

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.

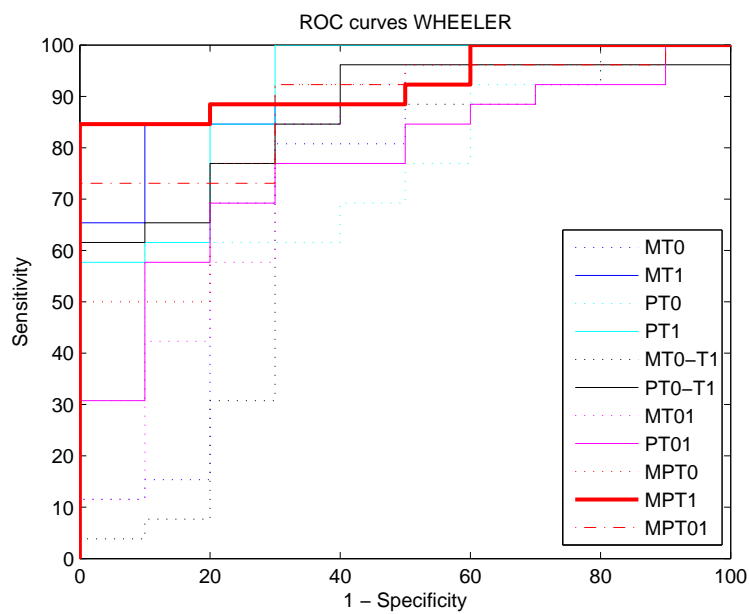


Figure 1: WHEELER – MT_0 (4 genes, blue dotted), MT_1 (29 genes, blue solid), PT_0 (35 proteins, cyan dotted), PT_1 (11 proteins, cyan solid), $MT_0 - T_1$ (32 genes, black dotted), $PT_0 - T_1$ (5 proteins, black solid), MT_{01} (3 genes, magenta dotted), PT_{01} (21 proteins, magenta solid), MPT_0 (3 genes, 35 proteins, red dotted), MPT_1 (25 genes, 12 proteins, red solid), and MPT_{01} (2 genes, 31 proteins, red dashdotted)

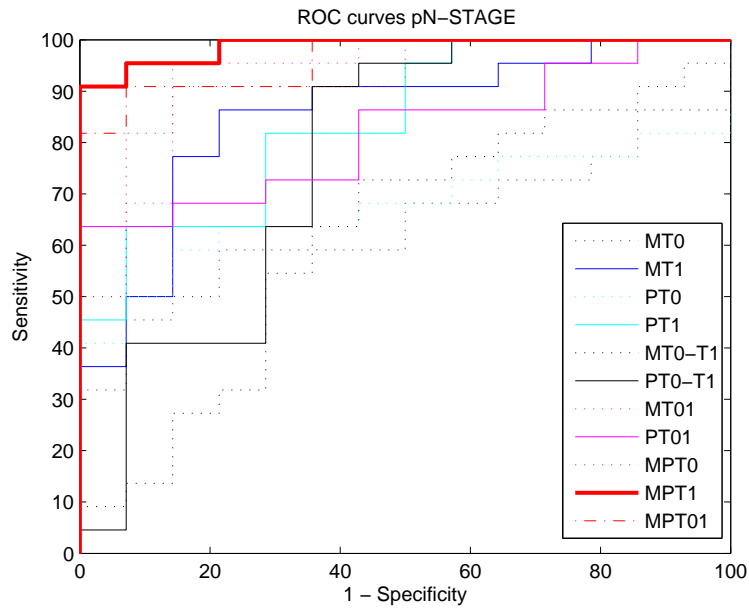


Figure 2: pN-STAGE – MT_0 (25 genes, blue dotted), MT_1 (22 genes, blue solid), PT_0 (2 proteins, cyan dotted), PT_1 (12 proteins, cyan solid), $MT_0 - T_1$ (4 genes, black dotted), $PT_0 - T_1$ (9 proteins, black solid), MT_{01} (24 genes, magenta dotted), PT_{01} (34 proteins, magenta solid), MPT_0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

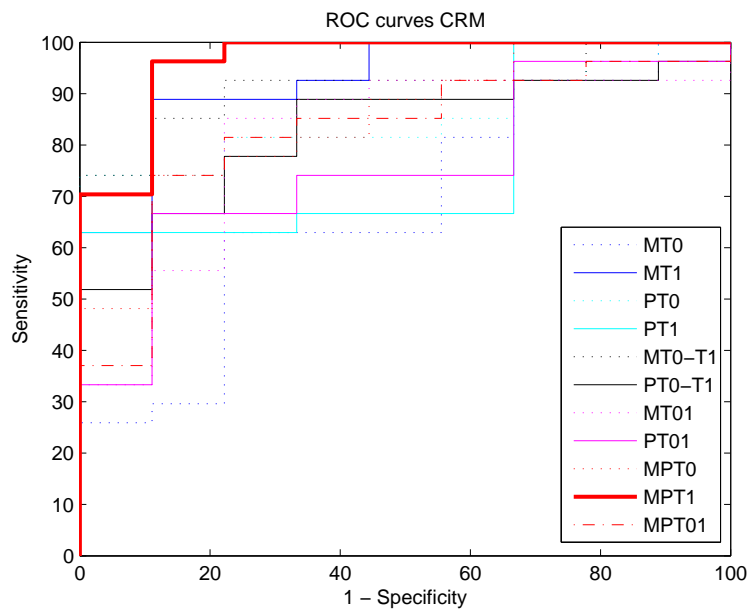


Figure 3: CRM – MT_0 (33 genes, blue dotted), MT_1 (9 genes, blue solid), PT_0 (34 proteins, cyan dotted), PT_1 (34 proteins, cyan solid), $MT_0 - T_1$ (6 genes, black dotted), $PT_0 - T_1$ (2 proteins, black solid), MT_{01} (16 genes, magenta dotted), PT_{01} (3 proteins, magenta solid), MPT_0 (7 genes, 27 proteins, red dotted), MPT_1 (7 genes, 33 proteins, red solid), and MPT_{01} (2 genes, 3 proteins, red dashdotted)

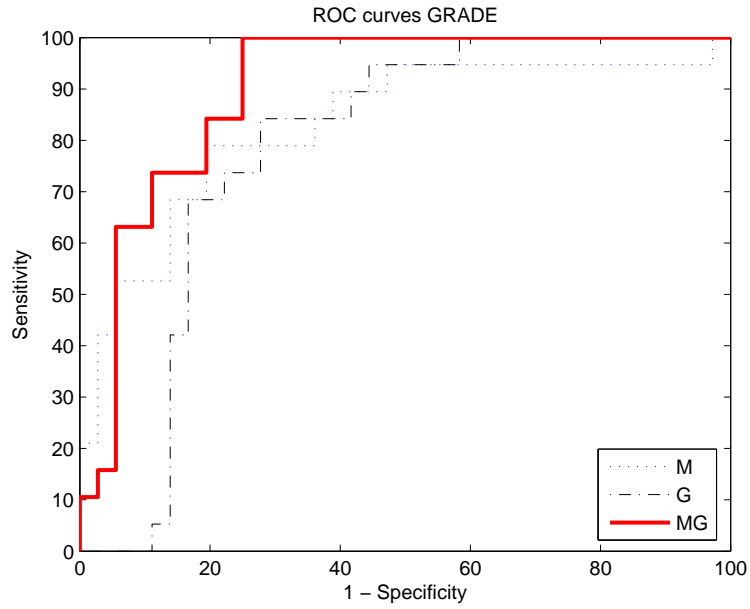


Figure 4: GRADE – *M* (24 genes, blue dotted), *G* (8 CNVs, black dashdotted), and *MG* (6 genes, 8 CNV, red solid)

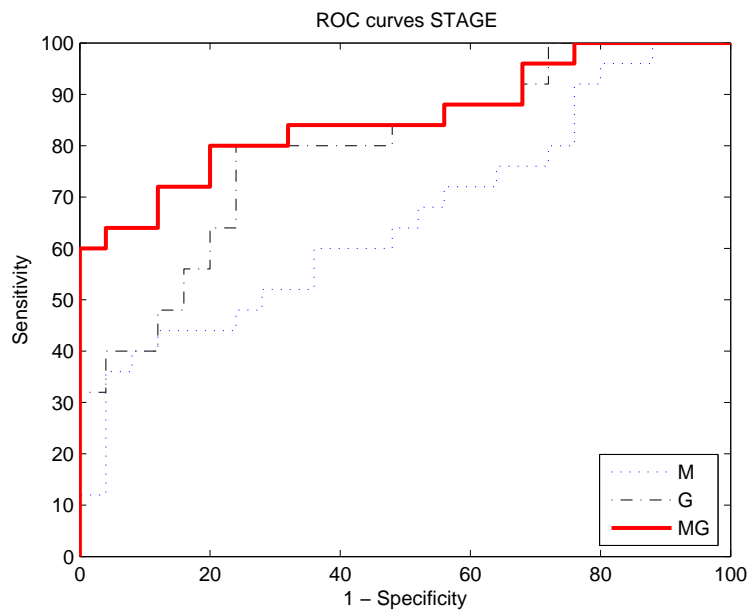


Figure 5: STAGE – *M* (18 genes, blue dotted), *G* (32 CNVs, black dashdotted), and *MG* (42 genes, 22 CNV, red solid)

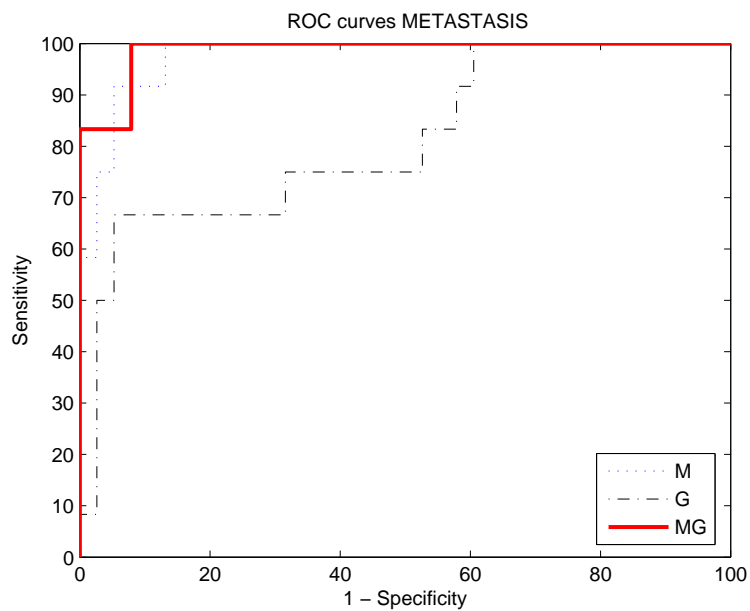


Figure 6: METASTASIS – M (18 genes, blue dotted), G (12 CNVs, black dashdotted), and MG (18 genes, 3 CNV, red solid)

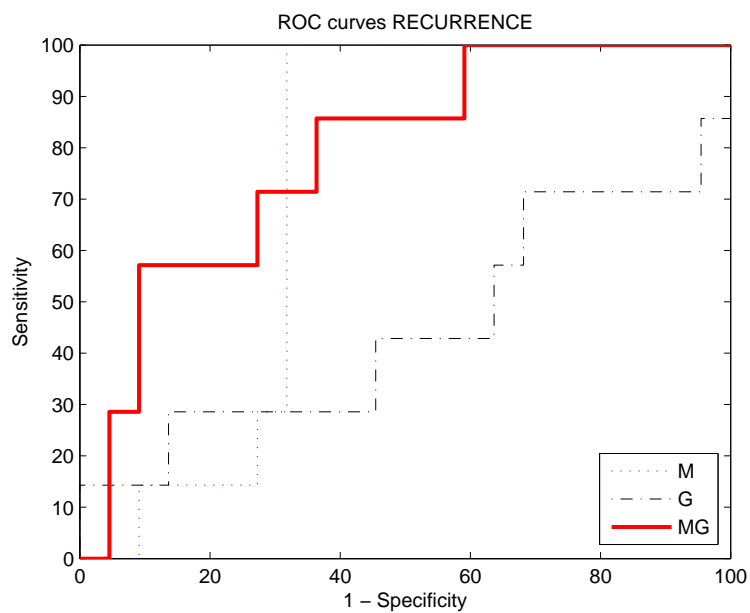


Figure 7: RECURRENCE – M (24 genes, blue dotted), G (26 CNVs, black dashdotted), and MG (32 genes, 2 CNV, red solid)