Anaquin: TransQuin Report

Contents

TransQuin Alignment

Summary statistics for: A1

Summary for file: K_RMXA1v2.accepted_hits.bam

```
Unmapped:    0 reads
Experiment: 11440146 (23.8709%) reads
Synthetic:  36484961 (76.1291%) reads

Reference:  1190 exons
Reference:  1028 introns
Reference:  149219 bases

Query:       85464855 exons
Query:       32195352 introns
Query:       161775 bases

Dilution:   0.761291


***
*** The following statistics are computed at the exon, intron and base level.
***
*** Exon level is defined by performance per exon. An alignment that
*** is not mapped entirely within an exon is considered as a FP. The
*** intron level is similar.
***
*** Base level is defined by performance per nucleotide. A partial
*** mapped read will have FP and TP.
***

-------------------- Exon level --------------------

Sensitivity: 0.997479
Specificity: 0.976043
Detection:   0.0590086 (R2_33)

-------------------- Intron level --------------------

Sensitivity: 0.993191
Specificity: 0.840372
Detection:   0.0590086 (R2_33)

-------------------- Base level --------------------

Sensitivity: 0.691812
Specificity: 0.932919
Detection:   0.0590086 (R2_33)

-------------------- Undetected --------------------

Exon:   0.002521
Intron: 0.006809
Gene:   0.026316
```

Sequin statistics for: A1

ID	Covered	Sensitivity (Exon)	Specificity (Exon)	Sensitivity (Intron)	Specificity (Intron)	Sens...	
R1_101	0.845083	1	0.999532	1	1	0.845083	0.998971
R1_102	0.721599	1	0.994156	1	0.901155	0.721599	0.998544
R1_103	0.628255	1	0.995319	1	0.977373	0.628255	0.99561
R1_11	0.645833	1	0.998799	1	0.998818	0.645833	0.997923
R1_12	0.591978	1	0.992884	1	0.9983	0.591978	0.997669
R1_13	0.920394	1	0.987685	0.909091	0.946898	0.920394	0.995898
R1_14	1	0.999823	--	--	1	0.995502	1
R1_21	0.630945	1	0.993234	1	0.916456	0.630945	0.942446
R1_22	0.528054	1	0.998358	1	0.0416689	0.528054	0.993191
R1_23	0.608499	1	0.988379	1	0.00621383	0.608499	0.997146
R1_24	0.999782	1	0.995249	1	0.998266	0.999782	0.997819
R1_31	0.688293	1	0.995473	1	0.244225	0.688293	0.994565
R1_32	0.545455	1	0.999737	1	1	0.545455	0.99894
R1_33	0.899202	1	0.993455	1	0.994169	0.899202	0.998359
R1_41	0.78125	1	0.996675	1	0.999808	0.78125	0.995575
R1_42	0.617479	1	0.980681	1	0.976687	0.617479	0.988844
R1_43	0.540369	1	0.990501	0.973684	0.96341	0.540369	0.996994
R1_51	0.607103	1	0.996288	1	0.999373	0.607103	0.993542
R1_52	0.622807	1	0.991475	1	1	0.622807	0.971446
R1_53	0.998489	1	0.99784	1	0.370359	0.998489	0.996482
R1_61	0.679466	1	1	1	1	0.679466	1
R1_62	0.774336	1	1	1	1	0.774336	1
R1_63	0.669443	1	0.995492	1	0.971203	0.669443	0.995741
R1_71	0.740968	1	0.994243	1	0.998708	0.740968	0.987705
R1_72	0.582844	1	1	1	1	0.582844	1
R1_73	0.731952	1	0.984041	1	0.98719	0.731952	0.996865
R1_81	0.747244	1	0.99754	1	0.995044	0.747244	0.996849
R1_82	0.587741	1	0.995744	1	0.992876	0.587741	0.991501
R1_83	0.644813	1	0.998373	1	0.997866	0.644813	0.997613
R1_91	0.685055	1	1	1	1	0.685055	1
R1_92	0.777919	1	0.980772	1	0.995753	0.777919	0.99513
R1_93	0.625086	1	0.996054	1	0.999554	0.625086	0.996156
R2_1	1	1	--	--	0.99196	1	0.99196
R2_105	1	0.967742	--	--	0.874667	0.99696	0.874667
R2_115	0.837412	1	0.988931	1	0.996079	0.837412	0.923815
R2_116	0.584726	1	0.987644	1	1	0.584726	0.997557
R2_117	0.711066	1	0.999248	1	0.998209	0.711066	0.996411
R2_14	0.719569	1	0.988252	1	0.987247	0.719569	0.991507
R2_150	0.835063	1	0.998167	1	0.518953	0.835063	0.991781
R2_151	0.578303	1	0.983911	1	0.000681453	0.578303	0.999244
R2_152	0.603856	1	0.99729	1	0.0120943	0.603856	0.998386
R2_153	0.677873	1	0.995311	1	0.359343	0.677873	0.999099
R2_154	0.855658	1	0.989621	1	0.547718	0.855658	0.994631
R2_18	0.628326	1	0.9853	1	0.852844	0.628326	0.985276
R2_19	0.811493	1	0.992328	1	0.98788	0.811493	0.998432
R2_20	0.735871	1	0.997986	1	0.997017	0.735871	0.997394
R2_24	0.586003	0.979592	0.991056	0.957447	0.693273	0.586003	0.998239
R2_26	0.916638	1	0.994978	1	0.994222	0.916638	0.997942
R2_27	0.754167	1	0.995777	1	1	0.754167	0.999606
R2_28	0.68506	1	1	1	1	0.68506	1
R2_32	0.671486	1	0.98234	1	1	0.671486	0.997715

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R2_33   0.879859    1   1   1   0.000191773 0.879859     1
R2_37   0.719465    1   0.993295    1   0.982877    0.719465    0.998428
R2_38   0.391233    1   0.989899    1   1   0.391233    0.995805
R2_41   0.837384    1   0.991692    1   0.995112    0.837384    0.989443
R2_42   0.882171    1   0.998311    1   1   0.882171    0.999561
R2_45   0.462072    1   1   1   1   0.462072    1
R2_46   0.688515    1   0.993056    1   1   0.688515    0.967061
R2_47   0.887733    1   0.996614    1   0.997939    0.887733    0.998675
R2_53   0.396308    1   0.989455    1   0.997009    0.396308    0.997744
R2_54   0.864703    1   0.982539    1   0.996987    0.864703    0.996936
R2_55   0.880804    1   0.987179    1   0.873955    0.880804    0.99142
R2_57   0.65303 1   0.996765    1   1   0.65303 0.998819
R2_59   0.588824    1   0.988263    1   0.993952    0.588824    0.999726
R2_6    0.702025    1   0.996212    1   0.990037    0.702025    0.98913
R2_60   0.605403    1   0.996636    1   1   0.605403    0.997073
R2_63   0.879982    1   0.987448    1   0.997983    0.879982    0.997517
R2_65   1   1   --  --  0.995595    1   0.995595
R2_66   0.529254    1   0.999748    1   0.999936    0.529254    0.985015
R2_67   0.959847    1   1   1   1   0.959847    1
R2_68   0.705317    1   0.998856    1   1   0.705317    0.999367
R2_7    0.760474    1   0.994878    1   0.994215    0.760474    0.994466
R2_71   0.72861 1   0.986272    1   1   0.72861 0.998168
R2_72   0.320416    0.866667    0.993094    0.727273    1   0.320416    0.99815
R2_73   0.94562 1   0.988466    1   0.996508    0.94562 0.999279
R2_76   0.470652    1   1   1   1   0.470652    1
```

Summary statistics for: A2

Summary for file: K_RMXA2v2.accepted_hits.bam

```
   Unmapped:   0 reads
   Experiment: 10700630 (23.3808%) reads
   Synthetic:  35066089 (76.6192%) reads

   Reference:  1190 exons
   Reference:  1028 introns
   Reference:  149219 bases

   Query:      82814262 exons
   Query:      34992686 introns
   Query:      162619 bases

   Dilution:   0.766192


   ***
   *** The following statistics are computed at the exon, intron and base level.
   ***
   *** Exon level is defined by performance per exon. An alignment that
   *** is not mapped entirely within an exon is considered as a FP. The
   *** intron level is similar.
   ***
   *** Base level is defined by performance per nucleotide. A partial
   *** mapped read will have FP and TP.
   ***

   -------------------- Exon level --------------------

   Sensitivity: 0.997479
   Specificity: 0.974098
   Detection:   0.0590086 (R2_33)

   -------------------- Intron level --------------------

   Sensitivity: 0.986381
   Specificity: 0.745193
   Detection:   0.0590086 (R2_33)

   -------------------- Base level --------------------

   Sensitivity: 0.691909
   Specificity: 0.928206
   Detection:   0.0590086 (R2_33)

   -------------------- Undetected --------------------

   Exon:   0.002521
   Intron: 0.013619
   Gene:   0.026316
```

Sequin statistics for: A2

ID	Covered	Sensitivity (Exon)	Specificity (Exon)	Sensitivity (Intron)	Specificity (Intron)	Sens
R1_101	0.843342	1	0.997495	1	0.995816	0.843342	0.995889
R1_102	0.721599	1	0.995219	1	0.00552418	0.721599	0.998544
R1_103	0.628532	1	0.995586	1	0.185487	0.628532	0.995612
R1_11	0.647177	1	0.999245	1	0.0529042	0.647177	0.997927
R1_12	0.590595	1	0.9933	0.956522	1	0.590595	0.998247
R1_13	0.920394	1	0.988579	0.909091	0.661924	0.920394	0.995082
R1_14	1	0.999844	--	--	1	0.991045	1
R1_21	0.630945	1	0.994394	1	0.942939	0.630945	0.942446
R1_22	0.527602	1	0.998493	1	0.101617	0.527602	0.994032
R1_23	0.604667	1	0.989406	1	0.0153541	0.604667	0.997701
R1_24	1	1	0.995351	1	0.995767	1	0.99782
R1_31	0.687823	1	0.994739	1	0.998694	0.687823	0.995916
R1_32	0.545455	1	0.998386	1	1	0.545455	0.995772
R1_33	0.911321	1	0.998728	1	0.99726	0.911321	0.999676
R1_41	0.78125	1	0.996939	1	0.932387	0.78125	0.994695
R1_42	0.617479	1	0.981914	1	0.891942	0.617479	0.986842
R1_43	0.541274	1	0.990613	0.973684	0.989699	0.541274	0.996335
R1_51	0.607103	1	0.995118	1	0.988762	0.607103	0.99446
R1_52	0.623188	1	0.979032	1	0.992218	0.623188	0.977858
R1_53	0.998489	1	0.995792	1	0.726932	0.998489	0.996983
R1_61	0.676962	1	0.99811	1	0.00262261	0.676962	0.998768
R1_62	0.767383	1	0.992147	1	0.00112939	0.767383	0.999177
R1_63	0.669964	1	0.995761	1	0.964477	0.669964	0.995745
R1_71	0.740968	1	0.993449	1	0.964899	0.740968	0.987705
R1_72	0.600451	1	1	1	0.000569401	0.600451	1
R1_73	0.732371	1	0.989559	0.96	0.531614	0.732371	0.996583
R1_81	0.747244	1	0.998029	1	0.994022	0.747244	0.996849
R1_82	0.587741	1	0.992549	1	0.995822	0.587741	0.991501
R1_83	0.645199	1	0.999418	1	0.999628	0.645199	0.99702
R1_91	0.685696	1	1	1	1	0.685696	1
R1_92	0.781726	1	0.980355	1	0.995561	0.781726	0.995153
R1_93	0.625086	1	0.996684	1	0.998378	0.625086	0.996156
R2_1	1	1	--	--	0.98995	1	0.98995
R2_105	1	1	--	--	0.68	1	0.68
R2_115	0.840131	1	0.989271	1	0.996256	0.840131	0.99549
R2_116	0.524582	1	0.996665	1	1	0.524582	0.998183
R2_117	0.710041	1	0.999708	1	0.999328	0.710041	0.997122
R2_14	0.719569	1	0.988161	1	0.737964	0.719569	0.991507
R2_150	0.835448	1	0.998619	1	0.673702	0.835448	0.991785
R2_151	0.565179	1	0.981308	0.85	0.00120631	0.565179	0.998454
R2_152	0.603368	1	0.998585	1	0.028801	0.603368	0.997981
R2_153	0.669927	1	0.981132	1	1	0.669927	0.999088
R2_154	0.855658	1	0.986231	1	0.753071	0.855658	0.994631
R2_18	0.628326	1	0.982418	1	0.932695	0.628326	0.986486
R2_19	0.811493	1	0.994275	1	0.395306	0.811493	0.998717
R2_20	0.732026	1	0.998159	1	0.998462	0.732026	0.998951
R2_24	0.586299	0.979592	0.987268	0.957447	0.764632	0.586299	0.998994
R2_26	0.916638	1	0.994996	1	0.995074	0.916638	0.997755
R2_27	0.750595	1	0.994545	1	1	0.750595	0.999208
R2_28	0.686747	1	0.996957	1	1	0.686747	0.979381
R2_32	0.671486	1	0.992126	1	1	0.671486	0.998171

