Supplementary plots to Figure 5

Below are some supplementary plots to Figure 5 of: Madeleine Darbyshire, Zachary du Toit, Mark F. Rogers, Tom Gaunt and Colin Campbell. Estimating the Frequency of Single Point Driver Mutations across Common Solid Tumours, *Scientific Reports* (Nature) 9, article number: 13452, (2019). In the plots below, a driver gene is labelled as such if it has at least one embedded high confidence SNV-driver. By *high confidence* we mean that we are using a false discovery rate of 5% which translates into a threshold cutoff on the p-score of 0.88 for *CScape*. Most of these genes are discussed in the text of the paper, and well studied in their respective contexts. Some comments are:

1-4 **TP53**, **KRAS**, **PIK3CA** and **CTC-297N7.11** are examples of genes with an important influence across multiple cancer types.

5,6 **SPOP** and **IDH1** are examples of genes with more restricted influence by cancer type: **SPOP** is relevant to prostate cancer (PRAD) but less so to early onset prostate cancer (EOPC), while also relevant to Uterine Corpus Endometrial Carcinoma (UCEC). **IDH1** has a more restricted role in brain lower grade glioma (LGG), among the cancers we consider.

7 **BRAF** as a driver gives a pointer towards *drug repurposing*: melanoma and thyroid cancer are obviously relevant. However, *BRAF* mutations are given as relevant to more than 10% of colon cancers (COAD). This is documented in the cancer literature. Currently two BRAF inhibitors are approved for clinical use: vemurafenib and dabrafenib, principally targeted at melanoma, but can be repurposed for other contexts. This gives support for the further development of predictors such as *CScape*, since they can highlight rare targets, infrequent for the given cancer type, but nonetheless a driver for the given tumour.

8 An unexpected result was for **TTN** and **TTN-AS1**, the latter transcribed from the opposite strand to **TTN** (*Titin*). Though commonly dismissed as a driver due to function and expression profile in the cell cycle, **TTN** may be conferring driver status through association with the long non-coding RNA gene **TTN-AS1**. The latter appears with a frequency, equal to, or slightly lower, than that for **TTN**.

