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1. Summary mapping report

1.1 Summary statistics

	Count	Average length	Total bases
Reads	167,281,082	97.94	16,384,061,821
Matched	137,598,424	98.2	13,511,755,617
Not matched	29,682,658	96.77	2,872,306,204
Contigs	174,178	1,653	288,085,806
Reads in pairs	27,496,752	326.53	
Broken paired reads	110,101,672	98.24	

1.2 General algorithm parameters

Parameter	Value
Conflict resolution	Unknown nucleotide (N)
Non specific matches	ignore

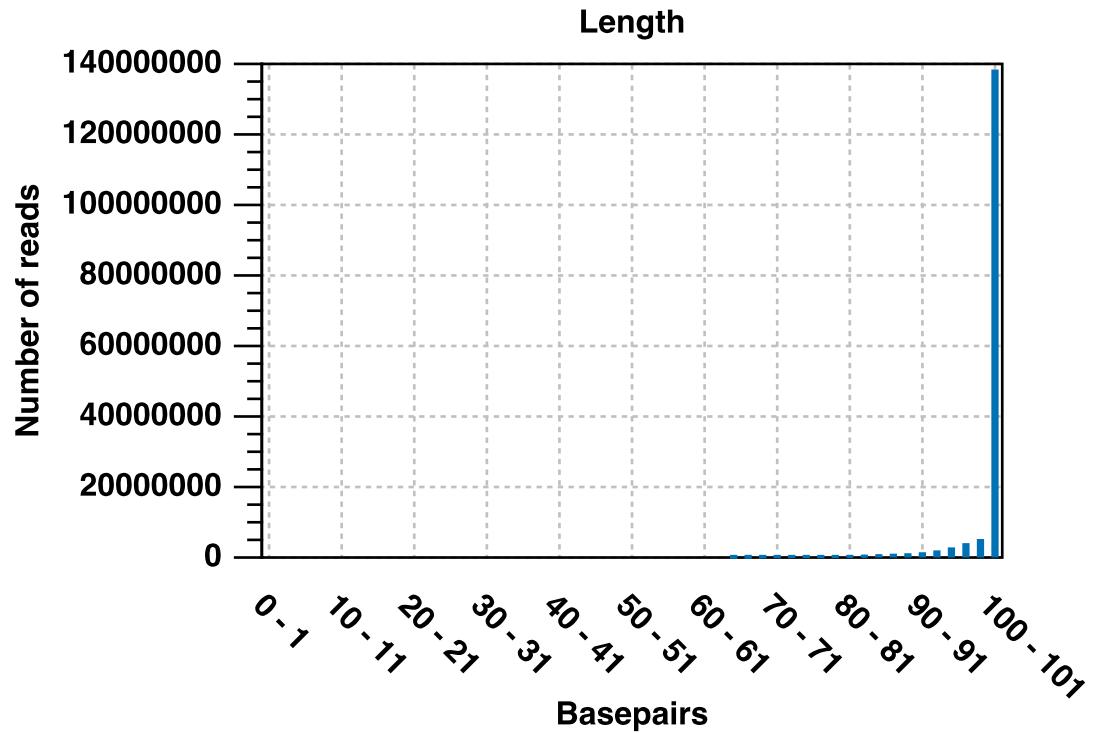
1.3 Reads parameters

Reads	Length	Type	Parameters
Prep7_1-3_1_sequence (paired)	Long	Paired	Similarity=0.9

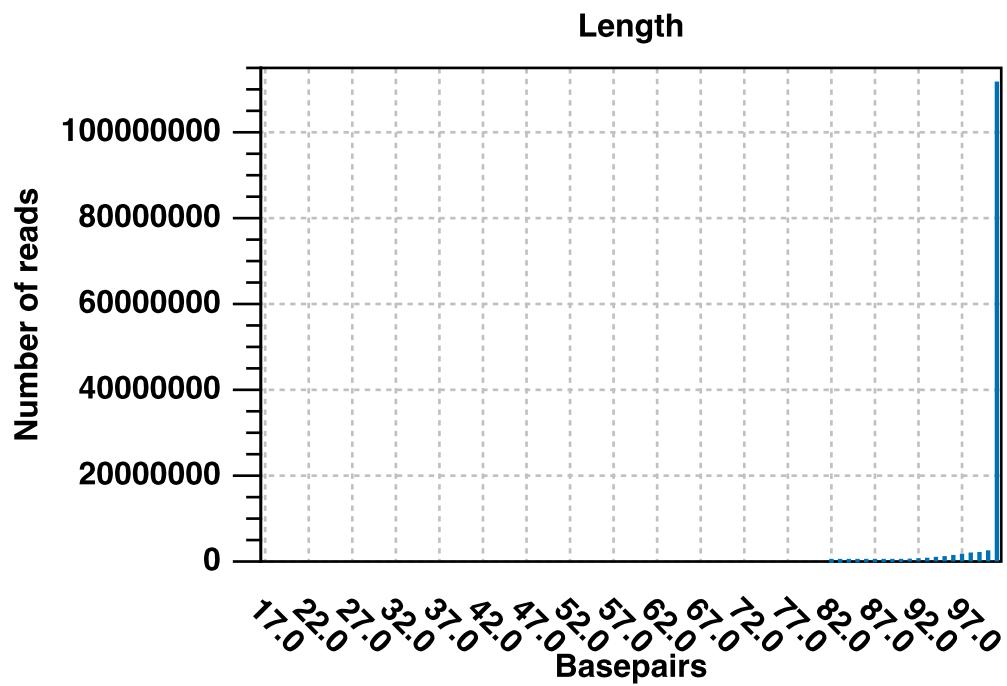
1.4 Quality measurement

Length	
N75	1,151
N50	2,299
N25	4,488

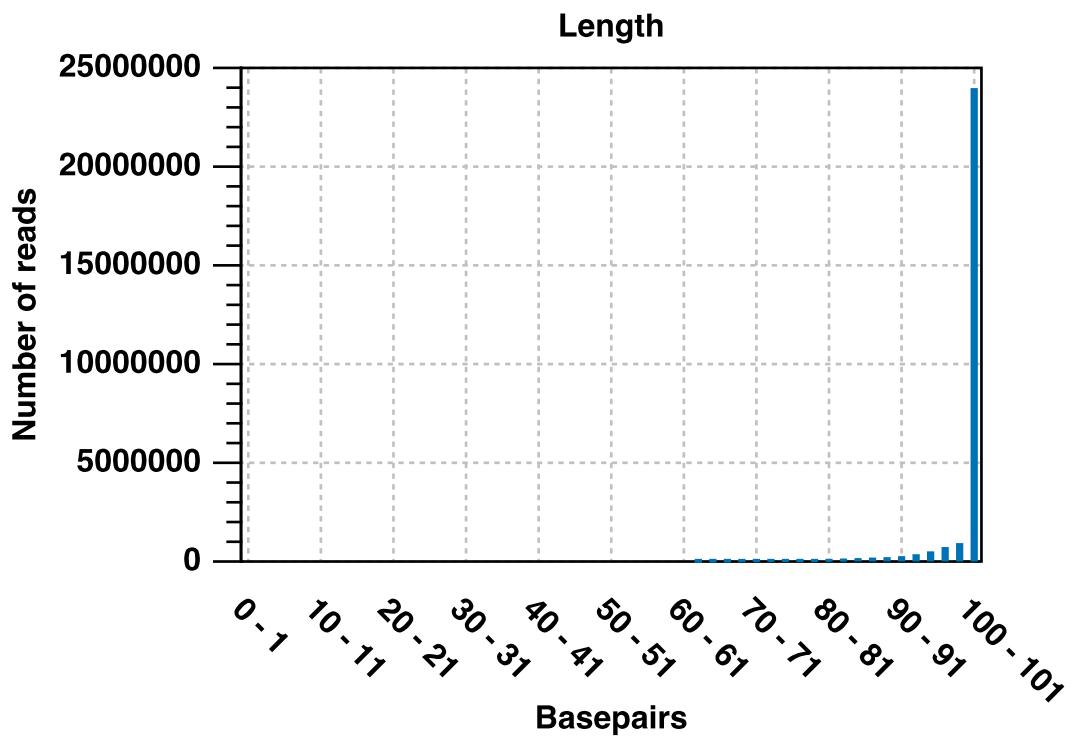
1.5 Distribution of read length



1.6 Distribution of matched read length



1.7 Distribution of non-matched read length



1.8 Paired reads distance distribution

