Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 15:39:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068189.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_SRR6068189 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068189.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 15:39:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068189.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,592,272
Mapped reads	1,409,855 / 88.54%
Unmapped reads	182,417 / 11.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,791 / 0.61%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	151,482 / 9.51%
Duplication rate	7.87%
Clipped reads	593,580 / 37.28%

2.2. ACGT Content

Number/percentage of A's	27,138,210 / 28.66%
Number/percentage of C's	17,194,178 / 18.16%
Number/percentage of T's	30,375,386 / 32.08%
Number/percentage of G's	19,872,281 / 20.99%
Number/percentage of N's	103,165 / 0.11%
GC Percentage	39.15%

2.3. Coverage

Mean	0.0306

Standard Deviation	0.6038

2.4. Mapping Quality

Mean Mapping Quality	44.91

2.5. Mismatches and indels

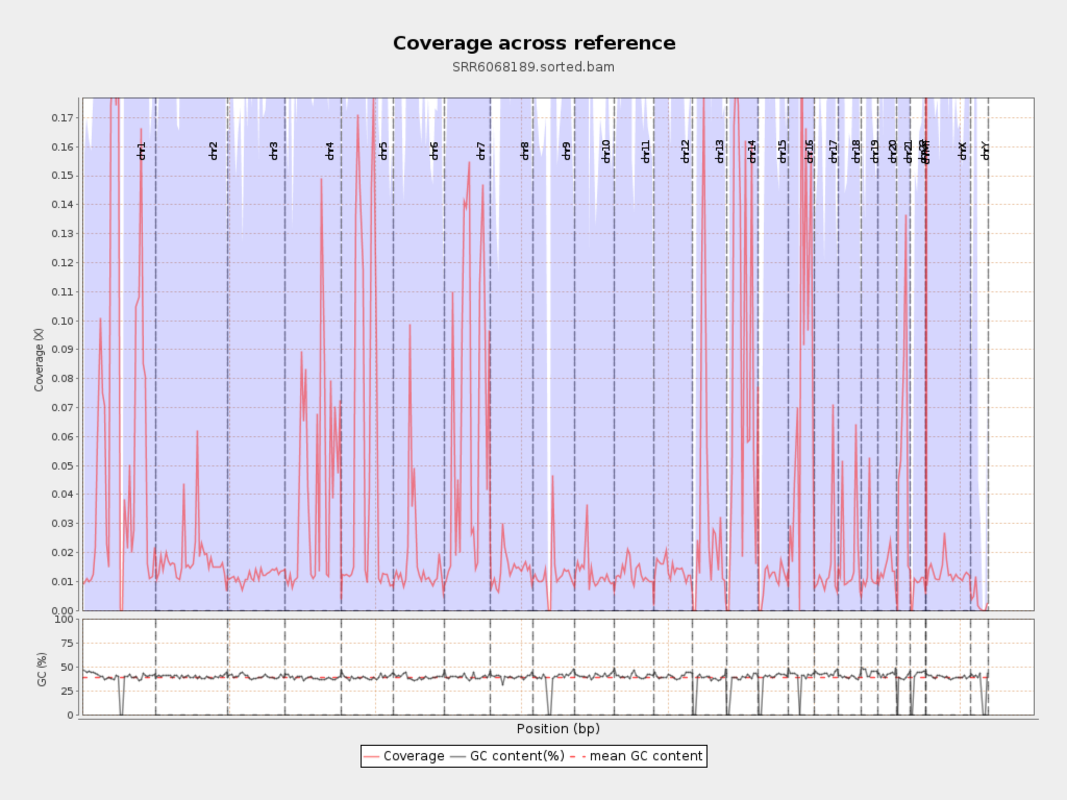
General error rate	0.9%
Mismatches	841,158
Insertions	7,126
Mapped reads with at least one insertion	0.5%
Deletions	23,544
Mapped reads with at least one deletion	1.65%
Homopolymer indels	48.42%

