



Thermo Fisher Scientific

QC Report

Analysis

V005-DNA2_v1_0a781a41-c9d1-4a31-90b5-d100bad40aa8			
Ion Reporter Version 5.18	Launched by Ion User	Launched on Oct 27 2021 07:07 PM	Workflow CMOL Oncomine Comprehensive Plus - w2.3 - DNA and Fusions - Single Sample_ec806cfb-2d79-4176-a5cd- 3f71636ed838 r.0
Annotations Oncomine Comprehensive Plus Annotations v1.2 r.0	Reference Oncomine Comprehensive Plus DNA MSI v1.2, Oncomine Comprehensive Plus RNA Fusions v1.2, (Ion) tumor_ fraction_params, (Ion) 1000_genome_ OCAv4_intersection_HS_20200527, (Ion) hrr_gene_list, Oncomine Comprehensive Plus DNA Mask v1. 2, Oncomine Comprehensive Plus DNA Regions v1.4, (Ion) chrom_ info, (Ion) ocaplus_20210825, hg19, Oncomine Comprehensive Plus DNA MSI In-Silico Control v3.0, (Ion) ocaplus_panel2genome, Oncomine Comprehensive Plus RNA Fusions Config v1.2, Oncomine Comprehensive Plus DNA Hotspots v1.2	Copy Number Baseline Oncomine Comprehensive Plus DNA 550 Baseline v2.2	Exon Tile Fusion Baseline Oncomine Comprehensive Plus Fusion Baseline v1.1

Samples

V005-DNA2_v1			
Gender Female	Relationship DNA Sample	Chip Type 550	Sample ID F-TKGC GGAW
Cancer Type Unknown	Percentage Cellularity 20	Sample Type DNA	

V005-RNA2_RNA_v1			
Gender Unknown	Relationship Fusions Sample	Chip Type 550	Cancer Type Unknown
Percentage Cellularity 20	Sample Type RNA		

QC Metrics

This section provides coverage metrics for hotspots, amplicons, and genes are available via export package.

Metric	V005-DNA2_v1 (DNA Sample)	V005-RNA2_RNA_v1 (Fusions Sample)
% BED region > threshold	99.8308	
% amplicons > threshold	99.7175	
Coverage Threshold	0	
Total number of Reads	28777620	
Total number of Bases(Mbp)	3478.2937	
Total number of Bases(AQ20)(Mbp)	3173.4162	
Mean Coverage Depth(fold)	2332.4928	
Coverage within Target Region	99.8308	

Metric	V005-DNA2_v1 (DNA Sample)	V005-RNA2_RNA_v1 (Fusions Sample)
Mean Read Length(AQ20)	115.6984	
Mean Read Length(AQ30)	104.2309	
Number of Homozygous SNVs	700	
Number of Homozygous INDELs	12	
Number of Heterozygous SNVs	1321	
Number of Homozygous MNVs	4	
Number of Heterozygous MNVs	9	
Number of Heterozygous INDELs	49	
Ti/Tv Ratio (SNPs)	3.893	
dbSNP concordance	0.975	
Heterozygotes/Homozygotes	1.913	
Indels/Total	0.015	
Indels/kb	0.043	
SNPs/kb	1.412	
CNV/Total	0.141	
LongDels/Total	0.000	
Number of CNVs	567	
Number of LongDels	0	
MAPD	0.31626433215264793	
BRCA CNV QC	Passed	Passed
Fusions/Total		0.000
Number of Fusions		0
Total Mapped Fusion Panel Reads		939
Fusion Sample QC		FAIL,[TotalMappedFusionPanelReads<=500000 OR MinReadLength<=50]
Fusion Overall Call		NOCALL,[FusionSampleQC=FAIL]
Total Unmapped Reads		1170669
Average Read Length		43
POOL-1 Mapped Fusion Reads		13
POOL-2 Mapped Fusion Reads		926
POOL-1,2 Mapped Fusion Reads		0
Expression Controls Total Reads		8
POOL-1 Expression Control Total Reads		4
POOL-2 Expression Control Total Reads		4

Coverage metrics

This section provides the sample name, barcode and coverage report information.

Sample Name	BarCode	Mapped Reads	On Target	Mean Depth	Uniformity
V005-DNA2_v1	IonCode_0102	31670988	90.95%	2339	94.17%

Coverage Analysis Report

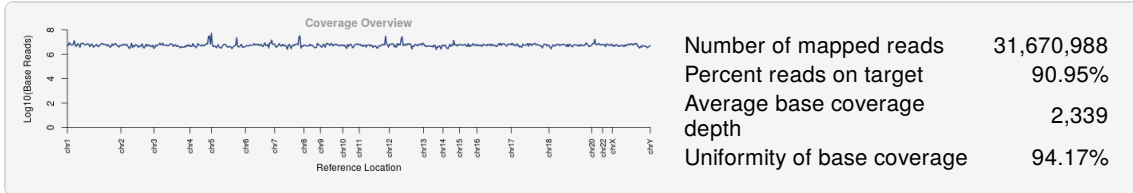
Sample Name: V005-DNA2

IonCode_0102_Auto_V005_pool_1_JC_torrent-server_30

Library type: AmpliSeq DNA and Fusions

Reference: hg19 (DNA)

Target regions: OCAPlus.20200727.designed

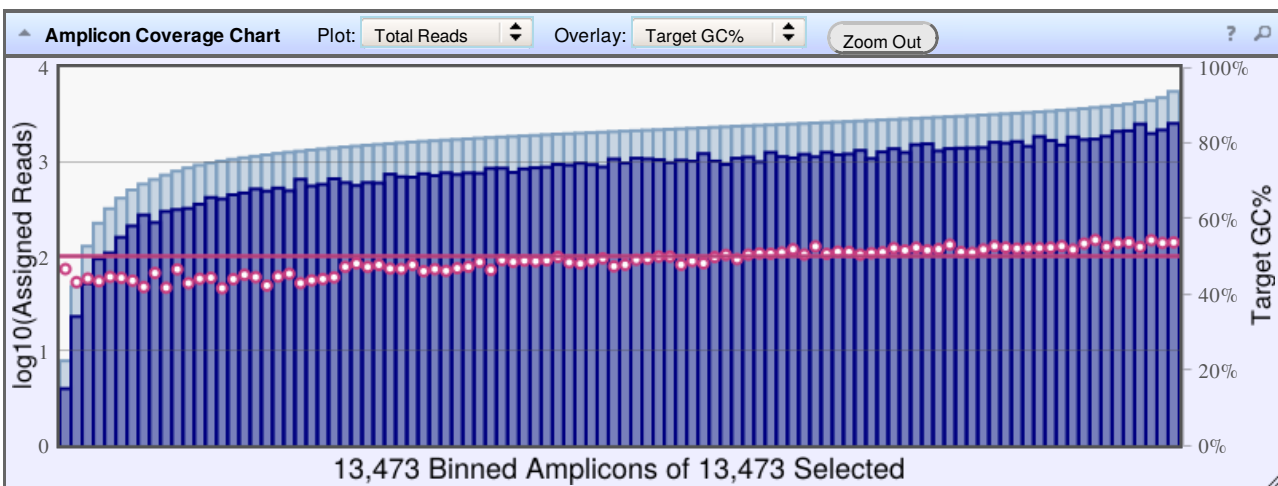
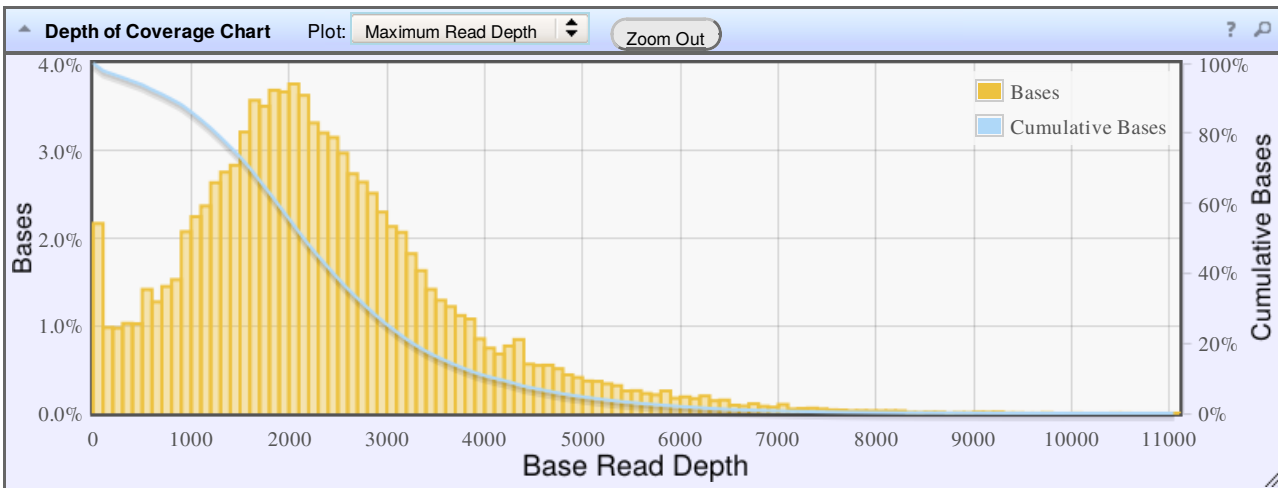


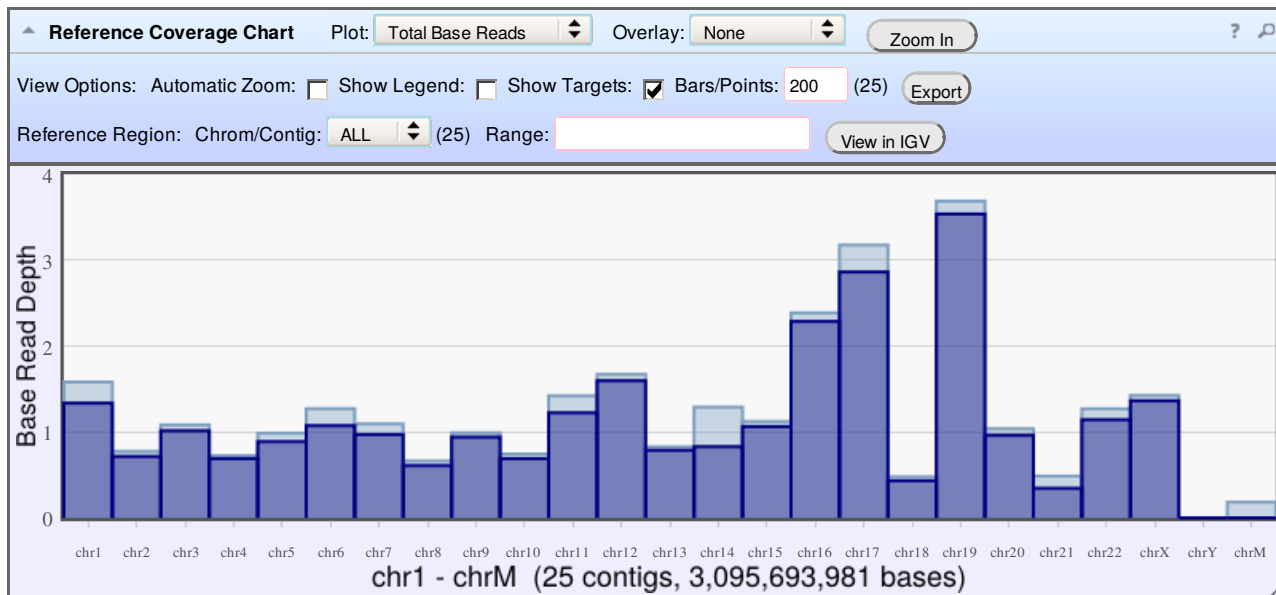
Amplicon Read Coverage

Number of amplicons	13,473
Percent assigned amplicon reads	90.95%
Average reads per amplicon	2,138
Uniformity of amplicon coverage	94.24%
Amplicons with at least 1 read	99.90%
Amplicons with at least 20 reads	99.00%
Amplicons with at least 100 reads	97.71%
Amplicons with at least 500 reads	93.52%
Amplicons with no strand bias	99.17%
Amplicons reading end-to-end	93.30%
Amplicon base composition bias	1.299

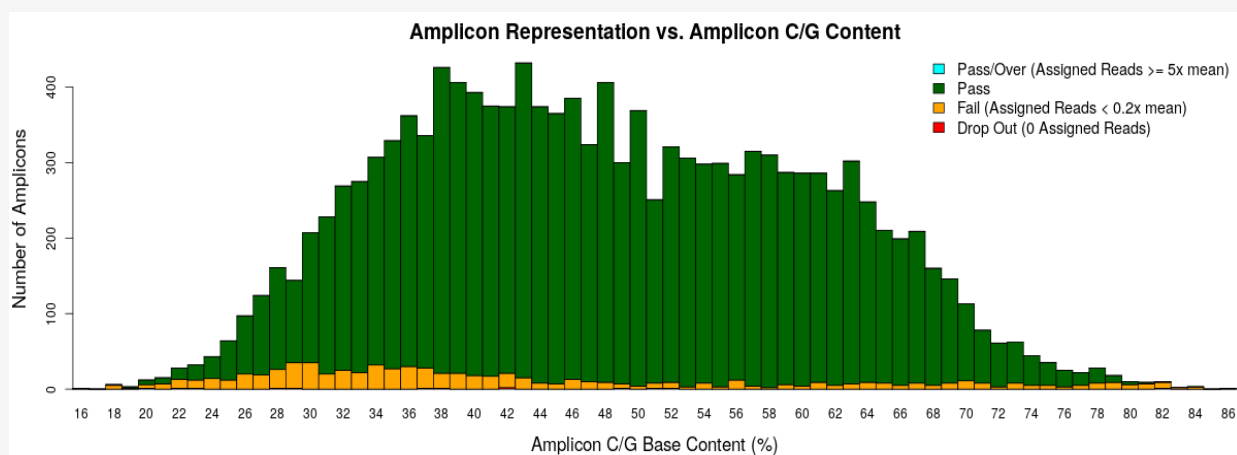
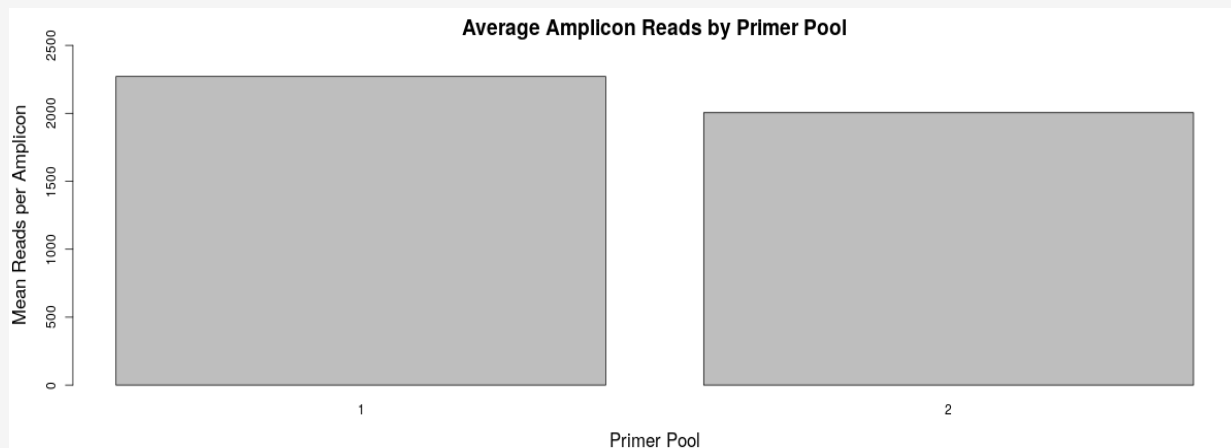
Target Base Coverage

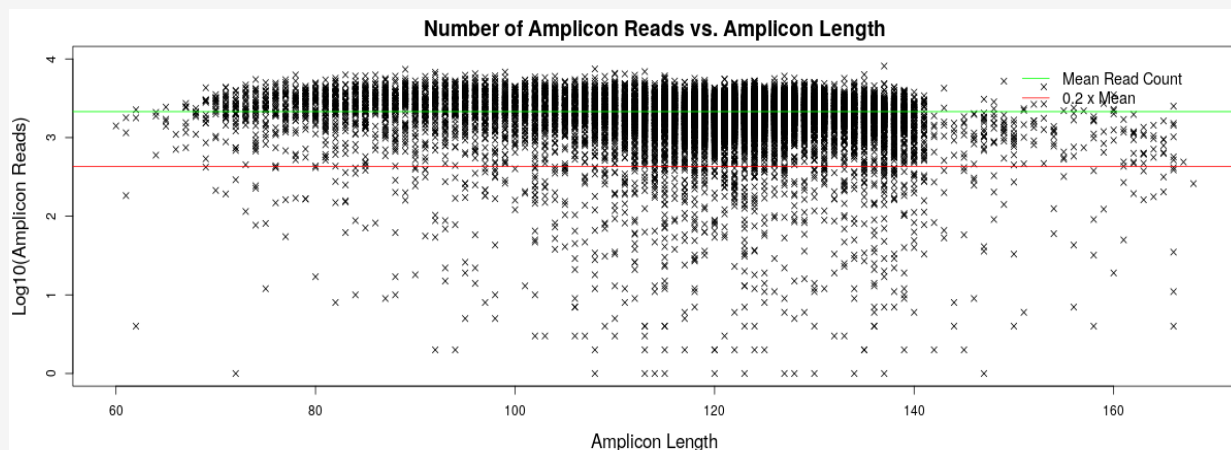
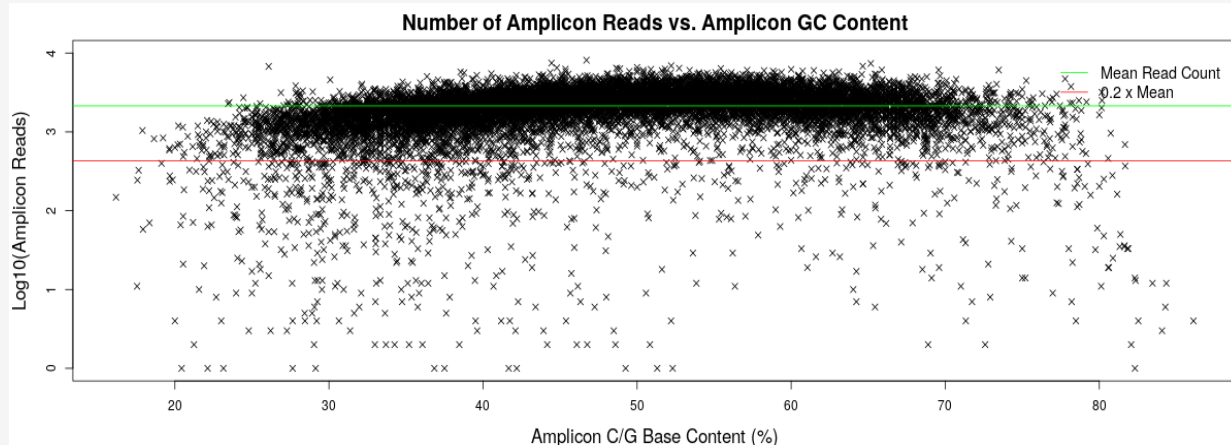
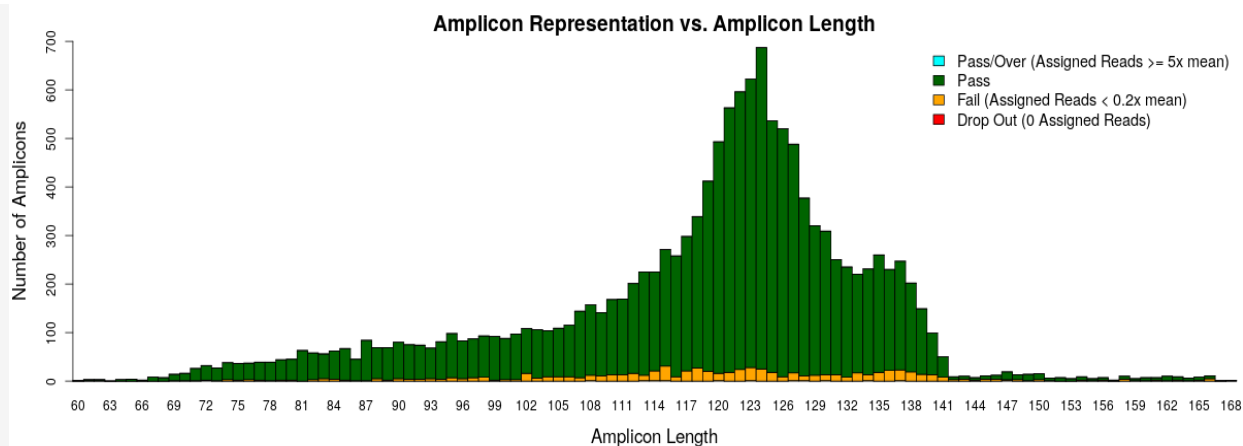
Bases in target regions	1,431,677
Percent base reads on target	90.27%
Average base coverage depth	2,339
Uniformity of base coverage	94.17%
Target base coverage at 1x	99.83%
Target base coverage at 20x	99.06%
Target base coverage at 100x	97.83%
Target base coverage at 500x	93.83%
Target bases with no strand bias	98.35%
Percent end-to-end reads	90.04%





Representation Plots





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