Med&Omix

Second Meeting Query-ing

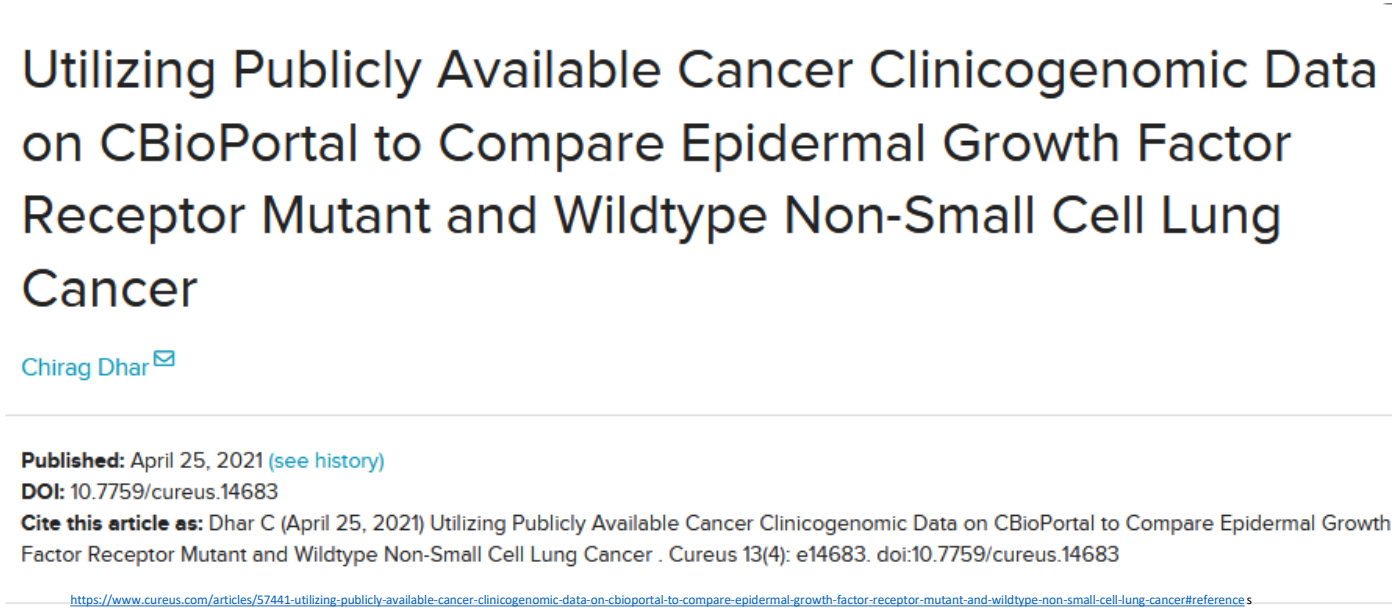
Previously Discussed in Med&Omix Meeting

- How to use cBioPortal
- How to apply on our hypothesis

So, I basically will do simple dry-testing of an hypothesis

Let’s Decide A Simple Hypothesis

- I found this article on «**Utilizing Publicly Available Cancer Clinicogenomic Data on CBioPortal to Compare Epidermal Growth Factor Receptor Mutant and Wildtype Non-Small Cell Lung Cancer»**



Utilizing Publicly Available Cancer Clinicogenomic Data on CBioPortal to Compare Epidermal Growth Factor Receptor Mutant and Wildtype Non-Small Cell Lung Cancer