2.6. Chromosome stats

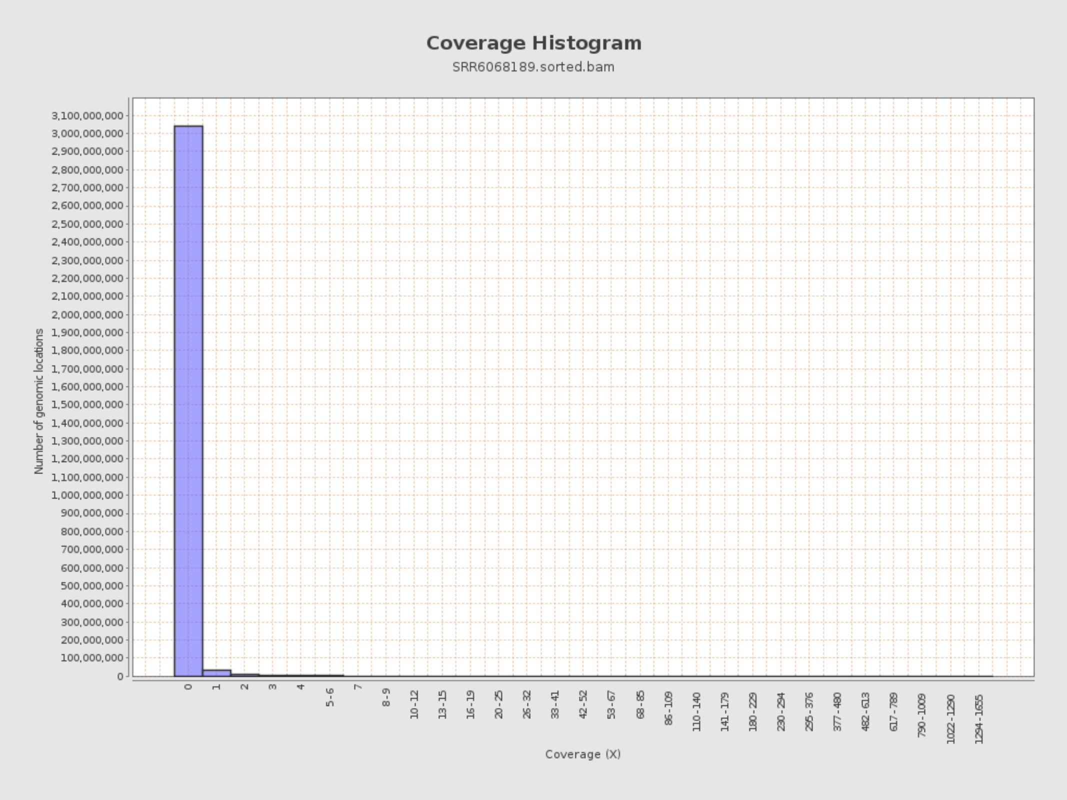
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15038690	0.0603	1.5396
chr2	243199373	4439688	0.0183	0.3402
chr3	198022430	2384561	0.012	0.1688
chr4	191154276	8264899	0.0432	0.3403
chr5	180915260	9314845	0.0515	0.3671
chr6	171115067	3211151	0.0188	0.3598
chr7	159138663	10472025	0.0658	0.6234

chr8	146364022	2086268	0.0143	0.6699
chr9	141213431	1768523	0.0125	0.4548
chr10	135534747	1787563	0.0132	0.2508
chr11	135006516	1712418	0.0127	0.3019
chr12	133851895	1886083	0.0141	0.2639
chr13	115169878	4183386	0.0363	0.3071
chr14	107349540	9669068	0.0901	0.5439
chr15	102531392	1067454	0.0104	0.1573
chr16	90354753	7300503	0.0808	0.5898
chr17	81195210	1302603	0.016	0.198
chr18	78077248	1638576	0.021	0.9759
chr19	59128983	916476	0.0155	1.0922
chr20	63025520	912554	0.0145	0.2669
chr21	48129895	2670733	0.0555	0.376
chr22	51304566	427418	0.0083	0.1344
chrMT	16571	53952	3.2558	3.4567
chrX	155270560	2029248	0.0131	0.2348
chrY	59373566	185951	0.0031	0.1111

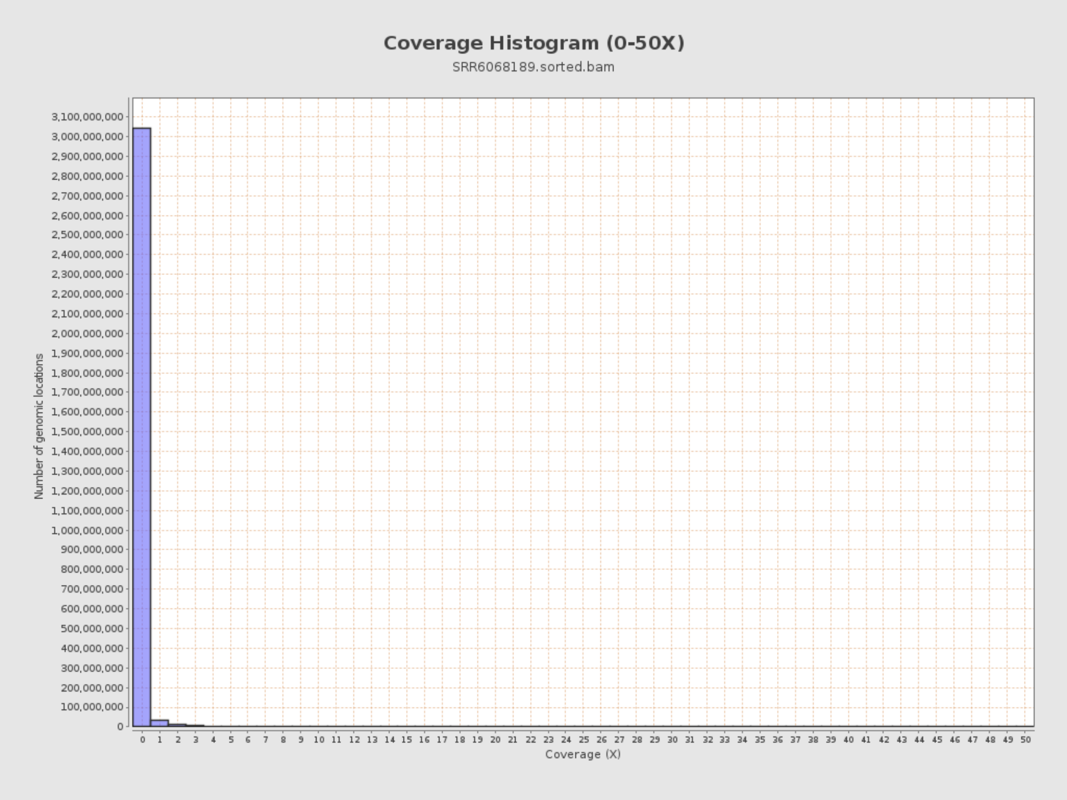
3. Results : Coverage across reference



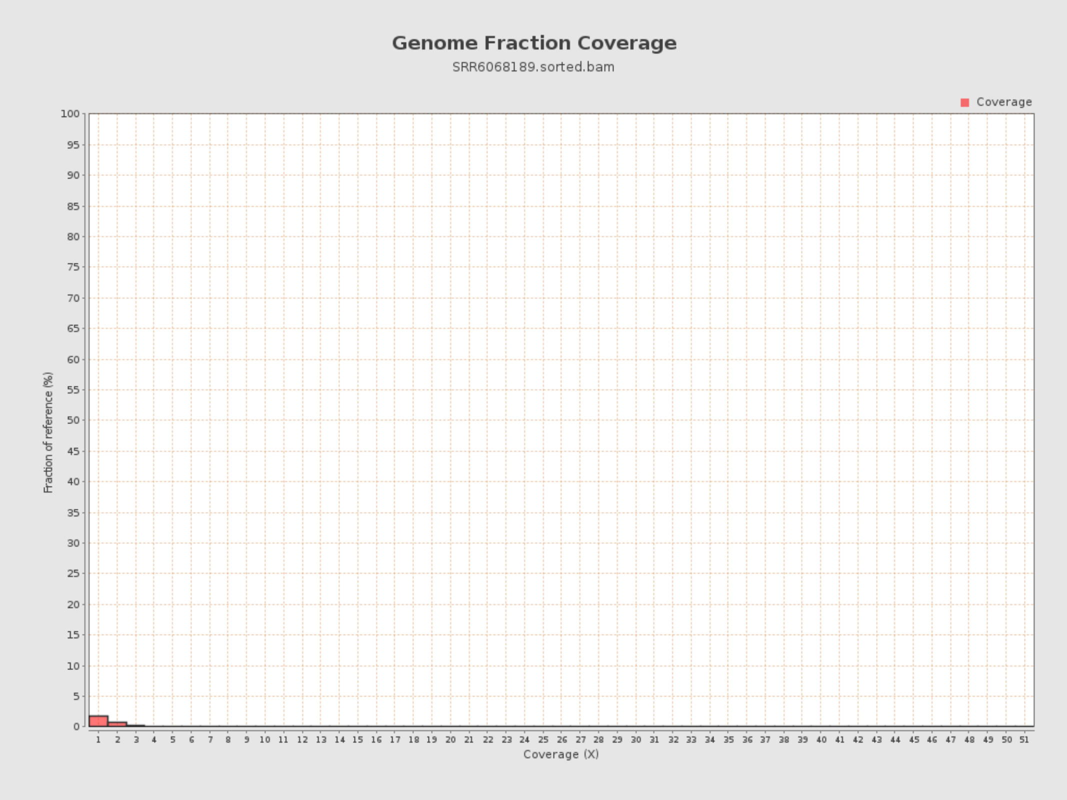
4. Results : Coverage Histogram



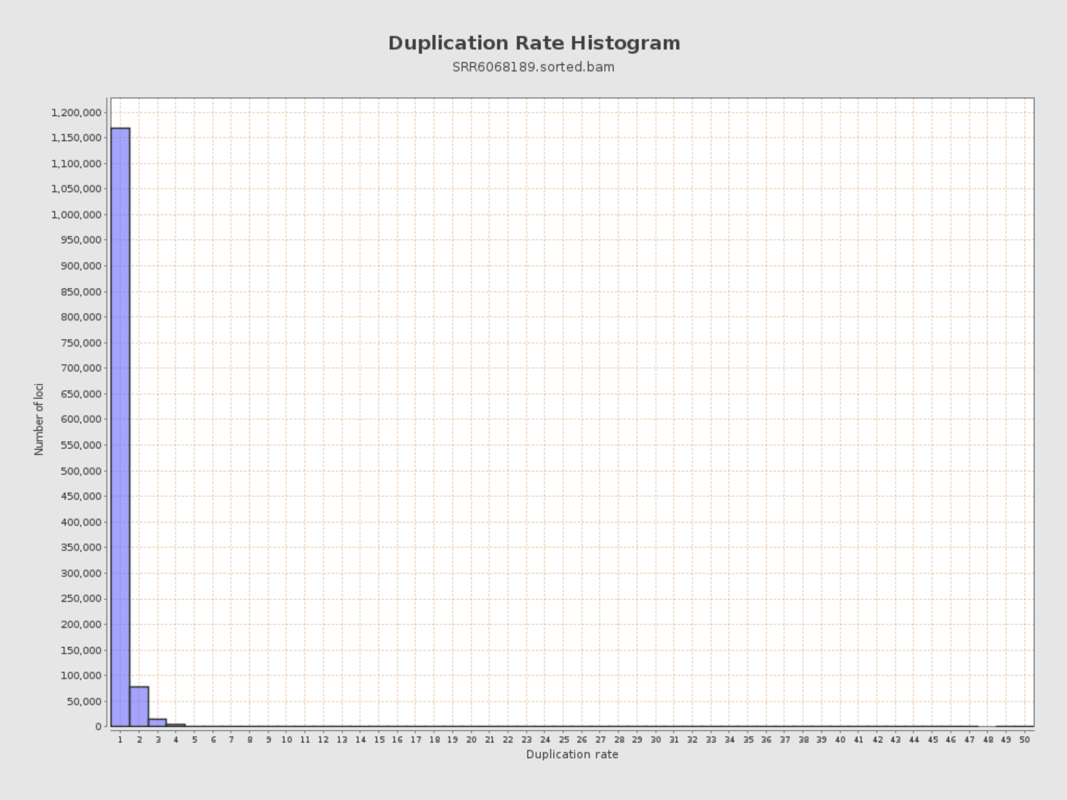
5. Results : Coverage Histogram (0-50X)



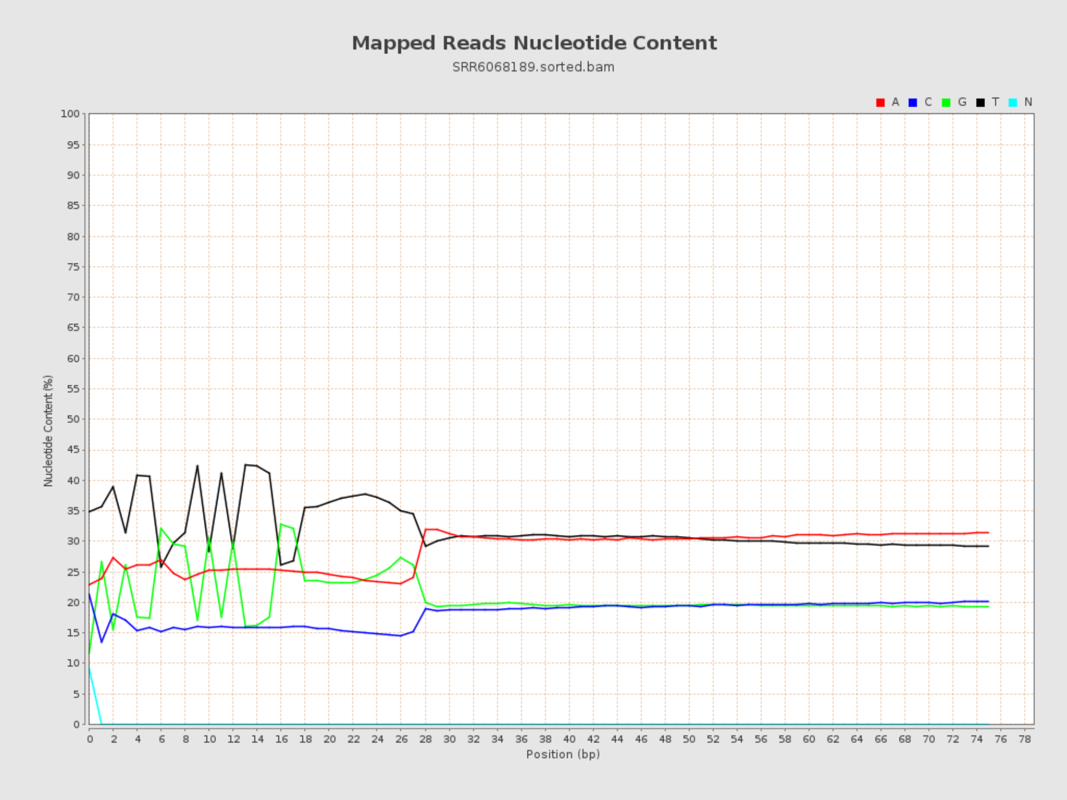
6. Results : Genome Fraction Coverage



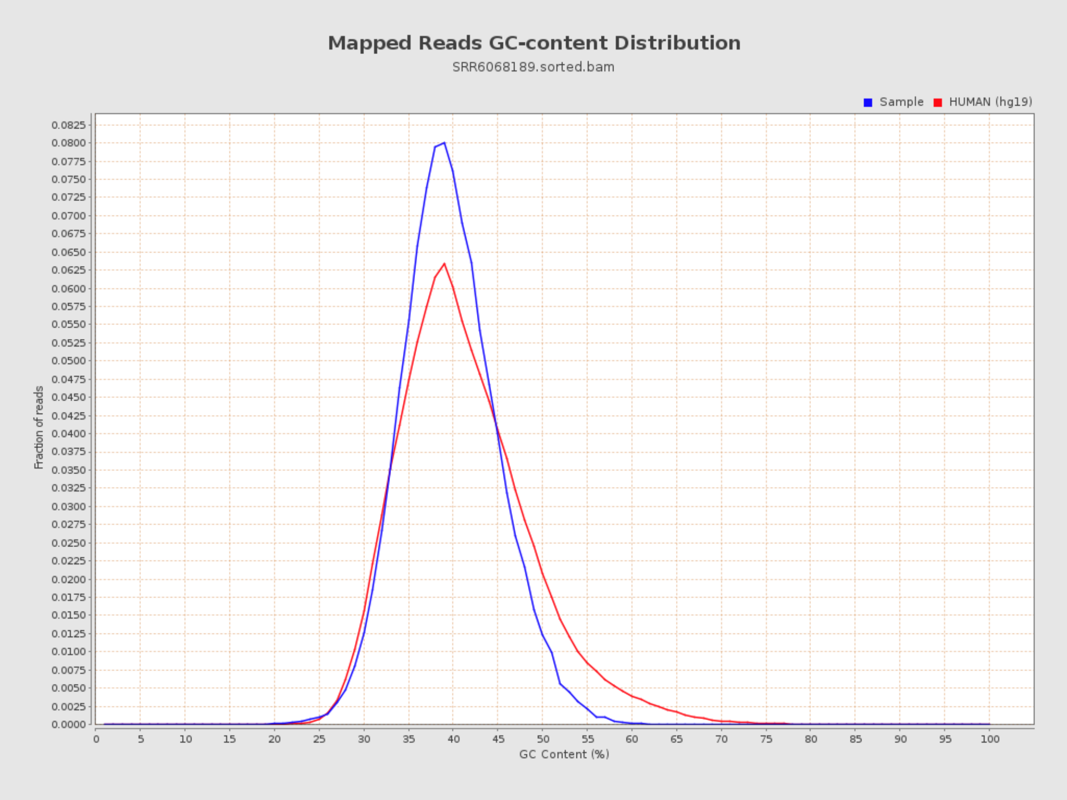
7. Results : Duplication Rate Histogram



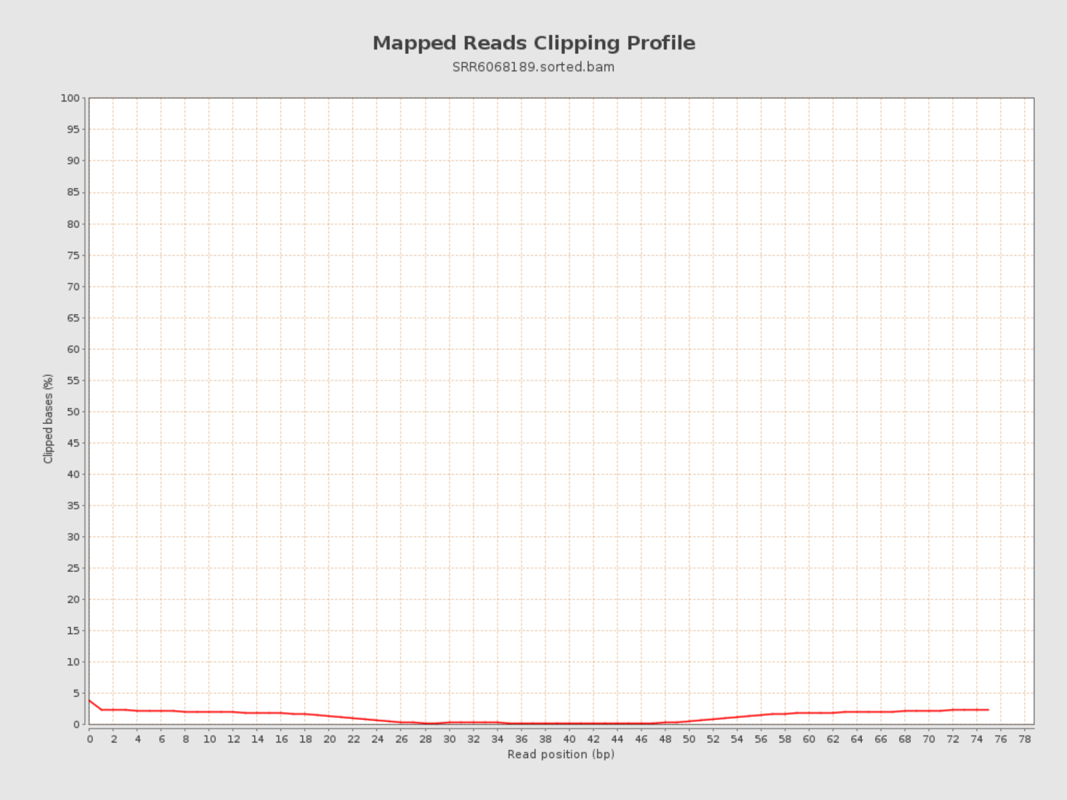
8. Results : Mapped Reads Nucleotide Content



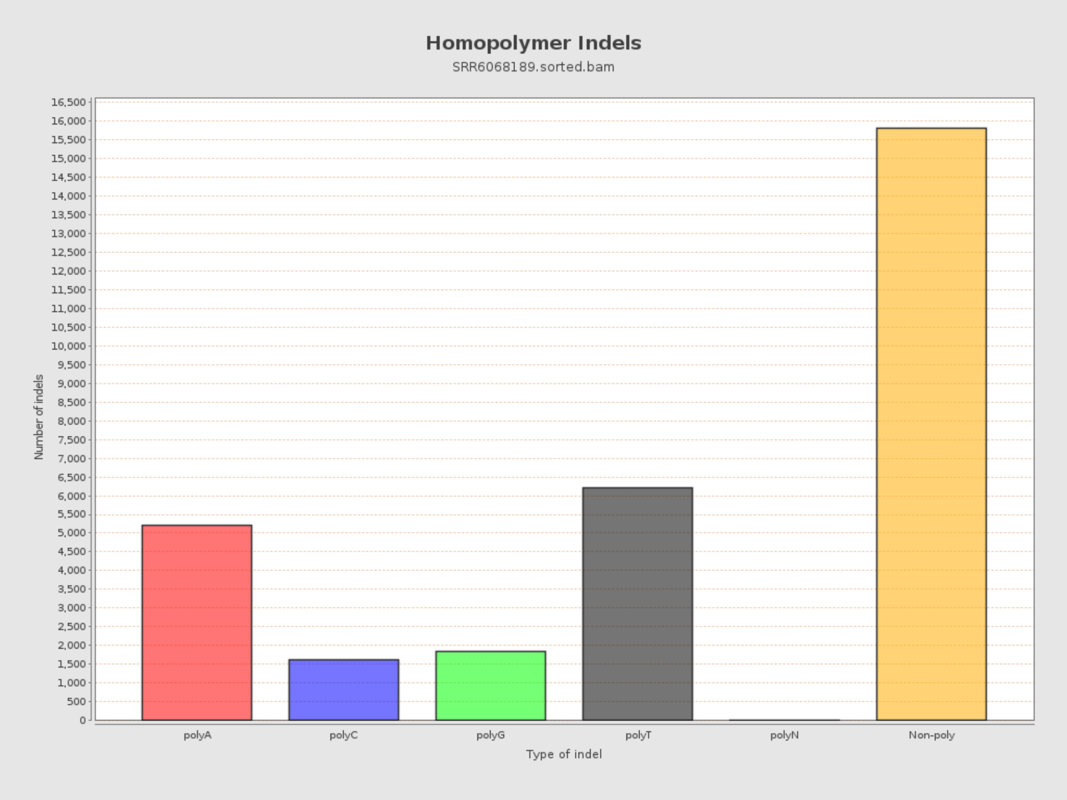
9. Results : Mapped Reads GC-content Distribution



