




Sex differences in oncogenic mutational processes

Constance H. Li, Stephenie D. Prokopec, Ren X. Sun, Fouad Yousif, Nathaniel Schmitz, Paul C. Boutros, Matthias Schlesner

Angaben zur Veröffentlichung / Publication details:

Li, Constance H., Stephenie D. Prokopec, Ren X. Sun, Fouad Yousif, Nathaniel Schmitz, Paul C. Boutros, and Matthias Schlesner. 2020. "Sex differences in oncogenic mutational processes." Nature Communications 11 (1): 4330.
<https://doi.org/10.1038/s41467-020-17359-2>.

Sex differences in oncogenic mutational processes

Constance H. Li ^{1,2,3}, Stephenie D. Prokopec ¹, Ren X. Sun^{1,4}, Fouad Yousif¹, Nathaniel Schmitz¹, PCAWG Tumour Subtypes and Clinical Translation*, Paul C. Boutros ^{2,3,4,5,6,7,8}✉ & PCAWG Consortium*

Sex differences have been observed in multiple facets of cancer epidemiology, treatment and biology, and in most cancers outside the sex organs. Efforts to link these clinical differences to specific molecular features have focused on somatic mutations within the coding regions of the genome. Here we report a pan-cancer analysis of sex differences in whole genomes of 1983 tumours of 28 subtypes as part of the ICGC/TCGA Pan-Cancer Analysis of Whole Genomes (PCAWG) Consortium. We both confirm the results of exome studies, and also uncover previously undescribed sex differences. These include sex-biases in coding and non-coding cancer drivers, mutation prevalence and strikingly, in mutational signatures related to underlying mutational processes. These results underline the pervasiveness of molecular sex differences and strengthen the call for increased consideration of sex in molecular cancer research.

¹Computational Biology Program, Ontario Institute for Cancer Research, Toronto, ON, Canada. ²Department of Medical Biophysics, University of Toronto, Toronto, ON, Canada. ³Department of Human Genetics, University of California, Los Angeles, CA, USA. ⁴Department of Pharmacology & Toxicology, University of Toronto, Toronto, ON, Canada. ⁵Vector Institute for Artificial Intelligence, Toronto, Canada. ⁶Department of Urology, University of California, Los Angeles, CA, USA. ⁷Jonsson Comprehensive Cancer Center, University of California, Los Angeles, CA, USA. ⁸Institute for Precision Health, University of California, Los Angeles, CA, USA. *List of authors and their affiliations appears at the end of the paper. ✉email: Paul.Boutros@mednet.ucla.edu

Sex disparities in cancer epidemiology include an increased overall cancer risk in males corresponding with higher incidence in most tumour types, even after adjusting for known risk factors^{1,2}. Cancer mortality is also higher in males, due in part to better survival for female patients in many cancer types, including those of the colon and head and neck³. Interestingly, female colorectal cancer patients respond better to surgery⁴ and adjuvant chemotherapy, though this is partially due to biases in tumour location and microsatellite instability⁵. Similarly, premenopausal female nasopharyngeal cancer patients have improved survival regardless of tumour stage, radiation or chemotherapy regimen⁶. There is a growing body of evidence for sex differences in cancer genomics^{7–12}, but their molecular origins and clinical implications remain largely elusive.

Previous studies have mostly focused on protein coding regions, leaving the vast majority of the genome unexplored. We hypothesise that there are uncharacterised sex differences in the non-coding regions of the genome. Using data from the Pan-cancer Analysis of Whole Genomes (PCAWG) project¹³, we perform a survey of sex-biased mutations in 1983 samples (1213 male, 770 female) from 28 tumour subtypes, excluding those of the sex organs (Supplementary Data 1). The PCAWG Consortium aggregated whole-genome sequencing data generated by the ICGC and TCGA projects. These data were re-analysed with standardised, high-accuracy pipelines to align to the human genome (reference build hs37d5). Our study leverages mutation calls generated by PCAWG working groups^{13–16} to identify molecular associations with sex. We exclude the X and Y chromosomes to focus on autosomal sex differences in cancers affecting both men and women, but there are known to be significant X-chromosome mutational differences between tumours arising in men and women⁸. Our analysis reveals sex differences in specific genes and in genome-wide phenomena including mutation signature activity. These sex-biases occur not only at the pan-cancer level across all 1983 tumours, but also in individual tumour subtypes.

Results

Sex-biases in driver genes, mutation load and tumour evolution. We began by investigating sex differences in driver gene mutation frequencies, focusing on 165 coding and nine non-coding mutation events¹⁴ (Supplementary Data 2). We used proportion tests to identify candidate sex-biased events with a false discovery rate (FDR) threshold of 10%. These putative sex-biased events were modelled using logistic regression (LGR) to adjust for tumour subtype-specific variables (model descriptions and variable breakdown in Supplementary Data 1). Finally, we vetted these sex-biased events in two ways: we assessed the impact of covariate imbalances in the data using repeated down-sampling analysis; we also implemented extended regression models to adjust for additional variables like stage or grade, which were only available for a greatly reduced subset of the data (see “Methods” section). We confirmed that all sex-biases remained significant under this additional scrutiny. This statistical framework formed the basis for our analysis of all genomic features.

Tumour subtype-specific sex-biased driver mutations included *CTNNB1* mutation frequency in liver hepatocellular cancer (Liver-HCC), with more male-derived samples harbouring *CTNNB1* mutations: (male: 31%, female: 13%, 95% CI: 8.1–28%, prop-test $q = 0.048$, LGR $q = 1.4 \times 10^{-3}$, Fig. 1a, Supplementary Fig. 1). This mirrors our previous finding of sex-biased *CTNNB1* mutation frequency in liver cancer from TCGA exome sequencing data, with similar effect sizes (male: 33% vs. female: 12%¹¹). We also identified a large sex-disparity in a non-coding driver event in

thyroid cancer (Thy-AdenoCA): *TERT* promoter mutations were observed in 64% of male-derived samples compared with only 11% of female-derived samples (95% CI: 17–89%, prop-test $q = 6.9 \times 10^{-3}$, LGR $q = 0.074$, Fig. 1a, Supplementary Fig. 1), again supporting a previous finding¹⁷. We did not find pathogenic germline variants in *TERT* or *CTNNB1* that might bias the detection of sex-associated somatic mutations in these genes. Other putative sex-biased events were detected, but were either not statistically significant after multivariate adjustment at present sample sizes (Supplementary Data 2), or were attributed to over-represented tumour subtypes (Supplementary Fig. 2).

Our previous work¹¹ found sex-biased mutation density across a number of tumour subtypes, including cancers of the liver, kidney and skin. We therefore investigated mutation density here to identify tumour subtypes where the cancer genomes of one sex accumulate more somatic single nucleotide variants (SNVs) than those of the other sex. Returning to our statistical framework, we first used Mann–Whitney *U*-tests to identify putative sex-biases, and then applied multivariate linear regression (LNR) on Box–Cox transformed mutation load to adjust for possible confounders. The Box–Cox transformation applies a power function to modify the shape of a variable’s distribution to better approximate a normal distribution. It preserves monotonicity and is often applied to make data more suitable for regression analysis (see “Methods” section). We also compared the total number of somatic SNVs and further divided mutations by coding and non-coding SNVs to determine whether sex-biases may be influenced by specific genomic contexts. Across all pan-cancer samples, we identified higher mutation prevalence in male-derived samples in all three contexts (coding LNR $q = 7.3 \times 10^{-4}$, non-coding LNR $q = 6.4 \times 10^{-4}$, overall LNR $q = 1.9 \times 10^{-6}$; Supplementary Data 3). These sex-biases remained significant even after adjusting for tumour subtype, ancestry and age in multivariate analysis, and after evaluating the effects of imbalanced tumour subtype and sex sample sizes (Fig. 1b, left; Supplementary Figs. 2, 3).

We investigated somatic SNV burden in each of the 23 individual tumour subtypes with at least 15 samples ($n_{\text{male}} + n_{\text{female}} \geq 15$), applying the same statistical approach using tumour subtype-specific models (Supplementary Data 1). We found sex-biased mutation load in three tumour subtypes (Fig. 1b, right), with trending higher male coding mutation load in thyroid cancer (difference in location = 0.26 mut/Mbp, 95% CI = 0.12–0.43 mut/Mbp, *U*-test $q = 0.028$, LNR $q = 0.10$), and higher male SNV load in hepatocellular cancer and kidney renal cell cancer (Kidney-RCC) for all three genomic contexts (Supplementary Data 3). We compared the group rank differences of coding and non-coding mutation load between the sexes and found that in renal cell cancer, the differences were similar at 0.40 mut/Mbp for non-coding mutations and 0.37 mut/Mbp for coding mutations. In hepatocellular cancer however, the median sex-difference in non-coding mutation load was higher than the difference in coding mutation load (non-coding difference = 0.84 mut/Mbp vs. coding difference = 0.53 mut/Mbp). There was a similar effect for pan-cancer mutations (non-coding difference = 0.60 mut/Mbp vs. coding difference = 0.41 mut/Mbp) suggesting mutation context may have a role in sex-biased SNVs in some tumour subtypes.

On detecting sex differences in both the mutation frequency of specific drivers as well as SNV density in the same tumour subtypes, we asked whether one may bias the other. For instance, higher *CTNNB1* mutation frequency in male-derived tumours may simply be due to more mutations occurring in those same samples. We therefore looked for associations between SNV burden with *CTNNB1* mutation in hepatocellular cancer, and with *TERT* promoter mutation in thyroid cancer.

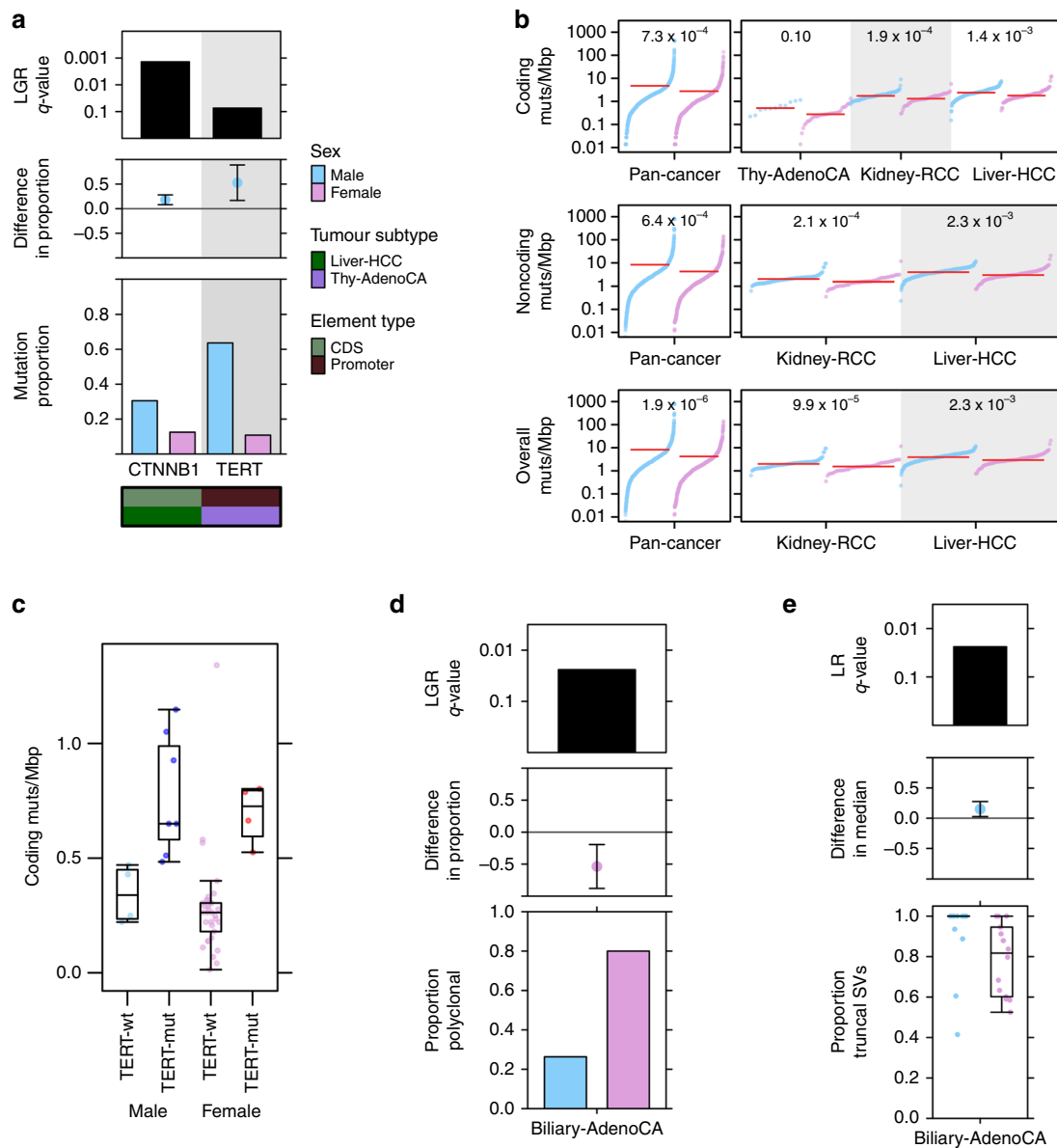


Fig. 1 Sex-biases in mutation frequency of driver genes, SNV density and tumour evolution. **a** From top to bottom, each plot shows the logistic regression q -value for the sex effect; difference in proportion of mutated samples between the sexes with blue denoting male-dominated bias; and mutation proportion for each gene. Covariate bars indicate mutation context and tumour subtype of interest. **b** The burden of somatic SNVs for coding, non-coding and overall mutation load. Linear regression q -values are shown. **c** Coding mutation load for thyroid adenocarcinoma samples compared by sex and presence or absence of *TERT* promoter mutations. **d** The proportion of polyclonal samples and **e** the proportion of truncal structural variants in biliary cancer. Tukey boxplots are shown with the box indicating quartiles and the whiskers drawn at the lowest and highest points within 1.5 interquartile range of the lower and upper quartiles, respectively. Error bars show the 95% confidence interval for the difference in proportions or medians between the sexes.

We did not find a significant association between SNV burden and *CTNNB1* mutation in hepatocellular cancer. In thyroid cancer however, *TERT* promoter mutation was associated with increased overall mutation burden (median_{TERT-wt} = 0.32 mut/Mbp vs. median_{TERT-mut} = 0.82 mut/Mbp, U -test $p = 7.9 \times 10^{-8}$). We further confirmed the association using a linear regression model (linear regression $p_{TERT} = 2.4 \times 10^{-5}$, $p_{sex} = 0.37$, Fig. 1c). To assess whether the sex-bias in *TERT* promoter mutation frequency might be due to sex-biased accumulation of SNVs, we examined tumour-matched mutation timing data generated by the PCAWG consortium¹⁵. We found that of eleven polyclonal samples with *TERT* promoter mutations, nine of these were earlier occurring truncal events.

We continued investigating whether sex-biased driver mutations might occur at different stages of tumour evolution between men and women and examined tumour subclonal architecture. Focusing only on thyroid tumours with *TERT* promoter mutations and liver tumours with *CTNNB1* mutations, we compared the proportions of polyclonal vs. monoclonal tumours between the sexes (Supplementary Fig. 4). We did not find sex-biased polyclonality in *TERT* promoter-mutated tumours, but did detect a putative bias in the proportion of polyclonal *CTNNB1*-mutated tumours (80% of male-derived tumours are polyclonal vs. 46% of female-derived tumours, 95% CI = -0.019-0.70, prop-test $p = 0.039$). We therefore accounted for polyclonality when comparing the timings of the mutations in these driver events. On

subsequently examining the frequency of clonal vs. subclonal driver mutation events between the sexes, we found that while there were differences in the proportions of truncal mutations (e.g. 100% of *TERT* promoter mutations were truncal events in male-derived vs. 50% truncal events in female-derived thyroid cancer patients), no comparisons were statistically significant.

We expanded our clonality analysis to perform a general survey of clonal structure and mutation timing across all tumour subtypes and mutations (Supplementary Data 4). We found that female-derived biliary adenocarcinoma (Biliary-AdenoCA) tumours were frequently polyclonal, whereas most male-derived tumours were monoclonal (26% male-derived samples are polyclonal vs. 80% female-derived, 95% CI = 19–88%, prop-test $q = 0.063$, LGR $q = 0.026$; Fig. 1d). In addition, we found intriguing evidence suggesting there may be sex differences in the mutation timing of structural variants (SVs) in this tumour subtype. Structural variants in male-derived samples were more frequently truncal events than in female-derived samples (median male percent truncal SVs = 100% vs. median female = 82%, 95% CI = 0.9–32%, U -test $q = 0.081$, LNR $q = 8.6 \times 10^{-3}$; Fig. 1e). Though other comparisons did not reach our statistical significance threshold, we found some interesting trends that may merit future study, including in oesophageal cancer (Eso-AdenoCA) where SVs in female-derived samples were more frequently truncal events while SVs in male-derived samples occurred more frequently in subclones (median male percent truncal SVs = 55%, median female = 100%; Supplementary Fig. 5), and in medulloblastoma, where insertion-deletions (indels) were more frequently truncal events in female-derived samples than male (median male percent of truncal indels = 65%, median female proportion of truncal indels = 70%; Supplementary Fig. 6). Our analysis of sex differences in tumour evolution identified some sex-biased events and hint at putative sex-biases that should be further explored in future analyses.

Sex-biases in genome instability and CNAs. Next, we examined percent genome altered (PGA), which provides a summary of copy number aberration (CNA) load. A proxy for genome instability, PGA is a complementary measure of mutation density to somatic SNV burden. Although we did not find associations between sex and autosome-wide PGA, we observed sex-biases in the copy number burden for specific chromosomes (Fig. 2a). In pan-cancer analysis, male-derived samples exhibited a slight but significant higher percent chromosome altered for chromosome 7 even after accounting for tumour subtype, ancestry and age (median male PGA-7 = 5.4%, median female PGA-7 = 0.37%, 95% CI = 9.4×10^{-4} – 2.4×10^{-3} %, U -test $q = 5.0 \times 10^{-3}$, LNR $q = 0.024$; Supplementary Data 5). In individual tumour subtypes, we found sex-biased PGA in renal cell cancer (chromosomes 7 & 12) and hepatocellular cancer (chromosomes 1 & 16). On further scrutinising these sex-PGA associations using extended models, we found that grade was a likely confounder in renal cell cancer, though the sex effect after correcting for this variable was still trending (extended LNR $q = 0.17$). By looking at copy number gains and losses separately, we additionally identified chromosomes with sex-biases in the burden of copy number gains and losses (Supplementary Fig. 7 and Supplementary Data 5), including sex-biased percent copy gained on chromosomes 5, 8 and 17 in pan-cancer tumours. These biases in chromosome instability were robust to imbalanced sex sample sizes (Supplementary Fig. 8).

We next compared CNA frequency on the gene level to identify specific genes lost or gained at sex-biased rates. Across all pan-cancer samples, we found 2,502 genes with sex-biased gains across 13 chromosomes (LGR q -value < 10%, Fig. 2b,

Supplementary Data 6, 7, Supplementary Figs. 2, 9). These genes were all more frequently gained in male-derived samples than female, with differences in copy number gain frequency up to 10% on chromosomes 7 and 8. Genes with male-dominated copy number gains include the oncogene *MYC* (male gain frequency = 37% vs. female gain frequency = 28%, 95% CI = 5.2–14%, prop-test $q = 2.5 \times 10^{-3}$, LGR $q = 0.068$). The driver *CTNNB1* was also more frequently gained in male samples (male gain frequency = 8.9% vs. female gain frequency = 5.2%, 95% CI = 1.4–6.1%, prop-test $q = 0.016$, LGR $q = 0.053$). We did not find pan-cancer sex-biased copy number losses.

We repeated this analysis for every tumour subtype independently and found sex-biased CNAs in renal cell and hepatocellular cancer (Supplementary Data 6 and 7). In renal cell cancer (Kidney-RCC), 1,986 sex-biased gains all occurred more frequently in male-derived samples, with differences in frequency up to 35% (Fig. 2c). They spanned across chromosomes 7 and 12, agreeing with our finding of male-dominated genome instability in these chromosomes (Fig. 2a; Supplementary Fig. 7). Using an extended renal cell cancer model accounting for grade, we obtained a high confidence set of 969 genes altered by sex-biased gains (extended model $q < 0.1$), with the remaining 1017 genes having a trending sex effect (extended model $q < 0.17$). In contrast to the male-dominated gains in pan-cancer and renal cell findings, we found higher female frequency of copy number losses in hepatocellular cancer (Fig. 2d). We identified 2226 genes with higher copy number loss rates in female-derived samples. As observed in renal cell cancer some of these losses span whole chromosomes, in this case chromosomes 3 and 16. Extended modelling in Liver-HCC incorporating stage and grade resulted in a list of 1797 high confidence sex-biased genes (extended model $q < 0.1$).

The concurrence between sex-biased PGA and gene-specific events in renal cell and hepatocellular cancer suggested that PGA could be used to guide identification of additional sex-biased CNAs on the gene level. We more closely examined regions of interest in tumour subtypes of that did not have sex-biased CNAs in our general CNA analysis, but did have putatively sex-biased genome instability (U -test $q < 0.2$): biliary cancer, B-cell non-Hodgkin lymphoma (Lymph-BNHL), and chronic lymphocytic leukaemia (Lymph-CLL). We identified an additional 203 genes on the p-arm of chromosome 8 that were more frequently lost in female-derived biliary tumours (Supplementary Fig. 10). These copy number losses were 50% more common in female-derived tumours and affect genes such as *DLCL1*, a known tumour suppressor gene in hepatocellular cancer that is thought to have a similar role in gallbladder cancer¹⁸. Although we did not identify additional sex-biased CNAs in non-Hodgkin lymphoma, chronic lymphocytic leukaemia or melanoma, our sex-biased PGA results suggest these as regions of interest for future work.

