MELANOMA SAMPLES

Percentage of BRAF V600E mutation obtained by pyrosequencing

475 samples from 428 patients. All consecutive samples with stage III or IV melanomas received in Ambroise Paré hospital pathology department from March 2010 to May 2014

 \rightarrow 368 samples with at least 80% of tumor cells of whom 142 with *BRAF* V600E

Fluorescence *in situ* hybridization (FISH) with BRAF (RP11-129G9
BAC)/chromosome 7 centromere probes
141 melanoma samples available on TMA (140 patients)
16 not interpretable because of lack of tumor on TMA sections, high lymphocytic infiltration or high background fluorescent signals.

 \rightarrow 125 samples with interpretable results

59 BRAF WT

56 BRAF V600E

10 with another *BRAF* exon 15 mutations (V600K n=7, K601E n=2, 600-601delinsE n=1).

 \rightarrow 44 samples analyzed with another BRAF probe (SureFISH 7q34 BRAF)



Single nucleotide polymorphism (SNP) array analysis

- 18 frozen samples available
- \rightarrow 17 samples with FISH results

 \rightarrow 1 sample with non interpretable FISH result

MELANOCYTIC NEVI (dermic and/or junctional)

FISH with BRAF (RP11-129G9 BAC)/chromosome 7 centromere probes and immunohistochemitry (IHC) with VE1 antibody

 \rightarrow 42 samples from 42 patients

| IHC | FISH analysis |
|--|---|
| \rightarrow 42 samples interpretable | \rightarrow 33 samples with interpretable FSIH results |
| 9 BRAF p.V600E negative | 6 BRAF p.V600E negative |
| 33 BRAF p.V600E positive | 27 BRAF p.V600E positive |
| | 9 FISH not interpretable because of lack of tumor on TMA sections |