

HiSeq High Output Mode Calculations

TruSeq v3 Reagents (one flow cell)

Clusters/mm ² (800K @85%PF) %PF may vary based on library	680,000
Area of a lane (mm ²)	273.6
Reads/lane	186,048,000
Genome or region size (in bases)	Enter your value here
Coverage	Enter your value here
Total number of cycles (e.g. 200 for 2x100)	Enter your value here
Total output required (in bases)	
Output/lane (bases/lane)	
Number of lanes	
Number of samples/lane	

The numbers in this spreadsheet are reasonable expectations assuming flow cells are clustered at the proper density. Output may vary based on sample quality, cluster density and other experimental factors. Use these calculations as estimates for planning your runs.

For more information about calculating coverage estimates, see the [Coverage Calculation Tech](#)

HiSeq v4 Reagents (one flow cell)

Clusters/mm ² (1050K @87%PF) %PF may vary based on library	913,500
Area of a lane (mm ²)	273.6
Reads/lane	249,933,600
Genome or region size (in bases)	Enter your value here
Coverage	Enter your value here
Total number of cycles (e.g. 250 for 2x125)	Enter your value here
Total output required (in bases)	
Output/lane (bases/lane)	
Number of lanes	
Number of samples/lane	

HiSeq Rapid Mode Output Calculations

HiSeq 1500/2500 rapid run (one flow cell)

Clusters/mm ² (900K @91%PF) %PF may vary based on library	819,000
Area of a lane (mm ²)	184
Reads/ lane (Use cBot duo sample loading kit to deliver different samples to each lane)	150,696,000
Genome or region size (in bases)	Enter your value here
Coverage	Enter your value here
Total number of cycles (e.g. 300 for 2x150)	Enter your value here
Total output required (in bases)	
Output/lane (bases/lane)	
Number of lanes	
Number of samples/lane	

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For more information about calculating coverage estimates, see the [Coverage Calculation](#)

Clusters/mm ² (900K @91%PF) %PF may vary based on library	819,000
Area of a lane (mm ²)	184
Reads/ flow cell (OBCG, same sample deliver to both lanes)	300,000,000
Genome or region size (in bases)	Enter your value here
Coverage	Enter your value here
Total number of cycles (e.g. 300 for 2x150)	Enter your value here
Total output required (in bases)	
Output/flow cell (bases/flow cell)	
Number of flow cells	
Number of samples/flow cell	

Genome Analyzer Ix Output Calculations

Clusters/mm ² (750K @85%PF) %PF may vary based on library	637,500
Area of a lane (mm ²)	66
Reads/lane	42,075,000
Genome or region size (in bases)	Enter your value here
Coverage	Enter your value here
Total number of cycles (e.g. 300 for 2x150)	Enter your value here
Total output required (in bases)	
Output/lane (bases/lane)	
Number of lanes	
Number of samples/lane	

The numbers in this spreadsheet are reasonable expectations assuming flow cells are clustered at the proper density. Output may vary based on sample quality, cluster density and other experimental factors. Use these calculations as estimates for planning your runs.

For more information about calculating coverage estimates, see the [Coverage Calculation Tech Note](#).

HiScanSQ Output Calculations

TruSeq v3 Reagents

Clusters/mm ² (800K @85%PF) %PF may vary based on library	680,000
Area of a lane (mm ²)	136.8
Reads/lane	93,024,000
Genome or region size (in bases)	Enter your value here
Coverage	Enter your value here
Total number of cycles (e.g. 200 for 2x100)	Enter your value here
Total output required (in bases)	
Output/lane (bases/lane)	
Number of lanes	
Number of samples/lane	

The numbers in this spreadsheet are reasonable expectations assuming flow cells are clustered at the proper density. Output may vary based on sample quality, cluster density and other experimental factors. Use these calculations as estimates for planning your runs.

For more information about calculating coverage estimates, see the [Coverage Calculation Tech Note](#).

MiSeq Output Calculations

	MiSeq V3 with: - Upgraded software, - MCS v2.3 or later - MiSeq Reagent Kit v3 (150/600)
Reads/flow cell	25,000,000
Genome or region size (in bases)	Enter your value here
Coverage	Enter your value here
Total number of cycles (e.g. 300 for 2x150)	Enter your value here
Total output required (in bases)	
Output/flow cell (bases/flow cell)	
Number of flow cells	
Number of samples per flow cell	

The numbers in this spreadsheet are reasonable expectations assuming flow cells a calculations as estimates for planning your runs.

For more information about calculating coverage estimates, see the [Coverage Calcul](#)

MiSeq V2 with: - Upgraded hardware, or from September 2012 and later - MCS v2.0 or later - MiSeq Reagent Kit v2 (50/300/500)	MiSeq V2 Nano: - Upgraded hardware, or from September 2012 and later - MCS v2.0 or later - MiSeq Reagent Nano Kit v2 (300/500)	MiSeq V2 Micro: - Upgraded hardware, or from September 2012 and later - MCS v2.0 or later - MiSeq Reagent Micro Kit v2 (300)
15,000,000	1,000,000	4,000,000
Enter your value here	Enter your value here	Enter your value here
Enter your value here	Enter your value here	Enter your value here
Enter your value here	Enter your value here	Enter your value here

are clustered at the proper density. Output may vary based on sample quality, cluster density and other experim

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MiSeq v1 run configurations.
5,000,000
Enter your value here
Enter your value here
Enter your value here

ental factors. Use these

NextSeq Output Calculations

	NextSeq High Output:
Reads/flow cell	400,000,000
Genome or region size (in bases)	Enter your value here
Coverage	Enter your value here
Total number of cycles (e.g. 300 for 2x150)	Enter your value here
Total output required (in bases)	
Output/flow cell (bases/flow cell)	
Number of flow cells	
Number of samples per flow cell	

The numbers in this spreadsheet are reasonable expectations assuming flow cells are clustered at the proper density, cluster density and other experimental factors. Use these calculations as estimates for planning your run.

For more information about calculating coverage estimates, see the [Coverage Calculation Tech Note](#).

NextSeq Mid Output kit
130,000,000
Enter your value here
Enter your value here
Enter your value here

lensity. Output may vary based on sample
ns.