Sex-biases in mutational signatures. We hypothesised that sex differences in mutation density and tumour evolution characteristics might be driven by sex differences in mutational processes. In addition to single base substitution (SBS) signatures, which have been well annotated and linked to tumour aetiology^{19,20}, we also examined doublet base substitution (DBS) and small insertion-deletion (ID) signatures. Sex differences in a mutational signature could shine insight on molecular differences between the sexes. For each of 47 validated PCAWG SBS, 11 DBS and 17 ID signatures¹⁶, we performed a two-stage analysis. We first compared the proportions of signature-positive samples between the sexes; that is, we looked at the proportions of samples with any mutations attributed to the signature to determine

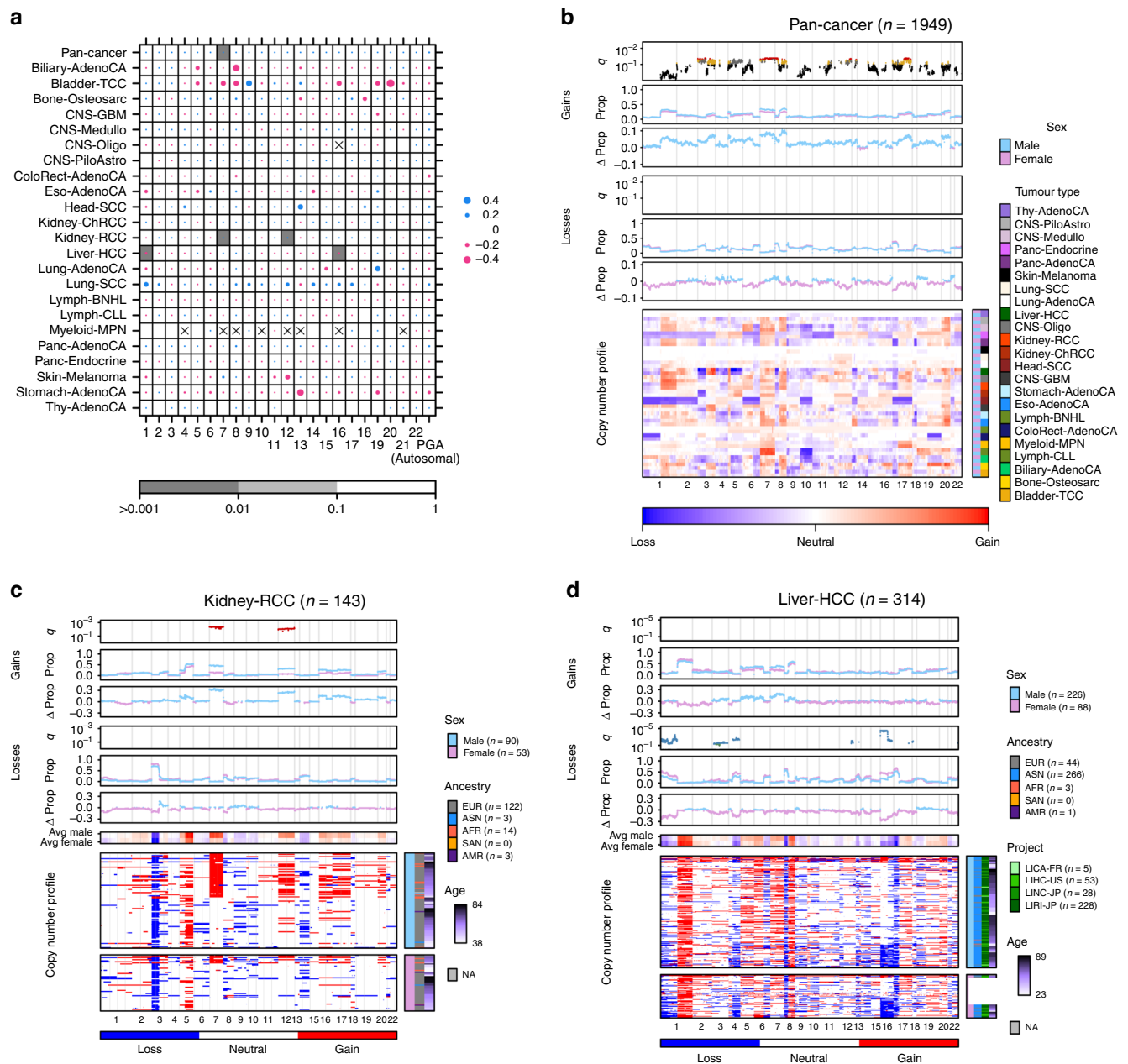


Fig. 2 Sex-biases in percent chromosome altered are reflected in gene-specific events. **a** A summary of associations between sex and genome instability across tumour subtypes. Dot size shows difference in median percent genome altered or percent chromosome altered between the sexes. Dot colour shows direction of bias, with blue indicating higher instability in male-derived tumours and pink indicating higher instability in female-derived tumours. Background shading shows q -values from multivariate linear regression. Sex differences in CNAs for **b** pan-cancer, **c** kidney renal cell cancer, and **d** hepatocellular cancer. Each plot shows, from top to bottom: the q -value showing significance of sex from multivariate linear modelling with yellow/green points corresponding to $0.1 < q < 0.05$, deep blue/red points corresponding to $q < 0.05$, and grey points indicating hits that were attributed to covariate sample size imbalances and rejected; the proportion of samples with aberration; the difference in proportion between male and female groups for copy number gain events; the same repeated for copy number loss events; and the copy number aberration (CNA) profile heatmap. The columns represent genes ordered by chromosome. Light blue and pink points represent data for male- and female-derived tumours respectively.

whether there was a relationship between each signature and sex. Then, we focused on signature-positive samples and compared the percentage of mutations attributed to each signature between the sexes to assess relative signature activity. For both analyses we used univariate techniques to identify putative events, adjusted for additional variables using linear models with SNV density as a variable, and compared the distributions of attributed mutations with Kolmogorov–Smirnov tests. We also evaluated hits using the added scrutiny of down-sampling and extended regression models (see “Methods” section; Supplementary Figs. 11, 12).

At the pan-cancer level, we identified three signatures that occurred more frequently in one sex over the other (Fig. 3a; Supplementary Data 8). SBS1 was more commonly detected in female-derived samples (88% of male-derived vs. 97% of female-derived, χ^2 -test $q = 9.2 \times 10^{-10}$, LGR $q = 3.0 \times 10^{-6}$) and was also associated with higher signature activity in these samples (male median percent mutations attributed to SBS1 = 8.6%, female median = 10%, U -test $q = 5.5 \times 10^{-3}$, LNR $q = 0.059$). Conversely, signatures SBS17a and SBS17b were detected in a larger proportion of male-derived samples (16% of male-derived vs.

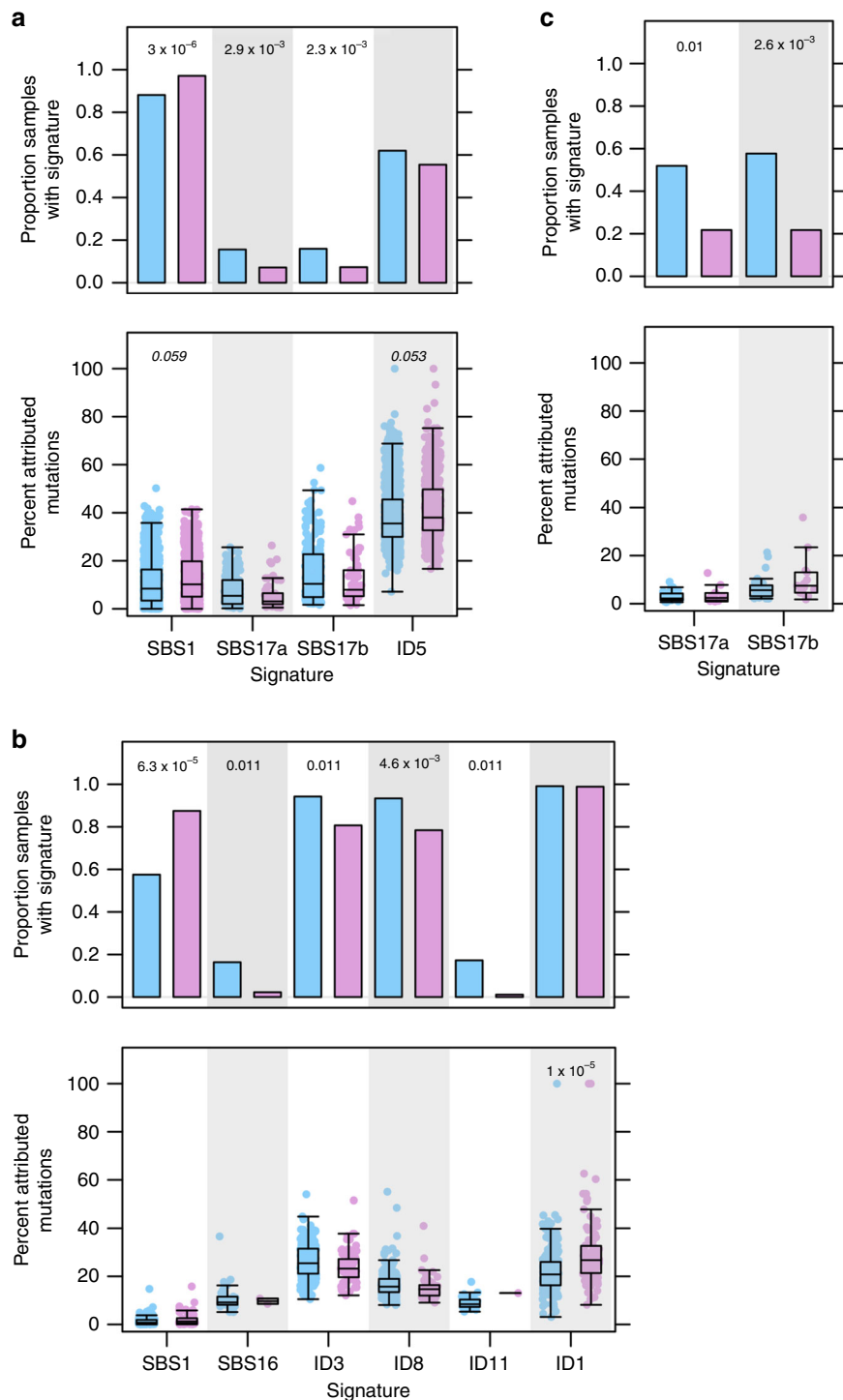


Fig. 3 Sex differences in mutational signatures related to mutational processes. Comparisons between proportions of signature-positive samples (top) and signature activity (bottom) for **a** pan-cancer comparisons, **b** liver hepatocellular cancer, and **c** B-cell non-Hodgkin lymphoma. FDR-adjusted q -values for multivariate logistic regression (top) and multivariate linear regression (bottom) shown only for significant comparisons. Blue shows male- and pink shows female-derived tumours. Tukey boxplots are shown with the box indicating quartiles and the whiskers drawn at the lowest and highest points within 1.5 interquartile range of the lower and upper quartiles, respectively.

7.2% of female-derived). SBS1 is thought to be caused by deamination of 5-methylcytosine to thymine, resulting in base substitutions. Signatures SBS17a and SBS17b are of unknown aetiology. We also identified a sex-bias in indel signature ID5, which had higher activity in female-derived tumours (male median percent attributed mutations = 35%, female median = 38%, U -test $q = 1.1 \times 10^{-3}$, LNR $q = 0.053$). ID5 mutations are

clock-like and may accumulate in normal cells. Both SBS1 and ID5 are correlated with age, but our multivariate model accounts for this variable and sex-bias remains significant.

Since mutational processes are disease-specific, we repeated the mutational signatures analysis in each tumour subtype. We identified six sex-biased signatures in hepatocellular cancer (Fig. 3b; Supplementary Data 8). We again detected a

female-dominated bias in the proportion of SBS1-positive samples (58% of male-derived vs. 88% of female-derived, χ^2 -test $q = 3.5 \times 10^{-5}$, LGR $q = 6.3 \times 10^{-5}$). We also detected a male-dominated bias in SBS16 (16% of male-derived vs. 2.2% of female-derived, χ^2 -test $q = 9.8 \times 10^{-3}$, LGR $q = 0.011$). A previous study²¹ described this sex-biased signature and an association between more *CTNNB1* mutations and higher activity of SBS16 in an independent dataset; these findings agree with what we report here for PCAWG data. There were also four sex-biased ID signatures in hepatocellular cancer: ID3 (94% of male-derived vs. 81% of female-derived, χ^2 -test $q = 5.0 \times 10^{-3}$, LGR $q = 0.011$), ID8 (93% of male-derived vs. 78% of female-derived, χ^2 -test $q = 3.5 \times 10^{-3}$, LGR $q = 4.6 \times 10^{-3}$) and ID11 (17% of male-derived vs. 1.1% of female-derived, χ^2 -test $q = 3.5 \times 10^{-3}$, LGR $q = 0.011$) occurred more frequently in male-derived samples. ID3 is associated with tobacco smoke, and ID8 with double-stranded break repair. ID11 has unknown aetiology. Although ID1 was detected at similar rates between the sexes, a greater proportion of ID1-attributed mutations were found in female-derived than male-derived samples (male median percent mutations attributed to ID1 = 21%, female median = 27%, U -test $q = 2.4 \times 10^{-6}$, LR $q = 1.0 \times 10^{-5}$). Using our extended hepatocellular model to further scrutinise these signatures, we found that all remained sex-biased after accounting for these variables except in ID3, where the effect was trending (extended model q -value = 0.12). Mutations associated with ID1 are thought to result from slippage during DNA replication and are associated with defective DNA mismatch repair, suggesting that while male- and female-derived tumours harbour defective DNA repair at similar rates, it is responsible for a larger proportion of mutations in female-derived tumours. Taken together, sex-biases in the aetiology underlying the molecular landscape of hepatocellular cancer begin to emerge. In this tumour subtype, spontaneous or enzymatic deamination of 5-methylcytosine to thymine and defective mismatch repair occur more frequently in female patients and are also responsible for more mutations. Conversely, tobacco smoking is more common in male patients though the number of mutations attributed to tobacco smoke is not different between the sexes; this leads to more tobacco-associated male hepatocellular tumours.

In B-cell non-Hodgkin lymphoma, we identified significant differences in the proportions of SBS17a- and SBS17b-positive tumours (Fig. 3c; Supplementary Data 8). More male-derived samples had mutations associated with these signatures. There were also several intriguing sex differences in mutational signatures that did not meet our significance threshold. For instance in thyroid cancer, DBS2 accounts for a higher percentage of mutations in male-derived samples (male median percent mutations attributed to DBS2 = 50%, female median = 33%, Supplementary Data 8). The association of DBS2 with tobacco smoking suggests that future insight in this signature may provide molecular explanations for the sex-specific associations between smoking and thyroid cancer risk²². As the aetiologies of these mutational signatures become better known, we can better understand how underlying mutational processes lead to molecular sex-biases. We may also be able to discern environmental and lifestyle factors even in the absence of reported data, allowing us to better account for confounding factors.

Finally, to ensure that our findings were not skewed by differences in sequencing quality, we checked for sex-biases in quality control (QC) metrics. These included comparing the coverage, read length, and overall quality summaries of both tumour and normal genomes. We mirrored our main analyses and used Mann–Whitney U -tests or χ^2 tests and linear modelling to check each QC metric. We did not find sex-biases in any QC metric in pan-cancer or tumour subtype analysis after multiple adjustment except in raw somatic mutation calling (SMC)

coverage. SMC coverage was higher in male-derived samples in six tumour subtypes including thyroid cancer and oesophageal cancer, and was higher in female-derived samples in lung adenocarcinoma and B-cell non-Hodgkin lymphoma (Supplementary Data 9 and Supplementary Fig. 13). Although we do not find sex differences in comparing the SMC coverage pass/fail rates using a recommended minimum of 2.6 gigabases covered, it is prudent to consider sex-biased SMC in relation to our findings.

Discussion

Our analysis of whole-genome sequencing data from the PCAWG project uncovered sex differences in the largely unexplored non-coding autosomal genome. In addition to validating previously reported findings in a novel dataset, we present sex-biases in measures of non-coding mutation density, tumour evolution and mutation signatures. These sex-biases suggest differences in the origins and trajectories of tumours between men and women, and that they are influenced by different endogenous and environmental factors. Although many of our findings describe pan-cancer differences, we have also uncovered an intriguing glimpse into tumour subtype-specific differences in cancers such as those of the liver and kidney.

These results should be taken within context of a number of caveats. As we use techniques like the Box–Cox transformation to make the data better suited for our statistical methods, there are likely characteristics that our models are unable to account for. An alternate approach using robust modelling may be better suited for future analyses. Secondly, the tumour subtype-specific results are bound by subtype sample size, and lack of annotation data restricts the ability to account for confounding variables. It is therefore important to consider these results within context of the multivariable models used, which do not directly capture characteristics such as tobacco smoking history. Many of our core multivariate regression models omit stage and grade due to a large number of missing values. We follow up this core regression with extended modelling as an additional level of scrutiny. Although these extended models do include stage or grade, they are run on a much smaller (up to 50%) subset of the data and there is a corresponding loss of statistical power. Finally, there are imbalances across covariate sample sizes, such as overrepresentation of some tumour types in pan-cancer analysis. We evaluated these imbalances using down-sampling analysis and rejected results that were biased by these imbalances. Nevertheless, pan-cancer analysis is dependent on the tumour subtypes included in the cohort and some findings may reflect subtype-specific trends rather than general characteristics across all cancers.

Future increases in sample size and robust associated annotation will allow for the detection of smaller effects and the control of more confounders. Such large datasets are critical in validating the preliminary findings we have described in this study. Increasing the diversity of donors will also allow the study of intriguing cross-variable questions such as investigating whether sex differences are universal across races, or if there are race-specific sex differences. Our results are based on single region sequencing, which can bias the clonal reconstruction for these tumours. Future work sampling multiple regions will allow us to detect sex differences in more precise reconstructions at a greater resolution. We will also be able to leverage germline data to assess whether there are sex-biases in inherited variants that affect the variants we observe in somatic mutation profiles.

Nevertheless, our analyses of driver genes and copy number alterations suggest functional impacts of genomic sex-biases on the transcriptome and tumorigenesis. By using signatures to distinguish between mutations attributed to lifestyle factors such

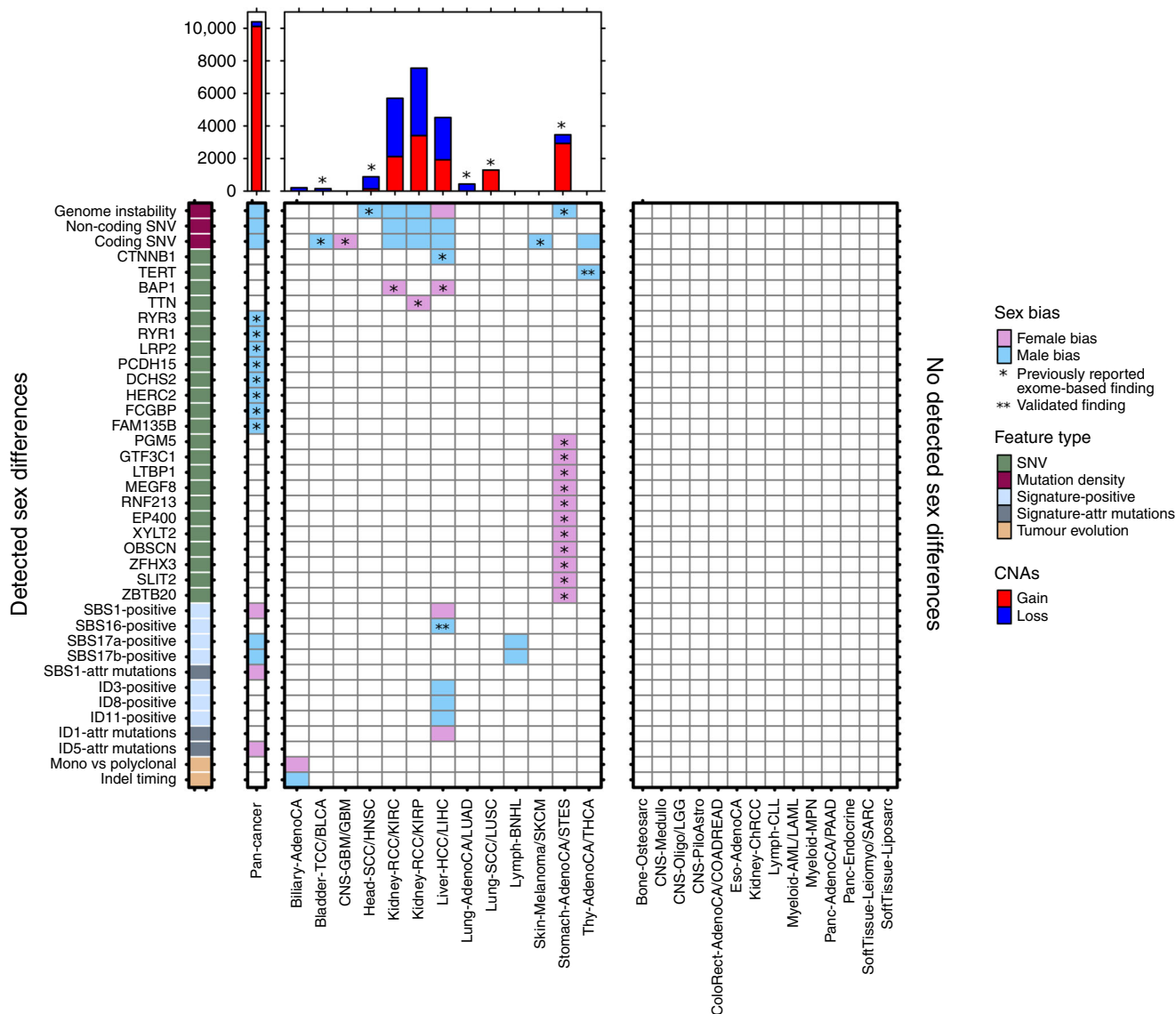


Fig. 4 The landscape of sex differences in cancer genomics. Summary of genomic features found to be sex-biased in pan-cancer analysis or in specific tumour subtypes. Results from both PCAWG and TCGA analyses are shown. Direction of sex-bias is shown in coloration denoting which sex has higher or more frequent aberration of the genomic feature. Top plot shows union of genes found to be involved in sex-biased CNAs. Starred indicate findings exclusively from exome sequencing data ($n = 7131$), un-starred indicate findings from PCAWG data ($n = 1983$), and double-starred indicate findings also described in other studies.

as smoking history, we can better describe sex differences related to biological factors such as hormone activity. And despite low tumour subtype-specific sample numbers, our mutation timing and mutational signatures findings at both the pan-cancer and tumour-subtype level hint at underlying mutational processes that may give rise to molecular sex-biases. Combined with our previous work in whole-exome sequencing, we present a landscape of sex-biases in cancer genomics and mutational processes (Fig. 4).

It is becoming clear that sex differences occur across many mutation classes and the portrait of differences for each tumour subtype is a unique reflection of active mutational processes and tumour evolution. We have performed here a pan-cancer analysis of sex differences in whole-genome sequencing data and catalogued previously undescribed sex-biases. However, increased study of molecular sex differences in future large-scale sequencing efforts is needed to strengthen the findings we present here, to determine why men and women have molecularly different

tumours, and to determine how this information can be leveraged to improve patient care.

Methods

General statistical framework. We only included non-sex-specific tumour subtypes in our analysis and focused on the autosome, excluding the sex chromosomes. Covariate data include genomically matched sex, age at diagnosis, and imputed ancestry.

For each genomic feature of interest, we performed three stages of analysis. At stage one, we use non-parametric univariate tests (Pearson’s χ^2 proportion or Mann–Whitney U -test) first, followed by false discovery rate adjustment to identify putative sex-biases of interest ($q < 0.1$).

At stage two, we further investigate these putative sex-biases by using multivariate linear or logistic modelling to account for potential confounders using bespoke models for each tumour subtype. Confounders were included as independent variables in each model. Supplementary Data 1 describes the model variables for each tumour context, as well as detail on when analyses included multivariate modelling. Variables were included based on availability of data (<15% missing), sufficient variability (at least two levels) and collinearity.

Discrete data were modelled using logistic regression. Continuous data were first transformed using the Box–Cox family and modelled using linear regression.

The Box–Cox family of transformations is a formalised method to select a power transformation to better approximate a normal-like distribution and stabilise variance. We used the Ye–Johnson extension to the Box–Cox transformation that allows for zeros and negative values²³:

$$y_i^\lambda = \begin{cases} \frac{(y_i+1)^\lambda - 1}{\lambda}, & \text{if } \lambda \neq 0, y \geq 0 \\ \log(y_i + 1), & \text{if } \lambda = 0, y \geq 0 \\ \frac{-(-y_i+1)^{2-\lambda} - 1}{2-\lambda}, & \text{if } \lambda \neq 2, y < 0 \\ -\log(-y_i + 1), & \text{if } \lambda = 2, y < 0 \end{cases}$$

FDR adjustment was performed for p -values for the sex variable significance estimate and an FDR threshold of 10% was used to determine statistical significance. For some tumour subtypes, the multivariate step is never performed because there are no univariate hits to evaluate.

The third stage of analysis involves re-evaluating our stage two sex-biases with a battery of additional modelling:

For pan-cancer findings, we evaluate the effect of unbalanced tumour subtype sample sizes by repeatedly and randomly down-sampling to the median subtype sample size with replacement ($n_{\text{median}} = 48$). For each down-sampled dataset, we record the difference between the male and female median/proportion, as well as the p -value from the relevant univariate test (Supplementary Fig. 2). We repeat this 10,000 times for each finding to generate distributions of male–female differences and p -values. We calculate a 95% confidence interval using the male–female difference distribution and reject findings where this confidence interval overlaps with 0. We also reject findings where the median down-sampled p -value is greater than the $p = 0.05$ threshold.

For both pan-cancer and tumour subtype-specific findings, we evaluate the effect of unbalanced sexes when either female or male donors account for >60% of samples. We down-sample to the smaller number of samples with replacement and record the difference between the male and female median/proportion, as well as the p -value from the relevant univariate test (Supplementary Figs. 1, 3, 8, 9 and 11). We repeat this 10,000 times for each finding to generate distributions of male–female differences and p -values. We calculate a 95% confidence interval using the male–female difference distribution and reject findings where this confidence interval overlaps with 0. We also reject findings where the median down-sampled p -value is greater than the $p = 0.05$ threshold. We present the median down-sampled p -values throughout Supplementary Data 2–8.

