

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 08:21:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777268.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_SRR1777268 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777268_1.fastq.gz SRR1777268_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 08:21:56 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777268.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,283,582
Mapped reads	3,067,914 / 93.43%
Unmapped reads	215,668 / 6.57%
Mapped paired reads	3,067,914 / 93.43%
Mapped reads, first in pair	1,539,459 / 46.88%
Mapped reads, second in pair	1,528,455 / 46.55%
Mapped reads, both in pair	3,043,454 / 92.69%
Mapped reads, singletons	24,460 / 0.74%
Secondary alignments	0
Supplementary alignments	54,730 / 1.67%
Read min/max/mean length	30 / 76 / 76.59
Duplicated reads (estimated)	63,205 / 1.92%
Duplication rate	1.86%
Clipped reads	417,571 / 12.72%

2.2. ACGT Content

Number/percentage of A's	68,161,798 / 29.78%
Number/percentage of C's	46,543,453 / 20.33%
Number/percentage of T's	66,716,996 / 29.15%
Number/percentage of G's	47,463,154 / 20.74%
Number/percentage of N's	13,393 / 0.01%

GC Percentage	41.07%
---------------	--------

2.3. Coverage

Mean	0.074
Standard Deviation	0.3809

2.4. Mapping Quality

Mean Mapping Quality	52.52
----------------------	-------

2.5. Insert size

Mean	195,064.9
Standard Deviation	4,265,921.71
P25/Median/P75	120 / 164 / 225

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	1,289,535
Insertions	50,153
Mapped reads with at least one insertion	1.62%
Deletions	21,300
Mapped reads with at least one deletion	0.69%
Homopolymer indels	49.53%

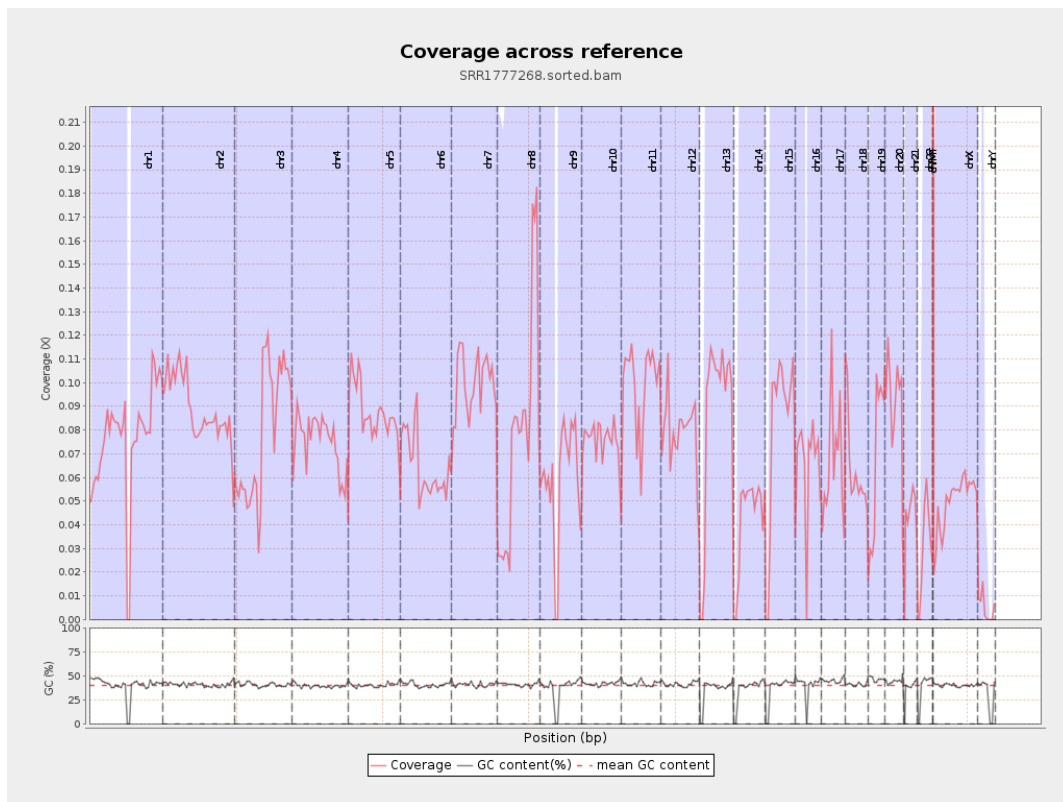
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

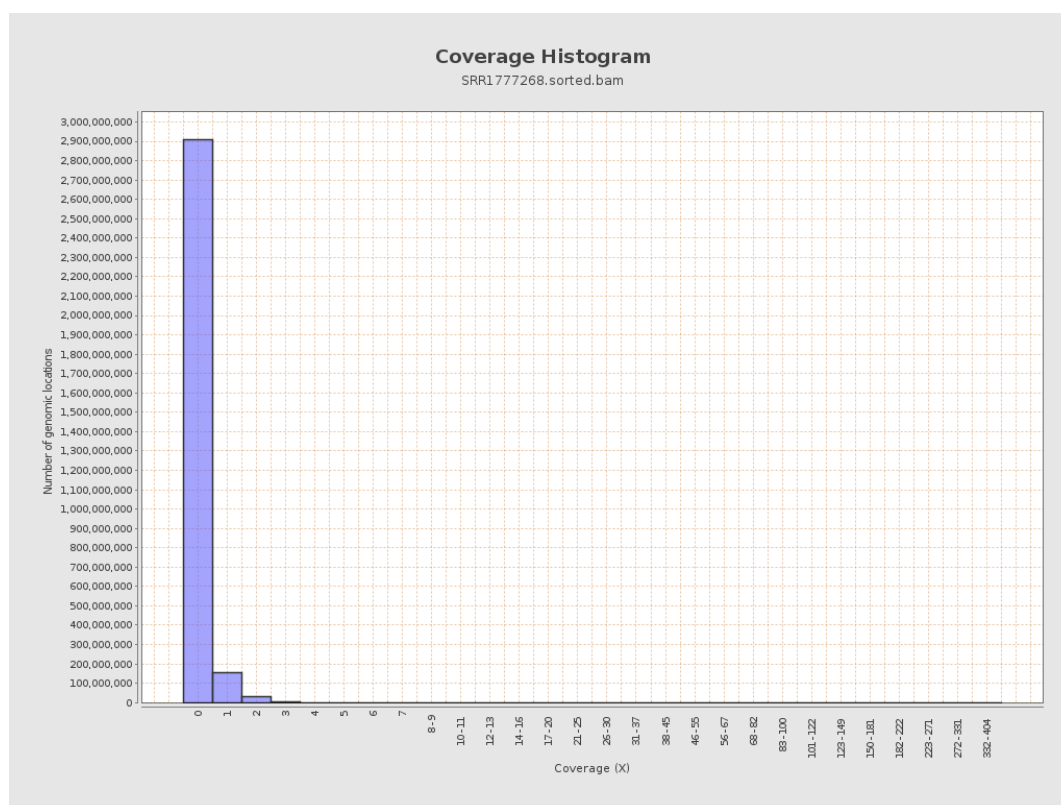
		bases	coverage	deviation
chr1	249250621	19043804	0.0764	0.5063
chr2	243199373	21669921	0.0891	0.3618
chr3	198022430	15554924	0.0786	0.3198
chr4	191154276	14381312	0.0752	0.3165
chr5	180915260	15754552	0.0871	0.3347
chr6	171115067	11042818	0.0645	0.318
chr7	159138663	15736420	0.0989	0.406
chr8	146364022	11637957	0.0795	0.3276
chr9	141213431	8400447	0.0595	0.4636
chr10	135534747	10303835	0.076	0.416
chr11	135006516	13356736	0.0989	0.3729
chr12	133851895	10646337	0.0795	0.3198
chr13	115169878	10024323	0.087	0.3358
chr14	107349540	4575975	0.0426	0.2347
chr15	102531392	8284687	0.0808	0.3242
chr16	90354753	5790795	0.0641	0.3201
chr17	81195210	5337566	0.0657	0.3161
chr18	78077248	4949433	0.0634	0.4018
chr19	59128983	3993209	0.0675	0.3782
chr20	63025520	5937089	0.0942	0.3497
chr21	48129895	2047152	0.0425	0.243
chr22	51304566	1591869	0.031	0.2002
chrMT	16571	932442	56.2695	13.5963
chrX	155270560	7651947	0.0493	0.2563

chrY	59373566	295798	0.005	0.1287
------	----------	--------	-------	--------

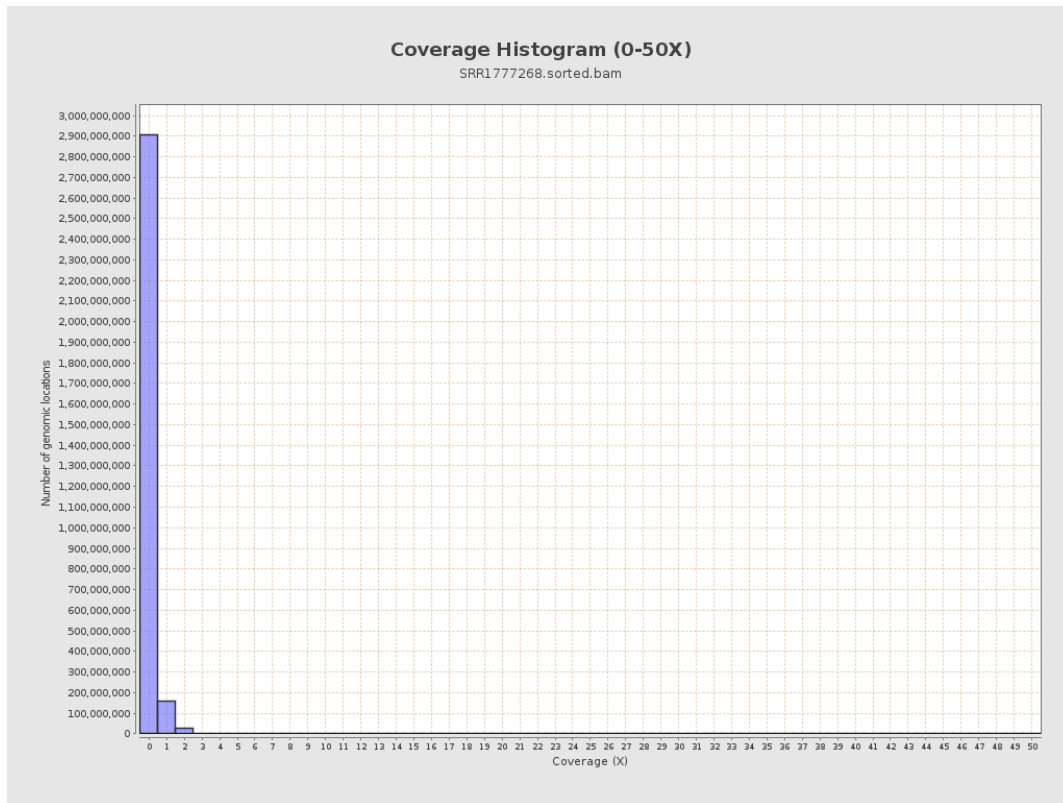
3. Results : Coverage across reference



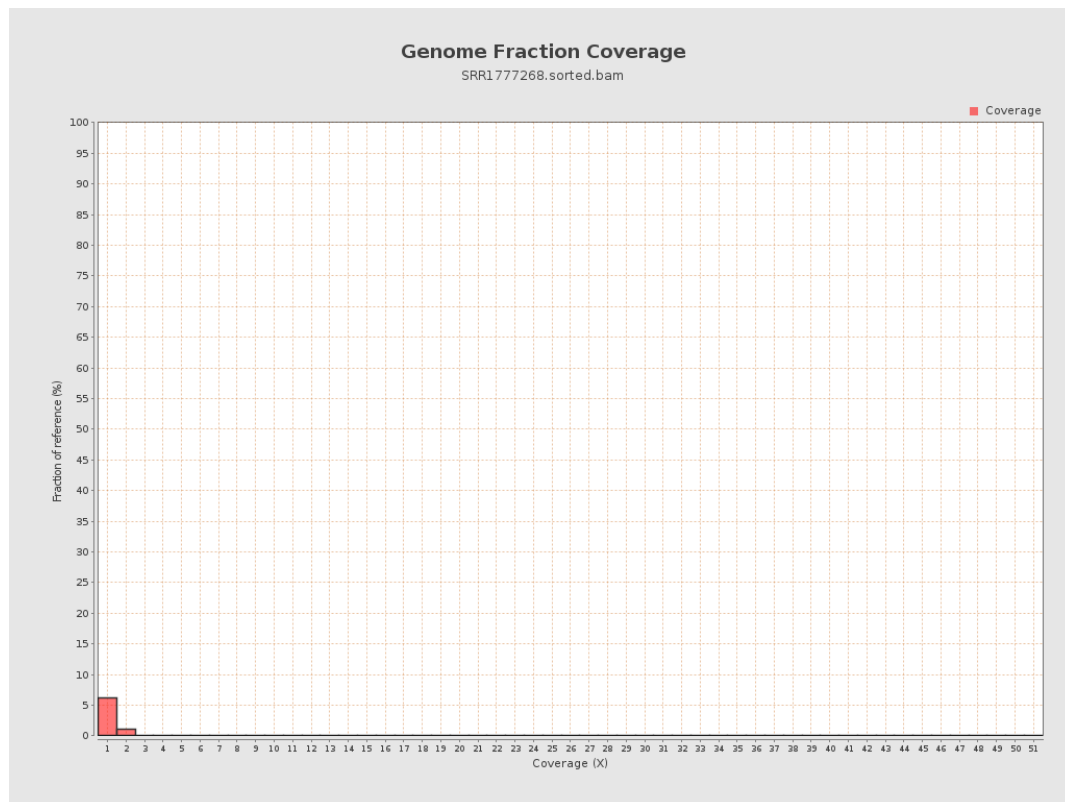
4. Results : Coverage Histogram



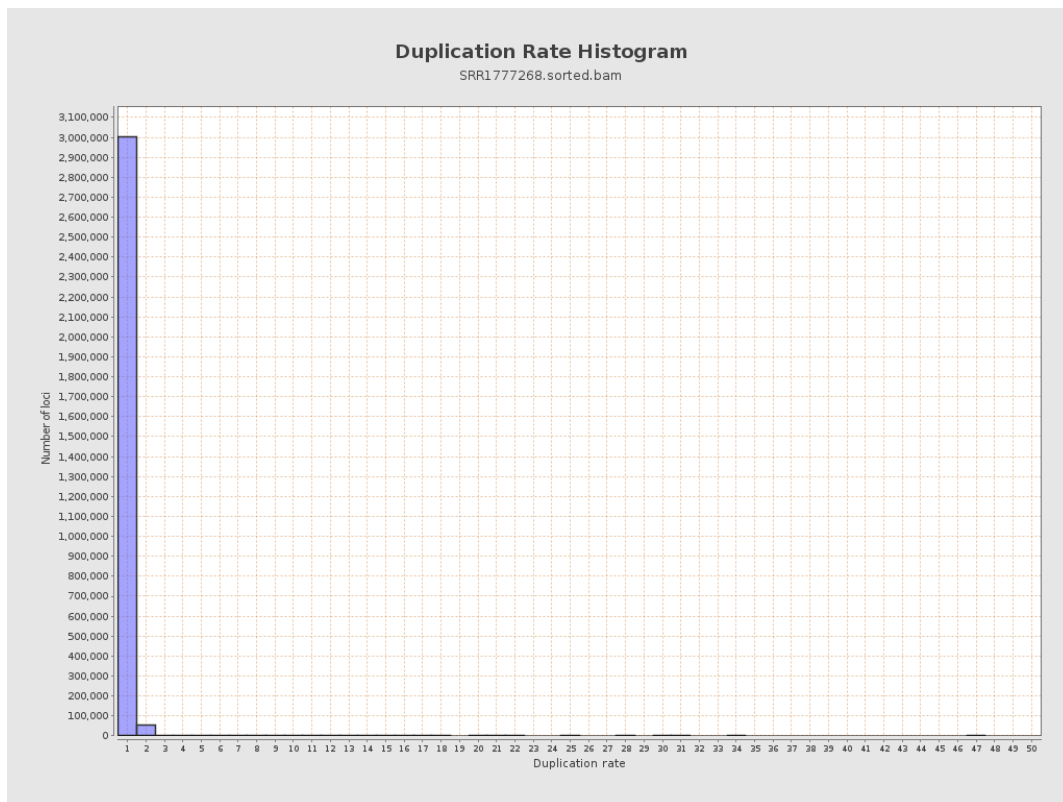
5. Results : Coverage Histogram (0-50X)



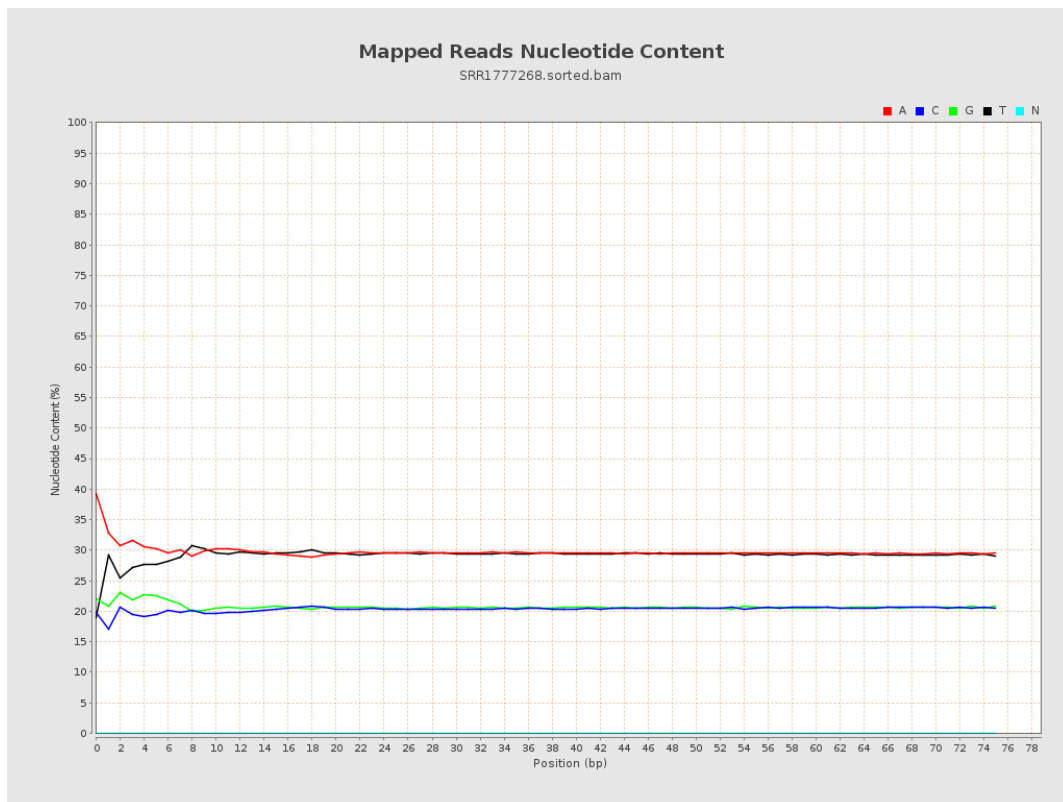
6. Results : Genome Fraction Coverage



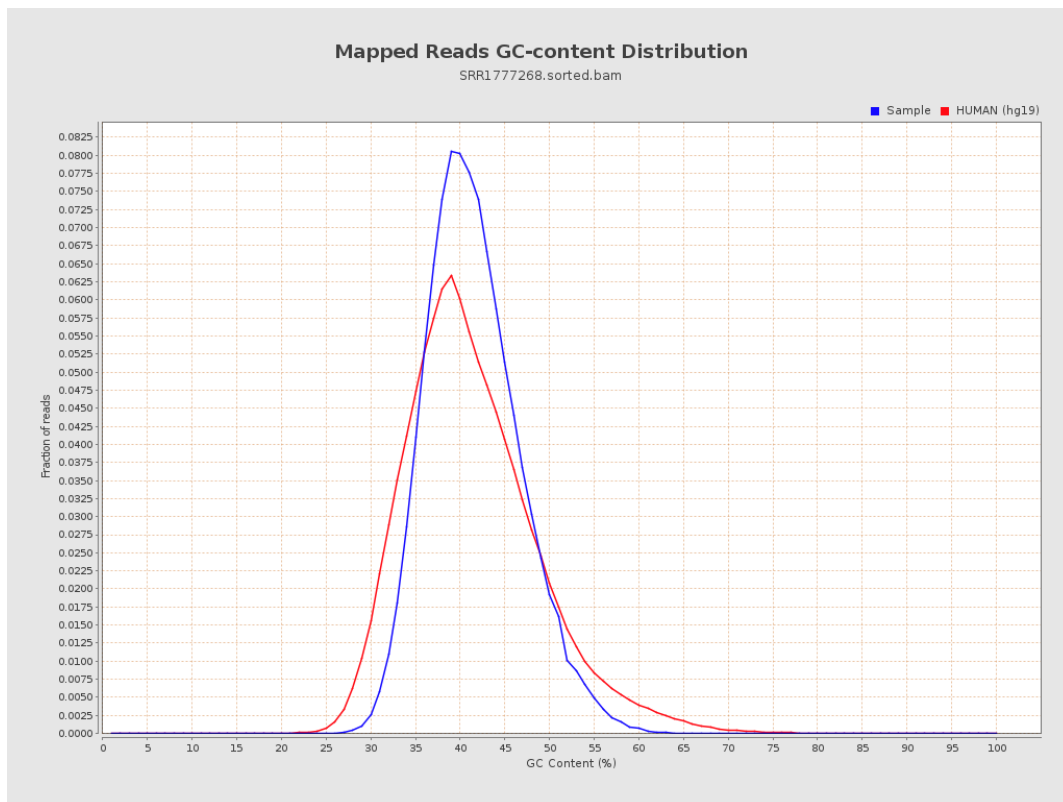
7. Results : Duplication Rate Histogram



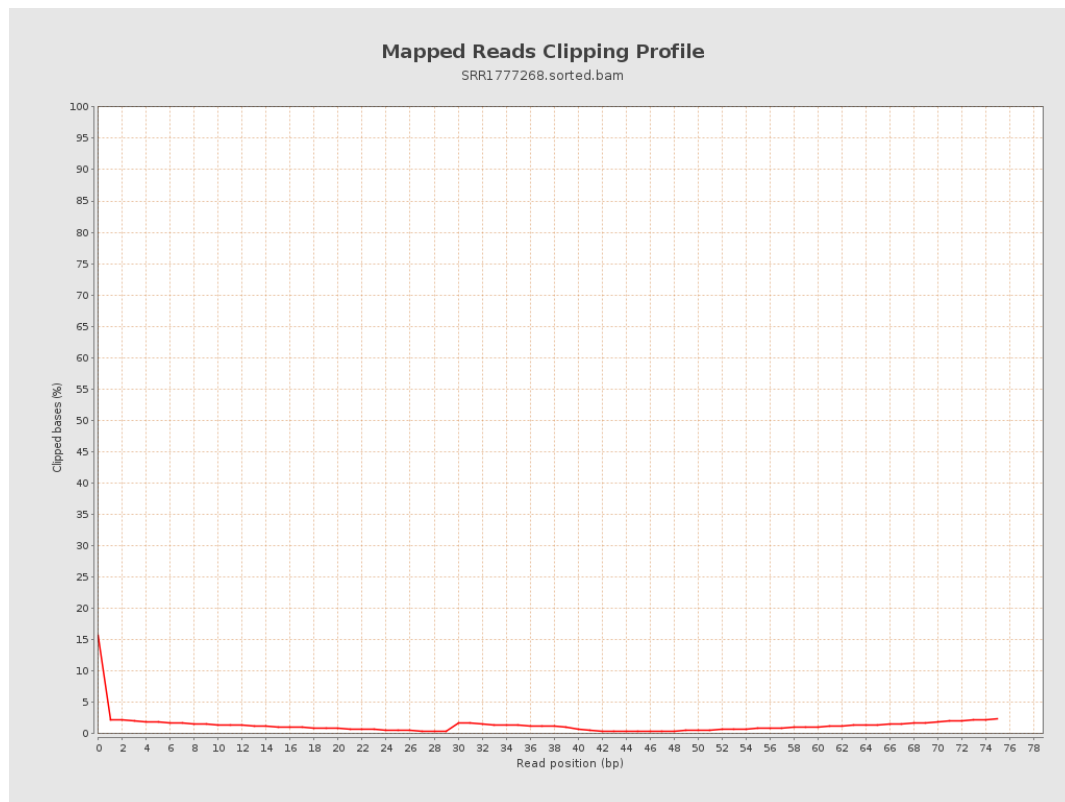
8. Results : Mapped Reads Nucleotide Content



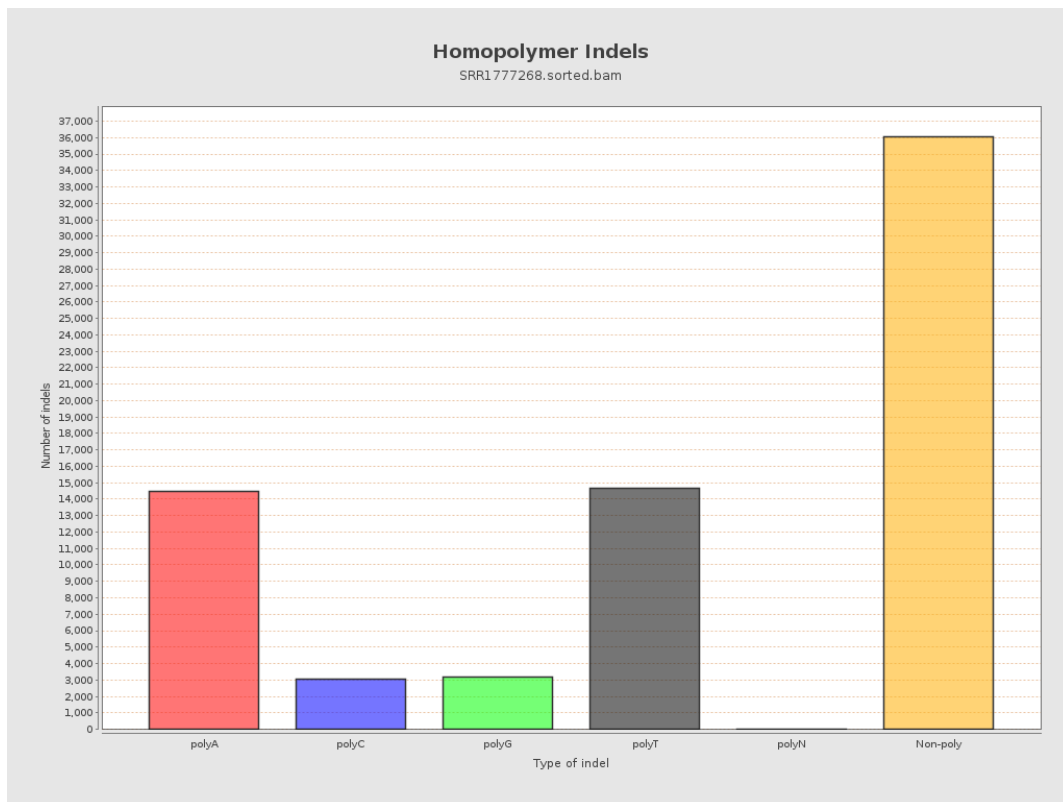
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



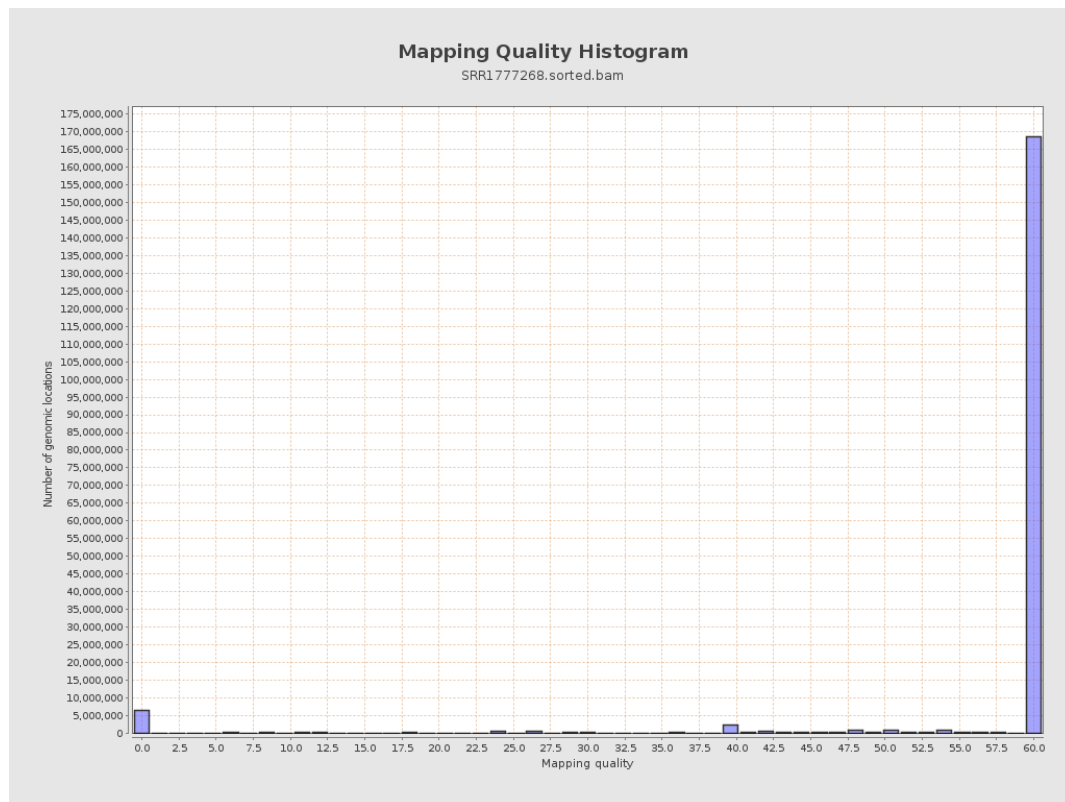
11. Results : Homopolymer Indels



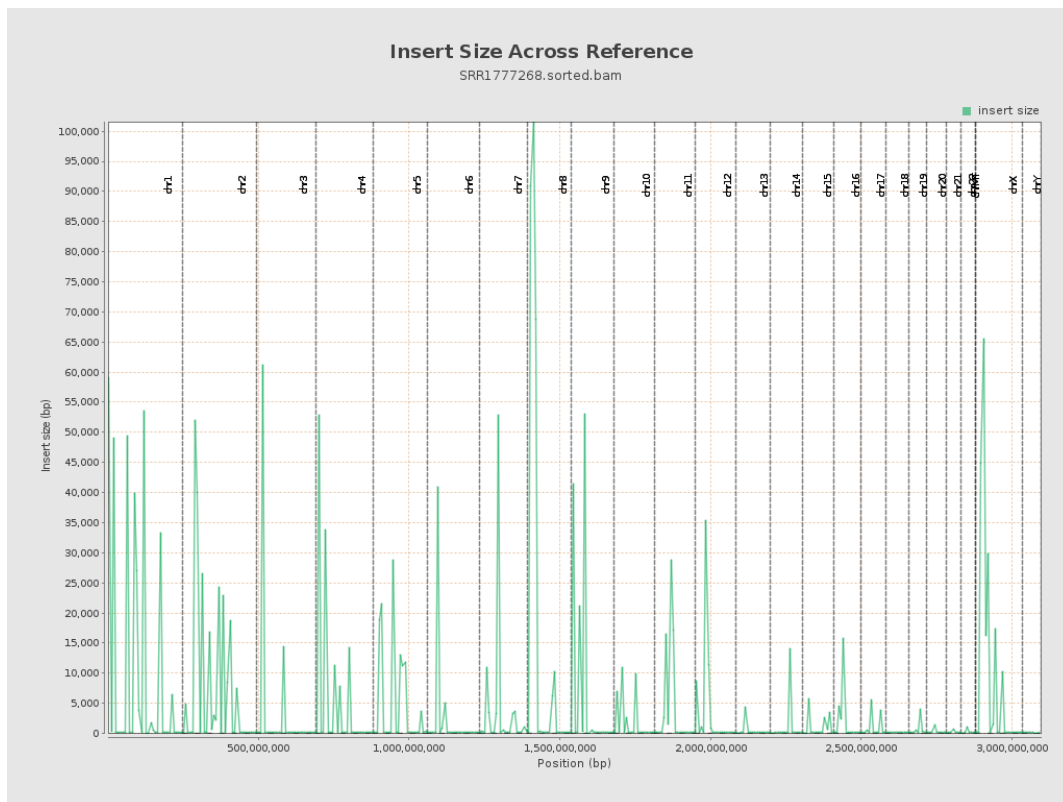
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

