SI A. Label changes in relation to vent settings changes

Table A.3 shows that most vent settings changes are accompanied by changes in labels. However, very few phenotype label changes correspond to changes in vent settings. *Over 64% of ventilator settings changes are identified in label changes.* A larger proportion (>87%) are identified when limited to PEEP, tidal volume, and model changes, which induce significant waveforms changes compared with other settings such as mandatory breath rate (set_rate). *Few (8%) identified changes in label, however, are directly associated in time with ventilator settings changes.*

Table A.3: N_s indicate the number of ventilator settings changes in set_PEEP, set_ptrigger, set_qtrigger, set_rate, set_fio2, set_ie, set_flowpat, set_mode, set_vt, and vt_set. N_l indicates the number of persistent label changes, counting those lasting longer than 30 seconds, to omit isolated transient changes and variability occurring as mixed-breath types (*e.g.*, FigB.7 during 11–14 hours, characterized by both alternation between labels #10 and #13 labels and changes in ML-identified VD type.) Column 's2l' indicates the percentage of vent settings changes that occur with a label change within 100 secondsColumn 'l2s' indicate the number of label changes that occur within 100 seconds of vent changes.

ID	N_s	s2l (%)	N_l	l2s (%)	ID	N_s	s2l (%)	N_l	l2s (%)
101	45	73.33	66	16.67	129	11	45.45	138	3.62
102	1	-	1	-	130	14	85.71	296	6.42
103	2	100.00	35	8.57	131	10	70.00	25	20.00
104	25	36.00	356	1.97	133	37	78.38	154	18.83
105	1	100.00	46	4.35	134	76	5.26	175	0.57
107	99	56.57	288	9.72	135	104	86.54	695	6.47
108	20	75.00	342	2.92	136	222	59.01	590	6.78
110	3	33.33	73	1.37	137	137	54.01	166	14.46
111	23	78.26	328	7.01	138	10	60.00	38	21.05
112	59	45.76	177	6.21	139	24	70.83	451	3.99
113	14	78.57	260	6.15	140	47	100.00	629	1.75
114	48	29.17	50	24.00	141	73	45.21	431	7.42
115	0	-	4	0	143	37	62.16	713	2.66
116	83	80.72	370	12.70	144	83	77.11	421	9.03
117	13	76.92	1000	1.40	145	50	62.00	380	8.42
119	51	98.04	265	8.30	146	220	42.27	650	9.38
120	57	40.35	246	8.94	149	39	25.64	296	4.73
123	18	88.89	460	3.91	150	12	75.00	424	2.12
					mean	52	64.57	325	8.00

SI B. Individual Experiments, continued

This supplement continues illustrated examples of §3.1.

Figure B.6 panels a–d illustrate the analysis of Patient #103 whose data consists of 7 record hours with one simple ventilator setting change. Only ventilator PEEP (a) is changed while there are three primary behaviors identified (b,d). The reduction of PEEP occurs about 2 hours following a rise in early flow limited breaths (eFL, panel c). This PEEP change (from 8 to 5 cm H_2O) shifts peak pressure from 16 to 12 cm H_2O for about an hour, at which time higher esophageal pressures returns. These breaths are identified as normal (NL) [11]. Increased specificity may be pursued by local segmentation or other dimensional reduction methods.

A closer look at label 1 of patient #103:. The first principal component loadings (panel e, black) for LVS descriptors over the first 5-hour period track the sequence of normal and eFL VD labels (f, shown as 5 minute statistics for clarity). Within the same breath phenotype (label 1), the *sign* of the component loading statistically the eFL VD labels (AUROC=0.8718); high positive values are associated with eFL breaths (f,g; green) where pressure maxima proceed volume maxima. These LVS variations result from changes in the patient component, as there is no change of ventilator settings. Note that direct correlation between continuous loading values on 10 second windows and statistical breath-wise binary VD label is not well-defined while binary-to-binary comparison is.

The patient #113 (Figure B.7) dataset is nearly twice as long with again only one PEEP change occurring after 10.5 hours of the 15.6 hour record. Breaths are stably identified as normal-type until about 8 hours,

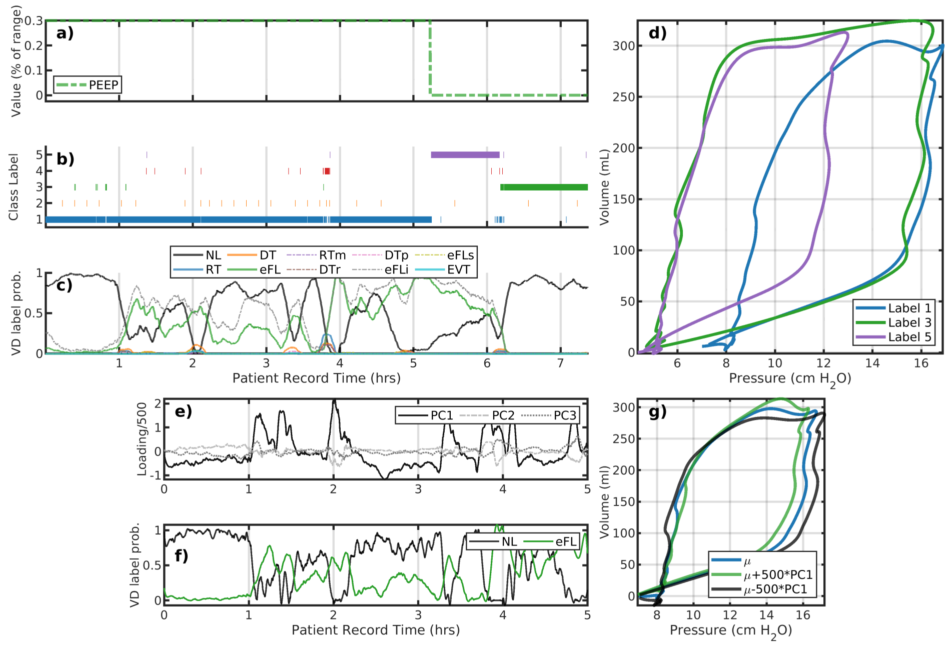

Figure B.6: Analysis of patient #103 LVS data (a–d) and the initial a 5-hour interval (e–g). Panels a–c correspond to changes in ventilator settings, segmentation labels, and identified VD type, respectively. The horizontal axis for these panels is the patient record time in hours. The panel (d) shows the model image of segmented data median parameters, which characterize the pV loops of breaths with that label (shown with the same color). Evolution of the LVS can be parsed pictorially from these figures. Large positive variations in the first principal component loading (e, black) for the initial 5-hour period align with VD labels indicating eFL type breaths (f) for this period. Specifically, this suggests discrimination of breaths shapes (g) can be differentiated using qualitatively criterion on local loadings or other segmentation.

occupying two cluster-identified similar breath shapes. This is followed briefly by eFL breaths and a transition to a new characterization (label 8, light green) for about 30 minutes. In the following period (9–14 hours), breaths are characterized by lower pressure maxima (label 10, gold); these are associated/identified with reverse-trigger breaths (primarily RTm) and waveforms featuring pronounced inspiratory pressure drop. The reduction in PEEP slightly increases the incidence of normal breaths during 11–14 hours although this results in the more frequent appearance of shallow breaths (label 13, red).

SI B.1. Intracluster normal and eFL in p111, label2

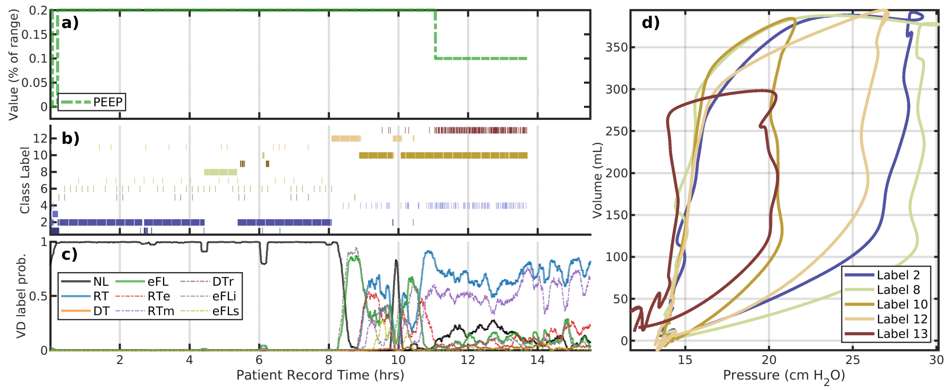

Figure B.7: The patient #113 evolution also includes only PEEP changed. The layout is the same as panels a–d of the previous figure. Under constant ventilator settings, breaths undergo transition several times including intervals of VD prior to PEEP change around 10.5 hours. A 1-hour long shift from label 2 to 8 occurs around 8 hours during which breaths decrease peak pressure and includes an increase in eFL and RT VD occurrence. After the PEEP change, breaths remain highly dyssynchronous and primarily centered around the characterization with label 10.

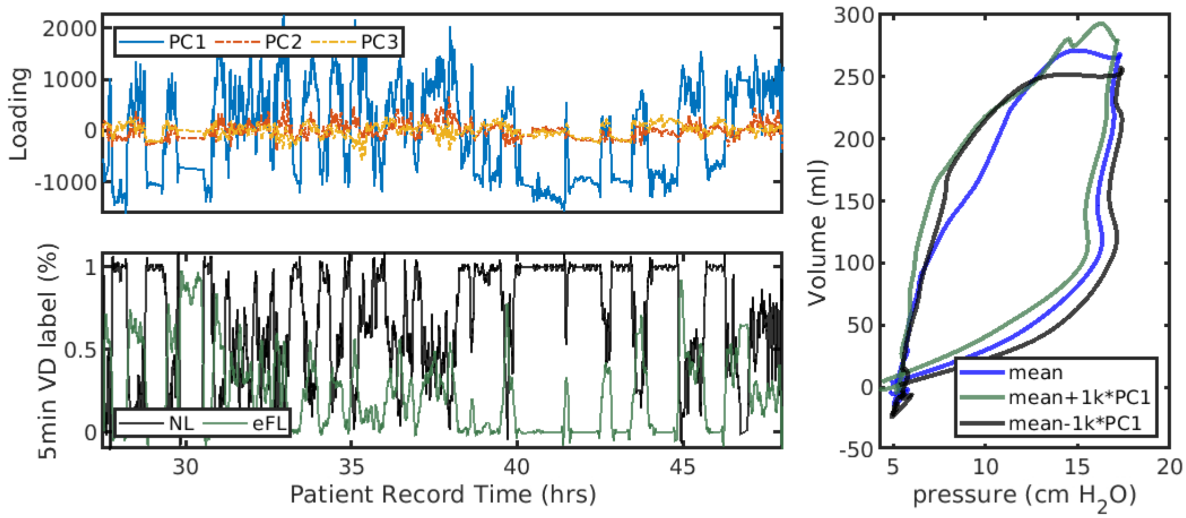

Figure B.8: The sign of PC1 loading roughly divides the VD classes in p111, label2. A threshold for the PC1 loading at zero roughly separates NL and eFL labels by 34%/65% and 85%/14%, respectively, with NL labels strongly associated with negative loadings. The optimal threshold (∼0.05) offers only subtle improvement. The right panel illustrates low fidelity changes in the cluster median pV loop (blue) when modified by these negative (black, more associated with NL) and positive (green, eFL) loadings. Note that this involves comprising 10-second properties (representing typically ∼3–4 breaths) to breath-wise labels, and some representation errors thus arise from summarizing binary VD labels over all breaths intersecting a 10-second analysis window.

SI B.2. Qualitiative equivalence of labels via tSNE & UMAP

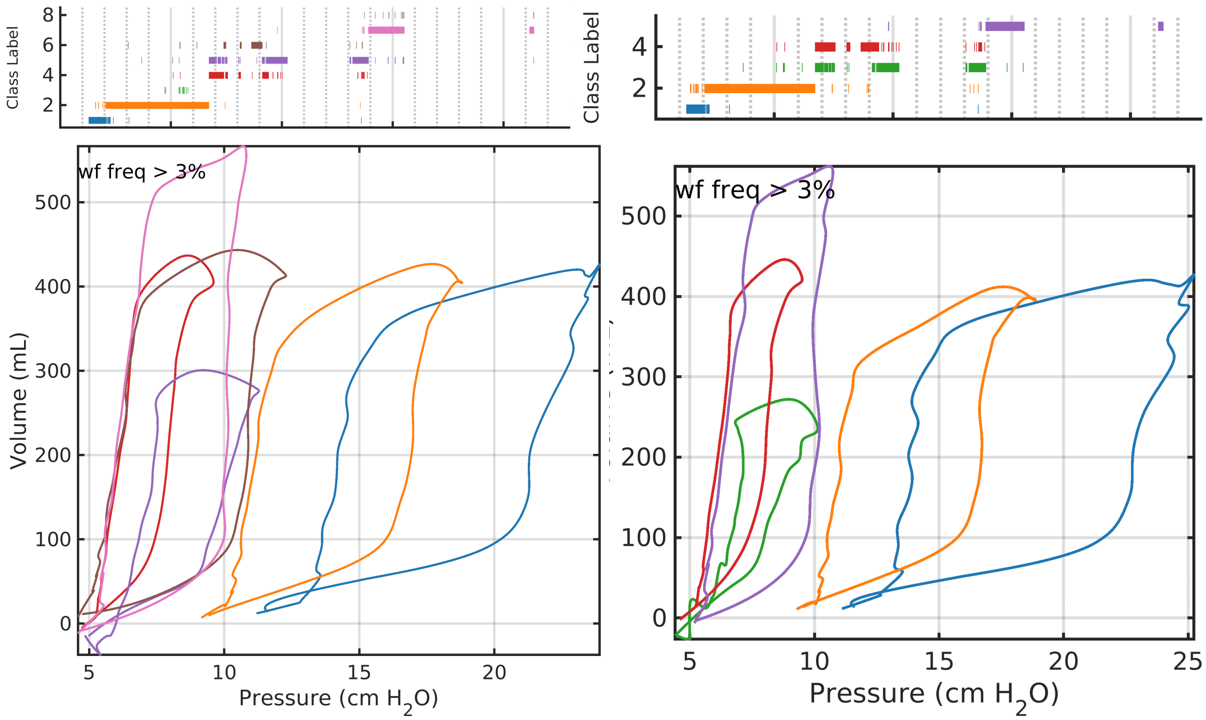

Figure B.9: Patient 101 clustering using tSNE (left) and UMAP (right) feature reduction stages, as an example. Temporal evolution of the LVS is qualitatively similar regardless of whether UMAP (neighbor size=5, minimum distance=0.01) or tSNE (exaggeration=20, perplexity=50, 5000 iterations) projection is used. DBSCAN parameter must also be adjusted as coordinate scales differ between the projections. For the plot shown, DBSCAN hyper-parameters (N_{pts}, ε) are (10,4) following tSNE and (4,1.5) following UMAP. Mild variations in pV characterizations result from medians of different point distributions.

