Supplementary Information for

Quantifying the Influence of Mutation Detection on Tumour Subclonal Reconstruction

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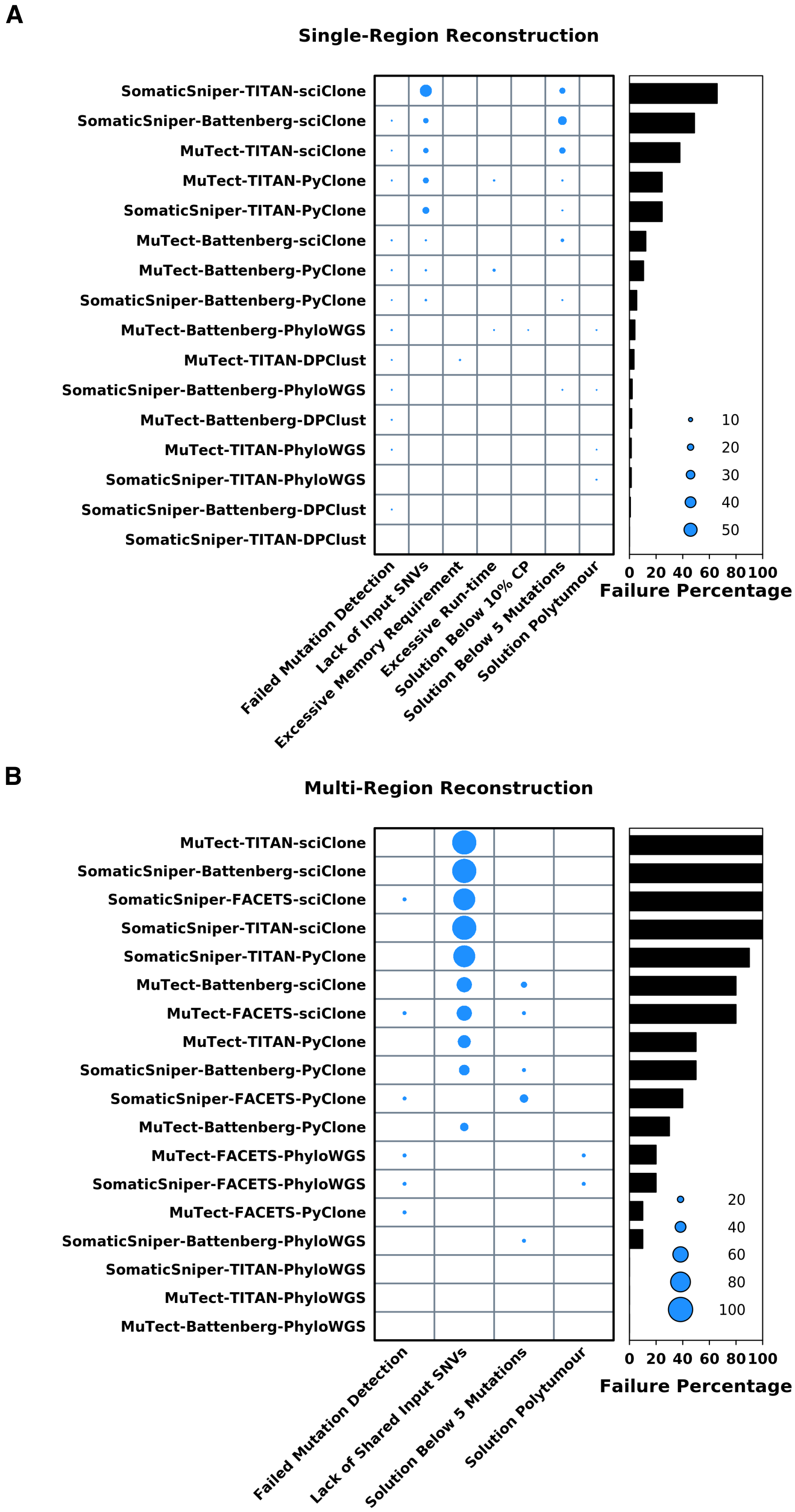
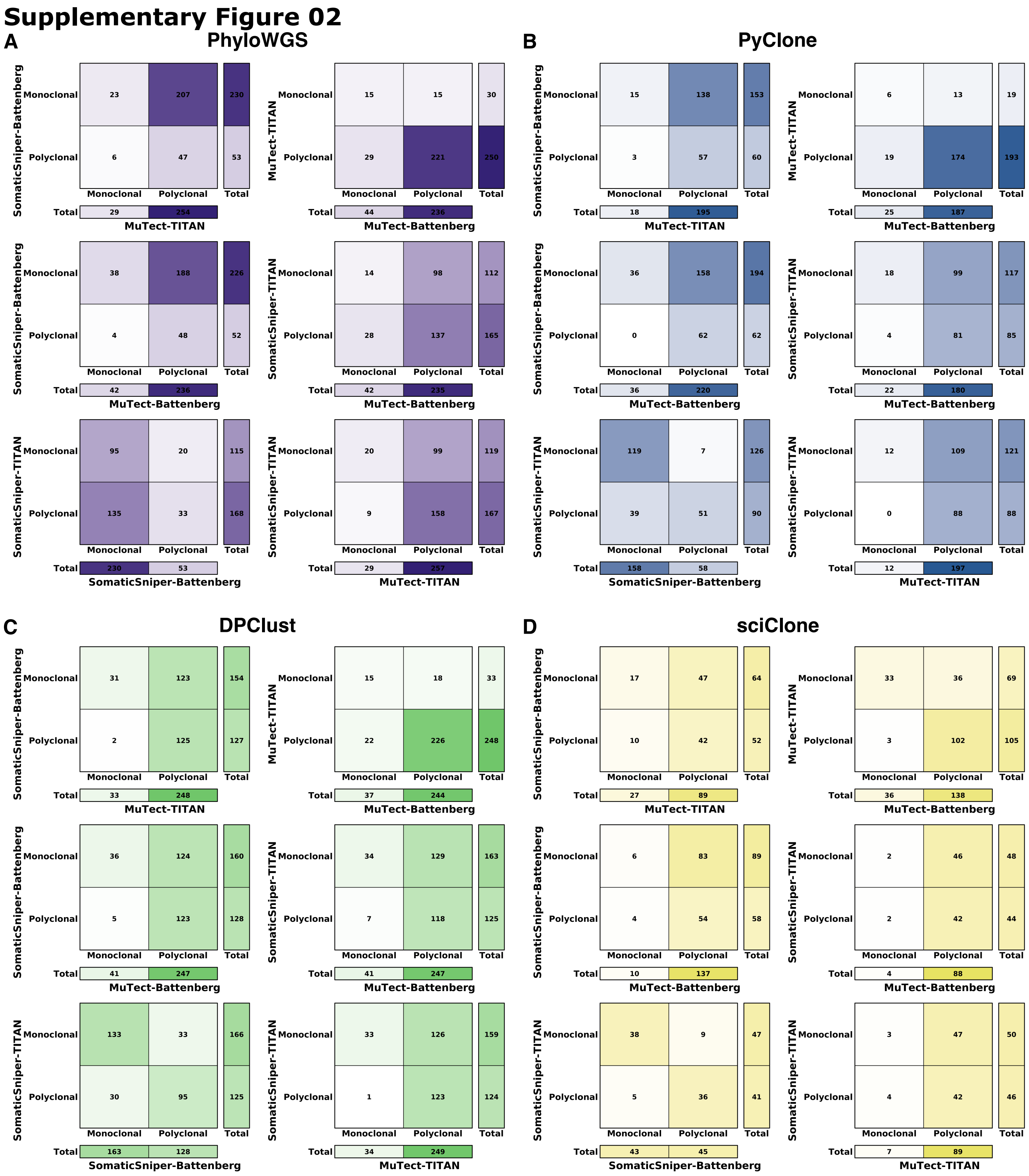
Supplementary Figure 01



Supplementary Figure 1 – Reconstruction Failures

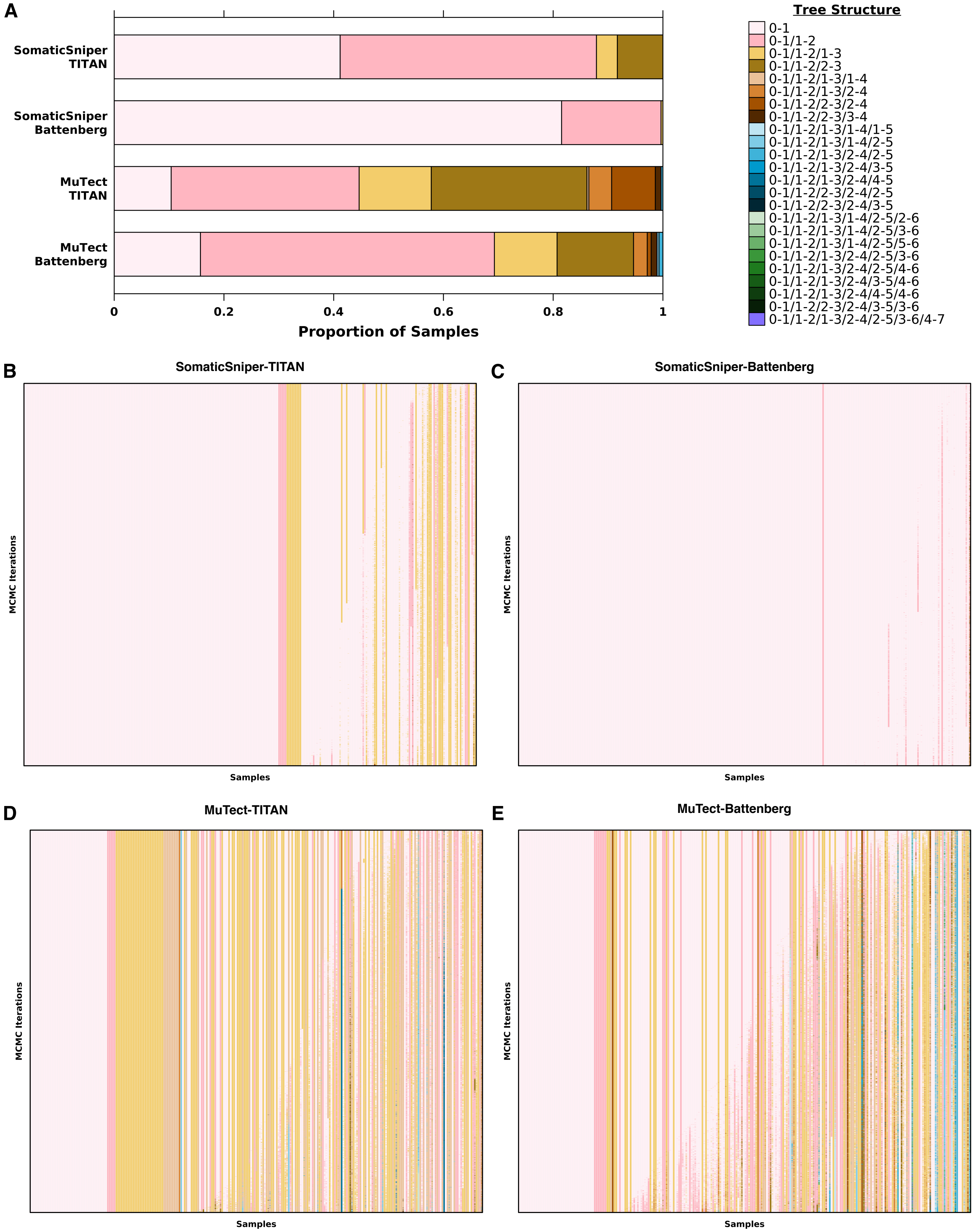
Percentage of 293 samples that failed single-region reconstruction (n=293 biologically independent samples) **A**) and percentage of 10 samples that failed multi-region reconstruction (n=10) **B**). Information is represented by pipeline and reason of failure, where the size of the dot corresponds to percentage of samples.



Supplementary Figure 2 – Clonality between Mutation Detection Tool Combinations

Comparison of clonality (monoclonal or polyclonal) for shared successfully executed samples between pipeline pairs using the same subclonal reconstruction algorithms PhyloWGS **A**), PyClone **B**), DPClust **C**), SciClone **D**). Darkness of background corresponds to number of samples.

