

Supplementary files

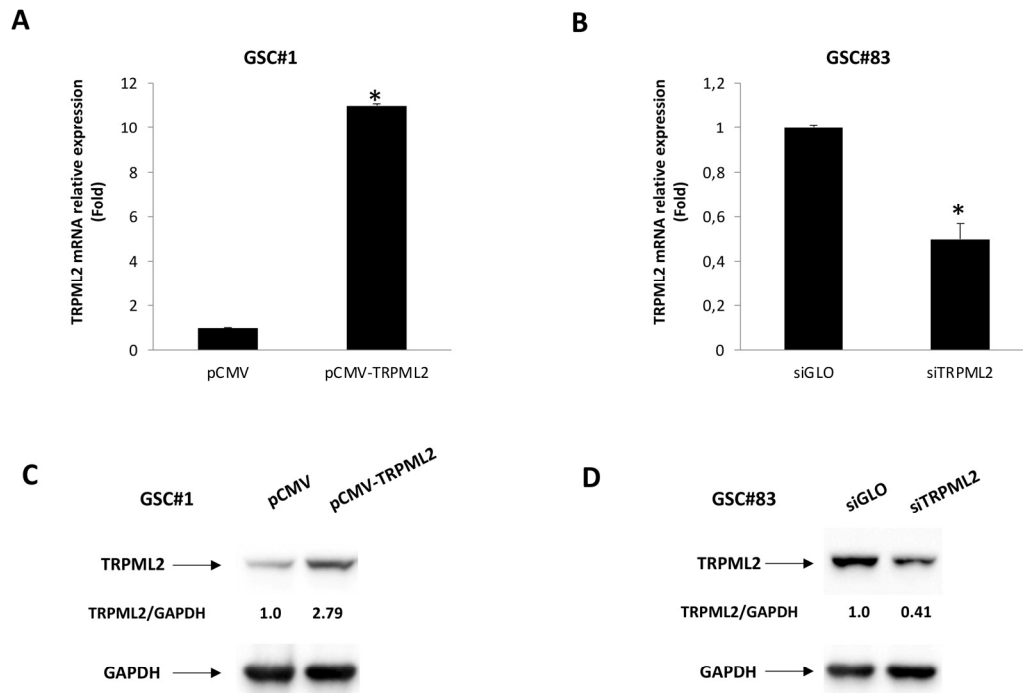


Figure S1. TRPML2 transfection models in GSC#1 and GSC#83 lines. (**A,B**) TRPML2 mRNA levels were evaluated by qRT-PCR after 72 h of pCMV-TRPML2 transfection in GSC#1 (**A**) and siTRPML2 transfection in GSC#83 (**B**). Relative TRPML2 expression, normalized to GAPDH mRNA levels, was calculated using siGLO as calibrator. * $p < 0.05$ vs control cells. (**C,D**) Representative immunoblots reflecting TRPML2 protein levels in pCMV and pCMV-TRPML2 GSC#1 (**C**) and in siGLO and siTRPML2 GSC#83 (**D**) after 72 h of transfection. Densitometry values were normalized to GAPDH, which was used as loading control.

Table S1. The clinico-pathologic characteristics of patients with GBM.

Variables	Patients (n=16)
<i>Age, years</i>	
range	40-77
median	57.5
<i>Sex</i>	
Male	13/16 (81.25%)
Female	3/16 (18.75%)
<i>Tumor localization</i>	
Temporal	3/16 (18.75%)
Parietal	6/16 (37.50%)
Frontal	6/16 (37.50%)
Occipital	1/16 (6.25%)
<i>Tumor dimention</i>	
ND	4/16 (25.00%)
< 3 cm	3/16 (18.75%)
> 3 cm	9/16 (56.25%)
<i>RxTP preop</i>	
No	15/16 (93.75%)
Yes	6.25 (6.25%)
<i>ASP TOT</i>	
No	3/16 (18.75%)
Yes	13/16 (82.25%)
<i>5-ALA</i>	
No	16/16 (100.00%)
Yes	0/16 (0.00%)
<i>KPSS</i>	
20	1/16 (6.25%)
60-70	8/16 (50.00%)
80-90	7/16 (43.75%)
<i>Recidive</i>	
No	15/16 (93.75%)
Yes	1/16 (6.25%)
<i>MGMT promoter status</i>	
Unmethylated	10/16 (62.25%)
Methylated	6/16 (37.75%)
<i>EGFRvIII</i>	
Negative	9/16 (56.25%)
Positive	7/16 (43.75%)
<i>PTEN</i>	
ND	1/16 (6.25%)
Normal	11/16 (68.75%)
Hypophosphorilated	4/16 (25.00%)
<i>Ki67</i>	
≤ 20	10/16 (62.25%)
> 20	6/16 (37.50%)

Table S2. Drug Transporters expression in GSC#1 and GSC#83 lines.

GSC#1			GSC#83		
Target genes	mRNA relative expression	mRNA relative expression	Target genes	mRNA relative expression	mRNA relative expression
ABCA1	0,0000 ± 0,0000	0,0226 ± 0,0060	SLC19A1	0,0065 ± 0,0026	0,0133 ± 0,0038
ABCA12	0,0011 ± 0,0038	0,0045 ± 0,0013	SLC19A2	0,0138 ± 0,0075	0,0185 ± 0,0053
ABCA13	0,0000 ± 0,0000	0,0036 ± 0,0010	SLC19A3	0,0040 ± 0,0018	0,0037 ± 0,0011
ABCA2	0,0184 ± 0,0630	0,0402 ± 0,0014	SLC22A1	0,0000 ± 0,0000	0,0022 ± 0,0006
ABCA3	0,0306 ± 0,1051	0,0382 ± 0,0019	SLC22A2	0,0000 ± 0,0000	0,0000 ± 0,0000
ABCA4	0,0046 ± 0,0159	0,0012 ± 0,0003	SLC22A3	0,0000 ± 0,0000	0,0064 ± 0,0018
ABCA5	0,0122 ± 0,0418	0,0168 ± 0,0048	SLC22A6	0,0000 ± 0,0000	0,0000 ± 0,0000
ABCA9	0,0000 ± 0,0000	0,0077 ± 0,0012	SLC22A7	0,0003 ± 0,0001	0,0000 ± 0,0000
ABCB1	0,0000 ± 0,0000	0,0000 ± 0,0000	SLC22A8	0,0003 ± 0,0002	0,0024 ± 0,0007
ABCB11	0,0000 ± 0,0000	0,0000 ± 0,0000	SLC22A9	0,0000 ± 0,0000	0,0000 ± 0,0000
ABCB4	0,0008 ± 0,0029	0,0027 ± 0,0008	SLC25A13	0,0192 ± 0,0058	0,0449 ± 0,0028
ABCB5	0,0000 ± 0,0000	0,0000 ± 0,0000	SLC28A1	0,0006 ± 0,0002	0,0013 ± 0,0004
ABCB6	0,0320 ± 0,1097	0,0505 ± 0,0044	SLC28A2	0,0011 ± 0,0004	0,0015 ± 0,0004
ABCC1	0,0093 ± 0,0321	0,0310 ± 0,0088	SLC28A3	0,0011 ± 0,0003	0,0016 ± 0,0004
ABCC10	0,0042 ± 0,0146	0,0179 ± 0,0051	SLC29A1	0,0220 ± 0,0055	0,0399 ± 0,0013
ABCC11	0,0010 ± 0,0037	0,0016 ± 0,0005	SLC29A2	0,0127 ± 0,0037	0,0102 ± 0,0029
ABCC12	0,0000 ± 0,0000	0,0000 ± 0,0000	SLC2A1	0,3037 ± 0,0147	0,1110 ± 0,0015
ABCC2	0,0003 ± 0,0002	0,0096 ± 0,0007	SLC2A2	0,0000 ± 0,0000	0,0000 ± 0,0000
ABCC3	0,0077 ± 0,0065	0,0360 ± 0,0012	SLC2A3	0,1508 ± 0,0068	0,0235 ± 0,0067