For tumour subtype-specific results, we also use extended models that incorporate additional variables such as tumour stage. Because this leads to up to 50% data loss, we only investigate a subset of results in this way. All extended modelling results are presented in Supplementary Data 2–8.

Specific details are provided for each analysis below.

Driver event analysis. We focused on driver events (syn11639581) described by the PCAWG consortium¹⁴. Driver mutation data were binarized to indicate presence or absence of the driver event in each patient. For the first stage of our analysis, we compared proportions of mutated genes between the sexes using univariate proportion tests. A q -value threshold of 0.1 was used to select genes for further multivariate analysis in stage two using binary logistic regression. FDR correction was again applied and genes with significant pan-cancer sex terms were extracted from the models (q -value < 0.1). Driver event analysis was performed separately for pan-cancer analysis and for each tumour subtype.

Clonal structure and mutation timing analysis. Subclonal structure and mutation timing calls¹⁵ were downloaded from Synapse (syn8532460). Subclonal structure data were binarized from number of subclonal clusters per sample to monoclonal (one cluster) or polyclonal (more than one cluster). The proportion of polyclonal samples was calculated per sex and compared in the first stage of analysis using proportion tests for both pan-cancer and tumour subtype analysis. The univariate p -values were FDR-adjusted across all tumour subtypes to identify putatively sex-biased clonal structure. These cases were further scrutinised in stage two using logistic regression. A multivariate q -value threshold of 0.1 was used to determine statistically significant sex-biased clonal structure.

Mutation timing data classified SNVs, indels and SVs into clonal (truncal) or subclonal groups. The proportion of truncal variants was calculated for each mutation type ($\frac{\text{Number truncal SNVs}}{\text{Total SNVs}}$, etc) to obtain proportions of truncal SNVs, indels and SVs for each sample. These proportions were compared in stage one of analysis between the sexes using two-sided Mann–Whitney U -tests and univariate p -values were FDR-adjusted to identify putatively sex-biased mutation timing. In stage two, linear regression was used to adjust for confounding factors and a multivariate q -value threshold of 0.1 was used to determine statistically significant sex-biased mutation timing. The mutation timing analysis was performed separately for SNVs, indels and SVs.

SNV density analysis. Consensus SNV calls were downloaded from Synapse (syn7357330). Overall SNV density per patient was calculated as the sum of SNVs across all genes on the autosomes and scaled to mutations/Mbp. Coding mutation prevalence only considers the coding regions of the genome, and non-coding prevalence only considers the non-coding regions. Mutation load was first

compared between the sexes using Mann–Whitney U -tests for both pan-cancer and tumour-type specific analysis. Comparisons with U -test q -values meeting an FDR threshold of 10% were further analysed using linear regression to adjust for tumour subtype-specific variables. Mutation load analysis was performed separately for each mutation context, with pan-cancer and tumour subtype p -values adjusted together.

Chromosome and genome instability analysis. Consensus copy number data were obtained from Synapse (syn8042988). Ploidy-adjusted calls were used to identify segments with copy number gains and losses. The number of bases in copy number gained or lost segments were summed per chromosome and divided by chromosome size to obtain percent chromosome gained and lost, respectively. All segments affected by any copy number aberration were also summed and treated in the same way to calculate percent chromosome altered. Percent copy number gained, lost and altered were also calculated over the autosomes. In stage one, genome and chromosome instability were compared in pan-cancer and tumour-subtype analysis using Mann–Whitney U -tests to identify putatively sex-biased chromosome and genome instability. In stage two, putatively sex-biased events were further analysed using linear regression modelling. Genome instability analysis was performed separately for each tumour subtype with FDR adjustment performed over percent copy gained, loss and altered comparisons together.

Genome-spanning CNA analysis. Consensus copy number data (syn8042988) were processed to gain/neutral/loss calls per gene. For each gene, we compared the proportion of gains for each sex using proportion tests. For putative sex-biased genes that passed an FDR threshold of 10%, we followed up with multivariate logistic regression to adjust for tumour subtype-specific covariates (Supplementary Data 1). We repeated this analysis for copy number loss. This genome-spanning analysis was performed separately for losses and gains for each tumour subtype.

Mutational signatures analysis. The number of mutations attributed to each SBS (syn11738669), DBS (syn11738667) and ID (syn11738668) signature¹⁶ per sample was downloaded from Synapse. For each signature, we compared the proportion of samples with any mutations attributed to the signatures (“signature-positive”) using χ^2 -square tests to identify univariately significant sex-biases. Signatures with putative sex-biases were further analysed using logistic regression.

We also compared the proportions of mutations attributed to each signature. The numbers of mutations per signature were divided by total number of mutations for each sample to obtain the proportion of mutations attributed to the signature. In the first stage of analysis, we used Mann–Whitney U -tests to compare these proportions of attributed mutations, and Kolmogorov–Smirnov tests to compare their distributions between the sexes. Putative sex-biased signatures were further analysed using linear regression after Box–Cox adjustment.

In addition to tumour subtype-specific covariates, we included SNV density in all multivariate mutational signatures models to account for bias in calling more signatures in SNV-dense samples. Signatures that were not detected in a tumour subtype were omitted from analysis for that tumour subtype. We also used Kolmogorov–Smirnov tests to compare the distributions of attributed mutations and kept results where the sex-difference was significant or trending.

Reporting summary. Further information on research design is available in the Nature Research Reporting Summary linked to this article.

Data availability

Somatic and germline variant calls, mutational signatures, subclonal reconstructions, transcript abundance, splice calls and other core data generated by the ICGC/TCGA Pan-cancer Analysis of Whole Genomes Consortium are described in the marker paper¹³ and available for download at <https://dcc.icgc.org/releases/PCAWG>. Additional information on accessing the data, including raw read files, can be found at <https://docs.icgc.org/pcawg/data/>. In accordance with the data access policies of the ICGC and TCGA projects, most molecular, clinical and specimen data are in an open tier that does not require access approval. To access potentially identification information, such as germline alleles and underlying sequencing data, researchers will need to apply to the TCGA Data Access Committee (DAC) via dbGaP for access to the TCGA portion of the dataset, and to the ICGC Data Access Compliance Office (DACO) for the ICGC portion. To access somatic single nucleotide variants derived from TCGA donors, researchers will also need to obtain dbGaP authorisation. In addition, the analyses in this paper used a number of datasets that were derived from raw PCAWG sequencing data and variant calls (Supplementary Data 10). The individual datasets are available at Synapse (<https://www.synapse.org/>), and are denoted with synXXXXX accession numbers (listed under Synapse ID); all these datasets are also mirrored at <https://dcc.icgc.org>, with full links, filenames, accession numbers and descriptions detailed in Supplementary Data 10. Tumour histological classifications were reviewed and assigned by the PCAWG Pathology and Clinical Correlates Working Group (annotation version 9; syn10389158, syn10389164). Ancestry imputation was performed using an ADMIXTURE²⁴-like algorithm by the PCAWG Germline Cancer Genome Working Group based on germline SNP profiles

determined by whole-genome sequencing of the reference sample and are available in Supplementary Table 1 of the PCAWG marker paper¹³. The consensus somatic SNV and indel (<syn7357330>) file covers 2778 whitelisted samples from 2583 donors. Driver events were called by the PCAWG Drivers and Functional Interpretation Group (<syn11639581>). Consensus CNA calls from the PCAWG Structural Variation Working Group were downloaded in VCF format (<syn8042988>). Subclonal reconstruction was performed by the PCAWG Evolution and Heterogeneity Working Group (<syn8532460>). SigProfiler mutation signatures were determined by the PCAWG Mutation Signatures and Processes Working Group for single base substitution (<syn11738669>), doublet base substitution (<syn11738667>) and indel (<syn11738668>) signatures.

Code availability

The core computational pipelines used by the PCAWG Consortium for alignment, quality control and variant calling are available to the public at <https://dockstore.org/search?search=pcawg> under the GNU General Public License v3.0, which allows for reuse and distribution. All statistical analyses and data visualisation were performed in the R statistical environment (v3.4.3) using the BPG²⁵ (v5.9.8) and car (v3.0-2) packages.

Received: 18 April 2019; Accepted: 30 January 2020;

Published online: 28 August 2020

References

- Cook, M. B. et al. Sex disparities in cancer incidence by period and age. *Cancer Epidemiol. Biomark. Prev.* **18**, 1174–1182 (2009).
- Edgren, G., Liang, L., Adami, H.-O. & Chang, E. T. Enigmatic sex disparities in cancer incidence. *Eur. J. Epidemiol.* **27**, 187–196 (2012).
- Cook, M. B., McGlynn, K. A., Devesa, S. S., Freedman, N. D. & Anderson, W. F. Sex disparities in cancer mortality and survival. *Cancer Epidemiol. Biomark. Prev.* **20**, 1629–1637 (2011).
- Wichmann, M. W., Muller, C., Hornung, H. M., Lau-Werner, U. & Schildberg, F. W. Gender differences in long-term survival of patients with colorectal cancer. *Br. J. Surg.* **88**, 1092–1098 (2001).
- Elsaleh, H. et al. Association of tumour site and sex with survival benefit from adjuvant chemotherapy in colorectal cancer. *Lancet Lond. Engl.* **355**, 1745–1750 (2000).
- OuYang, P.-Y. et al. The significant survival advantage of female sex in nasopharyngeal carcinoma: a propensity-matched analysis. *Br. J. Cancer* **112**, 1554–1561 (2015).
- Sun, T., Plutynski, A., Ward, S. & Rubin, J. B. An integrative view on sex differences in brain tumors. *Cell. Mol. Life Sci.* **72**, 3323–3342 (2015).
- Dunford, A. et al. Tumor-suppressor genes that escape from X-inactivation contribute to cancer sex bias. *Nat. Genet.* <https://doi.org/10.1038/ng.3726> (2016).
- Yuan, Y. et al. Comprehensive characterization of molecular differences in cancer between male and female patients. *Cancer Cell* **29**, 711–722 (2016).
- Warrington, N. M. et al. The cyclic AMP pathway is a sex-specific modifier of glioma risk in type I neurofibromatosis patients. *Cancer Res.* **75**, 16–21 (2015).
- Li, C. H., Haider, S., Shiah, Y.-J., Thai, K. & Boutros, P. C. Sex differences in cancer driver genes and biomarkers. *Cancer Res.* **78**, 5527 (2018).
- Lopes-Ramos, C. M. et al. Gene regulatory network analysis identifies sex-linked differences in colon cancer drug metabolism. *Cancer Res.* **78**, 5538–5547 (2018).
- The ICGC/TCGA Pan-Cancer Analysis of Whole Genomes Network. Pan-cancer analysis of whole genomes. *Nature* **578**, 82–93 (2020).
- Rheinbay, E. et al. Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. *Nature* **578**, 102–111 (2020).
- Gerstung, M. et al. The evolutionary history of 2,658 cancers. *Nature* **578**, 122–128 (2019).
- Alexandrov, L. B. et al. The repertoire of mutational signatures in human cancer. *Nature* **578**, 94–101 (2020).
- Liu, R. & Xing, M. TERT promoter mutations in thyroid cancer. *Endocr. Relat. Cancer* <https://doi.org/10.1530/ERC-15-0533> (2016).
- Qin, Y. et al. The inhibitory effects of deleted in liver cancer 1 gene on gallbladder cancer growth through induction of cell cycle arrest and apoptosis. *J. Gastroenterol. Hepatol.* **29**, 964–972 (2014).
- Nik-Zainal, S. et al. Mutational processes molding the genomes of 21 breast cancers. *Cell* **149**, 979–993 (2012).
- Alexandrov, L. B. et al. Signatures of mutational processes in human cancer. *Nature* **500**, 415–421 (2013).
- Letouze, E. et al. Mutational signatures reveal the dynamic interplay of risk factors and cellular processes during liver tumorigenesis. *Nat. Commun.* **8**, 1315 (2017).
- Cho, A., Chang, Y., Ahn, J., Shin, H. & Ryu, S. Cigarette smoking and thyroid cancer risk: a cohort study. *Br. J. Cancer* **119**, 638–645 (2018).
- Yeo, I.-K. & Johnson, R. A. A New Family Of Power Transformations To Improve Normality Or Symmetry. *Biometrika* **87**, 954–959 (2000).
- Alexander, D. H., Novembre, J. & Lange, K. Fast model-based estimation of ancestry in unrelated individuals. *Genome Res.* **19**, 1655–1664 (2009).
- P'ng, C. et al. BPG: Seamless, automated and interactive visualization of scientific data. *BMC Bioinformatics* **20**, 42 (2019).

Acknowledgements

We thank all the members of the Boutros lab for insightful discussions. This study was conducted with the support of the Ontario Institute for Cancer Research to P.C.B. through funding provided by the Government of Ontario. This work was supported by the Discovery Frontiers: Advancing Big Data Science in Genomics Research program, which is jointly funded by the Natural Sciences and Engineering Research Council (NSERC) of Canada, the Canadian Institutes of Health Research (CIHR), Genome Canada and the Canada Foundation for Innovation (CFI). P.C.B. was supported by a Terry Fox Research Institute New Investigator Award and a CIHR New Investigator Award. This work was supported by an NSERC Discovery grant and by Canadian Institutes of Health Research, grant #SVB-145586, to P.C.B. This work was supported by the NIH/NCI under award number P30CA016042 and an operating grant from the National Cancer Institute Early Detection Research Network (1U01CA214194-01). We acknowledge the contributions of the many clinical networks across ICGC and TCGA who provided samples and data to the PCAWG Consortium, and the contributions of the Technical Working Group and the Germline Working Group of the PCAWG Consortium for collation, realignment and harmonised variant calling of the cancer genomes used in this study. We thank the patients and their families for their participation in the individual ICGC and TCGA projects.

Author contributions

C.H.L. and P.C.B. initiated the project. C.H.L., S.D.P., R.X.S., F.Y. and N.S. analysed data. P.C.B. supervised research. C.H.L. and P.C.B. wrote the first draft of the manuscript, which all authors edited and approved. The PCAWG Tumour Subtypes and Clinical Translation working group and the PCAWG Consortium network provided variant calls, clinical annotation data and insightful commentary.

Competing interests

The authors declare no competing interests.

Additional information

Supplementary information is available for this paper at <https://doi.org/10.1038/s41467-020-17359-2>.

Correspondence and requests for materials should be addressed to P.C.B.

Peer review information *Nature Communications* thanks Joshua Rubin, Melissa Wilson and the other, anonymous, reviewer(s) for their contribution to the peer review of this work. Peer reviewer reports are available.

Reprints and permission information is available at <http://www.nature.com/reprints>

Publisher's note Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.



Open Access This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons license, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons license, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons license and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this license, visit <http://creativecommons.org/licenses/by/4.0/>.

© The Author(s) 2020

PCAWG Tumour Subtypes and Clinical Translation

Fatima Al-Shahrour⁹, Gurnit Atwal^{1,5,10}, Peter J. Bailey¹¹, Andrew V. Biankin^{11,12,13,14}, Paul C. Boutros^{1,2,3,4}, Peter J. Campbell^{15,16}, David K. Chang^{11,12}, Susanna L. Cooke¹¹, Vikram Deshpande¹⁷, Bishoy M. Faltas¹⁸, William C. Faquin¹⁷, Levi Garraway¹⁹, Gad Getz^{20,21,22,23}, Sean M. Grimmond²⁴, Syed Haider¹, Katherine A. Hoadley^{25,26}, Wei Jiao¹, Vera B. Kaiser²⁷, Rosa Karlič²⁸, Mamoru Kato²⁹, Kirsten Kübler^{17,20,21}, Alexander J. Lazar^{30,31}, Constance H. Li^{1,2}, David N. Louis¹⁷, Adam Margolin³², Sancha Martin^{15,33}, Hardeep K. Nahal-Bose³⁴, G. Petur Nielsen¹⁷, Serena Nik-Zainal^{15,35,36,37}, Larsson Omberg³⁸, Christine P'ng¹, Marc D. Perry^{34,39}, Paz Polak^{20,21,22}, Esther Rheinbay^{17,20,21}, Mark A. Rubin^{40,41,42,43,44}, Colin A. Semple²⁷, Dennis C. Sgroi¹⁷, Tatsuhiro Shibata^{45,46}, Reiner Siebert^{47,48}, Jaclyn Smith⁴⁹, Lincoln D. Stein^{1,10}, Miranda D. Stobbe^{50,51}, Ren X. Sun¹, Kevin Thai³⁴, Derek W. Wright^{11,52}, Chin-Lee Wu¹⁷, Ke Yuan^{53,54,55} & Junjun Zhang³⁴

⁹Bioinformatics Unit, Spanish National Cancer Research Centre (CNIO), Madrid 28029, Spain. ¹⁰Department of Molecular Genetics, University of Toronto, Toronto, ON M5S 1A8, Canada. ¹¹Wolfson Wohl Cancer Research Centre, Institute of Cancer Sciences, University of Glasgow, Glasgow, UK. ¹²Cancer Division, Garvan Institute of Medical Research, Kinghorn Cancer Centre, University of New South Wales (UNSW Sydney), Sydney, NSW, Australia. ¹³South Western Sydney Clinical School, Faculty of Medicine, University of New South Wales (UNSW Sydney), Liverpool, NSW, Australia. ¹⁴West of Scotland Pancreatic Unit, Glasgow Royal Infirmary, Glasgow, UK. ¹⁵Wellcome Sanger Institute, Wellcome Genome Campus, Hinxton, Cambridge CB10 1SA, UK. ¹⁶Department of Haematology, University of Cambridge, Cambridge CB2 2XY, UK. ¹⁷Massachusetts General Hospital, Boston, MA 02114, USA. ¹⁸Weill Cornell Medical College, New York, NY 10065, USA. ¹⁹Department of Medical Oncology, Dana-Farber Cancer Institute, Boston, MA 02215, USA. ²⁰Broad Institute of MIT and Harvard, Cambridge, MA 02142, USA. ²¹Harvard Medical School, Boston, MA 02115, USA. ²²Center for Cancer Research, Massachusetts General Hospital, Boston, MA 02129, USA. ²³Department of Pathology, Massachusetts General Hospital, Boston, MA 02115, USA. ²⁴Centre for Cancer Research, Victorian Comprehensive Cancer Centre, University of Melbourne, Melbourne, VIC 3052, Australia. ²⁵Lineberger Comprehensive Cancer Center, University of North Carolina at Chapel Hill, Chapel Hill, NC 27599, USA. ²⁶Department of Genetics, University of North Carolina at Chapel Hill, Chapel Hill, NC 27599, USA. ²⁷MRC Human Genetics Unit, MRC IGMM, University of Edinburgh, Edinburgh EH4 2XU, UK. ²⁸Bioinformatics Group, Division of Molecular Biology, Department of Biology, Faculty of Science, University of Zagreb, Zagreb, Croatia. ²⁹Department of Bioinformatics, Research Institute, National Cancer Center Japan, Tokyo 104-0045, Japan. ³⁰Departments of Pathology, The University of Texas MD Anderson Cancer Center, Houston, TX 77030, USA. ³¹Department of Genomic Medicine, The University of Texas MD Anderson Cancer Center, Houston, TX 77030, USA. ³²Computational Biology Program, School of Medicine, Oregon Health & Science University, Portland, OR 97239, USA. ³³Hematology, Hospital Clinic, Institut d'Investigacions Biomediques August Pi i Sunyer (IDIBAPS), University of Barcelona, Barcelona, Spain. ³⁴Genome Informatics Program, Ontario Institute for Cancer Research, Toronto, ON M5G 0A3, Canada. ³⁵Academic Department of Medical Genetics, University of Cambridge, Addenbrooke's Hospital, Cambridge CB2 0QQ, UK. ³⁶MRC Cancer Unit, University of Cambridge, Cambridge CB2 0XZ, UK. ³⁷The University of Cambridge School of Clinical Medicine, Cambridge, UK. ³⁸Sage Bionetworks, Seattle, WA 98109, USA. ³⁹Department of Radiation Oncology, University of California San Francisco, San Francisco, CA 94518, USA. ⁴⁰Department for Biomedical Research, University of Bern, Bern 3008, Switzerland. ⁴¹Bern Center for Precision Medicine, University Hospital of Bern, University of Bern, Bern 3008, Switzerland. ⁴²Englander Institute for Precision Medicine, Weill Cornell Medicine and New York Presbyterian Hospital, New York, NY 10021, USA. ⁴³Meyer Cancer Center, Weill Cornell Medicine, New York, NY 10065, USA. ⁴⁴Pathology and Laboratory, Weill Cornell Medical College, New York, NY 10021, USA. ⁴⁵Division of Cancer Genomics, National Cancer Center Research Institute, Tokyo 104-0045, Japan. ⁴⁶Department of Oncologic Pathology, Dana-Farber Cancer Institute, Harvard Medical School, Boston, MA, USA. ⁴⁷Institute of Human Genetics, Ulm University and Ulm University Medical Center, Ulm 89081, Germany. ⁴⁸Human Genetics, University of Kiel, Kiel 24118, Germany. ⁴⁹Oregon Health and Science University, Portland, OR, USA. ⁵⁰CNAG-CRG, Centre for Genomic Regulation (CRG), Barcelona Institute of Science and Technology (BIST), Barcelona 08028, Spain. ⁵¹Universitat Pompeu Fabra (UPF), Barcelona 08003, Spain. ⁵²MRC-University of Glasgow Centre for Virus Research, Glasgow G61 1QH, UK. ⁵³Li Ka Shing Centre, Cancer Research UK Cambridge Institute, University of Cambridge, Cambridge, UK. ⁵⁴University of Glasgow, Glasgow G61 1BD, UK. ⁵⁵School of Computing Science, University of Glasgow, Glasgow G12 8RZ, UK.