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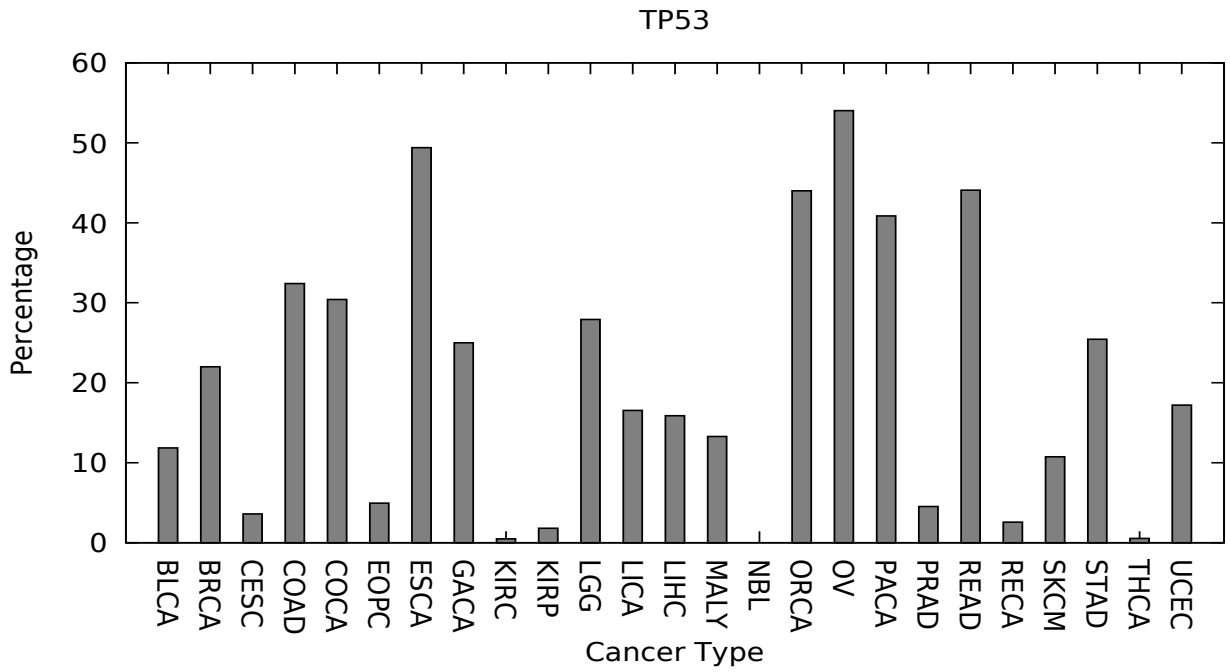
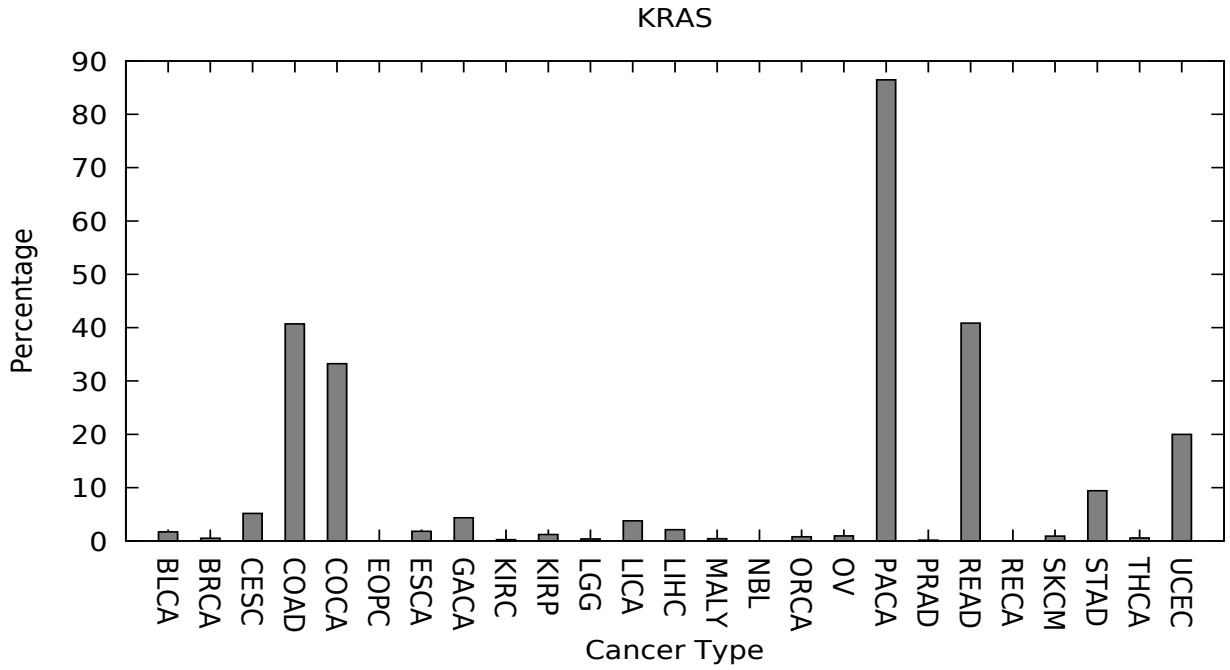
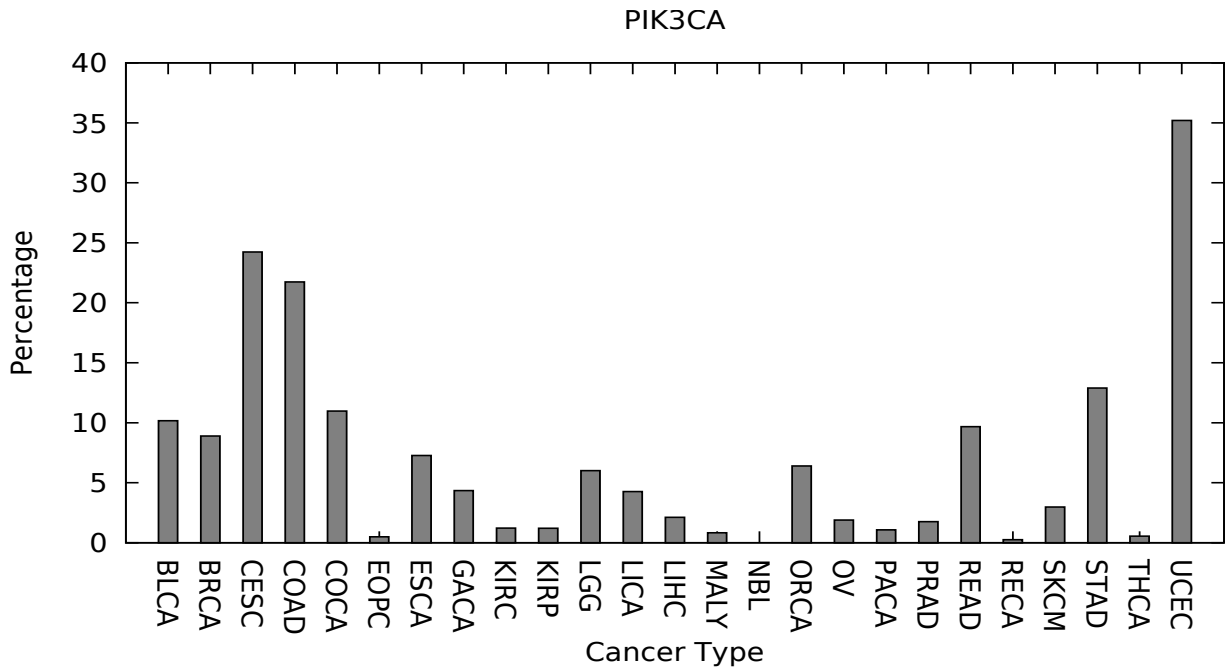
1. TP53


TP53
Percentage
0
10
20
30
40
50
60
BLCA
BRCA
CESC
COAD
COCA
EOPC
ESCA
GACA
KIRC
KIRP
LGG
LICA
LIHC
MALY
NBL
ORCA
OV
PACA
PRAD
READ
RECA
SKCM
STAD
THCA
UCEC
Cancer Type

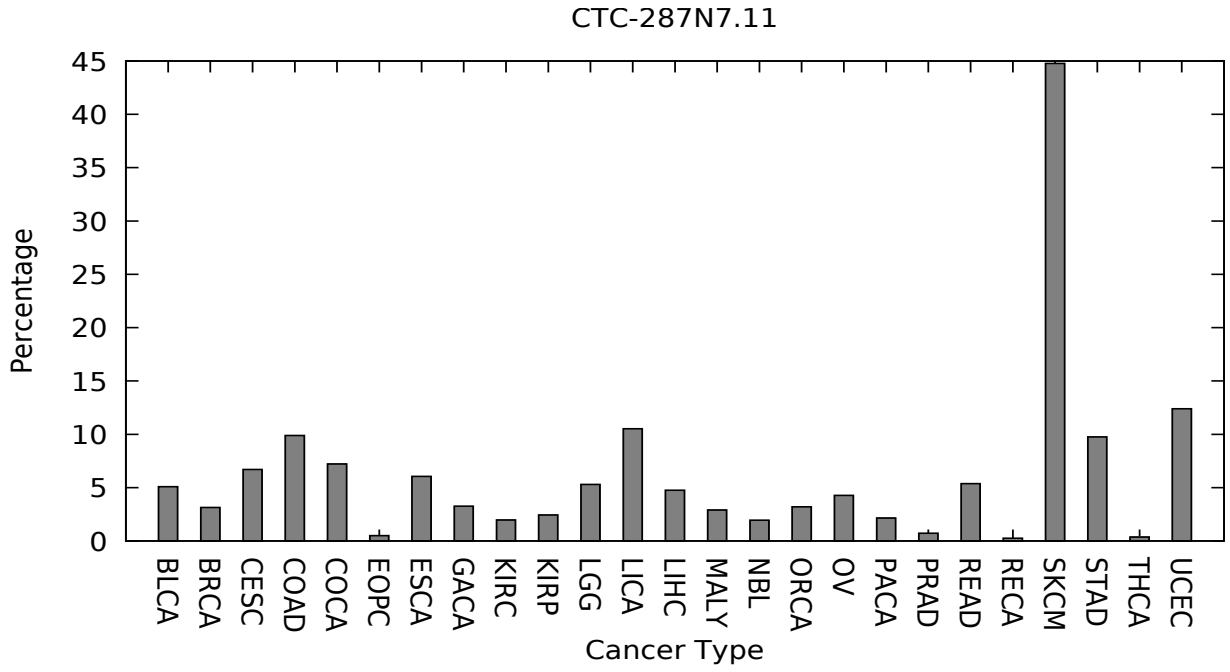
2. KRAS


KRAS
Percentage
0
10
20
30
40
50
60
70
80
90
BLCA
BRCA
CESC
COAD
COCA
EOPC
ESCA
GACA
KIRC
KIRP
LGG
LICA
LIHC
MALY
NBL
ORCA
OV
PACA
PRAD
READ
RECA
SKCM
STAD
THCA
UCEC
Cancer Type

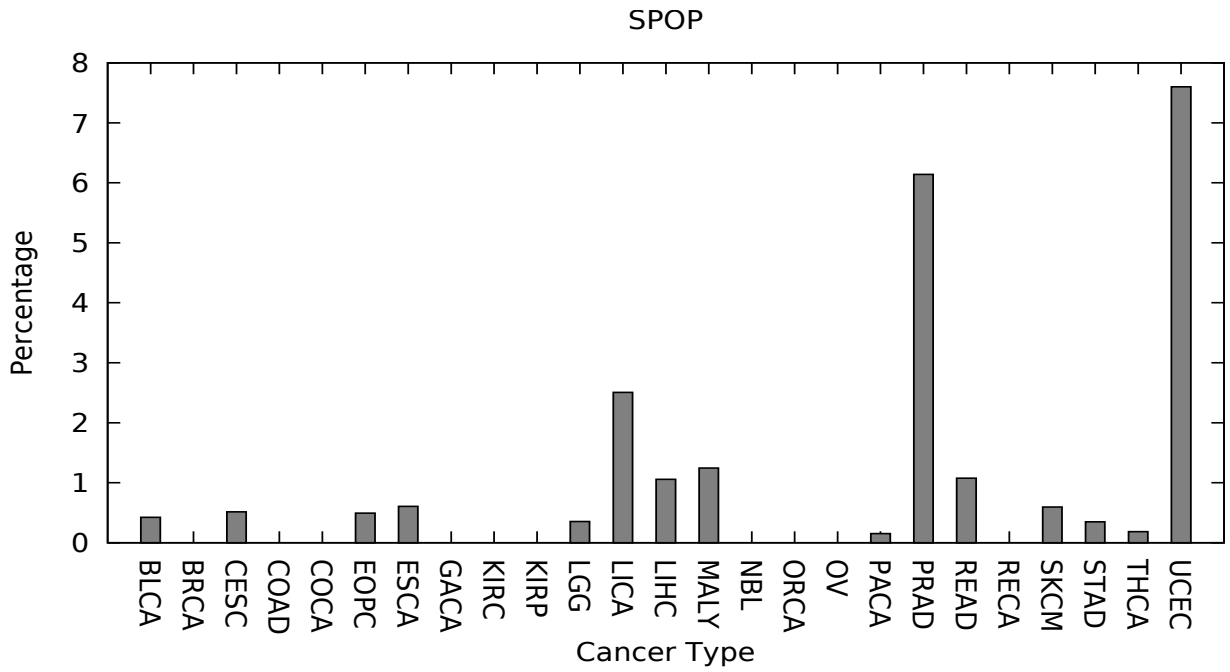
3. PIK3CA



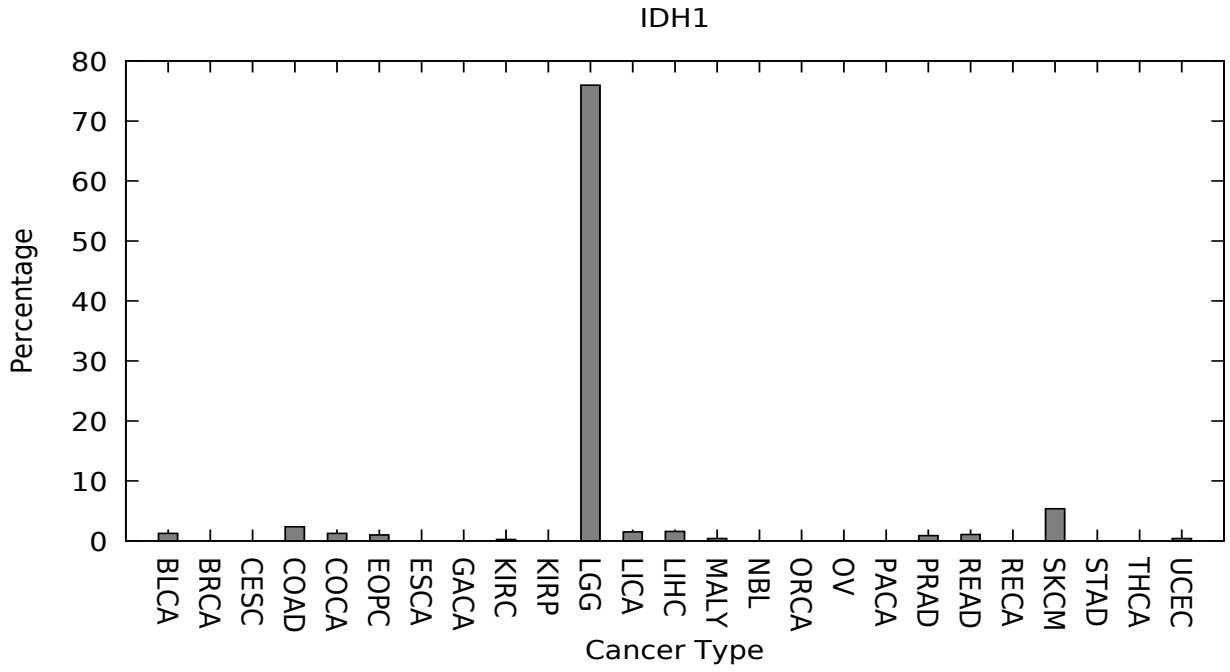
4. CTC-297N7.11



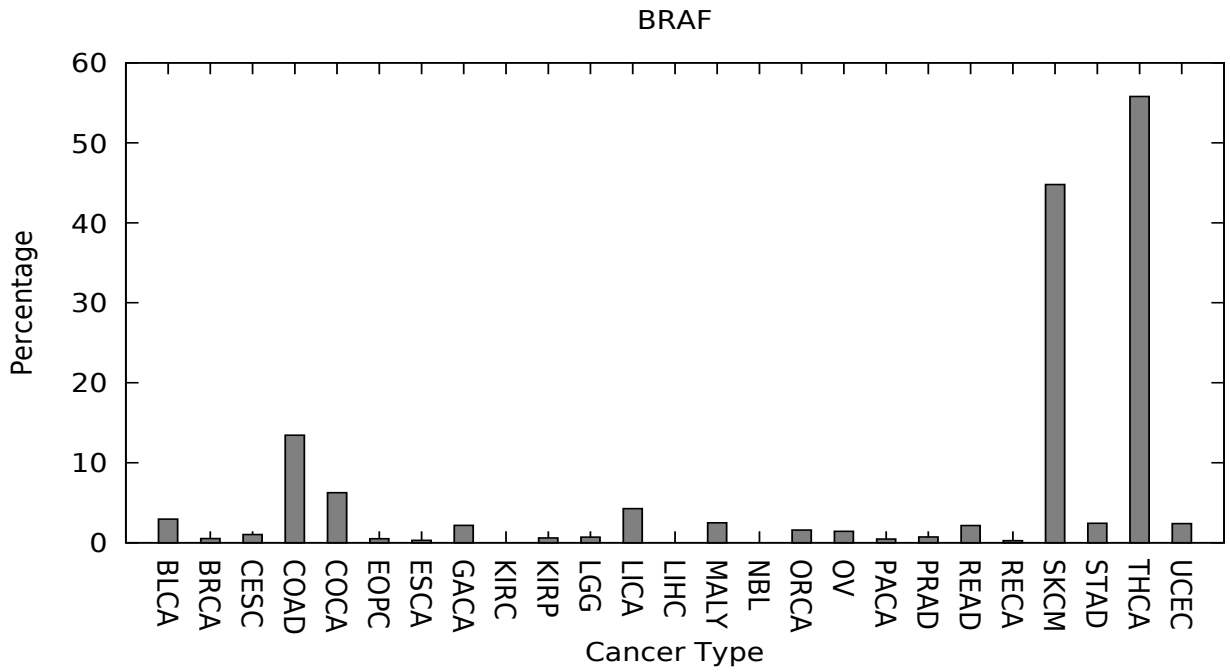
5. SPOP


SPOP
Percentage
0
1
2
3
4
5
6
7
8
BLCA
BRCA
CESC
COAD
COCA
EOPC
ESCA
GACA
KIRC
KIRP
LGG
LICA
LIHC
MALY
NBL
ORCA
OV
PACA
PRAD
READ
RECA
SKCM
STAD
THCA
UCEC
Cancer Type

6. IDH1


IDH1
Percentage
0
10
20
30
40
50
60
70
80
BLCA
BRCA
CESC
COAD
COCA
EOPC
ESCA
GACA
KIRC
KIRP
LGG
LICA
LIHC
MALY
NBL
ORCA
OV
PACA
PRAD
READ
RECA
SKCM
STAD
THCA
UCEC
Cancer Type

7. BRAF



8. TTN and TTN-AS1