

RNASeq

id	sum-lncRNA(lnc)	sum-protein-coding(pc)	ratio-lnc/pc(percent)
GM12878 _{Rep1} <i>PolyARNA</i>	13349	797031	1.67484
GM12878 _{Rep2} <i>PolyARNA</i>	13934	808673	1.72307
GM12878 _{Rep3} <i>PolyARNA</i>	14128	797404	1.77175
GM12891 _{Rep1} <i>PolyARNA</i>	11198	827839	1.35268
GM12891 _{Rep2} <i>PolyARNA</i>	10921	819825	1.33211
GM12891 _{Rep3} <i>PolyARNA</i>	10356	824319	1.25631

RP

id	sum-lncRNA(lnc)	sum-protein-coding(pc)	ratio-lnc/pc(percent)
SRR1803148	477912	869935	54.9365
SRR1803151	237654	925538	25.6774

RNASeq - Total

id	sum _{lncRNA} (lnc)	sum _{protein_coding} (pc)	ratio _{lnc/pc} (
H000.2T.7305	15955	793260	2.01132
H000.3T.9857	10802	728367	1.48304
H003.2T.7306	14688	815928	1.80016
H003.3T.9858	9418.6	748292	1.25868
H006.2T.7307	11829	825798	1.43243
H006.3T.9859	8805.9	737896	1.19338
H009.2T.7308	11358	795112	1.42848
H009.3T.12108	8892.7	726807	1.22353
H012.2T.7309	11076	758863	1.45955
H012.3T.9861	10771	883194	1.21955
H018.2T.7383	11467	778990	1.47203
H018.3T.9862	9295.8	721733	1.28798
H024.2T.7384	11403	743191	1.53433
H024.3T.9863	8829.4	729061	1.21106
H036.2T.7443	10314	820256	1.25741
H036.3T.9864	8958.2	725228	1.23523
H048.2T.7444	9809.9	801333	1.2242
H048.3T.9865	8214	718885	1.1426
H072.2T.7445	7245.4	772403	0.938034
H072.3T.9866	6704.3	712192	0.941361
H120.2T.7446	6576.7	759301	0.866152
H120.3T.9867	7800.2	715442	1.09026
H168.2T.7447	8484.3	827355	1.02547
H168.3T.9868	8630.3	773405	1.11588

RP

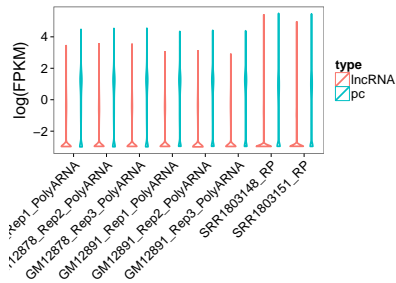
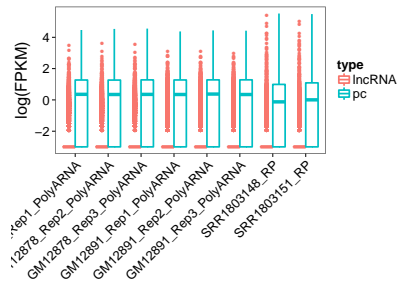
id	sum _{lncRNA} (lnc)	sum _{protein_coding} (pc)	ratio _{lnc/pc} (
H006.1RP.11895	821368	1002966	81.8939
H018.1RP.11896	144690	1149118	12.5914
H120.1RP.11897	94444	1072901	8.80268

RNASeq - Cytoplasm

id	sum _{lncRNA} (<i>lnc</i>)	sum _{protein_coding} (<i>pc</i>)	ratio _{lnc/pc} (
H000.2C.8986	12822	986133	1.30023
H000.3C.9539	11941	1087439	1.09808
H003.2C.8987	8935.8	995406	0.897704
H003.3C.9540	12004	1096988	1.09427
H006.2C.8988	9817.3	991627	0.990019
H006.3C.9541	9777	1035817	0.943893
H009.2C.8989	8859.3	975828	0.907875
H009.3C.9542	9098.3	998428	0.911263
H012.2C.8990	9019.3	964975	0.934667
H012.3C.9543	8832.8	964230	0.916047
H018.2C.8991	10109	989046	1.0221
H018.3C.9544	9249.3	954880	0.968635
H024.2C.8992	9487.4	928758	1.02151
H024.3C.9911	9302	990018	0.939579
H036.2C.8993	9339.5	945639	0.987639
H036.3C.9912	9148.1	1064567	0.859326
H048.2C.8994	7623.6	941293	0.809907
H048.3C.9913	8157.8	1026083	0.795043
H072.2C.8995	5930.2	936454	0.633261
H072.3C.9914	6577.1	1026260	0.64088
H120.2C.8996	9942.8	1004718	0.989611
H120.3C.9915	7199.2	1020129	0.705715
H168.2C.8997	12182	1024853	1.18866
H168.3C.9916	9996.8	1098374	0.910145

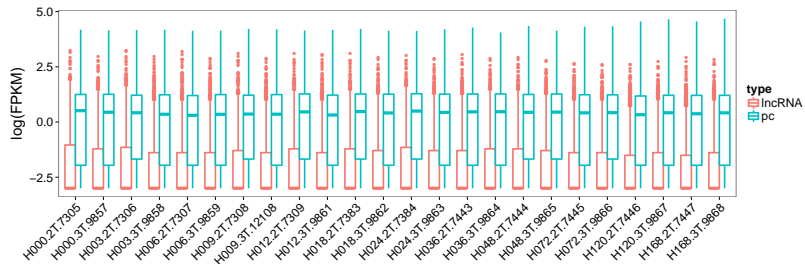
RNAseq - nucleus

id	sum _l ncRNA(<i>lnc</i>)	sum _p protein _c oding(<i>pc</i>)	ratio _l nc/ <i>pc</i> (
H000.2N.8998	26231	608031	4.31409
H000.3N.9845	27182	904210	3.00616
H003.2N.8999	24290	573806	4.23314
H003.3N.9846	25051	813617	3.07897
H006.2N.9000	26886	543965	4.9426
H006.3N.9847	17045	702063	2.42784
H009.2N.9001	22321	530339	4.20882
H009.3N.9848	16369	633340	2.58455
H012.2N.9002	24536	668684	3.6693
H012.3N.12109	18008	654835	2.75001
H018.2N.9003	24915	622039	4.00538
H018.3N.9850	16233	723133	2.24482
H024.2N.9004	24319	577529	4.21087
H024.3N.9851	19722	647133	3.0476
H036.2N.9005	24146	597786	4.03924
H036.3N.9852	15859	698159	2.27155
H048.2N.9006	19861	582878	3.4074
H048.3N.9853	11872	616362	1.92614
H072.2N.9007	13212	593984	2.2243
H072.3N.9854	11126	738629	1.5063
H120.2N.9008	17385	801007	2.17039
H120.3N.9855	12961	720797	1.79815
H168.2N.9009	18902	925825	2.04164
H168.3N.9856	13140	851323	1.54348

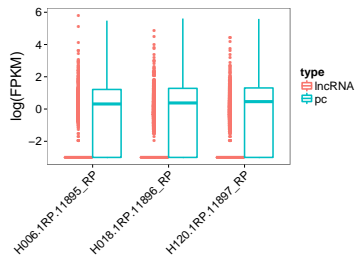


ERC

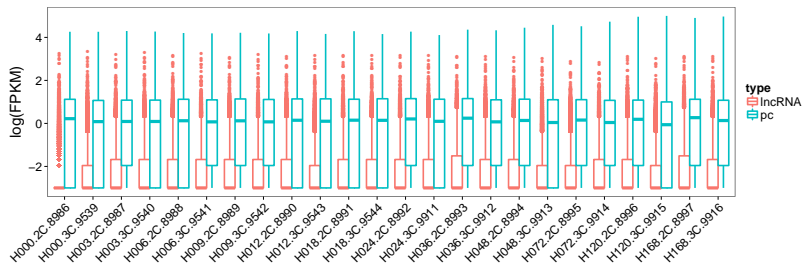
RNaseq total fraction



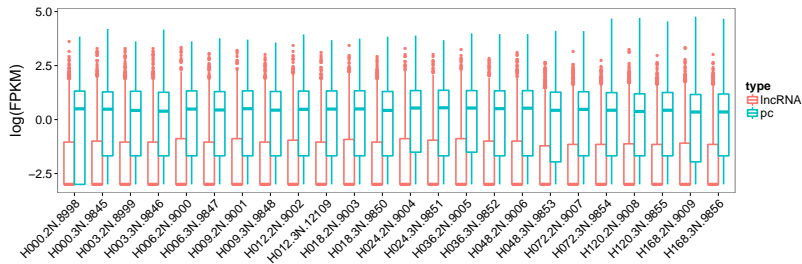
Riboprofiling



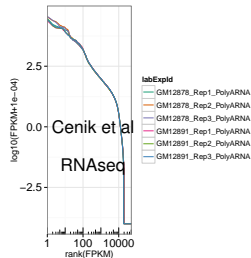
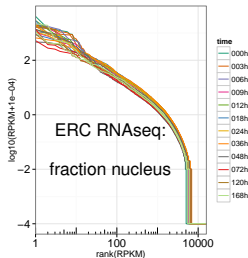
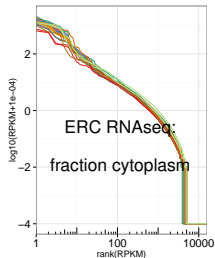
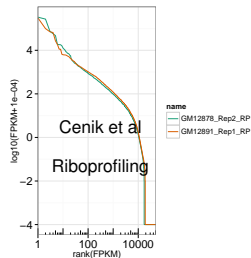
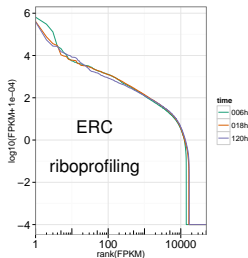
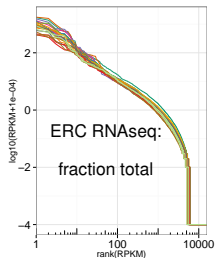
RNAseq cytoplasmic fraction



RNAseq nucleus fraction

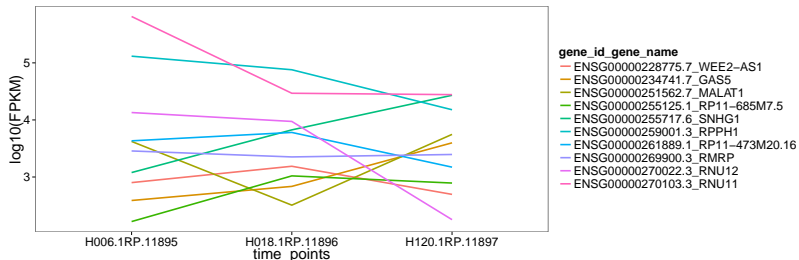


ERC VS Cenik et al, 2015



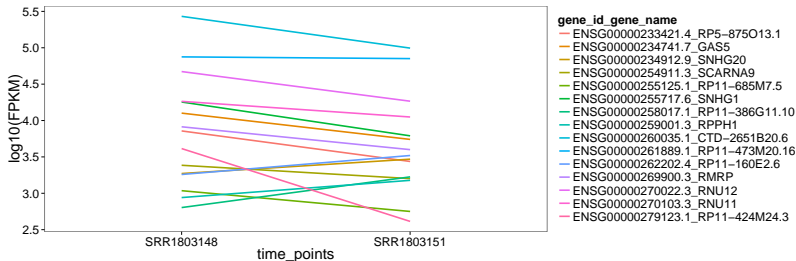
ERC - gene expression > 1000 FPKM in at least in RP sample

gene-id	H006.1RP.11895	H018.1RP.11896	H120.1RP.11897	classif
ENSG00000234741.7	387.63	684.69	3970.16	shortRNA
ENSG00000228775.7	797.58	1542.59	496.05	shortRNA
ENSG00000255125.1	165.72	1046.07	783.64	shortRNA
ENSG00000255717.6	1197.13	6694.68	27041.69	shortRNA
ENSG00000261889.1	4304.4	6037.68	1488.18	mm
ENSG00000270103.3	649682.6	29344.94	27750.05	mm+signal
ENSG00000269900.3	2860.36	2248.04	2481.17	signal
ENSG00000251562.7	4200.8	321.13	5581.65	signal
ENSG00000259001.3	131023.29	75755.26	15088.81	signal
ENSG00000270022.3	13480.13	9413.11	178.84	signal



Cenik et al - gene expression > 1000 FPKM in at least in RP sample

gene-id	SRR1803148	SRR1803151	classif
ENSG00000234741.7	12639.79	5502.08	shortRNA
ENSG00000255125.1	1085.6	562.74	shortRNA
ENSG00000255717.6	17970.55	6160.38	shortRNA
ENSG00000254911.3	2426.66	1591.96	shortRNA
ENSG00000234912.9	1868.62	2944.52	shortRNA
ENSG00000258017.1	636.4	1680.4	overlapping gene
ENSG00000233421.4	7194.4	2737.51	mm
ENSG00000260035.1	270303.41	98952.3	mm
ENSG00000279123.1	4116.18	410.76	mm
ENSG00000262202.4	1812.75	3305.11	mm
ENSG00000261889.1	74933.75	70953.92	mm+signal
ENSG00000270103.3	18346.52	11181.63	signal
ENSG00000269900.3	8201.85	3980.89	signal
ENSG00000259001.3	873.3	1506.44	signal
ENSG00000270022.3	47100.93	18434.31	signal



ERC - signal: ENSG00000269900.3 - RMRP - lincRNA

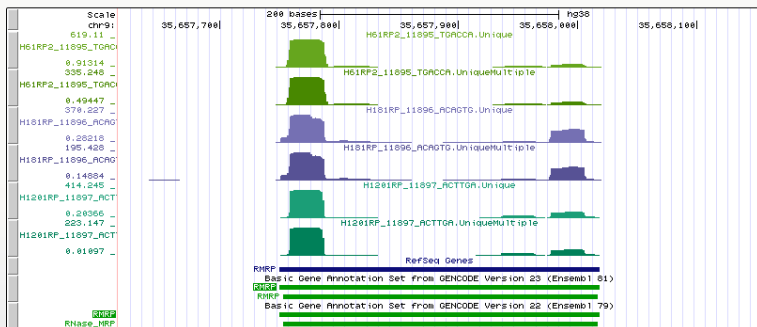
RNA component of mitochondrial RNA processing endoribonuclease

UCSC Genome Browser on Human Dec. 2013 (GRCh38/hg38) Assembly

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x

chr9:35,657,617-35,658,152 536 bp. enter position, gene symbol or search terms

go



ERC - signal: ENSG00000251562.7 - MALAT1 - lincRNA

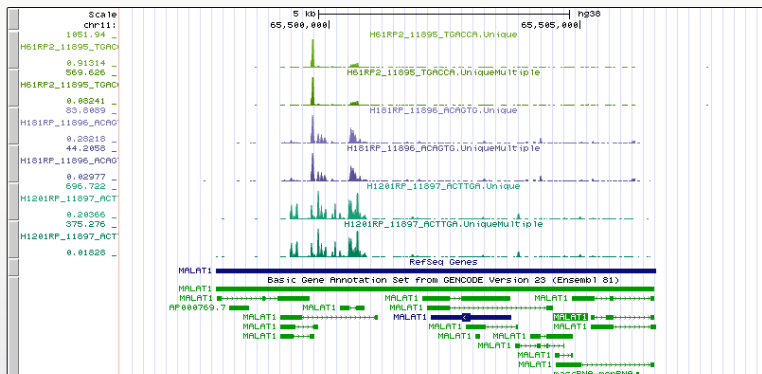
metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)

UCSC Genome Browser on Human Dec. 2013 (GRCh38/hg38) Assembly

move <<<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x

chr11:65,495,870-65,508,691 12,822 bp. enter position, gene symbol or search terms go

chr11 (q13.1) p15.4 p13 p12 q14.1 q21 q22.3 23.3 25



ERC - signal: ENSG00000259001.3 - RPPH1 - antisense

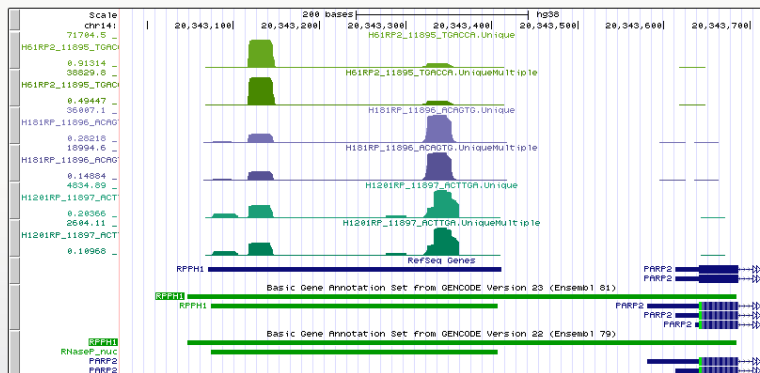
antisense of PARP2 ENSG00000129484 - poly(ADP-ribose) polymerase 2

