

Original Article

HOXD13 methylation status is a prognostic indicator in breast cancer

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Abstract: Homeobox protein Hox-D13 is encoded by *HOXD13* gene which is frequently methylated in cancer and has been recognized as a tumor suppressor in pancreatic cancer. In this study, we examined *HOXD13* mRNA expression in 40 pairs of breast cancers and corresponding normal breast tissues. Bisulfite sequencing of *HOXD13* promoter was performed in 6 pairs of breast tumors and corresponding normal breast tissues to examine the potential *HOXD13* CpG methylated sites. *HOXD13* DNA methylation frequency analysis was performed using MethyLight in 196 pairs of breast cancers and corresponding normal breast samples. DNA methylation status and clinicopathological features were investigated. Kaplan-Meier survival analysis and Cox proportional hazards models were utilized to assess the effect of methylation status on overall survival. We found that 60% (24/40) of breast cancers showed low *HOXD13* mRNA expression when compared with corresponding normal breast tissue. The predicted CpG island was located in the -1325 bp to +675 bp region. Next, the -332 bp site in *HOXD13* gene promoter was further examined and in 57.7% (113/196) samples methylation was detected at this site. *HOXD13* methylation was correlated with larger tumor size ($P = 0.004$), but not with other clinico-pathological parameters. In addition, patients with methylated *-HOXD13* promoter had worse overall survival (OS) ($P = 0.005$). Based on our results we conclude that *HOXD13* methylation is a common event in primary breast cancer and is associated with poor survival of breast cancer patients. *HOXD13* methylation could therefore potentially be used as a prognostic factor for breast cancer.

Keywords: *HOXD13*, breast cancer, DNA methylation, epigenetics, prognosis

Introduction

Breast cancer is the most common cancer in women world-wide and it is responsible for approximately 29% of new cancer cases and 15% of total cancer-related mortality in the United States [1]. It is also the primary cancer-related mortality cause among women in the developing countries [2].

Homeobox (*HOX*) genes encode transcription factors which were first discovered as important mediators of *Drosophila* development [3]. *HOX* genes belong to a highly conserved gene family which in humans consists of four gene clusters *HOX A-D* [4]. They have a pivotal role in the morphogenesis and development, and their abnormal expression during developmental processes may give rise to dysplasia [5]. Moreover, many *HOX* genes have been reported to be aberrantly expressed in different tumors,

thereby indicating that *HOX* genes have a role in tumor development and progression [6-9]. This is not surprising since in embryogenesis cell proliferation and differentiation have to be tightly controlled and coordinated while in tumorigenesis this balance is often disrupted.

Mutations of *HOXD13* have first been described in synpolydactyly [10]. When it comes to *HOXD13* role in cancer, *NUP98-HOXD13* gene fusion was reported in acute myelogenous leukemia [11] and *HOXD13* hypermethylation has been reported in extrahepatic cholangiocarcinoma [12] and malignant melanomas [13]. In addition, it has been shown that pancreatic cancer patients with low *HOXD13* expression have poorer prognosis than patients with high *HOXD13* expression, and this finding indicated that *HOXD13* possibly acts as a tumor suppressor gene in pancreatic cancer [14].

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Epigenetic changes such as DNA methylation, histone modification, X-chromosome inactivation, genome imprinting and RNA interference play a significant role in cancer onset and development. Indeed, epigenetic alterations like hypermethylation of CpG islands in the promoter regions of tumor-suppressor genes have frequently been observed as an early event in tumorigenesis [15].

In this study we have decided to examine the role of *HOXD13* gene in sporadic breast cancer by examining its expression as well as promoter methylation status and its association to clinicopathological characteristics of patients and their prognosis.

Materials and methods

Patients and sample collection

Breast cancer specimens and corresponding normal breast tissues were obtained from patients who underwent breast cancer surgery at the Affiliated Tumor Hospital of Harbin Medical University. A total of 236 sporadic breast cancer patients were included in this study. Clinicopathological data were obtained from patients' medical records. All patients were female and had not received prior therapy, such as radio- or chemotherapy. The median age of the patients was 47 years (range 23-77 years). Patients were followed up for at least 19 months and up to 67 months (median 61 months). Overall survival (OS) time was defined as the time interval from the date of surgery to the date of death, which was the assessment used for prognostic analyses. Informed consent was obtained from all subjects, and the study was performed with the approval of the Ethical Committee of the Harbin Medical University. During surgery, a section (1 to 3 cm) of the tumor and the matched normal tissue (≥ 5 cm distant from the tumor) were immediately sliced off and placed in liquid nitrogen and then stored at -80°C . From each tissue block, 3- μm sections were cut and stained with haematoxylin and eosin (H&E) for pathological evaluation. All H&E slides were reviewed by two pathologists independently. Almost all the carcinoma specimens had more than 70% of tumor content.

Immunohistochemistry and molecular subtype classification

Each tumor sample was routinely tested for estrogen receptor (ER), progesterone receptor

(PR), human epidermal growth factor receptor 2 (HER2), Ki-67 and P53 expression. Immunohistochemical markers were assayed in paraffin-embedded, formalin-fixed tumor tissue section stained with antibodies to ER, PR, Her-2, Ki-67 and P53 (Zhong shan -Bio Co., Beijing, China). Tumor samples in which ER or PR nuclear staining was detected in more than 1% of cells were considered as ER-positive or PR-positive, respectively [16]. Positive staining for HER2 was defined based on the percentage of tumor cells and intensity of the membrane staining. HER2 was scored from 0 to 3+ based on the method recommended for the Dako Hercep Test. Tumors were defined positive for HER2 if immunostaining was scored as 3+ or if HER-2 fluorescence *in situ* hybridization (GP medical technologies Co Ltd. Beijing, China) amplification ratio was greater than 2.2 [17]. Ki-67 and P53 positively stained cells were counted and samples with Ki-67 < 14% [18] and P53 < 25% [19] were identified as low expression.

Molecular subtypes of breast cancer were classified according to the St Gallen International Breast Cancer Conference 2011 criteria [20]: Luminal A type: ER and/or PR-positive and HER2-negative and low Ki-67 (< 14%); Luminal B type: (HER2-negative) ER and/or PR positive and HER2 negative and high Ki-67 ($\geq 14\%$); (HER2 positive) ER and/or PR positive and HER2 overexpressed or amplified and any Ki67; HER2 positive type: ER and PR negative and HER2-overexpressed or amplified; and triple-negative breast cancer (TNBC) type: ER-, PR- and HER2-negative.

RNA isolation and reverse transcription

Total RNA was extracted from 40 pairs of fresh frozen samples (tumor and corresponding normal tissue) using TRIzol reagent (Invitrogen, Burlington, USA) according to the manufacturer's instruction. RNA quality and concentration were determined by a spectrophotometer (Gene Quant Pro, Amersham Biosciences, England). Complementary DNA (cDNA) was synthesized from 2.0 μg of total RNA using a Transcriptor First Strand cDNA Synthesis Kit (Roche Diagnostics GmbH, Mannheim, Germany).

Real-time quantitative reverse transcriptase-polymerase chain reaction (RT-PCR)

Real-time quantitative RT-PCR was performed using Light Cycler[®] 480 SYBR Green I Master

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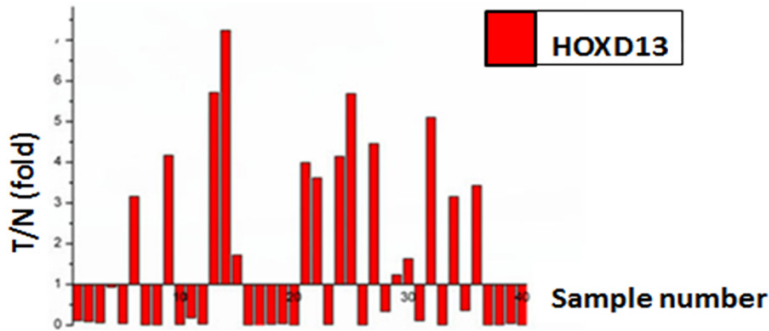


Figure 1. Histogram of *HOXD13* mRNA expression in breast cancer. *HOXD13* mRNA expression was calculated by the $2^{-\Delta\Delta Ct}$ method. X axis represents the sample number, from no. 1 to 40. Y axis represents the relative mRNA expression in each patient as ratio of T (tumor tissue)/N (normal tissue). Samples with T/N value < 0.5 were considered as samples with low *HOXD13* expression.

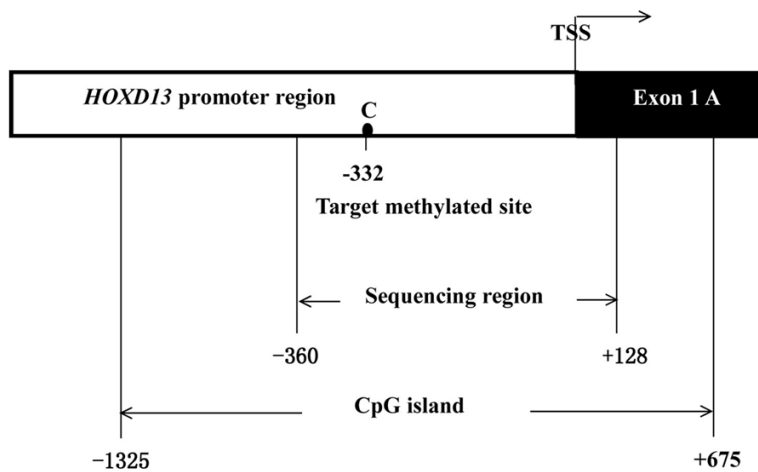


Figure 2. Schematic diagram of the CpG island region, the sequencing region and the target methylated site. TSS, transcription starting site.

Mix (Roche Diagnostics GmbH, Mannheim, Germany) on an ABI 7000 sequence detection system (Applied Biosystems, Foster City, USA) according to the manufacturer's instructions. The primers to *HOXD13* were as follows: forward, 5'-CTTCGGCAACGGCTACTACAG-3'; reverse, 5'-TGACACGTCCATGTACTTCTCC-3'. *GAPDH* was used as the internal reference, and its primers were as follows: forward, 5'-GGAGCG-AGATCCCTCCAAAT-3'; reverse, 5'-GGCTGTTGT-CATACTTCTCATGG-3'. Amplification was performed under the following conditions: 95°C for 10 min followed by 40 cycles of 9°C for 30 s, 55°C for 30 s, and 72°C for 30 s. The relative mRNA expression was calculated using the $2^{-\Delta\Delta Ct}$ method. Fold change > 2 in mRNA expression between breast cancer tissues and co-

responding normal breast tissues was considered as biologically relevant [21]. Samples with T (tumor tissues)/N (normal tissue) fold ratio < 0.5 were defined as samples with low *HOXD13* expression. All experiments were performed in triplicate.

HOXD13 CpG island prediction

To define the *HOXD13* promoter and first exon region we visited [http://genome.ucsc.edu/\(UCSC\)](http://genome.ucsc.edu/(UCSC)). Methyl Primer Express Software v1.0 (Applied Biosystems, Foster city, USA) was used to predict *HOXD13* CpG islands. The criteria for a potential *HOXD13* CpG island were as follows: a. ≥ 500 bp length; b. C+G content $> 55\%$; c. Observed CpG/Expected CpG $> 65\%$ as described previously [22].

DNA extraction, bisulfite conversion and sequencing

Genomic DNA was isolated from 6 pairs of fresh frozen primary breast tumors and corresponding normal tissues using an AxyPrep™ Multisource Genomic DNA Miniprep

Kit (Axygen Scientific, San Francisco, USA) following the manufacturer's instructions. DNA was quantified using a spectrophotometer (Gene Quant Pro, Amersham Biosciences, England).

Genomic DNA (500 ng) was used for bisulfite conversion using the EZ DNA Methylation-Gold kit (Zymo Research, Orange, USA) following the manufacturer's protocol. Converted DNA was amplified in a PCR reaction. The primers for *HOXD13* were as follows: forward, 5'-GAGTGG-GTGGGTTTAGTTAGGT-3'; reverse, 5'-AAACCRC-RACACTAACCTAAC-3'. PCR reaction mixture consisted of: 1.5 mM $MgCl_2$, 200 μ M dNTP, 1 μ M of forward and reverse primers, 2.5 units of Platinum Taq and 1 \times Platinum Taq buffer

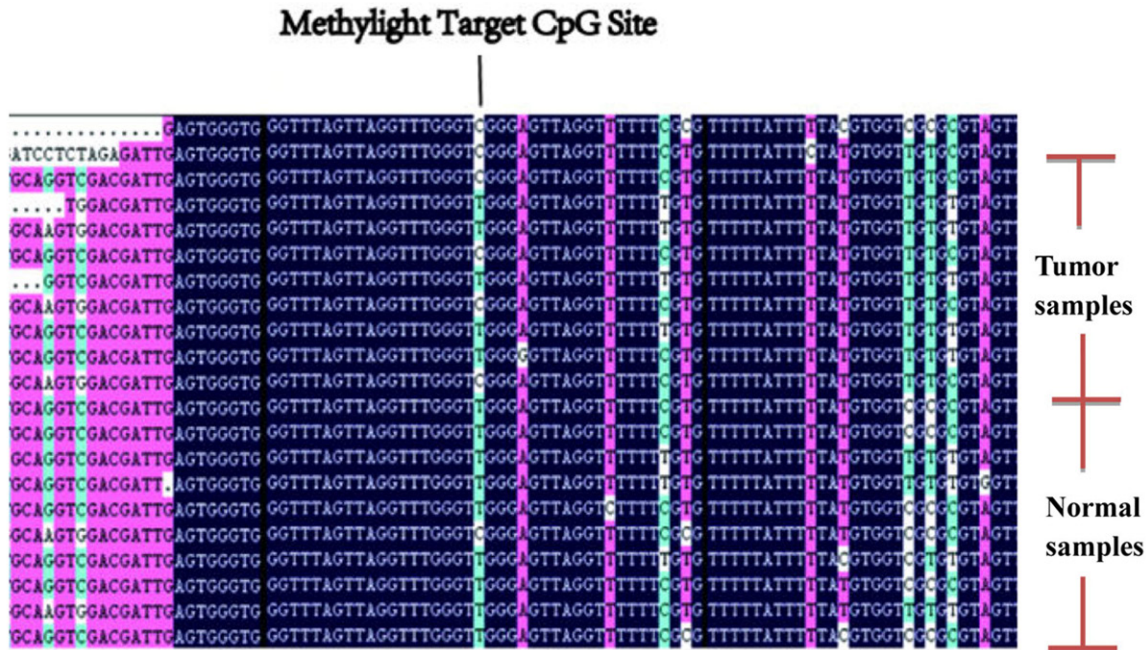


Figure 3. Part of the sequencing region in breast cancer samples and corresponding normal breast tissues. The -332 'C' was chosen for further analysis because of its high methylation frequency in breast tumor samples and the low methylation frequency in normal breast samples.

(Invitrogen, Burlington, USA) in a total reaction volume of 50 μ L. The PCR conditions were as follows: initial denaturation at 95°C for 5 min; 40 cycles of 95°C for 30 s, 56°C for 30 s and 72°C for 1 min; and final extension at 72°C for 5 min. The product size was 488 bp.

Next, PCR products were purified by gel extraction, ligated into the pGEM-T vector (Promega, Madison, USA) in a 3:1 vector: PCR product ratio and transformed into competent *Escherichia coli* (strain DH5 α). Blue-white screening was used to select at least 10 positive bacterial clones from which plasmid DNA was then isolated using a QIAprep Spin Miniprep Kit (Qiagen, Mississauga, USA). Clones were screened by digesting 1 μ g of plasmid DNA with Bst-ZI (Promega, Madison, USA), and by resolving the digestion products by agarose gel electrophoresis to verify the insertions. Positive clones were sequenced by the Life Technologies Lab (Invitrogen, Burlington, USA).

Methylight assay

Based on the DNA sequencing results of the *HOXD13* promoter we selected a probable CpG methylation site to design a specific probe. Sodium bisulfite-treated genomic DNA was

analyzed by Methylight, a fluorescence-based, real-time PCR assay, as described previously [23, 24]. TaqMan Minor Groove Binder (MGB) (Applied Biosystems, Foster City, USA) PCR was performed with primers specific for the bisulfite-converted methylated sequence and *globin* was used as internal reference gene. The primers for *HOXD13* were as follows: forward primer: 5'-GGGAATGGGAGGTGGATTTT-3'; reverse primer: 5'-CCGCCGAAAACGTACCATT-3'; product size, 145 bp; probe sequence, 5'-TTGGGTCGGGAGTTAG-3'. For each PCR, 0.5 μ l of 50 mM MgCl₂, 10 μ M dNTP, 0.25 μ l of 10 μ M forward and reverse primers, 0.1 μ l of 10 μ M probe, 0.1 μ l of 5 units of Platinum Taq polymerase and 1 μ l of 10 \times Platinum Taq buffer (Invitrogen, Burlington, USA) were used in a total reaction volume of 10 μ l. PCR was performed under the following conditions: 95°C for 3 min; followed by 40 cycles of 95°C for 10 s and 60°C for 30 s. The primers for *globin* were as follows: forward primer, 5'-AGGTAGAAAAGAGAATGAAGATAAA-3'; reverse primer, 5'-CTT-TCCACTCTTTTCTCATTCTCTC-3'; product size, 143 bp; probe sequence, 5'-AGGAGGATAAGGAAGAGGGGAAATAGG-3'. PCR was performed under the following conditions: 95°C, 3 min; followed by 40 cycles of 95°C for 10 s and 60°C

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Table 1. Correlation between *HOXD13* methylation with different clinicopathological parameters

Variables	Total no.	Unmethylated <i>HOXD13</i>		Methylated <i>HOXD13</i>		χ^2	P value
		n	%	n	%		
Age						0.798	0.372
< 45	64	30	36.1	34	30.1		
≥ 45	132	53	63.9	79	69.9		
Grade						0.168	0.682
I+II	180	77	92.8	103	91.2		
III	16	6	7.2	10	8.8		
Tumor size						8.325	0.004*
< 2 cm	63	36	43.4	27	23.9		
≥ 2 cm	133	47	56.6	86	76.1		
LNM						0.040	0.841
Negative	107	46	55.4	61	54.0		
Positive	89	37	44.6	52	46.0		
ER						0.221	0.638
Negative	53	21	25.3	32	28.3		
Positive	143	62	74.1	81	71.1		
PR						0.950	0.330
Negative	69	26	31.3	43	38.1		
Positive	127	57	68.7	70	61.9		
Her2						2.276	0.131
Negative	140	64	77.1	76	67.3		
Positive	56	19	22.9	37	32.7		
P53						0.285	0.594
Negative	162	70	84.3	92	81.4		
Positive	34	13	15.7	21	18.6		
Ki-67						0.791	0.374
Negative	99	45	54.2	54	47.8		
Positive	97	38	45.8	59	52.2		
Molecular subtype						3.399	0.334
Luminal A	113	51	61.4	62	54.9		
Luminal B	32	12	14.5	20	17.7		
Her-2	25	7	8.4	18	15.9		
TNBC	26	13	15.7	13	11.5		

* $P < 0.05$.

for 30 s. Values obtained in these two TaqMan MGB analyses were used as a measure of the degree of methylation at the analyzed locus. Relative quantification was performed based on the threshold cycles of the gene of interest (*HOXD13*) and internal reference gene (*globin*). The value of methylation at a specific locus was calculated by the $2^{-\Delta\Delta Ct}$ method, where $\Delta\Delta Ct = (Ct_{(Target)} - Ct_{(Reference)})_{sample} - (Ct_{(Target)} - Ct_{(Reference)})_{control}$ (corresponding normal tissue of the same

patient) [25]. The cut-off value of ≥ 1.5 [26] was delineated as methylation positive. All amplification efficiencies were similar. All samples were assayed in triplicate.

Statistical analysis

Statistical analyses were performed using SPSS software (version 17.0; SPSS Inc., Chicago, USA). The chi-square test was used to examine differences in categorical variables. Kaplan-Meier survival curves and log-rank statistics were employed to evaluate the association of *HOXD13* methylation and death using OS. The influence of different variables on survival was assessed using Cox univariate and multivariate regression analyses. Hazard ratios and their 95% confidence intervals (CIs) were recorded for each marker. A P -value < 0.05 was considered statistically significant for all analyses.

Results

HOXD13 mRNA expression in breast cancer tissues

HOXD13 mRNA expression was examined in 40 pairs of breast cancer tissues and corresponding normal breast tissues. Samples with the T/N fold ratio < 0.5 were considered as samples with low *HOXD13* expression. According to this criterion 60% (24/40) of the breast cancers samples showed low *HOXD13* mRNA expression

when compared with corresponding normal breast tissue samples (**Figure 1**).

HOXD13 CpG island, sequencing region and the target methylated CpG site

The predicted *HOXD13* CpG island was located in the -1325 bp to +675 bp with the length of 2000 bp. The sequencing region in our study was -360 bp to +128 bp. In this region we have

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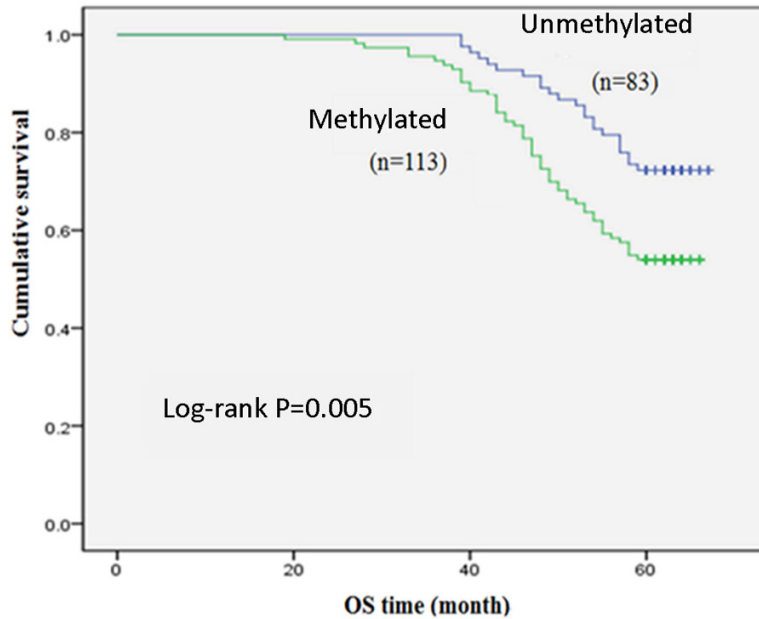


Figure 4. Kaplan-Meier curves for *HOXD13* methylation status in association with overall survival of 196 sporadic breast cancer patients. Patients with methylated *HOXD13* had a significantly worse prognosis than those with unmethylated *HOXD13* ($P=0.005$, log-rank test).

detected several methylated CpG sites, and we choose the -332 'C' as our target methylated site (See **Figure 2** and [Supplementary material 1](#)) due to its high methylation frequency in sequenced tumor samples and the low methylation frequency in corresponding normal breast samples (**Figure 3**). The results of sequencing are presented in the [Supplementary material 2](#).

Prevalence of HOXD13 methylation in breast cancer tissues

MethylLight assay was used to evaluate *HOXD13* methylation in sporadic breast cancer and corresponding normal breast tissues taken from the same patient. Out of 196 examined sample pairs, *HOXD13* methylation was detected in 113 of 196 tumor samples (57.7%).

Association of HOXD13 methylation with clinico-pathological characteristics

Next, the relationship between *HOXD13* methylation and various clinico-pathological characteristics was examined (**Table 1**). *HOXD13* methylation was significantly associated with larger tumor size ($P = 0.004$). However, no association between *HOXD13* methylation and other clinico-pathological factors was detected.

Kaplan-Meier survival analysis

Among the 196 patients, those with *HOXD13* methylation positive tumor showed poorer outcomes (56.788 ± 1.083 months) in terms of OS ($P = 0.005$, log rank test) compared with patients in whose tumors no *HOXD13* methylation was detected (62.313 ± 0.914). Kaplan-Meier survival curves are presented in **Figure 4**.

