

Annotation	Survey	Fisher's exact test			overlap		no overlap	
		Odds ratio	P-value	95% CI	DE-Probes	BG	DE-Probes	BG
Overlap with protein coding genes and intergenic space (all DE-probes)								
Normal vs. Tumor								
CDS (antisense)	Normal > Tumor	0.86	1.87e-02	[0.76, 0.98]	259	6159	9497	194434
	Normal < Tumor	2.06	3.40e-56	[1.90, 2.24]	665	6159	10182	194434
CDS (sense)	Normal > Tumor	3.96	0.00e+00	[3.76, 4.16]	2229	13972	7527	186621
	Normal < Tumor	1.29	1.17e-12	[1.21, 1.38]	957	13972	9890	186621
intergenic	Normal > Tumor	0.27	0.00e+00	[0.25, 0.28]	992	59919	8764	140674
	Normal < Tumor	0.91	5.65e-06	[0.87, 0.95]	3019	59919	7828	140674
introns (antisense)	Normal > Tumor	0.32	9.74e-267	[0.29, 0.34]	739	41391	9017	159202
	Normal < Tumor	0.91	3.06e-04	[0.87, 0.96]	2083	41391	8764	159202
introns (sense)	Normal > Tumor	0.99	5.94e-01	[0.94, 1.04]	1909	39702	7847	160891
	Normal < Tumor	0.72	9.27e-35	[0.68, 0.76]	1640	39702	9207	160891
3'UTRs (antisense)	Normal > Tumor	0.53	2.52e-31	[0.47, 0.60]	300	11280	9456	189313
	Normal < Tumor	1.29	1.97e-10	[1.19, 1.39]	773	11280	10074	189313
3'UTRs (sense)	Normal > Tumor	3.44	0.00e+00	[3.29, 3.60]	3159	24480	6597	176113
	Normal < Tumor	1.17	8.30e-08	[1.10, 1.24]	1515	24480	9332	176113
5'UTRs (antisense)	Normal > Tumor	0.77	6.77e-02	[0.56, 1.02]	48	1288	9708	199305
	Normal < Tumor	2.04	2.69e-13	[1.70, 2.43]	141	1288	10706	199305
5'UTRs (sense)	Normal > Tumor	2.60	1.32e-30	[2.24, 3.01]	209	1673	9547	198920
	Normal < Tumor	1.69	9.51e-09	[1.42, 2.00]	152	1673	10695	198920
Basal-like vs. Luminal Tumors								
CDS (antisense)	BL > Luminal	2.49	1.44e-24	[2.12, 2.91]	176	6159	2230	194434
	BL < Luminal	1.66	1.37e-03	[1.21, 2.22]	48	6159	914	194434
CDS (sense)	BL > Luminal	5.97	6.39e-263	[5.46, 6.52]	743	13972	1663	186621
	BL < Luminal	2.99	2.58e-31	[2.52, 3.53]	176	13972	786	186621
intergenic	BL > Luminal	0.12	3.38e-208	[0.10, 0.15]	120	59919	2286	140674
	BL < Luminal	0.52	8.68e-17	[0.44, 0.61]	174	59919	788	140674
introns (antisense)	BL > Luminal	0.22	2.07e-99	[0.18, 0.26]	129	41391	2277	159202
	BL < Luminal	0.49	1.55e-14	[0.39, 0.60]	108	41391	854	159202
introns (sense)	BL > Luminal	0.22	2.39e-95	[0.18, 0.26]	123	39702	2283	160891
	BL < Luminal	0.54	3.90e-11	[0.44, 0.66]	113	39702	849	160891
3'UTRs (antisense)	BL > Luminal	1.17	6.16e-02	[0.99, 1.38]	157	11280	2249	189313
	BL < Luminal	1.10	4.83e-01	[0.83, 1.43]	59	11280	903	189313
3'UTRs (sense)	BL > Luminal	5.20	4.21e-288	[4.79, 5.65]	1010	24480	1396	176113
	BL < Luminal	2.98	5.03e-45	[2.59, 3.44]	282	24480	680	176113
5'UTRs (antisense)	BL > Luminal	0.58	1.20e-01	[0.26, 1.11]	9	1288	2397	199305
	BL < Luminal	1.13	6.83e-01	[0.45, 2.35]	7	1288	955	199305
5'UTRs (sense)	BL > Luminal	1.45	5.48e-02	[0.97, 2.10]	29	1673	2377	198920
