History for:

solid0078_20110412_SB_METH trimmed report

RNA-Seq Analysis
3 Oct 2013 16:37:45

Version:	CLC Genomics Workbench 6.5
Modified by:	sr320
Use annotations for gene and transcript identification	Yes
References	oyster.v9
Additional upstream bases	0
Additional downstream bases	0
Maximum number of mismatches allowed (applies to short reads)	2
Minimum length fraction (applies to long reads)	0.9
Minimum similarity fraction (applies to long reads)	0.8
Unspecific match limit	10
Use colorspace encoding	No
Use strand specific assembly	No
Strand	Forward
Minimum paired distance	180
Maximum paired distance	250
Count paired reads as two	No
Organism type	EUKARYOTE
Exon discovery	Yes
Minimum exon coverage fraction	0.2
Minimum number of reads	10
Minimum length of putative exons	50
Create list of unmapped reads	Yes
Create report	Yes
Create fusion gene table	No
Minimum read count fusion gene table	5
Expression level	Genes
Expression value	RPKM
Calculate RPKM for genes without transcripts	No
Expression value	Read Per Kilobase of exon Model value
Comments:	Found: 28027 genes. Total number of reads : 102788767 (single reads: 102788767, paired reads: 0) Total number of mapped reads : 27125079 (single reads: 27125079, paired reads: 0) Total number of unmapped reads : 75663688 (single reads: 75663688, paired reads: 0)
Originates from:	

	oyster.v9

Trim Sequences
3 Oct 2013 15:55:41

Version:	CLC Genomics Workbench 6.5
Modified by:	sr320
Ambiguous trim	Yes
Ambiguous limit	2
Quality trim	Yes
Quality limit	0.05
Create report	No
Save discarded sequences	No
Remove 5' terminal nucleotides	No
Discard short reads	No
Remove 3' terminal nucleotides	No
Discard long reads	No
Save broken pairs	No
Comments:	Processed a total of 103,083,505 sequences. 294,738 sequences have been completely removed during trimming. 2,319,512,439 nucleotides have been trimmed, altogether.

Originates from:

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