```
R2_33  0.90106 1   1   1    1    0.90106 1
R2_37  0.719239  1   1   1   1    0.719239    1
R2_38  0.399143  1   0.984831  1   1    0.399143    0.998351
R2_41  0.839171  1   0.991918  1   0.998755    0.839171    0.990299
R2_42  0.874031  1   1   1   1    0.874031    1
R2_45  0.464239  1   0.999817  1   0.998319    0.464239    0.999689
R2_46  0.70475 1   0.988748    1   1    0.70475 0.967396
R2_47  0.887733  1   0.997391  1   0.998014    0.887733    0.998675
R2_53  0.396487  1   0.997205  1   0.997577    0.396487    0.999097
R2_54  0.864703  1   0.983372  1   0.996267    0.864703    0.997191
R2_55  0.880804  1   0.987741  1   0.862818    0.880804    0.990647
R2_57  0.659591  1   0.996748  1   0.00525698  0.659591    0.998248
R2_59  0.583656  1   1   1   1    0.583656    1
R2_6   0.702989  1   0.998334  1   0.994613    0.702989    0.995902
R2_60  0.604692  1   0.996744  1   0.00539659  0.604692    0.997069
R2_63  0.884363  1   0.984499  1   0.985809    0.884363    0.997037
R2_65  1   1    --   --   0.995595    1   0.995595
R2_66  0.529254  1   0.999748  1   0.999958    0.529254    0.985015
R2_67  0.992352  1   1   1   1    0.992352    1
R2_68  0.707775  1   0.996954  1   1    0.707775    0.999684
R2_7   0.760474  1   0.997273  1   0.999218    0.760474    0.993367
R2_71  0.69385 1   0.992081    1   0.992248    0.69385 0.997118
R2_72  0.338827  0.866667    0.985673    0.545455    1    0.338827    0.999124
R2_73  0.950398  1   0.991652  1   0.99652 0.950398    0.975023
R2_76  0.477536  1   0.99809 1   1    0.477536    0.999242
```

Summary statistics for: A3

Summary for file: K_RMXA3v2.accepted_hits.bam

```
   Unmapped:   0 reads
   Experiment: 9781841 (22.7411%) reads
   Synthetic:  33232155 (77.2589%) reads

   Reference:  1190 exons
   Reference:  1028 introns
   Reference:  149219 bases

   Query:      78415783 exons
   Query:      29409848 introns
   Query:      166617 bases

   Dilution:   0.772589


   ***
   *** The following statistics are computed at the exon, intron and base level.
   ***
   *** Exon level is defined by performance per exon. An alignment that
   *** is not mapped entirely within an exon is considered as a FP. The
   *** intron level is similar.
   ***
   *** Base level is defined by performance per nucleotide. A partial
   *** mapped read will have FP and TP.
   ***

   -------------------- Exon level --------------------

   Sensitivity: 0.997479
   Specificity: 0.971556
   Detection:   0.0590086 (R2_33)

   -------------------- Intron level --------------------

   Sensitivity: 0.992218
   Specificity: 0.840566
   Detection:   0.0590086 (R2_33)

   -------------------- Base level --------------------

   Sensitivity: 0.696877
   Specificity: 0.912440
   Detection:   0.0590086 (R2_33)

   -------------------- Undetected --------------------

   Exon:   0.002521
   Intron: 0.007782
   Gene:   0.026316
```

Sequin statistics for: A3

ID	Covered	Sensitivity (Exon)	Specificity (Exon)	Sensitivity (Intron)	Specificity (Intron)	Sens...
R1_101	0.844212	1	0.999087	1	1	0.844212	0.99897
R1_102	0.723352	1	0.995112	1	0.0284201	0.723352	0.998065
R1_103	0.629086	1	0.995227	1	0.535702	0.629086	0.99518
R1_11	0.646505	1	0.998816	1	0.0505829	0.646505	0.997925
R1_12	0.591978	1	0.993087	1	0.999141	0.591978	0.997669
R1_13	0.920394	1	0.988092	0.909091	0.909266	0.920394	0.995082
R1_14	1	0.999779	--	--	1	0.995502	1
R1_21	0.630945	1	0.993913	1	0.951111	0.630945	0.941599
R1_22	0.528054	1	0.998712	1	0.201023	0.528054	0.994037
R1_23	0.610589	1	0.987265	1	0.0338936	0.610589	0.997156
R1_24	1	1	0.995487	1	0.998898	1	0.99782
R1_31	0.687823	1	0.994534	1	0.998714	0.687823	0.995916
R1_32	0.544876	1	0.997818	1	1	0.544876	0.995767
R1_33	0.912504	1	0.997554	1	0.996416	0.912504	0.998706
R1_41	0.78125	1	0.99667	1	0.999697	0.78125	0.996457
R1_42	0.617479	1	0.980701	1	0.897666	0.617479	0.985844
R1_43	0.540731	1	0.99053	0.973684	0.984815	0.540731	0.996331
R1_51	0.607103	1	0.996042	1	0.992969	0.607103	0.993542
R1_52	0.623951	1	0.989971	1	1	0.623951	0.969769
R1_53	0.998489	1	0.998404	1	0.973515	0.998489	0.996983
R1_61	0.709516	1	0.993926	1	1	0.709516	0.998825
R1_62	0.776233	1	1	1	1	0.776233	1
R1_63	0.669703	1	0.995554	1	0.974728	0.669703	0.995743
R1_71	0.740968	1	0.993971	1	0.988434	0.740968	0.985685
R1_72	0.604966	1	1	1	1	0.604966	1
R1_73	0.731743	1	0.983855	0.96	0.986432	0.731743	0.996864
R1_81	0.747638	1	0.996786	1	0.994027	0.747638	0.99685
R1_82	0.587741	1	0.992415	1	0.997628	0.587741	0.993612
R1_83	0.644427	1	0.997372	1	0.996722	0.644427	0.998208
R1_91	0.684413	1	0.998495	1	1	0.684413	0.998129
R1_92	0.778765	1	0.980597	1	0.995994	0.778765	0.995135
R1_93	0.625086	1	0.995437	1	0.998834	0.625086	0.996703
R2_1	1	1	--	--	0.994975	1	0.994975
R2_105	1	0.979167	--	--	0.981333	0.994595	0.981333
R2_115	0.837955	1	0.989482	1	0.997475	0.837955	0.923861
R2_116	0.583771	1	0.988752	1	1	0.583771	0.997553
R2_117	0.709016	1	0.999618	1	0.99934	0.709016	0.9964
R2_14	0.719569	1	0.989328	1	0.838494	0.719569	0.991507
R2_150	0.835832	1	0.997978	1	0.821556	0.835832	0.996334
R2_151	0.589676	1	0.990974	1	0.00596157	0.589676	0.997779
R2_152	0.603368	1	0.998327	1	0.0588556	0.603368	0.997981
R2_153	0.685208	1	0.995346	1	0.983165	0.685208	0.998219
R2_154	0.855658	1	0.986493	1	0.834231	0.855658	0.994631
R2_18	0.628326	1	0.984271	1	0.935806	0.628326	0.986486
R2_19	0.811493	1	0.994731	1	0.753652	0.811493	0.998574
R2_20	0.733948	1	0.996812	1	0.99733	0.733948	0.996347
R2_24	0.586741	0.979592	0.990687	0.957447	0.842066	0.586741	0.998743
R2_26	0.916982	1	0.995763	1	0.994951	0.916982	0.997942
R2_27	0.755357	1	0.993405	1	0.999065	0.755357	0.998426
R2_28	0.68988	1	0.999127	1	1	0.68988	0.980144
R2_32	0.671486	1	0.989034	1	1	0.671486	0.988678

```
R2_33   0.971731    1   0.947368    1   1   0.971731    0.99278
R2_37   0.727623    1   0.993796    1   0.993171    0.727623    0.997825
R2_38   0.399473    1   0.995508    1   1   0.399473    0.998353
R2_41   0.839171    1   0.992037    1   0.998985    0.839171    0.968247
R2_42   0.885659    1   0.997419    1   1   0.885659    0.949709
R2_45   0.464528    1   0.997782    1   1   0.464528    0.998447
R2_46   0.719784    1   0.99254 1   1   0.719784    0.967273
R2_47   0.888518    1   0.996762    1   0.996155    0.888518    0.998676
R2_53   0.397025    1   0.994321    1   0.994027    0.397025    0.997748
R2_54   0.864703    1   0.982499    1   0.997465    0.864703    0.997446
R2_55   0.880804    1   0.988265    1   0.838564    0.880804    0.990647
R2_57   0.659205    1   0.99747 1   0.00678764  0.659205    0.99883
R2_59   0.596415    1   0.9968  1   0.998424    0.596415    0.999459
R2_6    0.702025    1   0.995403    1   0.991333    0.702025    0.993179
R2_60   0.605759    1   0.995309    1   0.00940813  0.605759    0.997074
R2_63   0.884801    1   0.985674    1   0.988104    0.884801    0.996547
R2_65   1   0.997792    --  --  0.994493    0.998894    0.994493
R2_66   0.529254    1   0.988763    1   0.999892    0.529254    0.986
R2_67   0.967495    1   1   1   1   0.967495    1
R2_68   0.717828    1   0.996747    1   0.998457    0.717828    0.999378
R2_7    0.76132 1   0.99719 1   0.999558    0.76132 0.994472
R2_71   0.916444    1   0.993642    1   0.997036    0.916444    0.986331
R2_72   0.347439    0.866667    0.991036    0.727273    1   0.347439    0.997017
R2_73   0.943572    1   0.985888    1   0.998646    0.943572    0.999759
R2_76   0.477536    1   0.994867    1   1   0.477536    0.998485
```

Summary statistics for: B1

Summary for file: G_RMXB1v2.accepted_hits.bam

```
   Unmapped:   0 reads
   Experiment: 6299276 (15.7506%) reads
   Synthetic:  33694649 (84.2494%) reads

   Reference:  1190 exons
   Reference:  1028 introns
   Reference:  149219 bases

   Query:      86364151 exons
   Query:      42105718 introns
   Query:      158128 bases

   Dilution:   0.842494

   ***
   *** The following statistics are computed at the exon, intron and base level.
   ***
   *** Exon level is defined by performance per exon. An alignment that
   *** is not mapped entirely within an exon is considered as a FP. The
   *** intron level is similar.
   ***
   *** Base level is defined by performance per nucleotide. A partial
   *** mapped read will have FP and TP.
   ***

   ------------------- Exon level --------------------

   Sensitivity: 0.993277
   Specificity: 0.977562
   Detection:   0.0590086 (R2_33)

   ------------------- Intron level --------------------

   Sensitivity: 0.984436
   Specificity: 0.793287
   Detection:   1.88828 (R1_72)

   ------------------- Base level --------------------

   Sensitivity: 0.683749
   Specificity: 0.943312
   Detection:   0.0590086 (R2_33)

   ------------------- Undetected --------------------

   Exon:   0.006723
   Intron: 0.015564
   Gene:   0.052632
```

Sequin statistics for: B1

```
ID  Covered Sensitivity (Exon)  Specificity (Exon)  Sensitivity (Intron)    Specificity (Intron)    Sen
R1_101  0.787641    1   0.996774    1   1   0.787641    0.998896
R1_102  0.721248    1   0.98946 1   0.108223    0.721248    0.999514
R1_103  0.627978    1   0.992978    1   0.959322    0.627978    0.996484
R1_11   0.644489    1   0.989534    1   1   0.644489    0.997919
R1_12   0.569848    1   0.992637    1   0.991467    0.569848    0.998788
R1_13   0.920394    1   0.988299    0.909091    0.983353    0.920394    0.995082
R1_14   1   0.999917    --  --  0.996988    0.996988    0.996988
R1_21   0.630945    1   0.993465    1   0.902076    0.630945    0.941599
R1_22   0.526697    1   0.999028    1   0.0033303   0.526697    0.997429
R1_23   0.609892    1   0.983464    1   0.00570884  0.609892    0.997153
R1_24   0.999345    1   0.995356    1   0.998841    0.999345    0.998472
R1_31   0.688764    1   0.99394 1   0.997605    0.688764    0.992547
R1_32   0.541401    1   1   1   1   0.541401    1
R1_33   0.88324 1   0.997831    1   1   0.88324 0.999331
R1_41   0.78125 1   0.99979 1   0.997007    0.78125 0.995575
R1_42   0.617479    1   0.989977    1   0.975927    0.617479    0.990854
R1_43   0.541999    1   0.986484    0.973684    0.348855    0.541999    0.996339
R1_51   0.603157    1   0.995454    1   0.855858    0.603157    0.995349
R1_52   0.622807    1   0.994252    1   1   0.622807    0.998166
R1_53   0.998993    1   0.997143    1   0.718094    0.998993    0.996985
R1_61   0.718698    1   1   1   1   0.718698    1
R1_62   0.697219    1   1   1   1   0.697219    1
R1_63   0.670484    1   0.994539    1   0.857561    0.670484    0.995748
R1_71   0.740968    1   0.99358 1   0.848788    0.740968    0.986694
R1_72   0.544921    1   1   1   1   0.544921    1
R1_73   0.731115    1   0.991175    0.96    0.993206    0.731115    0.997431
R1_81   0.747244    1   0.996891    1   0.991853    0.747244    0.996325
R1_82   0.587741    1   0.999352    1   0.987979    0.587741    0.992908
R1_83   0.647513    1   0.998826    1   0.998681    0.647513    0.998216
R1_91   0.66517 1   1   1   1   0.66517 1
R1_92   0.778765    1   0.980861    1   0.995714    0.778765    0.995135
R1_93   0.625086    1   0.996681    1   0.99831 0.625086    0.996156
R2_1    1   1   --  --  0.994975    1   0.994975
R2_105  1   0.992857    --  --  0.946667    0.994398    0.946667
R2_115  0.842849    1   0.991243    1   0.99245 0.842849    0.923719
R2_116  0.573747    1   0.984551    1   1   0.573747    0.999169
R2_117  0.71209 1   0.998192    1   0.997355    0.71209 0.994989
R2_14   0.719569    1   0.984461    1   0.904376    0.719569    0.991507
R2_150  0.831603    1   0.999201    1   0.0928247   0.831603    0.997694
R2_151  0.56343 1   1   1   0.000648549 0.56343 1
R2_152  0.606541    1   0.99787 1   0.0104632   0.606541    0.997992
R2_153  0.680318    1   0.991786    1   1   0.680318    0.988016
R2_154  0.853349    1   0.98975 1   0.345297    0.853349    0.994616
R2_18   0.628326    1   0.98623 1   0.852354    0.628326    0.986486
R2_19   0.811146    1   0.99566 1   0.940862    0.811146    0.999001
R2_20   0.733948    1   0.998092    1   0.995501    0.733948    0.997388
R2_24   0.586003    0.979592    0.990261    0.957447    0.846247    0.586003    0.998239
R2_26   0.916982    1   0.992369    1   0.957098    0.916982    0.997569
R2_27   0.752976    1   0.992291    1   1   0.752976    0.99921
R2_28   0.689157    1   1   1   1   0.689157    1
R2_32   0.66964 1   0.996432    1   1   0.66964 0.998624
```