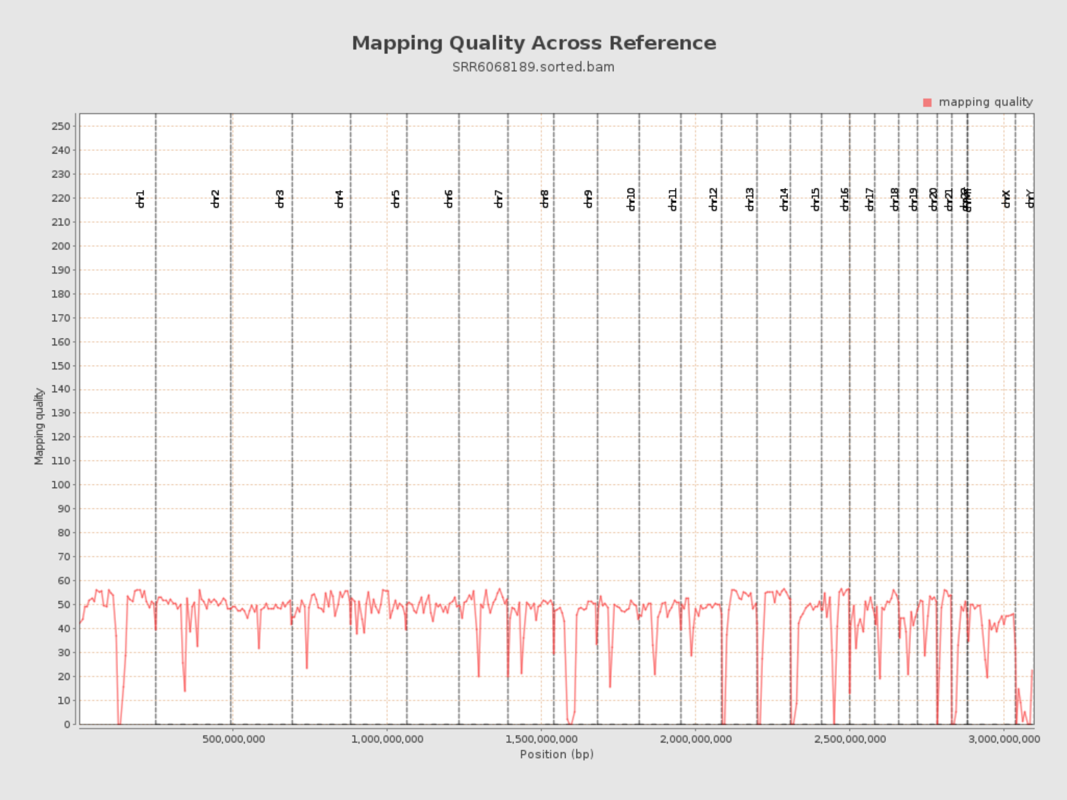
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram