Supplementary Table S5. Differential gene expression according to histologic subtype grouping

	logFC	P-Value	FDR
DNAJB5	0.973	0.000	0.001
DNAJC16	-0.903	0.000	0.007
XRCC6BP1	1.115	0.000	0.007
MMS19	-0.410	0.000	0.012
DNAJC10	-0.397	0.001	0.012
DNAJB2	-0.428	0.001	0.012
DNAJC7	-0.538	0.002	0.029
PMS1	0.636	0.002	0.029
DNAJA2	-0.418	0.002	0.032
BRIP1	0.632	0.003	0.037
PMS2	-0.395	0.006	0.060
XRCC2	0.330	0.010	0.088
ERCC3	-0.213	0.010	0.088
PARP3	0.834	0.011	0.089
ATM	-0.337	0.011	0.089
XPC	-0.463	0.012	0.092
NEIL2	-0.405	0.016	0.108
POLD3	0.349	0.017	0.108
DDB2	-0.261	0.019	0.108
DNAJC8	-0.297	0.019	0.108
ERCC1	-0.236	0.019	0.108
MLH3	-0.235	0.024	0.130
DNAJC14	-0.306	0.026	0.133
DNAJB14	-0.320	0.032	0.156
ERCC6	-0.210	0.034	0.162
SMUG1	-0.320	0.040	0.179
RAD23A	0.268	0.041	0.179
PARP1	-0.251	0.045	0.190

FC: fold change; FDR: false discovery rate. A negative fold change means that the gene is overexpressed in non-L-sarcomas.