**Supplementary Table 1. Melanocytic archival specimens analyzed for PD-L1 expression, BRAF mutational status, and inflammatory infiltrate.**

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| --- |
| **NEVI (N=14)** |
| **Case** | **Histologic subtype** | **BRAF** **codon 600** | **%PD-L1****by tumor cellsa** | **Inflammation****Scoreb** |
| 1 | Spitz | WT | 0 | 0 |
| 2 | Common | V600E | 0 | 1 |
| 3 | Common | V600E | 0 | 0 |
| 4 | Spitz | WT | 0 | 1 |
| 5 | Spitz | WT | 0 | 3 |
| 6 | Spitz | WT | 0 | 0 |
| 7 | Spitz | WT | 20 | 2 |
| 8 | Common | V600E | 0 | 0 |
| 9 | Common | V600E | 0 | 0 |
| 10 | Common | V600E | 0 | 0 |
| 11 | Common | WT | 0 | 0 |
| 12 | Blue | WT | 0 | 0 |
| 13 | Common | WT | 0 | 0 |
| 14 | Spitz | WT | 0 | 1 |
|  |
| **PRIMARY MALIGNANT MELANOMA (N=23)** |
| **Case** | **Histologic Subtype** | **BRAF** **codon 600** | **%PD-L1****by tumor cells** | **Inflammation****Score** |
| 1 | acral lentiginous | WT | 10 | 2 |
| 2 | nodular | WT | 0 | 2 |
| 3 | nodular | WT | 0 | 0 |
| 4 | acral lentiginous | WT | 0 | 0 |
| 5 | desmoplasic | WT | 0 | 2 |
| 6 | nodular | WT | 0 | 1 |
| 7 | nodular | WT | 5 | 1 |
| 8 | nodular | V600E | 10 | 2 |
| 9 | nodular | WT | 0 | 1 |
| 10 | acral lentiginous | WT | 0 | 0 |
| 11 | acral lentiginous | WT | 0 | 0 |
| 12 | nodular | WT | 5 | 1 |
| 13 | nodular | WT | 0 | 0 |
| 14 | superficial spreading | V600E\* | 0 | 0 |
| 15 | desmoplastic | WT | 0 | 0 |
| 16 | superficial spreading | V600E | 10 | 1 |
| 17 | spindle cell | WT | 50 | 0 |
| 18 | nodular | WT | 5 | 1 |
| 19 | nodular | WT | 5 | 1 |
| 20 | acral lentiginous | WT | 0 | 0 |
| 21 | nodular | V600E | 0 | 1 |
| 22 | spindle cell | V600E | 5 | 2 |
| 23 | nodular | WT | 20 | 1 |
|  |
| **METASTATIC MELANOMA (N=15)** |
| **Case** | **Location of metastasis** | **BRAF****codon 600** | **%PD-L1****by tumor** | **Inflammation****Score** |
| 1 |  lymph node | V600E\* | 5 | 1 |
| 2 |  lung | V600E | 5 | 1 |
| 3 |  lung | WT | 5 | 1 |
| 4 |  skin/subcutaneous soft tissue | WT | 5 | 1 |
| 5 |  brain | V600E | 0 | 0 |
| 6 |  soft tissue, neck | V600E | 5 | 1 |
| 7 |  lymph node | V600E | 5 | 1 |
| 8 |  lymph node | V600E | 5 | 1 |
| 9 |  lymph node | V600E | 0 | 1 |
| 10 |  skin/subcutaneous soft tissue | V600E | 0 | 0 |
| 11 |  lymph node | V600E | 5 | 1 |
| 12 |  lymph node | V600E | 0 | 1 |
| 13 |  lymph node | V600E | 5 | 1 |
| 14 |  lung | WT | 5 | 1 |
| 15 |  soft tissue, groin | V600E | 0 | 0 |

a Tumor cells were considered PD-L1(+) if >5% of cells demonstrated membranous (cell surface) PD-L1 expression.

b Immune score includes TILs and accompanying histiocytes. Infiltrates were scored as “none” (0), “focal” (1), “moderate” (2), or “severe” (3; see Materials and Methods).

\*One patient had both a primary and a metastasis that were studied, and both lesions demonstrated c.1799\_1800delinsAA, also resulting in V600E at the protein level.

**Supplementary Table 2. PD-L1 and MHC I induction by IFN-g on cultured human melanoma cell lines, according to BRAF codon 600 genotype**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **BRAF**  |   | **PD-L1 (**∆MFI)a |  | **MHC I (**∆MFI) |
| **codon 600b** | **Melanoma cell line**  | **Media** | **IFN-gc** |  | **Media** | **IFN-g** |
| **V** (wild type) | 537-mel | 0.3  | 56.3  |  | 163.3  | 785.6  |
| 697-mel | 3.3  | 52.3  |  | 288.8  | 882.9  |
| 1011-mel | 1.5  | 50.1  |  | 204.1  | 597.8  |
| 1088-mel | 5.1  | 52.7  |  | 137.2  | 511.7  |
| 1102-mel | 0.3  | 52.5  |  | 382.0  | 839.8  |
| 1330-mel | 3.7  | 88.3  |  | 378.7  | 1068.8  |
| 1350-mel | 0.6  | 18.1  |  | 123.3  | 406.7  |
| 1363-mel | 1.3  | 17.1  |   | 400.2  | 919.7  |
| **Mean (SEM)d** |  | 2.0 ( 0.6) | 48.4 (8.0) |  | 259.7 (41.3) | 751.6 (79.6) |
| **E** (mutant) | 397-mel | 5.2  | 23.3  |  | 197.3  | 562.6  |
| 553B-mel | 2.1  | 7.3  |  | 62.4  | 342.9  |
| 586-mel | 0.5  | 16.0  |  | 85.0  | 351.9  |
| 624-mel | 5.5  | 11.6  |  | 319.5  | 927.5  |
| 938-mel | 3.6  | 66.9  |  | 287.8  | 1279.5  |
| 1558-mel | 1.1  | 14.0  |  | 75.0  | 371.3  |
| 1844-mel | 0.2 | 45.6  |  | 74.1 | 463.4  |
| 1898-mel | 0.6 | 44.9  |  | 471.7 | 756.4  |
| 2048-mel | 0.5 | 74.0  |  | 284.7 | 1160.1  |
| 2104-mel | 1.1 | 80.3  |   | 643.1 | 1628.9  |
| **Mean (SEM)** |  | 2.0 (0.6) | 38.4 (8.8) |  | 250.1 (61.3) | 784.5 (142.4) |

a∆MFI, mean fluorescence intensity of isotype control mAb subtracted from intensity of specific mAb.

bBRAF mutational status was determined by direct sequencing of PCR amplicons, as described in Sharkey MS, et al. CD4+ T cell recognition of mutated B-RAF in melanoma patients harboring the V599E mutation. Cancer Res 2004;64:1595-99.

cCultured cells were incubated in the presence or absence of 500 IU/ml of IFN-g for 48 hr.

dSEM, standard error of the mean