

Genetic characterization of sellar metastasis from primary bronchial carcinoid tumor of neuroendocrine pathology



INTRODUCTION

Metastasis to the pituitary gland from neuroendocrine tumors is a rare occurrence that may originate from primary tumors the lung, gastrointestinal tract, thyroid, and pancreas, among others. Patients may present with signs of endocrine dysfunction secondary to pituitary involvement, as well as mass effect-related symptoms including headaches and visual deficits. Despite a small but accumulating body of literature describing the clinical and hispathological correlates for pituitary metastases from neuroendocrine tumors, the genetic basis underlying this presentation remains poorly characterized.

CASE DESCRIPTION

We report the case of a 68 year-old with a history of lung carcinoid tumor who developed a suprasellar lesion, causing mild visual deficits but otherwise without clinical or biochemical endocrine abnormalities (Figure 1). She underwent endoscopic endonasal resection of her tumor with final pathology confirming metastasis from her original neuroendocrine tumor (Figure 2).

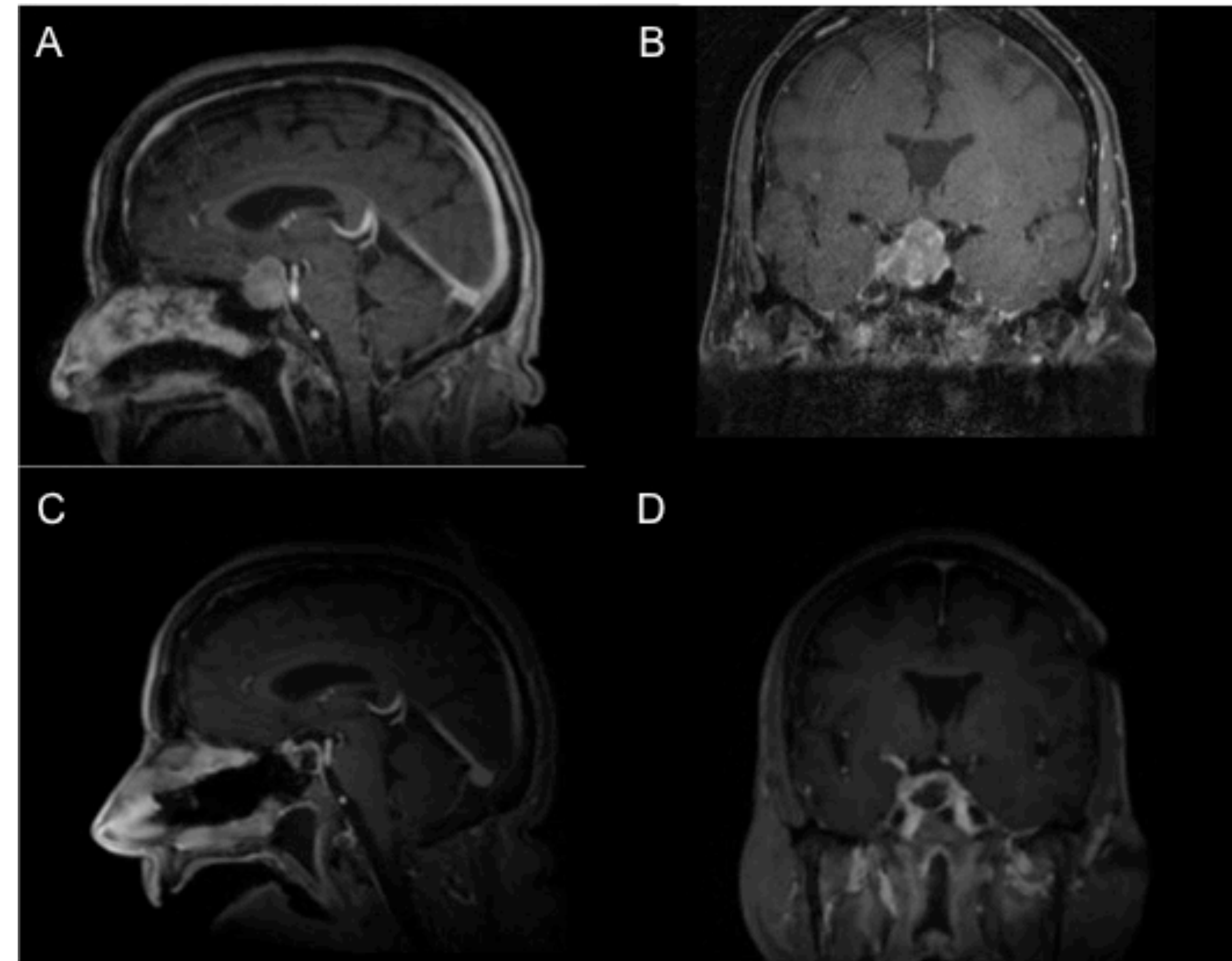


Figure 1. Magnetic resonance imaging pre- and post-operatively. Representative (A) sagittal and (B) coronal images of T1-weighted post-contrast MRI are shown at time of presentation. Intra-operative MRI was obtained, demonstrative gross total resection of the sellar tumor, as seen on representative (C) sagittal and (D) coronal images of T-weighted post-contrast MRI.

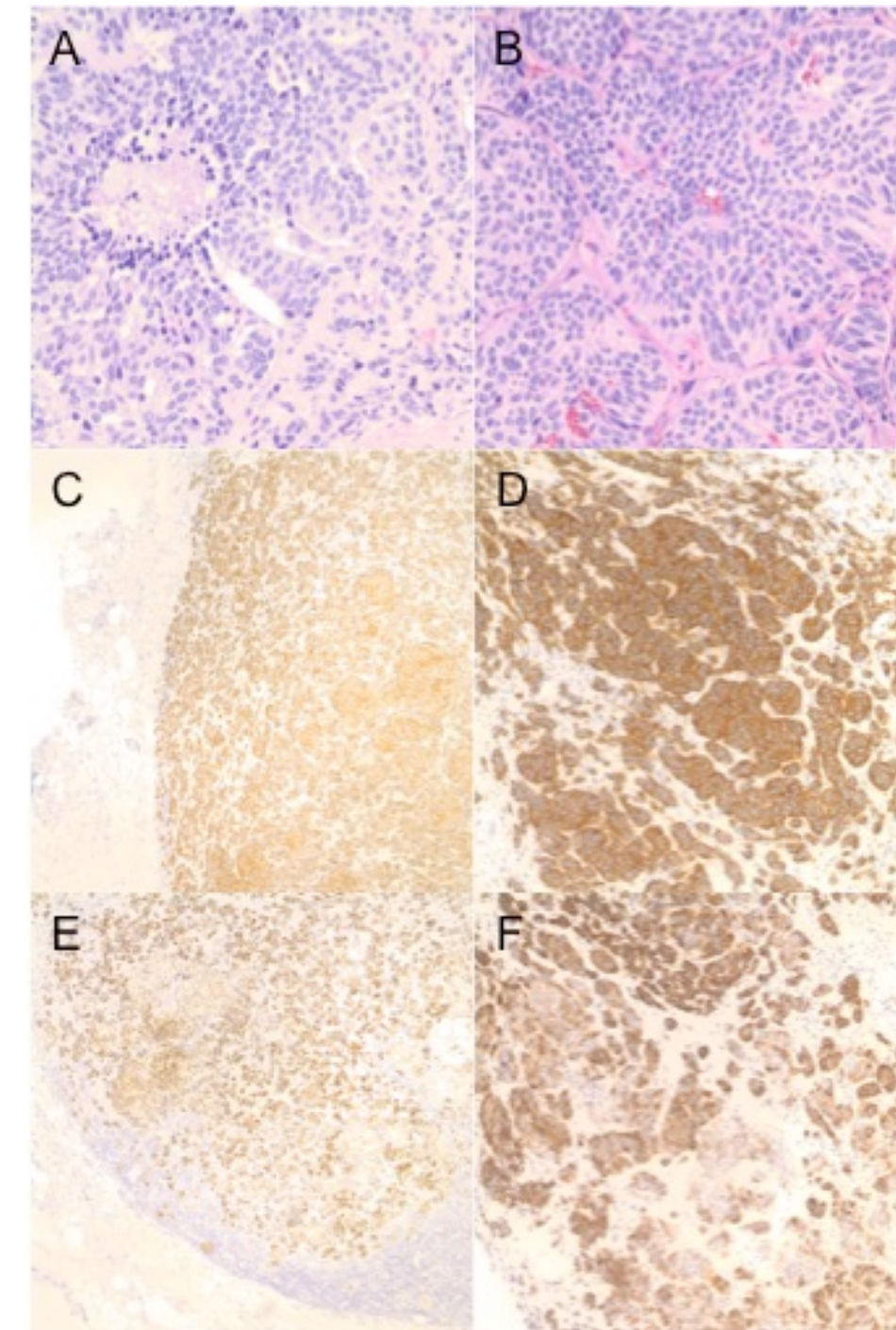


Figure 2. Histopathology of primary lung and sellar metastasis specimens. Routine H&E stains from the (A) lung and (B) sellar tumors demonstrate elevated mitotic activity and areas of focal necrosis (magnification, 400x). Neuroendocrine origin was confirmed via positive immunohistochemistry for synaptophysin in the (C) lung (magnification, 100x) and (D) sellar tumors (magnification, 200x), as well as for CK7 in the (E) lung (magnification, 100x) and (F) sellar tumors (magnification, 200x).

GENOMIC ANALYSIS

Whole-exome sequencing (WES) was performed on the resected sellar tumor and the matching blood sample (Figure 3). There was not enough tissue from the original lung specimen for similar analysis. There were a total of 91 somatic alterations identified, only 7 of which were previously reported to be implicated in oncogenesis (*MYO18A*, *PTCH1*, *BCOR*, *CLIC6*, *TLL2*, *COL1A1*, *PTPRK*). Notably, mutations in *BCOR* and *PTCH1* have been previously implicated in both systemic neuroendocrine tumors as well as primary tumors of the pituitary gland [1, 11, 13, 14, 25-27, 29, 35, 36]. Mutational signatures of all somatic alterations revealed an abundance of C>T transitions followed by C>A transversions. Further analysis of the mutational signatures in relation to the well-established COSMIC signatures, identified an interesting pattern for enrichment of Signature 4, which is seen in lung adenocarcinoma, lung squamous cell carcinoma, and small cell lung carcinoma.^[10] The other dominant signatures were signatures 16 and 23, for which the etiology remains unknown. Copy number variation (CNV) analysis revealed increased rate of genomic instability with 18.7% of the genome being deleted. Identified CNV events included large-scale deletions of chromosomes 3, 6, and 9 and focal deletions on chromosomes 1, 2, 11, 15, and 16. Interestingly, acquisition of increased CNV events in non-small cell lung cancer metastases to the brain has been reported before with both amplifications and deletions [19].

DISCUSSION

The genetic changes underlying sellar metastases from systemic cancer remain poorly characterized. We found a deleterious mutation of *PTCH1*, which encodes patched-1 protein, a receptor for sonic hedgehog (SHH) signaling that suppresses the release of *SMO* (smoothened)-mediated cell proliferation, thus acting as a tumor suppressor [1] and previously reported in neuroendocrine carcinomas of the gastrointestinal system [14, 29]. *PTCH1* has also been shown to be important in pituitary embryogenesis, giving rise to normal pituitary development through proliferation of normal Rathke's pouch progenitors and differentiation of pituitary cell types [7]. Downstream consequences of *PTCH1* inactivation have been implicated in the pathogenesis of adamantinomatous craniopharyngiomas [13] and pituitary adenomas [35]. Clinically, vismodegib and sonidegib are SHH pathway inhibitors, approved for the use of treating advanced basal cell carcinoma^[9] and is being tested in phase 2 clinical trials for medulloblastoma [34]. They have also been proposed as novel therapies for *PTCH1*-staining neuroendocrine cancers [14]. We also identified a deleterious loss-of-function mutation in *BCOR*, which encodes a co-repressor of the apoptotic protein, BCL6. *BCOR* acts as an epigenetic regulator through polycomb repressor complex-1 [3] and somatic *BCOR* mutations have been reported in neuroendocrine tumors such as small cell lung cancer [11, 26, 27], gastroenteropancreatic tumors [25], and pulmonary carcinoid. While targeted therapies for *BCOR*-mutated cancers have not been tested clinically, several preclinical studies have demonstrated abrogation of tumor growth through selective targeting with small molecule inhibitors of upregulated oncogenic signaling pathways, such as SHH, WNT, and JAK-STAT [24, 37]. We also found a mutation in *PTPRK*, which encodes receptor-type tyrosine-protein phosphatase kappa, a protein tyrosine phosphatase with broad downstream signaling implications, whose downregulation or absence has been reported in numerous cancers, including melanoma [21], lymphoma [23], colorectal cancer [32], breast cancer [33], and glioma [2].

