Humanizing Genomics
macrogen

Run report

Order No. : sample

Sample Information

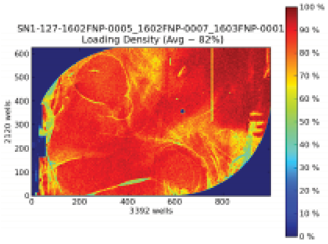
Order number	sample	Name of Customer	sample	Date of Order	sample

RUN Summary

499 M Total Bases　**95** Key Signal

82%
ISP Loading

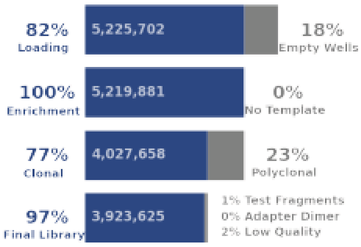
ISP Density



3,923,625
Total Reads

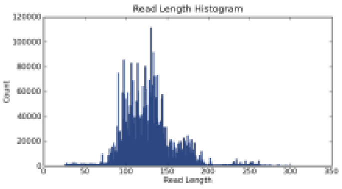
76%
Usable Reads

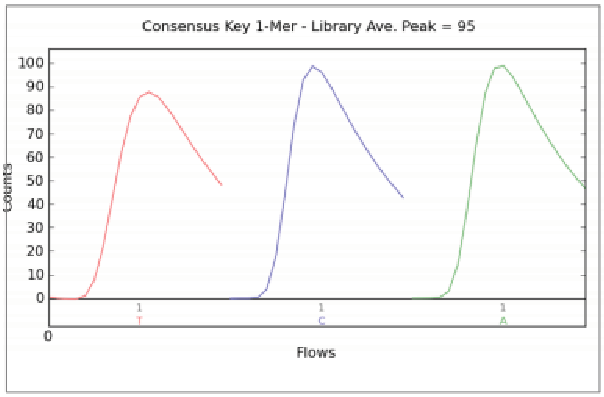
ISP Summary



127 bp Mean　**124 bp** Median　**129 bp** Mode

Read Length





Addressable Wells	**6,337,389**	
With ISPs	5,225,702	82.5%
Live	5,219,881	99.9%
Test Fragment	27,524	00.5%
Library	5,192,357	99.5%

Library ISPs	**5,192,357**	
Filtered: Polyclonal	1,192,223	23.0%
Filtered: Low Quality	67,591	01.3%
Filtered: Adapter Dimer	8,918	00.2%
Final Library ISPs	**3,923,625**	**75.6%**

Software Version

Torrent_Suite	5.0.4
host	MGpgm
ion-analysis	5.0.13-1
ion-chefupdates	5.0.3
ion-dbreports	5.0.33-1
ion-gpu	5.0.0-1
ion-pipeline	5.0.16-1
ion-plugins	5.0.28-1
ion-torrentr	5.0.0-1
Script	22.0.0
LiveView	643
DataCollect	488
OS	21
Graphics	36

Coverage Analysis Report

수주번호		Barcode	Sample	qPCR (pM)	Throughput (Mb)	On Target	Depth (X)	20X (%)	100X (%)	Variants (Hotspot)
1	sample1	4	sample1	2,125	1,622	99.29%.	913	95.70	89.01	1056 (3)
2	sample2	5	sample2	2,127	1,494	99.30%	838	97.39	93.07	1070 (5)
3	sample3	6	sample3	1,374	1,598	99.29%	900	95.98	90.12	1041 (8)

Variants_ sample name1

Chrom	Position	Ref	Variant	Allele Call	Frequency	Quality	Type	Allele Source	Allele Name	Gene ID
chr3	178917005	A	G	Heterozygous	52.2	1992.61	SNP	Novel	---	PIK3CA
chr4	1807894	G	A	Homozygous	100	13563	SNP	Novel	---	FGFR3
chr4	55141055	A	G	Homozygous	100	10404.6	SNP	Novel	---	PDGFRA
chr4	55152040	C	T	Heterozygous	50.9	5397.72	SNP	Hotspot	COSM22413	PDGFRA
chr5	112175162	C	T	Heterozygous	48.9	2994.58	SNP	Hotspot	COSM19072	APC
chr5	112175179	-	A	Heterozygous	51.1	1849.23	INS	Novel	---	APC
chr5	112175770	G	A	Homozygous	100	18072.8	SNP	Novel	---	APC
chr5	149433596	TG	GA	Heterozygous	23.8	572.921	MNP	Novel	---	CSF1R
chr9	139399409	CAC	-	Heterozygous	1.8	6.29494	DEL	Hotspot	COSM13047	NOTCH1
chr10	89720837	A	G	Heterozygous	51.7	3684.79	SNP	Novel	---	PTEN
chr11	534242	A	G	Heterozygous	43.8	1829.05	SNP	Hotspot	COSM249860	HRAS
chr12	25398284	C	T	Heterozygous	49.2	5391.28	SNP	Hotspot	COSM521	KRAS
chr17	7579472	G	C	Heterozygous	97.8	10293.9	SNP	Novel	---	TP53
chr19	1220321	T	C	Heterozygous	49.1	1662.93	SNP	Novel	---	STK11
chr19	1221318	CC	T	Heterozygous	51.7	5772.91	COMPLEX	Hotspot	COSM28298	STK11
chr19	1221319	C	T	Heterozygous	51.6	6410.11	SNP	Hotspot	COSM21355	STK11
chr19	1223125	C	G	Heterozygous	47.5	3657.73	SNP	Hotspot	COSM21360	STK11

Variants_ sample name2

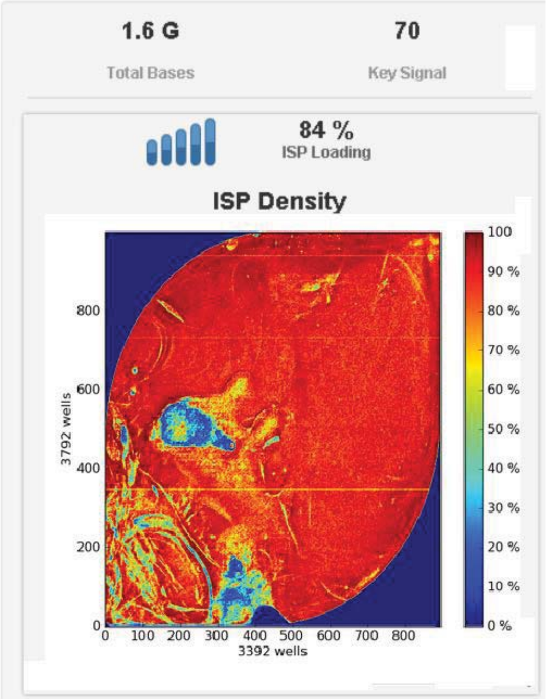
Chrom	Position	Ref	Variant	Allele Call	Frequency	Quality	Type	Allele Source	Allele Name	Gene ID
chr3	178917005	A	G	Heterozygous	52.2	1992.61	SNP	Novel	---	PIK3CA
chr4	1807894	G	A	Homozygous	100	13563	SNP	Novel	---	FGFR3
chr4	55141055	A	G	Homozygous	100	10404.6	SNP	Novel	---	PDGFRA
chr4	55152040	C	T	Heterozygous	50.9	5397.72	SNP	Hotspot	COSM22413	PDGFRA
chr5	112175162	C	T	Heterozygous	48.9	2994.58	SNP	Hotspot	COSM19072	APC
chr5	112175179	-	A	Heterozygous	51.1	1849.23	INS	Novel	---	APC
chr5	112175770	G	A	Homozygous	100	18072.8	SNP	Novel	---	APC
chr5	149433596	TG	GA	Heterozygous	23.8	572.921	MNP	Novel	---	CSF1R
chr9	139399409	CAC	-	Heterozygous	1.8	6.29494	DEL	Hotspot	COSM13047	NOTCH1
chr10	89720837	A	G	Heterozygous	51.7	3684.79	SNP	Novel	---	PTEN
chr11	534242	A	G	Heterozygous	43.8	1829.05	SNP	Hotspot	COSM249860	HRAS
chr12	25398284	C	T	Heterozygous	49.2	5391.28	SNP	Hotspot	COSM521	KRAS
chr17	7579472	G	C	Heterozygous	97.8	10293.9	SNP	Novel	---	TP53
chr19	1220321	T	C	Heterozygous	49.1	1662.93	SNP	Novel	---	STK11
chr19	1221318	CC	T	Heterozygous	51.7	5772.91	COMPLEX	Hotspot	COSM28298	STK11
chr19	1221319	C	T	Heterozygous	51.6	6410.11	SNP	Hotspot	COSM21355	STK11
chr19	1223125	C	G	Heterozygous	47.5	3657.73	SNP	Hotspot	COSM21360	STK11

Variants_ sample name3

Chrom	Position	Ref	Variant	Allele Call	Frequency	Quality	Type	Allele Source	Allele Name	Gene ID
chr3	178917005	A	G	Heterozygous	52.2	1992.61	SNP	Novel	---	PIK3CA
chr4	1807894	G	A	Homozygous	100	13563	SNP	Novel	---	FGFR3
chr4	55141055	A	G	Homozygous	100	10404.6	SNP	Novel	---	PDGFRA
chr4	55152040	C	T	Heterozygous	50.9	5397.72	SNP	Hotspot	COSM22413	PDGFRA
chr5	112175162	C	T	Heterozygous	48.9	2994.58	SNP	Hotspot	COSM19072	APC
chr5	112175179	-	A	Heterozygous	51.1	1849.23	INS	Novel	---	APC
chr5	112175770	G	A	Homozygous	100	18072.8	SNP	Novel	---	APC
chr5	149433596	TG	GA	Heterozygous	23.8	572.921	MNP	Novel	---	CSF1R
chr9	139399409	CAC	-	Heterozygous	1.8	6.29494	DEL	Hotspot	COSM13047	NOTCH1
chr10	89720837	A	G	Heterozygous	51.7	3684.79	SNP	Novel	---	PTEN
chr11	534242	A	G	Heterozygous	43.8	1829.05	SNP	Hotspot	COSM249860	HRAS
chr12	25398284	C	T	Heterozygous	49.2	5391.28	SNP	Hotspot	COSM521	KRAS
chr17	7579472	G	C	Heterozygous	97.8	10293.9	SNP	Novel	---	TP53
chr19	1220321	T	C	Heterozygous	49.1	1662.93	SNP	Novel	---	STK11
chr19	1221318	CC	T	Heterozygous	51.7	5772.91	COMPLEX	Hotspot	COSM28298	STK11
chr19	1221319	C	T	Heterozygous	51.6	6410.11	SNP	Hotspot	COSM21355	STK11
chr19	1223125	C	G	Heterozygous	47.5	3657.73	SNP	Hotspot	COSM21360	STK11

*Index

▣ ISP Density



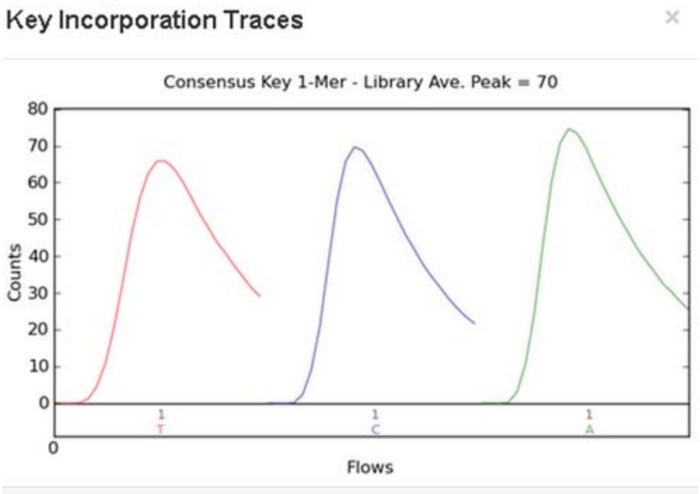
1.6 G
Total Bases

70
Key Signal

84 %
ISP Loading

This table describes the Ion Sphere™ Particle (ISP) density metrics:

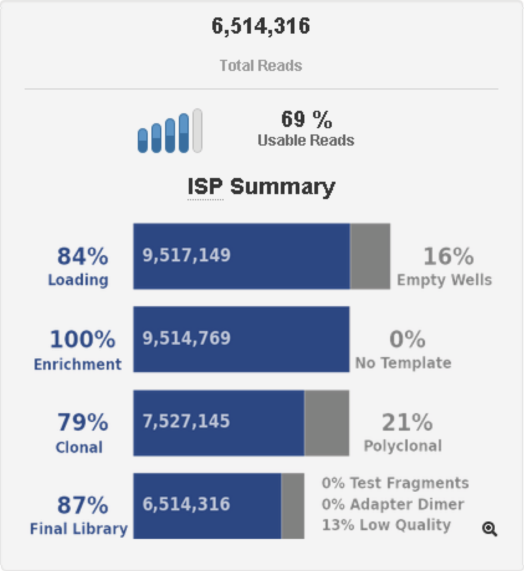
Metric	Description
Total Bases	Number of filtered and trimmed base pairs reported in the output BAM file.
Key Signal	Percentage of Live ISPs with a key signal that is identical to the library key signal.
Bead Loading	Percentage of chip wells that contain a live ISP. (The percentage value Considers only potentially addressable wells.)



The key incorporation graph show the average signal readings for flows of the bases T, C, and A in the library key.

▣ ISP Summary

In the lower rows, the percentages are relative to the total in the next higher row. The first row gives percentages of loaded wells and empty wells, relative to the number of potentially addressable wells on the chip.

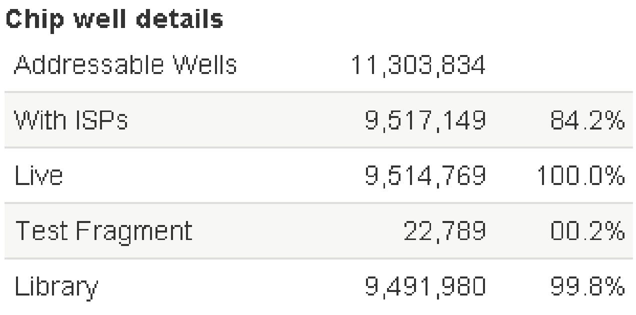


This table describes the ISP summary metrics:

Metric	Description	Calculation
Total Reads	Total number of filtered and trimmed reads independent of length reported in the output BAM file.	(Not calculated)
Usable Sequence	The percentage of library ISPs that pass the polyclonal, low quality and primer dimer filters.	Final Library ISPs / Library ISPs
Loading	Percentage of chip wells that contain a live ISP. (The percentage value considers only potentially addressable wells.)	No. of Loaded ISPs / No. of potentially addressable wells
Empty Wells	Percentage of chip wells that do not contain an ISP. (The percentage value considers only potentially addressable wells.)	(No. of potentially addressable wells minus No. of Loaded ISPs) / No. of potentially addressable wells
Enrichment	Predicted number of Live ISPs that have a key signal identical to the library key signal. The Percent Enrichment value reported is the number of loaded ISPs that are Library ISPs, after taking out Test Fragment ISPs.	Library ISPs / (No. of Loaded ISPs minus TF ISPs)

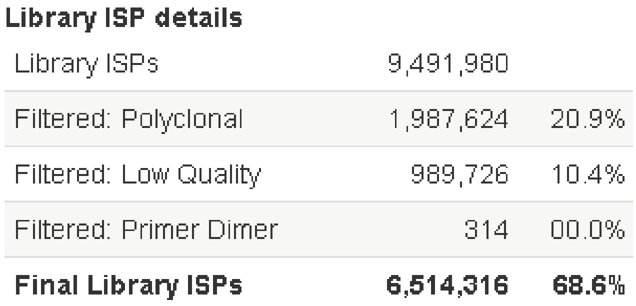
Metric	Description	Calculation
No Template	Percentage of chip wells that do not contain a DNA template.	(No. of Loaded ISPs minus TF ISPs) minus (Library ISPs) / (No. of Loaded ISPs minus TF ISPs)
Clonal	Percentage of chip wells that do not contain a DNA template.	No. of ISPs with single beads / No. of Live Wells
Polyclonal	Percentage of polyclonal ISPs (ISPs carrying clones from two or more templates).	Polyclonal ISPs / Live ISPs
Final Library	Percentage of reads which pass all filters and which are recorded in the output BAM file. This value may be different from the Total Reads due to technicalities associated with read trimming beyond a minimal requirement resulting in Total Reads being slightly less than Final Library.	Final Library / Clonal ISPs
% Test Fragments	Percentage of Live ISPs with a key signal that is identical to the test fragment key signal.	Final Library / Clonal ISPs
% Adapter Dimer	Percentage of ISPs with an insert length of less than 8 bp.	Primer dimer ISPs / Clonal ISPs
% Low Quality	Percentage of ISPs with a low or unrecognizable signal.	Low quality ISPs / Clonal ISPs

▣ Chip well details and Library ISP details



Chip well details

Addressable Wells	11,303,834	
With ISPs	9,517,149	84.2%
Live	9,514,769	100.0%
Test Fragment	22,789	00.2%
Library	9,491,980	99.8%



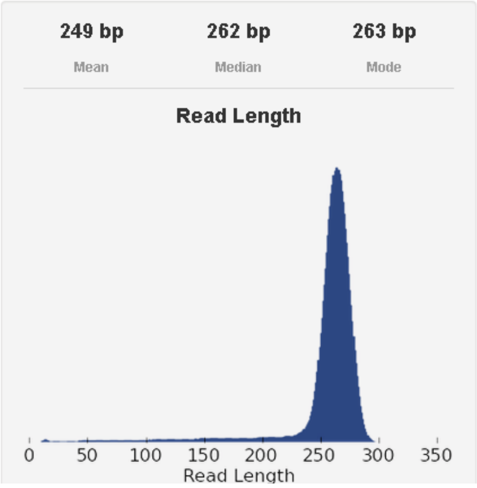
Library ISP details

Library ISPs	9,491,980	
Filtered: Polyclonal	1,987,624	20.9%
Filtered: Low Quality	989,726	10.4%
Filtered: Primer Dimer	314	00.0%
Final Library ISPs	**6,514,316**	**68.6%**

These metrics are described in this table:

Metric	Description	Calculation
Addressable Wells	Total number of addressable wells.	(Not calculated)
With ISPs	Number (and percentage of addressable wells) of wells that were determined to be "positive" for the presence of an ISP within the well. "Positive" is determined by measuring the diffusion rate of a flow with a different pH. Wells containing ISPs have a delayed pH change due to the presence of an ISP slowing the detection of the pH change from the solution.	Wells with ISPs /Total Addressable Wells
Live	Number (and percentage of wells with ISPs) of wells that contained an ISP with a signal of sufficient strength and composition to be associated with the library or Test Fragment key. This value is the sum of the following categories: -Test Fragment -Library	Live ISPs / Wells with ISPs
Test Fragment	Number (and percentage of Live ISPs) of Live ISPs with a key signal that was identical to the Test Fragment key signal.	Test Fragment ISPs /Live ISPs
Library	Number (and percentage of Live ISPs) of Live ISPs with a key signal that was identical to the library key signal.	Library ISPs / Live ISPs
Library ISPs	Predicted number of Live ISPs that have a key signal identical to the library key signal (the same value as shown in the well information table on the right).	Library ISPs
Filtered: Polyclonal	ISPs carrying clones from two or more templates.	Polyclonal ISPs / Library ISPs
Filtere: Low quality	Low or unrecognizable signal.	Low quality ISPs / Library ISPs
Filtered: Primer dimer	Insert length of less than 8 bp.	Primer dimer ISPs /Library ISPs
Final Library ISPs	Number (and percentage of Library ISPs) of reads passing all filters, which are recorded in the output BAM file. This value may be different from the **Total number of reads** located in the Library Summary Section due to technicalities associated with read trimming beyond a minimal requirement resulting in **Total number of reads** be ing slightly less than **Final ibrary Reads**.	Primer dimer ISPs /Library ISPs

▣ Read Length



This table describes the read length metrics:

Metric	Description
Mean Read Length	Average length, in base pairs, of called reads.
Median Read Length	Median length of called reads
Mode Read Length	Mode length of called reads.

Alignment Summary

This table describes the read length metrics:

Metric	Description
Total Aligned Bases	Number of filtered and trimmed aligned base pairs reported in the output BAM file. Total number of bases aligned to thereference sequence. Excludes the library key, barcodes, and 3' adaptersequences.
Reference Coverage	The average of the number of reads that cover each reference position: total aligned bases divided by the number of bases in the reference sequence. Does not consider enrichment.
% Aligned Bases	Percentage of Total Aligned Bases out of all reads.
% Unaligned	Percentage of bases not aligned to references.
Total Reads	Number of reads generated during basecalling.
Aligned Reads	Number of reads that aligned to the reference genome.
Unaligned Reads	Number of reads that did not align to the reference genome.
Mean Raw Accuracy 1x	Average raw accuracy of 1-mers plotted by their position in the read.
AQ17	An error rate of 2% or less.
AQ20	An error rate of 1% or less.
Perfect	The longest perfectly aligned segment.
Total Number of Bases	Total number of bases at the quality level.
Mean Length	Average segment length at the quality level.
Mean Coverage Depth	Average coverage at the quality level.