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1. After selection MSK-IMPACT Clinical Sequencing Cohort and filtering the results down to Lung Adenocarcinoma, I was able to find the most common mutated genes. I would design a gene panel to give information on tumor genetics for most cases by taking into account the frequency percentage of the genes that are displayed. For example, TP53 has 51.2% frequency percentage with the most number of mutated gene results in the database, so I would definitely want to include that in my gene panel. The top 5 genes displayed are TP53, KRAS, EGFR, STK11 and KEAP1.

2. I would say in terms of mutated genes the panel would be useful mainly because of the shared common gene of TP53. This is because TP53 has 51.2% frequency in Lung Adenocarcinoma while it has 81.2% for Lung Squamous Cell Carcinoma. Other than this gene where they both share a majority frequency percentage. But other than TP53 they dont really share any other mutated genes

Lung Adenocarcinoma

Mutated Genes (1357 profiled samples)

Gene	# Mut	#	Freq
TP53	748	695	51.2%
KRAS	413	405	29.8%
EGFR	497	388	28.6%
STK11	246	239	17.6%
KEAP1	217	208	15.3%

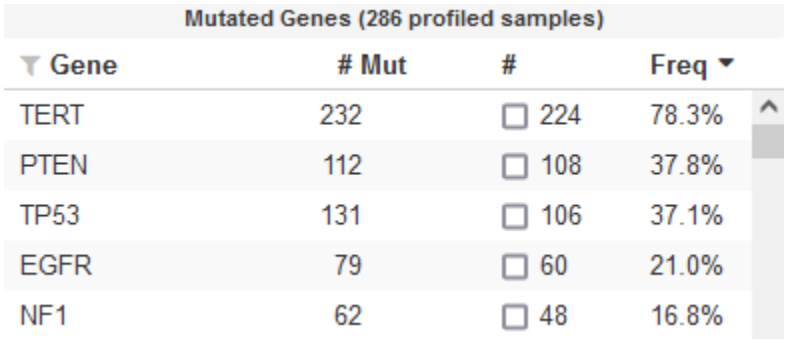
Lung Squamous Cell Carcinoma

Mutated Genes (170 profiled samples)

Gene	# Mut	#	Freq
TP53	151	138	81.2%
CDKN2A	35	34	20.0%
KMT2D	40	29	17.1%
FAT1	28	23	13.5%
NFE2L2	28	22	12.9%

3. Looking at Glioblastoma Multiforme we can see that it shares the genes TP53 and EGFR in the top 5 frequencies (Lung Adenocarcinoma TP53: 51.2%, EGFR: 28.6%) (Glioblastoma Multiforme TP53: 37.1%, EGFR: 21.0%)

Glioblastoma Multiforme



Mutated Genes (286 profiled samples)

Gene	# Mut	#	Freq
TERT	232	224	78.3%
PTEN	112	108	37.8%
TP53	131	106	37.1%
EGFR	79	60	21.0%
NF1	62	48	16.8%

4. I would most likely use NGS for mutations and copy number changes for one of the NGS methods known as Archer FusionPlex Lung Panel, some of the most common fusions found are *ALK*, *ROS1*, *RET*, *BRAF*, *MET*, *FGFR1-3*, *NTRK1-3*

Reference:

https://bmcmedgenomics.biomedcentral.com/articles/10.1186/s12920-021-00909-y