Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 11:21:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR090213.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_SRR090213 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR090213.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 11:21:36 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR090213.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	29,073,567
Mapped reads	25,315,407 / 87.07%
Unmapped reads	3,758,160 / 12.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,364 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	4,637,146 / 15.95%
Duplication rate	12.07%
Clipped reads	2,265,643 / 7.79%

2.2. ACGT Content

Number/percentage of A's	355,529,697 / 29.79%
Number/percentage of C's	239,273,262 / 20.05%
Number/percentage of T's	349,761,264 / 29.31%
Number/percentage of G's	248,770,297 / 20.85%
Number/percentage of N's	4,108 / 0%
GC Percentage	40.9%

2.3. Coverage

Mean	0.3856

Standard Deviation	1.8799

2.4. Mapping Quality

Mean Mapping Quality	44.85

2.5. Mismatches and indels

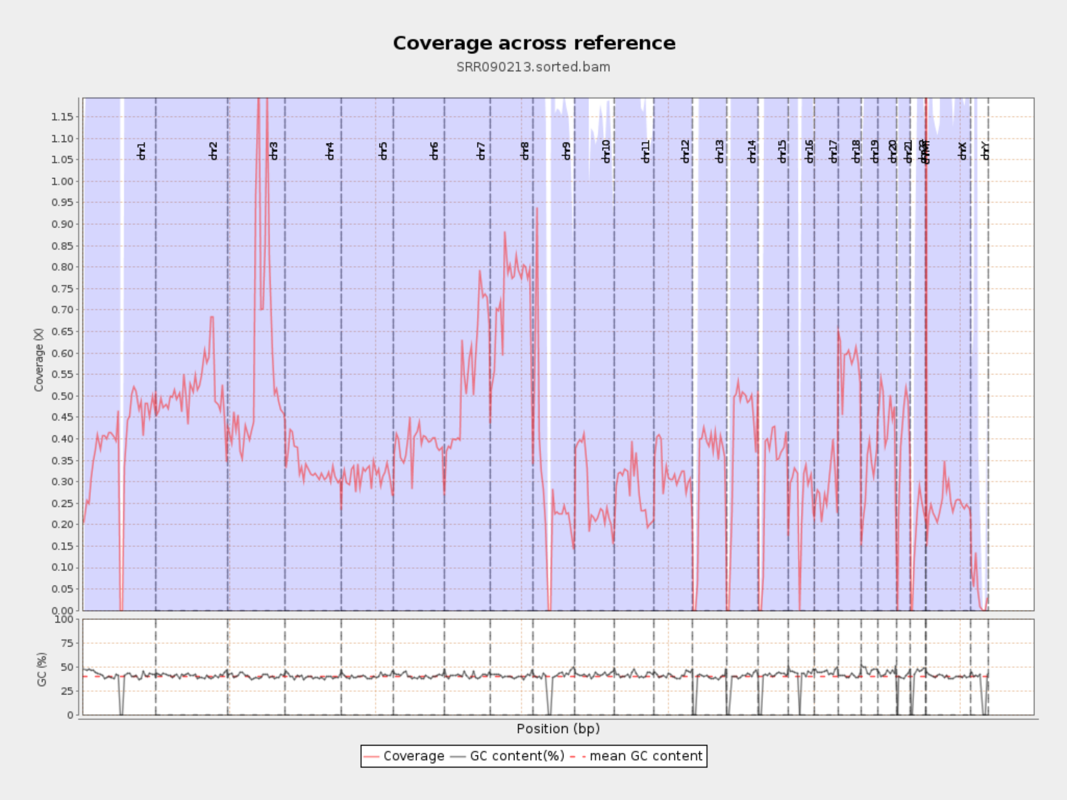
General error rate	0.37%
Mismatches	4,319,040
Insertions	43,468
Mapped reads with at least one insertion	0.17%
Deletions	149,476
Mapped reads with at least one deletion	0.59%
Homopolymer indels	48.28%

