Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 11:35:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008788.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_SRR6008788 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008788.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 11:35:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008788.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,640,357
Mapped reads	1,092,416 / 66.6%
Unmapped reads	547,941 / 33.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,261 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	40,545 / 2.47%
Duplication rate	2.78%
Clipped reads	521,363 / 31.78%

2.2. ACGT Content

Number/percentage of A's	19,715,040 / 27.6%
Number/percentage of C's	13,265,211 / 18.57%
Number/percentage of T's	22,462,935 / 31.45%
Number/percentage of G's	15,882,693 / 22.24%
Number/percentage of N's	97,916 / 0.14%
GC Percentage	40.81%

2.3. Coverage

Mean	0.0231

Standard Deviation	0.2713

2.4. Mapping Quality

Mean Mapping Quality	45.4

2.5. Mismatches and indels

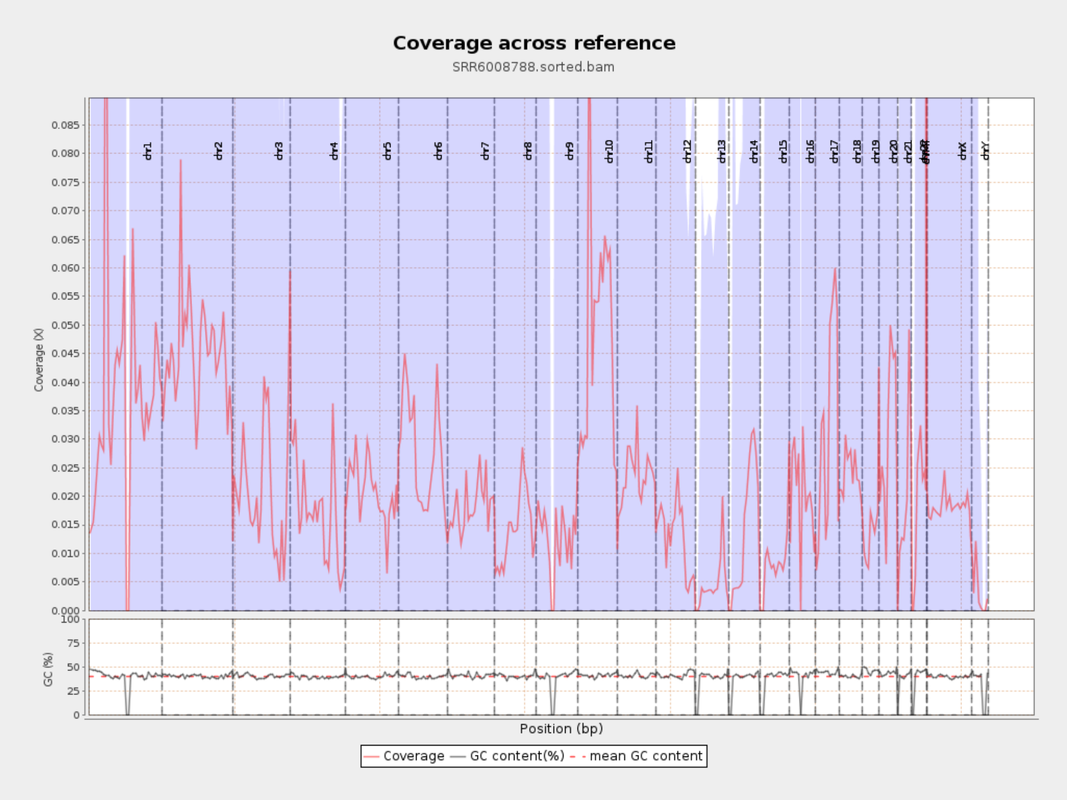
General error rate	0.82%
Mismatches	574,663
Insertions	4,946
Mapped reads with at least one insertion	0.45%
Deletions	19,070
Mapped reads with at least one deletion	1.73%
Homopolymer indels	45.43%

