Barcode	Pool	Sample_ID	Collab_ID	Patient_ID	Class	Sample_type
bc405	Project_05500_EF	ZS−msi−4506−pl−T01_IGO_05500_EF_41	–	–	Normal	–

Innovation QC Report

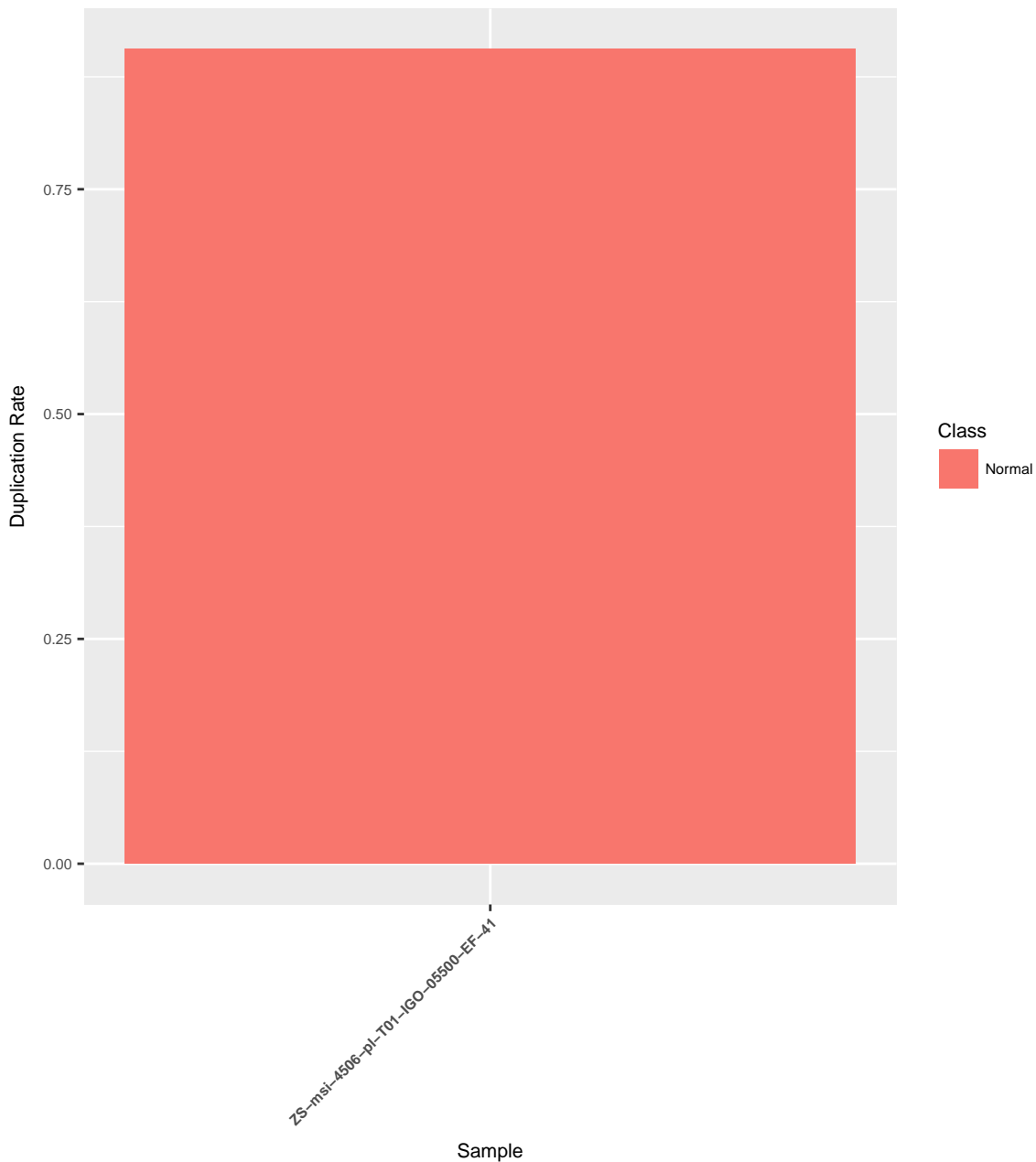| Sample_type	Input_ng	Library_yield	Pool_input	Bait_version	Gender	PatientName	MAccession	Extracted_DNA_Yield
–	–	–	–	–	–	–	–	–

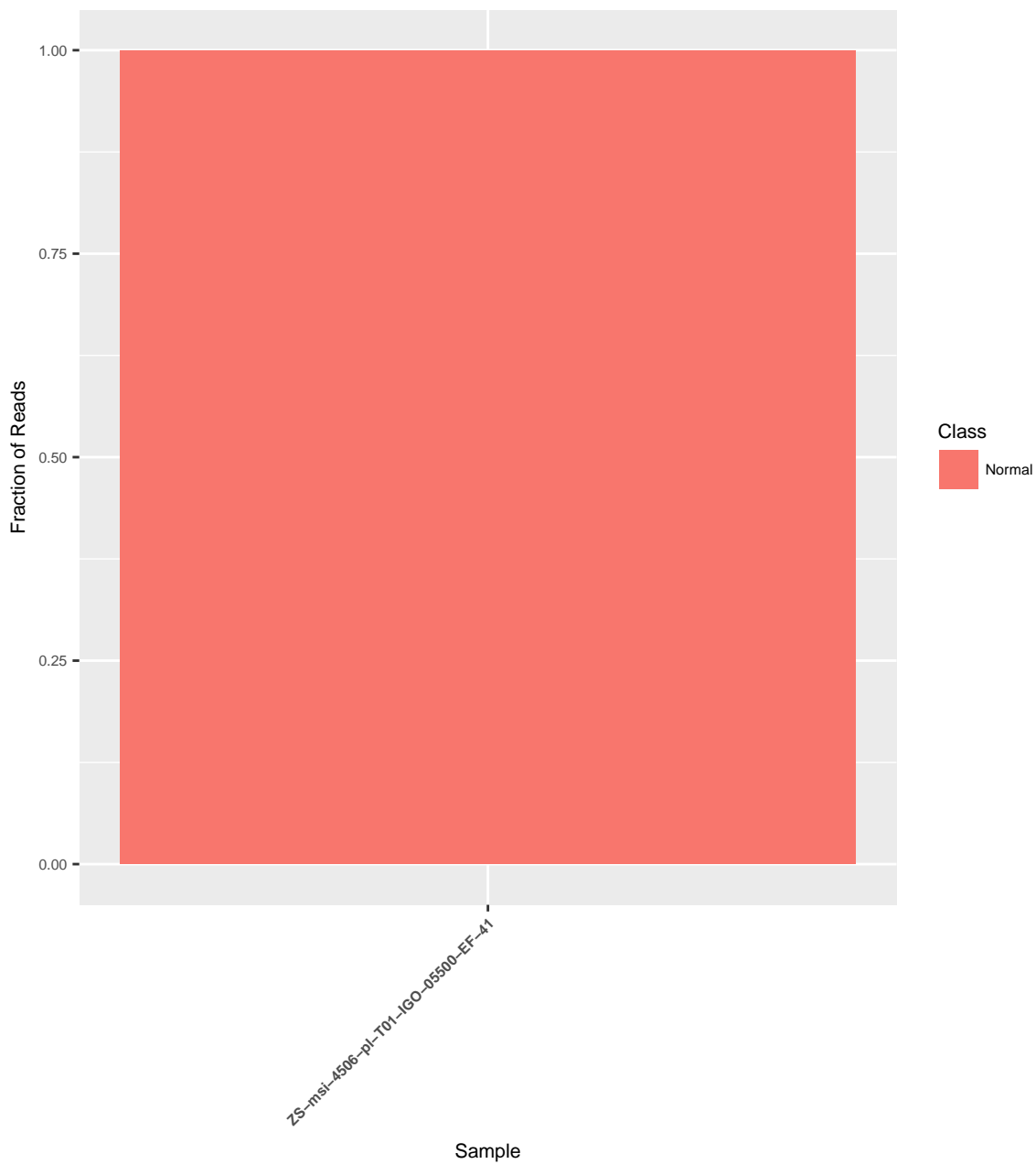