

Floragenex Sequencing Quality Control Report:

Analysis Rundate: 2013/09/25 20:07
Folder: /home/data/Project_Folders/Deagle_Krill_201308/Raw_Illumina_Sequence
Number of Samples: 148
Expected Reads / Sample: 2000000

Sample Name	% of Reads Obtained	(Remaining)	# of Reads Needed	RAD Clusters (<500x >5x)	Seq Depth (30x)	Median Depth	Tag Seq Distribution	(<20x Median)	Median Base Q Scores (Phred)	(Flag)
Deagle_Krill_S1CasF07_sequence_1.txt	1696996		303004	85702		13				
Deagle_Krill_S7RS49_sequence_1.txt	1734656		265344	51050		22				
Deagle_Krill_S2MawF09_sequence_1.txt	2430727		0	105373		15				
Deagle_Krill_S1CasM14_sequence_1.txt	2639912		0	88779		20				
Deagle_Krill_S2MawM01_sequence_1.txt	2771084		0	154289		11				
Deagle_Krill_S6WAPA11b_sequence_1.txt	2793772		0	85404		22				
Deagle_Krill_S2MawF01_sequence_1.txt	3052015		0	112112		18				
Deagle_Krill_S6WAPA07_sequence_1.txt	3084178		0	95794		21				
Deagle_Krill_S2MawF06_sequence_1.txt	3193435		0	126955		17				
Deagle_Krill_S6WAP12_sequence_1.txt	3227969		0	107643		20				
Deagle_Krill_S1CasM13_sequence_1.txt	3259559		0	109706		20				
Deagle_Krill_S7RS31c_sequence_1.txt	3363228		0	101194		22				
Deagle_Krill_S2MawF07_sequence_1.txt	3428585		0	103184		22				
Deagle_Krill_S3LazE14_sequence_1.txt	3632649		0	108970		22				
Deagle_Krill_S1CasF09_sequence_1.txt	3642460		0	171467		14				
Deagle_Krill_S2MawF10_sequence_1.txt	3671603		0	119530		20				
Deagle_Krill_S1CasF10_sequence_1.txt	3751957		0	169167		15				
Deagle_Krill_S2MawM04_sequence_1.txt	3777461		0	180877		14				
Deagle_Krill_S6WAPA06_sequence_1.txt	4008015		0	117692		22				
Deagle_Krill_S6WAP11_sequence_1.txt	4052734		0	121854		21				
Deagle_Krill_S4MawE12_sequence_1.txt	4061718		0	120343		22				
Deagle_Krill_19_sequence_1.txt	4082276		0	123589		22				
Deagle_Krill_S1CasF13_sequence_1.txt	4098751		0	183631		15				
Deagle_Krill_S6WAPB01_sequence_1.txt	4118675		0	140860		19				
Deagle_Krill_S2MawM02_sequence_1.txt	4151542		0	174895		15				
Deagle_Krill_S2MawM08_sequence_1.txt	4152087		0	181450		15				
Deagle_Krill_11_sequence_1.txt	4178219		0	141757		19				
Deagle_Krill_S3LazE16_sequence_1.txt	4186591		0	123024		21				
Deagle_Krill_S3LazE12_sequence_1.txt	4193041		0	130564		21				
Deagle_Krill_S2MawM06_sequence_1.txt	4199791		0	202906		13				

Floragenex Sequencing Quality Control Report:

Analysis Rundate: 2013/09/25 20:53
Folder: /home/data/Project_Folders/Deagle_Krill_201308/Raw_Illumina_Sequence
Number of Samples: 148
Expected Reads / Sample: 2000000

