Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 07:06:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063607.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_SRR6063607 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063607.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 07:06:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063607.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,150,237
Mapped reads	3,895,729 / 93.87%
Unmapped reads	254,508 / 6.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,981 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	366,216 / 8.82%
Duplication rate	7.42%
Clipped reads	2,018,862 / 48.64%

2.2. ACGT Content

Number/percentage of A's	66,522,836 / 26.43%
Number/percentage of C's	45,031,137 / 17.89%
Number/percentage of T's	82,173,538 / 32.65%
Number/percentage of G's	57,900,193 / 23.01%
Number/percentage of N's	28,671 / 0.01%
GC Percentage	40.9%

2.3. Coverage

Mean	0.0813

Standard Deviation	0.9381

2.4. Mapping Quality

Mean Mapping Quality	45.31

2.5. Mismatches and indels

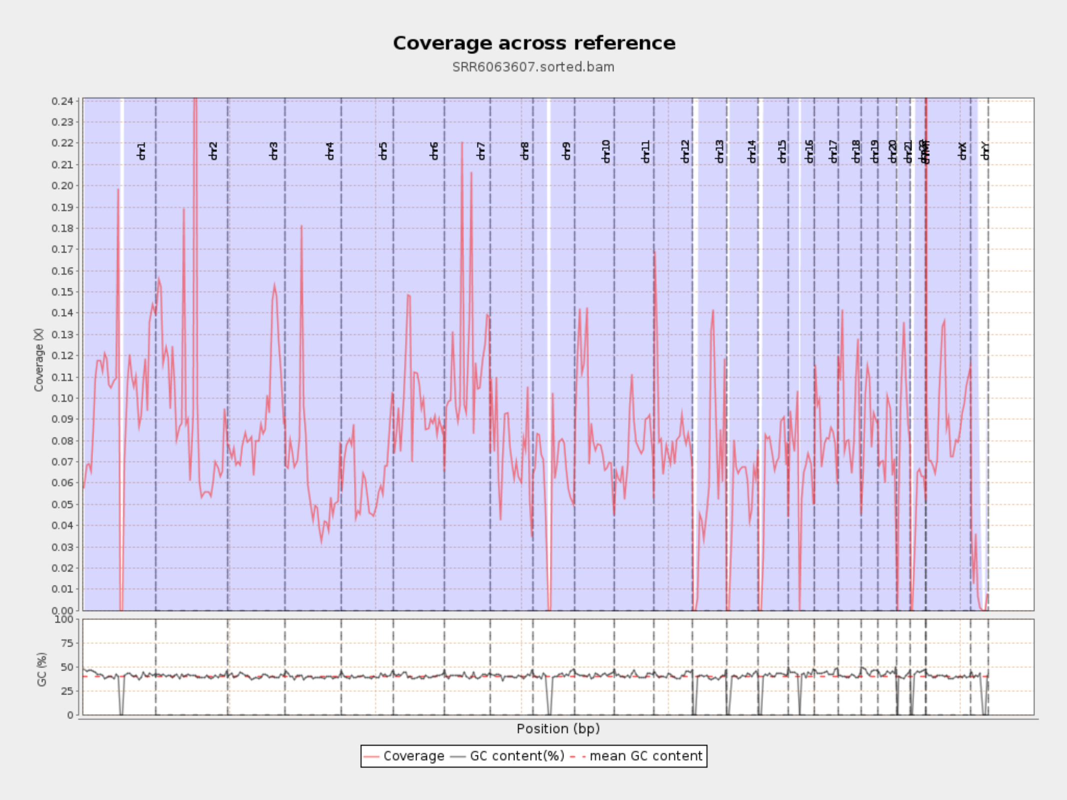
General error rate	0.57%
Mismatches	1,405,673
Insertions	16,417
Mapped reads with at least one insertion	0.42%
Deletions	60,297
Mapped reads with at least one deletion	1.53%
Homopolymer indels	44.39%

