Bespoke Circulating Tumor DNA (ctDNA) Analysis as a Predictive Biomarker in Solid Tumor Patients (pts) Treated with Single Agent Pembrolizumab (P)

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HSA primary tumour patients treated with single agent pembrolizumab (P).

**Table 1. Patient Demographics and Outcome**

| Subgroup | N | Mean Age (yr) | Sex (F:M) | Race (C:A) | BIctDNA Status Positive (%) | BIctDNA Measured Molecules/mL | BIctDNA Median (SD) | BIctDNA Mean (SD) | BIctDNA Increase from Baseline % | CIctDNA Status Positive (%) | CIctDNA Measured Molecules/mL | CIctDNA Median (SD) | CIctDNA Mean (SD) | CIctDNA Increase from Baseline % | CRctDNA Status Positive (%) | CRctDNA Measured Molecules/mL | CRctDNA Median (SD) | CRctDNA Mean (SD) | CRctDNA Increase from Baseline % |
|----------|---|---------------|-----------|-----------|----------------------------|-------------------------------|---------------------------|-------------------|---------------------------------|----------------------------|-----------------------------|---------------------------|----------------|----------------------------|----------------------------|-----------------------------|-----------------------------|----------------|----------------|----------------------------|
| Cohort A | 6 | 63.0 (7.9)    | 5:1       | 4:2       | 40.0%                       | 0.69 (0.58)                  | 1000                      | 1000              | -96.1%                          | 20.0%                      | 0.20 (0.16)                | 1000                      | 1000          | 96.1%                        | 20.0%                      | 1000                      | 1000          | 96.1%                        | 20.0%                      |
| Cohort B | 10 | 63.5 (7.9)   | 6:4       | 8:2       | 20.0%                       | 0.69 (0.58)                  | 1000                      | 1000              | -96.1%                          | 20.0%                      | 0.20 (0.16)                | 1000                      | 1000          | 96.1%                        | 20.0%                      | 1000                      | 1000          | 96.1%                        | 20.0%                      |
| Cohort C | 10 | 63.5 (7.9)   | 6:4       | 8:2       | 20.0%                       | 0.69 (0.58)                  | 1000                      | 1000              | -96.1%                          | 20.0%                      | 0.20 (0.16)                | 1000                      | 1000          | 96.1%                        | 20.0%                      | 1000                      | 1000          | 96.1%                        | 20.0%                      |
| Cohort D | 10 | 63.5 (7.9)   | 6:4       | 8:2       | 20.0%                       | 0.69 (0.58)                  | 1000                      | 1000              | -96.1%                          | 20.0%                      | 0.20 (0.16)                | 1000                      | 1000          | 96.1%                        | 20.0%                      | 1000                      | 1000          | 96.1%                        | 20.0%                      |

**Conclusions**
- All clinical correlation exists between ctDNA with QOL, PRS, CR, ORR and CR to patients treated with pembrolizumab.
- ctDNA can predict radiographic response.
- Limitations of study include small sample size and heterogeneous histologies.
- Future plans include:
  - Complete additional ctDNA analysis between baseline and cycle 3.
  - Conduct additional ctDNA analysis between baseline and cycle 3.
  - Contact the lead investigator after the CT scan.
  - Contact oncology and radiation oncology.
  - Conduct follow-up using a larger and more heterogeneous cohort.

**References**