

**Taylor et al. Frequent alterations and epigenetic silencing in differentiation pathway genes in structurally rearranged liposarcomas**  
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**Table S1:** Clinical characteristics of sequenced patient tumors.

<b>Case</b>	<b>DLPS1</b>	<b>DLPS2</b>
<b>Data related to patient's primary tumor</b>		
Age at presentation	60	74
Gender	Male	Female
Primary grade	High	Low
Primary depth	Deep depth	Deep depth
Size (largest dimension--primary tumor)	25	9
Histology for primary tumor	Liposarcoma	Liposarcoma
Variant for primary tumor	Dedifferentiated	Well-differentiated
Primary site	Retro-intrabdominal	Retro-intrabdominal
Primary subsite	Retroperitoneum	Retroperitoneum
Diagnosis date	22-Dec-04	19-Jan-07
<b>Data related to patient's first surgery at MSKCC</b>		
Presentation date	21-Jan-05	10-May-07
Presentation status	Primary-only (biopsy)	Local recurrence
First MSK surgery date	27-Jan-05	23-Oct-07
First MSK surgery status	Primary-only	First local recurrence
First surgery at MSK status--MICRO margins	Positive	Positive
First surgery at MSK status--GROSS margins	Negative	Negative
First surgery at MSK status--R0,R1,R2	R1	R1
Local recurrence since presentation	11-Jul-05	4-Dec-08
Time to local recurrence after presentation	6.60	22.51
Metastasis since presentation	-	-
Time to distant recurrence after presentation	-	-
<b>Data related to patient's sample</b>		
Stage of sample	Primary	First local recurrence
Surgery date of sample	27-Jan-05	23-Oct-07
Sample status-- R0,R1,R2	R1	R1
Histology of the sample	Liposarcoma	Liposarcoma
Variant of the sample	Dedifferentiated	Dedifferentiated
Grade of the sample	High	High
Largest dimension size of the sample	25	9
First LR post-sample	11-Jul-05	4-Dec-08
Time to LR from sample date	5.42	13.40
First DR post-sample	None	None
Time to DR from sample date	-	-
<b>General follow-up</b>		
Comorbidities	None reported	None reported
Survival date (FUP)	17-Feb-11	12-Apr-11
Status	AWD	AWD
Overall survival (months from diagnosis)	73.86	50.73
Overall survival (months from presentation)	72.87	47.08
Overall survival (months from sample)	72.67	41.63

