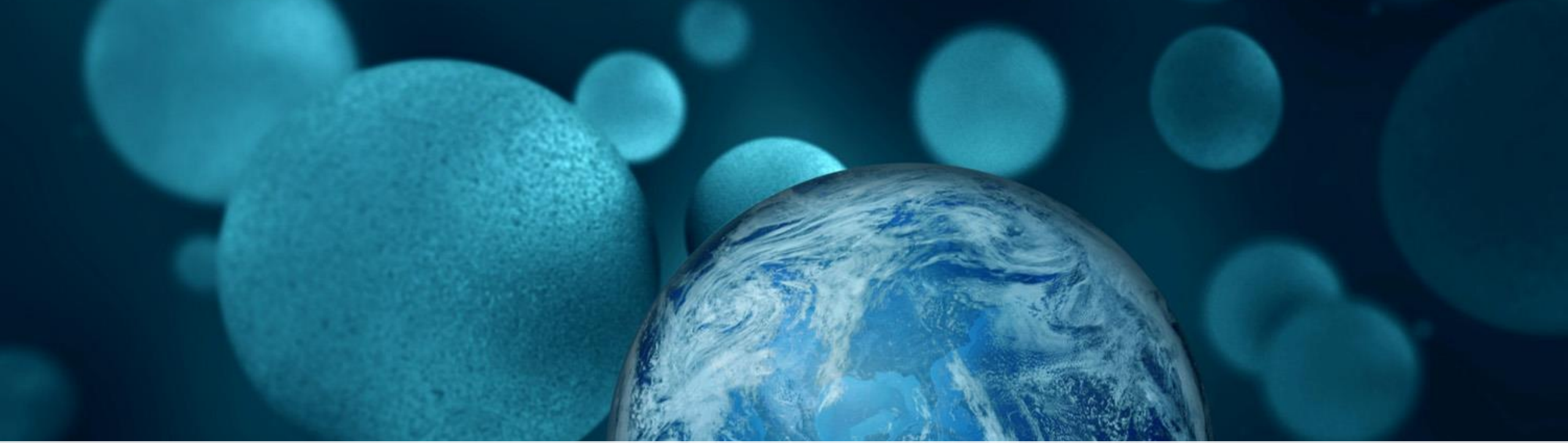

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Oncomine Childhood Cancer Research Assay

Customer Facing PPt

April 16 2018

Oncomine Childhood Cancer Research Assay

- Background
- Workflow
- Benefits
- Performance
- Content
- Summary

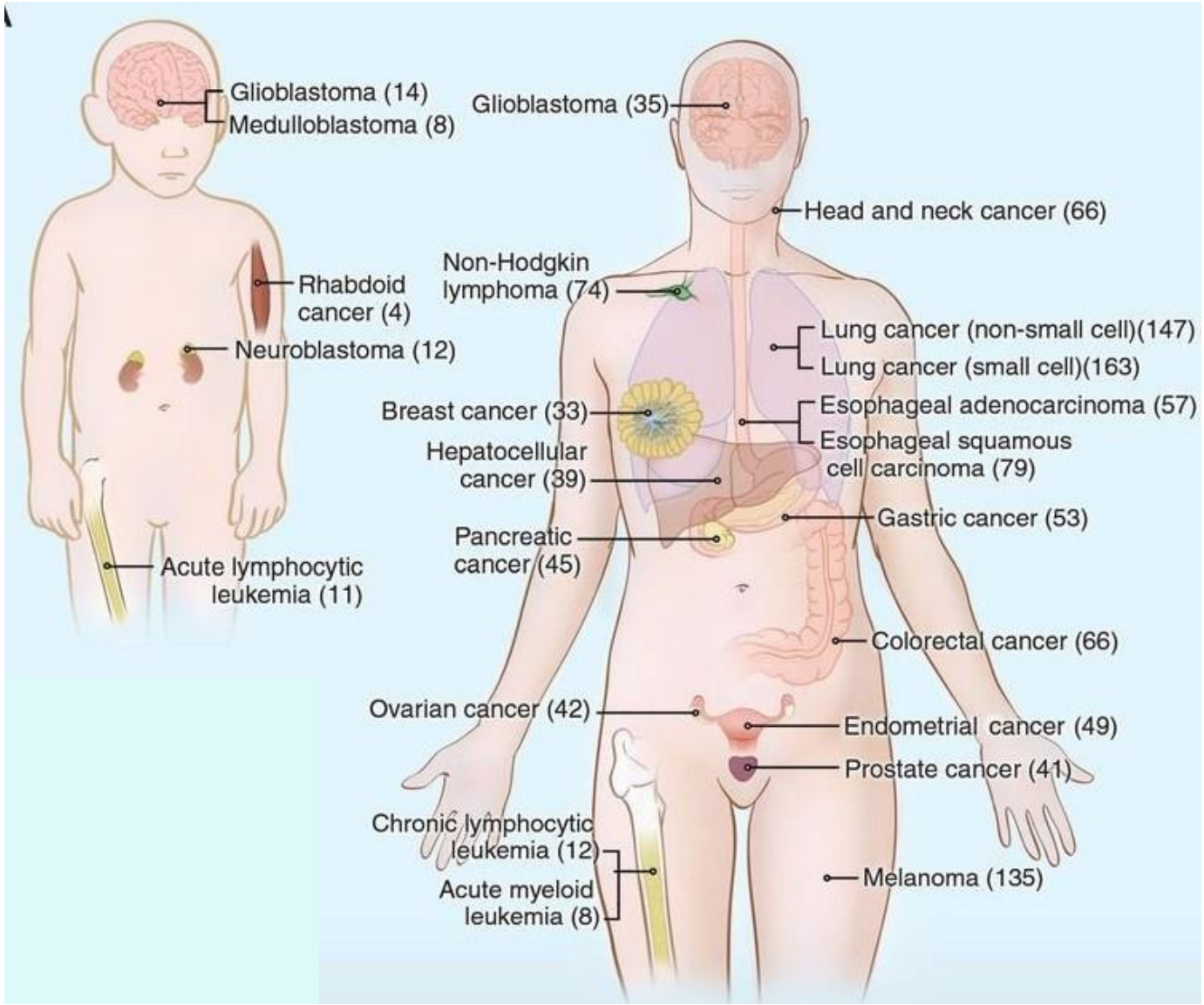
Childhood Cancer Is Different

- Every year, 300,000 cases of cancer are diagnosed in children and teens under the age of 19 globally (over 15,000 cases are diagnosed annually in the United States, where cancer remains the most common cause of death by disease for children).
- Cancers impacting children and young adults (up to age 20) are fundamentally different from cancers impacting the adult population.
- Existing tools for comprehensive genomic profiling, developed for adult cancers, are not suitable for childhood and adolescent cancer research.

GAP

Childhood Cancer Is Different

- Adult cancers are largely carcinoma, derived from epithelia with the most common cause being the accumulation of mutations over time, often caused from external sources
- Childhood and young adult cancers are rarely carcinoma most usually being mesenchymal or neuro-ectodermal in origin, developmental in character with few mutations.
- Childhood and young adult cancers also have fewer genomic aberrations than cancer in adults.



- **Bert Vogelstein et al. Science 2013;339:1546-1558** . The genomes of a diverse group of adult (right) and pediatric (left) cancers. Numbers in parentheses indicate the median number of nonsynonymous mutations per tumor

The Oncomine Childhood Cancer Research Assay (OCCRA) Is Unique

Designed to enable comprehensive genetic profiling of the most common childhood and adolescent cancers

Includes tumor-specific gene fusions, over-expressed genes, amplified genes, known gene mutations, insertions, and deletions—based on collaboration with leading scientists and pediatric oncologists

Robust performance is verified for multiple sample types, including FFPE, blood, and bone marrow

Free access to the International Childhood Oncology Network (ICON) and to a variant database, enabling researchers to collect, compare, and interrogate results

New Addition to Broad Oncomine Solutions Portfolio

All Ion Torrent™ Oncomine™ solutions have a comprehensive end-to-end workflow that includes bioinformatics

- Scalable, flexible, and fully automated on Ion Torrent™ NGS systems
- Ion AmpliSeq™ and cfDNA technology
- End-to-end oncology research informatics

- All key applications including liquid biopsy
- Protocols tested on clinical research samples
- Specialized implementation support

For Research Use Only. Not for use in diagnostic procedures.

International Childhood Oncology Network (ICON)

All Oncomine Childhood Cancer Research Assay customers will be invited to become a member of ICON, established by Thermo Fisher Scientific and CHLA.

Membership in this network will be free, and offers:

1. Connection with all other members to facilitate the optional sharing of protocols, best practices, and samples to enable rapid validation and ongoing quality assessment

2. Access to the Variant Database Platform
   - Allows interrogation of variants and comparison to other site results
   - Accumulate all Oncomine Childhood Cancer Research Assay data to amass an invaluable database for future use
   - Link out to public databases
   - Future iterations of Ion Reporter Software intended to have a push button associated with OCCRA run files, allowing seamless upload

Unique Content

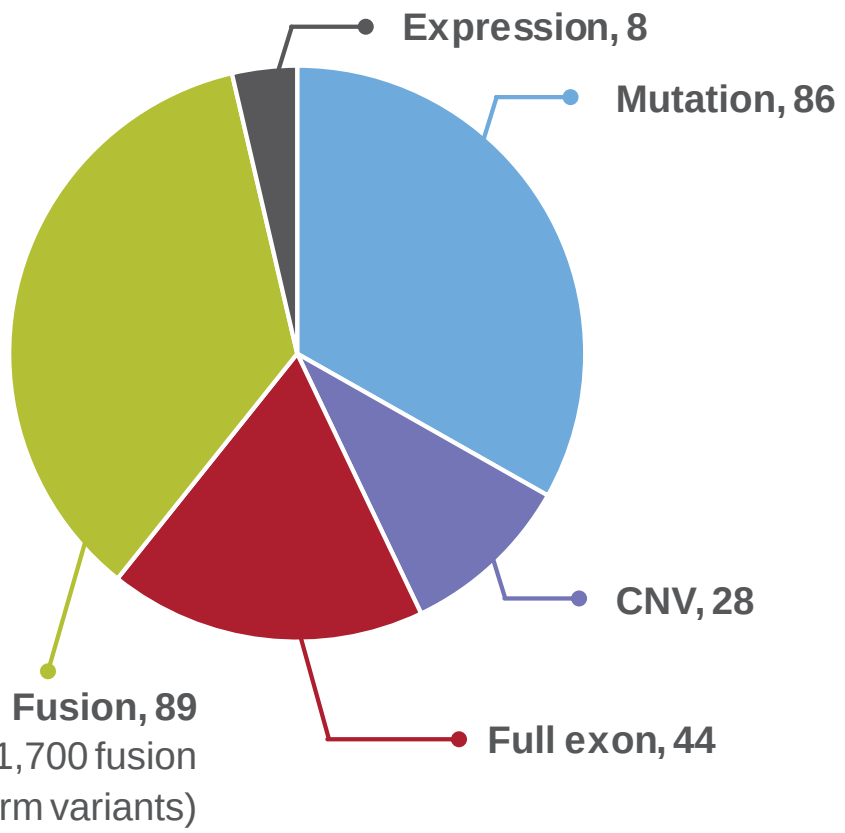
"The Ion Torrent Oncomine Childhood Cancer Research Assay is the first cancer panel designed for all forms of childhood cancer, including leukemia, brain tumors, and a diverse group of solid tumors. Of particular importance, it assays both RNA and DNA, allowing for the detection of both gene fusions and DNA mutations that are important in childhood cancer."

Timothy Triche, MD, PhD

Founding Director, Children's Hospital Los Angeles Center for Personalized Medicine

Key Facts About the Cancer Driver Aberrations Covered

203 unique genes, 3,069 DNA primer pairs (2 pools), and 1,701 (2) RNA isoforms (2 pools)



Comprehensive coverage of all relevant mutations in each of the 86 genes

Full-gene coverage specifically for tumor suppressor genes, as deleterious mutations can occur anywhere in the coding sequence

Fusion cancer drivers are relatively more common in many childhood cancers such as sarcomas and hematological malignancies, so they are covered by a large panel

Oncomine Childhood Cancer Research Assay Content

Comprehensive mutation coverage
(86 genes)

ABL1
ABL2
ALK
ACVR1
AKT1
ASXL1
ASXL2
BRAF
CALR
CBL
CCND1
CCND3
CCR5
CDK4
CIC
CREBBP
CRLF2
CSF1R
CSF3R
CTNNB1
DAXX
DNMT3A
EGFR
EP300
ERBB2
ERBB3
ERBB4
ESR1
EZH2
FASLG
FBXW7
FGFR1
FGFR2
FGFR3
FLT3
GATA2
GNA11
GNAQ
H3F3A
HDAC9
HIST1H3B
HRAS
IDH1
IDH2
IL7R
JAK1
JAK2
JAK3
KDM4C
KDR
KIT
KRAS
MAP2K1
MAP2K2
MET
MPL
MSH6
MTOR
MYC
MYCN
NCOR2
NOTCH1
NPM1
NRAS
NT5C2
PAX5
PDGFRA
PDGFRB
PIK3CA
PIK3R1
PPM1D
PTPN11
RAF1
RET
RHOA
SETBP1
SETD2
SH2B3
SH2D1A
SMO
STAT3
STAT5B
TERT
TPMT
USP7
ZMYM3

CNV
(28 genes)

ABL2
ALK
BRAF
CCND1
CDK4
CDK6
EGFR
ERBB2
ERBB3
FGFR1
FGFR2
FGFR3
FGFR4
GLI1
GLI2
IGF1R
JAK1
JAK2
JAK3
KIT
KRAS
MDM2
MDM4
MET
MYC
MYCN
PDGFRA
PIK3CA

Full exon coverage
(44 genes)

APC
ARID1A
ARID1B
ATRX
CDKN2A
CDKN2B
CEBPA
CHD7
CRLF1
DDX3X
DICER1
EBF1
EED
FAS
GATA1
GATA3
GNA13
ID3
IKZF1
KDM6A
KMT2D
MYOD1
NF1
NF2
PHF6
PRPS1
PSMB5
PTCH1
PTEN
RB1
RUNX1
SMARCA4
SMARCB1
SOCS2
SUFU
SUZ12
TCF3
TET2
TP53
TSC1
TSC2
WHSC1
WT1
XIAP

Fusion and expression
(97 genes)

ABL1
ABL2
AFF3
ALK
BCL11B
BCOR
BCR
BRAF
CAMTA1
CCND1
CIC
CREBBP
CRLF2
CSF1R
DUSP22
EGFR
ETV6
EWSR1
FGFR1
FGFR2
FGFR3
FLT3
FOSB
FUS
GLI1
GLIS2
HMGA2
JAK2
KAT6A
KMT2A
KMT2B
KMT2C
KMT2D
LMO2
MAML2
MAN2B1
MECOM
MEF2D
MET
MKL1
MLLT10
MN1
MYB
MYBL1
MYH11
MYH9
NCOA2
NCOR1
NOTCH1
NOTCH2
NOTCH4
NPM1
NR4A3
NTRK1
NTRK2
NTRK3
NUP214
NUP98
NUTM1
NUTM2B
PAX3
PAX5
PAX7
PDGFB
PDGFRA
PDGFRB
PLAG1
RAF1
RANBP17
RARA
RECK
RELA
RET
ROS1
RUNX1
SS18
SSBP2
STAG2
STAT6
TAL1
TCF3
TFE3
TP63
TSLP
TSPAN4
UBTF
USP6
WHSC1
YAP1
ZMYND11
ZNF384

Gene expression

BCL2
BCL6
FGFR1
FGFR4
IGF1R
MET
MYCN
MYC
TOP2A

>1,700 fusion isoform variants

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All Major Leukemia Translocations Represented

Acute lymphoblastic leukemia	ETV6-RUNX1, BCR-ABL1, MLL-AFF4, CDKN2A
Ph+ –like B-precursor ALL	ABL1, ABL2, CSF1R, PDGFRB, CRLF2, FLT3, KRAS
Acute myelogenous leukemia	FLT3, NPM1, KIT, IDH1, IDH2, DNMT3A, RUNX1, TET2, CEBPA
Acute promyelocytic leukemia	PML-RARα

Childhood/Adolescent Brain Tumors and Types

AT/RT, cribiform neuroepithelial tumor, schwannoma	Medulloblastoma, WNT, RT (rhabdoid tumor)	Medulloblastoma	Ependymoma	Ependymoma, meningioma
SMARCB1	SMARCA4	GLI2, MSH6, MYCN, PTCH1, SUFU	RELA	NF2

Astrocytoma	Glioblastoma	Glioma, astrocytoma grade I–IV, ependymoma grade 3–4	Glioma, astrocytoma grade I–IV, oligoastrocytoma	Pilocytic astrocytoma
FGFR1, HIST1H3B, MDM2, PTPN11, TERT, TP53	MDM4	PTEN	H3F3A	BRAF, NTRK2

Childhood/Adolescent Sarcoma Fusions

Rhabdomyosarcoma (embryonal and alveolar)	Ewing sarcoma	Synovial cell sarcoma	Infantile (congenital) fibrosarcoma	Desmoplastic small round cell tumor	Alveolar soft part sarcoma
PAX3/7-FOXO1	EWS-FLI1/ERG	SS18-SSX1/2/4	ETV6-NTRK	EWS-WT1	TFE3-ASPSCR1 (ASPL)

Clear cell sarcoma (melanoma of soft parts)	Inflammatory myofibroblastic tumor	Fibromyxoid sarcoma	Dermatofibrosarcoma protuberans	Epithelioid sarcoma	Angiomatoid fibrous histiocytoma
EWS-ATF1, EWS-CREB1	ALK-TPM3/4, CLTC	FUS-CREB3L2/1	COL1A-PDGFB	SMARCB1	EWS-CREB1

Epithelioid hemangioendothelioma	Mesenchymal chondrosarcoma	Malignant peripheral nerve sheath tumor	Undifferentiated sarcoma	Midline carcinoma
WWTR1-CAMTA1	HEY1-NCOA2	NF1/NF2 mut	BCOR-CCNB3, CIC-DUX4	NUTM1-BRD4

End-To-End Workflow Optimized for Childhood Cancer Research

- Variety of sample types verified: blood and bone marrow, fresh/frozen tissue, and FFPE tissue
- Up to 8 samples can be multiplexed on a single chip
- 2–3 days from sample to report—fast turnaround time is important in pediatric cancer research

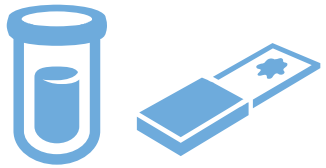
Powerful
Efficient with challenging samples

Simple
Automated library and templating options

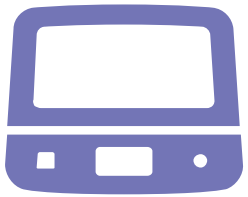
Flexible
1 to 8 samples can be run on the same chip with DNA and RNA

Streamlined
Built-in informatics

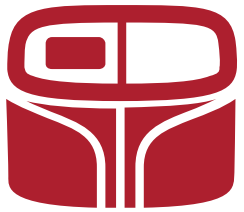
Ion AmpliSeq™ technology



Ion Chef™ System



Ion GeneStudio™ S5 System



Ion Reporter™ Software

The optimized bioinformatics pipeline will result in filtered lists of cancer driver mutations in .vcf file format that are uploadable to a dedicated childhood cancer variant platform

For Research Use Only. Not for use in diagnostic procedures.

Average Run-Level Performance Data

	Average Total Run Reads	Average Uniformity	Average Mapped Reads per Barcode (DNA)	Average Polyconality	Average Low Quality	Average Median Run Read Length
S5 Manual Library Prep	80 million	96.5%	8.5 million	26%	8%	117
S5 Chef Library Prep	70 million	96.5%	7.5 million	43%	14%	117

- Consistent performance across platforms
  - Ion S5 Manual Library Prep plexy = 7 samples + 1 NTC per Ion 540 Chip
  - Ion S5 Chef Library Prep plexy = 7 samples + 1 NTC per Ion 540 Chip

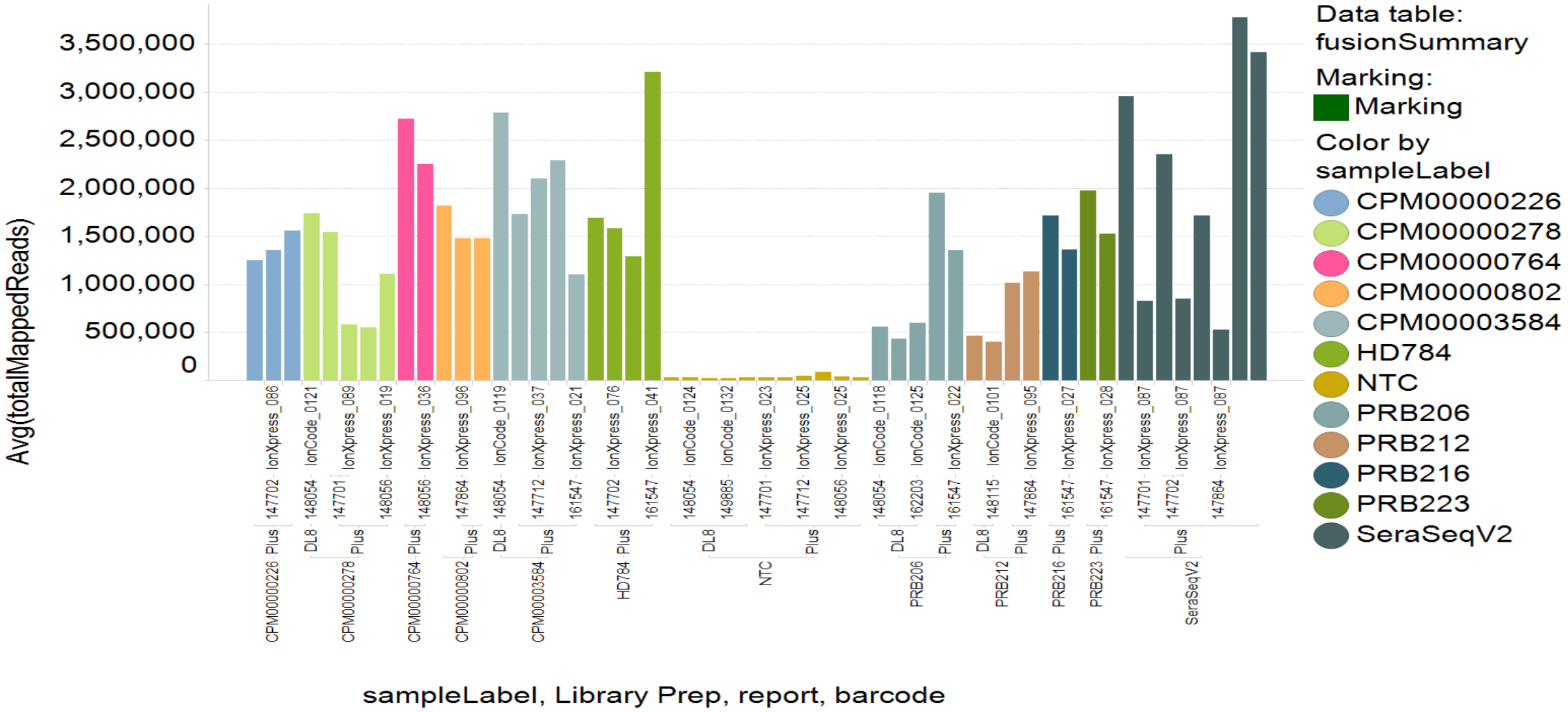
Results of verification in Children Hospital Los Angeles on over 500 samples *

- **>**5000X average coverage for DNA variants
- Average uniformity >95%
- Average mapped reads >2,000,000 for RNA fusions

*Data presented at AMP Europe Conference in April 2017

*verification data used as representative

DNA: Mapped Reads



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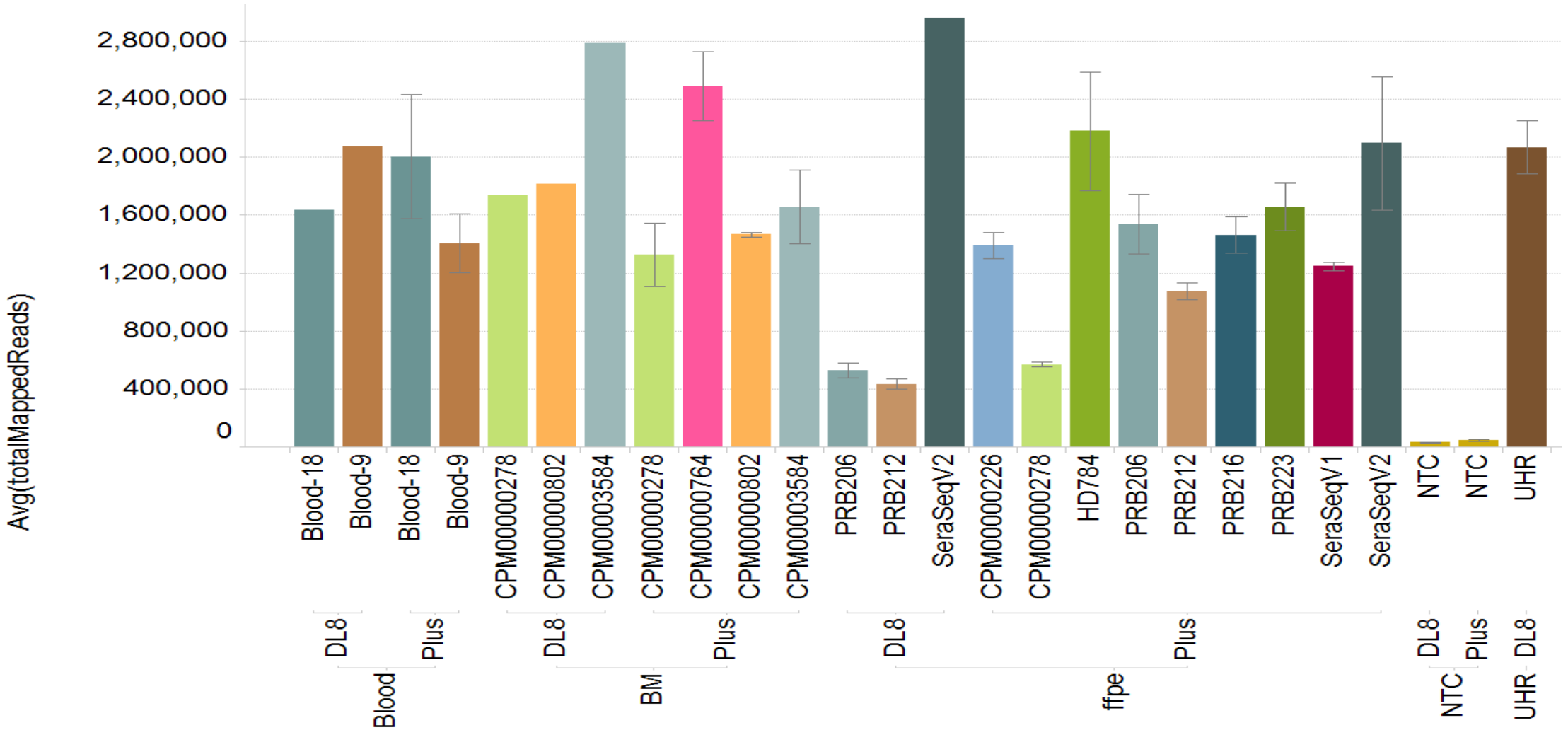
RNA: Total Mapped Reads



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Summary

Oncomine Childhood Cancer Research Assay & ICON will enable progress and standardization of the childhood and young adult cancer research across the world

This assay is a **unique tool** designed specifically for use in childhood and young adult cancer research

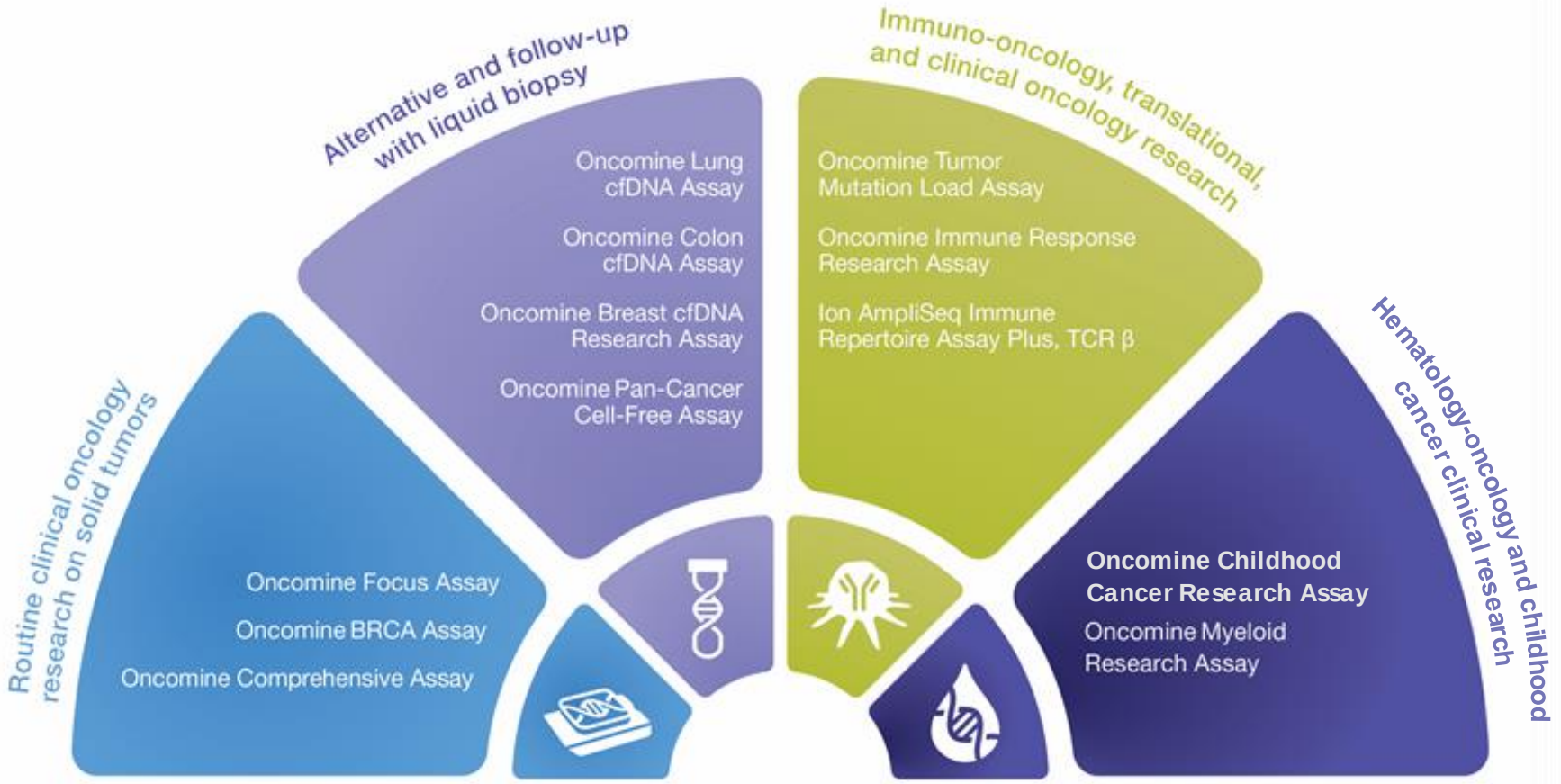
It has a **complete** end-to-end workflow, including informatics

The content, defined in collaboration with leading pediatric oncologists, covers key genetic aberrations across the whole spectrum of childhood cancers

Membership in **ICON** enables access to the variant database and collaboration with other researchers while collecting valuable findings, sharing protocols, best practices, and samples to enable rapid validation and ongoing quality assessment

Complete Set of Oncomine Assays for Clinical Research

Oncomine assays provide comprehensive tools not only for solid tumor clinical research but also for hematology-oncology clinical research and translational research in immuno-oncology.



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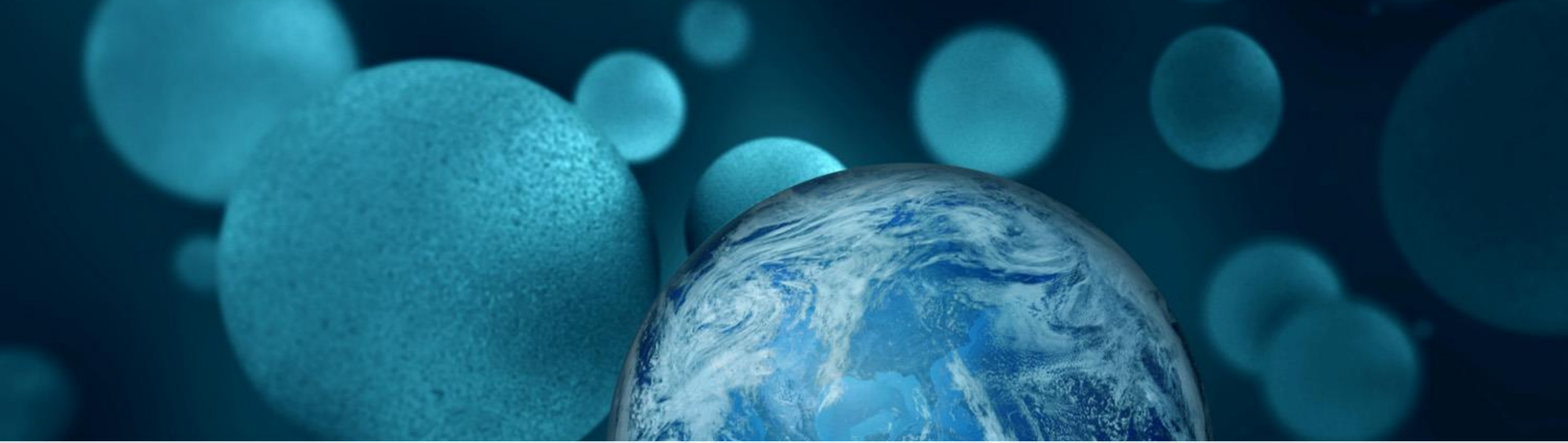

Thank you

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Kit Configuration and Ordering Information

Oncomine™ Childhood Cancer Research Assay
(Chef Ready Library x2, Equalizer and bar codes are included)

Content	Oligos & Library reagents
Number of pools	2 DNA, 2 RNA
Sample ID	Included
Blood/bone marrow compatible	Yes
FFPE compatible	Yes
Validation on clinical samples	Yes
Manufacturing QC	Enhanced

Oncomine™ Childhood Cancer Research Assay
(Manual Library).
Library Plus x2
Equalizer and bar codes NOT included

Part Number	SAP Description	Samples
A36114	ONCOMINE CH CANCER RESASSY DNA	x24
A36483	ONCOMINE CH CANCER RESASSY RNA	x24

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Small Variant Detection

SNV Detection

Hotspot

True Pos	False Pos	False Neg	%Sens	%PPV	%Repr*
387	1	8	**98.0**	**99.7**	**96.5**

Samples: AOHC synthetic control (MegaMix 5%) with 102 SNV Hotspot variants and Horizon 200, 728, and AF10 cell lines with 20 SNV Hotspot variants among them.

De novo

True Pos	False Pos	False Neg	%Sens	%PPV	%Repr*
342	1	0	**100**	**99.7**	**100**

Samples: AOHC synthetic control (MegaMix 5%) with 112 SNV De novo variants and Horizon 200, and AF10 cell lines with 2 SNV De novo variants among them.

Indel Detection

Hotspot

True Pos	False Pos	False Neg	%Sens	%PPV	%Repr*
52	0	0	**100**	**100**	**100**

Samples: AOHC synthetic control (MegaMix 10%) with 5 Indel Hotspot variants and AF10 cell line with 3 Indel Hotspot variants.

De novo

True Pos	False Pos	False Neg	%Sens	%PPV	%Repr*
137	0	19	**87.8**	**100**	**91.0**

Samples: CPM00000028 bone marrow samples with 1 Indel De novo variant, AOHC synthetic control (MegaMix 20%) with 11 Indel De novo variants and Horizon 200 cell line with 1 Indel De novo variant.

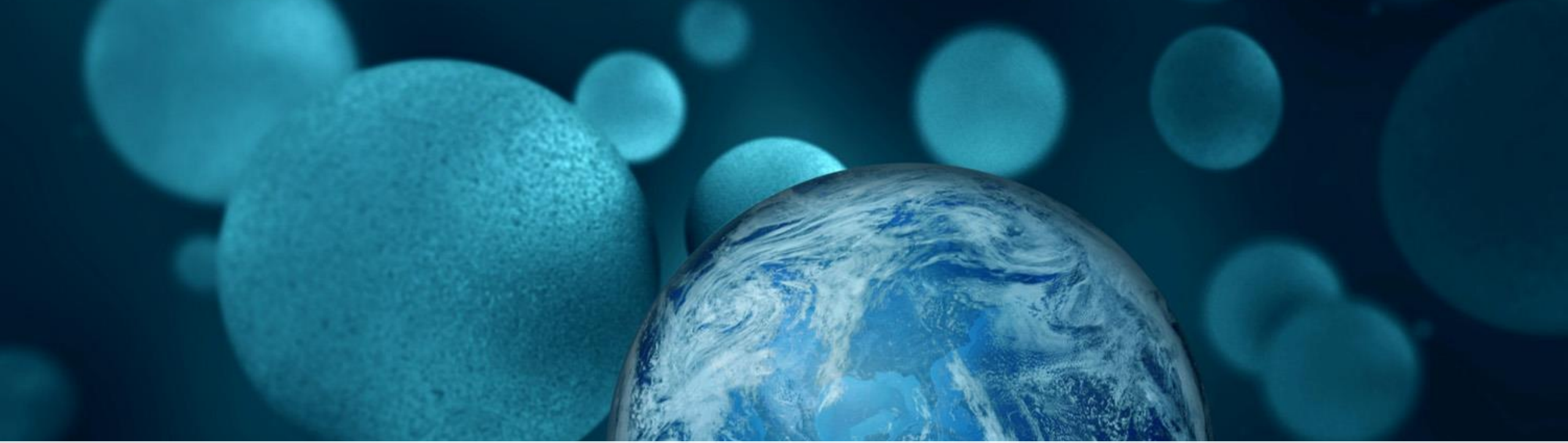
*Reproducibility calculated between manual and automated library prep

Copy Number Variants Detection in FFPE samples

True Pos	False Pos	False Neg	True Neg	%Sens	%Spec	%Repr*
40	0	0	32	**100**	**100**	**100**

Clinical Research Sample	Cellularity (LL)	Amplified Gene	FISH CNV	OCCRA	Neutral Gene	FISH CNV	OCCRA	Novel AMPs	
								Gene	OCCRA
365	90%	**CCND1**	13	13.14, 13.61, 13.03, 12.28	**CDK4**	1.9	1.93, 1.84, 1.93, 1.90		
1181615B	99%	**EGFR**	52.9	77.78, 78.42, 79.46, 81.80	**MET**	ND	2.77, 2.86, 2.87, 2.82		
		CDK4	14	14.09, 13.24, 13.31, 13.82	**FGFR1**	1.9	1.98, 1.73, 1.98, 1.89		
1193124B	100%	**CDK6**	16.8	7.86, 7.90, 7.82, 8.13	**CDK4**	3.3	2.24, 2.26, 2.23, 2.23	PDGFRA	8.74, 8.61, 8.66, 9.00
								KIT	6.34, 6.29, 6.59, 6.34
1196647B	80%	**PIK3CA**	10.5	8.80, 9.50, 9.88, 10.56	**MET**	3.2	2.15, 2.24, 2.30, 2.38		
1197046B	65%	**CCND1**	6.1	7.12, 7.69, 7.11, 7.66	**EGFR**	2.1	2.49, 2.43, 2.48, 2.58		
1198367B	70%	**MYC**	12.1	10.96, 10.41, 10.71, 11.27	**CDK6**	2.4	2.03, 2.03, 2.03, 2.11	CCND1	25.66, 26.76, 25.04, 25.73
1194253B	75%	**PIK3CA**	13.2	10.61, 11.41, 12.11, 11.17	**MYC**	2.5	1.56, 1.61, 1.63, 1.67		
1197339B	70%	**CCND1**	12.0	8.04, 8.13, 8.33, 8.84	**PIK3CA**	ND	2.44, 2.84, 2.54, 2.57	FGFR2	15.79, 15.86, 15.80, 16.09
1199087B	75%	**CCND1**	6.2	8.00, 7.77, 6.84, 8.12	**CDK6**	3.2	2.93, 2.76, 2.93, 2.93	EGFR	5.32, 5.51, 5.71, 5.37
								IL7R	6.41, 7.04, 7.48, 7.52
								PIK3CA	5.29, 5.41, 5.32, 5.19
								TERT	7.07, 12.59, 9.11, 7.25

*Reproducibility calculated between manual and automated library prep



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Oncomine Childhood Cancer Research Assay

Performance Data

April 11 2018

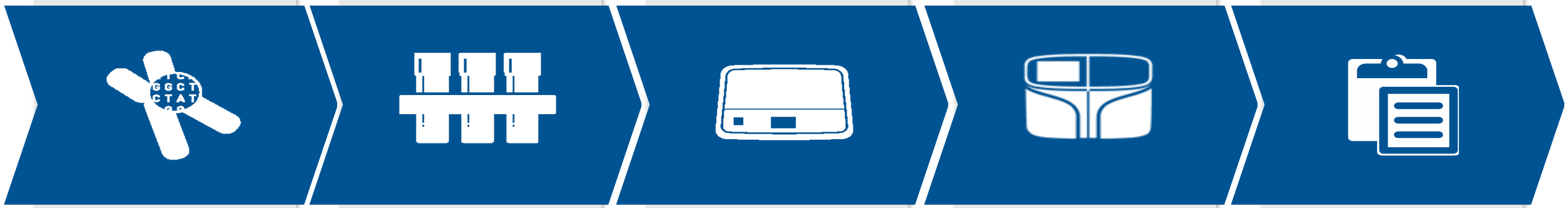
Panel Design: Amplicon Pools

Oncomine™ Childhood Cancer Research Assay	
Number of pools	4
Total Amplicons	DNA: 3,060 (excluding Sample ID) RNA: 1,701
Amplicons/pool	DNA pool 1: 1537 DNA pool 2: 1532 RNA pool 1: 1006 (950 primers) RNA pool 2: 695 (581 primers)
Avg. Amplicon insert length (range)	DNA: 114 bp (52 - 216) RNA: 97 bp (34 - 222)
Sample ID	Included, +9 amplicons
Libraries per sample	2 (1 DNA, 1 RNA)
Sample Input	10ng per pool (20ng DNA, 20ng RNA)

Hotspot	537
CDS	2205
CNV	142
CNV/Hotspot	176

OCCRA Workflow

- RNA and DNA from same sample
  - Seven DNA samples plus one negative control –PLUS-
  - Seven RNA samples plus one negative control per chip



Sample Input	Prepare Library	Prepare Template	Run Sequence	Analyze
RNA and DNA extracted from Blood, Bone marrow or FFPE tissue	Oncomine™ Childhood Cancer Research Assay Manual or Automated Library Prep	Ion Chef™ System	Ion S5™ System (540)	Ion Reporter™ Software
	Day 1 6 hr. process	Day 2 17 hr. process	Days 3 & 4 13 hr. sequencing & analysis + 5 hr. IR	

PASS

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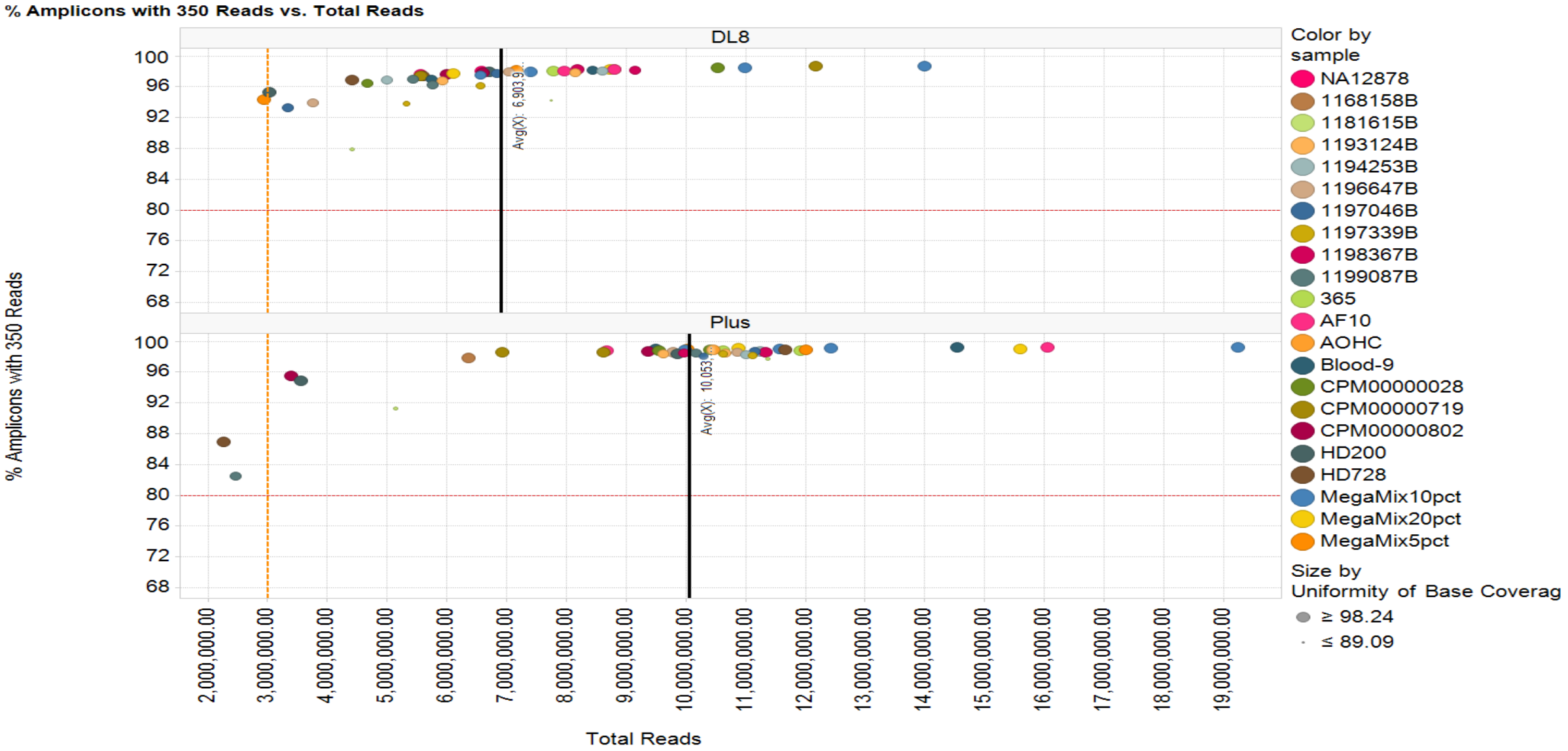
Average Run-Level Performance Data

	Average Total Run Reads	Average Uniformity	Average Mapped Reads per Barcode (DNA)	Average Polyconality	Average Low Quality	Average Median Run Read Length
S5 Manual Library Prep	80 million	96.5%	8.5 million	26%	8%	117
S5 Chef Library Prep	70 million	96.5%	7.5 million	43%	14%	117

- Consistent performance across platforms
  - Ion S5 Manual Library Prep plexy = 7 samples + 1 NTC per Ion 540 Chip
  - Ion S5 Chef Library Prep plexy = 7 samples + 1 NTC per Ion 540 Chip

*verification data used as representative

DNA: Amplicon Coverage vs Total Reads



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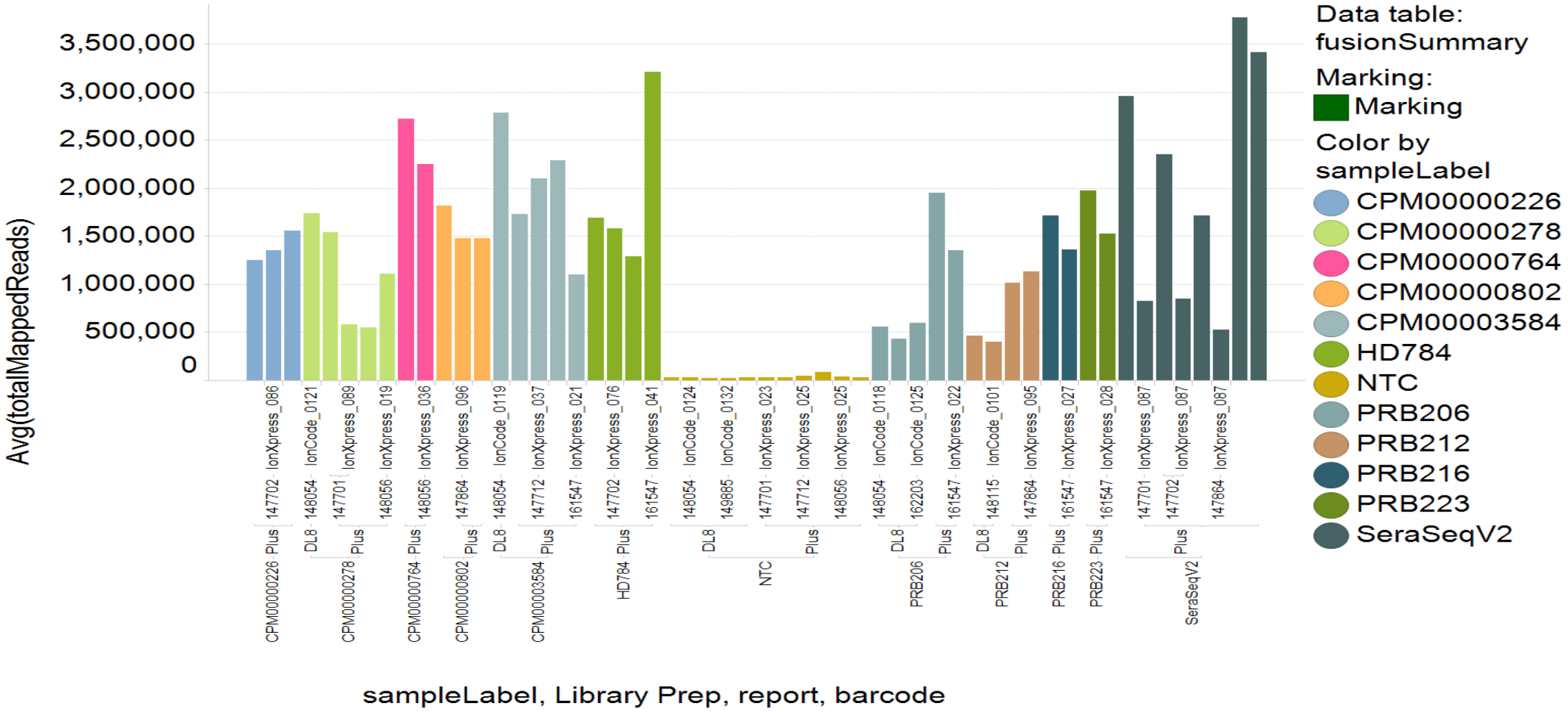
DNA: Mapped Reads



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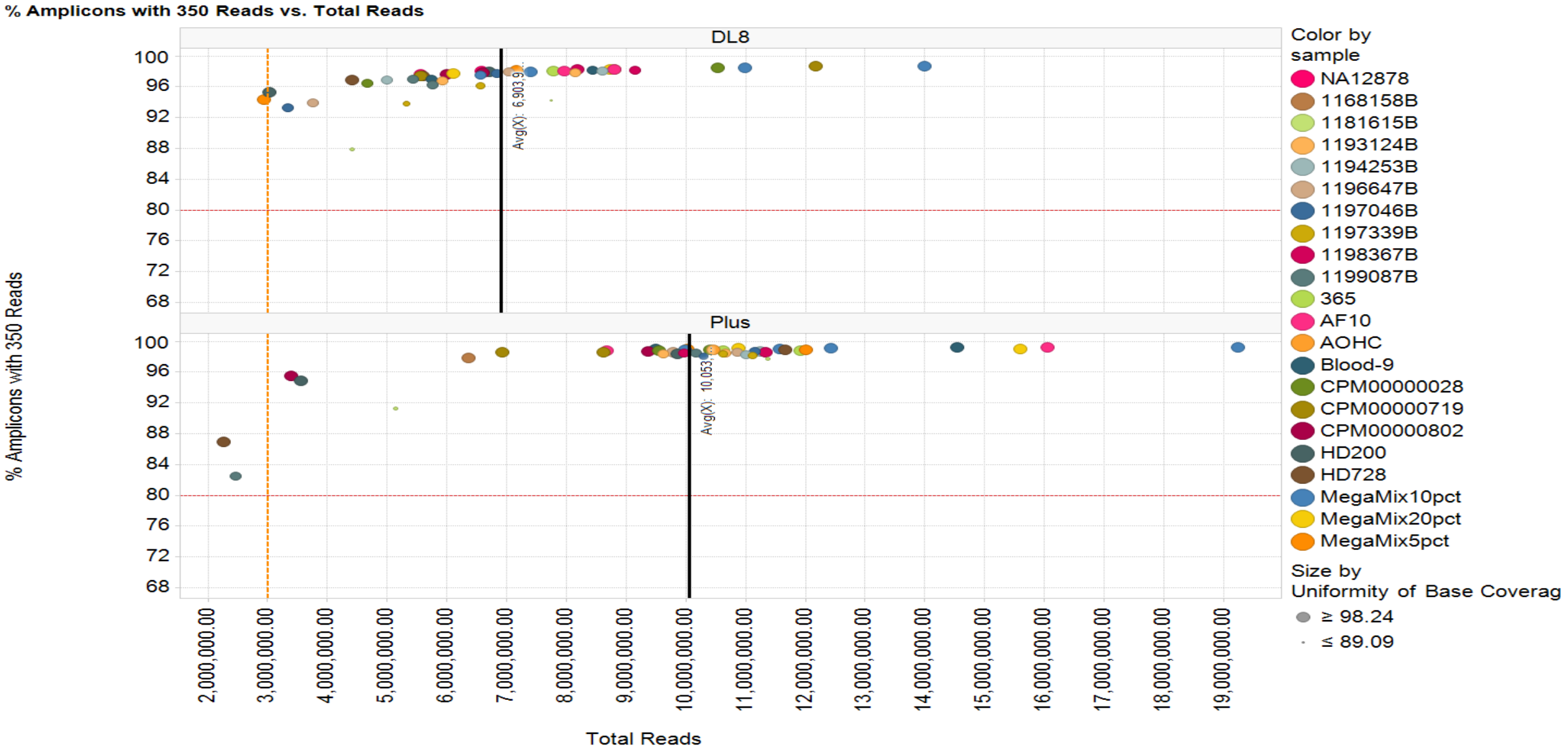
DNA: Amplicon Coverage vs Total Reads



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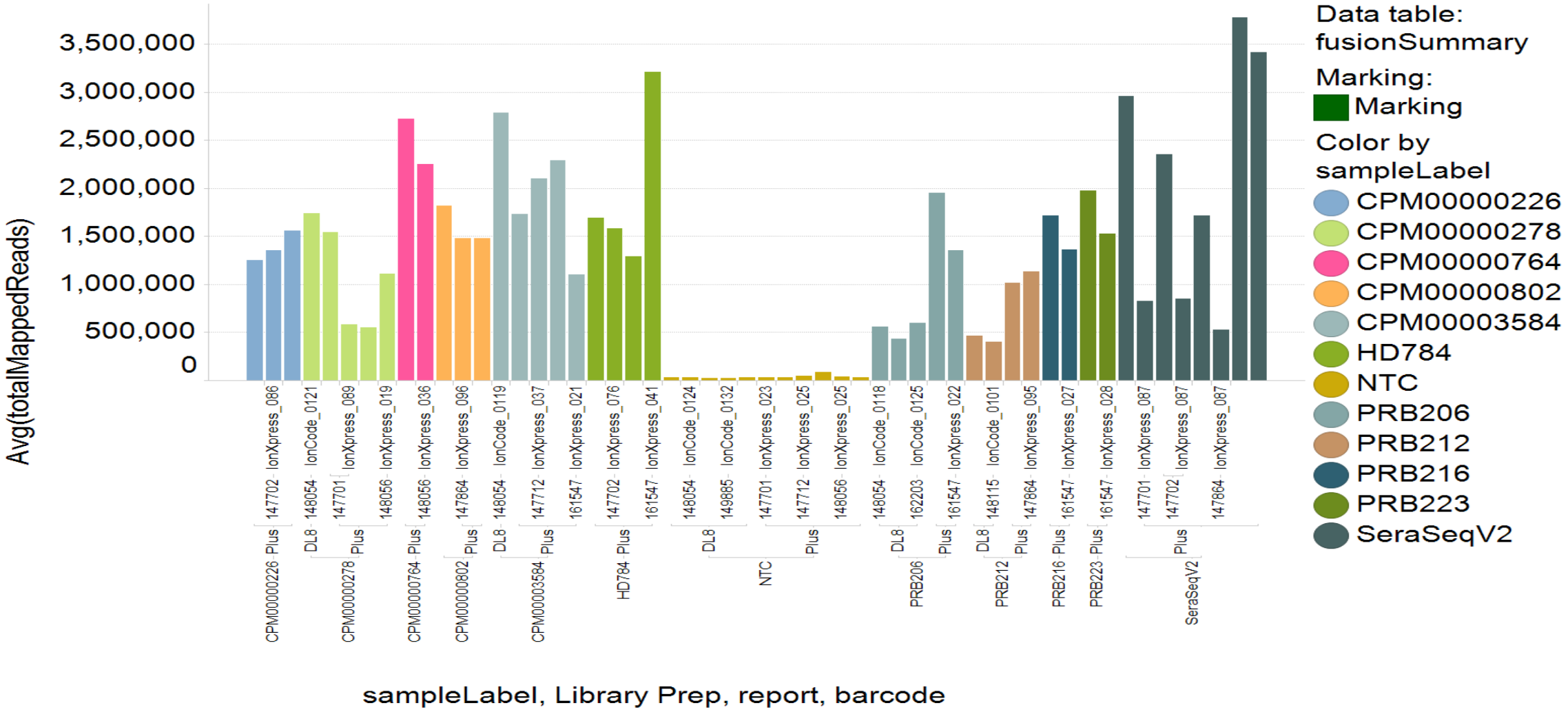
DNA: Mapped Reads



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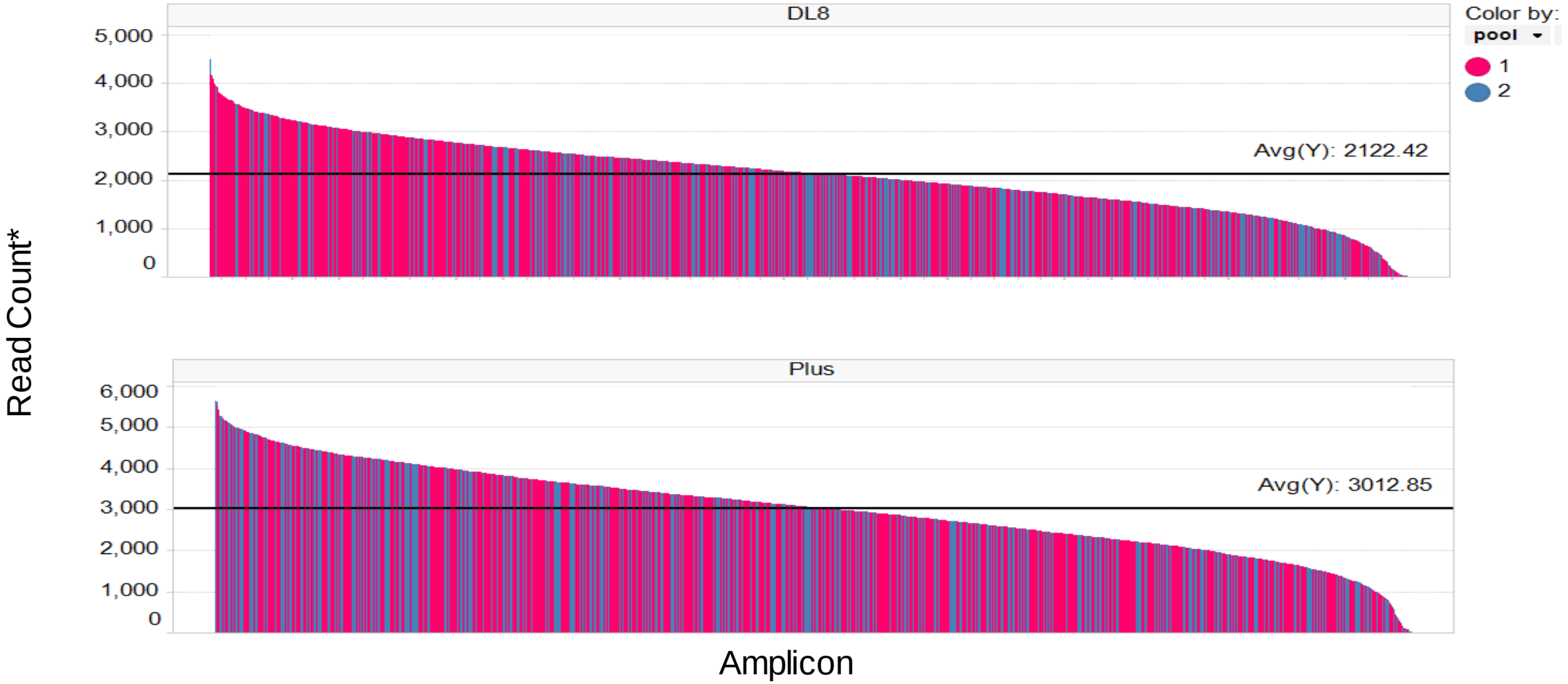
DNA: Amplicon Coverage Depth



*High outlier values stemming from high-level amplicifcation removed

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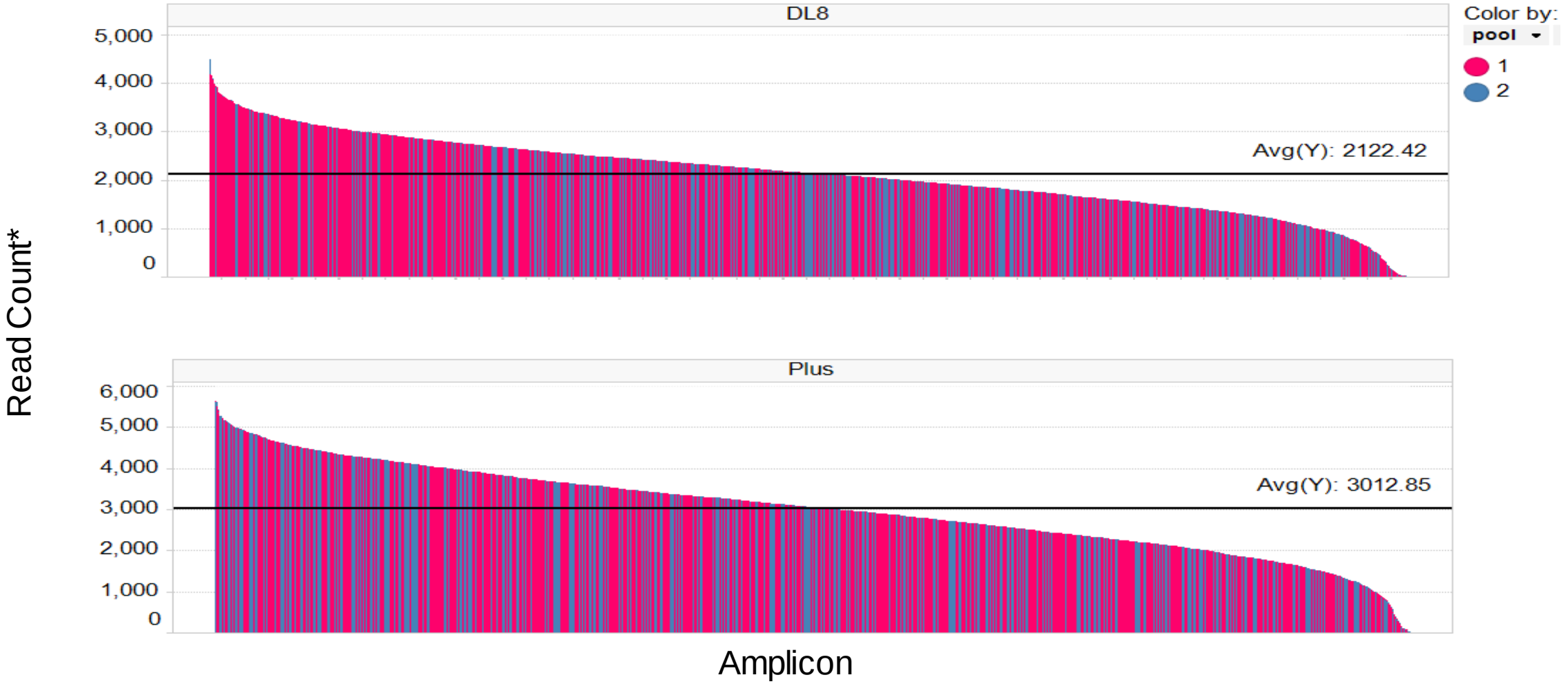
DNA: Amplicon Coverage Depth



*High outlier values stemming from high-level amplicifcation removed

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Small Variant Detection

SNV Detection

Hotspot

True Pos	False Pos	False Neg	%Sens	%PPV	%Repr*
387	1	8	**98.0**	**99.7**	**96.5**

Samples: AOHC synthetic control (MegaMix 5%) with 102 SNV Hotspot variants and Horizon 200, 728, and AF10 cell lines with 20 SNV Hotspot variants among them.

De novo

True Pos	False Pos	False Neg	%Sens	%PPV	%Repr*
342	1	0	**100**	**99.7**	**100**

Samples: AOHC synthetic control (MegaMix 5%) with 112 SNV De novo variants and Horizon 200, and AF10 cell lines with 2 SNV De novo variants among them.

Indel Detection

Hotspot

True Pos	False Pos	False Neg	%Sens	%PPV	%Repr*
52	0	0	**100**	**100**	**100**

Samples: AOHC synthetic control (MegaMix 10%) with 5 Indel Hotspot variants and AF10 cell line with 3 Indel Hotspot variants.

De novo

True Pos	False Pos	False Neg	%Sens	%PPV	%Repr*
137	0	19	**87.8**	**100**	**91.0**

Samples: CPM00000028 bone marrow samples with 1 Indel De novo variant, AOHC synthetic control (MegaMix 20%) with 11 Indel De novo variants and Horizon 200 cell line with 1 Indel De novo variant.

*Reproducibility calculated between manual and automated library prep

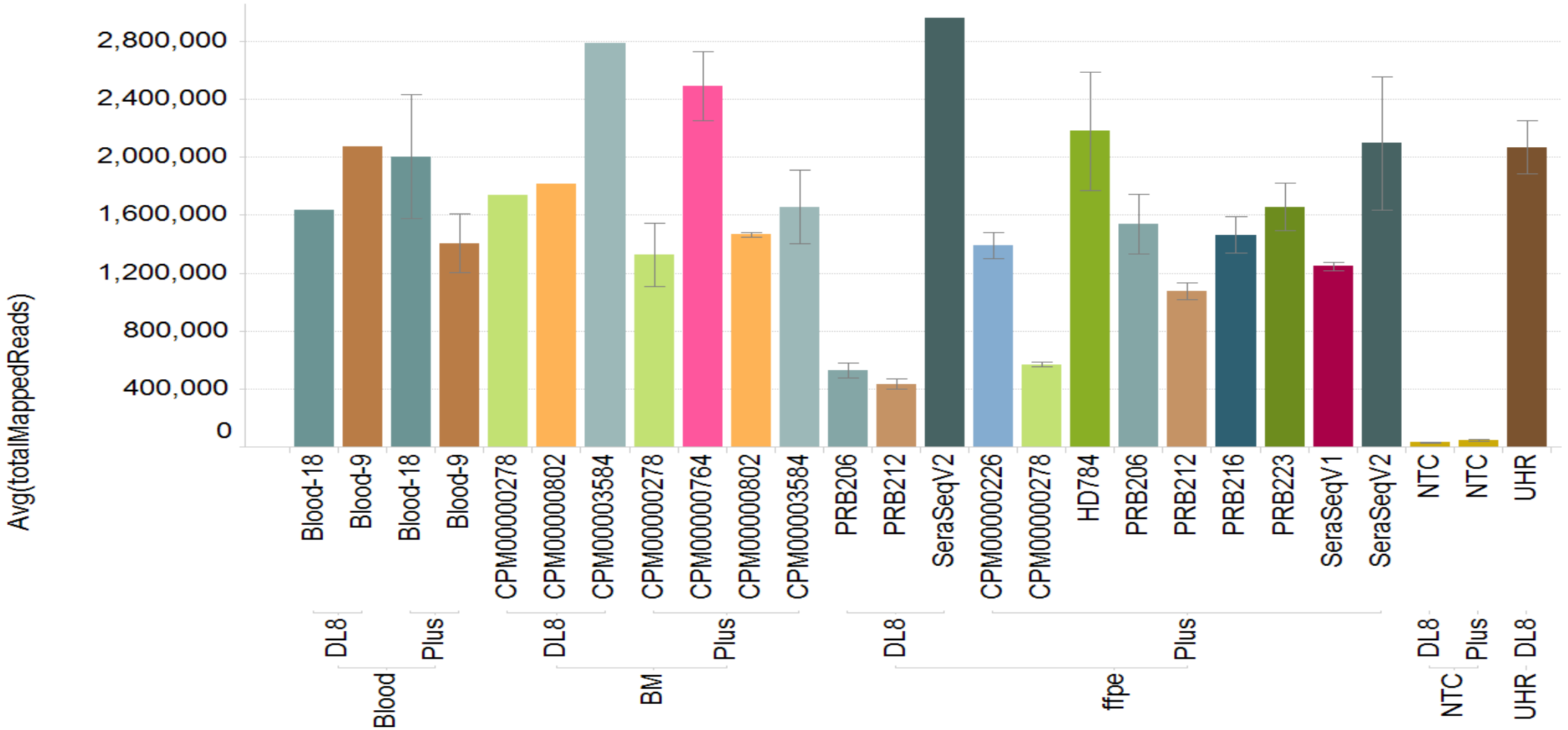
Copy Number Variants Detection in FFPE samples

True Pos	False Pos	False Neg	True Neg	%Sens	%Spec	%Repr*
40	0	0	32	**100**	**100**	**100**

Clinical Research Sample	Cellularity (LL)	Amplified Gene	FISH CNV	OCCRA	Neutral Gene	FISH CNV	OCCRA	Novel AMPs	
								Gene	OCCRA
365	90%	**CCND1**	13	13.14, 13.61, 13.03, 12.28	**CDK4**	1.9	1.93, 1.84, 1.93, 1.90		
1181615B	99%	**EGFR**	52.9	77.78, 78.42, 79.46, 81.80	**MET**	ND	2.77, 2.86, 2.87, 2.82		
		CDK4	14	14.09, 13.24, 13.31, 13.82	**FGFR1**	1.9	1.98, 1.73, 1.98, 1.89		
1193124B	100%	**CDK6**	16.8	7.86, 7.90, 7.82, 8.13	**CDK4**	3.3	2.24, 2.26, 2.23, 2.23	PDGFRA	8.74, 8.61, 8.66, 9.00
								KIT	6.34, 6.29, 6.59, 6.34
1196647B	80%	**PIK3CA**	10.5	8.80, 9.50, 9.88, 10.56	**MET**	3.2	2.15, 2.24, 2.30, 2.38		
1197046B	65%	**CCND1**	6.1	7.12, 7.69, 7.11, 7.66	**EGFR**	2.1	2.49, 2.43, 2.48, 2.58		
1198367B	70%	**MYC**	12.1	10.96, 10.41, 10.71, 11.27	**CDK6**	2.4	2.03, 2.03, 2.03, 2.11	CCND1	25.66, 26.76, 25.04, 25.73
1194253B	75%	**PIK3CA**	13.2	10.61, 11.41, 12.11, 11.17	**MYC**	2.5	1.56, 1.61, 1.63, 1.67		
1197339B	70%	**CCND1**	12.0	8.04, 8.13, 8.33, 8.84	**PIK3CA**	ND	2.44, 2.84, 2.54, 2.57	FGFR2	15.79, 15.86, 15.80, 16.09
1199087B	75%	**CCND1**	6.2	8.00, 7.77, 6.84, 8.12	**CDK6**	3.2	2.93, 2.76, 2.93, 2.93	EGFR	5.32, 5.51, 5.71, 5.37
								IL7R	6.41, 7.04, 7.48, 7.52
								PIK3CA	5.29, 5.41, 5.32, 5.19
								TERT	7.07, 12.59, 9.11, 7.25

*Reproducibility calculated between manual and automated library prep

RNA: Total Mapped Reads



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Fusions Detected

Clinical Research Samples

Sample	Expected Fusion	Sample Type
CPM00000226	KIAA1549-BRAF.K14B9.COSF483	BM
CPM00000278	ETV6-RUNX1.E5R3	BM
CPM00000764	ETV6-RUNX1.E5R4	BM
CPM00000802	PML-RARA.P3R3	BM
CPM00003584	ETV6-RUNX1.E5R4	BM
PRB206	PML-RARA.P6R3	FFPE
PRB212	EWSR1-FLI1.E7F6	FFPE
PRB216	ETV6-NTRK3.E5N15.COSF571.1	FFPE
PRB223	BCR-ABL1.B14A2	FFPE

Controls

Sample	Expected Fusion
HD784	CCDC6-RET.C1R12.COSF1271
	EML4-ALK.E13A20.COSF408.1
	SLC34A2-ROS1.S4R32.COSF1196
Seraseq FFPE v2	CD74-ROS1.C6R34.COSF1200
	EGFR-SEPT14.E24S10
	EML4-ALK.E13A20.COSF408.1
	ETV6-NTRK3.E5N15.COSF571.1
	FGFR3-BAIAP2L1.F17B2.COSF1346
	FGFR3-TACC3.F17T11.COSF1348
	KIF5B-RET.K24R11.COSF1262
	LMNA-NTRK1.L2N11
	NCOA4-RET.N7R12.COSF1491
	SLC34A2-ROS1.S4R34.COSF1198
	SLC45A3-BRAF.S1B8.COSF871
	TPM3-NTRK1.T7N10.COSF1329
	EGFR-EGFR.E1E8.DelPositive.2
	MET-MET.M13M15

True Pos	False Pos*	False Neg	%Sens	%PPV	%Repr
140	0	0	**100**	**100**	**100**

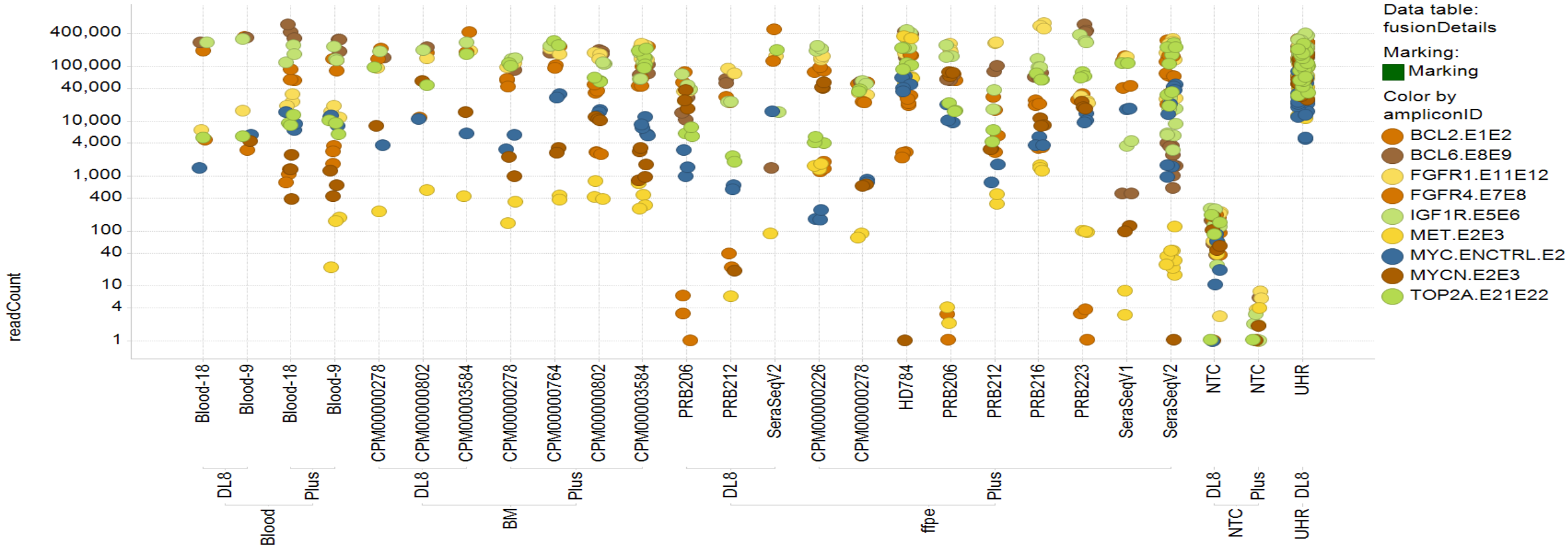
Seraseq FFPE Control Truth

Fusion RNA
EML4-ALK
KIF5B-RET
NCOA4-RET
CD74-ROS1
SLC34A2-ROS1
TPM3-NTRK1
FGFR3-BAIAP2L1
~~PAX8-PPARG1~~ — Not assayed
FGFR3-TACC3
ETV6-NTRK3
LMNA-NTRK1
SLC45A3-BRAF
~~TMPRSS2-ERG~~ — Not assayed
EGFR-SEPT14
MET exon 14 skipping
EGFR Variant III
(del exons 2-7)

Replicates

	Plus		Plus		Plus		Plus		Plus		Plus		Plus		DL8	
	Avg([r...	Avg(re...	Avg([r...	Avg(re...	Avg([r...	Avg(re...	Avg([r...	Avg(re...	Avg([r...	Avg(re...	Avg([r...	Avg(re...	Avg([r...	Avg(re...	Avg([r...	Avg(re...
TPM3-NTRK1.T7N10.COSF1329	6.60 %	54,685	5.66 %	85,413	6.46 %	34,235	4.85 %	183,235	4.13 %	141,029	4.07 %	134,420	6.11 %	104,941	7.63 %	225,789
FGFR3-TACC3.F17T11.COSF1348	4.78 %	39,602	4.65 %	72,359	4.91 %	26,034	4.01 %	151,669	3.93 %	134,167	3.95 %	130,291	2.04 %	35,101	5.67 %	167,821
KIF5B-RET.K24R11.COSF1262	3.29 %	27,294	3.51 %	57,325	3.33 %	17,662	4.03 %	152,458	3.87 %	132,217	3.91 %	129,140	3.87 %	66,469	4.07 %	120,439
ETV6-NTRK3.E5N15.COSF571.1	4.33 %	35,923	4.72 %	78,129	4.37 %	23,162	2.69 %	101,767	3.18 %	108,786	3.20 %	105,521	3.65 %	62,755	4.20 %	124,191
EGFR-SEPT14.E24S10	2.52 %	20,858	2.75 %	46,517	2.53 %	13,424	2.73 %	103,257	3.21 %	109,647	3.15 %	103,974	2.33 %	40,060	3.17 %	93,909
LMNA-NTRK1.L2N11	1.88 %	15,607	1.58 %	23,203	1.98 %	10,513	1.77 %	66,731	2.03 %	69,283	2.01 %	66,320	1.24 %	21,368	2.20 %	65,188
FGFR3-BAIAP2L1.F17B2.COSF1346	1.41 %	11,669	1.54 %	25,358	1.36 %	7,223	1.83 %	69,085	2.00 %	68,200	1.95 %	64,452	1.57 %	27,037	1.45 %	42,800
SLC45A3-BRAF.S1B8.COSF871	1.26 %	10,419	1.27 %	20,354	1.39 %	7,363	1.31 %	49,669	1.23 %	42,112	1.25 %	41,436	1.13 %	19,386	1.76 %	52,147
EML4-ALK.E13A20.COSF408.1	0.57 %	4,765	0.87 %	16,192	0.57 %	3,022	1.41 %	53,339	1.57 %	53,507	1.56 %	51,509	1.03 %	17,719	0.82 %	24,293
NCOA4-RET.N7R12.COSF1491	1.10 %	9,115	1.17 %	18,950	1.05 %	5,547	1.23 %	46,662	1.40 %	47,835	1.36 %	44,797	0.78 %	13,366	0.39 %	11,419
SLC34A2-ROS1.S4R34.COSF1198	0.49 %	4,067	0.52 %	8,718	0.47 %	2,470	0.62 %	23,357	0.66 %	22,615	0.66 %	21,816	0.54 %	9,269	0.26 %	7,811
CD74-ROS1.C6R34.COSF1200	0.24 %	2,010	0.29 %	5,079	0.24 %	1,269	0.59 %	22,220	0.65 %	22,230	0.65 %	21,336	0.28 %	4,888	0.18 %	5,240
FGFR3-TACC3.F17T10	0.01 %	76	0.07 %	1,660	0.01 %	46	0.04 %	1,360	0.04 %	1,510	0.05 %	1,584	0.01 %	194	0.02 %	549
EML4-ALK.E20A20.COSF409.1	0.00 %	0	0.01 %	332	0.00 %	0	0.00 %	0	0.00 %	0	0.00 %	0	0.05 %	857	0.03 %	748
EML4-ALK.E6aA20.AB374361	0.00 %	0	0.00 %	48	0.00 %	0	0.00 %	0	0.00 %	0	0.00 %	0	0.00 %	45	0.01 %	282
FGFR3-TACC3.F18T11del5	0.01 %	64	0.00 %	45	0.01 %	34	0.00 %	72	0.00 %	49	0.00 %	43	0.00 %	0	0.00 %	69
FGFR3-TACC3.F17ins1T10	0.00 %	0	0.00 %	7	0.00 %	0	0.00 %	10	0.00 %	11	0.00 %	11	0.00 %	1	0.00 %	2
ETV6-RUNX1.E5R4	0.00 %	0	0.00 %	1	0.00 %	0	0.00 %	1	0.00 %	0	0.00 %	1	0.00 %	0	0.00 %	10
EML4-ALK.E13A20.COSF1062.2	0.00 %	2	0.00 %	1	0.00 %	0	0.00 %	0	0.00 %	0	0.00 %	0	0.00 %	0	0.00 %	1
ETV6-RUNX1.E5R3	0.00 %	1	0.00 %	0	0.00 %	0	0.00 %	3	0.00 %	0	0.00 %	0	0.00 %	0	0.00 %	0
EGFR-EGFR.E1E8.DelPositive.2	1.09 %	9,035	1.05 %	16,886	1.09 %	5,759	1.56 %	58,933	1.92 %	65,653	1.99 %	65,711	0.97 %	16,622	1.47 %	43,452
MET-MET.M13M15	0.05 %	443	0.17 %	3,670	0.05 %	269	0.62 %	23,249	0.77 %	26,231	0.75 %	24,793	0.27 %	4,668	0.13 %	3,957

RNA: Gene Expression (Raw Reads)



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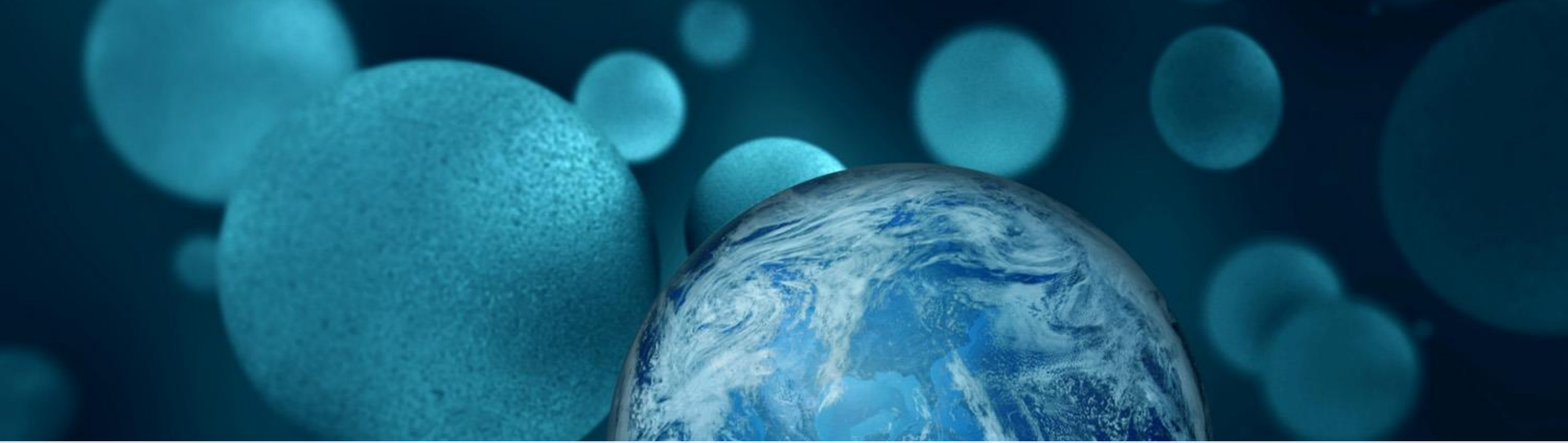

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Oncomine Childhood Cancer Research Assay

Content Details

April 11 2018

Expression Controls, Gene Expression, Transcript Variants

Assay Type	Genes
GeneExpression	BCL2, BCL6, FGFR1, FGFR4, IGF1R, MET, MYC, MYCN, TOP2A
ExpressionControl	ABCF1, ARF1, EIF2B1, FBXW2, HMBS, ITGB7, LRP1, PSMB2, PUM1, RAB7A, SYMPK, TBP, TRIM27, VPS29
RNAExonVariant	BRAF, EGFR, MET, NOTCH1, RELA

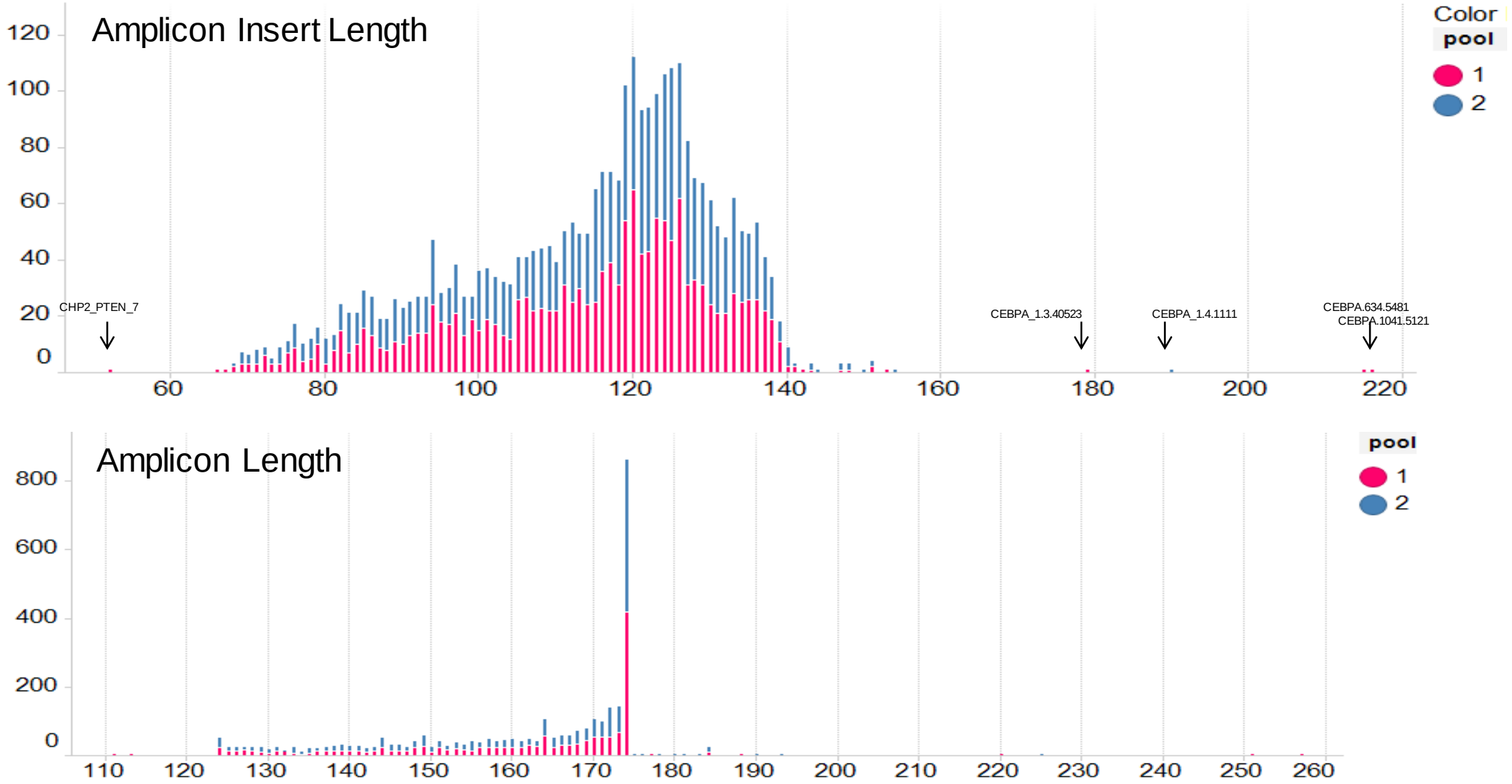
Expression Gene Pool Assignment:

Type	Pool 1	Pool 2
GeneExpression	FGFR1 FGFR4 MYCN MET IGF1R TOP2A BCL2 BCL6 MYC	None
ExpressionControl	TRIM27 RAB7A SYMPK VPS29 ARF1	EIF2B1 PUM1 PSMB2 FBXW2 ABCF1 LRP1 HMBS TBP ITGB7
	Total: 14	Total: 9

RNAExonVariant Isoforms:

Gene	Transcript Variants	Comment
BRAF	exon18-exon10	kinase domain duplication
BRAF	exon1-exon11	
BRAF	exon1-exon9	
EGFR	exon13-exon15	
EGFR	exon1-exon8	
EGFR	exon24-exon28	
EGFR	exon25-exon18	kinase domain duplication
EGFR	exon3-exon5	
MET	exon13-exon15	
MET	exon 17-exon20	
NOTCH1	exon2-exon28	
RELA	exon1-exon3	

DNA Size Distribution



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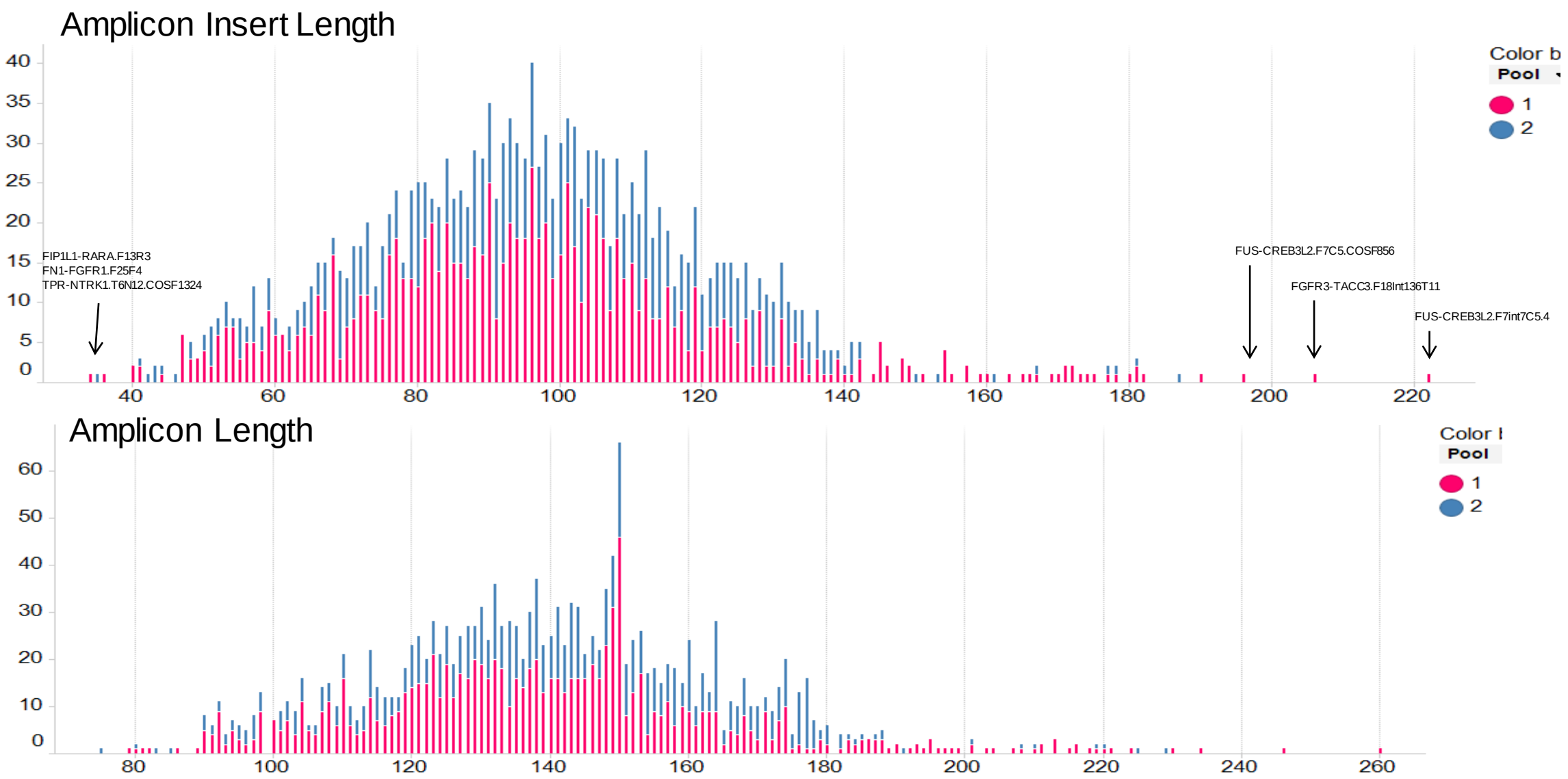
RNA Size Distribution



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Oncomine Childhood Cancer Fusion Assays (3' Acceptor, ABL1 to NCOA2)

3' Acceptor	5' Donor	# partners	# isoforms
ABL1	BCR, CABIN1, EML1, ETV6, FOXP1, INPP5D, NUP214, PRDM12, RALGPS1, RANBP2, RCSD1, RNF213, SFPQ, SNX2, SPECC1L, ZMIZ1	16	64
ABL2	ETV6, PAG1, RCSD1, ZC3HAV1	4	5
ALK	A2M, ACTG2, ATIC, ATRNL1, BEND5, BIRC6, C2orf44, CAD, CARS, CCDC88A, CENPF, CEPBZ, CLIP1, CLTC, COL25A1, DCTN1, EIF2AK3, EML4 , FN1, GFPT1, GTF2IRD1, GTF3C2, HIP1, ITSN2, KANK2, KCNQ5, KIF5B, KLC1, KTN1, LMNA, MALAT1, MAPRE3, MCFD2, MEMO1, MROH2B, MSN, MYH9, NCOA1, NPM1, PICALM, PPFIBP1, PPM1B, PPM1G, PPP1CB, PPP1R21, PPP4R3B, PRKAR1, PRKAR1A, PRKAR1B, RANBP2, RNF213, RRBP1, SATB1, SEC31A, SPTBN1, SQSTM1, STK32B, STRN, TERT, TFG, TPM1, TPM3, TPM4, TPR, TRAF1, VCL	66	119
BCL11B	ZEB2	1	2
BCOR	ZC3H7B	1	1
BRAF	AGAP3, AGK, AGTRAP, AKAP9, AP3B1, ARMC10, ATG7, BAIAP2L1, BBS9, BCL2L11, BTF3L4, C7orf73, CCDC6, CCDC91, CCNY, CDC27, CEP89, CLCN6, CLIP2, CUL1, CUX1, DGKI, DYNC1I2, EML4, EPS15, ERC1, FAM114A2, FAM131B, FCHSD1, FXR1, GATM, GHR, GNAI1, GTF2I, HERPUD1, KCTD7, KDM7A, KIAA1549, KLHL7, LSM12, LSM14A, MACF1, MAD1L 1, MKRN1, MKRN10, MYRIP, MZT1, NFIC, NRF1, NUB1, NUDCD3, NUP214, PAPSS1, PARP12, PICALM, PLIN3, PLXNA2, PPFIB2, RAD18, RBMS3, RNF11, RNF130, RP2, SLC12A7, SLC45A3, SND1, SOX6 , STRN3, TANK, TAX1BP1, TMEM178B, TMPRSS2, TRIM24, TRIM4, UBN2, ZC3HAV1, ZKSCAN5, ZNF767P, ZSCAN30	79	118
CAMTA1	WWTR1	1	10
CREBBP	KAT6A, KAT6B, KMT2A	3	13
CRLF2	P2RY8	1	4
CSF1R	MEF2D, RBM6, SSBP2	3	4
EGFR	CAND1, SEC61G	2	2
FGFR1	BAG4, BCR, CNTRL, CPSF6, CUX1, ERLIN2, ERVK3_1, FGFR1OP, FGFR1OP2, FN1, LRRFIP1, MYO18A, RANBP2, SQSTM1, TPR, TRIM24, WHSC1L1 , ZMYM2	18	28
FGFR2	APIP, CD44, COL25A1, CTNNB1, PARK2, PDHX, SLC45A3, SNX19	8	12
FGFR3	ETV6	1	1
FLT3	ETV6, SPTBN1	2	6
FOSB	SERPINE1, ZFP36	2	2
GLI1	ACTB	1	2
GLIS2	CBFA2T3	1	2
HMGA2	FHIT, LPP, RAD51B	3	3
JAK2	ATF7IP, BCR, BICD2, EBF1, ETV6, OFD1, PAX5, PCM1, PPFIBP1, RIC1, SEC31A, SPAG9, SSBP2, STRN3, TERF2, TPM3, TPR	17	38
KMT2A	NUP98	1	1
LMO2	RAG2	1	1
MAML2	C11orf95, CRTC1, CRTC3, KMT2A	4	5
MECOM	ETV6, PSMD2, RPN1, RUNX1	4	5
MET	BAIAP2L1, C8orf34, CAPZA2, CLIP2, DCTN1, EPS15, KIF5B, LRRFIP1, OXR1, PPFIBP1, PTPRZ1, SCAF11, SLC34A2, TFG, TPR, TRIM4, ZKSCAN1	17	21
MKL1	RBM15	1	2
MLLT10	DDX3X, HNRNPH1, KMT2A, NAP1L1, NUP98, PICALM	6	31
MN1	ETV6	1	2
MYBL1	C8orf34	1	1
MYH11	CBFB, KMT2A	2	20
NCOA2	AHRR, ETV6, HEY1, KAT6A, PAX3, SRF, TEAD1, VGLL2	8	11

Oncomine Childhood Cancer Fusion Assays (3' Acceptor, NCOR1 to ZNF384)

3' Acceptor	5' Donor	# partners	# isoforms
NCOR1	PAX5	1	1
NOTCH1	MIR143HG, SEC16A	2	3
NOTCH2	SEC22B	1	1
NOTCH4	NSD1	1	1
NR4A3	EWSR1, TAF15, TCF12, TFG	4	9
NTRK1	ARHGEF2, BCAN, CD74, CEL, CHTOP, EPHB2, EPS15, GSN, IRF2BP2, LMNA, MPRIP, MRPL24, NFASC, PPL, RNF213, SQSTM1, SSBP2, TFG, TP53, TPM3, TPR	21	50
NTRK2	AFAP1, AGBL4, DAB2IP, ETV6, NACC2, NAV1, QKI, SLMAP, SQSTM1, TP63, TRIM24, VCL	12	13
NTRK3	AKAP13, BTBD1, COX5A, EML4, ETV6, FAT1, LYN, MYO5A, RBPMS, TFG	10	15
NUP214	NOTCH1, SET	2	2
NUTM1	BRD3, BRD4, CIC, WHSC1L1	4	6
NUTM2B	YWHAE	1	1
PDGFB	COL1A1	1	42
PDGFRA	BCR, CDK5RAP2, DIP2C, ETV6, FIP1L1, FOXP1, KDR, KIF5B, SCAF11, STRN, TNKS2	11	30
PDGFRB	ATF7IP, BIN2, CAPRIN1, CCDC6, CCDC88C, CEP85L, CPSF6, DTD1, EBF1, ERC1, ETV6, GIT2, GOLGA4, GOLGB1, HIP1, KANK1, MPRIP, MYO18A, NDE1, NIN, PDE4DIP, PRKG2, RABEP1, SART3, SPECC1, TNIP1, TP53BP1, TPM3, TRIP11, WDR48, ZEB2	31	41
PLAG1	CHCHD7, COL1A2, COL3A1, CTNNB1, HAS2, LIFR, TCEA1	7	10
RAF1	AGGF1, ATG7, B4GALT1, CLCN6, CNTLN, ESRP1, FYCO1, GOLGA4, HACL1, LMNA, MPRIP, NFIA, PAPD7, PDZRN3, QKI, SRGAP3, TRAK1, TRIM33	18	19
RARA	ADAMTS17, BCOR, FIP1L1, IRF2BP2, MED1, NABP1, NPM1, NUMA1, PML, PRKAR1A, STAT5B, TBL1XR1, ZBTB16	13	45
RECK	PCSK5	1	1
RELA	C11orf95, ZMYND8	2	4
RET	ACBD5, AFAP1, AKAP13, BCR, CCDC6, CUX1, ERC1, FGFR1OP, FKBP15, FRDM4A, GOLGA5, HOOK3, KIAA1217, KIAA1468, KIF5B, KTN1, MYH10, MYH13, NCOA4, PCM1, PRKAR1A, RUFY2, SPECC1L, TBL1XR1, TRIM24, TRIM27, TRIM33	27	54
ROS1	CCDC30, CCDC6, CD74, CEP85L, CLIP1, CLTC, ERC1, EYS, EZR, GOPC, HLA_A, KIAA1598, LIMA1, LRIG3, MSN, MYO5A, NCOR2, NFKB2, PPFIBP1, PWWP2A, SDC4, SLC22A16, SLC34A2, TFG, TMEM106B, TPD52L1, TPM3, TSPAN3, YWHAE, ZCCHC8	30	47
RUNX1	ETV6	1	4
SS18	MEF2D	1	1
STAT6	NAB2	1	29
TAL1	STIL	1	3
TFE3	ASPSCR1, CLTC, DVL2, LUC7L3, MED15, NONO, PARP14, PRCC, SFPQ, YAP1	10	22
TP63	TBL1XR1	1	3
TSLP	IQGAP2	1	1
USP6	CDH11, CNBP, COL1A1, MYH9, OMD, THRAP3	6	11
WHSC1	ST6GAL1	1	1
YAP1	C11orf95	1	1
ZNF384	ARID1B, BMP2K, CREBBP, EP300, EWSR1, TAF15, TCF3	7	18

Oncomine Childhood Cancer Fusion Assays (5' Donor, AFF3 to NOTCH1)

5' Donor	3' Acceptor	# partners	# isoforms
AFF3	BCL2	1	1
ALK	PTPN3	1	1
BCOR	CCNB3, L3MBTL2, MAML3	3	3
BCR	LZTR1	1	1
CCND1	FSTL3	1	1
CIC	DUX4, FOXO4	2	6
CRLF2	CSF2RA	1	1
DUSP22	PTK7	1	1
EGFR	GNS, MCL, PSPH, RAD51, SEPT14, VOPP1	6	6
ETV6	ACSL6, ANLN, ARNT, ATP2B1, CDX2, CHIC2, DUSP16, FRK, GOT1, INO80D, ITPR2, LRP6, LYN, PER1, PRDM16, PTPRR, SYK	17	19
EWSR1	ATF1, CREB1, CREB3L1, CREB3L2, CREM, DDIT3, ERG, ETV1, ETV4, FEV, FLI1, KLF15, NFATC1, NFATC2, PATZ1, PBX1, PBX3, POU5F1, SMARCA5, SP3, WT1, YY1, ZNF444	23	68
FGFR1	ADAM32, HOOK3, TACC1, WHSC1L1	4	5
FGFR2	ACSL5, AFF3, AHCYL1, BICC1, CASP7, CCAR2, CCDC6, CIT, CLIP2, COL14A1, CREB5, FAM76A, KCTD1, KIAA1217, MGEA5, NOL4, OFD1, OGDH, OPTN, PCM1, PPHLN1, SHTN1, TACC3, WARS, ZMYM4	25	28
FGFR3	AES, BAIAP2L1, ELAVL3, FBXO28, JAKMIP1, TACC3	6	33
FUS	ATF1, CREB3L1, CREB3L2, DDIT3, ERG, FEV, KLF17, POU5F1	8	71
HMGA2	ALDH2, CCNB1IP1, CHMP1A, COX6C, EBF1, FHIT, LHFP, LPP, NFIB, PPAP2B, RAD51B, WIF1	12	19
KAT6A	EP300, NCOA3	2	3
KMT2A	ABI1, ABI2, ACACA, ACER1, ACTN4, ADARB2, AFF1, AFF3, AFF4, APBB1IP, ARHGAP26, ARHGEF12, ARHGEF17, ATG16L2, BTBD18, C11orf88, CASC5, CASP8AP2, CBL, CDK6, CEP170B, CT45A2, DAB2IP, DCP1A, DCPS, ELL, ENAH, EP300, EPS15, FLNA, FNBP1, FOXO3, FOXO4, FRYL, GAS7, GMPS, GPHN, KIAA1524, LASP1, LPP , MAPRE1, MEF2C, MLLT1, MLLT11, MLLT3, MLLT4, MLLT6, MYO18A, MYO1F, NCKIPSD, NEBL, NKAIN2, NRIP3, PDS5A, PICALM, RABGAP1L, RNF115, RPS3, SARNP, SEPT11, SEPT2, SEPT5 , SEPT6, SEPT9, SH3GL1, SMAP1, SORBS2, TECR, TET1, TIRAP, TOP3A, USP2, UVRAG, ZFYVE19	74	173
KMT2B	GPS2	1	1
KMT2C	PRKAG2	1	3
KMT2D	ADCY9	1	1
MAN2B1	RNASEH2A	1	1
MEF2D	BCL9, DAZAP1, HNRNPUL1	3	6
MN1	BEND2	1	1
MYB	NFIB, PCDHGA1, QKI, RAD51B, TYK2	5	18
MYBL1	NFIB	1	5
MYH9	IL2RB	1	1
NCOR1	LYN	1	1
NOTCH1	GABBR2, SDCCAG3, SNHG7	3	3

Oncomine Childhood Cancer Fusion Assays (5' Donor, NPM1 to ZMYND11)

5' Donor	3' Acceptor	# partners	# isoforms
NPM1	MLF1	1	1
NTRK1	DYNC2H1	1	1
NTRK3	ETV6, HOMER1	2	2
NUP214	DEK, XKR3	2	2
NUP98	ADD3, CCDC28A, CCT8, DDX10, GSX2, HHEX, HMGB3, HOXA11, HOXA13, HOXA9, HOXC11, HOXC13, HOXD11, HOXD13, IQCG, KDM5A, LNP1, NSD1 , PHF23, POU1F1, PRRX1, PRRX2, PSIP1, RAP1GDS1, RARG, SETBP1, TOP1, TOP2B, WHSC1L1	29	44
PAX3	FOXO1, FOXO4, MAML3, NCOA1	4	5
PAX5	ASXL1, AUTS2, BRD1, DACH1, DACH2, ELN, ESRRB, FOXP1, GOLGA6A, HIPK1, KIAA1549L, KIF3B, MLLT3, NOL4L, PML, POM121, SLCO1B3, SOX5, TAOK1, ZNF521	20	29
PAX7	FOXO1	1	1
RAF1	C9orf153	1	1
RANBP17	TLX3	1	1
RUNX1	AFF3, CBFA2T2, CBFA2T3, CEP76, CLCA2, EVX1, KIAA1549L, LPXN, MACROD1, MRPS6, NOL4L, PRDM16, PRDX4, RPL22, RUNX1T1, SH3D19, TRPS1, USP16, USP42, YTHDF2, ZFPM2, ZNF687	22	37
SS18	REPS2, SSX1, SSX2, SSX4	4	14
SSBP2	FER	1	1
STAG2	MAP7D3(5' Donor, AFF3 to NOTCH1)	1	2
TCF3	HLF, PBX1, TFPT	3	9
TFE3	GRIPAP1, SFPQ	2	2
TSPAN4	CD151	1	1
UBTF	MAML3	1	2
YAP1	FAM118B, MAMLD1	2	3
ZMYND11	MBTD1	1	1

Informatics Details

Oncomine Myeloid IR 5.6 and IR 5.10 TVC parameters

	SNP	Indel	Hotspot
Min AF	2%	2%	3%
Min Coverage	20	20	15
Strand Bias	0.9	0.85	0.96

ampliseq_childhood_cancer_research_panel_dna_540_w2.1_somatic_low stringency_parameters.json

Oncomine Myeloid IR 5.6 and IR 5.10 Fusion parameters

Parameter	Value
Min Read Count	40
Min Read Count Non-Targeted	1000
Total Mapped Reads	250,000
Total Mapped Reads per Pool	50,000
Min Read Length	60

AmpliSeq-childhood_cancer_research_panel_fusion_540_w2.1-RNACountsActor.ini

Oncomine Childhood Cancer Research Assay IR 5.6 Files

DNA	DNA Target BED file	OCCRA.20170711.designed.bed
	Hotspot/Blacklist BED file	OCCRA.20180306.hotspots.blist.bed
	Parameters	ampliseq_childhood_cancer_research_panel_dna_540_w2.1_somatic_lowstringency_parameters.json
RNA	Fusions FASTA file	OCCRA_030718_Reference_Reference.fasta
	Fusions target BED file	OCCRA_030718_Reference_Reference.bed
	Fusions properties file	OCCRA_030718_ReferenceReference.properties.txt

- IR 5.6 has a bug that will cause the blacklist file, if provided separately, to be deleted if workflow is copy-edited. We are thus providing a combined hotspot/blacklist BED.

Oncomine Childhood Cancer Research Assay IR 5.10 Files

DNA	DNA Target BED file	OCCRA.20170711.designed.bed
	Hotspot BED file	OCCRA.20180306.hotspots.bed
	Blacklist BED file	OCCRA.20170621.mask.bed
	Parameters	ampliseq_childhood_cancer_research_panel_dna_540_w2.1_somatic_lowstringency_parameters.json
RNA	Fusions FASTA file	OCCRA_030718_Reference_Reference.fasta
	Fusions target BED file	OCCRA_030718_Reference_Reference.bed
	Fusions properties file	OCCRA_030718_ReferenceReference.properties.txt