2.6. Chromosome stats

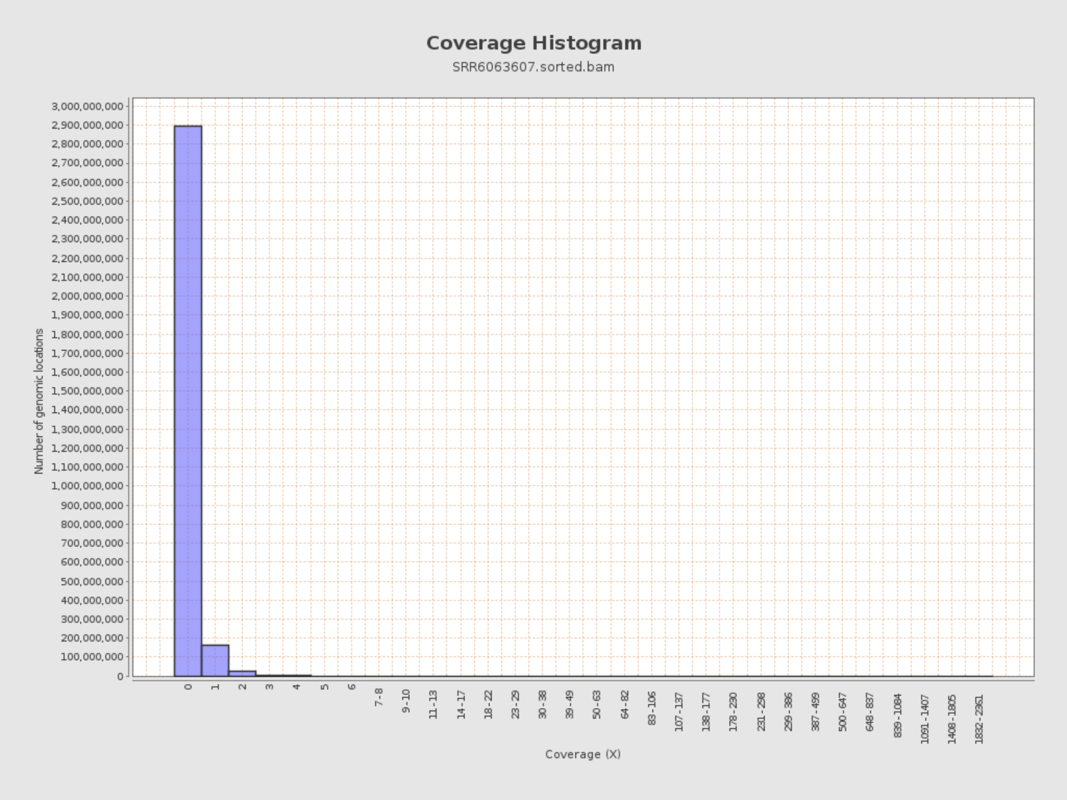
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25105433	0.1007	1.8897
chr2	243199373	24849862	0.1022	1.2674
chr3	198022430	18070770	0.0913	0.3709
chr4	191154276	12146961	0.0635	0.334
chr5	180915260	11538017	0.0638	0.3202
chr6	171115067	16659513	0.0974	0.5177
chr7	159138663	18775755	0.118	1.8715

chr8	146364022	10864304	0.0742	0.9944
chr9	141213431	8840549	0.0626	0.7914
chr10	135534747	12094362	0.0892	0.6561
chr11	135006516	10410981	0.0771	0.5847
chr12	133851895	11485867	0.0858	0.4141
chr13	115169878	7297948	0.0634	0.3383
chr14	107349540	5755353	0.0536	0.4128
chr15	102531392	6418396	0.0626	0.3504
chr16	90354753	5910808	0.0654	0.3963
chr17	81195210	6930623	0.0854	0.4304
chr18	78077248	7452713	0.0955	1.5398
chr19	59128983	5359377	0.0906	1.2227
chr20	63025520	4646692	0.0737	0.3725
chr21	48129895	4121937	0.0856	0.385
chr22	51304566	2277633	0.0444	0.2475
chrMT	16571	114630	6.9175	4.7359
chrX	155270560	13945627	0.0898	0.491
chrY	59373566	686877	0.0116	0.3431