2.6. Chromosome stats

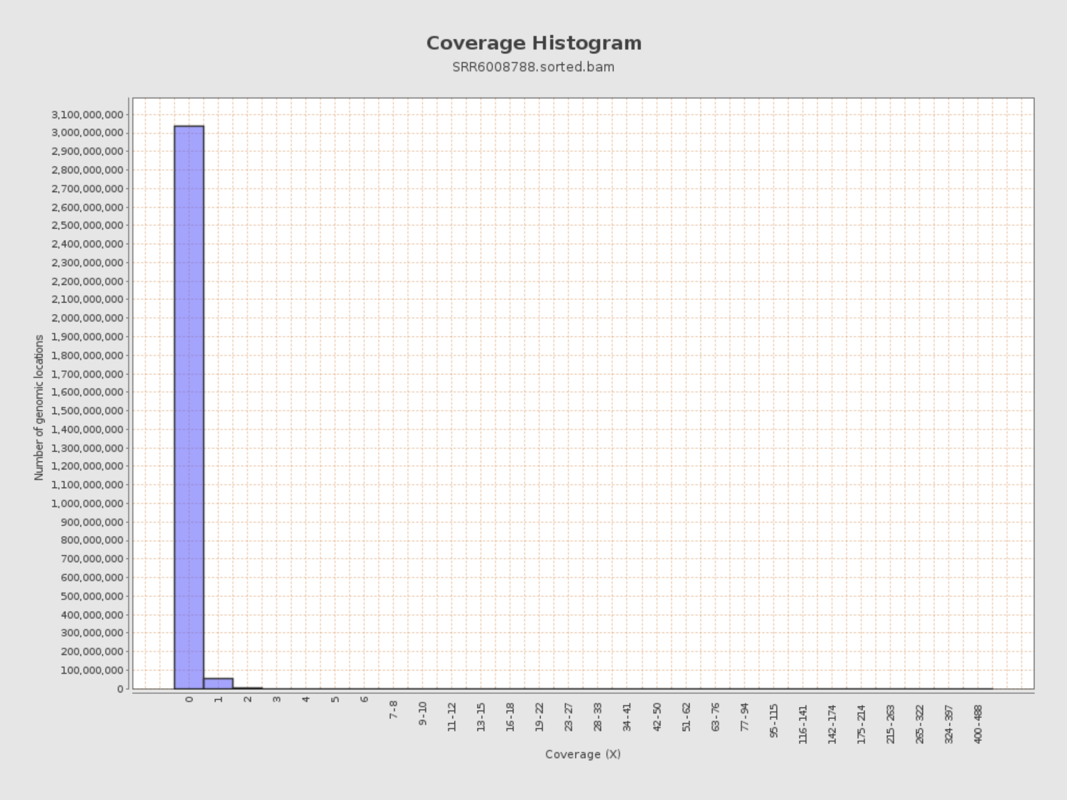
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9314897	0.0374	0.465
chr2	243199373	11046007	0.0454	0.2987
chr3	198022430	4088461	0.0206	0.2058
chr4	191154276	3267889	0.0171	0.1591
chr5	180915260	3777842	0.0209	0.1616
chr6	171115067	4718170	0.0276	0.212
chr7	159138663	2922142	0.0184	0.1826

chr8	146364022	2095049	0.0143	0.1906
chr9	141213431	1741059	0.0123	0.1537
chr10	135534747	6635853	0.049	0.7158
chr11	135006516	3172013	0.0235	0.2354
chr12	133851895	1727015	0.0129	0.1304
chr13	115169878	540988	0.0047	0.0756
chr14	107349540	1539387	0.0143	0.1378
chr15	102531392	832311	0.0081	0.1016
chr16	90354753	1806022	0.02	0.2153
chr17	81195210	2620049	0.0323	0.2491
chr18	78077248	1888310	0.0242	0.2382
chr19	59128983	828424	0.014	0.2959
chr20	63025520	1972742	0.0313	0.1997
chr21	48129895	952180	0.0198	0.18
chr22	51304566	904580	0.0176	0.1483
chrMT	16571	18925	1.1421	1.3047
chrX	155270560	2859134	0.0184	0.1656
chrY	59373566	189002	0.0032	0.127

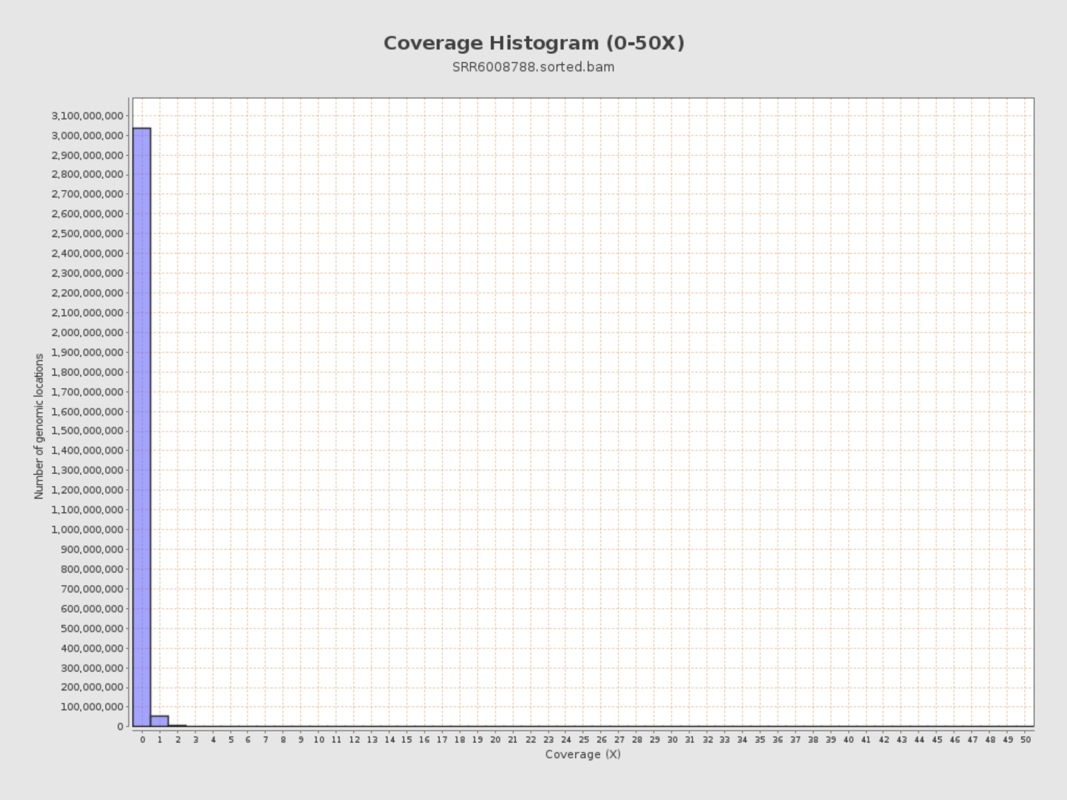
3. Results : Coverage across reference



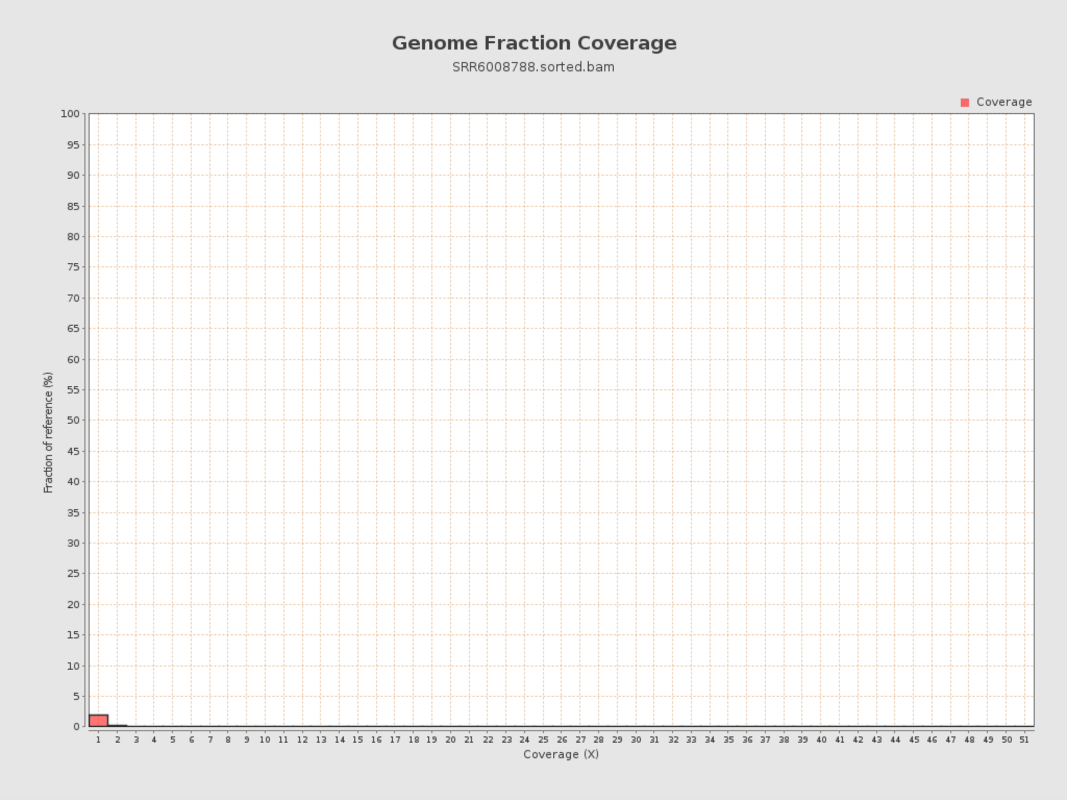
4. Results : Coverage Histogram



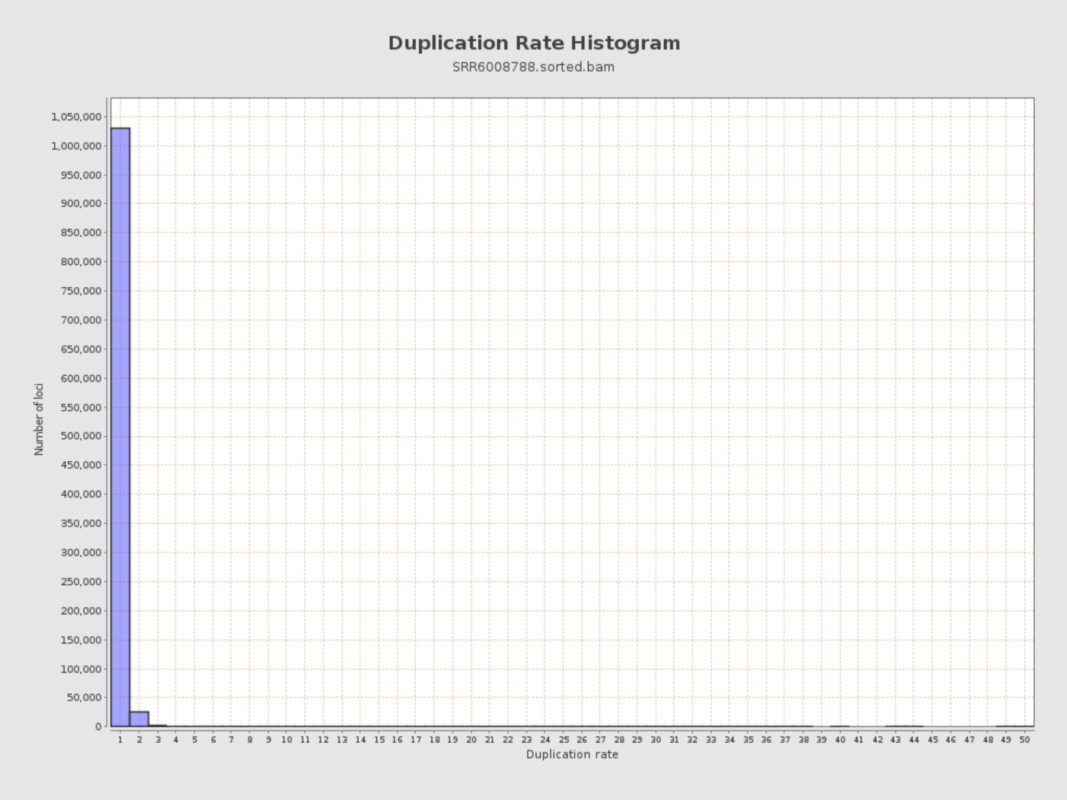
5. Results : Coverage Histogram (0-50X)



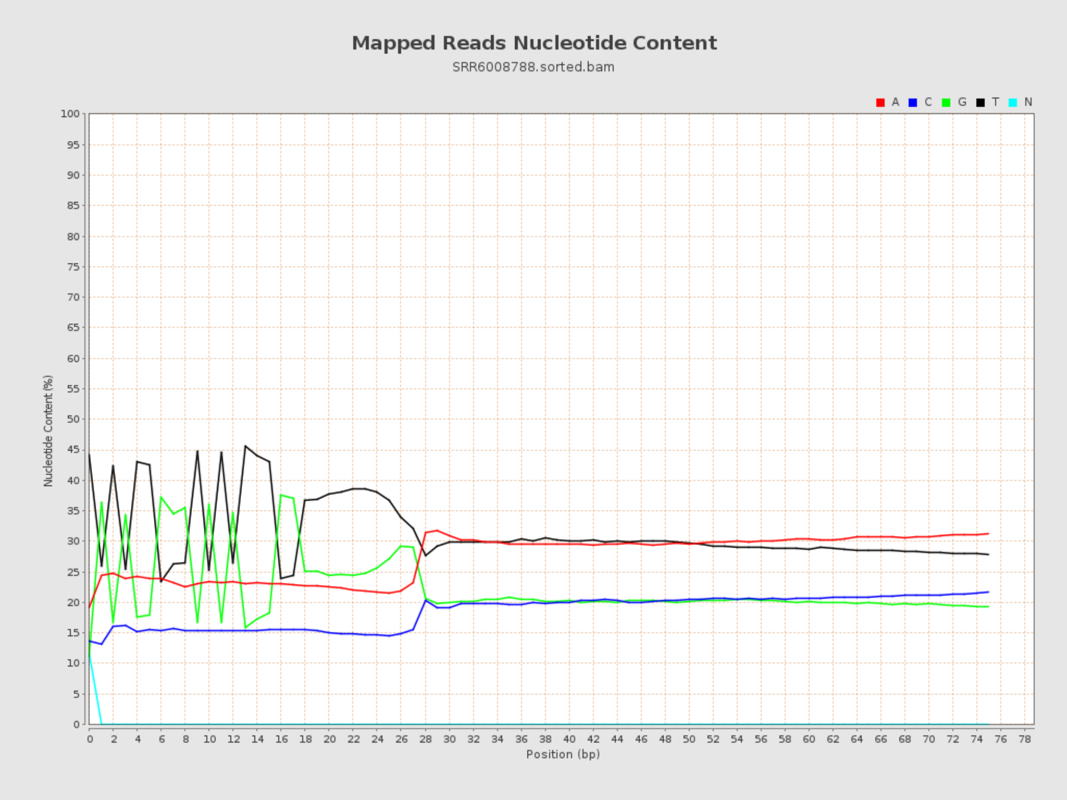
6. Results : Genome Fraction Coverage



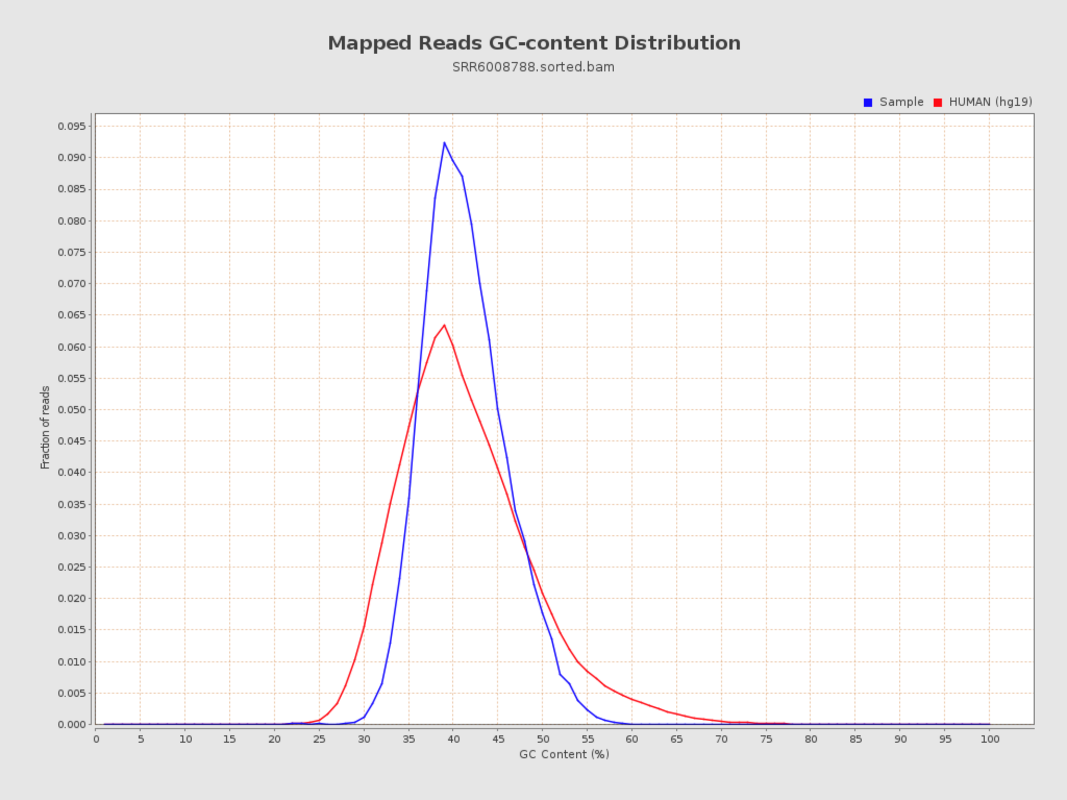
7. Results : Duplication Rate Histogram



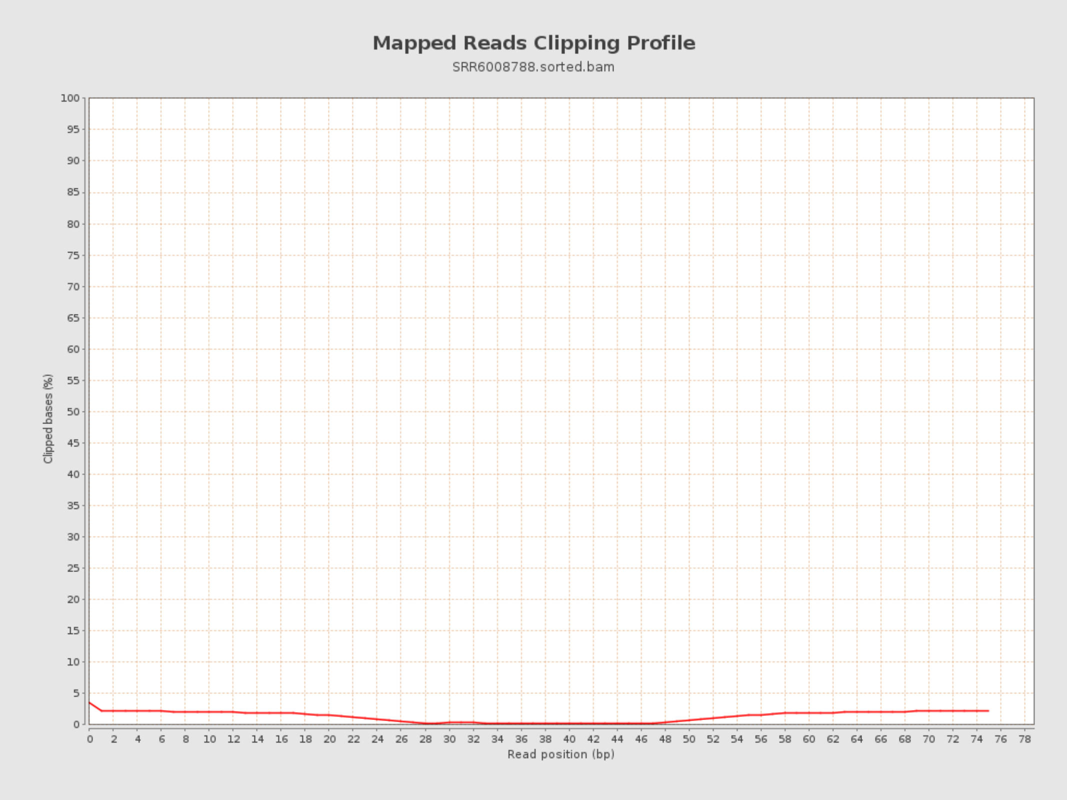
8. Results : Mapped Reads Nucleotide Content



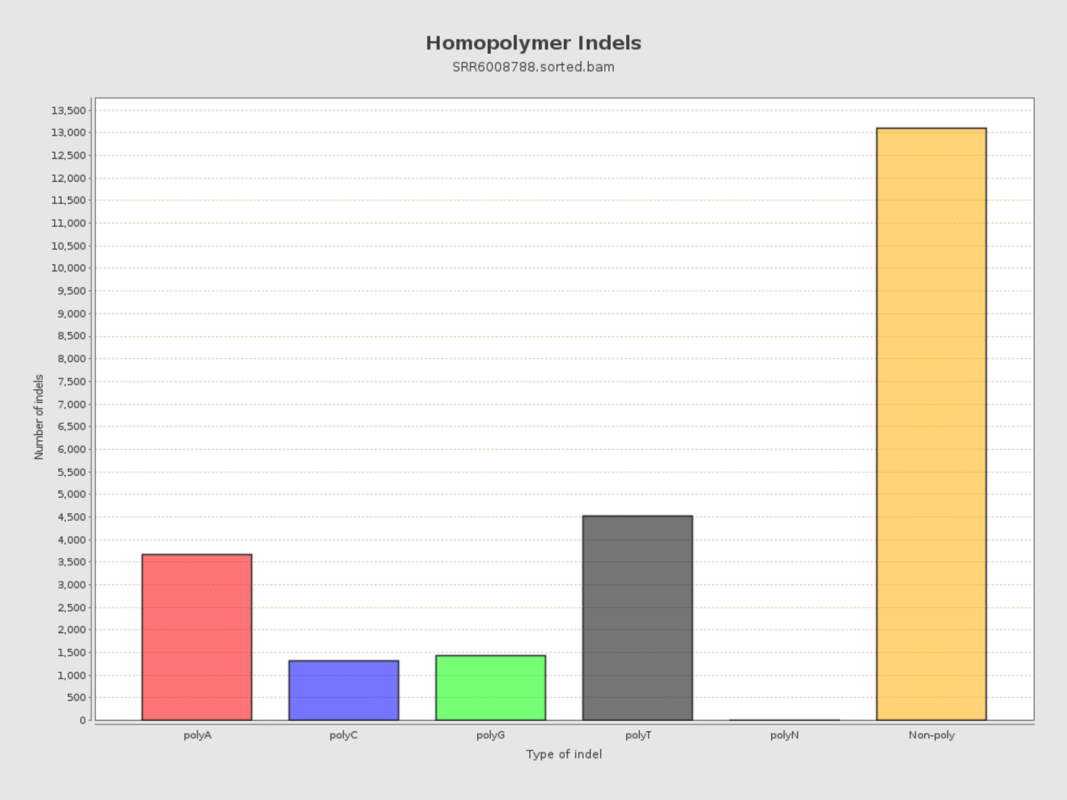
9. Results : Mapped Reads GC-content Distribution



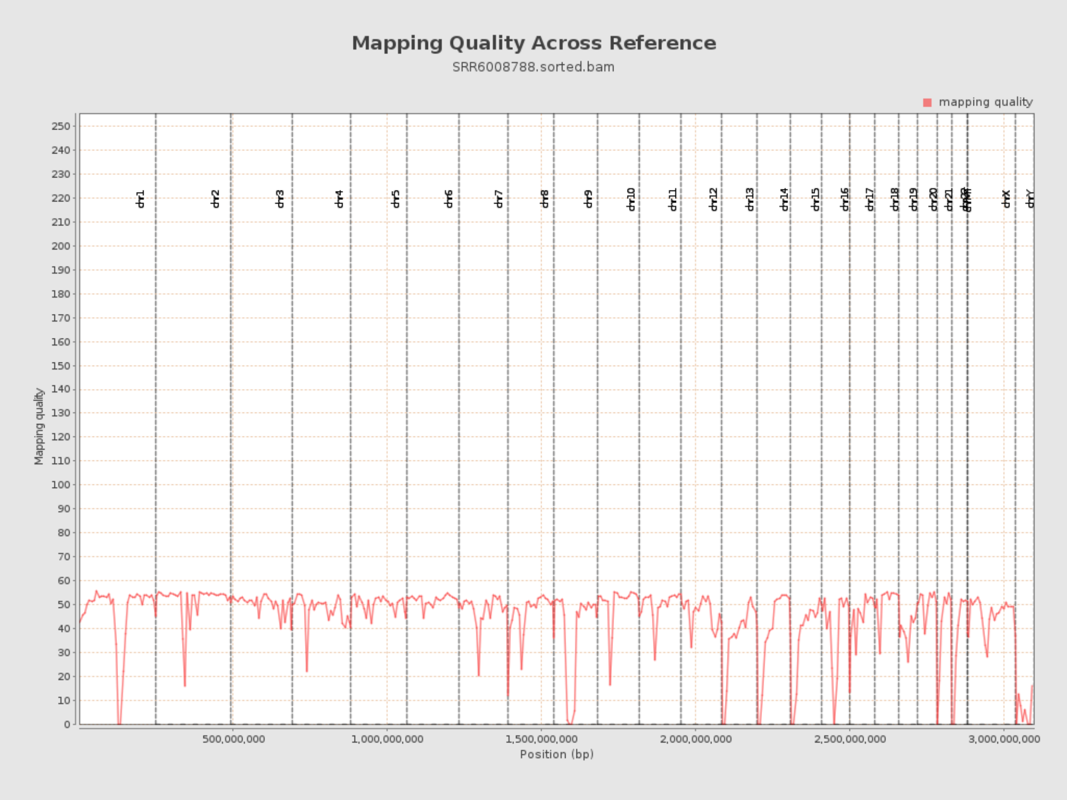
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram