

Tab. 1 | Quantitative evaluation of CHH methylation detection by DeepPlant and Dorado.

Species	Tool	Sequencing depth					
		5×	10×	15×	20×	25×	30×
<i>A. thaliana</i>	DeepPlant	0.6410	0.6611	0.6733	0.6853	0.6998	0.7139
	Dorado	0.5908	0.5828	0.5813	0.5795	0.5789	0.5787
<i>B. vulgaris</i>	DeepPlant	0.7655	0.7740	0.7826	0.7920	0.8006	0.8074
	Dorado	0.6385	0.6242	0.6123	0.6062	0.6054	0.6051
<i>O. sativa</i>	DeepPlant	0.6401	0.6535	0.6659	0.6796	0.6937	0.7051
	Dorado	0.3266	0.3292	0.3269	0.3247	0.3237	0.3240
<i>S. tuberosum</i>	DeepPlant	0.8048	0.8173	0.8251	-	-	-
	Dorado	0.6964	0.6899	0.6861	-	-	-
<i>R. communis</i>	DeepPlant	0.8340	0.8532	0.8592	0.8663	0.8742	0.8814
	Dorado	0.7849	0.7819	0.7752	0.7714	0.7713	0.7735
<i>S. miltiorrhiza</i>	DeepPlant	0.8472	0.8524	0.8601	0.8695	0.8780	-
	Dorado	0.7604	0.7500	0.7443	0.7420	0.7441	-
<i>V. vinifera</i>	DeepPlant	0.7268	0.7326	0.7445	0.7588	0.7719	0.7832
	Dorado	0.6499	0.6360	0.6284	0.6233	0.6201	0.6193
<i>C. sinensis</i>	DeepPlant	0.7616	0.7800	0.7949	0.8064	0.8175	0.8259
	Dorado	0.6644	0.6595	0.6563	0.6544	0.6538	0.6533

Note: each value represents the genome-wide Pearson correlation between the methylation callers and whole-genome BS-seq results at the corresponding sequencing depths of down-sampled nanopore datasets. For each species, the same BS-seq dataset (Supplementary Table 2) was used for all tests.

Tab. 2 | Single-molecule evaluation of CHH methylation detection.

Species	Tool	F1-score	Accuracy	Recall	Precision	AUC	AP
<i>A. thaliana</i>	DeepPlant	0.7883	0.8202	0.6697	0.9579	0.8662	0.9039
	Dorado	0.7722	0.8050	0.6611	0.9283	0.8481	0.8800
<i>B. vulgaris</i>	DeepPlant	0.8682	0.8775	0.8072	0.9392	0.9192	0.9405
	Dorado	0.8088	0.8217	0.7544	0.8717	0.8907	0.8942
<i>O. sativa</i>	DeepPlant	0.8867	0.8932	0.8355	0.9446	0.9375	0.9540
	Dorado	0.8186	0.8309	0.7632	0.8828	0.8887	0.9006
<i>S. tuberosum</i>	DeepPlant	0.8869	0.8925	0.8432	0.9355	0.9365	0.9518
	Dorado	0.8042	0.8076	0.7900	0.8188	0.8693	0.8695
<i>R. communis</i>	DeepPlant	0.9008	0.9064	0.8502	0.9578	0.9460	0.9595
	Dorado	0.8577	0.8694	0.7873	0.9419	0.9224	0.9332
<i>S. miltiorrhiza</i>	DeepPlant	0.9051	0.9083	0.8745	0.9378	0.9514	0.9617
	Dorado	0.7920	0.8000	0.7613	0.8252	0.8655	0.8526
<i>V. vinifera</i>	DeepPlant	0.8414	0.8566	0.7608	0.9411	0.8964	0.9227
	Dorado	0.8150	0.8349	0.7274	0.9267	0.8941	0.9096
<i>C. sinensis</i>	DeepPlant	0.8221	0.8433	0.7241	0.9508	0.9256	0.9375
	Dorado	0.7830	0.7788	0.7982	0.7684	0.8579	0.8646

Note: this table presents single-molecule methylation evaluation results of DeepPlant (13-mer model) and Dorado across different species. Corresponding ROC (Receiver Operating Characteristic) and PR (Precision-Recall) curves are provided in Supplementary Fig. 3. And AUC and AP denote area under ROC curve and area under PR curve, respectively.