2.6. Chromosome stats

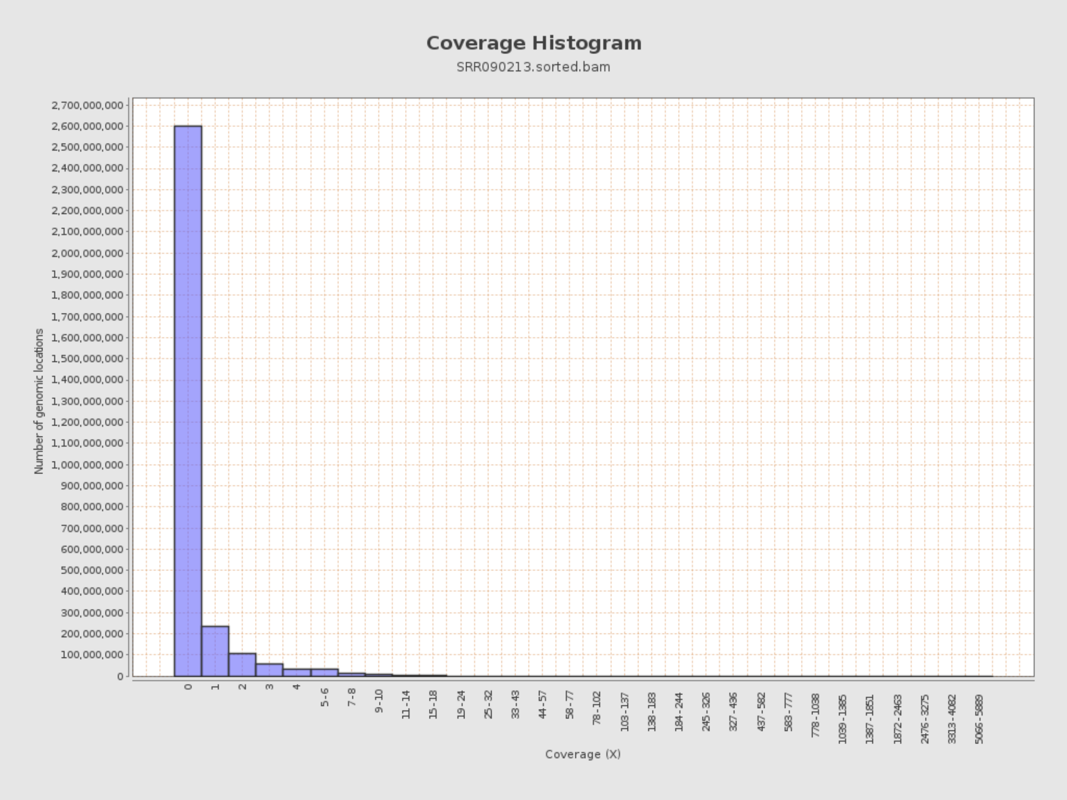
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	96402139	0.3868	2.7917
chr2	243199373	124865050	0.5134	2.0622
chr3	198022430	114367111	0.5775	1.61
chr4	191154276	63635193	0.3329	1.146
chr5	180915260	56722533	0.3135	1.115
chr6	171115067	66392018	0.388	1.3957
chr7	159138663	86451891	0.5432	3.1643

chr8	146364022	106928667	0.7306	3.6785
chr9	141213431	39099238	0.2769	1.5654
chr10	135534747	36581764	0.2699	1.3911
chr11	135006516	37910973	0.2808	1.3839
chr12	133851895	43343906	0.3238	1.1712
chr13	115169878	37401137	0.3247	1.1309
chr14	107349540	43429296	0.4046	1.331
chr15	102531392	31811706	0.3103	1.1199
chr16	90354753	23861003	0.2641	1.0509
chr17	81195210	23249401	0.2863	1.1561
chr18	78077248	45483279	0.5825	2.6554
chr19	59128983	18875635	0.3192	2.0571
chr20	63025520	28659876	0.4547	1.4154
chr21	48129895	17881805	0.3715	1.3137
chr22	51304566	9223533	0.1798	0.8221
chrMT	16571	138606	8.3644	6.8153
chrX	155270560	38239040	0.2463	1.1051
chrY	59373566	2610444	0.044	0.8897

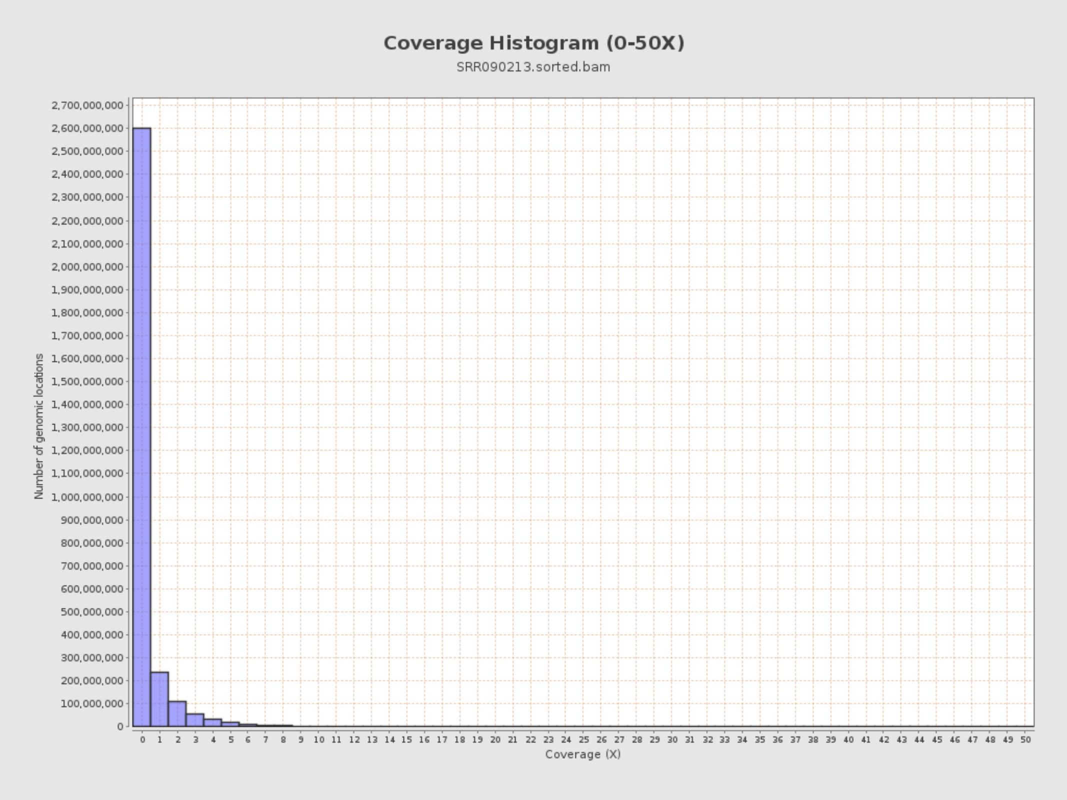
3. Results : Coverage across reference



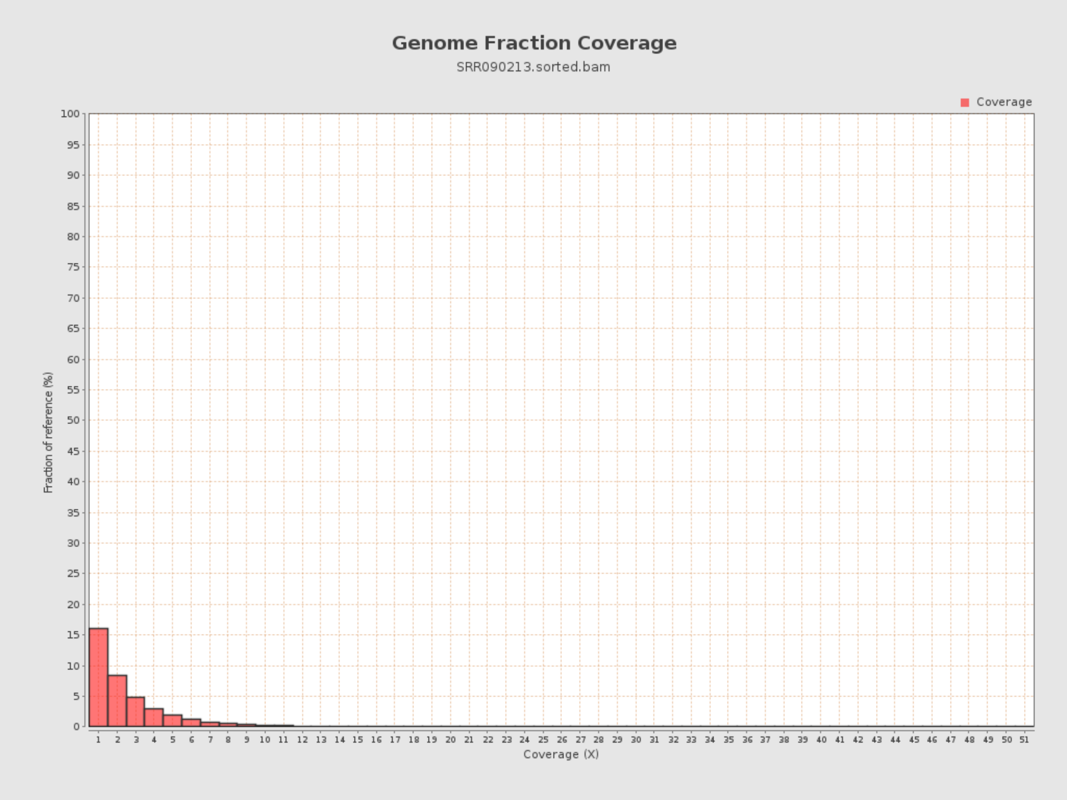