SI C. Influence of Hyperparameter choices on cohort phenotypes

For each of the 721 individual phenotypes, feature vectors defined by the 5-number summaries of period, PEEP, maxima of volume and pressure, ventilator settings, and estimated parameters of range-normalized waveform were assembled from the population of LVS windows with a given label. Ventilator mode was represented as a vector of percentages of each mode rather than a vector of binary categories, which eliminated the need for the Gower distance. UMAP applied to these cohort feature vectors with the scaled-euclidean metric produced a relatively stable point configuration across various hyper-parameter choices; 12 point neighborhoods (2% of data) with a minimum distance of 1 unit were adopted as values. Identified groups were more sensitive to DBSCAN labeling hyper-parameters. Figure C.10a shows the possibilities of different groupings based on the search neighborhood size (ε). Subsequent results in the main section employ a hyper-parameter choice at the 'knee-point' [39] to balance generalizability and specificity. A more specific labeling ($\varepsilon = 2.5$) shown in panel b, is qualitatively similar to that of main text.

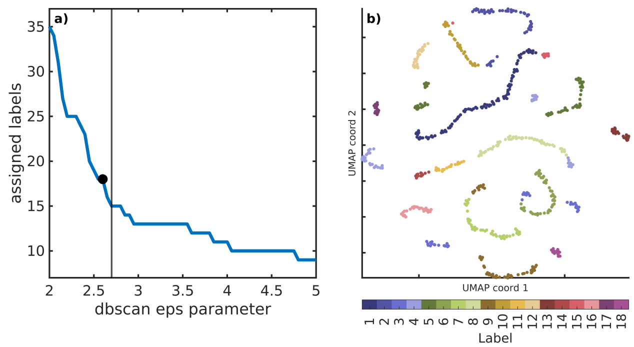

Figure C.10: DBSCAN search radius (ε) *v.* the number of identified groups. The black line indicates $\varepsilon = 2.7$ selected for cohort clustering. Choices of $\varepsilon \in [2.67, 2.82]$ yield equivalent results following increased granularity of groupings at ε lower values.

Table C.4: The equivalent of Table2 for the alternate choice of hyper-parameter $\varepsilon = 2.5$

Label	Total%	N_{pat}	N_{pheno}	p_{min}	p_{drive}	V_{max}	dp/dV	MV mode
1	15.5	11	101	8	12.7[4.1]	7.9[1.3]	1.5[0.4]	APVCMV
2	11.4	16	52	12	13.3[3.6]	6.2[2.1]	2.3[1.2]	PCMV*
3	8.4	5	37	10	13.5[1.9]	6.5[0.3]	2.1[0.4]	APVCMV*
4	7.7	8	45	14	12.6[2.9]	6.2[1.3]	1.9[0.7]	APVCMV
5	6.9	11	58	16	13.4[2.3]	6.0[0.6]	2.2[0.6]	APVCMV
6	6.3	7	49	11	16.6[12.5]	5.9[0.7]	3.4[2.4]	APVCMV
7	6.2	6	49	8	11.1[1.4]	6.6[1.0]	1.7[0.2]	APVCMV
8	6.2	23	56	10	12.1[3.7]	6.3[1.0]	1.9[0.6]	APVCMV
9	6.2	10	51	14	21.3[9.5]	5.6[1.8]	3.7[3.1]	APVCMV
10	4.1	12	34	14	12.2[6.9]	5.9[0.2]	2.0[1.3]	APVCMV*
11	4.0	14	20	5	8.9[4.1]	7.0[2.4]	1.2[0.8]	APVCMV
12	3.7	16	25	12	14.3[3.2]	6.0[0.4]	2.3[0.9]	PCMV**
13	3.4	17	22	11	13.1[2.9]	6.2[1.3]	2.1[0.5]	APVCMV***
14	3.3	11	12	8	9.7[2.7]	6.8[1.5]	1.6[0.4]	APVCMV
15	2.5	8	10	12	15.1[12.5]	5.9[0.1]	2.4[2.2]	APVCMV
16	1.7	11	27	14	13.3[2.9]	6.0[1.3]	2.0[0.8]	APVCMV
17	1.5	9	14	16	15.9[6.0]	5.9[2.8]	2.6[2.4]	APVCMV
18	1.1	5	16	5	10.7[0.2]	6.5[0.7]	1.7[0.2]	APVCMV