Table S1. Demographics and characteristics of patients with CM downloaded from TCGA.

Patient Characteristics	Classification	Number of Patients Primary CM (n=102)	Number of Patients Metastatic CM (n=366)
Gender	Male	60 (58.8 %)	228 (62.3%)
	Female	42 (41.2 %)	138 (37.7%)
Age at diagnosis (years)	Median	65	56
Tumor Stage	Stage I	2 (2%)	74 (20.2%)
	Stage II	66 (64.7%)	73 (20.0%)
	Stage III	26 (25.5%)	144 (39.3%)
	Stage IV	3 (2.9%)	21 (5.7%)
	Not reported	5 (4.9%)	54 (14.8%)
***BRAF* mutations**	Detected	43 (42.2%)	142 (38.8%)
	Not detected	59 (57.8%)	224 (61.2%)
***NRAS* mutations**	Detected	10 (9.8%)	88 (24%)
	Not detected	92 (90.2%)	278 (76%)
***NF1* mutations**	Detected	9 (8.8%)	37 (10.1%)
	Not detected	93 (91.2%)	329 (89.9%)

Table S2. Multivariable analysis of *ARL1* expression for overall survival of TCGA melanoma patients

	Classification (n)	Mean OS (years)	Standard Error	*p*-value	Exp(B)	95,0% CI for Exp(B) Lower	95,0% CI for Exp(B) Upper
Age	Mean=59		0,005	0,000	1,021	1,010	1,031
Gender	Male (254)		0,159	0,570	1,094	0,802	1,494
	Female (155)						
Tumor Stage	Stage I (79)		0,359	0,000	0,258	0,128	0,522
	Stage II (142)						
	Stage III (165)						
	Stage IV (23)						
Type of tumor	Primary (97)		0,248	0,002	2,143	1,317	3,487
	Metastatic (312)						
***BRAF* mutations**	Mutated (161)		0,173	0,990	1,002	0,714	1,406
	Wildtype (248)						
***NRAS* mutations**	Mutated (87)		0,184	0,411	0,860	0,599	1,233
	Wildtype (322)						
***NF1* mutations**	Mutated (40)		0,249	0,603	1,139	0,699	1,855
	Wildtype (369)						
ARL1			0,204	0,011	1,676	1,124	2,500
	Low expression (72)	4,8	0,598				
	High expression (337)	11,1	0,738				

Table S3. Multivariable analysis of *ARL3* expression for overall survival of TCGA CM patients.

	Classification (n)	Mean OS (years)	Standard Error	*p*-value	Exp(B)	95,0% CI for Exp(B)	
						Lower	Upper
Age	Mean=59		0,005	0,000	1,021	1,011	1,032
Gender	Male (254)		0,159	0,457	1,126	0,824	1,537
	Female (155)						
Tumor Stage	Stage I (79)		0,357	0,000	0,267	0,132	0,537
	Stage II (142)						
	Stage III (165)						
	Stage IV (23)						
Type of tumor	Primary (97)		0,245	0,001	2,334	1,445	3,760
	Metastatic (312)						
BRAF mutations	Mutated (161)		0,172	0,709	1,066	0,761	1,495
	Wildtype (248)						
NRAS mutations	Mutated (87)		0,184	0,471	0,876	0,611	1,256
	Wildtype (322)						
NF1 mutations	Mutated (40)		0,248	0,388	1,239	0,761	2,016
	Wildtype (369)						
ARL3			0,171	0,030	0,690	0,493	0,965
	Low expression (96)	11,1					
	High expression (313)	7,3					

Table S4. Multivariable analysis of *ARL5B* expression for overall survival of TCGA melanoma patients.

	Classification (n)	Mean OS (years)	Standard Error	*p*-value	Exp(B)	95,0% CI for Exp(B)	
						Lower	Upper
Age	Mean=59		0,005	0,000	1,020	1,010	1,031
Gender	Male (254)		0,159	0,512	1,109	0,813	1,513
	Female (155)						
Tumor Stage	Stage I (79)		0,357	0,000	0,264	0,131	0,532
	Stage II (142)						
	Stage III (165)						
	Stage IV (23)						
Type of tumor	Primary (97)		0,245	0,020	2,160	1,126	4,140
	Metastatic (312)						
BRAF mutations	Mutated (161)		0,172	0,635	1,085	0,774	1,521
	Wildtype (248)						
NRAS mutations	Mutated (87)		0,184	0,534	0,892	0,621	1,280
	Wildtype (322)						
NF1 mutations	Mutated (40)		0,248	0,454	1,204	0,741	1,957
	Wildtype (369)						
ARL5B			0,171	0,598	1,143	0,695	1,880
	Low expression (288)	10,8					
	High expression (121)	8,2					

Table S5. Multivariable analysis of *ARL8A* expression for overall survival of TCGA CM patients.

