**Table S1.** Clinical-pathological and genomic variable (*n* = 21) used to calculate the PAM50MET model.

PAM50MET, final model.

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| --- | --- | --- | --- |
|  | **Type of variable** | **Direction** | **Coefficient** |
| Performance status (PS) 0 | binary | PS 0 better outcome than PS1 | -0.178 |
| PAM50LumA | binary | PAM50 LumA subtype better outcome than the rest | -0.160 |
| SLC39A6 | continuous | High expression of SLC39A6 better outcome | -0.066 |
| MAPT | continuous | High expression of MAPT better outcome | -0.036 |
| PGR | continuous | High expression of PGR better outcome | -0.012 |
| NAT1 | continuous | High expression of NAT1 better outcome | -0.008 |
| ESR1 | continuous | High expression of ESR1 poorer outcome | -0.003 |
| AGE | continuous | High expression of AGE poorer outcome | -0.003 |
| TMEM45B | continuous | High expression of TMEM45B poorer outcome | -0.002 |
| UBE2T | continuous | High expression of UBE2T poorer outcome | 0.003 |
| GPR160 | continuous | High expression of GPR160 poorer outcome | 0.011 |
| NUF2 | continuous | High expression of NUF2 poorer outcome | 0.018 |
| FOXA1 | continuous | High expression of FOXA1 poorer outcome | 0.020 |
| GRB7 | continuous | High expression of GRB7 poorer outcome | 0.038 |
| FGFR4 | continuous | High expression of FGFR4 poorer outcome | 0.050 |
| PHGDH | continuous | High expression of PHGDH poorer outcome | 0.107 |
| CCNB1 | continuous | High expression of CCNB1 poorer outcome | 0.131 |
| FFPEPrimary | binary | FFPE Primary tumor biopsy poorer outcome than FFPE Metastatic tumor biopsy | 0.147 |
| Number of metastasis ≥3 | binary | Num. of metastases ≥3 poorer outcome than Num. of metastases <3  | 0.265 |
| PAM50 Basal-like signature | continuous | High expression of PAM50 Basal-like signature poorer outcome | 0.444 |
| PAM50HER2-E | binary | PAM50HER2-E subtype poorer outcome than nonPAM50HER2-E subtype | 0.678 |