



Classification Summary

This sample has the following classifications:

Sturgeon classification: Haematopoietic - LYMPHO - LYMPHO - 0.93

NanoDX classification: A IDH, HG - 0.09

PanNanoDX classification: DLBCL - 0.08

Forest classification: LYMPHO - 51.42

Estimated sex chromosome composition: XX

Coverage Depths - Global Estimated Coverage: 0.33x Targets Estimated Coverage: 1.22x

Target Coverage is below the recommended 10x threshold

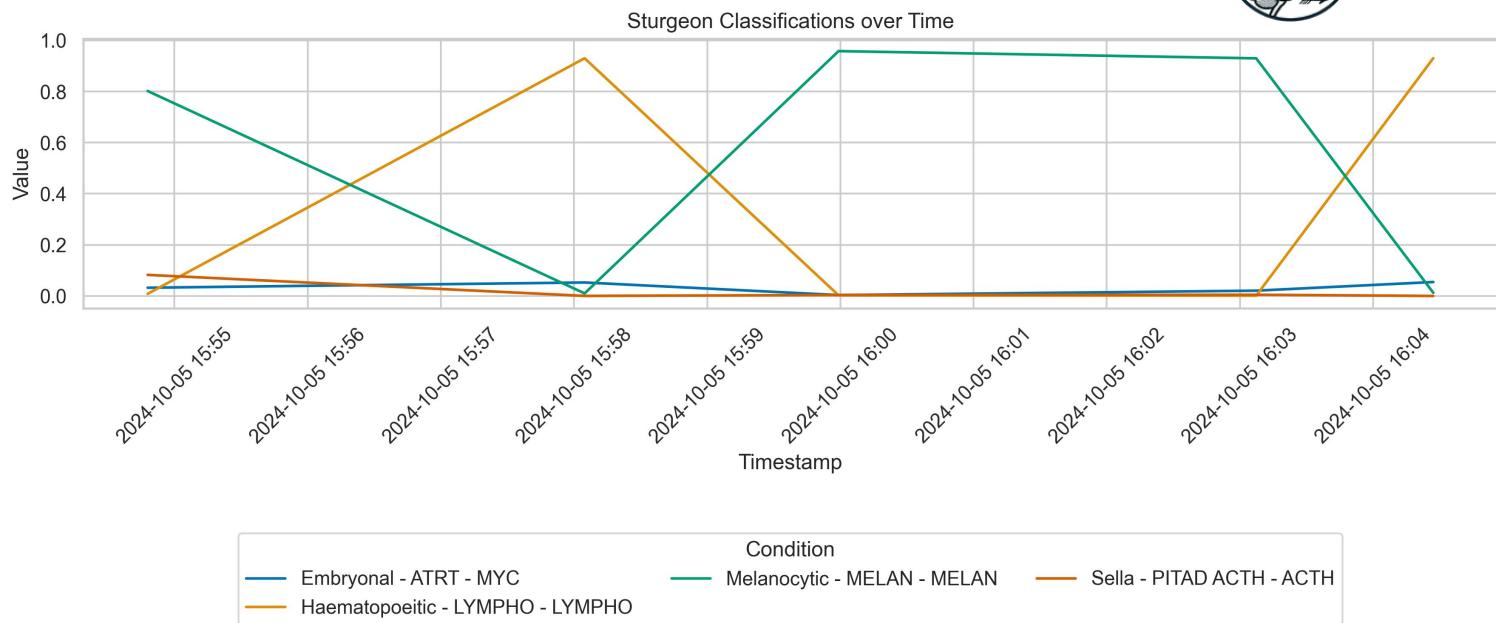
Outlier genes by coverage (high): GNAQ (4.0) - EGFR (3.7) - CASC11, MYC (3.6) - ALK (3.0) - CSF1R (3.0) - AKT3 (2.9) - FGFR4 (2.9) - BRAF (2.9) - MET (2.9) - CCND2, CCND2-AS1 (2.9) - FGFR2 (2.8) - SUZ12 (2.8) - CREBBP (2.7)

Outlier genes by coverage (low):

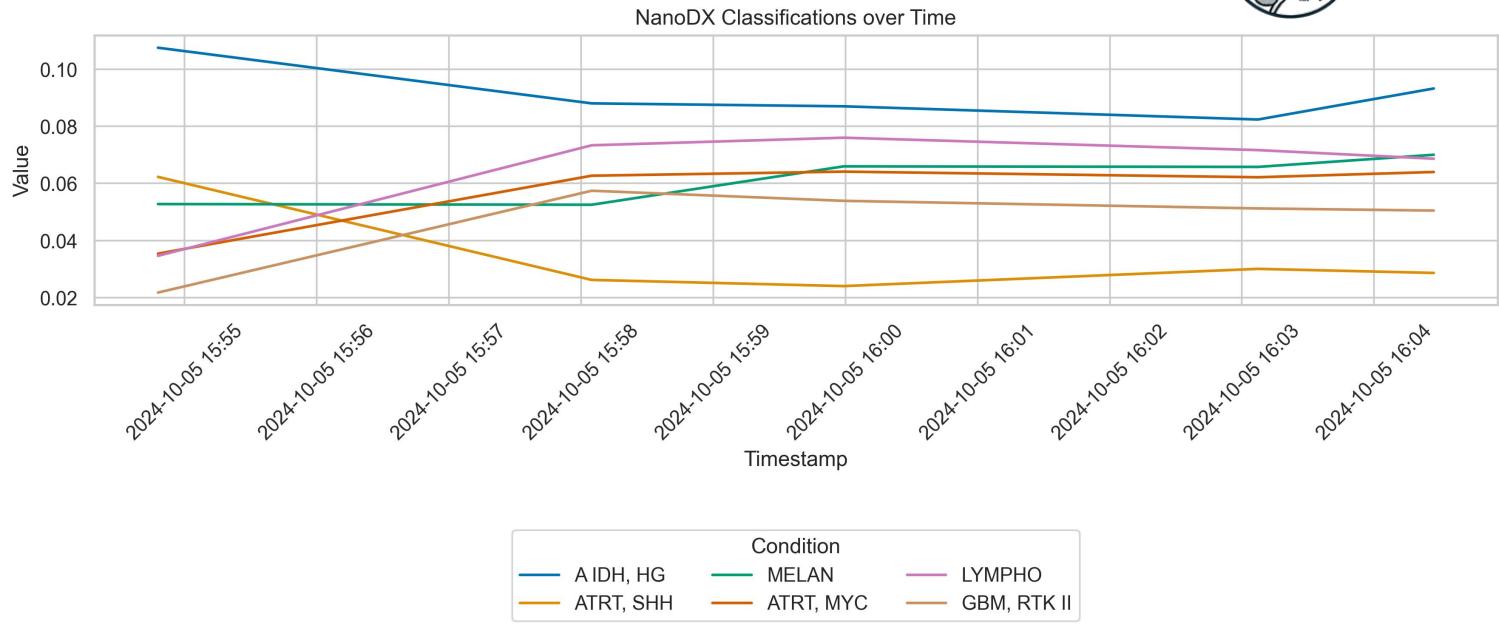
Fusion Candidates - using panel rCNS2 - 0 Low confidence fusions observed.

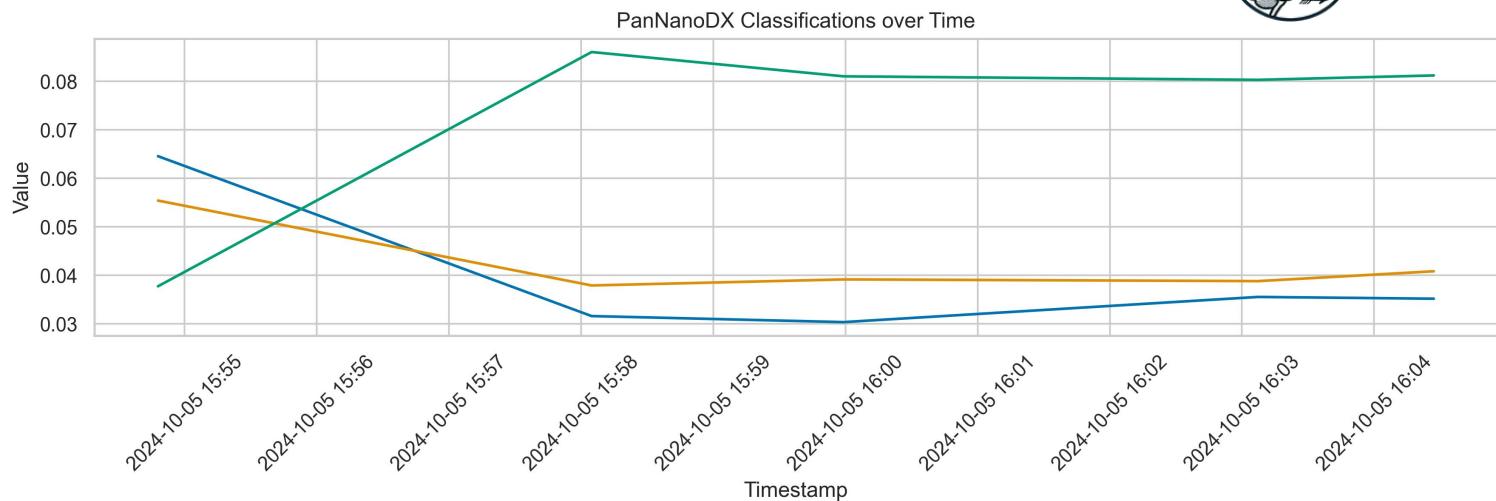
Run Data Summary

```
Sample ID: NA12878_05_NB4_06_22Rv1_07
Run Start: ['2022-03-17T17:06:42.262+00:00']
Run Folder: /Users/mattloose/datasets/test_data_set
Output Folder: /Users/mattloose/GIT/niceGUI/cnsmeth/robin_output_full
Target Panel: rCNS2
Reference: /Users/mattloose/references/hg38_simple.fa
Sequencing Device: ['PC24B243']
Flowcell ID: ['PAK09329']
Basecalling Model: ['modbase_models=dna_r9.4.1_e8_hac@v3.3_5mCG_5hmCG@v0']
bam_passed: 0
bam_failed: 360
mapped_count: 1197792
pass_mapped_count: 0
fail_mapped_count: 1197792
unmapped_count: 26572
pass_unmapped_count: 0
fail_unmapped_count: 26572
pass_bases_count: 0
fail_bases_count: 1108784305
bases_count: 1108784305
```



index	Haematopoietic - LYMPHO - LYMPHO	Embryonal - ATRT - MYC	Melanocytic - MELAN - MELAN	Mesenchymal - CHORDM - CHORDM	Embryonal - ATRT - SHH	Mesenchymal - EWS - EWS	Haematopoietic - PLASMA - PLASMA	Sella - PITAD STH - STH SPA	Sella - PITAD FSH LH - FSH LH	Embryonal - ETMR - ETMR
Score	0.92996	0.05449	0.01242	0.00076	0.00062	0.00048	0.00042	0.00027	0.00025	9e-05

