A typical cancer genome contains thousands of mutations , the overwhelming majority of which are in non-protein-coding sequences Classical models of tumour evolution posit that cancer progression is driven by only a few of these mutations But almost all known driver mutations are in coding sequences1,2, raising the question of how many drivers lurk in non-coding regions of the genome In a paper online in *Nature*, Rheinbay *et al*3 make a foray towards the answer

Identification of non-coding drivers is challenging, owing to the vastness of the non-coding genome and the difficulty of characterizing the positions of specific non-coding elements (regulatory regions such as promoters and enhancers that modulate gene expression), which might be predicted to contain driver mutations Coding drivers are easier to identify, because we have a better understanding of the start and end of coding regions, and of the impact that coding mutations might have on production and function of the protein encoded in that region It is possible that our understanding of coding regions creates an ascertainment bias and makes it more likely that researchers search for mutations in coding regions Nevertheless, there has been great interest in finding non-coding drivers4 Previous studies have provided a few examples5–7, but our understanding of non-coding drivers is far from complete

Rheinbay *et al* set out to identify coding and non-coding driver mutations in an unbiased fashion, using cells from a cohort of 360 people who had breast cancer To find non-coding drivers, the researchers measured the rate at which mutations typically arose across the whole genome, then searched for non-coding elements that harboured significantly more mutations than would be expected, or that contained clusters of mutations around sequences such as transcription-factor binding sites, which regulate the element’s activity

The authors identified putative driver mutations in nine promoters, and showed that three of these (those regulating expression of the genes *FOXA1, RMRP* and *NEAT1*) significantly altered gene-transcription levels Their analysis of mutational hotspots (single nucleotides that are mutated in multiple patients ) indicated that those in promoters are as common as those in coding genes Furthermore, the per-base mutation rate of promoters that contained drivers was similar to that of coding regions known to contain drivers This suggests that the reason that fewer drivers have been found in promoters than in coding regions can simply be attributed to the fact that they are smaller — they account for fewer nucleotides in the analysis

This work is state-of-the-art, but there is more still to do The authors’ power analysis — a statistical calculation that predicts the sample numbers needed to detect an effect of a given size — indicated that their sample size of 360 could be used to reliably identify drivers only if they occurred in at least 10% of patients in the cohort To understand the directions for improvement, it is worth considering how non-coding elements are defined, and how this plays into statistical power (Fig 1)

Currently, most non-coding elements are annotated as being fairly large (about one kilobase long) However, this is at least partly attributable to the fact that the techniques used to determine the positions of non-coding elements — which involve looking for characteristic features, such as specific molecular modifications, bound proteins or DNA-packaging signatures — are typically noisy The functional territory of a regulatory element can therefore be considerably smaller than is annotated Calculations of mutation rates that take into account oversized regions can hinder driver identification Power calculations show that restricting annotation to smaller, functionally relevant regions enhances power

One approach to better define the functional territories of non-coding elements is to identify evolutionary conserved regions, which are likely to be functionally important and so are more likely to contain driver mutations It should also be noted that non-coding elements, like genes, consist of discontinuous blocks of functional territories The connections between these territories are well understood for genes, because coding regions are joined up during processing of messenger RNA, making links readily apparent But the connections between non-coding elements and between these elements and the genes they regulate are less well understood, and are complex — genes can be connected to multiple promoters and enhancers, and one enhancer can affect multiple genes

Thus, the best way to increase the power of driver detection in non-coding elements is, perhaps non-intuitively, not to investigate every base in the genome Rather, it is to analyse a compact and highly accurate annotation set containing as few elements as possible, in which each element corresponds closely to an underlying functional territory More information might also be gained by analysing discontinuous functional regions that regulate one gene, increasing statistical power by enabling testing of just one hypothesis — that a mutation alters regulation of that gene In this way, rarer drivers can be uncovered

Once driver mutations are identified , the next challenge is to evaluate their effect In some circumstances it is clear what effect a mutation will have — if it breaks a transcription-factor binding site or creates a new one, for instance8 Nonetheless, better metrics of functional impact are needed over the whole genome to find non-coding equivalents of the coding mutations known to alter protein production or behaviour Finally, the power to detect drivers in non-coding regions is currently dependent on a uniform background-mutation rate However, this is not the case for wide expanses of the genome9, so the approach will require further refinement

An exhaustive but expensive approach to deal with some of these challenges is sequencing many patients This approach is feasible only through large-scale collaborations Such efforts will generate comprehensive catalogues of non-coding variants, which can be leveraged to detect more driver mutations However, these large-scale studies require the assembly of uniform cohorts, which can be challenging owing to the highly heterogeneous nature of cancer An alternative approach would be to develop a more compact functional annotation of the non-coding genome by precisely defining functional territories Here, large-scale annotation compendiums such as the ENCODE project10 have a vital role to play