ABCC4	0,0138 ± 0,0073	0,0241 ± 0,0069	SLC31A1	0,0164 ± 0,0064	0,0714 ± 0,0003
ABCC5	0,0100 ± 0,0045	0,0297 ± 0,0085	SLC38A2	0,0782 ± 0,0080	0,2731 ± 0,0377
ABCD1	0,0096 ± 0,0032	0,0333 ± 0,0095	SLC38A5	0,0019 ± 0,0008	0,0026 ± 0,0007
ABCD3	0,0474 ± 0,0026	0,0679 ± 0,0193	SLC3A1	0,0027 ± 0,0002	0,0031 ± 0,0008
ABCD4	0,0191 ± 0,0055	0,0363 ± 0,0003	SLC3A2	0,1294 ± 0,0133	0,2270 ± 0,0446
ABCF1	0,0224 ± 0,0067	0,0681 ± 0,0194	SLC5A1	0,0010 ± 0,0005	0,0000 ± 0,0000
ABCG2	0,0037 ± 0,0019	0,0059 ± 0,0017	SLC5A4	0,0000 ± 0,0000	0,0018 ± 0,0005
ABCG8	0,0000 ± 0,0000	0,0000 ± 0,0000	SLC7A11	0,0039 ± 0,0005	0,0329 ± 0,0093
AQP1	0,0346 ± 0,0087	0,1644 ± 0,0468	SLC7A5	0,1054 ± 0,0113	0,2235 ± 0,0136
AQP7	0,0000 ± 0,0000	0,0014 ± 0,0004	SLC7A6	0,0080 ± 0,0007	0,0324 ± 0,0092
AQP9	0,0000 ± 0,0000	0,0014 ± 0,0004	SLC7A7	0,0027 ± 0,0003	0,0052 ± 0,0005
ATP6VOC	0,0645 ± 0,0010	0,1268 ± 0,0361	SLC7A8	0,0104 ± 0,0009	0,0066 ± 0,0019
ATP7A	0,0067 ± 0,0031	0,021 ± 0,0060	SLC7A9	0,0000 ± 0,0000	0,0008 ± 0,0002
ATP7B	0,0037 ± 0,0018	0,002 ± 0,0006	SLC01A2	0,0000 ± 0,0000	0,0000 ± 0,0000
MVP	0,0157 ± 0,0038	0,1101 ± 0,0313	SLC01B1	0,0005 ± 0,0002	0,0008 ± 0,0002
SLC10A1	0,0005 ± 0,0018	0,0009 ± 0,0003	SLC01B3	0,0000 ± 0,0000	0,0000 ± 0,0000
SLC10A2	0,0000 ± 0,0000	0,0000 ± 0,0000	SLC02A1	0,0009 ± 0,0001	0,0174 ± 0,0049
SLC15A1	0,0000 ± 0,0000	0,0007 ± 0,0002	SLC02B1	0,0000 ± 0,0000	0,0005 ± 0,0001
SLC15A2	0,0061 ± 0,0009	0,0017 ± 0,0005	SLC03A1	0,0004 ± 0,0001	0,0671 ± 0,0090
SLC16A1	0,0791 ± 0,0010	0,1034 ± 0,0294	SLC04A1	0,0449 ± 0,0039	0,0904 ± 0,0257
SLC16A2	0,0059 ± 0,0003	0,0265 ± 0,0075	VDAC1	0,0445 ± 0,0027	0,1383 ± 0,0393
SLC16A3	0,0124 ± 0,0025	0,0405 ± 0,0015	VDAC2	0,0911 ± 0,0024	0,1433 ± 0,0408