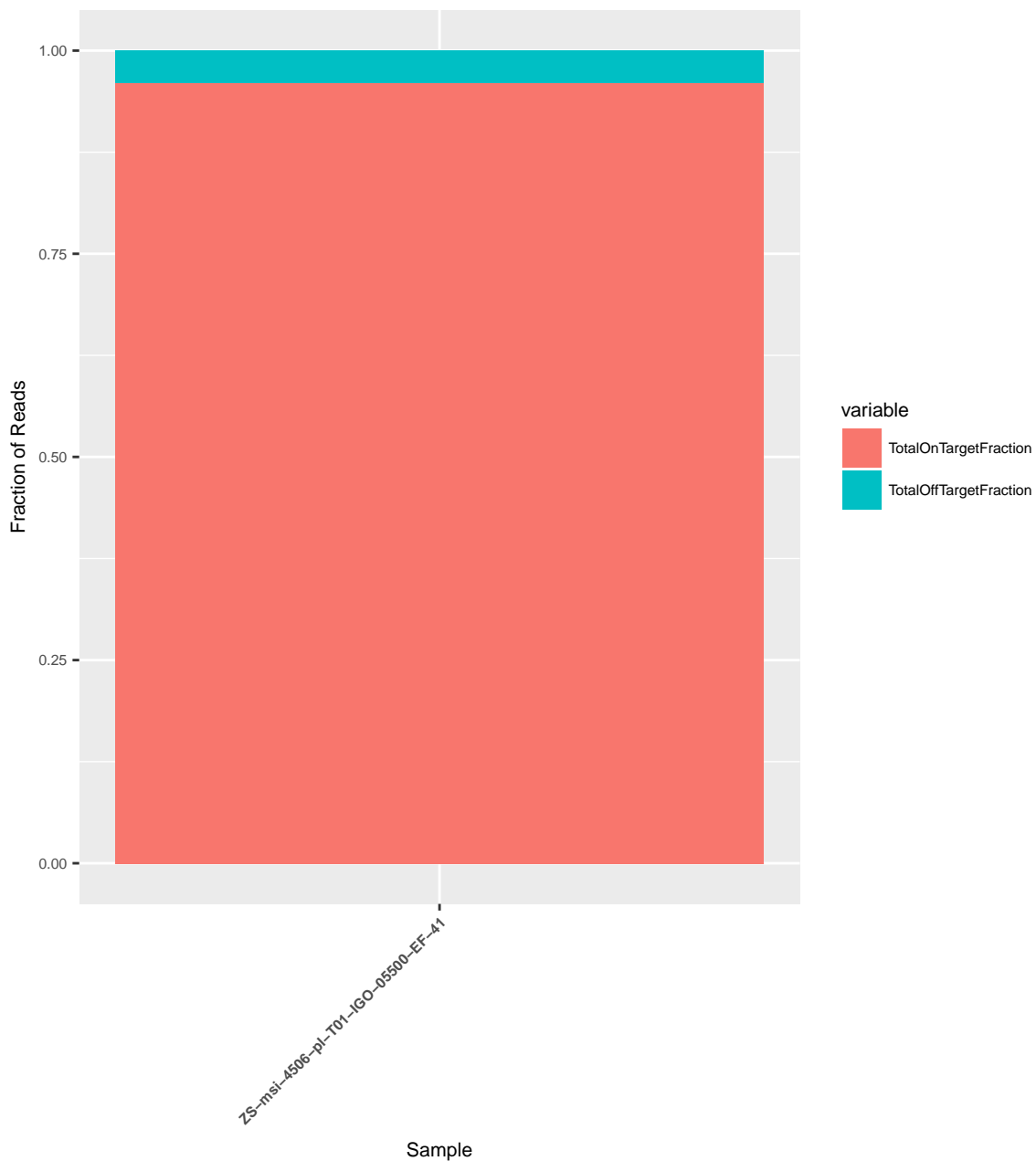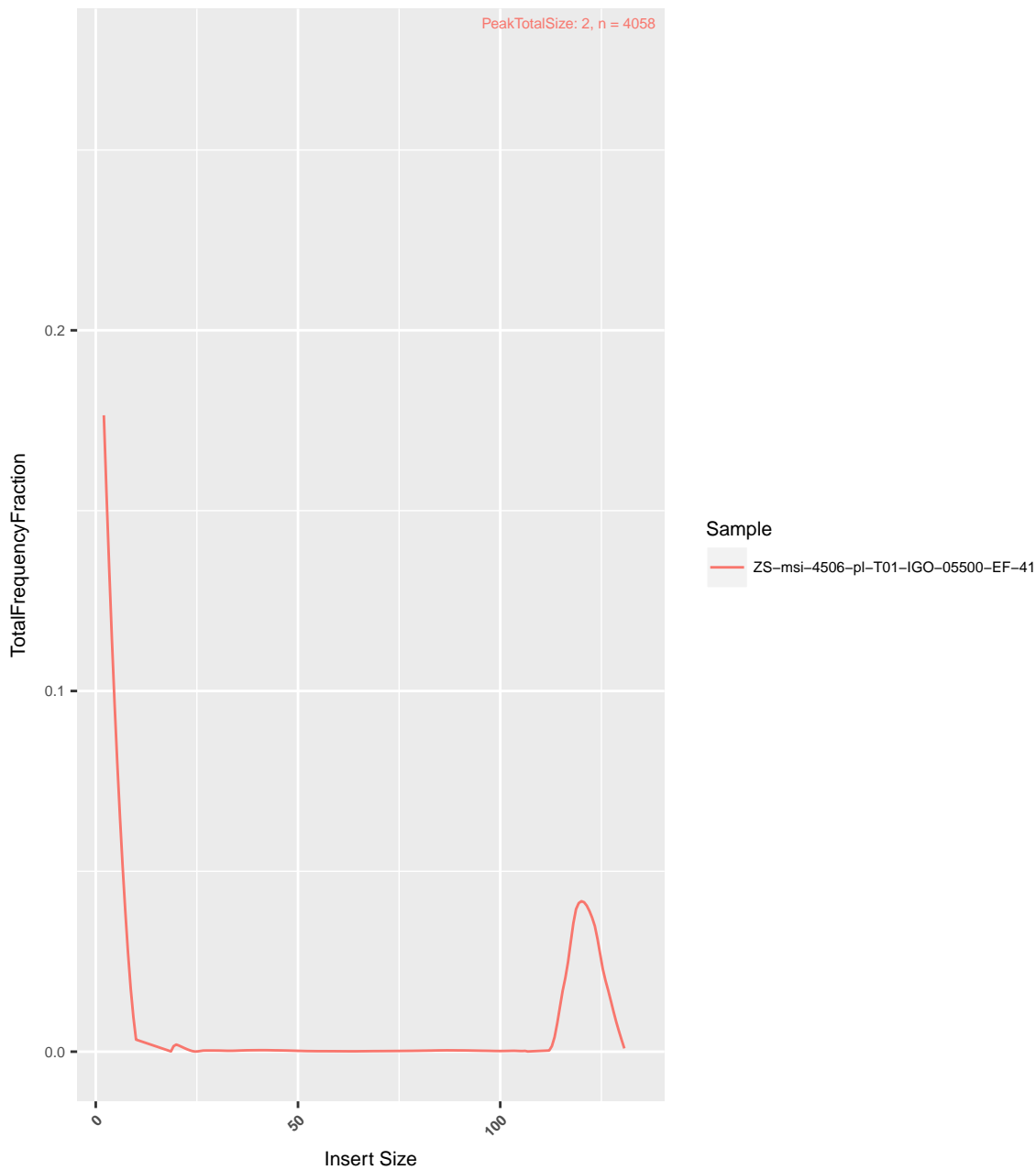# Duplication Rate per Sample

Fraction of Total Reads that Align to the Human Genome

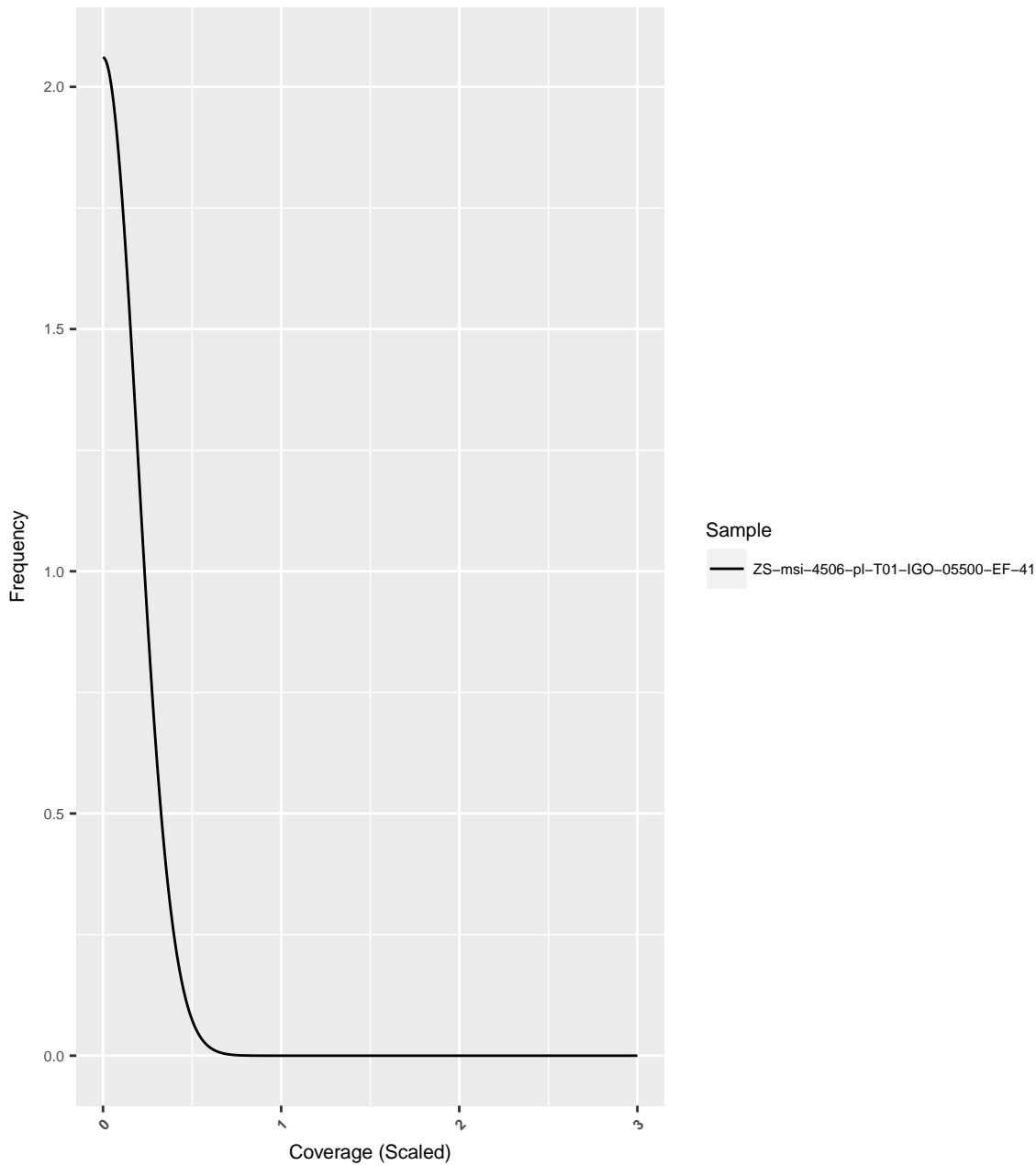Fraction of