4. Results : Coverage Histogram



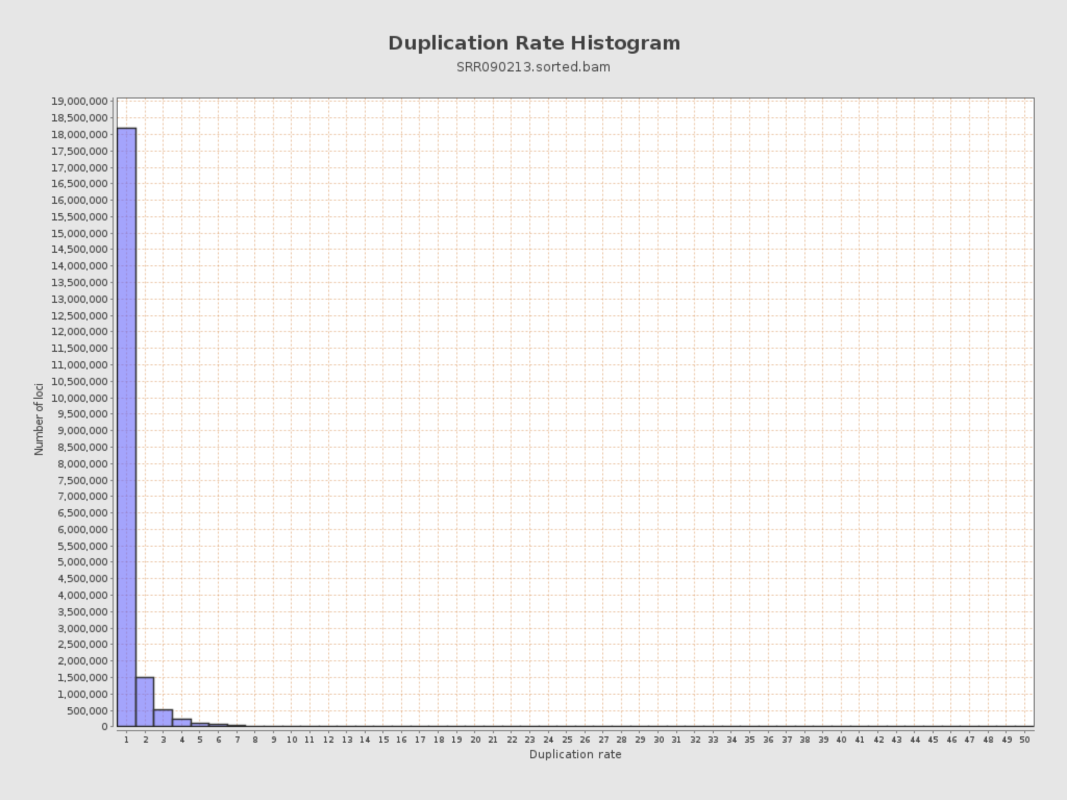
5. Results : Coverage Histogram (0-50X)



