**Supplementary Materials and Methods**

**Cell Lines and Cell Culture Conditions:** KYSE150 and Colo824 cell lines were obtained from DSMZ (Braunschweig, Germany). The KYSE150 cell line was established from the poorly differentiated esophageal squamous cell carcinoma resected from upper (cervical) esophagus of a 49-year-old Japanese woman after receiving radiotherapy (the tumor was invading contiguous structures) (Shimada *et al.*, 1992). KYSE 150 cells were cultured in 49% RPMI-1640 + 49% Ham's F12 + 2% fetal bovine serum (FBS). Colo824 cell line was established from the pleural fluid of a 52-year-old patient with breast carcinoma. Colo824 cells were cultured in 15% FBS RPMI-1640. HCC70 and HCC1954 cell lines were obtained from ATCC (Manassas, VA, USA). HCC70 and HCC1954 cells were cultured in 10% FBS RPMI-1640. MCF10A is a spontaneously immortalized, but nontransformed human mammary epithelial cell line derived from the breast tissue of a 36-year-old patient with fibrocystic changes (Soule *et al.*, 1990). MCF10A cells were cultured in Ham's F-12 medium supplemented with 0.1% bovine serum albumin, fungizone (0.5 µg/mL), gentamicin (5 µg/mL), ethanolamine (5 mmol/L), HEPES (10 mmol/L), transferrin (5 µg/mL), 3,3,'5-Triiodo-L-Thyronine (T3 ) (10 µmol/L), selenium (50 µmol/L), hydrocortisone (1 µg/mL), insulin (5 µg/mL) and 10 ng/ml epidermal growth factor (EGF). The isolation and culture of the SUM series of HBC cell lines have been described in detail previously (Forozan *et al.*, 2000; Forozan *et al.*, 1999). SUM-44 and SUM-190 cells were cultured in Ham's F-12 medium supplemented with 0.1% bovine serum albumin, fungizone (0.5 µg/mL), gentamicin (5 µg/mL), ethanolamine (5 mmol/L), HEPES (10 mmol/L), transferrin (5 µg/mL), 3,3,'5-Triiodo-L-Thyronine (T3 ) (10 µmol/L), selenium (50 µmol/L), hydrocortisone (1 µg/mL), and insulin. SUM-52, SUM-149 and SUM-225 cells were cultured with 5% fetal bovine serum, fungizone (0.5 µg/mL), gentamicin (5 µg/mL), hydrocortisone (1 µg/mL) and insulin (5 µg/mL).

**References**

Forozan F, Mahlamaki EH, Monni O, Chen Y, Veldman R, Jiang Y *et al* (2000). CGH analysis of 38 breast cancer cell lines: A basis for interpreting cDNA mircroarray data. *Cancer Res* **60:** 4519-4525.

Forozan F, Veldman R, Ammerman CA, Parsa NZ, Kallioniemi A, Kallioniemi O *et al* (1999). Molecular cytogenetic analysis of 11 new human breast cancer cell lines. *Br J Cancer* **81:** 1328-1334.

Shimada Y, Imamura M, Wagata T, Yamaguchi N, Tobe T (1992). Characterization of 21 newly established esophageal cancer cell lines. *Cancer* **69:** 277-84.

Soule HD, Maloney TM, Wolman SR, Peterson WD, Jr., Brenz R, McGrath CM *et al* (1990). Isolation and characterization of a spontaneously immortalized human breast epithelial cell line, MCF-10. *Cancer Res* **50:** 6075-86.

**Supplementary Table 1:** Array CGH data on chromosome 9p using an Agilent 244K chip (A) or 44K chip (B) in 9 cancer cell lines.

**Supplementary Figure Legend**

Figure S1. A summary of GASC1 amplification across multiple GISTIC analyses performed on the entire dataset (copy-number profiles of 3131 cancer samples) or subsets representing different cancer types.

Figure S2. Genome view of the PTPRD locus analyzed on the Agilent oligonucleotide array (Agilent Technology) in KYSE150 cells.

Figure S3. Schematic representation of PTPRD primers for genomic real-time PCR.

Figure S4. Relative copy number of the PTPRD gene in KYSE150, HCC1954 and control cells determined by genomic real time-PCR. Genomic DNA was used as a template and PCR amplification of PTPRD fragments of intron 7-exon 8 and intron 8-exon 9 were normalized against the PCR amplification of β-actin. Copy numbers in control cells are set as 0 arbitrarily. Relative copy numbers were shown as log2 values.