```
R2_33   0.416961    0.5 1   0    nan 0.416961     1
R2_37   0.694992    1   0.994852    1   0.981481    0.694992    0.999348
R2_38   0.379038    1   0.992625    1   1   0.379038    0.997398
R2_41   0.837026    1   0.993443    1   0.9981  0.837026    0.990694
R2_42   0.874031    1   1   1   1   0.874031    1
R2_45   0.462216    1   0.996477    1   1   0.462216    0.998439
R2_46   0.702646    1   1   1   1   0.702646    1
R2_47   0.888911    1   0.996626    1   0.995795    0.888911    0.998237
R2_53   0.387345    1   0.995233    1   1   0.387345    0.999075
R2_54   0.864703    1   0.985219    1   0.996922    0.864703    0.997701
R2_55   0.880804    1   0.983178    1   0.99546 0.880804    0.990647
R2_57   0.625241    1   1   0.941176    1   0.625241    1
R2_59   0.553456    1   0.993644    1   0.984615    0.553456    0.999708
R2_6    0.702989    1   0.996895    1   0.999525    0.702989    0.990489
R2_60   0.607892    1   0.997855    1   0.998146    0.607892    0.997085
R2_63   0.886991    1   0.998694    1   0.999702    0.886991    0.997046
R2_65   1   1   --  --  0.993392    1   0.993392
R2_66   0.528717    1   0.99979 1   0.999945    0.528717    0.987964
R2_67   0.782027    1   1   1   1   0.782027    1
R2_68   0.568811    0.846154    0.996553    0.833333    0.998019    0.568811    0.998823
R2_7    0.76132 1   0.996266    1   0.999624    0.76132 0.994472
R2_71   0.77139 1   0.977113    1   0.975684    0.77139 0.99827
R2_72   0.313586    0.866667    0.985308    0.636364    1   0.313586    0.99811
R2_73   0.921274    1   0.989642    0.952381    0.997619    0.921274    0.999506
R2_76   0.463043    1   0.996114    1   1   0.463043    0.999218
```

Summary statistics for: B2

Summary for file: G_RMXB2v2.accepted_hits.bam

```
   Unmapped:    0 reads
   Experiment: 6434036 (16.0152%) reads
   Synthetic:  33740540 (83.9848%) reads


   Reference:  1190 exons
   Reference:  1028 introns
   Reference:  149219 bases


   Query:       85746594 exons
   Query:       43266445 introns
   Query:       157833 bases


   Dilution:   0.839848


   ***
   *** The following statistics are computed at the exon, intron and base level.
   ***
   *** Exon level is defined by performance per exon. An alignment that
   *** is not mapped entirely within an exon is considered as a FP. The
   *** intron level is similar.
   ***
   *** Base level is defined by performance per nucleotide. A partial
   *** mapped read will have FP and TP.
   ***

   ------------------- Exon level --------------------

   Sensitivity: 0.994118
   Specificity: 0.976567
   Detection:   0.0590086 (R2_33)

   ------------------- Intron level -------------------

   Sensitivity: 0.986381
   Specificity: 0.756517
   Detection:   1.88828 (R1_72)

   ------------------- Base level --------------------

   Sensitivity: 0.685982
   Specificity: 0.948160
   Detection:   0.0590086 (R2_33)

   ------------------- Undetected --------------------

   Exon:   0.005882
   Intron: 0.013619
   Gene:   0.039474
```

Sequin statistics for: B2

ID	Covered	Sensitivity (Exon)	Specificity (Exon)	Sensitivity (Intron)	Specificity (Intron)	Sens
R1_101	0.832898	1	1	1	1	0.832898	1
R1_102	0.698107	1	0.985276	1	0.244275	0.698107	0.999498
R1_103	0.628532	1	0.993265	1	0.970835	0.628532	0.996924
R1_11	0.644489	1	1	1	1	0.644489	1
R1_12	0.590941	1	0.995051	1	1	0.590941	0.998831
R1_13	0.920394	1	0.987888	0.909091	0.995075	0.920394	0.995082
R1_14	1	0.999876	--	--	1	0.995502	1
R1_21	0.630945	1	0.99394	1	0.839282	0.630945	0.942446
R1_22	0.527149	1	0.999506	1	0.0015311	0.527149	0.999142
R1_23	0.609892	1	0.986752	1	0.00298525	0.609892	0.997721
R1_24	0.999563	1	0.995545	1	0.998693	0.999563	0.998037
R1_31	0.688764	1	0.992008	1	0.997879	0.688764	0.99322
R1_32	0.544296	1	1	1	1	0.544296	1
R1_33	0.896837	1	0.983193	1	1	0.896837	0.999341
R1_41	0.78125	1	0.999876	1	0.874219	0.78125	0.995575
R1_42	0.617479	1	0.990803	1	0.985162	0.617479	0.993884
R1_43	0.541636	1	0.985438	0.973684	0.803818	0.541636	0.996005
R1_51	0.604284	1	0.996225	1	0.0829933	0.604284	0.997209
R1_52	0.622807	1	0.994399	1	1	0.622807	0.997557
R1_53	0.998489	1	0.997344	1	0.0360915	0.998489	0.996482
R1_61	0.687813	1	0.986755	1	0.959677	0.687813	0.998788
R1_62	0.686473	1	1	0.8	0.8	0.686473	1
R1_63	0.670484	1	0.993684	1	0.877702	0.670484	0.996133
R1_71	0.740968	1	0.993425	1	0.997341	0.740968	0.984678
R1_72	0.600903	1	1	1	0.8	0.600903	1
R1_73	0.731115	1	0.991099	0.96	0.985267	0.731115	0.997716
R1_81	0.748031	1	0.997639	1	0.992314	0.748031	0.996329
R1_82	0.587741	1	0.99715	1	0.988495	0.587741	0.9908
R1_83	0.647127	1	0.998647	1	0.99802	0.647127	0.998215
R1_91	0.668377	1	1	1	1	0.668377	1
R1_92	0.778342	1	0.983037	1	0.996622	0.778342	0.994595
R1_93	0.625086	1	0.996003	1	0.996222	0.625086	0.996156
R2_1	1	1	--	--	0.99397	1	0.99397
R2_105	1	0.954887	--	--	0.981333	0.994595	0.981333
R2_115	0.837412	1	0.99107	1	0.992674	0.837412	0.923261
R2_116	0.582339	1	0.99	1	1	0.582339	0.997547
R2_117	0.711066	1	0.99903	1	0.997962	0.711066	0.996411
R2_14	0.719569	1	0.984606	1	0.928543	0.719569	0.991507
R2_150	0.82699	1	0.998974	1	0.046194	0.82699	0.993075
R2_151	0.549431	1	0.996042	1	0.000351715	0.549431	0.996035
R2_152	0.603368	1	0.998164	1	0.00536784	0.603368	0.999192
R2_153	0.672983	1	1	1	1	0.672983	1
R2_154	0.855658	1	0.988501	1	0.339719	0.855658	0.994631
R2_18	0.628326	1	0.984501	1	0.951897	0.628326	0.986486
R2_19	0.811146	1	0.996182	1	0.957324	0.811146	0.999001
R2_20	0.733564	1	0.997507	1	0.994503	0.733564	0.997386
R2_24	0.585856	0.979592	0.989461	0.957447	0.828288	0.585856	0.998239
R2_26	0.916982	1	0.99228	1	0.640148	0.916982	0.997569
R2_27	0.748512	1	0.981896	1	1	0.748512	0.999205
R2_28	0.687711	1	1	1	1	0.687711	1
R2_32	0.669948	1	0.993046	1	1	0.669948	0.998624

R2_33	0.95053	1	1	1	1	0.95053	1
R2_37	0.706322	1	0.98032	1	0.981481	0.706322	0.998718
R2_38	0.380026	1	0.97554	1	1	0.380026	0.998268
R2_41	0.836669	1	0.991694	1	0.998627	0.836669	0.995746
R2_42	0.851163	1	0.997821	1	1	0.851163	0.999545
R2_45	0.461061	1	0.996591	1	0.995166	0.461061	0.999061
R2_46	0.694227	1	1	1	1	0.694227	1
R2_47	0.888518	1	0.996794	1	0.975142	0.888518	0.998456
R2_53	0.39111	1	0.999066	1	1	0.39111	0.999542
R2_54	0.864703	1	0.986481	1	0.997388	0.864703	0.997956
R2_55	0.880804	1	0.987022	1	0.998648	0.880804	0.99142
R2_57	0.624855	1	0.993583	0.941176	1	0.624855	0.998766
R2_59	0.559432	1	1	1	1	0.559432	1
R2_6	0.702025	1	0.995921	1	0.998458	0.702025	0.990476
R2_60	0.607892	1	0.997107	1	0.996965	0.607892	0.995923
R2_63	0.886991	1	0.998679	1	0.999706	0.886991	0.997046
R2_65	1	0.984615	--	--	0.994493	0.99779	0.994493
R2_66	0.528717	1	0.999833	1	1	0.528717	0.987964
R2_67	0.944551	1	1	1	1	0.944551	1
R2_68	0.568811	0.846154	0.995703	0.833333	0.996352	0.568811	0.998431
R2_7	0.760474	1	0.994988	1	0.999414	0.760474	0.993367
R2_71	0.676471	1	0.99635	1	1	0.676471	0.999013
R2_72	0.337491	0.866667	0.989529	0.727273	1	0.337491	0.998682
R2_73	0.944937	1	0.986542	1	0.998453	0.944937	0.999519
R2_76	0.470652	1	1	1	1	0.470652	1

Summary statistics for: B3

Summary for file: G_RMXB3v2.accepted_hits.bam

```
   Unmapped:   0 reads
   Experiment: 7941201 (17.1508%) reads
   Synthetic:  38361013 (82.8492%) reads

   Reference:  1190 exons
   Reference:  1028 introns
   Reference:  149219 bases

   Query:      98520610 exons
   Query:      50973179 introns
   Query:      157888 bases

   Dilution:   0.828492

   ***
   *** The following statistics are computed at the exon, intron and base level.
   ***
   *** Exon level is defined by performance per exon. An alignment that
   *** is not mapped entirely within an exon is considered as a FP. The
   *** intron level is similar.
   ***
   *** Base level is defined by performance per nucleotide. A partial
   *** mapped read will have FP and TP.
   ***

   -------------------- Exon level --------------------

   Sensitivity: 0.994958
   Specificity: 0.978198
   Detection:   0.0590086 (R2_33)

   -------------------- Intron level --------------------

   Sensitivity: 0.983463
   Specificity: 0.751422
   Detection:   1.88828 (R1_72)

   -------------------- Base level --------------------

   Sensitivity: 0.684753
   Specificity: 0.946133
   Detection:   0.0590086 (R2_33)

   -------------------- Undetected --------------------

   Exon:   0.005042
   Intron: 0.016537
   Gene:   0.052632
```

Sequin statistics for: B3

ID	Covered	Sensitivity (Exon)	Specificity (Exon)	Sensitivity (Intron)	Specificity (Intron)	Sens
R1_101	0.841601	1	0.99403	1	1	0.841601 0.998967
R1_102	0.717742	1	0.980746	1	0.0221654	0.717742 0.999024
R1_103	0.627978	1	0.992148	1	0.835009	0.627978 0.996922
R1_11	0.645161	1	0.999461	1	1	0.645161 0.998959
R1_12	0.590595	1	0.991325	1	0.99781	0.590595 0.99883
R1_13	0.920394	1	0.988254	0.909091	0.987014	0.920394 0.995898
R1_14	1	0.999656	--	--	1	0.989568 1
R1_21	0.630945	1	0.993922	1	0.822178	0.630945 0.942446
R1_22	0.525792	1	1	1	0.00123868	0.525792 1
R1_23	0.60815	1	0.98571	1	0.00229028	0.60815 0.997714
R1_24	0.999563	1	0.995155	1	0.998935	0.999563 0.997819
R1_31	0.689234	1	0.991529	1	0.983869	0.689234 0.991881
R1_32	0.544296	1	1	1	1	0.544296 1
R1_33	0.890038	1	0.996205	1	1	0.890038 0.999005
R1_41	0.78125	1	0.999946	1	0.996632	0.78125 0.998225
R1_42	0.617479	1	0.991638	1	0.949859	0.617479 0.992872
R1_43	0.541818	1	0.986158	0.973684	0.604672	0.541818 0.996007
R1_51	0.60372	1	0.995606	1	0.831258	0.60372 0.996279
R1_52	0.62357	1	0.993546	1	0.999107	0.62357 0.997559
R1_53	0.998489	1	0.99506	1	0.72554	0.998489 0.995982
R1_61	0.686144	1	1	1	0.911765	0.686144 1
R1_62	0.716182	1	1	1	0.842105	0.716182 1
R1_63	0.670484	1	0.9934	1	0.879043	0.670484 0.995363
R1_71	0.740968	1	0.991256	1	0.984353	0.740968 0.987705
R1_72	0.586456	1	1	1	0.666667	0.586456 1
R1_73	0.731325	1	0.99045	0.96	0.991894	0.731325 0.997432
R1_81	0.749606	1	0.997294	1	0.989216	0.749606 0.996337
R1_82	0.587741	1	0.995803	1	0.987377	0.587741 0.991501
R1_83	0.644813	1	0.998136	1	0.995882	0.644813 0.998209
R1_91	0.679282	1	1	1	1	0.679282 1
R1_92	0.77665	1	0.97995	1	0.996986	0.77665 0.995122
R1_93	0.625086	1	0.996497	1	0.998423	0.625086 0.996156
R2_1	1	1	--	--	0.988945	1 0.988945
R2_105	1	0.983471	--	--	0.984	0.994609 0.984
R2_115	0.842849	1	0.989942	1	0.993289	0.842849 0.92427
R2_116	0.521718	1	0.996266	1	1	0.521718 0.998174
R2_117	0.711066	1	0.999352	1	0.997792	0.711066 0.997126
R2_14	0.719569	1	0.984373	1	0.944812	0.719569 0.991507
R2_150	0.833141	1	0.999017	1	0.0395501	0.833141 0.997698
R2_151	0.584864	1	0.997917	1	0.000290904	0.584864 0.999253
R2_152	0.603856	1	0.997058	1	0.00392735	0.603856 0.998386
R2_153	0.668093	1	0.997268	0.95	1	0.668093 0.99863
R2_154	0.855658	1	0.991371	1	0.158151	0.855658 0.994631
R2_18	0.628326	1	0.985099	1	0.89836	0.628326 0.986486
R2_19	0.811146	1	0.996027	1	0.769173	0.811146 0.998716
R2_20	0.732795	1	0.998371	1	0.998409	0.732795 0.997906
R2_24	0.586151	0.979592	0.988855	0.957447	0.904814	0.586151 0.99824
R2_26	0.916982	1	0.992311	1	0.984013	0.916982 0.997569
R2_27	0.749702	1	0.994169	1	1	0.749702 0.99881
R2_28	0.686747	1	1	1	1	0.686747 1
R2_32	0.667795	1	0.990257	1	1	0.667795 0.997244