Univariate and multivariate survival analysis

Utilizing Cox proportional hazards regression model, both univariate and multivariate survival analyses were applied to assess the association between *HOXD13* methylation and clinicopathological

features and prognosis. Univariate analyses of OS demonstrated tumor size ($P < 0.001$), LNM ($P < 0.001$), ER ($P = 0.023$) and *HOXD13* methylation ($P = 0.006$) as effective prognostic factors. Other factors were not significantly associated with overall survival. Applying multivariate analysis, tumor size ($P < 0.001$), LNM ($P < 0.001$), and *HOXD13* methylation ($P = 0.012$) were independent prognostic predictors (**Table 2**).

Discussion

The breast cancer is one of the leading types of cancer worldwide. Although much has been learned about its molecular pathology and significant progress has been achieved in its prevention as well as therapy, it still remains one of the major public health problems of the female population. The most worthy prognostic factors for breast cancer patients are the axillary lymph node status and tumor size, but they have become clinically less useful in breast cancer [27]. New potential markers such as DNA methylation have emerged in recent years and could possibly be used as prognostic marker in breast cancer [27-29].

The role of some HOX gene family members has been previously examined in development and progression of various tumors. Many HOX

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Table 2. Prognostic factors in the Cox proportional hazards model

Variables	Univariate analysis			Multivariate analysis		
	HR	95% CI	P	HR	95% CI	P
Age (≥ 45 vs. < 45)	0.878	(0.546, 1.413)	0.592			
Grade (III vs. II+I)	0.722	(0.292, 1.790)	0.482			
Tumor size (≥ 2 cm vs. < 2 cm)	3.912	(2.009, 7.619)	< 0.001*	3.315	(1.697, 6.474)	< 0.001*
LNM (Positive vs. Negative)	2.731	(1.703, 4.381)	< 0.001*	2.637	(1.639, 4.242)	< 0.001*
ER (Positive vs. Negative)	0.582	(0.364, 0.929)	0.023*			
PR (Positive vs. Negative)	0.694	(0.439, 1.097)	0.117			
Her2 (Positive vs. Negative)	1.447	(0.903, 2.319)	0.125			
P53 (Positive vs. Negative)	1.331	(0.766, 2.314)	0.310			
Ki-67 (Positive vs. Negative)	1.189	(0.756, 1.872)	0.454			
HOXD13 methylation (methylated vs. unmethylated)	1.980	(1.212, 3.237)	0.006*	1.889	(1.151, 3.099)	0.012*

*P < 0.05.

genes were found to be expressed at lower levels in breast cancer tissues when compared to normal breast tissues and the aberrant expression of HOX genes was shown to be associated with malignant behavior of breast cancer cells [30]. Moreover, it has been shown that *HOXD13* may be a tumor suppressor gene in pancreatic cancer [14]. In addition, *HOXD13* methylation status has been examined in some cancer types [12, 13, 31], however, *HOXD13* methylation status has not been detected in breast cancer. Therefore our study is the first to examine *HOXD13* methylation in breast cancer.

In our study the methylation rate of *HOXD13* promoter in sporadic breast tumors was 57.7%. In previous studies, *HOXD13* promoter methylation was examined in extrahepatic cholangiocarcinoma [12] and malignant melanomas [13] and the methylation rate observed was 94.38% and 30.8%, respectively. Since, to our knowledge, there are no other studies to which we could compare our results, we can only conclude that the *HOXD13* methylation rate in different tumors varies probably due to the tissue specific methylation differences [32, 33].

Moreover, in our study *HOXD13* low expression was observed in approximately 60% of breast cancer tumors. As DNA methylation is a common mechanism of tumor suppressor inactivation, we speculate that *HOXD13* low expression may be attributed to its methylation.

Thoraia Shinawi et al. [31] found that short-term glioblastoma survivors had significantly increased *HOXD13* methylation when compared to long-term survivors. These findings are

similar to ours since in our study patients with *HOXD13* methylation positive tumors had significantly poor OS than patients with *HOXD13* methylation negative tumors ($P = 0.005$, log rank test). Thus, in our study *HOXD13* methylation was an independent unfavorable survival factor for patients with invasive breast cancer.

Since DNA methylation status can be reversed by demethylation agents, *HOXD13* methylation could be considered as potential therapeutic target. Indeed, it has been shown that 5-aza-2-deoxycytidine (decitabine) can increase the sensitivity of breast cancer cells to chemotherapeutic drugs [34, 35]. Stella Tommasi et al. [36] detected DNA methylation in breast cancer and showed that some homeobox genes may be used as diagnostic biomarkers. Therefore, the determination of the *HOXD13* methylation status in serum might be examined in future studies to possibly evaluate its diagnosis value.

In conclusion, our study for the first time showed that *HOXD13* methylation is a common event in sporadic breast cancer. Furthermore, in our study *HOXD13* methylation was correlated with poor survival of breast cancer patients. Our results suggested that *HOXD13* methylation may be a prognostic factor in breast cancer.

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Disclosure of conflict of interest

The authors declare that they have no competing interests.

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HOXD13 methylation and prognosis of breast cancer

