Supplemental Table 2. Relative lane fraction needed to achieve optimal data on an under-duplicated sample.

If your peak family size is…	Re-run the sample on this relative lane fraction*
>12-16	Family size too large. On future experiments, use larger amount of input DNA for PCR (see TROUBLESHOOTING)
5-11	family size already optimal
4	.5X
3	1X
2	2X
1	Repeat PCR with 6X less input DNA

*As an example, suppose a sample was sequenced with 8,000,000 paired-reads, which resulted in a peak family size of 2. To increase the peak family size to 6, re-run the sample on 8,000,000 * **2** = 16,000,000 reads of a lane and then pool the raw reads from both sequencing runs and reprocess according to the PROCEDURE section. This will give a final peak family size of 2 + 4 = 6.

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