PCAWG Consortium

Lauri A. Aaltonen⁵⁶, Federico Abascal¹⁵, Adam Abeshouse⁵⁷, Hiroyuki Aburatani⁵⁸, David J. Adams¹⁵, Nishant Agrawal⁵⁹, Keun Soo Ahn⁶⁰, Sung-Min Ahn⁶¹, Hiroshi Aikata⁶², Rehan Akbani⁶³, Kadir C. Akdemir⁶⁴, Hikmat Al-Ahmadie⁵⁷, Sultan T. Al-Sedairy⁶⁵, Fatima Al-Shahrour⁹, Malik Alawi^{66,67}, Monique Albert⁶⁸, Kenneth Aldape^{30,69}, Ludmil B. Alexandrov^{15,70,71}, Adrian Ally⁷², Kathryn Alsop⁷³, Eva G. Alvarez^{74,75,76}, Fernanda Amary⁷⁷, Samirkumar B. Amin^{31,78,79}, Brice Aminou³⁴, Ole Ammerpohl^{80,47}, Matthew J. Anderson⁸¹, Yeng Ang⁸², Davide Antonello⁸³, Pavana Anur⁸⁴, Samuel Aparicio⁸⁵, Elizabeth L. Appelbaum^{86,87}, Yasuhito Arai⁴⁵, Axel Aretz⁸⁸, Koji Arihiro⁶², Shun-ichi Ariizumi⁸⁹, Joshua Armenia⁹⁰, Laurent Arnould⁹¹, Sylvia Asa^{92,93}, Yassen Assenov⁹⁴, Gurnit Atwal^{1,5,10}, Sietse Aukema^{47,95}, J. Todd Auman⁹⁶, Miriam R. Aure⁹⁷, Philip Awadalla^{1,10}, Marta Aymerich⁹⁸, Gary D. Bader¹⁰, Adrian Baez-Ortega⁹⁹, Matthew H. Bailey^{86,100},

Peter J. Bailey¹¹, Miruna Balasundaram⁷², Saianand Balu²⁵, Pratiti Bandopadhyay^{20,101,102}, Rosamonde E. Banks¹⁰³, Stefano Barbi¹⁰⁴, Andrew P. Barbour^{105,106}, Jonathan Barenboim¹, Jill Barnholtz-Sloan^{107,108}, Hugh Barr¹⁰⁹, Elisabet Barrera¹¹⁰, John Bartlett^{68,111}, Javier Bartolome¹¹², Claudio Bassi⁸³, Oliver F. Bathe^{113,114}, Daniel Baumhoer¹¹⁵, Prashant Bavi¹¹⁶, Stephen B. Baylin^{117,118}, Wojciech Bazant¹¹⁰, Duncan Beardsmore¹¹⁹, Timothy A. Beck^{120,121}, Sam Behjati¹⁵, Andreas Behren¹²², Beifang Niu¹²³, Cindy Bell¹²⁴, Sergi Beltran^{50,51}, Christopher Benz¹²⁵, Andrew Berchuck¹²⁶, Anke K. Bergmann¹²⁷, Erik N. Bergstrom^{70,71}, Benjamin P. Berman^{128,129,130}, Daniel M. Berney¹³¹, Stephan H. Bernhart^{132,133,134}, Rameen Beroukhim^{20,19,21}, Mario Berrios¹³⁵, Samantha Bersani¹³⁶, Johanna Bertl^{137,138}, Miguel Betancourt¹³⁹, Vinayak Bhandari^{1,2}, Shriram G. Bhosle¹⁵, Andrew V. Biankin^{11,12,13,14}, Matthias Bieg^{140,141}, Darell Bigner¹⁴², Hans Binder^{132,133}, Ewan Birney¹¹⁰, Michael Birrer¹⁴³, Nidhan K. Biswas¹⁴⁴, Bodil Bjerkehagen^{115,145}, Tom Bodenheimer²⁵, Lori Boice¹⁴⁶, Giada Bonizzato¹⁴⁷, Johann S. De Bono¹⁴⁸, Arnaud Boot^{149,150}, Moiz S. Bootwalla¹³⁵, Ake Borg¹⁵¹, Arndt Borkhardt¹⁵², Keith A. Boroevich^{153,154}, Ivan Borozan¹, Christoph Borst¹⁵⁵, Marcus Bosenberg¹⁵⁶, Mattia Bosio^{112,51,157}, Jacqueline Boulwood¹⁵⁸, Guillaume Bourque^{159,160}, Paul C. Boutros^{1,2,3,4}, G. Steven Bova¹⁶¹, David T. Bowen^{15,162}, Reanne Bowlby⁷², David D. L. Bowtell⁷³, Sandrine Boyault¹⁶³, Rich Boyce¹¹⁰, Jeffrey Boyd¹⁶⁴, Alvis Brazma¹¹⁰, Paul Brennan¹⁶⁵, Daniel S. Brewer^{166,167}, Arie B. Brinkman¹⁶⁸, Robert G. Bristow^{2,169,170,171,172}, Russell R. Broaddus³⁰, Jane E. Brock¹⁷³, Malcolm Brock¹⁷⁴, Annegien Broeks¹⁷⁵, Angela N. Brooks^{20,19,176,177}, Denise Brooks⁷², Benedikt Brors^{178,179,180}, Søren Brunak^{181,182}, Timothy J. C. Bruxner^{81,183}, Alicia L. Bruzos^{74,75,76}, Alex Buchanan¹⁸⁴, Ivo Buchhalter^{141,185,186}, Christiane Buchholz¹⁸⁷, Susan Bullman^{20,19}, Hazel Burke¹⁸⁸, Birgit Burkhardt¹⁸⁹, Kathleen H. Burns^{190,191}, John Busanovich^{20,192}, Carlos D. Bustamante^{193,194}, Adam P. Butler¹⁵, Atul J. Butte¹⁹⁵, Niall J. Byrne³⁴, Anne-Lise Børresen-Dale^{97,196}, Samantha J. Caesar-Johnson¹⁹⁷, Andy Cafferkey¹¹⁰, Declan Cahill¹⁹⁸, Claudia Calabrese^{110,199}, Carlos Caldas^{200,53}, Fabien Calvo²⁰¹, Niedzica Camacho¹⁴⁸, Peter J. Campbell^{15,16}, Elias Campo^{202,203}, Cinzia Cantù¹⁴⁷, Shaolong Cao⁶³, Thomas E. Carey²⁰⁴, Joana Carlevaro-Fita^{40,205,206}, Rebecca Carlsen⁷², Ivana Cataldo^{136,147}, Mario Cazzola²⁰⁷, Jonathan Cebon¹²², Robert Cerfolio²⁰⁸, Dianne E. Chadwick²⁰⁹, Dimple Chakravarty²¹⁰, Don Chalmers²¹¹, Calvin Wing Yiu Chan^{185,212}, Kin Chan²¹³, Michelle Chan-Seng-Yue¹¹⁶, Vishal S. Chandan²¹⁴, David K. Chang^{11,12}, Stephen J. Chanock²¹⁵, Lorraine A. Chantrill^{12,216}, Aurélien Chateigner^{34,217}, Nilanjan Chatterjee^{117,218}, Kazuaki Chayama⁶², Hsiao-Wei Chen^{82,90}, Jieming Chen¹⁹⁵, Ken Chen⁶⁴, Yiwen Chen⁶³, Zhaohong Chen²¹⁹, Andrew D. Cherniack^{20,19}, Jeremy Chien²²⁰, Yoke-Eng Chiew^{221,222}, Suet-Feung Chin^{200,53}, Juok Cho²⁰, Sunghoon Cho²²³, Jung Kyoong Choi²²⁴, Wan Choi²²⁵, Christine Chomienne²²⁶, Zechen Chong²²⁷, Su Pin Choo²²⁸, Angela Chou^{12,221}, Angelika N. Christ⁸¹, Elizabeth L. Christie⁷³, Eric Chuah⁷², Carrie Cibulskis²⁰, Kristian Cibulskis²⁰, Sara Cingarlini²²⁹, Peter Clapham¹⁵, Alexander Claviez²³⁰, Sean Cleary^{116,231}, Nicole Cloonan²³², Marek Cmero^{233,234,235}, Colin C. Collins²³⁶, Ashton A. Connor^{231,237}, Susanna L. Cooke¹¹, Colin S. Cooper^{148,167,238}, Leslie Cope¹¹⁷, Vincenzo Corbo^{104,147}, Matthew G. Cordes^{86,239}, Stephen M. Cordner²⁴⁰, Isidro Cortés-Ciriano^{241,242,243}, Kyle Covington²⁴⁴, Prue A. Cowin²⁴⁵, Brian Craft¹⁷⁷, David Craft^{20,246}, Chad J. Creighton²⁴⁷, Yupeng Cun²⁴⁸, Erin Curley²⁴⁹, Ioana Cutcutache^{149,150}, Karolina Czajka²⁵⁰, Bogdan Czerniak^{30,251}, Rebecca A. Dagg²⁵², Ludmila Danilova¹¹⁷, Maria Vittoria Davi²⁵³, Natalie R. Davidson^{18,254,255,256,257}, Helen Davies^{15,35,36}, Ian J. Davis²⁵⁸, Brandi N. Davis-Dusenbery²⁵⁹, Kevin J. Dawson¹⁵, Francisco M. De La Vega^{193,194,260}, Ricardo De Paoli-Iseppi¹⁸⁸, Timothy Defreitas²⁰, Angelo P. Dei Tos²⁶¹, Olivier Delaneau^{262,263,264}, John A. Demchok¹⁹⁷, Jonas Demeulemeester^{265,266}, German M. Demidov^{51,157,267}, Deniz Demircioğlu^{268,269}, Nening M. Dennis¹⁹⁸, Robert E. Denroche¹¹⁶, Stefan C. Dentro^{15,265,270}, Nikita Desai³⁴, Vikram Deshpande¹⁴³, Amit G. Deshwar²⁷¹, Christine Desmedt^{272,273}

Jordi Deu-Pons^{274,275}, Noreen Dhalla⁷², Neesha C. Dhani²⁷⁶, Priyanka Dhingra^{277,278}, Rajiv Dhir²⁷⁹, Anthony DiBiase²⁸⁰, Klev Diamanti²⁸¹, Li Ding^{86,100,282}, Shuai Ding²⁸³, Huy Q. Dinh¹²⁸, Luc Dirix²⁸⁴, HarshaVardhan Doddapaneni²⁴⁴, Nilgun Donmez^{236,285}, Michelle T. Dow²¹⁹, Ronny Drapkin²⁸⁶, Oliver Drechsel^{51,157}, Ruben M. Drews⁵³, Serge Serge¹⁵, Tim Dudderidge^{118,198}, Ana Dueso-Barroso¹¹², Andrew J. Dunford²⁰, Michael Dunn²⁸⁷, Lewis Jonathan Dursi^{1,288}, Fraser R. Duthie^{11,289}, Ken Dutton-Regester²⁹⁰, Jenna Eagles²⁵⁰, Douglas F. Easton^{291,292}, Stuart Edmonds²⁹³, Paul A. Edwards^{53,294}, Sandra E. Edwards¹⁴⁸, Rosalind A. Eeles^{148,198}, Anna Ehinger²⁹⁵, Juergen Eils^{296,297}, Roland Eils^{185,186,296,297}, Adel El-Naggar^{30,251}, Matthew Eldridge⁵³, Kyle Ellrott¹⁸⁴, Serap Erkek¹⁹⁹, Georgia Escaramis^{157,298,299}, Shadrielle M. G. Espiritu¹, Xavier Estivill^{157,300}, Dariush Etemadmoghadam⁷³, Jorunn E. Eyfjord³⁰¹, Bishoy M. Faltas¹⁸, Daiming Fan³⁰², Yu Fan⁶³, William C. Faquin¹⁴³, Claudiu Farcas²¹⁹, Matteo Fassan³⁰³, Aquila Fatima³⁰⁴, Francesco Favero³⁰⁵, Nodirjon Fayzullaev³⁴, Ina Felau¹⁹⁷, Sian Fereday⁷³, Martin L. Ferguson³⁰⁶, Vincent Ferretti^{34,307}, Lars Feuerbach¹⁷⁸, Matthew A. Field³⁰⁸, J. Lynn Fink^{81,112}, Gaetano Finocchiaro³⁰⁹, Cyril Fisher¹⁹⁸, Matthew W. Fittall²⁶⁵, Anna Fitzgerald³¹⁰, Rebecca C. Fitzgerald³⁶, Adrienne M. Flanagan³¹¹, Neil E. Fleshner³¹², Paul Flicek¹¹⁰, John A. Foekens³¹³, Kwun M. Fong³¹⁴, Nuno A. Fonseca^{110,315}, Christopher S. Foster^{316,317}, Natalie S. Fox¹, Michael Fraser¹, Scott Frazer²⁰, Milana Frenkel-Morgenstern³¹⁸, William Friedman³¹⁹, Joan Frigola²⁷⁴, Catrina C. Fronick^{86,239}, Akihiro Fujimoto¹⁵⁴, Masashi Fujita¹⁵⁴, Masashi Fukayama³²⁰, Lucinda A. Fulton⁸⁶, Robert S. Fulton^{86,100,282}, Mayuko Furuta¹⁵⁴, P. Andrew Futreal³²¹, Anja Füllgrabe¹¹⁰, Stacey B. Gabriel²⁰, Steven Gallinger^{116,231,237}, Carlo Gambacorti-Passerini³²², Jianjiong Gao⁹⁰, Shengjie Gao³²³, Levi Garraway¹⁹, Øystein Garred³²⁴, Erik Garrison¹⁵, Dale W. Garsed⁷³, Nils Gehlenborg^{20,325}, Josep L. L. Gelpi^{112,326}, Joshy George⁷⁹, Daniela S. Gerhard³²⁷, Clarissa Gerhauser³²⁸, Jeffrey E. Gershenwald^{329,330}, Mark Gerstein^{331,332,333}, Moritz Gerstung^{110,199}, Gad Getz^{20,21,22,23}, Mohammed Ghori¹⁵, Ronald Ghossein³³⁴, Nasra H. Giama³³⁵, Richard A. Gibbs²⁴⁴, Anthony J. Gill^{12,336}, Pelvender Gill³³⁷, Dilip D. Giri³³⁴, Dominik Glodzik¹⁵, Vincent J. Gnanapragasam^{338,339}, Maria Elisabeth Goebler³⁴⁰, Mary J. Goldman¹⁷⁷, Carmen Gomez³⁴¹, Santiago Gonzalez^{110,199}, Abel Gonzalez-Perez^{274,275,342}, Dmitry A. Gordenin³⁴³, James Gossage³⁴⁴, Kunihiro Gotoh³⁴⁵, Ramaswamy Govindan¹⁰⁰, Dorte Grabau³⁴⁶, Janet S. Graham^{11,347}, Robert C. Grant^{116,237}, Anthony R. Green²⁹⁴, Eric Green³⁴⁸, Liliana Greger¹¹⁰, Nicola Grehan³⁶, Sonia Grimaldi¹⁴⁷, Sean M. Grimmond²⁴, Robert L. Grossman³⁴⁹, Adam Grundhoff^{67,350}, Gunes Gundem⁵⁷, Qianyun Guo³⁵¹, Manaswi Gupta²⁰, Shailja Gupta³⁵², Ivo G. Gut^{50,51}, Marta Gut^{50,51}, Jonathan Göke^{268,353}, Gavin Ha²⁰, Andrea Haake⁸⁰, David Haan¹⁷⁶, Siegfried Haas¹⁵⁵, Kerstin Haase²⁶⁵, James E. Haber³⁵⁴, Nina Habermann¹⁹⁹, Faraz Hach^{236,355}, Syed Haider¹, Natsuko Hama⁴⁵, Freddie C. Hamdy³³⁷, Anne Hamilton²⁴⁵, Mark P. Hamilton³⁵⁶, Leng Han³⁵⁷, George B. Hanna³⁵⁸, Martin Hansmann³⁵⁹, Nicholas J. Haradhvala^{20,143}, Olivier Harismendy^{71,360}, Ivon Harliwong⁸¹, Arif O. Harmanci^{333,361}, Eoghan Harrington³⁶², Takanori Hasegawa³⁶³, David Haussler^{177,364}, Steve Hawkins⁵³, Shinya Hayami³⁶⁵, Shuto Hayashi³⁶³, D. Neil Hayes^{25,366,367}, Stephen J. Hayes^{368,369}, Nicholas K. Hayward^{188,290}, Steven Hazell¹⁹⁸, Yao He³⁷⁰, Allison P. Heath³⁷¹, Simon C. Heath^{50,51}, David Hedley²⁷⁶, Apurva M. Hegde³⁷², David I. Heiman²⁰, Michael C. Heinold^{185,186}, Zachary Heins⁵⁷, Lawrence E. Heisler¹²⁰, Eva Hellstrom-Lindberg³⁷³, Mohamed Helmy³⁷⁴, Seong Gu Heo³⁷⁵, Austin J. Hepperla²⁵, José María Heredia-Genestar³⁷⁶, Carl Herrmann^{185,186,377}, Peter Hersey¹⁸⁸, Julian M. Hess^{20,378}, Holmfridur Hilmarsdottir³⁰¹, Jonathan Hinton¹⁵, Satoshi Hirano³⁷⁹, Nobuyoshi Hiraoka³⁸⁰, Katherine A. Hoadley^{25,26}, Asger Hobolth^{137,351}, Ermin Hodzic²⁸⁵, Jessica I. Hoell¹⁵², Steve Hoffmann^{132,133,134,380,381}, Oliver Hofmann³⁸², Andrea Holbrook¹³⁵, Aliaksei Z. Holik¹⁵⁷, Michael A. Hollingsworth³⁸³, Oliver Holmes^{183,290}, Robert A. Holt⁷², Chen Hong^{178,212}, Eun Pyo Hong³⁷⁵, Jongwhi H. Hong³⁸⁴, Gerrit K. Hooijer³⁸⁵, Henrik Hornshøj¹³⁸, Fumie Hosoda⁴⁵, Yong Hou^{323,386},

Volker Hovestadt³⁸⁷, William Howat³³⁸, Alan P. Hoyle²⁵, Ralph H. Hruban¹¹⁷, Jianhong Hu²⁴⁴, Taobo Hu³⁸⁸, Xing Hua²¹⁵, Kuan-lin Huang^{86,389}, Mei Huang¹⁴⁶, Mi Ni Huang^{149,150}, Vincent Huang¹, Yi Huang^{390,391}, Wolfgang Huber¹⁹⁹, Thomas J. Hudson^{250,392}, Michael Hummel³⁹³, Jillian A. Hung^{221,222}, David Huntsman³⁹⁴, Ted R. Hupp³⁹⁵, Jason Huse⁵⁷, Matthew R. Huska³⁹⁶, Barbara Hutter^{141,180,397}, Carolyn M. Hutter³⁴⁸, Daniel Hübschmann^{186,296,398,399,400}, Christine A. Iacobuzio-Donahue³³⁴, Charles David Imbusch¹⁷⁸, Marcin Imielinski^{401,402}, Seiya Imoto³⁶³, William B. Isaacs⁴⁰³, Keren Isaev^{1,2}, Shumpei Ishikawa⁴⁰⁴, Murat Iskar³⁸⁷, S. M. Ashiqul Islam²¹⁹, Michael Ittmann^{405,406,407}, Sinisa Ivkovic²⁵⁹, Jose M. G. Izarzugaza⁴⁰⁸, Jocelyne Jacquemier⁴⁰⁹, Valerie Jakrot¹⁸⁸, Nigel B. Jamieson^{11,14,410}, Gun Ho Jang¹¹⁶, Se Jin Jang⁴¹¹, Joy C. Jayaseelan²⁴⁴, Reyka Jayasinghe⁸⁶, Stuart R. Jefferys²⁵, Karine Jegalian⁴¹², Jennifer L. Jennings⁴¹³, Seung-Hyup Jeon²²⁵, Lara Jerman^{199,414}, Yuan Ji^{415,416}, Wei Jiao¹, Peter A. Johansson²⁹⁰, Amber L. Johns¹², Jeremy Johns²⁵⁰, Rory Johnson^{205,417}, Todd A. Johnson¹⁵³, Clemency Jolly²⁶⁵, Yann Joly⁴¹⁸, Jon G. Jonasson³⁰¹, Corbin D. Jones⁴¹⁹, David R. Jones¹⁵, David T. W. Jones^{420,421}, Nic Jones⁴²², Steven J. M. Jones⁷², Jos Jonkers¹⁷⁵, Young Seok Ju^{15,224}, Hartmut Juhl⁴²³, Jongsun Jung⁴²⁴, Malene Juul¹³⁸, Randi Istrup Juul¹³⁸, Sissel Juul³⁶², Natalie Jäger¹⁸⁵, Rolf Kabbe¹⁸⁵, Andre Kahles^{254,255,256,257,425}, Abdullah Kahraman^{426,427,428}, Vera B. Kaiser²⁷, Hojabr Kakavand¹⁸⁸, Sangeetha Kalimuthu¹¹⁶, Christof von Kalle³⁹⁹, Koo Jeong Kang⁶⁰, Katalin Karasz³³⁷, Beth Karlan⁴²⁹, Rosa Karlic²⁸, Dennis Karsch⁴³⁰, Katayoon Kasaian⁷², Karin S. Kassahn^{81,431}, Hitoshi Katai⁴³², Mamoru Kato²⁹, Hiroto Katoh⁴⁰⁴, Yoshiiku Kawakami⁶², Jonathan D. Kay⁸⁷, Stephen H. Kazakoff^{183,290}, Marat D. Kazanov^{433,434,435}, Maria Keays¹¹⁰, Electron Kebebew^{436,437}, Richard F. Kefford⁴³⁸, Manolis Kellis^{20,439}, James G. Kench^{12,336,440}, Catherine J. Kennedy^{221,222}, Jules N. A. Kerssemakers¹⁸⁵, David Khoo²⁵¹, Vincent Khoo¹⁹⁸, Narong Khuntikeo^{83,441}, Ekta Khurana^{277,278,442,42}, Helena Kilpinen⁸⁷, Hark Kyun Kim⁴⁴³, Hyung-Lae Kim⁴⁴⁴, Hyung-Yong Kim⁴⁰⁹, Hyunghwan Kim²²⁵, Jaegil Kim²⁰, Jihoon Kim⁴⁴⁵, Jong K. Kim⁴⁴⁶, Youngwook Kim^{447,448}, Tari A. King^{449,450,451}, Wolfram Klapper⁹⁵, Kortine Kleinheinz^{185,186}, Leszek J. Klimczak⁴⁵², Stian Knappskog^{15,453}, Michael Kneba⁴³⁰, Bartha M. Knoppers⁴¹⁸, Youngil Koh^{454,455}, Jan Komorowski^{281,456}, Daisuke Komura⁴⁰⁴, Mitsuhiro Komura³⁶³, Gu Kong⁴⁰⁹, Marcel Kool^{420,457}, Jan O. Korbel^{110,199}, Viktoriya Korchina²⁴⁴, Andrey Korshunov⁴⁵⁷, Michael Koscher⁴⁵⁷, Roelof Koster⁴⁵⁸, Zsofia Kote-Jarai¹⁴⁸, Antonios Koures²¹⁹, Milena Kovacevic²⁵⁹, Barbara Kremeyer¹⁵, Helene Kretzmer^{133,134}, Markus Kreuz⁴⁵⁹, Savitri Krishnamurthy^{30,460}, Dieter Kube⁴⁶¹, Kiran Kumar²⁰, Pardeep Kumar¹⁹⁸, Sushant Kumar^{332,333}, Yogesh Kumar³⁸⁸, Ritika Kundra^{82,90}, Kirsten Kübler^{20,21,143}, Ralf Küppers⁴⁶², Jesper Lagergren^{373,463}, Phillip H. Lai¹³⁵, Peter W. Laird⁴⁶⁴, Sunil R. Lakhani⁴⁶⁵, Christopher M. Lalansingh¹, Emilie Lalonde¹, Fabien C. Lamaze¹, Adam Lambert³³⁷, Eric Lander²⁰, Pablo Landgraf^{466,467}, Luca Landoni⁸³, Anita Langerød⁹⁷, Andrés Lanzós^{205,206,417}, Denis Larsimont⁴⁶⁸, Erik Larsson⁴⁶⁹, Mark Lathrop¹⁶⁰, Loretta M. S. Lau⁴⁷⁰, Chris Lawerenz²⁹⁷, Rita T. Lawlor¹⁴⁷, Michael S. Lawrence^{20,143,153}, Alexander J. Lazar^{30,31}, Xuan Le⁴⁷¹, Darlene Lee⁷², Donghoon Lee³³³, Eunjung Alice Lee⁴⁷², Hee Jin Lee⁴¹¹, Jake June-Koo Lee^{241,243}, Jeong-Yeon Lee⁴⁷³, Juhee Lee⁴⁷⁴, Ming Ta Michael Lee³²¹, Henry Lee-Six¹⁵, Kjong-Van Lehmann^{254,255,256,257,425}, Hans Lehrach⁴⁷⁵, Dido Lenze³⁹³, Conrad R. Leonard^{183,290}, Daniel A. Leongamornlert^{15,148}, Ignaty Leshchiner²⁰, Louis Letourneau⁴⁷⁶, Ivica Letunic⁴⁷⁷, Douglas A. Levine^{57,478}, Lora Lewis²⁴⁴, Tim Ley⁴⁷⁹, Chang Li^{323,386}, Constance H. Li^{1,2}, Haiyan Irene Li⁷², Jun Li⁶³, Lin Li³²³, Shantao Li³³³, Siliang Li^{323,386}, Xiaobo Li^{323,386}, Xiaotong Li³³³, Xinyue Li³²³, Yilong Li¹⁵, Han Liang⁶³, Sheng-Ben Liang²⁰⁹, Peter Lichter^{387,397}, Pei Lin²⁰, Ziao Lin^{20,480}, W. M. Linehan⁴⁸¹, Ole Christian Lingjærde⁴⁸², Dongbing Liu^{323,386}, Eric Minwei Liu^{57,277,278}, Fei-Fei Liu^{172,483}, Fenglin Liu^{370,484}, Jia Liu^{58,109,485}, Xingmin Liu^{323,386}, Julie Livingstone¹, Dimitri Livitz²⁰, Naomi Livni¹⁹⁸, Lucas Lochovsky^{79,332,333}, Markus Loeffler⁴⁵⁹, Georgina V. Long¹⁸⁸, Armando Lopez-Guillermo³³, Shaoke Lou^{332,333}, David N. Louis¹⁴³,

