**S1 Table:** Short read libraries used to assemble the fin whale nuclear genome.

|  |  |  |
| --- | --- | --- |
| **Library type** | **Insert** | **Number of read pairs** |
| Short insert paired end | ~400bp | 578,742,088 |
| In-silico mate-pair | 1kb | 13,756,580 |
| In-silico mate-pair | 2kb | 13,175,593 |
| In-silico mate-pair | 5kb | 12,413,319 |
| In-silico mate-pair | 10kb | 12,063,091 |
| In-silico mate-pair | 20kb | 11,957,048 |