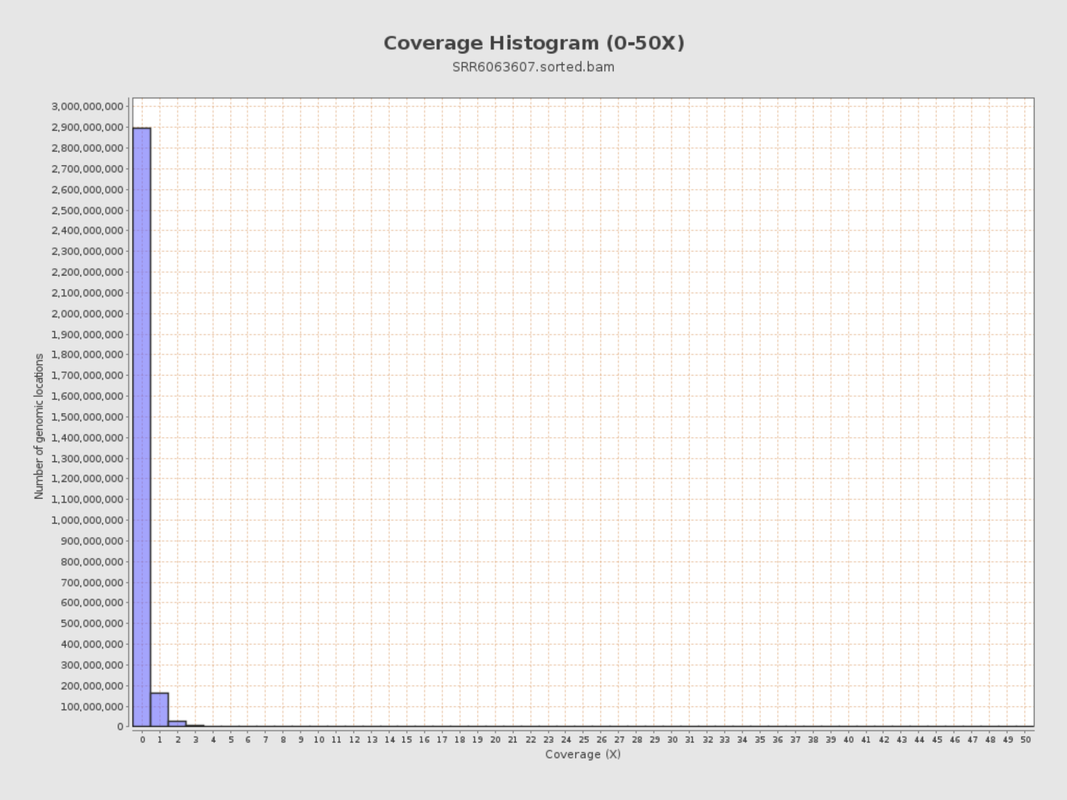
3. Results : Coverage across reference



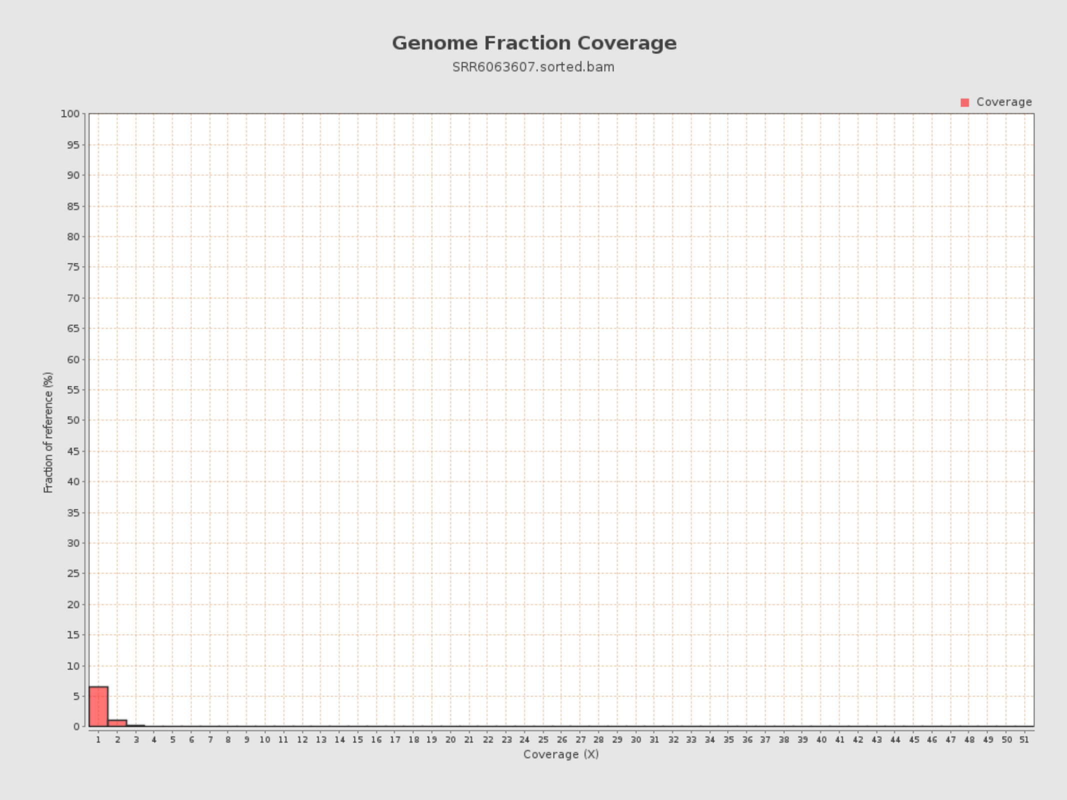