\* AWD; alive with disease





DLPS1	Intrachromosomal inverted orientation, mixed-type complex - non-amplified DNA	Somatic	19	13268365-13287080	19	17386375-17386410	36	CACNA1A	NM_00127221	-	CDS	Intron 11	1
DLPS1	Intrachromosomal inverted orientation, mixed-type complex - amplicon-to-amplicon	Somatic	19	13425396-13462482	19	22509503-22510471	52	CACNA1A	NM_00127221	-	CDS	Intron 2	0
DLPS1	Intrachromosomal inverted orientation, mixed-type complex - amplicon-to-amplicon	Somatic	19	13739913-13739575	19	33704373-33705036	5	MIR1	miR-102	+	5' UTR		
DLPS1	Intrachromosomal non-inverted orientation - amplicon-to-amplicon	Somatic	19	13865585-13868643	19	21270703-21272789	10	C1orf87	NM_003423	-	CDS	Intron 3	2
DLPS1	Intrachromosomal inverted orientation, mixed-type complex	Somatic	19	14022261-14022618	19	16241595-16241618	6			-			
DLPS1	Intrachromosomal inverted orientation, mixed-type complex	Somatic	19	16027296-16028875	19	16027811-16029392	6			-			
DLPS1	Intrachromosomal inverted orientation, non-amplified DNA-to-amplicon	Somatic	19	17296001-17287885	19	21528841-21529633	6	DDA1	NM_004050	+	CDS	Intron 3	0
DLPS1	Intrachromosomal inverted orientation, mixed-type complex - non-amplified DNA-to-amplicon	Somatic	19	18573859-18574482	19	18573859-18574482	6	CRF1	NM_004573	-	CDS	Intron 2	0
DLPS1	Intrachromosomal inverted orientation, mixed-type complex - non-amplified DNA-to-amplicon	Somatic	19	19060012-1906287	19	19746813-19747088	38	GNIP	NM_005650	-	CDS	Intron 18	2
DLPS1	Intrachromosomal inverted orientation, mixed-type complex - amplicon-to-amplicon	Somatic	19	19635630-19636606	19	21678352-21692311	39			-			
DLPS1	Intrachromosomal inverted orientation, mixed-type complex - amplicon-to-amplicon	Somatic	19	20012266-20013503	19	20055445-20057028	6			-			
DLPS1	Intrachromosomal inverted orientation, mixed-type complex - amplicon-to-amplicon	Somatic	19	20824092-20824456	19	21768069-21768433	40			-			
DLPS1	Intrachromosomal inverted orientation, mixed-type complex - amplicon-to-amplicon	Somatic	19	21203222-21204065	19	2128511-21227347	30			-			
DLPS1	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	21289302-21291137	19	21837445-21837376	12			-			
DLPS1	Intrachromosomal inverted orientation, mixed-type complex - amplicon-to-non-amplified DNA	Somatic	19	21378161-21379099	19	22710425-22710719	21	ZNF738	Non-coding RNA				
DLPS1	Intrachromosomal inverted orientation, mixed-type complex - amplicon-to-amplicon	Somatic	19	21384444-21385174	19	22551384-22554360	16	ZNF738	Non-coding RNA				
DLPS1	Intrachromosomal inverted orientation, mixed-type complex - amplicon-to-amplicon	Somatic	19	21910981-21911519	19	22434453-22435063	6			-			
DLPS1	Intrachromosomal inverted orientation, mixed-type complex - amplicon-to-amplicon	Somatic	19	22278870-22277875	19	22744729-22744883	6			-			
DLPS1	Intrachromosomal inverted orientation, mixed-type complex - amplicon-to-amplicon	Somatic	19	22442624-22433362	19	15442091-15446381	40			-			
DLPS1	Intrachromosomal inverted orientation, mixed-type complex - amplicon-to-amplicon	Somatic	19	23438034-23439164	19	34041942-34043072	6			-			
DLPS1	Intrachromosomal inverted orientation, mixed-type complex - amplicon-to-amplicon	Somatic	19	33473111-33474505	19	34268483-34269625	6			-			
DLPS1	Intrachromosomal inverted orientation, mixed-type complex - amplicon-to-amplicon	Somatic	19	37661783-37662788	19	38547195-38547195	1	DPY19L3	NM_207325	+	CDS	Intron 12	1
DLPS1	Intrachromosomal non-inverted orientation	Somatic	19	6102381-61023235	19	61043973-61045417	6	NLRP11	NM_145007	+	CDS	Intron 9	1
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	3251283-32517040	19	11551520-11552083	5	LCK	NM_003566	+	CDS	Intron 3	0
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	40071294-40072655	19	40464073-40464464	27			-			
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4100896-41001967	19	28891961-28892022	8	NFYC	NM_014223	+	CDS	Intron 6	0
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4100248-41002862	19	78616210-78616212	28	NFYC	NM_014223	+	CDS	Intron 7	0
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4100773-41009026	19	26892629-2689382	7	NFYC	NM_014223	+	CDS	Intron 8	0
DLPS2	Intrachromosomal inverted orientation, mixed-type complex - amplicon-to-amplicon	Somatic	19	4108334-41083516	19	61782463-61787658	128			-			
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4182298-41825862	19	2114073-2116338	7			-			
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4182244-41824772	19	11577245-11577458	6			-			
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4182521-41825470	19	11564811-11565204	86			-			
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4182533-41825688	19	11565203-11565236	6			-			
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4182599-41825767	19	35152948-35155166	7			-			
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4182771-41824752	19	27112040-27114021	7			-			
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4182883-41828217	19	4574384-45745265	6			-			
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4182734-41826282	19	4017786-42019314	5			-			
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4182673-41826643	19	2711815-27114023	9			-			
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	418274-41827008	19	35138-35184477	6	TESK2	NM_007170	-	CDS	Intron 1	1
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4182478-41826775	19	11391186-113914013	6	SUSD1	NM_002486	-	CDS	Intron 8	1
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4182478-41826775	19	4574384-4574384	6			-			
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4182478-41826775	19	11577222-115774488	18			-			
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4182478-41826775	19	27114103-27116382	10			-			
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4182478-41826775	19	11564808-11565236	81			-			
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4182478-41826775	19	115650431-11565235	60			-			
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4182478-41826775	19	11579974-115772207	8			-			
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4182478-41826775	19	11564808-11565236	15			-			
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4181583-41828281	19	11391009-113911307	22	HVEP3	NM_004503	-	CDS	Intron 3	0
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4181583-41828281	19	3515279-35153223	10	HVEP3	NM_004503	-	CDS	Intron 3	0
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4181583-41828281	19	4203172-42032951	35	HVEP3	NM_004503	-	CDS	Intron 3	0
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4181583-41828281	19	11565282-11565282	5	HVEP3	NM_004503	-	CDS	Intron 3	0
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4204698-42048820	19	4803294-48034881	647	HVEP3	NM_004503	-	CDS	Intron 1	1
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4205961-42059745	19	4205961-42059745	7	HVEP3	NM_004503	-	CDS	Intron 1	1
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4206373-42067387	19	11563720-115638231	19	HVEP3	NM_004503	-	CDS	Intron 1	1
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4206411-42070367	19	11563811-11563817	7	HVEP3	NM_004503	-	CDS	Intron 1	1
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4206428-42069549	19	42021520-42023643	10	HVEP3	NM_004503	-	CDS	Intron 1	1
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4206440-42068153	19	35104448-35142132	17	HVEP3	NM_004503	-	CDS	Intron 1	1
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4206568-42068581	19	27112095-27114082	6	HVEP3	NM_004503	-	CDS	Intron 1	1
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4207085-42069848	19	4574424-45745687	5	HVEP3	NM_004503	-	CDS	Intron 1	1
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4206873-4210078	19	11564810-115652297	17	HVEP3	NM_004503	-	CDS	Intron 1	1
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4206873-4210078	19	11565043-115652349	17	HVEP3	NM_004503	-	CDS	Intron 1	1
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4206873-4210078	19	11565235-11565238	171	HVEP3	NM_004503	-	CDS	Intron 1	1
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4206873-4210078	19	11565239-11565239	10	HVEP3	NM_004503	-	CDS	Intron 1	1
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4206873-4210078	19	11565240-11565261	8	HVEP3	NM_004503	-	CDS	Intron 1	1
DLPS2	Intrachromosomal inverted orientation, mixed-type complex - amplicon-to-amplicon	Somatic	19	4298488-42982676	19	14299260-14299978	12	LEPRE1	NM_022356	-	CDS	Intron 5	0
DLPS2	Intrachromosomal non-reciprocal orientation - non-amplified DNA-to-amplicon	Somatic	19	4301033-43019569	19	11564903-11564903	5			-			
DLPS2	Intrachromosomal non-reciprocal orientation - non-amplified DNA-to-amplicon	Somatic	19	4302217-43033960	19	4574384-45745474	6	CCDC23	NM_199442	-	CDS	Intron 2	0
DLPS2	Intrachromosomal non-reciprocal orientation - non-amplified DNA-to-amplicon	Somatic	19	4305392-43096156	19	11564808-11565288	6	CCDC23	NM_199442	-	CDS	Intron 2	0
DLPS2	Intrachromosomal non-reciprocal orientation - non-amplified DNA-to-amplicon	Somatic	19	4548493-45491665	19	11564808-11565288	6	CCDC23	NM_199442	-	CDS	Intron 2	0
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4548411-45491665	19	6780807-67811092	10	TESK2	NM_007170	-	CDS	Intron 3	2
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4548444-45491665	19	35162203-35164441	10	TESK2	NM_007170	-	CDS	Intron 3	2
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4548465-45491665	19	11577003-115771298	29	TESK2	NM_007170	-	CDS	Intron 3	2
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4548491-45491665	19	42021496-42023644	17	TESK2	NM_007170	-	CDS	Intron 3	2
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4548497-45491665	19	11564808-11565242	329	TESK2	NM_007170	-	CDS	Intron 3	2
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4548503-45491665	19	11565043-11565241	28	TESK2	NM_007170	-	CDS	Intron 3	2
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4548497-45491665	19	2711438-27116310	45	TESK2	NM_007170	-	CDS	Intron 3	2
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4548497-45491665	19	2711279-27116310	47	TESK2	NM_007170	-	CDS	Intron 3	2
DLPS2	Intrachromosomal non-reciprocal orientation - amplicon-to-amplicon	Somatic	19	4548497-45491665	19	11561228-11561289	5						



DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3493456-3493678	12	67387344-6738924	266	TTC23L	NM_144725	+	CDS	Intron 10	0		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3510396-3510520	9	61560901-6156308	93	PRLR	NM_000949	+	CDS	Intron 2	0		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3511861-3512007	6	61560901-6156308	93	PRLR	NM_000949	+	CDS	Intron 2	0		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3513485-3513549	9	61560901-6156308	93	PRLR	NM_000949	+	CDS	Intron 2	0		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3513493-3513576	8	61560901-6156308	93	PRLR	NM_000949	+	CDS	Intron 2	0		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3515885-3516121	9	61560901-6156308	93	PRLR	NM_000949	+	CDS	Intron 1	-1		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3515885-3516121	9	61560901-6156308	93	PRLR	NM_000949	+	CDS	Intron 1	-1		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3516217-3516431	9	61560901-6156308	93	PRLR	NM_000949	+	CDS	Intron 1	-1		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3516217-3516431	9	61560901-6156308	93	PRLR	NM_000949	+	CDS	Intron 1	-1		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3524175-3524265	5	38974540-3897543	15	PRLR	NM_000949	+	CDS	Intron 1	-1		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3524175-3524265	5	38974540-3897543	15	PRLR	NM_000949	+	CDS	Intron 1	-1		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3527218-3527431	9	3905356-3905700	136	PRLR	NM_000949	+	CDS	Intron 1	-1		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3527218-3527431	9	3905356-3905700	136	PRLR	NM_000949	+	CDS	Intron 1	-1		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3528265-3528553	9	11941442-11941710	21	PRLR	NM_000949	+	CDS	Intron 1	-1		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3531968-3531974	7	61560901-6156308	93	PRLR	NM_000949	+	CDS	Intron 1	-1		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3551842-3551869	12	67564484-6756411	13				CPM	NM_001874	CDS	Intron 3	0
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3555702-35559678	6	4625078-4625164	7				RICTOR	NM_152756	CDS	Intron 3	0
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3559253-3559275	5	3905356-3905700	23				CPM	NM_00114088	CDS	Intron 4	1
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3567962-3568061	12	6756269-6756128	20	SPEZF	NM_024867	+	CDS	Intron 3	2		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3574123-3574269	6	4601204-4601354	48				CLIC5	NM_00114088	CDS	Intron 4	1
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3578539-3580011	12	67778162-6777938	14	SPEZF	NM_024867	+	CDS	Intron 25	0		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3584584-3584589	9	11662924-1166296	25	SPEZF	NM_024867	+	CDS	Intron 30	0		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3600205-3600232	12	67639448-6764193	50	UGT3A1	NM_152404	+	CDS	Intron 4	0		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3600578-3600721	12	85324316-8532659	6	UGT3A1	NM_152404	+	CDS	Intron 2	-1		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3600793-3601037	19	5840204-5840155	107	UGT3A1	NM_152404	+	CDS	Intron 2	-1		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3602091-3602100	13	1932094-1932093	1	UGT3A1	NM_152404	+	CDS	Intron 2	-1		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3602490-3603126	9	11725614-11725748	13								
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3606006-3606097	6	4547016-4547541	11								
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3611920-36111105	19	6696330-6696532	71								
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3617599-3617621	9	11821770-11821792	12								
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3622054-3622261	12	6844289-6845034	44								
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3633438-3633583	12	68573185-6857419	12	LMBRD2	NM_00107827	+	CDS	Intron 4	2		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3644508-3644673	5	3646586-3646739	52								
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3644508-3644673	5	3646586-3646739	52								
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3645378-3645467	6	49750217-4975166	45								
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3645378-3645467	6	49750217-4975166	45								
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3645426-3645525	6	4974359-4974624	19								
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3646034-3646161	6	3646034-3646161	28								
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3646132-3646303	12	6838070-6838932	91								
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3646786-3646979	19	5089728-5089738	8								
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3652364-3652631	19	6696330-6696532	194								
DLPS2	Interhomosomal non-reciprocal - amplification to amplified DNA	Somatic	3657940-3657931	9	1225945-1225934	187								
DLPS2	Interhomosomal non-reciprocal - amplification to amplified DNA	Somatic	3658153-3658159	9	1224978-1224983	47								
DLPS2	Interhomosomal non-reciprocal - amplification to amplified DNA	Somatic	3658773-3658840	12	12285564-12285622	25								
DLPS2	Interhomosomal non-reciprocal - amplification to amplified DNA	Somatic	3663478-3663478	5	3663478-3663478	159								
DLPS2	Interhomosomal non-reciprocal - amplification to amplified DNA	Somatic	3663703-3663704	6	4214692-4214815	26								
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3663987-3664213	12	6929721-6929827	16								
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3667162-3667250	6	4899972-4897075	46	SLC1A3	NM_004172	+	CDS	Intron 3	1		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3668037-3668058	6	6737411-6737426	16	SLC1A3	NM_004172	+	CDS	Intron 3	1		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3668569-3668818	7	11848893-11848804	214	SLC1A3	NM_004172	+	CDS	Intron 3	1		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3669225-3669874	12	6831811-6831876	13								
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3672366-3672365	6	4498911-4498156	29								
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3676142-3676369	9	11574501-11574584	481								
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3691195-3691660	6	4203361-4203332	5	NFBL	NM_133433	+	CDS	Intron 1	-1		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3691195-3691660	6	4203361-4203332	5	NFBL	NM_133433	+	CDS	Intron 1	-1		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3691922-3691804	12	6073763-6073708	74	NFBL	NM_133433	+	CDS	Intron 1	-1		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3705920-3710363	12	6381723-6381863	32	NFBL	NM_133433	+	CDS	Intron 2	-1		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3724107-3724306	6	4983784-4984169	11	CSY42	NM_023073	+	CDS	Intron 18	1		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3728913-3729159	9	4444241-4444256	65								
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3744063-3744715	15	2143687-2143714	32	NUP155	NM_153485	+	CDS	Intron 22	0		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3737132-3737947	6	11393100-11393100	460	NUP155	NM_153485	+	CDS	Intron 10	1		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3738169-3738346	9	7805969-7807224	41	NUP155	NM_153485	+	CDS	Intron 9	2		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3748491-3749161	6	4961191-4961067	472	NUP155	NM_153485	+	CDS	Intron 2	-1		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3754406-3746201	14	10238428-10238478	334	WRD70	NM_180304	+	CDS	Intron 8	2		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3774558-3776218	14	10215762-10215426	18	WRD70	NM_180304	+	CDS	Intron 17	1		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3781893-3781893	6	6774485-6774580	19								
DLPS2	Interhomosomal non-reciprocal - amplification to amplified DNA	Somatic	3828327-3824063	5	4596159-4596216	799								
DLPS2	Interhomosomal non-reciprocal - amplification to amplified DNA	Somatic	3828748-3828969	6	4596159-4596216	675								
DLPS2	Interhomosomal non-reciprocal - amplification to amplified DNA	Somatic	3833450-3833710	19	4080260-4081138	675	EGFLAM	NM_152403	+	CDS	Intron 1	0		
DLPS2	Interhomosomal non-reciprocal - amplification to amplified DNA	Somatic	3835696-3836678	9	11379314-11379398	15	EGFLAM	NM_152403	+	CDS	Intron 1	0		
DLPS2	Interhomosomal non-reciprocal - amplification to amplified DNA	Somatic	3837504-3837518	38	3837504-3837518	38	EGFLAM	NM_152403	+	CDS	Intron 1	0		
DLPS2	Interhomosomal non-reciprocal - amplification to amplified DNA	Somatic	3841872-3841785	6	4572936-4573127	169	EGFLAM	NM_152403	+	CDS	Intron 6	2		
DLPS2	Interhomosomal non-reciprocal - amplified DNA to amplification	Somatic	3841892-3841775	12	6779452-6771876	158	EGFLAM	NM_152403	+	CDS	Intron 6	2		
DLPS2	Interhomosomal non-reciprocal - amplified DNA to amplification	Somatic	3842038-3842611	12	4137370-4136833	5	RICTOR	NM_152756	+	CDS	Intron 17	1		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3897529-3897611	6	3897529-3897611	6	RICTOR	NM_152756	+	CDS	Exon 38 Unknown	Unknown		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3909418-3909435	5	3909418-3909435	126	RICTOR	NM_152756	+	CDS	Exon 38 Unknown	Unknown		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3914001-3914521	12	3914001-3914521	51	RICTOR	NM_152756	+	CDS	Intron 2	1		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3914558-3914527	5	4075811-4074741	234	FYB	NM_199335	+	CDS	Intron 15	1		
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3925773-3925294	9	12251850-12251284	204								
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3925226-3925238	6	4837404-4837463	60								
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3925232-3925424	12	6751797-6752013	12								
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3925232-3925267	6	6862079-6862077	1								
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3964915-3964997	12	6759890-6759942	39								
DLPS2	Interhomosomal non-reciprocal - amplification to amplification	Somatic	3964972-3965182	9	11553631-11553786	206								
DLPS2	Interhomosomal non-reciprocal - amplification to amplified DNA	Somatic	3965246-3965603	14	7717981-7717873</									



**Table S3:** Expressed gene fusions.

Sample	5' Gene	Chromosome	Strand	3' Gene	Chromosome	Strand	No. of RNA reads spanning fusion junction	No. of atypical DNA mate pairs breakpoint	Frame	Validated?
DLPS2	<i>RCOR1</i>	14	+	<i>WDR70</i>	5	+	15	18	Out-of-frame	Yes
DLPS2	<i>CNOT2</i>	12	+	<i>ASTN2</i>	9	-	7	193	Out-of-frame	Yes
DLPS2	<i>FGGY</i>	1	+	<i>RTN1</i>	14	-	5	17	Out-of-frame	No
DLPS1	<i>CTDSP2</i>	12	-	<i>FAM19A2</i>	12	-	4	33	Out-of-frame	Yes
DLPS1	<i>NR6A1</i>	9	-	<i>TRHDE</i>	12	+	4	40	In-frame	Yes
DLPS2	<i>NUP107</i>	12	+	<i>PAPPA</i>	9	+	4	49	Out-of-frame	Yes
DLPS2	<i>BAZ2A</i>	12	-	<i>PTPRR</i>	12	-	3	305	Disrupted transcript	No