```
R2_33   0.40636 0.5 1    0    0    0.40636 1
R2_37   0.711761    1    0.994798    1    1    0.711761    0.999682
R2_38   0.387607    1    0.9946 1    1    0.387607    0.997455
R2_41   0.837384    1    0.991778    1    0.985197    0.837384    0.989861
R2_42   0.85814 1    1    1    1    0.85814 1
R2_45   0.454703    1    0.999465    1    0.98533 0.454703    0.999682
R2_46   0.683103    1    1    1    1    0.683103    1
R2_47   0.888911    1    0.996685    1    0.995092    0.888911    0.998237
R2_53   0.385374    1    0.998685    1    1    0.385374    0.999535
R2_54   0.864703    1    0.982419    1    0.996371    0.864703    0.997446
R2_55   0.880804    1    0.989737    1    0.973753    0.880804    0.989875
R2_57   0.639907    1    0.99214 0.941176    1    0.639907    0.997593
R2_59   0.562177    1    1    1    1    0.562177    1
R2_6    0.702025    1    0.9962 1    1    0.702025    0.991826
R2_60   0.607892    1    0.996822    1    0.998606    0.607892    0.996503
R2_63   0.886991    1    0.998578    1    1    0.886991    0.996555
R2_65   1    1    --    --    0.995595    1    0.995595
R2_66   0.527107    1    0.999792    1    0.999952    0.527107    0.986935
R2_67   0.804971    1    1    1    1    0.804971    1
R2_68   0.597632    0.923077    0.995682    0.875    0.997295    0.597632    0.99888
R2_7    0.76132 1    0.997063    1    0.99982 0.76132 0.993374
R2_71   0.679813    1    0.998536    1    1    0.679813    0.999018
R2_72   0.300965    0.866667    0.993569    0.454545    1    0.300965    0.999014
R2_73   0.950398    1    0.991451    1    0.997839    0.950398    0.999521
R2_76   0.477536    1    0.990426    1    1    0.477536    0.999242
```

TransQuin Assembly

Summary statistics for: A1

Summary for dataset: /Users/tedwong/Desktop/K_562/Cufflinks/A1/NotGuided/transcripts.gtf

```
   Experiment: 156131 features
   Synthetic:  1955 features

   Reference:  162 exons
   Reference:  1028 introns


   ***
   *** The following statistics are computed for exact and fuzzy.
   ***
   *** The fuzzy level is 10 nucleotides.
   ***


   ------------------- Exon level --------------------

   Sensitivity: 1 (1)
   Specificity: 1 (1)
   ------------------- Intron level --------------------

   Sensitivity: 0.996032 (0.996032)
   Specificity: 0.996032 (0.996032)
   ------------------- Base level --------------------

   Sensitivity: 1
   Specificity: 1
   ------------------ Intron Chain level -------------------

   Sensitivity: 1 (1)
   Specificity: 1 (1)


   ------------------- Transcript level -------------------

   Sensitivity: 1 (0.993939)
   Specificity: 1 (0.993939)

   Missing exons: 0/872 (0)
   Missing introns: 3/756 (0.00396825)

   Novel exons: 0/872 (0)
   Novel introns: 0/756 (0)
```

Summary statistics for: A2

Summary for dataset: /Users/tedwong/Desktop/K_562/Cufflinks/A2/NotGuided/transcripts.gtf

```
   Experiment: 144223 features
   Synthetic:  1928 features


   Reference:  162 exons
   Reference:  1028 introns


   ***
   *** The following statistics are computed for exact and fuzzy.
   ***
   *** The fuzzy level is 10 nucleotides.
   ***


   ------------------- Exon level --------------------

   Sensitivity: 1 (1)
   Specificity: 1 (1)
   ------------------- Intron level -------------------

   Sensitivity: 0.996032 (0.996032)
   Specificity: 0.996032 (0.996032)
   ------------------- Base level --------------------

   Sensitivity: 1
   Specificity: 1
   ------------------- Intron Chain level --------------------

   Sensitivity: 1 (1)
   Specificity: 1 (1)


   ------------------- Transcript level --------------------

   Sensitivity: 1 (0.993939)
   Specificity: 1 (0.993939)

   Missing exons: 0/872 (0)
   Missing introns: 3/756 (0.00396825)

   Novel exons: 0/872 (0)
   Novel introns: 0/756 (0)
```

Summary statistics for: A3

Summary for dataset: /Users/tedwong/Desktop/K_562/Cufflinks/A3/NotGuided/transcripts.gtf

```
   Experiment: 147191 features
   Synthetic:  2037 features


   Reference:  162 exons
   Reference:  1028 introns


   ***
   *** The following statistics are computed for exact and fuzzy.
   ***
   *** The fuzzy level is 10 nucleotides.
   ***


   ------------------- Exon level --------------------

   Sensitivity: 1 (1)
   Specificity: 1 (1)
   ------------------- Intron level -------------------

   Sensitivity: 0.996032 (0.996032)
   Specificity: 0.996032 (0.996032)
   ------------------- Base level --------------------

   Sensitivity: 1
   Specificity: 1
   ------------------- Intron Chain level --------------------

   Sensitivity: 1 (1)
   Specificity: 1 (1)


   ------------------- Transcript level --------------------

   Sensitivity: 1 (0.993939)
   Specificity: 1 (0.993939)

   Missing exons: 0/872 (0)
   Missing introns: 3/756 (0.00396825)

   Novel exons: 0/872 (0)
   Novel introns: 0/756 (0)
```

Summary statistics for: B1

Summary for dataset: /Users/tedwong/Desktop/K_562/Cufflinks/B1/NotGuided/transcripts.gtf

```
   Experiment: 108316 features
   Synthetic:  1691 features


   Reference:  162 exons
   Reference:  1028 introns


   ***
   *** The following statistics are computed for exact and fuzzy.
   ***
   *** The fuzzy level is 10 nucleotides.
   ***


   ------------------ Exon level --------------------

   Sensitivity: 1 (1)
   Specificity: 1 (1)
   ------------------ Intron level -------------------

   Sensitivity: 0.996032 (0.996032)
   Specificity: 0.996032 (0.996032)
   ------------------ Base level --------------------

   Sensitivity: 1
   Specificity: 1
   ------------------ Intron Chain level --------------------

   Sensitivity: 1 (1)
   Specificity: 1 (1)


   ------------------ Transcript level --------------------

   Sensitivity: 1 (0.993939)
   Specificity: 1 (0.993939)

   Missing exons: 0/872 (0)
   Missing introns: 3/756 (0.00396825)

   Novel exons: 0/872 (0)
   Novel introns: 0/756 (0)
```

Summary statistics for: B2

Summary for dataset: /Users/tedwong/Desktop/K_562/Cufflinks/B2/NotGuided/transcripts.gtf

```
   Experiment: 107544 features
   Synthetic:  1616 features


   Reference:  162 exons
   Reference:  1028 introns


   ***
   *** The following statistics are computed for exact and fuzzy.
   ***
   *** The fuzzy level is 10 nucleotides.
   ***


   ------------------- Exon level --------------------

   Sensitivity: 1 (1)
   Specificity: 1 (1)
   ------------------- Intron level -------------------

   Sensitivity: 0.996032 (0.996032)
   Specificity: 0.996032 (0.996032)
   ------------------- Base level --------------------

   Sensitivity: 1
   Specificity: 1
   ------------------- Intron Chain level --------------------

   Sensitivity: 1 (1)
   Specificity: 1 (1)


   ------------------- Transcript level --------------------

   Sensitivity: 1 (0.993939)
   Specificity: 1 (0.993939)

   Missing exons: 0/872 (0)
   Missing introns: 3/756 (0.00396825)

   Novel exons: 0/872 (0)
   Novel introns: 0/756 (0)
```

Summary statistics for: B3

Summary for dataset: /Users/tedwong/Desktop/K_562/Cufflinks/B2/NotGuided/transcripts.gtf

```
   Experiment: 107544 features
   Synthetic:  1616 features


   Reference:  162 exons
   Reference:  1028 introns


   ***
   *** The following statistics are computed for exact and fuzzy.
   ***
   *** The fuzzy level is 10 nucleotides.
   ***


   ------------------- Exon level --------------------

   Sensitivity: 1 (1)
   Specificity: 1 (1)
   ------------------- Intron level --------------------

   Sensitivity: 0.996032 (0.996032)
   Specificity: 0.996032 (0.996032)
   ------------------- Base level --------------------

   Sensitivity: 1
   Specificity: 1
   ------------------- Intron Chain level --------------------

   Sensitivity: 1 (1)
   Specificity: 1 (1)


   ------------------- Transcript level --------------------

   Sensitivity: 1 (0.993939)
   Specificity: 1 (0.993939)

   Missing exons: 0/872 (0)
   Missing introns: 3/756 (0.00396825)

   Novel exons: 0/872 (0)
   Novel introns: 0/756 (0)
```

TransQuin Expression (Gene)

Expression summary statistics for: A1

Expression scatter plot for: A1
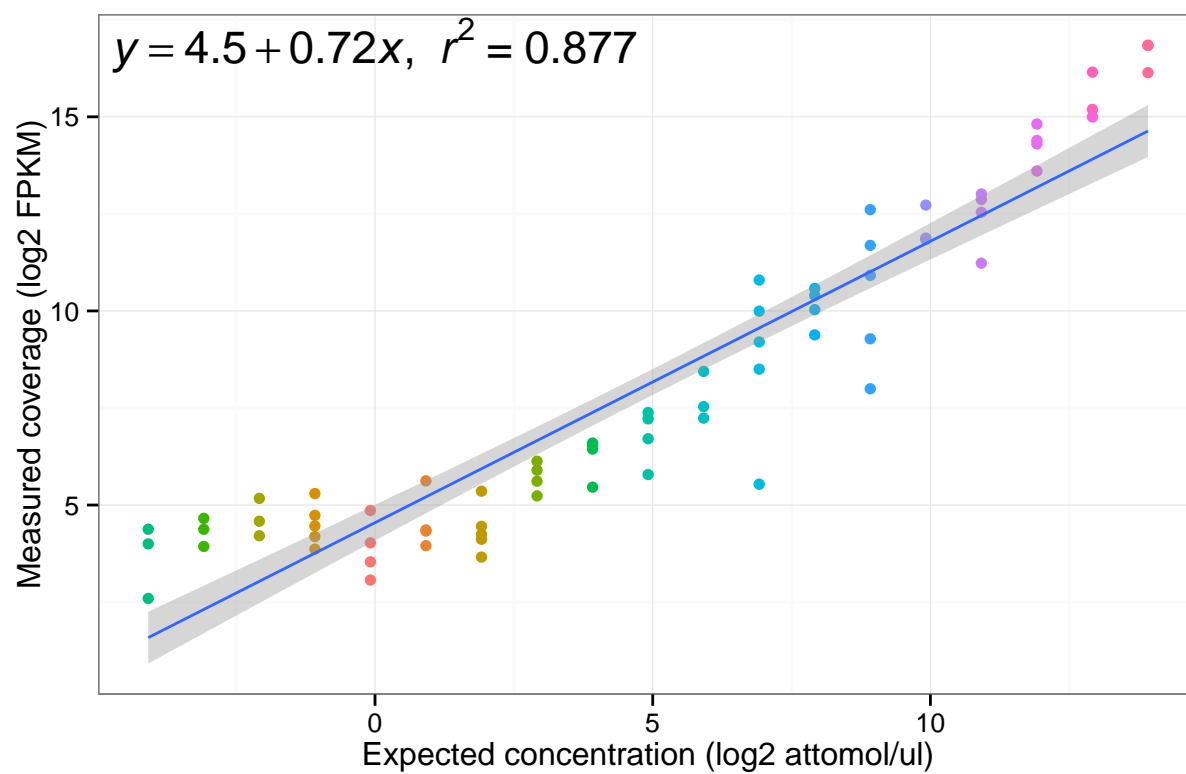
$y = 4.5 + 0.72x, \; r^2 = 0.877$

Measured coverage (log2 FPKM)

Expected concentration (log2 attomol/ul)

Expression summary statistics for: A2

Summary for dataset: /Users/tedwong/Desktop/K_562/Cufflinks/A2/genes.fpkm_tracking

```
   Experiment:  60570 gene
   Synthetic:   75 gene


   Reference:   76 gene
   Detected:    4.62321 gene


   ***
   *** Detection Limits
   ***


   Break: 3.77655 (R1_62)


   Left:  4.62321 + 0.0227324x (R2 = 0.00360572)
   Right: 2.20463 + 0.990951x (R2 = 0.91596)


   ***
   *** Statistics for linear regression
   ***


   Correlation: 0.960008
   Slope:       6.60733
   R2:          0.921615
   F-statistic: 834.781
   P-value:     0
   SSM:         3.663e+10, DF: 1
   SSE:         3.11546e+09, DF: 71
   SST:         3.97454e+10, DF: 72


