

Locus-specific LINE-1 expression in clinical ovarian cancer specimens at the single-cell level

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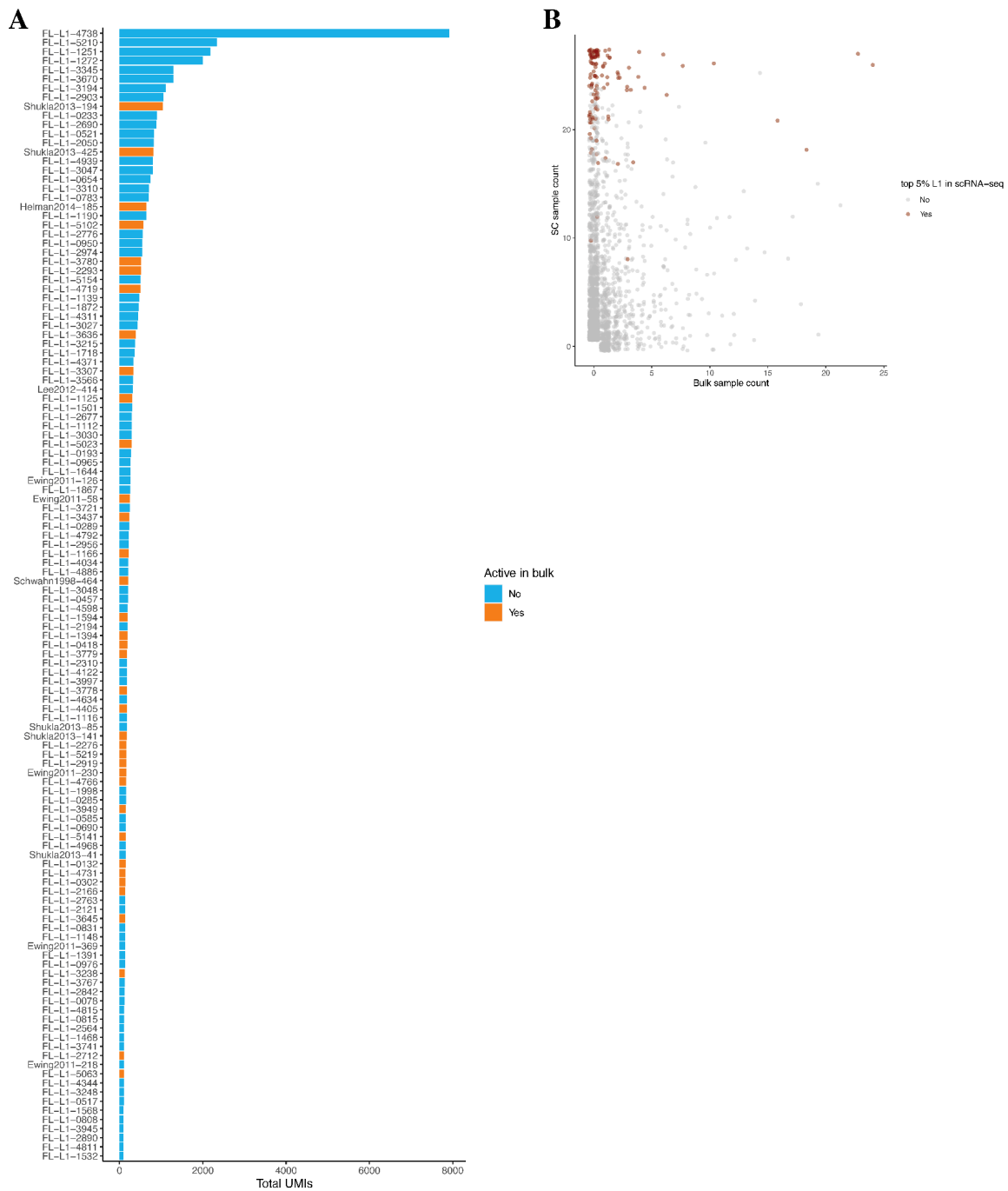
