcoxon test). In general, there is no significant difference in the doses between drugs predicted to be effective or ineffective. Box plots show the median (central line), 25th and 75th percentiles (box edges), and the range within 1.5 times the interquartile range from the box (whiskers). Source data are provided in Source Data file. (b) Correlation between the predicted drug doses and the measured PAX8+ (left) or PAX8- (right) cell inhibition across the 18 predicted treatments in the HGSC patient samples. Non-significant correlation based on the correlation test in every patient.



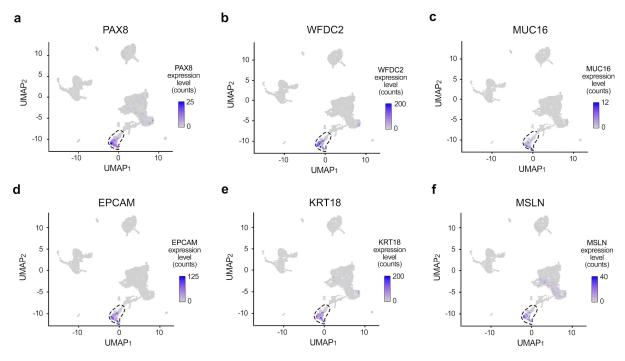
Supplementary Fig. 2 | Predicted effective drugs and doses for the diagnosis and refractory samples of the same AML patient. No significant (NS) differences were found in the predicted effective doses between the paired AML patient samples 2 and 3 from the same individual. (a) Predicted doses of all predicted drugs, difference assessed with two-sample Wilcoxon test. Box plots show the median (central line), 25th and 75th percentiles (box edges), and the range within 1.5 times the interquartile range from the box (whiskers). (b) Predicted doses of common drugs predicted for both the diagnostic and refractory samples, difference assessed with paired signed rank test. (c) Predicted effective drugs in diagnosis and refractory samples of the same individual. scTherapy predicted a total of 27 monotherapies both in the diagnosis and refractory samples, out of which 15 are common between the two samples. Drugs in boldface are those predicted to elicit a high-to-moderate response, while those in italics are expected to produce a moderate response. Epirubicin was predicted in diagnosis and refractory samples with moderate and high-to-moderate responses, respectively. Source data are provided in Source Data file.



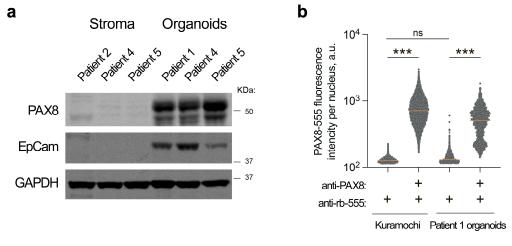
Supplementary Fig. 3 | Schematic workflow of the experimental-computational approach to predicting multi-targeting treatments for an individual AML patient/sample. See Online Methods for details of steps 1-5.

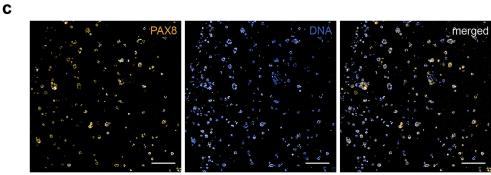


Supplementary Fig. 4 | InferCNV copy number variation analysis of malignant cells from the four AML samples. The heatmaps show a graphical representation of the CNV across the genomic regions, denoted as chromosomes (Chr) at the top of each heatmap. Shades of blue indicate lower levels of modified gene expression, suggesting genomic loss, while shades of red indicate higher levels of modified gene expression, indicative of genomic gain.



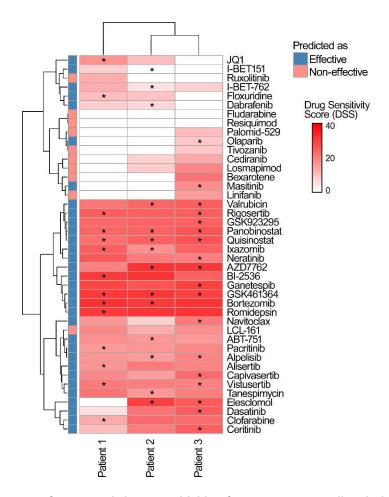
Supplementary Fig. 5 | Expression of the PAX8+ marker genes for the detection of ovarian cancer cell populations. (a) PAX8, (b) WFDC2, (c) MUC16, (d) EPCAM, (e) KRT18, and (f) MSLN. These markers were utilized for the detection of cancer cell populations in the HGSC Patient 1 (highlighted with dashed circles). The number of cells analyzed in Patient 1 as shown on UMAP plots is 4,706 cells.



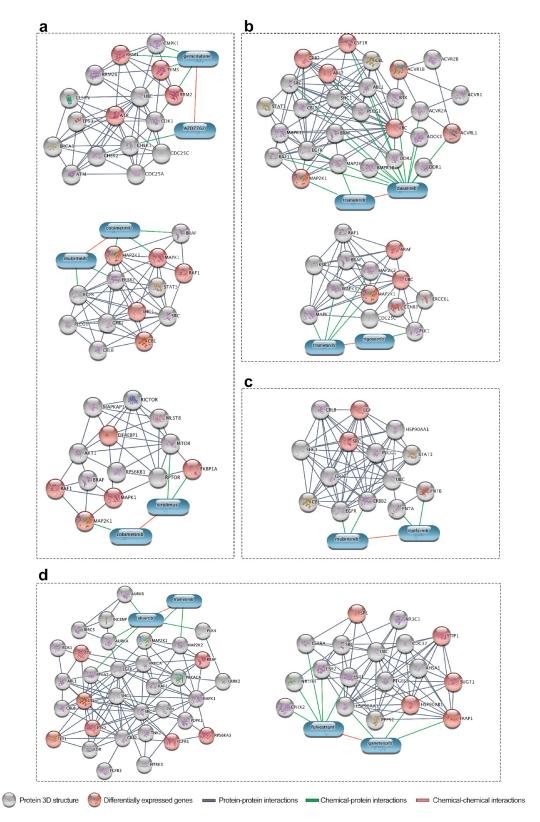


Statistical parameter	Kuramo	chi (control)	Organoids (patient 1)		
Statistical parameter	only 2ry-555	anti-PAX8+2ry-555	only 2ry-555	anti-PAX8+2ry-555	
N of nuclei scored	13721	13604	2040	1784	
Minimum	113,5	167,3	114,2	140,7	
Median	125,6	712,4	129,6	503,5	
Maximum	225,9	2986	598,3	1832	
10% Percentile	117	386	117,8	206,3	
90% Percentile	141,4	1273	169,9	883,7	
Mean	127,7	782,3	138,9	523,1	
Std. Deviation	10,14	362,2	28,63	267,3	
Std. Error of Mean	0,0866	3,105	0,6339	6,328	
Coefficient of variation	7,941%	46,30%	20,61%	51,10%	
% of PAX8+	1 %	100 %	1 %	84 %	

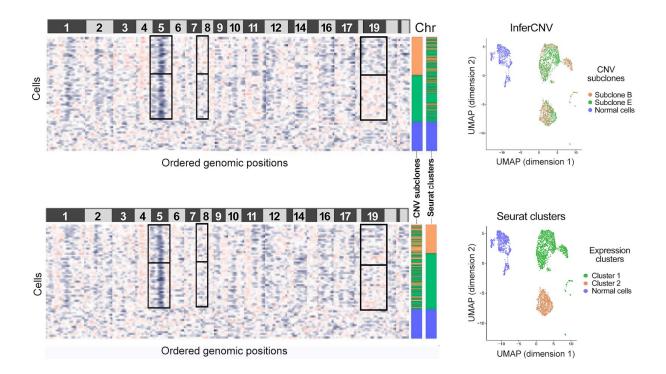
Supplementary Fig. 6 | Experimental analyses in the HGSC patient samples and organoids. (a) Immunoblotting for PAX8 and Epcam proteins in the stroma-derived and organoid samples from the representative individual HGSC patients (one experiment). The uncropped images with molecular weight markers are provided in the Source Data file. (b) Quantification of the imaging data for PAX8 nuclear expression in Patient 1-derived HGSC organoids (related to Fig. 3e), and in one control HGSC cell line, Kuramochi. Statistical significance was determined using a two-sided Wilcoxon signed-rank test; *** p < 0.001. Anti-rb-555, secondary goat-anti-rabbit-Alexa555 antibody conjugates. (c) Representative images of the immunofluorescence imaging of the nuclear PAX8 expression for the Patient 1 organoids. Scale bar equals to 250 μ m. (d) Statistical analysis of the imaging data presented in panels b and c. The fraction of PAX8+ objects correspond to the nuclei with PAX8-555 signal higher than mean+3SD for the respective control without PAX8 primary antibodies.



