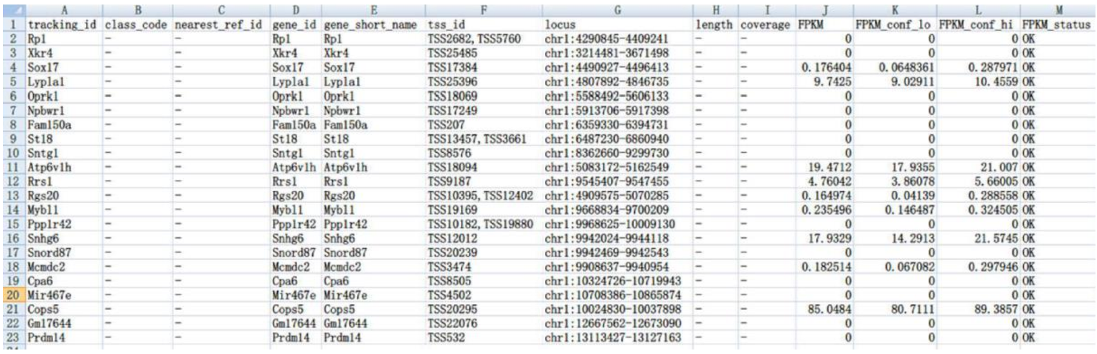
A

```
cufflinks -p 16 -o ../cufflinks_out/ --max-bundle-frag 10000000 -G
/home/ken/BioSoft/GeneGTFs/mm9_genes.gtf
-M /home/ken/BioSoft/GeneGTFs/mm9_repeatMasker.gtf -b
/home/ken/BioSoft/GenomeSeqMM9/ -u tophat_out/accepted_hits.bam
```

B

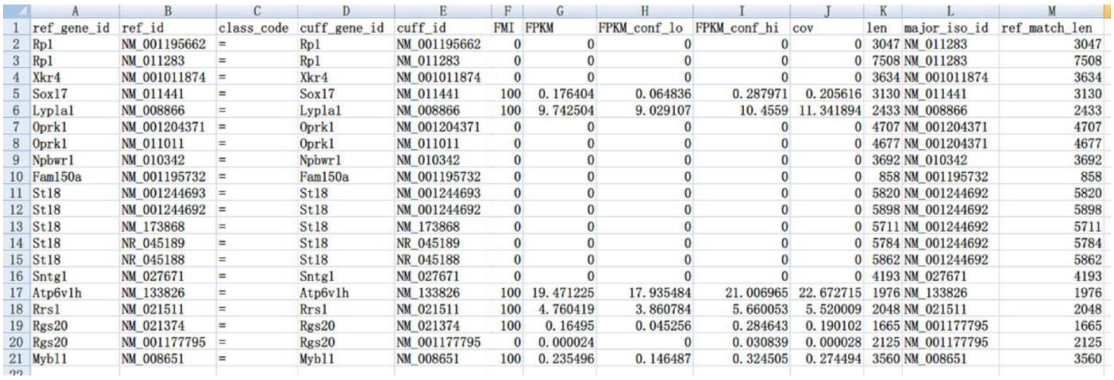


	A	B	C	D	E	F	G	H	I	J	K	L	M
1	tracking_id	class_code	nearest_ref_id	gene_id	gene_short_name	tss_id	locus	length	coverage	FPKM	FPKM_conf_lo	FPKM_conf_hi	FPKM_status
2	Rpl	–	–	Rpl	Rpl	TSS2682, TSS5760	chr1:4290845-4409241	–	–	0	0	0	OK
3	Xkr4	–	–	Xkr4	Xkr4	TSS25485	chr1:3214481-3671498	–	–	0	0	0	OK
4	Sox17	–	–	Sox17	Sox17	TSS17384	chr1:4490927-4496413	–	–	0.176404	0.0648361	0.287971	OK
5	Lypla1	–	–	Lypla1	Lypla1	TSS25396	chr1:4807892-4846735	–	–	9.7425	9.02911	10.4559	OK
6	Oprk1	–	–	Oprk1	Oprk1	TSS18069	chr1:5588492-5606133	–	–	0	0	0	OK
7	Npbwr1	–	–	Npbwr1	Npbwr1	TSS17249	chr1:5913706-5917398	–	–	0	0	0	OK
8	Fam150a	–	–	Fam150a	Fam150a	TSS207	chr1:6359330-6394731	–	–	0	0	0	OK
9	St18	–	–	St18	St18	TSS13457, TSS3661	chr1:6487230-6860940	–	–	0	0	0	OK
10	Sntg1	–	–	Sntg1	Sntg1	TSS8576	chr1:8362660-9299730	–	–	0	0	0	OK
11	Atp6v1h	–	–	Atp6v1h	Atp6v1h	TSS18094	chr1:5083172-5162549	–	–	19.4712	17.9355	21.007	OK
12	Rrs1	–	–	Rrs1	Rrs1	TSS9187	chr1:9545407-9547455	–	–	4.76042	3.86078	5.66005	OK
13	Rgs20	–	–	Rgs20	Rgs20	TSS10395, TSS12402	chr1:4909575-5070285	–	–	0.164974	0.04139	0.288558	OK
14	Mybl1	–	–	Mybl1	Mybl1	TSS19169	chr1:9668834-9700209	–	–	0.235496	0.146487	0.324505	OK
15	Ppp1r42	–	–	Ppp1r42	Ppp1r42	TSS10182, TSS19880	chr1:9968625-10009130	–	–	0	0	0	OK
16	Snhg6	–	–	Snhg6	Snhg6	TSS12012	chr1:9942024-9944118	–	–	17.9329	14.2913	21.5745	OK
17	Snord87	–	–	Snord87	Snord87	TSS20239	chr1:9942469-9942543	–	–	0	0	0	OK
18	Mcmdc2	–	–	Mcmdc2	Mcmdc2	TSS3474	chr1:9908637-9940954	–	–	0.182514	0.067082	0.297946	OK
19	Cpa6	–	–	Cpa6	Cpa6	TSS8505	chr1:10324726-10719943	–	–	0	0	0	OK
20	Mir467e	–	–	Mir467e	Mir467e	TSS4502	chr1:10708386-10865874	–	–	0	0	0	OK
21	Cops5	–	–	Cops5	Cops5	TSS20295	chr1:10024830-10037898	–	–	85.0484	80.7111	89.3857	OK
22	Gm17644	–	–	Gm17644	Gm17644	TSS22076	chr1:12667562-12673090	–	–	0	0	0	OK
23	Prdm14	–	–	Prdm14	Prdm14	TSS532	chr1:13113427-13127163	–	–	0	0	0	OK