Chirag Dhar

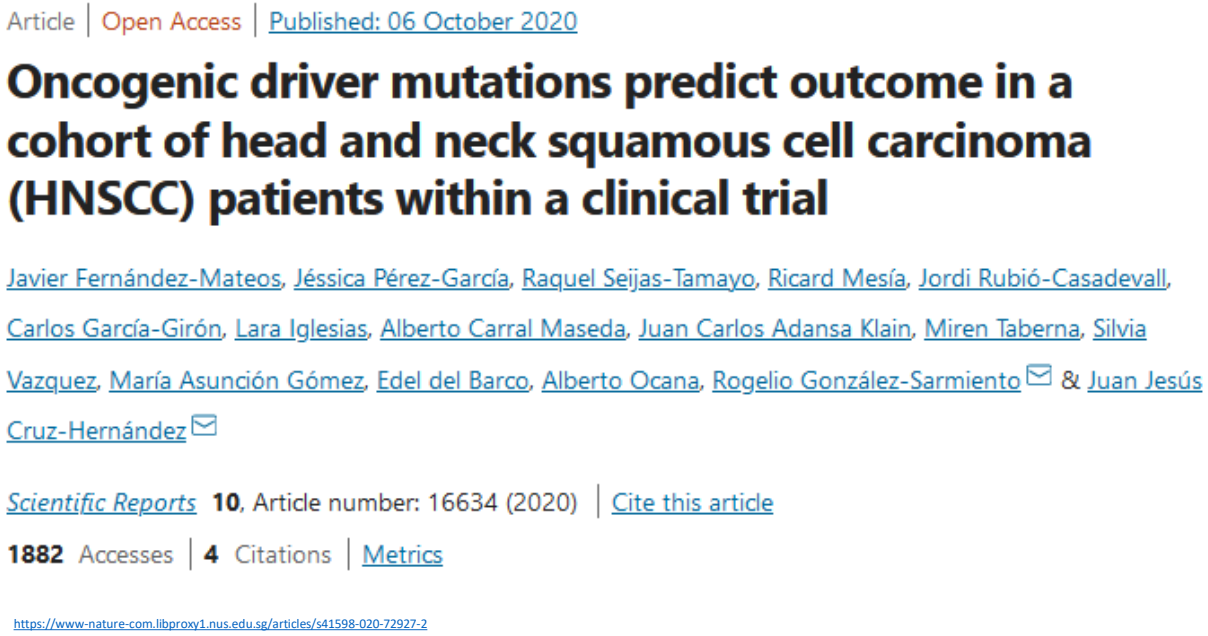
Published: April 25, 2021 (see history)
DOI: 10.7759/cureus.14683
Cite this article as: Dhar C (April 25, 2021) Utilizing Publicly Available Cancer Clinicogenomic Data on CBioPortal to Compare Epidermal Growth Factor Receptor Mutant and Wildtype Non-Small Cell Lung Cancer . Cureus 13(4): e14683. doi:10.7759/cureus.14683

https://www.cureus.com/articles/57441-utilizing-publicly-available-cancer-clinicogenomic-data-on-cbioportal-to-compare-epidermal-growth-factor-receptor-mutant-and-wildtype-non-small-cell-lung-cancer#references

Let’s Decide A Simple Hypothesis

- Then looked for an alternative disease with alternative mutation... Later, found this «**Oncogenic driver mutations predict outcome in a cohort of head and neck squamous cell carcinoma (HNSCC) patients within a clinical trial»**

HPV status



Article | Open Access | Published: 06 October 2020

Oncogenic driver mutations predict outcome in a cohort of head and neck squamous cell carcinoma (HNSCC) patients within a clinical trial

Javier Fernández-Mateos, Jéssica Pérez-García, Raquel Seijas-Tamayo, Ricard Mesía, Jordi Rubió-Casadevall, Carlos García-Girón, Lara Iglesias, Alberto Carral Maseda, Juan Carlos Adansa Klain, Miren Taberna, Silvia Vazquez, María Asunción Gómez, Edel del Barco, Alberto Ocana, Rogelio González-Sarmiento & Juan Jesús Cruz-Hernández