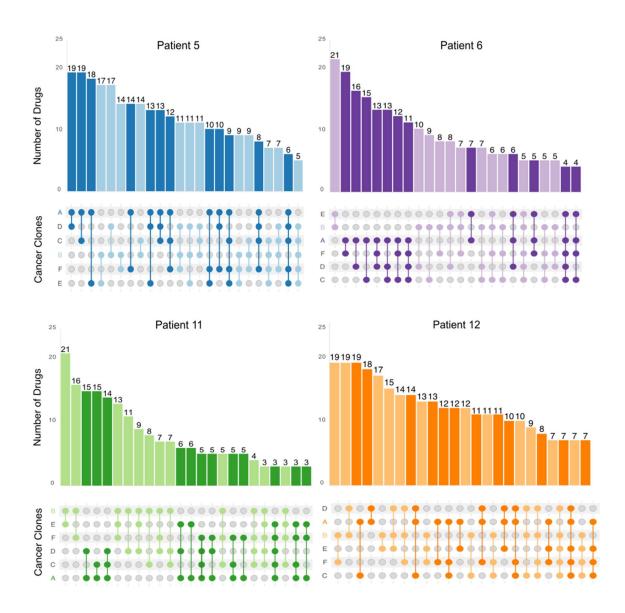
Suppl. Fig. 7 | Heatmap of measured drug sensitivities for treatments predicted either as effective or ineffective in ovarian cancer patients. Blue annotation in the left-hand column indicates that the drug was predicted to be effective in one or multiple ovarian cancer patients. Red color indicates those drugs predicted as non-effective in all the patient samples. *Drug treatments for which high efficacy class was predicted by the scTherapy model, showcasing the accuracy of our predictive model across the three patient-derived organoid lines. Source data are provided as a Source Data file. Scale bar represents Drug Sensitivity Score (DSS) values from 0 to 40 (white to red).



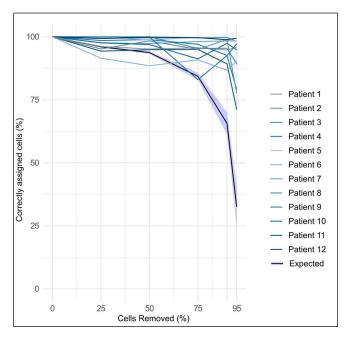
Supplementary Fig. 8 | Interaction networks for the predicted and experimentally validated AML patient-specific combinations. Representative drug combinations, where multiple drug targets were identified as differentially expressed genes between normal and malignant cells for the 4 AML patients: (a) Patient 5, (b) Patient 6, (c) Patient 11, and (d) Patient 12. The protein nodes in the networks include the nominal and potent off-targets of the compounds in the combinations, along with differentially expressed genes in the target pathways that may partly explain the observed combination effects in the particular patient cases. The network visualizations were done using the STITCH web-tool (Szklarczyk, D. et al. STITCH 5: augmenting protein-chemical interaction networks with tissue and affinity data. Nucleic Acids Res. 44, D380-384 (2016).



Supplementary Fig. 9 | Genetic clone detection vs. cell clustering. Comparison of cancer subclone characterization using inferred Copy Number Variation (CNV) profiles (upper panel) versus expression-based cell clusters (lower panel) in an AML patient sample 12. Bold rectangles highlight areas with pronounced expression differences, underscoring the effectiveness of CNV-based analysis in uncovering genetic subclonal diversity essential for designing clone-specific treatment options. The number of cells analyzed in Patient 12 as shown on UMAP plots is 3,610 cells.



Supplementary Fig. 10 | Overlap in scTherapy treatment predictions among the major and minor subclones across four AML patient samples. The darker bars highlight drug prediction overlaps with the first major subclone, and the lighter bars with the another. The colored subclone labels denote the major subclones, while those in gray denoted minor subclones. The four patient samples correspond to those used in the experimental validation. Source data are provided as a Source Data file.



Supplementary Fig. 11 | Stability of the subclone detection process at distinguishing normal and malignant cells. In this sub-sampling analysis, 25%, 50%, and 75% of cells were first randomly removed at increments of 25% from the 12 AML patient samples (traces). Then, using increments of 5% from 75% to 95%, we studied breaking point of the clone detection procedure. After each removal of cells without replacement, scTherapy Step was rerun. The y-axis illustrates the percentage of correctly assigned cells before and after the cell removal. The expected curve is an anticipated percentage of correctly assigned cells from a beta binomial distribution and the shaded areas depict 95% quantile for each point estimate, providing confidence interval for the expected values under random cell assignment. Beta-binomial distribution was used to account for the varying proportion of malignant/healthy cell types due to removal of different cell percentages.

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