Gene expression profile association with poor prognosis in epithelial ovarian cancer patients

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Supplementary information

Supplementary Table S1

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| Histologic | HSPA1A | | CD99 | | RAB3A | | POM121L9P | |
|--------------|--------|----------|--------|----------|--------|----------|-----------|----------|
| subtype | Median | Std.Dev. | Median | Std.Dev. | Median | Std.Dev. | Median | Std.Dev. |
| Clear Cell | 9.456 | 0.812 | 9.348 | 0.611 | 5.789 | 0.292 | 3.364 | 0.437 |
| Endometrioid | 9.121 | 0.576 | 9.248 | 1.049 | 5.718 | 0.420 | 3.153 | 0.461 |
| Mucinous | 9.668 | 0.629 | 9.188 | 0.268 | 5.781 | 0.431 | 3.498 | 0.389 |
| Serous | 9.933 | 0.724 | 8.949 | 0.623 | 5.929 | 0.427 | 3.284 | 0.714 |

Supplementary Table S1. Median expression values of *HSPA1A*, *CD99*, *RAB3A* and *POM121L9P* in each histologic subtype. Std.Dev.= standard deviation.



Supplementary Figure S1. Gene expression in "low risk" (blue) and "high risk" (orange) groups. Values are normalized and provided as log2 and P-value is presented above.

0.0

1.0

0.8







Supplementary Figure S2. Overal survival curves for each candidate (*HSPA1A*, *CD99*, *RAB3A* and *POM121L9P*) individually in "high risk" (red) and "low risk" (blue) groups (a-d). (e)ROC/AUC for RAB3A alone for 60 months patient OS. P-values are presented above.

AUC: 0.694

0.2

0.0

0.4

Specificity

0.6





С



Supplementary Figure S3. (a) Survival curve between "high risk" (red) and "low risk" (blue) in serous adenocarcinoma subtype. (b) Survival curve between serous adenocarcinoma and other OC subtypes. (c) AUC/ROC curve of combination of HSPA1A, CD99, RAB3A and POM121L9P in serous adenocarcinoma x other OC subtypes. P-values and AUC are presented above.



Supplementary Figure S4. Gene expression in all OC subtypes for *HSPA1A* (a), *CD99* (b), *RAB3A* (c) and *POM121L9P* (d). Values are normalized and provided as log2 and P-values are presented above.



Supplementary Figure S5. Survival curve between "high risk" (red) and "low risk" (blue) in high grade serous adenocarcinoma subtype. P-value is presented above.



Supplementary Figure S6. (a) Progression-free survival curve between "high risk" (red) and "low risk" (blue) in serous adenocarcinoma subtype. (b) Progression-free survival curve between serous adenocarcinoma and other OC subtypes. P-values are presented above.







| | 1 | 96 patient | GSE26193 cohort | | | | |
|----------------|----------------|------------|-----------------|-------|--------|-------|-------|
| | Classification | median | lower | upper | median | lower | upper |
| 4 targets | High_risk | 19.74 | 9.86 | 44.38 | 13.03 | 6.37 | |
| signature | Low_risk | 51.98 | 44.52 | 64.93 | 41.89 | 32.49 | 57.10 |
| Matondo et al. | High_risk | 26.60 | 18.38 | 42.87 | 29.08 | 20.73 | 50.69 |
| signature | Low_risk | 55.38 | 47.61 | 72.93 | 45.77 | 33.68 | 75.10 |

Supplementary Figure S7. Validation study. (a) Survival curve shows that "high risk" (all candidates overexpressed) group has a shorter survival compared to "low risk" OC patients, and (b) AUC/ROC curve of combination of HSPA1A, CD99, RAB3A and POM121L9P for 5-year OS in cohort GSE26193 (n= 107). The 97-gene signature performance from Matondo et al. (2017) in our current cohort (n=196) showing (c) Heatmap and classification of "high-" (red) and "low risk" (high) groups. (d) K-M curve for the "high-" and "low risk" groups, and table with median OS of patients on both cohorts and both signature panels. P-values and AUC are presented above.

а

b



GSE26193 Heatmap (Matondo classification)



Supplementary Figure S8. Assessment of the 97-gene signature panel from Matondo and colleagues on cohort GSE26193 (n= 107). (a) Survival curve shows that "high risk" group has a shorter survival compared to "low risk" OC patients. (b) Heatmap and classification of "high-" (red) and "low risk" (high) groups. P-value is presented above.