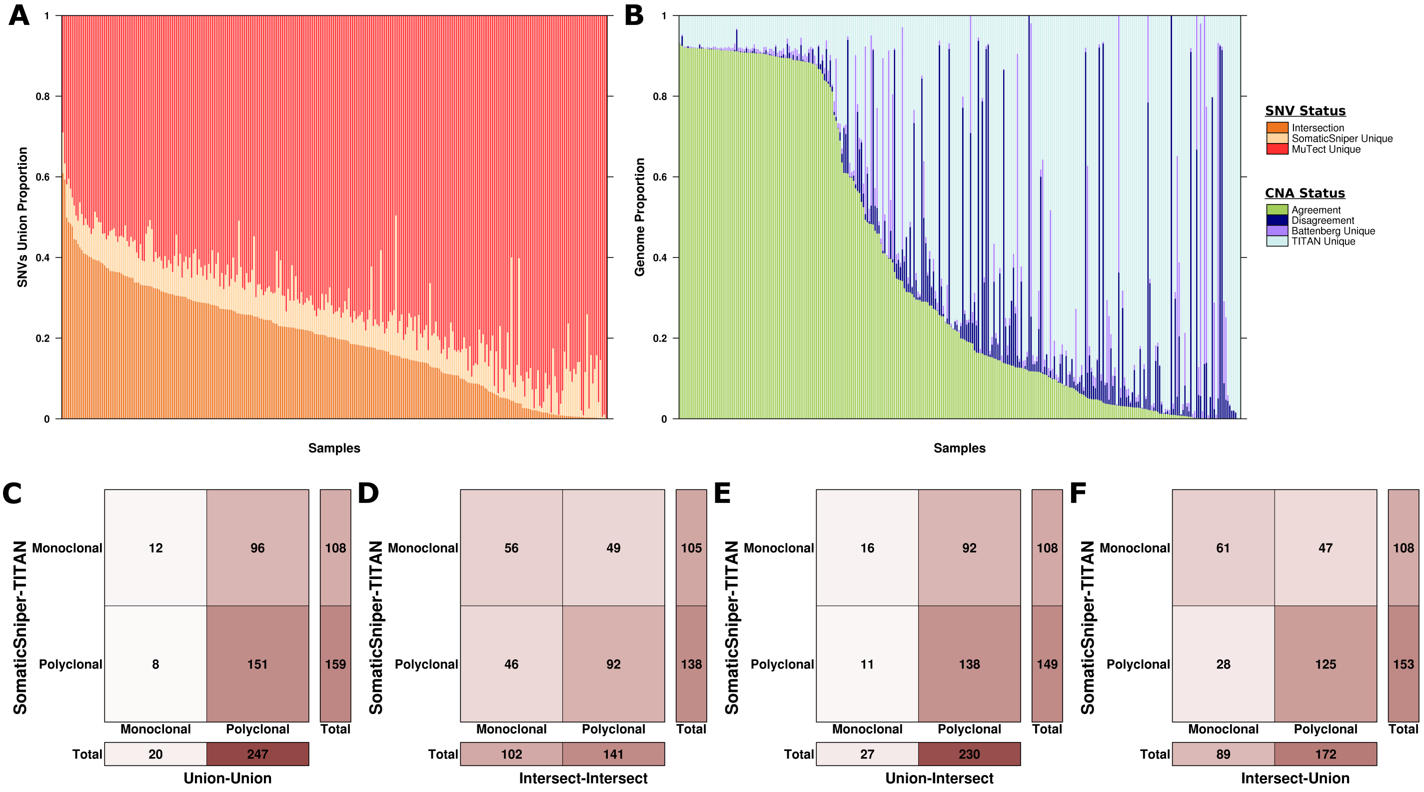
Supplementary Figure 03



Supplementary Figure 3 – Clone Tree Structures between Mutation Detection Tool Combinations

A) Proportion of samples with each clone tree structure as predicted by pipelines using PhyloWGS, with each stacked bar representing a pipeline. Tree structures are indicated by color of the stacked bar. SomaticSniper-TITAN: n=289 biologically independent samples; SomaticSniper-Battenberg: n=287; MuTect-TITAN: n=289; MuTect-Battenberg: n=280. Samples with polyclonal solutions SomaticSniper-TITAN: n=170; SomaticSniper-Battenberg: n=53; MuTect-TITAN: n=259; MuTect-Battenberg: n=236. All clone tree structures estimated across 2500 Markov chain Monte Carlo (MCMC) iterations of PhyloWGS for each sample are shown in **B-E**). Each column represents all clone tree structures predicted by 2500 iterations of MCMC for a sample, ordered top to bottom by decreasing log likelihood. Samples are ordered in increasing order by the first ordered iteration where a different clone tree structure was predicted, then by the complexity of the tree structure. Only samples with 2500 complete iterations of MCMC and harboring only the clone tree structures listed are considered. SomaticSniper-TITAN: n=274; SomaticSniper-Battenberg: n=262; MuTect-TITAN: n=265; MuTect-Battenberg: n=252. Number of samples with alternative phylogeny SomaticSniper-TITAN: n=106; SomaticSniper-Battenberg: n=85; MuTect-TITAN: n=176; MuTect-Battenberg: n=199. Number of samples with solutions only differing in clone tree structures SomaticSniper-TITAN: n=8; SomaticSniper-Battenberg: n=8; MuTect-TITAN: n=68; MuTect-Battenberg: n=95. Source data for presented and not presented samples are all provided as a Source Data file.

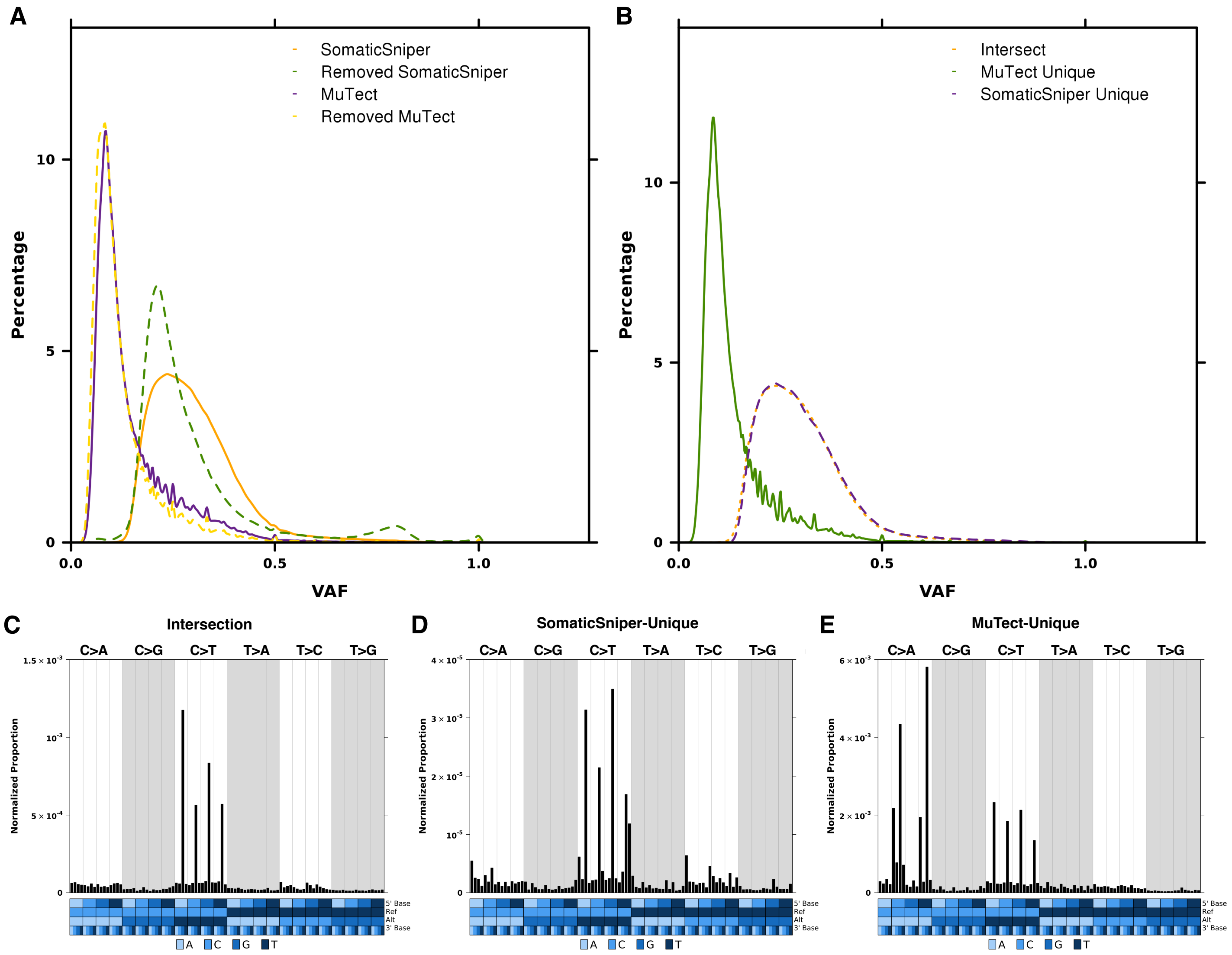
Supplementary Figure 04



Supplementary Figure 4 –Union and Intersection of SNVs and CNAs

A) Proportion of unique and intersecting SNVs detected by MuTect and SomaticSniper (n=288 biologically independent samples). **B**) Proportion of the genome covered by unique and intersecting CNAs detected by TITAN and Battenberg (n=288). Each stacked bar represents a sample and the color of the stack bar represents the status of the mutation. **C-F**) Comparing predictions of clonality by the SomaticSniper-TITAN-PhyloWGS pipeline to PhyloWGS-comprising pipelines that had inputs based on the union or intersection of SNVs and CNAs. Darkness of the background corresponds to the number of samples. Source data are provided as a Source Data file.

Supplementary Figure 05

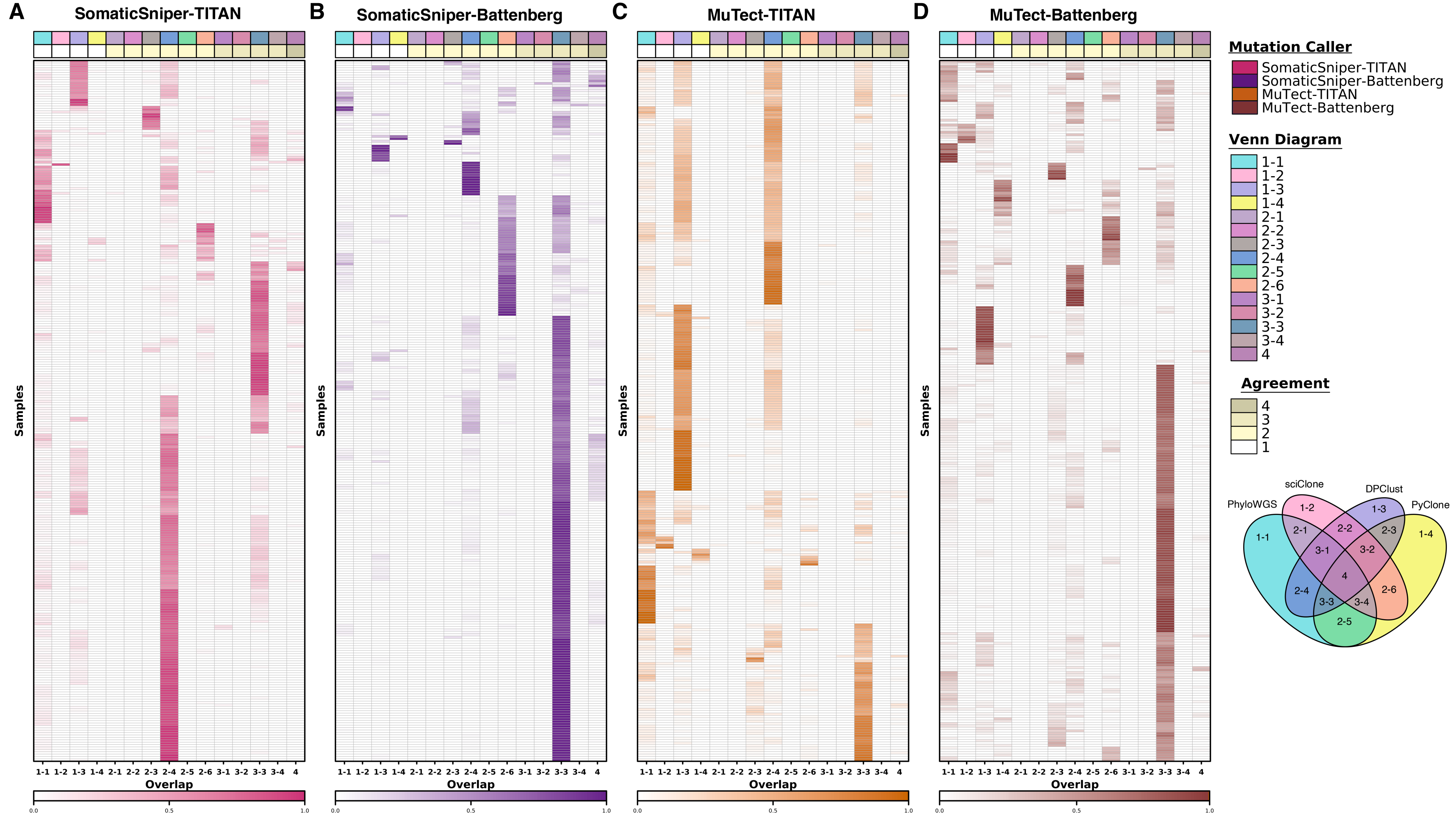


Supplementary Figure 5 – Effect of SNV Filtering

A) Density plots of variant allele frequencies (VAFs) for SNVs across all samples that were detected by SomaticSniper and MuTect post-filtering (SomaticSniper - long dash yellow line, MuTect - solid purple line), and SNVs that were removed by custom deny-list and allow-list filtering (Removed SomaticSniper - long dash green line, Removed MuTect - solid orange line). **B**) Considering only post-filtering SNVs, density plots of variant allele frequencies (VAFs) for SNVs across all samples that were detected by both SomaticSniper and MuTect (Intersect - short dash orange line), MuTect only (MuTect Unique - solid green line) and SomaticSniper only (SomaticSniper Unique - long dash purple line). **C**) Trinucleotide profile of post-filter SNVs that were detected by both SomaticSniper and MuTect, where the number of SNVs was normalized by the expected number of each trinucleotide context across the hg19 genome. Trinucleotide profiles for post-filter SomaticSniper-unique SNVs **D**) MuTect-unique SNVs **E**). Colors in the covariate bar indicate the 5', reference, alternative and 3' nucleotides in each trinucleotide context. Ref, reference nucleotide; Alt, alternative nucleotide of variant. Number of post-filtering SNVs across all samples in SomaticSniper: n=332,961 independent observations; Removed SomaticSniper: n=319,517; MuTect: n=2,246,971; Removed

MuTect: n=1,008,430; Intersect: n=185,044; SomaticSniper Unique: n=147,917; MuTect Unique: n=2,061,927. Source data are provided as a Source Data file.