UCSC Genome Browser on Human Dec. 2013 (GRCh38/hg38) Assembly

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x

chr14:20,342,971-20,343,714 744 bp.

chr14 (q11.2) p13 p12 14p11.2 q11.2 14q12 21.1 24.3 31.3 32.2



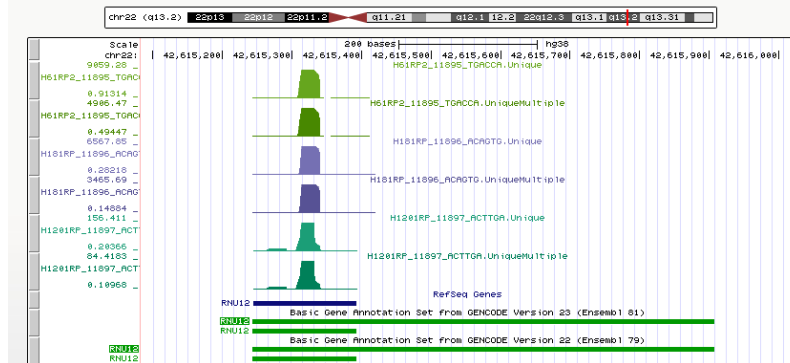
ERC - signal: ENSG00000270022.3 - RNU12 - lincRNA

Overlapping RefSeq Gene ID 267010 matches but different biotype of snRNA

UCSC Genome Browser on Human Dec. 2013 (GRCh38/hg38) Assembly

novel <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x

chr22:42,615,086-42,616,020 935 bp.



ERC - mm + signal: ENSG00000270103.3

UCSC Genome Browser on Human Dec. 2013 (GRCh38/hg38) Assembly

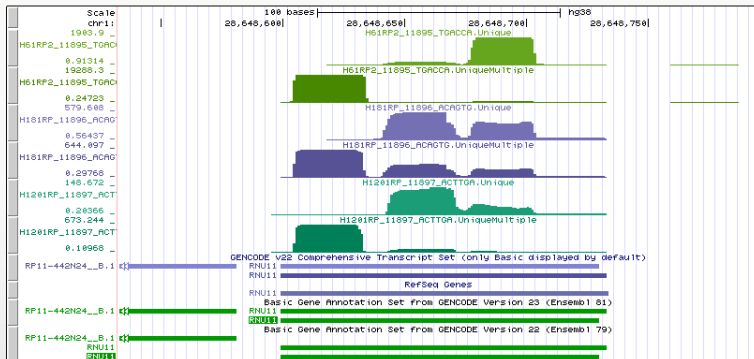
move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x

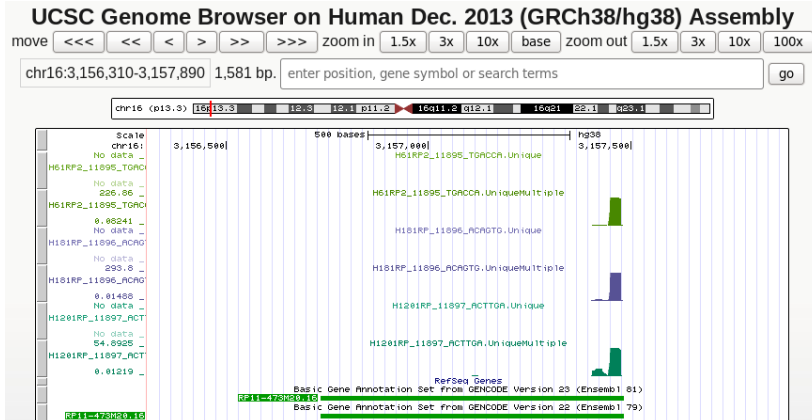
chr1:28,648,534-28,648,795 262 bp.