Laurence B. Lovat⁸⁷, Yiling Lu³⁷², Yong-Jie Lu^{131,486}, Youyong Lu^{487,488,489}, Claudio Luchini¹³⁶, Ilinca Lungu^{111,116}, Xuemei Luo¹²⁰, Hayley J. Luxton⁸⁷, Andy G. Lynch^{53,294,490}, Lisa Lype⁴⁹¹, Cristina López^{80,47}, Carlos López-Otín⁴⁹², Eric Z. Ma³⁸⁸, Yussanne Ma⁷², Gaetan MacGrogan⁴⁹³, Shona MacRae⁴⁹⁴, Geoff Macintyre⁵³, Tobias Madsen¹³⁸, Kazuhiro Maejima¹⁵⁴, Andrea Mafficini¹⁴⁷, Dennis T. Maglinte^{135,495}, Arindam Maitra¹⁴⁴, Partha P. Majumder¹⁴⁴, Luca Malcovati²⁰⁷, Salem Malikic^{236,285}, Giuseppe Malleo⁸³, Graham J. Mann^{188,221,496}, Luisa Mantovani-Löffler⁴⁹⁷, Kathleen Marchal^{498,499}, Giovanni Marchegiani⁸³, Elaine R. Mardis^{86,164,500}, Adam A. Margolin³², Maximillian G. Marin¹⁷⁶, Florian Markowetz^{53,294}, Julia Markowski³⁹⁶, Jeffrey Marks⁵⁰¹, Tomas Marques-Bonet^{50,376,502,503}, Marco A. Marra⁷², Luke Marsden³³⁷, John W. M. Martens³¹³, Sancha Martin^{15,54}, Jose I. Martin-Subero^{503,504}, Iñigo Martincorena¹⁵, Alexander Martinez-Fundichely^{277,278,42}, Yosef E. Maruvka^{20,143,378}, R. Jay Mashl^{86,505}, Charlie E. Massie⁵³, Thomas J. Matthew¹⁷⁶, Lucy Matthews¹⁴⁸, Erik Mayer^{198,506}, Simon Mayes⁵⁰⁷, Michael Mayo⁷², Faridah Mbabaali²⁵⁰, Karen McCune⁵⁰⁸, Ultan McDermott¹⁵, Patrick D. McGillivray³³², Michael D. McLellan^{86,100,282}, John D. McPherson^{116,250,509}, John R. McPherson^{149,150}, Treasa A. McPherson²³⁷, Samuel R. Meier²⁰, Alice Meng⁵¹⁰, Shaowu Meng²⁵, Andrew Menzies¹⁵, Neil D. Merrett^{83,511}, Sue Merson¹⁴⁸, Matthew Meyerson^{20,19,21}, William Meyerson^{333,512}, Piotr A. Mieczkowski⁵¹³, George L. Mihaiescu³⁴, Sanja Mijalkovic²⁵⁹, Ana Mijalkovic Mijalkovic-Lazic²⁵⁹, Tom Mikkelsen⁵¹⁴, Michele Milella²²⁹, Linda Mileskin⁷³, Christopher A. Miller⁸⁶, David K. Miller^{81,12}, Jessica K. Miller²⁵⁰, Gordon B. Mills⁵¹⁵, Ana Milovanovic¹¹², Sarah Minner⁵¹⁶, Marco Miotto⁸³, Gisela Mir Arnau²⁴⁵, Lisa Mirabello²¹⁵, Chris Mitchell⁷³, Thomas J. Mitchell^{15,294,338}, Satoru Miyano³⁶³, Naoki Miyoshi³⁶³, Shinichi Mizuno⁵¹⁷, Fruzsina Molnár-Gábor⁵¹⁸, Malcolm J. Moore²⁷⁶, Richard A. Moore⁷², Sandro Morganella¹⁵, Quaid D. Morris^{5,483}, Carl Morrison^{519,520}, Lisle E. Mose²⁵, Catherine D. Moser³³⁵, Ferran Muiños^{274,275}, Loris Mularoni^{274,275}, Andrew J. Mungall⁷², Karen Mungall⁷², Elizabeth A. Musgrove¹¹, Ville Mustonen^{521,522,523}, David Mutch⁵²⁴, Francesc Muyas^{51,157,267}, Donna M. Muzny²⁴⁴, Alfonso Muñoz¹¹⁰, Jerome Myers⁵²⁵, Ola Myklebost⁴⁵³, Peter Möller⁵²⁶, Genta Nagae⁵⁸, Adnan M. Nagrial¹², Hardeep K. Nahal-Bose³⁴, Hitoshi Nakagama⁵²⁷, Hidewaki Nakagawa¹⁵⁴, Hiromi Nakamura⁴⁵, Toru Nakamura³⁷⁹, Kaoru Nakano¹⁵⁴, Tannistha Nandi⁵²⁸, Jyoti Nangalia¹⁵, Mia Nastic²⁵⁹, Arcadi Navarro^{50,376,502}, Fabio C. P. Navarro³³², David E. Neal^{53,338}, Gerd Nettekoven⁵²⁹, Felicity Newell^{183,290}, Steven J. Newhouse¹¹⁰, Yulia Newton¹⁷⁶, Alvin Wei Tian Ng⁵³⁰, Anthony Ng⁵³¹, Jonathan Nicholson¹⁵, David Nicol¹⁹⁸, Yongzhan Nie^{302,532}, G. Petur Nielsen¹⁴³, Morten Muhlig Nielsen¹³⁸, Serena Nik-Zainal^{15,35,36,37}, Michael S. Noble²⁰, Katia Nones^{183,290}, Paul A. Northcott⁵³³, Faiyaz Notta^{116,534}, Brian D. O'Connor^{34,535}, Peter O'Donnell⁵³⁶, Maria O'Donovan³⁶, Sarah O'Meara¹⁵, Brian Patrick O'Neill⁵³⁷, J. Robert O'Neill⁵³⁸, David Ocana¹¹⁰, Angelica Ochoa⁵⁷, Layla Oesper⁵³⁹, Christopher Ogden¹⁹⁸, Hideki Ohdan⁶², Kazuhiro Ohi³⁶³, Lucila Ohno-Machado²¹⁹, Karin A. Oien^{519,540}, Akinyemi I. Ojesina^{541,542,543}, Hidenori Ojima⁵⁴⁴, Takuji Okusaka⁵⁴⁵, Larsson Omberg³⁸, Chovon Kiat Ong^{57,546}, Stephan Ossowski^{51,157,267}, German Ott⁵⁴⁷, B. F. Francis Ouellette^{34,548}, Christine P'ng¹, Marta Paczkowska¹, Salvatore Paiella⁸³, Chawalit Pairojkul⁵¹⁹, Marina Pajic¹², Qiang Pan-Hammarström^{323,549}, Elli Papaemmanuil¹⁵, Irene Papatheodorou¹¹⁰, Nagarajan Paramasivam^{141,185}, Ji Wan Park³⁷⁵, Joong-Won Park⁵⁵⁰, Keunchil Park^{551,552}, Kiejung Park⁵⁵³, Peter J. Park^{241,243}, Joel S. Parker⁵¹³, Simon L. Parsons⁹³, Harvey Pass⁵⁵⁴, Danielle Pasternack²⁵⁰, Alessandro Pastore²⁵⁴, Ann-Marie Patch^{183,290}, Iris Pauporte²²⁶, Antonio Pea⁸³, John V. Pearson^{183,290}, Chandra Sekhar Pedomallu^{20,19,21}, Jakob Skou Pedersen^{138,351}, Paolo Pederzoli⁸³, Martin Peifer²⁴⁸, Nathan A. Pennell⁵⁵⁵, Charles M. Perou^{96,513}, Marc D. Perry^{34,57}, Gloria M. Petersen⁵⁵⁶, Myron Peto⁸⁴, Nicholas Petrelli⁵⁵⁷, Robert Petryszak¹¹⁰, Stefan M. Pfister^{420,457,558}, Mark Phillips⁴¹⁸, Oriol Pich^{274,275}, Hilda A. Pickett⁴⁷⁰, Todd D. Pihl⁵⁵⁹, Nischalan Pillay⁵⁶⁰, Sarah Pinder⁵⁶¹, Mark Pinese¹², Andreia V. Pinho⁵⁶²,

Esa Pitkänen¹⁹⁹, Xavier Pivot⁵⁶³, Elena Piñeiro-Yáñez¹⁹, Laura Planko⁵²⁹, Christoph Plass³²⁸, Paz Polak^{20,21,22}, Tirso Pons⁵⁶⁴, Irinel Popescu⁵⁶⁵, Olga Potapova⁵⁶⁶, Aparna Prasad⁵¹, Shaun R. Preston⁵⁶⁷, Manuel Prinz¹⁸⁵, Antonia L. Pritchard²⁹⁰, Elena Provenzano⁵⁶⁸, Xose S. Puente⁴⁹², Sonia Puig¹⁴⁶, Montserrat Puiggròs¹¹², Sergio Pulido-Tamayo^{498,499}, Gulietta M. Pupo²²¹, Colin A. Purdie⁵⁶⁹, Michael C. Quinn^{183,290}, Raquel Rabionet^{51,157,570}, Janet S. Rader⁵⁷¹, Bernhard Radlwimmer³⁸⁷, Petar Radovic²⁵⁹, Benjamin Raeder¹⁹⁹, Keiran M. Raine¹⁵, Manasa Ramakrishna¹⁵, Kamna Ramakrishnan¹⁵, Suresh Ramalingam⁵⁷², Benjamin J. Raphael⁵⁷³, W. Kimryn Rathmell⁵⁷⁴, Tobias Rausch¹⁹⁹, Guido Reifenberger⁴⁶⁷, Jüri Reimand^{1,2}, Jorge Reis-Filho³³⁴, Victor Reuter³³⁴, Iker Reyes-Salazar²⁷⁴, Matthew A. Reyna⁵⁷³, Sheila M. Reynolds⁴⁹¹, Esther Rheinbay^{20,21,143}, Yasser Riazalhosseini¹⁶⁰, Andrea L. Richardson³⁰⁴, Julia Richter^{80,95}, Matthew Ringel⁵⁷⁵, Markus Ringné¹⁵¹, Yasushi Rino⁵⁷⁶, Karsten Rippe³⁹⁹, Jeffrey Roach⁵⁷⁷, Lewis R. Roberts³³⁵, Nicola D. Roberts¹⁵, Steven A. Roberts⁵⁷⁸, A. Gordon Robertson⁷², Alan J. Robertson⁸¹, Javier Bartolomé Rodríguez¹¹², Bernardo Rodríguez-Martin^{74,75,76}, F. Germán Rodríguez-González^{313,579}, Michael H. A. Roehrl^{2,92,116,209,580,581}, Marius Rohde⁵⁸², Hirofumi Rokutan²⁹, Gilles Romieu⁵⁸³, Ilse Rooman¹², Tom Roques²³⁹, Daniel Rosebrock²⁰, Mara Rosenberg^{20,143}, Philip C. Rosenstiel⁵⁸⁴, Andreas Rosenwald⁵⁸⁵, Edward W. Rowe^{198,586}, Romina Royo¹¹², Steven G. Rozen^{149,150,587}, Yulia Rubanova^{5,588}, Mark A. Rubin^{417,41,589,43,44}, Carlota Rubio-Perez^{274,275,590}, Vasilisa A. Rudneva¹⁹⁹, Borislav C. Rusev¹⁴⁷, Andrea Ruzzenente⁵⁹¹, Gunnar Rättsch^{18,254,255,256,257,425}, Radhakrishnan Sabarinathan^{274,275,592}, Veronica Y. Sabelnykova¹, Sara Sadeghi⁷², S. Cenk Sahinalp^{236,285,593}, Natalie Saini³⁴³, Mihoko Saito-Adachi²⁹, Gordon Saksena²⁰, Adriana Salcedo¹, Roberto Salgado⁵⁹⁴, Leonidas Salichos^{332,333}, Richard Sallari²⁰, Charles Saller⁵⁹⁵, Roberto Salvia⁸³, Michelle Sam²⁵⁰, Jaswinder S. Samra^{83,596}, Francisco Sanchez-Vega^{82,90}, Chris Sander^{254,597,598}, Grant Sanders²⁵, Rajiv Sarin⁵⁹⁹, Iman Sarrafi^{236,285}, Aya Sasaki-Oku¹⁵⁴, Torill Sauer⁴⁸², Guido Sauter⁵¹⁶, Robyn P. M. Saw¹⁸⁸, Maria Scardoni¹³⁶, Christopher J. Scarlett^{112,600}, Aldo Scarpa¹⁴⁷, Ghislaine Scelo¹⁶⁵, Dirk Schadendorf^{397,601}, Jacqueline E. Schein⁷², Markus B. Schilhabel⁵⁸⁴, Matthias Schlesner^{185,602}, Thorsten Schlomm^{603,604}, Heather K. Schmidt⁸⁶, Sarah-Jane Schramm²²¹, Stefan Schreiber⁶⁰⁵, Nikolaus Schultz⁹⁰, Steven E. Schumacher^{20,304}, Roland F. Schwarz^{110,396,399,606}, Richard A. Scolyer^{188,440,596}, David Scott⁴²², Ralph Scully⁶⁰⁷, Raja Seethala⁶⁰⁸, Ayellet V. Segre^{20,609}, Iris Selander²³⁷, Colin A. Semple²⁷, Yasin Senbabaoglu²⁵⁴, Subhjit Sengupta⁶¹⁰, Elisabetta Sereni⁸³, Stefano Serra⁵⁸⁰, Dennis C. Sgroi¹⁴³, Mark Shackleton⁷³, Nimish C. Shah³³⁸, Sagedeh Shahabi²⁰⁹, Catherine A. Shang³¹⁰, Ping Shang¹⁸⁸, Ofer Shapira^{20,20,304}, Troy Shelton²⁴⁹, Ciyue Shen^{597,598}, Hui Shen⁶¹¹, Rebecca Shepherd¹⁵, Ruian Shi⁴⁸³, Yan Shi²⁵, Yu-Jia Shiah¹, Tatsuhiro Shibata^{45,612}, Juliann Shih^{20,19}, Eigo Shimizu³⁶³, Kiyo Shimizu⁶¹³, Seung Jun Shin⁶¹⁴, Yuichi Shiraishi³⁶³, Tal Shmaya²⁶⁰, Ilya Shmulevich⁴⁹¹, Solomon I. Shorser¹, Charles Short¹¹⁰, Raunak Shrestha²³⁶, Suyash S. Shringarpure¹⁹⁴, Craig Shriver⁶¹⁵, Shimin Shuai^{1,10}, Nikos Sidiropoulos⁵⁷⁹, Reiner Siebert^{47,10}, Anieta M. Sieuwerts³¹³, Lina Sieverling^{178,212}, Sabina Signoretti^{173,94}, Katarzyna O. Sikora¹⁴⁷, Michele Simbolo¹⁰⁴, Ronald Simon⁵¹⁶, Janae V. Simons²⁵, Jared T. Simpson^{1,588}, Peter T. Simpson⁴⁶⁵, Samuel Singer^{83,450}, Nasa Sinnott-Armstrong^{20,194}, Payal Sipahimalani⁷², Tara J. Skelly²⁶, Marcel Smid³¹³, Jaclyn Smith⁵, Karen Smith-McCune⁵⁰⁸, Nicholas D. Succi²⁵⁴, Heidi J. Sofia³⁴⁸, Matthew G. Soloway²⁵, Lei Song²¹⁵, Anil K. Sood^{616,617,618}, Sharmila Sothi⁶¹⁹, Christos Sotiriou²¹⁹, Cameron M. Soulette¹⁷⁶, Paul N. Span⁶²⁰, Paul T. Spellman⁸⁴, Nicola Sperandio¹⁴⁷, Andrew J. Spillane¹⁸⁸, Oliver Spiro²⁰, Jonathan Spring⁶²¹, Johan Staaf¹⁵¹, Peter F. Stadler^{132,133,134}, Peter Staib⁶²², Stefan G. Stark^{255,257,614,623}, Lucy Stebbings¹⁵, Ólafur Andri Stefánsson⁶²⁴, Oliver Stegle^{110,199,625}, Lincoln D. Stein^{1,10}, Alasdair Stenhouse⁶²⁶, Chip Stewart²⁰, Stephan Stilgenbauer⁶²⁷, Miranda D. Stobbe^{50,51}, Michael R. Stratton¹⁵, Jonathan R. Stretch¹⁸⁸, Adam J. Struck³², Joshua M. Stuart^{176,177}, Henk G. Stunnenberg^{386,628}, Hong Su^{323,386}, Xiaoping Su³⁰, Ren X. Sun¹,

Stephanie Sungalee¹⁹⁹, Hana Susak^{51,157}, Akihiro Suzuki^{58,629}, Fred Sweep⁶³⁰, Monika Szczepanowski⁹⁵, Holger Sültmann^{180,631}, Takashi Yugawa⁶¹³, Angela Tam⁷², David Tamborero^{274,275}, Benita Kiat Tee Tan⁶³², Donghui Tan⁵¹³, Patrick Tan^{150,528,587,633}, Hiroko Tanaka³⁶³, Hirokazu Taniguchi⁶¹², Tomas J. Tanskanen⁶³⁴, Maxime Tarabichi^{15,265}, Roy Tarnuzzer¹⁹⁷, Patrick Tarpey⁶³⁵, Morgan L. Taschuk¹²⁰, Kenji Tatsuno⁵⁸, Simon Tavaré^{53,636}, Darrin F. Taylor⁸¹, Amaro Taylor-Weiner²⁰, Jon W. Teague¹⁵, Bin Tean Teh^{150,587,633,637,638}, Varsha Tembe²²¹, Javier Temes^{74,75}, Kevin Thai³⁴, Sarah P. Thayer³⁸³, Nina Thiessen⁷², Gilles Thomas⁶³⁹, Sarah Thomas¹⁹⁸, Alan Thompson¹⁹⁸, Alastair M. Thompson⁶²⁶, John F. Thompson¹⁸⁸, R. Houston Thompson⁶⁴⁰, Heather Thorne⁷³, Leigh B. Thorne¹⁴⁶, Adrian Thorogood⁴¹⁸, Grace Tiao²⁰, Nebojsa Tijanic²⁵⁹, Lee E. Timms²⁵⁰, Roberto Tirabosco⁶⁴¹, Marta Tojo⁷⁶, Stefania Tommasi⁶⁴², Christopher W. Toon¹², Umut H. Toprak^{186,643}, David Torrents^{112,502}, Giampaolo Tortora^{644,645}, Jörg Tost⁶⁴⁶, Yasushi Totoki⁴⁵, David Townend⁶⁴⁷, Nadia Traficante⁷³, Isabelle Treilleux^{648,649}, Jean-Rémi Trotta⁵⁰, Lorenz H. P. Trümper⁴⁶¹, Ming Tsao^{93,534}, Tatsuhiko Tsunoda^{153,650,651,652}, Jose M. C. Tubio^{74,75,76}, Olga Tucker⁶⁵³, Richard Turkington⁶⁵⁴, Daniel J. Turner⁵⁰⁷, Andrew Tutt³⁰⁴, Masaki Ueno³⁶⁵, Naoto T. Ueno⁶⁵⁵, Christopher Umbricht^{119,190,656}, Husen M. Umer^{281,657}, Timothy J. Underwood⁶⁵⁸, Lara Urban^{110,199}, Tomoko Urushidate⁶¹², Tetsuo Ushiku³²⁰, Liis Uusküla-Reimand^{659,660}, Alfonso Valencia^{112,502}, David J. Van Den Berg¹³⁵, Steven Van Laere²⁸⁴, Peter Van Loo^{265,266}, Erwin G. Van Meir⁶⁶¹, Gert G. Van den Eynden²⁸⁴, Theodorus Van der Kwast⁹², Naveen Vasudev¹⁰³, Miguel Vazquez^{112,662}, Ravikiran Veduru²⁴⁵, Umadevi Veluvolu⁵¹³, Shankar Vembu^{483,663}, Lieven P. C. Verbeke^{499,664}, Peter Vermeulen²⁸⁴, Clare Verrill^{337,665}, Alain Viari¹⁴⁷, David Vicente¹¹², Caterina Vicentini¹⁴⁷, K. Vijay Raghavan³⁵², Juris Viksna⁶⁶⁶, Ricardo E. Vilain⁶⁶⁷, Izar Villasante¹¹², Anne Vincent-Salomon⁶²⁸, Tapio Visakorpi¹⁶¹, Douglas Voet²⁰, Paresh Vyas^{290,337}, Ignacio Vázquez-García^{15,668,669,670}, Nick M. Waddell¹⁸³, Nicola Waddell^{183,290}, Claes Wadelius⁶⁷¹, Lina Wadi¹, Rabea Wagener^{80,47}, Jeremiah A. Wala^{20,19,21}, Jian Wang³²³, Jiayin Wang^{86,391,672}, Linghua Wang²⁴⁴, Qi Wang⁴⁵⁷, Wenyi Wang⁶³, Yumeng Wang⁶³, Zhining Wang¹⁹⁷, Paul M. Waring⁵¹⁹, Hans-Jörg Warnatz⁴⁷⁵, Jonathan Warrell^{332,333}, Anne Y. Warren^{338,673}, Sebastian M. Waszak¹⁹⁹, David C. Wedge^{15,270,674}, Dieter Weichenhan³²⁸, Paul Weinberger⁶⁷⁵, John N. Weinstein³⁷², Joachim Weischenfeldt^{199,579,603}, Daniel J. Weisenberger¹³⁵, Ian Welch⁶⁷⁶, Michael C. Wendl^{86,282,677}, Johannes Werner^{185,678}, Justin P. Whalley^{50,679}, David A. Wheeler^{244,680}, Hayley C. Whitaker⁸⁷, Dennis Wigle⁶⁸¹, Matthew D. Wilkerson⁵¹³, Ashley Williams²¹⁹, James S. Wilmott¹⁸⁸, Gavin W. Wilson^{1,116}, Julie M. Wilson¹¹⁶, Richard K. Wilson^{86,682}, Boris Winterhoff⁶⁸³, Jeffrey A. Wintersinger^{5,374,588}, Maciej Wiznerowicz^{684,685}, Stephan Wolf⁶⁸⁶, Bernice H. Wong⁶⁸⁷, Tina Wong^{72,86}, Winghing Wong⁶⁸⁸, Youngchoon Woo²²⁵, Scott Wood^{183,290}, Bradley G. Wouters², Adam J. Wright¹, Derek W. Wright^{11,97}, Mark H. Wright¹⁹⁴, Chin-Lee Wu¹⁴³, Dai-Ying Wu²⁶⁰, Guanming Wu⁶⁸⁹, Jianmin Wu¹², Kui Wu^{323,386}, Yang Wu^{149,150}, Zhenggang Wu³⁸⁸, Liu Xi²⁴⁴, Tian Xia⁶⁹⁰, Qian Xiang³⁴, Xiao Xiao³⁹¹, Rui Xing⁴⁸⁹, Heng Xiong^{323,386}, Qinying Xu^{183,290}, Yanxun Xu⁶⁹¹, Hong Xue³⁸⁸, Shinichi Yachida^{45,692}, Sergei Yakneen¹⁹⁹, Rui Yamaguchi³⁶³, Takafumi N. Yamaguchi¹, Masakazu Yamamoto⁸⁹, Shogo Yamamoto⁵⁸, Hiroki Yamaue³⁶⁵, Fan Yang⁴⁸³, Huanming Yang³²³, Jean Y. Yang⁶⁹³, Liming Yang¹⁹⁷, Lixing Yang⁶⁹⁴, Shanlin Yang²⁸³, Tsun-Po Yang²⁴⁸, Yang Yang³⁵⁷, Xiaotong Yao^{402,695}, Marie-Laure Yaspo⁴⁷⁵, Lucy Yates¹⁵, Christina Yau¹²⁵, Chen Ye^{323,386}, Kai Ye^{672,696}, Venkata D. Yellapantula^{282,669}, Christopher J. Yoon²²⁴, Sung-Soo Yoon⁴⁵⁵, Jun Yu⁶⁹⁷, Kaixian Yu⁶⁹⁸, Willie Yu⁶⁹⁹, Yingyan Yu⁷⁰⁰, Ke Yuan^{53,54,55}, Yuan Yuan⁶³, Denis Yuen¹, Takashi Yugawa⁶¹³, Christina K. Yung³⁴, Olga Zaikova⁷⁰¹, Jorge Zamora^{15,74,75,76}, Marc Zapatka³⁸⁷, Jean C. Zenklusen¹⁹⁷, Thorsten Zenz¹⁸⁰, Nikolajs Zeps^{702,703}, Cheng-Zhong Zhang^{20,704}, Fan Zhang³⁷⁰, Hailei Zhang²⁰, Hongwei Zhang⁴⁸⁶, Hongxin Zhang⁹⁰, Jiashan Zhang¹⁹⁷, Jing Zhang³³³, Junjun Zhang³⁴, Xiuqing Zhang³²³,

Xuanping Zhang^{357,391}, Yan Zhang^{333,705,706}, Zemin Zhang^{370,707}, Zhongming Zhao⁷⁰⁸, Liangtao Zheng³⁷⁰, Xiuqing Zheng³⁷⁰, Wanding Zhou⁶¹¹, Yong Zhou³²³, Bin Zhu²¹⁵, Hongtu Zhu^{698,709}, Jingchun Zhu¹⁷⁷, Shida Zhu^{323,386}, Lihua Zou⁷¹⁰, Xueqing Zou¹⁵, Anna deFazio^{221,222,711}, Nicholas van As¹⁹⁸, Carolien H. M. van Deurzen⁷¹², Marc J. van de Vijver⁵¹⁹, L. van't Veer⁷¹³ & Christian von Mering^{428,714}

⁵⁶Applied Tumor Genomics Research Program, Research Programs Unit, University of Helsinki, Helsinki, Finland. ⁵⁷Memorial Sloan Kettering Cancer Center, New York, NY, USA. ⁵⁸Genome Science Division, Research Center for Advanced Science and Technology, University of Tokyo, Tokyo, Japan. ⁵⁹Department of Surgery, University of Chicago, Chicago, IL, USA. ⁶⁰Department of Surgery, Division of Hepatobiliary and Pancreatic Surgery, School of Medicine, Keimyung University Dongsan Medical Center, Daegu, South Korea. ⁶¹Department of Oncology, Gil Medical Center, Gachon University, Incheon, South Korea. ⁶²Hiroshima University, Hiroshima, Japan. ⁶³Department of Bioinformatics and Computational Biology, The University of Texas MD Anderson Cancer Center, Houston, TX, USA. ⁶⁴University of Texas MD Anderson Cancer Center, Houston, TX, USA. ⁶⁵King Faisal Specialist Hospital and Research Centre, Al Maather, Riyadh, Saudi Arabia. ⁶⁶Bioinformatics Core Facility, University Medical Center Hamburg, Hamburg, Germany. ⁶⁷Heinrich Pette Institute, Leibniz Institute for Experimental Virology, Hamburg, Germany. ⁶⁸Ontario Tumour Bank, Ontario Institute for Cancer Research, Toronto, ON, Canada. ⁶⁹Laboratory of Pathology, Center for Cancer Research, National Cancer Institute, Bethesda, MD, USA. ⁷⁰Department of Cellular and Molecular Medicine and Department of Bioengineering, University of California San Diego, La Jolla, CA, USA. ⁷¹UC San Diego Moores Cancer Center, San Diego, CA, USA. ⁷²Canada's Michael Smith Genome Sciences Centre, BC Cancer, Vancouver, BC, Canada. ⁷³Sir Peter MacCallum Department of Oncology, Peter MacCallum Cancer Centre, University of Melbourne, Melbourne, VIC, Australia. ⁷⁴Centre for Research in Molecular Medicine and Chronic Diseases (CiMUS), Universidade de Santiago de Compostela, Santiago de Compostela, Spain. ⁷⁵Department of Zoology, Genetics and Physical Anthropology, (CiMUS), Universidade de Santiago de Compostela, Santiago de Compostela, Spain. ⁷⁶The Biomedical Research Centre (CINBIO), Universidade de Vigo, Vigo, Spain. ⁷⁷Royal National Orthopaedic Hospital - Bolsover, London, UK. ⁷⁸Quantitative and Computational Biosciences Graduate Program, Baylor College of Medicine, Houston, TX, USA. ⁷⁹The Jackson Laboratory for Genomic Medicine, Farmington, CT, USA. ⁸⁰Institute of Human Genetics, Christian-Albrechts-University, Kiel, Germany. ⁸¹Queensland Centre for Medical Genomics, Institute for Molecular Bioscience, University of Queensland, St. Lucia, Brisbane, QLD, Australia. ⁸²Salford Royal NHS Foundation Trust, Salford, UK. ⁸³Department of Surgery, Pancreas Institute, University and Hospital Trust of Verona, Verona, Italy. ⁸⁴Molecular and Medical Genetics, OHSU Knight Cancer Institute, Oregon Health and Science University, Portland, OR, USA. ⁸⁵Department of Molecular Oncology, BC Cancer Research Centre, Vancouver, BC, Canada. ⁸⁶The McDonnell Genome Institute at Washington University, St. Louis, MO, USA. ⁸⁷University College London, London, UK. ⁸⁸DLR Project Management Agency, Bonn, Germany. ⁸⁹Tokyo Women's Medical University, Tokyo, Japan. ⁹⁰Center for Molecular Oncology, Memorial Sloan Kettering Cancer Center, New York, NY, USA. ⁹¹Los Alamos National Laboratory, Los Alamos, NM, USA. ⁹²Department of Pathology, University Health Network, Toronto General Hospital, Toronto, ON, Canada. ⁹³Nottingham University Hospitals NHS Trust, Nottingham, UK. ⁹⁴Epigenomics and Cancer Risk Factors, German Cancer Research Center (DKFZ), Heidelberg, Germany. ⁹⁵Hematopathology Section, Institute of Pathology, Christian-Albrechts-University, Kiel, Germany. ⁹⁶Department of Pathology and Laboratory Medicine, School of Medicine, University of North Carolina at Chapel Hill, Chapel Hill, NC, USA. ⁹⁷Department of Cancer Genetics, Institute for Cancer Research, Oslo University Hospital, The Norwegian Radium Hospital, Oslo, Norway. ⁹⁸Pathology, Hospital Clinic, Institut d'Investigacions Biomediques August Pi i Sunyer (IDIBAPS), University of Barcelona, Barcelona, Spain. ⁹⁹Department of Veterinary Medicine, Transmissible Cancer Group, University of Cambridge, Cambridge, UK. ¹⁰⁰Alvin J. Siteman Cancer Center, Washington University School of Medicine, St. Louis, MO, USA. ¹⁰¹Dana-Farber/Boston Children's Cancer and Blood Disorders Center, Boston, MA, USA. ¹⁰²Department of Pediatrics, Harvard Medical School, Boston, MA, USA. ¹⁰³Leeds Institute of Medical Research @ St. James's University of Leeds, St. James's University Hospital, Leeds, UK. ¹⁰⁴Department of Pathology and Diagnostics, University and Hospital Trust of Verona, Verona, Italy. ¹⁰⁵Department of Surgery, Princess Alexandra Hospital, Brisbane, QLD, Australia. ¹⁰⁶Surgical Oncology Group, Diamantina Institute, University of Queensland, Brisbane, QLD, Australia. ¹⁰⁷Department of Population and Quantitative Health Sciences, Case Western Reserve University School of Medicine, Cleveland, OH, USA. ¹⁰⁸Research Health Analytics and Informatics, University Hospitals Cleveland Medical Center, Cleveland, OH, USA. ¹⁰⁹Gloucester Royal Hospital, Gloucester, UK. ¹¹⁰European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI), Cambridge, UK. ¹¹¹Diagnostic Development, Ontario Institute for Cancer Research, Toronto, ON, Canada. ¹¹²Barcelona Supercomputing Center (BSC), Barcelona, Spain. ¹¹³Arnie Charbonneau Cancer Institute, University of Calgary, Calgary, AB, Canada. ¹¹⁴Departments of Surgery and Oncology, University of Calgary, Calgary, AB, Canada. ¹¹⁵Department of Pathology, Oslo University Hospital, The Norwegian Radium Hospital, Oslo, Norway. ¹¹⁶PanCuRx Translational Research Initiative, Ontario Institute for Cancer Research, Toronto, ON, Canada. ¹¹⁷Department of Oncology, Sidney Kimmel Comprehensive Cancer Center at Johns Hopkins University School of Medicine, Baltimore, MD, USA. ¹¹⁸University Hospital Southampton NHS Foundation Trust, Southampton, UK. ¹¹⁹Royal Stoke University Hospital, Stoke-on-Trent, UK. ¹²⁰Genome Sequence Informatics, Ontario Institute for Cancer Research, Toronto, ON, Canada. ¹²¹Human Longevity Inc, San Diego, CA, USA. ¹²²Olivia Newton-John Cancer Research Institute, La Trobe University, Heidelberg, VIC, Australia. ¹²³Computer Network Information Center, Chinese Academy of Sciences, Beijing, China. ¹²⁴Genome Canada, Ottawa, ON, Canada. ¹²⁵Buck Institute for Research on Aging, Novato, CA, USA. ¹²⁶Duke University Medical Center, Durham, NC, USA. ¹²⁷Department of Human Genetics, Hannover Medical School, Hannover, Germany. ¹²⁸Center for Bioinformatics and Functional Genomics, Cedars-Sinai Medical Center, Los Angeles, CA, USA. ¹²⁹Department of Biomedical Sciences, Cedars-Sinai Medical Center, Los Angeles, CA, USA. ¹³⁰The Hebrew University Faculty of Medicine, Jerusalem, Israel. ¹³¹Barts Cancer Institute, Barts and the London School of Medicine and Dentistry, Queen Mary University of London, London, UK. ¹³²Department of Computer Science, Bioinformatics Group, University of Leipzig, Leipzig, Germany. ¹³³Interdisciplinary Center for Bioinformatics, University of Leipzig, Leipzig, Germany. ¹³⁴Transcriptome Bioinformatics, LIFE Research Center for Civilization Diseases, University of Leipzig, Leipzig, Germany. ¹³⁵USC Norris Comprehensive Cancer Center, University of Southern California, Los Angeles, CA, USA. ¹³⁶Department of Diagnostics and Public Health, University and Hospital Trust of Verona, Verona, Italy. ¹³⁷Department of Mathematics, Aarhus University, Aarhus, Denmark. ¹³⁸Department of Molecular Medicine (MOMA), Aarhus University Hospital, Aarhus N, Denmark. ¹³⁹Instituto Carlos Slim de la Salud, Mexico City, Mexico. ¹⁴⁰Center for Digital Health, Berlin Institute of Health and Charité - Universitätsmedizin Berlin, Berlin, Germany. ¹⁴¹Heidelberg Center for Personalized Oncology (DKFZ-HIPO), German Cancer Research Center (DKFZ), Heidelberg, Germany. ¹⁴²The Preston Robert Tisch Brain Tumor Center, Duke University Medical Center, Durham, NC, USA. ¹⁴³Massachusetts General Hospital, Boston, MA, USA. ¹⁴⁴National Institute of Biomedical Genomics, Kalyani, West Bengal, India. ¹⁴⁵Institute of Clinical Medicine and Institute of Oral Biology, University of Oslo, Oslo, Norway. ¹⁴⁶University of North Carolina at Chapel Hill, Chapel Hill, NC, USA. ¹⁴⁷ARC-Net Centre for Applied Research on Cancer, University and Hospital Trust of Verona, Verona, Italy. ¹⁴⁸The Institute of Cancer Research, London, UK. ¹⁴⁹Centre for Computational Biology, Duke-NUS Medical School,

Singapore, Singapore. ¹⁵⁰Programme in Cancer and Stem Cell Biology, Duke-NUS Medical School, Singapore, Singapore. ¹⁵¹Division of Oncology and Pathology, Department of Clinical Sciences Lund, Lund University, Lund, Sweden. ¹⁵²Department of Pediatric Oncology, Hematology and Clinical Immunology, Heinrich-Heine-University, Düsseldorf, Germany. ¹⁵³Laboratory for Medical Science Mathematics, RIKEN Center for Integrative Medical Sciences, Yokohama, Japan. ¹⁵⁴RIKEN Center for Integrative Medical Sciences, Yokohama, Japan. ¹⁵⁵Department of Internal Medicine/Hematology, Friedrich-Ebert-Hospital, Neumünster, Germany. ¹⁵⁶Departments of Dermatology and Pathology, Yale University, New Haven, CT, USA. ¹⁵⁷Centre for Genomic Regulation (CRG), The Barcelona Institute of Science and Technology, Barcelona, Spain. ¹⁵⁸Radcliffe Department of Medicine, University of Oxford, Oxford, UK. ¹⁵⁹Canadian Center for Computational Genomics, McGill University, Montreal, QC, Canada. ¹⁶⁰Department of Human Genetics, McGill University, Montreal, QC, Canada. ¹⁶¹Faculty of Medicine and Health Technology, Tampere University and Tays Cancer Center, Tampere University Hospital, Tampere, Finland. ¹⁶²Haematology, Leeds Teaching Hospitals NHS Trust, Leeds, UK. ¹⁶³Translational Research and Innovation, Centre Léon Bérard, Lyon, France. ¹⁶⁴Fox Chase Cancer Center, Philadelphia, PA, USA. ¹⁶⁵International Agency for Research on Cancer, World Health Organization, Lyon, France. ¹⁶⁶Earlham Institute, Norwich, UK. ¹⁶⁷Norwich Medical School, University of East Anglia, Norwich, UK. ¹⁶⁸Department of Molecular Biology, Faculty of Science, Radboud Institute for Molecular Life Sciences, Radboud University, Nijmegen, HB, The Netherlands. ¹⁶⁹CRUK Manchester Institute and Centre, Manchester, UK. ¹⁷⁰Department of Radiation Oncology, University of Toronto, Toronto, ON, Canada. ¹⁷¹Division of Cancer Sciences, Manchester Cancer Research Centre, University of Manchester, Manchester, UK. ¹⁷²Radiation Medicine Program, Princess Margaret Cancer Centre, Toronto, ON, Canada. ¹⁷³Department of Pathology, Brigham and Women's Hospital, Harvard Medical School, Boston, MA, USA. ¹⁷⁴Department of Surgery, Division of Thoracic Surgery, The Johns Hopkins University School of Medicine, Baltimore, MD, USA. ¹⁷⁵Division of Molecular Pathology, The Netherlands Cancer Institute, Oncode Institute, Amsterdam, CX, The Netherlands. ¹⁷⁶Department of Biomolecular Engineering, University of California Santa Cruz, Santa Cruz, CA, USA. ¹⁷⁷UC Santa Cruz Genomics Institute, University of California Santa Cruz, Santa Cruz, CA, USA. ¹⁷⁸Division of Applied Bioinformatics, German Cancer Research Center (DKFZ), Heidelberg, Germany. ¹⁷⁹German Cancer Genome Consortium (DKTK), Heidelberg, Germany. ¹⁸⁰National Center for Tumor Diseases (NCT) Heidelberg, Heidelberg, Germany. ¹⁸¹Center for Biological Sequence Analysis, Department of Bio and Health Informatics, Technical University of Denmark, Lyngby, Denmark. ¹⁸²Novo Nordisk Foundation Center for Protein Research, University of Copenhagen, Copenhagen, Denmark. ¹⁸³Institute for Molecular Bioscience, University of Queensland, St. Lucia, Brisbane, QLD, Australia. ¹⁸⁴Biomedical Engineering, Oregon Health and Science University, Portland, OR, USA. ¹⁸⁵Division of Theoretical Bioinformatics, German Cancer Research Center (DKFZ), Heidelberg, Germany. ¹⁸⁶Institute of Pharmacy and Molecular Biotechnology and BioQuant, Heidelberg University, Heidelberg, Germany. ¹⁸⁷Federal Ministry of Education and Research, Berlin, Germany. ¹⁸⁸Melanoma Institute Australia, University of Sydney, Sydney, NSW, Australia. ¹⁸⁹Pediatric Hematology and Oncology, University Hospital Muenster, Muenster, Germany. ¹⁹⁰Department of Pathology, Johns Hopkins University School of Medicine, Baltimore, MD, USA. ¹⁹¹McKusick-Nathans Institute of Genetic Medicine, Sidney Kimmel Comprehensive Cancer Center at Johns Hopkins University School of Medicine, Baltimore, MD, USA. ¹⁹²Foundation Medicine, Inc, Cambridge, MA, USA. ¹⁹³Department of Biomedical Data Science, Stanford University School of Medicine, Stanford, CA, USA. ¹⁹⁴Department of Genetics, Stanford University School of Medicine, Stanford, CA, USA. ¹⁹⁵Baker Computational Health Sciences Institute and Department of Pediatrics, University of California, San Francisco, CA, USA. ¹⁹⁶Institute of Clinical Medicine, Faculty of Medicine, University of Oslo, Oslo, Norway. ¹⁹⁷National Cancer Institute, National Institutes of Health, Bethesda, MD, USA. ¹⁹⁸Royal Marsden NHS Foundation Trust, Sutton, London, UK. ¹⁹⁹Genome Biology Unit, European Molecular Biology Laboratory (EMBL), Heidelberg, Germany. ²⁰⁰Department of Oncology, University of Cambridge, Cambridge, UK. ²⁰¹Institut Gustave Roussy, Villejuif, France. ²⁰²Anatomia Patológica, Hospital Clinic, Institut d'Investigacions Biomèdiques August Pi i Sunyer (IDIBAPS), University of Barcelona, Barcelona, Spain. ²⁰³Spanish Ministry of Science and Innovation, Madrid, Spain. ²⁰⁴University of Michigan Comprehensive Cancer Center, Ann Arbor, MI, USA. ²⁰⁵Department of Medical Oncology, Inselspital, University Hospital and University of Bern, Bern, Switzerland. ²⁰⁶Graduate School for Cellular and Biomedical Sciences, University of Bern, Bern, Switzerland. ²⁰⁷University of Pavia, Pavia, Italy. ²⁰⁸University of Alabama at Birmingham, Birmingham, AL, USA. ²⁰⁹UHN Program in BioSpecimen Sciences, Toronto General Hospital, Toronto, ON, Canada. ²¹⁰Department of Urology, Icahn School of Medicine at Mount Sinai, New York, NY, USA. ²¹¹Centre for Law and Genetics, University of Tasmania, Sandy Bay Campus, Hobart, TAS, Australia. ²¹²Faculty of Biosciences, Heidelberg University, Heidelberg, Germany. ²¹³Department of Biochemistry, Microbiology and Immunology, Faculty of Medicine, University of Ottawa, Ottawa, ON, Canada. ²¹⁴Division of Anatomic Pathology, Mayo Clinic, Rochester, MN, USA. ²¹⁵Division of Cancer Epidemiology and Genetics, National Cancer Institute, National Institutes of Health, Bethesda, MD, USA. ²¹⁶Illawarra Shoalhaven Local Health District L3 Illawarra Cancer Care Centre, Wollongong Hospital, Wollongong, NSW, Australia. ²¹⁷BioForA, French National Institute for Agriculture, Food, and Environment (INRAE), ONF, Orléans, France. ²¹⁸Department of Biostatistics, Bloomberg School of Public Health, Johns Hopkins University, Baltimore, MD, USA. ²¹⁹University of California San Diego, San Diego, CA, USA. ²²⁰Division of Experimental Pathology, Mayo Clinic, Rochester, MN, USA. ²²¹Centre for Cancer Research, The Westmead Institute for Medical Research, University of Sydney, Sydney, NSW, Australia. ²²²Department of Gynaecological Oncology, Westmead Hospital, Sydney, NSW, Australia. ²²³PDXen Biosystems Inc, Seoul, South Korea. ²²⁴Korea Advanced Institute of Science and Technology, Daejeon, South Korea. ²²⁵Electronics and Telecommunications Research Institute, Daejeon, South Korea. ²²⁶Institut National du Cancer (INCA), Boulogne-Billancourt, France. ²²⁷Department of Genetics, Informatics Institute, University of Alabama at Birmingham, Birmingham, AL, USA. ²²⁸Division of Medical Oncology, National Cancer Centre, Singapore, Singapore. ²²⁹Medical Oncology, University and Hospital Trust of Verona, Verona, Italy. ²³⁰Department of Pediatrics, University Hospital Schleswig-Holstein, Kiel, Germany. ²³¹Hepatobiliary/Pancreatic Surgical Oncology Program, University Health Network, Toronto, ON, Canada. ²³²School of Biological Sciences, University of Auckland, Auckland, New Zealand. ²³³Department of Surgery, University of Melbourne, Parkville, VIC, Australia. ²³⁴The Murdoch Children's Research Institute, Royal Children's Hospital, Parkville, VIC, Australia. ²³⁵Walter and Eliza Hall Institute, Parkville, VIC, Australia. ²³⁶Vancouver Prostate Centre, Vancouver, BC, Canada. ²³⁷Lunenfeld-Tanenbaum Research Institute, Mount Sinai Hospital, Toronto, ON, Canada. ²³⁸University of East Anglia, Norwich, UK. ²³⁹Norfolk and Norwich University Hospital NHS Trust, Norwich, UK. ²⁴⁰Victorian Institute of Forensic Medicine, Southbank, VIC, Australia. ²⁴¹Department of Biomedical Informatics, Harvard Medical School, Boston, MA, USA. ²⁴²Department of Chemistry, Centre for Molecular Science Informatics, University of Cambridge, Cambridge, UK. ²⁴³Ludwig Center at Harvard Medical School, Boston, MA, USA. ²⁴⁴Human Genome Sequencing Center, Baylor College of Medicine, Houston, TX, USA. ²⁴⁵Peter MacCallum Cancer Centre, University of Melbourne, Melbourne, VIC, Australia. ²⁴⁶Physics Division, Optimization and Systems Biology Lab, Massachusetts General Hospital, Boston, MA, USA. ²⁴⁷Department of Medicine, Baylor College of Medicine, Houston, TX, USA. ²⁴⁸University of Cologne, Cologne, Germany. ²⁴⁹International Genomics Consortium, Phoenix, AZ, USA. ²⁵⁰Genomics Research Program, Ontario Institute for Cancer Research, Toronto, ON, Canada. ²⁵¹Barking Havering and Redbridge University Hospitals NHS Trust, Romford, UK. ²⁵²Children's Hospital at Westmead, University of Sydney, Sydney, NSW, Australia. ²⁵³Section of Endocrinology, Department of Medicine, University and Hospital Trust of Verona, Verona, Italy. ²⁵⁴Computational Biology Center, Memorial Sloan Kettering Cancer Center, New York, NY, USA. ²⁵⁵Department of Biology, ETH Zurich, Zürich, Switzerland. ²⁵⁶Department of Computer Science, ETH Zurich, Zurich, Switzerland. ²⁵⁷SIB Swiss Institute of Bioinformatics, Lausanne, Switzerland. ²⁵⁸Departments of Pediatrics and Genetics, University of North Carolina at Chapel Hill, Chapel Hill, NC, USA. ²⁵⁹Seven Bridges Genomics, Charlestown, MA, USA. ²⁶⁰Annai

