Supplementary Table 3. Whole-genome sequencing coverage and mapping in PCD-141 I:1 and PCD-141 I:2

Sample	**PCD-141 I:1**	**PCD-141 I:2**
raw total sequences:	734,863,374	1,308,739,964
filtered sequences:	0	0
sequences:	734,863,374	1,308,739,964
is paired:	1	1
is sorted:	1	1
1st fragments:	367,431,687	654,369,982
last fragments:	367,431,687	654,369,982
reads mapped:	671,669,065	1,255,769,100
reads unmapped:	63,194,309	52,970,864
reads unpaired:	15,167,979	7,577,254
reads paired:	656,501,086	1,248,191,846
reads duplicated:	50,311,409	79,234,487
reads MQ0:	41,096,250	49,594,070
reads QC failed:	39,344	71,048
non-primary alignments:	0	0
total length:	73,486,337,400	1.3087×10^{11}
bases mapped:	67,166,906,500	1.2558×10^{11}
bases mapped (cigar):	66,105,105,897	1.2518×10^{11}
bases trimmed:	0	0
bases duplicated:	5,031,140,900	7,923,448,700
mismatches:	550,066,806	649,526,457
error rate:	0.00832	0.00519
average length:	100	100
maximum length:	100	100
average quality:	25.3	30.7
insert size average:	282.5	292.4
insert size standard deviation:	76.6	78.4
inward oriented pairs:	299,286,061	618,344,004
outward oriented pairs:	1,066,964	867,841
pairs with other orientation:	1,250,938	211,994
pairs on different chromosomes:	26,638,573	4,656,276