4. Results : Coverage Histogram



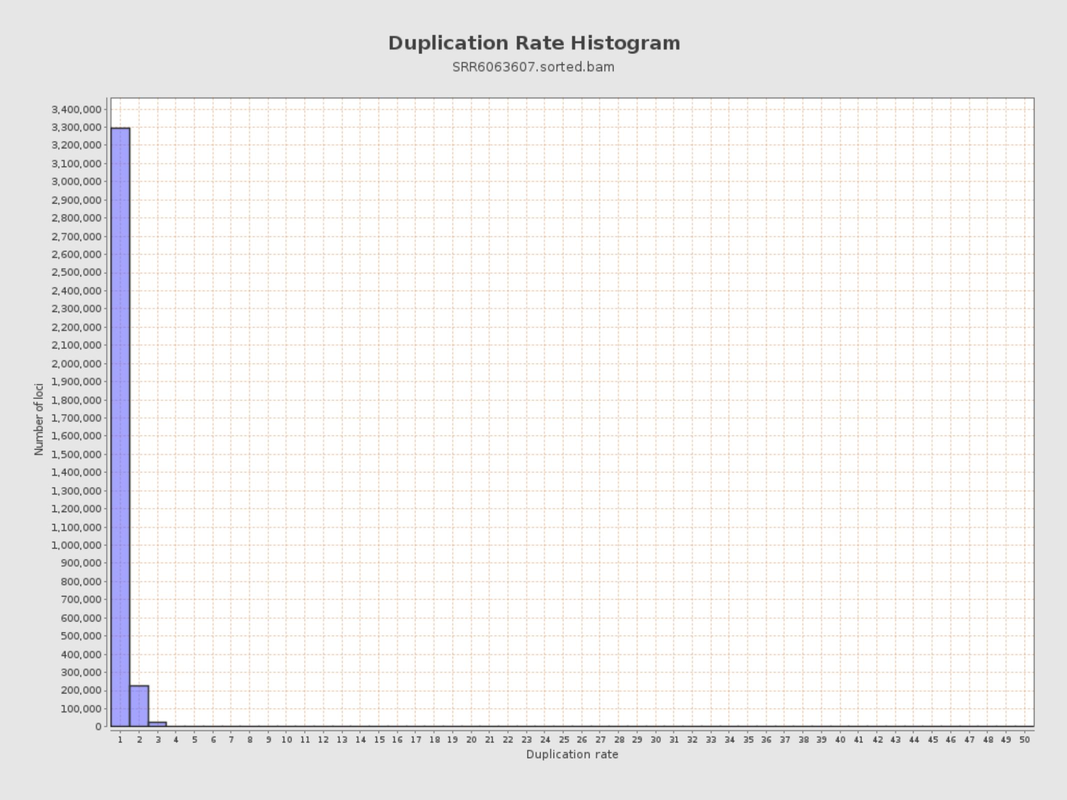
5. Results : Coverage Histogram (0-50X)



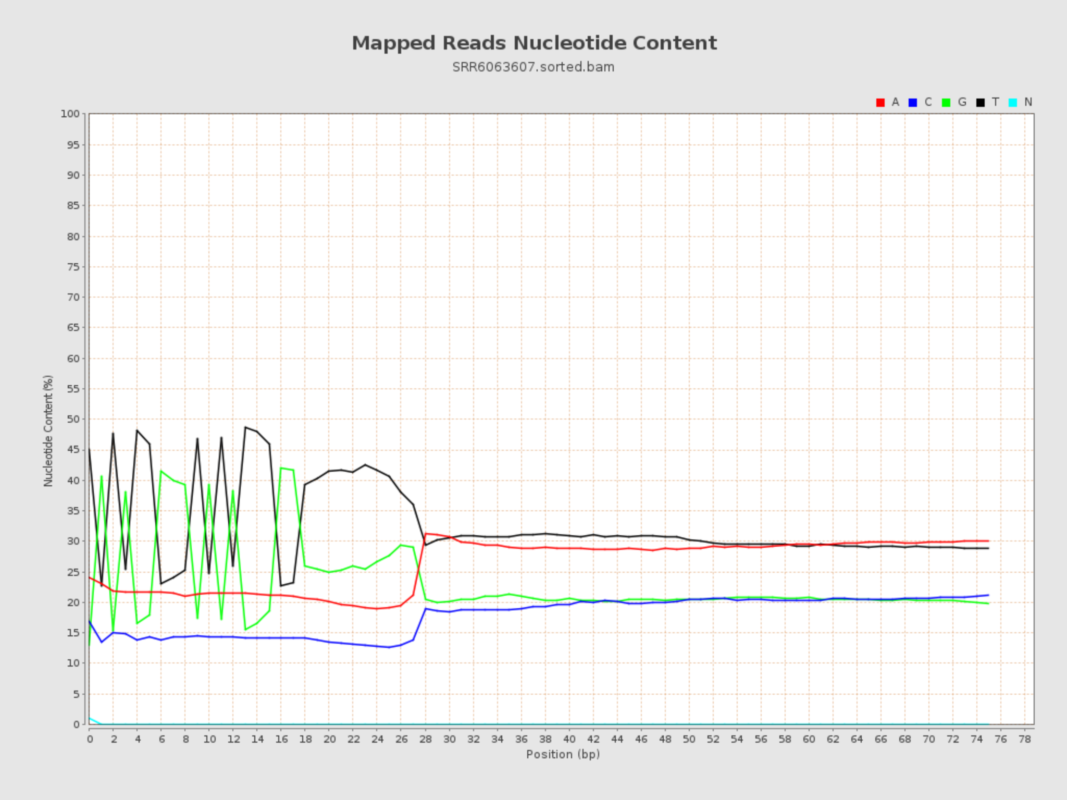
6. Results : Genome Fraction Coverage



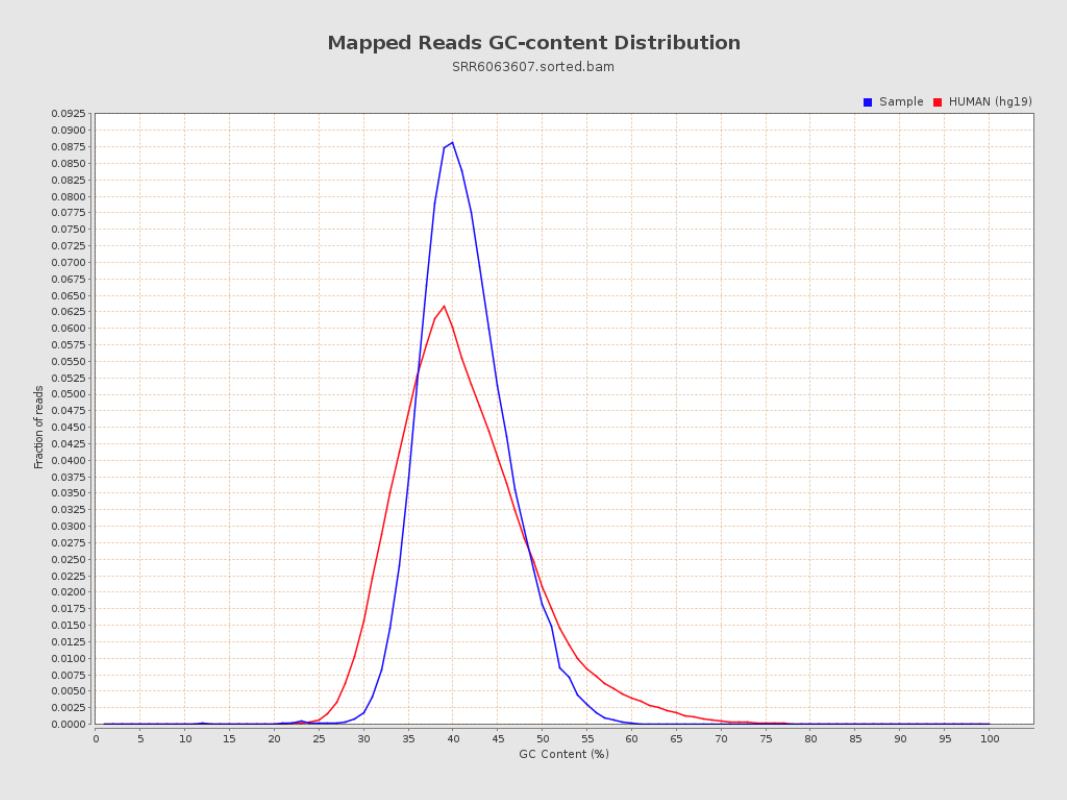
7. Results : Duplication Rate Histogram



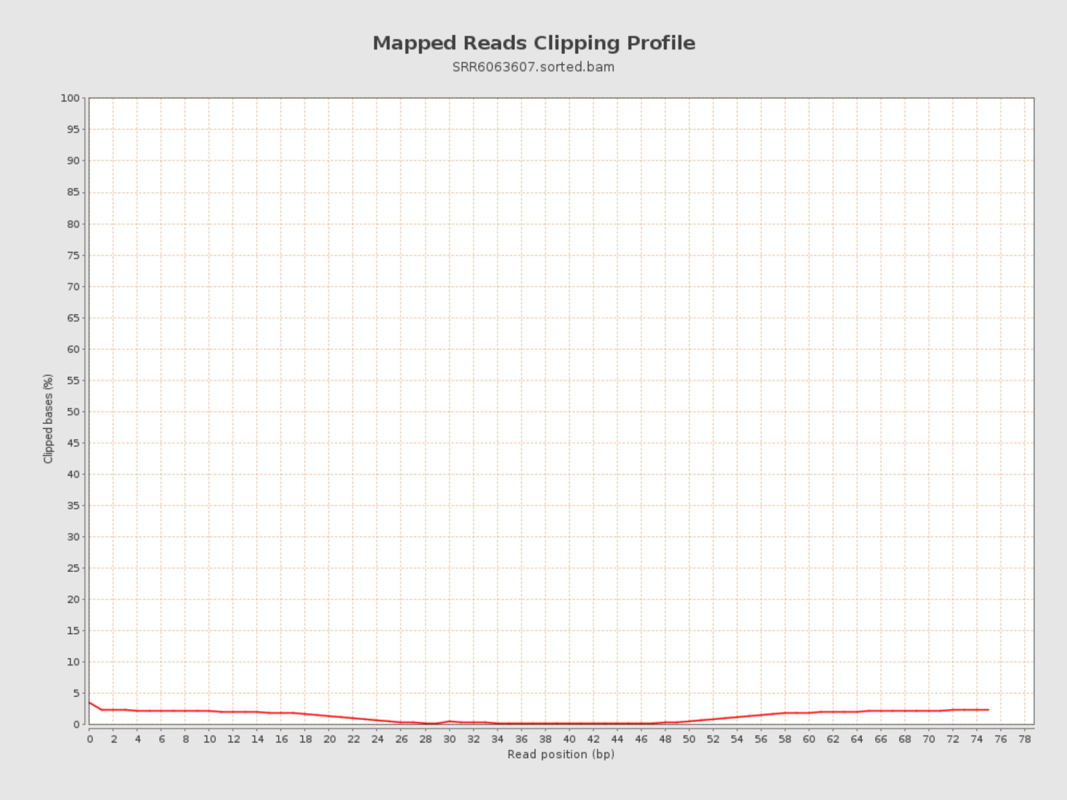
8. Results : Mapped Reads Nucleotide Content



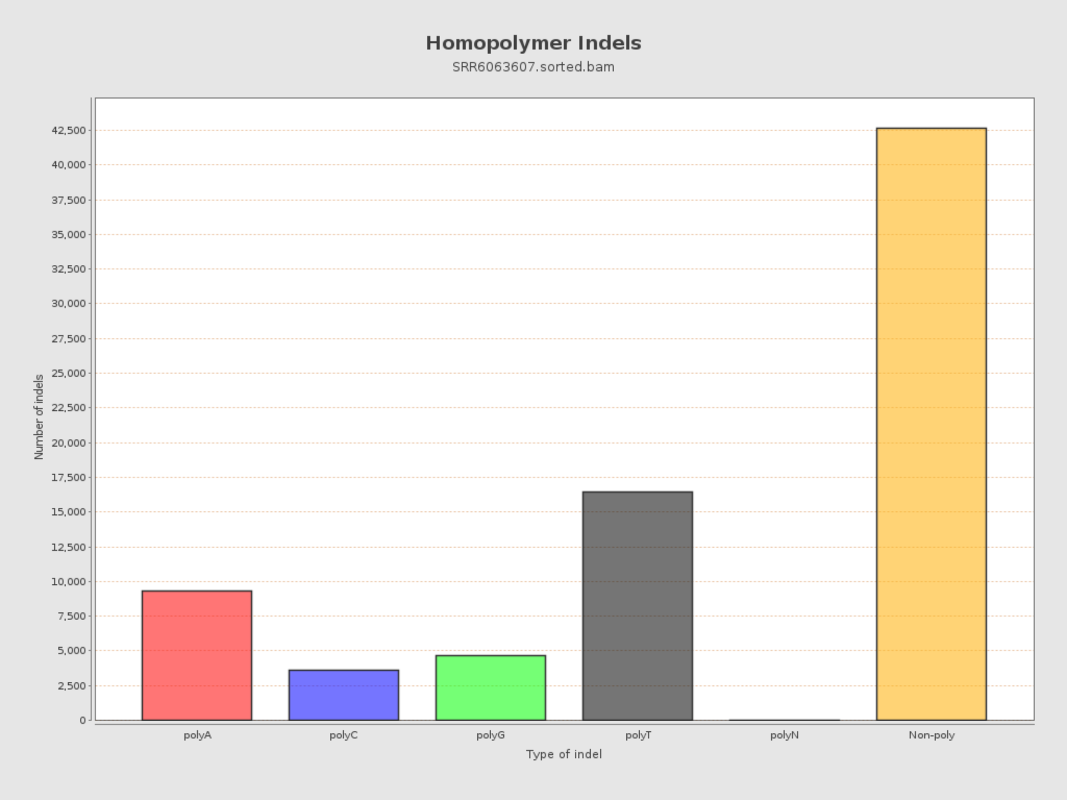
9. Results : Mapped Reads GC-content Distribution



