**Table 1.** Clinical demographics of the 38 metastatic osteosarcomas.

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| --- | --- | --- | --- | --- |
| Characteristic | Group A | Group B | Statistical method | *p* value |
| n (%) | 12 (31.6) | 26 (68.4) |  |  |
| Age at diagnosis (in years) |  |  | T test | 0.060 |
| Range | 6-61 | 6-57 |  |  |
| Median (Q1, Q3) | 19.5 (13.25, 38.75) | 14 (11, 17.5) |  |  |
| Gender, n (%) |  |  | Chi-square | 1.000 |
| Male | 9 (23.7) | 20 (52.6) |  |  |
| Female | 3 (7.9) | 6 (15.8) |  |  |
| Paired primary osteosarcoma, n (%) |  |  | Chi-square | 0.033a |
| Yes | 8 (21.1) | 7 (18.4) |  |  |
| No | 4 (10.5) | 19 (50.0) |  |  |
| Primary sample site, n (%) |  |  | Chi-square | 0.280 |
| Femur | 8 (21.1) | 16 (42.1) |  |  |
| Humerus | 0 (0.0) | 3 (7.9) |  |  |
| Tibia | 2 (5.3) | 6 (15.8) |  |  |
| Pelvis | 1 (2.6) | 1 (2.6) |  |  |
| Spine | 1 (2.6) | 0 (0.0) |  |  |
| Metastatic sample site, n (%) |  |  | Chi-square | 0.000a |
| Femur | 2 (5.3) | 3 (7.9) |  |  |
| Fibula | 2 (5.3) | 1 (2.6) |  |  |
| Tibia | 0 (0.0) | 2 (5.3) |  |  |
| Pelvis | 4 (10.5) | 0 (0.0) |  |  |
| Rib | 1 (2.6) | 0 (0.0) |  |  |
| Sacrum | 1 (2.6) | 0 (0.0) |  |  |
| Spine | 2 (5.3) | 1 (2.6) |  |  |
| Lung | 0 (0.0) | 19 (50.0) |  |  |
| Genomic type, n (%) |  |  | Chi-square | 0.018a |
| SNV | 10 (26.3) | 11 (28.9) |  |  |
| SV or mixed | 2 (5.3) | 15 (39.5) |  |  |
| TMB |  |  | Wilcoxon | 0.010a |
| Range | 1.1-32.9 | 0-14.2 |  |  |
| Median (Q1, Q3) | 4.85 (2.75, 11.98) | 2.4 (1.38, 4.45) |  |  |
| MSI status, n (%) |  |  | Chi-square | 0.316 |
| MSS | 11 (29.0) | 26 (68.4) |  |  |
| MSI-H | 1 (2.6) | 0 (0.0) |  |  |
| Neoantigen |  |  | Wilcoxon | 0.0028a |
| Range | 57-2084 | 0-1539 |  |  |
| Median (Q1, Q3) | 743 (316.5, 1034.5) | 128.5 (49, 200.5) |  |  |
| HED status, n (%) |  |  | Chi-square | 1.000 |
| Low | 10 (26.3) | 22 (57.9) |  |  |
| High | 2 (5.3) | 4 (10.5) |  |  |
| Adjuvant therapy, n (%) |  |  |  |  |
| First-line treatment | 11 (29.0) | 25 (65.8) | Chi-square | 0.538 |
| Second-line treatment | 9 (23.7) | 22 (57.9) | Chi-square | 0.656 |
| Third-line treatment | 5 (13.2) | 10 (26.3) | Chi-square | 1.000 |
| Fourth-line treatment | 2 (5.3) | 5 (13.2) | Chi-square | 1.000 |
| Vital status, n (%) |  |  | Chi-square | 0.108 |
| Alive | 7 (18.4) | 22 (57.9) |  |  |
| Dead | 5 (13.2) | 4 (10.5) |  |  |
| PFS (mo) |  |  | T test | 0.596 |
| Range | 0-48.23 | 2.23-34.43 |  |  |
| Median (Q1, Q3) | 12.4 (7.45, 21.22) | 13.95 (8.00, 19.75) |  |  |
| OS or follow-up time (mo) |  |  | T test | 0.856 |
| Range | 7-59 | 9-54 |  |  |
| Median (Q1, Q3) | 23.5 (15.25, 46.5) | 27 (16.75, 38.25) |  |  |

Abbreviations: SNV, single nucleotide variation; Amp, amplification; Fus, fusion; TMB, tumor mutation burden; MSI, microsatellite instability; MSS, microsatellite stability; MSI-H, microsatellite instability-high; PFS, progression free survival; Mo, month; OS, overall survival.

HED, human leukocyte antigen-I evolutionary divergence. HED score> 7.887, defined as HED high; HED score ≤ 7.887, defined as HED low.

a *p* value less than 0.05.