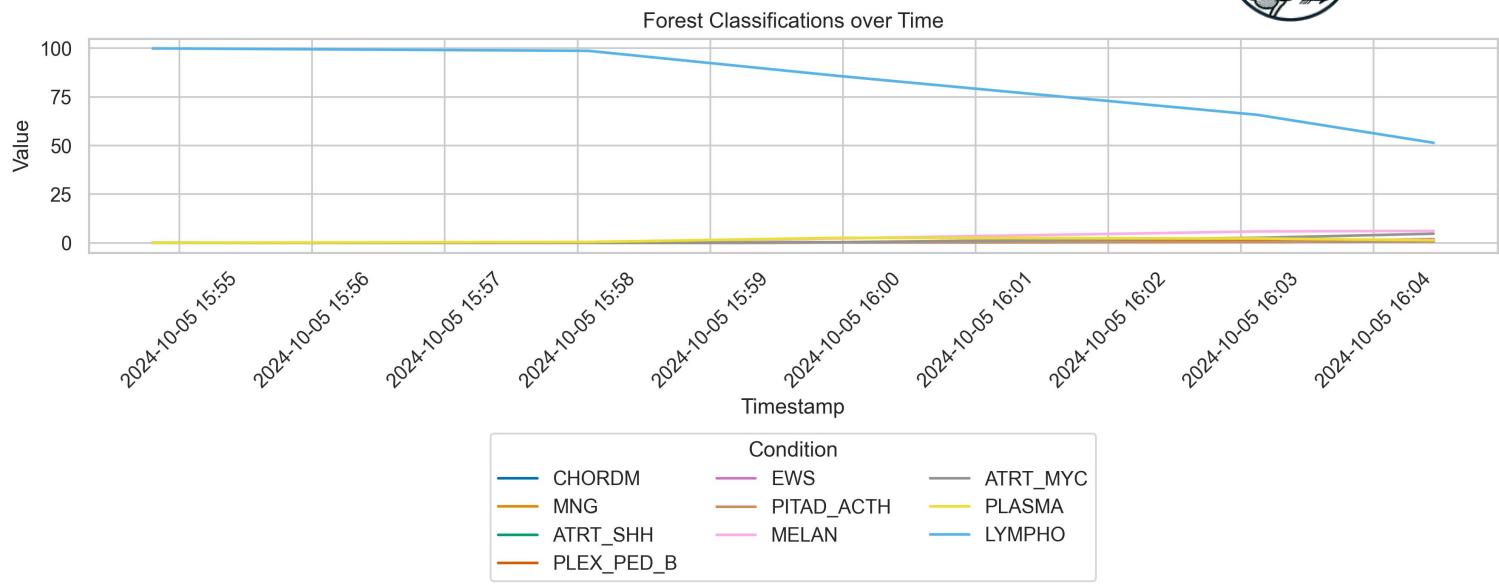




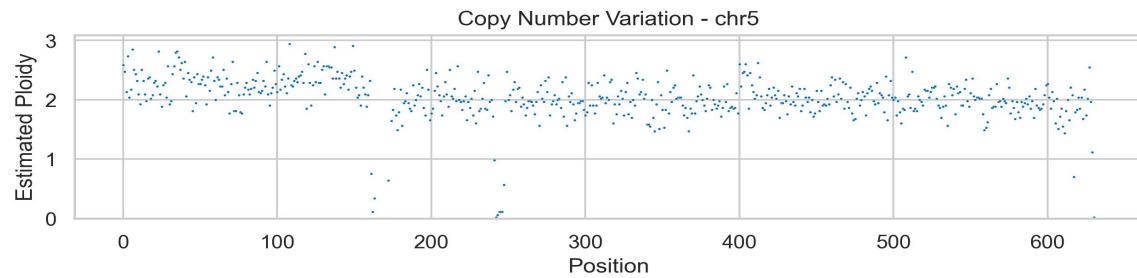
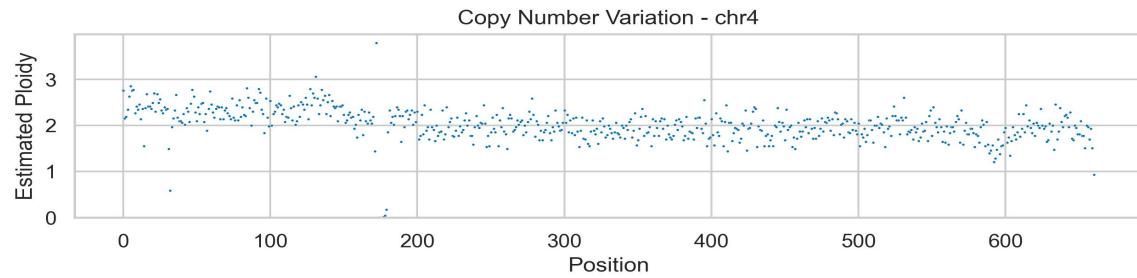
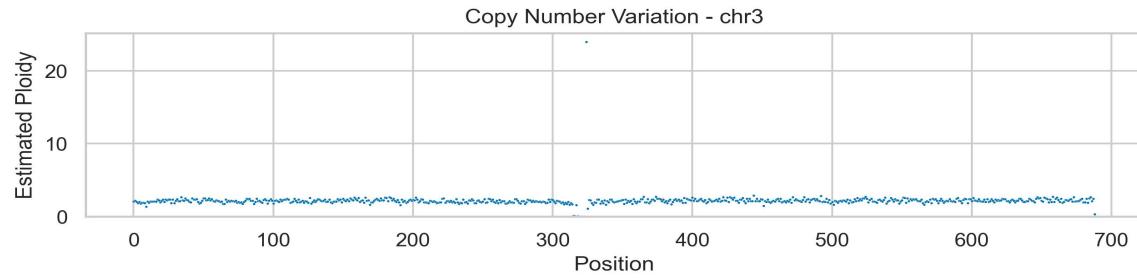