	BL < Luminal	1.76	4.76e-02	[0.95, 2.97]	14	1673	948	198920
Overlap with known non-coding RNAs (non-coding DE-probes)								
Normal vs. Tumor								

Annotation	Survey	Fisher's exact test			overlap		no overlap	
		Odds ratio	P-value	95% CI	DE-Probes	BG	DE-Probes	BG
CARs	Normal > Tumor	5.75	8.22e-95	[4.99, 6.60]	250	2073	2574	122732
	Normal < Tumor	0.84	1.39e-01	[0.67, 1.06]	81	2073	5685	122732
Evofold	Normal > Tumor	0.36	6.00e-22	[0.27, 0.46]	65	7726	2759	117079
	Normal < Tumor	0.32	2.11e-48	[0.27, 0.39]	120	7726	5646	117079
lincRNAs	Normal > Tumor	2.81	1.24e-13	[2.18, 3.57]	73	1167	2751	123638
	Normal < Tumor	0.91	5.74e-01	[0.67, 1.21]	49	1167	5717	123638
lncRNAdb	Normal > Tumor	10.09	3.88e-47	[7.78,12.95]	79	355	2745	124450
	Normal < Tumor	0.61	1.26e-01	[0.29, 1.13]	10	355	5756	124450
lncRNAs (Gencode)	Normal > Tumor	1.81	1.60e-03	[1.24, 2.56]	34	834	2790	123971
	Normal < Tumor	1.38	2.67e-02	[1.02, 1.82]	53	834	5713	123971
PINs	Normal > Tumor	3.69	2.16e-10	[2.55, 5.20]	36	435	2788	124370
	Normal < Tumor	0.70	2.05e-01	[0.38, 1.18]	14	435	5752	124370
RNAz	Normal > Tumor	0.97	1.00e+00	[0.56, 1.57]	17	773	2807	124032
	Normal < Tumor	0.45	4.65e-04	[0.25, 0.73]	16	773	5750	124032
miRNAs	Normal > Tumor	0.94	1.00e+00	[0.30, 2.22]	5	236	2819	124569
	Normal < Tumor	1.19	5.34e-01	[0.63, 2.08]	13	236	5753	124569
snoRNAs or scaRNAs	Normal > Tumor	3.65	4.29e-08	[2.37, 5.42]	27	329	2797	124476
	Normal < Tumor	4.92	2.63e-25	[3.76, 6.36]	74	329	5692	124476
SISSlz	Normal > Tumor	1.01	9.39e-01	[0.73, 1.36]	45	1976	2779	122829
	Normal < Tumor	1.51	1.11e-05	[1.26, 1.80]	137	1976	5629	122829
TINs	Normal > Tumor	2.28	4.41e-14	[1.87, 2.77]	114	2260	2710	122545
	Normal < Tumor	0.80	4.78e-02	[0.64, 1.00]	84	2260	5682	122545
TUCP	Normal > Tumor	4.58	4.02e-13	[3.16, 6.44]	37	361	2787	124444
	Normal < Tumor	0.72	3.12e-01	[0.37, 1.27]	12	361	5754	124444
Basal-like vs. Luminal Tumors								
CARs	BL > Luminal	0.37	5.31e-01	[0.01, 2.10]	1	2073	162	122732
	BL < Luminal	1.90	6.32e-02	[0.86, 3.70]	9	2073	281	122732
Evofold	BL > Luminal	0.38	4.90e-02	[0.10, 1.00]	4	7726	159	117079
	BL < Luminal	0.60	1.11e-01	[0.29, 1.10]	11	7726	279	117079
lincRNAs	BL > Luminal	1.32	6.67e-01	[0.16, 4.80]	2	1167	161	123638
	BL < Luminal	1.11	7.55e-01	[0.23, 3.30]	3	1167	287	123638
lncRNAdb	BL > Luminal	11.09	1.20e-04	[3.53,26.70]	5	355	158	124450
	BL < Luminal	0.00	1.00e+00	[0.00, 4.50]	0	355	290	124450
lncRNAs (Gencode)	BL > Luminal	6.67	1.31e-04	[2.63,14.10]	7	834	156	123971
	BL < Luminal	1.03	7.21e-01	[0.12, 3.80]	2	834	288	123971
PINs	BL > Luminal	0.00	1.00e+00	[0.00, 6.60]	0	435	163	124370
	BL < Luminal	0.99	1.00e+00	[0.02, 5.60]	1	435	289	124370
RNAz	BL > Luminal	3.01	8.19e-02	[0.61, 9.00]	3	773	160	124032