Figure S5: Summary of regions at chromosome 9 with signigicant copy number alterations in basal-like primary breast tumor, brain metastasis and xenograft samples that were adopted from Ding et al's published Supplementary Information .

Figure S6: Protein levels of p53 in HCC1954 cells stably expressing control shRNA, UHRF2 shRNA#1 or shRNA#2 were analyzed by Western blot.

Figure S7: Detection of RB protein in HCC1954 cells stably expressing non-silencing shRNA (lane 1), UHRF2 shRNA#1 (lane 2), or UHRF2 shRNA#2 (lane 3). Whole cell extracts of MCF10A cells were resolved on the same gel to serve as a migration control for the hypophosporylated (p) form and the

hyperphosporylated (pp) form of RB protein. MCF10A cells were either EGF-starved (-EGF) for 24 hours or EGF-starved for 24 hours followed by stimulation with EGF (+EGF) for 24 hours.

# Figure S1

Summary | Amplifications | Deletions

JMJD2C (chr9:6747653-7165648)

| Cancer Subset | In Peak? | Nearest Peak | #Genes in Peak | Q-value | Frequency of Amplification | | |
|---|---|---|---|---|---|---|---|
| | | | | | Overall | Focal | High-level |
| all_cancers | No | chr9:137916695-140207187 | 76 | 1.0 | 0.115 | 0.0287 | 0.0105 |
| Lung SC | Yes | chr9:235706-8362053 | 41 | 1.0 | 0.4 | 0.1 | 0.05 |
| Breast | Yes | chr9:235706-18592403 | 56 | 1.0 | 0.1564 | 0.0453 | 0.0453 |
| all_lung | Yes | chr9:235706-8548331 | 41 | 1.0 | 0.1344 | 0.0478 | 0.0065 |
| Esophageal squamous | No | No peak on chromosome | 0 | 1.0 | 0.2045 | 0.0227 | 0.0 |
| Myeloproliferative disorder | No | No peak on chromosome | 0 | 1.0 | 0.0558 | 0.0 | 0.0 |
| Ovarian | No | No peak on chromosome | 0 | 1.0 | 0.1942 | 0.068 | 0.0194 |
| all_neural | No | No peak on chromosome | 0 | 1.0 | 0.1198 | 0.0046 | 0.0046 |
| Acute lymphoblastic leukemia | No | chr9:36988416-36998984 | 0 | 1.0 | 0.0307 | 0.0 | 0.0 |
| Colorectal | No | chr9:135358506-140207187 | 101 | 1.0 | 0.1925 | 0.0062 | 0.0124 |
| Glioma | No | No peak on chromosome | 0 | 1.0 | 0.122 | 0.0 | 0.0 |
| Hepatocellular | No | No peak on chromosome | 0 | 1.0 | 0.0826 | 0.0165 | 0.0 |
| Lung NSC | No | No peak on chromosome | 0 | 1.0 | 0.1201 | 0.045 | 0.0041 |
| Medulloblastoma | No | No peak on chromosome | 0 | 1.0 | 0.1328 | 0.0078 | 0.0078 |
| Melanoma | No | chr9:26573226-29470065 | 11 | 1.0 | 0.0811 | 0.045 | 0.0090 |
| Prostate | No | No peak on chromosome | 0 | 1.0 | 0.1087 | 0.0217 | 0.0 |
| Renal | No | No peak on chromosome | 0 | 1.0 | 0.0238 | 0.0159 | 0.0 |
| all_epithelial | No | chr9:34233377-36127464 | 49 | 1.0 | 0.133 | 0.0388 | 0.0119 |
| all_hematologic | No | chr9:4648449-5698176 | 13 | 1.0 | 0.0515 | 0.0043 | 0.0043 |

# Figure S2

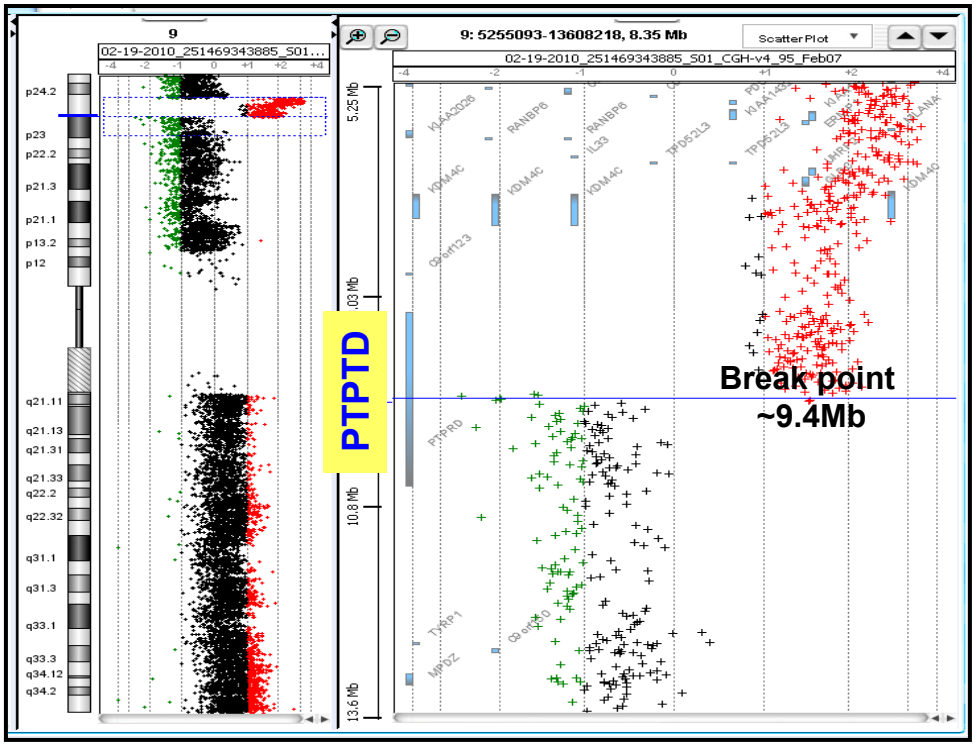
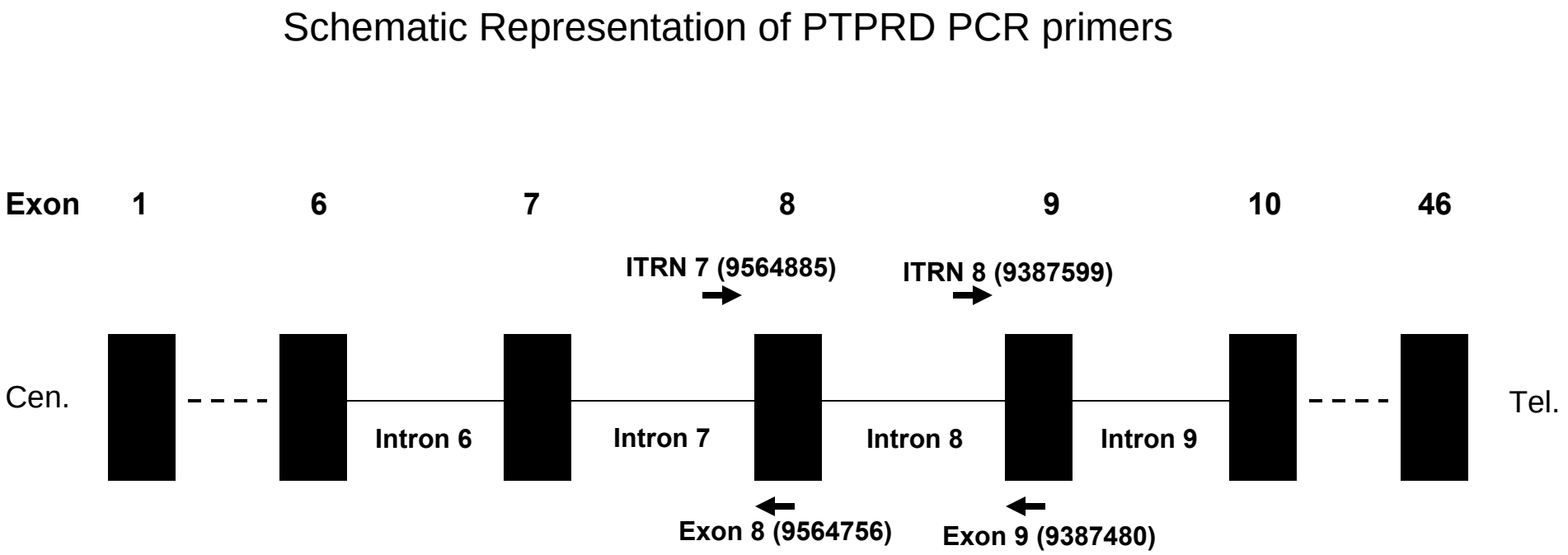
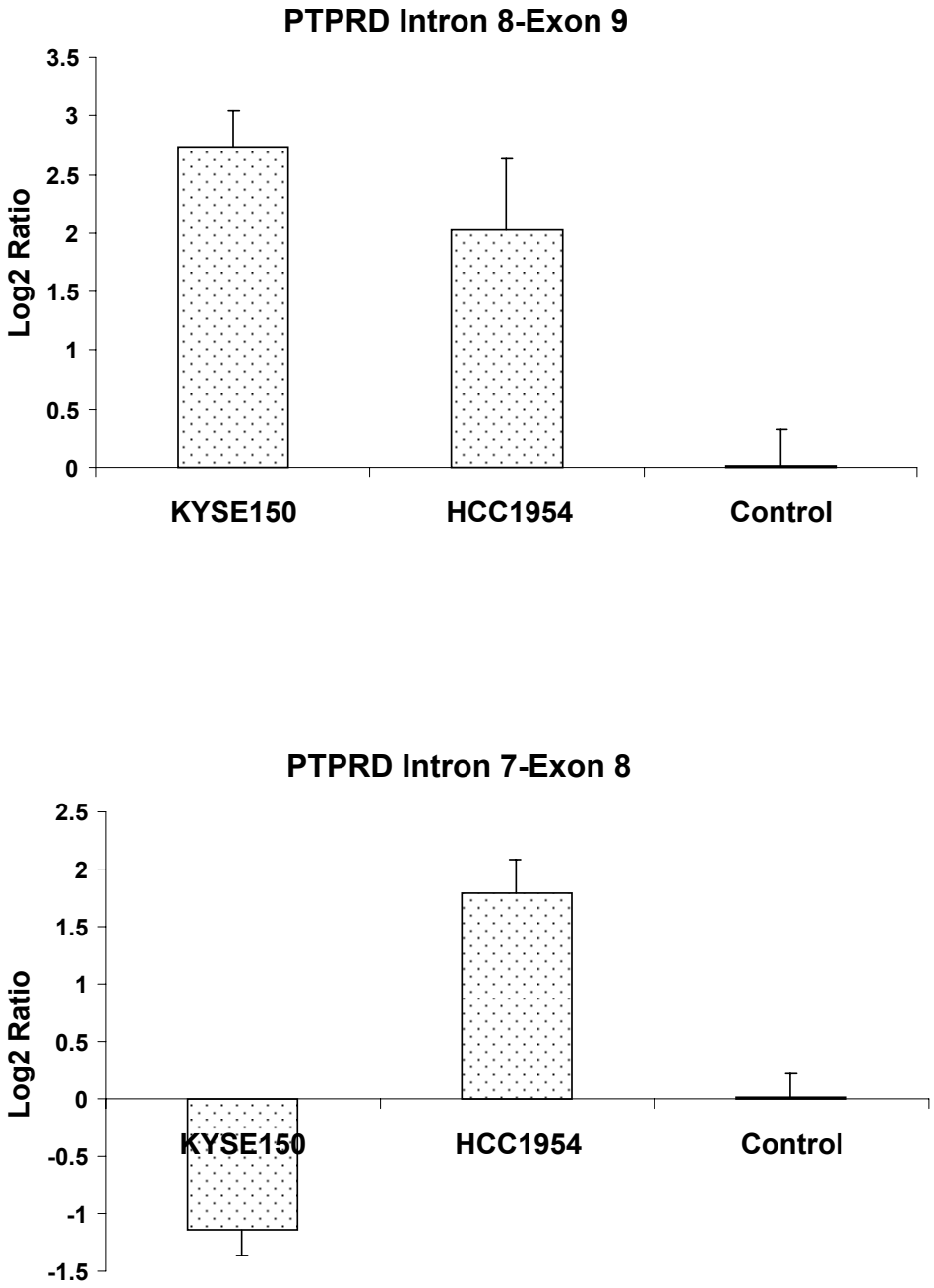

9
02-19-2010_251469343885_S01...
9: 5255093-13608218, 8.35 Mb
Scatter Plot
02-19-2010_251469343885_S01_CGH-v4_95_Feb07
p24.2
p23
p22.2
p21.3
p21.1
p13.2
p12
q21.11
q21.13
q21.31
q21.33
q22.2
q22.32
q31.1
q31.3
q33.1
q33.3
q34.12
q34.2
5.25 Mb
10.8 Mb
13.6 Mb
PTPTD
Break point
~9.4Mb

**Figure S3**


Schematic Representation of PTPRD PCR primers
Exon
1
6
7
8
9
10
46
ITRN 7 (9564885)
ITRN 8 (9387599)
Cen.
Tel.
Intron 6
Intron 7
Intron 8
Intron 9
Exon 8 (9564756)
Exon 9 (9387480)

# Figure S4


PTPRD Intron 8-Exon 9
Log2 Ratio
3.5
3
2.5
2
1.5
1
0.5
0
KYSE150
HCC1954
Control
PTPRD Intron 7-Exon 8
Log2 Ratio
2.5
2
1.5
1
0.5
0
-0.5
-1
-1.5
KYSE150
HCC1954
Control

# Figure S5

Supplementary Information for Genome Remodeling in a Basal-like Breast Cancer Metastasis and Xenograft (Ding et al. 2010)

**Supplementary Table 5.** Summary of regions with significant copy number alterations in primary tumor.

| Chromosome | Start position | End position | Size | Number of markers | HMM state | Copy Number | LLR score |
|---|---|---|---|---|---|---|---|
| 9 | 200000 | 8280000 | 8080000 | 809 | 3 | 2.83 | 42.04 |
| 9 | 17560000 | 20390000 | 2830000 | 284 | 3 | 2.8 | 12.37 |
| 9 | 139030000 | 140130000 | 1100000 | 111 | 3 | 3.1 | 12.88 |

**Supplementary Table 6.** Summary of regions with significant copy number alterations in brain metastasis.

| Chromosome | Start position | End position | Size | Number of markers | HMM state | Copy Number | LLR score |
|---|---|---|---|---|---|---|---|
| 9 | 200000 | 8880000 | 8680000 | 869 | 3 | 2.67 | 36.97 |
| 9 | 13350000 | 15370000 | 2020000 | 203 | 3 | 2.73 | 10.38 |
| 9 | 16000000 | 20580000 | 4580000 | 459 | 3 | 2.64 | 16.29 |
| 9 | 139020000 | 140130000 | 1110000 | 112 | 3 | 3.44 | 21.78 |

**Supplementary Table 7.** Summary of regions with significant copy number alterations in xenograft.

| Chromosome | Start position | End position | Size | Number of markers | HMM state | Copy Number | LLR score |
|---|---|---|---|---|---|---|---|
| 9 | 200000 | 7780000 | 7580000 | 759 | 3 | 2.84 | 48.75 |
| 9 | 12990000 | 19670000 | 6680000 | 669 | 3 | 2.74 | 30.2 |
| 9 | 138340000 | 140130000 | 1790000 | 180 | 3 | 4.9 | 80.77 |

**Figure S6**

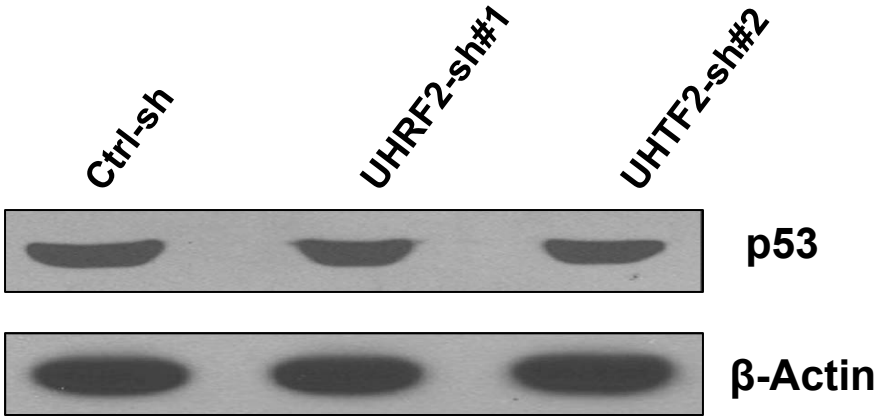


**Figure S7**