

A

Feature Name	Formula
Normalized Hi-C Read Counts	$10^6 \times R / \sqrt{l_1 \times l_2}$
Difference in Sequencing Coverage	$ \log_2(d_1/d_2) $
Total Sequencing Coverage	$\log_{10}(d_1 \times d_2)$
Variance of Total Sequencing Coverage	$\log_{10}(v_1 \times v_2)$
Total Connectivity	$\log_{10}(c_1 \times c_2)$
Hi-C Reads Connecting Two Scaffolds	R

B

Normalized Hi-C Read Counts	Difference in Sequencing Coverage	Total Sequencing Coverage	Variance of Total Sequencing Coverage	Total Connectivity	Hi-C Reads Connecting Two Scaffolds
17.81	0.03	2.36	2.57	2.59	2
8.76	4.96	3.86	4.48	4.38	4
19.37	0.09	2.34	2.22	2.55	2