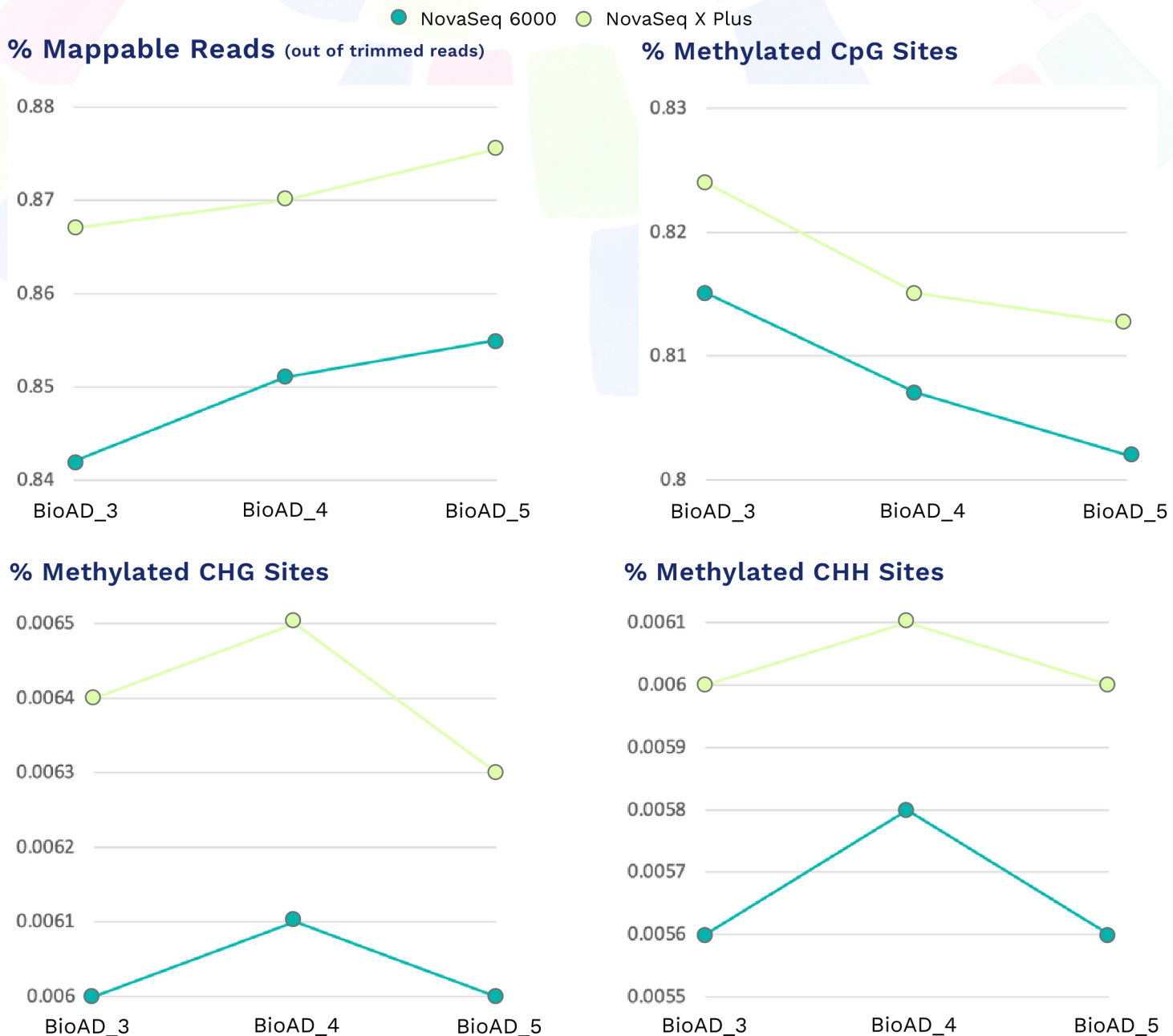


NovaSeq X Plus Concordance Data Whole Genome Methylation

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



The above 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.