

A novel high-throughput post-PCR DNA purification system for improving lab productivity

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Overview

The continued growth in the fields of genomic research and molecular diagnostics has created the need to improve the productivity of the mainframe liquid handling systems used in core research and clinical testing laboratories. Diffinity Genomics Inc.® has developed a novel molecular separation technology and functional pipette tip, the RapidTip®, which can be utilized with the Beckman Coulter Biomek® and other mainframe liquid handling systems to purify DNA from PCR samples at a dramatically improved rate of throughput with no additional capital investment.

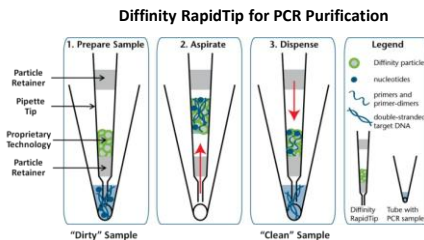
Introduction

The single-step RapidTip technology enables the DNA purification process to begin and end with the same single (functional) pipette tip. DNA samples requiring purification are aspirated into the RapidTip, mixed for 60 seconds wherein proprietary materials within the RapidTip bind and immobilize impurities, such as unincorporated dNTP and primers from post-PCR reactions. The purified DNA is then dispensed from the RapidTip into the same sample plate for subsequent analysis. On-instrument purification time is reduced to 1 ½ minutes for up to 96 samples at a time.

Method

Manufacturer-recommended protocols for several existing purification products were identified and are shown below. The time required to execute these workflows on an 8 and 96-channel Beckman-Coulter Biomek FX® liquid handling system was then measured and reported as time to purified sample availability and samples purified per hour. We also reported the number of consumables used by each method as well as any additional items required to complete the purification process. Representative RapidTip purification performance data is shown at right.

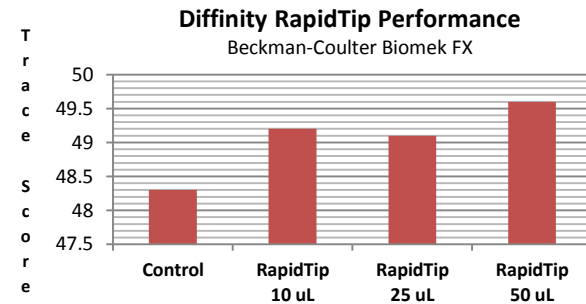
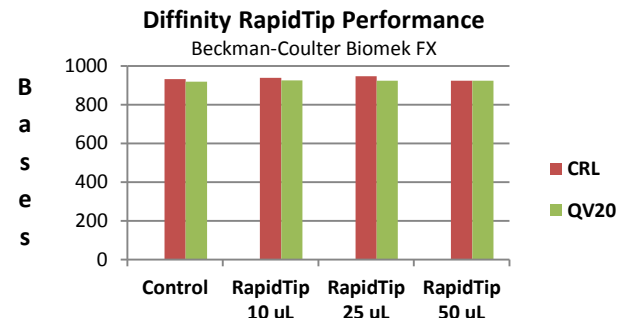
#	AMPure®	QIAquick®	ExoSAP-IT®	RapidTip®
1	Load Sample Plate	Load Sample Plate	Load Sample Plate	Load Sample Plate
2	Load Receiver Plate	Load PM Buffer Plate	Load Enzyme Plate	Load RapidTips
3	Load Buffer Plate	Load PE Buffer Plate	Load pipette tips	Mix Sample 60 Sec
4	Load Eluent Plate	Load EB Buffer Plate	Add Enzyme to Sample	Remove Sample Plate
5	Load Bead Plate	Load QIA-Vac Plate	Incubate 15 Min (37C)	
6	Load pipette tips	Load QIA-Quick Plate	Incubate 15 Min (80C)	
7	Add Beads / Mix	Load pipette tips	Remove Sample Plate	
8	Incubate 5 Min	Add PM Buffer		
9	Move to Magnet	Vacuum 60 Sec		
10	Incubate 2 Min	Add PE Buffer		
11	Aspirate Supernatant	Vacuum 60 Sec		
12	Remove Magnet	Dry for 10 Min		
13	Add Wash Buffer	Blot QIA-Quick Plate		
14	Incubate 30 Sec	Load Receiver Plate		
15	Remove Wash Buffer	Add EB Buffer		
16	Add Wash Buffer	Incubate 60 Sec		
17	Incubate 30 Sec	Vacuum 5 Min		
18	Remove Wash Buffer	Remove Receiver Plate		
19	Add Wash Buffer			
20	Incubate 30 Sec			
21	Remove Wash Buffer			
22	Dry 5 Min			
23	Add Elution Buffer/Mix			
24	Move to Magnet			
25	Incubate 1 Min			
26	Transfer Eluent			
27	Remove Eluent Plate			



Conclusions

- A 12-24X reduction in sample turn-around time relative to existing purification systems
- Dramatic increase in sample throughput at no additional capital cost, operator interventions, reagents or consumables
- Shorter overall time to analysis and results due to rapid sample turn-around time and reduced interruption to sample workflows
- Significantly reduced waste and environmental impact

Results – Sample Purification



Results – Sample Handling

Performance Metric	AMPure	QIAquick	ExoSAP-IT	RapidTip
Time to first sample (Minutes):	20	27	35	1.5
Samples/Hour - 8 Channels :	≈ 220 ¹	≈ 180 ²	≈ 150 ³	320
Samples/Hour - 96 Channels :	≈ 290 ¹	≈ 220 ²	≈ 180 ³	3840
# Reagents:	3	3	1	-
# Pipette Tips per Sample:	13	6	2	1
# Plates per 96 samples:	4	6	2	1
Other Requirements:	Cold Storage	Vacuum Manifold	Cold Storage	
	Magnetic Plate	Plate Mover	Thermo Cycler	
	Plate Mover		Plate Mover	

Note 1: Limited by number of magnetic plates and plate manipulators (One each is assumed above)

Note 2: Limited by number of vacuum manifolds (One is assumed above)

Note 3: Limited by number of thermo-cycling manifolds (One is assumed above)