	Classification (n)	Mean OS (years)	Standard Error	*p*-value	Exp(B)	95,0% CI for Exp(B)	
						Lower	Upper
Age	Mean=59		0,005	0,000	1,021	1,011	1,031
Gender	Male (254)		0,159	0,486	1,117	0,819	1,524
	Female (155)						
Tumor Stage	Stage I (79)		0,358	0,000	0,266	0,132	0,535
	Stage II (142)						
	Stage III (165)						
	Stage IV (23)						
Type of tumor	Primary (97)		0,322	0,048	1,889	1,006	3,548
	Metastatic (312)						
BRAF mutations	Mutated (161)		0,170	0,678	1,073	0,769	1,499
	Wildtype (248)						
NRAS mutations	Mutated (87)		0,185	0,441	0,867	0,604	1,246
	Wildtype (322)						
NF1 mutations	Mutated (40)		0,250	0,372	1,250	0,766	2,041
	Wildtype (369)						
ARL8A			0,331	0,192	0,649	0,340	1,242
	Low expression (65)	4,0					
	High expression (344)	10,6					

Table S6. Multivariable analysis of *ARL10* expression for overall survival of TCGA CM patients.

	Classification (n)	Mean OS (years)	Standard Error	*p*-value	Exp(B)	95,0% CI for Exp(B)	
						Lower	Upper
Age	Mean=59		0,005	0,000	1,021	1,011	1,032
Gender	Male (254)		0,159	0,548	1,100	0,806	1,501
	Female (155)						
Tumor Stage	Stage I (79)		0,357	0,000	0,271	0,135	0,547
	Stage II (142)						
	Stage III (165)						
	Stage IV (23)						
Type of tumor	Primary (97)		0,276	0,023	1,875	1,091	3,221
	Metastatic (312)						
BRAF mutations	Mutated (161)		0,172	0,722	1,063	0,759	1,490
	Wildtype (248)						
NRAS mutations	Mutated (87)		0,184	0,490	0,881	0,615	1,262
	Wildtype (322)						
NF1 mutations	Mutated (40)		0,249	0,391	1,238	0,760	2,015
	Wildtype (369)						
ARL10			0,190	0,050	1,452	1,283	2,413
	Low expression (263)	11,4					
	High expression (146)	6,7					

Table S7. Multivariable analysis of *ARL11* expression for overall survival of TCGA melanoma patients.

	Classification (n)	Mean OS (years)	Standard Error	*p*-value	Exp(B)	95,0% CI for Exp(B)	
						Lower	Upper
Age	Mean=59		0,005	0,000	1,020	1,010	1,031
Gender	Male (254)		0,159	0,519	1,108	0,811	1,513
	Female (155)						
Tumor Stage	Stage I (79)		0,358	0,000	0,267	0,132	0,538
	Stage II (142)						
	Stage III (165)						
	Stage IV (23)						
Type of tumor	Primary (97)		1,020	0,427	2,248	0,304	16,603
	Metastatic (312)						
BRAF mutations	Mutated (161)		0,171	0,677	1,074	0,768	1,502
	Wildtype (248)						
NRAS mutations	Mutated (87)		0,184	0,510	0,866	0,618	1,270
	Wildtype (322)						
NF1 mutations	Mutated (40)		0,248	0,452	1,205	0,742	1,958
	Wildtype (369)						
ARL11			1,035	0,936	0,920	0,121	6,995
	Low expression (95)	2,8					
	High expression (314)	10,7					

Table S8. Multivariable analysis of *ARL13A* expression for overall survival of TCGA melanoma patients.

	Classification (n)	Mean OS (years)	Standard Error	*p*-value	Exp(B)	95,0% CI for Exp(B)	
						Lower	Upper
Age	Mean=59		0,005	0,000	1,022	1,011	1,032
Gender	Male (254)		0,159	0,619	1,082	0,792	1,478
	Female (155)						
Tumor Stage	Stage I (79)		0,359	0,000	0,250	0,124	0,506
	Stage II (142)						
	Stage III (165)						
	Stage IV (23)						
Type of tumor	Primary (97)		0,254	0,000	2,561	1,583	4,143
	Metastatic (312)						
BRAF mutations	Mutated (161)		0,172	0,849	1,033	0,738	1,447
	Wildtype (248)						
NRAS mutations	Mutated (87)		0,185	0,427	0,864	0,601	1,241
	Wildtype (322)						
NF1 mutations	Mutated (40)		0,248	0,392	1,237	0,760	2,012
	Wildtype (369)						
ARL13A			0,278	0,029	0,544	0,316	0,938
	Low expression (384)	10,6					
	High expression (25)	5,5					

Table S9. Multivariable analysis of *ARL15* expression for overall survival of TCGA melanoma patients.

	Classification (n)	Mean OS (years)	Standard Error	*p*-value	Exp(B)	95,0% CI for Exp(B)	
						Lower	Upper
Age	Mean=59		0,005	0,000	1,021	1,011	1,032
Gender	Male (254)		0,159	0,440	1,131	0,828	1,544
	Female (155)						
Tumor Stage	Stage I (79)		0,357	0,000	0,262	0,130	0,528
	Stage II (142)						
	Stage III (165)						
	Stage IV (23)						
Type of tumor	Primary (97)		0,822	0,001	2,275	1,407	3,680
	Metastatic (312)						
BRAF mutations	Mutated (161)		0,163	0,713	1,065	0,760	1,494
	Wildtype (248)						
NRAS mutations	Mutated (87)		0,138	0,452	0,871	0,607	1,249
	Wildtype (322)						
NF1 mutations	Mutated (40)		0,224	0,368	1,251	0,768	2,037
	Wildtype (369)						
ARL15			0,494	0,003	0,610	0,443	0,841
	Low expression (297)	10,3					
	High expression (112)	6,8					

Table S10. Multivariable analysis of *ARL16* expression for overall survival of TCGA melanoma patients.

	Classification (n)	Mean OS (years)	Standard Error	*p*-value	Exp(B)	95,0% CI for Exp(B)	
						Lower	Upper
Age	Mean=59		0,005	0,000	1,021	1,011	1,032
Gender	Male (254)		0,159	0,525	1,106	0,810	1,510
	Female (155)						
Tumor Stage	Stage I (79)		0,357	0,000	0,271	0,135	0,546
	Stage II (142)						
	Stage III (165)						
	Stage IV (23)						
Type of tumor	Primary (97)		0,327	0,101	1,709	0,900	3,247
	Metastatic (312)						
BRAF mutations	Mutated (161)		0,171	0,728	1,061	0,759	1,485
	Wildtype (248)						
NRAS mutations	Mutated (87)		0,183	0,501	0,884	0,617	1,266
	Wildtype (322)						
NF1 mutations	Mutated (40)		0,249	0,361	1,256	0,771	2,047
	Wildtype (369)						
ARL16			0,256	0,110	0,665	0,402	1,098
	Low expression (282)	11,2					
	High expression (127)	4,9					

Table S11. Correlation between *ARL* genes expression and the infiltration of distinct immune cell subsets, in SKCM, primary and metastatic melanoma samples. Data obtained from the TIMER2.0 resource, including *p*-values and Spearman's rank correlation coefficients (cor) according to different algorithms applied. Only significant correlations were presented in the table.

