



Streamlining NGS Data Management & Analysis

Reads to Discovery

MeDIP-Seq

RNA-Seq

DNA-Seq

ChIP-Seq

Small
RNA-Seq

Methyl-Seq

MeDIP-Seq

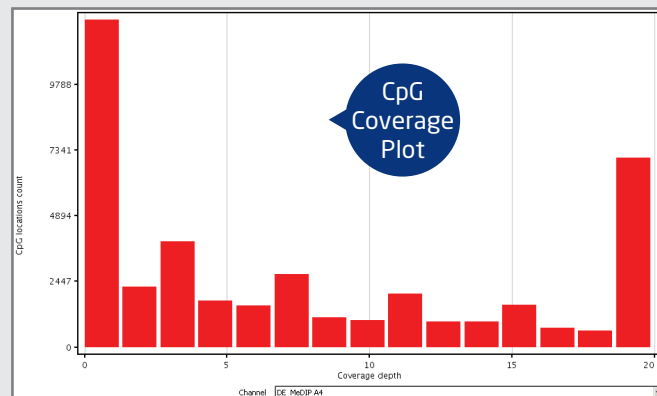
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Analyze | Visualize | Annotate | Discover

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New Generation Healthcare

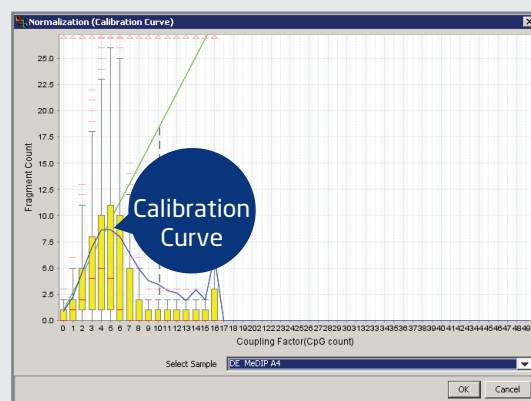
QC and CpG coverage analysis

- Quality metrics for pre- and post-alignment, target enrichment and library complexity.
- Compute CpG sites coverage for your samples.



Normalization (Calibration curve)

- Estimate the linear dependency of methylation signals and CpG counts by calculating the slope and the intercept for every sample.



Methylation Detection

- Identifies methylated regions across the genome or within regions of interest.
- Computes for every region, the reads per million (RPM), relative methylation score (RMS) and absolute methylation score (AMS).

RegionListInspector

Parameters

Name

Methylation report for whole genome 1000 bp regions

Organism

Homo sapiens

Notes

NESC_MEIP_C1 (0.1077867, 0.1085382)
DE_MEIP_A1 (1.4833077, 0.781151)
DE_MEIP_A2 (1.315605, 0.75719994)
DE_MEIP_A3 (1.624247, 0.31140063)
NESC_MEIP_C3

Creation date

Fri May 29 11:13:19 IST 2015

Last modified date

Fri May 29 11:13:19 IST 2015

Owner

gisner

Number of Regions

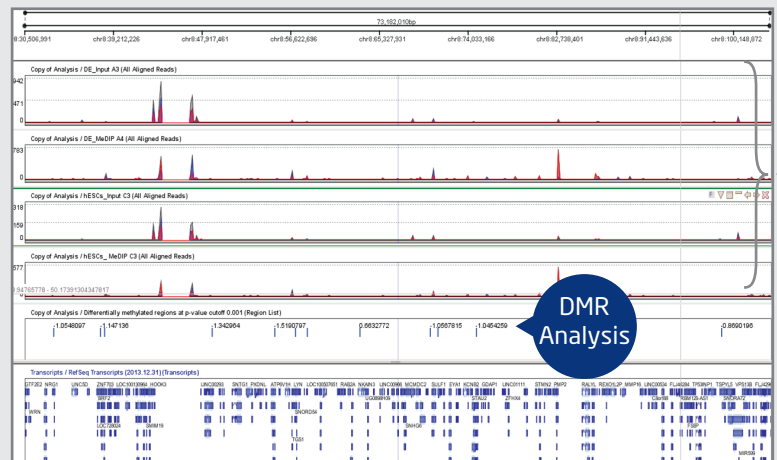
5,945,927

Regions | Histogram | Summary Statistics

Chromos.	Start	End	RPM dhes.	RMS dhes.	AMS dhes.	RPM dhes.	RMS dhes.	AMS dhes.	RPM dhes.	RMS dhes.	AMS dhes.	RPM dhes.	RMS dhes.	AMS dhes.	AN
chr1	9001	10000	0.216000	2.610373	0.163578	2.420690	0.114140	1.288409	0.189200	3.382971	0.189200	3.382971	0.189200	3.382971	5
chr1	10001	11000	3.210552	26.281551	2.986540	2.256018	22.27793	2.531583	2.777396	21.88340	2.486750	4.575810	47.27667	5	
chr1	11001	12000	0.314182	1.107453	0.246101	0.255815	1.322877	0.251750	0.101457	0.374934	0.083318	0.058695	2.358232	0	
chr1	12001	13000	0.147273	1.022907	0.464958	0.115866	0.914856	0.415844	0.101457	0.743495	0.337952	0.343362	3.252307	1	
chr1	13001	14000	0.157091	0.687792	0.458528	0.123500	0.720710	0.480473	0.000000	0.000000	0.000000	0.212444	0.025282	0	
chr1	14001	15000	0.382910	1.319577	0.581425	0.327157	1.261559	0.479510	0.638327	0.277511	0.406429	1.259074	0		
chr1	15001	16000	0.579274	2.021381	0.748660	0.477104	1.773232	0.149286	0.552913	0.651688	2.026542	0			
chr1	16001	17000	0.490910	3.170025	1.509536	0.298894	1.563788	0.533970	0.254271	0.212444	1.048126	0			
chr1	17001	18000	0.942547	3.880712	1.621130	0.736103	3.175900	0.766078	0.319198	0.953066	3.449862	1			
chr1	18001	19000	0.019636	0.079005	0.046474	0.088605	0.651100	0.259870	0.152865	0.056059	0.628664	0			
chr1	20001	21000	0.147273	0.814968	0.542312	0.122684	0.653944	0.157869	1.049112	0.133141	0.800468	0			
chr1	21001	22000	0.589022	2.405388	0.925148	0.565708	2.086433	1.997410	0.768235	0.728769	2.604138	1			
chr1	30001	31000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0
chr1	33001	34000	0.000000	0.000000	0.000000	0.047710	0.363118	1.407739	0.612682	0.143156	0.357891	0.035037	0.464440	1	
chr1	34001	35000	0.117818	0.938750	0.853409	0.054526	0.505681	0.459710	0.000000	0.000000	0.168178	1.781511	1		

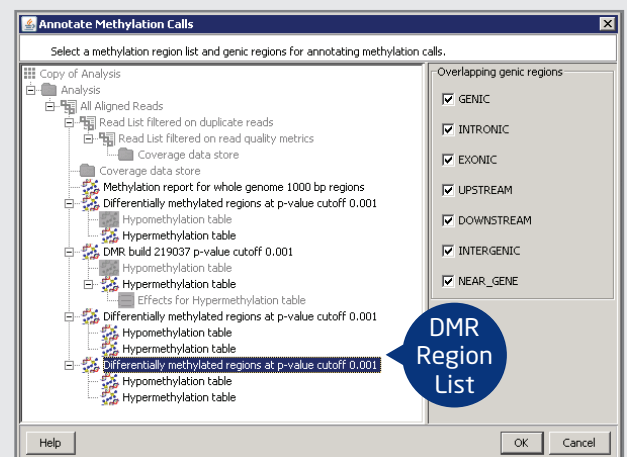
Differential methylation analysis (DMR)

- Identifies DMRs based on selected RMS ratio and p-value thresholds.
- Merges consecutive hypo and hyper-methylated regions if the new region still satisfies the specified threshold.
- Filters DMRs based on RPM, RMS or AMS and p-value thresholds.
- Creates separate lists for hypermethylated and hypomethylated regions from the identified DMRs.
- Creates associated gene lists based on an upstream / downstream padding (bp) selected for the genes.



Annotate methylation calls

- Determines the genomic context of the methylated or differentially methylated regions.
- Annotates the methylation calls for the selected genic region.

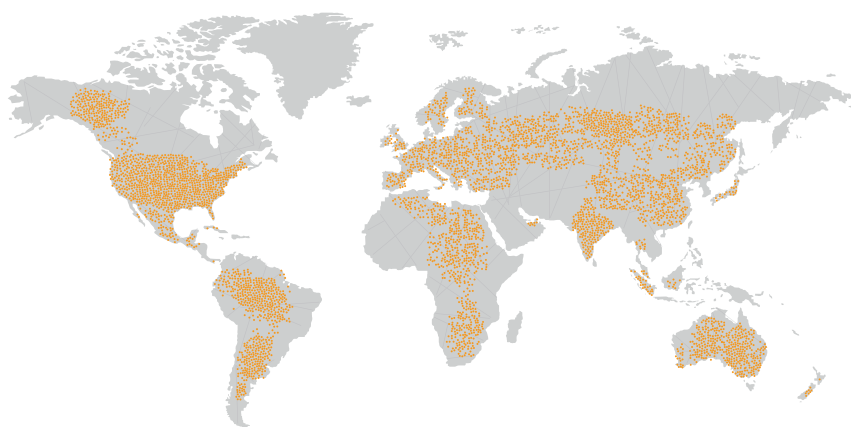


About Strand

A History of Innovative Genomic Research

Strand Life Sciences is a global genomic profiling company and leader in precision medicine diagnostics, aimed at empowering cancer care and genetic testing for inherited diseases. Strand works with physicians and hospitals to enable faster clinical decision support for accurate molecular diagnosis, prognosis, therapy recommendations, and clinical trials. The Strand Center for Genomics & Personalized Medicine is India's 1st and only CAP & NABL accredited NGS laboratory.

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For 15 years, our genomics products and solutions have facilitated the work of leading researchers and medical geneticists in over 2,000 laboratories and 100 hospitals around the world.

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