

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/18 07:32:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618583.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR618583 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618583_1.fastq.gz SRR618583_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 18 07:32:12 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618583.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	64,441,766
Mapped reads	60,141,089 / 93.33%
Unmapped reads	4,300,677 / 6.67%
Mapped paired reads	60,141,089 / 93.33%
Mapped reads, first in pair	30,750,869 / 47.72%
Mapped reads, second in pair	29,390,220 / 45.61%
Mapped reads, both in pair	57,746,104 / 89.61%
Mapped reads, singletons	2,394,985 / 3.72%
Secondary alignments	0
Supplementary alignments	178,281 / 0.28%
Read min/max/mean length	30 / 100 / 100.11
Duplicated reads (estimated)	27,126,489 / 42.09%
Duplication rate	34.39%
Clipped reads	12,821,766 / 19.9%

2.2. ACGT Content

Number/percentage of A's	1,543,000,273 / 27.15%
Number/percentage of C's	1,268,260,228 / 22.31%
Number/percentage of T's	1,557,527,499 / 27.4%
Number/percentage of G's	1,313,187,637 / 23.1%
Number/percentage of N's	1,742,874 / 0.03%

GC Percentage	45.42%
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2.3. Coverage

Mean	1.8373
Standard Deviation	7.8568

2.4. Mapping Quality

Mean Mapping Quality	52.31
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2.5. Insert size

Mean	87,372.54
Standard Deviation	2,969,908.24
P25/Median/P75	199 / 225 / 254

2.6. Mismatches and indels

General error rate	1.54%
Mismatches	85,826,498
Insertions	1,047,439
Mapped reads with at least one insertion	1.71%
Deletions	2,881,136
Mapped reads with at least one deletion	4.67%
Homopolymer indels	52.22%

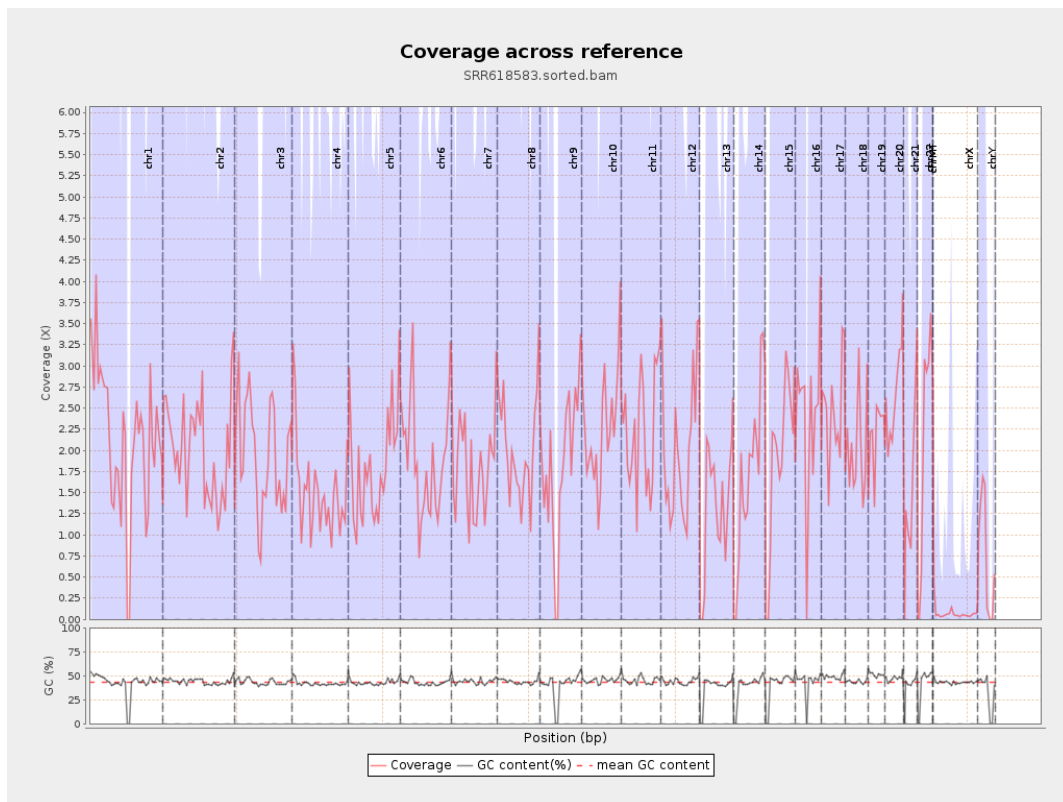
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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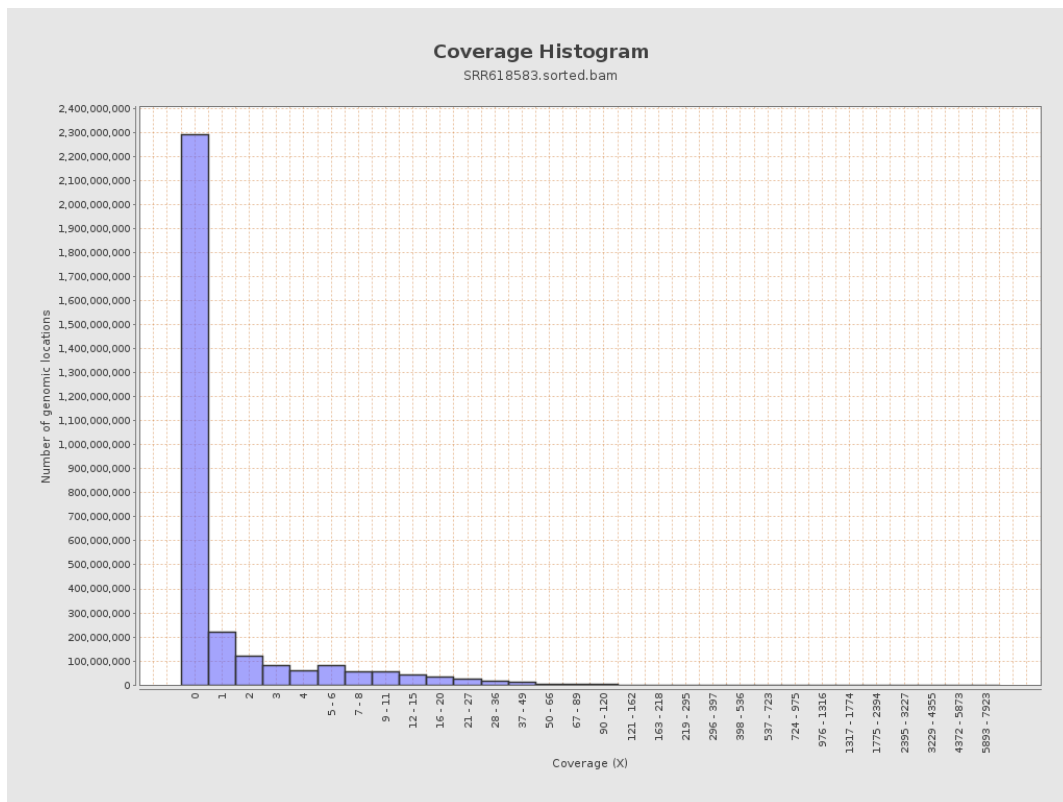
		bases	coverage	deviation
chr1	249250621	524820289	2.1056	9.8171
chr2	243199373	487546296	2.0047	8.9213
chr3	198022430	383043574	1.9343	6.6395
chr4	191154276	289426734	1.5141	6.2277
chr5	180915260	331949877	1.8348	6.9983
chr6	171115067	320713204	1.8743	6.7545
chr7	159138663	288718941	1.8143	6.7296
chr8	146364022	292592517	1.9991	7.0331
chr9	141213431	256208911	1.8143	8.2946
chr10	135534747	303234550	2.2373	7.4777
chr11	135006516	301060129	2.23	8.3298
chr12	133851895	271355859	2.0273	7.6689
chr13	115169878	150476196	1.3066	5.4003
chr14	107349540	183351489	1.708	6.5947
chr15	102531392	194145822	1.8935	7.4841
chr16	90354753	215628691	2.3865	14.3695
chr17	81195210	199400910	2.4558	9.3391
chr18	78077248	155770941	1.9951	8.5036
chr19	59128983	129099969	2.1834	8.8263
chr20	63025520	166524923	2.6422	8.3009
chr21	48129895	76989609	1.5996	9.9124
chr22	51304566	107850512	2.1022	8.3782
chrMT	16571	41968	2.5326	11.0382
chrX	155270560	10984486	0.0707	1.7403

chrY	59373566	46627402	0.7853	6.1169
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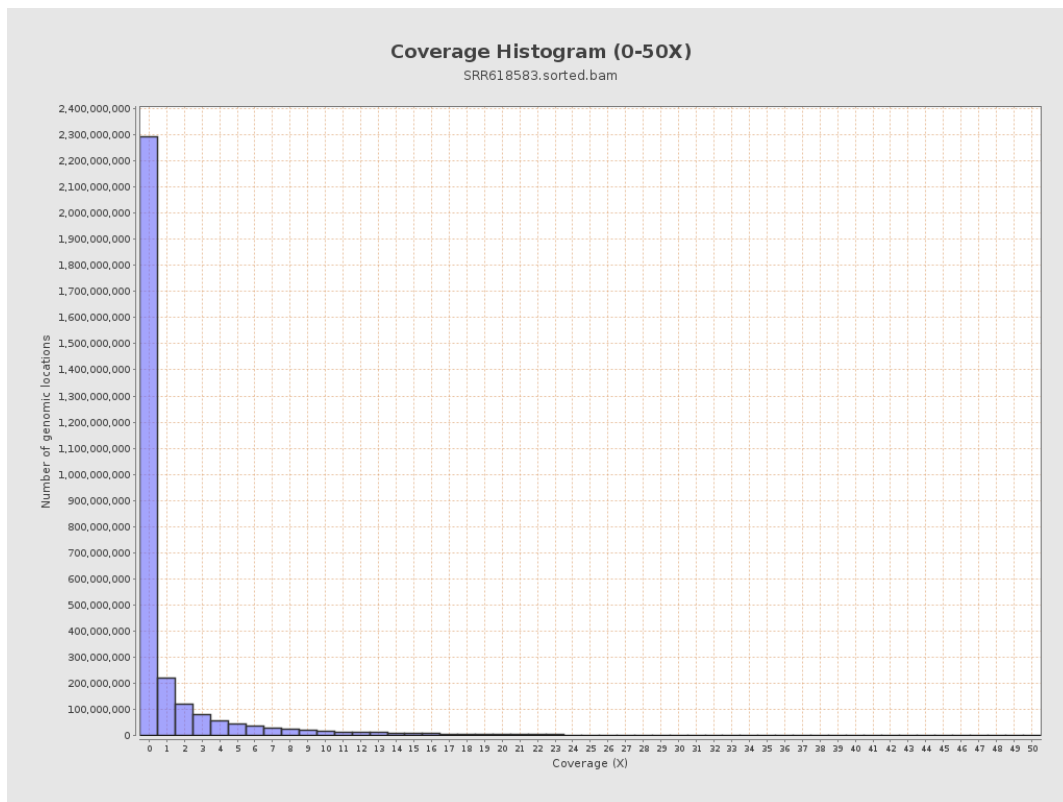
3. Results : Coverage across reference



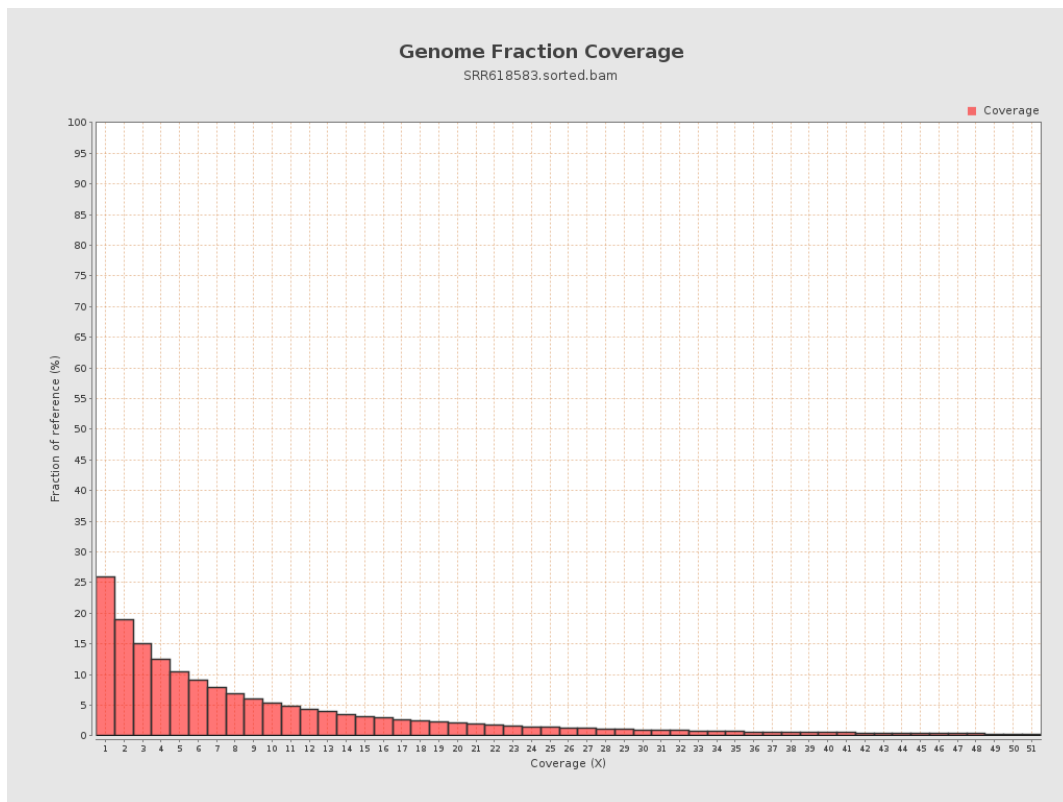
4. Results : Coverage Histogram



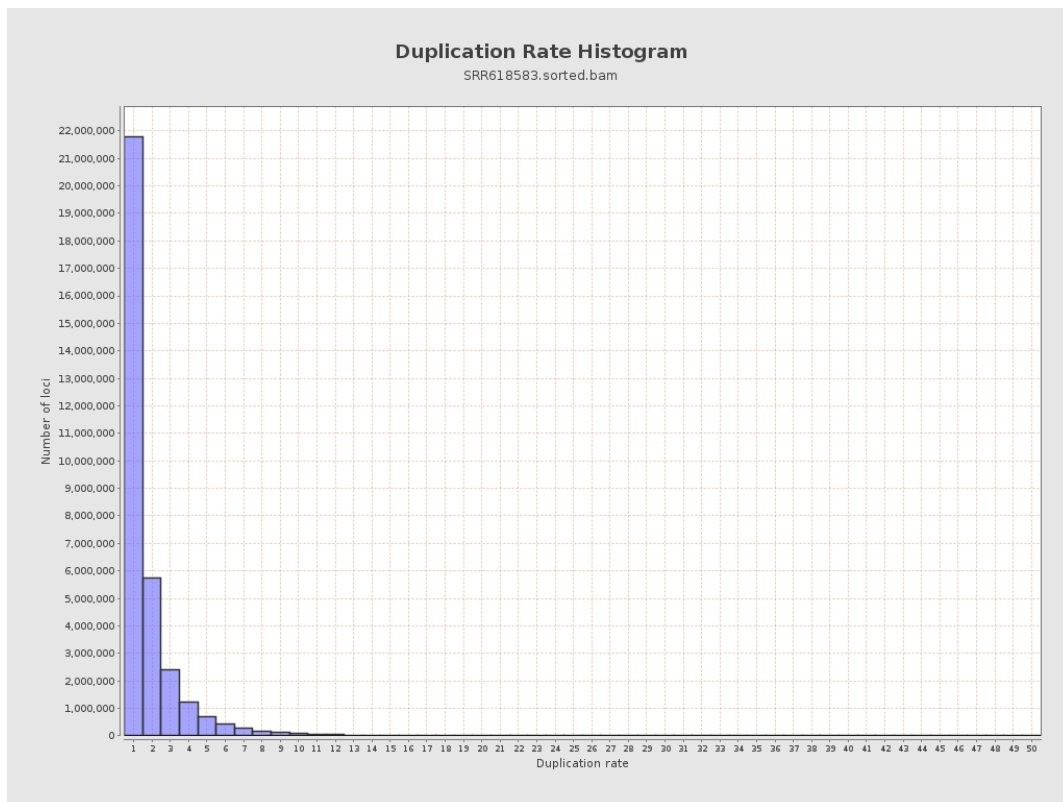
5. Results : Coverage Histogram (0-50X)



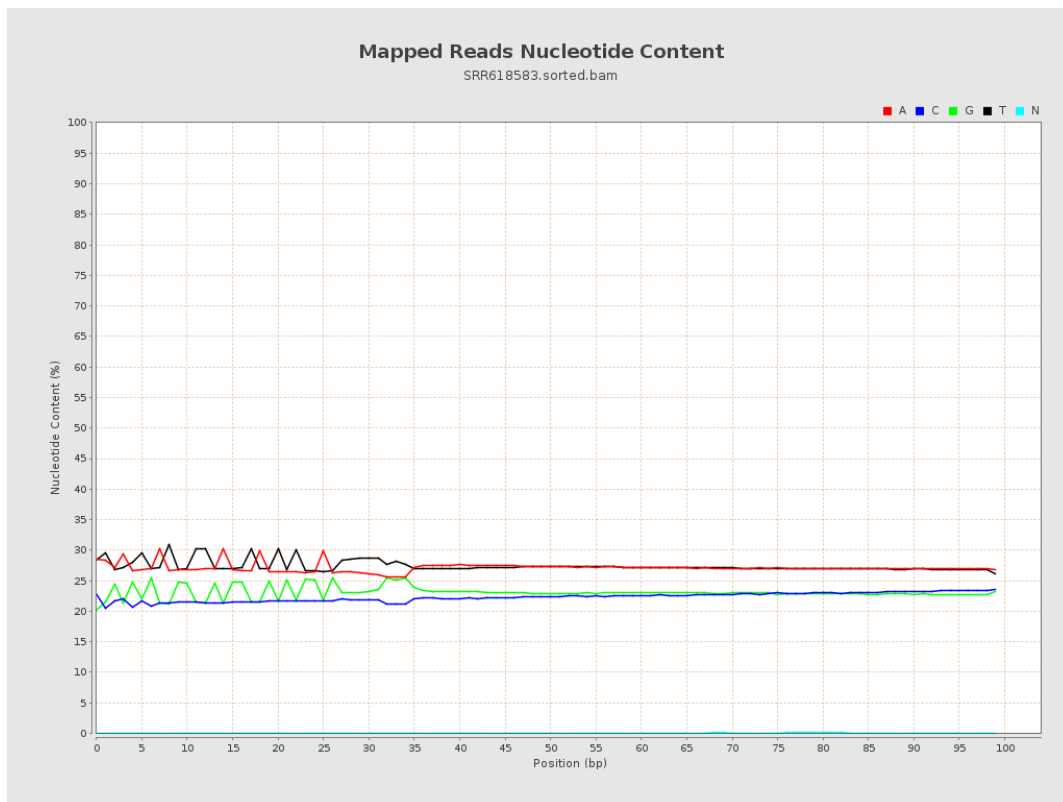
6. Results : Genome Fraction Coverage



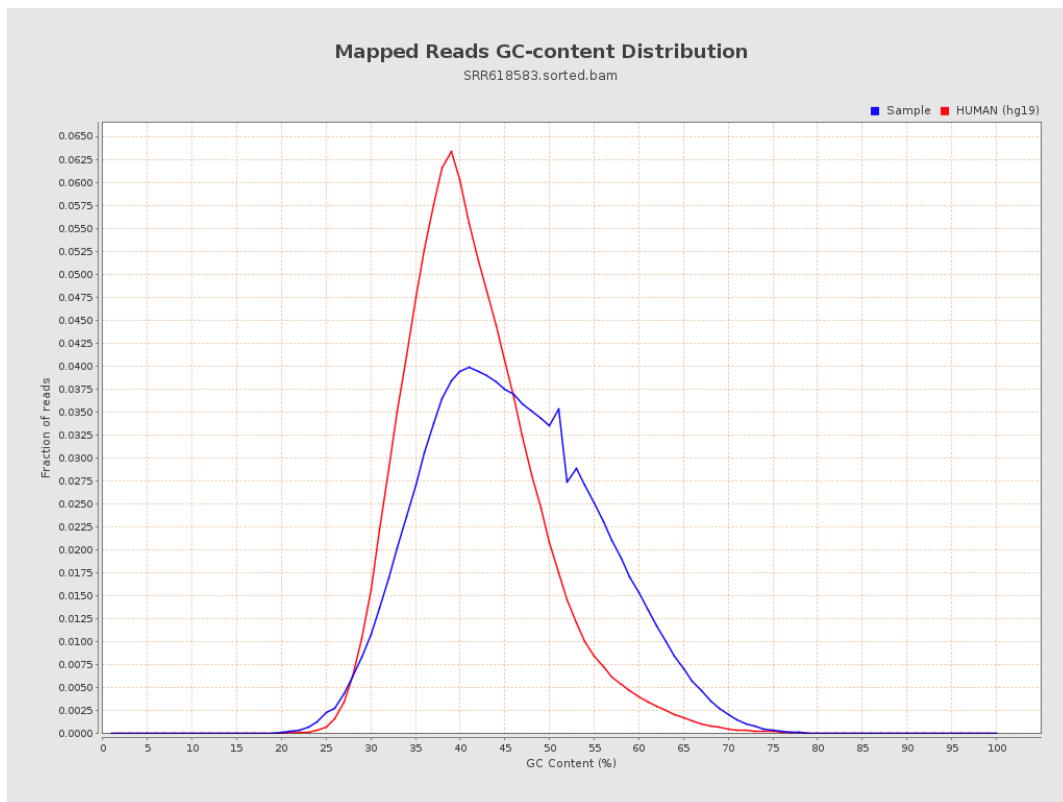
7. Results : Duplication Rate Histogram



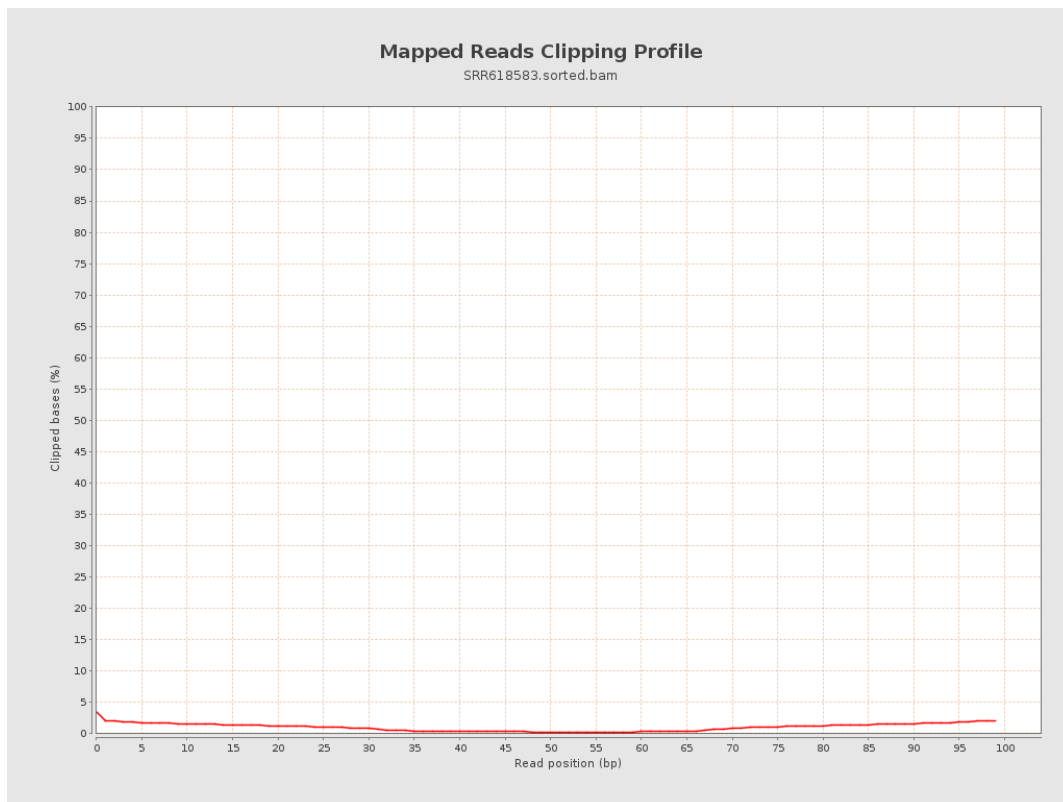
8. Results : Mapped Reads Nucleotide Content



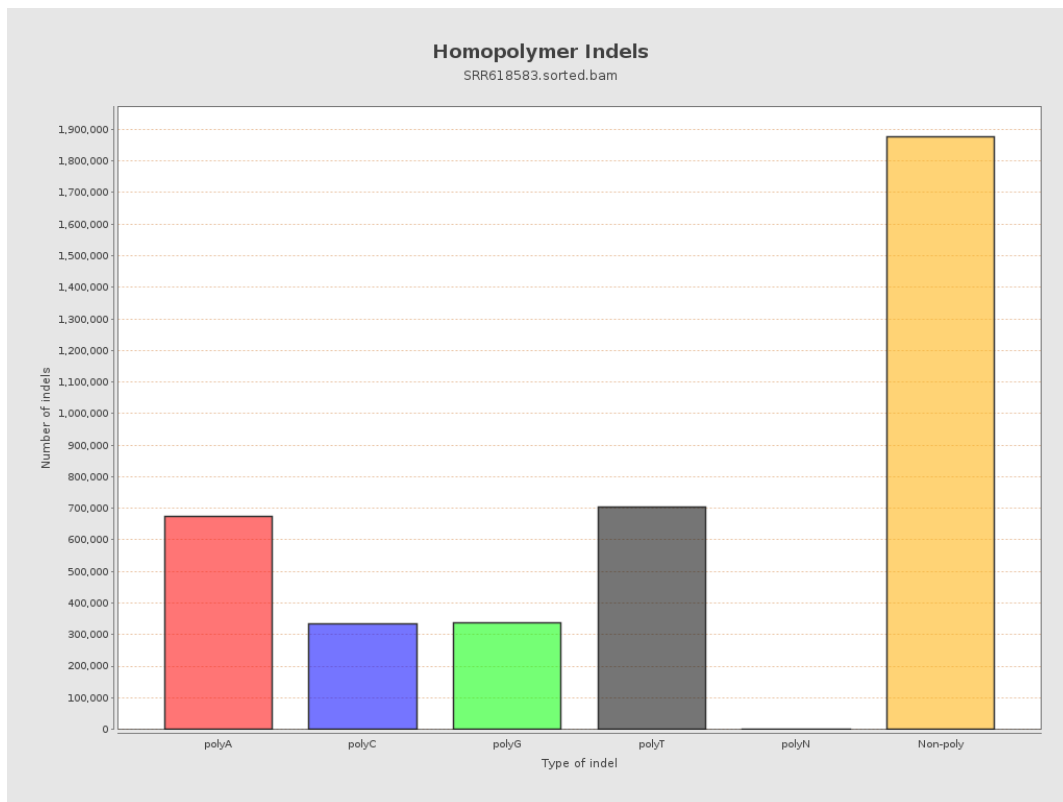
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



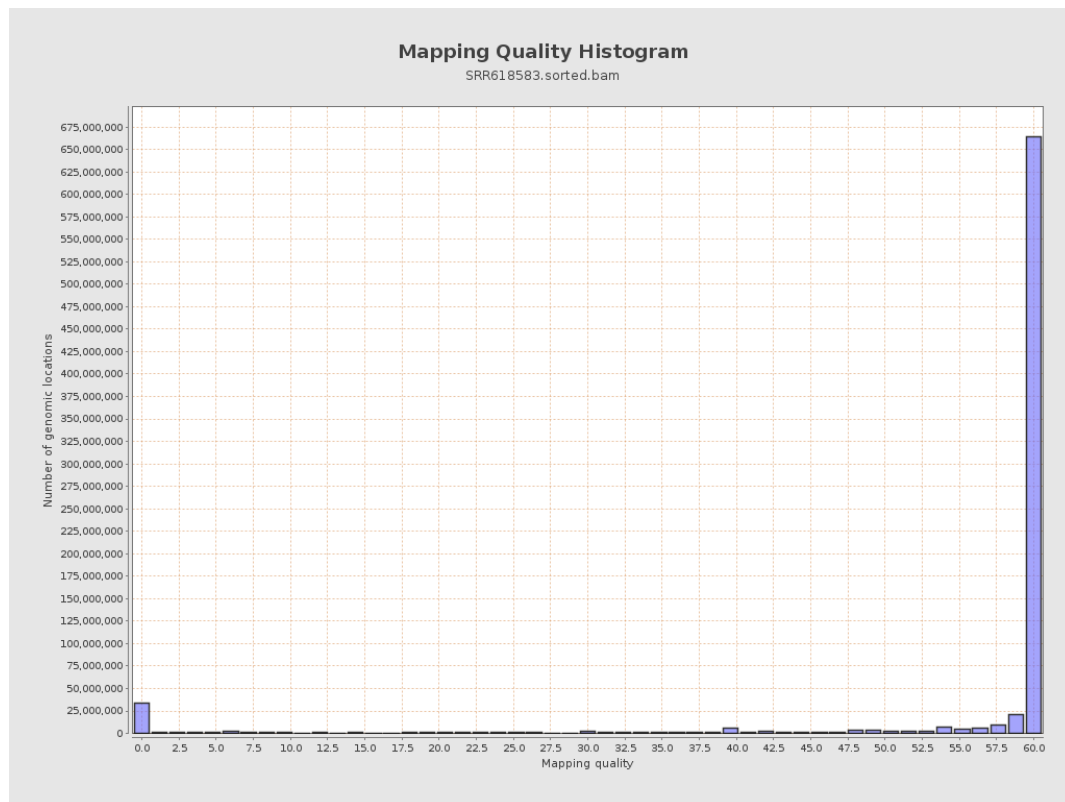
11. Results : Homopolymer Indels



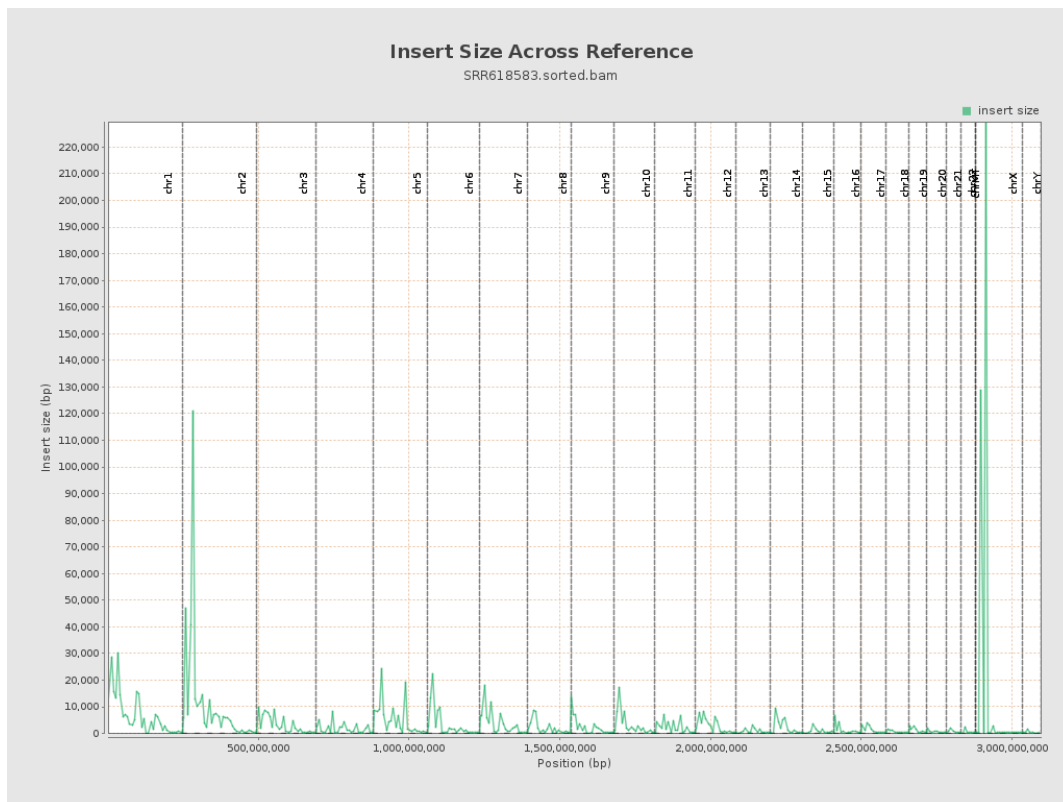
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