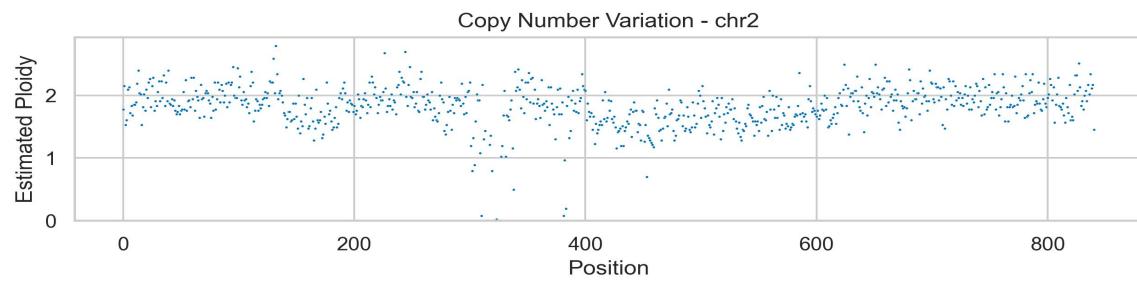
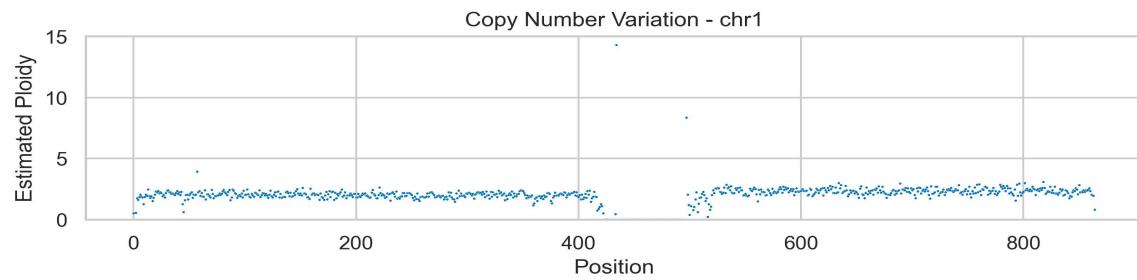
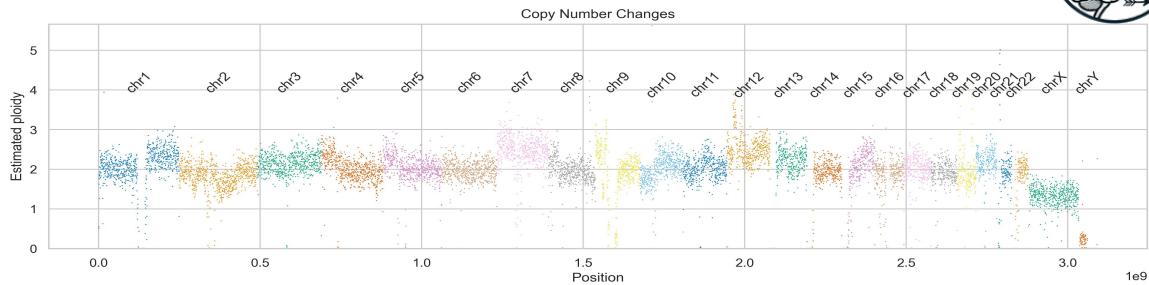
Condition