**Table S4:** Somatic mutations in liposarcoma.

Gene	Nucleotide	Protein	Sample <sup>[a]</sup>	Source <sup>[b]</sup>	Type	Copy Number <sup>[c]</sup>	Promoter status <sup>[d]</sup>	Predicted functional impact <sup>[e]</sup>
HDAC1	c.G1387T	p.E463*	DLPS2	Discoverv	Nonsense	2.01	Increased (10 <sup>12</sup> )	---
	c.G406A	p.A136T	DD442	Prevalence	Missense	---	---	Medium (1.64)
	c.T451C	p.C151R	DD344	Prevalence	Missense	---	---	High (3.41)
	c.T458C	p.V153A	DD5590p0	Prevalence	Missense	---	---	Medium (1.9)
	c.A608G	p.E203G	DD611	Prevalence	Missense	---	---	Medium (1.71)
	c.T736C	p.S246P	DD6960-1A	Prevalence	Missense	---	---	Medium (1.45)
	c.G790A	p.D264N	DD914	Prevalence	Missense	---	---	High (2.85)
	c.G1360A	p.E454K	DD391	Prevalence	Missense	---	---	Low (0.49)
	c.A577G	p.M193V	DLPS2	Discoverv	Missense	1.08	None	Low (0.94)
	c.A977C	p.E326A	DD2213	Prevalence	Missense	---	---	Medium (1.30)
MAPKAP1	c.A311G	p.K104R	DD846	Prevalence	Missense	---	---	Low (0.77)
	c.A265G	p.R89G	DD846	Prevalence	Missense	---	---	Low (0.71)
	c.C1045T	p.R349*	DLPS1	Discoverv	Nonsense	0.86	None	---
PTPN9	c.A1472G	p.Q491R	RWD8000-2	Prevalence	Missense	---	---	Low (0.80)
	c.A1027G	p.R343G	WDD171	Prevalence	Missense	---	---	High (3.38)
DAZAP2	c.G474T	p.M158I	DLPS1	Discoverv	Missense	0.94	None	Low (0.82)
	chr12:49922753A>G	---	ALT9070	Prevalence	Non-coding, 3' UTR	---	---	---
ABCG2	chr12:49922779T>C	---	ALT9070	Prevalence	Non-coding, 3' UTR	---	---	---
	c.1874_1875insT	p.G625fs	DLPS1	Discoverv	Frameshift insertion	1.01	None	---
AHNAK	c.G16487A	p.G5496E	DLPS2	Discoverv	Missense	0.92	None	Neutral (-0.34)
ATF6B	c.A421C	p.T141P	DLPS1	Discoverv	Missense	0.87	None	Low (0.55)
CADM2	c.G248A	p.R83H	DLPS1	Discoverv	Missense	1.06	None	Low (0.14)
CSPG4	c.G3853A	p.G1285S	DLPS1	Discoverv	Missense	0.86	None	High (2.59)
HYDIN	c.C5A	p.T2K	DLPS1	Discoverv	Missense	0.92	None	Low (0.39)
HYOU1 <sup>[f]</sup>	c.G2029A	p.V677I	DLPS1	Discoverv	Missense	0.62	None	Low (0.79)
MAP3K4	chr6:161458265T>C	---	DLPS2	Discoverv	Non-coding, 3' UTR	0.99	None	---
MLK4	c.C2195T	p.S732L	DLPS2	Discoverv	Missense	0.99	None	Medium (1.03)
MLK4	c.G2196T	p.S732S	DLPS2	Discoverv	Silent	0.99	None	Neutral (-0.01)
PDE4DIP	c.C424A	p.L142I	DLPS2	Discoverv	Missense	0.98	None	Medium (1.24)
PTCHD1	c.C1254A	p.L418L	DLPS2	Discoverv	Silent	---	None	Neutral (-0.01)
RAB11FIP2	chr10:119754620A>G	---	DLPS2	Discoverv	Non-coding, 3' UTR	1.01	None	---
SACS <sup>[g]</sup>	c.G973A	p.G325R	DLPS2	Discoverv	Missense	0.89	None	Medium (1.22)
TBX4	c.C1214G	p.S405C	DLPS2	Discoverv	Missense	1.04	Increased (10 <sup>4</sup> )	Medium (1.36)
TBX11	c.C405T	p.A135A	DLPS2	Discoverv	Silent, splice-site	---	None	Neutral (-0.18)
XIRP2	c.A8674T	p.S2892C	DLPS2	Discoverv	Missense	0.96	None	Low (0.00)

[a] DD5590p0, DD6960-1A, RWD8000-2, and ALT9070 are cell lines established at MSK from consenting DLPS patients and tested somatic from available matched normals, as with mutations in the primary tumors.

[b] Discoverv includes mutations from either exome or transcriptome sequence data validated with orthogonal 454 sequencing.

[c] Inferred from segmentation of matched whole-genome sequence

[d] The status of differential methylation; in parentheses, the statistical significance (multiple hypothesis corrected q-value).

[e] The prediction of functional impact available for coding point mutations only (FI score in parentheses; <http://mutationassessor.org/>)

[f] Loss of heterozygosity (LOH)

**Table S5:** Allele-specific expression in liposarcoma transcriptomes.

Sample	Chromosome	Position	SNP	Alleles	Gene	Reads (normal)	Reads (tumor) <sup>a</sup>	Zygoty	Context	Protein	Type	Q-value	Copy number <sup>b</sup>	Promoter methylation
DLPS2	chr7	5533638	rs7612	C/T	ACTB	11/23	0/26	Hom	3' UTR	--	--	0.202	1.11	None
DLPS2	chr1	980669	rs2799073	G/A	AGRN	5/6	15/0	Hom	3' UTR	--	--	0.243	1.31	None
DLPS2	chrX	152427617	rs11538656	C/A	BGN	13/19	20/1	Hom	3' UTR	--	--	0.023	--	None
DLPS2	chr19	533927	rs8259	T/A	BSG	17/8	26/0	Hom	3' UTR	--	--	0.222	1.64	None
DLPS2	chr19	6628989	rs17030	G/A	C3	21/22	3/34	Hom	Exonic	p.P1632P	Silent	0.026	1.32	None
DLPS2	chr5	41017932	rs16870568	T/C	C7	21/9	1/14	Hom	3' UTR	--	--	0.027	4.85	None
DLPS1	chr19	38565275	rs2772	T/G	CEBPG	11/8	2/19	Hom	3' UTR	--	--	0.241	3.92	None
DLPS2	chr5	39407907	rs1046033	A/G	DAB2	20/12	7/38	Het	3' UTR	--	--	0.023	14.05	None
DLPS2	chr5	39409010	rs4578	C/T	DAB2	16/8	7/30	Het	3' UTR	--	--	0.065	14.05	None
DLPS2	chr10	5848092	rs1129614	G/A	GDI2	18/12	21/0	Hom	Exonic	p.T407T	Silent	0.108	1.07	None
DLPS1	chr12	56295639	rs2277323	G/A	GEFT	8/8	1/30	Hom	Exonic	p.L411L	Silent	0.064	13.59	None
DLPS2	chr20	56912202	rs7121	C/T	GNAS	14/14	0/18	Hom	Exonic	p.I131I	Silent	0.053	1.06	None
DLPS1	chr12	63394427	rs1061743	G/C	GNS	13/11	1/27	Hom	3' UTR	--	--	0.026	2.72	None
DLPS2	chr6	31430890	rs1051488	C/T	HLA-B	13/31	0/35	Hom	Exonic	p.T329T	Silent	0.065	1.05	None
DLPS2	chr6	31432495	rs1131215	C/A	HLA-B	21/10	0/23	Hom	Exonic	p.Y98Y	Silent	1.82E-04	1.05	None
DLPS2	chr6	31430282	rs2308655	C/G	HLA-B	13/17	0/27	Hom	Exonic/splicing	p.C349S	Missense	0.026	1.05	None
DLPS2	chr6	31345765	rs41556617	A/T	HLA-C	24/9	3/16	Hom	Exonic	p.X324X	Silent	0.036	1.05	None
DLPS2	chr6	31345781	rs17413387	A/G	HLA-C	23/13	1/29	Hom	Exonic	p.L319P	Missense	1.82E-04	1.05	None
DLPS2	chr6	31345812	rs1050180	T/C	HLA-C	9/13	0/20	Hom	Exonic	p.W309G	Missense	0.207	1.05	None
DLPS2	chr6	32654648	rs1064708	C/T	HLA-DRB1	13/14	1/30	Hom	3' UTR	--	--	0.029	1.08	None
DLPS2	chr6	32595380	rs1136795	C/A	HLA-DRB5	11/6	0/10	Hom	Exonic	p.A133S	Missense	0.161	1.08	None
DLPS2	chr12	67524002	rs7970778	T/C	MDM2	19/4	8/32	Het	3' UTR	--	--	0.003	22.13	None
DLPS1	chr12	56449006	rs703842	A/G	METTL1	7/8	1/32	Hom	3' UTR	--	--	0.106	11.84	None
DLPS1	chr14	21037756	rs1139130	A/G	METTL3	3/21	14/7	Het	Exonic	p.N445N	Silent	0.060	1.23	None
DLPS2	chr1	61700464	rs2499543	G/A	NFIA	4/11	21/1	Hom	3' UTR	--	--	0.015	6.01	None
DLPS1	chr12	56398456	rs799265	A/G	OS9	17/16	43/0	Hom	Exonic	p.E465E	Silent	1.82E-04	11.84	None
DLPS2	chr4	152811641	rs4571	T/C	PET112L	6/10	15/0	Hom	3' UTR	--	--	0.060	1.00	None
DLPS2	chr11	118033676	rs7389	T/G	PHLDB1	12/15	23/2	Hom	3' UTR	--	--	0.064	1.06	None
DLPS2	chr2	170201349	rs1050354	T/A	PIIG	7/7	0/16	Hom	Exonic	p.D445E	Missense	0.222	1.00	None
DLPS1	chr19	5156718	rs1129626	C/T	PTPRS	7/27	12/6	Het	3' UTR	--	--	0.243	0.82	None
DLPS2	chr3	23936766	rs1133926	A/G	RPL15	16/9	31/0	Hom	3' UTR	--	--	0.062	1.09	None
DLPS1	chr21	43659235	rs62932362	G/A	SIK1	23/11	3/21	Hom	3' UTR	--	--	0.023	2.67	None
DLPS1	chr21	43659253	rs3366	G/A	SIK1	29/11	6/22	Het	3' UTR	--	--	0.026	2.67	None
DLPS2	chr5	36723613	rs2269272	C/T	SLC1A3	17/12	33/2	Hom	3' UTR	--	--	0.122	16.23	None
DLPS2	chrX	47329607	rs1043428	C/T	TIMP1	25/16	35/3	Hom	Exonic	p.P87P	Silent	0.202	--	None
DLPS2	chrX	12903207	rs41311479	C/T	TMSB4X	27/9	6/19	Het	Splicing	--	Splice-site	0.053	--	None
DLPS2	chr17	20844368	rs1044420	T/C	USP22	8/8	0/18	Hom	3' UTR	--	--	0.120	1.06	None
DLPS1	chr19	21480335	rs73017722	C/T	ZNF429	6/10	16/1	Hom	5' UTR	--	--	0.125	2.79	None

<sup>a</sup> Actual read counts in tumor underestimated in the presence of genomic amplification due to de-duplication during mutation detection

<sup>b</sup> Ratio of tumor to normal, inferred from segmentation of whole genome sequencing data