enter position, gene symbol or search terms

go

chr1 (p35.3) p31.1 1q12 q41 4844





ERC - shortRNA: ENSG00000255125.1

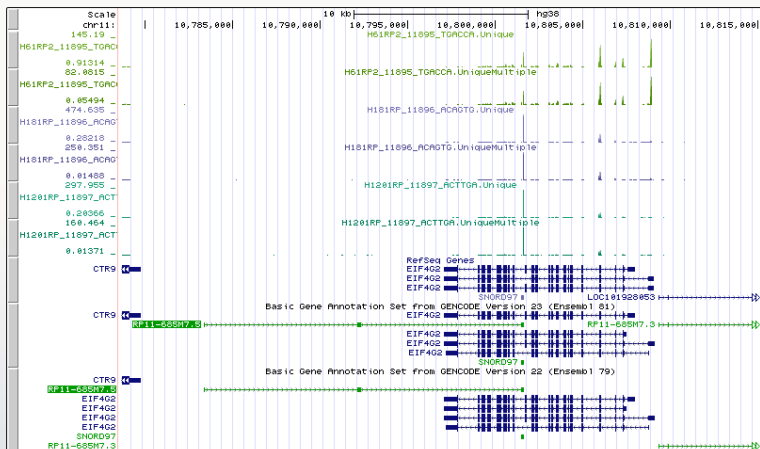
UCSC Genome Browser on Human Dec. 2013 (GRCh38/hg38) Assembly

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x

chr11:10,778,553-10,815,178 36,626 bp. enter position, gene symbol or search terms

go

chr11 (p15.4) p15.4 p15 p12 q14.1 q21 q22.3 23.3 26

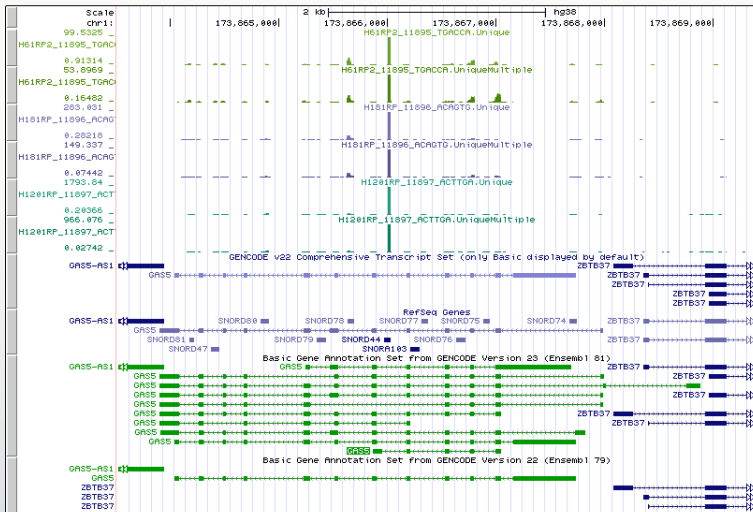


ERC - shortRNA: ENSG00000234741.7

UCSC Genome Browser on Human Dec. 2013 (GRCh38/hg38) Assembly

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x

chr1:173,863,519-173,869,388 5,870 bp. enter position, gene symbol or search terms go



gene expression $> 500 < 1000$ FPKM in at least in
RP sample

ERC

gene-id	H006.1RP.11895	H018.1RP.11896	H120.1RP.11897	classif
ENSG00000233421.4	894.08	172.55	59.51	mm
ENSG00000254144.3	987.07	178.57	37.6	mm
ENSG00000258017.1	500.19	941.97	69.15	mm (neighbor gene)
ENSG00000260035.1	650.48	256.69	489.69	mm
ENSG00000262202.4	840.59	961.48	462.44	mm

Cenik et al. 2015

gene-id	SRR1803148	SRR1803151
ENSG00000242125.3	191.82	663.7
ENSG00000203875.10	808.23	637.71
ENSG00000251562.7	375.4	911.55
ENSG00000253701.2	525.96	0.16
ENSG00000175061.17	658.37	219.71
ENSG00000243655.2	567.57	65.25