Supplementary material 1

1. HOXD13 promoter region and the first exon region were predicted in <http://genome.ucsc.edu/> (UCSC).

```
ggttgaactttcattgctgacttttgccttctttcccaaatagtgaaaa
aaatcttctcatcagcaaacttctattccctatgatttctgtaaattca
ggccctcccattcctcaaatgatcatgaacatgctagaactcaaaaac
gatgaaacgaatttcttctgcttttcttccaacaccctctcataact
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gtggtgctgggtgacaagcttcaccaatcacaggcttaggggagtgatt
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gccccattagttgctgagattgagggatgggtgggctggagctctgaggct
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CCGGAG
GCTCCCCAGCCAAAGAGTGCCAGCACCCACGCCTGCAGCGGCCGCTGC
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CTCAAGTCATCGCCGCACGCCTCGCTGGGAGGCTTCCCGTGGAGAAGTA
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CAGCACGTGCCCGGTATATCGACATGGTGTCCACTTTCGGCTCCGGGGA
GCCTCGGCACGAGGCCTACATCTCCATGGAGGGGTACCAGTCTGGACGC
TGGCTAACGGGTGGAACAGCCAGGTGTACTGCACCAAGGACCAGCCACAG
GGGTCCCACTTTTGAAATCTTCCTTTCCAG

2. CpG island was predicted by Methyl Primer Express Software v1.0.

CpG Island

ACCTAGCCCCACCAGCACTGCCCTGAGCCACCTAACCCCTTGAAGTCAGACCGTTTCTCTGGGCTGCTCCTA-
TCACAAAATCCGAATTTGCTTGAACAAGCGCCCTTAAATTTGCCCTCTCAGTTCTCTGCAGTTGACAGCTT-
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CGCGCAATCAACTCGTGGGGTGGCTGCAGCGCTACGCCTGGTTCGGGGGGAGGGCGGGAATGGGAGGT-
GGACCCTGCAAGGGGCGAGAGAGGGTGGGGCCG**EAGTGGGTGGGTCCAGCCAGGCCTGGGC****GGGAGCC-**
AGGCTCCCCCGCTTCTACCCCCACGTGGCCGCGCGCAGCCAATGGCACGCCCCCGGGCGGGGCCCTCG-
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CCCCAGCCAAAGAGTGGCCAGACCCACGCCTGACGCGGCGCTGCAGCGCCCCGAGCGGCTCCAGC-
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GTCAGGCCTGGCGAGCAGCAGCGTACCGGCCAACGAGGTGCCAGCGGAGCCAAGGAGGTATCCTTCT-
ACCAGGGCTATACGAGCCCTTACCAGCACGTGCCCGGCTATATCGACATGGTGTCCACTTTCGGCTCCGGGGAGC-
CTCGGCACGAGGCCTACATCTCC

Start: -1325 End: 675 Length: 2000
A%: 17.70 -- T%: 17.50 -- C%: 29.95 -- G%: 34.85
C+G%: 64.80 -- CpG%: 8.45
A+T/C+G%: 0.54

The green region was chosen to be examined by bisulfite sequencing PCR in six breast cancers and paired normal tissues. The yellow site is the targeted methylation site (-332). The blue region "ATG" is the transcription starting site.

Supplementary material 2

Bisulfite sequencing results of HOXD13 methylation was detected in six breast cancer tissues and paired normal breast tissues.

HOXD13 methylation and prognosis of breast cancer

From No.1-6 are P774, P203, P252, P738, P226, and P847.

From No.7-12 are C774, C203, C252, C738, C226 and C847.

They are matched normal breast tissues and breast cancer tissues.

"C" means breast cancer and "P" means pairwise normal breast tissue.

1. The sequencing results from the normal breast tissue of the first breast cancer patient.

A07_58610.83.S1208222354.SM-P2-1-1.M13(-48)

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CATAAAAAATAAAAAACACAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCGACCT-
GCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTT-
AATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCC-
AACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATTTCA-
CACCGCATATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAAC-
CCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGA-
GCTGCATGTGTCAGAGGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCTCGTGATACGCCTATT-
TTTATAGGTTAATGTCATGATAATAATGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGAA-
ACCCCTATTTGTTTATTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTT-
CAATAATTTGAAAATGAAGAGTATGAGTATCAACATTTTCGTGTCGCCTATCCCTTTTTCGCGCATTTGCTCTGTTT-
TGCTCACCAGAAACGCTGTGAAGTAAAGATGCTGAAGAATCAGTGGGTGCACGGAGTGTTACATCGAAACTGGA-
ATCT

B02_58610.90.S1208222361.SM-P2-1-8.M13(-48)

AACTCGTCTCGGTTCCCGGCGATCCTCTGGAGATTACCCGTCCATATCCCAACTCCCGACGCGACTCATAACCC-
GACCTAACCCAACCCCGACCCTGACCCTAACCCCGCGCAAAACACCGTAACGCGACACACCTCCTCCCTCCTC-
TCCTTTCTCTCTAATTCACCTCGCTCCCGCCCTCTTCCCTAACCCCTCTCTCCCTCTATAAACCTCCCACCTCCG-
ACCCGCTACCCTCCAACAAATTAACCTATCGCGAAACATTTATAAAAAACAAAATTCAAATTA AAAAAAAAACCT-
AAACCAATCAAAAAACCACCTCCCACCCCAAAAACCCCCACCAAAAACATACCATTA ACTACACACAACCACAT-
AAAAATAAAAAACACAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCCACTTGC-
CGTCATGCTTCTTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAAT-
CGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAAC-
AGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATTTACAC-
CGCATATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACACCC-
GCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGAC
CGTCTCCGGGAGCTGCATGTGTCAGAGGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCTCGT-
GATACGCCTATTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAA-
ATGTGCGCGGAACCCCTATTTGTTATTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACATACCCTGAT-
AAATGCTTCAATAATGAAAAGGAGAGTATGAGTATCACATTTTCGTGTCGCCTATCCCTTTTTCGCGCATTTGC-
TCTGTTTTGCTCACCAGACGCTGTGAAAGTAAAGATGCTGAGATCAGTGTGCACGAGTGGGATCTCGACTGAATC-
TCACAGCGTAGATCTTCAT

B03_58610.91.S1208222362.SM-P2-1-9.M13(-48)

CGAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCCAACACAACCTCATAACC-
CAACCTAACCCAACCCCAACCCTAACCCCAACCAAAAACACCATAACACAACACACCTCCTCCCTCCTCTC-

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CTTTCTCTCTAATTCACCTACTCCCACCCTCTTCTCTAACCCTCTCTCCCTCTATAAACCTCCCACCTCCGACCCGC-
CTACCCTCCAACAAATTAACCTCATCACAAAACATTTATAAAAAACAAAATTCAAATTAACCAATCA-
AAAAACCACCTCCCACCCCAAAAACCCCCACCAAAAACATAACCATTAACCTACACACAACCACATAAAAAATAAAAC-
ACAAAAAACCTAACTCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCGACCTGCAGGCATGCAAGCTT-
GGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACCTAATCGCCTTGCAGCACA-
TCCCCCTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCT-
GAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTATTTACACCCGCATATGGTGCAC-
CTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCAACACCCCGCTGACGCGCCC-
TGACGGGCTTGTCTGCTCCCGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAG-
GTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCTCGTGATACGCCTATTTTTATAGGTTAATGTCA-
TGATAATAATGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGAAATGTGCGCGGAACCCCTATTTGTTATTTTT-
CTAAATACATTCAAATATGTATCCGCTCATGAGACATAACCCTGATAATGCTTCAATAATATTGAAAAAGGAGAGT-
ATGAGTATTCACATTTTCGTGTCGCCTATCCCTTTTTGCGCATTTGCTCTGTTTTGCTCACCAGAACGCTTGTGAGT-
TAAGATGCTGAGATCAGTGGGTGCACGAGTGGTACATCGAACTGATCTCAACAGCGTAGAATCCTTG

B04_58610.92.S1208222363.SM-P2-1-10.M13(-48)

CAAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCATCCATATCCCAACTCCCAACACAGCTCATAACCC-
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CTTTCTCTCTAATTCACCTACTCCCACCCTCTTCTCTAACCCTCTCTCCCTCTATAAACCTCCCACCTCCAACCCAC-
CTACCCTCCAACAAATTAACCTCATCACAAAACATTTATAAAAAACAAAATTCAAATTAACCAATCA-
AAAAACCACCTCCCACCCCAAAAACCCCCACCAAAAACATAACCATTAACCTACACACAACCACATAAAAAATAAAAC-
ACAAAAAACCTAACTCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCGACCTGCAGGCATGCAAGCTT-
TGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACCTAATCGCCTTGCAGCAC-
ATCCCCCTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCT-
GAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTATTTACACCCGCATATGGTGCAC-
CTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCAACACCCCGCTGACGCGCCCTG-
ACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTG
ACCGTCTCCGGGAGCTGCATGTGTCAGAGGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCTCGT-
GATACGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGAAAT-
GTGCGCGGAACCCCTATTTGTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACATAACCCTGATAA-
ATGCTTCATAATATGAAAAGGAGAGTATGAGTATCACATTTTCGTGTCGCCCTATCCCTTTTTGCGCATTTGCTCTGT-
TTTTGCTCACCAGAACGCTGTGAAGTAAAGATGCTGAAGAATCAGTTGTTTCGAGTGGTACATCGAACTGATCTCCA-
CAGCGTAGAATCTTGAAGTTCTCGCCGAGAGAAGCGTTCTCATGTAGTC

2. The sequencing results from the normal breast tissue of the second breast cancer patient.

B07_58610.95.S1208222366.SM-P2-2-1.M13(-48)

AATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCATATCCCAACTCCCAACACAACCTCATAACCCA-
ACCTAACCCAACCCCAACCCTAACCCTAACCCACACAAAACACCATAACACAACACACCTCCTCCCTCCTCTCCTT-
TCTCTCTAATTCACCTACTCCCACCCTCTTCTCTAACCCTCTCTCCCTCTATAAACCTCCCACCTCCAACCCACCTA-
CCCTCCAACAAATTAACCTCATCACAAAACATTTATAAAAAACAAAATTCAAATTAACCAATCA-
AAAAACCACCTCCCACCCCAAAAACCCCCACCAAAAACATAACCATTAACCTACACACAACCACATAAAAAATAAAACACA-
AAAAAACCTAACTCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCGACCTGCAGGCATGCAAGCTTGG-
CACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACCTAATCGCCTTGCAGCACAT-
CCCCCTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGA-
ATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTATTTACACCCGCATATGGTGCAC-
CAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCAACACCCCGCTGACGCGCCCTGAC-
GGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTCAG-
GAGGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCTCGTGATACGCCTATTTTTATAGGTTA-
ATGTCATGATAATAATGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGAAATGTGCGCGGAACCCCTATT-
TGTTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACATAACCCTGATAAATGCTTCAATAATATTG-
AAAAGGAGAGTATGAGTATTCACATTTTCGTGTCGCCCTATCCCTTTTTGCGGCATTTGCTTCTGTTTTGTC-
TACCCAGAACGCTGTGAAAGTAAAGATGCTGAAGATCAGTGGGGTGCACGAGTTGTACATCGGACTGGAT-
CCAACAGCGGTTAGAATCTTTGGAGAGTTTTGCTCCGGA

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B08_58610.96.S1208222367.SM-P2-2-2.M13(-48)

ACGAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCCAACACAACCTCACA-
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TCCTCTCCTTTCTCTCTAACTCGCTCACTCCCGCCCTCTTCTCTAACCCCTCTCTCCCTCTATAAACCTCCCAC-
CTCCGACCCGCTACCCTCCAACAAATTAACTCATCGCGAAACGTTTATAAAAAACAAAATTCAAATTAAAAAA-
AACCTAAACCAATCAAAAAACACCTCCCACCCCAAAAAACCCCAACGAAAACGTACCATTAACCACACACAA-
CCACATAAAAAATAAAAAACAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTAATCGTCGAC-
CTGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCAA-
CTTAATCGCCTTGCAGCACATCCCCCTTTCCGCGAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTT-
CCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATT-
TCACACCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCA-
ACACCCGCTGACGCGCCCTGACGGGCTTGCTGCTCCCGCATCCGCTTACAGACAAGCTGTGACCGTCTCCG-
GGAGCTGCATGTGTCAGAGTTTTACCGTCATACCCGAAACGCGCGAGACGAAAGGGCCTCGTGATACGCCT-
ATTTTATAGGTTAATGTCATGATAATAATGGTTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCGC-
GGAACCCCTATTTGTTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACATACCCTGATAATGCT-
CATATATGAAAAGGAGAGTATGAGTATCACATTTTCGTGTCGCCTATCCCTTTTGCGCATTTGCTCTGTTTTGCTC-
ACCCAGACGCTGTGAGTAAAGATGCTGAGAATCAGTGGGTGCACGAGTGGTACATCGACTGGATCTCAACAGGG-
GGTGAAGATCCTGAA

B09_58610.97.S1208222368.SM-P2-2-3.M13(-48)

TCGAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCCGACGCGACTCATAA-
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CCTCTCCTTTCTCTCTAATTCGCTCGCTCCACCCTCTTCTCTAACCCCTCTCTCCCTCTATAAACCTCCCACC-
TCCAACCCACCTACCCTCCAACAAATTAACTCATCGCGAAACGTTTATAAAAAACAAAATTCAAATTAAAAAA-
ACCTAAACCAATCAAAAAACACCTCCCACCCCAAAAAACCCCAACCAAAAAACATAACCATTAACCTACGCGGACC-
ACATAAAAAATAAAAAACAGAAAAGACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCGACC-
TGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCAACT-
TAATCGCCTTGCAGCACATCCCCCTTTCCGCGAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCC-
CAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATTTCC-
ACACCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAAC-
ACCCGCTGACGCGCCCTGACGGGCTTGCTGCTCCCGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGG-
AGCTGCATGTGTCAGAGTTTTACCGTCATACCCGAAACGCGCGAGACGAAAGGGCCTCGTGATACGCCTAT-
TTTTATAGGTTAATGTCATGATAATAATGGTTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGG-
AACCCCTATTTGTTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACATACCCTGATAATGCTTC-
ATATATTGAAAAGAGAGTATGAGTATCACATTTTCGTGTCGCCTTATCCCTTTTGCGCATTTGCTTCTGTTTTG-
GCTCACCAGAACGCTGTGAAGTAAAGAATGCTGAGATCAGTTGGGGTGCACGAGTGGTTTACATTCGAACTGGAT-
CTTACCACGCGGGTGAGA

B10_58610.98.S1208222369.SM-P2-2-4.M13(-48)

TCGAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCCGACACAACCTCATA-
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CCTCTCCTTTCTCTCTAATTCACTCACTCCCACCCTCTTCTCTAACCCCTCTCTCCCTCTATAAACCTCCCACC-
TCCAACCCACCTACCCTCCAACAAATTAACTCATCGCGAAACGTTTATAAAAAACAAAATTCAAATTAAAAAA-
CCTAAACCGATCGAAAAACCGCCCCCGCCCCGAAAACCCCGCGCAAAAACGTACCATTAACCTACGCGCGAC-
CACATAAAAAATAAAAAACGCGAAAAACCTAACTCCCGACCCAAACCTAACTAAACCCACCCACTCAATCGTCCA-
CTTGCCGTCATGCTTCTTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCAA-
CTTAATCGCCTTGCAGCACATCCCCCTTTCCGCGAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTT-
CCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATT-
TCACACCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCA-
ACACCCGCTGACGCGCCCTGACGGGCTTGCTGCTCCCGCATCCGCTTACAGACAAGCTGTGACCGTCTCCG-
GGAGCTGCATGTGTCAGAGTTTTACCGTCATACCCGAAACGCGCGAGACGAAAGGGCCTCGTGATACGCC-
TATTTTTATAGGTTAATGTCATGATAATAATGGTTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCG-

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CGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAGGGAGAGTATGAGTATTCAACATTTCCGTGTGCCCCTATCCCTTTTTGCGGCATTTGCTTCTCTGTTTTGCTCACAGAAAACGCTGGGTGAAAGTAAAGATGCTGAAGAATCAGTGGGTGCCACGAGGTGGGTTACTCGGAACCTGGATTTTACA

B11_58612.1.S1208222370.SM-P2-2-5.M13(-48)

AGATTACGAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCCAGCGGACTCATAACCCGACCTAACCCGACCCCGACCCTAACCCCTAACCCCGCGCAAAACACCATAACGCGACGCGCCTCCTCCCTCCTCCTTTCTCTCTAGTTTCGCTCGCTCCCACCCTCTTCCCTAACCCCTCCTCCTCTACAAACCTCCACCTCCAACCCACCTACCCTCCAACAAATTAACCTCATCAGAAAACATTTATAAAAAACAAATTCAAATTAACAAAACCTAAACCAATCAAAAAACACCTCCCACCCCAAAAACCCCCACCGAAAACATACCATTAACCTACACACGACCACGTAATAAAAAACACAAAAAACCTAACTCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCGACCTGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCAACTTAATCGCCTTGACGACATCCCCCTTTGCCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATTCACACCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACCCCGTACGCGCCCTGACGGGCTTGCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGCAGAGTTTTACCCGTCATACCGAAACGCGCGAGACGAAAGGGCCCTCGTGATACGCCTATTTTATAGGTTAATGTCATGATAATAATGTTTTCTTAGACGTCAGTGGCACTTTTCGGGGAAATGTGCGCGAACCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACATACCCTGATAATGCTCATATATGAAAAGAGAGTATGAGTATCACATTCGTGTGCTATCCCTTTTTGCGCATTGCTCTGTTTTGCTCACCCGAAACGCTGGTGAAGTAAAGAAT

C01_58612.3.S1208222372.SM-P2-2-7.M13(-48)

ACGAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCGACGCGACTCATAACCCGACCTAACCCGACCCCGACCCTAACCCCTAACCCCGCGCAAAACACCATAACGCGACGCGCCTCCTCCTCCTCCTTTCTCTCTAATTCGCTCGCTCCCACCCTCTTCCCTAACCCCTCCTCCTCTATAAACCTCCCACCTCCAACCCACCTACCCTCCAACAAATTAACCTCATCGAAAAACGTTTTATAAAAAACAAAGTTCAAATTAACAAAAACCTAAACCAATCAAAAAACACCTCCCAGCCCAAAAACCCCCACCAAAAACATACCATTAACCTACGCGGACCCACATAAAAAATAAAAAACAGAAAAACCTAACTCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCGACCTGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCAACTTATCGCCTTGACGACATCCCCCTTTGCCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATTTACACCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACACCCGCTGACGCGCCCTGACGGGCTTGCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGCAGAGTTTTACCCGTCATACCGAAACGCGCGAGACGAAAGGGCCCTCGTGATACGCCTATTTTATAGGTTAATGTCATGATAATAATGTTTTCTTAGACGTCAGTGGCACTTTTCGGGGAAATGTGCGCGGAAACCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAGGAAGAGTATGAGTATCACATTCGTGTGCTTATTCCCTTTTTGCGCATTTGCTCTGTTTGCTACCAGAACGCTGGTGAAGTAAAGAATGCTGAGAACAGTGGGGGCACGAAGTGGGTTACTCGACCTGGATCTTACCAACG

C03_58612.5.S1208222374.SM-P2-2-9.M13(-48)

CTCGTCTCGGTTCCCGGCATCCTCTGGAGATTACCCGTCCATATCCCAACTCCCAACACAACCTCATAACCCAACCTAACCCAACCCCAACCCTAACCCCTAACCCACACAAAACACCATAACACAACACACCTCCTCCCTCCTCCTTTCTCTCTAATTCACTACTCCCACCCTCTTCCCTAACCCCTCCTCCTCTATAAACCTCCCGCCTCCAAACCACCTACCCTCCAACAAATTAACCTCATCAGAAAACGTTTTATAAAAAACAAATTCAAATTAACAAAAACCTAAACCAATCAAAAAACACCTCCCACCCCAAAAACCCCCACCGAAAACGTACCATTAACCTACACACAACCACATAAAATAAAAAACAGAAAAACCTAACTCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCCACTTGCCGTCATGCTTCTTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCAACTTAACTGCCTTGACGACATCCCCCTTTGCCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATTTACACCG

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CATATGGTGCACCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACACCCCGCT-
GACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCG
TCTCCGGGAGCTGCATGTGTGAGAGGTTTTACCGTCATACCGAAAACGCGGAGACGAAAGGGCCTCGTGAT-
ACGCCTATTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAGACGTCAGGGGCACTTTTCGGGGAAATGT-
GCGCGAACCCCTATTTGTTTTTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATACCCTGATA-
AATGCTTCAATAATATTGAAAAGGAGAGTATGAGTATTCAACATTCCGCTGTCCGCCCTTATCCCTTTTTGCGCA-
TTTGCTTCTGTTTTGCTCACCAGAACGCTGTGAAAGTAAAGATGCTGAAGATCAGTGGTGCCACGAGGTGGT-
AATCGACTGATTCCACAGCGTAGATCTTGGGAGTTCGCCCGGAGACGTTTTCAATGATGT

C04_58612.6.S1208222375.SM-P2-2-10.M13(-48)

TTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCCGACGCGACTCATAACCCGA-
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CTTCTCTCTAATTCGCTCGCTCCCGCCCTCTTCTCTAACCCCTCTCCTCTATAAACCTCCCGCCTCCGAC-
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AAATAAAAACGCGAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCGACCTGCAG-
GCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCAACCTAATC-
GCCTTGCAGCACATCCCCCTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACA-
GTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATTTACACC-
GCATATGGTGCACCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACACCCG-
CTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTG-
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TTGAAAAGAGAGTATGAGTATTCAACATTCGTGTGCGCCTATCCTTTTTGCGCATTTGCTCTGTTTTGCTCAC-
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C05_58612.7.S1208222376.SM-P2-2-11.M13(-48)

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TCTCCTTTCTCTCTAATTCGCTCGCTCCCGCCCTCTTCTCTAACCCCTCTCCTCTATAAACCTCCCGCCTC-
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ATAAAAATAAAAACACGAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCGACCTG-
CAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCAACCTA-
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ACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATTTAC-
ACCGCATATGGTGCACCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACAC-
CCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAG-
CTGCATGTGTCAGAGTTTTACCCGTCATACCGAAAACGCGCGAGACGAAAGGGCCTCGTGATACGCCTATTT-
TTATAGGTTAATGTCATGATAATAATGGTTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGA-
ACCCCTATTTGTTTTATTTTTCTAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCT-
TCAATAATATGAAAATGAGAGTATGAGTTTTACATTTCCGCTGTGCGCCTTATTCCTTTTTGCGCATTTGCTTC-
TGTTTTGCTCACCAGAACGCTGTGAAGTAAAGATGCTGAGATCAGTGGGGCACGAGTGGGTACTCGAACTGAATC-
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C06_58612.8.S1208222377.SM-P2-2-12.M13(-48)

ATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCCGACGCGACTCATAACC-
CGACCTAACCCGACCCCGACCCTAACCCCTAACCCCGCGCAAAACACCATAACGCGACATGCCTCCTCCCTCC-
TCTCCTTTCTCTCTAATTCGCTCGCTCCACCCCTCTTCTCTAACCCCTCTCCTCTATAAACCTCCACCTC-
CAACCCACCTACCCTCCAACAAATTAACCTATCGCGAAACGTTTATAAAAACAAAATTCAAATTAACCAACCTAA-
ACCAACCTAACCCGACCCCGACCCTAACCCCTAACCCCGCGCAAAACACCATAACGCGACATGCCTCCTCCCTCC-

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CTAAACCAATCAAAAAACCACCTCCCGCCCCAAAAACCCCAACAAAAACATACCATTAACCTACGCGCGACCA-CATAAAAAATAAAAAACACGAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCGACC-TGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAAC-TTAATCGCCTTGCAGCACATCCCCCTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTC-CCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTATT-TCACACCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCC-AACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCC-GGGAGCTGCATGTGTGAGAGGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCTCGTGATACGC-CTATTTTATAGGTTAATGTCATGATAATAATGGTTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGC-GCGGAACCCCTATTTGTTTTTTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACATACCCTGATAAA-TGCTTCATAATATGAAAGGGAGAGTATGAGTATTCACATTCCGTGTGCGCTTATTCCTTTTTGCGGCATTTGCT-TTGTGCTACAGAACGCTGGGTGAAGTAAAGATGCTGAGATCAGTGGGTGCACGAGTGGTAATCGAACTGGAAT-TCACACAGCGTAGATCTGAGTCGTCGAGAACGGATTCCATGAGTGAGGCACTTA

3. The sequencing results from the normal breast tissue of the third breast cancer patient.

C07_58612.9.S1208222378.SM-P2-3-1.M13(-48)

AATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTGAGTGGGTGGGTTTAGTTAGGTTTGGGTTGGGAGTT-AGGTTTTTTCGTGCTTTTATTTTTATGTGGTCGCGCTAGTTAATGGTATGTTTTTGGTGGGGTTTTTGGGG-CGGGAGGTGGTTTTTGGATTGGTTTAGGTTTTTTTTAATTTGAATTTGTTTTATAAACGTTTCGCGATGAGTT-AATTTGTTGGAGGTAGGCGGGTTCGGAGGTGGGAGGTTATAGAGGGAGAGAGGGTTAGAGGAAGAGGGCGG-GAGTGAGCGAATTAGAGAGAAAGGAGAGGGAGGAGGCGCGTCGCGTTATGGTGTGTTGCGCGGGTTAG-GGTTAGGGTTCGGGGTTCGGTTAGGTCGGGTTATGAGTCGCGTCGGGAGTTGGGATATGGACGGGTAATCGTC-GACCTGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTAC-CCAACCTAATCGCCTTGCAGCACATCCCCCTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCC-CTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTATTTACACCCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTA-AGCCAGCCCCGACACCCGCCAACACCCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTAC-AGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAGGTTTTACCGTCATCACCGAAACGCGCGAG-ACGAAAGGGCCTCGTGATACGCCTTATTTTTATAGGTTAATGTCATGATAATAATGGTTTTCTTAGACGTCA-GGTGCCTTTTTTCGGGGAAATGTGCGCGGACCCTATTTGTTATTTTTCTAAATACATTCAAATATGTATCCG-CCTCATGAGACAATAACCCTGATAAATGCTTCAATAATTTGAAAAGGAGAGTATGAGTATTCACATTCGTGTC-CGCCCTATTCCTTTTTGCGGCATTTGCTTCTGTTGCTCACCCAGAACGCTGGAGGTAAGATGCTGAAAGATCAGT-GGGCAAGTGTACTCGACTGAATCTCAACGCGTAAGAATCTTTGGAAGTTTCCCGGA

C08_58612.10.S1208222379.SM-P2-3-2.M13(-48)

CAAACCTCGTCTCGGTTCCGGCGATCCTCTGGAGATTGAGTGGGTGGGTTTAGTTAGGTTTGGGTTGGGAGTT-AGGTTTTTTCGCGTTTTTATTTTTACGTGGTCGCGCTAGTTAATGGTACGTTTTTCGGCGGGGTTTTTCGGG-GCGGGAGGCGGTTTTTGTATCGGTTTAGGTTTTTTTTAATTTGAATTCGTTTTTATAAACGTTTCGCGATGAG-TTAATTTGTTGGAGGTTAGGCGGGTTCGGAGGCGGGAGGTTATAGAGGGAGAGAGGGTTAGAGGAAGAGGGC-GGGAGCGAGCGAATTAGAGAGAAAGGAGAGGGAGGAGGCGTGTGTTATGGTGTGTTGCGTGGGGTT-AGGGTTAGGGTTCGGGGCCGGTTAGGTCGGGTTATGAGTCGCGTCGGGAGTTGGGATATGGACGGGTAATCG-TCCACTTGCCGTCATGCTTCTTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTA-CCCAACTAATCGCCTTGCAGCACATCCCCCTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGC-CCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGG-TATTTACACCCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCC-GCCAACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCT-CCGGGAGCTGCATGTGTGAGAGGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCCTCGTGATA-CGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATG-TGCGCGGAACCCCTATTTGTTTTTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCTTG-ATAAATGCTTCATAATTTGAAAAGGAGAGTATGAGTATTCACATTTTCGTGTGCGCTTATTCCTTTTTTTCG-GCATTTTGCTTCTGTTTTGCTACAGAACGCTGGGTGAAGTAAAGATGCTTGAAGATCAGGTGGTGCACGAAGTGT-TACATTCGACTGGAATCTCACACGCGTTAGAATATCTTGTGAGAGAT

HOXD13 methylation and prognosis of breast cancer

C09_58612.11.S1208222380.SM-P2-3-3.M13(-48)

TCGAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCCGACGCGACTCATAA-
CCCAGACCTAACCCGACCCCGACCCCTGACCCTAACCCCGCGCAAACACCATAGCGCGACGCGCCTCCTCCCT-
CCTCTCCTTTCTCTCTAATTCGCTCGCTCCCGCCCTCTTCCTCTAACCCCTCTCCTCTATAAACCTCCCACC-
TCCGACCCGCTACCCTCCAACAAATTAACCTCATCGCGAAACGTTTATAAAAACAAAATTCAAATTAAAAAAAAA-
CCTAAACCGATCAAAAAACCGCCTCCCGCCCCGAAAACCCCGCCGAAAACGTACCATTAACCTACGCGCGACC-
ACGTAAAAATAAAAAACGCGAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCGAC-
CTGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCAAC-
TTAATCGCCTTGAGCACATCCCCCTTTCCGACGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCC-
AACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTC
TCCTTACGCATCTGTGCGGTATTTCACACCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTT-
AAGCCAGCCCCGACACCCGCCAACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTAC-
AGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAGTTTTACCCGTCATCACCGAAAACGCGCGAGA-
CGAAAGGGCCTCGTGATACGCCTATTTTATAGGTTAATGTCATGATAATAATGTTTCTTAGACGTCAGGTG-
GCACTTTTCGGGAAATGTGCGCGGAACCCCTATTTGTTATTTTTCTAAATACATTCAAATATGTATCCGCT-
CATGAGACAATACCCTGATAAATGCTTCAATAATATTGAAAAGGAGAGTATGAGTATTCAACATTTCGTGTGCC-
TATCCCTTTTTGCGGCATTTGCTCTGTTTTGCTCACCAGACGCTGTGAAAGTAAAAGATGCTGAGATCAGTGGGTG-
CCACGAGGGTTAAATCGAACCTGGAAT

C10_58612.12.S1208222381.SM-P2-3-4.M13(-48)

TCGACTCGTCCCTCGGTTCCCGGCGATCCTCTGGAGATTACCCGTCCATATCCCAACTCCCGACGCGACTCATAA-
CCCAGACCTAACCCGACCCCGACCCCTAACCCCTAACCCCGCGCAAACACCATAACGCGACACGCCTCCTCCCT-
CCTCTCCTTTCTCTCTAATTCGCTCGCTCCACCCCTCTTCCTCTAACCCCTCTCCTCTATAAACCTCCCACC-
TCCAACCCACCTACCCTCCAACAAATTAACCTCATCGCGAAACGTTTATAAAAACAAAATTCAAATTAAAAAAAA-
ACCTAAACCAATCAAAAAACCACTCCCGCCCCAAAAACCCCAACAAAAACATAACCTAACTACGCGCGAC-
CACATAAAAAATAAAAAACGAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCCA-
CTTGCCGTCATGCTTTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCAA-
CTTAATCGCCTTGAGCACATCCCCCTTTCCGACGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTT-
CCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTAT-
TTCACACCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCC-
AACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCC-
GGGAGCTGCATGTGTCAGAGGTTTTACCCGTCATCACCGAAAACGCGCGAGACGAAAGGGCCTCGTGATACGC-
CTATTTTATAGGTTAATGTCATGATAATAATGTTTTCTTAGACGTCAGGTGGCACTTTTCGGGAAATGTGC-
GCGGAACCCCTATTTGTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACATAACCTGATAAATG-
CTTCAATATATTGAAAAGGAGAGTATGAGTATCACATTTCGTGTGCTATCCCTTTTTGCGCATTTGCTCTGTTTTGCT-
CACCAGACGCTGTGAAGTAAAGATGCTGAGATCAGTGGGTGCCGAGTGATACATCGACCTGGATTCTCA

C12_58612.14.S1208222383.SM-P2-3-6.M13(-48)

TACATGCATTACGAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCCGAC-
GCGACTCATAACCCGACCTAACCCGACCCCAACCCTAACCCCTAACCCACGCAAACACCATAACGCGACGCG-
CCTCCTCCCTCCTCTCCTTTCTCTCTAATTCGCTCGCTCCCGCCCTCTTCCTCTAACCCCTCTCCTCTATAA-
ACCTCCCGCCTCCGTCCCGCCTACCCTCCAACAAATTAACCTCATCGCGAAACGTTTATAAAAACGAAATTCAA-
TAAAAAAAACCTAAACCGATCAAAAAACCGCCTCCCGCCCCGAAAACCCCGCCGAAAACGTACCATTAAC-
TACGCGCAACCACGTAATAAAAAACGCGAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACT-
CAATCGTCGACCTGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTG-
GCGTTACCCAACCTAATCGCCTTGAGCACATCCCCCTTTCCGACGCTGGCGTAATAGCGAAGAGGCCCGCAC-
CGATCGCCCTTCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCAT-
CTGTGCGGTATTTACACCCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCC-
CGACACCCGCCAACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGT-
GACCGTCTCCGGGAGCTGCATGTGTCAGAGGTTTTACCCGTCATCACCGAAAACGCGCGAGACGAAAGGGCC-
TCGTGATACGCCTATTTTATAGGTTAATGTCATGATAATAATGTTTTCTTAGACGTCAGTGGCACTTTTCGGG-
GAAATGTGCGCGGAACCCCTATTTGTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACATAACCTG-
ATAAATGCTTCATATATGAAAAGAGAGTATGAGTATCAACATTTCCGTGTGCGCCCTTATTCCTTTTTGCGGCATAGC

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D01_58612.15.S1208222384.SM-P2-3-7.M13(-48)

ATCGAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAA_cTc_cTACGCGACTCAT-
AACCCGACCTAACCCGACCCCAACCCTAACCCACGCCAAAACACCATAACGCGACGCGCCTCCTCC-
CTCCTCTCCTTTCTCTCTAATTCGCTCACTCCCGCCCTCTTCTCTAACCCTCTCTCCCTCTATAAACCTCCCA-
CCTCCGACCCGCTACCCTCCAACAAATTAATCATCGCGAAACGTTTATAAAAAACAAAATTCAAATTAAAAA-
AAACCTAAACCAATCAAAAAACCACCTCCCGCCCCAAAAACCCCAACAAAAACATACCATTAATACGCGCG-
ACCACATAAAAAATAAAGCACGAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTC-
GACCTGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACC-
CAACTTAATCGCCTTGCAACACATCCCCCTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGC-
CCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTG-
GGTATTTACACCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACA-
CCCGCCAACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACC-
GTCTCCGGGAGCTGCATGTGTCAGAGGTTTACCCGTCATCACC_GAAACGCGCGAGACGAAAGGGCCTCGT-
GATACGCCTATTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAGACGTCAGGGGCACTTTTCGGGGA-
AATGTGCGCGGAACCCCTATTTGTTATTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACATACCCT-
GATAATGCTTCATAATATTGAAAAGGAGAGTATGAGTATTCAACATTTCCGGTTCGCCTTATCCCTTTTTCGGGCAT-
TTTGCTTCTGTTTGGCTCAC
CCAGAACGCTGGTGAAGTAAAGATGCGTGGAAGATCAGGTGGGGGGCACGAGGTGGGTACCATCCGAACCTT-
GAATCTCCA

D03_58612.17.S1208222386.SM-P2-3-9.M13(-48)

GAACGTCCTCGGTTCCCGGCGATCCTCTGGAGATTGAGTGGGTGGGTTTAGTTAGGTTTGGGTTGGGAGTT-
AGGTTTTTTCGCGTTTTTCATTTTTACGTGGTTGCGCGTAGTTAATGGTACGTTTTCGGCGGGGGTTTTTCGGG-
GCGGGAGGCGGTTTTTGTATCGGTTTAGGTTTTTTTTAATTTGAATTTCTGTTTTATAAACGTTTCGCGATGAG-
TTAATTTGTTGGAGGGTAGGCGGGACGGAGGCGGGAGGTTTATAGAGGGAGAGAGGGTTAGAGGAAGAGGGCG-
GGAGCGAGCGAATTAGAGAGAAAGGAGAGGAGGGAGGAGGCGCGTTCGCGTTATGGTGTGTTTTCGCGGGGTTA-
GGGTTAGGGTTGGGGTCGGGTTAGGTCGGGTTATGAGTTCGCGTCCGGAGTTGGGATATGGACGGGTAATCGT-
CCACTTGCCGTCATGCTTCTTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTAC-
CCAACCTAATCGCCTTGCAACACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCG-
CCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTG-
CGGTATTTACACCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGAC-
ACCCGCCAACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGA-
CCGTCTCCGGGAGCTGCATGTGTCAGAGGTTTACCCGTCATCACC_GAAACGCGCGAGACGAAAGGGCCC-
TCGTGATACGCCTATTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAGACGTCAGGTGGCACTTTTCG-
GGGAAATGTGCGCGGAACCCCTATTTGTTATTTTCTAATACATTCAAATATGTATCGCTCATGAGACAAT-
ACCTGAATAAATGCTTCATATATGAAAAGAGAGTATGGTATCAACATTTCCGTGTTTCGCCTATCCTTTTCGGC-
ATTTGCTCTTTTTGCTCACCAGACGCTGTGAAGTTAAGATGCTGAGATCAGTGTACAAGTGTACTCGGAACCTGGA-
TCTCACACCCGCTAGATCTGAAGTTTGACA

D04_58612.18.S1208222387.SM-P2-3-10.M13(-48)

AATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTGAGTGGGTGGGTTTAGTTAGGTTTGGGTCGGGAGTT-
AGGTTTTTTCGCGTTTTTATTTTTACGTGGTTCGCGTAGTTAATGGTACGTTTTCGGTGGGGGTTTTTGGG-
GTGGGAGGTGGTTTTTACTGGTTTAGGTTTTTTTTAATTTGAATTTGTTTTATAAACGTTTCGCGATGAG-
TTAATTTGTTGGAGGGTAGGCGGGTTGGAGGCGGGAGGTTTATAGAGGGAGAGAGGGTTAGAGGAAGAGGGCG-
GGAGCGAGCGAATTAGAGAGAAAGGAGAGGAGGGAGGAGGCGCGTTCGCGTTATGGTGTGTTTTCGCGGGGTTA-
GGGTTAGGGTTGGGGTCGGGTTAGGTCGGGTTATGAGTTCGCGTCCGGAGTTGGGATATGGACGGGTAATCGTC-
GACCTGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTAC-
CCAACCTAATCGCCTTGCAACACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCG-
CCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTG-
CGGTATTTACACCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGAC-
ACCCGCCAACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGA-
CCGTCTCCGGGAGCTGCATGTGTCAGAGGTTTACCCGTCATCACC_GAAACGCGCGAGACGAAAGGGCCTC-

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GTGATACGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAGACGTCAGGTGGCACTTTTCGG-
GGAAATGTGCGCGGAACCCCTATTTGTTATTTTCTAATACATTCAATATGTATCCGCTCATGAGACATACCC-
TGATAAATGCTCATTAAATATTGAAAAGAGAGTTTGTAGATTCAACATTCCGTGTGCGTATCCCTTTTGCGCATT-
TGCTCTGTTTTGCTCACCAGGACGCTGTGAAGTAAGATGCTGAGATTCAGTGTGTCGATGGTACTCGACTGGAT-
CCAACCGTAGATCCTGGAGTTTCCGCGAAACGTTCCATGTT

D05_58612.19.S1208222388.SM-P2-3-11.M13(-48)

ATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCCGACGCGACTCATAACC-
CGACCTAACCCGACCCCGACCCTAACCCCTAACCCCGCGCAAAACACCATAACGCAACGCGCCTCCTCCCTC-
CTCTCCTTTCTCTAATTCGCTCGCTCCCGCCCTCTTCTCTAACCCCTCTCTCCCTCCATAAACCTCCCGCC-
TCCGACCCGCTACCCTCCAACAAATTAACCTATCGCGAAACGTTTATAAAAAACAAAATTCAAATTAACAAAAA-
CCTAAACCGATCGAAAAACCGCCTCCCGCCCCGAAAACCCCGCCGAAAACGTACCATTAACCTACGCGCGAC-
CACGTAATAAAAAACAGGAAAAACCTAACTCCCGACCCAAACCTAACTAAACCCACCCACTCAATCGTCG-
ACCTGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACC-
CAACTAATCGCCTTGCAACACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGC-
CCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGC-
GGTATTTACACCCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACA-
CCCGCCAACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGAC-
CGTCTCCGGGAGCTGCATGTGTGAGAGTTTTACCCTCATCACCGAAACGCGCGAGACGAAAGGGCCTCG-
TGATACGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAGACGTCAGGTGGCACTTTTCGGG-
GAAATGTGCGCGGAACCCCTATTTGTTATTTTCTAAATACATTCAATATGTATCCGCTCATGAGACATACC-
TGATAAATGCTTCATATATTGAAAAGGAGAGTATGAGTATCACATTTCCGTGTGCGCCTATCCCTTTTTCGCGA-
TTTGCTCTGTTTTGGCTCACCAGAACGCTGTGAGGTAAGATGCTGAGATCAGTGGTGCACGAGTGGATACTCGACT-
GATTCACAGCGGTAAGATCTTGAAGTTGCCTGAGACGGTCCATGTAGTGACCACTTTTAAAG

D06_58612.20.S1208222389.SM-P2-3-12.M13(-48)

ACTCGTCTCGGTTCCCGGGGATCCTCTGGAGATTACCCGTCCATATCCCAACTCCCGACGCGACTCATAACC-
CGACCTAACCCGACCCCGACCCTAACCCCTAACCCCGCGCAAAACACCATAACGCAACGCGCCTCCTCCCTCC-
TCTCCTTTCTCTAATTCGCTCGCTCCCGCCCTCTTCTCTAACCCCTCTCTCCCTCCATAAACCTCCCGCCT-
CCGACCCGCTACCCTCCAACAAATTAACCTATCGCGAAACGTTTATAAAAAACAAAATTCAAATTAACAAAAA-
CCTAAACCGATCGAAAAACCGCCTCCCGCCCCGAAAACCCCGCCGAAAACGTACCATTAACCTACGCGCGAC-
CACGTAATAAAAAACAGGAAAAACCTAACTCCCGACCCAAACCTAACTAAACCCACCCACTCAATCGTCC-
ACTTGCCGTCATGCTTCTTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCC-
AACTAATCGCCTTGCAACACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCC-
CTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCG-
GTATTTACACCCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACAC-
CCGCCAACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCG-
TCTCCGGGAGCTGCATGTGTGAGAGTTTTACCCTCATCACCGAAACGCGCGAGACGAAAGGGCCTCGTG-
ATACGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAGACGTCAGTGGCACTTTTCGGGAAATGTG-
CGCGGAACCCCTATTTGTTATTTTCTAAATACATTCAATATGTATCCGCTCATGAGACAATAACCTGATAAATG-
CTTCAATAATATTGAAAAGGAGAGTATGAGTATTCATTTTCGTGTTCCGCTTATTCCCTTTTTCGCGCATTGCCTT-
CTGTTTTGCTCACC
AGAACGCTGTGAAGTAAGATGCTGAGAATCAGTGGTGCCGAGTGGGATACTCGACTGGATTCAACGCGTAGATCT-
GAAGTTTCCCGGAGAACGGTTCATGTATAGACACCTTTAAAG

4. The sequencing results from the normal breast tissue of the fourth breast cancer patient.

D07_58612.21.S1208222390.SM-P2-4-1.M13(-48)

GAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCATCCATATCCCAACTCCCAACACAACCTCATAACC-
CAACCTAACCCAAACCCCAACCCCTAACCCCTAACCCACACAAAACACCATAACACAACACACCTCCTCCCTCCTC-
TCTTTTCTCTAGTTCACTCACTCCACCCCTTCTCTAACCCCTCTCTCCCTCTATAAACCTCCACCTCCAA-
CCCGCCTACCCTCCAACAAATTAACCTATCACAACAAATTTATAAAAAACAAAATTCAAATTAACAAAAAACCTAA-

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ACCAATCAAAAAACCACCTCCCACCCCAAAAACCCCCACCAAAAACATACCATTAACCTACACACAACCACATAAA-
AATAAAAAACAAAAAACCTAGCTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCGACCTGCAGGC-
ATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCAACCTAATCGCC-
TTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTT-
GCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATTTACACCCGCA-
TATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACACCCGCTG-
ACGCGCCCTGACGGGCTTGTCTGCTCCCGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATG-
TGTCAGAGGTTTTACCGTCATCACCGAAACGCGGAGACGAAAGGGCCTCGTGATACGCCTATTTTTATAGGT-
TAATGTCATGATAATAATGGTTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATT-
TGTTTTATTTTTCTAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTG-
AAAAGGAAGAGTATGAGTATTCACATTTCCGTGTGCGCGTATCCCTTTTTGCGCGCATTGTCTGTGTTGCTCAC-
CAGAACGCTGGTGAAGTAAAGATGCTTGAATCAGTGGTGCACGAGTGGTAATCGACTGGATCCACAGCGTAAG-
ATCCTGGGAGTTCGCTCGAGAACGGTTCCAATAGATGAGACACTTTTTTA

D08_58612.22.S1208222391.SM-P2-4-2.M13(-48)

CAACTCGTCCTCGGTTCCCGGCGATCCTCTGGAGATTACCCGTCCATATCCCAACTCCCAACACAACCTCATAAC-
CCAACCTAACCCAACCCCAACCCTAACCCCTAACCCACACAAAAACCCATAACACAACACACCTCCTCCCTCC-
TCTCCTTTCTCTCTAATCACTCACTCCCACCCCTTCTCCTAACCCCTCTCTCCCTCTATAAACCTCCCACCTCC-
AACCCGCCTACCCTCCAACAAATTAACCTCATCACAAAACATTTATAAAAAACAAAATCAAATTAACAAAAAACCT-
AAACCAATCAAAAAACCACCTCCCACCCCAAAAACCCCCACCAAAAACATACCATTAACCTACACACAACCACATA-
AAAATAAAAAACAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCCACTTGGCG-
TCATGCTTCTTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCAACCTAATCG-
CCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGT-
TGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATTTACACCCG-
ATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACACCCGCT-
GACGCGCCCTGACGGGCTTGTCTGCTCCCGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCAT-
GTGTCAGAGGTTTTACCGTCATCACCGAAACGCGGAGACGAAAGGGCCTCGTGATACGCCTATTTTTATAGG-
TTAATGTCATGATAATAATGGTTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTAT-
TTGTTATTTTTCTAATACATTCAAATATGTATCCGCTCATGAGACATACCCTGATAAATGCTCATAATATGAAAAGAGA-
GTATGAGTATTCACATTTCCGTGTGCGCTATCCCTTTTGGCATTGCTCTGTTTGTCTACCAAACGCTGTGAGGTAA-
GATGCTGAGATCAGTGTGCACGATGGTACTCGGACTGGATTCAAACGGTAGATCCTGGAAGGTTGCCGAGAACGT-
TCAATGTGATGAGACT

D09_58612.23.S1208222392.SM-P2-4-3.M13(-48)

AGAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCCAACACAACCTCATAA-
CCCAACCTAACCCAACCCCAACCCTAACCCCTAACCCACACAAAAACCCATAACACAACACACCTCCTCCCTC-
CTCTCCTTTCTCTCTAATCACTCACTCCCGCCCTTCTCCTAACCCCTCTCTCCCTCTATAAACCTCCCACCTC-
CAACCCACCTACCCTCCAACAAATTAACCTCATCACAAAACATTTATAAAAAACAAAATCAAATTAACAAAAAAC-
TAAACCAATCAAAAAACCACCTCCCACCCCAAAAACCCCCACCAAAAACATACCATTAACCTACACACAACCACAT-
AAAAATAAAAAACAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCGACCTGCA-
GGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCAACCTAAT-
CGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACA-
GTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATTTACACCC-
GCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACACCCG-
CTGACGCGCCCTGACGGGCTTGTCTGCTCCCGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGC-
ATGTGTCAGAGGTTTTACCGTCATCACCGAAACGCGGAGACGAAAGGGCCTCGTGATACGCCTATTTTTATA-
GGTTAATGTCATGATAATAATGGTTTTCTTAGACGTCAGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTA-
TTTTGTTATTTTTCTAATACATTCAAATATGTATCCGCTCATGAGACATACCCTGATAAATGCTTCAATAATATTGA-
AAAAGGAGAGTATGAGTATTCACATTTCCGTGTGCGTAATCCCTTTTTGCGCATTGCTCTGTTTTGCTCCCCAG-
AACGCTGTGAGTAAAGATGCTGAGATCAGTGGTGCACGAGGGGTACATCGGACTGATTCTCACAGCGGTAGATCTT-
GGAGAGTTTTG

D11_58612.25.S1208222394.SM-P2-4-5.M13(-48)

HOXD13 methylation and prognosis of breast cancer

TAATTTACGAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCATCCATATCCCAACTCCCAACACAA-
CTCATAACCCAACCTAACCCAACCCCAACCCTAACCCCTAACCCACACAAAAACACCATAACACAACACACCTC-
CTCCCTCCTCTCCTTTCTCTCTAATTCACCTACTCCCACCCTCTTCCTCTAACCCCTCTCTCCCTCTATAAACCT-
CCCGCCTCCAACCCACCTACCCTCCAACAAATTAACCTCATCACAAAACATTTATAAAAAACAAAATTCAAATTA-
AAAAAACCTAAACCAATCAAAAAACCACCTCCCACCCCAAAAACCCCAACCAAAAACATAACCATTAACACAC-
CACAACCACATAAAAAATAAAAAACAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATC-
GTGCACCTGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTA-
CCCAACTTAATCGCCTTGAGCACATCCCCCTTTCCGACAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGC-
CCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCG-
GTATTTACACCCGCATATGGTGCACCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACC-
CGCAACACCCCGCTGACGCGCCCTGACGGGCTTGCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTC-
TCCGGGAGCTGCATGTGTGAGAGGTTTTACCCTCATCACCAGAAACGCGCGAGACGAAAGGGCCTCGTGATA-
CGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTTCTTAGACGTCAGTGGCACTTTTCCGGGAAATGT-
GCGCGGAACCCCTATTTGTTTTATTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACATACCCTGATAA-
ATGCTTCATAATATTGAAAAGGAGAGTATGAGTATTCACATTTCCGTGTCGCCCTTATCCCTTTTTGCGGCATTTGC-
TTCTGTTTTGCCTCACCCAGAAACCCCTGGGTGAAAGATAAAAAAGTTGCTTGAAGATCAGTG

D12_58612.26.S1208222395.SM-P2-4-6.M13(-48)

AACCTGATTACGATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCATATCCCAACTCCCAACAC-
AACTCATAACCCAACCTAACCCAACCCCGACCCCTAACCCCTAACCCACACAAAAACACCATAACACAACACACC-
TCCTCCCTCCTCTCCTTTCTCTCTAATTCACCTACTCCCACCCTCTTCCTCTAACCCCTCTCTCCCTCTATAAAC-
CTCCACCTCCAACCCACCTACCCTCCAACAAATTAACCTCATCACAAAACATTTATAAAAAACAAAATTCAAATTA-
AAAGAAAACCTAAACCAATCAAAGAACCACCTCCCACCCCAAAAACCCCAACCAAAAACATAACCATTAACACAC-
ACACAACCACATAAAAAATAAAAAACAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAAT-
CGTCGACCTGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTT-
ACCCAACTTAATCGCCTTGAGCACATCCCCCTTTCCGACAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGC-
CCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCG
GTATTTCTCCTTACGCATCTGTGCGGTATTTACACCCGCATATGGTGCACCTCTCAGTACAATCTGCTCTGATGCC-
GCATAGTTAAGCCAGCCCCGACACCCGCAACACCCGCTGACGCGCCCTGACGGGCTTGCTGCTCCCGGCAT-
CCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTGAGAGGTTTTACCCTCATCACCAGAAACG-
CGCGAGACGAAAGGGCCTCGTGATACGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTTCTTAGACGT-
CAGTGGCACTTTTCCGGGAAATGTGCGCGGAACCCCTATTTGTTTTATTTTCTAAATACATTCAAATATGTATCC-
GCTCATGAGACATACCCTGATAAATGCTCATATATGAAAAGGAGAGTATGAGTATTCACATTTCCGTGTCGCCCTTA-
TTCCCTTTTTGCGGCATTTTGG

E02_58612.28.S1208222397.SM-P2-4-8.M13(-48)

TCGAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCATATCCCAACTCCCAACACAACCTCATA-
ACCCAACCTAACCCAACCCCAACCCTAACCCCTAACCCACACAAAAACACCATAACACAACACACCTCCTCCCT-
CCTCTCCTTTCTCTCTAATTCACCTACTCCCACCCTCTTCCTCTAACCCCTCTCTCCCTCTATAAACCTCCCACC-
TCCAACCCGCTACCCTCCAACAAATTAACCTCATCACAAAACATTTATAAAAAACAAAATTCAAATTAACAAAAA-
AACCTAAACCAATCAAAAAACCACCTCCCACCCCAAAAACCCCAACCAAAAACGTACCATTAACACACACAAC-
CACATAAAAAATAAAAAACAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCGAC-
CTGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCAAC-
TTAATCGCCTTGAGCACATCCCCCTTTCCGACAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCC-
AACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTT
CTCCTTACGCATCTGTGCGGTATTTACACCCGCATATGGTGCACCTCTCAGTACAATCTGCTCTGATGCCGCATAGT-
TAAGCCAGCCCCGACACCCGCAACACCCGCTGACGCGCCCTGACGGGCTTGCTGCTCCCGGCATCCGCTTA-
CAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTGAGAGGTTTTACCCTCATCACCAGAAACGCGCGAG-
ACGAAAGGGCCTCGTGATACGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTTCTTAGACGTCAGTGG-
CACTTTTCCGGGAAATGTGCGCGGAACCCCTATTTGTTTTATTTTCTAAATACATTCAAATATGTATCCGCTCATG-
AGACATACCCTGATAAATGCTTCAATAATATGAAAAGGAGAGTATGAGTATCACATTTCCGTGTCGCCCTTATCC-
CTTTTTGCGCATTTGCTCTGTTTTGCTCACCCAGAACGCTGTGAAGTAAAGATGCTGAGATCAGTTGTGCACGAGGT-
GGTACTCGGACTGATCTCAACAGGCGTAAGATTCTTGAGT

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E03_58612.29.S1208222398.SM-P2-4-9.M13(-48)

GAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCATCCATATCCCAACTCCCAACACAACCTCATAAC-
CCAACCTAACCCAACCCCGACCCTAACCCCTAACCCACACAAAACACCATAACACAACACACCTCCTCCCTCC-
TCTCCTTTCTCTCTAATTCGCTCACTCCACCCCTCTTCTCTAACCCCTCTCTCCCTCTATAAACCTCCCACCTC-
CAACCCACCTACCCTCCAACAAATTAACATCACAAAACATTTATAAAAACAAAATTCAAATTAAAAAAACC-
CTAAACCAATCAAAAAACCACCTCCCACCCCAAAAAACCCCAACAAAACATACCATTAACATACACACAACCTAC-
ATAAAAATAAAAAACAAAAAACCTAGCTCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCGACCT-
GCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCAACCT-
AATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCCGATCGCCCTTCCC-
AACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATTTCA-
CACCGCATATGGTGCACCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACA-
CCCCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGA-
GCTGCATGTGTCAGAGGTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCCTCGTGATACGCCTATT-
TTTATAGGTTAATGTCATGATAATAATGGTTTCTTAGACGTCAGTGGCACTTTTCGGGGAAATGTGCGCGGA-
ACCCCTATTTGTTATTTTTCTAATACATTCAATATGTATCCGCTCATGAGACAATACCCTGATAAATGCTTCAT-
ATATTGAAAGGAGAGTATGAGTTTACATTCCGTGTCGCCCTTATCCCTTTTTGCGGCATTTTGCTTCTGTTTT-
TGCTCACCCAGAACGCTGTGAGTAAAGATGCTGAGATCAGTGTGCACGAGGGTACTCGACTGATCCCACACGTAGAT-
CTGGAAGTTCGCCGAAGACGTTCAATGGTAGTGAGACT

E04_58612.30.S1208222399.SM-P2-4-10.M13(-48)

CAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCATATCCCAACTCcCAACACAACCTCATAAC-
CCAACCTAACCCAACCCCAACCCTAACCCCTAACCCACACAAAACACCATAACACAACACACCTCCTCCCTCC-
TCTCCTTTCTCCCTAATTCGCTCACTCCACCCCTCTTCTCTAACCCCTCTCTCCCTCTATAAACCTCCCACCTC-
CAACCCACCTACCCTCCAACAAATTAACATCACAAAACATTTATAAAAACAAAATTCAAATTAAAAAAACC-
CTAAACCAATCAAAAAACCACCTCCCACCCCAAAAAACCCCAACAAAACATACCATTAACATACACACAGCCAC-
ATAAAAATAAAAAACAAAAAACCTAACTCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCGACCT-
GCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCAACCT-
AATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCCGATCGCCCTTCCC-
AACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATTTCA-
CACCGCATATGGTGCACCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACA-
CCCCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGA-
GCTGCATGTGTCAGAGGTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCCTCGTGATACGCCTATT-
TTTATAGGTTAATGTCATGATAATAATGGTTTCTTAGACGTCAGTGGCACTTTTCGGGGAAATGTGCGCGGA-
ACCCCTATTTGTTATTTTTCTAATACATTCAAATATGTATCCGCTCATGAGACATAACCCTGATAAATGCTTCAT-
AATATGAAAGGAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTTATCCCTTTTTGCGGCATTTTGCTCTGTTT-
TGCTCACCCAGAACGCTTGTGAGTAAAGAATGCTGAGATCAGTGGGTGCACGAGTGGATAACATCGACTGGATCCAA-
CCGGTAGATCCTGAGTCGCCGAGAACGTTCAAGTAGTAGACACTTTAG

E05_58612.31.S1208222400.SM-P2-4-11.M13(-48)

CTCGTCTCGGTTCCCGGCATCCTCTGGAGATTGAGTGGGTGGGTTTAGTTAGGTTTGGGTTGGGAGTTAG-
GTTTTTTGTGTTTTATTTTTATGTGGTTGTGTATAGTTAATGGTACGTTTTTGGTGGGGGTTTTTGGGGTG-
GGAGGTGGTTTTTGTATTGGTTAGGTTTTTTTTAATTTGAATTTGTTTTATAAATGTTTTGTGATGAGTTAATTT-
GTTGGAGGGTAGGTGG
GTTGGAGGTGGGAGGTTTATAGAGGGAGAGAGGGTTAGAGGAAGAGGGCGGGAGTGAGTGAATTAGAGAGAAA-
GGAGAGGAGGGAGGAGGTGTGTTGTGTTATGGTGTGTTGTGTTGGGGTTAGGGTTAGGGTTGGGGTTGGGTTA-
GGTTGGGTTATGAGTTGTGTTGGGAGTTGGGATATGGACGGGTAATCGTCCACTTGCCGTCATGCTTCTTTGG-
CACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCAACCTAATCGCCTTGCAGCACAT-
CCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCCGATCGCCCTTCCCAACAGTTGCGCAGCCTG-
AATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATTTACACCCGCATATGGTGCAC-
TCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACACCCGCTGACGCGCCC-
TGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTCAG-
AGGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCCTCGTGATACGCCTATTTTTATAGGTTAATG-

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TCATGATAATAATGGTTTTCTTAGACGTCAGGTGGCACTTTTCGGGAATGGGCGCGGACCCCTATTTTGT-TATTTTTCTAATACATTCAATATGTATCCGCTCATGAGACATACCCTGATAATGCTCCATATATTGAAAAGAGAGTAT-GAGTATTTCAACATTTTCGTGTTTCGCTTATTCTTTTTGGCGCATTTGGCTCTGTTTTGCTCACCGAGGCTTGT-GAGTTAAGATGCTGAGATCAGTGCCTCATGTACTCGACTGATTCCACCGTAGATCTGGAGTTTTGCCCGAAACGT-TCAG

E06_58612.32.S1208222401.SM-P2-4-12.M13(-48)

CTCGTCTCGGTTCCCGGCGATCCTCTGGAGATTACCCGTCCATATCCCAACTCCCAACACAACCTCATAACCC-AACCTGACCCAACCCCAACCCTAACCCCTAACCCACACAAAAACCCATAACACAACACACCTCCTCCCTCCT-CTCCTTTCTCTAATTACTCACTCCCACCCTCTTCTCTAACCCCTCTCTCCCTCTATAAACCTCCCACCTC-CAACCCACCTACCCTCCAACAAATTAACCTCATCACAAAACATTTATAAAAACAAAATTCAAATTAACAAAAAAC-CTAAACCAATCAAAAAACCACCTCCCACCCCAAAAACCCCAACCAAAAACATAACCATTAACCTACACACAACCA-CATAAAAAATAAAAAACAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCCAC-TTGCCGTATGCTTCTTTGGCACTGGCCGTGTTTTACAACGTCTGACTGGGAAAACCCTGGCGTTACCCAA-CTTAATCGCCTTGCAGCACATCCCCCTTTCCGCGAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTT-CCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTAT-TTACACCCGCATATGGTGCACCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGC-CAACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGCATCCGCTTACAGACAAGCTGTGACCGTCTC-CGGGAGCTGCATGTGTGAGAGTTTTACCCGTATCACCAGAACGCGCGAGACGAAAGGGCCCTCGTGATA-CGCCTATTTTATAGGTTAATGTCATGATAATAATGGTTTTCTTAGACGTGAGGTGGCACTTTTCGGGAAATGT-GCGCGGAACCCCTATTGTTATTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACATACCTGATAAATGC-TTCATAATATTGAAAAGAGAGTATGAGTATCACATTTCCGGTGTTCGCCCTTATCCCTTTTGGCGGCATTGCC-TCTGTTTTGCTCACCAGAACGCTGGTAAGTAAAGGATGCTGAGATCAGTTGGTGCCGATGGTACTTCGACTGATTC-CAACGGTAGATCTGAAGTTTCCCGAGACGTTCTAATGATGGACACTTTTAAGTCGC

5. The sequencing results from the normal breast tissue of the fifth breast cancer patient.

E08_58612.34.S1208222403.SM-P2-5-2.M13(-48)

TAATTCGAGCTCGGTACCCGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCCAACACAACCTCATAA-CCCAACCTAACCCAACCCCAACCCTAACCCCTAACCCACACAGAACACCATAACACAACACACCTCCTCCCT-CCTCTCCTTTCTCTAATTACTCACTCCCACCCTCTTCTCTAACCCCTCTCTCCCTCTATAAACCTCCCAC-CTCCAACCCACCTACCCTCCAACAAATTAACCTCATCACAAAACATTTATAAAAACAAAATTCAAATTAACAAAAA-AACCTAAACCAATCAAAAAACCACCTCCCACCCCAAAAACCCCAACCAAAAACATAACCATTAACCTACACACGA-CCACATAAAAAATAAAAAACAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCG-ACCTGCAGGCATGCAAGCTTGGCACTGGCCGTGTTTTACAACGTCTGACTGGGAAAACCCTGGCGTTACCC-AACTTAATCGCCTTGCAGCACATCCCCCTTTCCGCGAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCC-CTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCG-GTATTTACACCCGCATATGGTGCACCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACAC-CCGCCAACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGCATCCGCTTACAGACAAGCTGTGACCG-TCTCCGGGAGCTGCATGTGTGAGAGTTTTACCCGTATCACCAGAACGCGCGAGACGAAAGGGCCTCGTGA-TACGCCTATTTTATAGGTTAATGTCATGATAATAATGGTTTTCTTAGACGTGAGGTGGCACTTTTCGGGAAA-TGTGCGCGGAACCCCTATTGTTATTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACATACCCTGATAAA-TGCTTCATAATATTGAAAAGAGAGTATGAGTATCACATTTTCGTGTCGCCTAATCCCTTTTGGCGATTGCTTCTG-TTTTTGCTCCCCAGAACGCTGTGAAGTTAAAGATGCTGAGATCAGTTGTGCACGAGTGGTACTCGGAGCTGGATC-CCACAGCGTAGATCTGGAGTTCCGCCGAGAAGCGTTTCCATGTATG

E09_58612.35.S1208222404.SM-P2-5-3.M13(-48)

AGAACTCGTCTCGGTTCCCGGCGATCCTCTGGAGATTACCCGTCCATATCCCAACTCCCAACACAACCTCATA-AACCAACCTAACCCAACCCCAACCCTAACCCCTAACCCACACAGAACACCATAACACAACACACCTCCTCCC-TCCTCTCCTTTCTCTAATTACTCACTCCCACCCTCCTCCTCTAACCCCTCTCTCCCTCTATAAACCTCCCA-CCTCCAACCCACCTACCCTCCAACAAATTAACCTCATCACAAAACATTTATAAAAACAAAATTCAAATTAACAAAA-AAACCTAAACCAATCAAAAAACCACCTCCCACCCCAAAAACCCCAACCAAAAACATAACCATTAACCTACACACG-ACCACATAAAAAATAAAAAACAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTC-

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CACTTGCCGTCATGCTTCTTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACC-
CAACTTAATCGCCTTGACGACATCCCCCTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCC-
CTTCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGG-
TATTTACACCCGCATATGGTGCACCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACC-
CGCCAACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGT-
CTCCGGGAGCTGCATGTGTGAGAGGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCTCGTGAT-
ACGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAAT-
GTGCGCGGAACCCTATTTGTTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACATACTGATAA-
ATGCTTCAATAATATTGAAAGGAGAGTATGGAGTATTCACATTTTCGTGTGCGCTATCCTTTTTGCGCATTGCT-
TCTGTTTTGCCCACCCAGAACGCTGTGAGTAAAGATGCTGAGATCAGTTGTGCACGAGTGGTACATCGACTGATC-
TCACGGCGTAGAATCCTTGAGAGTTTG

E10_58612.36.S1208222405.SM-P2-5-4.M13(-48)

AACTTCGTCCTCGGTTCCCGGGGATCCTCTGGAGATTACCCGTCCATATCCCAACTCCCAACACAACCTCATAA-
CCCAACCTAACCCAACCCCAACCCTAACCCTAACCCTAACCCACACAAAAACACCATAACACAACACACCTCCTCCCT-
CCTCTCCTTTCTCTCTAATTCGCTCACTCCCACCCTCTTCTCTAACCCTCTCTCCCTCTATAAACCTCCCAC-
CTCCAACCCACCTACCCTCCAACAAATTAACTCATCACAAAACATTTATAAAAAACAAAATTCAAATTAACAAAA-
AACCTAAACCAATCAAAAAACCACCTCCCACCCCAAAAACCCCCACCAAAAACATACCATTAACACACACAA-
CCACATAAAAAATAAAAAACAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCC-
ACTTGCCGTCATGCTTCTTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCC-
AACTTAATCGCCTTGACGACATCCCCCTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCC-
CTTCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCG-
GTATTTACACCCGCATATGGTGCACCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACAC-
CCGCCAACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCG-
TCTCCGGGAGCTGCATGTGTGAGAGGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCTCGTG-
ATACGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAA-
ATGTGCGCGGAACCCTATTTGTTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACATAACC-
CTGATAATGCTTCAATATATTGAAAAGGAGAGTATGAGTATTCACATTTCCGTGTGCGCTATCCCTTTTTGCGG-
CATTGCTTCTGTTTTGCTCCCAGACGCTGTGAAAGTAAAGATGCTGAGATCAGTGGGGTGCACGAGTGGTTACA-
TCGACCTGATC

E11_58612.37.S1208222406.SM-P2-5-5.M13(-48)

TTACGAaTTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCATCCATATCCCAACTCCCAACACAACCTC-
ATAACCCAACCTAACCCAACCCCGACCCTAACCCTAACCCTAACCCACACAAAAACACCATAACACAACACACCTCCT-
CCCTCCTCTCCTTTCTCTCTAATTCACCTCACTCCCACCCTCTTCTCTAACCCTCTCTCCCTCTATAAACCTCC-
CACCTCCGACCCACCTACCCTCCAACAAATTAACTCATCACAAAACATTTATAAAAAACAAAATTCAAATTAACAA-
AAAGACCTAAACCAATCAAAAAACCACCTCCCACCCCAAAAACCCCCACCGAAAACATACCATTAACACGCG-
CGACCAGTAAATAAAAAACAAAAAACCTAACTCCCGACCCAAACCTAACTAAACCCACCCACTCAATC-
GTGACCTGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGT-
TACCAACTTAATCGCCTTGACGACATCCCCCTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGAT-
CGCCCTTCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTG-
TGCGGTATTTACACCCGCATATGGTGCACCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCG-
ACACCCGCCAACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTG-
ACCGTCTCCGGGAGCTGCATGTGTGAGAGGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCC-
TCGTGATACGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTTCTTAGACGTCAGGTGGCACTTTTCGG-
GGAAATGTGCGCGGAACCCTATTTGTTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACATAAC-
CCTGATAAATGCTTCAATAATATGAAAAGGAGAGTATGAGTATCACATTTCCGTGTGCGCTTATTCCCTTTGCGCAT-
TTGCTCCTGTTTTGCTCACCCAGAAACGCTGGGTGAAGTAAAGATTCTTGA

E12_58612.38.S1208222407.SM-P2-5-6.M13(-48)

CGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCCAACACAACCTCATAACCCAACCTAAC-
CCAACCCCAACCTAACCCTAACCCTAACCCACACAGAACACCATAACACAACACACCTCCTCCCTCCTCTCCTTTCT-
TCTCTAATTCACCTCACTCCCACCCTCTTCTCTAACCCTCTCTCCCTCTATAAACCTCCCACCTCCAACCCA-

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CCTACCCTCCAACAAATTAACCTCATCACAAAACATTTATAAAAACAAAATTCAAATTAACAAAAAACCTAAAC-
CAATCAAAAAACCACCTCCCACCCCAAAAACCCACCAAAAACATACCATTAACCTACACACGACCACATAAA-
AATAAAAAACAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCGACCTGCAG-
GCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCAACCTAAT-
CGCCTTGCAACATCCCCCTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAA-
CAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATTTAC-
ACCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAAC-
CCCCTGACGCGCCCTGACGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGG-
AGCTGCATGTGTCAGAGGTTTTACCCTCATCACCGAAACGCGCGAGACGAAAGGGCCCTCGTGATACGCC-
TATTTTATAGGTTAATGTCATGATAAATGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGC-
GCGGAACCCCTATTTGTTTTTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATACCCTGATAAATGCTC-
ATATATGAAAAGAGAGATGAGTATTCAACATTTCCGTGTCGCCTATTCTTTTTGCGCATTGCGCTTCCCTG

F01_58612.39.S1208222408.SM-P2-5-7.M13(-48)

TAATTACGAACTCGTCCTCGGTTCCCGGCATCCTCTGGAGATTGAGTGGGTGGGTTTAGTTAGGTTTGGGT-
TGGGAGTTAGGTTTTTTGTGTTTTATTTTACGTGGTCGCGCTAGTTAATGGTATGTTTTTGGTGGGG-
TTTTTGGGTGGGAGGTGGTTTTTATTGGTTAGGTTTTTTAATTTGAATTTGTTTTATAAATGTTTTGTA-
TGAGTTAATTTGTTGGAG
GGTAGCGGGTCGGAGGTGGGAGGTTTATAGAGGGAGAGGGTTAGAGGAAGAGGGTGGGAGTGAGTGAAT-
CAGAGAGAGAGGAGAGGAGGGAGGAGGTGTGTTGTGTTATGGTGTGTTTGTGTTGGGTTAGGTTAGGTTGG-
GTTGGGTTAGGTTGGGTTATGAGTTGTGTTGGGAGTTGGGATATGGACGGGTAATCGTCCACTTGCCGTCAT-
GCTTCTTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCAACCTAATCGCC-
TTGCAGCACATCCCCCTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGT-
TGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTATTTACACCG-
CATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACACCC-
GCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGC-
TGCATGTGTCAGAGGTTTTACCCTCATCACCGAACGCGCGAGACGAAAGGGCCCTCGTGATACGCCTATTTT-
TATAGTTAATGTCATGATAAATGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGA-
ACCCCTTTTTTGTGTTTTTTTTCTAAATACATTCAAATATGTATCCGCTCATGAAACATACCTGATAAATGCTTCATATG-
AAAAGGAGAGATGAGTATTCAACAATTCGTGTCGCCTATCGTTTTGCGCATTGCTCTGTTGCTCACCAGAACG-
CTGGTGAAGTAACA

F02_58612.40.S1208222409.SM-P2-5-8.M13(-48)

AATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAAcTccCAACAAAACCTCATAACCC-
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TCCTTTCTCTCTAATTCGCTCGCTCCACCCTCTTCTCTAACCCCTCTCCTCCTATAAACCTCCCACCTCCA-
ACCCACCTACCCTCCAACAAATTAACCTCATCACAAAACATTTATAAAAACAAAATTCAAATTAACAAAAAACCTAA-
ACCAATCAAAAAACCACCCCCACCCCAAAAACCCCAACAAAAACATACCATTAACCTACACACAACCACATAA-
AAATAAAAAACAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCGACCTGCAGG-
CATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCAACCTAATCG-
CCTTGCAACATCCCCCTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGT-
TGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTATTTACACCCG-
ATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACACCCGCT-
GACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCAT-
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TTGTTTTATTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACATACCCTGATAAATGCTTCATAAATTT-
GAAAAGAGAGATGAGTATTCAACATTTTCGTGTTCCGCCCTATTCCCTTTTTGCGCATTGCTCTGTTTTGCTC-
CACCCAGAACGCTGGTGAAGTAAGATGCTGAGATCAGTGGGTGCACGGAGTGATAACTCGACTGGATCTCACA-
GCGTAGAATC

F03_58612.41.S1208222410.SM-P2-5-9.M13(-48)

AATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAAcTccCAACAAAACCTCATAACCC-
AACCTAACCAACCCCAACCCTAACCCCTAACCCCAACAAAACACCATAACACAACACACCTCCTCCCTCCTCT-

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CCTTTCTCTAATTCACCTACTCCCACCCTCTTCTCTAACCCTCTCTCCCTCTATAAACCTCCCGCCTCCGA-
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ACCAATCAAAAAACCACCTCCCACCCCAAAAACCCCCACCGAAAACATACCATTAACCTACGCGCGACCACGTAA-
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GTATGAGTATTCACATTTTCGTGTCGCCCTATCCCTTTTTGCGCATTTGCTTCTGTTTTGCTCACCAGAACGCTGGT
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GCCCGAGAC

F04_58612.42.S1208222411.SM-P2-5-10.M13(-48)

AACTCCGTCCTCGGTTCCCGGCGATCCTCTGGAGATTACCCGTCCATATCCCAACTCCCAACACAACCTCATAAC-
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TCTCCTTTCTCTAATTCGCTCGCTCCCACCCTCTTCTCTAACCCTCTCTCCCTCTATAAACCTCCCACCTCC-
GACCCACCTACCCTCCAACAAATTAACCTCATCACAAAACATTTATAAAAACAAAATTCAAATTAAGACCTAA-
AACCAATCAAAAAACCACCTCCCACCCCAAAAACCCCCACCGAAAACATACCATTAACCTACGCGCGACCACGT-
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CGTCATGCTTCTTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCAACCTAAT-
CGCCTTGACGACATCCCCCTTTCCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAAC-
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CGCATATGGTGCACCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACACCC-
GCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCT-
GCATGTGTCAGAGGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCTCGTGATACGCCTATTTTTA-
TAGGTTAATGTCATGATAATAATGGTTTTCTTAGACGTCAGGTGGCACTTTTCGGGAAATGTGCCGCGGAAC-
CCCTATTTGTTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACATACCCTGATAATGCTTCATA-
TATTGAAAAAGAGAGTATGAGTATTCACATTTCCGTGTCGCCCTTATCCCTTTTTGCGCATTTTGCTCTGTTTG-
CCTCACCCAGAAACGCCTGTGAAAGTTAAGAATGCTGAAGATCAGTGGTGCACGAGTGGTTACTCGAACTGGAT-
CCCAACGCGTTAGATCTGGAGAGTTCGCCCCGAAGAACGTTCCAAGGATGAGAACA

F05_58612.43.S1208222412.SM-P2-5-11.M13(-48)

CGAATTCGAGCTCGGTACCCGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCCAACACAACCTCATAACC-
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CCTTTCTCTAATTCACCTACTCCCACCCTCTTCTCTAACCCTCTCTCCCTCTATAAACCTCCCACCTCCGACC-
CACCTACCCTCCAACAAATTAACCTCATCACAAAACATTTATAAAAACAAAATTCAAATTAAGACCTAAACCA-
ATCAAAAAACCACCTCCCACCCCAAAAACCCCCACCAAAAACATACCATTAACCTACACACAACCACATAAAAATAA-
AAACACAAAAAACCTAACTCCCAACCCAAACCTAATAAACCACCCACTCAATCGTCGACCTGCAGGCATGCA-
AGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCAACCTAATCGCCTTGCA-
GCACATCCCCCTTTCCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCA-
GCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATTTACACCCGCATATGGT-
GCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACACCCCGCTGACGCGC-
CCTGACGGGCTTGTCTGCTCCCGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTCAG-
AGGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCTCGTGATACGCCTATTTTTATAGGTTAATG-
TCATGATAATAATGGTTTTCTTAGACGTCAGGTGGCACTTTTCGGGAAATGTGCGCGGAACCCCTATTTGTTT-
ATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATACCCTGATAAATGCTTCAATAATATTGAAAAAG-
GAAGAGTATGAGTATTCACATTTCCGGTGTGCCCTTATCCCTTTTTGGCGGCATTTGCTCTGTTTTGCTCACC-
AGACGCTGGGTGAGTAAAGATGCTGAGATCAGTGGTGCACGAGTGTACTCGACTGATTTACAGCGGTTAAG-
AATCTGAAGAGTTCGCCCGGAGAGAGCGTTTTCCAATGGGTGAGTGGG

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6. The sequencing results from the normal breast tissue of the sixth breast cancer patient.

F07_58612.45.S1208222414.SM-P2-6-1.M13(-48)

TGAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCATCCATATCCCAACTCCCAACACAACCTCATAAC-
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TCTCCTTTCTCTCTAATCACTCACTCCCACCCTCTTCTCTAACCCCTCTCTCCCTCTATAAACCTCCCACCTCC-
AACCCACCTACCCTCCAACAAATTAACCTCATCACAAAACATTTATAAAAACAAAATTCAAATTAACCAACCT-
AAACCAATCAAAAAACACCTCCCACCCCAAAAACCCCAACCAAAAACATACCATTAACCTACACACAACCACATA-
AAAATAAAAACACAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCGACCTGCAG-
GCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCAACCTAATCG-
CCTTGCAGCACATCCCCCTTTCCGACGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGT-
TGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATTTACACCCGCA-
TATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACACCCGCTG-
ACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATG-
TGTCAGAGTTTTACCGTCATACCGAAACGCGGAGACGAAAGGGCCTCGTGATACGCCTATTTTATAGGT-
TAATGTCATGATAATAATGTTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATT-
TGTTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATACCCTGATAAATGCTCAAAATATTGA-
AAAGGAAGAGTATGAGTATTCACATTCGTGTGCTATCCCTTTTGCGCATTTGCTCTGTTTGTCTACCAGAAAC-
GCTGTGAGTAAGATGCTGAGATCAGTTGTGCCGAGTGTTACTCCGAACCTGAATCCACAGCGTTAGATCTTGAG-
AGTTCCGCCGGAGAGAAGCGTTCCCA

F08_58612.46.S1208222415.SM-P2-6-2.M13(-48)

GAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCATCCATATCCCAACTCCCAACACAACCTCATAACC-
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TCCTTTCTCTCTAATTCGCTCGCTCCCGCCCTCTTCTCTAACCCCTCTCTCCCTCTATAAACCTCCCGCCTCCG-
ACCCACCTACCCTCCAACAAATTAACCTCATCGCAAAACATTTATAAAAACAAAATTCAAATTAACCAACCTA-
AACCAATCAAAAAACACCTCCCACCCCAAAAACCCCAACCAAAAACATACCATTAACCTACACACAACCACATAA-
AAATAAAAACACAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCGACCTGCAGG-
CATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCAACCTAATCGC-
CTTGCAGCACATCCCCCTTTCCGACGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTT-
GCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATTTACACCCGCAT-
ATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACACCCGCTGA-
CGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGT-
GTCAGAGTTTTTACCGTCATACCGAAACGCGGAGACGAAAGGGCCTCGTGATACGCCTATTTTATAGGTT-
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GTTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATGA-
AAAGGAGAGTATGAGTATTCACATTCGTGTGCTATCCCTTTTGCGCATTTGCTCTGTTTTGCTACCAGAAC-
GCTGTGAAGTAAAGATGCTGAGATCAGTTGGGGCAGAGTGTACTCGACTGGATCCACAGCGTTAAGAATCTGGA-
AGTTCCGCCGAAGACGTTTTCCA

F09_58612.47.S1208222416.SM-P2-6-3.M13(-48)

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CTCTCCTTTCTCTCTAATTCGCTCGCTCCCGCCCTCTTCTCTAACCCCTCTCTCCCTCTATAAACCTCCCGCCTC-
CGACCCACCTACCCTCCAACAAATTAACCTCATCGCAAAACATTTATAAAAACGAAATTCAAATTAACCAACCT-
AAACCGATCAAAAAACACCTCCCACCCCAAAAACCCCGCGCAAAACGTAACCTAACCTACGCGCGACCCACAT-
AAAAATAAAAACACGAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCCACTTGC-
CGTCATGCTCTTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCAACCTAAT-
CGCCTTGCAGCACATCCCCCTTTCCGACGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACA-
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GCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACACCCG-
CTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGC-

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ATGTGTCAGAGGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCTCGTGATACGCCTATTTTTATA-
GGTTAATGTCATGATAATAATGGTTTCTTAGACGTGAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCT-
ATTTGTTTATTTTTCTAAATACATTCAATATGTATCCGCTCATGAGACATACCCTGATAATGCTTCATAATATGAA-
AAGAGAGTATGAGTATCACATTTTCGTGTCGGCGTATCCCTTTTTCGCGCATTTGCTCCTGTTTTGGCTCACCAGAACG-
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F10_58612.48.S1208222417.SM-P2-6-4.M13(-48)

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CCTCCTCTCCTTTCTCTCTAATTCGCTCGCTCCCGCCCTCTTCTCTAACCCCTCTCTCCCTCTATAAACCTCCC-
GCCTCCGACCCACCTACCCTCCAACAAATTAATCATCGCAAAACATTTATAAAAAACGAAATTCAAATTAAAAAA-
AAACCTAAACCGATCAAAAAACACCTCCCGCCCCGAAAACCCCGCGGAAAACGTACCATTAACCTACGCGCG-
ACCACATAAAAAATAAAAAACACGAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCG-
ACCTGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTGCTGACTGGGAAAACCCCTGGCGTTACCCA-
ACTTAATCGCCTTGCAGCACATCCCCCTTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTC-
CCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATT
TTCTCCTTACGCATCTGTGCGGTATTTACACCCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATA-
GTTAAGCCAGCCCCGACACCCGCCAACACCCGCTGACGCGCCCTGACGGGCTTGCTGCTCCCGGCATCCGCT-
TACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTGAGAGGTTTTACCCGTATCACCGAAACGCGCGA-
GACGAAAGGGCCTCGTGATACGCCTATTTTTATAGGTTAATGTATGATAATAATGGTTTCTAGACGTGAGTGG-
CACTTTTCGGGGAAATGTGCGCGGAACCCATTTGTTTATTTCTAAATACATTCAAATATGTATCCGCTCATG-
AGACATACCCTGATAAATGCTCAATATATGAAAAGAGAGTATGAGTATTCACATTTTCGTGTCGCTTATCCTTTTTG-
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GATATACGC

F11_58612.49.S1208222418.SM-P2-6-5.M13(-48)

ATTACGAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCCGACGCGACTC-
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CCTCCTCTCCTTTCTCTCTAATTCGCTCGCTCCCGCCCTCTTCTCTAACCCCTCTCTCCCTCTATAAACCTCCC-
GCCTCCGACCCACCTACCCTCCAACAAATTAATCATCACAAAACATTTATAAAAAACAAATTCAAATTAAAAAA-
AAACCTAAACCAATCAAAAAACACCTCCCACCCCAAAAACCCCAACCAAAAACATAACCATTAACCTACACGCAA-
CCACATAAAAAATAAAAAACAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCGA-
CCTGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTGCTGACTGGGAAAACCCCTGGCGTTACCCAA-
CTTAATCGCCTTGCAGCACATCCCCCTTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTT-
CCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATT-
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GAGCTGCATGTGTCAGAGGTTTTACCCGTATCACCGAAACGCGCGAGACGAAAGGGCCTCGTGATACGCCTA-
TTTTTATAGGTTAATGTATGATAATAATGGTTTCTTAGACGTGAGTGGCACTTTTCGGGGAAATGTGCGCGG-
AACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACATACCCTGATAAATGCTTC-
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CCAGAAACCCTGGTGAAGTAAAGATGCTGGAGATCAGTTTGGGTG

G01_58612.51.S1208222420.SM-P2-6-7.M13(-48)

TCGGAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAAcTccGACGCGACTCATA-
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CCTCTCCTTTCTCTCTAATTCGCTCGCTCCCGCCCTCTTCTCTAACCCCTCTCTCCCTCTATAAACCTCCCGCCT-
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TAAACCGATCAAAAAACACCTCCCGCCCCGAAAACCCCGCGGAAAACGTACCATTAACCTACGCGCGACCACA-
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AGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTGCTGACTGGGAAAACCCCTGGCGTTACCCAACTTAAT-
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GTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTATTTACACCCG
GCATATGGTGCACCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACACCCGC
TGACGCGCCCTGACGGGCTTGCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCA
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TGCTCCACCCAGAAACGCCTGGGTGAAAGTAAAAGATTGCTTGGGA

G02_58612.52.S1208222421.SM-P2-6-8.M13(-48)

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CTCCAACCCACCTACCCTCCAACAAATTAACCTCATCACAAAACATTTATAAAAAACAAAATTCAAATTA
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CACCGCATATGGTGCACCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAAC
CCGCTGACGCGCCCTGACGGGCTTGCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAG
CTGCATGTGTCAGAGGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCTCGTGATACGCCTATTTT
TATAGGTTAATGTCATGATAATAATGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAAC
CCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAA
AATATTGAAAAGGAGAGTATGAGTATTCAACATTTCCGTGTGCGCCTATCCCTTTTTGCGGCATTGCTCCTGTTTTG
CTCACCGAACGCTGTGAAGTAAAGATGCTGAAGATCAGTGGGTGCCACGAGTGTTACATCGG

G03_58612.53.S1208222422.SM-P2-6-9.M13(-48)

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CCCGACCTAACCCGACCCCGACCCTAACCCCTAACCCCGCGCAAAACACCATAACGCGACACACCTCCTCCCTC
CTCTCCTTTCTCTAATTCGCTCGCTCCCGCCCTTCTCCTAACCCCTCTCTCCCTCTATAAACCTCCCACCT
CCAACCCACCTACCCTCCAACAAATTAACCTCATCGCAAAACATTTATAAAAAACGAAATTCAAATTA
AAAAAAAACCTAAACCAATCAAAAAACACCTCCCACCCCAAAAAACCCCAACCAAAAAACATACCATTA
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CCGTCATGCTTCTTTGGCACTGGCCGTGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCA
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GCATATGGTGCACCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACACCCGC
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TGTGTCAGAGGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCTCGTGATACGCCTATTTTTATAG
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TTTGTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACATAACCCTGATAAATGCTTCAATAATAT
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CCCAGAAACGCTGTGAAAGTAAAGATGCTGAGATCAGTGTGCACGAGTGGATACTTCGACTGATCCTCAACAGCGT
TAAGAATCTTG

G05_58612.55.S1208222424.SM-P2-6-11.M13(-48)

AGAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCCAACACAACCTCATAAC
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CTCCTTTCTCTCTAATTCACCTACTCCCACCCCTTCTCCTAACCCCTCTCTCCCTCTATAAACCTCCCACCTCCA
ACCCACCTACCCTCCAACAAATTAACCTCATCACAAAACATTTATAAAACCAAAATCAAATTA
AAAAAAAACCTAAACCAATCAAAAAACACCTCCCACCCCAAAAAACCCCAACCAAAAAACATGCCATTA
ACTACACACAACCAACATAA

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CCAACCCACCTACCCTCCAACAAATTA ACTCATCACAAAACATTTATAAAAACAAAATTCAAATTA AAAAAAAAAA
ACCTAAACCAATCAAAAAACCACTCCCACCCCAAAAACCCCAACAAAACATAACCATTAAC TACACGCGAC
CACATAAAAATAAAAACACAAAAAACCTAACTCCCGACCCAAACCTAACTAAACCCACCCACTCAATCGT CGA
CCTGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCA
ACTTAATCGCCTTG CAGCACATCCCCCTTTCCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTC
CCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTC
TCCTTACGCATCTGTGCGGTATTTACACCCGCATATGGTGC ACTCTCAGTACAATCTGCTCTGATGCCGCATAGTT
AAGCCAGCCCCGACACCCGCCAACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTAC
AGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAGTTTTACCCGTCATCACCGAAAACGCGCGAGA
CGAAAGGGCCTCGTGATACGCCTATTTTATAGGTTAATGT CATGATAATAATGGTTTTCTTAGACGTCAGGTGG
CACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTTTTTTCTAAATACATTCAAATATGTATCCGCTCA
TGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAGAGAGTATGAGTATTCACATTTTCGTGTCCCCTTAT
TCCCTTTTTGCGCATTTGCTCTGTTTTGCTCACCAGAATGCTGTGAAGTAAAGATGCTGAGATCAGTGTGCACGA
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G10_58612.60.S1208222429.SM-P2-7-4.M13(-48)

ATACGAACTCGTCTCGGTTCCCGGCGATCCTCTGGAGATTACCCGTCCATATCCCAACTCCCAACACA ACTCA
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CTCCTCTCCTTTCTCTCTAATTCACTCACTCCCACCCTCTTCCTCTAACCCCTCTCTCCCTCTATAAACCTCCG
CCTCCAACCCACCTACCCTCCAACAAATTA ACTCATCACAAAACATTTATAAAAACAAAATTCAAATTA AAAAAA
AACCTAAACCGATCGAAAAACCGCCTCCCACCCCAAAAACCCCAACAAAACGTAACCTAACTACGCGCGA
CCACGTAAAAATAAAAACGCGAAAAAACCTAACTCCCGACCCAAACCTAACTAAACCCACCCACTCAATCGTCC
ACTTGCCGTCATGCTTCTTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCA
ACTTAATCGCCTTG CAGCACATCCCCCTTTCCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCT
TCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTAT
TTCACACCCGCATATGGTGC ACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCC
AACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCC
GGGAGCTGCATGTGTCAGAGGTTTTACCCGTCATCACCGAAAACGCGCGAGACGAAAGGGCCTCGTGATACGC
CTATTTTATAGGTTAATGTCATGATAATAATGGTTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGC
GCGGAACCCCTATTTGTTTTATTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATACCCTGATAAA
TGCTTCAATAATATTGAAAAAGGAGAGTATGAGTATTCAACATTTCCGTGTGCGCCCTATCCCTTTTTGCGCATTTGC
TCTGTTTTTTGCCACCCAGAAACGCTGTGAAAGTAAAAAATGCTGAAGGATCAAGTTGGGTTGCACAGAGTTGG

G11_58612.61.S1208222430.SM-P2-7-5.M13(-48)

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CCTCCTCTCCTTTCTCTCTAATTCACTCACTCCCACCCTCTTCCTCTAACCCCTCTCTCCCTCTATAAACCTCCCA
CCTCCAACCCACCTACCCTCCAACAAATTA ACTCATCACAAAACATTTATAAAAACAAAATTCAAATTA AAAAAA
ACCTAAACCGATCGAAAAACCGCCTCCCACCCCAAAAACCCCAACAAAACGTAACCTAACTACGCGCGACC
ACGTAAAAATAAAAACGCGAAAAAACCTAACTCCCGACCCAAACCTAACTAAACCCACCCACTCAATCGTCCGACC
TGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCA ACTT
AATCGCCTTG CAGCACATCCCCCTTTCCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCA
ACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATTTAC
ACCGCATATGGTGC ACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACAC
CCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAG
CTGCATGTGTCAGAGGTTTTACCCGTCATCACCGAAAACGCGCGAGACGAAAGGGCCTCGTGATACGCCTATTTT
TATAGGTTAATGTCATGATAATAATGGTTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAAC
CCCTATTTGTTTTATTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACATAACCCTGATAATGCTTCATAA
TATTGAAAAGGAAGAGTATGAGTATTACATTTTCGTGTGCGCCTTATTCCCTTTTTGCGCATTTGCTTCTGTTTTGCTC
ACCAGAACGCTGGGTGAAAGTAAAAGAATGC

G12_58612.62.S1208222431.SM-P2-7-6.M13(-48)

AGGAAAATTTTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCCGACGCGACT
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CCCTCCTCCTTTCTCTCTAATTGCTCGCTCCACCCCTTCTCCTAACCCTCTCTCCCTCTATAAACCTCCC-
GCCTCCGACCCGCCTACCCTCCAACAAATTAACCTCATCGCGAAACGTTTATAAAAAACAAAATTCAAATTAAAAA-
AAACCTAAACCAATCAAAAAACCGCTCCACCCCAAAAACCCCGCCGAAGACGTACCATTAACCTACGCGCGA-
CCACGTAAAAATAAAAAACGCGAAAAAACCTAACCCTCCGACCCAAACCTAACTAAACCCACCCACTCAATCGTCGA-
CCTGCAGGCATGCAAGCTTGGCACTGGCCGTGTTTTACAACGTGCTGACTGGGAAAACCCCTGGCGTTACCCAA-
CTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTC-
CCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTATTT-
CACACCGCATATGGTGCACCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAA-
CACCCGCTGACGCGCCCTGACGGGCTTGCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGG-
AGCTGCATGTGTCAGAGGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCCTCGTGATACGCCTA-
TTTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAGACGTGAGGTGGCACTTTTCGGGGAAATGTGCGCG-
GAACCCCTATTTGTTTATTTTCTAAATACATTCAATATGTATCCGCTCATGAGACAATAACCTGATAAATGTCATAAT-
ATGAAAAGGAGAGTATGAGTACACATTCGTGTCGCCTTATCCCTTTTTGGGGCATTGCT

H02_58612.64.S1208222433.SM-P2-7-8.M13(-48)

TTGATTTACGAAACTCGTCTCGGTTCCCGGCGATCCTCTGGAGATTACCCGTCCATATCCCAACTCCCAACAC-
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CCTCCCTCCTCTCCTTTCTCTCTAATTAACCTACTACTCCACCCCTTCTCCTAACCCTCTCTCCCTCTATAAACCT-
CCCACCTCCAACCCACCTACCCTCCAACAAATTAACCTATCACAAAACATTTATAAAAAACAAAATTCAAATTA-
AAAAAACCTAAACCAATCAAAAAACACCTCCACCCCAAAAACCCCGACCAAAAACATACCATTAACCTACACA-
CAACCACATAAAAAATAAAACACAAAAAACCTAACCCTAACCCAAACCTAACTAAACCCACCCACTCAATCGT-
CCACTTGCCGTCATGCTTCTTTGGCACTGGCCGTGTTTTACAACGTGCTGACTGGGAAAACCCCTGGCGTTACC-
CAACTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCC-
TTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTA-
TTTACACCCGCATATGGTGCACCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGC-
CAACACCCGCTGACGCGCCCTGACGGGCTTGCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCC-
GGGAGCTGCATGTGTCAGAGGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCCTCGTGATACGC-
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CGGAACCCCTATTTGTTTATTTTCTAAATACATTCAATATGTATCCGCTCATGAGACAATAACCCTGATAAATG-
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TGTTTTGCTCACCCAGAAACGCTGGTGAAAGTAAAAGAATTGCCTGAGATC

H03_58612.65.S1208222434.SM-P2-7-9.M13(-48)

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CCTCCTCTCCTTTCTCTCTAATTAACCTACTACTCCACCCCTTCTCCTAACCCTCTCTCCCTCTATAAACCTCCC-
ACCTCCAACCCACCTACCTTCCAACAAATTAACCTATCACAAAACATTTATAAAAAACAAAATTCAAATTA-
AAAAAACCTAAACCGATCGAAAAACACCTCCACCCCAAAAACCCCGACCAAAAACGTACCATTAACCTACGCGCG-
ACCACATAAAAAATAAAACACGAAAAAACCTAACCCTAACCCAAACCTAACTAAACCCACCCACTCAATCGTC-
GACCTGCAGGCATGCAAGCTTGGCACTGGCCGTGTTTTACAACGTGCTGACTGGGAAAACCCCTGGCGTTACC-
CAACTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCC-
CTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGG-
TATTTACACCCGCATATGGTGCACCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCC-
GCCAACACCCGCTGACGCGCCCTGACGGGCTTGCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTC-
TCCGGGAGCTGCATGTGTCAGAGGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCCTCGTGATA-
CGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAGACGTGAGGTGGCACTTTTCGGGGAAATG-
TGCGCGGAACCCCTATTTGTTTATTTTCTAAATACATTCAATATGTATCCGCTCATGAGACAATAACCCTGAT-
AAATGCTTCAATAATGAAAAGGAGAGTATGAGTATTACATTTTCGTGTCGCCTATCCCTTTTTGCGCATTGCTC-
TGTTTTGCTCACCCAGAAACGCTGGGTGAAGTAAAAGGCTGGAAGATCAGTTTGGGGTGCACGAGGTGGCTC

H04_58612.66.S1208222435.SM-P2-7-10.M13(-48)

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CCCTCCTCTCCTTTCTCTCTAATTAACCTACTACTCCACCCCTTCTCCTAACCCTCTCTCCCTCTATAAACCTCC-
CACCTCCGACCCACCTACCCTCCAACAAATTAACCTATCACAAAACATTTATAAAAAACAAAATTCAAATCA-
AAAAAACCTAAACCGATCGAAAAACACCTCCACCCCAAAAACCCCGACCAAAAACGTACCATTAACCTACGCGCG-

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AAAAACCTAAACCAATCAAAAAACACCTCCCACCCCAAAAACCCCGCCAAAAACATAACCATTAECTACGCA-
CAACCACATAAAAAATAAAAACACAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCG-
TCGACCTGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTA-
CCCAACTTAATCGCCTTGCGCAGCATCCCCCTTTCCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCC-
CTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATT
TTCTCCTTACGCATCTGTGCGGTATTTACACCCGCATATGGTGCACCTCTCAGTACAATCTGCTCTGATGCCGCAT-
AGTTAAGCCAGCCCCGACACCCGCCAACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCG-
CTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAGGTTTTACCGTCATCACCGAAACGCG-
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AGTGGCACTTTTCGGGAAATGTGCGCGGAACCCCTATTTGTTTTATTTTCTAAATACATTCAAATATGTATC-
CGCTCATGAGACAATAACCCCTGATAAATGCTTCAATAATATTGAAAAAGGAGAGTATGAGTATCACATTTCCGT-
GTCGCCTTATCCCTTTTGGCATTGCTCTGTTTTGCTCACCAGAACGCTTGTGAAGTAAAGATGCTGAGAATCA-
GTGGGGTGCACGAGGGGTAATCGACTGATTCTAA

H05_58612.67.S1208222436.SM-P2-7-11.M13(-48)

CTTACGAATTCGAGCTCGGTACCCGGGATCCTCTAGAGATTGAGTGGGTGGGTTTAGTTAGGTTTGGGTCCG-
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TGGGGTGGGAGGCGTTTTTTGATTGGTTTAGGTTTTTTTTAATTTGAATTTGTTTTATAAACGTTTCGCGA-
TGAGTTAATTTGTTGGAGGGTAGCCGGTCCGAGGCGGGAGGTTTATAGAGGGAGAGAGGGTTAGAGGAAGAG-
GGTGGGAGCGAGCGAATTAGAGAGAAAGGAGAGGGAGGAGGCGCGTTCGCGTTATGGTGTGTTTTCGCGGG-
GTTAGGGTTAGGTCGGGGTCCGGTTAGGTCGGGTTATGAGTCGCGTCCGGAGTTGGGATATGGACGGGTAAT-
CGTCGACCTGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCG-
TTACCCAACTTAATCGCCTTGCGCAGCATCCCCCTTTCCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGA-
TCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCT-
GTGCGGTATTTACACCCGCATATGGTGCACCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCC-
GACACCCGCCAACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGT-
GACCGTCTCCGGGAGCTGCATGTGTCAGAGGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCC-
TCGTGATACGCCTATTTTATAGGTTAATGTCATGATAATAATGGGTTCTTAGACGTCAGGTGGCACTTTTTCG-
GGGAAATGTGCCGCGGAACCCCTATTGTTATTTTTCTAATACATTCAAATATGTATCCGCTCATGAA-
ACAATAACCCCTGATAAATGCTTCATATATGAAAAGAGAGTATGAGTATCAACATTTTCGTGTCGCCTATCATTTTGGC-
GCATTGCTCTTTTTGCTCACCAGAACCTGGTGAAGTTAAGAATGCTGAGAATCAGTTGGTGCCCGA

H06_58612.68.S1208222437.SM-P2-7-12.M13(-48)

ACGAAACTCCGTCCTCGGTTCCCGGGCAGTCTCTGGAGATTACCCGTCCATATCCCAACTCCCAACACAACCTCA-
TAACCCAACCTAACCCAACCCCAACCCTAACCCCTAACCCACACAAAACACCATAACACAACACACCTCCTCC-
CTCCTCTCCTTTCTCTCTAATTCACCTACTCCCACCCTCTCCTCTAACCCCTCTCTCCCTCTATAAACCTCCCA-
CCTCCAACCCACCTACCCTCCAACAAATTAACCTATCACAAAACATTTATAAAAAACAAAATTCAAATTAAAAAA-
AACCTAAACCAATCAAAAAACACCTCCCACCCCAAAAACCCCAACAAAACGTACCATTAECTACGCACAAC-
CACATAAAAAATAAAAACACGAAAAACCTAACTCCCACCCAAACCTAACTAAACCCACCCACTCAATCGTCCA-
CTTGCCGTCATGCTTCTTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCAA-
CTTAATCGCCTTGCGCAGCATCCCCCTTTCCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTT-
CCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTATT-
TCACACCCGCATATGGTGCACCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCA-
ACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCG-
GGAGCTGCATGTGTCAGAGTTTTACCGTCATCACCGAACGCGCGAGACGAAAGGGCCTCGTGATACGCCTA-
TTTTATAGGTTAATGTCATGATAATAATGGTTTCTAGACGTCAGGTGGCACTTTTCGGGAAATGTGCGCGG-
ACCCCTATTTGTTATTTTTCTAATACATCAATATGTATCCGCTCATGGAGACAATACCCTGATAATGCTCATATAT-
GAAAAGAGAGTATGAGTATCACATTCGTGTCGCCTATCTTTTGGCATTGCTCCTGTTTGGTACGGAAGTGTGAGG-
TAAGATGCTGAGATCAGTTGTGCCATGTAATCGGACTGAATCTCACAGCGGTTAGA

8. The sequencing results from the breast cancer tissue of the second breast cancer patient.

A02_58612.76.S1208222445.SM-P2-8-8.M13(-48)

GGGACATAGGACAATGATTACGACTCGTCTCGGTTCCGGCGATCCTCTGGAGATTACCCGTCCATATCCCAAT-
GGACAGCACAACCTATAACCCAACCTAACCTAACCCCAACCCTAACCCCAACCCCAACCCCAACAAAACACCATAACA-

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TCTATAAACCTCCCACCTCCAACCCACCTACCCTCCAACAAATTAACATCATCACAAAACATTTATAAAAAACAAAA-
TTCAAATTAATAAAAAAACCTAAACCAATCAAAAAACCACCTCCCACCCCAAAAACCCCAACAAAACGTACCA-
TAACTACGCACAACCACATAAAAAATAAAAAACGAAAAAACCTAACTCCCGACCCAAACCTAACTAAACCCAC-
CCACTCAATCGTCCACTTGCCGTATGCTTCTTTGGCACTGGCCGTGTTTTACAACGTCGTGACTGGGAAAAC-
CCTGGCGTTACCCAACCTAATCGCCTTGAGCACATCCCCCTTCGCCAGCTGGCGTAATAGCGAAGAGGCC-
GCACCGATCGCCCTTCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTAC-
GCATCTGTGCGGTATTTACACCCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCA-
GCCCCGACACCCGCAACACCCGCTGACGCGCCCTGACGGGCTTGCTGCTCCCGCATCCGCTTACAGACAA-
GCTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAG-
GGCCTCGTGATACGCTATTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAGACGTCAGTGGCACTTTT-
CGGGGAAATGTGCGCGGAACCCCTATTTGTTATTTTCTAAATACATTCAATATGTATCCGCTCATGAGACAATAAC-
CCTGATAAATGCTTCAATAATATTGAAAAGGGAAGAGTATGGAGTATTCAACATTTCCGTGGTCCGCC

A04_58612.78.S1208222447.SM-P2-8-10.M13(-48)

CGAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCCAACACAACCTCATAG-
CCCAACCTAACCCAACCCCAACCCTAACCCCAACACAAAACACCATAACACAACACACCTCCTCCTCCT-
CCTCTCCTTTCTCTCTAATTCACCTCACTCCCACCCTCTTCTCTAACCCCTCTCTCCCTCTATAAACCTCCCACC-
TCCAACCCACCTACCCTCCAACAAATTAACATCATCACAAAACATTTATAAAAAACAAAATTTCAAATTAATAAAAA-
ACCTAAACCAATCAAAAAACCACCTCCCACCCCAAAAACCCCAACAAAACATAACCTAACTACACACAAC-
CACATAAAAAATAAAAAACAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCGA-
CCTGCAGGCATGCAAGCTTGGCACTGGCCGTGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCA-
ACTAATCGCCTTGAGCACATCCCCCTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCT-
TCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTA-
TTTACACCCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCG-
CAACACCCGCTGACGCGCCCTGACGGGCTTGCTGCTCCCGCATCCGCTTACAGACAAGCTGTGACCGTCTC-
CGGGAGCTGCATGTGTCAGAGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCTCGTGATACG-
CCTATTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAGACGTCAGTGGCACTTTTCGGGGAAATGTG-
GCGGACCCCTATTTGTTATTTTCTAAATACATTCAATATGTATCGCTCATGAGACATACCTGATAAATGCTCATAATG-
AAAAGAGAGTATGAGTATCACATTCGTGTCGCCCTTATTCCTTTTTGCG

A05_58612.79.S1208222448.SM-P2-8-11.M13(-48)

CAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCCAACACAACCTCATAGC-
CCAACCTAACCCAACCCCAACCCTAACCCCAACACAAAACACCATAACACAACACGCCTCCTCCTCC-
TCTCCTTTCTCTCTAATTCACCTCACTCCCACCCTCTTCTCTAACCCCTCTCTCCCTCTATAAACCTCCCGCCTC-
CGACCCACCTACCCTCCAACAAATTAACATCATCACAAAACATTTATAAAAAACAAAATTTCAAATTAATAAAAAAAC-
CTAAACCAATCAAAAAACCACCTCCCACCCCAAAAACCCCAACAAAACATAACCTAACTACACACAACCAC-
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CAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATTT-
CACACCCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCA-
ACACCCGCTGACGCGCCCTGACGGGCTTGCTGCTCCCGCATCCGCTTACAGACAAGCTGTGACCGTCTCCG-
GGAGCTGCATGTGTCAGAGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCTCGTGATACGCC-
TATTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCG-
CGGAACCCCTATTTGTTATTTTCTAAATACATTCAATATGTATCGCTCATGAGACAATACCTGATAAATGCTTCAAT-
AATATGAAAAGGAGAGTATGAGTATCACATTTCCCGTGTGCCCTTATTCATGTG

A06_58612.80.S1208222449.SM-P2-8-12.M13(-48)

CCCTGCTTTGTTTTGCCATTATCTTACTGATTGCAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTGA-
GTGGGTGGGTTTAGTTAGGTTTGGGTGCGGAGTTAGGTTTTTTCGTGTTTTTATTTCTATGTGGTTGTGCGTA-
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TTTGAATTTTGT TTTTATAAATGTTTGTGATGAGTTAATTTGTTGGAGGGTAGGTGGGTTGGAGGTGGGAGGTT-
TATAGAGGGAGAGAGGGTTAGAGGAAGAGGGTGGGAGTGAGTGAATTCAGAGAAAGGAGAGGGAGGGAGGAG-
GTGTGTTGTGTATGGCGTTTTGTGTGGGGTTAGGGTTAGGGTTGGGGTTGGGTTAGGTTGGGTTATGAGTTGT-
GTTGGCAGTTGGGATATGGACGGCTAATCGTCGACCTGCCGGCATGCAAGCCTGCCACTGGCCGTGTTTTAC-
AACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACCTATCGCCTTGCAGCACATCCCCCTTTTCGCCAGCTGG-
CGTAAATAGCGACAGAGGCCCGCACCGATCGCCCTCCCAACAGTTGCCGCAGCCTGAATGGCCAATGGCGC-
CTGATGCGGTATTTTTCTCCCTACGCATCTGTGCGTATTTACACCCGCATATGGGGCACTCACAGTACAATCT-
GCTCTGATGCCGCACAGTTAAGCCAGCCCCGACACCCGCCAACACCCGCTGAAGCGCCCTGACGGGTTTGTG-
CGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGCCACTGCATGTGTCAGACGCTCTCCCCC-
TCATCACCGACAACGCGCCGAGACCGAAAGCGCCTCGATGATACGCCATATTTTAACGTAACAGGCCACG-
AAATATAAAGGGTTTCTTACACGCCAGGTGGCACTTTTCGGGATAATGTCGGCGTAACCCCTATTTGGTCTAATA-
TTCCAAACTACCTCCAATACGGTATCCACACCATGACGACCATATACCCTTGAA

E03_58612.76.S1208222445.SM-P2-8-8.M13(-48)

ACTTCGTCCTCGGTTCCCGGCGATCCTCTGGAGATTACCCGTCCATATCCCAACTCCCAACACAACCTCATAAC-
CCAACCTAACCTAACCCCAACCCTAACCCTAACCCACACAAAACACCATAACACAACACACCTCCTCCCTC-
CTCTCCTTTCTCTAATTCACTCACTCCCACCCTCTTCCCTAACCCTCTCTCCCTCTATAAACCTCCCACCT-
CCAACCCACCTACCCTCCAACAAATTAACTCATCACAAAACATTTATAAAAACAAAATTCAAATTAACAAAAA-
CCTAAACCAATCAAAAAACCACCTCCCACCCCAAAAACCCCAACCAAAAACGTACCATTAACACGCACAACC-
ACATAAAAATAAAAACACGAAAAAACCTAATCCCGACCCAAACCTAATAACCCACCCACTCAATCGTCCAC-
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CTTAATCGCTTGCAGCACATCCCCCTTTCCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTT-
CCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTAT-
TTCACACCCGCATATGGTGCATCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGC-
CAACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGCATCCGCTTACAGACAAGCTGTGACCGTCTC-
CGGGAGCTGCATGTGTCAGAGTTTTACCCTCATCACCGAAACGCGCGAGACGAAAGGGCCTCGTGATACG-
CCTATTTTATAGGTTAATGTGATGATAATAATGTTTTCTTAGACGTGAGTGGCACTTTTCGGGAAATGTGC-
GCGGAACCCTATTTGTTTTATTTTCTAATACATCAATATGTATCCGCTCATGAGACAATAACCCTGATAATGCTTCA-
TAATATTGAAAAAGGAAGAGTTTGAGTATTCAACATTT

H07_58612.69.S1208222438.SM-P2-8-1.M13(-48)

GTCGATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCCAACACAACCTCATA-
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CCTCTCCTTTCTCTAATTCACTCACTCCCACCCTCTTCCCTAACCCTCTCTCCCTCTATAAACCTCCCACC-
TCCAACCCACCTACCCTCCAACAAATTAACTCATCAGAAAACATTTATAAAAACAAAATTCAAATTAACAAAAA-
CCTAAACCAATCAAAAAACCACCTCCCACCCCAAAAACCCCAACCAAAAACGTACCATTAACACGCACAACCA-
CATAAAAATAAAAACACGAAAAACCTAATCCCGACCCAAACCTAATAACCCACCCACTCAATCGTGCACCT-
GCAGGCATGCAAGCTTGGCACTGGCCGTGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACCT-
AATCGCCTTGCAGCACATCCCCCTTTCCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCA-
CAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTC
TCCTTACGCATCTGTGCGGTATTTACACCCGCATATGGTGCATCTCAGTACAATCTGCTCTGATGCCGCATAGTT-
AAGCCAGCCCCGACACCCGCCAACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTAC-
AGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAGTTTTACCCTCATCACCGAAACGCGCGAGA-
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GCACTTTTCGGGAAATGTGCGCGGAACCCTATTTGTTTTATTTTCTAATACATCAAAATATGTATCCGCTCA-
TGAGACAATACCCTGATAAATGCTTCAATAATTTGAAAAAGGAGATGAGATCACATTCCGTGTTCCGCTTA-
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H08_58612.70.S1208222439.SM-P2-8-2.M13(-48)

ATTACGAAACTCGTCTCGGTTCCCGGCGATCCTCTGGAGATTACCCGTCCATATCCCAACTCCCAACACAACCT-
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CCCTCCTCTCCTTTCTCTCTAATTCACCTACTCCCACCCTCTTCCTCTAACCTCTCTCCCTCTATAAACCTCC-
CACCTCCAACCCACCTACCCTCCAACAAATTAACCTATCACAAAAACATTTATAAAAAACAAAATTCAAATTAAAAA-
AAAACCTAAACCAATCAAAAAACACCTCCCACCCCAAAAAACCCCAACAAAAACATACCATTAACCTACACACA-
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CACTTGCCGTCATGCTTCTTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCC-
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CCAACACCCGCTGACGCGCCCTGACGGGCTTGCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTC-
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GCGGAACCCCTATTTGTTTTATTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAA-
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H10_58612.72.S1208222441.SM-P2-8-4.M13(-48)

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CCTCCTCTCCTTTCTCTCTAATTCACCTACTCCCACCCTCTTCCTCTAACCTCTCTCCCTCTATAAACCTCCC-
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CCACATAAAAAATAAAAAACAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCC-
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CTGTGAGTAAAGATGCTG

H11_58612.73.S1208222442.SM-P2-8-5.M13(-48)

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CCACCTCCAACCCACCTACCCTCCAACAAATTAACCTATCACAAAAACATTTATAAAAAACAAAATTCAAATTAAAAA-
AAAACCTAAACCAATCAAAAAACACCTCCCACCCCAAAAAACCCCAACAAAAACGTTACCATTAACCTACGCACA-
ACCACATAAAAAATAAAAAACGAAAAAACCTAACTCCCGACCCAAACCTAACTAAACCCACCCACTCAATCGTCG-
ACCTGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCA-
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CCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATT-
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ACACCCGCTGACGCGCCCTGACGGGCTTGCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGG-
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TGCTAACA

H12_58612.74.S1208222443.SM-P2-8-6.M13(-48)

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AAAAAAAACCTAAACCAATCAAAAAACACCTCCCACCCCAAAAACCCCCACCAAAAACATACCATTAACACTAC-
ACACAACCACATAAAAAATAAAAAACAAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAAT-
CGTCGACCTGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTT-
ACCCAACTTAATCGCCTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCG-
GTATTTACACCCGCATATGGTGCACCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAAGCCAGCCCCGACAC-
CCGCCAACCCCGCTGACGCGCCCTGACGGGCTGTCTGCTCCCGGCATCCGCTTACAGACAGCTTGTGACCGT-
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ACGCCTTATTTTATAGGTTAATGTCATGATAAATGGTTTTCTTAGACGTCAGGTGGCACTTTTTTCGGGGAAAT-
GTGCGGCGGAACCCCTATTTGTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCCTTGATA-
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9. The sequencing results from the breast cancer tissue of the third breast cancer patient.

A07_58612.81.S1208222450.SM-P2-9-1.M13(-48)

AGATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCCAGCGGACTCATAAC-
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CGACCCGCTACCCTCCAACAAATTAACCCATCACGAAACGTTTATAAAAAACAAAATTCAAATTAAAAAAACCC-
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GCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCAAC-
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CCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTATT-
TCACACCCGCATATGGTGCACCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCC-
AACACCCGCTGACGCGCCCTGACGGGCTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCC-
GGGAGCTGCATGTGTGAGAGGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCTCGTGATACG-
CCTATTTTATAGGTTAATGTCATGATAAATGGTTTTCTTAGACGTCAGGTGGCACTTTTTTCGGGGAAATGT-
GCGCGAACCCCTATTTGTTATTTTTCTAAATACATTCAAATATGTATCGCTCATGAGACATAACCTGATAATGCTCCATTATAT-
GAAAAGAGAGTATGAGTATTCACATTCGTGTCGCCCTTATTCGGTTTTGGCGCATTTCCTTC

A08_58612.82.S1208222451.SM-P2-9-2.M13(-48)

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CCTCCTCTCCTTTCTCTCTAATTCGCTCGCTCCCGCCCTCTTCTCCAACCCCTCTCTCCCTCTATAAACCTCC-
CGCCTCCGACCCGCTACCCTCCAACAAATTAACACTATCGCGAAACATTTATAAAAAACAAAATTCAAATTA AAA-
AAAAACCTAAGCCAATCAAAAAACACCTCCCGCCCCGAAAACCCCGCCGAAAACGTACCATTAACACTACG-
GCGACCACGTAAAAATAAAAACGCGAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAAT-
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GCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTT
CTCCTTACGCATCTGTGCGGTATTTACACCCGCATATGGTGCACCTCAGTACAATCTGCTCTGATGCCGCATA-
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TTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTGAGAGGTTTTACCGTCATCACCGAAACGCGC-
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GGTGGCACTTTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTATTTTTCTAAATACATTCAAATATGTATCCGCT-
CATGAGACATAACCCCTGATAAATGCTTCATAATATTGAAAAGGAAGAAGTATGAGTATTCACATTTTC

A09_58612.83.S1208222452.SM-P2-9-3.M13(-48)

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CTCCTCTCCTTTCTCTCTAATTCGCTCGCTCCCGCCCTTTCCTCTAACCCCTCTCTCCCTCTATAAACCTCCC-
GCCTCCGACCCGCTACCCTCCAACAAATTAATCATCGCGAAACATTTATAAAAAACAAATTCAAATTAATAAA-
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GCTCATGAGACAATAACCTGAATAAATGCTTCATAATTTGAAAAAGGGAGAGTATGAGTATTCAAACATTCGGTGGT-
CGCCCCCTTATGGT

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ATACGAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCCAACACAACCTC-
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CTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTT
TCTCCTTACGCATCTGTGCGGTATTTACACCCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAG-
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CACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTATTTTTCTAAATAACATTCAATATGTATCCGCTCATGAG-
ACAATAACCCCTGATAAATGCTTCAATAATATTGAAAAAGGGAAGAGTATGAGTATTCACATTCCCGTGTGCGCCTA

A11_58612.85.S1208222454.SM-P2-9-5.M13(-48)

TAACATGAATTACGATTTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCATCCATATCCCAACTCCCAACA-
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CGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATG-
TGCGCGGACCCCTATTTGTTATTTTTCTAAATACATTCAATATGTATCCGCTCATGAGACAATAACCCCTGATAAATG-
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A12_58612.86.S1208222455.SM-P2-9-6.M13(-48)

GCCTGGGACATGATTACGAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTC-
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ACACACCTCCTCCCTCCTCTCCTTTCTCTCTAATTAACACTCACTCCCACCCTCTTCCTCTAACCCCTCTCTCCCTC-
TATAAACCTCCCACCTCCAACCCACCTACCCTCCAACAAATTAACATCATCAAAAACATTTATAAAAACAAAATT-
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CACTCAATCGTCGACCTGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACC-
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CATCTGTGCGGTATTTACACCCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAG-
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B01_58612.87.S1208222456.SM-P2-9-7.M13(-48)

AGAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCCGACACGACTCATAA-
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CACCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAAC-
CCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGA-
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B02_58612.88.S1208222457.SM-P2-9-8.M13(-48)

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TCCTCTCCTTTCTCTCTAATTCGCTCGCTCCCGCCCTCTTCTCTAACCCCTCTCTCCCTCTATAAACCTCCCGCC-
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CAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTGAGAGTTTTACCGTCATCACCGAAACGCGCGAG-
ACGAAAGGGCCTCGTGATACGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTTCTTAGACGTCAGGTG-
GCACTTTTCGGGAAATGTGCGCGGAACCCCTATTTGTTATTTTCTAAATACATTCAAATATGTATCCGCTCA-
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B03_58612.89.S1208222458.SM-P2-9-9.M13(-48)

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CCGCCTACCCTCCAACAAATTAACCTCATCAGGAAACATTTATAAAAACAAAATTCAAATTAACAAAAAACCTAAAC-
CAATCAAAAAACCACTCCCACCCCAAAAACCCACCGAAAACGTACCATTAACCTACGCGGACTACGTAAAA-
ATAAAAACACGAAAAAACCTAACTCCCGACCCAAACCTAACTAAACCCACCCACTCAATCGTCCACTTGCCGTCA-
TGCTTCTTTGGCACTGGCCGTGTTTTACAACGTGCTGACTGGGAAAACCCCTGGCGTTACCCAACCTTAATCGCCT-
TGCAGCACATCCCCCTTTCCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGC-
GCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATTTACACCCGCATAT-
GGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACACCCCGCTGACG-
CGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGT-
CAGAGTTTTACCGTCATCACCGAAAACGCGCGAGACGAAAGGGCCTCGTGATACGCCTATTTTATAGGTTAA-
TGTCATGATAATAATGGTTTTCTTAGACGTCAGGTGGCACTTTTCGGGAAATGTGCGCGGAACCCCTATTTGT-
TTATTTTTCTAAATACATTCAAATATGTATCGCTCATGAGACATACCCTGATAAATGCTCATATATGAAAAGAGAGTATG-
AGTATCACATTCGTGTCGGCGTATCCCTTTTTGCGCATTTGCTCTGTTTTGCTCACCCAGAACGCCTG

B04_58612.90.S1208222459.SM-P2-9-10.M13(-48)

AATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCCAACACAACCTCATAACCC-
AACCTAACCCAACCCCAACCCTAACCCCTAACCCACACAAAAACACCATAACACAACACACCTCCTCCCTCCTCT-
CCTTTCTCTAATTAACCTACTCCACCCCTCTTCTCTAACCCCTCTCCTCTATAAACCTCCACCTCCAAC-
CCACCTACCCTCCAACAAATTAACCTATCACAAAAATTTATAAAAACAAAATCAAATTAACAAAAAACCTAAA-
CAAATCAAAAAACCACTCCCACCCCAAAAACCCCAACAAAAACATAACCTAACTACACACAACCCACATAAAA-
ATAAAAACAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCCGACTGCAGGCA-
TGCAAGCTTGGCACTGGCCGTGTTTTACAACGTGCTGACTGGGAAAACCCCTGGCGTTACCCAACCTTAATCGCC-
TTGCAGCACATCCCCCTTTCCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTT-
GCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATTTACACCCGCA-
TATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACACCCCGTG-
ACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCAT-
GTGTGAGAGTTTTACCGTCATCACCGAAAACGCGCGAGACGAAAGGGCCTCGTGATACGCCTATTTTATAG-
GTTAATGTCATGATAATAATGGTTTTCTTAGACGTCAGGTGGCACTTTTCGGGAAATGTGCGCGGAACCCCT-
ATTTGTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATACCCTGATAAATGCTTCCATAAT-
ATTGAAAAGAAGAGTATGAGTATTCACATTCGTGTCGCCCTTATCCCTTTTTGCGGCATTTGCTTCCCTGTTTT-
TGCTCCACCAGAATCGCTGGGTGA

10. The sequencing results from breast cancer tissue of the fourth breast cancer patients.

B07_58612.93.S1208222462.SM-P2-10-1.M13(-48)

AGATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCCGACGCGACTCATAAC-
CCGACCTAACCCGACCCCAACCCTAACCCCTAACCCCGCGAAAACACCATAACGCGACACGCCTCCTCCCTC-
CTCTCCTTTCTCTAATTCGCTCGCTCCCGCCCTCTTCTCTAACCCCTCTCCTCTATAAACCTCCCGCCT-
CCGACCCGCCTACCCTCCAACAAATTAACCTATCGCGAAACGTTTATAAAAACGAAATTCAAATTAACAAAAAAC-
CTAAGCCGATCAAAAAACCGCCTCCCGCCCCGAAAACCCCGCCGAAAACGTACCATTAACCTACGCGCGACCA-
CGTAAAAATAAAAACGCGAAAAAACCTGACTCCCGACCCAAACCTAACTAAACCCACCCACTCAATCGTCCGACC-
TGCAGGCATGCAAGCTTGGCACTGGCCGTGTTTTACAACGTGCTGACTGGGAAAACCCCTGGCGTTACCCAAC-
TAATCGCCTTGCAGCACATCCCCCTTTCCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCC-
CAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATTTCC-
ACACCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAAC-
ACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGG-
AGCTGCATGTGTCAGAGTTTTACCGTCATCACCGAAAACGCGCGAGACGAAAGGGCCTCGTGATACGCCTAT-
TTTTATAGGTTAATGTCATGATAATAATGGTTTTCTTAGACGTCAGGTGGCACTTTTCGGGAAATGTGCGCGG-
AACCCCTATTGTTTTTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCTGATAAATGCTCATAAT-
TGAAAAGGAGAGTATGAGTATCACATTCGTGTCGCCCTTATTCCTTTTTGCGGCATTTGCTTCTGTTTTGCT

B08_58612.94.S1208222463.SM-P2-10-2.M13(-48)

CAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTGAGTGGGTGGGTTAGTTAGGTTTGGGTCCGGGAGTCA-
GGTTTTTTTCGCGTTTTTATTTTTACGTGGTCGCGCGTAGTTAATGGTACGTTTTTCGGCGGGGTTTTTCGGGGC-

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GGGAGGCGGTTTTTGTATCGGCTTAGGTTTTTTTTAATTTGAATTCGTTTTTATAAACGTTTCGCGATGAGTTA-
ATTTGTTGGAGGGTAGGCGGGTCGGAGGCGGGAGGTTTATAGAGGGAGAGAGGGTTAGAGGAAGAGGGCGGG-
AGCGAGCGAATTAGAGAGAAAGGAGAGGAGGGAGGAGCGTGTGCGGTTATGGTGTTCGCGGGGTTAGG-
GTTAGGGTTGGGGTCGGTTAGGTCGGTTATGAGTCGCGTCGGGAGTTGGGATATGGACGGGTAATCGTCG-
ACCTGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACC-
CAACTAATCGCCTTGACGACATCCCCCTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGC-
CCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGC-
GGTATTTACACCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACA-
CCCCCAACACCCGCTGACGCGCCCTGACGGGCTTGCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGAC-
CGTCTCCGGGAGCTGCATGTGTCAGAGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCTC-
GTGATACGCCTATTTATAGGTTAATGTCATGATAATAATGGTTTCTTAGACGTCAGGTGGCACTTTTCGGG-
GAAATGTGCGGACCCCTATTTGTTATTTTCTAAATACATCAATATGTATCCGCTCATGAGAACAATAACCTGATAA-
TGCTCATATATTGAAAAGAGAGTATGAGTATTCACATTCGTGTCCGCC

B09_58612.95.S1208222464.SM-P2-10-3.M13(-48)

CGAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCCAGCGGACTCATA-
ACCCGACCTAACCCGACCCCAACCCTAACCCACGCAAAACACCATAACGCGACGCGCCTCCTCC-
CTCCTCTCCTTTCTCTCTAATTCGCTCGCTCCCGCCCTCTTCTCTGACCCTCTCTCCCTCTATAAACCTCCC-
GCCTCCGACCCGCTACCCTCCAACAAATTAATCATCGCGAAACGTTTACAAAAACGAAATTCAAATAAAA-
AAAAACCTAAACCGATCAAAAAACCGCCTCCCGCCCCGAAAACCCCGCGAAAACGTACCATTAATACGCGC-
AACCACGTAATAAAAAACGCGAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTC-
GACCTGCAGGCATGCAAGCTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCA-
ACTTAATCGCCTTGACGACATCCCCCTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTT-
CCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATT-
TCACACCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACCCCGCCAA-
CACCCGCTGACGCGCCCTGACGGGCTTGCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGG-
AGCTGCATGTGTCAGAGGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCTCGTGATACGCCTATT-
TTTATAGGTTAATGTCATGATAATAATGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGAA-
CCCCTATTTGTTATTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACATACCCTGATAAATGCTTCAATAAT-
ATTGAAAAGGAAGAGTATGAGTATTCACATTTCCGTGTGCGCCCTATTCCAT

B10_58612.96.S1208222465.SM-P2-10-4.M13(-48)

GATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCCAGCGGACTCATAACCC-
GACCTGACCCAACCCGACCCCTAACCCCTAACCCACACAAAACACCATAACGCGACGCGCCTCCTCCCTCCTCT-
CCTTTCTCTCTAATTCGCTCGCTCCCGCCCTTCTCTAACCCTCTCTCCCTCTATAAACCTCCCGCCTCCGA-
CCCGCCTACCCTCCAACAAATTAATCATCGCGAAACGTTTATAAAAACAAAATTCAAATTAACAAAAACCTAA-
CCGATCAAAAAACCCCTCCACCCCAAAAACCCCAACAAAACATAACCATTAATACACACAACCACATAAAAA-
ATAAAAACAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCGACCTGCAGGCA-
TGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCT-
TGCAGCACATCCCCCTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTG-
CGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATTTACACCCGATA-
TGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCAACACCCGCTGAC-
GCGCCCTGACGGGCTTGCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTG-
TCAGAGGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCTCGTGATACGCCTATTTTATAGGTTA-
ATGTCATGATAATAATGGTTTTCTTAGACGTCAGGTGGCACTTTTCGGGCAAATGTGCGCGGAACCCCTATTT-
GTTTATTTTCTAATACATTCAATATGTATCCGCTCATGAGACATACCCTGATAAATGCTTCAATAATTGAAAAAGGAG-
AGTATGAGTATTCACATTCGCTGTGCGCCCTATC

B11_58612.97.S1208222466.SM-P2-10-5.M13(-48)

ATTACGAACTCGTCCTCGGTTCCCGGGGATCCTCTGGAGATTGAGTGGGTGGGTTTAGTTAGGTTTGGGCCGGG-
AGTTAGGTTTTTTCGCGTTTTTATTTTACGTGGTCGCGGTAGTCAATGGTACGTTTTTCGGCGGGGTTTTTCG-
GGGCGGGAGGCGGTTTTTCGATCGGTTTAGGTTTTTTTTAATTTGAACCTTTGTTTTTATAAATGTTTTGCGATGA-

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GTTAATTTGTTGGAGGGTAGGCCGGTTCGGAGGCGGGAGGTTTATAGAGGGAGAGAGGGTTAGAGGAAGAGGGC-
GGGAGCGAGCGAATTAGAGAGAAAGGAGAGGAGGGAGGAGGTGTGTTGTGTTATGTTGTTTTGTGTGGGGTTA-
GGGTTAGGGTTGGGGTTGGGTTAGGTTCGGGTTATGAGTTGCGTCGGGAGTTGGGATATGGACGGGTAATCGTC-
CACTTGCCGTCATGCTTCTTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACC-
CAACTTAATCGCCTTGCAGCACATCCCCCTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCC-
CTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGG-
TATTTACACCCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCC-
GCCAACACCCGCTGACGCGCCCTGACGGGCTTGCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCT-
CCGGGAGCTGCATGTGTGAGAGGTTTTACCGTCATCACCGAAAACGCGCGAGACGAAAGGGCCTCGTGATAC-
GCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGT-
GCGCGAACCCCTATTTGTTATTTCTAATACATCAATATGTATCCGCTCATGAGAACAATAACCTGATAAATGCTTCATA-
ATATTGAAAAAGGAGA

B12_58612.98.S1208222467.SM-P2-10-6.M13(-48)

TATTACGACTCGTCCTCGGTTCCCGGCGATCCTCTGGAGATTACCCGTCCATATCCCAACTCCCGACGCGACTC-
ATAACCCAACCTAACCCAACCCCGACCCTAACCCTAACCCACACAAAACACCATAACGCGACGCGCCTCCT-
CCCTCCTCCTTTCTCTCTAATTCGCTCGCTCCCGCCCTCTTCTCTAACCCCTCCTCCCTCTATAAACCTCC-
CGCCTCCAACCCGCTACCCTCCAACAAATTAACCTCATCGCGAAAACGTTTATAAAAAACAAAATTCAAATTA AAA-
AAAAACCTAAACCGATCAAAGAACCACCTCCCGCCCCGAAAACCCCGCGAAAACATACCATTAACCTACGC-
GCGACCACATAAAAAATAAAAACGCAAAAAAACCTAACCCCAACCCAAACCTAACCTAACCCACCCACTCAATC-
GTCCACTTGCCGTCATGCTTCTTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTA-
CCCAACTTAATCGCCTTGCAGCACATCCCCCTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGC-
CCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCG-
GTATTTACACCCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACC-
CGCCAACACCCGCTGACGCGCCCTGACGGGCTTGCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTC-
TCCGGGAGCTGCATGTGTGAGAGGTTTTACCGTCATCACCGAAAACGCGCGAGACGAAAGGGCCTCGTGATA-
CGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTTCTTAGACGTCAGTGGCACTTTTCGGGGAAATGT-
GCGCGAACCCCTATTTGTTATTTCTAATACATCAATATGTATCCGCTCATGAGACATACCCTGATAAATGCTTC-
ATAAATATTGA

C01_58613.1.S1208222468.SM-P2-10-7.M13(-48)

TCGAATTCGAGCTCGGTACCCGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCCGACGCGACTCATA-
ACCCGACCTAACCCGACCCCAACCCTAACCCTAACCCCGCGAAAACACCATAACGCGACACGCTCCTCCC-
TCCTCCTCTTTCTCTCTAATTCGCTCGCTCCCGCCCTCTTCTCTAACCCCTCCTCCCTCTATAAACCTCCCGC-
CTCCGACCCGCTACCCTCCAACAAATTAACCTCATCGCGAAAACGTTTATAAAAAACGAAATCAAATTA AAAAAA-
ACCTAAGCCGATCAAAAAACCGCCTCCCGCCCCGAAAACCCCGCGAAAACGTACCATTAACCTACGCGCGAC-
CACGTA AAAAATAAAAACGCGAAAAAACCTGACTCCCGACCCAAACCTAACCTAACCCACCCACTCAATCGTCGA-
CCTGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCAA-
CTTAATCGCCTTGCAGCACATCCCCCTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTCC-
CAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTC
TCCTTACGCATCTGTGCGGTATTTACACCCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTT-
AAGCCAGCCCCGACACCCGCCAACACCCGCTGACGCGCCCTGACGGGCTTGCTGCTCCCGGCATCCGCTTAC-
AGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTGAGAGGTTTTACCGTCATCACCGAAAACGCGCGAGA-
CGAAAGGGCCTCGTGATACGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTTCTTAGACGTCAGGTGG-
CACTTTTCGGGGAAATGTGCGCGGACCCCTATTTGTTATTTCTAATACATCAATATGTATCCGCTCATGAGACA-
TACCTGATAAATGCTTCATATATTGAAAAGAGAGTATGAGTATTCAACATTCGCTGT

C02_58613.2.S1208222469.SM-P2-10-8.M13(-48)

AGATTCGAGCTCGGTACCCGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCCGACGCAACTCATAACC-
CGACCTAACCCAACCCCAACCCTAACCCTAACCCACACAAAACACCATAACACAACACACCTCCTCCCTCCT-
CTCCTTTCTCTCTAATTCGCTCGCTCCCGCCCTCTTCTCTAACCCCTCCTCCCTCTATAAACCTCCCGCCTCC-
GACCCGCTACCCTCCAACAAATTAACCTCATCAAAAACATTTATAAAAAACAAAATTCAAATTA AAAAAAACCT-
AAACCAATCGAAAAACCGCCTCCACCCCGAAAACCCCGCGAAAACATACCATTAACCTACGCGCGACCCAG-

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TAAAAATAAAAACGCGAAAAAACCTAACTCCCGACCCAAACCTAACTAAACCCACCCACTCAATCGTCGACCTG-CAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCAACCTA-ATCGCCTTGCAGCACATCCCCCTTTCCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCA-ACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATTTAC-ACCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACAC-CCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAG-CTGCATGTGTCAGAGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCTCGTGATACGCCTATTT- TTATAGTTAATGTCATGATAATAATGTTTTCTTAGACGTCAGGTGCACTTTTCGGGAAATGTGCGCGGAA-CCCCTATTTGTTATTTCTAATACATTCAAATATGTATCCGCTCATGAGACATACCCTGATAAATGCTTCATATATTGAA-AAGGAAGAGTATGAGTATCACATTTCTGTGTCGCCTTATTC

C03_58613.3.S1208222470.SM-P2-10-9.M13(-48)

ATCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCCGACGCGACTCATAACCCA-ACCTAACCCAACCCCAACCCTAACCCCAACCCACACAAAACACCATAACGCGACGCGCCTCCTCCCTCCTCT-CTTTCTCTCTAATTCGCTCGCTCCCGCCCTCTTCTCTAACCCCTCTCTCCCTCTATAAACCTCCCGCCTCCAA-CCCGCCTACCCTCCAACAAATTAACCTCATCGCGAAACGTTATAAAAACAAAATTCAAATTAACCAAAACCTAA-ACCGATCAAAGAACCACCTCCCGCCCCGAAAACCCCGCCGAAAACATACCATTAACCTACGCGCGACCACATA-AAAATAAAAACGCAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCGACCTGCA-GGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCAACCTA-ATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCC-CAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATT-TCACACCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGC-CAACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGCATCCGCTTACAGACAAGCTGTGACCGTCT-CCGGGAGCTGCATGTGTCAGAGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCTCGTGAT-ACGCCTATTTTTATAGTTAATGTCATGATAATAATGTTTTCTTAGACGTCAGGTGGCACTTTTCGGGGA-AATGTGCGCGGACCCCTATTTGTTATTTCTAATACATTCAAATATGTATCCGCTCATGAGACATACCCTGATAAATGCC-TCATATGAAAAGAGAGTATGAGTATCCACATTCGTGTGCGCTATCCTTTTTGCGCATTTGCTCTGTTTTGCTCAC-CCAGAAA

C04_58613.4.S1208222471.SM-P2-10-10.M13(-48)

ATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCCGACGCGACTCATAAC-CCGACCTGACCCAACCCCGACCCTAACCCTAACCCACACAAAACACCATAACGCGACGCGCCTCCTCCCT-CTCTCCTTTCTCTCTAATTCGCTCGCTCCCGCCCTCTTCTCTAACCCCTCTCTCCCTCTATAAACCTCCCG-CCTCCGACCCGCTACCCTCCAACAAATTAACCTCATCGCGAAACGTTATAAAAACAAAATTCAAATTAACCA-AAAACCTAAACCGATCAAAAAACACCTCCCACCCCAAAAACCCCAACAAAACATACCATTAACCTACAC-ACAACCACATAAAAAACAAAAACAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAAT-CGTCGACCTGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGC-GTTACCCAACCTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCAC-CGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGC-ATCTGTGCGGTATTTACACACCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCA-GCCCCGACACCCGCCAACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGCATCCGCTTACAGAC-AAGCTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAGTTTTACCGTCATCACCGAAACGCGCGAGACG-AAAGGGCCTCGTGATACGCCTATTTTTATAGTTAATGTCATGATAATAATGTTTTCTTAGACGTCAGTGGC-ACTTTTCGGGAAATGTGCGCGGAACCCCTATTTGTTATTTTCTAATACATTCAAATATGTATCCGCTCA-TGAGACATACCCTGATAAATGCTCATAATGAAAAGAGAGTATGAGTATCCACATTTCTGTTGCGCTATCCCTTTTG-CGATTTGCTCTGTTTTGCTCACCG

11. The sequencing results from the breast cancer tissue of the fifth breast cancer patient.

C07_58613.7.S1208222474.SM-P2-11-1.M13(-48)

ATCGTCTCGGTTCCCGGCGATCCTCTGGAGATTACCCGTCCATATCCCAACTCCCGACGCGACTCATAACC-GACCTAACCCGACCCCGACCCTAACCCGACCCACACAAAACACCATAACGCGACGCGACCTCCTCCCT-

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CCTCTCCTTTCTCTCTAATTCACCTACTCCCACCTCTTCTCTAACCCTCTCTCCCTCTATAAACCTCCCA-
CCTCCAACCCACCTACCCTCCAACAAATTAACCTCATCGCGAAACGTTTATAAAAACGAAATTCAAATAAAA-
AAAAACCTAAACCAATCAAAAAACCACCTCCCACCCCAAAAACCCCAACAAAAACATACCATTAACCTACGC-
GCGACCACGTAAAAATAAAAACGCGAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAA-
TCGTCCACTTGCCGTATGCTTCTTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCTGGC-
GTTACCCAACCTAATCGCCTTGCAGCACATCCCCCTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCAC-
CGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGC-
ATCTGTGCGGTATTTACACCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCA-
GCCCCGACACCCGCCAACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGAC-
AAGCTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAGGTTTTACCGTCATCACCGAAACGCGCGAGACG-
AAAGGGCCTCGTGATACGCCTATTTTATAGGTTAATGTCATGATAATAATGGTTTTCTTAGACGTCAGGTGG-
CACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTTATTTTTCTAAATACATTCAAATATGTATCCGC-
TCATGAGACAATACCCTGATAATGCCTCATATATGAAAAGAGAGTATGAGTATCACATTCGTGTCGCCTATCCTTTTT-
GCGCATTTGCCTTCTGTTTTTGCTAACA

C08_58613.8.S1208222475.SM-P2-11-2.M13(-48)

ATTACGATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCCGACGCGACT-
CATAACCCGACCTAGCCCAACCCCAACCCTAACCCTAACCCACACAAAAACCCATAACGCGACGCGCCTC-
CTCCCTCCTCCTTTCTCTCTAATTCGCTCACTCCCGCCCTCTTCTCTAACCCTCTCTCCCTCTATAAACCT-
CCCGCCTCCGACCCGCTACCCTCCAACAAATTAACCTCATCGCGAAACATTTATAAAAACGAAATTCAAATTA-
AAAAAACCTAAACCAATCAAAAAACCACCTCCCACCCCAAAAACCCCGCGGAAAACGTACCATTAACCTACG-
CGCGACCACGTAAAAATAAAAACGCGAAAAAACCTAACTCCCGACCCAAACCTAACTAAACCCACCCACTCAAT-
CGTCGACCTGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCTGGCGT-
TACCCAACCTAATCGCCTTGCAGCACATCCCCCTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGAT-
CGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGT-
GCGGTATTTACACCCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGAC-
ACCCGCCAACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGAC-
CGTCTCCGGGAGCTGCATGTGTCAGAGGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCTCG-
TGATACGCCTATTTTATAGGTTAATGTCATGATAATAATGCTTTCTTAGACGTCAGGTGGCACTTTTCGGGG-
AAATGTGCGCGGAACCCCTATTTGTTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATACCTGATA-
AATTGCTCAATAATGAAAAGGAAGAGTATGAGTATCAACATTTCCCGTGTGCGCTTAATCCCTTTTTTGCGGCGAT

C09_58613.9.S1208222476.SM-P2-11-3.M13(-48)

GAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTGAGTGGGTGGGTTTAGTTAGGTTTGGGTGCGGGAGTT-
AGGTTTTTTCGTGTTTTTATTTTTACGTGGTTCGCGCGTAGTTAATGGTACGTTTTTCGGCGGGGGTTTTCGGGG-
CGGGAGGCGGTTTTTCGATCGGTTTCAAGTTTTTTTTAATTTGAATTTTCGTTTTTATAACGTTTCGCGATGAGT-
TAATTTGTTGGAGGGTAGGCGGGTTCGAGGTTGGGAGGTTTATAGAGGGAGAGAGGTTAGAGGAAGAGGGCGG-
GAGCGAGCGAATTAGAGAGAAAGGAGAGGAGGGAGGAGGCGCGTCGCGTTATGGTGTGTTGCGCGGGGTTAG-
GGTTAGGTTGGGGTTCGGGTTAGGTCGGGTTATGAGTCGCGTCGGGAGTTGGGATATGGACGGGTAATCGTCG-
ACCTGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCTGGCGTTACCC-
AACTTAATCGCCTTGCAGCACATCCCCCTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTT-
CCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTC
CTTACGCATCTGTGCGGTATTTACACCCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTA-
AGCCAGCCCCGACACCCGCCAACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACA-
GACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAGGTTTTACCGTCATCACCGAAACGCGCGAGA-
CGAAAGGGCCTCGTGATACGCCTATTTTATAGGTTAATGTCATGATAATAATGGTTTTCTTAGACGTCAGGTGC-
ACTTTTCGGGGAAATGTGCGCGAACCCCTATTTGTTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAAT-
ACCCTGATAATGCTCATATATGAAAAGAGAGTATGGAGTATTCAACATTTCCGGTGTGCGCCCTTATTCC

C10_58613.10.S1208222477.SM-P2-11-4.M13(-48)

AGATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCCGACGCGACTCATAA-
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CCTCTCCTTTCTCTCTAATTCGCTCGCTCCCGCCCTCTTCTCTAACCCTCTCTCCCTCTATAAACCTCCCGC-

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CTCCGACCCGCCTACCCTCCAACAAATTA ACTCATCGCGAAACGTTTATAAAAACGAAATTC AAATTA AAAAAA
AACCTAAACCGATCAAAAAACACCTCCACCCCGAAAACCCCGCCGAAAACGTACCATTA ACTACGCGCG
ACCACGTA AAAAATAAAAAACACGAAAAAACCTAACTCCCGACCCAAACCTAACTAAACCCACCCACTCAATCGTC
GACCTGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACC
CAACTTAATCGCCTTGCAGCACATCCCCCTTTCCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGC
CCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGC
GGTATTTACACCGCATATGGTGC ACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACA
CCCCCAACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACC
GTCTCCGGGAGCTGCATGTGT CAGAGGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCTCGT
GATACGCCTATTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGG
AAATGTGCGCGGAACCCCTATTTGTTATTTTCTAAATACATTCAATATGTATCCGCTCATGAGACAATACCCTGATA
AATGCTTCATATATGAAAAGGAGATATGAGTATCACATTCCGTGTCGCCCTTATTCCTTTTTGGCGGCATTTGCCCT

C11_58613.11.S1208222478.SM-P2-11-5.M13(-48)

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TCCTCTCCTTTCTCTCTAATTCGCTCGCTCCCGCCCTCTTCCTCTAACCCCTCTCTCCCTCTATAAACCTCCCGC
CTCCGACCCGCCTACCCTCCAACAAATTA ACTCATCGCGAAACATTTATAAAAACAAAATTC AAATTA AAAAAA
AACCTAAACCAATCAAAAAACACCTCCACCCCAAAAACCCCAACCAAAAACATAACCATTA ACTACGCGCAAC
CACATAAAAATAAAAACGCGAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCGAC
CTGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCAAC
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CAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTATTT
ACACCGCATATGGTGC ACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAAC
ACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGA
GCTGCATGTGT CAGAGGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCTCGTGATACGCCTATT
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TGAAAAGGAAGATATGAGTATCAACATTTCCGTGTCGCCCTTATTCCT

C12_58613.12.S1208222479.SM-P2-11-6.M13(-48)

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CCTCCCTCCTCTCCTTTCTCTCTAATTCGCTCACTCCCGCCCTCTTCCTCTAACCCCTCTCTCCCTCTATAAACCT
CCCGCCTCCGACCCGCTACCCTCCAACAAATTA ACTCATCGCGAAACATTTATAAAAACGAAATTC AAATTA AAAAA
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GCGACCACGTA AAAAATAAAAAACGCGAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCG
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CCA ACTTAATCGCCTTGCAGCACATCCCCCTTTCCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGC
CCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCG
GTATTTACACCGCATATGGTGC ACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACC
CGCCAACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTC
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CTTCATATAG

D01_58613.13.S1208222480.SM-P2-11-7.M13(-48)

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CTCCCTCCTCTCCTTTCTCTCTAATTCGCTCGCTCCCGCCCTCTTCCTCTAACCCCTCTCTCCCTCTATAAACCT
CCCGCCTCCGACCCACCTACCCTCCAACAAATTA ACTCATCACGAAACGTTTATAAAAACAAAATTC AAATTA AAAAA

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GTGACCTGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTA-
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CCCTTCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGC-
GGTATTTACACCCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCGACAC-
CCGCCAACCCCGCTGACGCGCCCTGACGGGCTTGCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGT-
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ACGCCTATTTTTATAGTTAATGTCATGATAAATGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGAAATGTGCGC-
GACCCTATTGTTATTTCTAATACATTCAATATGTATCCGCTCATGAGACATACCTGATAAATGCTTCAATATATG

D02_58613.14.S1208222481.SM-P2-11-8.M13(-48)

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CCTCTCCTTTCTCTCTAATTCGCTCGCTCCCGCCCTCTTCCTCTAACCCCTCTCTCCCTCTATAAACCTCCCACCT-
CCGACCCGCTACCCTCCAACAAATTAATCATCGCGAAACGTTTATAAAAAACGAAATCAAATTAIAAAAAAAAA-
CCTAAACCGATGCAAAAAACGCGCTCCCGCCCCGAAAACCCCGCCGAAAACGTACCATTAACCTACGCGCGACC-
ACGTAIAAATAAAAACGCGCAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCCAC-
TTGCCGTCATGCTTCTTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCAAC-
TTAATGCTTGCAGCACATCCCCCTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTC-
CCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATT-
TCACACCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCGACACCCGCC-
AACACCCGCTGACGCGCCCTGACGGGCTTGCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCC-
GGGAGCTGCATGTGTGAGAGGTTTTACCGTCATCACCGAAAACGCGCGAGACGAAAGGGCCTCGTGATACGC-
CTATTTTTATAGTTAATGTCATGATAAATGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGAAATGTGCG-
GCGAACCCTATTTGTTATTTTCTAAATACATTCAATATGTATCCGCTCATGAGACATAACCTGATAAATGCTTCA-
TAATATTGAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTAATC

D03_58613.15.S1208222482.SM-P2-11-9.M13(-48)

CGAACTCGTCTCGGTTCCCGGCGATCCTCTGGAGATTACCCGTCCATATCCCAACTCCCAACGCGACTCATAA-
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CCTCTCCTTTCTCTCTAATTCGCTCGCTCCCGCCCTCTTCCTCTAACCCCTCTCTCCCTCTATAAACCTCCCGCC-
TCCGACCCGCTACCCTCCAACAAATTAATCATCGCGAAACATTTATAAAAAACAAAATCAAATTAIAAAAAAAAA-
ACCTAAACCAATCAAAAAACCACCTCCCACCCCAAAAACCCCGCCGAAAACGTACCATTAACCTACGCGCGAC-
CACGTAIAAATAAAAACAGCAAAAAACCTAACTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCCA-
CTTGCCGTCATGCTTCTTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCA-
ACTTAATCGCCTTGCAGCACATCCCCCTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCT-
TCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTA-
TTTCACACCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCGACACCCG-
CCAACACCCGCTGACGCGCCCTGACGGGCTTGCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCT-
CCGGGAGCTGCATGTGTGAGAGGTTTTACCGTCATCACCGAAAACGCGCGAGACGAAAGGGCCTCGTGATAC-
GCCTATTTTTATAGTTAATGTCATGATAAATGGTTTCTTAGACGTCAGTGGCACTTTTCGGGAAATGTG-
CGCGGAACCCTATTTGTTATTTTCTAAATACATTCAATATGTATCCGCTCATGAGACAATAACCTGATAAATGCT-
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D04_58613.16.S1208222483.SM-P2-11-10.M13(-48)

ATCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTCCCGACGCGACTCATAACCCG-
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CCTTTCTCTCTAATTCGCTCGCTCCCGCCCTCTTCCTCTAACCCCTCTCTCCCTCTATAAACCTCCCGCCTCCG-
ACCCGCTACCCTCCAACAAATTAATCATCAGAAAACATTTATAAAAAACAAAATCAAATTAIAAAAAAAAAACCTA-
AACCAATCAAAAAACCACCTCCCACCCCAAAAACCCCGCCGAAAACGTACCATTAACCTACGCGCGACCACGT-
AAAAATAAAAACGCGCAAAAAACCTAACTCCCGACCCAAACCTAACTAAACCCACCCACTCAATCGTGCACCTG-

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CAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACCTTA-
ATCGCCTTGCAGCACATCCCCCTTTCCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTCCCA-
ACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTATTTCA-
CACCGCATATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAAC-
ACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGG-
AGCTGCATGTGTCAGAGGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCTCGTGATACGCCTA-
TTTTTATAGTTAATGTCATGATAATAATGTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCGC-
GGAACCCCTATTTGTTTATTTTCTAAATACATTCAAATATGTATCCGCCTCATGAGACAATAACCCTGATAAA-
TGCTTCAATAAATATTGAAAAAGGAAGAGTATGAGTATCAACATTTTCGTGTGCGCGTATCCCTTTTTGCGCATTG-
CTCTGTTTTGCTCACCCAG

12. The sequencing results from the breast cancer tissue of the sixth breast cancer patient.

D07_58613.19.S1208222486.SM-P2-12-1.M13(-48)

GACTCGTCTCGGTTCCCGGCGATCCTCTGGAGATTACCGTCCATATCCCAACTCCCAACACAACCTCATAACC-
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TCTCCTTTCTCTCTAATTCGCTCGCTCCCGCCCTCTTCTCTAACCCCTCTCCTCTATAAACCTCCCGCCTC-
CGACCCGCTACCCTCCAACAAATTAACCTCATCGCGAAACGTTTATAAAAAACAAAATTCAAATTAACAAAAAAC-
CTAACCAATCAAAAAACCACTCCACCCCAAAAAACCCCAACCAAAAAACATAACCTAACCTACACACAACCCAC-
ATAAAAAATAAAAAACAGAAAAAACCTAACCTCCCAACCCAAACCTAACCTAACCCACCCACTCAATCGTCCACTTG-
CCGTGCATGCTTCTTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACCTAA-
TCGCTTGCAGCACATCCCCCTTTCCGCGAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAAC-
AGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTATTTTACACC-
GCATATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACACCCG-
CTGACGCGCCCTGACGGGCTTGTCTGCTCCCGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTG-
CATGTGTCAGAGGTTTTACCGTCATACCGAAACGCGCGAGACGAAAGGGCCTCGTGATACGCCTATTTTAT-
AGGTTAATGTCATGATAATAATGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGACCC-
TATTTGTTTATTTTCTAAATACATTCAAATATGTATCCGCCTCATGAGACATAACCCTGATAATGCTCCATATATGAAAAGA-
GAGTATGAGTATCACATTTTCGTGTGCGCCTATCCCTTTTTTGGCGCATTGTCCTG

D08_58613.20.S1208222487.SM-P2-12-2.M13(-48)

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CTCCTTCCCTCCCTAATTCACTCACTCCACCCCTCTTCTCTAACCCCTCTCCTCCTATAAACCTCCACCTCC-
AACCCACCTACCCTCCAACAAATTAACCTCATCACAAAAACATTTATAAAAAACAAAATTCAAATTAACAAAAAACCT-
AAACCAATCAAAAAACCACTCCACCCCAAAAAACCCCAACCAAAAAACATAACCTAACCTACACACAACCCACAT-
AAAAATAAAAAACACAAAAAACCTAACCTCCCAACCCAAACCTAACCTAACCCACCCACTCAATCGTCCACTTGC-
CGTCATGCTTCTTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACCTAAT-
CGCCTTGCAGCACATCCCCCTTTCCGCGAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAAC-
AGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTATTTTACAC-
CGCATATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACACCC-
GCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCT-
GCATGTGTCAGAGGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCTCGTGATACGCCTATTTTAT-
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CTATTTGTTTATTTTCTAAATACATTCAAATATGTATCCGCCTCATGAGACAATAACCTGATAATGCTTCAATAATTTG-
AAAAGAGAGTATGAGTATCAACATTTCCGTGTGCGCCTTATCCCTTTTTTGGCGCATTGTCCTG

D09_58613.21.S1208222488.SM-P2-12-3.M13(-48)

GAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCATCCATATCCCAACTCCCAACACAACCTCATAAC-
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TCTCCTTTCTCTCTAATTCACTCACTCCACCCCTCTTCTCTAACCCCTCTCCTCCTATAAACCTCCACCTCC-
AACCCACCTACCCTCCAACAAATTAACCTCATCACAAAAACATTTATAAAAAACAAAATTCAAATTAACAAAAAACCT-

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AAACCAATCAAAAAACACCTCCCACCCCAAAAAACCCCGCCAAAAACATACCATTAACCTACACACAACCACAT-
AAAAATAAAAAACACAAAAAACCTAACCCTCCCAACCCAAACCTAACTAAACCCACCCACTCAATCGTCGACCTGCA-
GGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCAACCTTAATC-
GCCTTGACAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAG-
TTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTATTTACACCG-
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TTGTTTTATTTTCTAAATACATTCAAATATGTATCGCTCATGAGACATAACCTGATAAATGCTCCATAATATGAAAGAGA-
GATGAGTATCACATTCGTGTGCCTTATCCTTTTTTGCGGCATTTGCCTCCTGCATG

D10_58613.22.S1208222489.SM-P2-12-4.M13(-48)

GTTACGAAGCTCGCTCGGTTCCCGGCGATCCTCTGGAGATTACCCATCCATATCCCAACTCCCAACACAACCTC-
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CCACATAAAAAATAAAAAACACAAAAAACCTAACCCTAACCCCAACCCCTAACCTAAACCCACCCACTCAATCGTCC-
ACTTGGCGTCATGCTTCTTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCA-
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CCAACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCT-
CCGGGAGCTGCATGTGTCAGAGGTTTTACCGTCATCACCGAAACGCGCGAGACGAAAGGGCCTCGTGATAC-
GCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTTCTTAGACGTCAGGTGGCACTTTTCGGGAAATGT-
GCGCGGACCCCTATTTGTTATTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACATAACCCGATAAATGCTCATA-
TATGAAAAGGAGAGTATGAGTATTCACATTCGGGTGTCG

D11_58613.23.S1208222490.SM-P2-12-5.M13(-48)

GCACCATGACATGATTACGATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTC-
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GCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTCCTTAC-
GCATCTGTGCGGTATTTACACCCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCA-
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GGGCCCTCGTGATACGCCTATTTTTATAGGTTATGTCATGATAATAATGGTTTTCTTAGACGTCAGGTGGCACTT-
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D12_58613.24.S1208222491.SM-P2-12-6.M13(-48)

GATTACGATTCGAGCTCGGTACCCGGGGATCCTCTAGAGATTACCCGTCCATATCCCAACTTCCGACGCGACTC-
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CCCTCCTCTCCTTTCTCTCTAATTCGCTCGCTCCCGCCCTCTTCCCTCTAACCCCTCTCTCCCTCTATAAACCTCC-
CGCCTCCGACCCGCTACCCTCCAACAAATTAATCATCGCGAAACGTTTTATAAAAAACGAAATTCAAATTA AAA-
AAAAACCTAAACCAATCGAAAAACACCTCCCACCCCGAAAAACCCCGCCAAAGACATACCATTAACCTACGCG-

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CCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATT
TTCTCCTTACGCATCTGTGCGGTATTTACACCCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCAT-
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GAGACGAAAGGGCCTCGTGATACGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTTCTTAGACGTCA-
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E01_58613.25.S1208222492.SM-P2-12-7.M13(-48)

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CCTCCCTCCTCTCCTTTCTCTCTAATTCGCTCGCTCCCGCCCTCTTCTCTAACCCCTCTCTCCCTCTATAAAC-
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ATCGTCCACTTGCCGTCATGCTTCTTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGG-
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