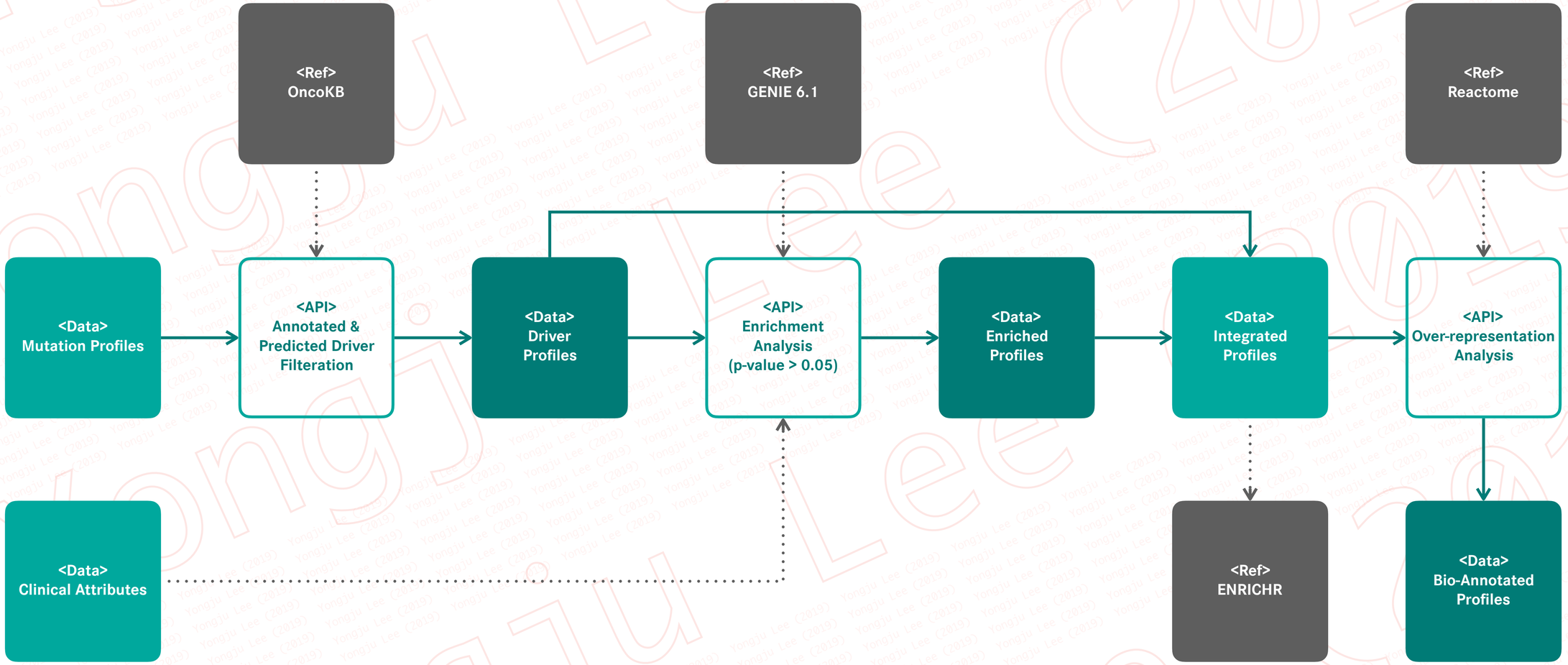
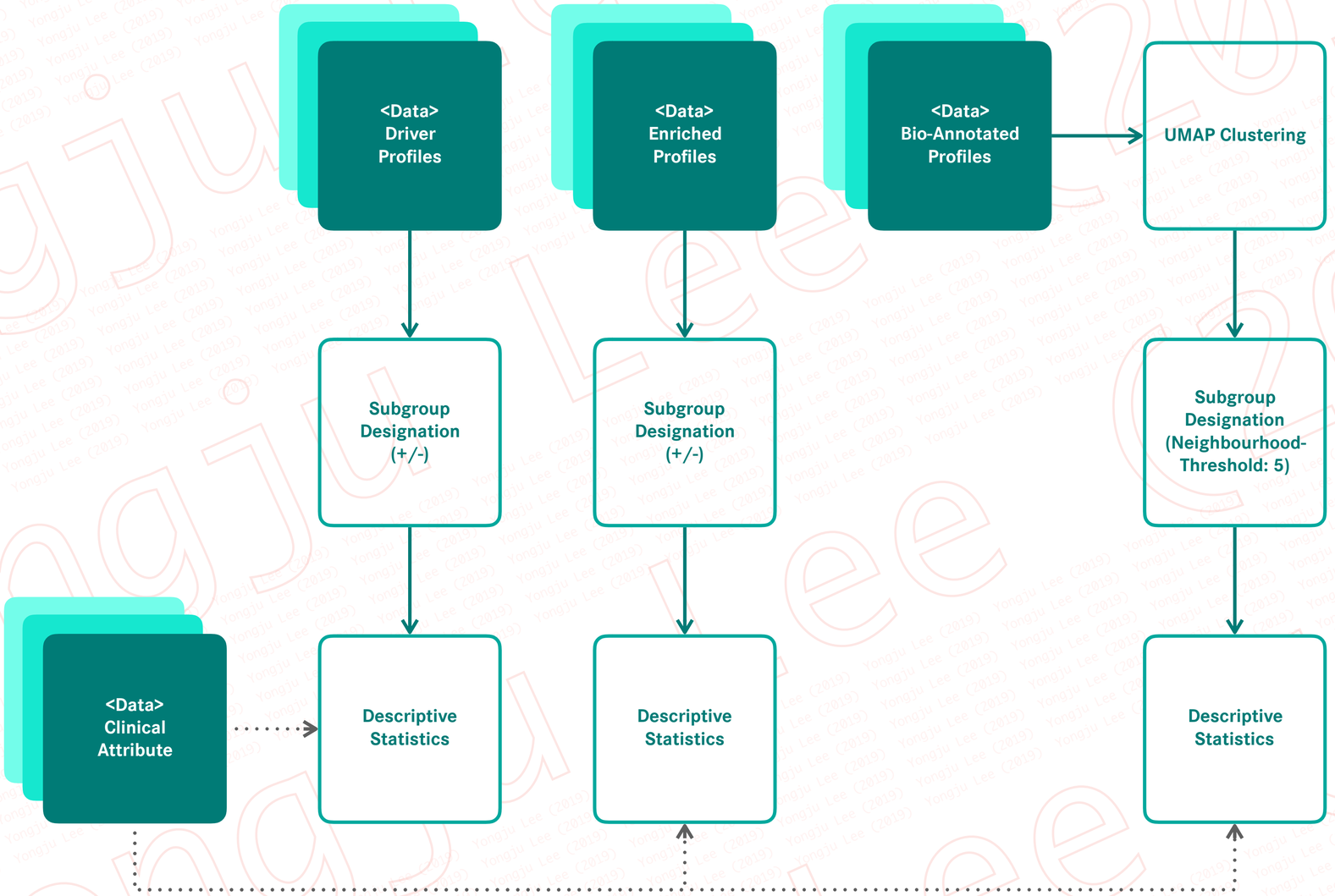
Patient-level



Study-level

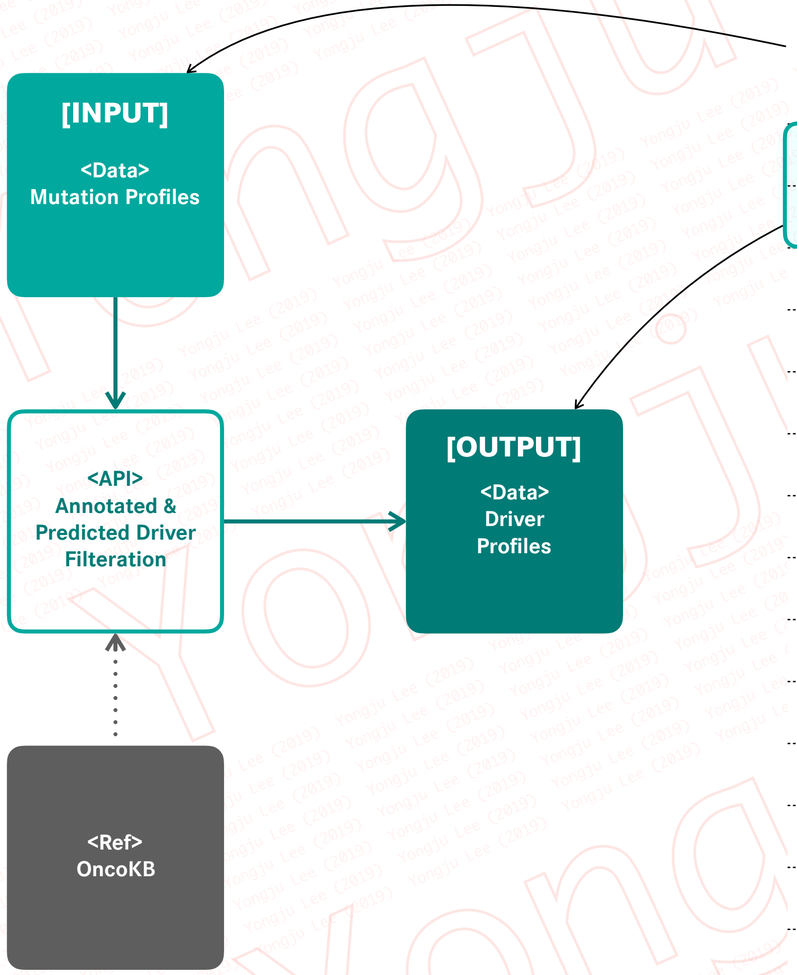

<Data>
Driver
Profiles
<Data>
Enriched
Profiles
<Data>
Bio-Annotated
Profiles
UMAP Clustering
Subgroup
Designation
(+/-)
Subgroup
Designation
(+/-)
Subgroup
Designation
(Neighbourhood-
Threshold: 5)
<Data>
Clinical
Attribute
Descriptive
Statistics
Descriptive
Statistics
Descriptive
Statistics

1. 환자별 Mutation 리스트 & OncoKB Annotation

[INPUT] 환자별 Mutation을 Gene과 해당 Gene의 Protein Change를 받아

[FILTER] OncoKB 최신 Annotation dataset을 맵핑하여

[OUTPUT] 1) Oncogenic이거나 2) Likely Oncogenic인 “Driver Gene”들만 추림



Gene	Protein Change	Annotation
BRAF	KIAA1549-BRAF	**OncoKB: Oncogenic, level_3b**;CIViC: Predictive: 8, Functional: 1, Diagnostic: 2, Prognostic: 2;MyCancerGenome: no
PTEN	X85_splice	**OncoKB: Likely Oncogenic, level_4**;CIViC: NA;MyCancerGenome: not present;CancerHotspot: no;3DHotspot: no
TSC2	D1644N	OncoKB: Unknown, level NA;CIViC: NA;MyCancerGenome: not present;CancerHotspot: no;3DHotspot: no
VAV1	D295N	OncoKB: Unknown, level NA;CIViC: NA;MyCancerGenome: not present;CancerHotspot: no;3DHotspot: no
ARID1B	R1062Q	OncoKB: Unknown, level NA;CIViC: NA;MyCancerGenome: not present;CancerHotspot: no;3DHotspot: no
ADGRB1	A214T	OncoKB: NA;CIViC: NA;MyCancerGenome: not present;CancerHotspot: no;3DHotspot: no
CETP	S275Y	OncoKB: NA;CIViC: NA;MyCancerGenome: not present;CancerHotspot: no;3DHotspot: no
DES	N311del	OncoKB: NA;CIViC: NA;MyCancerGenome: not present;CancerHotspot: no;3DHotspot: no
GYPA	R116*	OncoKB: NA;CIViC: NA;MyCancerGenome: not present;CancerHotspot: no;3DHotspot: no
TMPRSS15	T685M	OncoKB: NA;CIViC: NA;MyCancerGenome: not present;CancerHotspot: no;3DHotspot: no
GDF5	N483Y	OncoKB: NA;CIViC: NA;MyCancerGenome: not present;CancerHotspot: no;3DHotspot: no
PKP4	S959L	OncoKB: NA;CIViC: NA;MyCancerGenome: not present;CancerHotspot: no;3DHotspot: no
SCAF11	R788H	OncoKB: NA;CIViC: NA;MyCancerGenome: not present;CancerHotspot: no;3DHotspot: no
PLCH2	R207Q	OncoKB: NA;CIViC: NA;MyCancerGenome: not present;CancerHotspot: no;3DHotspot: no
ARHGAP32	G1366S	OncoKB: NA;CIViC: NA;MyCancerGenome: not present;CancerHotspot: no;3DHotspot: no

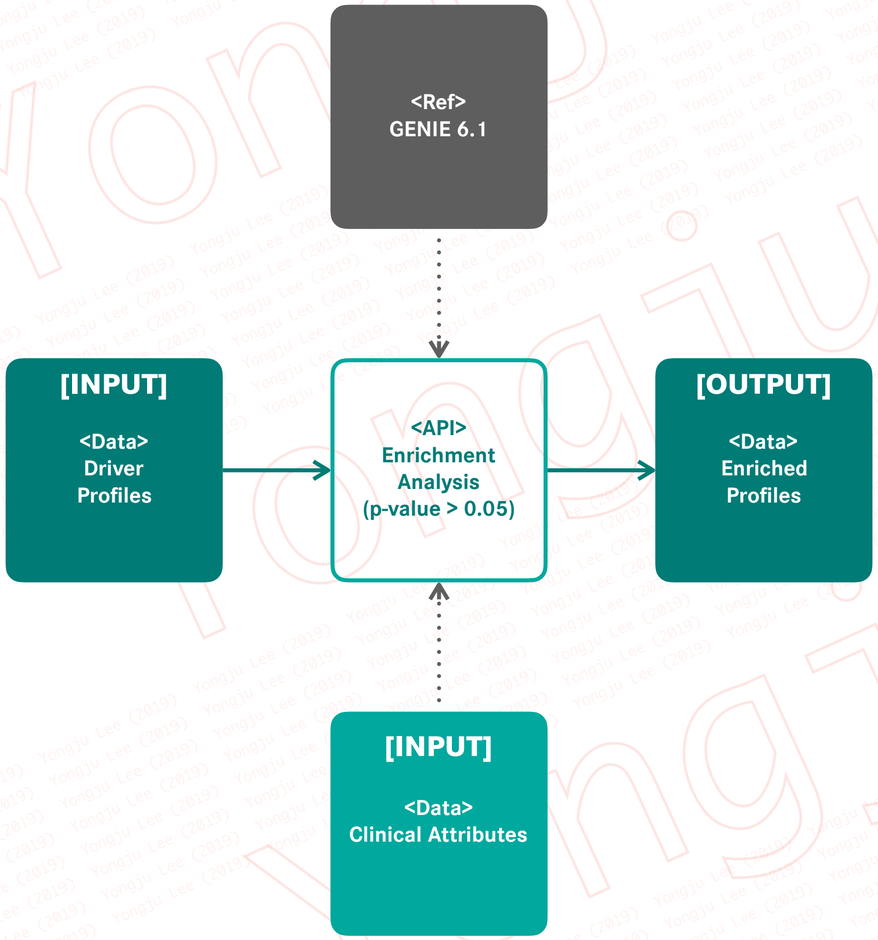
2. Enrichment Analysis

[INPUT] 1) 추려진 “Driver Gene”들과, 2) 환자의 a. Oncotree(i.e., BRCA, ICD, ILC, PRAD, etc.) 코드와, b. Sample type(i.e., Primary or Metastasis)를

[FILTER] CBioPortal Genie에서 동일한 a. Oncotree code와 b. Sample type 조건을 준 뒤,

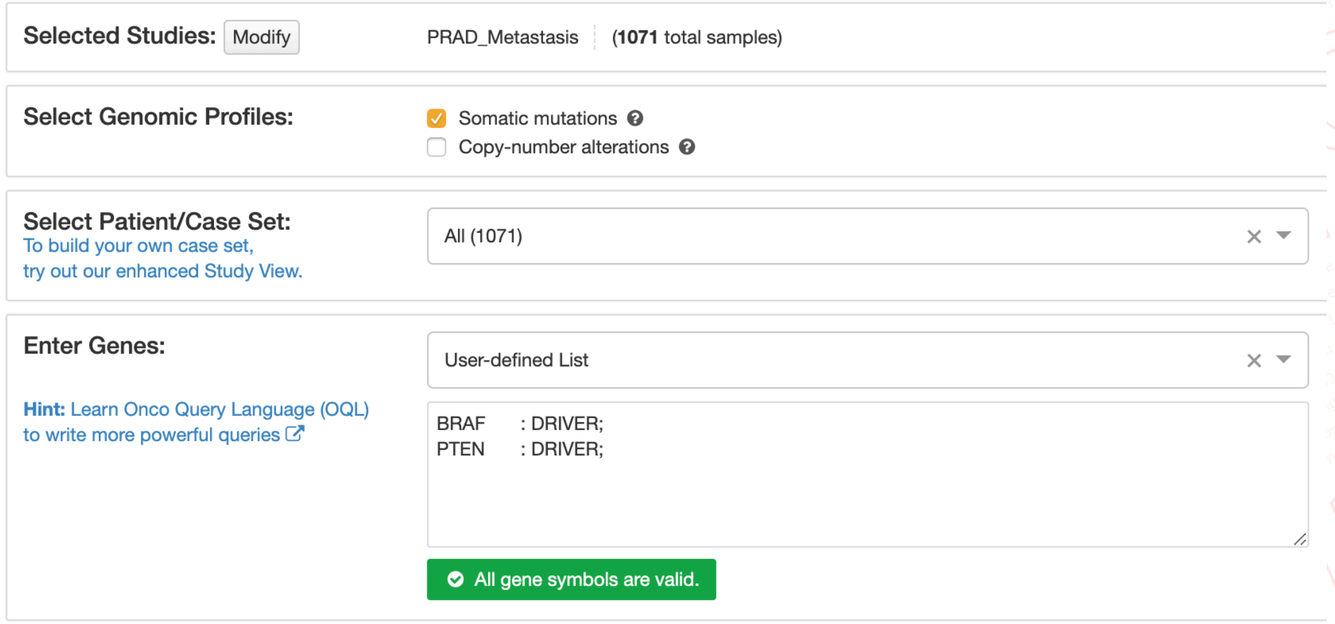
“Driver Gene”당 “: MUT_DRIVER;” 스트링을 붙여 (OQL; Oncology Query Language) Enrichment 분석 (이때, Genomic profile은 Somatic mutations만)

[OUTPUT] 1) Patient-level Enrichment, 2) Enrichment group 은 Mutual Exclusivity로 지정한 뒤, 3) p-value < 0.05인 Gene symbol을 가져옴



[INPUT]

BRAF	: DRIVER;
PTEN	: DRIVER;



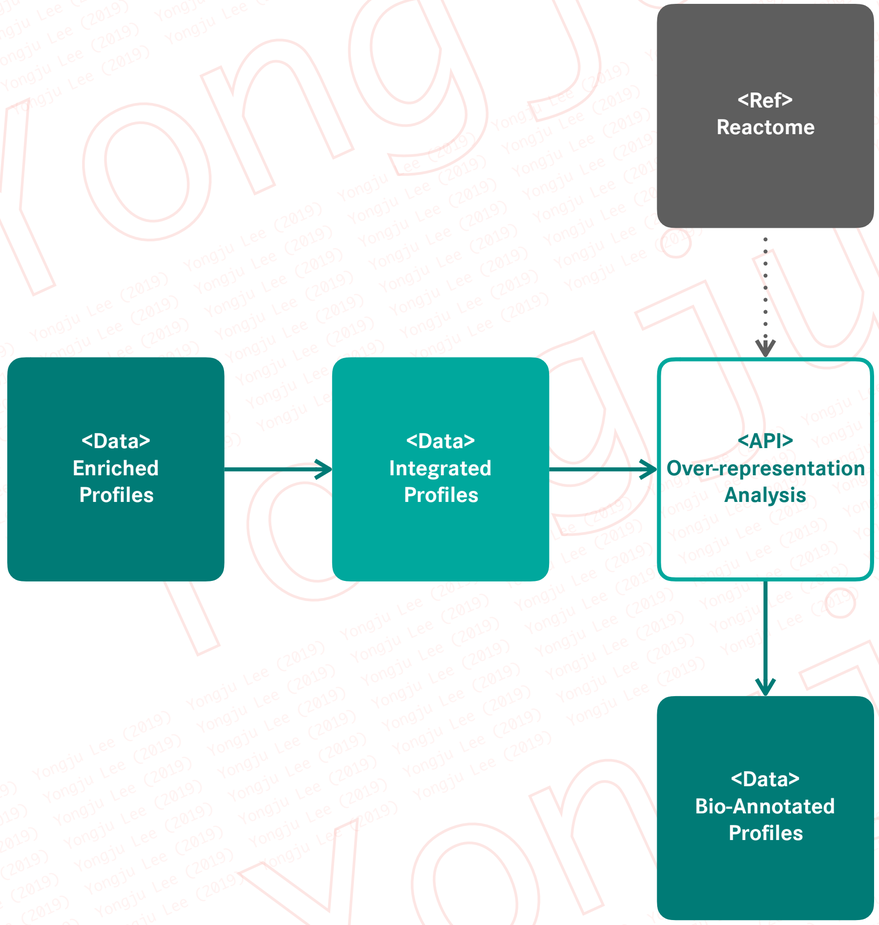
3. 환자별 Mutation 리스트 & OncoKB Annotation

[INPUT] 1) Mutated Gene 프로필과, 2) Enriched Gene 프로필이 병합된 Integrated 프로필(Gene symbol만)을

[FILTER] Reactome GSEA(Gene set enrichment analysis)로 분석 (이때, parameter 설정을 a. Project to human & b. Include interactors를 TRUE로 분석)

랭킹된 Pathway list에서 “Entities pValue”와 “Entities FDR”의 값을 -log10값으로 치환하여

[OUTPUT] 환자별 패스웨이 랭킹을 가져옴 (Bio-annotated ranked profile)



Step 2: Select your preferred options.

Project to human

All non-human identifiers are converted to their human equivalents (expand for more info...)

Include interactors

IntAct interactors are used to increase the analysis background (expand for more info...)

Pathway identifier	Pathway name	#Entities	#Entities	#Interact	#Interact	Entities ratio	Entities pValue	Entities FDR
R-HSA-5628897	TP53 Regulates Metabolic Genes	3	125	1	69	0.00877316	7.31030055	0.00113309
R-HSA-8943723	Regulation of PTEN mRNA translation	2	29	1	23	0.00203537	6.25975645	0.00482007
R-HSA-6807070	PTEN Regulation	3	171	2	503	0.01200168	3.16910341	0.01616242
R-HSA-8943724	Regulation of PTEN gene transcription	2	70	0	102	0.00491297	6.71466183	0.02551571
R-HSA-1257604	PIP3 activates AKT signaling	3	316	2	781	0.02217855	0.00127971	0.03967123
R-HSA-9006925	Intracellular signaling by second messengers	3	362	2	881	0.02540707	0.00181936	0.04548424
R-HSA-8986944	Transcriptional Regulation by MECP2	2	100	1	353	0.00701852	0.00456343	0.08407179
R-HSA-3700989	Transcriptional Regulation by TP53	3	486	2	1472	0.03411005	0.00639118	0.08407179
...	...	...	...	...	...	...	...	...

4. UMAP-based 클러스터링 Preparation

[INPUT] Bio-annotated ranked profile에서 a. -LOG10(Entities pValue) 버전과, b. -LOG10(Entities FDR) 버전을 나눠

[OUTPUT] 1) vector와 2) label 리스트 tsv 생성

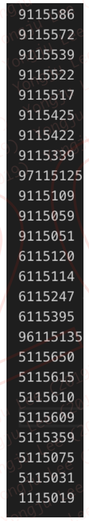
환자리스트

HSA_NAME	HSA_CODE	STDEV	AVG	CNT	9115586	9115572	9115539
Defective Mismatch Repair Associated With MLH1	R-HSA-5545483	⚠️	1.4055506	1	1.405550654493160		
Resolution of D-loop Structures through Synthesis-Dependent S	R-HSA-5693554	0.2039106	0.8533256	17	1.229146916723810	0.754337392352587	0.879823343399318
Resolution of D-loop Structures through Holliday Junction Interr	R-HSA-5693568	0.2020603	0.8524245	17	1.229146916723810	0.754337392352587	0.879823343399318
Resolution of D-Loop Structures	R-HSA-5693537	0.2014205	0.8518870	17	1.229146916723810	0.754337392352587	0.879823343399318
HDR through Single Strand Annealing (SSA)	R-HSA-5685938	0.3092483	0.8995658	19	1.229146916723810	0.672630280305592	0.879823343399318
Processing of DNA double-strand break ends	R-HSA-5693607	0.2144646	0.7749681	17	1.229146916723810	0.630004274129010	0.816978853976554
HDR through Homologous Recombination (HRR)	R-HSA-5685942	0.1993074	0.7821921	17	1.229146916723810	0.590856054495176	0.775590112742391
Meiotic recombination	R-HSA-912446	0.2184479	0.7518827	17	1.229146916723810	0.585624564469399	0.770039850544110
Transcriptional Regulation by E2F6	R-HSA-8953750	0.2871504	0.7176407	15	1.229146916723810	0.515963152367605	0.695636053797126
SUMO E3 ligases SUMOylate target proteins	R-HSA-3108232	0.4393138	0.4551416	23	1.229146916723810	0.264650651162941	0.516064715395482
SUMOylation	R-HSA-2990846	0.4390480	0.4475852	23	1.229146916723810	0.254496116843433	0.502298482580464
Metabolism of proteins	R-HSA-392499	0.4951786	0.2633776	24	1.229146916723810	0.066480159992483	0.044547689690695
TP53 Regulates Transcription of DNA Repair Genes	R-HSA-6796648	2.0919406	3.6150411	17	1.229146916723810		4.29997324972002E
G2/M DNA damage checkpoint	R-HSA-69473	0.4657978	1.1867209	16	1.229146916723810		0.879823343399318
G2/M Checkpoints	R-HSA-69481	0.3154110	1.1020147	15	1.229146916723810		0.879823343399318
Regulation of TP53 Activity through Phosphorylation	R-HSA-6804756	0.3010464	1.0730907	18	1.229146916723810		0.879823343399318
Homologous DNA Pairing and Strand Exchange	R-HSA-5693579	0.1820286	0.8502934	14	1.229146916723810		0.879823343399318
Presynaptic phase of homologous DNA pairing and strand excha	R-HSA-5693616	0.1821164	0.8442072	14	1.229146916723810		0.879823343399318
Meiotic synapsis	R-HSA-1221632	0.2493609	0.6870204	15	1.229146916723810		0.700141795961886

-LOG10(FDR)값

Pivot된 벡터

벡터 순으로 나열된 환자 id



4. UMAP-based 클러스터링

[INPUT] Vector와 Label 리스트 tsv를,

[PROCESS] Neighborhood parameter를 최솟값이 5로 지정한뒤, UMAP clustering

[OUTPUT] Cluster group별 리스트 가져오기

1	1.405550654	1.229146917	1.229146917	1.229146917	1.229146917	1.229146917	1.
2	0	0.754337392	0.754337392	0.754337392	0.67263028	0.630004274	0.59085605
3	0	0.879823343	0.879823343	0.879823343	0.879823343	0.816978854	0.77559011
4	0	0	0	0	0	0	0	0.084607889	0.079360377	7.566E-05	4.
5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6	0	0	0	0	1.403568034	0	0	0	0	1.414996791	1.414996791	1.4149
7	0	0	0	0	0.884457004	0	0	0	0.646277146	0.366462845	0.35148081
8	0	0.683539988	0.683539988	0.683539988	0.683539988	0.683539988	0.564794148	0.68353998
9	0	0	0	0	0	0	0	1.025544325	1.366544469	1.025544325	1.02554432
10	0	0	0	0	0	0	0	0	0.891488505	0.891488505	0.597070818	0.
11	0	0.904915122	0.904915122	0.904915122	0.904915122	0.894130778	0.84905199	0.90491512
12	0	0.808416197	0.808416197	0.808416197	0.808416197	0.808416197	0.668179673	0.62847941
13	0	0.892110401	0.892110401	0.887955178	0.812566628	0.711170702	0.81256662
14	0	1.252824627	1.237505999	1.232523412	1.81101513	1.075948279	1.02675944
15	0	0	0	0	0	0	0.750537141	0	0.25900116	0.252258512	0.0264
16	0	0.649690695	0.649690695	0.649690695	0.649690695	0.649690695	0.595762688	0.64969069
17	0	0.600928448	0.600928448	0.600928448	0.600928448	0.600928448	0.579904013	0.54157377
18	0	0.836561138	0.836561138	0.836561138	0.836561138	0.832002844	0.787477293	0.74637333
19	0	0.957861341	0.957861341	0.957861341	0.957861341	0.957861341	0.922837747	0.88058655
20	0	0.685993135	0.685993135	0.685993135	0.685993135	0.685993135	0.685993135	0.64902855
21	0	0.683539988	0.683539988	0.683539988	0.683539988	0.683539988	0.564794148	0.68353998
22	0	0.679030141	0.679030141	0.679030141	0.679030141	0.679030141	0.612437282	0.67903014
23	0	0.816846642	0.816846642	0.816846642	0.816846642	0.73243996	0.689006864	0.64902855
24	0	0	0	0	0	0	0	0	0.101121417	0.00E+00	0	0
25	0	1.190970032	1.190970032	1.190970032	1.190970032	1.190970032	1.190970032	1.16656087

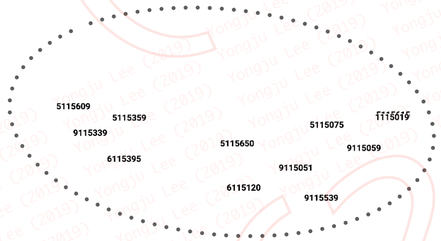
Pivot된 벡터

9115586
9115572
9115539
9115522
9115517
9115425
9115422
9115339
97115125
9115109
9115059
9115051
6115120
6115114
6115247
6115395
96115135
5115650
5115615
5115610
5115609
5115359
5115075
5115031
1115019

벡터 순으로 나열된 환자 id

Cluster 1

Cluster 2



5. 클러스터 기반 Group Analysis

[INPUT] 클러스터된 환자들을 기준으로 그룹을 생성하여,

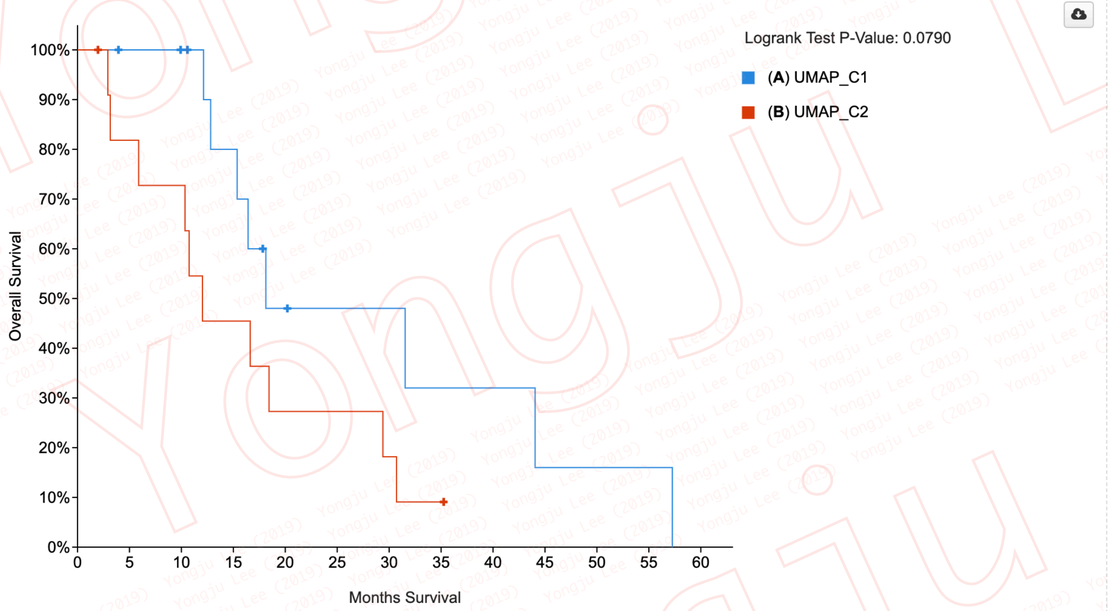
[OUTPUT] CBioPortal에서 제공되는 모든 탭의 Group Analysis결과 가져오기

Metastatic Prostate Adenocarcinoma (SU2C/PCF Dream Team, PNAS 2019)

Groups: (drag to reorder) (A) UMAP_C1 (13) (B) UMAP_C2 (14/12) Select all | Deselect all

Overlap | Survival | Clinical | Mutations | Copy-number | mRNA

Overall Survival Kaplan-Meier Estimate (Overall patient survival status.)



	Number of Cases, Total	Number of Cases, Deceased	Median Months Survival
(A) UMAP_C1	**13**	**8**	**18.13403417**
(B) UMAP_C2	**12**	**10**	**12.02365309**

Metastatic Prostate Adenocarcinoma (SU2C/PCF Dream Team, PNAS 2019)

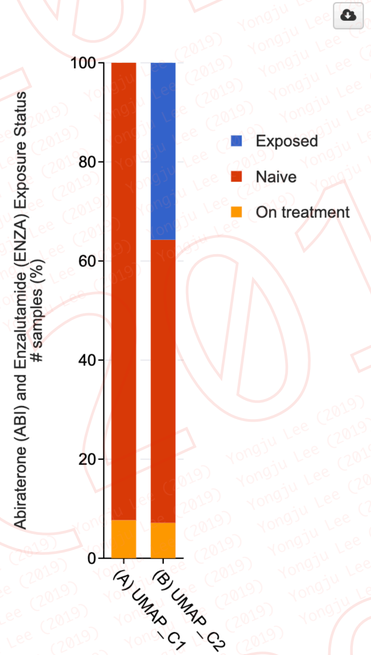
Groups: (drag to reorder) (A) UMAP_C1 (13) (B) UMAP_C2 (14/12) Select all | Deselect all

Overlap | Survival | Clinical | Mutations | Copy-number | mRNA

Clinical Attribute	Attribute Type	Statistical Test	p-Value	q-Value ▲
Fraction Genome Altered	Sample	Kruskal Wallis Test	0.0369	0.651
Abiraterone (ABI) and Enzalutamide (ENZA) Exposure Status	Sample	Chi-squared Test	0.0558	0.651
Neuroendocrine Features	Sample	Chi-squared Test	0.109	0.651
polyA ARV7 SRPM spliced reads per million	Sample	Kruskal Wallis Test	0.125	0.651
Pathology Classification	Sample	Chi-squared Test	0.126	0.651
Capture ARV7 SRPM spliced reads per million	Sample	Kruskal Wallis Test	0.150	0.651
Tissue Site	Sample	Chi-squared Test	0.216	0.698
Overall Survival (Months)	Patient	Kruskal Wallis Test	0.231	0.698
Other Sample ID	Sample	Chi-squared Test	0.310	0.698
ETS Fusion SEQ	Sample	Chi-squared Test	0.310	0.698
Tissue Source Site	Sample	Chi-squared Test	0.314	0.698
Prostate-specific antigen	Patient	Chi-squared Test	0.341	0.698
ETS Fusion Details	Sample	Chi-squared Test	0.353	0.698
Number of Samples Per Patient	Patient	Chi-squared Test	0.426	0.698
Overall Survival Status	Patient	Chi-squared Test	0.443	0.698
NEPC Score (Capture)	Sample	Kruskal Wallis Test	0.450	0.698

Plot Type: 100% stacked bar chart

Swap Axes Horizontal Bars



SUMMIT TRIAL (2018)

Driver Only

With Enriched Entities (CO*s & ME*s)

With Enriched Entities (ME* only)

without Over-representation*

DRIVER_TP53+/-

Clinical Attribute	Attribute Type	Statistical Test	p-Value	q-Value
Mutation Count	Sample	Kruskal Wallis Test	4.6E-03	0.0462
Mutation Burden	Sample	Kruskal Wallis Test	4.62E-03	0.0462
Duration of Therapy Days	Patient	Kruskal Wallis Test	0.0143	0.0954
Progress Free Survival (Months)	Patient	Kruskal Wallis Test	0.0650	0.288
Waterfall Group	Sample	Chi-squared Test	0.0821	0.288
Coverage	Sample	Kruskal Wallis Test	0.0864	0.288
Bubble Group	Sample	Chi-squared Test	0.159	0.453
Qualifying Mutation	Sample	Chi-squared Test	0.252	0.554
Central	Sample	Chi-squared Test	0.256	0.554
Local Test	Sample	Chi-squared Test	0.277	0.554
Best objective response rate	Patient	Chi-squared Test	0.392	0.712
Clonality	Sample	Chi-squared Test	0.494	0.732
IMPACT	Sample	Chi-squared Test	0.494	0.732
Data	Sample	Chi-squared Test	0.535	0.732
Criteria	Sample	Chi-squared Test	0.549	0.732
MSI Status	Sample	Chi-squared Test	0.714	0.840
Oncoprint	Sample	Chi-squared Test	0.714	0.840
Amplification Status	Sample	Chi-squared Test	0.788	0.846
Purity	Sample	Kruskal Wallis Test	0.808	0.846
ER_PR	Sample	Chi-squared Test	0.846	0.846

DRIVER_PIK3CA+/-

Clinical Attribute	Attribute Type	Statistical Test	p-Value	q-Value
Mutation Count	Sample	Kruskal Wallis Test	0.0354	0.239
Mutation Burden	Sample	Kruskal Wallis Test	0.0357	0.239
Progress Free Survival (Months)	Patient	Kruskal Wallis Test	0.0359	0.239
Waterfall Group	Sample	Chi-squared Test	0.0920	0.460
Best objective response rate	Patient	Chi-squared Test	0.189	0.696
Purity	Sample	Kruskal Wallis Test	0.234	0.696
Bubble Group	Sample	Chi-squared Test	0.244	0.696
Qualifying Mutation	Sample	Chi-squared Test	0.363	0.744
Central	Sample	Chi-squared Test	0.371	0.744
Local Test	Sample	Chi-squared Test	0.372	0.744
Duration of Therapy Days	Patient	Kruskal Wallis Test	0.514	0.801
MSI Status	Sample	Chi-squared Test	0.585	0.801
Oncoprint	Sample	Chi-squared Test	0.585	0.801
Criteria	Sample	Chi-squared Test	0.653	0.801
Clonality	Sample	Chi-squared Test	0.661	0.801
IMPACT	Sample	Chi-squared Test	0.661	0.801
Coverage	Sample	Kruskal Wallis Test	0.695	0.801
Data	Sample	Chi-squared Test	0.721	0.801
ER_PR	Sample	Chi-squared Test	0.836	0.880
Amplification Status	Sample	Chi-squared Test	0.954	0.954

N/A

ME_GATA3+/-

Clinical Attribute	Attribute Type	Statistical Test	p-Value	q-Value
Duration of Therapy Days	Patient	Kruskal Wallis Test	1.46E-03	0.0293
Progress Free Survival (Months)	Patient	Kruskal Wallis Test	9.20E-03	0.0642
Mutation Count	Sample	Kruskal Wallis Test	0.0127	0.0642
Mutation Burden	Sample	Kruskal Wallis Test	0.0128	0.0642
Coverage	Sample	Kruskal Wallis Test	0.0451	0.181
Waterfall Group	Sample	Chi-squared Test	0.0567	0.189
Bubble Group	Sample	Chi-squared Test	0.125	0.338
Best objective response rate	Patient	Chi-squared Test	0.135	0.338
Central	Sample	Chi-squared Test	0.162	0.361
Data	Sample	Chi-squared Test	0.191	0.372
Qualifying Mutation	Sample	Chi-squared Test	0.205	0.372
IMPACT	Sample	Chi-squared Test	0.356	0.594
Local Test	Sample	Chi-squared Test	0.509	0.783
ER_PR	Sample	Chi-squared Test	0.576	0.823
Amplification Status	Sample	Chi-squared Test	0.642	0.856
Clonality	Sample	Chi-squared Test	0.693	0.866
Purity	Sample	Kruskal Wallis Test	0.808	0.876
MSI Status	Sample	Chi-squared Test	0.833	0.876
Oncoprint	Sample	Chi-squared Test	0.833	0.876
Criteria	Sample	Chi-squared Test	0.933	0.933

ME_ESR1+/-

Clinical Attribute	Attribute Type	Statistical Test	p-Value	q-Value
Duration of Therapy Days	Patient	Kruskal Wallis Test	2E-03	0.0440
Progress Free Survival (Months)	Patient	Kruskal Wallis Test	9.8E-03	0.0978
Best objective response rate	Patient	Chi-squared Test	0.0384	0.256
Waterfall Group	Sample	Chi-squared Test	0.0821	0.282
Mutation Count	Sample	Kruskal Wallis Test	0.0842	0.282
Mutation Burden	Sample	Kruskal Wallis Test	0.0847	0.282
Bubble Group	Sample	Chi-squared Test	0.159	0.425
Central	Sample	Chi-squared Test	0.170	0.425
Coverage	Sample	Kruskal Wallis Test	0.221	0.490
Qualifying Mutation	Sample	Chi-squared Test	0.252	0.504
ER_PR	Sample	Chi-squared Test	0.333	0.574
Local Test	Sample	Chi-squared Test	0.345	0.574
Clonality	Sample	Chi-squared Test	0.494	0.663
IMPACT	Sample	Chi-squared Test	0.494	0.663
Purity	Sample	Kruskal Wallis Test	0.497	0.663
Data	Sample	Chi-squared Test	0.535	0.669
MSI Status	Sample	Chi-squared Test	0.714	0.794
Oncoprint	Sample	Chi-squared Test	0.714	0.794
Amplification Status	Sample	Chi-squared Test	0.788	0.830
Criteria	Sample	Chi-squared Test	0.861	0.861

with Over-representation*

2 GROUP CLUSTERING (DRIVER)

Clinical Attribute	Attribute Type	Statistical Test	p-Value	q-Value
Duration of Therapy Days	Patient	Kruskal Wallis Test	1.46E-03	0.0293
Progress Free Survival (Months)	Patient	Kruskal Wallis Test	9.20E-03	0.0642
Mutation Count	Sample	Kruskal Wallis Test	0.0127	0.0642
Mutation Burden	Sample	Kruskal Wallis Test	0.0128	0.0642
Coverage	Sample	Kruskal Wallis Test	0.0451	0.181
Waterfall Group	Sample	Chi-squared Test	0.0567	0.189
Bubble Group	Sample	Chi-squared Test	0.125	0.338
Best objective response rate	Patient	Chi-squared Test	0.135	0.338
Central	Sample	Chi-squared Test	0.162	0.361
Data	Sample	Chi-squared Test	0.191	0.372
Qualifying Mutation	Sample	Chi-squared Test	0.205	0.372
IMPACT	Sample	Chi-squared Test	0.356	0.594
Local Test	Sample	Chi-squared Test	0.509	0.783
ER_PR	Sample	Chi-squared Test	0.576	0.823
Amplification Status	Sample	Chi-squared Test	0.642	0.856
Clonality	Sample	Chi-squared Test	0.693	0.866
Purity	Sample	Kruskal Wallis Test	0.808	0.876
MSI Status	Sample	Chi-squared Test	0.833	0.876
Oncoprint	Sample	Chi-squared Test	0.833	0.876
Criteria	Sample	Chi-squared Test	0.933	0.933

2 GROUP CLUSTERING (ENR)

Clinical Attribute	Attribute Type	Statistical Test	p-Value	q-Value
Mutation Count	Sample	Kruskal Wallis Test	0.0191	0.138
Central	Sample	Chi-squared Test	0.0220	0.138
Mutation Burden	Sample	Kruskal Wallis Test	0.0227	0.138
Progress Free Survival (Months)	Patient	Kruskal Wallis Test	0.0365	0.138
Best objective response rate	Patient	Chi-squared Test	0.0384	0.138
Purity	Sample	Kruskal Wallis Test	0.0415	0.138
Duration of Therapy Days	Patient	Kruskal Wallis Test	0.0662	0.189
Local Test	Sample	Chi-squared Test	0.174	0.399
Amplification Status	Sample	Chi-squared Test	0.179	0.399
Data	Sample	Chi-squared Test	0.253	0.496
Waterfall Group	Sample	Chi-squared Test	0.273	0.496
Clonality	Sample	Chi-squared Test	0.494	0.744
IMPACT	Sample	Chi-squared Test	0.494	0.744
Criteria	Sample	Chi-squared Test	0.549	0.744
Bubble Group	Sample	Chi-squared Test	0.558	0.744
Qualifying Mutation	Sample	Chi-squared Test	0.677	0.794
MSI Status	Sample	Chi-squared Test	0.714	0.794
Oncoprint	Sample	Chi-squared Test	0.714	0.794
ER_PR	Sample	Chi-squared Test	0.846	0.891
Coverage	Sample	Kruskal Wallis Test	0.903	0.903

3 GROUP CLUSTERING (ENR)

Clinical Attribute	Attribute Type	Statistical Test	p-Value	q-Value
Central	Sample	Chi-squared Test	0.0389	0.284
Purity	Sample	Kruskal Wallis Test	0.0498	0.284
Duration of Therapy Days	Patient	Kruskal Wallis Test	0.0524	0.284
Mutation Count	Sample	Kruskal Wallis Test	0.0639	0.284
Mutation Burden	Sample	Kruskal Wallis Test	0.0745	0.284
Progress Free Survival (Months)	Patient	Kruskal Wallis Test	0.0933	0.284
Amplification Status	Sample	Chi-squared Test	0.0995	0.284
Data	Sample	Chi-squared Test	0.136	0.307
Best objective response rate	Patient	Chi-squared Test	0.143	0.307
Clonality	Sample	Chi-squared Test	0.153	0.307
MSI Status	Sample	Chi-squared Test	0.229	0.382
Oncoprint	Sample	Chi-squared Test	0.229	0.382
Waterfall Group	Sample	Chi-squared Test	0.249	0.382
Local Test	Sample	Chi-squared Test	0.267	0.382
IMPACT	Sample	Chi-squared Test	0.318	0.424
Bubble Group	Sample	Chi-squared Test	0.501	0.599
ER_PR	Sample	Chi-squared Test	0.509	0.599
Coverage	Sample	Kruskal Wallis Test	0.630	0.701
Qualifying Mutation	Sample	Chi-squared Test	0.676	0.712
Criteria	Sample	Chi-squared Test	0.825	0.825

2 GROUP CLUSTERING (ME)

Clinical Attribute	Attribute Type	Statistical Test	p-Value	q-Value
Mutation Count	Sample	Kruskal Wallis Test	0.0191	0.138
Central	Sample	Chi-squared Test	0.0220	0.138
Mutation Burden	Sample	Kruskal Wallis Test	0.0227	0.138
Progress Free Survival (Months)	Patient	Kruskal Wallis Test	0.0365	0.138
Best objective response rate	Patient	Chi-squared Test	0.0384	0.138
Purity	Sample	Kruskal Wallis Test	0.0415	0.138
Duration of Therapy Days	Patient	Kruskal Wallis Test	0.0662	0.189
Local Test	Sample	Chi-squared Test	0.174	0.399
Amplification Status	Sample	Chi-squared Test	0.179	0.399
Data	Sample	Chi-squared Test	0.253	0.496
Waterfall Group	Sample	Chi-squared Test	0.273	0.496
Clonality	Sample	Chi-squared Test	0.494	0.744
IMPACT	Sample	Chi-squared Test	0.494	0.744
Criteria	Sample	Chi-squared Test	0.549	0.744
Bubble Group	Sample	Chi-squared Test	0.558	0.744
Qualifying Mutation	Sample	Chi-squared Test	0.677	0.794
MSI Status	Sample	Chi-squared Test	0.714	0.794
Oncoprint	Sample	Chi-squared Test	0.714	0.794
ER_PR	Sample	Chi-squared Test	0.846	0.891
Coverage	Sample	Kruskal Wallis Test	0.903	0.903

3 GROUP CLUSTERING (ME)

Clinical Attribute	Attribute Type	Statistical Test	p-Value	q-Value
Duration of Therapy Days	Patient	Kruskal Wallis Test	6.3E-03	0.127
Mutation Count	Sample	Kruskal Wallis Test	0.0242	0.133
Progress Free Survival (Months)	Patient	Kruskal Wallis Test	0.0260	0.133
Mutation Burden	Sample	Kruskal Wallis Test	0.0266	0.133
Best objective response rate	Patient	Chi-squared Test	0.0530	0.171
Purity	Sample	Kruskal Wallis Test	0.0599	0.171
Coverage	Sample	Kruskal Wallis Test	0.0603	0.171
Central	Sample	Chi-squared Test	0.0683	0.171
Amplification Status	Sample	Chi-squared Test	0.0995	0.221
Waterfall Group	Sample	Chi-squared Test	0.211	0.408
ER_PR	Sample	Chi-squared Test	0.241	0.408
IMPACT	Sample	Chi-squared Test	0.245	0.408
Bubble Group	Sample	Chi-squared Test	0.277	0.426
Data	Sample	Chi-squared Test	0.342	0.488
Qualifying Mutation	Sample	Chi-squared Test	0.435	0.527
MSI Status	Sample	Chi-squared Test	0.448	0.527
Oncoprint	Sample	Chi-squared Test	0.448	0.527
Local Test	Sample	Chi-squared Test	0.494	0.548
Criteria	Sample	Chi-squared Test	0.825	0.869
Clonality	Sample	Chi-squared Test	0.949	0.949

- CO : Co-occurrent mutations
- ME : Mutually exclusive mutations
- Over-representation : Reactome based enrichment analysis

CCRCC (2019)

DV_VHL+/-

Clinical Attribute	Attribute Type	Statistical Test	p-Value	q-Value
Sex	Patient	Chi-squared Test	0.0350	0.484
NonSynonymous Uneval	Sample	Kruskal Wallis Test	0.0561	0.484
First Line Therapy	Patient	Chi-squared Test	0.0781	0.484
Progress Free Survival (Months)	Patient	Kruskal Wallis Test	0.0815	0.484
Cell Membrane PDL1 3%+	Patient	Kruskal Wallis Test	0.0956	0.484
Treatment Group	Patient	Chi-squared Test	0.112	0.484
Mutations Subclonal	Sample	Kruskal Wallis Test	0.133	0.484
Mutations Clonal	Sample	Kruskal Wallis Test	0.139	0.484
Purity	Sample	Kruskal Wallis Test	0.152	0.484
NonSynonymous Subclonal	Sample	Kruskal Wallis Test	0.170	0.484
Nonsynonymous Clonal	Sample	Kruskal Wallis Test	0.184	0.484
FrameShift Indels	Sample	Kruskal Wallis Test	0.193	0.484
Cell Membrane PDL1 2%+	Patient	Kruskal Wallis Test	0.250	0.571
PDL1 Positive 1%	Patient	Kruskal Wallis Test	0.277	0.571
Mutations Uneval	Sample	Kruskal Wallis Test	0.285	0.571
Response to Immunotherapy	Patient	Chi-squared Test	0.370	0.668
Overall Survival Censor	Patient	Chi-squared Test	0.378	0.668
Overall Survival (Months)	Patient	Kruskal Wallis Test	0.433	0.722
Genome Doublings	Sample	Chi-squared Test	0.498	0.784
Nonsynonymous Mutation Count	Sample	Kruskal Wallis Test	0.571	0.784
Cell Membrane PDL1 0%	Patient	Kruskal Wallis Test	0.576	0.784
Age	Patient	Kruskal Wallis Test	0.601	0.784
Mutation Count	Sample	Kruskal Wallis Test	0.601	0.784
All Synonymous Mutations	Sample	Kruskal Wallis Test	0.647	0.809
Cell Membrane PDL1 1%+	Patient	Kruskal Wallis Test	0.695	0.826
RECIST	Patient	Chi-squared Test	0.716	0.826
PDL1 Positive 5%	Patient	Kruskal Wallis Test	0.787	0.862
Progression Free Censor	Patient	Chi-squared Test	0.805	0.862
All Mutations	Sample	Kruskal Wallis Test	0.862	0.891
Ploidy	Sample	Kruskal Wallis Test	0.981	0.981

DV_PBRM1+/-

Clinical Attribute	Attribute Type	Statistical Test	p-Value	q-Value
Progress Free Survival (Months)	Patient	Kruskal Wallis Test	5.37E-03	0.161
Response to Immunotherapy	Patient	Chi-squared Test	0.0131	0.196
RECIST	Patient	Chi-squared Test	0.0275	0.275
Overall Survival Censor	Patient	Chi-squared Test	0.0584	0.438
Sex	Patient	Chi-squared Test	0.0774	0.465
Mutations Uneval	Sample	Kruskal Wallis Test	0.144	0.633
Purity	Sample	Kruskal Wallis Test	0.175	0.633
Overall Survival (Months)	Patient	Kruskal Wallis Test	0.186	0.633
Cell Membrane PDL1 2%+	Patient	Kruskal Wallis Test	0.190	0.633
Ploidy	Sample	Kruskal Wallis Test	0.280	0.815
Age	Patient	Kruskal Wallis Test	0.327	0.815
Cell Membrane PDL1 3%+	Patient	Kruskal Wallis Test	0.376	0.815
FrameShift Indels	Sample	Kruskal Wallis Test	0.393	0.815
PDL1 Positive 5%	Patient	Kruskal Wallis Test	0.398	0.815
PDL1 Positive 1%	Patient	Kruskal Wallis Test	0.408	0.815
Nonsynonymous Mutation Count	Sample	Kruskal Wallis Test	0.454	0.851
NonSynonymous Subclonal	Sample	Kruskal Wallis Test	0.501	0.885
Mutation Count	Sample	Kruskal Wallis Test	0.552	0.891
All Mutations	Sample	Kruskal Wallis Test	0.564	0.891
Mutations Subclonal	Sample	Kruskal Wallis Test	0.645	0.903
Nonsynonymous Clonal	Sample	Kruskal Wallis Test	0.659	0.903
First Line Therapy	Patient	Chi-squared Test	0.662	0.903
Treatment Group	Patient	Chi-squared Test	0.757	0.907
Mutations Clonal	Sample	Kruskal Wallis Test	0.759	0.907
Progression Free Censor	Patient	Chi-squared Test	0.765	0.907
NonSynonymous Uneval	Sample	Kruskal Wallis Test	0.786	0.907
All Synonymous Mutations	Sample	Kruskal Wallis Test	0.908	0.960
Cell Membrane PDL1 0%	Patient	Kruskal Wallis Test	0.921	0.960
Genome Doublings	Sample	Chi-squared Test	0.948	0.960
Cell Membrane PDL1 1%+	Patient	Kruskal Wallis Test	0.960	0.960

ME_SMAD3+/-

Clinical Attribute	Attribute Type	Statistical Test	p-Value	q-Value
Treatment Group	Patient	Chi-squared Test	0.0334	0.519
First Line Therapy	Patient	Chi-squared Test	0.0498	0.519
FrameShift Indels	Sample	Kruskal Wallis Test	0.0617	0.519
Cell Membrane PDL1 3%+	Patient	Kruskal Wallis Test	0.0956	0.519
Progress Free Survival (Months)	Patient	Kruskal Wallis Test	0.102	0.519
Sex	Patient	Chi-squared Test	0.128	0.519
Mutations Subclonal	Sample	Kruskal Wallis Test	0.142	0.519
NonSynonymous Subclonal	Sample	Kruskal Wallis Test	0.186	0.519
Overall Survival (Months)	Patient	Kruskal Wallis Test	0.201	0.519
NonSynonymous Uneval	Sample	Kruskal Wallis Test	0.204	0.519
Mutations Clonal	Sample	Kruskal Wallis Test	0.232	0.519
Nonsynonymous Clonal	Sample	Kruskal Wallis Test	0.240	0.519
Purity	Sample	Kruskal Wallis Test	0.248	0.519
Cell Membrane PDL1 2%+	Patient	Kruskal Wallis Test	0.250	0.519
Age	Patient	Kruskal Wallis Test	0.266	0.519
PDL1 Positive 1%	Patient	Kruskal Wallis Test	0.277	0.519
Response to Immunotherapy	Patient	Chi-squared Test	0.307	0.541
Nonsynonymous Mutation Count	Sample	Kruskal Wallis Test	0.543	0.763
Overall Survival Censor	Patient	Chi-squared Test	0.560	0.763
Genome Doublings	Sample	Chi-squared Test	0.566	0.763
Mutation Count	Sample	Kruskal Wallis Test	0.571	0.763
Cell Membrane PDL1 0%	Patient	Kruskal Wallis Test	0.576	0.763
Mutations Uneval	Sample	Kruskal Wallis Test	0.585	0.763
Ploidy	Sample	Kruskal Wallis Test	0.635	0.787
Progression Free Censor	Patient	Chi-squared Test	0.656	0.787
Cell Membrane PDL1 1%+	Patient	Kruskal Wallis Test	0.695	0.802
All Mutations	Sample	Kruskal Wallis Test	0.769	0.843
PDL1 Positive 5%	Patient	Kruskal Wallis Test	0.787	0.843
RECIST	Patient	Chi-squared Test	0.816	0.844
All Synonymous Mutations	Sample	Kruskal Wallis Test	0.916	0.916

ME_EP300+/-

Clinical Attribute	Attribute Type	Statistical Test	p-Value	q-Value
Progress Free Survival (Months)	Patient	Kruskal Wallis Test	3.29E-03	0.0593
Response to Immunotherapy	Patient	Chi-squared Test	4.0E-03	0.0593
Sex	Patient	Chi-squared Test	8.90E-03	0.0890
FrameShift Indels	Sample	Kruskal Wallis Test	0.0217	0.132
RECIST	Patient	Chi-squared Test	0.0220	0.132
Overall Survival (Months)	Patient	Kruskal Wallis Test	0.0321	0.160
NonSynonymous Uneval	Sample	Kruskal Wallis Test	0.0568	0.244
PDL1 Positive 1%	Patient	Kruskal Wallis Test	0.0921	0.345
Age	Patient	Kruskal Wallis Test	0.107	0.357
First Line Therapy	Patient	Chi-squared Test	0.120	0.359
Treatment Group	Patient	Chi-squared Test	0.161	0.438
Cell Membrane PDL1 2%+	Patient	Kruskal Wallis Test	0.190	0.475
Mutations Uneval	Sample	Kruskal Wallis Test	0.310	0.716
Cell Membrane PDL1 3%+	Patient	Kruskal Wallis Test	0.376	0.769
PDL1 Positive 5%	Patient	Kruskal Wallis Test	0.398	0.769
Cell Membrane PDL1 0%	Patient	Kruskal Wallis Test	0.410	0.769
Overall Survival Censor	Patient	Chi-squared Test	0.447	0.782
Cell Membrane PDL1 1%+	Patient	Kruskal Wallis Test	0.469	0.782
Purity	Sample	Kruskal Wallis Test	0.497	0.784
Progression Free Censor	Patient	Chi-squared Test	0.568	0.845
Nonsynonymous Mutation Count	Sample	Kruskal Wallis Test	0.592	0.845
Nonsynonymous Clonal	Sample	Kruskal Wallis Test	0.620	0.845
Mutation Count	Sample	Kruskal Wallis Test	0.691	0.901
Mutations Clonal	Sample	Kruskal Wallis Test	0.721	0.901
Mutations Subclonal	Sample	Kruskal Wallis Test	0.781	0.937
All Mutations	Sample	Kruskal Wallis Test	0.842	0.953
NonSynonymous Subclonal	Sample	Kruskal Wallis Test	0.858	0.953
All Synonymous Mutations	Sample	Kruskal Wallis Test	0.889	0.953
Genome Doublings	Sample	Chi-squared Test	0.933	0.965
Ploidy	Sample	Kruskal Wallis Test	1.00	1.00

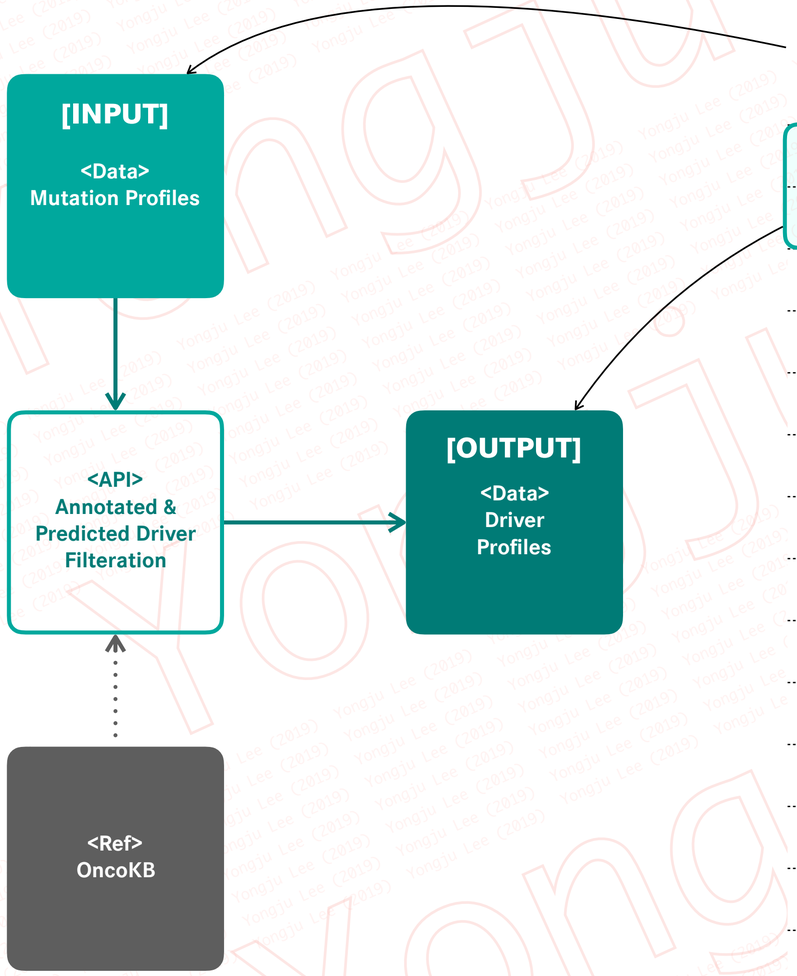
UMAP_C1 vs C2

Clinical Attribute	Attribute Type	Statistical Test	p-Value	q-Value
Progress Free Survival (Months)	Patient	Kruskal Wallis Test	2.84E-03	0.0515
Response to Immunotherapy	Patient	Chi-squared Test	3.43E-03	0.0515
Sex	Patient	Chi-squared Test	5.78E-03	0.0578
RECIST	Patient	Chi-squared Test	0.0171	0.128
NonSynonymous Uneval	Sample	Kruskal Wallis Test	0.0367	0.220
FrameShift Indels	Sample	Kruskal Wallis Test	0.0497	0.249
Overall Survival (Months)	Patient	Kruskal Wallis Test	0.0627	0.269
PDL1 Positive 1%	Patient	Kruskal Wallis Test	0.0921	0.345
First Line Therapy	Patient	Chi-squared Test	0.149	0.498
Age	Patient	Kruskal Wallis Test	0.189	0.518
Cell Membrane PDL1 2%+	Patient	Kruskal Wallis Test	0.190	0.518
Mutations Uneval	Sample	Kruskal Wallis Test	0.231	0.577
Treatment Group	Patient	Chi-squared Test	0.281	0.648
Cell Membrane PDL1 3%+	Patient	Kruskal Wallis Test	0.376	0.724
Overall Survival Censor	Patient	Chi-squared Test	0.387	0.724
PDL1 Positive 5%	Patient	Kruskal Wallis Test	0.398	0.724
Cell Membrane PDL1 0%	Patient	Kruskal Wallis Test	0.410	0.724
Purity	Sample	Kruskal Wallis Test	0.451	0.741
Cell Membrane PDL1 1%+	Patient	Kruskal Wallis Test	0.469	0.741
Nonsynonymous Mutation Count	Sample	Kruskal Wallis Test	0.608	0.856
Nonsynonymous Clonal	Sample	Kruskal Wallis Test	0.608	0.856
Progression Free Censor	Patient	Chi-squared Test	0.628	0.856
Mutations Clonal	Sample	Kruskal Wallis Test	0.676	0.880
Mutation Count	Sample	Kruskal Wallis Test	0.704	0.880
All Synonymous Mutations	Sample	Kruskal Wallis Test	0.775	0.894
Mutations Subclonal	Sample	Kruskal Wallis Test	0.819	0.894
Ploidy	Sample	Kruskal Wallis Test	0.851	0.894
All Mutations	Sample	Kruskal Wallis Test	0.879	0.894
Genome Doublings	Sample	Chi-squared Test	0.891	0.894
NonSynonymous Subclonal	Sample	Kruskal Wallis Test	0.894	0.894

Yongju Lee (2019)

1. Retrieving patient's mutated gene profiles filtered by OncoKB annotations

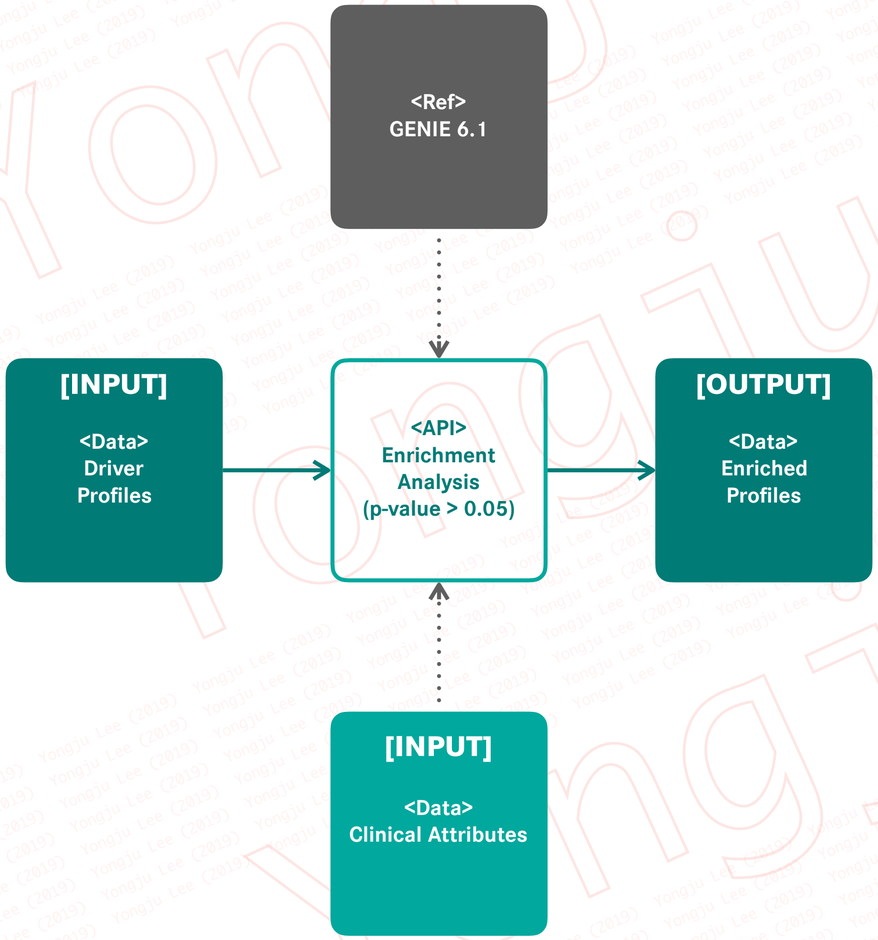
[INPUT] Patient's mutated genes and their protein change retrieval
[FILTER] Identify gene-protein change from OncoKB for their status of oncogenesis (either 1. Oncogenic or 2. Likely oncogenic)
[OUTPUT] Patient's driver mutation profile



Gene	Protein Change	Annotation
BRAF	KIAA1549-BRAF	**OncoKB: Oncogenic, level_3b**;CIViC: Predictive: 8, Functional: 1, Diagnostic: 2, Prognostic: 2;MyCancerGenome: no
PTEN	X85_splice	**OncoKB: Likely Oncogenic, level_4**;CIViC: NA;MyCancerGenome: not present;CancerHotspot: no;3DHotspot: no
TSC2	D1644N	OncoKB: Unknown, level NA;CIViC: NA;MyCancerGenome: not present;CancerHotspot: no;3DHotspot: no
VAV1	D295N	OncoKB: Unknown, level NA;CIViC: NA;MyCancerGenome: not present;CancerHotspot: no;3DHotspot: no
ARID1B	R1062Q	OncoKB: Unknown, level NA;CIViC: NA;MyCancerGenome: not present;CancerHotspot: no;3DHotspot: no
ADGRB1	A214T	OncoKB: NA;CIViC: NA;MyCancerGenome: not present;CancerHotspot: no;3DHotspot: no
CETP	S275Y	OncoKB: NA;CIViC: NA;MyCancerGenome: not present;CancerHotspot: no;3DHotspot: no
DES	N311del	OncoKB: NA;CIViC: NA;MyCancerGenome: not present;CancerHotspot: no;3DHotspot: no
GYPA	R116*	OncoKB: NA;CIViC: NA;MyCancerGenome: not present;CancerHotspot: no;3DHotspot: no
TMPRSS15	T685M	OncoKB: NA;CIViC: NA;MyCancerGenome: not present;CancerHotspot: no;3DHotspot: no
GDF5	N483Y	OncoKB: NA;CIViC: NA;MyCancerGenome: not present;CancerHotspot: no;3DHotspot: no
PKP4	S959L	OncoKB: NA;CIViC: NA;MyCancerGenome: not present;CancerHotspot: no;3DHotspot: no
SCAF11	R788H	OncoKB: NA;CIViC: NA;MyCancerGenome: not present;CancerHotspot: no;3DHotspot: no
PLCH2	R207Q	OncoKB: NA;CIViC: NA;MyCancerGenome: not present;CancerHotspot: no;3DHotspot: no
ARHGAP32	G1366S	OncoKB: NA;CIViC: NA;MyCancerGenome: not present;CancerHotspot: no;3DHotspot: no

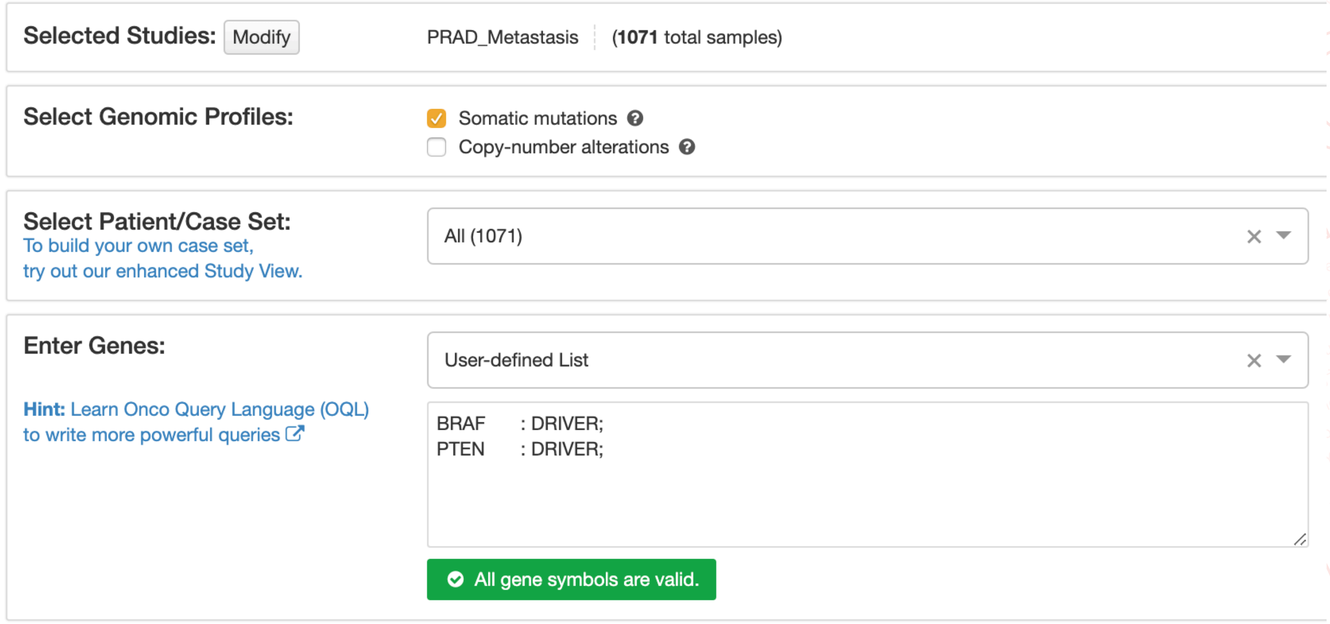
2. Enrichment Analysis

[INPUT] Based on extracted driver mutations and patient's clinical attribute (inc. oncotree code and sample type of tumor sample),
[FILTER]
A. Perform enrichment analysis with GENIE 6.1. CBioPortal Enrichment Tab with certain conditions applied.
***Conditions (1. Filter GENIE 6.1. patients with same clinical attribute; 2. Select somatic mutation profiles (not CNVs); 3. Enter driver genes with ': DRIVER;';)
B. Extract enriched genes with certain conditions applied.
1) Select patient-level enrichment, 2) Enrichment group : Mutual Exclusivity, 3) p-value cutoff : under 0.05



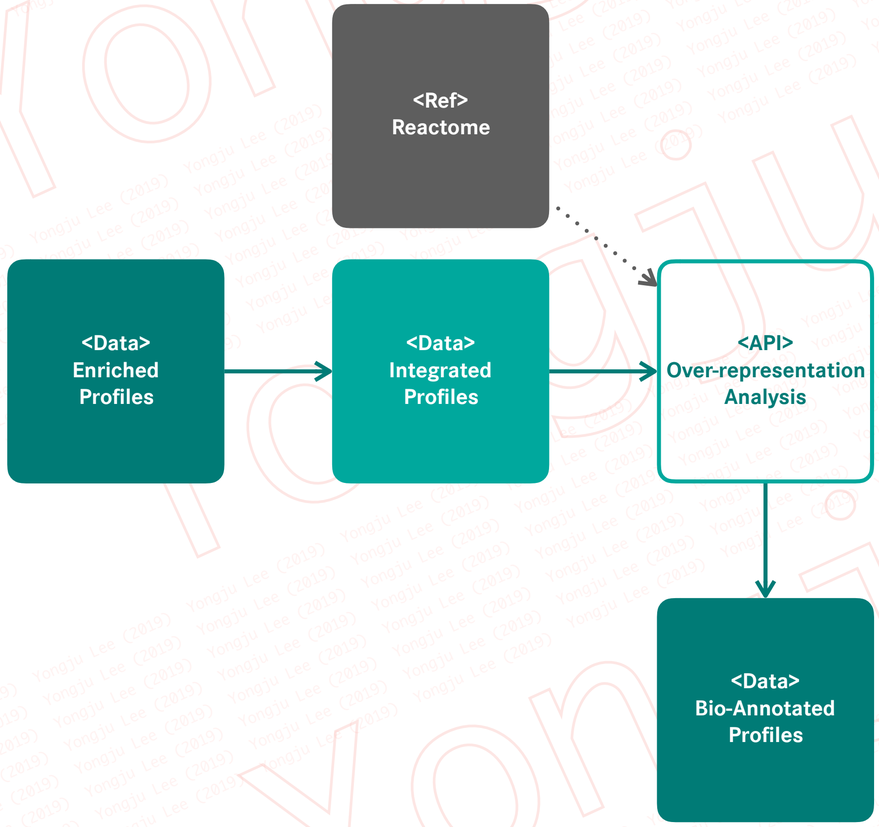
[INPUT]

BRAF	: DRIVER;
PTEN	: DRIVER;



3. Pathway enrichment analysis

[INPUT]
Integrate both 1) mutated and 2) enriched profiles (GENE symbol only)
[FILTER]
Perform pathway enrichment analysis with certain parameters applied.
A. Project to human = TRUE;
B. Include interactions = TRUE;
C. Apply -log10() for both p-value column and FDR column
[OUTPUT] Patient specific ranked over-representation with p-value and FDR



Step 2: Select your preferred options.

Project to human

All non-human identifiers are converted to their human equivalents (expand for more info...)

Include interactors

IntAct interactors are used to increase the analysis background (expand for more info...)

Pathway identifier	Pathway name	#Entities	#Entities	#Interact	#Interact	Entities ratio	Entities pValue	Entities FDR
R-HSA-5628897	TP53 Regulates Metabolic Genes	3	125	1	69	0.00877316	7.31030055	0.00113309
R-HSA-8943723	Regulation of PTEN mRNA translation	2	29	1	23	0.00203537	6.25975645	0.00482007
R-HSA-6807070	PTEN Regulation	3	171	2	503	0.01200168	3.16910341	0.01616242
R-HSA-8943724	Regulation of PTEN gene transcription	2	70	0	102	0.00491297	6.71466183	0.02551571
R-HSA-1257604	PIP3 activates AKT signaling	3	316	2	781	0.02217855	0.00127971	0.03967123
R-HSA-9006925	Intracellular signaling by second messengers	3	362	2	881	0.02540707	0.00181936	0.04548424
R-HSA-8986944	Transcriptional Regulation by MECP2	2	100	1	353	0.00701852	0.00456343	0.08407179
R-HSA-3700989	Transcriptional Regulation by TP53	3	486	2	1472	0.03411005	0.00639118	0.08407179
...	...	...	...	...	...	...	...	...

4. UMAP-based clustering Preparation

[INPUT]

Prepare both 1) -log10(Entities p-value) and 2) -log10(Entities FDR).

[OUTPUT]

Generate both vector and label tsv.

환자리스트

HSA_NAME	HSA_CODE	STDEV	AVG	CNT	9115586	9115572	9115539
Defective Mismatch Repair Associated With MLH1	R-HSA-5545483	⚠️	1.4055506	1	1.405550654493160		
Resolution of D-loop Structures through Synthesis-Dependent S	R-HSA-5693554	0.2039106	0.8533256	17	1.229146916723810	0.754337392352587	0.879823343399318
Resolution of D-loop Structures through Holliday Junction Interr	R-HSA-5693568	0.2020603	0.8524245	17	1.229146916723810	0.754337392352587	0.879823343399318
Resolution of D-Loop Structures	R-HSA-5693537	0.2014205	0.8518870	17	1.229146916723810	0.754337392352587	0.879823343399318
HDR through Single Strand Annealing (SSA)	R-HSA-5685938	0.3092483	0.8995658	19	1.229146916723810	0.672630280305592	0.879823343399318
Processing of DNA double-strand break ends	R-HSA-5693607	0.2144646	0.7749681	17	1.229146916723810	0.630004274129010	0.816978853975654
HDR through Homologous Recombination (HRR)	R-HSA-5685942	0.1993074	0.7821921	17	1.229146916723810	0.590856054495176	0.775590112742391
Meiotic recombination	R-HSA-912446	0.2184479	0.7518827	17	1.229146916723810	0.585624564469399	0.770039850544110
Transcriptional Regulation by E2F6	R-HSA-8953750	0.2871504	0.7176407	15	1.229146916723810	0.515963152367605	0.695636053797126
SUMO E3 ligases SUMOylate target proteins	R-HSA-3108232	0.4393138	0.4551416	23	1.229146916723810	0.264650651162941	0.516064715395482
SUMOylation	R-HSA-2990846	0.4390480	0.4475852	23	1.229146916723810	0.254496116843433	0.502298482580464
Metabolism of proteins	R-HSA-392499	0.4951786	0.2633776	24	1.229146916723810	0.066480159992483	0.044547689690695
TP53 Regulates Transcription of DNA Repair Genes	R-HSA-6796648	2.0919406	3.6150411	17	1.229146916723810		4.29997324972002E
G2/M DNA damage checkpoint	R-HSA-69473	0.4657978	1.1867209	16	1.229146916723810		0.879823343399318
G2/M Checkpoints	R-HSA-69481	0.3154110	1.1020147	15	1.229146916723810		0.879823343399318
Regulation of TP53 Activity through Phosphorylation	R-HSA-6804756	0.3010464	1.0730907	18	1.229146916723810		0.879823343399318
Homologous DNA Pairing and Strand Exchange	R-HSA-5693579	0.1820286	0.8502934	14	1.229146916723810		0.879823343399318
Presynaptic phase of homologous DNA pairing and strand excha	R-HSA-5693616	0.1821164	0.8442072	14	1.229146916723810		0.879823343399318
Meiotic synapsis	R-HSA-1221632	0.2493609	0.6870204	15	1.229146916723810		0.700141795961886

-LOG10(FDR)값

Pivot된 벡터

1	1.405550654	1.229146917	1.229146917	1.229146917	1.229146917	1.229146917	1.											
2	0	0.754337392	0.754337392	0.754337392	0.67263028	0.630004274	0.59085605											
3	0	0.879823343	0.879823343	0.879823343	0.879823343	0.816978854	0.77559011											
4	0	0	0	0	0	0	0	0.084607889	0.079360377	7.566E-05	4.							
5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6	0	0	0	0	1.403568034	0	0	0	0	1.414996791	1.414996791	1.4149						
7	0	0	0	0	0.884457004	0	0	0	0.646277146	0.366462845	0.35148081							
8	0	0.683539988	0.683539988	0.683539988	0.683539988	0.564794148	0.68353998											
9	0	0	0	0	0	0	0	1.025544325	1.366544469	1.025544325	1.02554432							
10	0	0	0	0	0	0	0	0	0	0.891488505	0.891488505	0.597070818	0.					
11	0	0.904915122	0.904915122	0.904915122	0.904915122	0.894130778	0.84905199	0.90491512										
12	0	0.808416197	0.808416197	0.808416197	0.808416197	0.808416197	0.668179673	0.62847941										
13	0	0.892110401	0.892110401	0.887955178	0.812566628	0.711170702	0.81256662											
14	0	1.252824627	1.237505999	1.232523412	1.81101513	1.075948279	1.02675944											
15	0	0	0	0	0	0	0.750537141	0	0.25900116	0.252258512	0.0264							
16	0	0.649690695	0.649690695	0.649690695	0.649690695	0.595762688	0.64969069											
17	0	0.600928448	0.600928448	0.600928448	0.600928448	0.579904013	0.54157377											
18	0	0.836561138	0.836561138	0.836561138	0.836561138	0.832002844	0.787477293	0.74637333										
19	0	0.957861341	0.957861341	0.957861341	0.957861341	0.922837747	0.88058653											
20	0	0.685993135	0.685993135	0.685993135	0.685993135	0.685993135	0.64902855											
21	0	0.683539988	0.683539988	0.683539988	0.683539988	0.564794148	0.68353998											
22	0	0.679030141	0.679030141	0.679030141	0.679030141	0.612437282	0.67903014											
23	0	0.816846642	0.816846642	0.816846642	0.73243996	0.689006864	0.64902855											
24	0	0	0	0	0	0	0	0	0	0	0.101121417	0.00E+00	0	0				
25	0	1.190970032	1.190970032	1.190970032	1.190970032	1.190970032	1.16656087											

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벡터 순으로 나열된 환자 id

4. UMAP-based clustering

1	1.405550654 1.229146917 1.229146917 1.229146917 1.229146917 1.229146917 1.
2	0 0.754337392 0.754337392 0.754337392 0.67263028 0.630004274 0.5908560
3	0 0.879823343 0.879823343 0.879823343 0.879823343 0.816978854 0.7755901
4	0 0 0 0 0 0 0 0 0.084607889 0.079360377 7.566E-05 4.
5	0 0 0 0 0 0 0 0 0

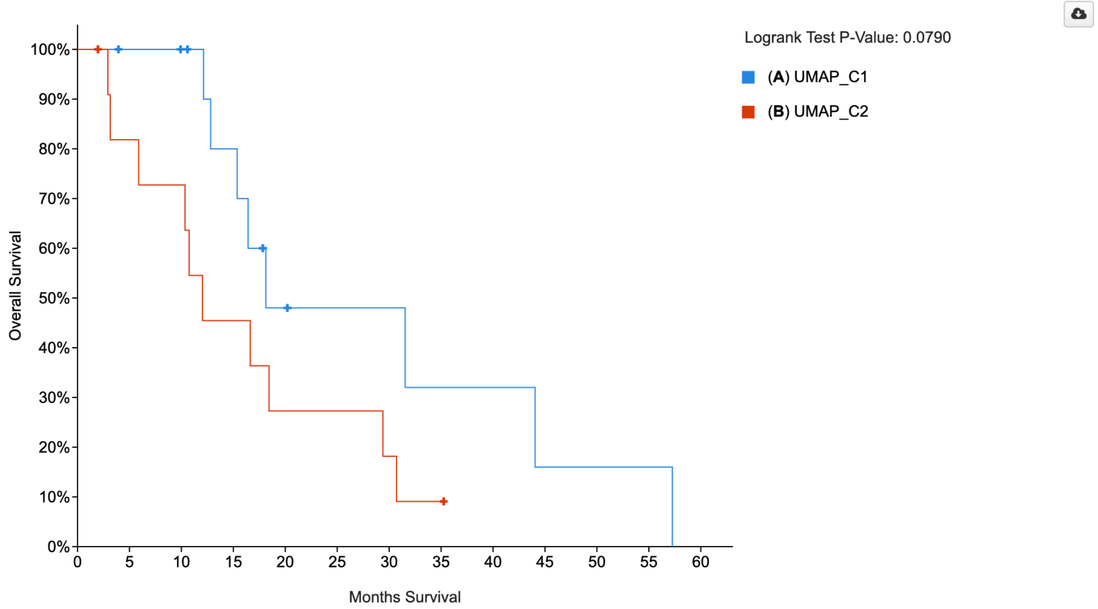
5. Cluster based group Analysis

Metastatic Prostate Adenocarcinoma (SU2C/PCF Dream Team, PNAS 2019)

Groups: (drag to reorder) (A) UMAP_C1 (13) (B) UMAP_C2 (14/12) Select all | Deselect all

Overlap | Survival | Clinical | Mutations | Copy-number | mRNA

Overall Survival Kaplan-Meier Estimate (Overall patient survival status.)



	Number of Cases, Total	Number of Cases, Deceased	Median Months Survival
(A) UMAP_C1	**13**	**8**	**18.13403417**
(B) UMAP_C2	**12**	**10**	**12.02365309**

Metastatic Prostate Adenocarcinoma (SU2C/PCF Dream Team, PNAS 2019)

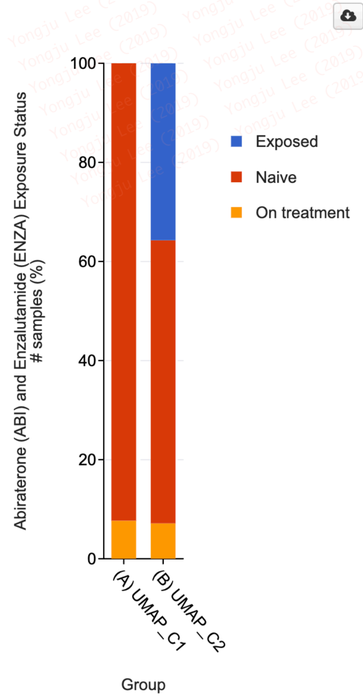
Groups: (drag to reorder) (A) UMAP_C1 (13) (B) UMAP_C2 (14/12) Select all | Deselect all

Overlap | Survival | Clinical | Mutations | Copy-number | mRNA

Plot Type: 100% stacked bar chart

Swap Axes | Horizontal Bars

Clinical Attribute	Attribute Type	Statistical Test	p-Value	q-Value ▲
Fraction Genome Altered	Sample	Kruskal Wallis Test	0.0369	0.651
Abiraterone (ABI) and Enzalutamide (ENZA) Exposure Status	Sample	Chi-squared Test	0.0558	0.651
Neuroendocrine Features	Sample	Chi-squared Test	0.109	0.651
polyA ARV7 SRPM spliced reads per million	Sample	Kruskal Wallis Test	0.125	0.651
Pathology Classification	Sample	Chi-squared Test	0.126	0.651
Capture ARV7 SRPM spliced reads per million	Sample	Kruskal Wallis Test	0.150	0.651
Tissue Site	Sample	Chi-squared Test	0.216	0.698
Overall Survival (Months)	Patient	Kruskal Wallis Test	0.231	0.698
Other Sample ID	Sample	Chi-squared Test	0.310	0.698
ETS Fusion SEQ	Sample	Chi-squared Test	0.310	0.698
Tissue Source Site	Sample	Chi-squared Test	0.314	0.698
Prostate-specific antigen	Patient	Chi-squared Test	0.341	0.698
ETS Fusion Details	Sample	Chi-squared Test	0.353	0.698
Number of Samples Per Patient	Patient	Chi-squared Test	0.426	0.698
Overall Survival Status	Patient	Chi-squared Test	0.443	0.698
NEPC Score (Capture)	Sample	Kruskal Wallis Test	0.450	0.698
Age At Procurement	Sample	Kruskal Wallis Test	0.457	0.698
RAF1/BRAF Status	Sample	Chi-squared Test	0.496	0.716
AR Score (PolyA)	Sample	Kruskal Wallis Test	0.556	0.725



SUMMIT TRIAL (2018)

Driver Only

With Enriched Entities (CO*s & ME*s)

With Enriched Entities (ME* only)

without Over-representation*

DRIVER_TP53+/-

Clinical Attribute	Attribute Type	Statistical Test	p-Value	q-Value
Mutation Count	Sample	Kruskal Wallis Test	4.6E-03	0.0462
Mutation Burden	Sample	Kruskal Wallis Test	4.62E-03	0.0462
Duration of Therapy Days	Patient	Kruskal Wallis Test	0.0143	0.0954
Progress Free Survival (Months)	Patient	Kruskal Wallis Test	0.0650	0.288
Waterfall Group	Sample	Chi-squared Test	0.0821	0.288
Coverage	Sample	Kruskal Wallis Test	0.0864	0.288
Bubble Group	Sample	Chi-squared Test	0.159	0.453
Qualifying Mutation	Sample	Chi-squared Test	0.252	0.554
Central	Sample	Chi-squared Test	0.256	0.554
Local Test	Sample	Chi-squared Test	0.277	0.554
Best objective response rate	Patient	Chi-squared Test	0.392	0.712
Clonality	Sample	Chi-squared Test	0.494	0.732
IMPACT	Sample	Chi-squared Test	0.494	0.732
Data	Sample	Chi-squared Test	0.535	0.732
Criteria	Sample	Chi-squared Test	0.549	0.732
MSI Status	Sample	Chi-squared Test	0.714	0.840
Oncoprint	Sample	Chi-squared Test	0.714	0.840
Amplification Status	Sample	Chi-squared Test	0.788	0.846
Purity	Sample	Kruskal Wallis Test	0.808	0.846
ER_PR	Sample	Chi-squared Test	0.846	0.846

DRIVER_PIK3CA+/-

Clinical Attribute	Attribute Type	Statistical Test	p-Value	q-Value
Mutation Count	Sample	Kruskal Wallis Test	0.0354	0.239
Mutation Burden	Sample	Kruskal Wallis Test	0.0357	0.239
Progress Free Survival (Months)	Patient	Kruskal Wallis Test	0.0359	0.239
Waterfall Group	Sample	Chi-squared Test	0.0920	0.460
Best objective response rate	Patient	Chi-squared Test	0.189	0.696
Purity	Sample	Kruskal Wallis Test	0.234	0.696
Bubble Group	Sample	Chi-squared Test	0.244	0.696
Qualifying Mutation	Sample	Chi-squared Test	0.363	0.744
Central	Sample	Chi-squared Test	0.371	0.744
Local Test	Sample	Chi-squared Test	0.372	0.744
Duration of Therapy Days	Patient	Kruskal Wallis Test	0.514	0.801
MSI Status	Sample	Chi-squared Test	0.585	0.801
Oncoprint	Sample	Chi-squared Test	0.585	0.801
Criteria	Sample	Chi-squared Test	0.653	0.801
Clonality	Sample	Chi-squared Test	0.661	0.801
IMPACT	Sample	Chi-squared Test	0.661	0.801
Coverage	Sample	Kruskal Wallis Test	0.695	0.801
Data	Sample	Chi-squared Test	0.721	0.801
ER_PR	Sample	Chi-squared Test	0.836	0.880
Amplification Status	Sample	Chi-squared Test	0.954	0.954

N/A

ME_GATA3+/-

Clinical Attribute	Attribute Type	Statistical Test	p-Value	q-Value
Duration of Therapy Days	Patient	Kruskal Wallis Test	1.46E-03	0.0293
Progress Free Survival (Months)	Patient	Kruskal Wallis Test	9.20E-03	0.0642
Mutation Count	Sample	Kruskal Wallis Test	0.0127	0.0642
Mutation Burden	Sample	Kruskal Wallis Test	0.0128	0.0642
Coverage	Sample	Kruskal Wallis Test	0.0451	0.181
Waterfall Group	Sample	Chi-squared Test	0.0567	0.189
Bubble Group	Sample	Chi-squared Test	0.125	0.338
Best objective response rate	Patient	Chi-squared Test	0.135	0.338
Central	Sample	Chi-squared Test	0.162	0.361
Data	Sample	Chi-squared Test	0.191	0.372
Qualifying Mutation	Sample	Chi-squared Test	0.205	0.372
IMPACT	Sample	Chi-squared Test	0.356	0.594
Local Test	Sample	Chi-squared Test	0.509	0.783
ER_PR	Sample	Chi-squared Test	0.576	0.823
Amplification Status	Sample	Chi-squared Test	0.642	0.856
Clonality	Sample	Chi-squared Test	0.693	0.866
Purity	Sample	Kruskal Wallis Test	0.808	0.876
MSI Status	Sample	Chi-squared Test	0.833	0.876
Oncoprint	Sample	Chi-squared Test	0.833	0.876
Criteria	Sample	Chi-squared Test	0.933	0.933

ME_ESR1+/-

Clinical Attribute	Attribute Type	Statistical Test	p-Value	q-Value
Duration of Therapy Days	Patient	Kruskal Wallis Test	2E-03	0.0440
Progress Free Survival (Months)	Patient	Kruskal Wallis Test	9.8E-03	0.0978
Best objective response rate	Patient	Chi-squared Test	0.0384	0.256
Waterfall Group	Sample	Chi-squared Test	0.0821	0.282
Mutation Count	Sample	Kruskal Wallis Test	0.0842	0.282
Mutation Burden	Sample	Kruskal Wallis Test	0.0847	0.282
Bubble Group	Sample	Chi-squared Test	0.159	0.425
Central	Sample	Chi-squared Test	0.170	0.425
Coverage	Sample	Kruskal Wallis Test	0.221	0.490
Qualifying Mutation	Sample	Chi-squared Test	0.252	0.504
ER_PR	Sample	Chi-squared Test	0.333	0.574
Local Test	Sample	Chi-squared Test	0.345	0.574
Clonality	Sample	Chi-squared Test	0.494	0.663
IMPACT	Sample	Chi-squared Test	0.494	0.663
Purity	Sample	Kruskal Wallis Test	0.497	0.663
Data	Sample	Chi-squared Test	0.535	0.669
MSI Status	Sample	Chi-squared Test	0.714	0.794
Oncoprint	Sample	Chi-squared Test	0.714	0.794
Amplification Status	Sample	Chi-squared Test	0.788	0.830
Criteria	Sample	Chi-squared Test	0.861	0.861

with Over-representation*

2 GROUP CLUSTERING (DRIVER)

Clinical Attribute	Attribute Type	Statistical Test	p-Value	q-Value
Duration of Therapy Days	Patient	Kruskal Wallis Test	1.46E-03	0.0293
Progress Free Survival (Months)	Patient	Kruskal Wallis Test	9.20E-03	0.0642
Mutation Count	Sample	Kruskal Wallis Test	0.0127	0.0642
Mutation Burden	Sample	Kruskal Wallis Test	0.0128	0.0642
Coverage	Sample	Kruskal Wallis Test	0.0451	0.181
Waterfall Group	Sample	Chi-squared Test	0.0567	0.189
Bubble Group	Sample	Chi-squared Test	0.125	0.338
Best objective response rate	Patient	Chi-squared Test	0.135	0.338
Central	Sample	Chi-squared Test	0.162	0.361
Data	Sample	Chi-squared Test	0.191	0.372
Qualifying Mutation	Sample	Chi-squared Test	0.205	0.372
IMPACT	Sample	Chi-squared Test	0.356	0.594
Local Test	Sample	Chi-squared Test	0.509	0.783
ER_PR	Sample	Chi-squared Test	0.576	0.823
Amplification Status	Sample	Chi-squared Test	0.642	0.856
Clonality	Sample	Chi-squared Test	0.693	0.866
Purity	Sample	Kruskal Wallis Test	0.808	0.876
MSI Status	Sample	Chi-squared Test	0.833	0.876
Oncoprint	Sample	Chi-squared Test	0.833	0.876
Criteria	Sample	Chi-squared Test	0.933	0.933

2 GROUP CLUSTERING (ENR)

Clinical Attribute	Attribute Type	Statistical Test	p-Value	q-Value
Mutation Count	Sample	Kruskal Wallis Test	0.0191	0.138
Central	Sample	Chi-squared Test	0.0220	0.138
Mutation Burden	Sample	Kruskal Wallis Test	0.0227	0.138
Progress Free Survival (Months)	Patient	Kruskal Wallis Test	0.0365	0.138
Best objective response rate	Patient	Chi-squared Test	0.0384	0.138
Purity	Sample	Kruskal Wallis Test	0.0415	0.138
Duration of Therapy Days	Patient	Kruskal Wallis Test	0.0662	0.189
Local Test	Sample	Chi-squared Test	0.174	0.399
Amplification Status	Sample	Chi-squared Test	0.179	0.399
Data	Sample	Chi-squared Test	0.253	0.496
Waterfall Group	Sample	Chi-squared Test	0.273	0.496
Clonality	Sample	Chi-squared Test	0.494	0.744
IMPACT	Sample	Chi-squared Test	0.494	0.744
Criteria	Sample	Chi-squared Test	0.549	0.744
Bubble Group	Sample	Chi-squared Test	0.558	0.744
Qualifying Mutation	Sample	Chi-squared Test	0.677	0.794
MSI Status	Sample	Chi-squared Test	0.714	0.794
Oncoprint	Sample	Chi-squared Test	0.714	0.794
ER_PR	Sample	Chi-squared Test	0.846	0.891
Coverage	Sample	Kruskal Wallis Test	0.903	0.903

3 GROUP CLUSTERING (ENR)

Clinical Attribute	Attribute Type	Statistical Test	p-Value	q-Value
Central	Sample	Chi-squared Test	0.0389	0.284
Purity	Sample	Kruskal Wallis Test	0.0498	0.284
Duration of Therapy Days	Patient	Kruskal Wallis Test	0.0524	0.284
Mutation Count	Sample	Kruskal Wallis Test	0.0639	0.284
Mutation Burden	Sample	Kruskal Wallis Test	0.0745	0.284
Progress Free Survival (Months)	Patient	Kruskal Wallis Test	0.0933	0.284
Amplification Status	Sample	Chi-squared Test	0.0995	0.284
Data	Sample	Chi-squared Test	0.136	0.307
Best objective response rate	Patient	Chi-squared Test	0.143	0.307
Clonality	Sample	Chi-squared Test	0.153	0.307
MSI Status	Sample	Chi-squared Test	0.229	0.382
Oncoprint	Sample	Chi-squared Test	0.229	0.382
Waterfall Group	Sample	Chi-squared Test	0.249	0.382
Local Test	Sample	Chi-squared Test	0.267	0.382
IMPACT	Sample	Chi-squared Test	0.318	0.424
Bubble Group	Sample	Chi-squared Test	0.501	0.599
ER_PR	Sample	Chi-squared Test	0.509	0.599
Coverage	Sample	Kruskal Wallis Test	0.630	0.701
Qualifying Mutation	Sample	Chi-squared Test	0.676	0.712
Criteria	Sample	Chi-squared Test	0.825	0.825

2 GROUP CLUSTERING (ME)

Clinical Attribute	Attribute Type	Statistical Test	p-Value	q-Value
Mutation Count	Sample	Kruskal Wallis Test	0.0191	0.138
Central	Sample	Chi-squared Test	0.0220	0.138
Mutation Burden	Sample	Kruskal Wallis Test	0.0227	0.138
Progress Free Survival (Months)	Patient	Kruskal Wallis Test	0.0365	0.138
Best objective response rate	Patient	Chi-squared Test	0.0384	0.138
Purity	Sample	Kruskal Wallis Test	0.0415	0.138
Duration of Therapy Days	Patient	Kruskal Wallis Test	0.0662	0.189
Local Test	Sample	Chi-squared Test	0.174	0.399
Amplification Status	Sample	Chi-squared Test	0.179	0.399
Data	Sample	Chi-squared Test	0.253	0.496
Waterfall Group	Sample	Chi-squared Test	0.273	0.496
Clonality	Sample	Chi-squared Test	0.494	0.744
IMPACT	Sample	Chi-squared Test	0.494	0.744
Criteria	Sample	Chi-squared Test	0.549	0.744
Bubble Group	Sample	Chi-squared Test	0.558	0.744
Qualifying Mutation	Sample	Chi-squared Test	0.677	0.794
MSI Status	Sample	Chi-squared Test	0.714	0.794
Oncoprint	Sample	Chi-squared Test	0.714	0.794
ER_PR	Sample	Chi-squared Test	0.846	0.891
Coverage	Sample	Kruskal Wallis Test	0.903	0.903

3 GROUP CLUSTERING (ME)

Clinical Attribute	Attribute Type	Statistical Test	p-Value	q-Value
Duration of Therapy Days	Patient	Kruskal Wallis Test	6.3E-03	0.127
Mutation Count	Sample	Kruskal Wallis Test	0.0242	0.133
Progress Free Survival (Months)	Patient	Kruskal Wallis Test	0.0260	0.133
Mutation Burden	Sample	Kruskal Wallis Test	0.0266	0.133
Best objective response rate	Patient	Chi-squared Test	0.0530	0.171
Purity	Sample	Kruskal Wallis Test	0.0599	0.171
Coverage	Sample	Kruskal Wallis Test	0.0603	0.171
Central	Sample	Chi-squared Test	0.0683	0.171
Amplification Status	Sample	Chi-squared Test	0.0995	0.221
Waterfall Group	Sample	Chi-squared Test	0.211	0.408
ER_PR	Sample	Chi-squared Test	0.241	0.408
IMPACT	Sample	Chi-squared Test	0.245	0.408
Bubble Group	Sample	Chi-squared Test	0.277	0.426
Data	Sample	Chi-squared Test	0.342	0.488
Qualifying Mutation	Sample	Chi-squared Test	0.435	0.527
MSI Status	Sample	Chi-squared Test	0.448	0.527
Oncoprint	Sample	Chi-squared Test	0.448	0.527
Local Test	Sample	Chi-squared Test	0.494	0.548
Criteria	Sample	Chi-squared Test	0.825	0.869
Clonality	Sample	Chi-squared Test	0.949	0.949

- CO : Co-occurrent mutations
- ME : Mutually exclusive mutations
- Over-representation : Reactome based enrichment analysis

CCRCC (2019)

DV_VHL+/-

Clinical Attribute	Attribute Type	Statistical Test	p-Value	q-Value
Sex	Patient	Chi-squared Test	0.0350	0.484
NonSynonymous Uneval	Sample	Kruskal Wallis Test	0.0561	0.484
First Line Therapy	Patient	Chi-squared Test	0.0781	0.484
Progress Free Survival (Months)	Patient	Kruskal Wallis Test	0.0815	0.484
Cell Membrane PDL1 3%+	Patient	Kruskal Wallis Test	0.0956	0.484
Treatment Group	Patient	Chi-squared Test	0.112	0.484
Mutations Subclonal	Sample	Kruskal Wallis Test	0.133	0.484
Mutations Clonal	Sample	Kruskal Wallis Test	0.139	0.484
Purity	Sample	Kruskal Wallis Test	0.152	0.484
NonSynonymous Subclonal	Sample	Kruskal Wallis Test	0.170	0.484
Nonsynonymous Clonal	Sample	Kruskal Wallis Test	0.184	0.484
FrameShift Indels	Sample	Kruskal Wallis Test	0.193	0.484
Cell Membrane PDL1 2%+	Patient	Kruskal Wallis Test	0.250	0.571
PDL1 Positive 1%	Patient	Kruskal Wallis Test	0.277	0.571
Mutations Uneval	Sample	Kruskal Wallis Test	0.285	0.571
Response to Immunotherapy	Patient	Chi-squared Test	0.370	0.668
Overall Survival Censor	Patient	Chi-squared Test	0.378	0.668
Overall Survival (Months)	Patient	Kruskal Wallis Test	0.433	0.722
Genome Doublings	Sample	Chi-squared Test	0.498	0.784
Nonsynonymous Mutation Count	Sample	Kruskal Wallis Test	0.571	0.784
Cell Membrane PDL1 0%	Patient	Kruskal Wallis Test	0.576	0.784
Age	Patient	Kruskal Wallis Test	0.601	0.784
Mutation Count	Sample	Kruskal Wallis Test	0.601	0.784
All Synonymous Mutations	Sample	Kruskal Wallis Test	0.647	0.809
Cell Membrane PDL1 1%+	Patient	Kruskal Wallis Test	0.695	0.826
RECIST	Patient	Chi-squared Test	0.716	0.826
PDL1 Positive 5%	Patient	Kruskal Wallis Test	0.787	0.862
Progression Free Censor	Patient	Chi-squared Test	0.805	0.862
All Mutations	Sample	Kruskal Wallis Test	0.862	0.891
Ploidy	Sample	Kruskal Wallis Test	0.981	0.981

DV_PBRM1+/-

Clinical Attribute	Attribute Type	Statistical Test	p-Value	q-Value
Progress Free Survival (Months)	Patient	Kruskal Wallis Test	5.37E-03	0.161
Response to Immunotherapy	Patient	Chi-squared Test	0.0131	0.196
RECIST	Patient	Chi-squared Test	0.0275	0.275
Overall Survival Censor	Patient	Chi-squared Test	0.0584	0.438
Sex	Patient	Chi-squared Test	0.0774	0.465
Mutations Uneval	Sample	Kruskal Wallis Test	0.144	0.633
Purity	Sample	Kruskal Wallis Test	0.175	0.633
Overall Survival (Months)	Patient	Kruskal Wallis Test	0.186	0.633
Cell Membrane PDL1 2%+	Patient	Kruskal Wallis Test	0.190	0.633
Ploidy	Sample	Kruskal Wallis Test	0.280	0.815
Age	Patient	Kruskal Wallis Test	0.327	0.815
Cell Membrane PDL1 3%+	Patient	Kruskal Wallis Test	0.376	0.815
FrameShift Indels	Sample	Kruskal Wallis Test	0.393	0.815
PDL1 Positive 5%	Patient	Kruskal Wallis Test	0.398	0.815
PDL1 Positive 1%	Patient	Kruskal Wallis Test	0.408	0.815
Nonsynonymous Mutation Count	Sample	Kruskal Wallis Test	0.454	0.851
NonSynonymous Subclonal	Sample	Kruskal Wallis Test	0.501	0.885
Mutation Count	Sample	Kruskal Wallis Test	0.552	0.891
All Mutations	Sample	Kruskal Wallis Test	0.564	0.891
Mutations Subclonal	Sample	Kruskal Wallis Test	0.645	0.903
Nonsynonymous Clonal	Sample	Kruskal Wallis Test	0.659	0.903
First Line Therapy	Patient	Chi-squared Test	0.662	0.903
Treatment Group	Patient	Chi-squared Test	0.757	0.907
Mutations Clonal	Sample	Kruskal Wallis Test	0.759	0.907
Progression Free Censor	Patient	Chi-squared Test	0.765	0.907
NonSynonymous Uneval	Sample	Kruskal Wallis Test	0.786	0.907
All Synonymous Mutations	Sample	Kruskal Wallis Test	0.908	0.960
Cell Membrane PDL1 0%	Patient	Kruskal Wallis Test	0.921	0.960
Genome Doublings	Sample	Chi-squared Test	0.948	0.960
Cell Membrane PDL1 1%+	Patient	Kruskal Wallis Test	0.960	0.960

ME_SMAD3+/-

Clinical Attribute	Attribute Type	Statistical Test	p-Value	q-Value
Treatment Group	Patient	Chi-squared Test	0.0334	0.519
First Line Therapy	Patient	Chi-squared Test	0.0498	0.519
FrameShift Indels	Sample	Kruskal Wallis Test	0.0617	0.519
Cell Membrane PDL1 3%+	Patient	Kruskal Wallis Test	0.0956	0.519
Progress Free Survival (Months)	Patient	Kruskal Wallis Test	0.102	0.519
Sex	Patient	Chi-squared Test	0.128	0.519
Mutations Subclonal	Sample	Kruskal Wallis Test	0.142	0.519
NonSynonymous Subclonal	Sample	Kruskal Wallis Test	0.186	0.519
Overall Survival (Months)	Patient	Kruskal Wallis Test	0.201	0.519
NonSynonymous Uneval	Sample	Kruskal Wallis Test	0.204	0.519
Mutations Clonal	Sample	Kruskal Wallis Test	0.232	0.519
Nonsynonymous Clonal	Sample	Kruskal Wallis Test	0.240	0.519
Purity	Sample	Kruskal Wallis Test	0.248	0.519
Cell Membrane PDL1 2%+	Patient	Kruskal Wallis Test	0.250	0.519
Age	Patient	Kruskal Wallis Test	0.266	0.519
PDL1 Positive 1%	Patient	Kruskal Wallis Test	0.277	0.519
Response to Immunotherapy	Patient	Chi-squared Test	0.307	0.541
Nonsynonymous Mutation Count	Sample	Kruskal Wallis Test	0.543	0.763
Overall Survival Censor	Patient	Chi-squared Test	0.560	0.763
Genome Doublings	Sample	Chi-squared Test	0.566	0.763
Mutation Count	Sample	Kruskal Wallis Test	0.571	0.763
Cell Membrane PDL1 0%	Patient	Kruskal Wallis Test	0.576	0.763
Mutations Uneval	Sample	Kruskal Wallis Test	0.585	0.763
Ploidy	Sample	Kruskal Wallis Test	0.635	0.787
Progression Free Censor	Patient	Chi-squared Test	0.656	0.787
Cell Membrane PDL1 1%+	Patient	Kruskal Wallis Test	0.695	0.802
All Mutations	Sample	Kruskal Wallis Test	0.769	0.843
PDL1 Positive 5%	Patient	Kruskal Wallis Test	0.787	0.843
RECIST	Patient	Chi-squared Test	0.816	0.844
All Synonymous Mutations	Sample	Kruskal Wallis Test	0.916	0.916

ME_EP300+/-

Clinical Attribute	Attribute Type	Statistical Test	p-Value	q-Value
Progress Free Survival (Months)	Patient	Kruskal Wallis Test	3.29E-03	0.0593
Response to Immunotherapy	Patient	Chi-squared Test	4.0E-03	0.0593
Sex	Patient	Chi-squared Test	8.90E-03	0.0890
FrameShift Indels	Sample	Kruskal Wallis Test	0.0217	0.132
RECIST	Patient	Chi-squared Test	0.0220	0.132
Overall Survival (Months)	Patient	Kruskal Wallis Test	0.0321	0.160
NonSynonymous Uneval	Sample	Kruskal Wallis Test	0.0568	0.244
PDL1 Positive 1%	Patient	Kruskal Wallis Test	0.0921	0.345
Age	Patient	Kruskal Wallis Test	0.107	0.357
First Line Therapy	Patient	Chi-squared Test	0.120	0.359
Treatment Group	Patient	Chi-squared Test	0.161	0.438
Cell Membrane PDL1 2%+	Patient	Kruskal Wallis Test	0.190	0.475
Mutations Uneval	Sample	Kruskal Wallis Test	0.310	0.716
Cell Membrane PDL1 3%+	Patient	Kruskal Wallis Test	0.376	0.769
PDL1 Positive 5%	Patient	Kruskal Wallis Test	0.398	0.769
Cell Membrane PDL1 0%	Patient	Kruskal Wallis Test	0.410	0.769
Overall Survival Censor	Patient	Chi-squared Test	0.447	0.782
Cell Membrane PDL1 1%+	Patient	Kruskal Wallis Test	0.469	0.782
Purity	Sample	Kruskal Wallis Test	0.497	0.784
Progression Free Censor	Patient	Chi-squared Test	0.568	0.845
Nonsynonymous Mutation Count	Sample	Kruskal Wallis Test	0.592	0.845
Nonsynonymous Clonal	Sample	Kruskal Wallis Test	0.620	0.845
Mutation Count	Sample	Kruskal Wallis Test	0.691	0.901
Mutations Clonal	Sample	Kruskal Wallis Test	0.721	0.901
Mutations Subclonal	Sample	Kruskal Wallis Test	0.781	0.937
All Mutations	Sample	Kruskal Wallis Test	0.842	0.953
NonSynonymous Subclonal	Sample	Kruskal Wallis Test	0.858	0.953
All Synonymous Mutations	Sample	Kruskal Wallis Test	0.889	0.953
Genome Doublings	Sample	Chi-squared Test	0.933	0.965
Ploidy	Sample	Kruskal Wallis Test	1.00	1.00

UMAP_C1 vs C2

Clinical Attribute	Attribute Type	Statistical Test	p-Value	q-Value
Progress Free Survival (Months)	Patient	Kruskal Wallis Test	2.84E-03	0.0515
Response to Immunotherapy	Patient	Chi-squared Test	3.43E-03	0.0515
Sex	Patient	Chi-squared Test	5.78E-03	0.0578
RECIST	Patient	Chi-squared Test	0.0171	0.128
NonSynonymous Uneval	Sample	Kruskal Wallis Test	0.0367	0.220
FrameShift Indels	Sample	Kruskal Wallis Test	0.0497	0.249
Overall Survival (Months)	Patient	Kruskal Wallis Test	0.0627	0.269
PDL1 Positive 1%	Patient	Kruskal Wallis Test	0.0921	0.345
First Line Therapy	Patient	Chi-squared Test	0.149	0.498
Age	Patient	Kruskal Wallis Test	0.189	0.518
Cell Membrane PDL1 2%+	Patient	Kruskal Wallis Test	0.190	0.518
Mutations Uneval	Sample	Kruskal Wallis Test	0.231	0.577
Treatment Group	Patient	Chi-squared Test	0.281	0.648
Cell Membrane PDL1 3%+	Patient	Kruskal Wallis Test	0.376	0.724
Overall Survival Censor	Patient	Chi-squared Test	0.387	0.724
PDL1 Positive 5%	Patient	Kruskal Wallis Test	0.398	0.724
Cell Membrane PDL1 0%	Patient	Kruskal Wallis Test	0.410	0.724
Purity	Sample	Kruskal Wallis Test	0.451	0.741
Cell Membrane PDL1 1%+	Patient	Kruskal Wallis Test	0.469	0.741
Nonsynonymous Mutation Count	Sample	Kruskal Wallis Test	0.608	0.856
Nonsynonymous Clonal	Sample	Kruskal Wallis Test	0.608	0.856
Progression Free Censor	Patient	Chi-squared Test	0.628	0.856
Mutations Clonal	Sample	Kruskal Wallis Test	0.676	0.880
Mutation Count	Sample	Kruskal Wallis Test	0.704	0.880
All Synonymous Mutations	Sample	Kruskal Wallis Test	0.775	0.894
Mutations Subclonal	Sample	Kruskal Wallis Test	0.819	0.894
Ploidy	Sample	Kruskal Wallis Test	0.851	0.894
All Mutations	Sample	Kruskal Wallis Test	0.879	0.894
Genome Doublings	Sample	Chi-squared Test	0.891	0.894
NonSynonymous Subclonal	Sample	Kruskal Wallis Test	0.894	0.894

Yongju Lee (2019)