Table S1. Details of single NGS library preparation steps in both canonical and optimized workflows

	Canonical	Optimized
1st amplification step (Molecule tagging) components:		
Breast cfDNA Panel v2	2µl	0.6µl
cfDNA Library PCR Master Mix	15µl	5µl
Nuclease-free water	0µl	1.4µl
DNA input	10µl normal genomic DNA (5ng) plus 3µl DNA from MDA sorted cells on DEPArray	3µl DNA from MDA sorted cells on DEPArray
Total volume	**30µl**	**10µl**
1st purification and elution steps:		
Agencourt Ampure XP Reagent beads	45µl	15µl
80% ethanol	150µl	100µl
Low TE	24µl	8µl
2nd amplification step (Library generation) components:		
DNA from 1st elution step	23µl	8µl
Tag Sequencing BC (1-24)	1µl	0.4µl
cfDNA Library Primer P1	1µl	0.4µl
cfDNA Library PCR Master Mix	25µl	8µl
Total volume	**50µl**	**16.8µl**
2nd purification and elution steps:		
Agencourt Ampure XP Reagent beads	57.5µl	19.3µl
80% ethanol	150µl	100µl
Low TE	50µl	16.8µl
Size selection step:		
DNA from 2nd elution step	50µl	16.8µl
Agencourt Ampure XP Reagent beads	50µl	16.8µl
80% ethanol	150µl	100µl
Low TE	30µl	22µl
Final transferred library volume	28µl	20µl