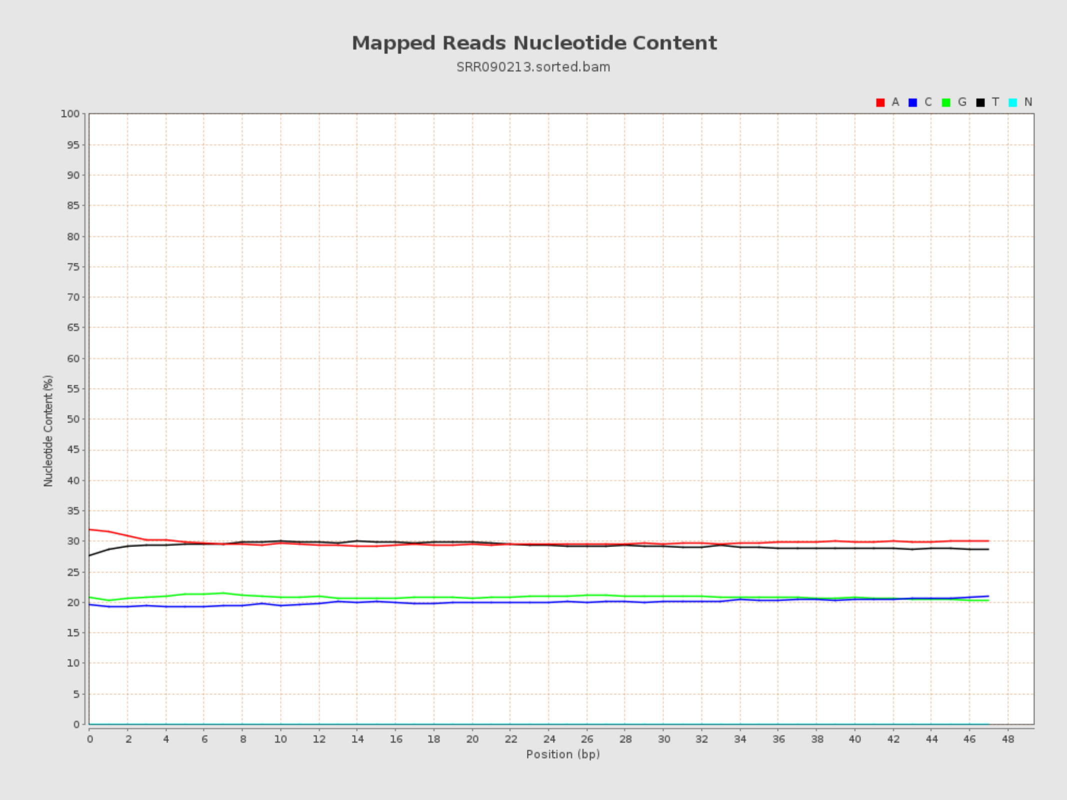
6. Results : Genome Fraction Coverage



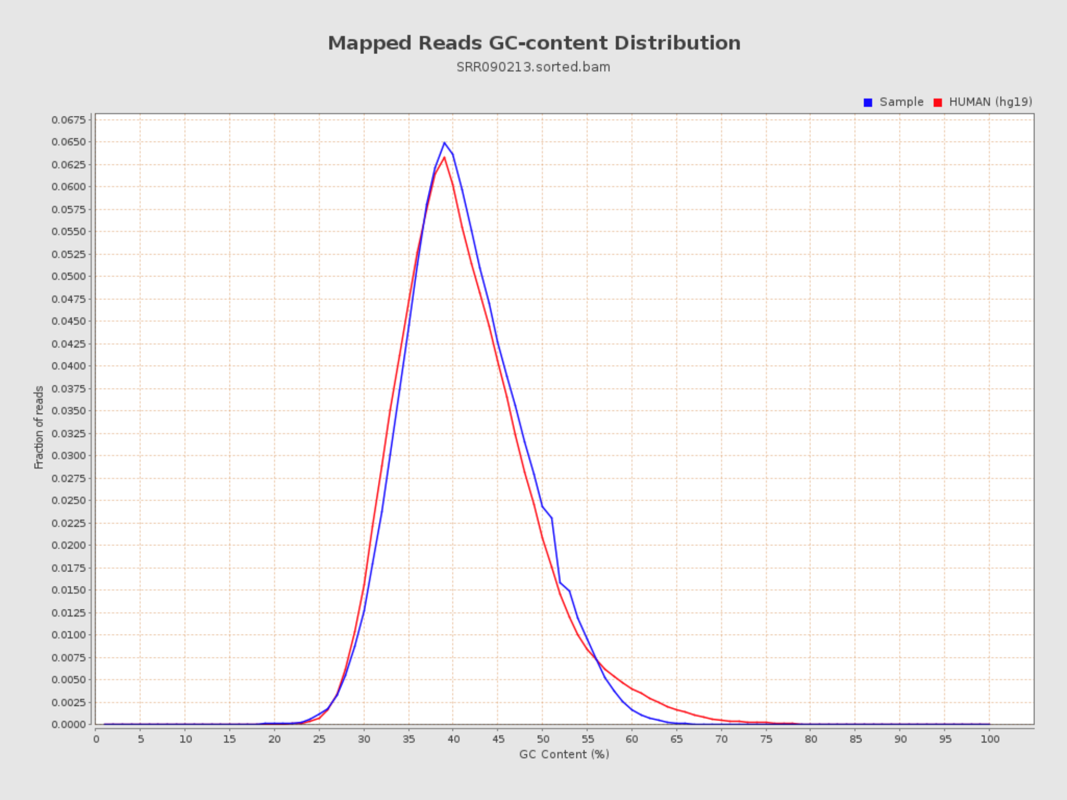
7. Results : Duplication Rate Histogram



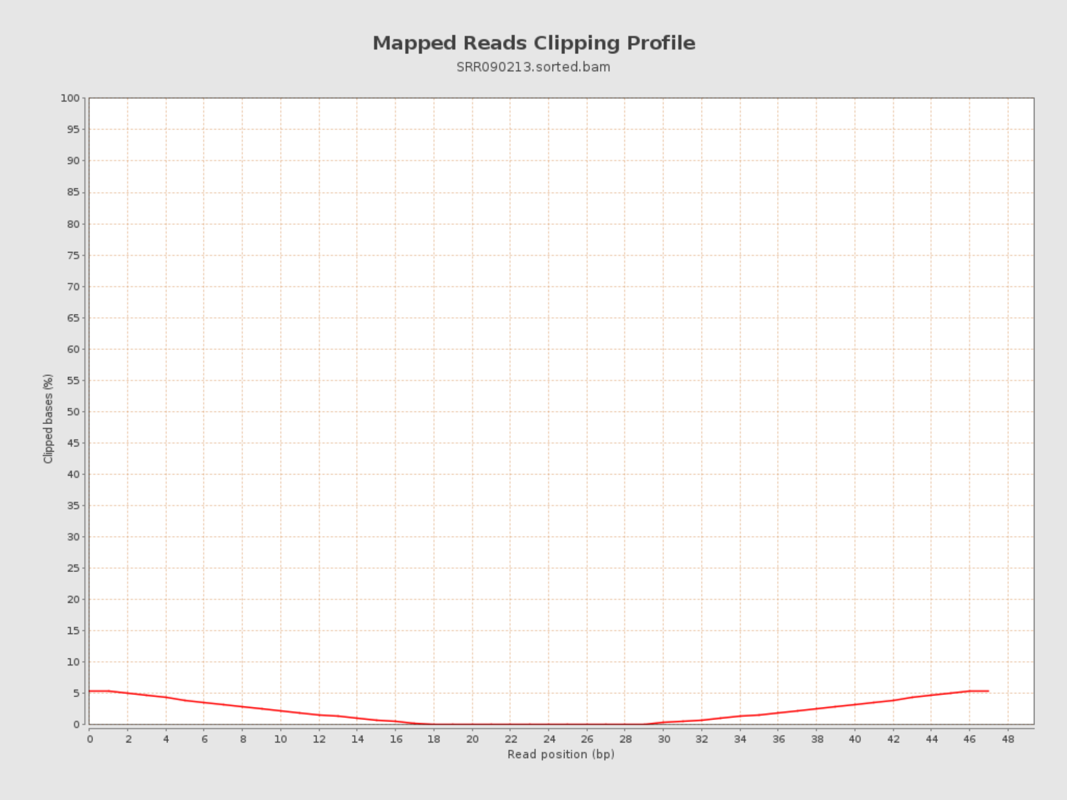
8. Results : Mapped Reads