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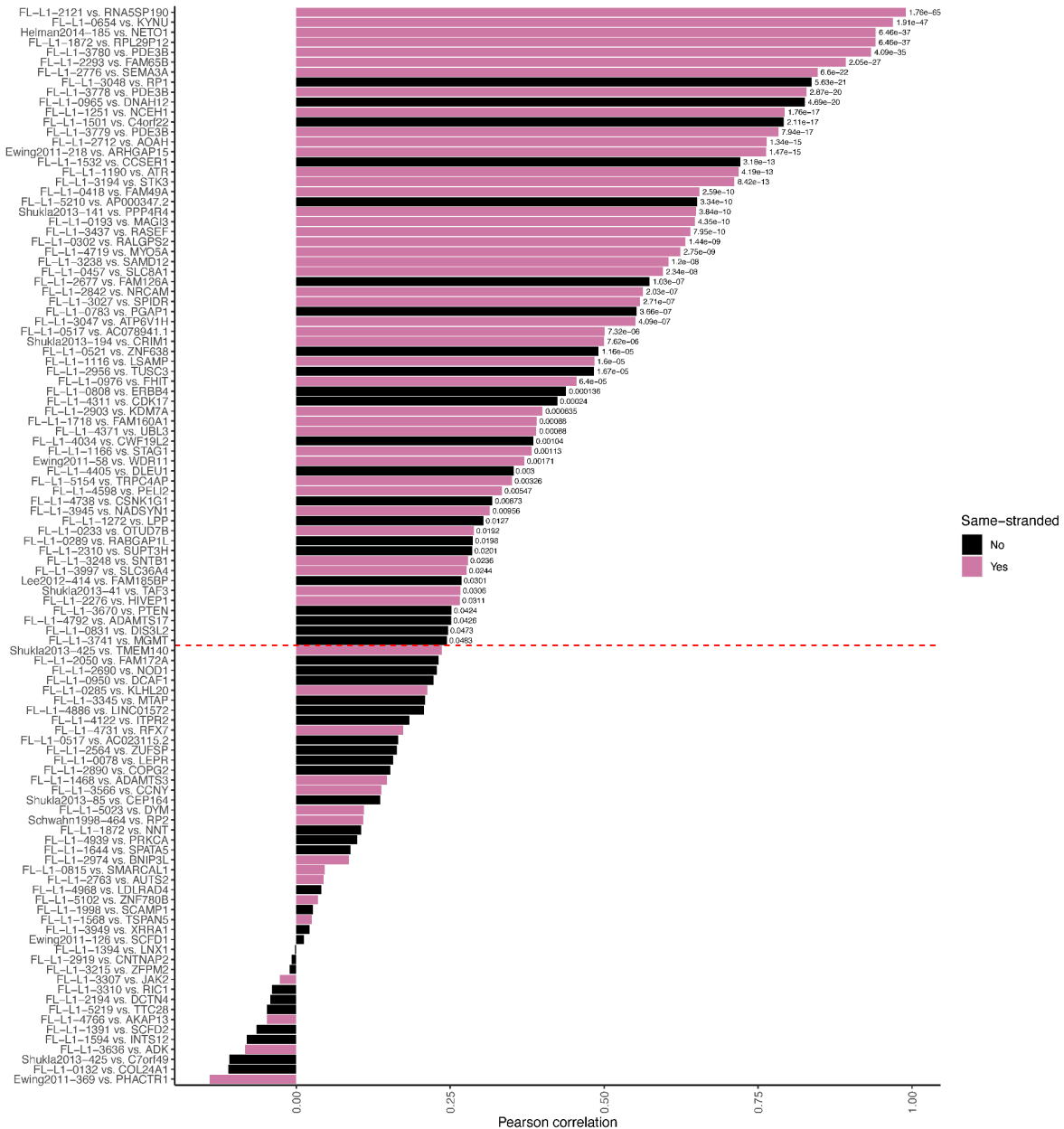
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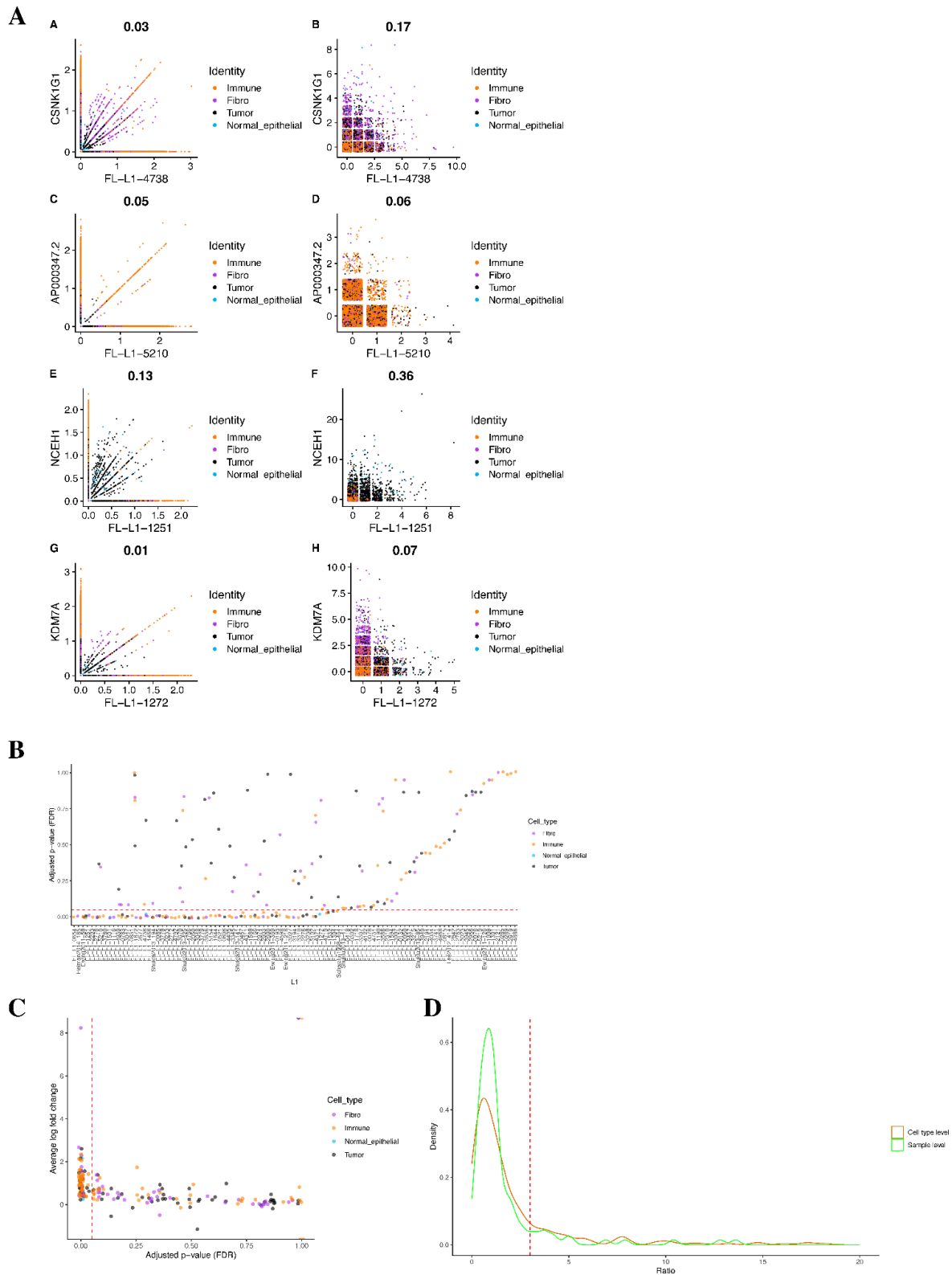
Supplementary information