Sample Name	% of Reads Obtained	(Remaining)	# of Reads Needed	RAD Clusters (<500x >5x)	Seq Depth (30x)	Median Depth	Tag Seq Distribution	<20x Median	Median Base Q Scores (Phred)	(Flag)
Deagle_Krill_13_sequence_1.txt	4375731		0	138639		21				
Deagle_Krill_S1CasF12_sequence_1.txt	4436943		0	203888		14				
Deagle_Krill_S3LazE10_sequence_1.txt	4542624		0	134427		22				
Deagle_Krill_S1CasF14_sequence_1.txt	4561460		0	191919		15				
Deagle_Krill_S2MawF08_sequence_1.txt	4579249		0	143477		21				
Deagle_Krill_S6WAP15_sequence_1.txt	4649165		0	159295		19				
Deagle_Krill_S4MawE03_sequence_1.txt	4677432		0	136022		22				
Deagle_Krill_S3LazE06_sequence_1.txt	4711998		0	134990		22				
Deagle_Krill_21_sequence_1.txt	4726633		0	152558		20				
Deagle_Krill_S6WAPB13_sequence_1.txt	4751494		0	155399		20				
Deagle_Krill_25_sequence_1.txt	4762292		0	149862		21				
Deagle_Krill_S3LazE02_sequence_1.txt	4791499		0	139937		22				
Deagle_Krill_S2MawF05_sequence_1.txt	4796703		0	159037		20				
Deagle_Krill_5_sequence_1.txt	4856709		0	158801		20				
Deagle_Krill_S6WAPA01_sequence_1.txt	4912065		0	148199		21				
Deagle_Krill_S6WAP16_sequence_1.txt	4956404		0	139637		23				
Deagle_Krill_12_sequence_1.txt	4970198		0	149958		22				
Deagle_Krill_23_sequence_1.txt	4998007		0	140964		23				
Deagle_Krill_S2MawM03_sequence_1.txt	5081393		0	218459		15				
Deagle_Krill_S6WAPA05_sequence_1.txt	5133468		0	145314		23				
Deagle_Krill_3_sequence_1.txt	5225627		0	163582		20				
Deagle_Krill_S1CasM04_sequence_1.txt	5230793		0	203537		16				
Deagle_Krill_10_sequence_1.txt	5238038		0	144623		24				
Deagle_Krill_S1CasF08_sequence_1.txt	5249687		0	225117		15				
Deagle_Krill_3c_sequence_1.txt	5272479		0	150249		22				
Deagle_Krill_S2MawF02_sequence_1.txt	5319275		0	159064		22				
Deagle_Krill_S2MawF04_sequence_1.txt	5334675		0	194417		18				
Deagle_Krill_2c_sequence_1.txt	5341649		0	158152		21				
Deagle_Krill_S6WAPA06b_sequence_1.txt	5332732		0	153417		22				
Deagle_Krill_S4MawE13_sequence_1.txt	5403423		0	151959		23				

Floragenex Sequencing Quality Control Report:

Analysis Rundate: 2013/09/25 21:56
Folder: /home/data/Project_Folders/Deagle_Krill_201308/Raw_Illumina_Sequence
Number of Samples: 148
Expected Reads / Sample: 2000000

Sample Name	% of Reads Obtained	(Remaining)	# of Reads Needed	RAD Clusters (<500x >5x)	Seq	Median Depth	Tag Seq Distribution	(<20x Median)	Median Base Q Scores (Phred)	(Flag)
					Depth (30x)					
	0 %	100 %			5x 20x 30x		20x 100x 500x 1000x			
Deagle_Krill_18_sequence_1.txt	5406329		0	152309		23				
Deagle_Krill_S2MawF03_sequence_1.txt	5463388		0	175323		20				
Deagle_Krill_S2MawM10_sequence_1.txt	5468909		0	232117		15				
Deagle_Krill_S3LazE01_sequence_1.txt	5481967		0	158353		22				
Deagle_Krill_S6WAPPS1_sequence_1.txt	5653067		0	168374		21				
Deagle_Krill_S1CasM07_sequence_1.txt	5718559		0	181083		20				
Deagle_Krill_15_sequence_1.txt	5816442		0	158400		23				
Deagle_Krill_6_sequence_1.txt	5839396		0	170647		22				
Deagle_Krill_20_sequence_1.txt	5898477		0	157484		24				
Deagle_Krill_S6WAPA02_sequence_1.txt	5899899		0	153635		23				
Deagle_Krill_S2MawF11_sequence_1.txt	5921429		0	168017		22				
Deagle_Krill_S7RS20_sequence_1.txt	5884375		0	166130		23				
Deagle_Krill_S4MawE10_sequence_1.txt	5987943		0	166567		23				
Deagle_Krill_S2MawM07_sequence_1.txt	6009908		0	261147		15				
Deagle_Krill_S6WAPPS5_sequence_1.txt	5990939		0	167524		23				
Deagle_Krill_S1CasM10_sequence_1.txt	6084332		0	189151		21				
Deagle_Krill_1a_sequence_1.txt	6090688		0	166778		23				
Deagle_Krill_S2MawM11_sequence_1.txt	6102318		0	168965		23				
Deagle_Krill_S7RS24_sequence_1.txt	6026091		0	170101		23				
Deagle_Krill_S1CasF01_sequence_1.txt	6128274		0	252109		16				
Deagle_Krill_9_sequence_1.txt	6228513		0	180175		22				
Deagle_Krill_S6WAPB11_sequence_1.txt	6260663		0	169254		23				
Deagle_Krill_S6WAP14_sequence_1.txt	6274249		0	176088		23				
Deagle_Krill_S6WAPB04_sequence_1.txt	6281708		0	175722		22				
Deagle_Krill_S6WAPPS2_sequence_1.txt	6299177		0	196155		20				
Deagle_Krill_S1CasM09_sequence_1.txt	6409582		0	232896		17				
Deagle_Krill_S1CasF05_sequence_1.txt	6591455		0	254005		17				
Deagle_Krill_17_sequence_1.txt	6618267		0	203365		21				
Deagle_Krill_S6WAPB09_sequence_1.txt	6649304		0	185113		22				
Deagle_Krill_S7RS05_sequence_1.txt	6667645		0	189325		23				