Scientific Reports **10**, Article number: 16634 (2020) | Cite this article

1882 Accesses | **4** Citations | Metrics

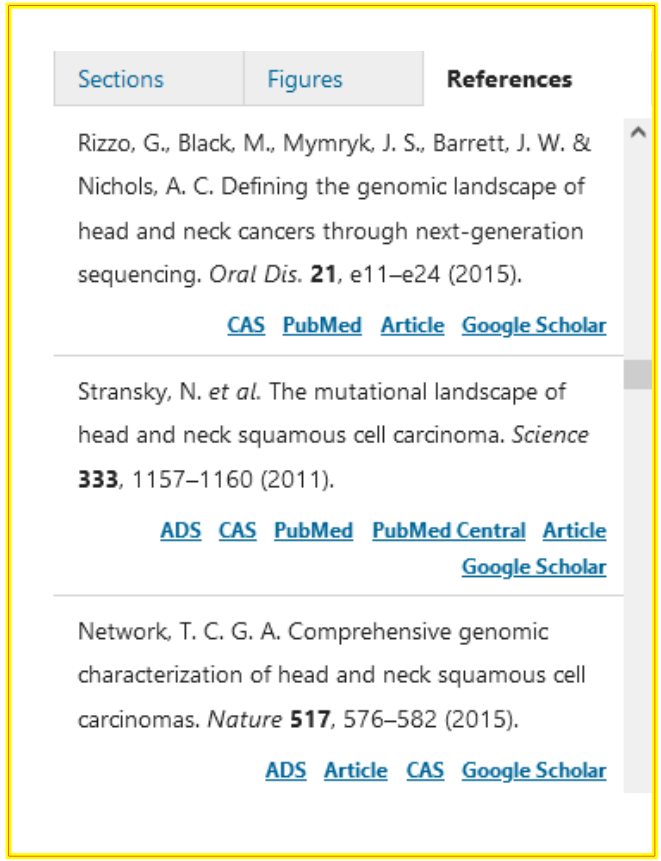
https://www-nature-com.libproxy1.nus.edu.sg/articles/s41598-020-72927-2

Let’s Decide A Simple Hypothesis

- They are the ones referred in the article, so I will test how much consistent across all these datasets

