



NOVASEQ X PLUS CONCORDANCE DATA WHOLE GENOME METHYLATION

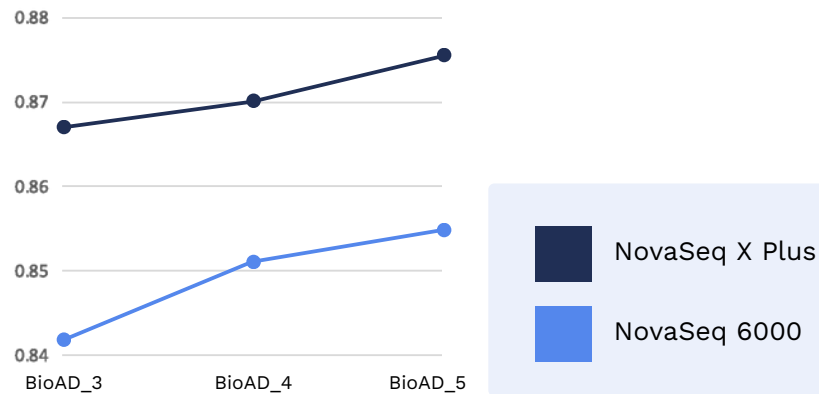
Psomagen labs conducted concordance analysis on our NovaSeq X Plus, and got results that are highly accurate, specific, and sensitive — at levels comparable to the NovaSeq 6000.

We're thrilled to gather positive results on the NovaSeq X Plus — our lab is continuing to improve our processes and get to know one of the newest members of our fleet. Please [visit our website](#) for additional concordance data, a white paper with further performance details, and much more. Here's to many successful runs to come!

Whole Genome Methylation Raw Data Statistics

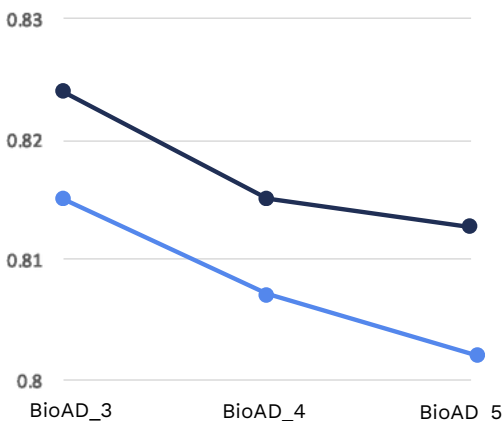
Platform	Q20 (%)	Q30 (%)	% Map Reads	Bisulfite Conversion Rate
NovaSeq X Plus	97.91	95.79	87.08	0.99
NovaSeq 6000	95.35	88.58	84.93	0.99

% Mappable Reads

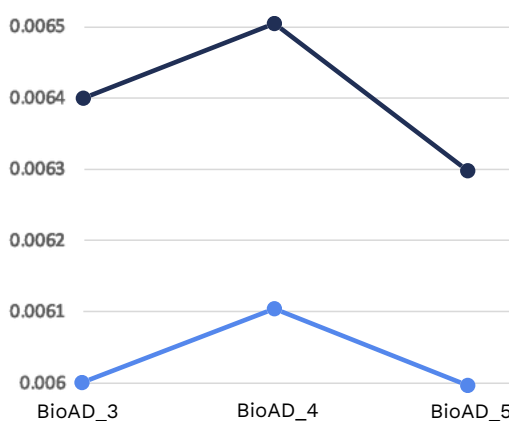


These graphs illustrate the percentage of methylated cytosine in the human genome (hg38). As anticipated, we observe that CHG and CHH types of methylation exhibit less than 5% methylated sites. Here, "H" represents any nucleotide from A, C, or T.

% Methylated CpG Sites



% Methylated CHG Sites



% Methylated CHH Sites