**Table S6:** Adenosine-to-inosine RNA editing events.

Gene	Edit	Context	Type	Sample(s)	Coverage in RNA sequencing	Reads from exome calling reference allele	Reads from exome calling alternative allele
<i>KHDRBS1</i>	chr1:32269716A>G	Exonic	Missense	N1	10	17	0
<i>CYR61</i>	chr1:85821301A>G	Exonic	Synonymous	N1,DLPS1,N2,DLPS2	22,17,17,6	61,73,43,63	0,2,0,0
<i>IFI16</i>	chr1:157251342A>G	Exonic	Missense	N1,N2	11,12	35,23	0,0
<i>PRDX6</i>	chr1:171722133A>G	Exonic	Synonymous	N1,N2,DLPS2	22,19,7	48,17,31	0,0,0
<i>EDARADD</i>	chr1:234713081A>G	3' UTR	--	N1	7	27	0
<i>EDARADD</i>	chr1:234713553A>G	3' UTR	--	N1	6	64	1
<i>FAHD2B</i>	chr2:97119785A>G	Exonic	Synonymous	N1,DLPS2	14,6	24,20	0,0
<i>XRCC5</i>	chr2:216721170A>G	Exonic	Synonymous	N1,DLPS1	15,13	20,32	0,0
<i>HDLBP</i>	chr2:241817707A>G	Exonic	Synonymous	N1	6	41	0
<i>LMCD1</i>	chr3:8553874A>G	Exonic	Synonymous	N1	9	15	0
<i>FLNB</i>	chr3:58116831A>G	Exonic	Missense	N1,DLPS1,N2,DLPS2	21,8,19,7	55,33,42,52	0,0,1,0
<i>LOC401127</i>	chr4:39159008A>G	ncRNA	--	N1	0	68	0
<i>FRG1</i>	chr4:191121250A>G	Exonic	Missense	DLPS2	16	17	0
<i>PARP8</i>	chr5:49999669A>G	Exonic	Synonymous	N1	5	99	0
<i>PFDN6</i>	chr6:33366203A>G	Exonic	Synonymous	N1,N2	12,5	41,28	0,0
<i>LYPLA2P1</i>	chr6:33441922A>G	ncRNA	--	N1,DLPS1,N2	11,7,5	49,27,16	0,0,0
<i>DDX43</i>	chr6:74174489A>G	Exonic	Missense	N1	7	53	0
<i>FAM26F</i>	chr6:116891436A>G	Exonic	Missense	N1,N2,DLPS2	7,7,11	28,29,38	0,0,0
<i>TWIST1</i>	chr7:19123032A>G	Exonic	Synonymous	N1,DLPS1,N2,DLPS2	17,8,10,15	65,48,28,56	2,0,1,0
<i>GARS</i>	chr7:30623275A>G	Exonic	Synonymous	N1	13	53	1
<i>CCT6A</i>	chr7:56091599A>G	Exonic	Synonymous	N1	5	40	0
<i>CHCHD7</i>	chr8:57291597A>G	Exonic	Missense	N2	9	14	0
<i>EDF1</i>	chr9:138876593A>G	Exonic	Synonymous	N2	33	42	0
<i>GRK5</i>	chr10:121197635A>G	Exonic	Missense	N2	7	17	0
<i>PDHX</i>	chr11:34944774A>G	Exonic	Missense	N1	8	20	0
<i>NDUFS3</i>	chr11:47560522A>G	Exonic	Missense	N2	8	36	1
<i>OTUB1</i>	chr11:63521590A>G	Exonic	Missense	N1	5	31	0
<i>RPL6</i>	chr12:111328177A>G	Exonic	Missense	N1	6	62	0
<i>ZNF84</i>	chr12:132144951A>G	Exonic	Missense	N1	9	44	1
<i>IPO5</i>	chr13:97464448A>G	Exonic	Synonymous	N1,N2	6,8	53,25	0,0
<i>RPL36AL</i>	chr14:49155239A>G	3' UTR	--	DLPS1	8	37	0
<i>SYNE2</i>	chr14:63758048A>G	Exonic;splicing	Missense	N1,DLPS1,N2,DLPS2	19,8,12,7	37,28,19,30	0,0,0,0
<i>ZBTB1</i>	chr14:64059472A>G	Exonic	Synonymous	N1	14	57	2
<i>MARK3</i>	chr14:103002522A>G	Exonic	Synonymous	N1	7	14	0
<i>SNX1</i>	chr15:62215643A>G	Exonic	Missense	DLPS2	12	43	1
<i>SNX33</i>	chr15:73729965A>G	Exonic	Synonymous	N1	6	24	0
<i>CLUAP1</i>	chr16:3516456A>G	Exonic	Missense	DLPS2	6	36	0
<i>C16orf62</i>	chr16:19619287A>G	Exonic	Synonymous	DLPS1	16	73	1
<i>CES8</i>	chr16:65600571A>G	3' UTR	--	N1	9	20	0
<i>SUZ12</i>	chr17:27327659A>G	Exonic	Missense	N1	6	22	0
<i>ZNF207</i>	chr17:27720910A>G	3' UTR	--	N1,DLPS1,N2	8,5,7	51,26,43	0,0,0
<i>C17orf71</i>	chr17:54645427A>G	Exonic	Missense	N1,DLPS2	6,5	146,126	0,0
<i>EXOC7</i>	chr17:71591929A>G	Exonic	Missense	N1,DLPS1	14,6	64,80	2,1
<i>RNF213</i>	chr17:75972237A>G	Exonic	Missense	N2	5	54	0
<i>TUBB6</i>	chr18:12300948A>G	Exonic	Missense	N1,N2	22,18	26,18	0,0
<i>DHPS</i>	chr19:12651285A>G	Exonic	Missense	N1	7	46	0
<i>TRIM28</i>	chr19:63753327A>G	Exonic;splicing	Missense	N1,DLPS1,N2,DLPS2	41,13,30,18	45,38,18,32	0,0,0,1
<i>ZNF343</i>	chr20:2411997A>G	Exonic	Missense	N1	7	102	0
<i>SAMHD1</i>	chr20:34981294A>G	Exonic	Missense	N1	5	17	0
<i>MX1</i>	chr21:41739914A>G	Exonic	Missense	DLPS2	9	23	0
<i>EGFL6</i>	chrX:13545986A>G	Exonic	Missense	DLPS1	6	13	0
<i>TTC3L</i>	chrX:74878249A>G	ncRNA	--	N1	7	26	0

**Table S7:** Primers used for mutation and methylation validation.

Experiment	Target	Primer	Sequence
Bisulfite	CEBPA	Ver1_peak_position	ATCTCCCTCACACTT (F:AGTTTGGGGATTTTAAAGT, R:CCTTACCAACCTAAAACCACATC)
Bisulfite	CEBPA	Ver2_upstream	GATAGTGGTTTAGGTTG (F:TGTTATAGGTGAGGGAAGATT, R:ACCCAAATAAATCTCTTCTT)
Bisulfite	miR-193b	S1	GATTTTGGTGAGATGAT (F:CAAGATTTTGGTATTTTGGTGAATGAG, R:CTCCAAAATAAATCCCAATTCA)
Bisulfite	miR-193b	S1	GATGGTGGGGGGAATTA (F:GGGAGTGGTTTGGTGAATGAG, R:TCCCTCCCAACCAATCAGCAATC)
Mutation validation (discovery)	ABC2G	591350_L_6927793_chr4_89232282	AAACAATTGCTGCTGGTCA
Mutation validation (discovery)	ABC2G	591350_R_6927794_chr4_89232606	TGACGGCTGATGAGTAA
Mutation validation (discovery)	AHNK4	602954_L_1613151_chr11_62041767	GATTTTGGGCGCTCAAGT
Mutation validation (discovery)	AHNK4	602954_R_1613152_chr11_62042096	AGCGCAAAAGTAAAGAGGA
Mutation validation (discovery)	ATF6B	728939_L_7637027_chr6_32201780	TGCACTTCCCTCATCTAC
Mutation validation (discovery)	ATF6B	728939_R_7637028_chr6_32202096	AAAGCTTTTGTTCGCTCTT
Mutation validation (discovery)	CADM2	110359_L_6428217_chr3_86015027	TGGCCAAAGAAACATTTATTG
Mutation validation (discovery)	CADM2	110359_R_6428218_chr3_86015365	TTTGTGTATGATGATGCTGCT
Mutation validation (discovery)	CSPG4	732758_L_3171181_chr15_73764830	CTCCAGCTCCCAAGGAC
Mutation validation (discovery)	CSPG4	732758_R_3171182_chr15_73765163	ACAGTGGACCCCTTGAGAC
Mutation validation (discovery)	DAZAP2	161490_L_2122907_chr12_49922297	TCTTACAGGCTCTGCTCT
Mutation validation (discovery)	DAZAP2	161490_R_2122908_chr12_49922639	CACCAAGAGACCCCAAGC
Mutation validation (discovery)	HDAC1	250269_L_212655_chr11_32570795	GTAGTGTGGGGAAGGGGTC
Mutation validation (discovery)	HDAC1	250269_R_212656_chr11_32571013	TTTCTCAGAGTGGGGAC
Mutation validation (discovery)	HYO1N	846524_L_3583829_chr16_69778082	TTTGTAGATGCAAGTAGCA
Mutation validation (discovery)	HYO1N	846524_R_3583830_chr16_69778418	AAATCTCTGATGAAAGAA
Mutation validation (discovery)	HYOU1	846816_L_1849901_chr11_118424532	ACTTGAGACTCTGGTCCGA
Mutation validation (discovery)	HYOU1	846816_R_1849902_chr11_118424865	TGGGAATGAGGAGGGCAG
Mutation validation (discovery)	MAP3K4	330140_L_7978811_chr6_161458124	TACTGTACAGCCATCCGTC
Mutation validation (discovery)	MAP3K4	330140_R_7978812_chr6_161458450	TGCTTGGCTCATAGTGTGTT
Mutation validation (discovery)	MAPKAP1	913725_L_9069125_chr9_127387559	CAGCCCAATGCTGAAAGA
Mutation validation (discovery)	MAPKAP1	913725_R_9069126_chr9_127387893	GGAGAGCAGTGGGGTCTGA
Mutation validation (discovery)	MLK4	297577_L_929221_chr11_231581393	CTTCTGGGAAAGATCTCAGA
Mutation validation (discovery)	MLK4	297577_R_929222_chr11_231581694	CTTCTGGGAAAGATCTCAGA
Mutation validation (discovery)	MLK4	297577_L_929221_chr11_231581393	CTTCTGGGAAAGATCTCAGA
Mutation validation (discovery)	MLK4	297577_R_929222_chr11_231581694	CTTCTGGGAAAGATCTCAGA
Mutation validation (discovery)	PDE4DIP	976531_L_530961_chr11_143727125	GGCAACTCATGGGTCATA
Mutation validation (discovery)	PDE4DIP	976531_R_530962_chr11_143727456	TGATTTCTGCTGAATGTGC
Mutation validation (discovery)	PTCHD1	433314_L_9232803_chrX_23320639	AGCGACATCCATCTCTCT
Mutation validation (discovery)	PTCHD1	433314_R_9232804_chrX_23320991	GTAGTGTCTCTCTCTCTCT
Mutation validation (discovery)	PTPN9	1007867_L_3169683_chr15_73569537	AAAGCTCTTGGGAAGAGC
Mutation validation (discovery)	PTPN9	1007867_R_3169684_chr15_73569785	GCACCCCTTAGCTGTGTC
Mutation validation (discovery)	RAB11FIP2	1012246_L_1331626_chr10_119754814	TCATCATCAGATGAAATATAC
Mutation validation (discovery)	RAB11FIP2	1012246_R_1331626_chr10_119754814	AGATGTGATGTTTCACTATTG
Mutation validation (discovery)	SACS	1035522_L_2438979_chr13_22827703	TTATAGAAATCGCCCTCA
Mutation validation (discovery)	SACS	1035522_R_2438980_chr13_22828016	CAGTTTGACCATTTGTTGG
Mutation validation (discovery)	TBK4	512410_L_4043977_chr17_56915101	CTTCTGATGATGATGATGTT
Mutation validation (discovery)	TBK4	512410_R_4043978_chr17_56915436	TAAAGTGGGCACTTCTGTT
Mutation validation (discovery)	TEX11	1091365_L_9341107_chrX_69989723	CAGACTTGGAAAATAAACCA
Mutation validation (discovery)	TEX11	1091365_R_9341108_chrX_69989980	TTTCTTCAATTTCCCCCA
Mutation validation (discovery)	XIRP2	136877_L_5254452_chr2_167814949	CTTCTGATGATGATGATGTT
Mutation validation (discovery)	XIRP2	136877_R_5254458_chr2_167814949	GGGATTTCTCACAGGAGAAA
Mutations (prevalence)	DAZAP2	96560_L_11839416_chr12_49918476	TGAATCGGTAGGTGGAAA
Mutations (prevalence)	DAZAP2	96560_R_11839417_chr12_49919557	CGCGTATTTGGTATGAGC
Mutations (prevalence)	DAZAP2	96561_L_14129918_chr12_49920905	CGCCAGGTAGCTTACAGCC
Mutations (prevalence)	DAZAP2	96561_R_14129919_chr12_49921023	GCTCAAGAAGCAAACTCA
Mutations (prevalence)	DAZAP2	96562_L_14309830_chr12_49920723	TGAATTTGGTGTGTGAGC
Mutations (prevalence)	DAZAP2	96562_R_14309831_chr12_49922044	GCAGAGCTGCAGACAGTGA
Mutations (prevalence)	DAZAP2	96563_L_14309832_chr12_49922044	CCGATGTTCTGATGATGTT
Mutations (prevalence)	DAZAP2	96563_R_chr12_49922850_notail	GCTCAAGTCCCTCCAAACC
Mutations (prevalence)	HDAC1	151511_L_12860342_chr11_32528886	GATCTCCAGCAGCCTTTTC
Mutations (prevalence)	HDAC1	151511_R_12860343_chr11_32531281	CACCTCCCTCTAGAGACTC
Mutations (prevalence)	HDAC1	151512_L_13052732_chr11_32540456	CCCCAGTACCTTTGGAATGA
Mutations (prevalence)	HDAC1	151512_R_13052733_chr11_32541327	AATGAATGCATATGGGGAA
Mutations (prevalence)	HDAC1	151513_L_chr11_32554749_notail	AGCAGCTAGCTCCATGCTG
Mutations (prevalence)	HDAC1	151513_R_chr11_32555887_notail	TGGGGAATCAGAGCTGTTA
Mutations (prevalence)	HDAC1	151514_L_chr11_32562156_notail	TGGGTGAGGTGGGATCAG
Mutations (prevalence)	HDAC1	151514_R_chr11_32562301_notail	GGACTGAACAGAGGAGCAT
Mutations (prevalence)	HDAC1	151515_L_14504910_chr11_32565612	CTGCTGAAGTAGGTTGGGAG
Mutations (prevalence)	HDAC1	151515_R_14504911_chr11_32565625	CTTCCAGAGACAGGAGCAG
Mutations (prevalence)	HDAC1	151516_L_chr11_32565594_notail	CCAGTCTCCAGCTCTCTGTT
Mutations (prevalence)	HDAC1	151516_R_chr11_32565970_notail	ATTGGGAAAGAGGCAAGAA
Mutations (prevalence)	HDAC1	151517_L_13010543_chr11_32566807	GTTCTGGTACTCTGCTGTT
Mutations (prevalence)	HDAC1	151517_R_13010543_chr11_32567908	ACTGACCAACAGAGATCCA
Mutations (prevalence)	HDAC1	151520_L_12182232_chr11_32568120	TTCAAAGGAGGCTTTGAATG
Mutations (prevalence)	HDAC1	151520_R_12182233_chr11_32569451	TGAGAACCTTACCCAGTCC
Mutations (prevalence)	HDAC1	151521_L_14515800_chr11_32568382	CTTGTGATCAACAGAGAGAC
Mutations (prevalence)	HDAC1	151521_R_14515801_chr11_32569155	ACCATCTTGTGCTACCTG
Mutations (prevalence)	HDAC1	151522_L_1430176_chr11_32568571	TGAAAAGTAGGAGTGGGTTG
Mutations (prevalence)	HDAC1	151522_R_1430177_chr11_32568982	CCCTCAGTCCCTACTGCTG
Mutations (prevalence)	HDAC1	151525_L_12416002_chr11_32569277	CTGGAATGCGGAGTGAAGGG
Mutations (prevalence)	HDAC1	151525_R_12416003_chr11_32570152	GGGCAAAACCAAGTCAAGGA
Mutations (prevalence)	HDAC1	151526_L_13636682_chr11_32569379	CTCACAGTGTCTTGGAGGCA
Mutations (prevalence)	HDAC1	151526_R_13636683_chr11_32570078	CCAGAGACACAGAGGAAAG
Mutations (prevalence)	HDAC1	151528_L_15047560_chr11_32570265	TTTCCCTGGTCTCTCTGG
Mutations (prevalence)	HDAC1	151528_R_15047561_chr11_32571038	GTCCAGGAGTCCAGTGAAG
Mutations (prevalence)	HDAC1	151530_L_chr11_32570895_notail	CTCCAGGCTCTAGGCTAA
Mutations (prevalence)	HDAC1	151530_R_chr11_32571017_notail	GTGCTTCTCCAGAGTGGT
Mutations (prevalence)	HDAC1	151534_L_chr11_32571140_notail	GCTGCACATTTGCCCTGAG
Mutations (prevalence)	HDAC1	151534_R_chr11_32571141_notail	CCAGTGGGAGGATGCAAAA
Mutations (prevalence)	MAPKAP1	554913_L_14789920_chr9_127474281	CTCCAGATGAGGAGTGTG
Mutations (prevalence)	MAPKAP1	554913_R_14789921_chr9_127475688	TGCAAGCCCTTCTCTGAT
Mutations (prevalence)	MAPKAP1	554917_L_chr9_127471817_notail	AACTCCAGAGGATTTAAAGGAT
Mutations (prevalence)	MAPKAP1	554917_R_chr9_127472067_notail	TGTTCTTTTATGGTAACTTCA
Mutations (prevalence)	MAPKAP1	554922_L_chr9_127458686_notail	CCAGACCACTCTGCTGCT
Mutations (prevalence)	MAPKAP1	554922_R_chr9_127460029_notail	CTGCATGCTCCAGCTGAA
Mutations (prevalence)	MAPKAP1	554928_L_1538483_chr9_127387504	CAGAGCTGGATGAGTACAGA
Mutations (prevalence)	MAPKAP1	554928_R_1538483_chr9_127388251	TACTCTGGAGTGTCTTTGG
Mutations (prevalence)	MAPKAP1	554934_L_14664410_chr9_127361554	TAGCTAGTGCAGAGGACAT
Mutations (prevalence)	MAPKAP1	554934_R_14664411_chr9_127362429	TCCTCAATTTGCTGCTGTT
Mutations (prevalence)	MAPKAP1	554940_L_14683910_chr9_127344950	CTTCTCAGATGCCCTGTA
Mutations (prevalence)	MAPKAP1	554940_R_14683911_chr9_127346629	CTCTGGATGATTTGGTCTG
Mutations (prevalence)	MAPKAP1	554946_L_12445782_chr9_127323267	TCTGTCACTAGTCAAGCCAG
Mutations (prevalence)	MAPKAP1	554946_R_12445783_chr9_127324550	GGCTCTAAGTGTGCTCTCA
Mutations (prevalence)	MAPKAP1	554947_L_15378756_chr9_127308205	AGGATCGAGCTCTCTACCA
Mutations (prevalence)	MAPKAP1	554947_R_15378759_chr9_127308880	CGCTTTTCCAGACTTCTCC
Mutations (prevalence)	MAPKAP1	554951_L_chr9_127286482_notail	CCCCATTTCCACCCAGTCT
Mutations (prevalence)	MAPKAP1	554951_R_chr9_127286736_notail	CATTTCGAGCCCTCATGTA
Mutations (prevalence)	MAPKAP1	554955_L_11915202_chr9_127269930	GGCAGCATATGAAAGTCCG
Mutations (prevalence)	MAPKAP1	554955_R_11915203_chr9_127270878	TTGTGTGGCCATTTGGAGT
Mutations (prevalence)	MAPKAP1	554960_L_12983932_chr9_127246336	GGCTGCTGTTGACTGAAGC
Mutations (prevalence)	MAPKAP1	554960_R_12983933_chr9_127247029	ACCAGAGCCCTCAACACAG
Mutations (prevalence)	MAPKAP1	554969_L_14804710_chr9_127241016	GTGACTCAGGCACTGGG
Mutations (prevalence)	MAPKAP1	554969_R_14804711_chr9_127241679	CAGTGTGCTGATGACTGG
Mutations (prevalence)	PTPN9	613219_L_12822996_chr15_73657675	CTGCCAATCTCGGGAAGAG
Mutations (prevalence)	PTPN9	613219_R_12822997_chr15_73659094	CTCCGGCTTAAAGATTTCC
Mutations (prevalence)	PTPN9	613221_L_14281290_chr15_73606201	CTGTACAGGACTCTCTCCG
Mutations (prevalence)	PTPN9	613221_R_14281291_chr15_73607168	CAGACTTGCTGGGAAAGGG
Mutations (prevalence)	PTPN9	613222_L_chr15_73603534_notail	TTTATCCAGAAATCTCTCC
Mutations (prevalence)	PTPN9	613222_R_chr15_73603769_notail	TTTATCCAGAAATCTCTCC
Mutations (prevalence)	PTPN9	613223_L_13891692_chr15_73602326	TAAAGAACGCCCAACTTCA
Mutations (prevalence)	PTPN9	613223_R_13891693_chr15_73603541	CCATTTGCGCAGGAAAGTGA
Mutations (prevalence)	PTPN9	613224_L_12717073_chr15_73597291	TTTATCCAGAAATCTCTCC
Mutations (prevalence)	PTPN9	613224_R_12717073_chr15_73597291	GTGTGCACTGAGGAGTGT
Mutations (prevalence)	PTPN9	613225_L_12173436_chr15_73588310	CTAGAAGCAAGCCAGGAGG
Mutations (prevalence)	PTPN9	613225_R_12173437_chr15_73588863	GGGGAAGAGAGGAGAAACC
Mutations (prevalence)	PTPN9	613226_L_14428974_chr15_73586092	CTAACCAAGTCAAGGAGTGG
Mutations (prevalence)	PTPN9	613226_R_14428975_chr15_73586085	CCCATCTCCAAACTTGA
Mutations (prevalence)	PTPN9	613227_L_14590474_chr15_73569135	ACTCACAAAGGAAATGGAC
Mutations (prevalence)	PTPN9	613227_R_14590475_chr15_73570178	CCATCTCTCCACCCTAAG
Mutations (prevalence)	PTPN9	613228_L_15230628_chr15_73558693	TCTCTGGGAAGTCCACTGCT
Mutations (prevalence)	PTPN9	613228_R_15230629_chr15_73559812	CTGGCCATTTCACTCTCAT
Mutations (prevalence)	PTPN9	613229_L_15302438_chr15_73553072	CAGGCTGACCTCATATT
Mutations (prevalence)	PTPN9	613229_R_15302439_chr15_73553877	AGCAGGAGTGGGAAGATG
Mutations (prevalence)	PTPN9	613230_L_14038140_chr15_73549917	TCTGTGCTGCAATGATGG
Mutations (prevalence)	PTPN9	613230_R_14038141_chr15_73550740	AGATGATGATGCTGCTGGG
Mutations (prevalence)	PTPN9	613231_L_12283452_chr15_73549629	ATTCTGGCATCACTGGCTC
Mutations (prevalence)	PTPN9	613231_R_12283453_chr15_73548894	AGCCAGAGGATGCTAGGGG
Mutations (prevalence)	PTPN9	613236_L_13451902_chr15_73547499	GGACTGAAATCACGCCCTA
Mutations (prevalence)	PTPN9	613236_R_13451903_chr15_73549046	CATTGATTTGCTGGTGGT
Gene fusions	RSO1-WDR70	1F/R	F:AGCCAGTCCAGGAGGGGG, R:CCCTCCCACTGCAAGAAAGCC
Gene fusions	CNOT2-ASTN2	2F/R	F:GGTCACTGCTCAGTTGGGG, R:ACAGGCGCTCCAGGGTCA
Gene fusions	FGFY-RTN1	3F/R	F:TACGACAGAAAGCTGGGAGCA, R:CCTGCTCAGTGGGGGCT
Gene fusions	CTDSP2-FAM19A2	4F/R	F:TCCGGGGGAGAAACAGAGGG, R:TCCGCTCTCTCCCAAGCC
Gene fusions	SNCA1-TRIM8	5F/R	F:TACCTCTCTCTCAGTGTGCT, R:TCCGCTGTCAGAGGTTGCTG
Gene fusions	HUP107-PAPPA	6F/R	F:TCCGGGTAGTGTGAGCACT, R:CAAGCAGCAATGCCAGCT
Gene fusions	BA22A-PTPRB	7F/R	F:ACTCTGCTCAGTCTCC, R:AGACAGGTAAGGCTCAGGAA