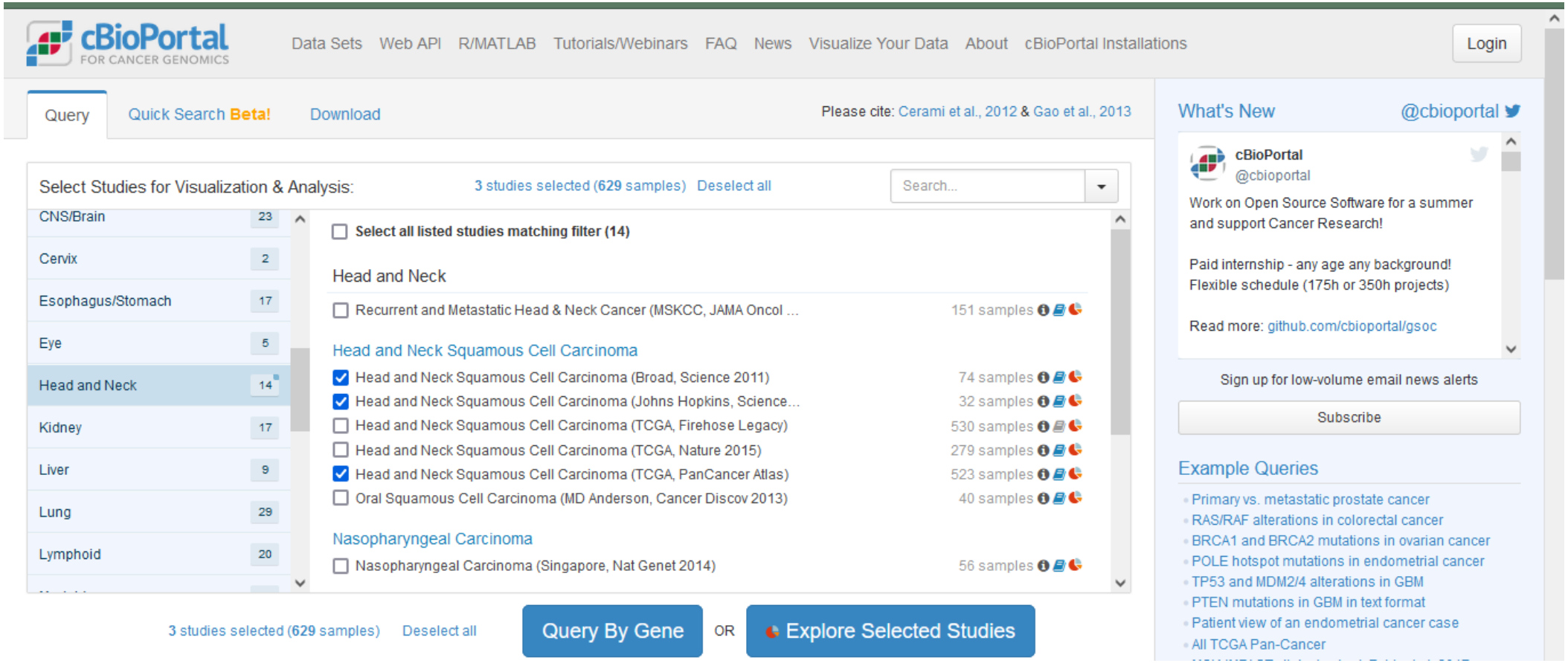
Next-generation sequencing (NGS) has helped to identify genetic alterations that could be used as a molecular vulnerability for therapeutic discovery and target optimization. In addition, they could have a prognosis utility as biomarkers of response in different tumour types including head and neck squamous cell carcinomas[16,17]. For instance, the analysis of *The Cancer Genome Atlas* (TCGA) described the molecular landscape of HPV-positive and HPV-negative HNSCC as having molecular alterations not reported before[18]. Since the first description of the recurrently mutated genes in HNSCC[19], additional studies have included other genes such as *TP53, NOTCH1, PIK3CA, CDKN2A, CCDN1, HRAS, FAT1, FBXW7* and *FGFR3*, among others[20,21]. For this reason, targeted sequencing has become a flexible tool to study those genes previously reported as mutated in HNSCC[21].

To contribute to the understanding of how somatic mutations influence the outcome of HNSCC treatment, we have studied a panel of 26 genes (Table S1) by next-generation sequencing in a homogenously treated locally advanced HNSCC Spanish cohort. In this study