   ***
   *** Statistics for linear regression (log2 scale)
   ***


   Correlation: 0.925689
   Slope:       0.699133
   R2:          0.8569
   F-statistic: 425.155
   P-value:     0
   SSM:         967.772, DF: 1
   SSE:         161.616, DF: 71
   SST:         1129.39, DF: 72
```

Expression scatter plot for: A2
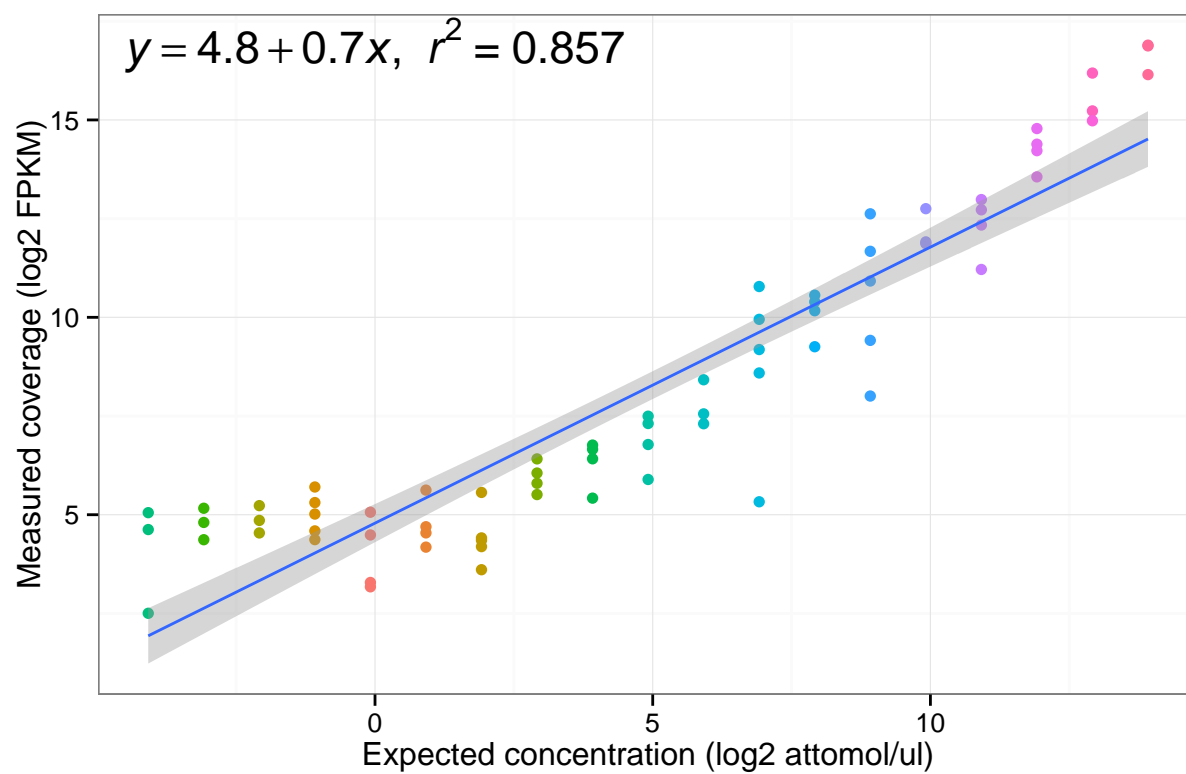
$y = 4.8 + 0.7x, \; r^2 = 0.857$

Measured coverage (log2 FPKM)

Expected concentration (log2 attomol/ul)

Expression summary statistics for: A3

Summary for dataset: /Users/tedwong/Desktop/K_562/Cufflinks/A3/genes.fpkm_tracking

```
    Experiment:  60569 gene
    Synthetic:   75 gene


    Reference:   76 gene
    Detected:    5.25776 gene


    ***
    *** Detection Limits
    ***


    Break: 15.1062 (R1_101)


    Left:  5.25776 + 0.16804x (R2 = 0.139073)
    Right: 1.51144 + 1.05768x (R2 = 0.903529)


    ***
    *** Statistics for linear regression
    ***


    Correlation: 0.961001
    Slope:       6.31637
    R2:          0.923522
    F-statistic: 857.371
    P-value:     0
    SSM:         3.34749e+10, DF: 1
    SSE:         2.7721e+09, DF: 71
    SST:         3.6247e+10, DF: 72


    ***
    *** Statistics for linear regression (log2 scale)
    ***


    Correlation: 0.915017
    Slope:       0.666601
    R2:          0.837255
    F-statistic: 365.266
    P-value:     0
    SSM:         879.802, DF: 1
    SSE:         171.015, DF: 71
    SST:         1050.82, DF: 72
```

Expression scatter plot for: A3
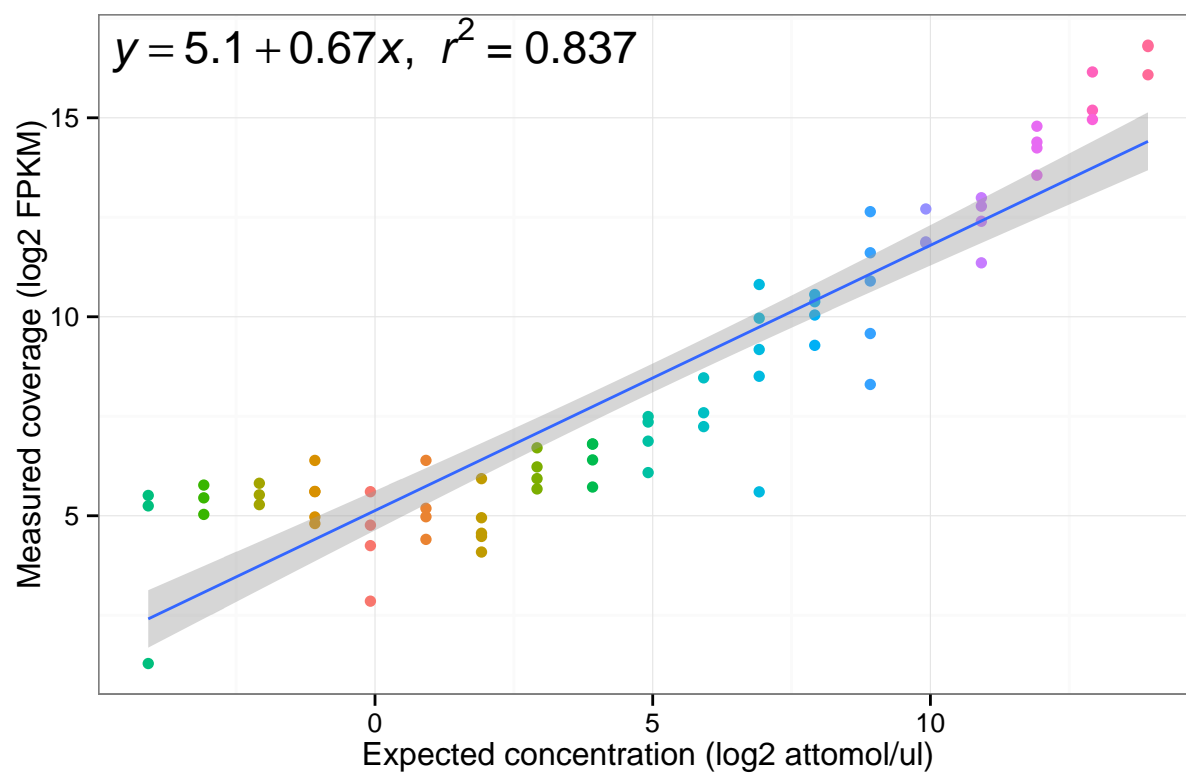
$y = 5.1 + 0.67x, \ r^2 = 0.837$

Measured coverage (log2 FPKM)

Expected concentration (log2 attomol/ul)

Expression summary statistics for: B1

Summary for dataset: /Users/tedwong/Desktop/K_562/Cufflinks/B1/genes.fpkm_tracking

```
Experiment:  60568 gene
Synthetic:   74 gene


Reference:   76 gene
Detected:    5.19759 gene


***
*** Detection Limits
***


Break: 1.88828 (R1_72)


Left:  5.19759 + 0.42932x (R2 = 0.278885)
Right: 2.76376 + 0.857773x (R2 = 0.701784)


***
*** Statistics for linear regression
***


Correlation: 0.87057
Slope:       3.70819
R2:          0.757893
F-statistic: 219.128
P-value:     0
SSM:         3.24184e+10, DF: 1
SSE:         1.0356e+10, DF: 70
SST:         4.27744e+10, DF: 71


***
*** Statistics for linear regression (log2 scale)
***


Correlation: 0.84233
Slope:       0.652163
R2:          0.709519
F-statistic: 170.98
P-value:     0
SSM:         856.494, DF: 1
SSE:         350.653, DF: 70
SST:         1207.15, DF: 71
```
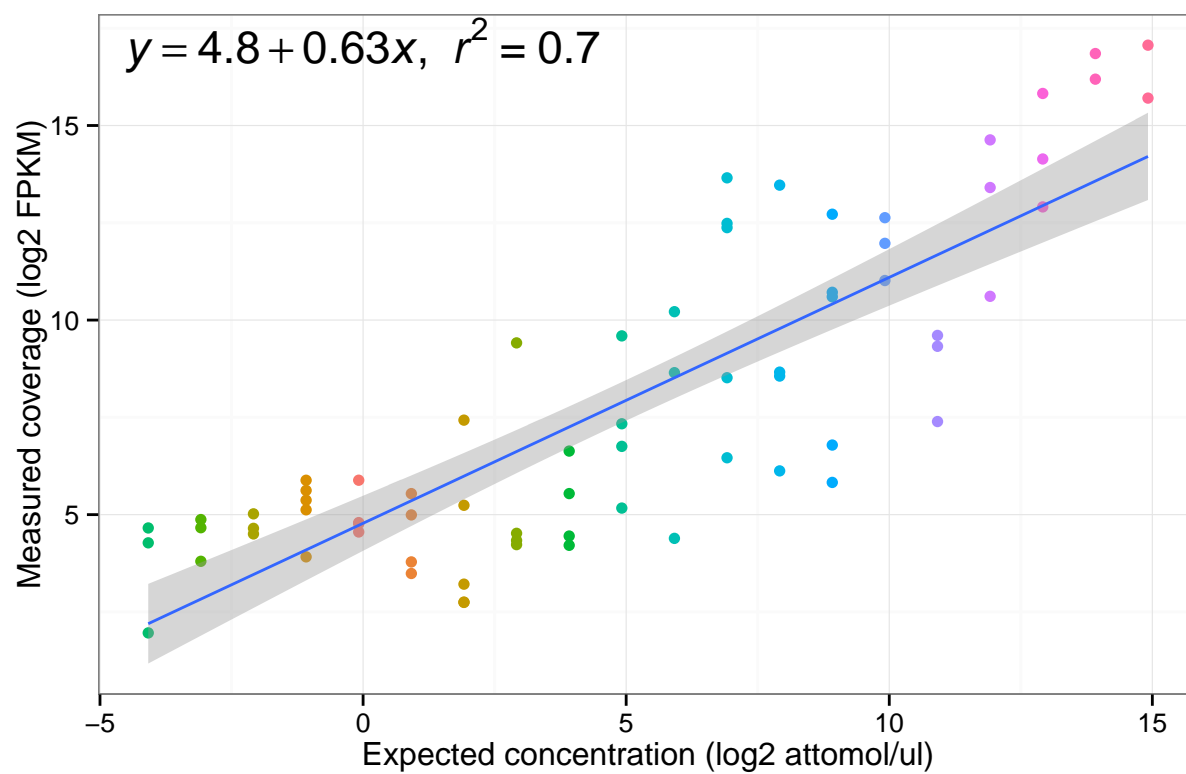
Expression scatter plot for: B1
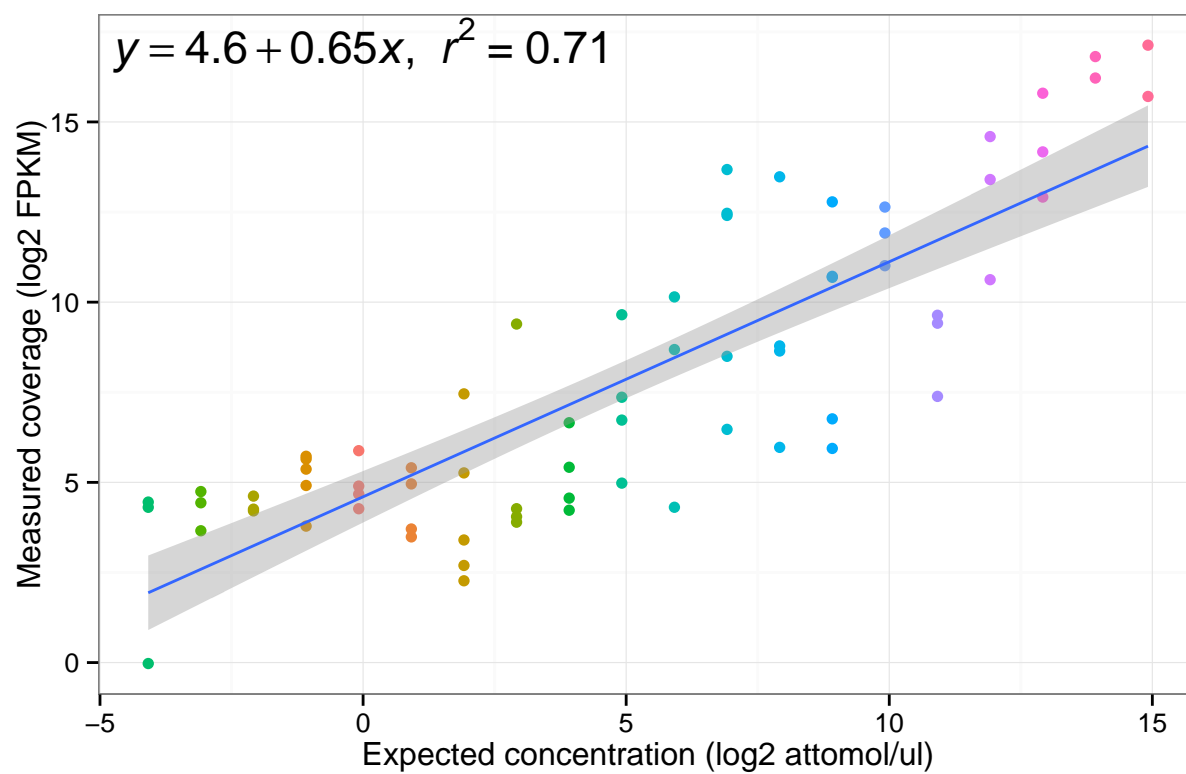
$y = 4.6 + 0.65x, \ r^2 = 0.71$

Measured coverage (log2 FPKM)

Expected concentration (log2 attomol/ul)

Expression summary statistics for: B2

Summary for dataset: /Users/tedwong/Desktop/K_562/Cufflinks/B2/genes.fpkm_tracking