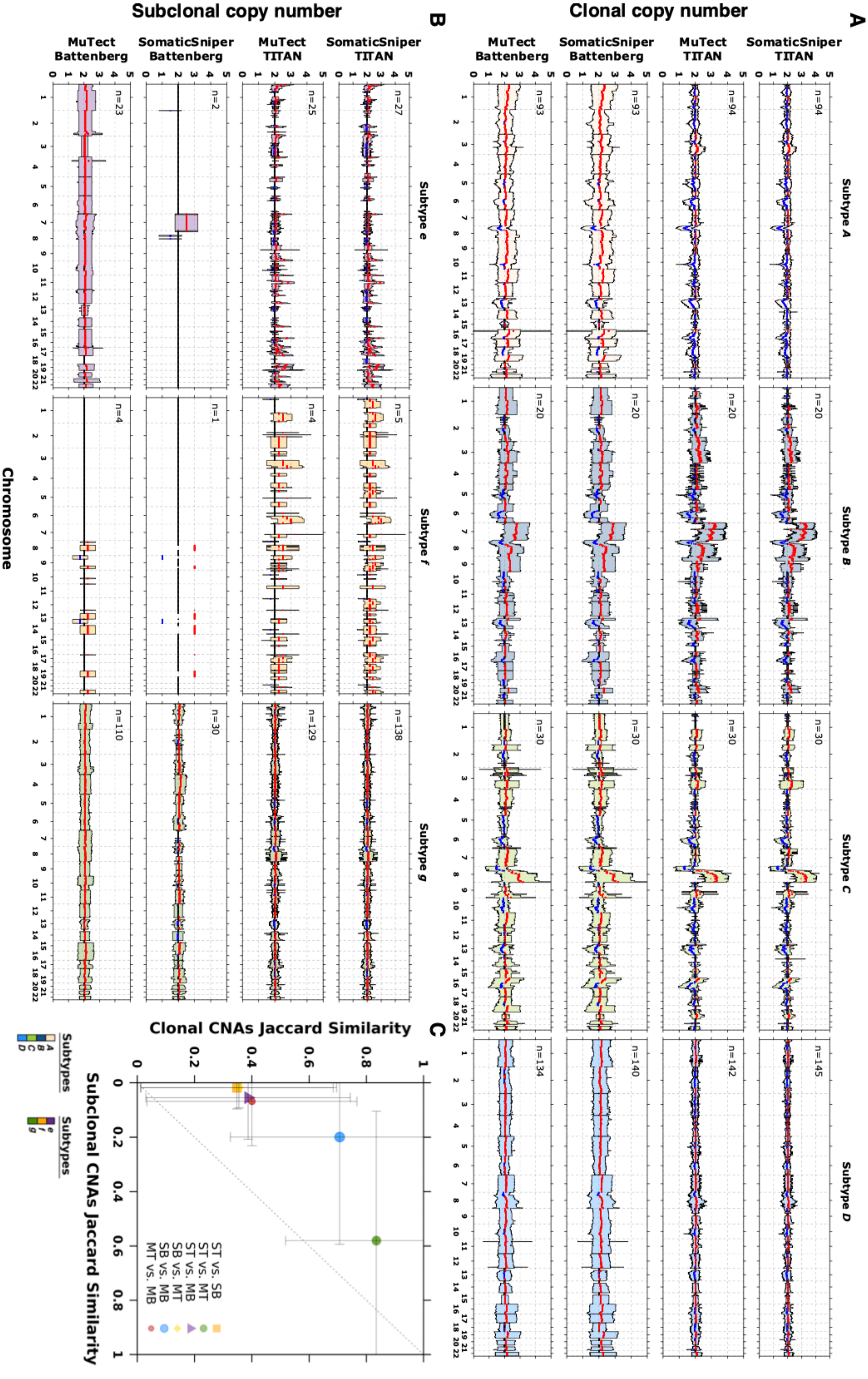
Supplementary Figure 06



Supplementary Figure 6 – Clonal SNVs by Subclonal Reconstruction Algorithm

Proportional overlap between clonal SNVs identified across pipelines using the same mutation detection tool combinations but different subclonal reconstruction algorithms **A-D**). Each row indicates clonal SNV overlap proportions for a sample. Venn diagram indicates the overlap groups of the SNVs, and the first number in the group name indicates the number of subclonal reconstruction algorithms in the overlap. Overlap groups are also represented by colors in the covariate bar, with both legend and Venn diagram reference provided. Covariate bar also indicates, by color, the number of subclonal reconstruction algorithms in agreement for each overlap group. Heatmap colors also correspond with mutation detection tool combinations, with intensity corresponding to proportion of clonal SNVs. SomaticSniper-TITAN: n=293 biologically independent samples; SomaticSniper-Battenberg: n=291; MuTect-TITAN: n=290; MuTect-Battenberg: n=288. Source data are provided as a Source Data file.

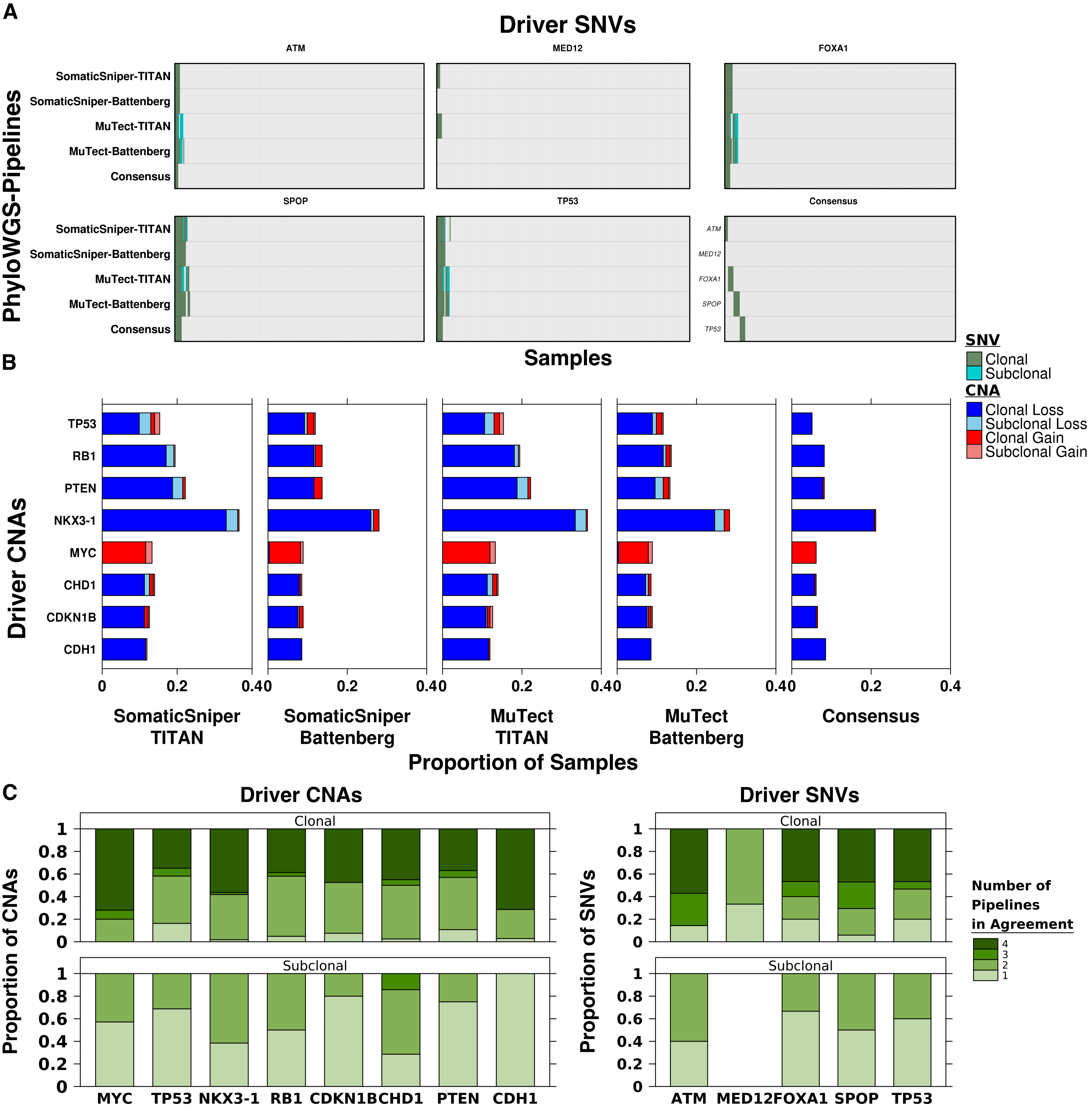
Supplementary Figure 07



Supplementary Figure 7 – Clonal and Subclonal CNAs

Average clonal and subclonal CNA profiles based on four subclonal reconstruction pipelines using PhyloWGS, organized into subtypes determined on the SomaticSniper-TITAN pipeline **A-B**). Chromosomes are shown along the *x*-axis and copy number on the *y*-axis, while each horizontal panel represents the mean clonal or subclonal copy numbers in the CNA profile of one pipeline, based on previously identified clonal and subclonal subtypes. Clonal CNA subtype average profiles are shown in **A**) and subclonal CNA subtypes are shown in **B**). Red indicates that the mean copy number is above the neutral copy number of two while blue indicates that the mean is below two. The shaded regions indicate one standard deviation and is colored to delineate each CNA clonal and subclonal subtype. Sample size is labeled within each panel. **C**) Each marker (delineated by shape and color) represents the comparison between a pair of pipelines and the Jaccard index of 1.0 Mbp genomic bins with clonal and subclonal CNAs. Mean agreement across samples is shown with error bars indicating one standard deviation. Dashed diagonal line represents the $y = x$ line. ST, SomaticSniper-TITAN; MT, MuTect-TITAN; SB, SomaticSniper-Battenberg; MB, MuTect-Battenberg. PhyloWGS ST vs. SB: n=290 independent observations; PhyloWGS ST vs. MT: n=290; PhyloWGS ST vs. MB: n=284; PhyloWGS SB vs. MT: n=287; PhyloWGS SB vs. MB: n=284; PhyloWGS MT vs. MB: n=284.

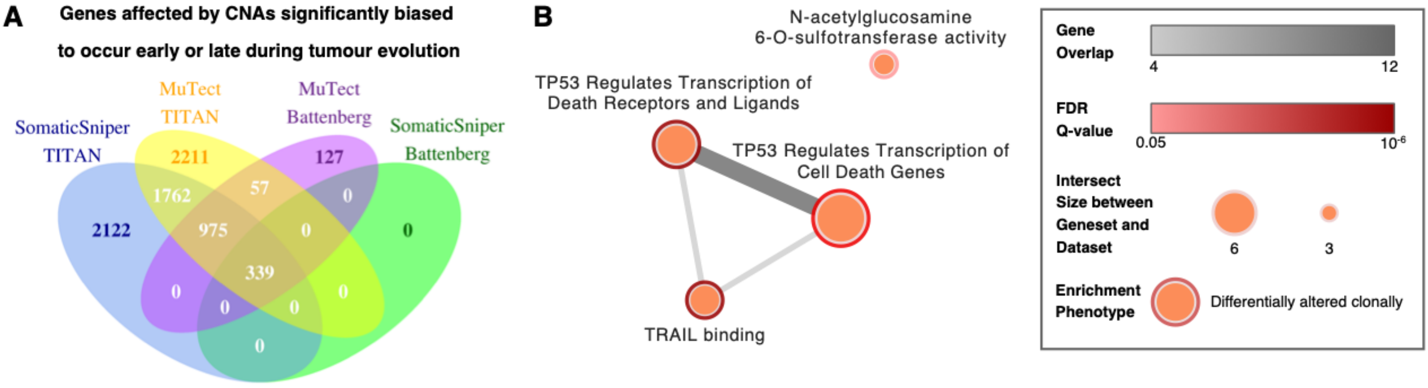
Supplementary Figure 08



Supplementary Figure 8 – Driver CNAs and SNVs

Clonal and subclonal identification of localized prostate cancer driver mutations (single nucleotide variants – SNVs; copy number aberrations - CNAs) based on four pipelines using PhyloWGS and a consensus. **A**) Sub-panels show data for five genes known to be recurrently altered by SNVs in localized prostate cancer. Each column within each sub-panel represent one sample and clonal (green) and subclonal (blue) SNVs detected by each pipeline are indicated by color. **B**) Sub-panels show data for eight genes known to be recurrently altered by CNAs in localized prostate cancer. Clonal and subclonal CNAs identified by each pipeline are shown along with a consensus. Each stacked bar represents a gene and color of the stack bar indicates the type of CNA. **C**) Proportion of samples where each number of pipelines agree on the clonality of driver mutations, assessed separately for clonal and subclonal driver mutations whenever the clonality was predicted by at least one pipeline. Each stacked bar represents information for a gene and darkness of the stacked bar corresponds to the number of pipelines in agreement. SomaticSniper-TITAN: n=289 biologically independent samples; SomaticSniper-Battenberg: n=287; MuTect-TITAN: n=289; MuTect-Battenberg: n=281. Number of SNV driver mutations SomaticSniper-TITAN: n=46 independent observations; SomaticSniper-Battenberg: n=39; MuTect-TITAN: n=59; MuTect-Battenberg: n=56. Number of CNA driver mutations SomaticSniper-TITAN: n=426 independent observations; SomaticSniper-Battenberg: n=299; MuTect-TITAN: n=426; MuTect-Battenberg: n=298. Source data are provided as a Source Data file.