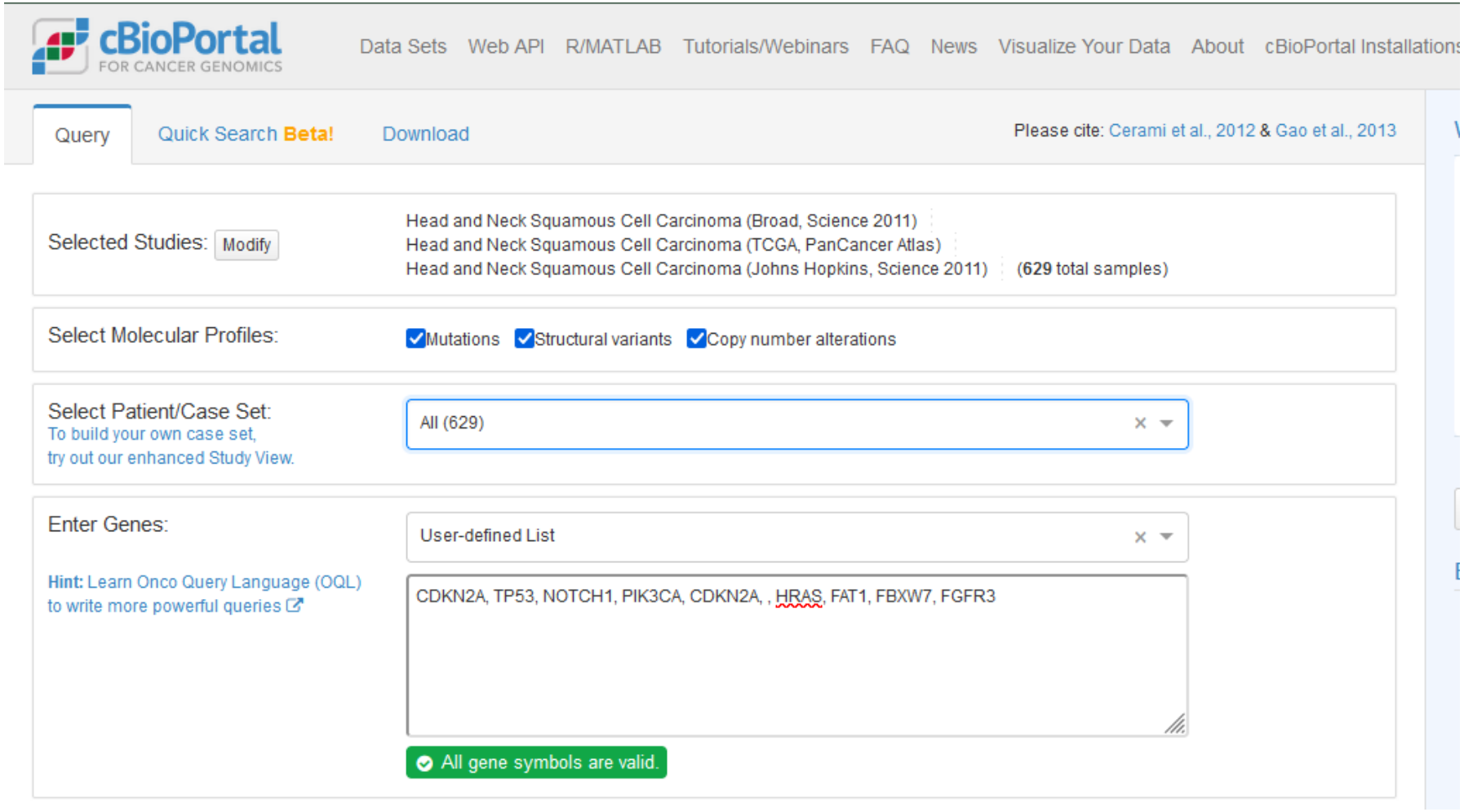


How to apply on

- Selected these datasets available

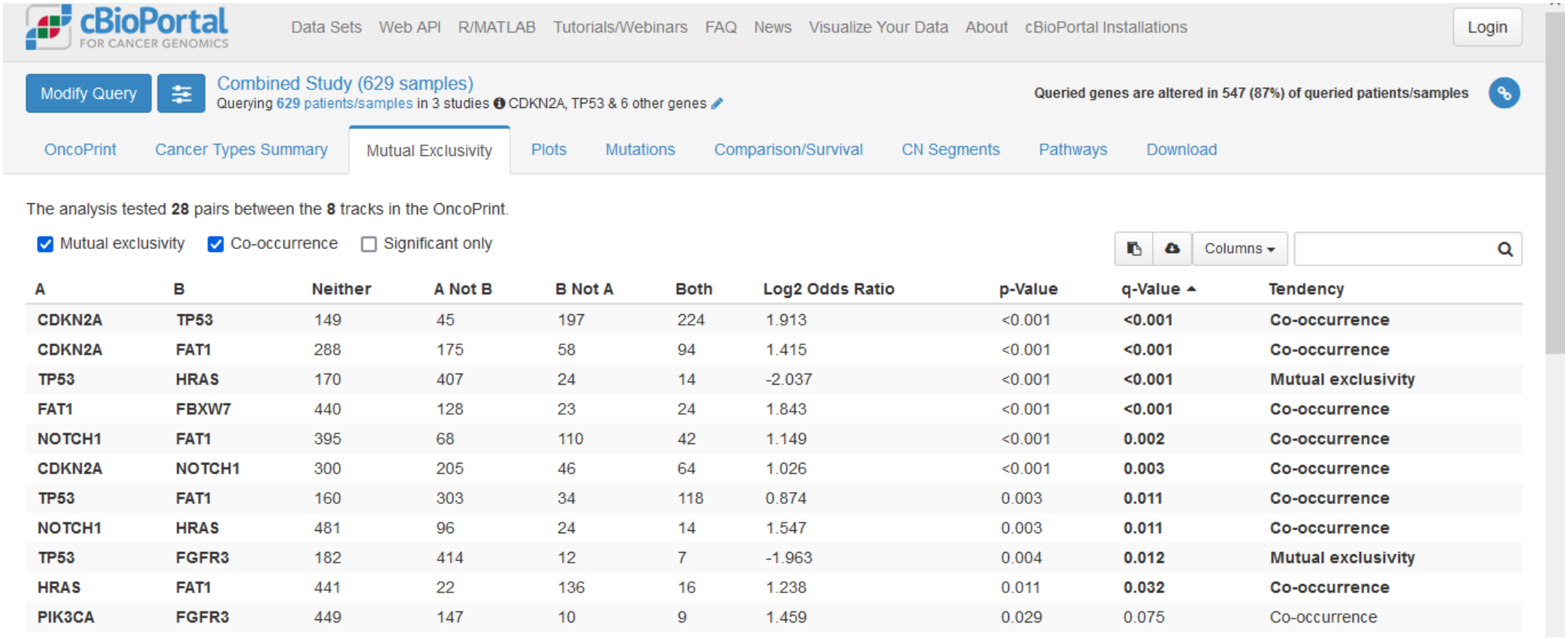