Supplementary Figure 1. A. Total number of UMIs per LI in unnormalized single cell dataset. LIs that were also detected in bulk RNA-seq are marked in orange. **B.** The number of LI-expressing samples in bulk and scRNA-seq data. One dot corresponds to a single LI locus. The most active LIs of the scRNA-seq (top 5% based on total UMI count) are marked in blue.



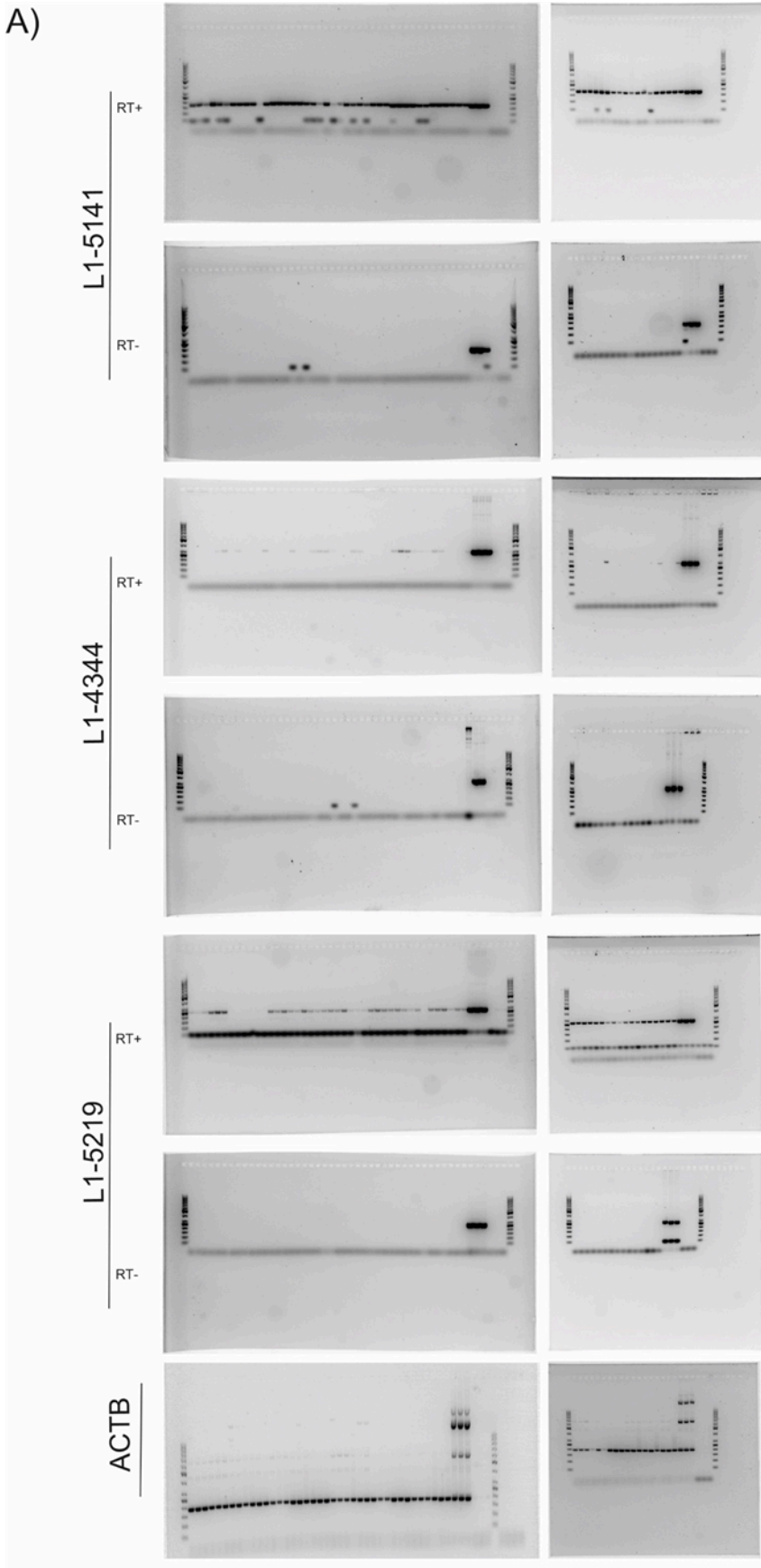
Supplementary Figure 2. Pearson's correlation coefficients between L1s and their host genes from highest to lowest. Each bar represents the correlation coefficient between a single L1-host pair, calculated based on their mean expression per sample per cell type. Numbers next to bars indicate false discovery rate -adjusted p-values (FDR). Pairs above the dashed red line are statistically significantly associated (FDR < 0.05).



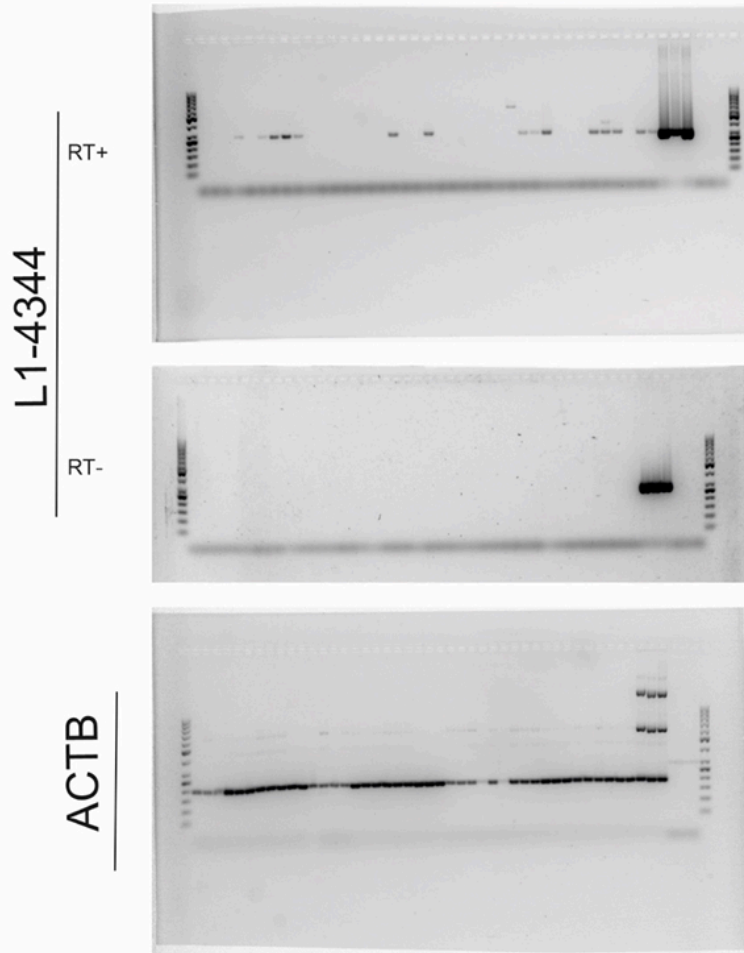
Supplementary Figure 3. A. Expression of the four most highly active L1s of scRNA-seq data and their host genes. The graphs on the left (A,C,E,G) are based on log-normalized counts, whereas graphs on the right (B,D,F,H) are based on unnormalized counts. **B.** Adjusted *p*-values of host gene differential expression analysis between cells that do and do not express the resident L1 in question. Dot denotes a host gene in a particular cell type. FDR = false discovery rate. **C.** Differential expression of L1 host genes between cells that do and do not express the corresponding resident L1.

Positive average log fold change values indicate higher host gene expression in the resident L1-expressing cells. **D.** Distribution of mean expression ratios between tumor and normal samples ('Sample level'), as well as between cancer cells and other cell types ('Cell type level'). A single value corresponds to a single L1 locus. Dashed red line indicates the selected threshold for the enrichment (3:1).

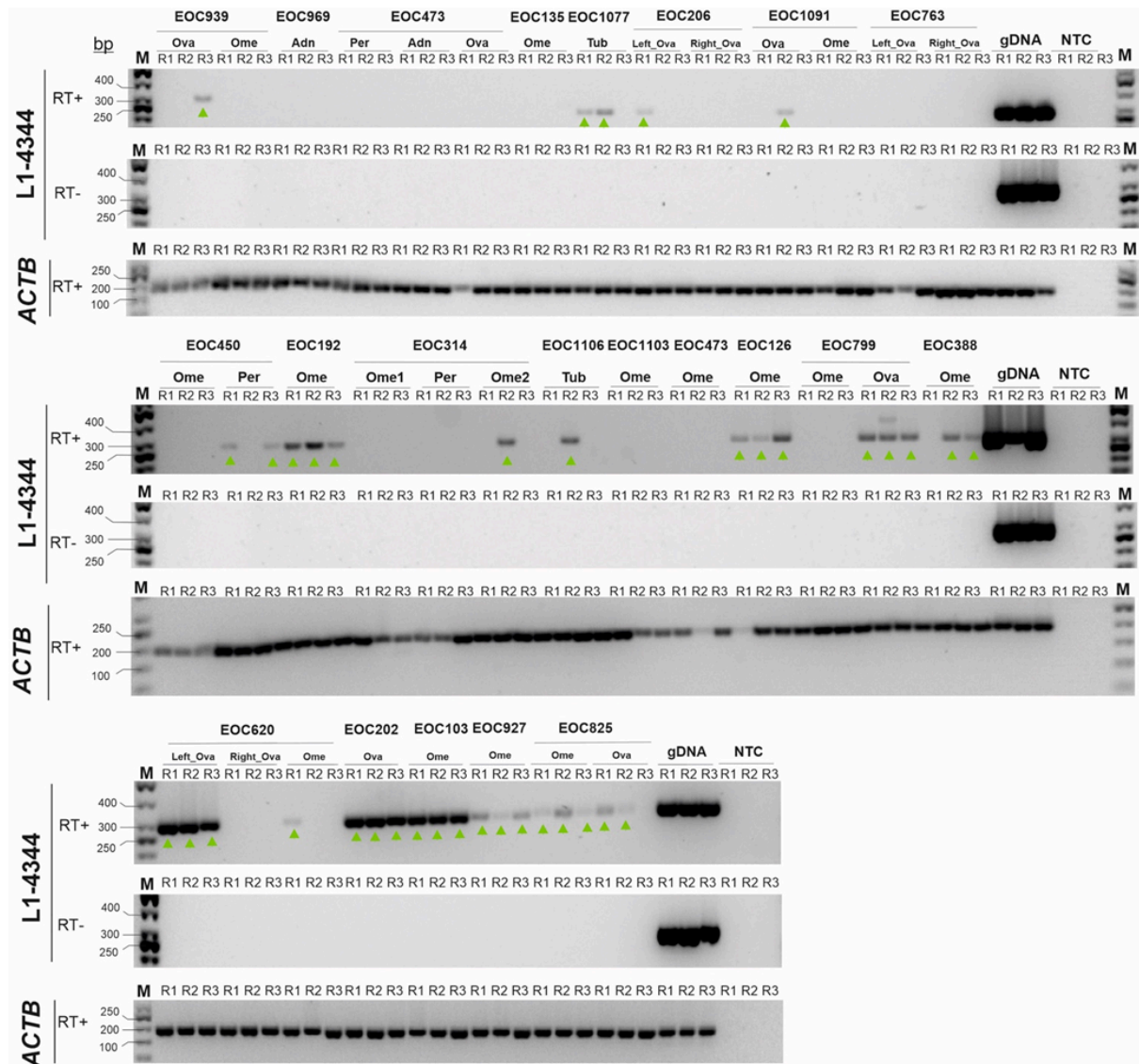
A)



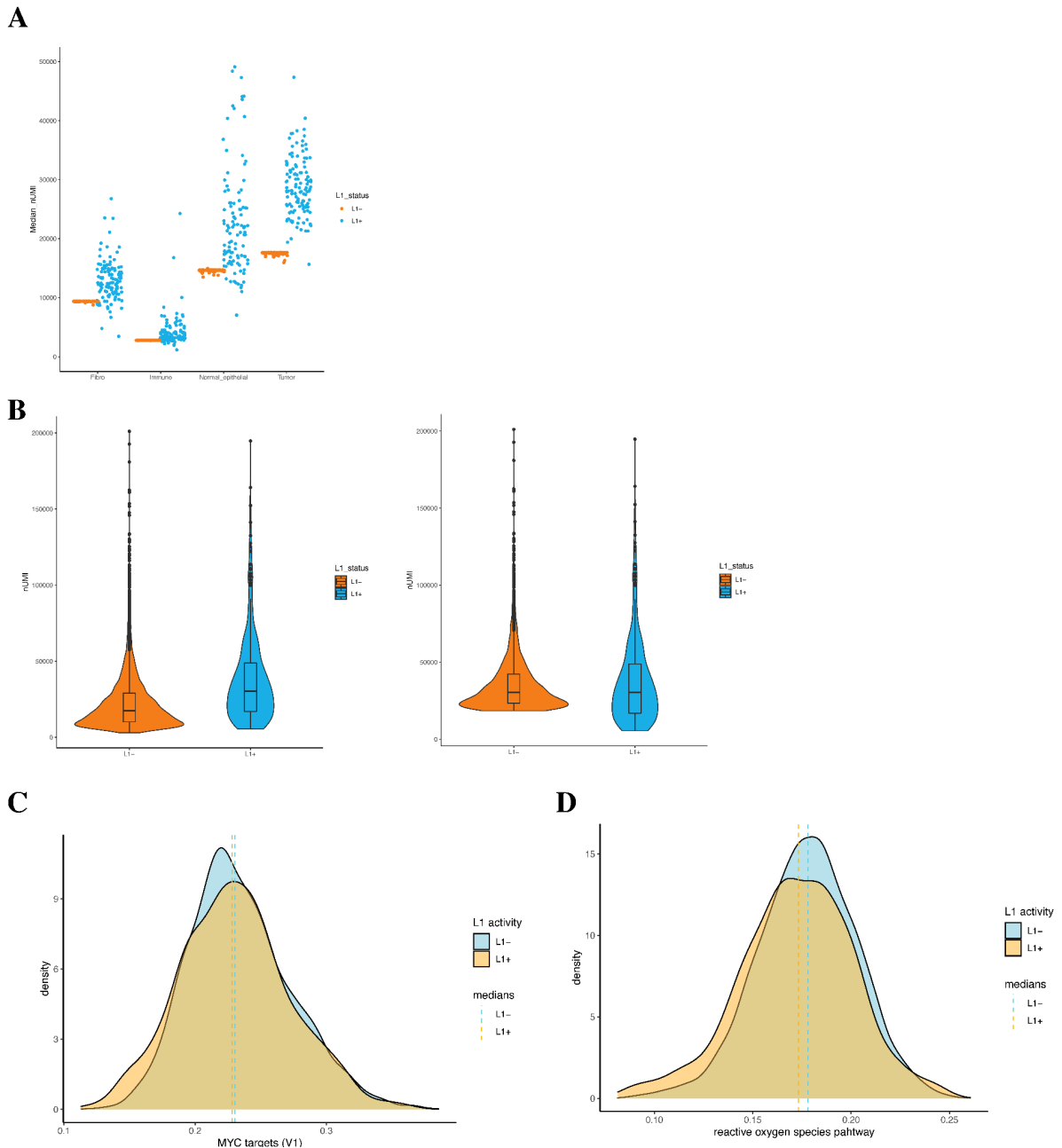
B)



Supplementary Figure 4. *Uncropped images of agarose gels shown in A) Figure 3 and B) Supplementary Figure 5.*



Supplementary Figure 5. Locus-specific RT-PCR to detect expression of L1-4344 in an independent HGSOc patient cohort. Agarose gel image is shown with inverted colors (white-on-black) for ease of visualizing amplification products. RT-PCRs positive for amplification (L1-4344 RT-PCR product is sized 291 bp) are marked with green arrowheads. Genomic DNA was included as a control (lane labeled “gDNA”). RT-PCR with primers against ACTB transcript reports on the integrity of RNA samples. Abbreviations: R1,R2 & R3 = replicate 1, 2 & 3 respectively; p = primary (pre-chemotherapy); i = interval (post-chemotherapy); gDNA = genomic DNA; NTC = no template control; M = GeneRuler™ 50 bp DNA ladder, Thermo Scientific™; anatomical sites of tumor sample origin: Ova = ovary, Ome = omentum, Per = peritoneum, Adn = Adnexus, Tub = fallopian tube



Supplementary Figure 6. UMI counts differ in L1+ and L1- cells. **A.** Median UMI count in L1-positive and L1-negative cells (based on the validated L1 loci). One dot denotes a median UMI count in cells that do/do not express a particular L1. **B.** Cell size bias in L1-positivity. Number of UMIs in cancer cells that do (L1+) and do not (L1-) express the validated L1s, FL_L1-5219 and/or FL_L1-5141. **C.** Cell size bias in L1-positivity is reduced with the “median matching” procedure. Number of UMIs in subsetted cancer cells that do (L1+) and do not express (L1-) the validated L1s FL_L1-5219 and/or FL_L1-5141. Area Under the Curve (AUC) scores for “MYC targets” (**C**) and “Reactive oxygen species pathway” (**D**) hallmark gene sets between L1-positive and L1-negative cells. L1-positivity was assigned based on all the L1s appearing to be genuinely expressed in the scRNA-seq.

Supplementary Table 1. Percentiles of the total number of unique molecular identifiers (UMIs) per LI locus, summed from all the samples of the dataset.

0%	25%	50%	75%	95%	100%
1	1	4	12	95	7924

Supplementary Table 2. Features of the top 5% most strongly expressed L1s of the scRNA-seq. Total UMI count = sum of UMIs from all the samples combined; Pearson's $r/p.adj$ = Pearson's correlation and FDR adjusted p -value from the L1-host gene expression association analysis; Host expression enrichment in L1+ cells = In which cell types (if any) a host gene is upregulated in the resident L1-expressing cells compared to cells that do not express the resident L1; L1 expression high = Sample/cell types in which an L1 has a minimum of 3-fold enrichment in expression when compared to other sample/cell types; scRNA-seq N = Number of samples in which an L1 was active in scRNA-seq; Bulk RNA-seq N = Number of samples in which an L1 was active in bulk RNA-seq.

L1 ID	location	Total UMI count	host gene(s)	Pearson's $r/p.adj$ (L1 vs. host)	Host expression enrichment In L1+ cells	L1 expression high	scRNA-seq N	Bulk RNA-seq N
Ewing2011-126	chr14:30679187-30683088	257	SCFD1 (antisense),	0.01/0.94	NA	NA	27	0
			UBE2CP1 (same-stranded)	NA/NA	NA			
Ewing2011-218	chr2:143250295-143254196	105	ARHGAP15 (same-stranded)	0.76/< 0.001	Yes (immune cells)	Yes (immune cells)	24	0
Ewing2011-230	chr2:190611556-190612556	158	NA	NA/NA	NA	NA	26	1
Ewing2011-369	chr6:13187873-13191774	130	PHACTR1 (same-stranded)	-0.14/0.29	Yes (tumor cells)	Yes (fibroblasts)	21	0
Ewing2011-58	chr10:120899751-120903652	253	WDR11 (same-stranded)	0.37/0.002	Yes (tumor cells, immune cells)	NA	25	2
FL-L1-0078	chr1:65449279-65457309	115	LEPR (antisense)	0.16/0.23	NA	Yes (tumor samples)	23	0
FL-L1-0132	chr1:85926070-85934100	144	COL24A1 (antisense)	-0.11/0.43	NA	Yes (tumor samples)	17	1
FL-L1-0193	chr1:113496220-113504257	281	MAGI3 (same-stranded)	0.65/< 0.001	Yes (tumor cells, immune cells)	NA	25	0
FL-L1-0233	chr1:149951052-149959158	899	OTUD7B (same-stranded)	0.29/0.02	Yes (tumor cells, fibroblasts, immune cells)	NA	27	0
FL-L1-0285	chr1:173724764-173732872	155	KLHL20 (same-stranded)	0.21/0.09	NA	NA	27	0

FL-L1-0289	chr1:174589352-174597377	229	RABGAP1L (antisense)	0.29/0.02	NA	Yes (normal samples)	23	0
FL-L1-0302	chr1:178836557-178844666	141	RALGPS2 (same-stranded)	0.63/< 0.001	NA	NA	24	1
FL-L1-0418	chr2:16592725-16600755	184	FAM49A (same-stranded)	0.65/< 0.001	NA	Yes (immune cells)	25	2
FL-L1-0457	chr2:40231600-40239627	201	SLC8A1 (same-stranded)	0.59/< 0.001	Yes (tumor cells, immune cells)	NA	26	0
			SLC8A1-AS1 (antisense)	NA/NA	NA			
FL-L1-0517	chr2:67188811-67196967	100	AC023115.2 (antisense),	0.17/0.21	NA	NA	22	0
			AC078941.1 (same-stranded)	0.50/< 0.001	NA			
FL-L1-0521	chr2:71410474-71418501	833	ZNF638 (antisense)	0.49/< 0.001	Yes (fibroblasts, immune cells)	NA	27	0
FL-L1-0585	chr2:110411395-110419526	153	AC108938.5 (same-stranded)	NA/NA	NA	Yes (normal samples, normal epithelial cells)	22	0
			RP13-1039J1.2 (same-stranded)	NA/NA	NA			
			RP13-1039J1.4 (same-stranded)	NA/NA	NA			
FL-L1-0654	chr2:143005044-143013076	742	KYNU (same-stranded)	0.97/< 0.001	Yes (immune cells)	Yes (tumor samples, immune cells)	27	0
FL-L1-0690	chr2:157396599-157397599	150	NA	NA/NA	NA	Yes (immune cells)	23	0
FL-L1-0783	chr2:196904589-196912619	702	PGAP1 (antisense)	0.55/< 0.001	Yes (tumor cells, immune cells)	NA	27	0
FL-L1-0808	chr2:212053824-212061959	97	ERBB4 (antisense)	0.44/< 0.001	Yes (tumor cells)	NA	18	0

FL-L1-0815	chr2:216453724-216461842	113	SMARCAL1 (same-stranded)	0.05/0.78	NA	NA	24	0
FL-L1-0831	chr2:232148196-232156229	136	DIS3L2 (antisense)	0.25/0.05	Yes (immune cells)	NA	25	0
FL-L1-0950	chr3:51454920-51463072	544	DCAF1 (antisense)	0.22/0.08	NA	NA	27	0
FL-L1-0965	chr3:57475938-57484084	263	DNAH12 (antisense)	0.83/< 0.001	Yes (tumor cells, fibro cells)	Yes (normal samples, normal epithelial cells)	27	0
FL-L1-0976	chr3:60959425-60967566	129	FHIT (same-stranded)	0.45/< 0.001	NA	NA	21	0
FL-L1-1112	chr3:112730267-112731267	295	NA	NA/NA	NA	Yes (tumor samples, tumor cells)	18	0
FL-L1-1116	chr3:116202385-116210424	174	LSAMP (same-stranded)	0.48/< 0.001	Yes (fibroblasts)	Yes (tumor samples, fibroblasts)	21	0
FL-L1-1125	chr3:119562180-119563180	303	NA	NA/NA	NA	Yes (tumor samples, immune cells)	24	1
FL-L1-1139	chr3:125848810-125856962	470	ENPP7P4 (same-stranded)	NA/NA	NA	NA	27	0
			RP11-379B18.5 (antisense)	NA/NA	NA			
FL-L1-1148	chr3:132370232-132371232	130	NA	NA/NA	NA	NA	22	0
FL-L1-1166	chr3:136478078-136486101	217	STAG1 (same-stranded)	0.38/0.001	Yes (tumor cells, immune cells)	NA	27	1
FL-L1-1190	chr3:142474105-142482225	640	ATR (same-stranded)	0.72/< 0.001	NA	NA	27	0
FL-L1-1251	chr3:172658987-172667103	2176	NCEH1 (same-stranded)	0.79/ < 0.001	Yes (all cell types)	NA	27	0
FL-L1-1272	chr3:188371709-188379858	2004	LPP (antisense)	0.30/0.01	Yes (normal epithelial cells)	NA	27	0

FL-L1-1391	chr4:53327731-5335762	129	SCFD2 (antisense)	-0.06/0.67	NA	NA	23	0
FL-L1-1394	chr4:53465373-53473500	189	LNK1 (antisense),	-0.002/0.98	Yes (tumor cells)	NA	25	1
			RP11-231C18.3 (same-stranded)	NA/NA	NA			
FL-L1-1468	chr4:72513834-72521993	111	ADAMTS3 (same-stranded)	0.15/0.27	Yes (fibroblasts)	Yes (fibroblasts)	17	0
FL-L1-1501	chr4:80668983-80677169	301	C4orf22 (antisense)	0.79/< 0.001	Yes (normal epithelial cells, fibroblasts)	Yes (normal samples, normal epithelial cells)	24	0
FL-L1-1532	chr4:90478376-90486523	95	CCSER1 (antisense)	0.72/< 0.001	Yes (tumor cells)	Yes (normal epithelial cells)	20	0
FL-L1-1568	chr4:98591435-98599461	97	TSPAN5 (same-stranded)	0.03/0.86	Yes (immune cells)	NA	24	0
FL-L1-1594	chr4:105879181-105887196	198	INTS12 (antisense)	-0.08/0.57	NA	Yes (normal epithelial cells)	25	1
FL-L1-1644	chr4:122938633-122946796	257	SPATA5 (antisense)	0.09/0.54	Yes (immune cells)	NA	27	0
FL-L1-1718	chr4:151510300-151518459	359	FAM160A1 (same-stranded)	0.39/< 0.001	NA	NA	25	0
FL-L1-1867	chr5:42937866-42938866	254	NA	NA/NA	NA	Yes (normal samples)	21	0
FL-L1-1872	chr5:43666275-43674422	464	NNT (antisense),	0.11/0.44	NA	NA	27	0
			RPL29P12 (same-stranded)	0.94/< 0.001	Yes (fibroblasts)			
FL-L1-1998	chr5:78434233-78442331	155	SCAMP1 (antisense)	0.03/0.86	NA	NA	21	0
FL-L1-2050	chr5:93760070-93768199	820	FAM172A (antisense)	0.23/0.06	Yes (fibroblasts, immune cells)	NA	27	0
FL-L1-2121	chr5:119438179-119446196	137	RNA5SP190 (same-stranded)	0.99/< 0.001	NA	Yes (tumor samples, fibroblasts)	21	0

FL-L1-2166	chr5:132519996-132520996	140	NA	NA/NA	NA	NA	24	4
FL-L1-2194	chr5:150741837-150749950	190	DCTN4 (antisense)	-0.04/0.79	NA	NA	25	0
FL-L1-2276	chr6:12138368-12146531	169	HIVEP1 (same-stranded)	0.27/0.03	Yes (tumor cells)	NA	27	6
FL-L1-2293	chr6:24810678-24818704	514	FAM65B (same-stranded)	0.89/< 0.001	Yes (immune cells)	Yes (normal samples)	26	1
FL-L1-2310	chr6:44869634-44877665	180	AL161905.1 (antisense),	NA/NA	NA	NA	24	0
			SUPT3H (antisense)	0.29/0.02	NA			
FL-L1-2564	chr6:116637699-116645834	111	ZUFSP (antisense)	0.16/0.21	NA	NA	25	0
FL-L1-2677	chr7:22923196-22931356	296	FAM126A (antisense)	0.57/< 0.001	Yes (fibroblasts, immune cells)	NA	27	0
FL-L1-2690	chr7:30438244-30446274	878	NOD1 (antisense)	0.23/0.07	Yes (immune cells)	NA	27	0
FL-L1-2712	chr7:36551968-36560126	107	AOAH (same-stranded)	0.76/< 0.001	Yes (immune cells)	Yes (normal samples, immune cells)	17	2
FL-L1-2763	chr7:70196331-70204357	139	AUTS2 (same-stranded)	0.04/0.78	NA	NA	23	0
FL-L1-2776	chr7:83988325-83996342	552	SEMA3A (same-stranded)	0.85/< 0.001	Yes (tumor cells, fibroblasts)	NA	24	0
FL-L1-2842	chr7:108386569-108394721	118	NRCAM (same-stranded)	0.56/< 0.001	NA	NA	18	0
FL-L1-2890	chr7:130576798-130584457	96	COPG2 (antisense)	0.15/0.25	NA	Yes (tumor samples)	23	0
FL-L1-2903	chr7:140102318-140110394	1049	KDM7A (same-stranded)	0.40/< 0.001	Yes (fibroblasts, immune cells)	NA	27	0
FL-L1-2919	chr7:147841591-147849620	159	CNTNAP2 (antisense)	-0.008/0.95	NA	NA	8	3

FL-L1-2956	chr8:15555008-1 5563026	222	TUSC3 (antisense)	0.48/< 0.001	NA	NA	26	0
FL-L1-2974	chr8:26394612-2 6402579	542	BNIP3L (same-stranded)	0.09/0.55	Yes (immune)	NA	27	0
FL-L1-3027	chr8:47483871-4 7492006	429	SPIDR (same-stranded)	0.56/ < 0.001	Yes (immune cells)	NA	27	0
FL-L1-3030	chr8:48333021-4 8334021	294	NA	NA/NA	NA	Yes (tumor samples)	12	0
FL-L1-3047	chr8:53779543-5 3787666	802	ATP6V1H (same-stranded)	0.55/< 0.001	Yes (tumor cells, immune cells)	NA	27	0
FL-L1-3048	chr8:54579988-5 4588142	207	RP1 (antisense)	0.84/< 0.001	Yes (tumor cells)	Yes (normal samples, normal epithelial cells)	26	0
FL-L1-3194	chr8:98693365-9 8701518	1114	STK3 (same-stranded)	0.71/< 0.001	Yes (fibroblasts)	NA	27	0
FL-L1-3215	chr8:105788089- 105796234	370	ZFPM2 (antisense),	-0.01/0.94	NA	NA	21	0
			ZFPM2-AS1 (same-stranded)	NA/NA	NA			
FL-L1-3238	chr8:118530003- 118537089	128	SAMD12 (same-stranded)	0.60/< 0.001	Yes (tumor cells)	Yes (tumor samples, tumor cells)	24	3
FL-L1-3248	chr8:120643161- 120651187	100	SNTB1 (same-stranded)	0.28/0.02	NA	NA	24	0
FL-L1-3307	chr9:5030773-50 38865	334	JAK2 (same-stranded)	-0.03/0.86	NA	NA	26	1
FL-L1-3310	chr9:5721562-57 29670	708	RIC1 (antisense)	-0.04/0.80	Yes (immune cells)	NA	27	0
FL-L1-3345	chr9:21818140-2 1826239	1295	MTAP (antisense),	0.21/0.10	Yes (immune cells)	NA	27	0
			RP11-145E5.5 (antisense)	NA/NA	NA			
FL-L1-3437	chr9:83048539-8 3056569	235	RASEF (same-stranded)	0.64/< 0.001	NA	NA	21	1
FL-L1-3566	chr10:35472782- 35480771	325	CCNY (same-stranded)	0.14/0.30	NA	NA	27	0

FL-L1-3636	chr10:74215882-74224021	384	ADK (same-stranded)	-0.08/0.56	Yes (fibroblasts)	NA	27	4
FL-L1-3645	chr10:78094479-78095479	136	NA	NA/NA	NA	NA	21	1
FL-L1-3670	chr10:87896804-87904979	1292	PTEN (antisense)	0.25/0.04	Yes (immune cells)	NA	27	0
FL-L1-3721	chr10:111049281-111050281	246	NA	NA/NA	NA	Yes (tumor samples)	25	0
FL-L1-3741	chr10:129731560-129739580	107	MGMT (antisense)	0.24/0.05	NA	Yes (normal samples)	20	0
FL-L1-3767	chr11:9539333-9540333	127	NA	NA/NA	NA	NA	21	0
FL-L1-3778	chr11:14660329-14668447	178	PDE3B (same-stranded)	0.83/< 0.001	Yes (immune cells)	Yes (immune cells)	24	3
FL-L1-3779	chr11:14714908-14722938	181	PDE3B (same-stranded)	0.78/< 0.001	Yes (immune cells)	Yes (immune cells)	23	6
FL-L1-3780	chr11:14776675-14784773	521	PDE3B (same-stranded)	0.93/< 0.001	Yes (immune cells)	Yes (immune cells)	26	8
FL-L1-3945	chr11:71510047-71518198	96	NADSYN1 (same-stranded)	0.31/0.01	NA	NA	22	0
FL-L1-3949	chr11:74886437-74894565	153	RP11-14713.1 (same-stranded)	NA/NA	NA	NA	25	2
			XRRA1 (antisense)	0.02/0.88	NA			
FL-L1-3997	chr11:93171447-93179521	178	RP11-573M3.2 (antisense),	NA/NA	NA	NA	23	0
			SLC36A4 (same-stranded)	0.27/0.02	NA			
FL-L1-4034	chr11:107371762-107379780	213	CWF19L2 (antisense)	0.38/0.001	NA	Yes (normal samples)	26	0
FL-L1-4122	chr12:26668557-26676709	179	ITPR2 (antisense)	0.18/0.15	NA	NA	27	0
FL-L1-4311	chr12:96314944-96322971	451	CDK17 (antisense)	0.42/< 0.001	Yes (immune cells)	NA	27	0
FL-L1-4344	chr12:126298010-126306038	103	RP4-809F18.1 (antisense)	NA/NA	NA	Yes (tumor samples, fibroblasts)	10	0

FL-L1-4371	chr13:29822715-29830837	337	UBL3 (same-stranded)	0.39/< 0.001	Yes (tumor cells)	NA	27	0
FL-L1-4405	chr13:50179295-50187327	174	DLEU1 (antisense)	0.35/0.003	Yes (immune cells)	Yes (tumor samples)	24	3
FL-L1-4598	chr14:56227636-56235747	198	PELI2 (same-stranded)	0.33/0.006	Yes (immune cells)	NA	27	0
FL-L1-4634	chr14:70546296-70554322	176	RP11-486O13.4 (antisense)	NA/NA	NA	NA	21	0
FL-L1-4719	chr15:52471398-52479553	496	MYO5A (same-stranded)	0.62/< 0.001	Yes (immune cells)	Yes (immune cells)	27	1
FL-L1-4731	chr15:56133618-56141628	142	RFX7 (same-stranded)	0.17/0.18	NA	NA	25	2
FL-L1-4738	chr15:64325660-64333700	7924	CSNK1G1 (antisense),	0.32/0.009	Yes (normal epithelial cells, fibroblasts)	NA	27	0
			CTD-2116N17.1 (antisense)	NA/NA	NA			
FL-L1-4766	chr15:85432963-85440965	156	AKAP13 (same-stranded)	-0.05/0.78	Yes (tumor cells)	NA	27	1
FL-L1-4792	chr15:100082863-100090998	223	ADAMTS17 (antisense)	0.25/0.04	Yes (immune cells)	NA	26	0
FL-L1-4811	chr16:31344038-31345038	95	NA	NA/NA	NA	Yes (tumor samples)	19	0
FL-L1-4815	chr16:31943726-31944726	113	NA	NA/NA	NA	NA	19	0
FL-L1-4886	chr16:72579798-72587932	212	LINC01572 (antisense)	0.21/0.10	NA	NA	27	0
FL-L1-4939	chr17:66595579-66603592	802	PRKCA (antisense)	0.10/0.47	Yes (immune cells)	Yes (tumor samples)	24	0
FL-L1-4968	chr18:13342089-13350216	146	LDLRAD4 (antisense)	0.04/0.79	NA	NA	26	0
FL-L1-5023	chr18:49101418-49109547	293	DYM (same-stranded)	0.11/0.43	NA	NA	26	10
FL-L1-5063	chr19:12003811-12011812	104	CTD-2006C1.2 (antisense)	NA/NA	NA	NA	26	3
FL-L1-5102	chr19:40036915-40045054	566	ZNF780B (same-stranded)	0.04/0.82	Yes (immune cells)	NA	27	1

FL-L1-5141	chr20:23432140-23433140	146	NA	NA/NA	NA	Yes (tumor samples, tumor cells)	21	16
FL-L1-5154	chr20:35070283-35078389	501	TRPC4AP (same-stranded)	0.35/0.003	Yes (immune cells)	NA	27	0
FL-L1-5210	chr22:23661983-23670138	2336	AP000347.2 (antisense),	0.65/< 0.001	Yes (immune cells)	NA	27	0
			GUSBP11 (antisense),	NA/NA	NA			
			KB-1572G7.2 (antisense)	NA/NA	NA			
FL-L1-5219	chr22:28662285-28670315	160	TTC28 (antisense)	-0.05/0.78	NA	Yes (tumor samples, tumor cells)	18	18
Helman2014-185	chr18:72844266-72848167	642	NETO1 (same-stranded)	0.94/< 0.001	Yes (fibroblasts)	Yes (tumor samples, fibroblasts)	17	3
Lee2012-414	chr7:77091735-77095636	323	FAM185BP (antisense),	0.27/0.03	NA	NA	27	0
			RP11-467H10.2 (same-stranded)	NA/NA	NA			
Schwahn1998-464	chrX:46834934-46838835	211	RP2 (same-stranded)	0.11/0.43	Yes (immune cells)	NA	26	24
Shukla2013-141	chr14:94173729-94177630	171	PPP4R4 (same-stranded)	0.65/< 0.001	Yes (fibroblasts)	NA	25	4
Shukla2013-194	chr2:36389671-36393572	1037	CRIM1 (same-stranded)	0.50/< 0.001	Yes (tumor cells, immune cells)	NA	27	1
Shukla2013-41	chr10:7980124-7984025	145	TAF3 (same-stranded)	0.27/0.03	NA	NA	25	0
Shukla2013-425	chr7:135157267-135161168	814	C7orf49 (antisense),	-0.11/0.43	NA	Yes (immune cells)	27	23
			TMEM140 (same-stranded)	0.24/0.06	Yes (tumor cells, immune cells)			
Shukla2013-85	chr11:117322084-117325985	173	AP000892.4 (same-stranded)	NA/NA	NA	NA	26	0
			CEP164 (antisense)	0.14/0.30	NA			

Supplementary Table 3. Primers used for RT-PCR.

Target locus	Primer name	Sequence (5'-3')
L1-5141	L1_008 (forward)	AGATATACCTAATGCTAGA TGACACA
L1-5141	L1_54A (reverse)	GCATCTTATCGACTGGTG CATG
L1-5219	L1_008 (forward)	AGATATACCTAATGCTAGA TGACACA
L1-5219	L1_003 (reverse)	ATTTTGGCCCTAACTGGT CACA
L1-4344	L1_008 (forward)	AGATATACCTAATGCTAGA TGACACA
L1-4344	L1_4344_dR2 (reverse)	AACATGTCAACCTGCAGA ACC
ACTB	MT_126 (forward)	AGAAAATCTGGCACCACA CC
ACTB	MT_127 (reverse)	AGAGGCGTACAGGGATAG CA