

**Table 5: Confusion matrix and statistical measures of the *MYBPC3* NCSS variants.**

Tool	Missing values	T P	F P	T N	F N	Accuracy	PP V	Sensitivity	Specificity	NP V	MCC
<b>Alamut Consensus 3/4</b>	0	23	5	22	11	74%	82%	68%	81%	67%	0.49
<b>CADD</b>	0	21	8	19	13	66%	72%	62%	70%	59%	0.32
<b>DSSP</b>	0	23	20	17	11	56%	53%	68%	46%	61%	0.14
<b>GeneSplicer</b>	0	25	7	20	9	74%	78%	74%	74%	69%	0.47
<b>MaxEntScan</b>	0	24	7	20	10	72%	77%	71%	74%	67%	0.44
<b>MMSplice</b>	0	27	14	13	7	66%	66%	79%	48%	65%	0.29
<b>MTSplice</b>	0	18	11	16	16	56%	62%	53%	59%	50%	0.12
<b>NNSplice</b>	0	23	7	20	11	70%	77%	68%	74%	65%	0.41
<b>SCAP</b>	18	20	10	17	14	61%	67%	59%	63%	55%	0.22
<b>Spidex</b>	3	6	3	24	28	49%	67%	18%	89%	46%	0.09
<b>SpliceAI</b>	0	22	8	19	12	67%	73%	65%	70%	61%	0.35
<b>SpliceRover</b>	0	20	10	17	14	61%	67%	59%	63%	55%	0.22
<b>SpliceSiteFinder-like</b>	0	25	7	20	9	74%	78%	74%	74%	69%	0.47

FN – false negatives, FP – false positives, MCC – Mathew’s correlation coefficient, NPV – negative predictive value - PPV – positive predictive value, TN – true negatives, TP – true positives