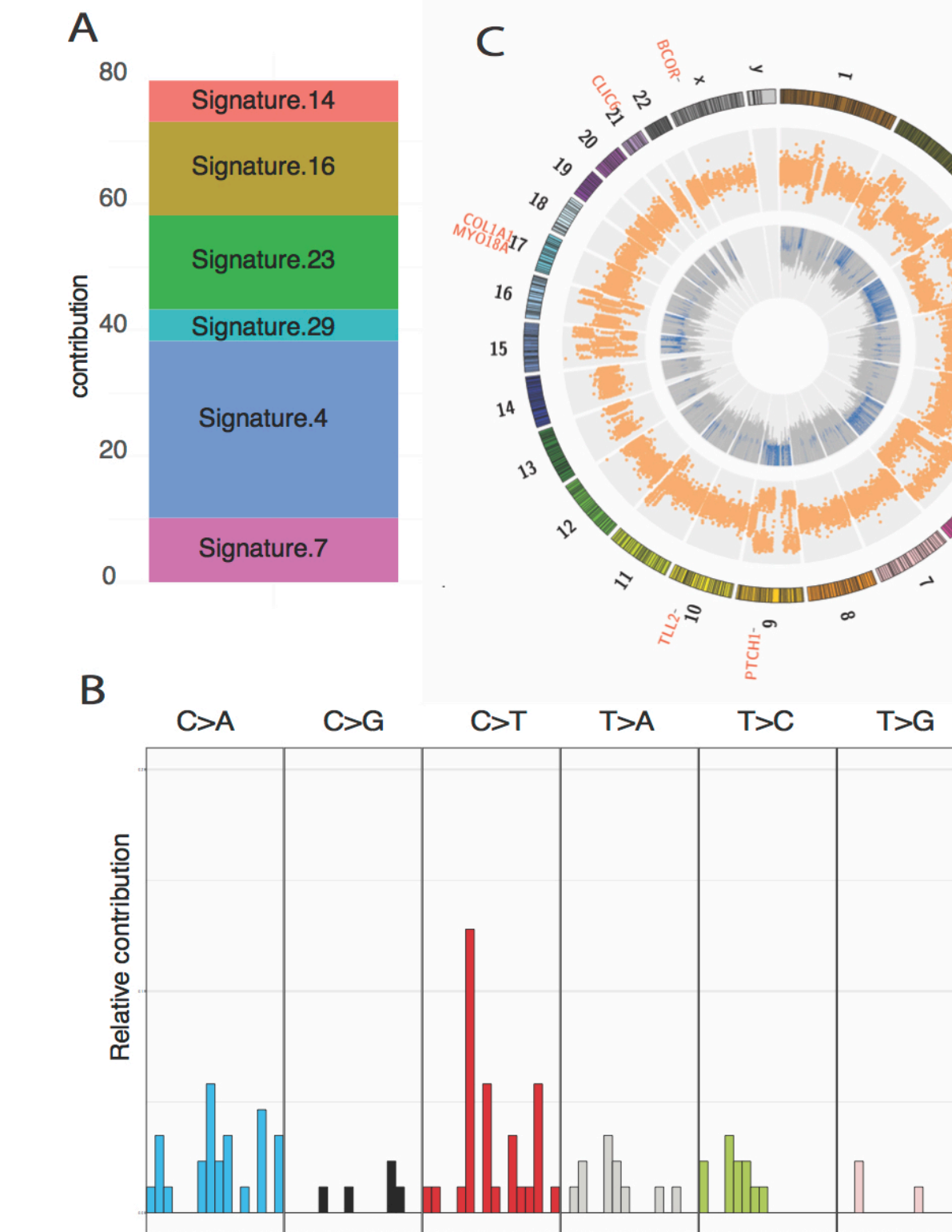


Figure 3. Genomics summary of the sellar specimen. (A) Mutation signature contribution to COSMIC signatures. (B) Distribution of 96 mutation signatures. (C) Circos plot depicting the CNV and LOH events in the inner and outer circles, respectively. The cancer associated somatic mutations are listed outside the karyotype.

CONCLUSION

In summary, sellar metastases from primary systemic tumors represent a small but growing pathology that arise as patients continue to live longer with modern oncologic therapies. While clinical features exist that may help differentiate patients with metastases from primary pituitary adenomas at time of presentation, such as the presence of diabetes insipidus, surgical intervention remains critical for definitive diagnosis to guide further therapy and to relieve symptoms secondary to endocrine dysfunction or mass effect on nearby cranial nerves. Genetic alterations underlying metastasis to the sellar region remain uncharacterized, but this report highlights a potential key role for mutations in *PTCH1* and *BCOR*, previously implicated in both primary neuroendocrine and pituitary tumors. Further genetic studies of these rare cases are needed to elucidate the mechanisms underlying sellar metastasis of systemic cancers.

REFERENCES

1. Alizadeh A, Brown K, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
2. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
3. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
4. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
5. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
6. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
7. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
8. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
9. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
10. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
11. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
12. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
13. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
14. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
15. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
16. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
17. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
18. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
19. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
20. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
21. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
22. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
23. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
24. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
25. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
26. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
27. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
28. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
29. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
30. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
31. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
32. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
33. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
34. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
35. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.
36. Alizadeh A, Miller F, Davis S, et al. Microarray analysis of primary myeloid leukemia. *Nature* 2000;403:858-868.