Gene	Description	Algorithm	SKCM		SKCM - Primary		SKCM - Metastasis	
			cor	*p*-value	cor	*p*-value	cor	*p*-value
ARL1	T cells CD4+ memory	XCELL	0.447	8.81×10^{-24}	0.725	6.76×10^{-18}	0.3	8.78×10^{-09}
	T cells CD4+ Th1	XCELL	-0.577	5.60×10^{-42}	-0.601	2.39×10^{-42}	-0.568	1.41×10^{-31}
	T cells CD4+ Th2	XCELL	0.261	1.56×10^{-08}	0.598	3.11×10^{-11}	0.098	6.68×10^{-02}
	Treg	QUANTISEQ	0.351	1.06×10^{-14}	0.458	1.31×10^{-06}	0.278	1.11×10^{-07}
	Neutrophils	TIMER	0.427	1.17×10^{-21}	0.501	8.17×10^{-08}	0.349	1.38×10^{-11}
	Common lymphoid progenitor	XCELL	0.485	2.25×10^{-28}	0.72	1.53×10^{-17}	0.411	7.87×10^{-16}
ARL2	T cells CD4+ Th1	XCELL	0.369	3.76×10^{-16}	0.52	4.80×10^{-09}	0.312	2.04×10^{-09}
ARL3	T cells CD8+	TIMER	0.231	5.80×10^{-07}	0.47	6.02×10^{-07}	0.133	1.25×10^{-02}
	T cells CD4+ memory	XCELL	0.348	2.01×10^{-14}	0.502	7.86×10^{-08}	0.263	5.35×10^{-07}
	T cells CD4+ Th2	XCELL	0.321	2.03×10^{-12}	0.47	6.29×10^{-07}	0.243	3.88×10^{-06}
	Common lymphoid progenitor	XCELL	0.325	1.02×10^{-12}	0.451	1.96×10^{-06}	0.287	3.89×10^{-08}
ARL4A	Common lymphoid progenitor	XCELL	0.28	1.05×10^{-09}	0.433	5.37×10^{-06}	0.23	1.25×10^{-05}
ARL4C	T cells CD4+ memory	XCELL	0.444	1.51×10^{-23}	0.364	1.43×10^{-4}	0.384	7.28×10^{-14}
	T cells CD4+ Th2	XCELL	0.307	2.06×10^{-11}	0.409	2.01×10^{-5}	0.22	3.10×10^{-05}
	Treg	QUANTISEQ	0.409	7.43×10^{-20}	0.363	1.79×10^{-04}	0.376	2.36×10^{-13}
	Neutrophils	TIMER	0.508	2.34×10^{-31}	0.362	1.87×10^{-04}	0.517	1.22×10^{-25}
	Macrophages M2	CIBERSORT-ABS	0.433	2.79×10^{-22}	0.363	1.80×10^{-04}	0.407	1.56×10^{-15}
	Monocyte	MCP-COUNTER	0.571	5.77×10^{-41}	0.321	1.01×10^{-03}	0.581	2.34×10^{-33}
ARL5A	T cells CD4+	EPIC	0.46	2.70×10^{-25}	0.595	4.09×10^{-11}	0.421	1.18×10^{-16}
	T cells CD4+ memory	XCELL	0.57	9.75×10^{-41}	0.603	1.95×10^{-11}	0.525	1.95×10^{-11}
	T cells CD4+ Th2	XCELL	0.388	7.87×10^{-18}	0.459	1.21×10^{-06}	0.32	6.88×10^{-10}
	Neutrophils	TIMER	0.556	1.88×10^{-38}	0.602	2.25×10^{-11}	0.508	1.19×10^{-24}

		MCP-COUNTER	0.405	1.93×10^{-19}	0.568	4.82×10^{-10}	0.377	2.25×10^{-13}
	Common lymphoid progenitor	XCELL	0.52	5.02×10^{-33}	0.657	6.23×10^{-14}	0.48	9.20×10^{-22}
ARL5B	**T cells CD4+**	EPIC	0.413	3.29×10^{-20}	0.402	2.78×10^{-05}	0.418	2.08×10^{-16}
	T cells CD4+ memory	XCELL	0.552	7.11×10^{-38}	0.679	4.43×10^{-15}	0.439	4.20×10^{-18}
	T cells CD4+ Th2	XCELL	0.417	1.12×10^{-20}	0.557	1.19×10^{-09}	0.315	1.28×10^{-09}
	Neutrophils	TIMER	0.51	1.46×10^{-31}	0.537	6.01×10^{-09}	0.447	8.39×10^{-19}
		MCP-COUNTER	0.4	5.99×10^{-19}	0.395	4.04×10^{-05}	0.431	1.90×10^{-17}
	Common lymphoid progenitor	XCELL	0.495	1.16×10^{-29}	0.644	2.82×10^{-13}	0.467	1.31×10^{-20}
	T cell NK	XCELL	-0.417	1.17×10^{-20}	-0.581	1.53×10^{-10}	-0.355	5.63×10^{-12}
ARL6	**T cells CD4+ memory**	XCELL	0.465	6.03×10^{-26}	0.679	4.34×10^{-15}	0.308	3.05×10^{-09}
	T cells CD4+ Th1	XCELL	-0.499	4.27×10^{-30}	-0.532	8.65×10^{-09}	-0.495	2.77×10^{-23}
	T cells CD4+ Th2	XCELL	0.266	7.76×10^{-09}	0.525	1.50×10^{-08}	0.12	2.41×10^{-02}
	Treg	QUANTISEQ	0.385	1.30×10^{-17}	0.411	1.76×10^{-05}	0.323	4.85×10^{-10}
	Neutrophils	TIMER	0.481	8.67×10^{-28}	0.519	2.23×10^{-08}	0.407	1.53×10^{-15}
		MCP-COUNTER	0.422	3.66×10^{-21}	0.388	5.51×10^{-05}	0.462	4.22×10^{-20}
	Common lymphoid progenitor	XCELL	0.577	6.02×10^{-42}	0.703	1.74×10^{-16}	0.543	1.67×10^{-28}
	T cell NK	XCELL	-0.419	6.80×10^{-21}	-0.554	1.56×10^{-09}	-0.365	1.32×10^{-12}
ARL8B	**Neutrophils**	TIMER	0.435	1.74×10^{-22}	0.548	2.44×10^{-09}	0.381	1.15×10^{-13}
		MCP-COUNTER	0.386	1.13×10^{-17}	0.48	3.23×10^{-07}	0.365	1.38×10^{-12}
	Common lymphoid progenitor	XCELL	0.413	2.70×10^{-20}	0.642	3.74×10^{-13}	0.337	7.5×10^{-11}
	T cell NK	XCELL	-0.228	8.43×10^{-07}	-0.484	2.61×10^{-07}	-0.135	1.12×10^{-02}
ARL11	**T cells CD8+**	EPIC	0.281	9.52×10^{-10}	0.469	6.68×10^{-07}	0.229	1.33×10^{-05}
		MCP-COUNTER	0.593	9.16×10^{-45}	0.373	1.14×10^{-04}	0.575	1.42×10^{-32}
		QUANTISEQ	0.571	6.75×10^{-41}	0.305	1.81×10^{-03}	0.565	3.41×10^{-31}
		CIBERSORT-ABS	0.576	9.37×10^{-42}	0.348	3.44×10^{-04}	0.576	1.18×10^{-32}
		XCELL	0.489	7.12×10^{-29}	0.376	9.88×10^{-05}	0.477	1.81×10^{-21}
	T cells CD8+ central memory	XCELL	0.572	5.16×10^{-41}	0.368	1.41×10^{-04}	0.564	3.83×10^{-31}
	T cells CD4+ memory	XCELL	0.602	2.48×10^{-46}	0.485	2.47×10^{-07}	0.542	1.87×10^{-28}
	B cell	QUANTISEQ	0.404	2.41×10^{-19}	0.242	1.44×10^{-02}	0.341	4.32×10^{-11}
		XCELL	0.498	4.50×10^{-30}	0.32	1.05×10^{-03}	0.434	1.18×10^{-17}

	Cell type	Method						
		MCP-COUNTER	0.443	2.46×10^{-23}	0.334	6.13×10^{-04}	0.359	3.47×10^{-12}
	Memory B cell	TIMER	0.463	1.03×10^{-25}	0.435	4.79×10^{-06}	0.387	4.36×10^{-14}
	Neutrophil	TIMER	0.697	8.74×10^{-68}	0.666	2.19×10^{-14}	0.667	5.93×10^{-47}
	Macrophage	EPIC	0.551	1.20×10^{-37}	0.327	7.93×10^{-04}	0.568	1.33×10^{-31}
		XCELL	0.603	1.58×10^{-46}	0.412	1.65×10^{-05}	0.573	2.58×10^{-32}
	Macrophage M1	CIBERSORT-ABS	0.612	2.28×10^{-48}	0.472	5.40×10^{-07}	0.583	1.49×10^{-33}
		QUANTISEQ	0.462	1.64×10^{-25}	0.377	9.38×10^{-05}	0.414	4.44×10^{-16}
		XCELL	0.662	6.25×10^{-59}	0.486	2.25×10^{-07}	0.64	2.89×10^{-42}
	Macrophage M2	CIBERSORT-ABS	0.739	5.21×10^{-80}	0.692	8.48×10^{-16}	0.718	2.71×10^{-57}
		QUANTISEQ	0.517	1.30×10^{-32}	0.225	2.27×10^{-02}	0.553	9.55×10^{-30}
		TIDE	-0.604	1.01×10^{-46}	-0.545	3.26×10^{-09}	-0.57	6.24×10^{-32}
	Monocyte	MCP-COUNTER	0.842	4.32×10^{-124}	0.863	2.41×10^{-31}	0.809	3.06×10^{-83}
		XCELL	0.605	4.92×10^{-47}	0.37	1.29×10^{-04}	0.647	2.19×10^{-43}
	Myeloid Dendritic Cell	TIMER	0.514	3.59×10^{-32}	0.275	5.13×10^{-03}	0.547	5.82×10^{-29}
		XCELL	0.429	6.58×10^{-22}	0.305	1.84×10^{-03}	0.465	2.08×10^{-20}
		MCP-COUNTER	0.624	1.29×10^{-50}	0.49	1.71×10^{-07}	0.614	5.24×10^{-38}
	Myeloid Dendritic Cell Activated	XCELL	0.612	2.42×10^{-48}	0.415	1.42×10^{-05}	0.585	7.72×10^{-34}
	Plasmocytoid Dendritic Cell	XCELL	0.496	9.91×10^{-30}	0.211	3.36×10^{-02}	0.519	7.82×10^{-26}
	NK cell	MCP-COUNTER	0.546	8.13×10^{-37}	0.433	5.62×10^{-06}	0.547	5.52×10^{-29}
	NK cell Actvated	MCP-COUNTER	0.467	4.14×10^{-26}	0.454	1.68×10^{-06}	0.445	1.26×10^{-18}
	T cell follicular helper	CIBERSORT-ABS	0.508	2.23×10^{-31}	0.42	1.14×10^{-05}	0.515	2.17×10^{-25}
ARL13B	**T cells CD4+ memory**	XCELL	0.522	2.68×10^{-33}	0.662	3.37×10^{-14}	0.428	3.27×10^{-17}
	T cells CD4+ Th2	XCELL	0.36	1.92×10^{-15}	0.534	7.35×10^{-09}	0.259	7.97×10^{-07}
	Treg	QUANTISEQ	0.463	1.24×10^{-25}	0.45	2.05×10^{-06}	0.431	2.04×10^{-17}
	Neutrophil	MCP-COUNTER	0.449	4.60×10^{-24}	0.452	1.89×10^{-06}	0.478	1.21×10^{-21}
		TIMER	0.545	9.86×10^{-37}	0.5	8.62×10^{-08}	0.518	9.65×10^{-26}
	Common lymphoid progenitor	XCELL	0.54	5.49×10^{-36}	0.77	3.23×10^{-21}	0.471	6.04×10^{-21}

	T cell NK	XCELL	-0.428	8.81×10^{-22}	-0.601	2.44×10^{-11}	-0.361	$2.29 \times 10\text{-}12$
ARL15	**T cell CD4+**	EPIC	0.431	4.43×10^{-22}	0.542	4.06×10^{-09}	0.393	1.72×10^{-14}
	T cell CD4+ memory	XCELL	0.419	7.47×10^{-21}	0.353	2.71×10^{-04}	0.36	3.01×10^{-12}
	T cells CD4+ Th1	XCELL	-0.506	4.26×10^{-31}	-0.541	4.20×10^{-09}	-0.5	8.59×10^{-24}
	Tregs	QUANTISEQ	0.392	3.29×10^{-18}	0.446	2.70×10^{-06}	0.342	3.70×10^{-11}
	Neutrophil	TIMER	0.559	6.21×10^{-39}	0.6	2.62×10^{-11}	0.511	5.58×10^{-25}
	Macrophage M2	CIBERSORT-ABS	0.504	7.57×10^{-31}	0.409	1.99×10^{-05}	0.515	2.37×10^{-25}
	Monocytes	QUANTISEQ	0.344	4.11×10^{-14}	0.477	4.02×10^{-07}	0.339	5.44×10^{-11}
	Myeloid Dendritic cell	MCP-COUNTER	0.444	1.68×10^{-23}	0.428	7.14×10^{-06}	0.403	2.94×10^{-15}
	NK cell	QUANTISEQ	0.405	1.98×10^{-19}	0.448	2.37×10^{-06}	0.424	7.05×10^{-17}
	T cell NK	XCELL	-0.383	1.96×10^{-17}	-0.541	4.43×10^{-09}	-0.31	2.57×10^{-09}

Table S12. Expression thresholds defined to divide patients into two non-overlapping groups with high or low *ARL* expression

Variables	Threshold
ARL1	10,72
ARL2	11.09
ARL3	9.50
ARL4A	11.125
ARL4C	10.43
ARL4D	10.25
ARL5A	11.04
ARL5B	10.03
ARL5C	1.13
ARL6	7.44
ARL8A	10.62
ARL8B	12.26
ARL9	4.80
ARL10	9.57
ARL11	4.27
ARL13A	1.70
ARL13B	8.01
ARL14	1.29
ARL15	9.54
ARL16	9.88
ARL17A	9.99
ARL17B	6.75