```
   Experiment:  60570 gene
   Synthetic:   74 gene


   Reference:   76 gene
   Detected:    5.22081 gene


   ***
   *** Detection Limits
   ***


   Break: 1.88828 (R1_72)


   Left:  5.22081 + 0.303379x (R2 = 0.28516)
   Right: 2.85593 + 0.848121x (R2 = 0.700146)


   ***
   *** Statistics for linear regression
   ***


   Correlation: 0.866031
   Slope:       3.64019
   R2:          0.750009
   F-statistic: 210.01
   P-value:     0
   SSM:         3.12402e+10, DF: 1
   SSE:         1.04129e+10, DF: 70
   SST:         4.16532e+10, DF: 71


   ***
   *** Statistics for linear regression (log2 scale)
   ***


   Correlation: 0.836934
   Slope:       0.63197
   R2:          0.700459
   F-statistic: 163.691
   P-value:     0
   SSM:         804.275, DF: 1
   SSE:         343.936, DF: 70
   SST:         1148.21, DF: 71
```
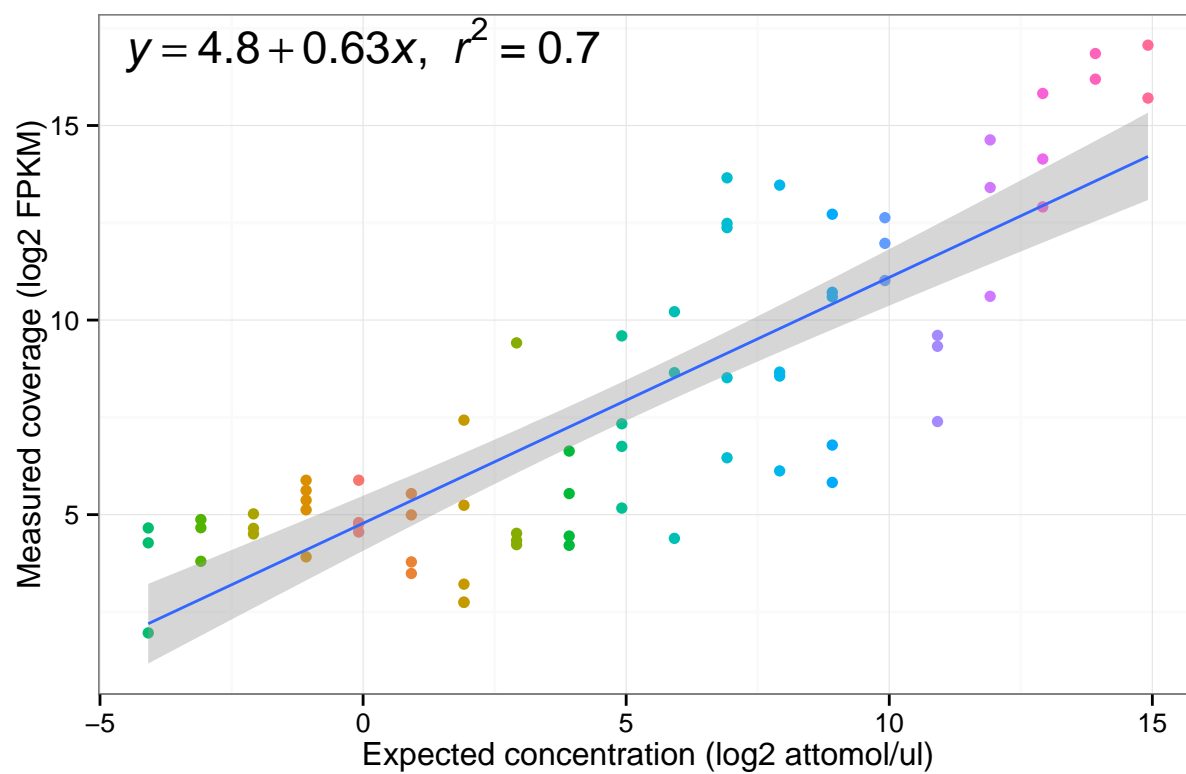
Expression scatter plot for: B2

$y = 4.8 + 0.63x, \ r^2 = 0.7$

Measured coverage (log2 FPKM)

Expected concentration (log2 attomol/ul)

Expression summary statistics for: B3

Summary for dataset: /Users/tedwong/Desktop/K_562/Cufflinks/B3/genes.fpkm_tracking

```
    Experiment:  60570 gene
    Synthetic:   74 gene


    Reference:   76 gene
    Detected:    5.22081 gene


    ***
    *** Detection Limits
    ***


    Break: 1.88828 (R1_72)


    Left:  5.22081 + 0.303379x (R2 = 0.28516)
    Right: 2.85593 + 0.848121x (R2 = 0.700146)


    ***
    *** Statistics for linear regression
    ***


    Correlation: 0.866031
    Slope:       3.64019
    R2:          0.750009
    F-statistic: 210.01
    P-value:     0
    SSM:         3.12402e+10, DF: 1
    SSE:         1.04129e+10, DF: 70
    SST:         4.16532e+10, DF: 71


    ***
    *** Statistics for linear regression (log2 scale)
    ***


    Correlation: 0.836934
    Slope:       0.63197
    R2:          0.700459
    F-statistic: 163.691
    P-value:     0
    SSM:         804.275, DF: 1
    SSE:         343.936, DF: 70
    SST:         1148.21, DF: 71
```

Expression scatter plot for: B3

$y = 4.8 + 0.63x, \ r^2 = 0.7$

Measured coverage (log2 FPKM)

Expected concentration (log2 attomol/ul)

TransQuin Expression (Isoform)

Expression summary statistics for: A1

Summary for dataset: /Users/tedwong/Desktop/K_562/StringTie/A1/t_data.ctab

```
Experiment:  100769 isoform
Synthetic:   164 isoform

Reference:   162 isoform
Detected:    1.25307 isoform


***
*** Detection Limits
***


Break: 3.5544 (R1_32_1)

Left:  1.25307 + 0.157653x (R2 = 0.0887965)
Right: 0.825739 + 1.06985x (R2 = 0.865753)


***
*** Statistics for linear regression
***


Correlation: 0.951062
Slope:       5.16984
R2:          0.904519
F-statistic: 1373.62
P-value:     0
SSM:         7.55327e+10, DF: 1
SSE:         7.97327e+09, DF: 145
SST:         8.35059e+10, DF: 146


***
*** Statistics for linear regression (log2 scale)
***


Correlation: 0.940142
Slope:       0.820425
R2:          0.883867
F-statistic: 1103.57
P-value:     0
SSM:         3387.56, DF: 1
SSE:         445.096, DF: 145
SST:         3832.65, DF: 146
```
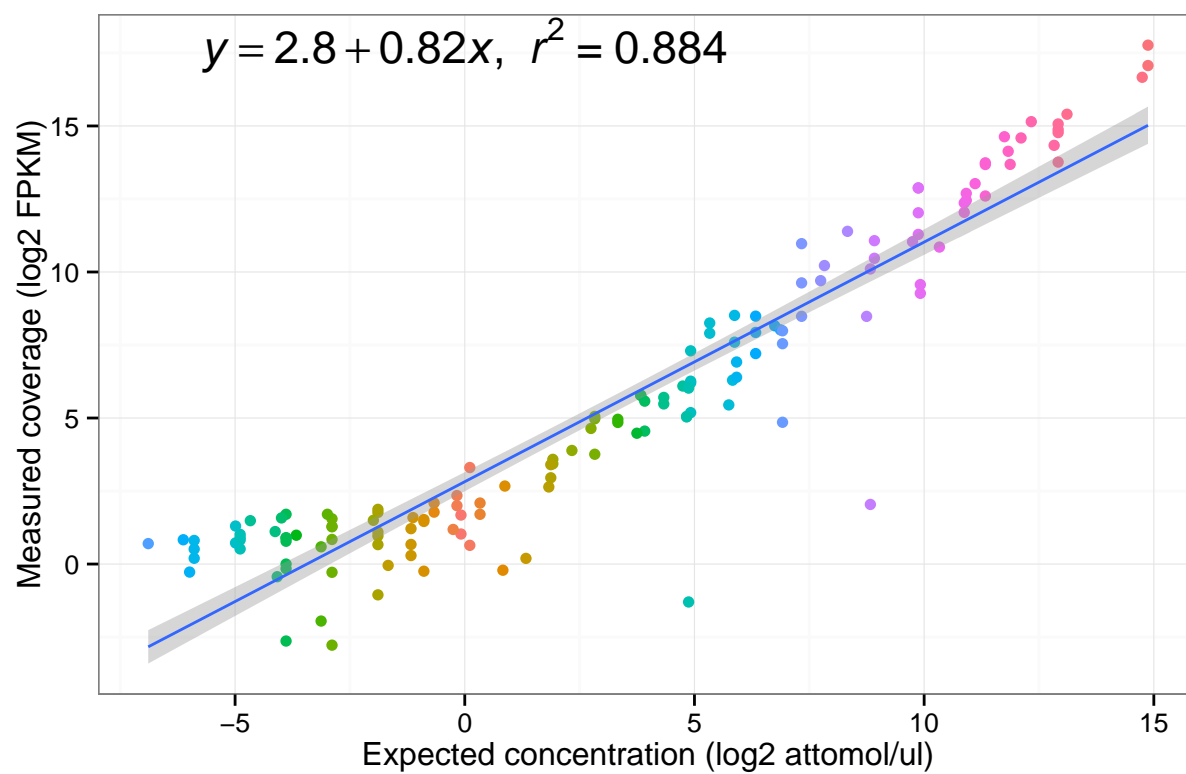
Minor/Major plot

Expression scatter plot for: A1

$y = 2.8 + 0.82x, \; r^2 = 0.884$

Measured coverage (log2 FPKM)

Expected concentration (log2 attomol/ul)

Expression summary statistics for: A2

Summary for dataset: /Users/tedwong/Desktop/K_562/StringTie/A1/t_data.ctab

```
   Experiment:  100769 isoform
   Synthetic:   164 isoform


   Reference:   162 isoform
   Detected:    1.25307 isoform


   ***
   *** Detection Limits
   ***


   Break: 3.5544 (R1_32_1)


   Left:  1.25307 + 0.157653x (R2 = 0.0887965)
   Right: 0.825739 + 1.06985x (R2 = 0.865753)


   ***
   *** Statistics for linear regression
   ***


   Correlation: 0.951062
   Slope:       5.16984
   R2:          0.904519
   F-statistic: 1373.62
   P-value:     0
   SSM:         7.55327e+10, DF: 1
   SSE:         7.97327e+09, DF: 145
   SST:         8.35059e+10, DF: 146


   ***
   *** Statistics for linear regression (log2 scale)
   ***


   Correlation: 0.940142
   Slope:       0.820425
   R2:          0.883867
   F-statistic: 1103.57
   P-value:     0
   SSM:         3387.56, DF: 1
   SSE:         445.096, DF: 145
   SST:         3832.65, DF: 146
```
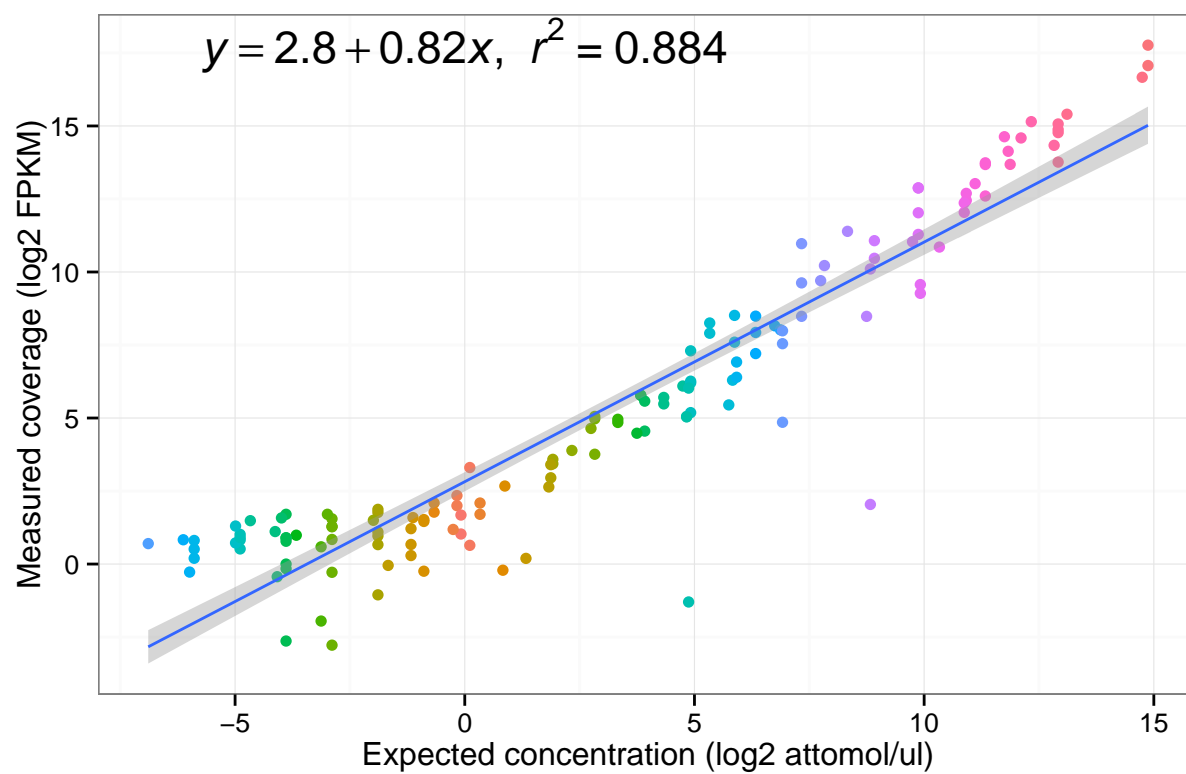
Expression scatter plot for: A2

$$y = 2.8 + 0.82x, \ r^2 = 0.884$$

Measured coverage (log2 FPKM)

Expected concentration (log2 attomol/ul)

Expression summary statistics for: A3

Summary for dataset: /Users/tedwong/Desktop/K_562/StringTie/A1/t_data.ctab

```
    Experiment:  100769 isoform
    Synthetic:   164 isoform


    Reference:   162 isoform
    Detected:    1.25307 isoform


    ***
    *** Detection Limits
    ***


    Break: 3.5544 (R1_32_1)


    Left:  1.25307 + 0.157653x (R2 = 0.0887965)
    Right: 0.825739 + 1.06985x (R2 = 0.865753)


    ***
    *** Statistics for linear regression
    ***


    Correlation: 0.951062
    Slope:       5.16984
    R2:          0.904519
    F-statistic: 1373.62
    P-value:     0
    SSM:         7.55327e+10, DF: 1
    SSE:         7.97327e+09, DF: 145
    SST:         8.35059e+10, DF: 146


    ***
    *** Statistics for linear regression (log2 scale)
    ***


    Correlation: 0.940142
    Slope:       0.820425
    R2:          0.883867
    F-statistic: 1103.57
    P-value:     0
    SSM:         3387.56, DF: 1
    SSE:         445.096, DF: 145
    SST:         3832.65, DF: 146
```
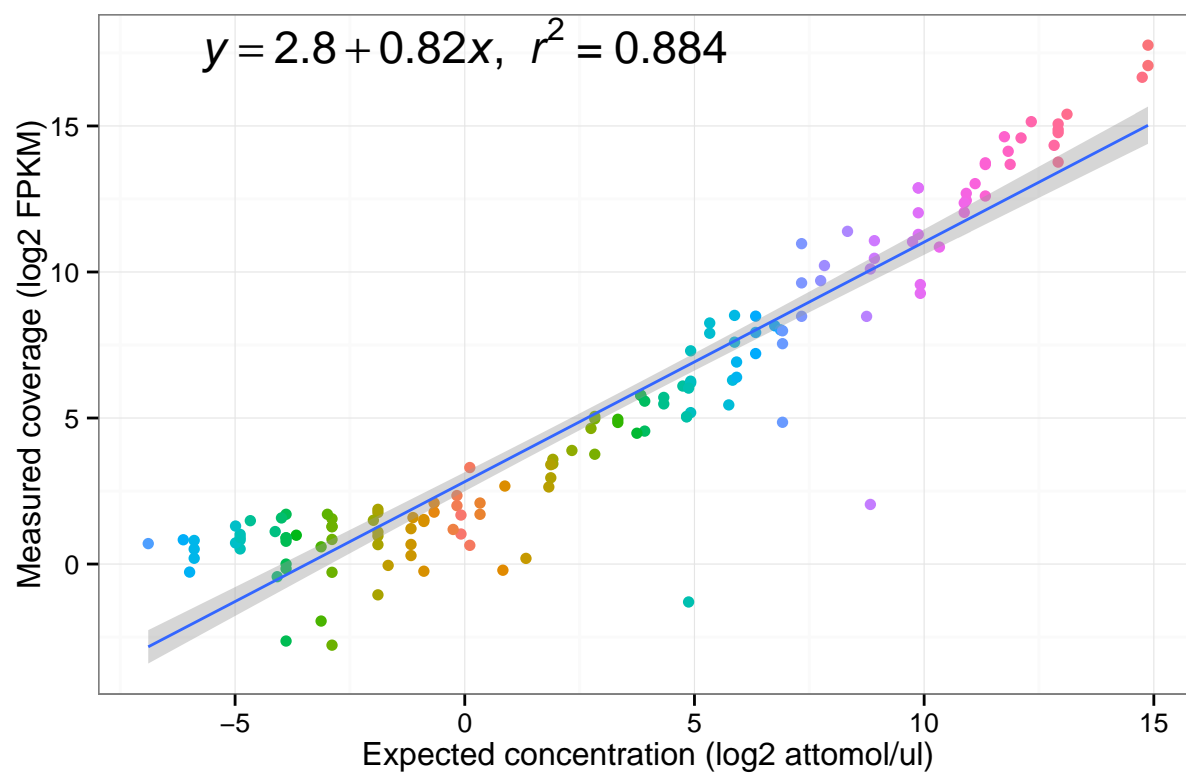
Expression scatter plot for: A3

$y = 2.8 + 0.82x, \ r^2 = 0.884$

Measured coverage (log2 FPKM)

Expected concentration (log2 attomol/ul)

Expression summary statistics for: B1

Summary for dataset: /Users/tedwong/Desktop/K_562/StringTie/A1/t_data.ctab

```
   Experiment:  100769 isoform
   Synthetic:   164 isoform


   Reference:   162 isoform
   Detected:    1.25307 isoform


   ***
   *** Detection Limits
   ***


   Break: 3.5544 (R1_32_1)


   Left:  1.25307 + 0.157653x (R2 = 0.0887965)
   Right: 0.825739 + 1.06985x (R2 = 0.865753)


   ***
   *** Statistics for linear regression
   ***


   Correlation: 0.951062
   Slope:       5.16984
   R2:          0.904519
   F-statistic: 1373.62
   P-value:     0
   SSM:         7.55327e+10, DF: 1
   SSE:         7.97327e+09, DF: 145
   SST:         8.35059e+10, DF: 146


   ***
   *** Statistics for linear regression (log2 scale)
   ***


   Correlation: 0.940142
   Slope:       0.820425
   R2:          0.883867
   F-statistic: 1103.57
   P-value:     0
   SSM:         3387.56, DF: 1
   SSE:         445.096, DF: 145
   SST:         3832.65, DF: 146
```
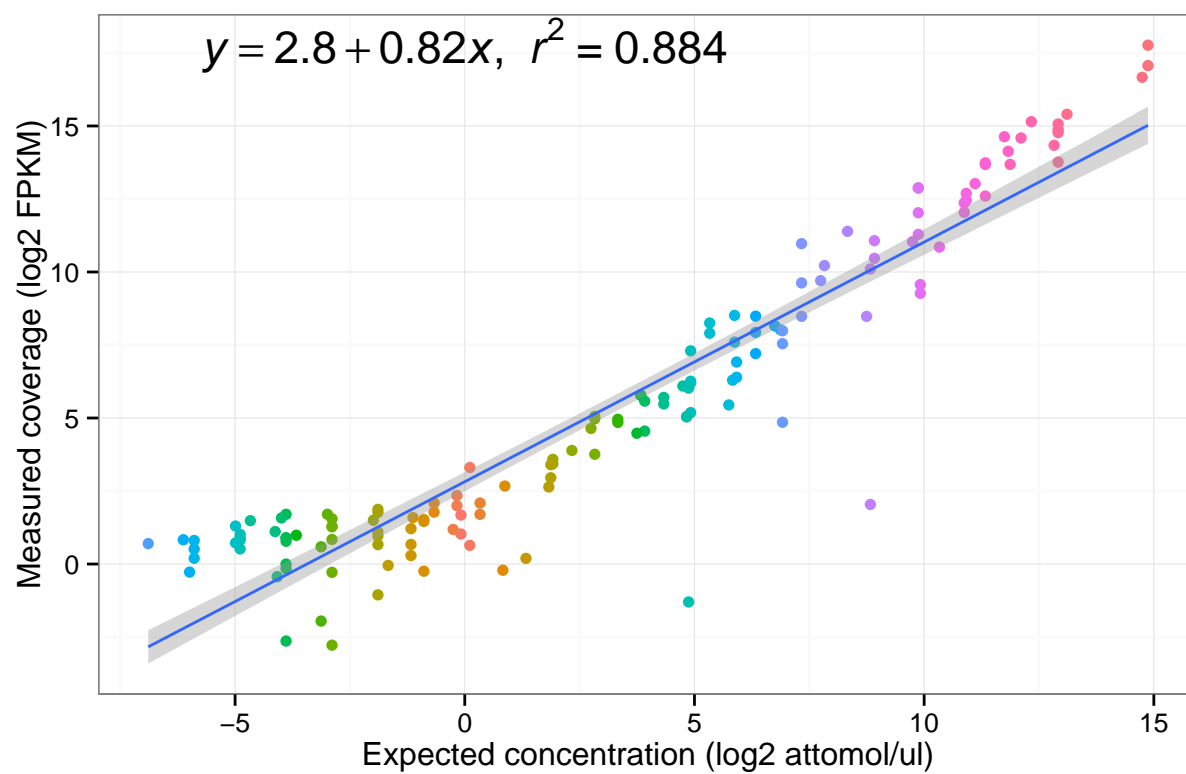
Expression scatter plot for: B1

$$y = 2.8 + 0.82x, \ r^2 = 0.884$$

(x-axis) Expected concentration (log2 attomol/ul)

(y-axis) Measured coverage (log2 FPKM)

Expression summary statistics for: B2

Summary for dataset: /Users/tedwong/Desktop/K_562/StringTie/A1/t_data.ctab

```
    Experiment:  100769 isoform
    Synthetic:   164 isoform


    Reference:   162 isoform
    Detected:    1.25307 isoform


    ***
    *** Detection Limits
    ***


    Break: 3.5544 (R1_32_1)


    Left:  1.25307 + 0.157653x (R2 = 0.0887965)
    Right: 0.825739 + 1.06985x (R2 = 0.865753)


    ***
    *** Statistics for linear regression
    ***


    Correlation: 0.951062
    Slope:       5.16984
    R2:          0.904519
    F-statistic: 1373.62
    P-value:     0
    SSM:         7.55327e+10, DF: 1
    SSE:         7.97327e+09, DF: 145
    SST:         8.35059e+10, DF: 146


    ***
    *** Statistics for linear regression (log2 scale)
    ***


    Correlation: 0.940142
    Slope:       0.820425
    R2:          0.883867
    F-statistic: 1103.57
    P-value:     0
    SSM:         3387.56, DF: 1
    SSE:         445.096, DF: 145
    SST:         3832.65, DF: 146
```
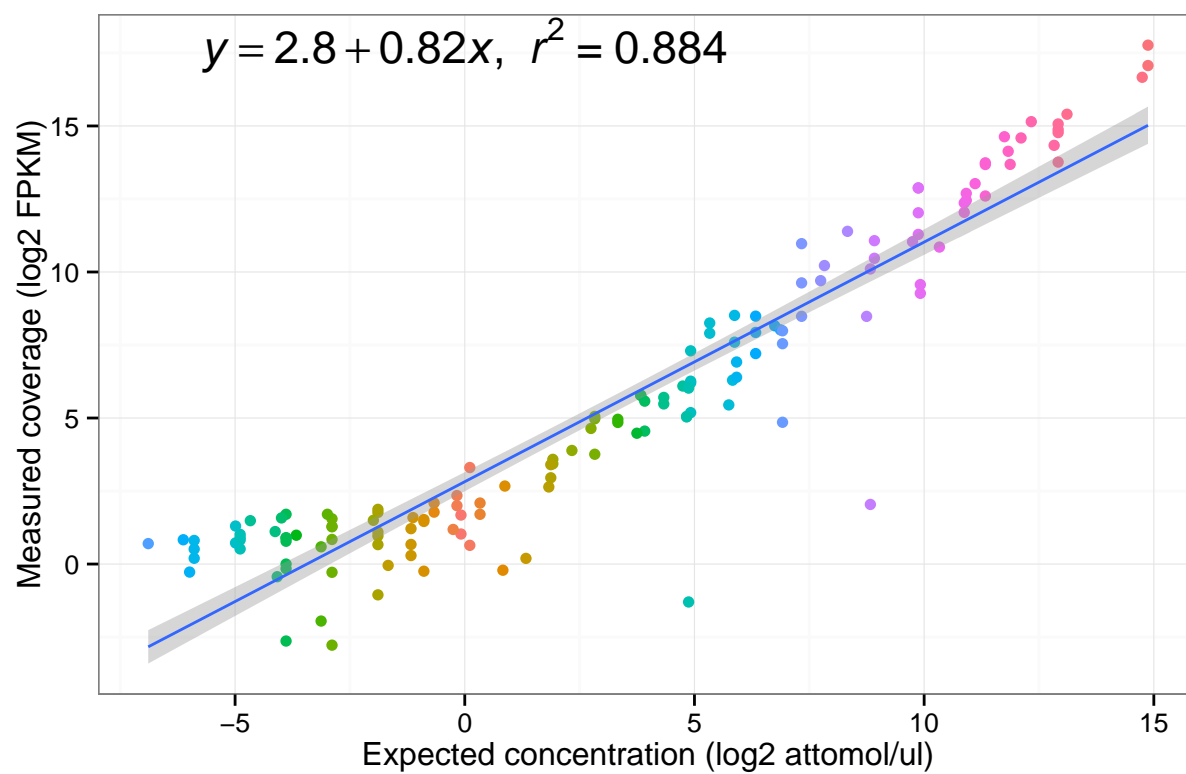
Expression scatter plot for: B2

$y = 2.8 + 0.82x, \ r^2 = 0.884$

Measured coverage (log2 FPKM)

Expected concentration (log2 attomol/ul)

Expression summary statistics for: B3

Summary for dataset: /Users/tedwong/Desktop/K_562/StringTie/A1/t_data.ctab

