

Medical Policy



An Independent Licensee of the
Blue Cross and Blue Shield Association.

Title: Gene Expression Assay for Breast Cancer Treatment

Professional

Original Effective Date: July 1, 2007

Revision Date(s):

Current Effective Date: July 1, 2007

Institutional

Original Effective Date: July 1, 2007

Revision Date(s):

Current Effective Date: July 1, 2007

DESCRIPTION

This policy addresses the use of genetic profiling of breast tumors as a technique of predicting breast cancer recurrence and response to therapy.

POLICY

Patient must meet all the following criteria:

A Gene Expression Survey such as Oncotype DX™, is a diagnostic test designed to assist in the decision making in regards to chemotherapy treatments based on the possibility of the recurrence of breast cancer in those women with newly diagnosed, early-stage breast cancer. The cancer diagnosis has all of the following characteristics:

- Estrogen-receptor positive (ER+)
- Newly diagnosed
- Node negative
- Stage I or II (based on size only - over 2 cm)

CODING

REVENUE CODE

0300

HCPCS

S3854 Gene expression profiling panel for use in the management of breast cancer treatment

DIAGNOSIS

These diagnoses are otherwise subject to medical policy as stated above

174.0 Malignant neoplasm of female breast; Nipple and areola
 174.1 Malignant neoplasm of female breast; Central portion
 174.2 Malignant neoplasm of female breast; Upper-inner quadrant
 174.3 Malignant neoplasm of female breast; Lower-inner quadrant
 174.4 Malignant neoplasm of female breast; Upper-outer quadrant

- 174.5 Malignant neoplasm of female breast; Lower-outer quadrant
- 174.6 Malignant neoplasm of female breast; Axillary tail
- 174.8 Malignant neoplasm of female breast; Other specified sites of female breast
- 175.0 Malignant neoplasm of male breast; Nipple and areola

REFERENCES

1. Ahr A, Holtrich U, Solback C, et al. Molecular classification of breast cancer patients by gene expression profiling. *J Pathol.* 2001; 195:312-320.
2. Ahr A, Karn T, Solback C, et al. Identification of high risk breast-cancer patients by gene expression profiling. *Lancet.* 2002; 359:131-132.
3. Ayers M, Symmans WF, Stec J, et al. Gene expression profiles predict complete pathological response to neoadjuvant paclitaxel and fluorouracil, doxorubicin, and cyclophosphamide chemotherapy in breast cancer. *J Clin Oncol.* 2004; 22:2284-2293.
4. Borie N, Bertucci F, Groulet-Martinec A, et al. Gene expression profiling defines new molecular classes and predicts prognosis in breast cancer patients treated with adjuvant chemotherapy: development of a clinical tool to improve management of breast cancer. *Breast Cancer Res Treat.* 2004; 88(Suppl 1):A5035.
5. Borie N, Birnbaum D, Bertucci F, et al. Breast cancer Profilechip: Utilization of microarray technology to predict prognosis and improve clinical management of breast cancer. *J Clin Oncol.* 2004; 22(14 Suppl):9658.
6. Chang JC, Wooten EC, Tsimelzon A, et al. Gene expression profiling for the prediction of therapeutic response to docetaxel in patients with breast cancer. *Lancet.* 2003; 362(9381):362-369.
7. Cobleigh MA, Bitterman P, Baker J, et al. Tumor gene expression predicts distant disease-free survival (DDFS) in breast cancer patients with 10 or more positive nodes: high throughput RT-PCR assay of paraffinembedded tumor tissues. *Prog Proc Am Soc Clin Oncol.* 2003; 22:850.
8. Cobleigh MA, Tabesh B, Bitterman P, et al. Tumor gene expression and prognosis in breast cancer patients with 10 or more positive nodes. *Clin Cancer Res.* 2005; 11(24 Pt 1):8623-8631.
9. Esteban J, Baker J, Cronin M, et al. Tumor gene expression and prognosis in breast cancer: multi-gene RTPCR assay of paraffin-embedded tissue. *Prog Proc Am Soc Clin Oncol.* 2003; 22:850.
10. Esteva FJ, Sahin AA, Coombes K, et al. Multi-gene RT=PCR assay for predicting recurrence in node negative breast cancer patients—MD Anderson Clinical Validation Study. *Breast Cancer Res Treat.* 2003; 82:A16.
11. Gianni L, Zambetti M, Clark K, et al. Gene expression profiles of paraffin-embedded core biopsy tissue predict response to chemotherapy in patients with locally advanced breast cancer. *J Clin Oncol.* 2004; 22(14 Suppl):501.
12. Hannemann J, Oosterkamp HM, Bosch CA, et al. Changes in gene expression profiling due to primary chemotherapy in patients with locally advanced breast cancer. *J Clin Oncol.* 2004; 22 (14 Suppl):502.

13. Iwao-Koizumi K, Matoba R, Ueno N, et al. Prediction of docetaxel response in human breast cancer by gene expression profiling. *J Clin Oncol*. 2005; 23:422-431.
14. Kaklamani, V., Gradishar, W. Gene expression in breast cancer. *Curr Treat Opt Oncol*. 2006; 7:123-128.
15. Klijn JG., Atkins D, Sieuwerts AM, et al. Validation of a 76-gene prognostic profile in clinically relevant subgroups of lymph-node-negative breast cancer patients. *Ann Oncol*. 2004; 15(Suppl 3):A2080. [Abstract].
16. Paik S, Shak S, Tang G, et al. Multi-gene RT-PCR assay for predicting recurrence in node negative breast cancer patients—NSABP studies B-20 and B-14. *Breast Cancer Res Treat*. 2003; 82:A16.
17. Paik S, Shak S, Tang G, et al. A multi-gene assay to predict recurrence of tamoxifen-treated, node-negative breast cancer. *N Engl J Med*. 2004; 351:2817-2826.
18. Paik S, Shak S, Tang G, et al. Risk classification of breast cancer patients by the Recurrence Score assay: comparison to guidelines based on patient age, tumor size, and tumor grade. *Breast Cancer Res Treat*. 2004; 88(Suppl 1):A104.
19. Paik S, Shak S, Tang G, et al. Expression of the 21 genes in the Recurrence Score assay and prediction of clinical benefit from tamoxifen in NSABP study B-14 and chemotherapy in NSABP study B-20. *Breast Cancer Res Treat*. 2004; 88(Suppl 1):A24.
20. Piccart MJ, Loi S, Van'tVeer L, et al. Multi-center external validation study of the Amsterdam 70-gene prognostic signature in node negative untreated breast cancer: are the results still outperforming the clinical/pathological criteria? *Breast Cancer Res Treat*. 2004; 88(Suppl 1):A38.
21. van de Vijver MJ, He YD, van't Veer LJ, et al. A gene-expression signature as a predictor of survival in breast cancer. *N Engl J Med*. 2002; 347 1999-2009.
22. van't Veer LJ, Dai H, He Y, et al. Gene expression profiles predicting outcome of disease are different for young and older age breast cancer patients. *Breast Cancer Res Treat*. 2004; 88(Suppl 1):A102].
23. Wang Y, Klijn J, Zhang Y, et al. Pathway analysis and validation of the 76-gene prognostic signature in lymph node negative (LNN) primary breast cancer. *Breast Cancer Res Treat*. 2004; 88(Suppl 1):A103.
24. Oncology Liaison Committee February 15, 2005 and Medical Advisory Committee April 19, 2007.

Government Agency; Medical Society; and Other Authoritative Publications

1. Blue Cross Blue Shield Association. Gene Expression Profiling for Managing Breast Cancer Treatment. *TEC Assessment*, 2005; 20(3).
2. Blue Cross and Blue Shield of Kansas Oncology Liaison Committee, February 20, 2007 (see Blue Cross and Blue Shield of Kansas Newsletter, Blue Shield Report. MAC-01-07).

3. Blue Cross and Blue Shield of Kansas Medical Advisory Committee meeting, April 19, 2007 (see Blue Cross and Blue Shield of Kansas Newsletter, Blue Shield Report. MAC-01-07).
4. Hayes Inc. Hayes alert-Technology Assessment Brief. *Gene Expression Profiling of Tumor Tissue to Predict Breast Cancer Recurrence*. Lansdale, PA: Hayes, Inc.: September 2005.

Web site

1. National Library of Medicine. Medical Encyclopedia: Breast Cancer. Available at: <http://www.nlm.nih.gov/medlineplus/ency/article/000913.htm>. Accessed on December 5, 2006.