C

```
cuffcompare -o compare_to_known_gene -r
/home/ken/BioSoft/GeneGTF/mm9_genes.gtf -s
/home/ken/BioSoft/GenomeSeqMM9/ transcripts.gtf
```

D



	A	B	C	D	E	F	G	H	I	J	K	L	M
1	ref_gene_id	ref_id	class_code	cuff_gene_id	cuff_id	FMI	FPKM	FPKM_conf_lo	FPKM_conf_hi	cov	len	major_iso_id	ref_match_len
2	Rpl	NM_001195662	=	Rpl	NM_001195662	0	0	0	0	0	3047	NM_011283	3047
3	Rpl	NM_011283	=	Rpl	NM_011283	0	0	0	0	0	7508	NM_011283	7508
4	Xkr4	NM_001011874	=	Xkr4	NM_001011874	0	0	0	0	0	3634	NM_001011874	3634
5	Sox17	NM_011441	=	Sox17	NM_011441	100	0.176404	0.064836	0.287971	0.205616	3130	NM_011441	3130
6	Lypla1	NM_008866	=	Lypla1	NM_008866	100	9.742504	9.029107	10.4559	11.341894	2433	NM_008866	2433
7	Oprk1	NM_001204371	=	Oprk1	NM_001204371	0	0	0	0	0	4707	NM_001204371	4707
8	Oprk1	NM_011011	=	Oprk1	NM_011011	0	0	0	0	0	4677	NM_001204371	4677
9	Npbwr1	NM_010342	=	Npbwr1	NM_010342	0	0	0	0	0	3692	NM_010342	3692
10	Fam150a	NM_001195732	=	Fam150a	NM_001195732	0	0	0	0	0	858	NM_001195732	858
11	St18	NM_001244693	=	St18	NM_001244693	0	0	0	0	0	5820	NM_001244692	5820
12	St18	NM_001244692	=	St18	NM_001244692	0	0	0	0	0	5898	NM_001244692	5898
13	St18	NM_173868	=	St18	NM_173868	0	0	0	0	0	5711	NM_001244692	5711
14	St18	NR_045189	=	St18	NR_045189	0	0	0	0	0	5784	NM_001244692	5784
15	St18	NR_045188	=	St18	NR_045188	0	0	0	0	0	5862	NM_001244692	5862
16	Sntg1	NM_027671	=	Sntg1	NM_027671	0	0	0	0	0	4193	NM_027671	4193
17	Atp6v1h	NM_133826	=	Atp6v1h	NM_133826	100	19.471225	17.935484	21.006965	22.672715	1976	NM_133826	1976
18	Rrs1	NM_021511	=	Rrs1	NM_021511	100	4.760419	3.860784	5.660053	5.520009	2048	NM_021511	2048
19	Rgs20	NM_021374	=	Rgs20	NM_021374	100	0.16495	0.045256	0.284643	0.190102	1665	NM_001177795	1665
20	Rgs20	NM_001177795	=	Rgs20	NM_001177795	0	0.000024	0	0.030839	0.000028	2125	NM_001177795	2125
21	Mybl1	NM_008651	=	Mybl1	NM_008651	100	0.235496	0.146487	0.324505	0.274494	3560	NM_008651	3560

E

```
tophat -p 16 -r 5 --mate-std-dev 90 --no-novel-juncs -G
/home/ken/BioSoft/GeneGTFs/mm9_genes.gtf
/home/ken/BioSoft/bowtie-0.12.7/indexes/mm9 Example1.read1 Example1.read2
```

F

```
cuffcompare -o compare_to_known_gene -r
/home/ken/BioSoft/GeneGTF/mm9_genes.gtf -s
/home/ken/BioSoft/GenomeSeqMM9/ transcripts.gtf
```