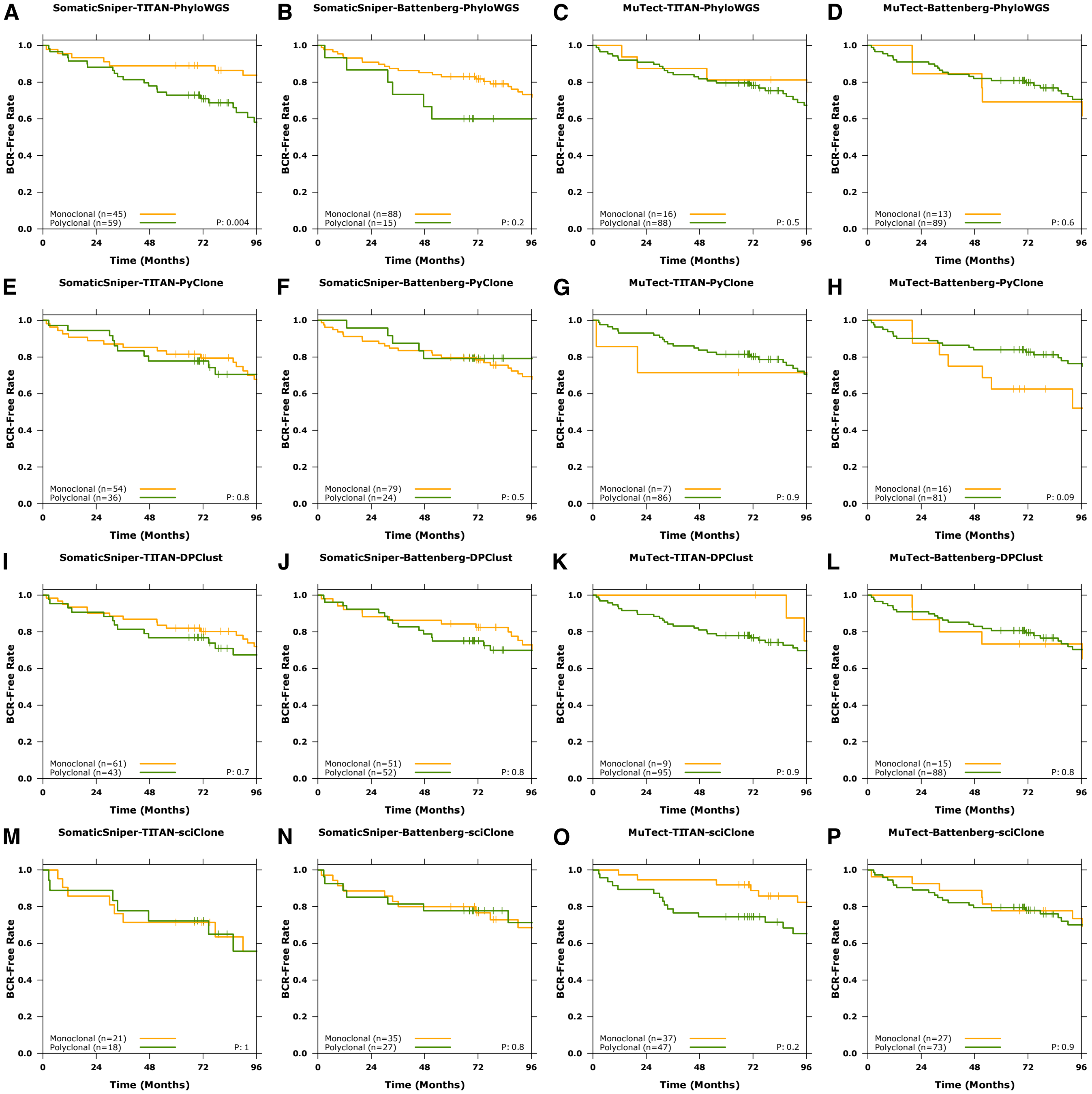
Supplementary Figure 09



Supplementary Figure 9 – Differentially Altered CNAs

A) Venn diagram of genes with CNAs that were significantly biased to be altered clonally (*i.e.,* early during tumour evolution) or subclonally (*i.e.,* late during tumour evolution) based on reconstructions from four pipelines using PhyloWGS. Numbers in overlapping areas correspond to the genes with biased timing with the same directionality (*i.e.,* consistent bias for the same gene towards early or late alterations). All 339 genes with biased timing based on all four pipelines were affected by alterations early during tumour evolution. Colors are used to help delineate between Venn's. **B**) Pathway enrichment map based on the 339 genes that were consistently differentially altered clonally. Legend indicates the number of gene overlaps between pathway gene sets (darkness of edges between vertices), false-discovery-rate (FDR) adjusted Q-values for each enriched pathway (darkness of the rims of vertices), and the number of shared genes between gene sets and the dataset (size of vertices).

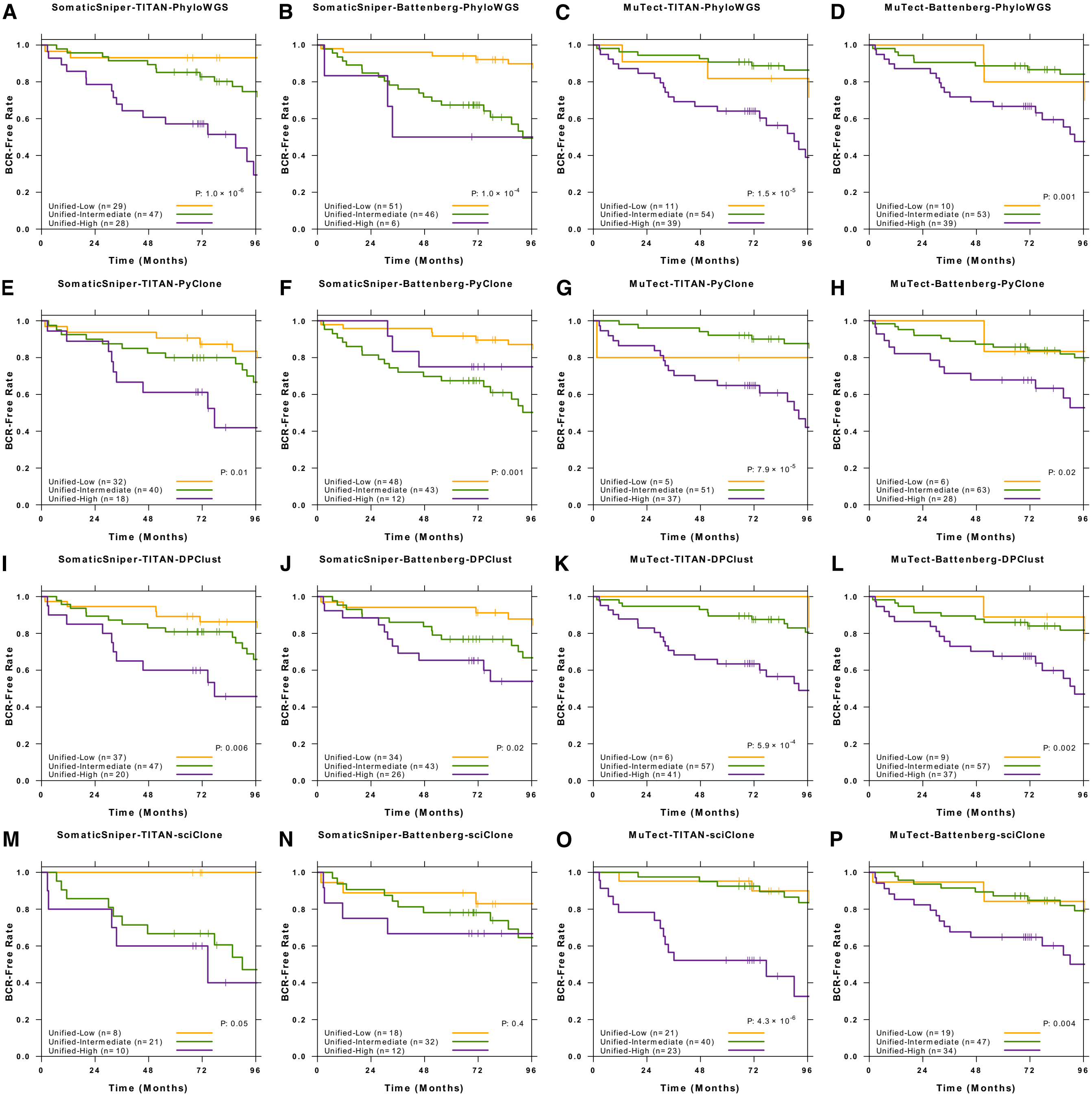
Supplementary Figure 10



Supplementary Figure 10 – Clonality Biomarker

Patients stratified using clonality (monoclonal or polyclonal) as a biomarker across all sixteen subclonal reconstruction pipelines for single-region reconstruction and groups were tested for associations with biochemical recurrence (BCR) **A-P**). Univariate modelling was carried out using log-rank tests, no covariates were included. Color of line in the KM-plots indicate patient groups, monoclonal - yellow, polyclonal - green. Sample size of each group is given as labeled.

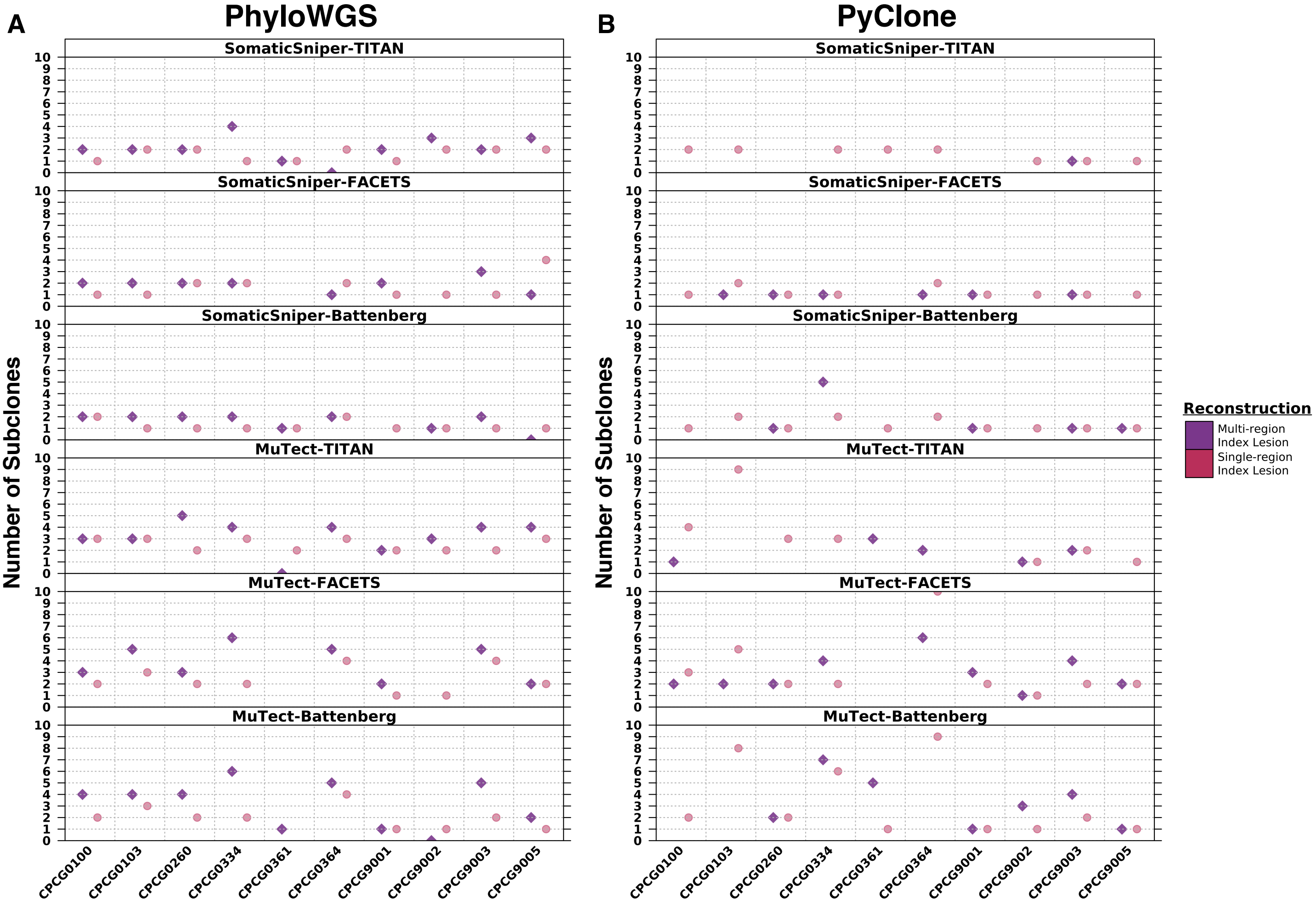
Supplementary Figure 11



Supplementary Figure 11 – Unified Biomarker

Patient recurrence outcomes stratified using a unified biomarker, combining a previously developed multi-modal biomarker with clonality predicted by sixteen pipelines for single-region reconstruction **A-P**). Univariate modelling was carried out using log-rank tests, no covariates were included. Color of line in the KM-plots indicate patient groups. Sample size of each group is given as labeled.

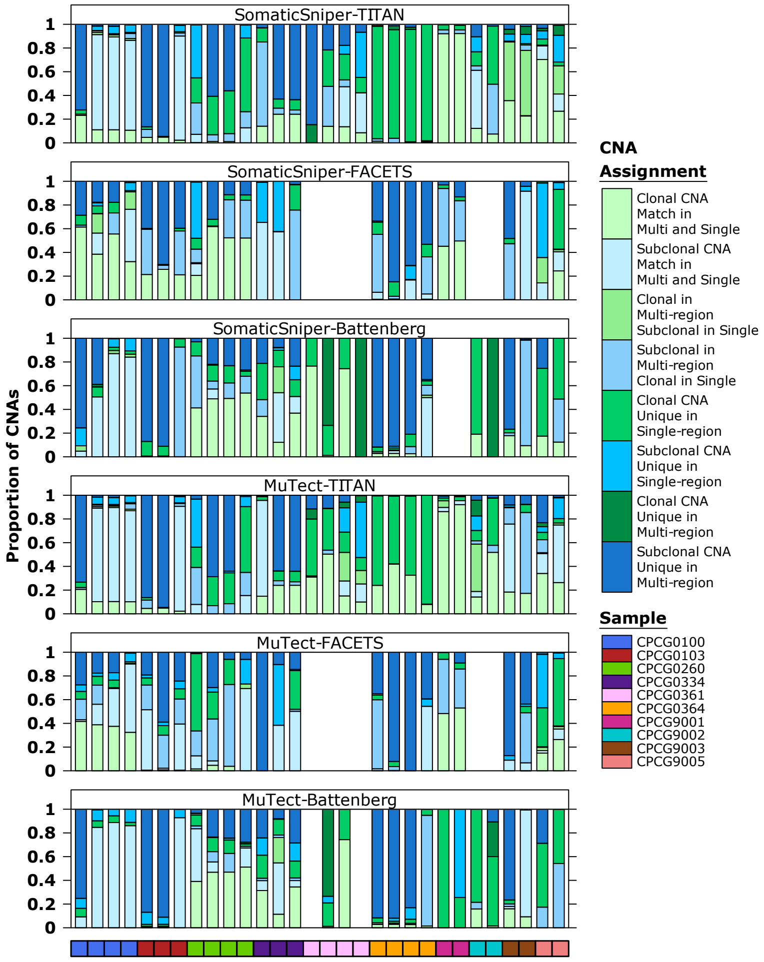
Supplementary Figure 12



Supplementary Figure 12 – Index Lesion in Multi-Region Reconstructions

Number of subclones detected in the index lesion in single-region (pink circle) and multi-region (purple diamond) reconstructions based on pipelines using PhyloWGS **A**) and PyClone **B**). Single-region reconstructions indicate the number of subclones detected in the index lesion using only single-region reconstruction of the index lesion. Multi-region reconstructions indicate the number of subclones detected in the index lesion through multi-region reconstruction of all samples from the tumour. Missing values indicate a failed reconstruction, either single- or multi-region. Multi-region reconstruction SomaticSniper-TITAN-PhyloWGS: n=10 biologically independent samples; SomaticSniper-FACETS-PhyloWGS: n=8; SomaticSniper-Battenberg-PhyloWGS: n=9; MuTect-TITAN-PhyloWGS: n=10; MuTect-FACETS-PhyloWGS: n=8; MuTect-Battenberg-PhyloWGS: n=10; SomaticSniper-TITAN-PyClone: n=1; SomaticSniper-FACETS-PyClone: n=6; SomaticSniper-Battenberg-PyClone: n=5; MuTect-TITAN-PyClone: n=5; MuTect-FACETS-PyClone: n=9; MuTect-Battenberg-PyClone: n=7. Single-region reconstruction SomaticSniper-TITAN-PhyloWGS: n=10; SomaticSniper-FACETS-PhyloWGS: n=9; SomaticSniper-Battenberg-PhyloWGS: n=10; MuTect-TITAN-PhyloWGS: n=10; MuTect-FACETS-PhyloWGS: n=9; MuTect-Battenberg-PhyloWGS: n=9; SomaticSniper-TITAN-PyClone: n=8; SomaticSniper-FACETS-PyClone: n=9; SomaticSniper-Battenberg-PyClone: n=10; MuTect-TITAN-PyClone: n=7; MuTect-FACETS-PyClone: n=9; MuTect-Battenberg-PyClone: n=10.

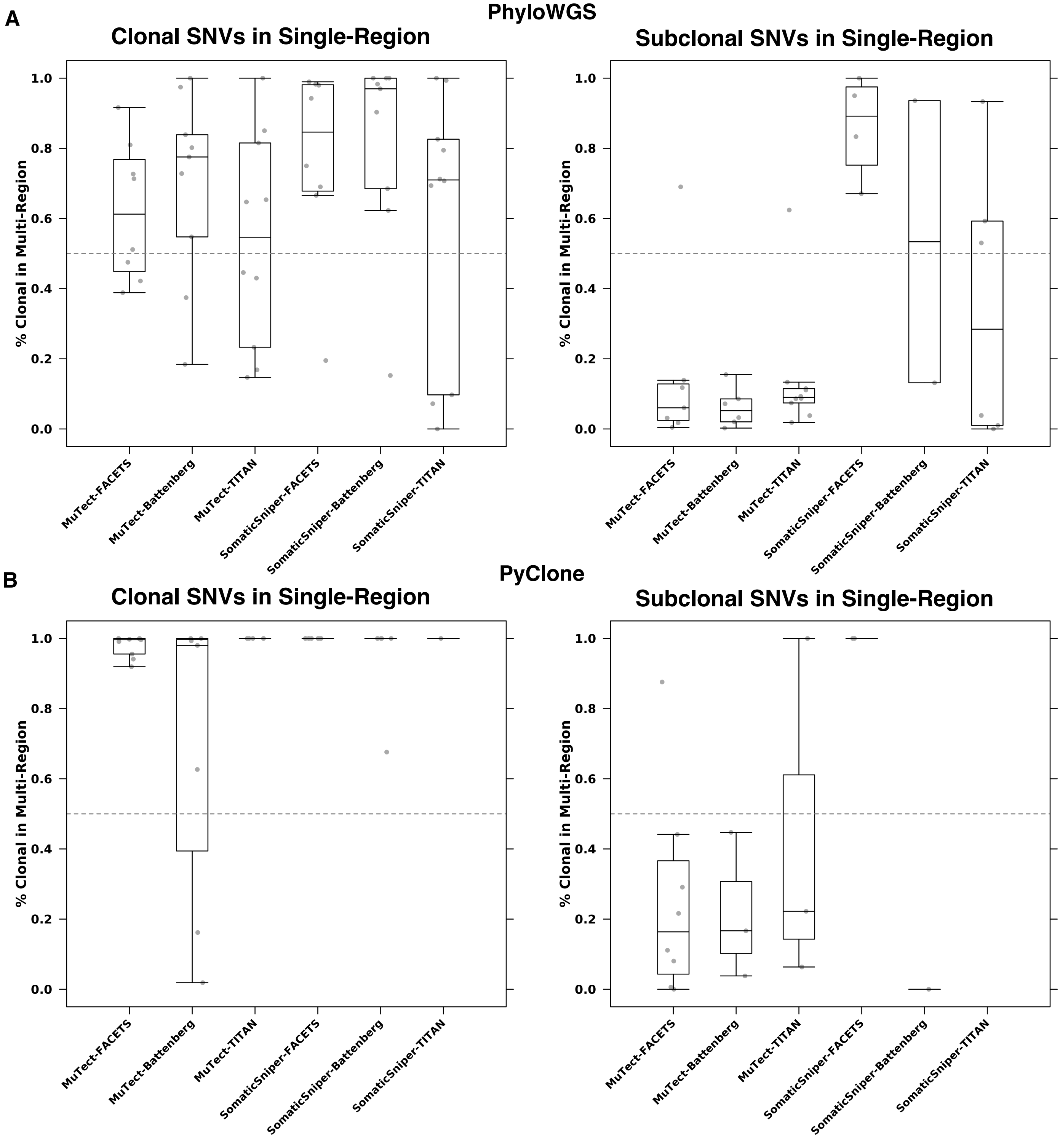
Supplementary Figure 13



Supplementary Figure 13 – Single- and Multi-Region CNA Clonality

Comparison of clonal and subclonal CNA clonality predictions by single- and multi-region subclonal reconstructions in pipelines using PhyloWGS. CNAs were compared by 1.0 Mbp genomic bins between single-region reconstructions and their corresponding multi-region reconstructions. Each stacked bar represents one single-region and the covariate bar color indicates the identity of the sample. Missing bars indicated failed reconstructions, either single- or multi-region. CNAs were grouped into eight categories, delineated by stacked bar color. “Clonal CNA Match in Multi and Single” if the CNA was predicted to be clonal in both single- and multi-region reconstructions and ‘Subclonal CNA Match in Multi and Single’ if the CNA was predicted to be subclonal in both. CNAs with disagreeing clonality predictions in single- and multi-region reconstructions were grouped as ‘Clonal in Multi-region Subclonal in Single’ or *vice versa* as ‘Subclonal in Multi-region Clonal in Single’. CNAs considered only in single- or multi-region reconstruction and thus did not have a clonality assignment in the reconstruction where it was not considered were given one of the categories: ‘Clonal CNA Unique in Single-region’, ‘Subclonal CNA Unique in Single-region’, ‘Clonal CNA Unique in Multi-region’, or ‘Subclonal CNA Unique in Multi-region’. SomaticSniper-TITAN-PhyloWGS: n=30 biologically independent samples; SomaticSniper-FACETS-PhyloWGS: n=24; SomaticSniper-Battenberg-PhyloWGS: n=28; MuTect-TITAN-PhyloWGS: n=30; MuTect-FACETS-PhyloWGS: n=24; MuTect-Battenberg-PhyloWGS: n=28.

Supplementary Figure 14



Supplementary Figure 14 – Index Lesion SNVs in Multi-Region Analyses

Clonal and subclonal mutation cluster composition as defined by SNVs in index lesion single-region reconstructions compared to multi-region reconstructions by pipelines using PhyloWGS **A**) and PyClone **B**). Proportion of SNVs that were predicted to be clonal or subclonal in single-region reconstructions of the index lesion but were predicted to be clonal in multi-region reconstructions. All boxplots show the median (center line, 50th percentile), upper and lower quartiles (box limits, 75th and 25th percentile, respectively), and whiskers extend to the minimum and maximum values within 1.5 times the interquartile range (Tukey boxplots). All data points are represented using grey circles and outliers are those beyond the whiskers. Clonal SNVs in single-region MuTect-FACETS-PhyloWGS: n=8 biologically independent samples; MuTect-Battenberg-PhyloWGS: n=9; MuTect-TITAN-PhyloWGS: n=10; SomaticSniper-FACETS-PhyloWGS: n=8; SomaticSniper-Battenberg-PhyloWGS: n=9; SomaticSniper-TITAN-PhyloWGS: n=10; MuTect-FACETS-PyClone: n=9; MuTect-Battenberg-PyClone: n=7; MuTect-TITAN-PyClone: n=4; SomaticSniper-FACETS-PyClone: n=6; SomaticSniper-Battenberg-PyClone: n=5; SomaticSniper-TITAN-PyClone: n=1. Subclonal SNVs in single-region MuTect-FACETS-PhyloWGS: n=7; MuTect-Battenberg-PhyloWGS: n=6; MuTect-TITAN-PhyloWGS: n=10; SomaticSniper-FACETS-PhyloWGS: n=4; SomaticSniper-Battenberg-PhyloWGS: n=2; SomaticSniper-TITAN-PhyloWGS: n=6; MuTect-FACETS-PyClone: n=8; MuTect-Battenberg-PyClone: n=3; MuTect-TITAN-PyClone: n=3; SomaticSniper-FACETS-PyClone: n=2; SomaticSniper-Battenberg-PyClone: n=1; SomaticSniper-TITAN-PyClone: n=0. Source data are provided as a Source Data file.

Supplementary Tables

Supplementary Table 1 – Failed Reconstructions

Number of reconstructions attempted, number of successful reconstructions and failure rate for all single- and multi-region subclonal reconstruction pipelines. Information is displayed separately for each of the twenty-two different mutation detection tool and subclonal reconstruction algorithm combinations. Summary information is calculated for single-region reconstruction of 293 tumours, single-region reconstruction of 30 samples from 10 tumours with multi-region sequencing, and multi-region reconstructions of the 10 tumours. Each sample that failed reconstruction is listed with the reason of failure.

SomaticSniper-TITAN	PhyloWGS
Single-Region	Reconstruction
Total Samples	293
Completed Samples	289
Failure Rate	0.0136518771331058
Sample	Failure Reason
CPCG0166	Polytumour
CPCG0520	Polytumour
CPCG0528	Polytumour
TCGA_7522_T1_wgs	Polytumour

SomaticSniper-TITAN	PhyloWGS
Multi-region	Tumours
Single-Region	Reconstruction
Total Samples	30
Completed Samples	30
Failure Rate	0
Multi-Region	Reconstruction
Total Samples	10
Completed Samples	10
Failure Rate	0
Sample	Failure Reason

SomaticSniper-Battenberg	PhyloWGS
Single-Region	Reconstruction
Total Samples	293
Completed Samples	287
Failure Rate	0.0204778156996587
Sample	Failure Reason
CPCG0117	Failed Battenberg
CPCG0124	Failed Battenberg
CPCG0205	Failed Battenberg
CPCG0567	Below 5 Mutations
CPCG0424	Below 5 Mutations
CPCG0074	Polytumour

SomaticSniper-Battenberg	PhyloWGS
Multi-region	Tumours
Single-Region	Reconstruction
Total Samples	30
Completed Samples	30
Failure Rate	0
Multi-Region	Reconstruction
Total Samples	10
Completed Samples	9
Failure Rate	0.1
Sample	Failure Reason
CPCG9001-MR	Below 5 Mutations

MuTect-TITAN	PhyloWGS
Single-Region	Reconstruction
Total Samples	293
Completed Samples	289
Failure Rate	0.0136518771331058
Sample	Failure Reason
CPCG0050	Failed MuTect
CPCG0090	Failed MuTect
CPCG0122	Failed MuTect
TCGA_7522_T1_wgs	Polytumour

MuTect-TITAN	PhyloWGS
Multi-region	Tumours
Single-Region	Reconstruction
Total Samples	30
Completed Samples	30
Failure Rate	0
Multi-Region	Reconstruction
Total Samples	10
Completed Samples	10
Failure Rate	0
Sample	Failure Reason

MuTect-Battenberg	PhyloWGS
Single-Region	Reconstruction
Total Samples	293
Completed Samples	281
Failure Rate	0.0409556313993174
Sample	Failure Reason
CPCG0117	Failed Battenberg
CPCG0124	Failed Battenberg
CPCG0205	Failed Battenberg
CPCG0050	Failed MuTect
CPCG0090	Failed MuTect
CPCG0122	Failed MuTect
CPCG0089	Excessive run-time
CPCG0587	Excessive run-time
CPCG0575	Excessive run-time
CPCG0361	Below 10% CP
CPCG0575	Polytumour
TCGA_5789_T1_wgs	Polytumour

MuTect-Battenberg	PhyloWGS
Multi-region	Tumours
Single-Region	Reconstruction
Total Samples	30
Completed Samples	28
Failure Rate	0.0666666666666667
Multi-Region	Reconstruction
Total Samples	10
Completed Samples	10
Failure Rate	0
Sample	Failure Reason
CPCG0361-F1	Below 10% CP
CPCG0361-F4	Polytumour

SomaticSniper-FACETS	PhyloWGS
Multi-region	Tumours
Single-Region	Reconstruction
Total Samples	30
Completed Samples	26
Failure Rate	0.133333333333333
Multi-Region	Reconstruction
Total Samples	10
Completed Samples	8
Failure Rate	0.2
Sample	Failure Reason
CPCG9002-MR	Polytumour
CPCG0361-F1	No FACETS
CPCG0361-F2	No FACETS
CPCG0361-F3	No FACETS
CPCG0361-F4	No FACETS
CPCG0361-MR	No FACETS

MuTect-FACETS	PhyloWGS
Multi-region	Tumours
Single-Region	Reconstruction
Total Samples	30
Completed Samples	26
Failure Rate	0.133333333333333
Multi-Region	Reconstruction
Total Samples	10
Completed Samples	8
Failure Rate	0.2
Sample	Failure Reason
CPCG9002-MR	Polytumour
CPCG0361-F1	No FACETS
CPCG0361-F2	No FACETS
CPCG0361-F3	No FACETS
CPCG0361-F4	No FACETS
CPCG0361-MR	No FACETS

SomaticSniper-TITAN	PyClone
Single-Region	Reconstruction
Total Samples	293
Completed Samples	221
Failure Rate	0.245733788395904

