**Supplementary Table 1.** **Characteristics of Study Participants with High Grade Serous Tubo-Ovarian Carcinoma by Contributing Study**

|  | **TCGA (N=372)** | **Mayo Clinic (N=325)** | **UCL****(N=158)** | **UIHC****(N=81)** | **AOCS****(N=68)** | **OHSU (N=36)** | **Total (N=1,040)** | **p value** |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Age at diagnosis, yrs** |  |  |  |  |  |  |  | 0.010 |
|    Mean  (range) | 60.0 (30ꟷ84) | 62.6 (33ꟷ86) | 59.0 (28ꟷ84) | 60.1 (29ꟷ85) | 60.7 (44ꟷ78) | 62.3 (20ꟷ80) | 60.8 (20ꟷ86) |  |
| **Stage** |  |  |  |  |  |  |  | 0.18 |
|    Early | 19 (5%) | 18 (6%) | 12 (8%) | 3 (4%) | 0 | 3 (11%) | 55 (5%) |  |
|    Advanced | 353 (95%) | 307 (94%) | 146 (92%) | 76 (96%) | 68 (100%) | 24 (89%) | 974 (95%) |  |
|    Unknown | 0 | 0 | 0 | 2 | 0 | 9 | 11 |  |
| **Debulking status** |  |  |  |  |  |  |  | 4.3 x 10-7 |
|    < 1 cm remaining | 276 (74%) | 260 (80%) | 88 (56%) | 53 (65%) | 42 (62%) | 28 (78%) | 747 (72%) |  |
|    >= 1 cm remaining | 96 (26%) | 65 (20%) | 70 (44%) | 28 (35%) | 26 (38%) | 8 (22%) | 293 (28%) |  |
| **Germline pathogenic** **deleterious *BRCA1/2*****mutation** |  |  |  |  |  |  |  | 0.61 |
|    *BRCA1* mutation | 16 (7%) | 18 (8%) | 0 | 0 | 7 (10%) | 0 (0%) | 41 (8%) |  |
|    *BRCA2* mutation | 15 (6%) | 15 (6%) | 0 | 0 | 2 (3%) | 1 (25%) | 33 (6%) |  |
|    *BRCA1* & *BRCA2* mutation | 2 (1%) | 0  | 0 | 0 | 0 (0%) | 0 (0%) | 2 (0%) |  |
|    Tested non-carrier | 199 (86%) | 198 (86%) | 0 | 0 | 59 (87%) | 3 (75%) | 459 (86%) |  |
|    Unknown | 140 | 94 | 158 | 81 | 0 | 32 | 505 |  |
| **Gene expression molecular**  **subtype** |  |  |  |  |  |  |  | 1.8 x 10-4 |
|  C1.MES | 89 (24%) | 82 (27%) | 0 | 0 | 32 (49%) | 0 | 203 (27%) |  |
|  C2.IMM | 79 (21%) | 83 (27%) | 0 | 0 | 10 (15%) | 0 | 172 (23%) |  |
|  C4.DIF | 105 (28%) | 64 (21%) | 0 | 0 | 17 (26%) | 0 | 186 (25%) |  |
|  C5.PRO | 98 (26%) | 80 (26%) | 0 | 0 | 7 (11%) | 0 | 185 (25%) |  |
|  Unknown | 1 | 16 | 158 | 81 | 2 | 36 | 294 |  |
| **CD8+ TIL level** |  |  |  |  |  |  |  | 0.20 |
|  Negative | 0 | 36 (19%) | 0 | 0 | 4 (29%) | 4 (24%) | 44 (20%) |  |
|  Low | 0 | 27 (14%) | 0 | 0 | 3 (21%) | 6 (35%) | 36 (16%) |  |
|  Moderate | 0 | 96 (50%) | 0 | 0 | 4 (29%) | 6 (35%) | 106 (48%) |  |
|  High | 0 | 32 (17%) | 0 | 0 | 3 (21%) | 1 (6%) | 36 (16%) |  |
|  Unknown | 372 | 134 | 158 | 81 | 54 | 19 | 818 |  |
| **Normalized TAP1 mRNA expression** |  |  |  |  |  |  |  | 0.43 |
|  Mean (Range) | 0.006(-3.53-3.11) | -0.04(-5.89-2.32) | NA | NA | -0.25(-2.67-1.45) | NA | -0.03(-5.89-3.11) |  |
|  Unknown | 112 | 13 | 158 | 81 | 35 | 36 | 435 |  |
| **Vital status** |  |  |  |  |  |  |  |  |
|  Deceased | 207 (56%) | 265 (81%) | 122 (77%) | 64 (87%) | 57 (84%) | 22 (61%) | 737 (71%) | 1.1 x 10-15 |
|  Alive | 165 (44%) | 60 (19%) | 36 (238%) | 10 (13%) | 11 (16%) | 14 (39%) | 296 (29%) |  |
|  Unknown | 0 | 0 | 0 | 7 | 0 | 0 | 7 |  |
| **Median overall survival, yrs** | 3.65 | 3.76 | 3.25 | 2.23 | 1.89 | 3.96 | 3.35 | 4.1 x 10-5 |
| **Median follow-up among living, yrs** |  |  |  |  |  |  |  | 1.0 x 10-65 |
|  Median  (Range) | 2.1(0.04 - 10) | 10.0(8.9 - 10) | 6.4(0.5 - 10) | 3.5(0.5 - 10) | 10.0(0.7 - 10) | 5.7(0.4 - 9.9) | 4.5(0.04 - 10) |  |
| **Detailed outcome event** |  |  |  |  |  |  |  | NE |
|  Death | 12 (3%) | 62 (19%) | 122 (77%) | 0 (0%) | 58 (85%) | 4 (11%) | 258 (25%) |  |
|  Persistent Disease | 0 (0%) | 39 (12%) | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 39 (4%) |  |
|  Progression | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 3 (4%) | 0 (0%) | 3 (0%) |  |
|  Recurrence | 0 (0%) | 195 (60%) | 0 (0%) | 0 (0%) | 0 (0%) | 25 (69%) | 220 (21%) |  |
|  Recurrence/Progression | 267 (72%) | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 267 (26%) |  |
|  Recurrence/Progression/ Death | 0 (0%) | 0 (0%) | 0 (0%) | 74 (91%) | 0 (0%) | 0 (0%) | 74 (7%) |  |
|  No Event | 93 (25%) | 29 (9%) | 36 (23%) | 7 (9%) | 7 (10%) | 7 (19%) | 179 (17%) |  |
| **Combined outcome event** |  |  |  |  |  |  |  | 7.3 x 10-8 |
|  First event (Death/ Persistence/ Progression/ Recurrence) | 279 (75%) | 296 (91%) | 122 (77%) | 74 (91%) | 61 (90%) | 29 (81%) | 861 (838%) |  |
|  None | 93 (25%) | 29 (9%) | 36 (23%) | 7 (9%) | 7 (10%) | 7 (19%) | 179 (17%) |  |
| **Median time to event, yrs** | 1.40 | 1.35 | 3.25 | 0.75 | 0.82 | 1.74 | 1.49 | 2.1 x 10-21 |
| **Median follow-up among those without event, yrs** |  |  |  |  |  |  |  | 1.5 x 10-43 |
|  Median (Range) | 0.7(0.04 - 7.6) | 10.0(8.9 - 10) | 6.4(0.5 - 10) | 1.3(0.5 - 10) | 10.0(5.5 - 10) | 5.2(0.4 - 9.9) | 3.9(0.04 - 10) |  |
| **Illumina Infinium BeadChip** |  |  |  |  |  |  |  | NE |
| HumanMethylation27 | 372 (100%) | 0 | 0 | 0 | 0 | 0 | 372 (36%) |  |
| HumanMethylation450 | 0 | 325 (100%) | 158 (100%) | 0 | 68 (100%) | 0 | 551 (53%) |  |
| MethylationEPIC | 0 | 0 | 0 | 81 (100%) | 0 | 36 (100%) | 117 (11%) |  |
| **Methylation signature** |  |  |  |  |  |  |  | 0.49 |
|  Mean (Range) | -0.032(-0.72-0.82) | -0.021(-0.81-0.80) | 0.007(-0.65-0.68) | -0.081(-0.73-0.52) | -0.019(-0.67-0.55) | -0.074(-0.64-0.55) | -0.027(-0.81-0.81) |  |

TCGA, Cancer Genome Atlas Research Network 2011, overlapping Mayo Clinic cases excluded; MAY participants were among those previously analyzed (Wang et al., 2014) and here are included with updated endpoints; UCL, Bartlett, Jones et al. 2015; UIHC, Reyes, Devor et al. 2019; AOCS, Patch, Christie et al. 2015; Moran, Martinez-Cardus et al. 2016, Curry, Zeller et al. 2018, Natanzon, Earp et al. 2018; OHSU, Pejovic, Pande et al. 2009, White, Vierkant et al. 2013; NE, not estimated; Levels of CD8+ TILs per high powered field: negative, low [1-2 CD8+ TILs], moderate [3-19 CD8+ TILs], high [>20 CD8+ TILs] ascertained by immunohistochemistry (Ovarian Tumor Tissue Analysis Consortium et al., 2017)