Total On/Off Target Reads

Insert Size Distribution for all Samples
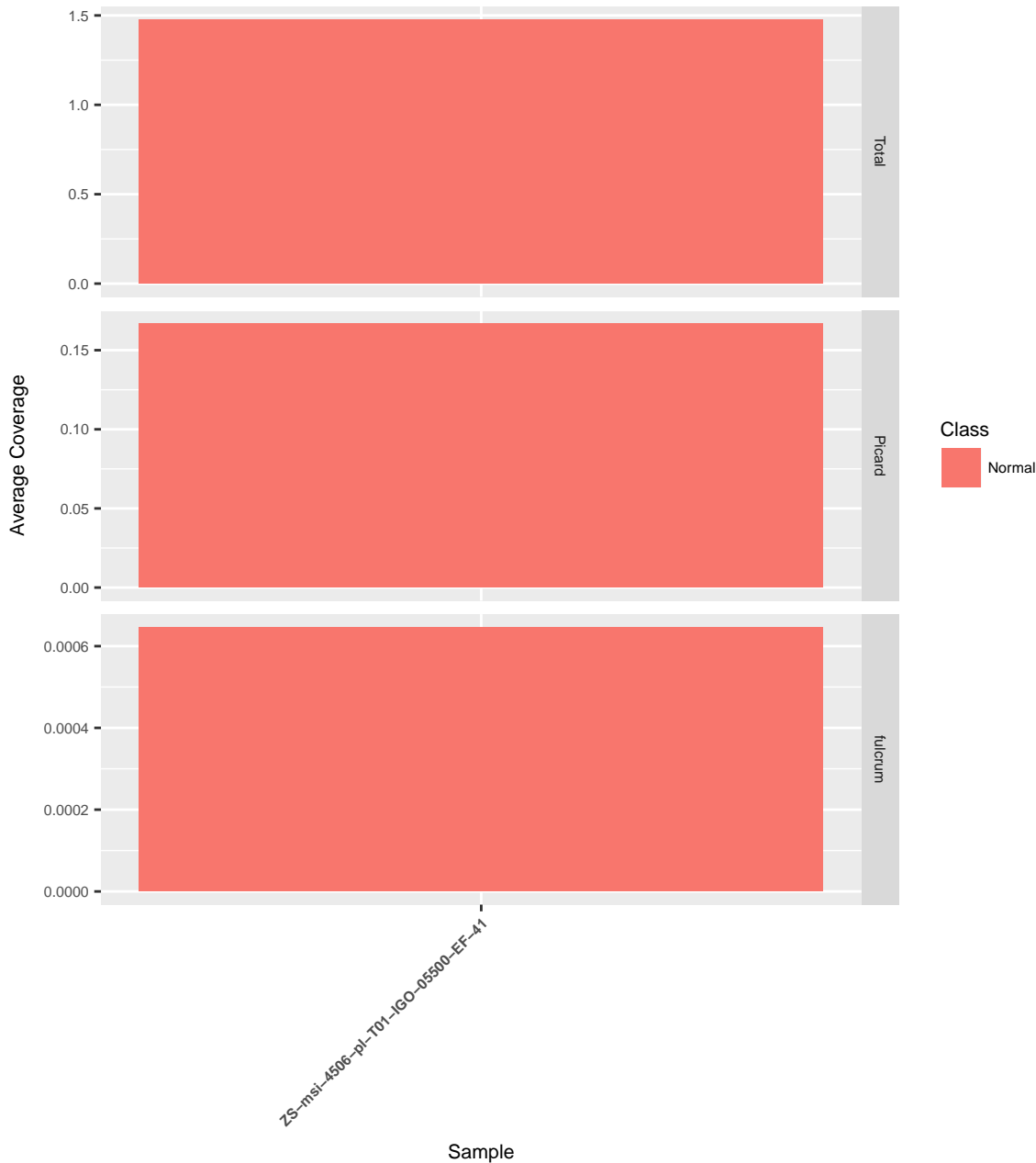

