

Supplemental Table S1. Genetic alterations and methylation patterns in cases with matched samples from tumor Series B

Case no.	Sample analysed	<i>SDHB</i> mutation of 1p#	loss	CIMP type	<i>DCR2</i> (% met)		<i>CDH1</i> (%)		NORE1A (%)		<i>P16</i> (%)		<i>RARB</i> (%)		<i>RASSF1A</i> (%)	
					MetI	range	MetI	range	MetI	range	MetI	range	MetI	range	MetI	range
BS-10	Blood	<i>SDHB</i>	-	-	3	2 - 4	5	2 - 8	2	1 - 4	1	1 - 2	2	1 - 4	1	1 - 2
BS-10*	Primary	<i>SDHB</i>	Loss	CIMP	62	40 - 75	4	2 - 9	1	0 - 3	36	13 - 59	18	8 - 39	58	6 - 84
BS-24	Blood	<i>SDHB</i>	-	-	2	1 - 4	5	2 - 8	2	1 - 4	1	1 - 2	2	0 - 4	1	0 - 2
BS-24*	Primary	<i>SDHB</i>	Loss	CIMP	49	9 - 73	7	0 - 29	0	0 - 2	65	55 - 70	-	-	57	5 - 72
BS-25	Blood	<i>SDHB</i>	-	-	2	1 - 4	6	2 - 8	2	1 - 6	3	1 - 4	-	-	1	1 - 2
BS-25*	Primary	<i>SDHB</i>	Loss	-	30	16 - 38	4	0 - 12	1	0 - 2	22	11 - 32	1	0 - 4	15	2 - 29
BS-15n	Normal	<i>SDHB</i>	-	-	2	1 - 3	4	2 - 6	3	1 - 9	3	2 - 4	2	1 - 4	18	13 - 23
BS-15a*	Primary	<i>SDHB</i>	Loss	CIMP	62	49 - 73	6	0 - 15	20	0 - 15	62	61 - 55	2	0 - 12	50	5 - 68
BS-15b*	Metastasis	<i>SDHB</i>	Loss	CIMP	40	13 - 58	5	1 - 10	12	2 - 33	58	57 - 60	14	0 - 33	58	5 - 73
BS-2n	Blood	wt	-	-	2	1 - 4	6	2 - 9	3	1 - 10	1	1 - 2	-	-	1	1 - 2
BS-2a*	Primary	wt	Loss	CIMP	67	56 - 81	11	1 - 52	2	0 - 4	52	33 - 60	26	16 - 33	50	5 - 62
BS-2b*	Metastasis	wt	Loss	CIMP	62	39 - 75	25	0 - 53	1	0 - 3	55	54 - 56	30	24 - 36	42	4 - 54

* = Data from Geli *et al.* 2008 and Kiss *et al.* 2008; # = Data from Sandgren *et al.* 2010 wt = wild-type sequence; Primary = Primary tumor