**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)