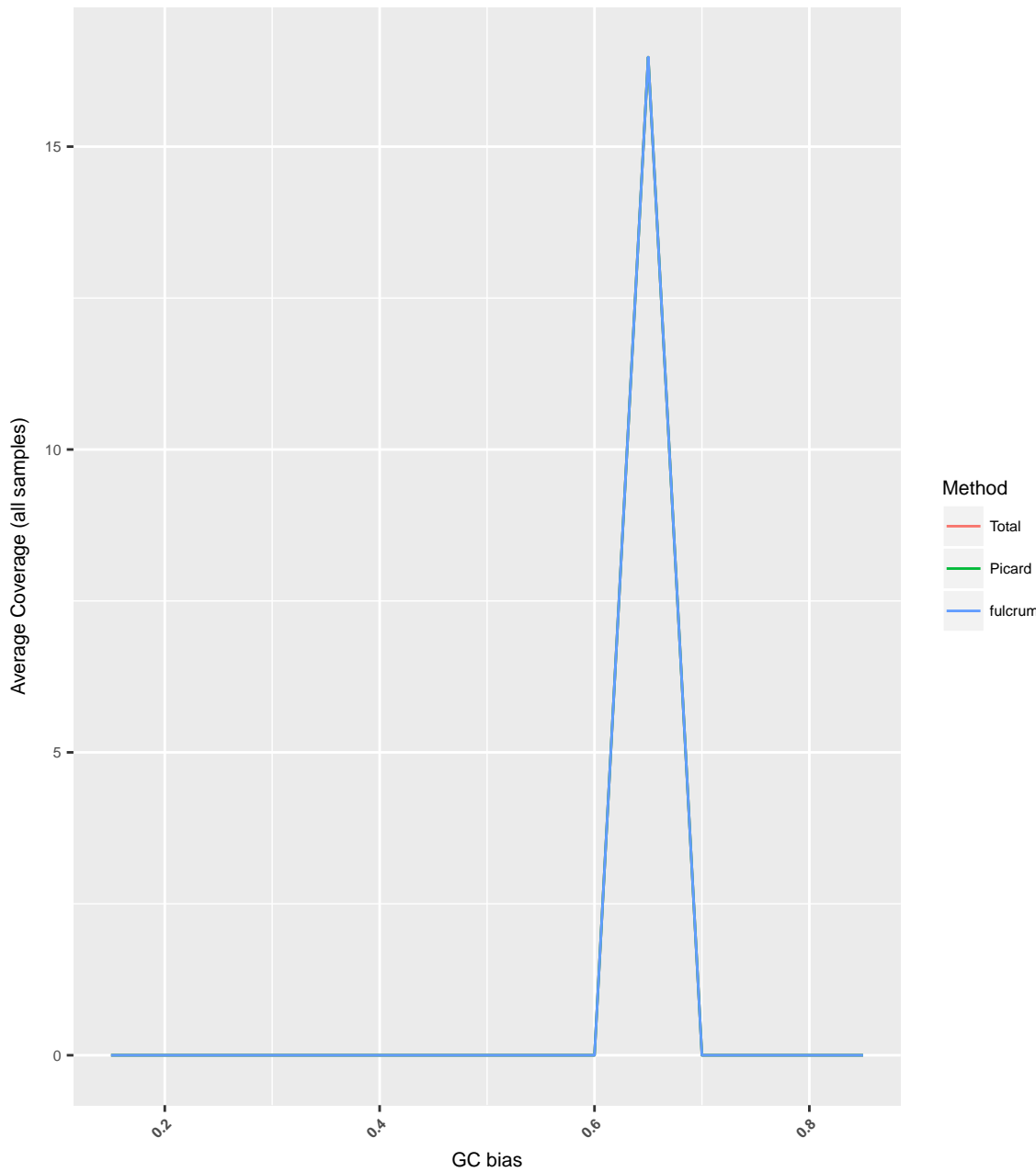PeakTotalSize: 2, n = 4058

Sample

ZS–msi–4506–pl–T01–IGO–05500–EF–41

TotalFrequencyFraction

Insert Size

Distribution of Coverages per Target Interval

Sample

— ZS–msi–4506–pl–T01–IGO–05500–EF–41

Frequency

Coverage (Scaled)

Average Coverage per Sample for Each Collapsing Method

Average Coverage versus GC bias for each Collapsing Method

Average Coverage versus GC bias for each Collapsing Method