## Supplement Table 2 Characteristics of Included studies

| Author Year | % Male | % Cutaneous Primary | % Ulceration | Breslow Thickness | Tissue tested for BRAFm status | Test type |
| --- | --- | --- | --- | --- | --- | --- |
| Akman 2015 [46] | 48% | 100% | 44% | 2-4mm: 28.0% >4mm: 72.0% | Primary tumour and metastatic tumour | DNA sequencing (microarray-based) |
| Algazi 2015 [59] | 68% | 79% | NR | NR | NR | Sanger sequencing of exon 15 |
| Amaravadi 2009 [61] | 69% | NR | NR | NR | Metastatic | PCR (BigDye Terminator v1.1 Cycle on an ABI PRISM 3130×l Genetic Analyzer (Applied Biosistem). S) |
| Barbour 2014 [39] | 60% | 100% | 33% | <2mm: 42.74% ≥2mm: 38.71% | Lymph node tissues | Multiplex PCR (MelanoCARTA panel) + MALDI-TOF (MassARRAY system) |
| Bhandaru 2014 [62] | 60% | 59% | 11% | For primary tumour (n=193): <=2mm: 47.2% >2mm: 52.8% | Primary tumour and metastatic tumour | IHC |
| Birkeland 2013 [63] | 57% | 67% | NR | <1mm: 9.0% 1-2mm: 18.0% 2-4mm: 29.0% >4mm: 35.0% | Metastatic samples collected prior to chemotherapy | PCR (DyNazyme) + DNA sequencing (BigDye v.1.1 and a capillary DNA sequencer (ABI 3700)) |
| Brown 2012 [64] | NR | 100% | NR | NR | Primary or metastatic lesions | PCR + RFLP |
| Capper 2012 [65] | 55% | 100% | NR | NR | Primary tumour and additional non-CNS metastases | IHC using antibody VE1 |
| Carlino 2014 [20] | 67% | 81% | NR | Mean: 2.5mm | Distant metastatic samples were preferentially sampled over lymph nodes or primaries where available. | Multiplex PCR (OncoCartaPanel) + MALDI-TOF (Sequenom MassArray platform) |
| Cheng 2015 [41] | 60% | NR | NR | For primary tumour (n=148):  <=2mm: 41% >2mm: 58% unspecified: 1% | Primary tumour and metastatic tumour | IHC |
| Davies 2012 [66] | 72% | NR | NR | NR | NR | Mass-spectroscopy based genotyping + RPPA |
| Devitt 2011 [47] | 54% | 100% | 17% | <1mm: 47.0% 1-2mm: 17.0% 2-4mm: 19.0% >4mm: 18.0% | Primary melanoma | PCR (duplex allele-specific) |
| Edlundh-Rose 2006 [67] | 55% | 100% | 37% | Mean: 4.9mm | Primary and metastatic | PCR (pyrosequencing) |
| Ekedahl 2013 | 61% | 100% | NR | <1mm: 8.0% 1-2mm: 28.0% 2-4mm: 18.0% >4mm: 38.0% | NR (based on frozen tissue from time of surgery) | PCR (Sanger) |
| Frauchiger 2016 [42] | 54% | 86% | NR | <1mm: 7.0% 1-2mm: 13.0% 2-4mm: 31.0% >4mm: 26.0% | Metastatic | PCR + Sanger sequencing |
| Gallaher 2016 [68] | 47% | NR | 17% | NR | Metastatic (brain) | NR (Routine clinical testing methods) |
| Gorayski 2015 [69] | 65% | NR | NR | NR | Primary, regional lymph node tissues and metastatic tissues | Real-time PCR |
| Griewank 2014 [70] | 54% | 100% | 8% | Mean: 3.7mm | Primary, metastatic and occult | PCR + Direct (Sanger) Sequencing |
| Gupta 2015 [71] | 62% | 100% | NA | NR | Metastatic (distant metastasis, regional lymph node or regional tissue) | NR |
| Hugdahl 2016 [72] | 54% | 100% | 57% | NR | Primary tissue of nodular cutaneous melanoma | Real-time PCR |
| Ide 2016 [73] | 50% | 100% | 47% | Median: 3.15mm, Range: 0.2-22mm | Primary or metastatic lesions | Direct sequencing (determining BRAF exon 15 mutations) + Quenching probe (QP) method (detection of BRAF V600E mutation) |
| Jacquelot 2016 [74] | 51% | NR | 44% | 0-3mm: 56.2% >3mm: 43.8% | NR | NR |
| Jakob 2012 [8] | 63% | 77% | 29% | Mean: 2.5mm | NR | PCR (pyrosequencing) |
| Joon 2015 [75] | NR | NR | 41% | NR | Nodal, metastatic and primary tissue | NGS sequencing |
| Joseph 2012 [76] | 60% | NR | NR | NR | NR | Mass-spectrometry (n=67) or pyrosequencing (n=34) |
| Jovanovic 2008 [77] | 68% | 100% | 28% | Mean: 1.3mm | Primary melanoma | PCR (single strand conformation polymorphism and direct sequencing) |
| Linardou 2015 [78] | 54% | 26% | NA | NR | Metastatic | Sanger sequencing of BRAF exon 15 |
| Lyubchenko 2016 [79] | 32% | 100% | 34% | < 1 mm: 7.5% | Primary cutaneous melanoma | Biochip analysis + Allele-specific real-time PCR + Sanger sequencing |
| Mar 2015 [80] | NR | NR | NR | NR | Primary cutaneous melanoma | PCR (duplex allele-specific) + Sanger sequencing to differentiate BRAF V600E and V600K mutations |
| Meckbach 2014a [21] | 53% | 100% | NR | <1mm: 58.0% 1-2mm: 29.0% 2-4mm: 10.0% >4mm: 3.0% | Primary melanoma | PCR (Sanger) |
| Meckbach 2014b [81] | 55% | 100% | 35% | NR | Tissue from patients receiving first-line treatment | PCR (Sanger) |
| Menzies 2012 [82] | NR | 84% | NR | <1mm: 17.0% 1-2mm: 24.0% 2-4mm: 14.0% >4mm: 28.0% | Distant metastatic tissue (most recent) first, then locoregional/in-transit metastasis, and finally primary melanoma (only if no metastatic tissue was available by biopsy) | High-resolution melting (HRM) + sequencing using M13 primers |
| Moreau 2012 [38] | 61% | 100% | 51% | <1mm: 7.0% 1-2mm: 26.0% 2-4mm: 34.0% >4mm: 32.5% | Metastatic (nodal tissues) | Direct sequencing + pyrosequencing |
| Nagore 2014 [35] | 46% | 100% | 39% | Mean: 1.71mm | Primary melanoma | Single-base primer extension MassARRAY (Sequenom) |
| Picard 2014 [37] | 64% | NR | NR | ≤1mm: 4% 1.01-2mm: 39% 2.01-4mm: 29% >4mm: 28% | Primary and intranodal metastatic tissue | PCR + Sanger Sequencing |
| Roh 2016 (KMC) [34] | 63% | NR | NR | Mean: 4.7mm | Primary melanoma | PCR +Pyrosequencing |
| Roh 2016 (TCGA) [34] | 50% | NR | 47% | Mean: 4.35mm | Primary, regional lymph node tissues and metastatic tissues | NR |
| Rutkowski 2014 [40] | 49% | 100% | 18% | ≤1mm: 4.2% 1.01-2mm: 17.8% 2.01-4mm: 31.4% >4mm: 17.8% | Metastatic tumour samples of lymph node | PCR + BigDye Terminator Cycle sequencing kit and ABI Prism 3100 Genetic Analyzer |
| Safaee 2013 [83] | 60% | NR | NA | NR | Primary and metastatic | IHC with a polyclonal anti-BRAF antibody (1: 100 dilution; Sigma, St. Louis, MO, USA.) |
| Saiag 2015 [84] | 53% | NR | 77% | <1mm: 13% 1-2mm: 29% 2-4mm: 35% >4mm: 6% | NR | Pyrosequencing |
| Schoenewolf 2014 [86] | 50% | NR | NR | NR | Primary melanoma | PCR (Sanger) |
| Sekulovic 2015 [87] | NR | 100% | 64% | NR | NR | NR |
| Shankar 2016 [88] | 57% | NR | NR | Mean: 4.2mm, Range: 0.8-25mm | Primary melanoma | PCR |
| Sheen 2016 [89] | NR | NR | NR | NR | NR | NR |
| Shinozaki 2007 [43] | 55% | 100% | NR | 2-4mm: 34.0% >4mm: 66.0% | Primary cutaneous melanoma | Real-time LightCycler polymerase chain reaction (LC PCR) |
| Si 2012 [51] | 76% | NR | NR | NR | Metastatic patient blood sample (blood was drawn within 1 week before the start of biochemotherapy and within 4 weeks after the last cycle) | Real-time PCR |
| Slingluff 2013 [90] | 47% | NR | 53% | Mean: 5.02mm | Primary melanoma | PCR + Sanger sequencing |
| Thomas 2015 [91] | 72% | 100% | 25% | NR | NR | NR |
| Ugurel 2007 [36] | 54% | 47% | NR | <1mm: 69.0% 1-2mm: 17.0% 2-4mm: 10.0% >4mm: 4.0% | First primary invasive melanoma | PCR (single strand conformation polymorphism and direct sequencing) |
| Ulivieri 2015 [45] | 54% | 77% | NR | NR | Metastatic | PCR (single strand conformation polymorphism [SSCP] and direct DNA sequencing) |
| von Moos 2012 [53] | 60% | 92% | NR | Mean: 2.7mm | Metastatic | PCR + Sanger Sequencing |
| Wilson 2015 [48] | 65% | NR | NR | NR | Metastatic | Real-Time PCR (TaqMan) |
| Wu 2014 [92] | 43% | NR | NR | NR | NR | NR |
| Xu 2016 [44] | NR | 100% | NR | < 1 mm: 59% | Primary melanoma | PCR + Pyrosequencing |
| Akman 2015 [46] | 67% | 100% | NR | <1mm: 8% 1-2mm: 15% 2-4mm: 23% >4mm: 14% | Primary tumours (brain metastasis for all) | Western blot or IHC/immunostaining or PCR (Sanger) |