Nucleotide Content



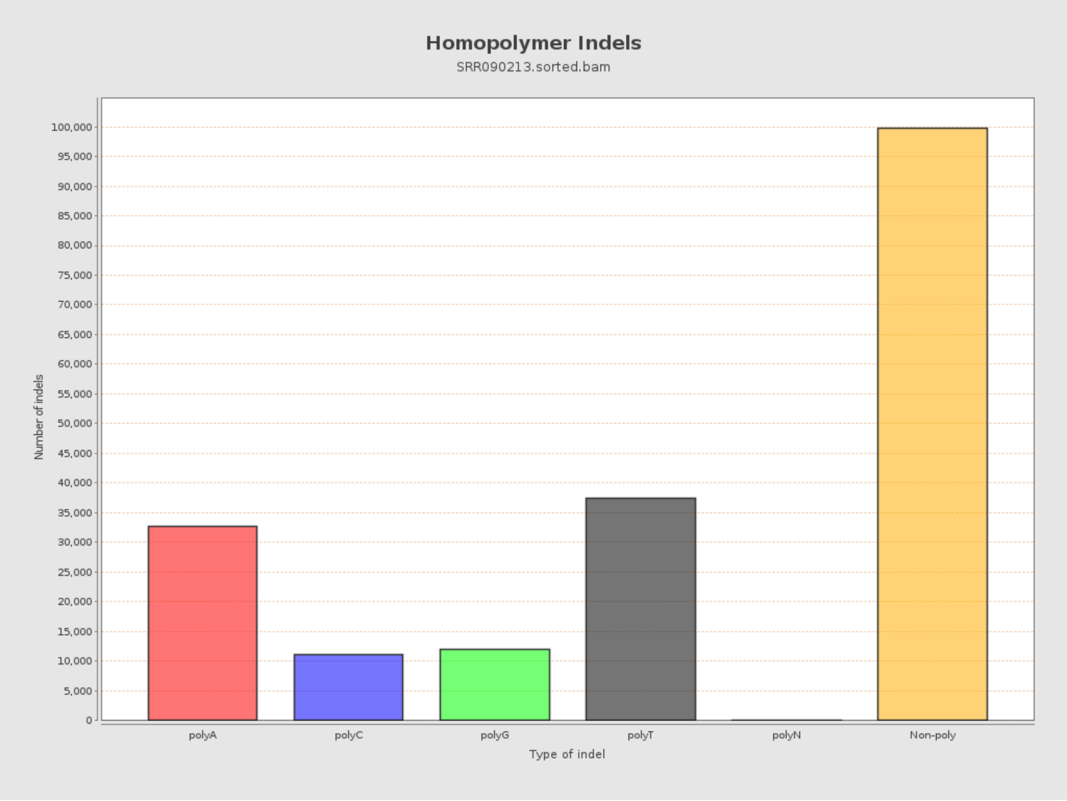
9. Results : Mapped Reads GC-content Distribution



