Supplemental Data Table S4. Sequencing quality and coverage summary of NewbornSeq

	Median	Range
Number of mapped reads	201,670	144,797-368,044
Percent reads on target	94.75%	88.42-95.93%
Number of amplicons	2,054	2,054
Total assigned amplicon reads	192,114	134,882-350,760
Percent assigned amplicon reads	94.75%	88.42-95.93%
Average reads per amplicon	94	66-171
Uniformity of amplicon coverage	92.61%	77.73-95.43%
Amplicons with at least 1 read	98.93%	97.08-95.46%
Amplicons with at least 20 reads	93.14%	70.4-95.28%
Total aligned base reads	27,527,377	17,715,111-50,206,887
Total base reads on target	25,640,376	15,212,164-46,971,364
Bases in target regions	289,005	289,005
Percent base reads on target	93.07%	85.87-94.69%
Average base coverage depth (X)	89	53-163
Uniformity of base coverage	92.23%	74.9-95.25%
Target base coverage at 1x	98.93%	96.47-99.45%
Target base coverage at 20x	92.52%	62.36-95.13%
Target base coverage at 100x	39.37%	14.99-70.64%