Systems, Inc, Carlsbad, CA, USA. ²⁶¹Department of Pathology, General Hospital of Treviso, Department of Medicine, University of Padua, Treviso, Italy. ²⁶²Department of Computational Biology, University of Lausanne, Lausanne, Switzerland. ²⁶³Department of Genetic Medicine and Development, University of Geneva Medical School, Geneva, CH, Switzerland. ²⁶⁴Swiss Institute of Bioinformatics, University of Geneva, Geneva, CH, Switzerland. ²⁶⁵The Francis Crick Institute, London, UK. ²⁶⁶University of Leuven, Leuven, Belgium. ²⁶⁷Institute of Medical Genetics and Applied Genomics, University of Tübingen, Tübingen, Germany. ²⁶⁸Computational and Systems Biology, Genome Institute of Singapore, Singapore, Singapore. ²⁶⁹School of Computing, National University of Singapore, Singapore, Singapore. ²⁷⁰Big Data Institute, Li Ka Shing Centre, University of Oxford, Oxford, UK. ²⁷¹The Edward S. Rogers Sr. Department of Electrical and Computer Engineering, University of Toronto, Toronto, ON, Canada. ²⁷²Breast Cancer Translational Research Laboratory JC Heuson, Institut Jules Bordet, Brussels, Belgium. ²⁷³Department of Oncology, Laboratory for Translational Breast Cancer Research, KU Leuven, Leuven, Belgium. ²⁷⁴Institute for Research in Biomedicine (IRB Barcelona), The Barcelona Institute of Science and Technology, Barcelona, Spain. ²⁷⁵Research Program on Biomedical Informatics, Universitat Pompeu Fabra, Barcelona, Spain. ²⁷⁶Division of Medical Oncology, Princess Margaret Cancer Centre, Toronto, ON, Canada. ²⁷⁷Department of Physiology and Biophysics, Weill Cornell Medicine, New York, NY, USA. ²⁷⁸Institute for Computational Biomedicine, Weill Cornell Medicine, New York, NY, USA. ²⁷⁹Department of Pathology, UPMC Shadyside, Pittsburgh, PA, USA. ²⁸⁰Independent Consultant, Wellesley, USA. ²⁸¹Department of Cell and Molecular Biology, Science for Life Laboratory, Uppsala University, Uppsala, Sweden. ²⁸²Department of Medicine and Department of Genetics, Washington University School of Medicine, St. Louis, St. Louis, MO, USA. ²⁸³Hefei University of Technology, Anhui, China. ²⁸⁴Translational Cancer Research Unit, GZA Hospitals St.-Augustinus, Center for Oncological Research, Faculty of Medicine and Health Sciences, University of Antwerp, Antwerp, Belgium. ²⁸⁵Simon Fraser University, Burnaby, BC, Canada. ²⁸⁶University of Pennsylvania, Philadelphia, PA, USA. ²⁸⁷The Wellcome Trust, London, UK. ²⁸⁸The Hospital for Sick Children, Toronto, ON, Canada. ²⁸⁹Department of Pathology, Queen Elizabeth University Hospital, Glasgow, UK. ²⁹⁰Department of Genetics and Computational Biology, QIMR Berghofer Medical Research Institute, Brisbane, QLD, Australia. ²⁹¹Department of Oncology, Centre for Cancer Genetic Epidemiology, University of Cambridge, Cambridge, UK. ²⁹²Department of Public Health and Primary Care, Centre for Cancer Genetic Epidemiology, University of Cambridge, Cambridge, UK. ²⁹³Prostate Cancer Canada, Toronto, ON, Canada. ²⁹⁴University of Cambridge, Cambridge, UK. ²⁹⁵Department of Laboratory Medicine, Translational Cancer Research, Lund University Cancer Center at Medicon Village, Lund University, Lund, Sweden. ²⁹⁶Heidelberg University, Heidelberg, Germany. ²⁹⁷New BIH Digital Health Center, Berlin Institute of Health (BIH) and Charité - Universitätsmedizin Berlin, Berlin, Germany. ²⁹⁸CIBER Epidemiología y Salud Pública (CIBERESP), Madrid, Spain. ²⁹⁹Research Group on Statistics, Econometrics and Health (GRECS), UdG, Barcelona, Spain. ³⁰⁰Quantitative Genomics Laboratories (qGenomics), Barcelona, Spain. ³⁰¹Icelandic Cancer Registry, Icelandic Cancer Society, Reykjavik, Iceland. ³⁰²State Key Laboratory of Cancer Biology, and Xijing Hospital of Digestive Diseases, Fourth Military Medical University, Shaanxi, China. ³⁰³Department of Medicine (DIMED), Surgical Pathology Unit, University of Padua, Padua, Italy. ³⁰⁴Department of Cancer Biology, Dana-Farber Cancer Institute, Boston, MA, USA. ³⁰⁵Rigshospitalet, Copenhagen, Denmark. ³⁰⁶Center for Cancer Genomics, National Cancer Institute, National Institutes of Health, Bethesda, MD, USA. ³⁰⁷Department of Biochemistry and Molecular Medicine, University of Montreal, Montreal, QC, Canada. ³⁰⁸Australian Institute of Tropical Health and Medicine, James Cook University, Douglas, QLD, Australia. ³⁰⁹Department of Neuro-Oncology, Istituto Neurologico Besta, Milano, Italy. ³¹⁰Bioplatforms Australia, North Ryde, NSW, Australia. ³¹¹Department of Pathology (Research), University College London Cancer Institute, London, UK. ³¹²Department of Surgical Oncology, Princess Margaret Cancer Centre, Toronto, ON, Canada. ³¹³Department of Medical Oncology, Josephine Nefkens Institute and Cancer Genomics Centre, Erasmus Medical Center, Rotterdam, CN, The Netherlands. ³¹⁴The University of Queensland Thoracic Research Centre, The Prince Charles Hospital, Brisbane, QLD, Australia. ³¹⁵CIBIO/InBIO - Research Center in Biodiversity and Genetic Resources, Universidade do Porto, Vairão, Portugal. ³¹⁶HCA Laboratories, London, UK. ³¹⁷University of Liverpool, Liverpool, UK. ³¹⁸The Azrieli Faculty of Medicine, Bar-Ilan University, Safed, Israel. ³¹⁹Department of Neurosurgery, University of Florida, Gainesville, FL, USA. ³²⁰Department of Pathology, Graduate School of Medicine, University of Tokyo, Tokyo, Japan. ³²¹National Genotyping Center, Institute of Biomedical Sciences, Academia Sinica, Taipei, Taiwan. ³²²University of Milano Bicocca, Monza, Italy. ³²³BGI-Shenzhen, Shenzhen, China. ³²⁴Department of Pathology, Oslo University Hospital Ullevål, Oslo, Norway. ³²⁵Center for Biomedical Informatics, Harvard Medical School, Boston, MA, USA. ³²⁶Department Biochemistry and Molecular Biomedicine, University of Barcelona, Barcelona, Spain. ³²⁷Office of Cancer Genomics, National Cancer Institute, National Institutes of Health, Bethesda, MD, USA. ³²⁸Cancer Epigenomics, German Cancer Research Center (DKFZ), Heidelberg, Germany. ³²⁹Department of Cancer Biology, The University of Texas MD Anderson Cancer Center, Houston, TX, USA. ³³⁰Department of Surgical Oncology, The University of Texas MD Anderson Cancer Center, Houston, TX, USA. ³³¹Department of Computer Science, Yale University, New Haven, CT, USA. ³³²Department of Molecular Biophysics and Biochemistry, Yale University, New Haven, CT, USA. ³³³Program in Computational Biology and Bioinformatics, Yale University, New Haven, CT, USA. ³³⁴Department of Pathology, Memorial Sloan Kettering Cancer Center, New York, NY, USA. ³³⁵Division of Gastroenterology and Hepatology, Mayo Clinic, Rochester, MN, USA. ³³⁶University of Sydney, Sydney, NSW, Australia. ³³⁷University of Oxford, Oxford, UK. ³³⁸Cambridge University Hospitals NHS Foundation Trust, Cambridge, UK. ³³⁹Department of Surgery, Academic Urology Group, University of Cambridge, Cambridge, UK. ³⁴⁰Department of Medicine II, University of Würzburg, Würzburg, Germany. ³⁴¹Sylvester Comprehensive Cancer Center, University of Miami, Miami, FL, USA. ³⁴²Institut Hospital del Mar d'Investigacions Mèdiques (IMIM), Barcelona, Spain. ³⁴³Genome Integrity and Structural Biology Laboratory, National Institute of Environmental Health Sciences (NIEHS), Durham, NC, USA. ³⁴⁴St. Thomas's Hospital, London, UK. ³⁴⁵Osaka International Cancer Center, Osaka, Japan. ³⁴⁶Department of Pathology, Skåne University Hospital, Lund University, Lund, Sweden. ³⁴⁷Department of Medical Oncology, Beatson West of Scotland Cancer Centre, Glasgow, UK. ³⁴⁸National Human Genome Research Institute, National Institutes of Health, Bethesda, MD, USA. ³⁴⁹Department of Medicine, Section of Hematology/Oncology, University of Chicago, Chicago, IL, USA. ³⁵⁰German Center for Infection Research (DZIF), Partner Site Hamburg-Borstel-Lübeck-Riems, Hamburg, Germany. ³⁵¹Bioinformatics Research Centre (BIRC), Aarhus University, Aarhus, Denmark. ³⁵²Department of Biotechnology, Ministry of Science and Technology, Government of India, New Delhi/Delhi, India. ³⁵³National Cancer Centre Singapore, Singapore, Singapore. ³⁵⁴Brandeis University, Waltham, MA, USA. ³⁵⁵Department of Urologic Sciences, University of British Columbia, Vancouver, BC, Canada. ³⁵⁶Department of Internal Medicine, Stanford University, Stanford, CA, USA. ³⁵⁷The University of Texas Health Science Center at Houston, Houston, TX, USA. ³⁵⁸Imperial College NHS Trust, Imperial College, London, INY, UK. ³⁵⁹Senckenberg Institute of Pathology, University of Frankfurt Medical School, Frankfurt, Germany. ³⁶⁰Division of Biomedical Informatics, Department of Medicine, UC San Diego School of Medicine, San Diego, CA, USA. ³⁶¹Center for Precision Health, School of Biomedical Informatics, The University of Texas Health Science Center, Houston, TX, USA. ³⁶²Oxford Nanopore Technologies, New York, NY, USA. ³⁶³Institute of Medical Science, University of Tokyo, Tokyo, Japan. ³⁶⁴Howard Hughes Medical Institute, University of California Santa Cruz, Santa Cruz, CA, USA. ³⁶⁵Wakayama Medical University, Wakayama, Japan. ³⁶⁶Division of Medical Oncology, Department of Internal Medicine, Lineberger Comprehensive Cancer Center, University of North Carolina at Chapel Hill, Chapel Hill, NC, USA. ³⁶⁷University of Tennessee Health Science Center for Cancer Research, Memphis, TN, USA. ³⁶⁸Department of Histopathology, Salford Royal NHS Foundation Trust, Salford, UK. ³⁶⁹Faculty of Biology, Medicine and Health, University of Manchester, Manchester, UK. ³⁷⁰Peking University, Beijing, China. ³⁷¹Children's Hospital of Philadelphia, Philadelphia, PA, USA. ³⁷²Department of Bioinformatics and Computational Biology and Department of Systems Biology, The University of Texas MD Anderson Cancer Center, Houston,

TX, USA. ³⁷³Karolinska Institute, Stockholm, Sweden. ³⁷⁴The Donnelly Centre, University of Toronto, Toronto, ON, Canada. ³⁷⁵Department of Medical Genetics, College of Medicine, Hallym University, Chuncheon, South Korea. ³⁷⁶Department of Experimental and Health Sciences, Institute of Evolutionary Biology (UPF-CSIC), Universitat Pompeu Fabra, Barcelona, Spain. ³⁷⁷Health Data Science Unit, University Clinics, Heidelberg, Germany. ³⁷⁸Massachusetts General Hospital Center for Cancer Research, Charlestown, MA, USA. ³⁷⁹Hokkaido University, Sapporo, Japan. ³⁸⁰Department of Pathology and Clinical Laboratory, National Cancer Center Hospital, Tokyo, Japan. ³⁸¹Computational Biology, Leibniz Institute on Aging - Fritz Lipmann Institute (FLI), Jena, Germany. ³⁸²University of Melbourne Centre for Cancer Research, Melbourne, VIC, Australia. ³⁸³University of Nebraska Medical Center, Omaha, NE, USA. ³⁸⁴Syntekabio Inc, Daejeon, South Korea. ³⁸⁵Department of Pathology, Academic Medical Center, Amsterdam, AZ, The Netherlands. ³⁸⁶China National GeneBank-Shenzhen, Shenzhen, China. ³⁸⁷Division of Molecular Genetics, German Cancer Research Center (DKFZ), Heidelberg, Germany. ³⁸⁸Division of Life Science and Applied Genomics Center, Hong Kong University of Science and Technology, Clear Water Bay, Hong Kong, China. ³⁸⁹Icahn School of Medicine at Mount Sinai, New York, NY, USA. ³⁹⁰Geneplus-Shenzhen, Shenzhen, China. ³⁹¹School of Computer Science and Technology, Xi'an Jiaotong University, Xi'an, China. ³⁹²AbbVie, North Chicago, IL, USA. ³⁹³Institute of Pathology, Charité - University Medicine Berlin, Berlin, Germany. ³⁹⁴Centre for Translational and Applied Genomics, British Columbia Cancer Agency, Vancouver, BC, Canada. ³⁹⁵Edinburgh Royal Infirmary, Edinburgh, UK. ³⁹⁶Berlin Institute for Medical Systems Biology, Max Delbrück Center for Molecular Medicine, Berlin, Germany. ³⁹⁷German Cancer Consortium (DKTK), Heidelberg, Germany. ³⁹⁸Department of Pediatric Immunology, Hematology and Oncology, University Hospital, Heidelberg, Germany. ³⁹⁹German Cancer Research Center (DKFZ), Heidelberg, Germany. ⁴⁰⁰Heidelberg Institute for Stem Cell Technology and Experimental Medicine (HI-STEM), Heidelberg, Germany. ⁴⁰¹Institute for Computational Biomedicine, Weill Cornell Medical College, New York, NY, USA. ⁴⁰²New York Genome Center, New York, NY, USA. ⁴⁰³Department of Urology, James Buchanan Brady Urological Institute, Johns Hopkins University School of Medicine, Baltimore, MD, USA. ⁴⁰⁴Department of Preventive Medicine, Graduate School of Medicine, The University of Tokyo, Tokyo, Japan. ⁴⁰⁵Department of Molecular and Cellular Biology, Baylor College of Medicine, Houston, TX, USA. ⁴⁰⁶Department of Pathology and Immunology, Baylor College of Medicine, Houston, TX, USA. ⁴⁰⁷Michael E. DeBakey Veterans Affairs Medical Center, Houston, TX, USA. ⁴⁰⁸Technical University of Denmark, Lyngby, Denmark. ⁴⁰⁹Department of Pathology, College of Medicine, Hanyang University, Seoul, South Korea. ⁴¹⁰Academic Unit of Surgery, School of Medicine, College of Medical, Veterinary and Life Sciences, University of Glasgow, Glasgow Royal Infirmary, Glasgow, UK. ⁴¹¹Department of Pathology, Asan Medical Center, College of Medicine, Ulsan University, Songpa-gu, Seoul, South Korea. ⁴¹²Science Writer, Garrett Park, MD, USA. ⁴¹³International Cancer Genome Consortium (ICGC)/ICGC Accelerating Research in Genomic Oncology (ARGO) Secretariat, Ontario Institute for Cancer Research, Toronto, ON, Canada. ⁴¹⁴University of Ljubljana, Ljubljana, Slovenia. ⁴¹⁵Department of Public Health Sciences, University of Chicago, Chicago, IL, USA. ⁴¹⁶Research Institute, NorthShore University HealthSystem, Evanston, IL, USA. ⁴¹⁷Department for Biomedical Research, University of Bern, Bern, Switzerland. ⁴¹⁸Centre of Genomics and Policy, McGill University and Génome Québec Innovation Centre, Montreal, QC, Canada. ⁴¹⁹Carolina Center for Genome Sciences, University of North Carolina at Chapel Hill, Chapel Hill, NC, USA. ⁴²⁰Hopp Children's Cancer Center (KiTZ), Heidelberg, Germany. ⁴²¹Pediatric Glioma Research Group, German Cancer Research Center (DKFZ), Heidelberg, Germany. ⁴²²Cancer Research UK, London, UK. ⁴²³Indivumed GmbH, Hamburg, Germany. ⁴²⁴Genome Integration Data Center, Syntekabio, Inc, Daejeon, South Korea. ⁴²⁵University Hospital Zurich, Zurich, Switzerland. ⁴²⁶Clinical Bioinformatics, Swiss Institute of Bioinformatics, Geneva, Switzerland. ⁴²⁷Institute for Pathology and Molecular Pathology, University Hospital Zurich, Zurich, Switzerland. ⁴²⁸Institute of Molecular Life Sciences, University of Zurich, Zurich, Switzerland. ⁴²⁹Women's Cancer Program at the Samuel Oschin Comprehensive Cancer Institute, Cedars-Sinai Medical Center, Los Angeles, CA, USA. ⁴³⁰Department for Internal Medicine II, University Hospital Schleswig-Holstein, Kiel, Germany. ⁴³¹Genetics and Molecular Pathology, SA Pathology, Adelaide, SA, Australia. ⁴³²Department of Gastric Surgery, National Cancer Center Hospital, Tokyo, Japan. ⁴³³A.A. Kharkevich Institute of Information Transmission Problems, Moscow, Russia. ⁴³⁴Oncology and Immunology, Dmitry Rogachev National Research Center of Pediatric Hematology, Moscow, Russia. ⁴³⁵Skolkovo Institute of Science and Technology, Moscow, Russia. ⁴³⁶Department of Surgery, The George Washington University, School of Medicine and Health Science, Washington, DC, USA. ⁴³⁷Endocrine Oncology Branch, Center for Cancer Research, National Cancer Institute, National Institutes of Health, Bethesda, MD, USA. ⁴³⁸Melanoma Institute Australia, Macquarie University, Sydney, NSW, Australia. ⁴³⁹MIT Computer Science and Artificial Intelligence Laboratory, Massachusetts Institute of Technology, Cambridge, MA, USA. ⁴⁴⁰Tissue Pathology and Diagnostic Oncology, Royal Prince Alfred Hospital, Sydney, NSW, Australia. ⁴⁴¹Cholangiocarcinoma Screening and Care Program and Liver Fluke and Cholangiocarcinoma Research Centre, Faculty of Medicine, Khon Kaen University, Khon Kaen, Thailand. ⁴⁴²Controlled Department and Institution, New York, NY, USA. ⁴⁴³National Cancer Center, Gyeonggi, South Korea. ⁴⁴⁴Department of Biochemistry, College of Medicine, Ewha Womans University, Seoul, South Korea. ⁴⁴⁵Health Sciences Department of Biomedical Informatics, University of California San Diego, La Jolla, CA, USA. ⁴⁴⁶Research Core Center, National Cancer Centre Korea, Goyang-si, South Korea. ⁴⁴⁷Department of Health Sciences and Technology, Sungkyunkwan University School of Medicine, Seoul, South Korea. ⁴⁴⁸Samsung Genome Institute, Seoul, South Korea. ⁴⁴⁹Breast Oncology Program, Dana-Farber/Brigham and Women's Cancer Center, Boston, MA, USA. ⁴⁵⁰Department of Surgery, Memorial Sloan Kettering Cancer Center, New York, NY, USA. ⁴⁵¹Division of Breast Surgery, Brigham and Women's Hospital, Boston, MA, USA. ⁴⁵²Integrative Bioinformatics Support Group, National Institute of Environmental Health Sciences (NIEHS), Durham, NC, USA. ⁴⁵³Department of Clinical Science, University of Bergen, Bergen, Norway. ⁴⁵⁴Center For Medical Innovation, Seoul National University Hospital, Seoul, South Korea. ⁴⁵⁵Department of Internal Medicine, Seoul National University Hospital, Seoul, South Korea. ⁴⁵⁶Institute of Computer Science, Polish Academy of Sciences, Warszawa, Poland. ⁴⁵⁷Functional and Structural Genomics, German Cancer Research Center (DKFZ), Heidelberg, Germany. ⁴⁵⁸Laboratory of Translational Genomics, Division of Cancer Epidemiology and Genetics, National Cancer Institute, National Institutes of Health, Bethesda, MD, USA. ⁴⁵⁹Institute for Medical Informatics Statistics and Epidemiology, University of Leipzig, Leipzig, Germany. ⁴⁶⁰Morgan Welch Inflammatory Breast Cancer Research Program and Clinic, The University of Texas MD Anderson Cancer Center, Houston, TX, USA. ⁴⁶¹Department of Hematology and Oncology, Georg-Augusts-University of Göttingen, Göttingen, Germany. ⁴⁶²Institute of Cell Biology (Cancer Research), University of Duisburg-Essen, Essen, Germany. ⁴⁶³King's College London and Guy's and St. Thomas' NHS Foundation Trust, London, UK. ⁴⁶⁴Center for Epigenetics, Van Andel Research Institute, Grand Rapids, MI, USA. ⁴⁶⁵The University of Queensland Centre for Clinical Research, Royal Brisbane and Women's Hospital, Herston, QLD, Australia. ⁴⁶⁶Department of Pediatric Oncology and Hematology, University of Cologne, Cologne, Germany. ⁴⁶⁷University of Düsseldorf, Düsseldorf, Germany. ⁴⁶⁸Department of Pathology, Institut Jules Bordet, Brussels, Belgium. ⁴⁶⁹Institute of Biomedicine, Sahlgrenska Academy at University of Gothenburg, Gothenburg, Sweden. ⁴⁷⁰Children's Medical Research Institute, Sydney, NSW, Australia. ⁴⁷¹ILSbio, LLC Biobank, Chestertown, MD, USA. ⁴⁷²Division of Genetics and Genomics, Boston Children's Hospital, Harvard Medical School, Boston, MA, USA. ⁴⁷³Institute for Bioengineering and Biopharmaceutical Research (IBBR), Hanyang University, Seoul, South Korea. ⁴⁷⁴Department of Statistics, University of California Santa Cruz, Santa Cruz, CA, USA. ⁴⁷⁵Department of Vertebrate Genomics/Otto Warburg Laboratory Gene Regulation and Systems Biology of Cancer, Max Planck Institute for Molecular Genetics, Berlin, Germany. ⁴⁷⁶McGill University and Genome Quebec Innovation Centre, Montreal, QC, Canada. ⁴⁷⁷biobyte solutions GmbH, Heidelberg, Germany. ⁴⁷⁸Gynecologic Oncology, NYU Laura and Isaac Perlmutter Cancer Center, New York University, New York, NY, USA. ⁴⁷⁹Division of Oncology, Stem Cell Biology Section, Washington University School of Medicine, St. Louis, MO, USA. ⁴⁸⁰Harvard University,