Floragenex Sequencing Quality Control Report:

Analysis Rundate: 2013/09/25 23:19
Folder: /home/data/Project_Folders/Deagle_Krill_201308/Raw_Illumina_Sequence
Number of Samples: 148
Expected Reads / Sample: 2000000

Sample Name	% of Reads Obtained	(Remaining)	# of Reads Needed	RAD Clusters (<500x >5x)	Seq Depth (30x)	Median Depth	Tag Seq Distribution	(<20x Median)	Median Base Q Scores (Phred)	(Flag)	
	0 %		100 %		5x	20x	30x	20x	100x	500x	1000x
Deagle_Krill_S7RS17_sequence_1.txt	6724987		0	193665		22					
Deagle_Krill_S6WAPB02_sequence_1.txt	6882456		0	191484		23					
Deagle_Krill_7_sequence_1.txt	6891093		0	191559		23					
Deagle_Krill_S6WAPB08_sequence_1.txt	6974448		0	183338		24					
Deagle_Krill_S2MawM05_sequence_1.txt	6976222		0	288212		15					
Deagle_Krill_S1CasF02_sequence_1.txt	7000068		0	198571		22					
Deagle_Krill_S3LazE26_sequence_1.txt	7096010		0	191546		23					
Deagle_Krill_8_sequence_1.txt	7117528		0	191775		24					
Deagle_Krill_S7RS33_sequence_1.txt	7080324		0	204585		22					
Deagle_Krill_S7RS30_sequence_1.txt	7170587		0	198333		23					
Deagle_Krill_S1CasM08_sequence_1.txt	7410106		0	240476		19					
Deagle_Krill_S7RS25_sequence_1.txt	7384962		0	207549		22					
Deagle_Krill_S3LazE03_sequence_1.txt	7487802		0	195696		24					
Deagle_Krill_S1CasF11_sequence_1.txt	7656855		0	297206		16					
Deagle_Krill_16_sequence_1.txt	7657179		0	196689		25					
Deagle_Krill_S7RS34_sequence_1.txt	7696480		0	209280		23					
Deagle_Krill_S7RS28_sequence_1.txt	7697176		0	212530		23					
Deagle_Krill_S1CasM01_sequence_1.txt	7803801		0	244794		20					
Deagle_Krill_S6WAPPS3_sequence_1.txt	7852643		0	220252		23					
Deagle_Krill_S1CasM06_sequence_1.txt	7968754		0	223788		22					
Deagle_Krill_S7RS43_sequence_1.txt	7881255		0	208411		24					
Deagle_Krill_2_sequence_1.txt	7985632		0	222904		22					
Deagle_Krill_S7RS31_sequence_1.txt	8038360		0	209692		25					
Deagle_Krill_S1CasM12_sequence_1.txt	8171929		0	226241		23					
Deagle_Krill_S7RS32_sequence_1.txt	8294108		0	218297		24					
Deagle_Krill_4_sequence_1.txt	8424820		0	250264		21					
Deagle_Krill_S7RS26_sequence_1.txt	8335453		0	219697		24					
Deagle_Krill_S7RS31b_sequence_1.txt	8419840		0	221750		24					
Deagle_Krill_S1CasM14b_sequence_1.txt	8422113		0	228248		23					
Deagle_Krill_S7RS36_sequence_1.txt	8539209		0	232864		23					

Floragenex Sequencing Quality Control Report:

Analysis Rundate: 2013/09/26 01:02
Folder: /home/data/Project_Folders/Deagle_Krill_201308/Raw_Illumina_Sequence
Number of Samples: 148
Expected Reads / Sample: 2000000

Sample Name	0 % 100 %	RAD Clusters (≤500x >5x)	Seq Depth (30x)	Median Depth	Tag Seq Distribution (≤20x Median)	Median Base Q Scores (Phred)	(Flag)
Deagle_Krill_S7RS37_sequence_1.txt	8830154	0	232296	24			
Deagle_Krill_S1CasF10b_sequence_1.txt	8903966	0	240106	24			
Deagle_Krill_S7RS21_sequence_1.txt	9004786	0	243579	24			
Deagle_Krill_S6WAPA16b_sequence_1.txt	9117270	0	239890	24			
Deagle_Krill_S7RS22_sequence_1.txt	9253391	0	241049	24			
Deagle_Krill_S7RS06_sequence_1.txt	9320757	0	240162	25			
Deagle_Krill_S2MawM02b_sequence_1.txt	9488637	0	244766	23			
Deagle_Krill_S3LazE25_sequence_1.txt	9544741	0	248654	24			
Deagle_Krill_S6WAPA07b_sequence_1.txt	9432187	0	247528	24			
Deagle_Krill_S7RS29_sequence_1.txt	10027994	0	264375	24			
Deagle_Krill_S7RS27_sequence_1.txt	10474957	0	271684	24			
Deagle_Krill_S7RS13_sequence_1.txt	10589597	0	273274	24			
Deagle_Krill_S2MawF10b_sequence_1.txt	10820562	0	277413	24			
Deagle_Krill_S1CasM13b_sequence_1.txt	10976522	0	276874	25			
Deagle_Krill_S7RS18_sequence_1.txt	11180188	0	290105	24			
Deagle_Krill_S2MawM09_sequence_1.txt	11595283	0	431951	16			
Deagle_Krill_S7RS23_sequence_1.txt	11579304	0	292821	25			
Deagle_Krill_Test02b_sequence_1.txt	11630750	0	292134	25			
Deagle_Krill_S6WAPPS4_sequence_1.txt	11705774	0	291701	25			
Deagle_Krill_S1CasF07b_sequence_1.txt	13055088	0	310231	26			
Deagle_KrillTest_S2F12Sbfl_sequence_1.txt	13542418	0	554219	15			
Deagle_KrillTest_Test04Sbfl_sequence_1.txt	15330584	0	590124	16			
Deagle_KrillTest_Test03Sbfl_sequence_1.txt	15635056	0	586497	16			
Deagle_Krill_S2MawF01b_sequence_1.txt	16395561	0	370078	27			
Deagle_Krill_S1CasM03_sequence_1.txt	17281976	0	391118	26			
Deagle_KrillTest_S2M12Sbfl_sequence_1.txt	17931949	0	622904	17			
Deagle_KrillTest_Test01Sbfl_sequence_1.txt	18507607	0	603871	20			
Deagle_KrillTest_Test02Sbfl_sequence_1.txt	18630601	0	615239	19			

Analysis Rundate: 2013/09/26 03:14
Folder: /home/data/Project_Folders/Deagle_Krill_201308/Raw_Illumina_Sequence
Number of Samples: 148
Expected Reads / Sample: 2000000

Sequencing Statistics Summary

Number of Samples Analyzed: 148
Sequence Threshold: 2,000,000 reads / sample
Number of Samples Meeting Designated Sequence Threshold: 146
Mean Number of Sequence Reads per Sample: 6,775,937
Total Number of Sequence Reads in Dataset: 1,002,838,684
Sequencing Standard Deviation: 3,274,878
Sequencing Coefficient of Variation: 0.48