

Supplementary Materials for

Tumor collection/processing under physioxia uncovers highly relevant signaling networks and drug sensitivity

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Tables S1 to S4

Supplementary Tables

Table S1: Global proteomic analysis of EpCAM⁺ tumor cells from PyMT and Her2/Neu mice collected and processed under physioxia and ambient air.

Table S2: Phospho-proteomic analysis of EpCAM⁺ tumor cells from PyMT mice collected and processed under physioxia and ambient air.

Table S3: RNA-seq analysis of cells from ascites fluids of three patients. Genes differentially expressed under physioxia compared to ambient air are listed.

Table S4: List of genes alternatively spliced along with splicing type and location under physioxia compared to ambient air.

Supplementary Figures

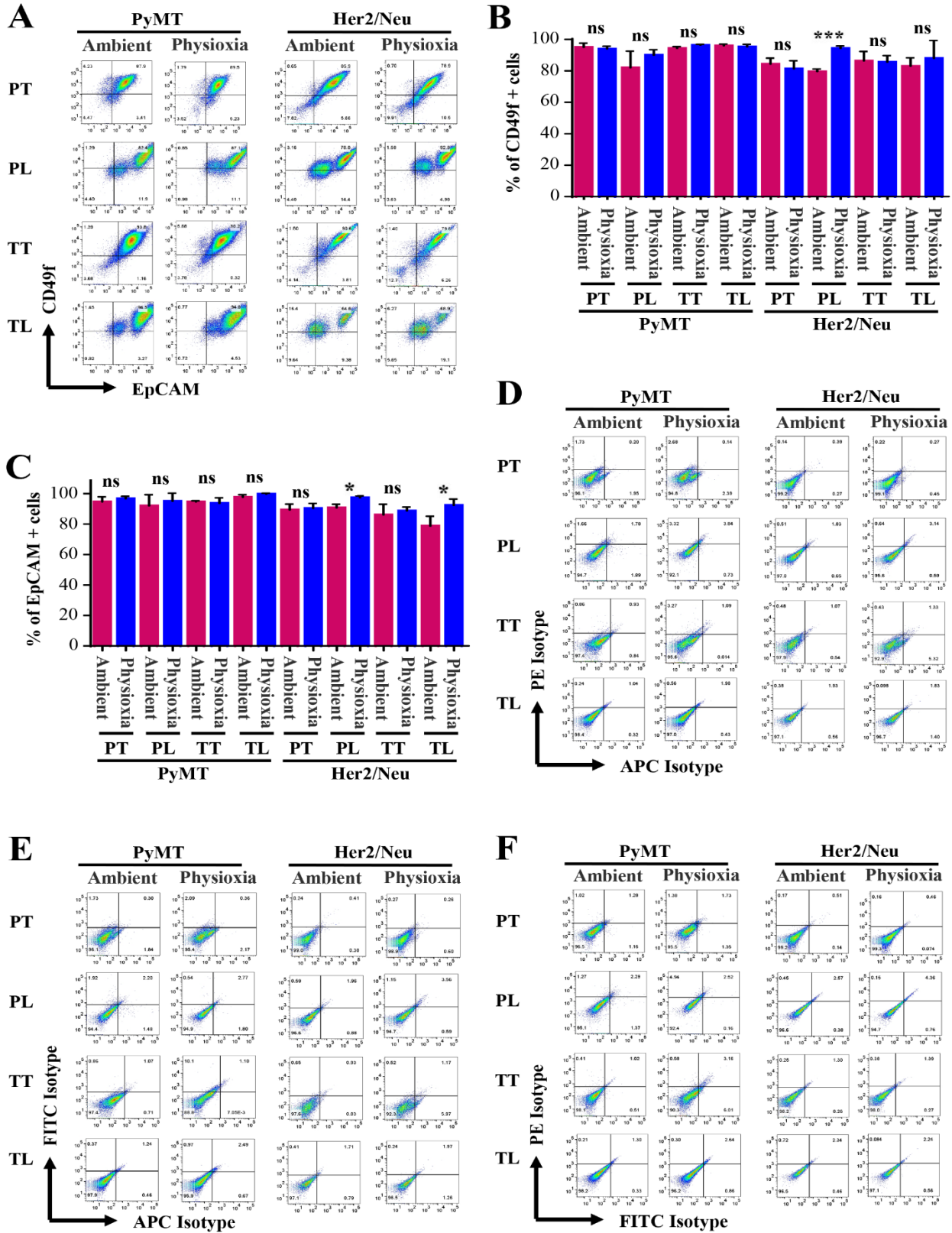


Figure S1

fig. S1: Physioxia minimally effected CD49f/EpCAM staining patterns. (A) CD49f/EpCAM staining patterns of tumor cells under physioxia and ambient air (n=3-6, one-way ANOVA). (B) Number of CD49f⁺ cells were similar under two conditions except in cultured Her2/Neu tumor cells (PL). (C) Number of EpCAM⁺ cells were similar under two conditions except in cultured Her2/Neu cells. (D-F) Staining patterns of isotype controls for the experiments that measured LGR5-PE/TSPAN8-APC, CD61-FITC/TSPAN8-APC, CD49f-PE/EpCAM-APC, CD274-PE/EpCAM-APC and CD24-APC/CD29-FITC. *p<0.05, ***p<0.001 by ANOVA. ns is not significant.

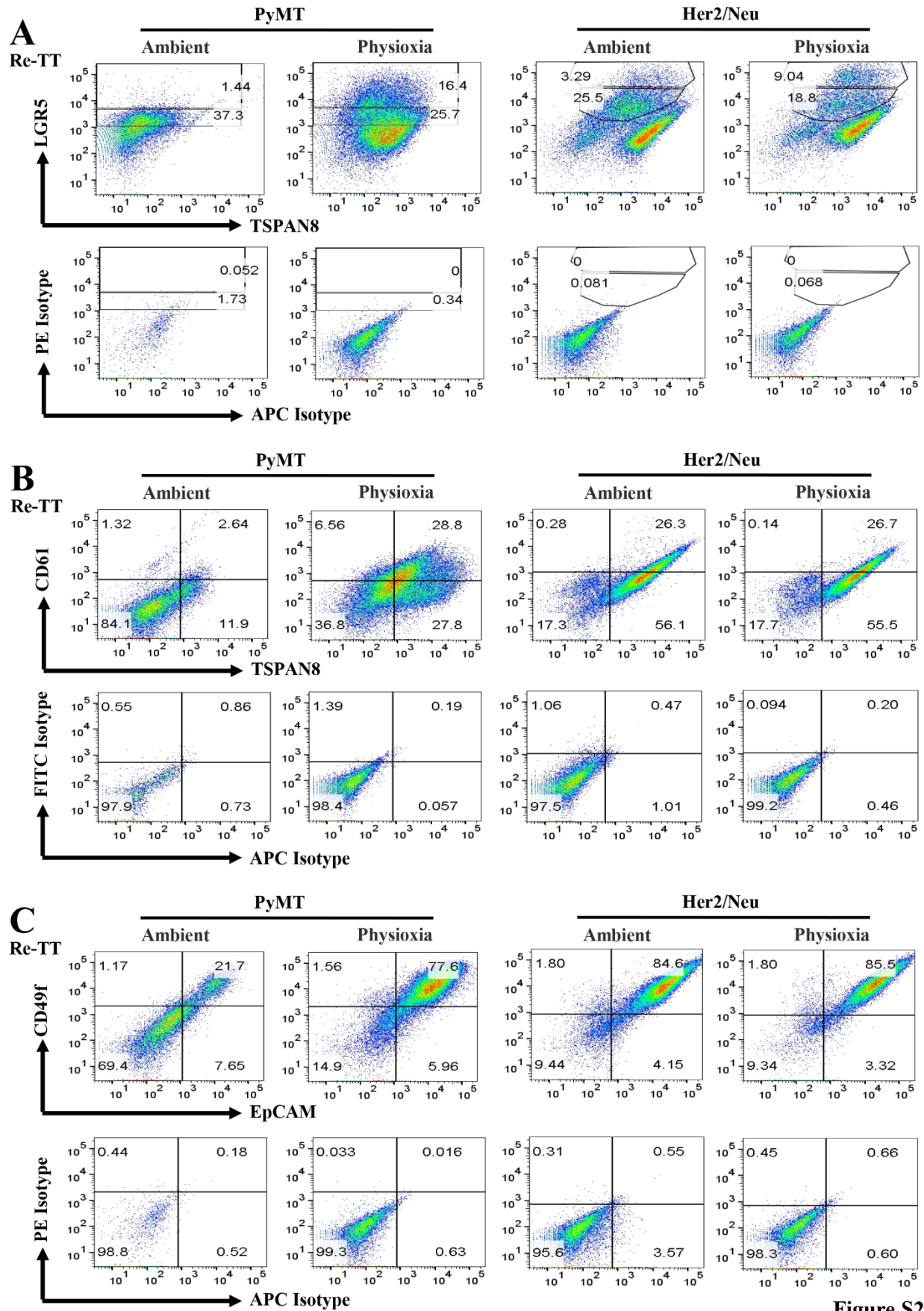


Figure S2

fig. S2: Analysis of tumors developed upon re-transplantation of cells derived from stage 3 tumors. (A) LGR5/TSPAN8 staining patterns of cells from tumors derived from stage 3 as described in Fig. 1A. (B) CD61/TSPAN8 staining patterns. (C) CD49f/EpCAM staining patterns. Representative staining patterns with isotype control antibodies are shown.

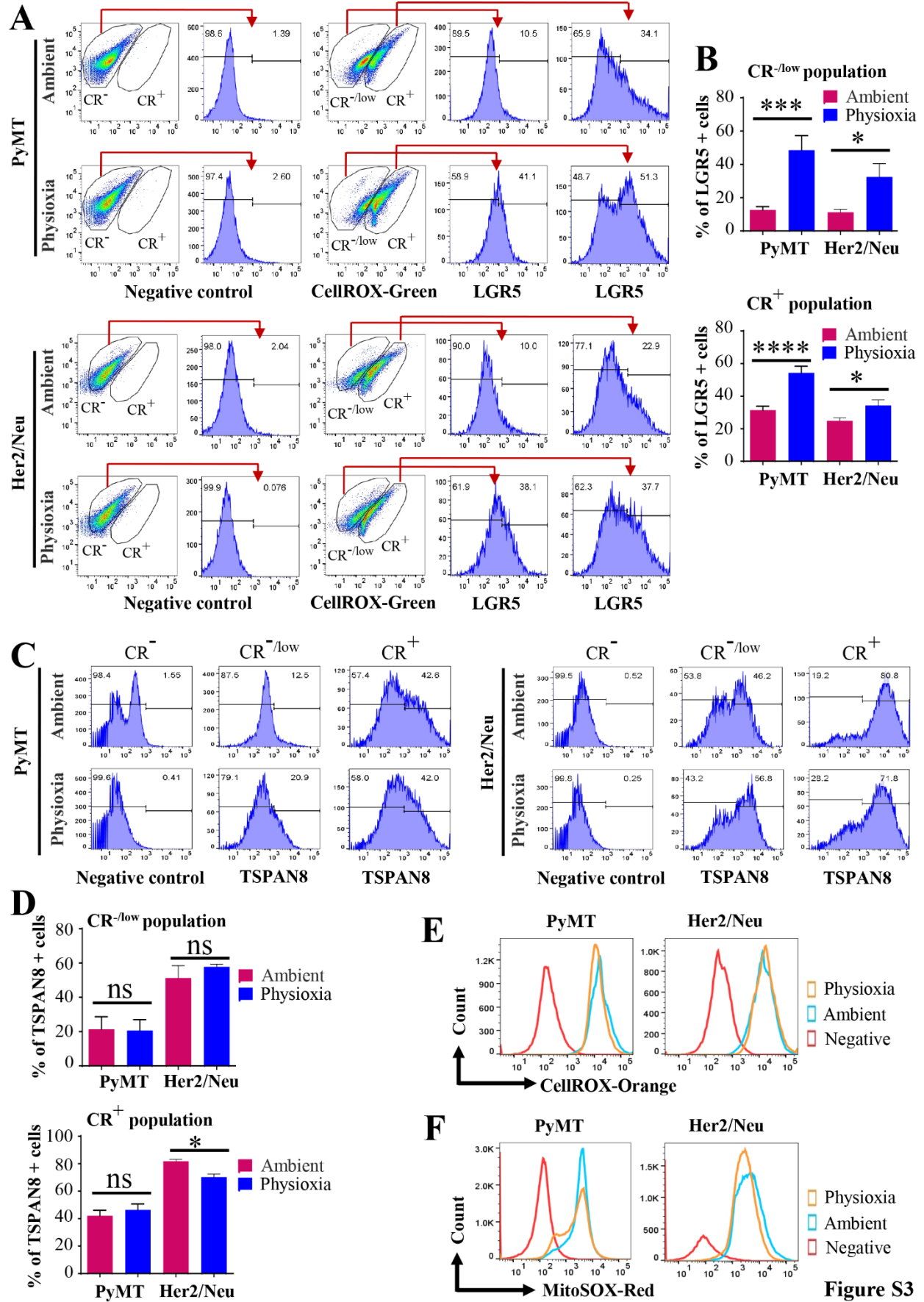


fig. S3: LGR5 positivity of CellROX-Green⁺ populations, representing cells with nuclear ROS, was higher under physioxia compared to ambient air. (A) Representative flow cytometry data showing staining patterns of CellROX-green^{-low} (CR^{-low}) and CellROX-green⁺ (CR⁺) populations in PyMT and Her2/Neu tumor cells and enrichment of LGR5⁺ cells in both populations. (B) Quantitation of LGR5⁺ cells in CellROX-green^{-low} and CellROX-green⁺ populations in PyMT and Her2/Neu tumor cells (n=3-4). (C) Representative flow cytometry data showing TSPAN8⁺ cells in CellROX-green^{-low} and CellROX-green⁺ populations in PyMT and Her2/Neu tumor cells. (D) Quantitation of TSPAN8⁺ cells in CellROX-green^{-low} and CellROX-green⁺ populations in PyMT and Her2/Neu tumor cells (n=3-4). (E) Tumor cells collected and processed under physioxia and processed under ambient air were stained with CellROX-orange and subjected to flow cytometry (n=4). (F) Tumor cells collected and processed under physioxia and processed under ambient air were stained with MitoSOX or vehicle control and analyzed by flow cytometry (n=4).

A

PyMT		Her2/Neu	
Ambient	Physioxia	Ambient	Physioxia
Carcinoma	Carcinoma	Carcinoma	Carcinoma
Carcinoma	Undifferentiated squamous cell carcinoma	Undifferentiated squamous cell carcinoma, Lymphoma	Undifferentiated squamous cell carcinoma, Lymphoma
Adeno squamous	Adeno squamous	Anaplastic squamous cell, Lymphoma	Undifferentiated squamous cell carcinoma, Lymphoma
		Undifferentiated squamous cell carcinoma, Lymphoma	Undifferentiated squamous cell carcinoma
		Carcinoma	Lymphoma, Carcinoma
		Lymphoma, Carcinoma	Carcinoma

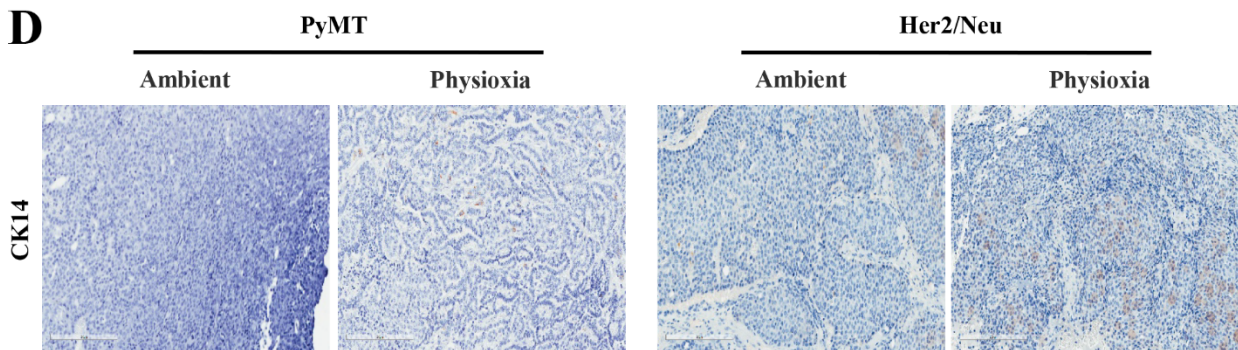
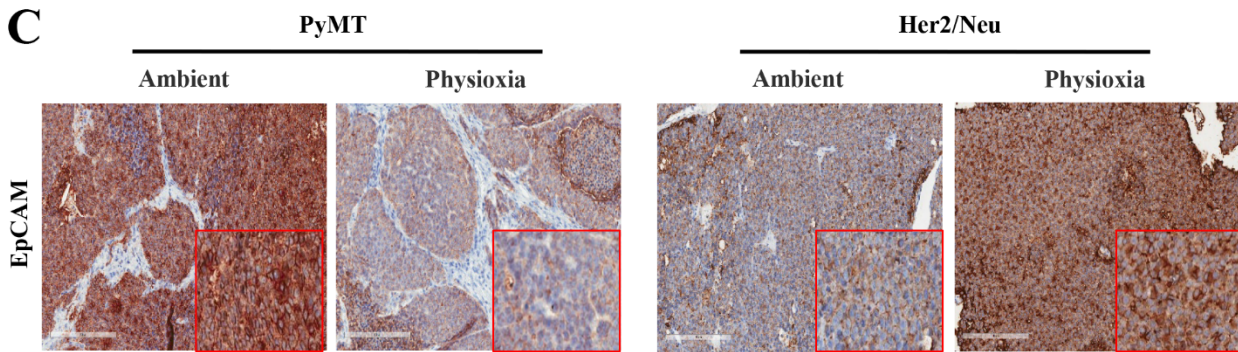
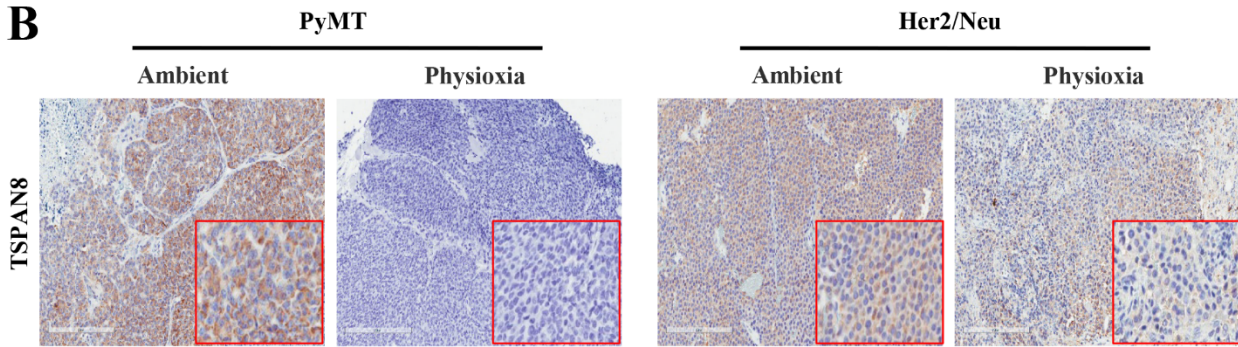
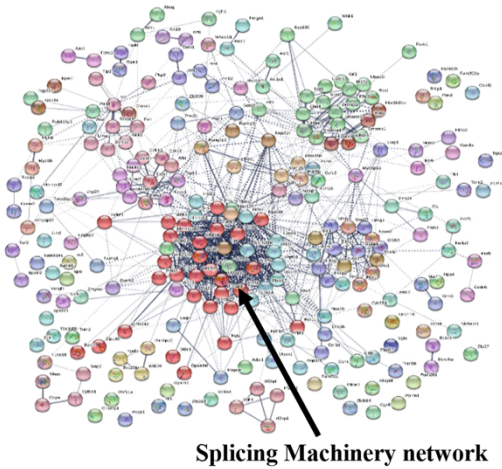


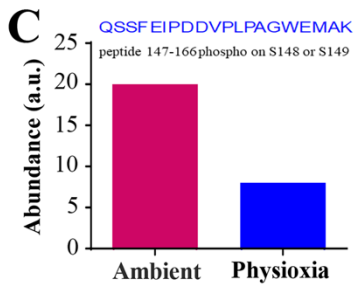
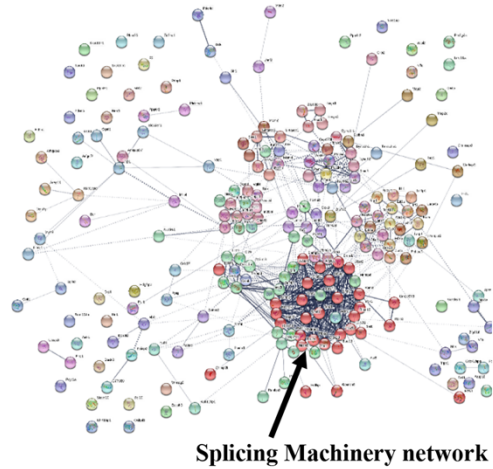
Figure S4

fig. S4: Histology of tumors developed from re-implanted tumor cells collected and processed under physioxia or processed under ambient air. (A) Tumor histotype designated by a pathologist based on H&E staining patterns (n=7). (B) Immunohistochemistry for TSPAN8 (n=7). (C) Immunohistochemistry for EpCAM (n=7). (D) Immunohistochemistry for CK14 (n=7). CK14 negativity suggests that tumors have retained luminal characteristics.

A
Networks of abundant phosphopeptides
in Physioxia



B
Networks of abundant phosphopeptides
in Ambient air



D

YAP1	Position of peptide (QSSFEIPDDVPLPAGWEMAK)	Position of phospho Serine
Mouse	147 - 166	S148 and S149
Human	162 - 181	S163 and S164

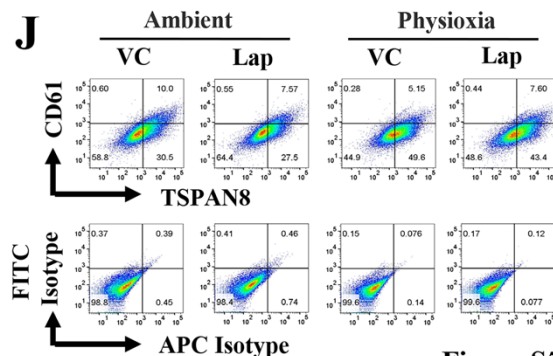
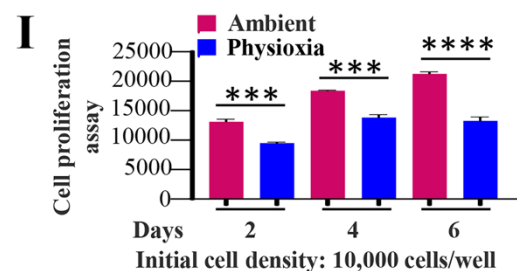
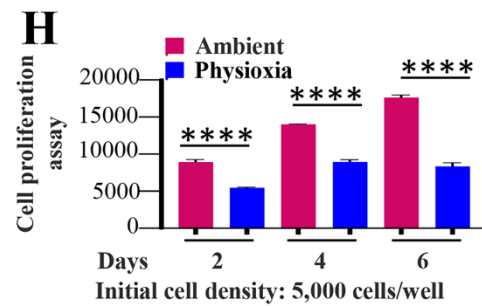
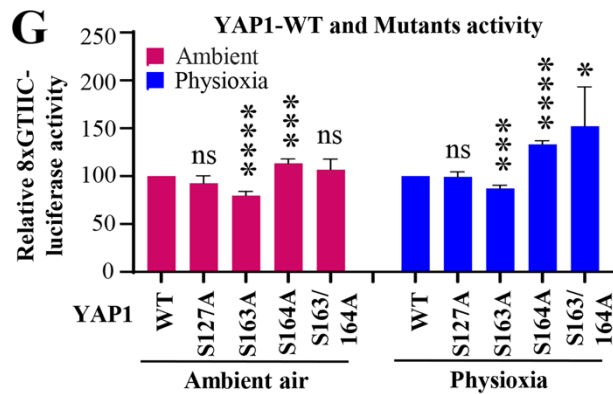
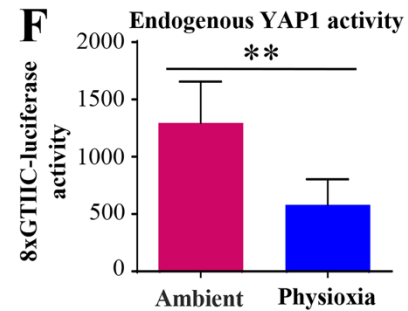
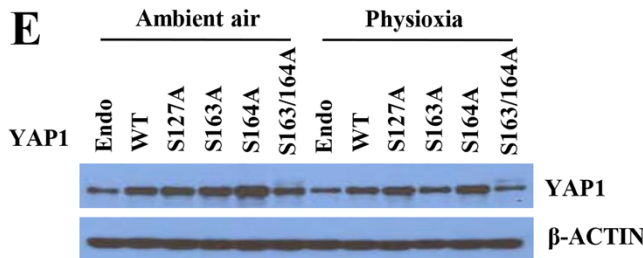


Figure S5

fig. S5: Phospho-proteomics reveal a specific effect of physioxia on splicing machinery and YAP1 signaling. (A) STRING network analysis of phospho-proteins abundant under physioxia. (B) STRING network analysis of phospho-proteins abundant under ambient air. (C) Phosphoproteomics show decreased phosphorylation on either S148 or S149 within the peptide spanning residues 147-166 under physioxia relative to ambient air. (D) Table shows phosphopeptide position in mouse YAP1 and position of the phosphoserines, including corresponding positions in human YAP1. (E) Western blots show expression of YAP1 in HEK293T cells transfected with the indicated plasmid constructs under ambient air and physioxia. HEK293T cells were grown and transfected with indicated plasmid constructs under physioxia, cells were split into two equal parts 24 hours post-transfection, with one portion grown in physioxia and the other in ambient air. Cells were lysed after 24 hours for western blotting. Endo, endogenous expression. (F) Decreased endogenous YAP1 activity under physioxia compared to ambient air as indicated by luciferase reporter activity (n=5). (G) Differential YAP1 activity in HEK293T cells co-transfected with indicated plasmid constructs and 8xGTIIC luciferase under physioxia and ambient air (n=5). Activity of wild type YAP1 was normalized to 100 and relative activity of mutants with specific non-phosphorylatable residues is shown. (H and I) Tumor cells processed and grown under ambient air showed higher proliferation rate. Indicated number of PyMT tumor cells were plated in 96 well plates and cell proliferation rates were measured on indicated days after plating (n=6). (J) CD61/TSPAN8 staining pattern of tumor cells from transplanted PyMT tumor xenografts developed from tumor cells collected and processed under ambient air and physioxia, and treated daily with 100 mg/kg body weight lapatinib (Lap) or vehicle control (VC) via oral gavage for 25 days (n=3). ***p<0.001, ****p<0.0001 by ANOVA.

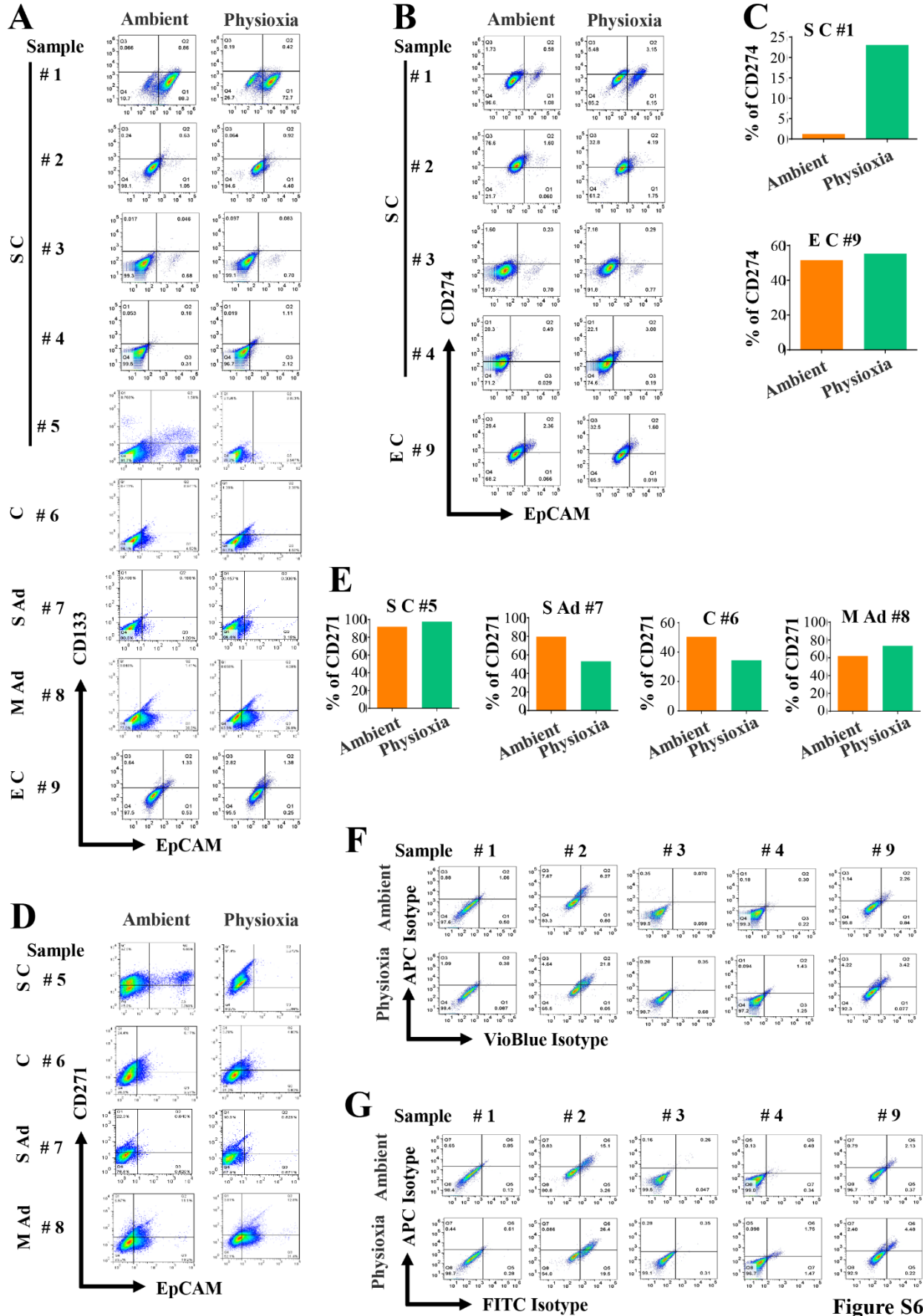


Figure S6

fig. S6: Characterization of cells from ascites fluids collected and processed under physioxia and ambient air. (A) CD133/EpCAM staining pattern of lineage-negative cells from ascites fluid (n=9). (B) CD274/EpCAM staining pattern of cells from ascites fluid (n=5). (C) Cells cultured from ascites fluid of a serous carcinoma under physioxia showed elevated levels of CD274⁺ cells. (D) CD271/EpCAM staining pattern of cells from ascites fluids (n=4). (E) Physioxia displayed tumor subtype-specific effects on CD271⁺ cells. (F and G). Isotype control antibody staining patterns for cells derived from ascites fluids that measured CD49f-APC/EpCAM-VioBlue, CD44-APC/CD24-FITC, CD133-APC/EpCAM-VioBlue, CD274-APC/EpCAM-VioBlue and CD271-APC/EpCAM-VioBlue.

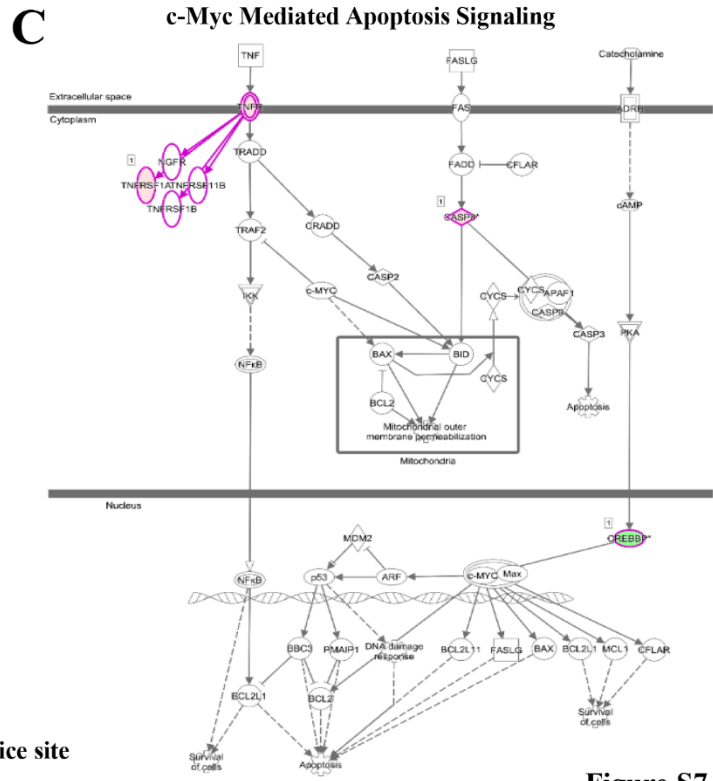
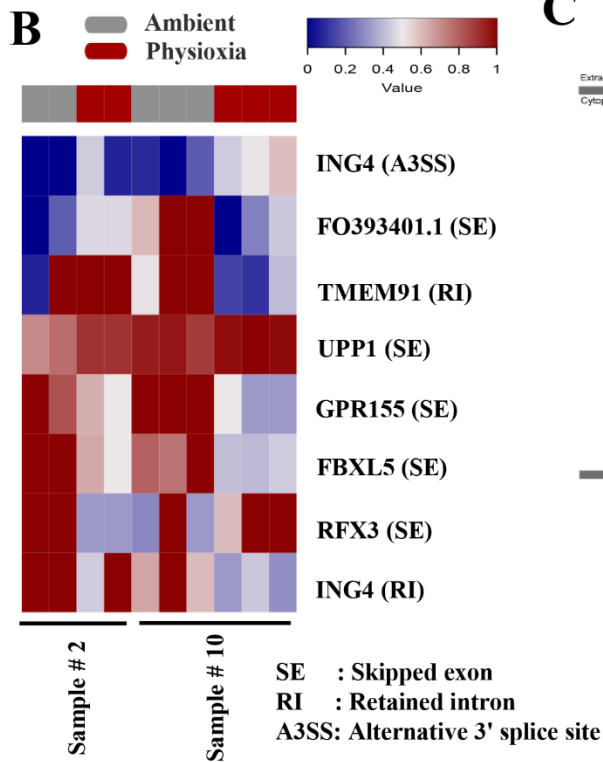
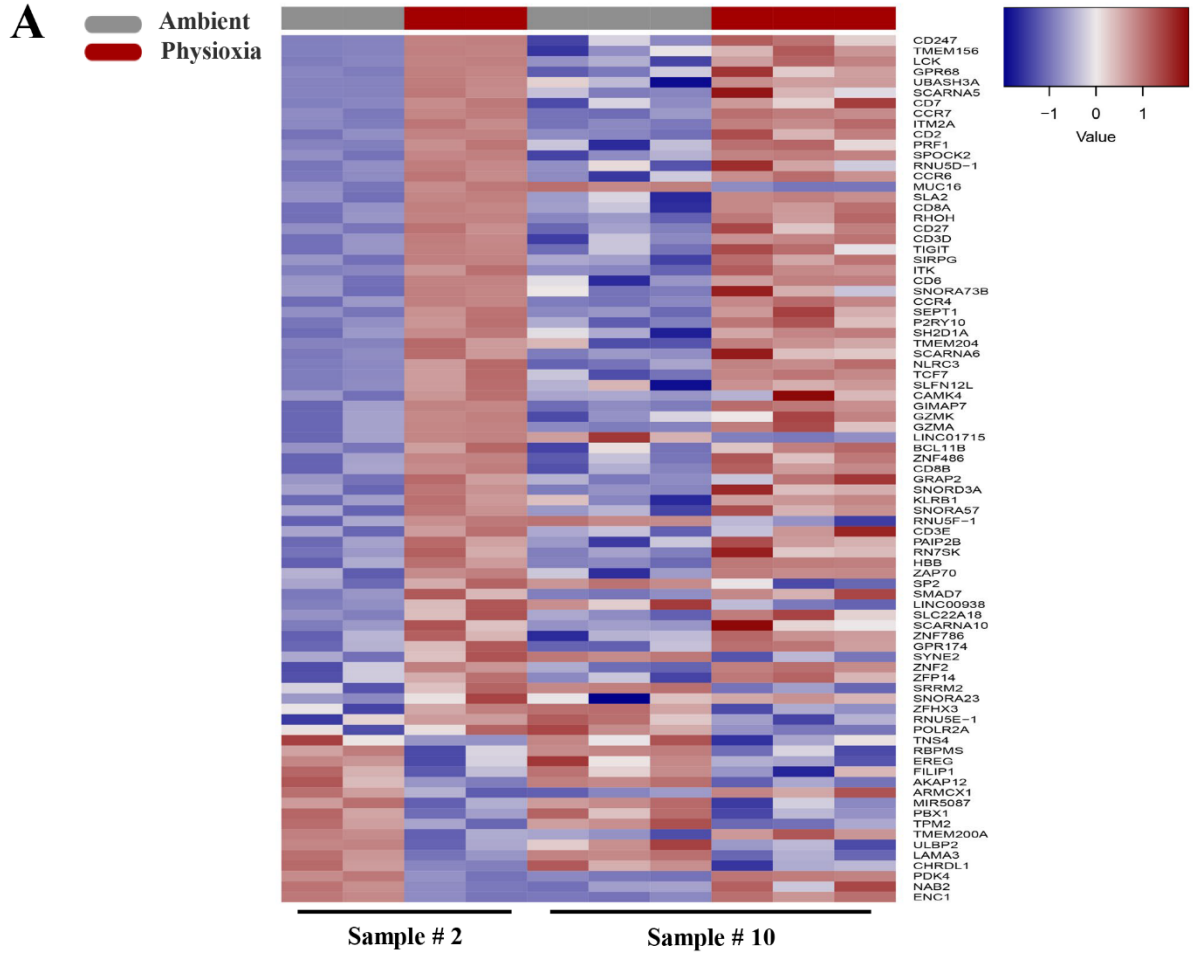


Figure S7

fig. S7: Heatmap of genes differentially expressed and alternatively spliced genes in cells of ascites fluid collected and processed under physioxia compared to that collected and processed under ambient air. (A) Heatmap of differentially expressed genes in cells collected and processed under physioxia compared to cells collected and processed under ambient air. Differentially expressed genes from independent analyses were filtered for $FDR \leq 0.05$ and absolute $\log_2FC \geq 0.5$. Genes passing filters and common in both patients were then used to generate the heatmap. \log_2FPKM values were centered and scaled by gene in each experiment separately. Color bar at the top denotes ambient air or physioxia condition. (B) Heatmap of differentially spliced genes in cells collected and processed under physioxia compared to cells collected and processed under ambient air. Differentially spliced events from all event types were merged and filtered in both experiments. Events having an $FDR \leq 0.05$ and a minimum number of 5 inclusion or exclusion reads across all replicates in a group, as well as having at least 1 inclusion or exclusion read in all replicates from both groups, were kept. These filters ensured events were significant, sufficiently covered and consistently present respectively. Inclusion levels of the remaining 8 exons were directly plotted for each gene and sample replicate. Color bar at the top denotes ambient air (gray) or physioxia (red) condition. (C) Ingenuity pathway analysis (IPA) of alternatively spliced genes under physioxia compared to ambient air. These genes are part of cMyc-mediated apoptotic pathways.