	BL < Luminal	1.11	7.02e-01	[0.13, 4.10]	2	773	288	124032
miRNAs	BL > Luminal	0.00	1.00e+00	[0.00,12.20]	0	236	163	124569
	BL < Luminal	0.00	1.00e+00	[0.00, 6.80]	0	236	290	124569
snoRNAs or scaRNAs	BL > Luminal	7.09	9.63e-03	[1.44,21.30]	3	329	160	124476
	BL < Luminal	2.63	1.79e-01	[0.32, 9.70]	2	329	288	124476
SISSlz	BL > Luminal	0.00	1.92e-01	[0.00, 1.40]	0	1976	163	122829
	BL < Luminal	1.99	5.32e-02	[0.90, 3.80]	9	1976	281	122829

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		Odds ratio	P-value	95% CI	DE-Probes	BG	DE-Probes	BG
TINs	BL > Luminal	3.54	8.60e-04	[1.66, 6.70]	10	2260	153	122545
	BL < Luminal	0.38	1.86e-01	[0.05, 1.40]	2	2260	288	122545
TUCP	BL > Luminal	4.28	8.19e-02	[0.51,15.80]	2	361	161	124444
	BL < Luminal	1.19	5.69e-01	[0.03, 6.70]	1	361	289	124444
Overlap with known non-coding RNAs regulated during cell cycle, upon TP53 or Stat3 induction (non-coding DE-probes)								
Normal vs. Tumor								
CC (intergenic)	Normal > Tumor	2.75	7.14e-06	[1.79, 4.06]	27	437	2797	124368
	Normal < Tumor	0.59	8.28e-02	[0.30, 1.05]	12	437	5754	124368
CC (intron)	Normal > Tumor	2.15	1.13e-12	[1.76, 2.60]	116	2440	2708	122365
	Normal < Tumor	0.63	4.45e-05	[0.49, 0.79]	71	2440	5695	122365
P53 (intergenic)	Normal > Tumor	3.33	7.85e-12	[2.42, 4.48]	48	645	2776	124160
	Normal < Tumor	1.01	9.25e-01	[0.67, 1.45]	30	645	5736	124160
P53 (intron)	Normal > Tumor	2.41	5.33e-40	[2.14, 2.72]	328	6445	2496	118360
	Normal < Tumor	0.52	2.36e-18	[0.44, 0.61]	160	6445	5606	118360
Stat3 (intergenic)	Normal > Tumor	0.50	2.98e-01	[0.10, 1.47]	3	266	2821	124539
	Normal < Tumor	0.49	7.62e-02	[0.18, 1.08]	6	266	5760	124539
Stat3 (intron)	Normal > Tumor	0.67	3.97e-01	[0.24, 1.47]	6	397	2818	124408
	Normal < Tumor	0.98	1.00e+00	[0.58, 1.57]	18	397	5748	124408
Basal-like vs. Luminal Tumors								
CC (intergenic)	BL > Luminal	7.16	2.79e-03	[1.92,18.80]	4	437	159	124368
	BL < Luminal	0.98	1.00e+00	[0.03, 5.60]	1	437	289	124368
CC (intron)	BL > Luminal	1.92	1.42e-01	[0.69, 4.30]	6	2440	157	122365
	BL < Luminal	1.42	2.87e-01	[0.61, 2.80]	8	2440	282	122365
P53 (intergenic)	BL > Luminal	11.25	2.44e-07	[5.03,22.00]	9	645	154	124160
	BL < Luminal	0.67	1.00e+00	[0.02, 3.80]	1	645	289	124160
P53 (intron)	BL > Luminal	3.33	1.19e-06	[2.08, 5.10]	25	6445	138	118360
	BL < Luminal	1.22	4.23e-01	[0.71, 2.00]	18	6445	272	118360
Stat3 (intergenic)	BL > Luminal	0.00	1.00e+00	[0.00,10.80]	0	266	163	124539
	BL < Luminal	1.62	4.62e-01	[0.04, 9.20]	1	266	289	124539
Stat3 (intron)	BL > Luminal	0.00	1.00e+00	[0.00, 7.20]	0	397	163	124408
	BL < Luminal	2.18	2.37e-01	[0.26, 8.00]	2	397	288	124408
Overlap with regulation tracks (non-coding DE-probes)								
Normal vs. Tumor								
CpG	Normal > Tumor	2.06	6.71e-08	[1.60, 2.62]	72	1565	2752	123240
	Normal < Tumor	2.92	5.06e-36	[2.50, 3.38]	206	1565	5560	123240
CpG and H3K4me3	Normal > Tumor	2.17	2.99e-08	[1.67, 2.78]	68	1402	2756	123403
	Normal < Tumor	2.95	1.82e-33	[2.51, 3.45]	187	1402	5579	123403
DNaseI	Normal > Tumor	1.51	2.68e-24	[1.39, 1.63]	1041	34856	1783	89949
	Normal < Tumor	1.34	7.21e-24	[1.26, 1.42]	1969	34856	3797	89949
H3K27ac	Normal > Tumor	2.81	7.82e-160	[2.61, 3.04]	1613	40108	1211	84697
	Normal < Tumor	1.34	9.55e-26	[1.27, 1.42]	2240	40108	3526	84697
H3k27me3	Normal > Tumor	0.51	1.26e-63	[0.48, 0.56]	1616	90135	1208	34670
	Normal < Tumor	1.34	1.63e-20	[1.26, 1.43]	4480	90135	1286	34670

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		Odds ratio	P-value	95% CI	DE-Probes	BG	DE-Probes	BG
H3K36me3	Normal > Tumor	4.86	1.40e-243	[4.35, 5.44]	2458	72412	366	52393
	Normal < Tumor	1.01	8.06e-01	[0.95, 1.06]	3355	72412	2411	52393
H3K4me1	Normal > Tumor	2.43	6.65e-89	[2.21, 2.68]	2281	79050	543	45755
	Normal < Tumor	1.48	5.28e-41	[1.39, 1.57]	4144	79050	1622	45755
H3K4me3	Normal > Tumor	2.54	2.48e-124	[2.36, 2.74]	1304	31493	1520	93312
	Normal < Tumor	1.62	3.04e-62	[1.53, 1.71]	2039	31493	3727	93312
Pol II	Normal > Tumor	4.15	2.04e-279	[3.84, 4.47]	1389	23618	1435	101187
	Normal < Tumor	1.41	1.26e-26	[1.33, 1.50]	1428	23618	4338	101187
TFBs (Encode)	Normal > Tumor	1.76	1.82e-39	[1.62, 1.91]	869	25175	1955	99630
	Normal < Tumor	1.53	9.03e-43	[1.44, 1.63]	1609	25175	4157	99630
Basal-like vs. Luminal Tumors								
CpG	BL > Luminal	1.48	4.63e-01	[0.30, 4.40]	3	1565	160	123240
	BL < Luminal	2.23	3.17e-02	[0.95, 4.47]	8	1565	282	123240
CpG and H3K4me3	BL > Luminal	1.65	4.36e-01	[0.34, 4.92]	3	1402	160	123403
	BL < Luminal	2.18	4.76e-02	[0.87, 4.56]	7	1402	283	123403
DNaseI	BL > Luminal	1.24	1.91e-01	[0.88, 1.74]	53	34856	110	89949
	BL < Luminal	1.42	4.80e-03	[1.11, 1.82]	103	34856	187	89949
H3K27ac	BL > Luminal	2.74	2.12e-10	[1.99, 3.78]	92	40108	71	84697
	BL < Luminal	1.29	3.77e-02	[1.01, 1.65]	110	40108	180	84697
H3k27me3	BL > Luminal	0.34	7.63e-12	[0.24, 0.46]	76	90135	87	34670
	BL < Luminal	1.26	1.01e-01	[0.95, 1.67]	222	90135	68	34670
H3K36me3	BL > Luminal	10.00	5.48e-24	[5.43,20.45]	152	72412	11	52393
	BL < Luminal	1.07	5.92e-01	[0.84, 1.36]	173	72412	117	52393
H3K4me1	BL > Luminal	2.37	2.88e-06	[1.60, 3.61]	131	79050	32	45755
	BL < Luminal	1.13	3.29e-01	[0.88, 1.46]	192	79050	98	45755
H3K4me3	BL > Luminal	1.82	3.90e-04	[1.30, 2.52]	62	31493	101	93312
	BL < Luminal	1.23	1.19e-01	[0.94, 1.59]	85	31493	205	93312
Pol II	BL > Luminal	4.23	9.39e-19	[3.07, 5.83]	81	23618	82	101187
	BL < Luminal	1.41	1.31e-02	[1.07, 1.86]	72	23618	218	101187
TFBs (Encode)	BL > Luminal	1.33	1.18e-01	[0.91, 1.91]	41	25175	122	99630
	BL < Luminal	1.75	2.61e-05	[1.35, 2.26]	89	25175	201	99630