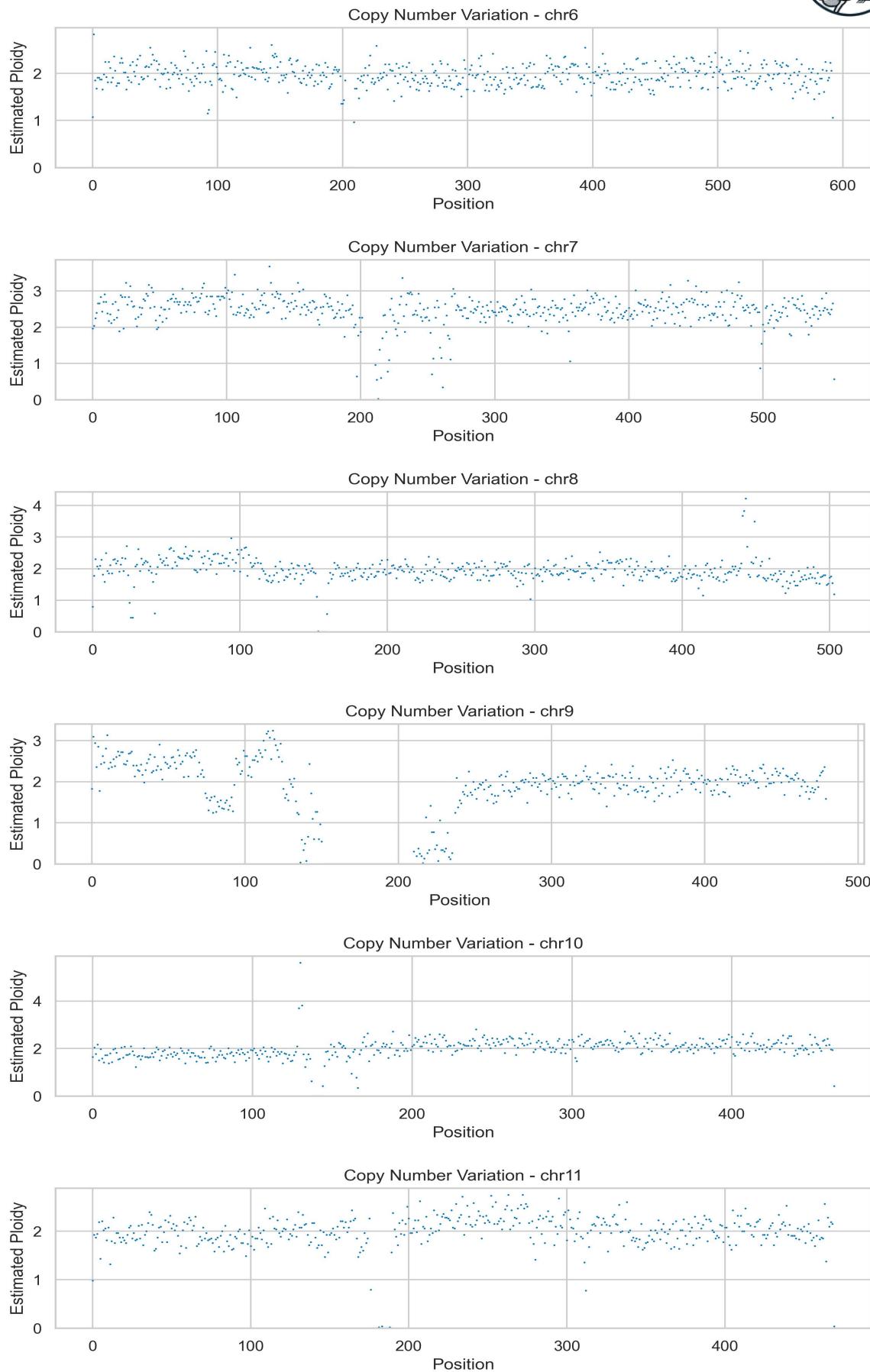
— STAD	— MELAN	— DLBCL
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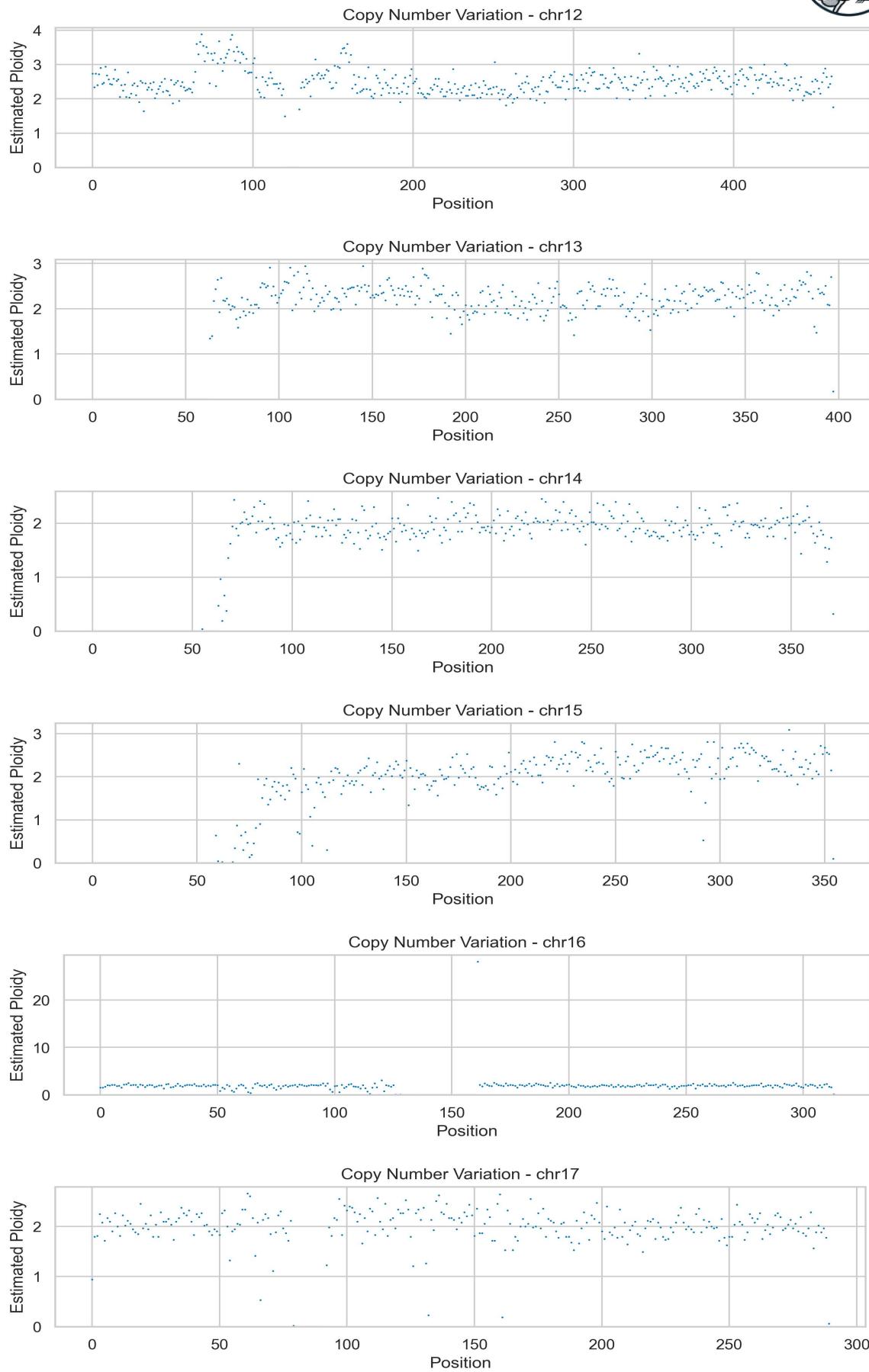
index	DLBCL	MELAN	STAD	CESC	ACC	ATRT, MYC	LUAD	LMS	LIHC	AIDH, HG
Score	0.08118	0.04084	0.03519	0.02966	0.02373	0.02311	0.02195	0.02116	0.02066	0.02048

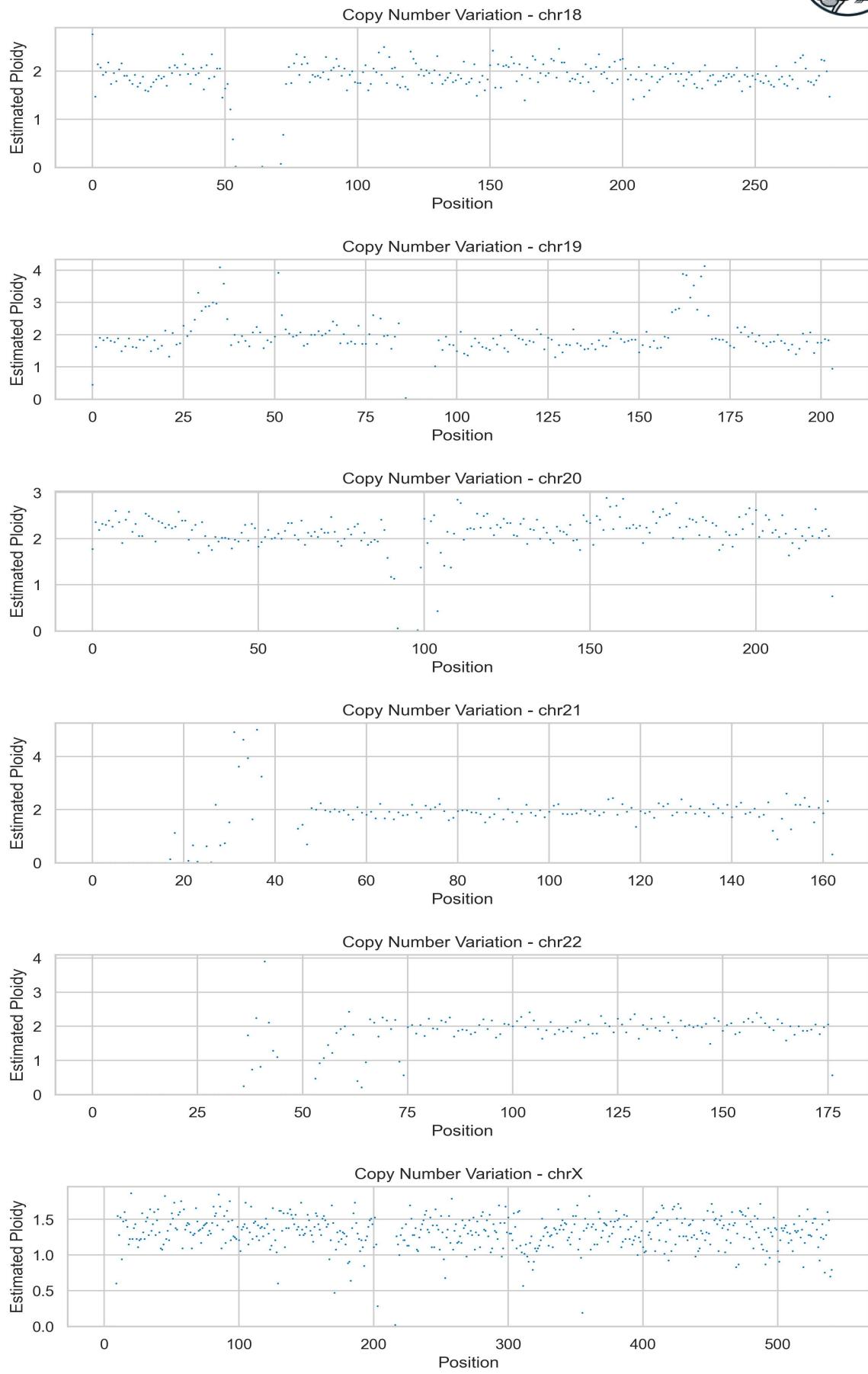


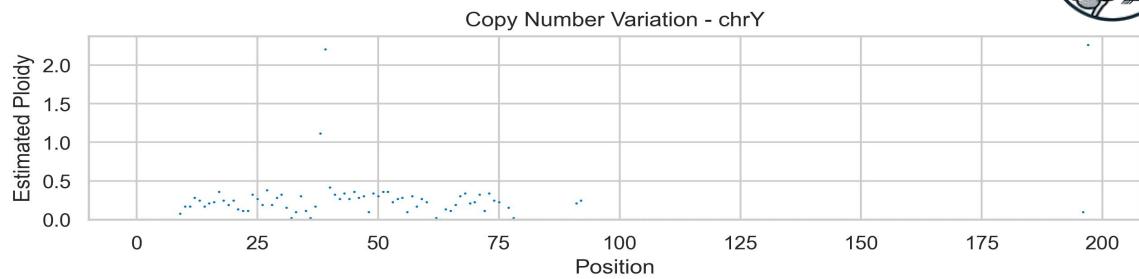
index	LYMPHO	MELAN	ATRT_MYC	EWS	MNG	PLASMA	ATRT_SHH	PITAD_ACTH	PLEX_PED_B	CHORDM
Score	51.42138	6.13105	4.70102	1.90572	1.51152	1.35244	1.16228	1.06312	0.89244	0.86039









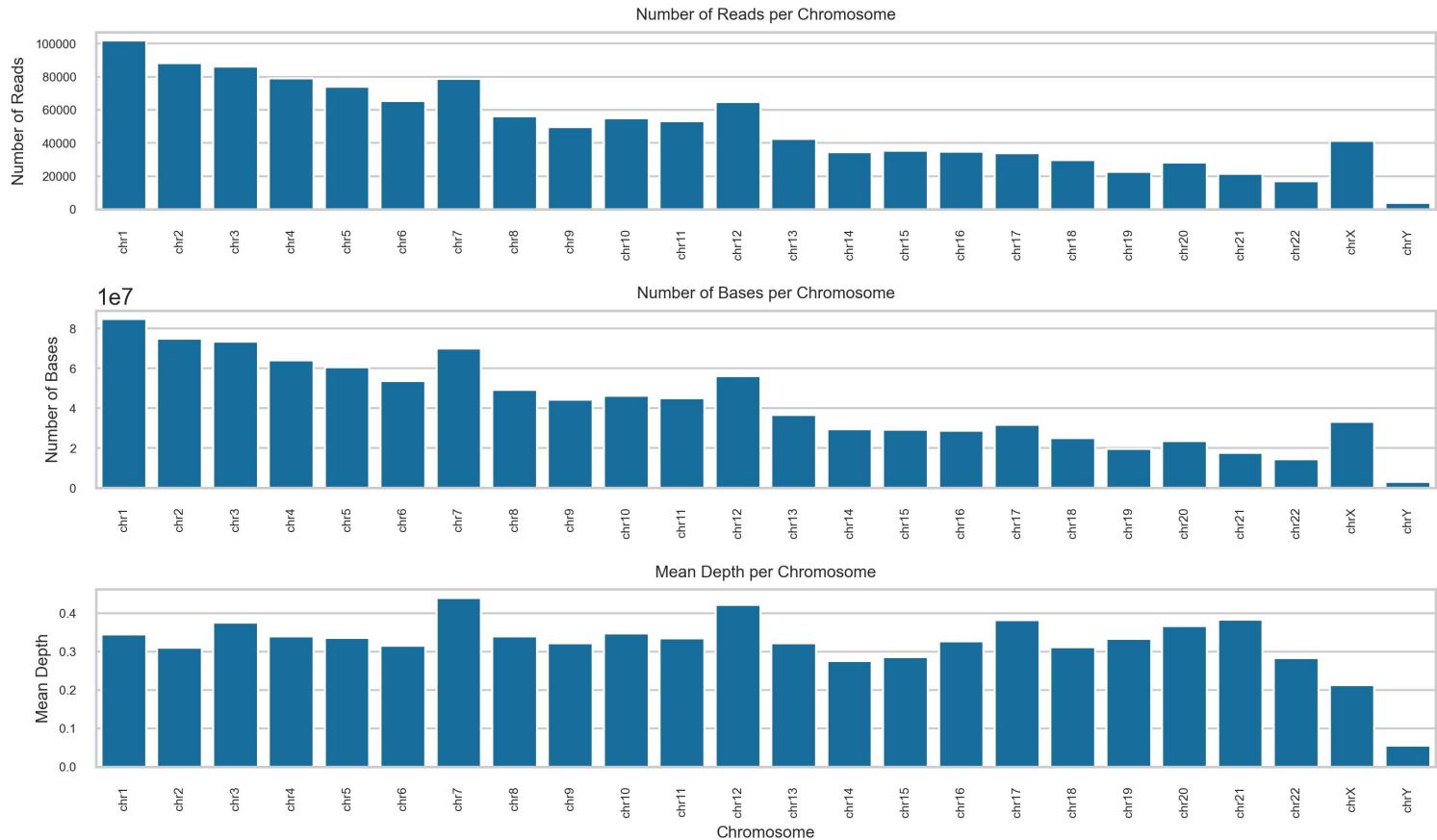


Estimated Genetic Sex: XX
Current Bin Width: 288000
Current Variance: 0.607

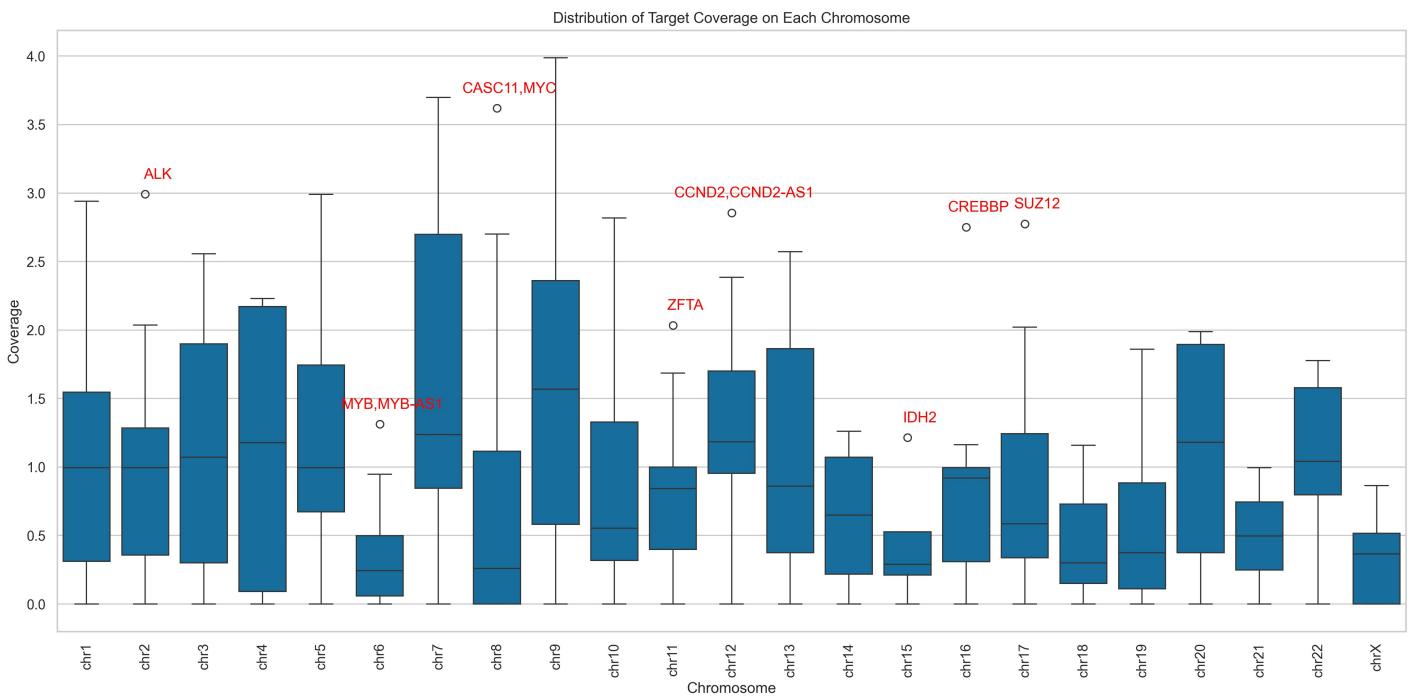


Target Coverage

This plot was generated by ROBIN.



Coverage over individual targets on each chromosome. Outliers are annotated by gene name.



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Sample ID: NA12878_05_NB4_06_22Rv1_07

R.O.B.I.N. Report Generated: 2024-10-05 17:27:09



The following table identifies potential outliers differing significantly from the mean coverage of 1.22x

chrom	startpos	endpos	name	length	coverage	bases
chr9	77922045	77922385	GNAQ	341	4.0	1360
chr7	55019175	55019380	EGFR	206	3.7	762
chr8	127736553	127740984	CASC11,MYC	4432	3.6	16041
chr2	29531853	29532207	ALK	355	3.0	1062
chr5	150054041	150086446	CSF1R	32406	3.0	96917
chr1	243843046	243843247	AKT3	202	2.9	594
chr5	177089482	177097792	FGFR4	8311	2.9	24332
chr7	140726418	140924779	BRAF	198362	2.9	584654
chr7	116695635	116796136	MET	100502	2.9	295603
chr12	4274094	4299976	CCND2,CCND2-AS1	25883	2.9	73919
chr10	121479482	121593891	FGFR2	114410	2.8	322385
chr17	31937307	31999110	SUZ12	61804	2.8	171466
chr16	3727587	3880143	CREBBP	152557	2.7	419512



Fusion Candidates - Low Confidence

This plot was generated by ROBIN.

