S9 Figure: A) Total, B) between, C) and within chromosome rearrangements identified that have 3 supporting independent read-pairs. There is no correlation between sequence coverage depth and total number of rearrangements ($R^2 = 0.009632$, $P = 0.3678$), between chromosomes rearrangements ($R^2 = 0.0132$, $P = 0.38$), and within chromosome rearrangements ($R^2 = 0.004914$, $P = 0.3226$). Lines CY04B, CY08A, CY17C, and CY21B3 have abnormally high amount of structure calls, most are rearrangements that have support of three read-pairs.