**SUPPLEMENTARY DATA**

**A randomized phase II trial of adjuvant hepatic arterial infusion and systemic therapy with or without panitumumab after hepatic resection of KRAS wild-type colorectal cancer**

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**Figure S1: OS according to randomization arm and PIk3CA alteration**



Abbreviations: A, arm A; B, arm B; HAI, hepatic arterial infusion; MUT, mutant; Pmab, panitumumab; Sys, systemic therapy; WT, wildtype.

**Table S1: Treatment Schedule**

|  |  |  |  |
| --- | --- | --- | --- |
| **Day 1** | **Day 15** | **Day 29** | **Day 36**  **(day 1 of next cycle)** |
| HAI FUDR\* + dexamethasone | Systemic chemotherapy† +/- Pmab‡ | Systemic chemotherapy†  +/- Pmab‡ | HAI FUDR + dexamethasone |

Abbreviations: FUDR, floxuridine; HAI, hepatic arterial infusion; Pmab, panitumumab.

\* FUDR: 0.12 mg/Kg x 30/flow rate, dexamethasone flat dose 25 mg.

‡ Irinotecan 125-150 mg/m2, 5FU (fluorouracil) 2000 mg/m2 48-hour infusion, leucovorin 400 mg/m2.

‡ Patients randomized to Pmab 6 mg/kg on days 15 and 29 only.

**Table S2: Genomic profile by randomization arm\***

|  |  |  |  |
| --- | --- | --- | --- |
| **Characteristic** | **Arm A**  **(+ Pmab)**  **n = 37** | **Arm B**  **(no Pmab)**  **n = 38** | ***P* value** |
| **APC** |  |  | 0.4 |
| Altered | 20 (83) | 18 (69) |  |
| WT | 4 (17) | 8 (31) |  |
| Unknown | 13 | 12 |  |
| **TP53** |  |  | 0.3 |
| Altered | 21 (88) | 19 (73) |  |
| WT | 3 (12) | 7 (27) |  |
| Unknown | 13 | 12 |  |
| **PIK3CA** |  |  | 0.2 |
| Altered | 3 (8.1) | 8 (21) |  |
| WT | 34 (92) | 30 (79) |  |
| **SOX9** |  |  | 0.5 |
| Altered | 5 (21) | 3 (12) |  |
| WT | 19 (79) | 23 (88) |  |
| Unknown | 13 | 12 |  |
| **SMAD4** |  |  | >0.9 |
| Altered | 3 (12) | 3 (12) |  |
| WT | 21 (88) | 23 (88) |  |
| Unknown | 13 | 12 |  |
| **CDK8** |  |  | >0.9 |
| Altered | 3 (12) | 3 (12) |  |
| WT | 21 (88) | 23 (88) |  |
| Unknown | 13 | 12 |  |
| **BCL2L1** |  |  | 0.7 |
| Altered | 4 (17) | 3 (12) |  |
| WT | 20 (83) | 23 (88) |  |
| Unknown | 13 | 12 |  |
| **FLT3** |  |  | >0.9 |
| Altered | 3 (12) | 3 (12) |  |
| WT | 21 (88) | 23 (88) |  |
| Unknown | 13 | 12 |  |
| **DNMT3B** |  |  | >0.9 |
| Altered | 3 (12) | 3 (12) |  |
| WT | 21 (88) | 23 (88) |  |
| Unknown | 13 | 12 |  |
| **SRC** |  |  | 0.093 |
| Altered | 5 (21) | 1 (3.8) |  |
| WT | 19 (79) | 25 (96) |  |
| Unknown | 13 | 12 |  |

Values are n (%). P value calculated by Fisher's exact test.

\* Only genes with ≥10% mutation rates in the tumor samples analyzed are included in this table. Mutations in *NRAS* and *BRAF* in patients enrolled before the protocol was updated to include 2 NRAS (1 in each arm and 2 BRAF; both in arm B) no mutations in *AKT1* or *MEK1* were found.

**Table S3:** **Association between frequently mutated gene and survival**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Variable** | **Obs.** | **RFS**  **36 months (95% CI)** | ***P* value** | **OS 36 months (95% CI)** | ***P* value** |
| **Overall** | 75 | 48.9 (36.9, 59.9) |  | 93.9 (84.5, 97.7) |  |
| **Any APC alteration** |  |  | 0.426 |  | 0.122 |
| WT | 12 | 33.3 (10.3, 58.8) |  | 81.8 (44.7, 95.1) |  |
| Altered | 38 | 48.2 (31.2, 63.2) |  | 97.3 (82.3, 99.6) |  |
| **Any TP53 alteration** |  |  | 0.576 |  | 0.493 |
| WT | 10 | 50.0 (18.4, 75.3) |  | 100.0 (100.0, 100.0) |  |
| Altered | 40 | 42.7 (26.7, 57.8) |  | 91.1 (74.9, 97.1) |  |
| **Any PIK3CA alteration** |  |  | 0.185 |  | **<.001** |
| WT | 64 | 49.9 (36.9, 61.6) |  | 98.1 (87.4, 99.7) |  |
| Altered | 11 | 45.5 (16.7, 70.7) |  | 68.2 (28.6, 88.9) |  |
| **Any SOX9 alteration** |  |  | 0.282 |  | 0.823 |
| WT | 42 | 40.3 (25.0, 55.1) |  | 91.6 (76.2, 97.2) |  |
| Altered | 8 | 62.5 (22.9, 86.1) |  | 100.0 (100.0, 100.0) |  |
| **Any SMAD4 alteration** |  |  | 0.347 |  | 0.939 |
| WT | 44 | 40.8 (25.8, 55.2) |  | 95.0 (81.2, 98.7) |  |
| Altered | 6 | 66.7 (19.5, 90.4) |  | 80.0 (20.4, 96.9) |  |
| **Any CDK8 alteration** |  |  | 0.124 |  | 0.438 |
| WT | 44 | 48.0 (32.2, 62.1) |  | 94.9 (80.9, 98.7) |  |
| Altered | 6 | 16.7 (0.8, 51.7) |  | 83.3 (27.3, 97.5) |  |
| **Any BCL2L1 alteration** |  |  | 0.506 |  | 0.259 |
| WT | 43 | 45.5 (30.0, 59.7) |  | 92.2 (77.8, 97.4) |  |
| Altered | 7 | 34.3 (4.8, 68.5) |  | 100.0 (NA, NA) |  |
| **Any FLT3 alteration** |  |  | 0.589 |  | 0.705 |
| WT | 44 | 46.1 (30.6, 60.2) |  | 92.2 (77.8, 97.4) |  |
| Altered | 6 | 33.3 (4.6, 67.6) |  | 100.0 (NA, NA) |  |
| **Any DNMT3B alteration** |  |  | 0.381 |  | 0.259 |
| WT | 44 | 45.9 (30.4, 60.1) |  | 92.2 (77.8, 97.4) |  |
| Altered | 6 | 33.3 (4.6, 67.6) |  | 100.0 (NA, NA) |  |
| **Any SRC alteration** |  |  | 0.236 |  | 0.417 |
| WT | 44 | 48.6 (32.9, 62.6) |  | 92.4 (78.2, 97.5) |  |
| Altered | 6 | 16.7 (0.8, 51.7) |  | 100.0 (NA, NA) |  |

P value calculated by log-rank test.

Abbreviations: Obs., observations; OS, overall survival; RFS, relapse-free survival.