```
   Experiment:  100769 isoform
   Synthetic:   164 isoform


   Reference:   162 isoform
   Detected:    1.25307 isoform


   ***
   *** Detection Limits
   ***


   Break: 3.5544 (R1_32_1)


   Left:  1.25307 + 0.157653x (R2 = 0.0887965)
   Right: 0.825739 + 1.06985x (R2 = 0.865753)


   ***
   *** Statistics for linear regression
   ***


   Correlation: 0.951062
   Slope:       5.16984
   R2:          0.904519
   F-statistic: 1373.62
   P-value:     0
   SSM:         7.55327e+10, DF: 1
   SSE:         7.97327e+09, DF: 145
   SST:         8.35059e+10, DF: 146


   ***
   *** Statistics for linear regression (log2 scale)
   ***


   Correlation: 0.940142
   Slope:       0.820425
   R2:          0.883867
   F-statistic: 1103.57
   P-value:     0
   SSM:         3387.56, DF: 1
   SSE:         445.096, DF: 145
   SST:         3832.65, DF: 146
```

Expression scatter plot for: B3

$$y = 2.8 + 0.82x, \quad r^2 = 0.884$$

Measured coverage (log2 FPKM)

Expected concentration (log2 attomol/ul)

TransQuin Differential

Differential summary statistics

Summary for dataset: /Users/tedwong/Desktop/K_562/DESeq2/DESeq2.csv

```
   Experiment:  60500 gene
   Synthetic:   75 gene


   Reference:   76 gene
   Detected:    75 gene


   ***
   *** Detection Limits
   ***


   Absolute:    0.0590086 (attomol/ul) (R2_38)


   ***
   *** Statistics for linear regression
   ***


   Correlation: 0.707428
   Slope:       0.426606
   R2:          0.500454
   F-statistic: 73.1328
   P-value:     1.29274e-12
   SSM:         302.202, DF: 1
   SSE:         301.653, DF: 73
   SST:         603.855, DF: 74


   ***
   *** Statistics for linear regression (log2 scale)
   ***


   Correlation: 0.790229
   Slope:       0.648599
   R2:          0.624462
   F-statistic: 121.388
   P-value:     0
   SSM:         183.058, DF: 1
   SSE:         110.087, DF: 73
   SST:         293.145, DF: 74
```
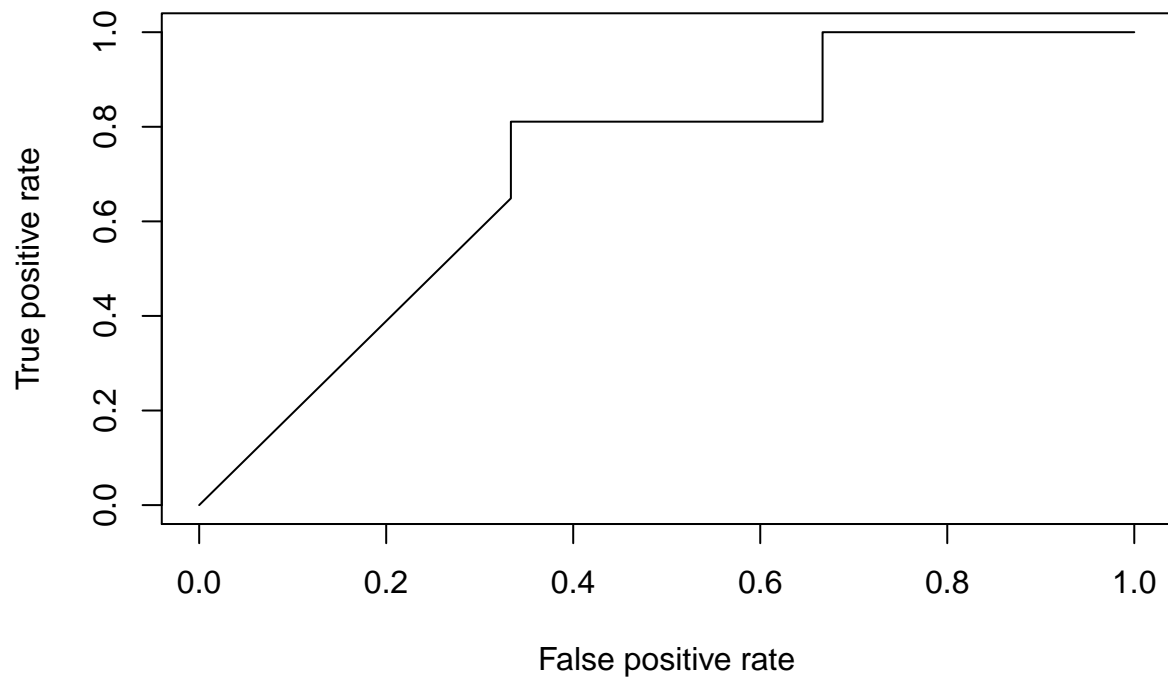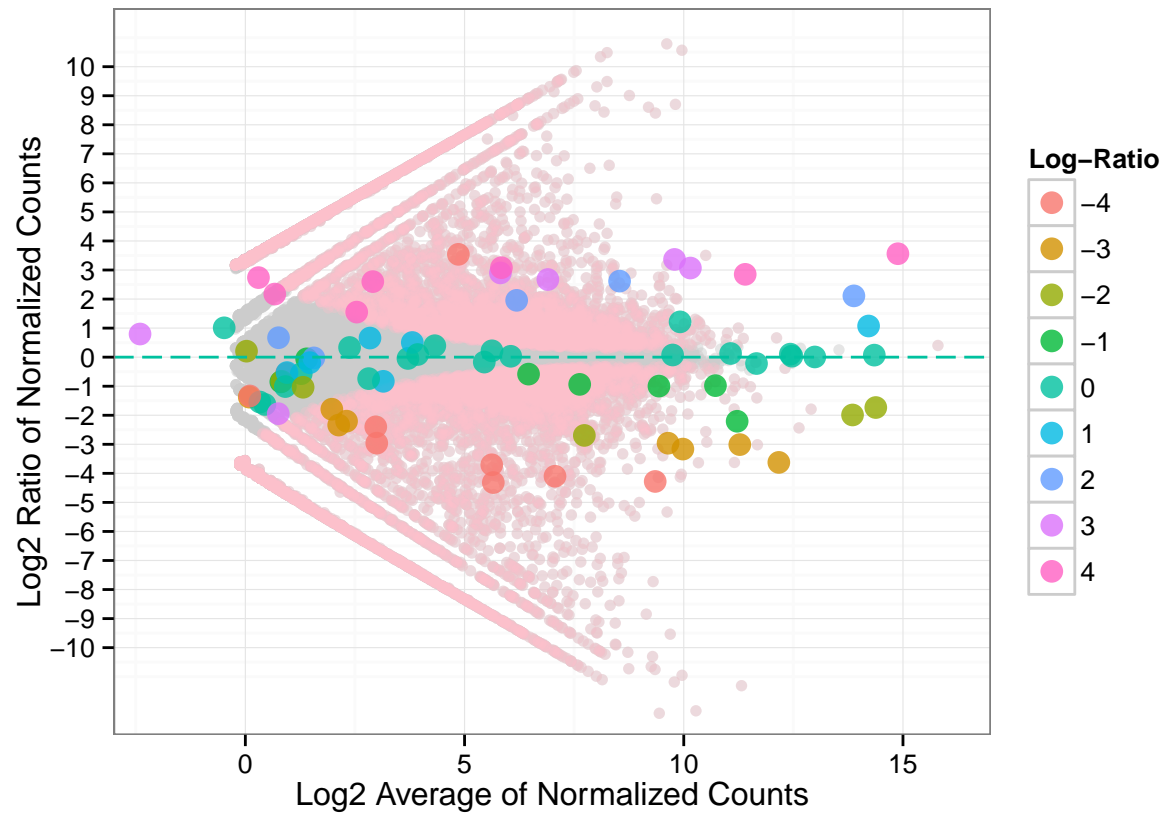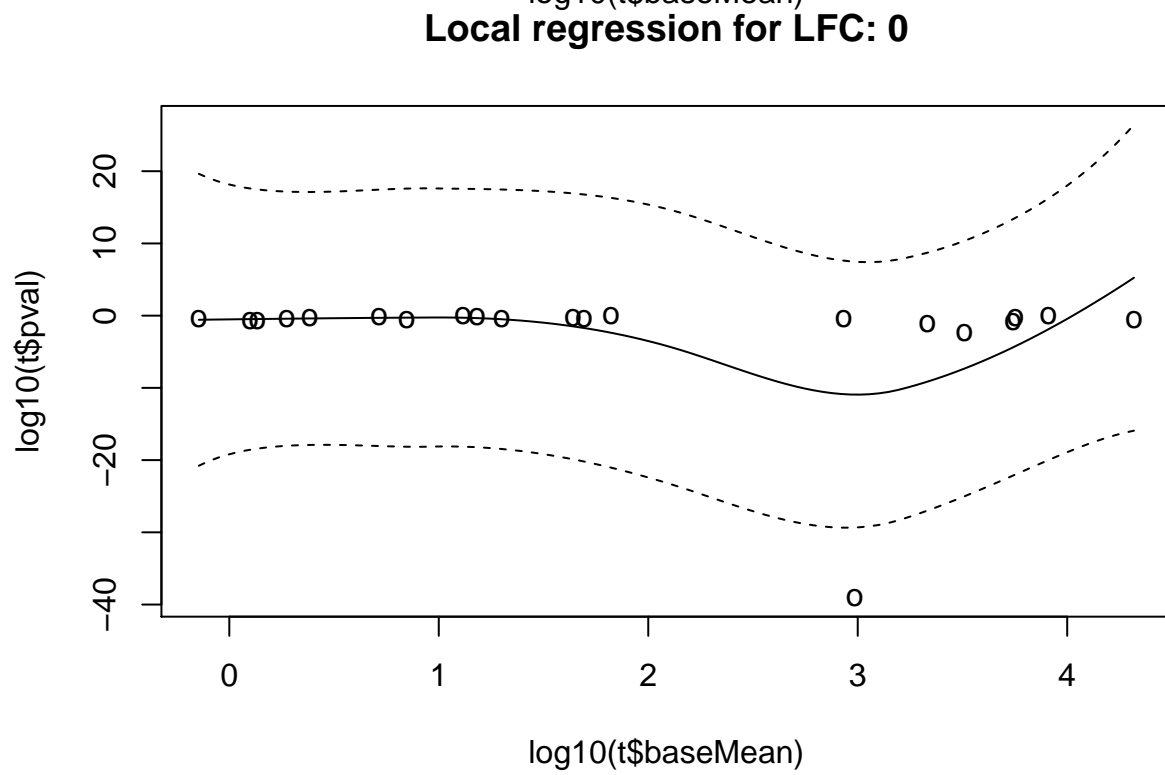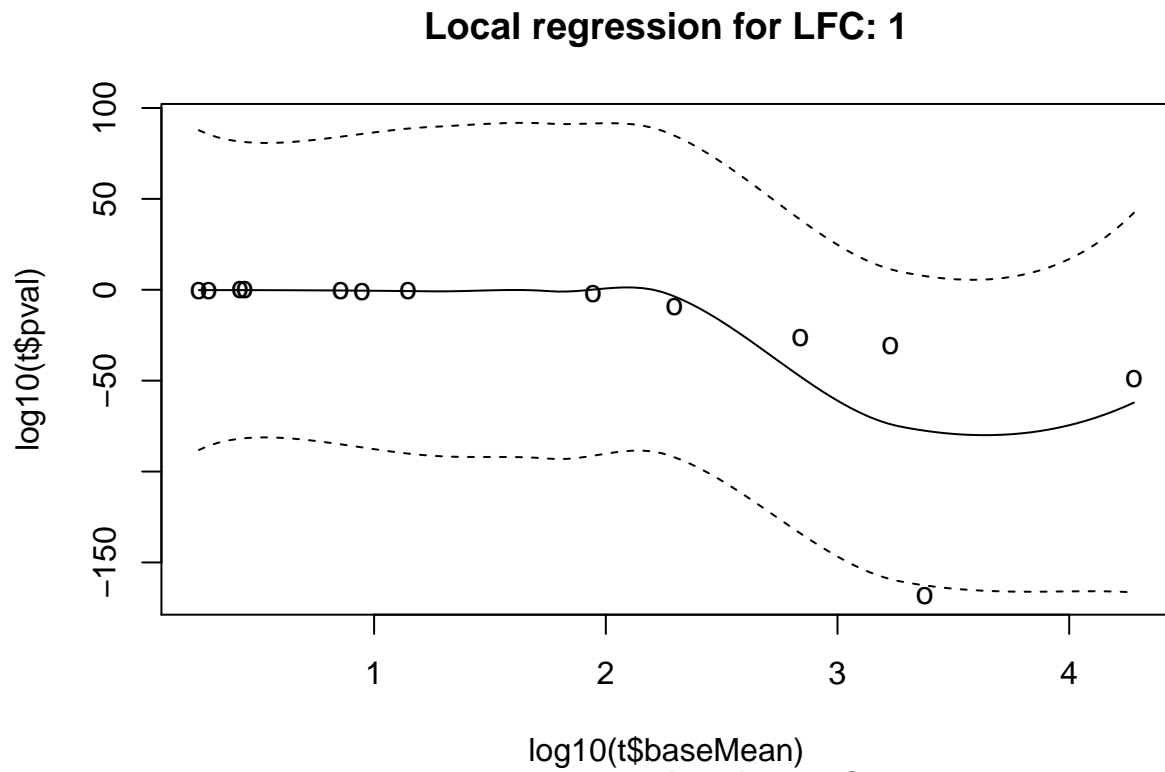
ROC plot

MA plot

LODR plot

Local regression for LFC: 1

log10(t$baseMean)

Local regression for LFC: 0

log10(t$baseMean)

Local regression for LFC: 2