Sample	Failure Reason
Baca_03-728_T_wgs	No Input
Baca_05-2709_T_wgs	No Input
Baca_09-3983_T_wgs	No Input
Baca_STID0000000410_T_wgs	No Input
Berger_1783_T_wgs	No Input
Berger_2832_T_wgs	No Input
CPCG0015	No Input
CPCG0019	No Input
CPCG0022	No Input
CPCG0027	No Input
CPCG0030	No Input
CPCG0046	No Input
CPCG0072	No Input
CPCG0074	No Input
CPCG0084	No Input
CPCG0089	No Input
CPCG0120	No Input
CPCG0123	No Input
CPCG0154	No Input
CPCG0199	No Input
CPCG0205	No Input
CPCG0212	No Input
CPCG0219	No Input
CPCG0234	No Input
CPCG0237	No Input
CPCG0246	No Input
CPCG0251	No Input
CPCG0259	No Input
CPCG0274	No Input
CPCG0342	No Input
CPCG0344	No Input
CPCG0353	No Input
CPCG0358	No Input
CPCG0373	No Input
CPCG0450	No Input
CPCG0458	No Input
CPCG0525	No Input
CPCG0529	No Input
CPCG0559	No Input
CPCG0562	No Input
CPCG0570	No Input
CPCG0580	No Input
CPCG0584	No Input
CPCG0590	No Input
CPCG0595	No Input

CPCG0597	No Input
CPCG0600	No Input
TCGA_5503_T1_wgs	No Input
TCGA_5506_T1_wgs	No Input
TCGA_5763_T1_wgs	No Input
TCGA_5771_T1_wgs	No Input
TCGA_6336_T1_wgs	No Input
TCGA_6370_T1_wgs	No Input
TCGA_7079_T1_wgs	No Input
TCGA_7233_T1_wgs	No Input
TCGA_7522_T1_wgs	No Input
TCGA_7737_T1_wgs	No Input
Weischenfeldt_02_T_wgs	No Input
Weischenfeldt_03_T_wgs	No Input
Weischenfeldt_06_T_wgs	No Input
Baca_07-5037_T_wgs	No Input
Baca_STID0000002621_T_wgs	No Input
CPCG0102	No Input
CPCG0452	No Input
CPCG0547	No Input
CPCG0560	No Input
CPCG0589	No Input
Baca_09-396_T_wgs	Below 5 Mutations
CPCG0127	Below 5 Mutations
CPCG0360	Below 5 Mutations
CPCG0363	Below 5 Mutations
CPCG0578	Below 5 Mutations

SomaticSniper-TITAN	PyClone
Multi-region	Tumours
Single-Region	Reconstruction
Total Samples	30
Completed Samples	18
Failure Rate	0.4
Multi-Region	Reconstruction
Total Samples	10
Completed Samples	1
Failure Rate	0.9
Sample	Failure Reason
CPCG0100-F3	Below 5 Mutations
CPCG0100-F6	No Input
CPCG0103-F4	No Input
CPCG0260-F1	No Input
CPCG0260-F4	No Input
CPCG0361-F3	No Input
CPCG0361-F4	No Input
CPCG0364-F3	No Input
CPCG9001-P1	No Input
CPCG9001-P2	No Input
CPCG9002-P2	No Input
CPCG9005-P2	Below 5 Mutations
CPCG0100-MR	No shared input

CPCG0103-MR	No shared input
CPCG0260-MR	No shared input
CPCG0334-MR	No shared input
CPCG0361-MR	No shared input
CPCG0364-MR	No shared input
CPCG9001-MR	No shared input
CPCG9002-MR	No shared input
CPCG9005-MR	No shared input

SomaticSniper-Battenberg	PyClone
Single-Region	Reconstruction
Total Samples	293
Completed Samples	277
Failure Rate	0.0546075085324232
Sample	Failure Reason
CPCG0117	Failed Battenberg
CPCG0124	Failed Battenberg
Baca_STID0000000410_T_wgs	No Input
CPCG0074	No Input
CPCG0120	No Input
CPCG0212	No Input
CPCG0219	No Input
CPCG0274	No Input
Weischenfeldt_011_T_wgs	No Input
Weischenfeldt_02_T_wgs	No Input
Weischenfeldt_09_T_wgs	No Input
CPCG0046	No Input
CPCG0089	No Input
Baca_09-396_T_wgs	Below 5 Mutations
Berger_1701_T_wgs	Below 5 Mutations
Berger_2832_T_wgs	Below 5 Mutations

SomaticSniper-Battenberg	PyClone
Multi-region	Tumours
Single-Region	Reconstruction
Total Samples	30
Completed Samples	25
Failure Rate	0.166666666666667
Multi-Region	Reconstruction
Total Samples	10
Completed Samples	5
Failure Rate	0.5
Sample	Failure Reason
CPCG0100-F3	Below 5 Mutations
CPCG0100-F5	No Input
CPCG0100-F6	No Input
CPCG0103-F4	No Input
CPCG0364-F4	No Input
CPCG0100-MR	No shared inputs
CPCG0103-MR	No shared inputs
CPCG0361-MR	Below 5 Mutations
CPCG0364-MR	No shared inputs
CPCG9002-MR	No shared inputs

MuTect-TITAN	PyClone
Single-Region	Reconstruction
Total Samples	293
Completed Samples	221
Failure Rate	0.245733788395904
Sample	Failure Reason
CPCG0006	Excessive Run-time
CPCG0020	Excessive Run-time
CPCG0040	Excessive Run-time
CPCG0047	Excessive Run-time
CPCG0063	Excessive Run-time
CPCG0166	Excessive Run-time
CPCG0424	Excessive Run-time
CPCG0451	Excessive Run-time
CPCG0574	Excessive Run-time
CPCG0050	Failed MuTect
CPCG0090	Failed MuTect
CPCG0122	Failed MuTect
Baca_05-2709_T_wgs	No Input
Baca_STID0000000410_T_wgs	No Input
Berger_1783_T_wgs	No Input
CPCG0022	No Input
CPCG0027	No Input
CPCG0030	No Input
CPCG0046	No Input
CPCG0084	No Input
CPCG0089	No Input
CPCG0120	No Input
CPCG0123	No Input
CPCG0154	No Input
CPCG0205	No Input
CPCG0219	No Input
CPCG0237	No Input
CPCG0246	No Input
CPCG0251	No Input
CPCG0259	No Input
CPCG0274	No Input
CPCG0342	No Input
CPCG0344	No Input
CPCG0353	No Input
CPCG0358	No Input
CPCG0450	No Input
CPCG0458	No Input
CPCG0529	No Input
CPCG0559	No Input
CPCG0580	No Input
CPCG0590	No Input
CPCG0595	No Input
CPCG0597	No Input
CPCG0600	No Input
TCGA_5503_T1_wgs	No Input

TCGA_5506_T1_wgs	No Input
TCGA_5763_T1_wgs	No Input
TCGA_5771_T1_wgs	No Input
TCGA_6370_T1_wgs	No Input
TCGA_7079_T1_wgs	No Input
TCGA_7233_T1_wgs	No Input
TCGA_7737_T1_wgs	No Input
Weischenfeldt_02_T_wgs	No Input
Baca_03-728_T_wgs	No Input
Baca_STID0000002621_T_wgs	No Input
CPCG0019	No Input
CPCG0072	No Input
CPCG0234	No Input
CPCG0525	No Input
CPCG0570	No Input
CPCG0584	No Input
CPCG0589	No Input
TCGA_6336_T1_wgs	No Input
TCGA_7522_T1_wgs	No Input
Weischenfeldt_03_T_wgs	No Input
Weischenfeldt_06_T_wgs	No Input
Baca_07-5037_T_wgs	Below 5 Mutations
Berger_2832_T_wgs	Below 5 Mutations
CPCG0015	Below 5 Mutations
CPCG0199	Below 5 Mutations
CPCG0560	Below 5 Mutations
CPCG0562	Below 5 Mutations

MuTect-TITAN	PyClone
Multi-region	Tumours
Single-Region	Reconstruction
Total Samples	30
Completed Samples	25
Failure Rate	0.166666666666667
Multi-Region	Reconstruction
Total Samples	10
Completed Samples	5
Failure Rate	0.5
Sample	Failure Reason
CPCG0103-F4	No Input
CPCG0260-F4	Below 5 Mutations
CPCG0364-F1	Excessive run-time
CPCG9001-P1	No Input
CPCG9001-P2	No Input
CPCG0103-MR	No shared input
CPCG0260-MR	No shared input
CPCG0334-MR	No shared input
CPCG9001-MR	No shared input
CPCG9005-MR	No shared input

MuTect-Battenberg	PyClone
Single-Region	Reconstruction
Total Samples	293
Completed Samples	262
Failure Rate	0.10580204778157
Sample	Failure Reason
CPCG0006	Excessive Run-time
CPCG0019	Excessive Run-time
CPCG0020	Excessive Run-time
CPCG0027	Excessive Run-time
CPCG0040	Excessive Run-time
CPCG0047	Excessive Run-time
CPCG0063	Excessive Run-time
CPCG0072	Excessive Run-time
CPCG0084	Excessive Run-time
CPCG0166	Excessive Run-time
CPCG0234	Excessive Run-time
CPCG0249	Excessive Run-time
CPCG0346	Excessive Run-time
CPCG0388	Excessive Run-time
CPCG0424	Excessive Run-time
CPCG0574	Excessive Run-time
CPCG0577	Excessive Run-time
CPCG0589	Excessive Run-time
CPCG0050	Failed MuTect
CPCG0090	Failed MuTect
CPCG0122	Failed MuTect
CPCG0117	Failed Battenberg
CPCG0124	Failed Battenberg
CPCG0046	No Input
CPCG0074	No Input
CPCG0120	No Input
CPCG0219	No Input
CPCG0274	No Input
Weischenfeldt_011_T_wgs	No Input
Weischenfeldt_02_T_wgs	No Input
Weischenfeldt_09_T_wgs	No Input

MuTect-Battenberg	PyClone
Multi-region	Tumours
Single-Region	Reconstruction
Total Samples	30
Completed Samples	28
Failure Rate	0.0666666666666667
Multi-Region	Reconstruction
Total Samples	10
Completed Samples	7
Failure Rate	0.3
Sample	Failure Reason
CPCG0100-F5	No Input
CPCG0100-F6	No Input

CPCG0103-MR	No Input
CPCG0100-MR	No shared input
CPCG0364-MR	No shared input

SomaticSniper-FACETS	PyClone
Multi-region	Tumours
Single-Region	Reconstruction
Total Samples	30
Completed Samples	26
Failure Rate	0.133333333333333
Multi-Region	Reconstruction
Total Samples	10
Completed Samples	6
Failure Rate	0.4
Sample	Failure Reason
CPCG0361-F1	No FACETS
CPCG0361-F2	No FACETS
CPCG0361-F3	No FACETS
CPCG0361-F4	No FACETS
CPCG0100-MR	Below 5 Mutations
CPCG9002-MR	Below 5 Mutations
CPCG9005-MR	Below 5 Mutations
CPCG0361-MR	No FACETS

MuTect-FACETS	PyClone
Multi-region	Tumours
Single-Region	Reconstruction
Total Samples	30
Completed Samples	25
Failure Rate	0.166666666666667
Multi-Region	Reconstruction
Total Samples	10
Completed Samples	9
Failure Rate	0.1
Sample	Failure Reason
CPCG0103-F4	Excessive Memory Requirementy
CPCG0361-F1	No FACETS
CPCG0361-F2	No FACETS
CPCG0361-F3	No FACETS
CPCG0361-F4	No FACETS
CPCG0361-MR	No FACETS

SomaticSniper-TITAN	DPClust
Single-Region	Reconstruction
Total Samples	293
Completed Samples	293
Failure Rate	0
Sample	Failure Reason

SomaticSniper-Battenberg	DPClust
Single-Region	Reconstruction
Total Samples	293
Completed Samples	291
Failure Rate	0.0068259385665529
Sample	Failure Reason
CPCG0124	Failed Battenberg
CPCG0117	Failed Battenberg

MuTect-TITAN	DPClust
Single-Region	Reconstruction
Total Samples	293
Completed Samples	283
Failure Rate	0.0341296928327645
Sample	Failure Reason
CPCG0050	Failed MuTect
CPCG0090	Failed MuTect
CPCG0122	Failed MuTect
CPCG0166	Excessive Memory Requirement
CPCG0574	Excessive Memory Requirement
CPCG0063	Excessive Memory Requirement
CPCG0089	Excessive Memory Requirement
CPCG0424	Excessive Memory Requirement
CPCG0084	Excessive Memory Requirement
CPCG0234	Excessive Memory Requirement

MuTect-Battenberg	DPClust
Single-Region	Reconstruction
Total Samples	293
Completed Samples	288
Failure Rate	0.0170648464163823
Sample	Failure Reason
CPCG0050	Failed MuTect
CPCG0090	Failed MuTect
CPCG0122	Failed MuTect
CPCG0117	Failed Battenberg
CPCG0124	Failed Battenberg

SomaticSniper-TITAN	sciClone
Single-Region	Reconstruction
Total Samples	293
Completed Samples	100
Failure Rate	0.658703071672355
Sample	Failure Reason
Baca_03-1426_T_wgs	Below 5 Mutations
Baca_07-4814_T_wgs	Below 5 Mutations
Baca_07-5318_T_wgs	Below 5 Mutations
Baca_08-2153_T_wgs	Below 5 Mutations
Baca_08-217_T_wgs	Below 5 Mutations
Baca_08-5852_T_wgs	Below 5 Mutations
Baca_09-146_T_wgs	Below 5 Mutations
Baca_09-628_T_wgs	Below 5 Mutations
Baca_STID0000003042_T_wgs	Below 5 Mutations
Berger_3027_T_wgs	Below 5 Mutations
CPCG0003	Below 5 Mutations
CPCG0007	Below 5 Mutations
CPCG0094	Below 5 Mutations
CPCG0095	Below 5 Mutations
CPCG0098	Below 5 Mutations
CPCG0122	Below 5 Mutations
CPCG0185	Below 5 Mutations
CPCG0189	Below 5 Mutations
CPCG0191	Below 5 Mutations
CPCG0194	Below 5 Mutations
CPCG0208	Below 5 Mutations
CPCG0213	Below 5 Mutations
CPCG0232	Below 5 Mutations
CPCG0237	Below 5 Mutations
CPCG0250	Below 5 Mutations
CPCG0260	Below 5 Mutations
CPCG0262	Below 5 Mutations
CPCG0263	Below 5 Mutations
CPCG0265	Below 5 Mutations
CPCG0341	Below 5 Mutations
CPCG0346	Below 5 Mutations
CPCG0356	Below 5 Mutations
CPCG0358	Below 5 Mutations
CPCG0365	Below 5 Mutations
CPCG0366	Below 5 Mutations
CPCG0371	Below 5 Mutations
CPCG0374	Below 5 Mutations
CPCG0378	Below 5 Mutations
CPCG0381	Below 5 Mutations
CPCG0387	Below 5 Mutations
CPCG0391	Below 5 Mutations
CPCG0411	Below 5 Mutations
CPCG0412	Below 5 Mutations
CPCG0451	Below 5 Mutations
CPCG0454	Below 5 Mutations

CPCG0520	Below 5 Mutations
CPCG0528	Below 5 Mutations
CPCG0551	Below 5 Mutations
CPCG0565	Below 5 Mutations
CPCG0574	Below 5 Mutations
CPCG0575	Below 5 Mutations
CPCG0581	Below 5 Mutations
CPCG0591	Below 5 Mutations
CPCG0592	Below 5 Mutations
TCGA_5789_T1_wgs	Below 5 Mutations
TCGA_7744_T1_wgs	Below 5 Mutations
Weischenfeldt_03_T_wgs	Below 5 Mutations
Baca_02-1431_T_wgs	No Input
Baca_03-728_T_wgs	No Input
Baca_05-1657_T_wgs	No Input
Baca_05-2709_T_wgs	No Input
Baca_07-3258_T_wgs	No Input
Baca_07-5021_T_wgs	No Input
Baca_07-5037_T_wgs	No Input
Baca_08-716_T_wgs	No Input
Baca_09-37_T_wgs	No Input
Baca_09-396_T_wgs	No Input
Baca_09-3983_T_wgs	No Input
Baca_STID0000000410_T_wgs	No Input
Baca_STID0000002525_T_wgs	No Input
Baca_STID0000002621_T_wgs	No Input
Berger_0508_T_wgs	No Input
Berger_0581_T_wgs	No Input
Berger_1701_T_wgs	No Input
Berger_1783_T_wgs	No Input
Berger_2832_T_wgs	No Input
Berger_3043_T_wgs	No Input
CPCG0001	No Input
CPCG0015	No Input
CPCG0019	No Input
CPCG0022	No Input
CPCG0027	No Input
CPCG0030	No Input
CPCG0046	No Input
CPCG0048	No Input
CPCG0057	No Input
CPCG0072	No Input
CPCG0074	No Input
CPCG0075	No Input
CPCG0078	No Input
CPCG0084	No Input
CPCG0087	No Input
CPCG0089	No Input
CPCG0102	No Input
CPCG0117	No Input
CPCG0120	No Input
CPCG0121	No Input

CPCG0123	No Input
CPCG0127	No Input
CPCG0154	No Input
CPCG0158	No Input
CPCG0166	No Input
CPCG0182	No Input
CPCG0198	No Input
CPCG0199	No Input
CPCG0205	No Input
CPCG0206	No Input
CPCG0210	No Input
CPCG0212	No Input
CPCG0219	No Input
CPCG0234	No Input
CPCG0236	No Input
CPCG0246	No Input
CPCG0251	No Input
CPCG0255	No Input
CPCG0259	No Input
CPCG0266	No Input
CPCG0267	No Input
CPCG0268	No Input
CPCG0274	No Input
CPCG0339	No Input
CPCG0340	No Input
CPCG0342	No Input
CPCG0344	No Input
CPCG0348	No Input
CPCG0350	No Input
CPCG0352	No Input
CPCG0353	No Input
CPCG0357	No Input
CPCG0360	No Input
CPCG0362	No Input
CPCG0363	No Input
CPCG0368	No Input
CPCG0373	No Input
CPCG0375	No Input
CPCG0380	No Input
CPCG0401	No Input
CPCG0413	No Input
CPCG0414	No Input
CPCG0424	No Input
CPCG0432	No Input
CPCG0433	No Input
CPCG0450	No Input
CPCG0452	No Input
CPCG0458	No Input
CPCG0492	No Input
CPCG0525	No Input
CPCG0529	No Input
CPCG0547	No Input

CPCG0559	No Input
CPCG0560	No Input
CPCG0562	No Input
CPCG0567	No Input
CPCG0570	No Input
CPCG0577	No Input
CPCG0578	No Input
CPCG0580	No Input
CPCG0584	No Input
CPCG0587	No Input
CPCG0588	No Input
CPCG0589	No Input
CPCG0590	No Input
CPCG0595	No Input
CPCG0596	No Input
CPCG0597	No Input
CPCG0600	No Input
TCGA_5503_T1_wgs	No Input
TCGA_5506_T1_wgs	No Input
TCGA_5750_T1_wgs	No Input
TCGA_5763_T1_wgs	No Input
TCGA_5771_T1_wgs	No Input
TCGA_6336_T1_wgs	No Input
TCGA_6365_T1_wgs	No Input
TCGA_6370_T1_wgs	No Input
TCGA_7075_T1_wgs	No Input
TCGA_7079_T1_wgs	No Input
TCGA_7169_T1_wgs	No Input
TCGA_7233_T1_wgs	No Input
TCGA_7522_T1_wgs	No Input
TCGA_7737_T1_wgs	No Input
TCGA_7740_T1_wgs	No Input
TCGA_7791_T1_wgs	No Input
TCGA_8258_T1_wgs	No Input
Weischenfeldt_010_T_wgs	No Input
Weischenfeldt_011_T_wgs	No Input
Weischenfeldt_01_T_wgs	No Input
Weischenfeldt_02_T_wgs	No Input
Weischenfeldt_04_T_wgs	No Input
Weischenfeldt_05_T_wgs	No Input
Weischenfeldt_06_T_wgs	No Input
Weischenfeldt_07_T_wgs	No Input
Weischenfeldt_08_T_wgs	No Input
Weischenfeldt_09_T_wgs	No Input

SomaticSniper-TITAN	sciClone
Multi-region	Tumours
Single-Region	Reconstruction
Total Samples	30
Completed Samples	3
Failure Rate	0.9
Multi-Region	Reconstruction

Total Samples	10
Completed Samples	0
Failure Rate	1
Sample	Failure Reason
CPCG0260-B1F2	Below 5 Mutations
CPCG0334-B1F3	Below 5 Mutations
CPCG0361-B1F1	Below 5 Mutations
CPCG0361-B1F2	Below 5 Mutations
CPCG0364-B1F2	Below 5 Mutations
CPCG0100-B1F3	No Input
CPCG0100-B1F5	No Input
CPCG0100-B1F6	No Input
CPCG0103-B1F2	No Input
CPCG0103-B1F4	No Input
CPCG0260-B1F1	No Input
CPCG0260-B1F3	No Input
CPCG0260-B1F4	No Input
CPCG0334-B1F1	No Input
CPCG0334-B1F2	No Input
CPCG0361-B1F3	No Input
CPCG0361-B1F4	No Input
CPCG0364-B1F3	No Input
CPCG0364-B1F4	No Input
CPCG9001-B1P1	No Input
CPCG9001-B1P2	No Input
CPCG9002-B1P1	No Input
CPCG9002-B1P2	No Input
CPCG9003-B1P1	No Input
CPCG9003-B1P2	No Input
CPCG9005-B1P1	No Input
CPCG9005-B1P2	No Input
CPCG0100-MR	No Input
CPCG0103-MR	No Input
CPCG0260-MR	No Input
CPCG0334-MR	No Input
CPCG0361-MR	No Input
CPCG0364-MR	No Input
CPCG9001-MR	No Input
CPCG9002-MR	No Input
CPCG9003-MR	No Input
CPCG9005-MR	No Input

SomaticSniper-Battenberg	sciClone
Single-Region	Reconstruction
Total Samples	293
Completed Samples	150
Failure Rate	0.488054607508532
Sample	Failure Reason
CPCG0117	Failed Battenberg
CPCG0124	Failed Battenberg
CPCG0205	Failed Battenberg
Baca_02-1431_T_wgs	Below 5 Mutations
Baca_03-1426_T_wgs	Below 5 Mutations
Baca_03-728_T_wgs	Below 5 Mutations
Baca_04-1243_T_wgs	Below 5 Mutations
Baca_05-2709_T_wgs	Below 5 Mutations
Baca_07-3258_T_wgs	Below 5 Mutations
Baca_07-4814_T_wgs	Below 5 Mutations
Baca_08-2153_T_wgs	Below 5 Mutations
Baca_08-5852_T_wgs	Below 5 Mutations
Baca_08-784_T_wgs	Below 5 Mutations
Baca_STID0000003127_T_wgs	Below 5 Mutations
Berger_3043_T_wgs	Below 5 Mutations
CPCG0006	Below 5 Mutations
CPCG0007	Below 5 Mutations
CPCG0019	Below 5 Mutations
CPCG0027	Below 5 Mutations
CPCG0046	Below 5 Mutations
CPCG0048	Below 5 Mutations
CPCG0057	Below 5 Mutations
CPCG0075	Below 5 Mutations
CPCG0078	Below 5 Mutations
CPCG0084	Below 5 Mutations
CPCG0087	Below 5 Mutations
CPCG0095	Below 5 Mutations
CPCG0098	Below 5 Mutations
CPCG0121	Below 5 Mutations
CPCG0127	Below 5 Mutations
CPCG0154	Below 5 Mutations
CPCG0158	Below 5 Mutations
CPCG0182	Below 5 Mutations
CPCG0189	Below 5 Mutations
CPCG0191	Below 5 Mutations
CPCG0194	Below 5 Mutations
CPCG0198	Below 5 Mutations
CPCG0199	Below 5 Mutations
CPCG0206	Below 5 Mutations
CPCG0213	Below 5 Mutations
CPCG0234	Below 5 Mutations
CPCG0250	Below 5 Mutations
CPCG0255	Below 5 Mutations
CPCG0265	Below 5 Mutations
CPCG0268	Below 5 Mutations

CPCG0341	Below 5 Mutations
CPCG0348	Below 5 Mutations
CPCG0352	Below 5 Mutations
CPCG0358	Below 5 Mutations
CPCG0363	Below 5 Mutations
CPCG0371	Below 5 Mutations
CPCG0373	Below 5 Mutations
CPCG0374	Below 5 Mutations
CPCG0380	Below 5 Mutations
CPCG0381	Below 5 Mutations
CPCG0387	Below 5 Mutations
CPCG0391	Below 5 Mutations
CPCG0401	Below 5 Mutations
CPCG0411	Below 5 Mutations
CPCG0412	Below 5 Mutations
CPCG0528	Below 5 Mutations
CPCG0529	Below 5 Mutations
CPCG0557	Below 5 Mutations
CPCG0561	Below 5 Mutations
CPCG0565	Below 5 Mutations
CPCG0575	Below 5 Mutations
CPCG0580	Below 5 Mutations
CPCG0581	Below 5 Mutations
CPCG0590	Below 5 Mutations
CPCG0591	Below 5 Mutations
CPCG0592	Below 5 Mutations
CPCG0595	Below 5 Mutations
TCGA_5506_T1_wgs	Below 5 Mutations
TCGA_5750_T1_wgs	Below 5 Mutations
TCGA_5763_T1_wgs	Below 5 Mutations
TCGA_5771_T1_wgs	Below 5 Mutations
TCGA_5789_T1_wgs	Below 5 Mutations
TCGA_6336_T1_wgs	Below 5 Mutations
TCGA_6365_T1_wgs	Below 5 Mutations
TCGA_6370_T1_wgs	Below 5 Mutations
TCGA_7075_T1_wgs	Below 5 Mutations
TCGA_7079_T1_wgs	Below 5 Mutations
TCGA_7169_T1_wgs	Below 5 Mutations
TCGA_7233_T1_wgs	Below 5 Mutations
TCGA_7522_T1_wgs	Below 5 Mutations
TCGA_7737_T1_wgs	Below 5 Mutations
TCGA_8258_T1_wgs	Below 5 Mutations
Weischenfeldt_01_T_wgs	Below 5 Mutations
Weischenfeldt_02_T_wgs	Below 5 Mutations
Weischenfeldt_03_T_wgs	Below 5 Mutations
Weischenfeldt_04_T_wgs	Below 5 Mutations
Weischenfeldt_05_T_wgs	Below 5 Mutations
Weischenfeldt_06_T_wgs	Below 5 Mutations
Weischenfeldt_08_T_wgs	Below 5 Mutations
Weischenfeldt_09_T_wgs	Below 5 Mutations
Baca_01-28_T_wgs	No Input
Baca_09-37_T_wgs	No Input

Baca_09-396_T_wgs	No Input
Baca_STID0000000410_T_wgs	No Input
Baca_STID0000003042_T_wgs	No Input
Berger_0508_T_wgs	No Input
Berger_0581_T_wgs	No Input
Berger_1701_T_wgs	No Input
Berger_1783_T_wgs	No Input
Berger_2832_T_wgs	No Input
Berger_3027_T_wgs	No Input
CPCG0074	No Input
CPCG0083	No Input
CPCG0089	No Input
CPCG0120	No Input
CPCG0166	No Input
CPCG0185	No Input
CPCG0196	No Input
CPCG0208	No Input
CPCG0212	No Input
CPCG0219	No Input
CPCG0274	No Input
CPCG0344	No Input
CPCG0353	No Input
CPCG0368	No Input
CPCG0375	No Input
CPCG0413	No Input
CPCG0414	No Input
CPCG0424	No Input
CPCG0433	No Input
CPCG0437	No Input
CPCG0450	No Input
CPCG0454	No Input
CPCG0492	No Input
CPCG0525	No Input
CPCG0550	No Input
CPCG0562	No Input
CPCG0567	No Input
CPCG0574	No Input
CPCG0578	No Input
CPCG0584	No Input
CPCG0587	No Input
TCGA_5503_T1_wgs	No Input
TCGA_7740_T1_wgs	No Input
TCGA_7791_T1_wgs	No Input
Weischenfeldt_010_T_wgs	No Input
Weischenfeldt_011_T_wgs	No Input
Weischenfeldt_07_T_wgs	No Input

SomaticSniper-Battenberg	sciClone
Multi-region	Tumours
Single-Region	Reconstruction
Total Samples	30
Completed Samples	5

Failure Rate	0.833333333333333
Multi-Region	Reconstruction
Total Samples	10
Completed Samples	0
Failure Rate	1
Sample	Failure Reason
CPCG0260-B1F2	Below 5 Mutations
CPCG0260-B1F3	Below 5 Mutations
CPCG0260-B1F4	Below 5 Mutations
CPCG0334-B1F3	Below 5 Mutations
CPCG0361-B1F2	Below 5 Mutations
CPCG0364-B1F2	Below 5 Mutations
CPCG0364-B1F3	Below 5 Mutations
CPCG9002-B1P2	Below 5 Mutations
CPCG9003-B1P1	Below 5 Mutations
CPCG9003-B1P2	Below 5 Mutations
CPCG9005-B1P1	Below 5 Mutations
CPCG9005-B1P2	Below 5 Mutations
CPCG0100-B1F3	No Input
CPCG0100-B1F5	No Input
CPCG0100-B1F6	No Input
CPCG0103-B1F2	No Input
CPCG0103-B1F4	No Input
CPCG0334-B1F2	No Input
CPCG0361-B1F1	No Input
CPCG0361-B1F3	No Input
CPCG0361-B1F4	No Input
CPCG0364-B1F4	No Input
CPCG9001-B1P1	No Input
CPCG9001-B1P2	No Input
CPCG9002-B1P1	No Input
CPCG0100-MR	No Input
CPCG0103-MR	No Input
CPCG0260-MR	No Input
CPCG0334-MR	No Input
CPCG0361-MR	No Input
CPCG0364-MR	No Input
CPCG9001-MR	No Input
CPCG9002-MR	No Input
CPCG9003-MR	No Input
CPCG9005-MR	No Input

MuTect-TITAN	sciClone
Single-Region	Reconstruction
Total Samples	293
Completed Samples	182
Failure Rate	0.378839590443686
Sample	Failure Reason
CPCG0050	Failed MuTect
CPCG0090	Failed MuTect
CPCG0122	Failed MuTect
Baca_02-1431_T_wgs	Below 5 Mutations
Baca_03-728_T_wgs	Below 5 Mutations
Baca_07-5037_T_wgs	Below 5 Mutations
Baca_08-217_T_wgs	Below 5 Mutations
Baca_08-784_T_wgs	Below 5 Mutations
Baca_09-37_T_wgs	Below 5 Mutations
Baca_09-396_T_wgs	Below 5 Mutations
Baca_STID0000000410_T_wgs	Below 5 Mutations
Baca_STID0000002525_T_wgs	Below 5 Mutations
Baca_STID0000002621_T_wgs	Below 5 Mutations
Berger_1701_T_wgs	Below 5 Mutations
CPCG0003	Below 5 Mutations
CPCG0006	Below 5 Mutations
CPCG0007	Below 5 Mutations
CPCG0015	Below 5 Mutations
CPCG0019	Below 5 Mutations
CPCG0022	Below 5 Mutations
CPCG0027	Below 5 Mutations
CPCG0030	Below 5 Mutations
CPCG0046	Below 5 Mutations
CPCG0072	Below 5 Mutations
CPCG0087	Below 5 Mutations
CPCG0102	Below 5 Mutations
CPCG0123	Below 5 Mutations
CPCG0154	Below 5 Mutations
CPCG0182	Below 5 Mutations
CPCG0199	Below 5 Mutations
CPCG0205	Below 5 Mutations
CPCG0206	Below 5 Mutations
CPCG0246	Below 5 Mutations
CPCG0251	Below 5 Mutations
CPCG0260	Below 5 Mutations
CPCG0268	Below 5 Mutations
CPCG0340	Below 5 Mutations
CPCG0342	Below 5 Mutations
CPCG0352	Below 5 Mutations
CPCG0353	Below 5 Mutations
CPCG0358	Below 5 Mutations
CPCG0362	Below 5 Mutations
CPCG0373	Below 5 Mutations
CPCG0413	Below 5 Mutations
CPCG0433	Below 5 Mutations

CPCG0450	Below 5 Mutations
CPCG0492	Below 5 Mutations
CPCG0565	Below 5 Mutations
CPCG0570	Below 5 Mutations
CPCG0577	Below 5 Mutations
CPCG0578	Below 5 Mutations
CPCG0588	Below 5 Mutations
CPCG0589	Below 5 Mutations
CPCG0592	Below 5 Mutations
CPCG0597	Below 5 Mutations
CPCG0600	Below 5 Mutations
TCGA_5750_T1_wgs	Below 5 Mutations
TCGA_5771_T1_wgs	Below 5 Mutations
TCGA_6365_T1_wgs	Below 5 Mutations
TCGA_7169_T1_wgs	Below 5 Mutations
TCGA_7522_T1_wgs	Below 5 Mutations
TCGA_8258_T1_wgs	Below 5 Mutations
Weischenfeldt_010_T_wgs	Below 5 Mutations
Baca_05-2709_T_wgs	No Input
Baca_07-3258_T_wgs	No Input
Baca_07-5318_T_wgs	No Input
Baca_09-3983_T_wgs	No Input
Berger_0581_T_wgs	No Input
Berger_1783_T_wgs	No Input
Berger_2832_T_wgs	No Input
Berger_3043_T_wgs	No Input
CPCG0001	No Input
CPCG0057	No Input
CPCG0074	No Input
CPCG0078	No Input
CPCG0089	No Input
CPCG0117	No Input
CPCG0120	No Input
CPCG0198	No Input
CPCG0212	No Input
CPCG0219	No Input
CPCG0274	No Input
CPCG0432	No Input
CPCG0458	No Input
CPCG0525	No Input
CPCG0529	No Input
CPCG0559	No Input
CPCG0560	No Input
CPCG0562	No Input
CPCG0580	No Input
CPCG0584	No Input
CPCG0590	No Input
CPCG0595	No Input
CPCG0596	No Input
TCGA_5503_T1_wgs	No Input
TCGA_5506_T1_wgs	No Input
TCGA_5763_T1_wgs	No Input

TCGA_6336_T1_wgs	No Input
TCGA_6370_T1_wgs	No Input
TCGA_7079_T1_wgs	No Input
TCGA_7233_T1_wgs	No Input
TCGA_7737_T1_wgs	No Input
Weischenfeldt_011_T_wgs	No Input
Weischenfeldt_01_T_wgs	No Input
Weischenfeldt_02_T_wgs	No Input
Weischenfeldt_04_T_wgs	No Input
Weischenfeldt_05_T_wgs	No Input
Weischenfeldt_06_T_wgs	No Input
Weischenfeldt_07_T_wgs	No Input
Weischenfeldt_08_T_wgs	No Input
Weischenfeldt_09_T_wgs	No Input

MuTect-TITAN	sciClone
Multi-region	Tumours
Single-Region	Reconstruction
Total Samples	30
Completed Samples	11
Failure Rate	0.633333333333333
Multi-Region	Reconstruction
Total Samples	10
Completed Samples	0
Failure Rate	1
Sample	Failure Reason
CPCG0260-B1F1	Below 5 Mutations
CPCG0260-B1F4	Below 5 Mutations
CPCG0334-B1F1	Below 5 Mutations
CPCG0361-B1F4	Below 5 Mutations
CPCG0364-B1F3	Below 5 Mutations
CPCG9002-B1P1	Below 5 Mutations
CPCG9003-B1P1	Below 5 Mutations
CPCG9003-B1P2	Below 5 Mutations
CPCG9005-B1P1	Below 5 Mutations
CPCG0100-B1F3	No Input
CPCG0100-B1F5	No Input
CPCG0100-B1F6	No Input
CPCG0103-B1F4	No Input
CPCG0361-B1F3	No Input
CPCG0364-B1F4	No Input
CPCG9001-B1P1	No Input
CPCG9001-B1P2	No Input
CPCG9002-B1P2	No Input
CPCG9005-B1P2	No Input
CPCG0100-MR	No Input
CPCG0103-MR	No Input
CPCG0260-MR	No Input
CPCG0334-MR	No Input
CPCG0361-MR	No Input
CPCG0364-MR	No Input
CPCG9001-MR	No Input

CPCG9002-MR	No Input
CPCG9003-MR	No Input
CPCG9005-MR	No Input

MuTect-Battenberg	sciClone
Single-Region	Reconstruction
Total Samples	293
Completed Samples	257
Failure Rate	0.122866894197952
Sample	Failure Reason
CPCG0050	Failed MuTect
CPCG0090	Failed MuTect
CPCG0122	Failed MuTect
CPCG0117	Failed Battenberg
CPCG0124	Failed Battenberg
CPCG0205	Failed Battenberg
Baca_05-2709_T_wgs	Below 5 Mutations
Baca_08-784_T_wgs	Below 5 Mutations
Baca_09-37_T_wgs	Below 5 Mutations
Baca_STID0000003042_T_wgs	Below 5 Mutations
Berger_0508_T_wgs	Below 5 Mutations
Berger_0581_T_wgs	Below 5 Mutations
Berger_1783_T_wgs	Below 5 Mutations
Berger_3027_T_wgs	Below 5 Mutations
Berger_3043_T_wgs	Below 5 Mutations
CPCG0006	Below 5 Mutations
CPCG0074	Below 5 Mutations
CPCG0083	Below 5 Mutations
CPCG0189	Below 5 Mutations
CPCG0212	Below 5 Mutations
CPCG0413	Below 5 Mutations
CPCG0437	Below 5 Mutations
CPCG0450	Below 5 Mutations
CPCG0492	Below 5 Mutations
CPCG0550	Below 5 Mutations
Weischenfeldt_010_T_wgs	Below 5 Mutations
Weischenfeldt_011_T_wgs	Below 5 Mutations
Weischenfeldt_05_T_wgs	Below 5 Mutations
Weischenfeldt_06_T_wgs	Below 5 Mutations
Berger_1701_T_wgs	No Input
Berger_2832_T_wgs	No Input
Weischenfeldt_01_T_wgs	No Input
Weischenfeldt_02_T_wgs	No Input
Weischenfeldt_04_T_wgs	No Input
Weischenfeldt_07_T_wgs	No Input
Weischenfeldt_09_T_wgs	No Input

MuTect-Battenberg	sciClone
Multi-region	Tumours
Single-Region	Reconstruction
Total Samples	30
Completed Samples	20
Failure Rate	0.333333333333333
Multi-Region	Reconstruction
Total Samples	10

Completed Samples	2
Failure Rate	0.8
Sample	Failure Reason
CPCG0100-B1F5	Below 5 Mutations
CPCG0103-B1F4	Below 5 Mutations
CPCG0364-B1F4	Below 5 Mutations
CPCG9001-B1P1	Below 5 Mutations
CPCG9001-B1P2	Below 5 Mutations
CPCG9002-B1P1	Below 5 Mutations
CPCG9005-B1P1	Below 5 Mutations
CPCG0100-B1F3	No Input
CPCG0100-B1F6	No Input
CPCG9005-B1P2	No Input
CPCG0100-MR	No Input
CPCG0103-MR	No Input
CPCG0260-MR	Below 5 Mutations
CPCG0364-MR	No Input
CPCG9001-MR	No Input
CPCG9002-MR	No Input
CPCG9003-MR	Below 5 Mutations
CPCG9005-MR	No Input

SomaticSniper-FACETS	sciClone
Multi-region	Tumours
Single-Region	Reconstruction
Total Samples	30
Completed Samples	5
Failure Rate	0.833333333333333
Multi-Region	Reconstruction
Total Samples	10
Completed Samples	0
Failure Rate	1
Sample	Failure Reason
CPCG0361-F1	No FACETS
CPCG0361-F2	No FACETS
CPCG0361-F3	No FACETS
CPCG0361-F4	No FACETS
CPCG0361-MR	No FACETS
CPCG0260-B1F3	Below 5 Mutations
CPCG0260-B1F4	Below 5 Mutations
CPCG0334-B1F3	Below 5 Mutations
CPCG0364-B1F2	Below 5 Mutations
CPCG0364-B1F3	Below 5 Mutations
CPCG9003-B1P1	Below 5 Mutations
CPCG9005-B1P1	Below 5 Mutations
CPCG9005-B1P2	Below 5 Mutations
CPCG0100-B1F3	No Input
CPCG0100-B1F5	No Input
CPCG0100-B1F6	No Input
CPCG0100-MR	No Input
CPCG0103-B1F2	No Input
CPCG0103-B1F4	No Input
CPCG0103-MR	No Input
CPCG0260-B1F2	No Input
CPCG0260-MR	No Input
CPCG0334-B1F2	No Input
CPCG0334-MR	No Input
CPCG0364-B1F4	No Input
CPCG0364-MR	No Input
CPCG9001-B1P1	No Input
CPCG9001-B1P2	No Input
CPCG9001-MR	No Input
CPCG9002-B1P1	No Input
CPCG9002-B1P2	No Input
CPCG9002-MR	No Input
CPCG9003-B1P2	No Input
CPCG9003-MR	No Input
CPCG9005-MR	No Input

MuTect-FACETS	sciClone
Multi-region	Tumours
Single-Region	Reconstruction
Total Samples	30
Completed Samples	20
Failure Rate	0.333333333333333
Multi-Region	Reconstruction
Total Samples	10
Completed Samples	2
Failure Rate	0.8
Sample	Failure Reason
CPCG0361-F1	No FACETS
CPCG0361-F2	No FACETS
CPCG0361-F3	No FACETS
CPCG0361-F4	No FACETS
CPCG0361-MR	No FACETS
CPCG0100-B1F6	Below 5 Mutations
CPCG0260-MR	Below 5 Mutations
CPCG9002-B1P1	Below 5 Mutations
CPCG9005-B1P1	Below 5 Mutations
CPCG9005-B1P2	Below 5 Mutations
CPCG0100-B1F3	No Input
CPCG0100-MR	No Input
CPCG0364-B1F4	No Input
CPCG0364-MR	No Input
CPCG0103-MR	No shared input
CPCG9001-MR	No shared input
CPCG9005-MR	No Input
CPCG9002-MR	No Input