Additional file 2 - ROC curves of the models shown in Tables 2 and 4

The ROC curves of the optimal LS-SVM models for all considered combinations of data sets shown in Tables 2 and 4 are shown in these additional figures. Additional figures 1 to 3 show the ROC curves for the prediction of WHEELER, pN-STAGE, and CRM in rectal cancer, respectively. For prostate cancer, the ROC curves for the prediction of GRADE, STAGE, METASTASIS, and RECURRENCE are shown in additional figures 4 to 7, respectively.

Figure 1: WHEELER – $MT_0$ (4 genes, blue dotted), $MT_1$ (29 genes, blue solid), $PT_0$ (35 proteins, cyan dotted), $PT_1$ (11 proteins, cyan solid), $MT_0 - T_1$ (32 genes, black dotted), $PT_0 - T_1$ (5 proteins, black solid), $MT_{01}$ (3 genes, magenta dotted), $PT_{01}$ (21 proteins, magenta solid), $MPT_0$ (3 genes, 35 proteins, red dotted), $MPT_1$ (25 genes, 12 proteins, red solid), and $MPT_{01}$ (2 genes, 31 proteins, red dashdotted)
Figure 2: pN-STAGE – \(MT_0\) (25 genes, blue dotted), \(MT_1\) (22 genes, blue solid), \(PT_0\) (2 proteins, cyan dotted), \(PT_1\) (12 proteins, cyan solid), \(MT_0 - T_1\) (4 genes, black dotted), \(PT_0 - T_1\) (9 proteins, black solid), \(MT_{01}\) (24 genes, magenta dotted), \(PT_{01}\) (34 proteins, magenta solid), \(MPT_0\) (27 genes, 27 proteins, red dotted), \(MPT_1\) (21 genes, 14 proteins, red solid), and \(MPT_{01}\) (23 genes, 16 proteins, red dashdotted).

Figure 3: CRM – \(MT_0\) (33 genes, blue dotted), \(MT_1\) (9 genes, blue solid), \(PT_0\) (34 proteins, cyan dotted), \(PT_1\) (34 proteins, cyan solid), \(MT_0 - T_1\) (6 genes, black dotted), \(PT_0 - T_1\) (2 proteins, black solid), \(MT_{01}\) (16 genes, magenta dotted), \(PT_{01}\) (3 proteins, magenta solid), \(MPT_0\) (7 genes, 27 proteins, red dotted), \(MPT_1\) (7 genes, 33 proteins, red solid), and \(MPT_{01}\) (2 genes, 3 proteins, red dashdotted).
Figure 4: GRADE – $M$ (24 genes, blue dotted), $G$ (8 CNVs, black dashdotted), and $MG$ (6 genes, 8 CNV, red solid)

Figure 5: STAGE – $M$ (18 genes, blue dotted), $G$ (32 CNVs, black dashdotted), and $MG$ (42 genes, 22 CNV, red solid)
Figure 6: METASTASIS – $M$ (18 genes, blue dotted), $G$ (12 CNVs, black dashdotted), and $MG$ (18 genes, 3 CNV, red solid)

Figure 7: RECURRENCE – $M$ (24 genes, blue dotted), $G$ (26 CNVs, black dashdotted), and $MG$ (32 genes, 2 CNV, red solid)