How to apply on



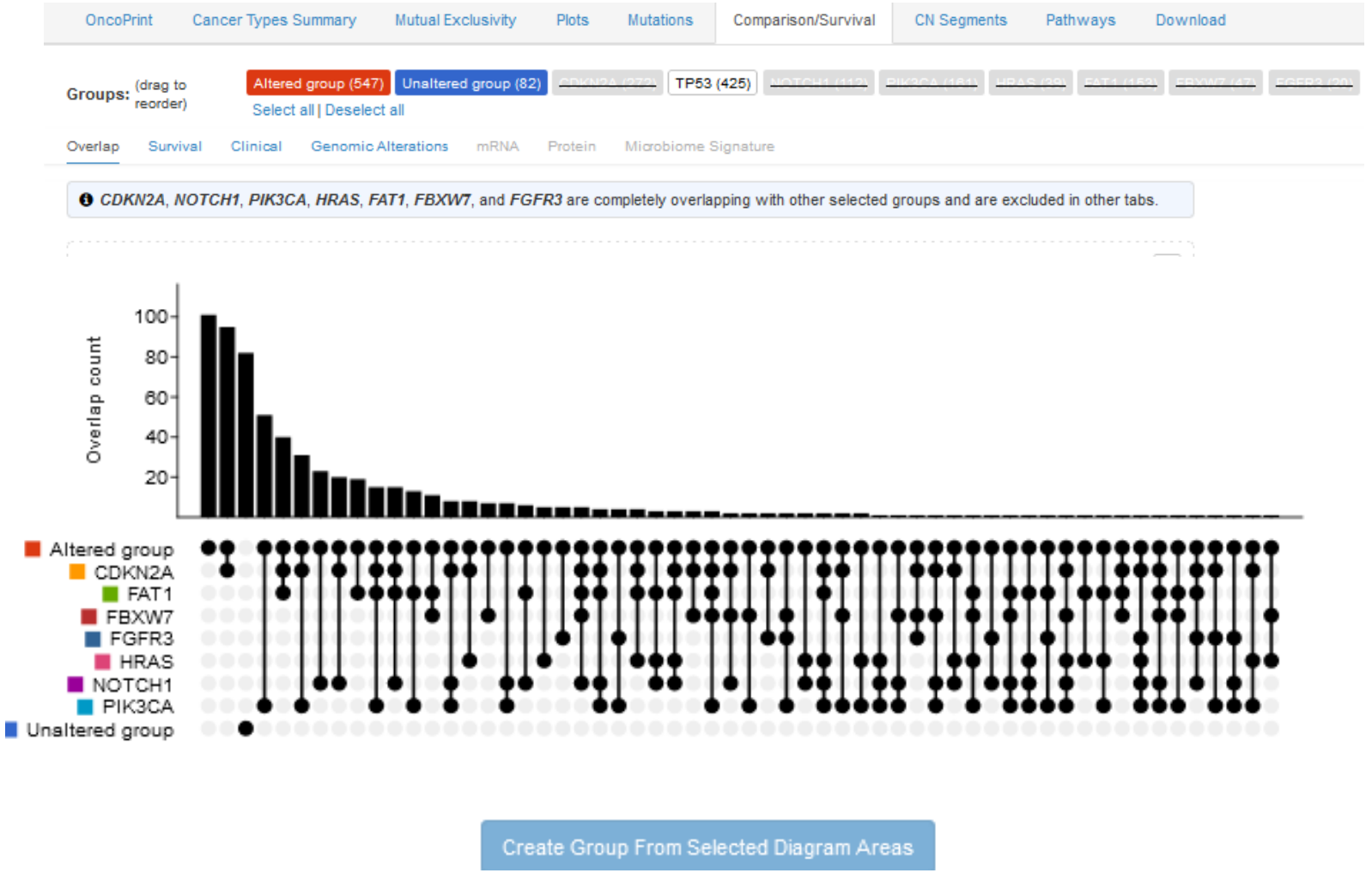
How to apply on

Interesting relationships... For example, TP53 and HRAS are mutually exclusive, and TP53 and FAT1 co-occurs. However, FAT1 and HRAS co-occurs, too. (Need to check pathway details for this)



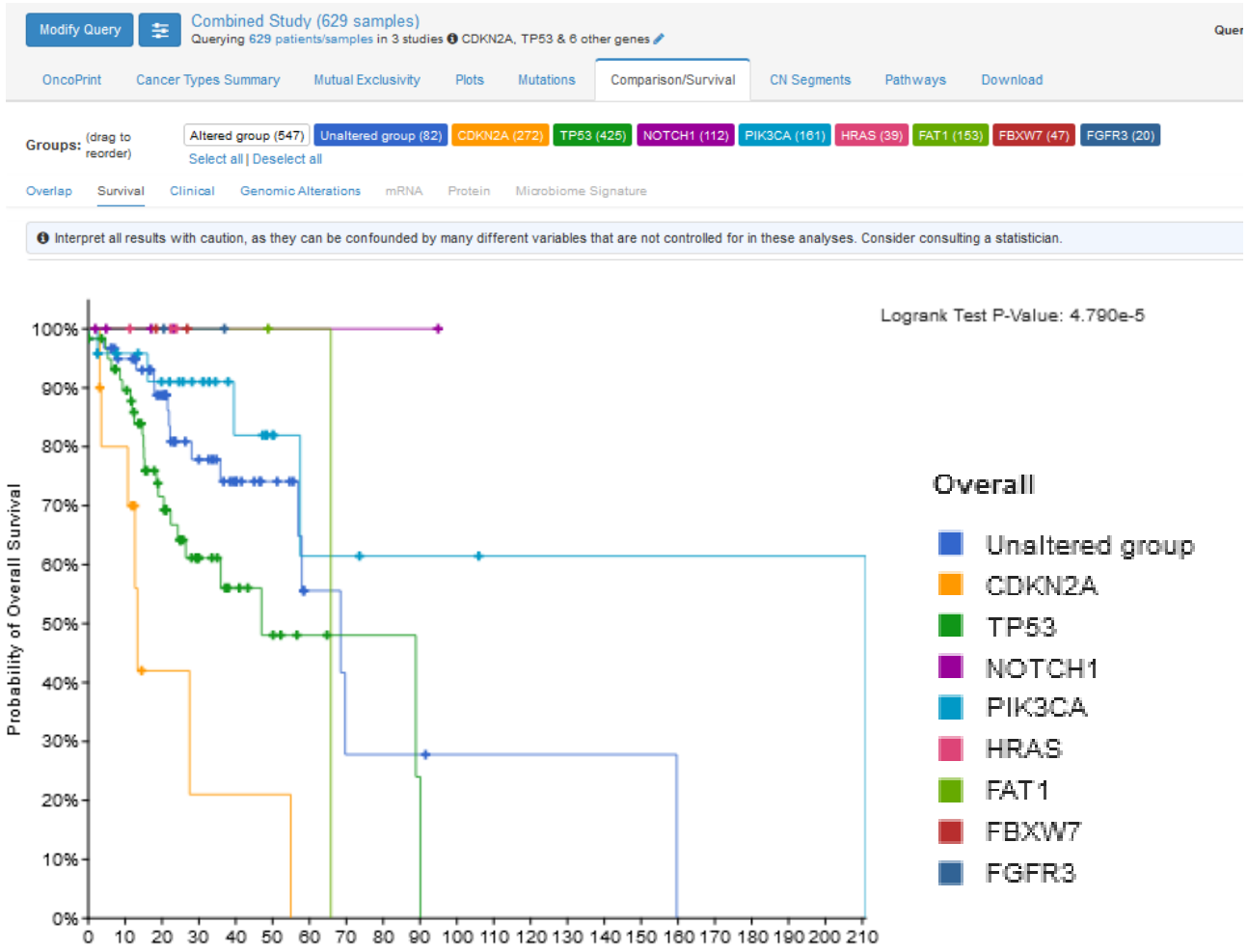
A	B	Neither	A Not B	B Not A	Both	Log2 Odds Ratio	p-Value	q-Value ▲	Tendency
CDKN2A	TP53	149	45	197	224	1.913	<0.001	<0.001	Co-occurrence
CDKN2A	FAT1	288	175	58	94	1.415	<0.001	<0.001	Co-occurrence
TP53	HRAS	170	407	24	14	-2.037	<0.001	<0.001	Mutual exclusivity
FAT1	FBXW7	440	128	23	24	1.843	<0.001	<0.001	Co-occurrence
NOTCH1	FAT1	395	68	110	42	1.149	<0.001	0.002	Co-occurrence
CDKN2A	NOTCH1	300	205	46	64	1.026	<0.001	0.003	Co-occurrence
TP53	FAT1	160	303	34	118	0.874	0.003	0.011	Co-occurrence
NOTCH1	HRAS	481	96	24	14	1.547	0.003	0.011	Co-occurrence
TP53	FGFR3	182	414	12	7	-1.963	0.004	0.012	Mutual exclusivity
HRAS	FAT1	441	22	136	16	1.238	0.011	0.032	Co-occurrence
PIK3CA	FGFR3	449	147	10	9	1.459	0.029	0.075	Co-occurrence

How altered group is selected



If I look the survival data for all the genes

- It seems CDKN2A (correlated to HPV stats) alteration might be related to poor outcome in 0-50months period of survival, whereas HRA& NOTCH1 alteration has minimal or no direct effect on the survival.



	Number of Cases, Total	Number of Events	Median Months Overall (95% CI)
Unaltered group	60	16	68.48 (56.94 - NA)
CDKN2A	10	7	13.35 (10.75 - NA)
TP53	59	23	47.01 (26.43 - NA)
NOTCH1	5	0	NA
PIK3CA	24	5	210.97 (57.47 - NA)
HRAS	3	0	NA
FAT1	2	1	65.82
FBXW7	2	0	NA
FGFR3	2	0	NA