Human Drug Transporters RT profiler PCR array in mRNA samples extracted from GSC#1 and GSC#83. The expression levels were normalized to the average Ct value of ACTB and calculated by the $\Delta\Delta Ct$ method. ABCA1, ATP-binding cassette, sub-family A (ABC1), member 1 (ABCA1); ABC1 member 12 (ABCA12); ABC1 member 13 (ABCA13); ABC1 member 2 (ABCA2); ABC1, member 3 (ABCA3); ABC1 member 4 (ABCA4); ABC1 member 5 (ABCA5); ABC1 member 9 (ABCA9); ATP-binding cassette, sub-family B (MDR/TAP), member 1 (ABCB1); MDR/TAP member 11 (ABCB11); MDR/TAP member 4 (ABCB4); MDR/TAP member 5 (ABCB5); MDR/TAP, member 6 (ABCB6); (CFTR/MRP), member 1 (ABCC1); CFTR/MRP member 10 (ABCC10); CFTR/MRP member 11 (ABCC11); CFTR/MRP member 12 (ABCC12); CFTR/MRP member 2

(ABCC2); CFTR/MRP member 3 (ABCC3); CFTR/MRP member 4 (ABCC4); CFTR/MRP member 5 (ABCC5); ATP-binding cassette, sub-family D (ALD), member 1 (ABCD1); ALD member 3 (ABCD3); ALD member 4 (ABCD4); ATP-binding cassette, sub-family F (GCN20), member 1 (ABCF1); ATP-binding cassette, sub-family G (WHITE), member 2 (ABCG2); WHITE member 8 (ABCG8); Aquaporin 1 (AQP1); Aquaporin 7 (AQP7); Aquaporin 9 (AQP9); ATPase, H⁺ transporting, lysosomal 16kDa, V0 subunit c (ATP6V0C); ATPase, Cu⁺⁺ transporting, alpha polypeptide (ATP7A); ATPase, Cu⁺⁺ transporting, beta polypeptide (ATP7B); Major vault protein (MVP); Solute carrier family 10 (sodium/bile acid cotransporter family), member 1 (SLC10A1); Solute carrier family 10 (sodium/bile acid cotransporter family), member 2 (SLC10A2); Solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1); Solute carrier family 15 (H⁺/peptide transporter), member 2 (SLC15A2); Solute carrier family 16, member 1 (monocarboxylic acid transporter 1) (SLC16A1); Solute carrier family 16, member 2 (monocarboxylic acid transporter 8) (SLC16A2); Solute carrier family 16, member 3 (monocarboxylic acid transporter 4) (SLC16A3); Solute carrier family 19 (folate transporter), member 1 (SLC19A1); Solute carrier family 19 (thiamine transporter), member 2 (SLC19A2); Solute carrier family 19, member 3 (SLC19A3); Solute carrier family 22 (organic cation transporter), member 1 (SLC22A1); Solute carrier family 22 (organic cation transporter), member 2 (SLC22A2); Solute carrier family 22 (extraneuronal monoamine transporter), member 3 (SLC22A3); Solute carrier family 22 (organic anion transporter), member 6 (SLC22A6); Solute carrier family 22 (organic anion transporter), member 7 (SLC22A7); Solute carrier family 22 (organic anion transporter), member 8 (SLC22A8); Solute carrier family 22 (organic anion transporter), member 9 (SLC22A9); Solute carrier family 25, member 13 (citrin) (SLC25A13); Solute carrier family 28 (sodium-coupled nucleoside transporter), member 1 (SLC28A1); Solute carrier family 28 (sodium-coupled nucleoside transporter), member 2 (SLC28A2); Solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3); Solute carrier family 29 (nucleoside transporters), member 1 (SLC29A1); Solute carrier family 29 (nucleoside transporters), member 2 (SLC29A2); Solute carrier family 2 (facilitated glucose transporter), member 1 (SLC2A1); Solute carrier family 2 (facilitated glucose transporter), member 2 (SLC2A2); Solute carrier family 2 (facilitated glucose transporter), member 3 (SLC2A3); Solute carrier family 31 (copper transporters), member 1 (SLC31A1); Solute carrier family 38, member 2 (SLC38A2); Solute carrier family 38, member 5 (SLC38A5); Solute carrier family 3 (cystine, dibasic and neutral amino acid transporters, activator of cystine, dibasic and neutral amino acid transport), member 1 (SLC3A1); Solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 (SLC3A2); Solute carrier family 5 (sodium/glucose cotransporter), member 1 (SLC5A1); Solute carrier family 5 (low affinity glucose cotransporter), member 4 (SLC5A4); Solute carrier family 7 (anionic amino acid transporter light chain, xc⁻ system), member 11 (SLC7A11); Solute carrier family 7 (amino acid transporter light chain, L system), member 5 (SLC7A5); Solute carrier family 7 (amino acid transporter light chain, y⁺L system), member 6 (SLC7A6); Solute carrier family 7 (amino acid transporter light chain, y⁺L system), member 7 (SLC7A7); Solute carrier family 7 (amino acid transporter light chain, L system), member 8 (SLC7A8); Solute carrier family 7 (glycoprotein-associated amino acid transporter light chain, bo⁺ system), member 9 (SLC7A9); Solute carrier organic anion transporter family, member 1A2 (SLCO1A2); Solute carrier organic anion transporter family, member 1B1 (SLCO1B1); Solute carrier organic anion transporter family, member 1B3 (SLCO1B3); Solute carrier organic anion transporter family, member 2A1 (SLCO2A1); Solute carrier organic anion transporter family, member 2B1 (SLCO2B1); Solute carrier organic anion transporter family, member 3A1 (SLCO3A1); Solute carrier organic anion transporter family, member 4A1 (SLCO4A1); Voltage-dependent anion channel 1 (VDAC1); Voltage-dependent anion channel 2 (VDAC2).

Table S3. Drug Transporters expression in pCMV-TRPML2 GSC#1 and siTRPML2 GSC#83 lines.

Target genes	pCMV-TRPML2 GSC#1	siTRPML2 GSC#83
	Fold expression	Fold expression
ABCA1	Induced	2.16 ± 0.41
ABCA12	3.72 ± 0.70	
ABCB1		Induced
ABCB4	Silenced	0.27 ± 0.05
ABCB5		Induced
ABCB11	Silenced	Induced
ABCC2	8.10 ± 1.51	
ABCC3	0.64 ± 0.03	1.61 ± 0.23
ABCC11	Silenced	
ABCD1	0.96 ± 0.17	2.10 ± 0.39
ABCD4	2.20 ± 0.41	
ABCG2	0.95 ± 0.13	1.34 ± 0.12
AQP1	0.85 ± 0.19	1.15 ± 0.12
AQP7		2.16 ± 0.40
AQP9	Induced	
ATP6VOC	0.85 ± 0.21	1.08 ± 0.31
ATP7B	0.91 ± 0.07	3.03 ± 0.56
SLC10A1	2.89 ± 0.53	1.3 ± 0.41
SLC15A1		Silenced
SLC15A2		Silenced
SLC16A1	0.87 ± 0.09	1.59 ± 0.21
SLC16A2	0.55 ± 0.10	
SLC22A1		2.20 ± 0.41
SLC22A2	Induced	
SLC22A7	5.78 ± 1.08	
SLC22A8	Silenced	Silenced
SLC25A13	0.85 ± 0.11	
SLC28A1	2.42 ± 0.45	0.91 ± 0.09
SLC28A2	4.02 ± 0.75	0.79 ± 0.12
SLC29A1	0.89 ± 0.05	1.64 ± 0.25
SLC29A2	0.91 ± 0.07	1.43 ± 0.17
SLC28A3	2.05 ± 0.38	
SLC38A5	2.55 ± 0.48	
SLC2A1	0.65 ± 0.12	1.47 ± 0.12
SLC2A2		Induced
SLC3A1	0.84 ± 0.08	1.71 ± 0.33
SLC5A1	Silenced	
SLC5A4	Induced	2.60 ± 0.49
SLC7A7	2.40 ± 0.36	
SLC7A8	0.87 ± 0.07	1.54 ± 0.23
SLC7A9	Induced	
SLC01B1	2.42 ± 0.36	2.81 ± 0.52
SLC02A1	0.85 ± 0.08	1.68 ± 0.26
SLC02B1	2.10 ± 0.39	
SLC03A1	Silenced	1.34 ± 0.11

Human Drug Transporters RT profiler PCR array in mRNA samples extracted from GSC#1. The expression levels were normalized to the average Ct value of two housekeeping genes (ACTB and RPLP0) and calculated by the $\Delta\Delta C_t$ method. Values represent fold differences of individual gene expression in pCMV-TRPML2 compared to pCMV GSC#1 and siTRPML2 compared to siGLO GSC#83 cells.

ABCA1, ATP-binding cassette, sub-family A (ABC1), member 1 (ABCA1); ABC1 member 12 (ABCA12); ATP-binding cassette, sub-family B (MDR/TAP), member 1 (ABCB1); ATP-binding cassette, sub-family B (MDR/TAP), member 11 (ABCB11); MDR/TAP member 4 (ABCB4); MDR/TAP member 5 (ABCB5); CFTR/MRP member 2

(ABCC2); CFTR/MRP member 3 (ABCC3); CFTR/MRP member 11 (ABCC11); ALD member 4 (ABCD4); ATP-binding cassette, sub-family G (WHITE), member 2 (ABCG2); Aquaporin 1 (AQP1); Aquaporin 7 (AQP7); Aquaporin 9 (AQP9); ATPase, H⁺ transporting, lysosomal 16kDa, V0 subunit c (ATP6V0C); ATPase, Cu⁺⁺ transporting, beta polypeptide (ATP7B); Solute carrier family 10 (sodium/bile acid cotransporter family), member 1 (SLC10A1); Solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1); Solute carrier family 15 (H⁺/peptide transporter), member 2 (SLC15A2); Solute carrier family 16, member 1 (monocarboxylic acid transporter 1) (SLC16A1); Solute carrier family 16, member 2 (monocarboxylic acid transporter 8)(SLC16A2); Solute carrier family 22 (organic cation transporter), member 1 (SLC22A1); Solute carrier family 22 (organic cation transporter), member 2 (SLC22A2); Solute carrier family 22 (organic anion transporter), member 7 (SLC22A7); Solute carrier family 22 (organic anion transporter), member 8 (SLC22A8); Solute carrier family 28 (sodium-coupled nucleoside transporter), member 1 (SLC28A1); Solute carrier family 28 (sodium-coupled nucleoside transporter), member 2 (SLC28A2); Solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3); Solute carrier family 29 (nucleoside transporters), member 1 (SLC29A1); Solute carrier family 29 (nucleoside transporters), member 2 (SLC29A2); Solute carrier family 2 (facilitated glucose transporter), member 1 (SLC2A1); Solute carrier family 2 (facilitated glucose transporter), member 2 (SLC2A2); Solute carrier family 31 (copper transporters), member 1 (SLC31A1); Solute carrier family 5 (sodium/glucose cotransporter), member 1 (SLC5A1); Solute carrier family 5 (low affinity glucose cotransporter), member 4 (SLC5A4); Solute carrier family 7 (amino acid transporter light chain, γ +L system), member 7 (SLC7A7); Solute carrier family 7 (amino acid transporter light chain, L system), member 8 (SLC7A8); Solute carrier family 7 (glycoprotein-associated amino acid transporter light chain, bo,+ system), member 9 (SLC7A9); Solute carrier organic anion transporter family, member 1B1 (SLCO1B1); Solute carrier organic anion transporter family, member 2A1 (SLCO2A1); Solute carrier organic anion transporter family, member 2B1 (SLCO2B1); Solute carrier organic anion transporter family, member 3A1 (SLCO3A1).

Table S4. Kaplan-Meier p-values.

OS, p value	Methylated MGMT TRPML2 negative	Methylated MGMT TRPML2 positive	Unmethylated MGMT TRPML2 negative	Unmethylated MGMT TRPML2 positive
Methylated MGMT TRPML2 negative		0.0295 *	0.9876	0.0094 *
Methylated MGMT TRPML2 positive	0.0295 *		0.0295 *	0.6392
Unmethylated MGMT TRPML2 negative	0.9876	0.0295 *		0.0094 *
Unmethylated MGMT TRPML2 positive	0.0094 *	0.6392	0.0094 *	

PFS, p value	Methylated MGMT TRPML2 negative	Methylated MGMT TRPML2 positive	Unmethylated MGMT TRPML2 negative	Unmethylated MGMT TRPML2 positive
Methylated MGMT TRPML2 negative		0.0295 *	0.8292	0.0168 *
Methylated MGMT TRPML2 positive	0.0295 *		0.2254	0.1048
Unmethylated MGMT TRPML2 negative	0.8292	0.2254		0.0094 *
Unmethylated MGMT TRPML2 positive	0.0168 *	0.1048	0.0094 *	

OS, p value	EGFRvIII negative TRPML2 negative	EGFRvIII negative TRPML2 positive	EGFRvIII positive TRPML2 negative	EGFRvIII positive TRPML2 positive
EGFRvIII negative TRPML2 negative		0.0027 *	0.0253 *	0.0023 *
EGFRvIII negative TRPML2 positive	0.0027 *		0.1161	0.0013 *
EGFRvIII positive TRPML2 negative	0.0253 *	0.1161		0.0928
EGFRvIII positive TRPML2 positive	0.0023 *	0.0013 *	0.0928	

PFS, p value	EGFRvIII negative TRPML2 negative	EGFRvIII negative TRPML2 positive	EGFRvIII positive TRPML2 negative	EGFRvIII positive TRPML2 positive
EGFRvIII negative TRPML2 negative		0.0047 *	0.7046	0.0109 *
EGFRvIII negative TRPML2 positive	0.0047 *		0.0455 *	0.0027 *
EGFRvIII positive TRPML2 negative	0.7046	0.0455 *		0.0895
EGFRvIII positive TRPML2 positive	0.0109 *	0.0027 *	0.0895	

OS, p value	Ki67 ≤ 20 TRPML2 negative	Ki67 ≤ 20 TRPML2 positive	Ki67 > 20 TRPML2 positive
Ki67 ≤ 20 TRPML2 negative		0.0013 *	0.0007 *
Ki67 ≤ 20 TRPML2 positive	0.0013 *		0.7824
Ki67 > 20 TRPML2 positive	0.0007 *	0.7824	

PFS, p value	Ki67 ≤ 20 TRPML2 negative	Ki67 ≤ 20 TRPML2 positive	Ki67 > 20 TRPML2 positive
Ki67 ≤ 20 TRPML2 negative		0.0140 *	0.0009 *
Ki67 ≤ 20 TRPML2 positive	0.0140 *		0.2449
Ki67 > 20 TRPML2 positive	0.0009 *	0.2449	

OS, p value	Normal PTEN TRPML2 negative	Normal PTEN TRPML2 positive	Hypo PTEN TRPML2 negative	Hypo PTEN TRPML2 positive
Normal PTEN TRPML2 negative		0.0089 *	0.2072	0.0389 *
Normal PTEN TRPML2 positive	0.0089 *		0.0253 *	0.0742
Hypo PTEN TRPML2 negative	0.2072	0.0253 *		0.0896
Hypo PTEN TRPML2 positive	0.0389 *	0.0742	0.0896	

PFS, p value	Normal PTEN TRPML2 negative	Normal PTEN TRPML2 positive	Hypo PTEN TRPML2 negative	Hypo PTEN TRPML2 positive
Normal PTEN TRPML2 negative		0.043 *	0.8864	0.0455 *
Normal PTEN TRPML2 positive	0.043 *		0.0228 *	0.0662
Hypo PTEN TRPML2 negative	0.8864	0.0228 *		0.0833
Hypo PTEN TRPML2 positive	0.0455 *	0.0662	0.0833	