A

Freeze List		
Sample (n)		467
Age at dx (years)		46.8 (range 15-89)
Year of collection		2009 (range 1993-2012)
Gender	Male	125 (27%)
	Female	342 (73%)
Race	White	299
	Black	19
	Asian	49
	American indian or alaska native	1
	Not Available	99
Ethnicity	Hispanic or latino	37
	Not hispanic or latino	322
	Not Available	108
Prior Tumor	Yes	26
	No	441
Laterality	Right lobe	196
	Left lobe	166
	Bilateral	82
	Isthmus	18
	NA	5
Tumor Size (cm)		2.92
Staging (TNM)	T1 : (t1(38) + t1a(20) + t1b(76))	134
	T2	158
	T3	154
	T4 : (t4(8) + t4a (10))	18
	TX	3
Nodes	Node- (N0)	214
	Node- (N1 : (n1(53) + n1a(88) + n1b(66)))	207
	Node unknown (NX)	46
Metastasis	Mets - (M0)	250
	Mets - (M1)	8
	MX	208
	NA	1
Clinical stage	Stage I	268
	Stage II	49
	Stage III	102
	Stage IV : ((IV (2) + Iva (39) + Ivc(5))	46
	NA	2

Table S1A. Clinical and pathology data summary of patients.

B

Data type	Platform	Primary Tumors	Metastatic Tumors	Normal Thyroid
Pathologic	n.a.	496	8	100
Clinical	n.a.	467	8	89
Whole exome DNA seq.	Illumina	402	4	73
Whole genome DNA seq.	Illumina	49*	0	49*
DNA copy number	Agilent	496	8	97
Low pass DNA sequence	Illumina	95	0	13
mRNA sequence	Illumina	482	8	58
miRNA sequence	Illumina	495	8	59
CpG DNA methylation	Illumina Infinium Methylation 450K	496	8	56
Functional proteomics	Reverse phase protein array	368	0	0

*indicates that whole genome DNA sequencing data from 49 tumours, while actually not part of the data freeze, was used to identify and confirm the presence of fusion genes.

Table S2B. Characterization platforms used, sample counts and data produced.

C

Center	SNP6 array analysis	Exomes	lowpass WGS	WGS	mRNA	miRNA	DNA methylation	RPPA	Other
Baylor		Mutation detection							
British Columbia Cancer Agency		Mutation detection				Expression Clustering			
Broad Institute	Genotyping, CNV detection, clustering, significance analysis	Mutation detection, CNV detection, mutation significance analysis	Mutation detection, Rearrangement/ fusion detection	Mutation detection, CNV detection, Rearrangement/fusion detection	Fusion Detection				Significance Analysis
Brown University									Pathyway Analysis
Harvard University			CNV detection, mutation detection						TERT genotyping
Institute for Systems Biology									Significance Analysis
Johns Hopkins							Clustering		
MD Anderson					Fusion Detection			Expression Clustering	
Memorial Sloan Kettering Cancer Center									Pathyway Analysis
University of California San Diego									Pathyway Analysis
University of California Santa Ciara		Mutation detection							
University of California Santa Cruz									Pathway Analysis
University of North Carolina					Fusion Detection, Expression Clustering				

Table S1C. Analyses performed by center.