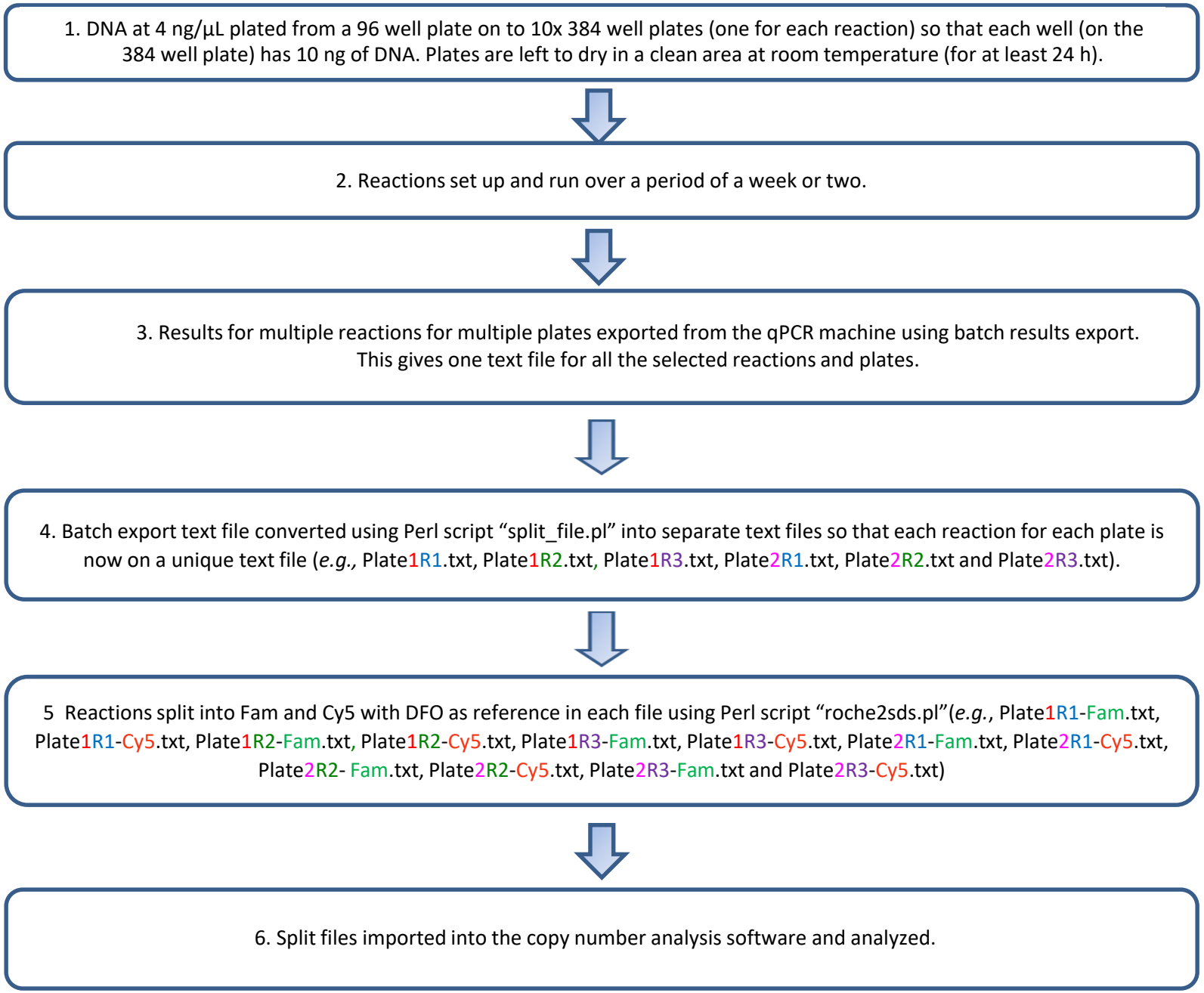
1. DNA at 4 ng/µL plated from a 96 well plate on to 10x 384 well plates (one for each reaction) so that each well (on the 384 well plate) has 10 ng of DNA. Plates are left to dry in a clean area at room temperature (for at least 24 h).
2. Reactions set up and run over a period of a week or two.
3. Results for multiple reactions for multiple plates exported from the qPCR machine using batch results export. This gives one text file for all the selected reactions and plates.
4. Batch export text file converted using Perl script "split_file.pl" into separate text files so that each reaction for each plate is now on a unique text file (e.g., Plate1R1.txt, Plate1R2.txt, Plate1R3.txt, Plate2R1.txt, Plate2R2.txt and Plate2R3.txt).
5 Reactions split into Fam and Cy5 with DFO as reference in each file using Perl script "roche2sds.pl"(e.g., Plate1R1-Fam.txt, Plate1R1-Cy5.txt, Plate1R2-Fam.txt, Plate1R2-Cy5.txt, Plate1R3-Fam.txt, Plate1R3-Cy5.txt, Plate2R1-Fam.txt, Plate2R1-Cy5.txt, Plate2R2- Fam.txt, Plate2R2-Cy5.txt, Plate2R3-Fam.txt and Plate2R3-Cy5.txt)
6. Split files imported into the copy number analysis software and analyzed.