

Devin™ is a fractionation filter that effectively removes host DNA interference from body fluids, such as whole blood, plasma, CSF, BALF etc. It utilizes a patent technology of Zwitterionic Interface Ultra-Self-assemble Coating (ZISC) which allows to deplete human nucleated cells from the sample (Fig. 1) while allowing most of microorganisms (including bacteria, viruses, fungi etc.) to go through the filter intact (Fig. 2).

Fig. 1 Leukocytes reduction efficiency

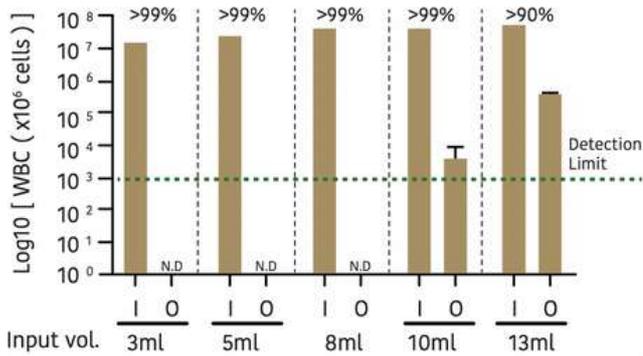
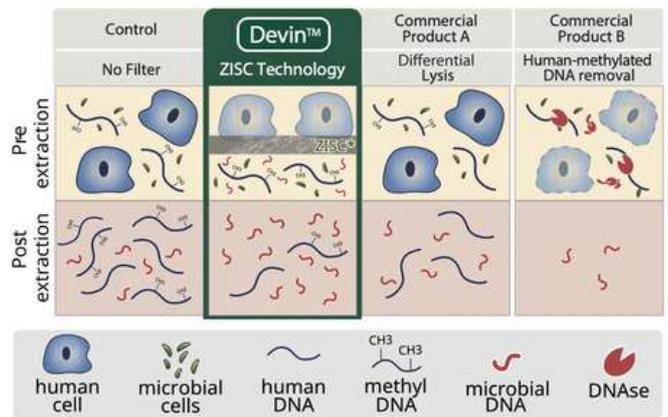


Fig 3. Contemporary depletion techniques



Devin™ filter's core technology is Zwitterionic Coating (ZISC) of membrane that effectively captures nucleated cells (over 99% for samples up to 10 ml within 5 minutes) and has high microbial passing efficiency (over 99%)

Fig 2. Microbial passing efficiency

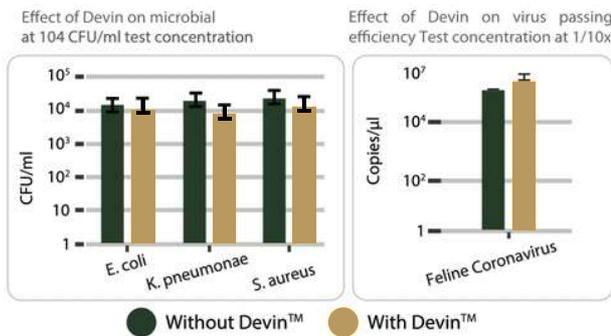
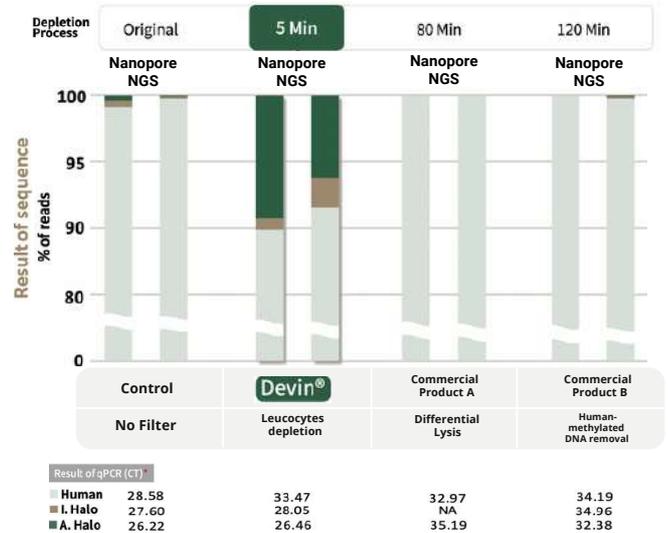


Fig 4. Comparison of different depletion methods



In comparison with other depletion methods (Fig. 3) Devin™ shows much faster processing time (less than 5 minutes) and greater ratio of microbial sequencing reads (Fig. 4)

Devin™ filter may be used for wide range of applications including genetic tests (DNA sequencing, PCR, qPCR, end-point PCR etc.), virology, immunology and other applications.

*Results of human and microbial identification using qPCR, NGS and Nanopore. Human blood samples (5 mL) were added. 10⁴ Genome Copies/mL spike in control from ZYMO Research and then processed using different depletion methods. Test results show that Devin™ filter increases ratio of microbial DNA and decreases the ratio of human (host) DNA.



Fig. 5 PaRTI-seq™ Test Workflow

Efficacy of Devin™ filter evaluated within PaRTI-Seq™ test with clinical samples show much better performance in comparison with Blood Culture test (Table 1)

Devin™ filter (column 5) significantly increased the microbial sequencing reads as compared to untreated samples (column 6), ranging from 10 up to 1000 fold.

Moreover, potential pathogens showed higher microbial sequencing reads as compared to the healthy reference database (column 8)

Pathogens identified in patients with positive blood culture results (patient C and D) were also detected by PaRTI-Seq™ test. In patient C, additional potentially disease-causative pathogens (n=9) were identified apart from *Proteus mirabilis*.

PaRTI-Seq™ also identified potential disease-causative pathogens in patient A and patient B who had negative blood culture results. The preliminary results using spike-in control showed detection sensitivity of PaRTI-Seq™ at min 102 genome copies/ml.

ABOUT PaRTI-Seq™

PaRTI-Seq™ test (Pathogen Real Time Identification by Sequencing) is an original solution developed by Micronbrane for rapid identification of pathogens in clinical setting (Fig. 5)

PaRTI-Seq™ includes reagents and consumables for sample preparation, extraction of microbial DNA, NGS Library preparation for downstream sequencing and proprietary software PaRTI-for analysis of sequencing data and pathogen analysis report.

Overall PaRTI-Seq™ (Fig. 5) enables the detection of disease causing pathogens within 24 hrs. and showed full consistency with the outcomes of positive blood culture. Most importantly, it also detects potential pathogens that will otherwise be missed by routine culture and thus could affect effectiveness of selected treatment and cause complications.

Sample	Pathogen Detected	Detected By		Microbial reads within 5M of total reads		Ratio of sequencing reads		Estimated GC
		PaRTI-Seq [®] Test	Blood Culture Test	With DEVIN	Without DEVIN	w/ DEVIN to w/o DEVIN	Infected Patients to Healthy Individual	
1	2	3	4	5	6	7	8	9
a	<i>Klebsiella oxytoca</i>	✓	✗	257	34	7.5	4.2	1*10 ²
	<i>Streptococcus suis</i>	✓	✗	899	118	7.6	9.7	5*10 ²
b	<i>Stenotrophomonas maltophilia</i>	✓	✗	2828	73	38.9	3.2	2*10 ³
c	<i>Corynebacterium tuberculostrictum</i>	✓	✗	28389	43	661.9	1976.1	2*10 ⁴
	<i>Corynebacterium amycolatum</i>	✓	✗	19270	26	752.8	2577.2	1*10 ⁴
	<i>Corynebacterium Kefirresidentii</i>	✓	✗	4984	9	555.2	270.9	3*10 ³
	<i>Corynebacterium aurimucosum</i>	✓	✗	1406	2	650.8	113.6	9*10 ²
	<i>Corynebacterium minutissimum</i>	✓	✗	390	0	2344.2	71.3	2*10 ²
	<i>Corynebacterium singulare</i>	✓	✗	271	0	1630.4	49.3	1*10 ²
	<i>Finogoldia magna</i>	✓	✗	1293	1	1296.8	236.7	8*10 ²
	<i>Proteus mirabilis</i>	✓	✓	1288	1	968.6	106.9	8*10 ²
	<i>Staphylococcus hominis</i>	✓	✗	983	1	1183.2	180.0	6*10 ²
	<i>Staphylococcus haemolyticus</i>	✓	✗	764	0	2298.1	63.4	5*10 ²
d	<i>Enterococcus faecalis</i>	✓	✓	4317	447	9.7	130.4	4*10 ⁴

Table 1. Clinical results of pathogens identified by PaRTI-Seq™ with Devin™ filter in comparison with Blood Culture Test.