

Information on sample sequencing, preparation protocol, read filtering, and assembly

Sample IDs	Number of samples	Sequencer
myc01 to 52 except 03, 28, 38, 41, & 44	47	HiSeq 2000
myc03	1	HiSeq 2000
myc44	1	HiSeq 2000
myc28, 38, & 41	3	HiSeq 2000
myc54 to 59 & 64 to 66	9	NextSeq 500
myc54 to 57 & 66	5	MiSeq
myc53, 60 to 63, 67, 69 to 115, 118, 120 to 123, & 126.run1	59	NextSeq 500
myc68, 116, 117, 119, & 125	5	NextSeq 500
myc124	1	NextSeq 500
myc126.run2 & 127 to 132	1	NextSeq 500
myc53	1	MiSeq
myc59, 61, 68, 85, 121, & 123	6	MiSeq

All Trimmomatic runs used LEADING:30

Trimmomatic runs with ILLUMINACLIP used TruSeq3-PE-2.fa:2:30:10

SPAdes k values for 21-77 were 21, 33, 55, & 77

SPAdes k values for 21-121 were 21, 33, 55, 77, 99, & 121

Read length	Preparation protocol	Trimmomatic ILLUMINACLIP	Trimmomatic CROP	Trimmomatic SLIDINGWINDOW
2x100 bp	Standard	No	No	10:20
2x100 bp	Standard	Raw reads		
2x100 bp	Standard	Raw reads		
2x100 bp	Standard	No	No	10:20
2x150 bp	Alternate	Yes	No	10:20
2x301 bp	Alternate	Yes	150	10:20
≤2x151 bp	Standard	No	No	10:20
2x150 bp	Standard	No	No	10:30
2x150 bp	Standard	Bad reads		
2x150 bp	Standard	No	No	10:20
2x301 bp	Standard	Yes	250	10:20
2x301 bp	Standard	Yes	150	10:20

Trimmomatic MINLEN	Usage of R2.unpaired	Velvet k	SPAdes k
100	Kept	63	
		45	21-77
		27	21-77
75	Kept	63	21-77
100	Neglected	99	21-121
100	Neglected	81	21-121
100	Kept	81	21-121
100	Kept	81	
100	Kept	81	
100	Neglected	81	21-121
100	Neglected	81	