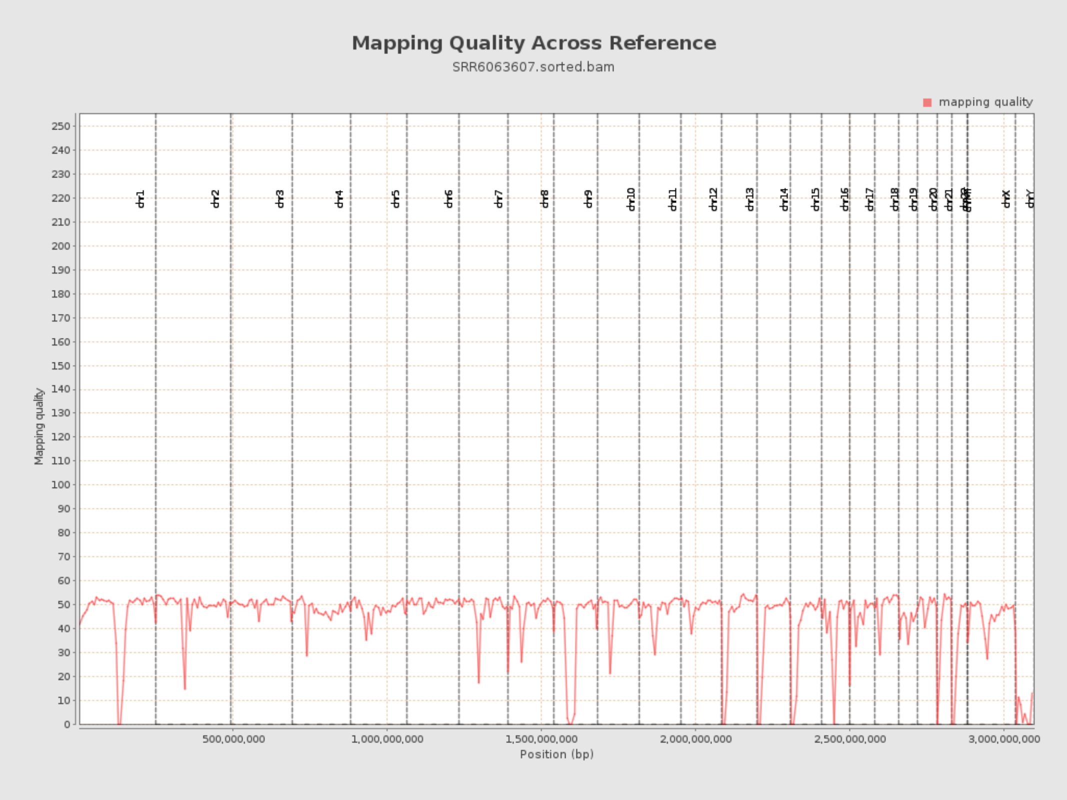
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram