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1. Summary mapping report

1.1 Summary statistics

	Count	Average length	Total bases
Reads	14,175,854	75	1,063,189,050
Matched	3,188,314	75	239,123,550
Not matched	10,987,540	75	824,065,500
Contigs	5,374	1,175	6,318,372
Reads in pairs	2,645,710	223.3	
Broken paired reads	542,604	75	

1.2 General algorithm parameters

Parameter	Value
Conflict resolution	Vote (A, C, G, T)
Non specific matches	ignore

1.3 Reads parameters

Reads	Length	Type	Parameters
MMLabsCulture4_CGAGGC TG- AAGGAGTA_L001_R1_001 (paired)	Long	Paired	Length=0.9,Similarity=0.98

1.4 Quality measurement

Length	
N75	608
N50	988
N25	169,402

1.5 Distribution of read length

Length	Count
75	14,175,854

1.6 Distribution of matched read length

Length	Count
75	3,188,314

1.7 Distribution of non-matched read length

Length	Count
75	10,987,540

1.8 Paired reads distance distribution

