

1 **Table S1: Mean methylation for TK mutant GIST and pSDH wtGIST**

Tumour ID	KIT/PDGF RA mutation status	SDH status	Germline gene mutation	Mean MGMT methylation% CpG 1-8
G0054	KIT	SDHp	NA	3%
G0064	KIT	SDHp	KIT c.1924A>G (p.K642E) homozygous ;c.2466T>A, (p.N822K)	1%
G0072	KIT	SDHp	KIT c.1504_1509 dupGCCTAT p.(Ala502_Tyr503dup)	3%
G0074	KIT	SDHp	KIT c.1701_1728del p.(Asn567_Leu576delinsLysGlu)	4%
G0075	KIT	SDHp	KIT c.1509_1510insGCCTAT p.(Ser501_AlA502insAlaTyr)	7%
G0101	KIT	SDHp	KIT c.1669T>C p.(Trp557Arg)	1%
G0103	KIT	SDHp	KIT p.(Leu576Pro)	3%
G0104	KIT	SDHp	KIT c.1669_1674del p.(Trp557_Lys558del)	4%
G0105	KIT	SDHp	KIT p.(Trp557Arg)	6%
G0106	KIT	SDHp	KIT E11 mutation	3%
G0112	KIT	SDHp	KIT c.1668_1724del p.(Trp557_Thr574del) c.2460T>G p. (Asp820Glu)	1%
G0113	KIT	SDHp	KIT c.1738_1739insTAGACCCAACACAACCTCCTTATGATC p.(Ile571_Asp572insAspProThrGlnLeuProTyrAspLeu)	1%
G0116	KIT	SDHp	KIT c.1679T>A p.(Val560Asp)	3%
G0145	KIT	SDHp	KIT E11 deletion	2%
G0146	KIT	SDHp	KIT c.1668_16679delGTGGAAGGTTGTinsTTCCAC p.(Glu556_Val560_insHisSerThr)	1%
G0264a2	KIT	SDHp	KIT p.(Trp557Gly) SDHA c1A>C, (p.MET1?) (p.MET1?)	2%
G0264b1	KIT	SDHp	KIT p.(Val559Asp)	2%
G0032	NF1	SDHp	NF1 c.7706dupA p.(His2569GlnfsTer6)	3%
G0039	NF1	SDHp	NA	3%
G0041	NF1	SDHp	NA	2%
G0044	NF1	SDHp	NA	3%
G0048b	NF1	SDHp	NA	2%
G0083	NF1	SDHp	NA	5%
G0109	NF1	SDHp	NA	4%
G0060	PDGFRA	SDHp	PDGFRA c.2525A>T p.(Asp842Val)	2%
G0061	PDGFRA	SDHp	PDGFRA c.2526_2537delCATCATGCATGA p.(Asp842_His845del)	6%
G0102	PDGFRA	SDHp	PDGFRA c.1977C>G p.(Asn659Lys)	4%
G0149	PDGFRA	SDHp	PDGFRA p.(Val561Asp)	2%
G0046	Quad.	SDHp	NA	3%
G0048a	Quad.	SDHp	NA	3%
G0052	Quad.	SDHp	NA	4%
G0056	Quad.	SDHp	NA	1%
G0110	Quad.	SDHp	NA	1%
G0138	NA	SDHp	NA	4%
G0139	NA	SDHp	NA	4%

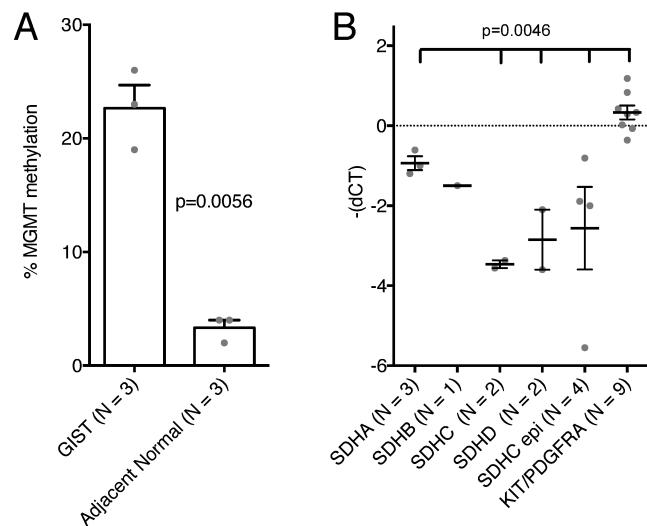
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3 Table S2: Mean methylation in tumour and adjacent tissue

Sample ID	KIT/PDGFR α mutation status	SDH status	Germline gene mutation	Mean MGMT methylation % of tumour CpG 1-8	Mean MGMT methylation % of adjacent normal CpG 1-8
G0002N	-	SDHp	Adjacent normal of SDHd	2%	4%
G0003N	-	SDHp	Adjacent normal of SDHd	23%	4%
G0013N	-	SDHp	Adjacent normal of SDHd	5%	2%
G0017N	-	SDHp	Adjacent normal of SDHd	3%	5%
G0018N	-	SDHp	Adjacent normal of SDHd	2%	3%
G0019N	-	SDHp	Adjacent normal of SDHd	5%	4%
G0024N	-	SDHp	Adjacent normal of SDHd	7%	8%
G0044N	-	SDHp	Adjacent normal of NF1	3%	10%
G0053N	-	SDHp	Adjacent normal of SDHd	4%	1%
G0054N	-	SDHp	Adjacent normal of KIT	3%	1%
G0074N	-	SDHp	Adjacent normal of KIT	4%	4%
G0081N	-	SDHp	Adjacent normal of SDHd	2%	2%
G0082N	-	SDHp	Adjacent normal of SDHd	19%	2%
G0083N	-	SDHp	Adjacent normal of NF1	5%	11%
G0085N	-	SDHp	Adjacent normal of SDHd	3%	4%
G0086N	-	SDHp	Adjacent normal of SDHd	3%	3%
G0101N	-	SDHp	Adjacent normal of KIT	1%	4%
G0138N	-	SDHp	Adjacent normal	4%	6%
G0150N	-	SDHp	Adjacent normal of SDHd	3%	2%
G0151N	-	SDHp	Adjacent normal of SDHd	26%	4%

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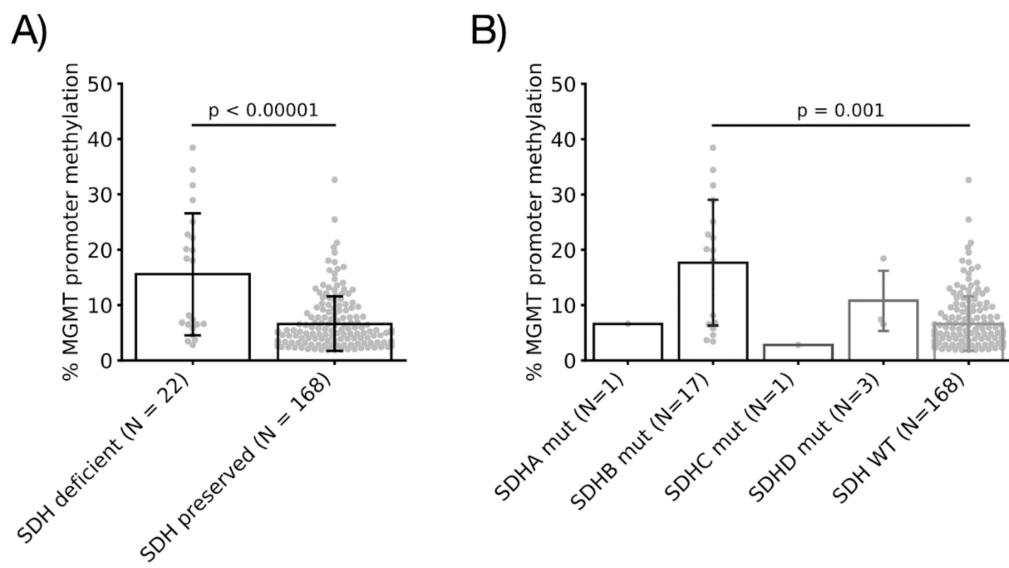
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6 **Figure S1**

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8 A) MGMT promoter methylation in GIST in comparison to adjacent normal tissue where elevated
9 methylation was observed in the tumour ($N = 3$; $p=0.0056$). B) Detailed listing of -dCT values in
10 GIST (q-RT-PCR). Kruskall-Wallis one way ANOVA for MGMT expression (SDHB excluded):
11 $p=0.0046$.

12 **Figure S2** (Related to Figure 2). MGMT promoter methylation for patients WT and mutant
13 for SDH.
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17 A) PPGL patients deficient for SDH show an increased MGMT promoter methylation; p represents
18 student's t-test. B) PPGL patients published by Hadoux et al show no differences between SDH
19 mutant patients. Patients mutant for SDHB show an increase in MGMT promoter methylation
20 compared to SDH WT. ANOVA p < 0.001; p represents multiple
21 test corrected Tukey post-hoc.