Cambridge, MA, USA. ⁴⁸¹Urologic Oncology Branch, Center for Cancer Research, National Cancer Institute, National Institutes of Health, Bethesda, MD, USA. ⁴⁸²University of Oslo, Oslo, Norway. ⁴⁸³University of Toronto, Toronto, ON, Canada. ⁴⁸⁴School of Life Sciences, Peking University, Beijing, China. ⁴⁸⁵Leidos Biomedical Research, Inc, McLean, VA, USA. ⁴⁸⁶Second Military Medical University, Shanghai, China. ⁴⁸⁷Chinese Cancer Genome Consortium, Shenzhen, China. ⁴⁸⁸Department of Medical Oncology, Beijing Hospital, Beijing, China. ⁴⁸⁹Laboratory of Molecular Oncology, Key Laboratory of Carcinogenesis and Translational Research (Ministry of Education), Peking University Cancer Hospital and Institute, Beijing, China. ⁴⁹⁰School of Medicine/School of Mathematics and Statistics, University of St. Andrews, St. Andrews, Fife, UK. ⁴⁹¹Institute for Systems Biology, Seattle, WA, USA. ⁴⁹²Department of Biochemistry and Molecular Biology, Faculty of Medicine, University Institute of Oncology-IUOPA, Oviedo, Spain. ⁴⁹³Institut Bergonié, Bordeaux, France. ⁴⁹⁴Cancer Unit, MRC University of Cambridge, Cambridge, UK. ⁴⁹⁵Department of Pathology and Laboratory Medicine, Center for Personalized Medicine, Children's Hospital Los Angeles, Los Angeles, CA, USA. ⁴⁹⁶John Curtin School of Medical Research, Canberra, ACT, Australia. ⁴⁹⁷MVZ Department of Oncology, PraxisClinic am Johannisplatz, Leipzig, Germany. ⁴⁹⁸Department of Information Technology, Ghent University, Ghent, Belgium. ⁴⁹⁹Department of Plant Biotechnology and Bioinformatics, Ghent University, Ghent, Belgium. ⁵⁰⁰Institute for Genomic Medicine, Nationwide Children's Hospital, Columbus, OH, USA. ⁵⁰¹Department of Surgery, Duke University, Durham, NC, USA. ⁵⁰²Institució Catalana de Recerca i Estudis Avançats (ICREA), Barcelona, Spain. ⁵⁰³Institut Català de Paleontologia Miquel Crusafont, Universitat Autònoma de Barcelona, Barcelona, Spain. ⁵⁰⁴Institut d'Investigacions Biomèdiques August Pi i Sunyer (IDIBAPS), Barcelona, Spain. ⁵⁰⁵Division of Oncology, Washington University School of Medicine, St. Louis, MO, USA. ⁵⁰⁶Department of Surgery and Cancer, Imperial College, London, INY, UK. ⁵⁰⁷Applications Department, Oxford Nanopore Technologies, Oxford, UK. ⁵⁰⁸Department of Obstetrics, Gynecology and Reproductive Services, University of California San Francisco, San Francisco, CA, USA. ⁵⁰⁹Department of Biochemistry and Molecular Medicine, University California at Davis, Sacramento, CA, USA. ⁵¹⁰STTARR Innovation Facility, Princess Margaret Cancer Centre, Toronto, ON, Canada. ⁵¹¹Discipline of Surgery, Western Sydney University, Penrith, NSW, Australia. ⁵¹²Yale School of Medicine, Yale University, New Haven, CT, USA. ⁵¹³Department of Genetics, Lineberger Comprehensive Cancer Center, University of North Carolina at Chapel Hill, Chapel Hill, NC, USA. ⁵¹⁴Departments of Neurology and Neurosurgery, Henry Ford Hospital, Detroit, MI, USA. ⁵¹⁵Precision Oncology, OHSU Knight Cancer Institute, Oregon Health and Science University, Portland, OR, USA. ⁵¹⁶Institute of Pathology, University Medical Center Hamburg-Eppendorf, Hamburg, Germany. ⁵¹⁷Department of Health Sciences, Faculty of Medical Sciences, Kyushu University, Fukuoka, Japan. ⁵¹⁸Heidelberg Academy of Sciences and Humanities, Heidelberg, Germany. ⁵¹⁹Department of Clinical Pathology, University of Melbourne, Melbourne, VIC, Australia. ⁵²⁰Department of Pathology, Roswell Park Cancer Institute, Buffalo, NY, USA. ⁵²¹Department of Computer Science, University of Helsinki, Helsinki, Finland. ⁵²²Institute of Biotechnology, University of Helsinki, Helsinki, Finland. ⁵²³Organismal and Evolutionary Biology Research Programme, University of Helsinki, Helsinki, Finland. ⁵²⁴Department of Obstetrics and Gynecology, Division of Gynecologic Oncology, Washington University School of Medicine, St. Louis, MO, USA. ⁵²⁵Penrose St. Francis Health Services, Colorado Springs, CO, USA. ⁵²⁶Institute of Pathology, Ulm University and University Hospital of Ulm, Ulm, Germany. ⁵²⁷National Cancer Center, Tokyo, Japan. ⁵²⁸Genome Institute of Singapore, Singapore, Singapore. ⁵²⁹German Cancer Aid, Bonn, Germany. ⁵³⁰Programme in Cancer and Stem Cell Biology, Centre for Computational Biology, Duke-NUS Medical School, Singapore, Singapore. ⁵³¹The Chinese University of Hong Kong, Shatin, NT, Hong Kong, China. ⁵³²Fourth Military Medical University, Shaanxi, China. ⁵³³St. Jude Children's Research Hospital, Memphis, TN, USA. ⁵³⁴University Health Network, Princess Margaret Cancer Centre, Toronto, ON, Canada. ⁵³⁵Center for Biomolecular Science and Engineering, University of California Santa Cruz, Santa Cruz, CA, USA. ⁵³⁶Department of Medicine, University of Chicago, Chicago, IL, USA. ⁵³⁷Department of Neurology, Mayo Clinic, Rochester, MN, USA. ⁵³⁸Cambridge Oesophagogastric Centre, Cambridge University Hospitals NHS Foundation Trust, Cambridge, UK. ⁵³⁹Department of Computer Science, Carleton College, Northfield, MN, USA. ⁵⁴⁰Institute of Cancer Sciences, College of Medical Veterinary and Life Sciences, University of Glasgow, Glasgow, UK. ⁵⁴¹Department of Epidemiology, University of Alabama at Birmingham, Birmingham, AL, USA. ⁵⁴²HudsonAlpha Institute for Biotechnology, Huntsville, AL, USA. ⁵⁴³O'Neal Comprehensive Cancer Center, University of Alabama at Birmingham, Birmingham, AL, USA. ⁵⁴⁴Department of Pathology, Keio University School of Medicine, Tokyo, Japan. ⁵⁴⁵Department of Hepatobiliary and Pancreatic Oncology, National Cancer Center Hospital, Tokyo, Japan. ⁵⁴⁶Lymphoma Genomic Translational Research Laboratory, National Cancer Centre, Singapore, Singapore. ⁵⁴⁷Department of Clinical Pathology, Robert-Bosch-Hospital, Stuttgart, Germany. ⁵⁴⁸Department of Cell and Systems Biology, University of Toronto, Toronto, ON, Canada. ⁵⁴⁹Department of Biosciences and Nutrition, Karolinska Institutet, Stockholm, Sweden. ⁵⁵⁰Center for Liver Cancer, Research Institute and Hospital, National Cancer Center, Gyeonggi, South Korea. ⁵⁵¹Division of Hematology-Oncology, Samsung Medical Center, Sungkyunkwan University School of Medicine, Seoul, South Korea. ⁵⁵²Samsung Advanced Institute for Health Sciences and Technology, Sungkyunkwan University School of Medicine, Seoul, South Korea. ⁵⁵³Cheonan Industry-Academic Collaboration Foundation, Sangmyung University, Cheonan, South Korea. ⁵⁵⁴NYU Langone Medical Center, New York, NY, USA. ⁵⁵⁵Department of Hematology and Medical Oncology, Cleveland Clinic, Cleveland, OH, USA. ⁵⁵⁶Department of Health Sciences Research, Mayo Clinic, Rochester, MN, USA. ⁵⁵⁷Helen F. Graham Cancer Center at Christiana Care Health Systems, Newark, DE, USA. ⁵⁵⁸Heidelberg University Hospital, Heidelberg, Germany. ⁵⁵⁹CSRA Incorporated, Fairfax, VA, USA. ⁵⁶⁰Research Department of Pathology, University College London Cancer Institute, London, UK. ⁵⁶¹Department of Research Oncology, Guy's Hospital, King's Health Partners AHSC, King's College London School of Medicine, London, UK. ⁵⁶²Faculty of Medicine and Health Sciences, Macquarie University, Sydney, NSW, Australia. ⁵⁶³University Hospital of Minjoo, INSERM UMR1098, Besançon, France. ⁵⁶⁴Spanish National Cancer Research Centre, Madrid, Spain. ⁵⁶⁵Center of Digestive Diseases and Liver Transplantation, Fundeni Clinical Institute, Bucharest, Romania. ⁵⁶⁶Cureline, Inc, South San Francisco, CA, USA. ⁵⁶⁷St. Luke's Cancer Centre, Royal Surrey County Hospital NHS Foundation Trust, Guildford, UK. ⁵⁶⁸Cambridge Breast Unit, Addenbrooke's Hospital, Cambridge University Hospital NHS Foundation Trust and NIHR Cambridge Biomedical Research Centre, Cambridge, UK. ⁵⁶⁹East of Scotland Breast Service, Ninewells Hospital, Aberdeen, UK. ⁵⁷⁰Department of Genetics, Microbiology and Statistics, University of Barcelona, IRSJD, IBUB, Barcelona, Spain. ⁵⁷¹Department of Obstetrics and Gynecology, Medical College of Wisconsin, Milwaukee, WI, USA. ⁵⁷²Hematology and Medical Oncology, Winship Cancer Institute of Emory University, Atlanta, GA, USA. ⁵⁷³Department of Computer Science, Princeton University, Princeton, NJ, USA. ⁵⁷⁴Vanderbilt Ingram Cancer Center, Vanderbilt University, Nashville, TN, USA. ⁵⁷⁵Ohio State University College of Medicine and Arthur G. James Comprehensive Cancer Center, Columbus, OH, USA. ⁵⁷⁶Department of Surgery, Yokohama City University Graduate School of Medicine, Kanagawa, Japan. ⁵⁷⁷Research Computing Center, University of North Carolina at Chapel Hill, Chapel Hill, NC, USA. ⁵⁷⁸School of Molecular Biosciences and Center for Reproductive Biology, Washington State University, Pullman, WA, USA. ⁵⁷⁹Finsen Laboratory and Biotech Research and Innovation Centre (BRIC), University of Copenhagen, Copenhagen, Denmark. ⁵⁸⁰Department of Laboratory Medicine and Pathobiology, University of Toronto, Toronto, ON, Canada. ⁵⁸¹Department of Pathology, Human Oncology and Pathogenesis Program, Memorial Sloan Kettering Cancer Center, New York, NY, USA. ⁵⁸²University Hospital Giessen, Pediatric Hematology and Oncology, Giessen, Germany. ⁵⁸³Oncologie Sénologie, ICM Institut Régional du Cancer, Montpellier, France. ⁵⁸⁴Institute of Clinical Molecular Biology, Christian-Albrechts-University, Kiel, Germany. ⁵⁸⁵Institute of Pathology, University of Wuerzburg, Wuerzburg, Germany. ⁵⁸⁶Department of Urology, North Bristol NHS Trust, Bristol, UK. ⁵⁸⁷SingHealth, Duke-NUS Institute of Precision Medicine, National Heart Centre Singapore, Singapore, Singapore. ⁵⁸⁸Department of Computer Science, University of Toronto, Toronto, ON, Canada. ⁵⁸⁹Englander Institute for Precision Medicine, Weill Cornell Medicine and New York Presbyterian Hospital, New York, NY, USA.

⁵⁹⁰Vall d'Hebron Institute of Oncology: VHIO, Barcelona, Spain. ⁵⁹¹General and Hepatobiliary-Biliary Surgery, Pancreas Institute, University and Hospital Trust of Verona, Verona, Italy. ⁵⁹²National Centre for Biological Sciences, Tata Institute of Fundamental Research, Bangalore, India. ⁵⁹³Indiana University, Bloomington, IN, USA. ⁵⁹⁴Department of Pathology, GZA-ZNA Hospitals, Antwerp, Belgium. ⁵⁹⁵Analytical Biological Services, Inc, Wilmington, DE, USA. ⁵⁹⁶Sydney Medical School, University of Sydney, Sydney, NSW, Australia. ⁵⁹⁷cBio Center, Dana-Farber Cancer Institute, Harvard Medical School, Boston, MA, USA. ⁵⁹⁸Department of Cell Biology, Harvard Medical School, Boston, MA, USA. ⁵⁹⁹Advanced Centre for Treatment Research and Education in Cancer, Tata Memorial Centre, Navi Mumbai, Maharashtra, India. ⁶⁰⁰School of Environmental and Life Sciences, Faculty of Science, The University of Newcastle, Ourimbah, NSW, Australia. ⁶⁰¹Department of Dermatology, University Hospital of Essen, Essen, Germany. ⁶⁰²Bioinformatics and Omics Data Analytics, German Cancer Research Center (DKFZ), Heidelberg, Germany. ⁶⁰³Department of Urology, Charité Universitätsmedizin Berlin, Berlin, Germany. ⁶⁰⁴Martini-Clinic, Prostate Cancer Center, University Medical Center Hamburg-Eppendorf, Hamburg, Germany. ⁶⁰⁵Department of General Internal Medicine, University of Kiel, Kiel, Germany. ⁶⁰⁶German Cancer Consortium (DKTK), Partner site Berlin, Berlin, Germany. ⁶⁰⁷Cancer Research Institute, Beth Israel Deaconess Medical Center, Boston, MA, USA. ⁶⁰⁸University of Pittsburgh, Pittsburgh, PA, USA. ⁶⁰⁹Department of Ophthalmology and Ocular Genomics Institute, Massachusetts Eye and Ear, Harvard Medical School, Boston, MA, USA. ⁶¹⁰Center for Psychiatric Genetics, NorthShore University HealthSystem, Evanston, IL, USA. ⁶¹¹Van Andel Research Institute, Grand Rapids, MI, USA. ⁶¹²Laboratory of Molecular Medicine, Human Genome Center, Institute of Medical Science, University of Tokyo, Tokyo, Japan. ⁶¹³Japan Agency for Medical Research and Development, Tokyo, Japan. ⁶¹⁴Korea University, Seoul, South Korea. ⁶¹⁵Murtha Cancer Center, Walter Reed National Military Medical Center, Bethesda, MD, USA. ⁶¹⁶Center for RNA Interference and Noncoding RNA, The University of Texas MD Anderson Cancer Center, Houston, TX, USA. ⁶¹⁷Department of Experimental Therapeutics, The University of Texas MD Anderson Cancer Center, Houston, TX, USA. ⁶¹⁸Department of Gynecologic Oncology and Reproductive Medicine, The University of Texas MD Anderson Cancer Center, Houston, TX, USA. ⁶¹⁹University Hospitals Coventry and Warwickshire NHS Trust, Coventry, UK. ⁶²⁰Department of Radiation Oncology, Radboud University Nijmegen Medical Centre, Nijmegen, GA, The Netherlands. ⁶²¹Institute for Genomics and Systems Biology, University of Chicago, Chicago, IL, USA. ⁶²²Clinic for Hematology and Oncology, St.-Antonius-Hospital, Eschweiler, Germany. ⁶²³Computational and Systems Biology Program, Memorial Sloan Kettering Cancer Center, New York, NY, USA. ⁶²⁴University of Iceland, Reykjavik, Iceland. ⁶²⁵Division of Computational Genomics and Systems Genetics, German Cancer Research Center (DKFZ), Heidelberg, Germany. ⁶²⁶Dundee Cancer Centre, Ninewells Hospital, Dundee, UK. ⁶²⁷Department for Internal Medicine III, University of Ulm and University Hospital of Ulm, Ulm, Germany. ⁶²⁸Institut Curie, INSERM Unit 830, Paris, France. ⁶²⁹Department of Gastroenterology and Hepatology, Yokohama City University Graduate School of Medicine, Kanagawa, Japan. ⁶³⁰Department of Laboratory Medicine, Radboud University Nijmegen Medical Centre, Nijmegen, GA, The Netherlands. ⁶³¹Division of Cancer Genome Research, German Cancer Research Center (DKFZ), Heidelberg, Germany. ⁶³²Department of General Surgery, Singapore General Hospital, Singapore, Singapore. ⁶³³Cancer Science Institute of Singapore, National University of Singapore, Singapore, Singapore. ⁶³⁴Department of Medical and Clinical Genetics, Genome-Scale Biology Research Program, University of Helsinki, Helsinki, Finland. ⁶³⁵East Anglian Medical Genetics Service, Cambridge University Hospitals NHS Foundation Trust, Cambridge, UK. ⁶³⁶Irving Institute for Cancer Dynamics, Columbia University, New York, NY, USA. ⁶³⁷Institute of Molecular and Cell Biology, Singapore, Singapore. ⁶³⁸Laboratory of Cancer Epigenome, Division of Medical Science, National Cancer Centre Singapore, Singapore, Singapore. ⁶³⁹Université Lyon, INCa-Synergie, Centre Léon Bérard, Lyon, France. ⁶⁴⁰Department of Urology, Mayo Clinic, Rochester, MN, USA. ⁶⁴¹Royal National Orthopaedic Hospital - Stanmore, Stanmore, Middlesex, UK. ⁶⁴²Giovanni Paolo II/I.R.C.C.S. Cancer Institute, Bari, BA, Italy. ⁶⁴³Neuroblastoma Genomics, German Cancer Research Center (DKFZ), Heidelberg, Germany. ⁶⁴⁴Fondazione Policlinico Universitario Gemelli IRCCS, Rome, Italy, Rome, Italy. ⁶⁴⁵University of Verona, Verona, Italy. ⁶⁴⁶Centre National de Génotypage, CEA - Institute de Génomique, Evry, France. ⁶⁴⁷CAPHRI Research School, Maastricht University, Maastricht, ER, The Netherlands. ⁶⁴⁸Department of Biopathology, Centre Léon Bérard, Lyon, France. ⁶⁴⁹Université Claude Bernard Lyon1, Villeurbanne, France. ⁶⁵⁰Core Research for Evolutional Science and Technology (CREST), JST, Tokyo, Japan. ⁶⁵¹Department of Biological Sciences, Laboratory for Medical Science Mathematics, Graduate School of Science, University of Tokyo, Yokohama, Japan. ⁶⁵²Department of Medical Science Mathematics, Medical Research Institute, Tokyo Medical and Dental University (TMDU), Tokyo, Japan. ⁶⁵³University Hospitals Birmingham NHS Foundation Trust, Birmingham, UK. ⁶⁵⁴Centre for Cancer Research and Cell Biology, Queen's University, Belfast, UK. ⁶⁵⁵Breast Medical Oncology, The University of Texas MD Anderson Cancer Center, Houston, TX, USA. ⁶⁵⁶Department of Surgery, Johns Hopkins University School of Medicine, Baltimore, MD, USA. ⁶⁵⁷Department of Oncology-Pathology, Science for Life Laboratory, Karolinska Institute, Stockholm, Sweden. ⁶⁵⁸School of Cancer Sciences, Faculty of Medicine, University of Southampton, Southampton, UK. ⁶⁵⁹Department of Gene Technology, Tallinn University of Technology, Tallinn, Estonia. ⁶⁶⁰Genetics and Genome Biology Program, SickKids Research Institute, The Hospital for Sick Children, Toronto, ON, Canada. ⁶⁶¹Departments of Neurosurgery and Hematology and Medical Oncology, Winship Cancer Institute and School of Medicine, Emory University, Atlanta, GA, USA. ⁶⁶²Department of Clinical and Molecular Medicine, Faculty of Medicine and Health Sciences, Norwegian University of Science and Technology, Trondheim, Norway. ⁶⁶³Argmix Consulting, North Vancouver, BC, Canada. ⁶⁶⁴Department of Information Technology, Ghent University, Interuniversitair Micro-Electronica Centrum (IMEC), Ghent, Belgium. ⁶⁶⁵Nuffield Department of Surgical Sciences, John Radcliffe Hospital, University of Oxford, Oxford, UK. ⁶⁶⁶Institute of Mathematics and Computer Science, University of Latvia, Riga, LV, Latvia. ⁶⁶⁷Discipline of Pathology, Sydney Medical School, University of Sydney, Sydney, NSW, Australia. ⁶⁶⁸Department of Applied Mathematics and Theoretical Physics, Centre for Mathematical Sciences, University of Cambridge, Cambridge, UK. ⁶⁶⁹Department of Epidemiology and Biostatistics, Memorial Sloan Kettering Cancer Center, New York, NY, USA. ⁶⁷⁰Department of Statistics, Columbia University, New York, NY, USA. ⁶⁷¹Department of Immunology, Genetics and Pathology, Science for Life Laboratory, Uppsala University, Uppsala, Sweden. ⁶⁷²School of Electronic and Information Engineering, Xi'an Jiaotong University, Xi'an, China. ⁶⁷³Department of Histopathology, Cambridge University Hospitals NHS Foundation Trust, Cambridge, UK. ⁶⁷⁴Oxford NIHR Biomedical Research Centre, University of Oxford, Oxford, UK. ⁶⁷⁵Georgia Regents University Cancer Center, Augusta, GA, USA. ⁶⁷⁶Wythenshawe Hospital, Manchester, UK. ⁶⁷⁷Department of Genetics, Washington University School of Medicine, St. Louis, MO, USA. ⁶⁷⁸Department of Biological Oceanography, Leibniz Institute of Baltic Sea Research, Rostock, Germany. ⁶⁷⁹Wellcome Centre for Human Genetics, University of Oxford, Oxford, UK. ⁶⁸⁰Department of Molecular and Human Genetics, Baylor College of Medicine, Houston, TX, USA. ⁶⁸¹Thoracic Oncology Laboratory, Mayo Clinic, Rochester, MN, USA. ⁶⁸²Institute for Genomic Medicine, Nationwide Children's Hospital, Columbus, OH, USA. ⁶⁸³Division of Gynecologic Oncology, Department of Obstetrics and Gynecology, Mayo Clinic, Rochester, MN, USA. ⁶⁸⁴International Institute for Molecular Oncology, Poznań, Poland. ⁶⁸⁵Poznan University of Medical Sciences, Poznań, Poland. ⁶⁸⁶Genomics and Proteomics Core Facility High Throughput Sequencing Unit, German Cancer Research Center (DKFZ), Heidelberg, Germany. ⁶⁸⁷NCCS-VARI Translational Research Laboratory, National Cancer Centre Singapore, Singapore, Singapore. ⁶⁸⁸Edison Family Center for Genome Sciences and Systems Biology, Washington University, St. Louis, MO, USA. ⁶⁸⁹Department of Medical Informatics and Clinical Epidemiology, Division of Bioinformatics and Computational Biology, OHSU Knight Cancer Institute, Oregon Health and Science University, Portland, OR, USA. ⁶⁹⁰School of Electronic Information and Communications, Huazhong University of Science and Technology, Wuhan, China. ⁶⁹¹Department of Applied Mathematics and Statistics, Johns Hopkins University, Baltimore, MD, USA. ⁶⁹²Department of Cancer Genome Informatics, Graduate School of Medicine, Osaka University,

Osaka, Japan. ⁶⁹³School of Mathematics and Statistics, University of Sydney, Sydney, NSW, Australia. ⁶⁹⁴Ben May Department for Cancer Research and Department of Human Genetics, University of Chicago, Chicago, IL, USA. ⁶⁹⁵Tri-Institutional PhD Program in Computational Biology and Medicine, Weill Cornell Medicine, New York, NY, USA. ⁶⁹⁶The First Affiliated Hospital, Xi'an Jiaotong University, Xi'an, China. ⁶⁹⁷Department of Medicine and Therapeutics, The Chinese University of Hong Kong, Shatin, NT, Hong Kong, China. ⁶⁹⁸Department of Biostatistics, The University of Texas MD Anderson Cancer Center, Houston, TX, USA. ⁶⁹⁹Duke-NUS Medical School, Singapore, Singapore. ⁷⁰⁰Department of Surgery, Ruijin Hospital, Shanghai Jiaotong University School of Medicine, Shanghai, China. ⁷⁰¹Division of Orthopaedic Surgery, Oslo University Hospital, Oslo, Norway. ⁷⁰²Eastern Clinical School, Monash University, Melbourne, VIC, Australia. ⁷⁰³Epworth HealthCare, Richmond, VIC, Australia. ⁷⁰⁴Department of Biostatistics and Computational Biology, Dana-Farber Cancer Institute and Harvard Medical School, Boston, MA, USA. ⁷⁰⁵Department of Biomedical Informatics, College of Medicine, The Ohio State University, Columbus, OH, USA. ⁷⁰⁶The Ohio State University Comprehensive Cancer Center (OSUCCC - James), Columbus, OH, USA. ⁷⁰⁷BIOPIIC, ICG and College of Life Sciences, Peking University, Beijing, China. ⁷⁰⁸The University of Texas School of Biomedical Informatics (SBMI) at Houston, Houston, TX, USA. ⁷⁰⁹Department of Biostatistics, University of North Carolina at Chapel Hill, Chapel Hill, NC, USA. ⁷¹⁰Department of Biochemistry and Molecular Genetics, Feinberg School of Medicine, Northwestern University, Chicago, IL, USA. ⁷¹¹Faculty of Medicine and Health, University of Sydney, Sydney, NSW, Australia. ⁷¹²Department of Pathology, Erasmus Medical Center Rotterdam, Rotterdam, GD, The Netherlands. ⁷¹³Division of Molecular Carcinogenesis, The Netherlands Cancer Institute, Amsterdam, CX, The Netherlands. ⁷¹⁴Institute of Molecular Life Sciences and Swiss Institute of Bioinformatics, University of Zurich, Zurich, Switzerland.