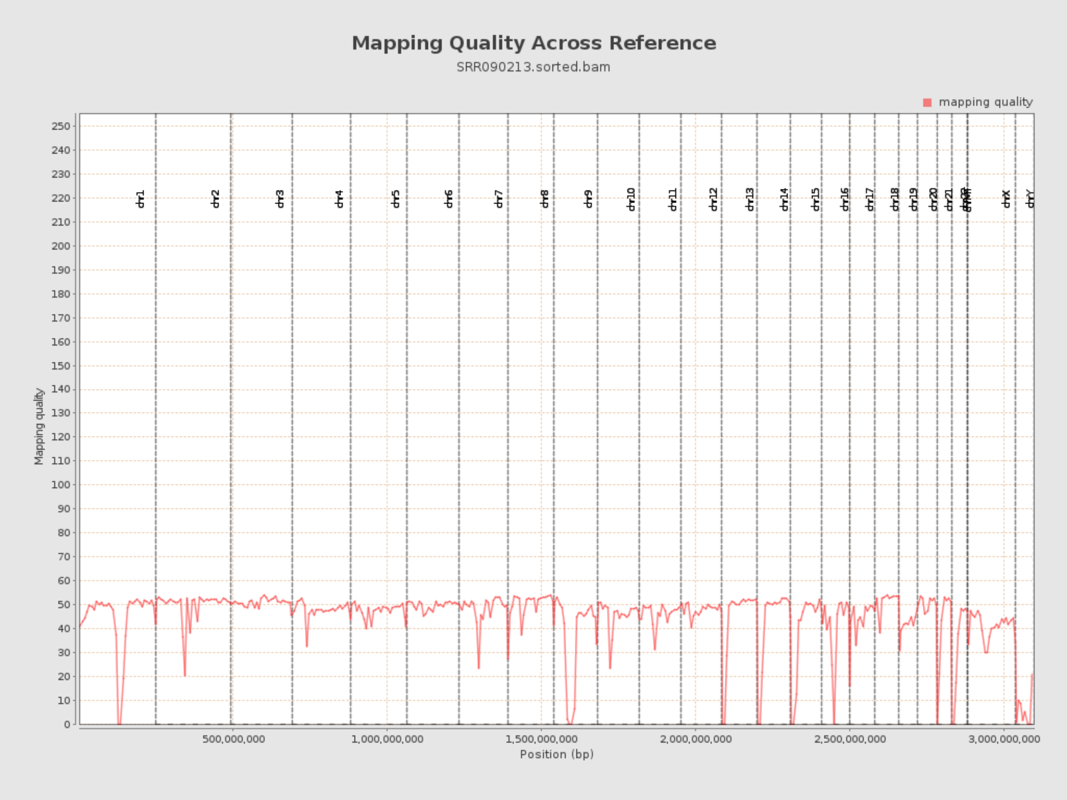
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram