Anaquin: TransQuin Report

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TransQuin Alignment

Alignment summary statistics for: A1

```
Summary for dataset: A1/TransAlign_summary.stats

   Unmapped:   0 reads
   Experiment: 6635268 (21.5363%) reads
   Synthetic:  24174356 (78.4637%) reads

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

   Query:      59421555 exons
   Query:      24855847 introns
   Query:      163383 bases

   Dilution:   0.784637

   ***
   *** 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: 0.973343
   Detection:   0.0590086 (R2_33)

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

   Sensitivity: 0.991245
   Specificity: 0.821653
   Detection:   0.0590086 (R2_33)

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

   Sensitivity: 0.692468
   Specificity: 0.924613
   Detection:   0.0590086 (R2_33)

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

   Exon:   0.005042
   Intron: 0.008755
   Gene:   0.052632
```

Alignment summary statistics for: A2

```
Summary for dataset: A2/TransAlign_summary.stats

   Unmapped:   0 reads
   Experiment: 5742035 (20.4187%) reads
   Synthetic:  22379420 (79.5813%) reads

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

   Query:      55184443 exons
   Query:      24887760 introns
   Query:      163986 bases

   Dilution:   0.795813

   ***
   *** 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: 0.996639
   Specificity: 0.975178
   Detection:   0.0590086 (R2_33)

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

   Sensitivity: 0.991245
   Specificity: 0.763722
   Detection:   0.0590086 (R2_33)

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

   Sensitivity: 0.693059
   Specificity: 0.921999
   Detection:   0.0590086 (R2_33)

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

   Exon:   0.003361
   Intron: 0.008755
   Gene:   0.039474
```

Alignment summary statistics for: A3

```
Summary for dataset: A3/TransAlign_summary.stats

   Unmapped:   0 reads
   Experiment: 5803436 (21.0203%) reads
   Synthetic:  21805238 (78.9797%) reads

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

   Query:      53748651 exons
   Query:      22830699 introns
   Query:      166153 bases

   Dilution:   0.789797

   ***
   *** 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: 0.996639
   Specificity: 0.974466
   Detection:   0.0590086 (R2_33)

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

   Sensitivity: 0.992218
   Specificity: 0.811167
   Detection:   0.0590086 (R2_33)

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

   Sensitivity: 0.695741
   Specificity: 0.913495
   Detection:   0.0590086 (R2_33)

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

   Exon:   0.003361
   Intron: 0.007782
   Gene:   0.039474
```

Alignment summary statistics for: B1

```
Summary for dataset: B1/TransAlign_summary.stats

   Unmapped:   0 reads
   Experiment: 3564555 (14.1897%) reads
   Synthetic:  21556180 (85.8103%) reads

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

   Query:      57069428 exons
   Query:      26914113 introns
   Query:      158601 bases

   Dilution:   0.858103

   ***
   *** 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: 0.992437
   Specificity: 0.981463
   Detection:   0.0590086 (R2_33)

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

   Sensitivity: 0.986381
   Specificity: 0.880564
   Detection:   1.88828 (R1_72)

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

   Sensitivity: 0.685079
   Specificity: 0.942327
   Detection:   0.0590086 (R2_33)

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

   Exon:   0.007563
   Intron: 0.013619
   Gene:   0.065789
```

Alignment summary statistics for: B2

```
Summary for dataset: B2/TransAlign_summary.stats

   Unmapped:   0 reads
   Experiment: 3673262 (14.5259%) reads
   Synthetic:  21614486 (85.4741%) reads

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

   Query:      57264502 exons
   Query:      28885125 introns
   Query:      160649 bases

   Dilution:   0.854741

   ***
   *** 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: 0.981653
   Detection:   0.0590086 (R2_33)

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

   Sensitivity: 0.984436
   Specificity: 0.818059
   Detection:   0.0590086 (R2_33)

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

   Sensitivity: 0.687879
   Specificity: 0.934117
   Detection:   0.0590086 (R2_33)

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

   Exon:   0.005882
   Intron: 0.015564
   Gene:   0.052632
```

Alignment summary statistics for: B3

```
Summary for dataset: B3/TransAlign_summary.stats

   Unmapped:   0 reads
   Experiment: 4705904 (15.6992%) reads
   Synthetic:  25269549 (84.3008%) reads

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

   Query:      67685272 exons
   Query:      37139930 introns
   Query:      162712 bases

   Dilution:   0.843008

   ***
   *** 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: 0.980831
   Detection:   0.0590086 (R2_33)

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

   Sensitivity: 0.986381
   Specificity: 0.759454
   Detection:   0.0590086 (R2_33)

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

   Sensitivity: 0.688292
   Specificity: 0.922827
   Detection:   0.0590086 (R2_33)

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

   Exon:   0.005042
   Intron: 0.013619
   Gene:   0.052632
```

Alignment sequin statistics for: A1

Summary for dataset: A1/TransAlign_quins.stats

ID	Covered	Sensitivity (Exon)	Specificity (Exon)	Sensitivity (Intron)	Specificity (Intron)	Sens
R1_101	0.847694	1	0.999322	1	1	0.847694	0.998974
R1_102	0.721248	1	0.996879	1	0.11205	0.721248	0.998544
R1_103	0.628255	1	0.996404	1	0.872516	0.628255	0.994737
R1_11	0.645161	1	0.999251	1	0.0622323	0.645161	0.996885
R1_12	0.590941	1	0.995265	1	0.998603	0.590941	0.996501
R1_13	0.920773	1	0.992209	0.909091	0.939559	0.920773	0.994269
R1_14	1	0.999757	--	--	1	0.995502	1
R1_21	0.630945	1	0.997646	1	0.91334	0.630945	0.942446
R1_22	0.528959	1	0.9983	1	0.0595461	0.528959	0.993203
R1_23	0.608847	1	0.994273	1	0.00824358	0.608847	0.997717
R1_24	1	1	0.995671	1	0.998218	1	0.997168
R1_31	0.688293	1	0.995361	1	0.179726	0.688293	0.994565
R1_32	0.545455	1	0.996002	1	0.997528	0.545455	0.990536
R1_33	0.88324	1	0.994233	1	0.997701	0.88324	0.998997
R1_41	0.78125	1	0.996444	1	0.950421	0.78125	0.994695
R1_42	0.617479	1	0.982642	1	0.89545	0.617479	0.986842
R1_43	0.526611	0.975	0.99293	0.973684	0.96402	0.526611	0.995551
R1_51	0.607666	1	0.996623	1	0.999144	0.607666	0.992634
R1_52	0.6209	1	0.994545	1	1	0.6209	0.970203
R1_53	0.998489	1	0.998138	1	0.567302	0.998489	0.997485
R1_61	0.686144	1	1	1	1	0.686144	1
R1_62	0.776233	1	1	1	1	0.776233	1
R1_63	0.669964	1	0.997411	1	0.987252	0.669964	0.99536
R1_71	0.740968	1	0.989782	1	0.996867	0.740968	0.985685
R1_72	0.605418	1	1	1	1	0.605418	1
R1_73	0.731952	1	0.990579	1	0.988759	0.731952	0.996297
R1_81	0.746457	1	0.996933	1	0.996006	0.746457	0.996322
R1_82	0.587741	1	0.991724	1	0.993417	0.587741	0.993612
R1_83	0.644813	1	0.998035	1	0.997838	0.644813	0.997018
R1_91	0.683772	1	1	1	1	0.683772	1
R1_92	0.777496	1	0.990108	1	0.997403	0.777496	0.995127
R1_93	0.625086	1	0.995626	1	0.997761	0.625086	0.997251
R2_1	1	1	--	--	0.996985	1	0.996985
R2_105	1	0.942857	--	--	0.874667	0.99696	0.874667
R2_115	0.837412	1	0.992879	1	0.996245	0.837412	0.922708
R2_116	0.584726	1	0.996656	1	1	0.584726	0.997557
R2_117	0.710041	1	0.997963	1	0.986627	0.710041	0.99569
R2_14	0.719569	1	0.986972	1	0.948655	0.719569	0.991507
R2_150	0.834679	1	0.996211	1	0.599452	0.834679	0.991777
R2_151	0.573928	1	0.97485	1	0.00142271	0.573928	0.994693
R2_152	0.60288	1	0.997882	1	0.017786	0.60288	0.99798
R2_153	0.671455	1	0.995719	1	1	0.671455	0.99909
R2_154	0.855658	1	0.988294	1	0.641379	0.855658	0.993964
R2_18	0.628326	1	0.984616	1	0.92933	0.628326	0.985276
R2_19	0.811493	1	0.992047	1	0.947606	0.811493	0.998147
R2_20	0.732411	1	0.998754	1	1	0.732411	0.997905
R2_24	0.586003	0.979592	0.994692	0.957447	1	0.586003	0.998491
R2_26	0.916294	1	0.995692	1	0.985066	0.916294	0.997941
R2_27	0.754464	1	0.998102	1	1	0.754464	0.999212

```
R2_28   0.685301    1   1   1   1   0.685301    1
R2_32   0.669025    1   0.986915    1   1   0.669025    0.998623
R2_33   0.879859    1   1   1   0.000207469 0.879859    1
R2_37   0.724904    1   0.994058    1   0.994505    0.724904    0.999687
R2_38   0.375412    0.888889    0.987441    0.857143    1   0.375412    0.9965
R2_41   0.838456    1   0.99339 1   0.995872    0.838456    0.967423
R2_42   0.883333    1   0.997452    1   1   0.883333    0.999123
R2_45   0.464239    1   1   1   1   0.464239    1
R2_46   0.706554    1   0.988095    1   0.984375    0.706554    0.96668
R2_47   0.888126    1   0.996247    1   0.997381    0.888126    0.998676
R2_53   0.389676    1   0.99433 1   0.990033    0.389676    0.997705
R2_54   0.864703    1   0.992248    1   0.857243    0.864703    0.997446
R2_55   0.880111    1   0.990548    1   0.850544    0.880111    0.988327
R2_57   0.64724 1   0.996649    1   0.00781695  0.64724 0.998809
R2_59   0.594477    1   0.997976    1   0.995441    0.594477    0.999728
R2_6    0.702025    1   0.995992    1   0.989247    0.702025    0.98913
R2_60   0.606114    1   0.9967  1   0.00853443  0.606114    0.997076
R2_63   0.883925    1   0.988671    1   0.98321 0.883925    0.996051
R2_65   1   1   --  --  0.995595    1   0.995595
R2_66   0.529254    1   0.992772    1   0.999104    0.529254    0.985015
R2_67   0.959847    1   1   1   1   0.959847    1
R2_68   0.699062    1   0.99951 1   1   0.699062    0.999681
R2_7    0.76132 1   0.998183    1   0.999392    0.76132 0.996124
R2_71   0.822193    1   0.991979    1   1   0.822193    0.999188
R2_72   0.343281    0.866667    0.987707    0.727273    1   0.343281    0.998704
R2_73   0.931968    1   0.997207    1   0.998643    0.931968    0.999512
R2_76   0.472826    1   0.997807    1   1   0.472826    0.999234
```

Alignment sequin statistics for: A2

Summary for dataset: A2/TransAlign_quins.stats

ID	Covered	Sensitivity (Exon)	Specificity (Exon)	Sensitivity (Intron)	Specificity (Intron)	Sens
R1_101	0.842472	1	0.997743	1	0.994398	0.842472	0.998968
R1_102	0.72195 1	0.996092	1	0.00745621	0.72195 0.998061	
R1_103	0.629363	1	0.996332	1	0.190876	0.629363	0.995182
R1_11	0.645833	1	0.999611	1	0.0609563	0.645833	0.99896
R1_12	0.591632	1	0.996195	1	0.999449	0.591632	0.997668
R1_13	0.920773	1	0.99341 0.909091	0.689422	0.920773	0.994676	
R1_14	1	0.999704	-- --	1	0.994012	1	
R1_21	0.630945	1	0.99783 1	0.94016 0.630945	0.940754		
R1_22	0.528959	1	0.99921 1	0.0886522	0.528959	0.995741	
R1_23	0.605016	1	0.990962	1	0.0131643	0.605016	0.996558
R1_24	1	1	0.995808	1	0.994776	1	0.99782
R1_31	0.689234	1	0.994005	1	0.99822 0.689234	0.995248	
R1_32	0.545455	1	0.996609	1	1	0.545455	0.99472
R1_33	0.911913	1	0.997009	1	1	0.911913	0.999028
R1_41	0.78125 1	0.996615	1	0.984857	0.78125 0.995575		
R1_42	0.617479	1	0.983941	1	0.918226	0.617479	0.990854
R1_43	0.526611	0.975	0.992939	0.973684	0.970546	0.526611	0.995551
R1_51	0.607103	1	0.995561	1	0.995538	0.607103	0.993542
R1_52	0.623951	1	0.986547	1	0.993277	0.623951	0.970344
R1_53	0.997986	1	0.995796	1	0.998658	0.997986	0.996982
R1_61	0.687813	1	0.996259	1	0.00393677	0.687813	0.997579
R1_62	0.766119	1	0.990741	1	0.00177231	0.766119	0.999176
R1_63	0.670224	1	0.997749	1	0.982678	0.670224	0.994977
R1_71	0.740968	1	0.990143	1	0.965202	0.740968	0.986694
R1_72	0.6 1	1	1	0.000771367 0.6 1			
R1_73	0.731952	1	0.990777	0.96	0.594568	0.731952	0.996014
R1_81	0.74685 1	0.997109	1	0.994664	0.74685 0.996847		
R1_82	0.587741	1	0.989888	1	0.996501	0.587741	0.993612
R1_83	0.644427	1	0.998518	1	0.998462	0.644427	0.996422
R1_91	0.68762 1	1	1	1	0.68762 1		
R1_92	0.779611	1	0.989036	1	0.997001	0.779611	0.99514
R1_93	0.625775	1	0.996087	1	0.997967	0.625775	0.997254
R2_1	1	1	-- --	0.990955	1	0.990955	
R2_105	1	1	-- --	0.690667	1	0.690667	
R2_115	0.840131	1	0.993099	1	0.995773	0.840131	0.992293
R2_116	0.52506 1	0.995198	1	1	0.52506 0.998185		
R2_117	0.711066	1	0.997799	1	0.986683	0.711066	0.995696
R2_14	0.719569	1	0.987726	1	0.762312	0.719569	0.990981
R2_150	0.835448	1	0.997498	1	0.637765	0.835448	0.991785
R2_151	0.559055	1	0.993207	1	0.00185397	0.559055	0.999218
R2_152	0.602636	1	0.998542	1	0.0249012	0.602636	0.998383
R2_153	0.679707	1	1	1	1	0.679707	1
R2_154	0.855658	1	0.991999	1	0.752922	0.855658	0.994631
R2_18	0.628326	1	0.98195 1	0.952684	0.628326	0.986486	
R2_19	0.811493	1	0.991557	1	0.412105	0.811493	0.99829
R2_20	0.732795	1	0.9974 1	0.997538	0.732795	0.997906	
R2_24	0.585856	0.979592	0.991346	0.957447	1	0.585856	0.997737
R2_26	0.916638	1	0.995474	1	0.994598	0.916638	0.997568
R2_27	0.752381	1	0.996593	1	1	0.752381	0.999209

```
R2_28   0.686747    1   0.992133    1   1   0.686747    0.979381
R2_32   0.671486    1   0.988811    1   0.995984    0.671486    0.997715
R2_33   0.922261    1   1   1   1   0.922261    1
R2_37   0.725357    1   0.994978    1   1   0.725357    0.996265
R2_38   0.394199    1   0.989486    1   0.976667    0.394199    0.998331
R2_41   0.839171    1   0.994146    1   0.995818    0.839171    0.990299
R2_42   0.871318    1   0.998773    1   0.996774    0.871318    0.999555
R2_45   0.464239    1   0.99862 1   0.998657    0.464239    0.999378
R2_46   0.705051    1   0.994681    1   1   0.705051    0.967409
R2_47   0.888126    1   0.99716 1   0.997684    0.888126    0.997795
R2_53   0.39093 1   0.998503    1   1   0.39093 0.999542
R2_54   0.864703    1   0.992071    1   0.99359 0.864703    0.997446
R2_55   0.880111    1   0.990367    1   0.877687    0.880111    0.987558
R2_57   0.659591    1   0.997113    1   0.00776074  0.659591    0.93286
R2_59   0.60449 1   0.999487    1   1   0.60449 0.999733
R2_6    0.693346    1   0.997899    1   1   0.693346    0.997226
R2_60   0.604692    1   0.999074    1   0.00876215  0.604692    0.998239
R2_63   0.86509 1   0.986341    0.666667    0.984241    0.86509 0.996971
R2_65   1   1   --  --  0.995595    1   0.995595
R2_66   0.529254    1   0.993527    1   0.998951    0.529254    0.986987
R2_67   0.988528    1   1   1   1   0.988528    1
R2_68   0.717828    1   0.99418 1   1   0.717828    0.999689
R2_7    0.76132 1   0.997537    1   0.998989    0.76132 0.996124
R2_71   0.808155    1   0.995012    1   0.993478    0.808155    0.998348
R2_72   0.341203    0.866667    0.991131    0.727273    1   0.341203    0.99913
R2_73   0.950171    1   0.994921    1   0.99508 0.950171    0.999282
R2_76   0.475725    1   0.996596    1   1   0.475725    0.998479
```

Alignment sequin statistics for: A3

Summary for dataset: A3/TransAlign_quins.stats

ID	Covered	Sensitivity (Exon)	Specificity (Exon)	Sensitivity (Intron)	Specificity (Intron)	Sens
R1_101	0.843342	1	0.998545	1	1	0.843342	0.998969
R1_102	0.724404	1	0.996659	1	0.0275419	0.724404	0.998068
R1_103	0.629086	1	0.99598 1	0.466926	0.629086	0.99518
R1_11	0.646505	1	0.999213	1	0.0613864	0.646505	0.998962
R1_12	0.591978	1	0.996492	1	0.999063	0.591978	0.998833
R1_13	0.921152	1	0.992714	0.909091	0.927537	0.921152	0.994272
R1_14	1	0.999661	-- --	1	0.996997	1
R1_21	0.630945	1	0.997923	1	0.932742	0.630945	0.941599
R1_22	0.528959	1	0.999234	1	0.0715257	0.528959	0.99659
R1_23	0.610589	1	0.991844	1	0.00939993	0.610589	0.996023
R1_24	1	1	0.995729	1	0.997156	1	0.997168
R1_31	0.688764	1	0.993699	1	0.998371	0.688764	0.995245
R1_32	0.545455	1	0.996925	1	0.997249	0.545455	0.992624
R1_33	0.911913	1	0.995448	1	0.998975	0.911913	0.998705
R1_41	0.78125 1	0.996329	1	0.949202	0.78125 0.995575
R1_42	0.617479	1	0.986143	1	0.911049	0.617479	0.990854
R1_43	0.526611	0.975	0.993215	0.973684	0.971656	0.526611	0.995892
R1_51	0.607103	1	0.996125	1	0.993582	0.607103	0.993542
R1_52	0.624333	1	0.991891	1	0.996644	0.624333	0.968639
R1_53	0.999496	1	0.995838	1	0.894373	0.999496	0.997487
R1_61	0.705342	1	0.996028	1	0.030201	0.705342	0.998818
R1_62	0.774968	1	0.996558	1	0.0173625	0.774968	0.999185
R1_63	0.669703	1	0.997245	1	0.984976	0.669703	0.995743
R1_71	0.740968	1	0.993089	1	0.991204	0.740968	0.985685
R1_72	0.604966	1	1	1	0.0175711	0.604966	1
R1_73	0.731534	1	0.986479	0.96	0.869319	0.731534	0.996295
R1_81	0.746457	1	0.996425	1	0.258511	0.746457	0.996845
R1_82	0.587741	1	0.995206	1	0.978119	0.587741	0.993612
R1_83	0.644427	1	0.99821 1	0.997789	0.644427	0.998805
R1_91	0.681206	1	1	1	1	0.681206	1
R1_92	0.774535	1	0.988785	1	0.997123	0.774535	0.99565
R1_93	0.625775	1	0.997114	1	0.998507	0.625775	0.997254
R2_1	1	1	-- --	0.99598 1	0.99598
R2_105	1	0.965517	-- --	0.930667	0.994302	0.930667
R2_115	0.837412	1	0.99224 1	0.997013	0.837412	0.922708
R2_116	0.582339	1	0.996341	1	1	0.582339	0.997547
R2_117	0.710041	1	0.99923 1	0.998468	0.710041	0.997122
R2_14	0.719569	1	0.987344	1	0.913125	0.719569	0.991507
R2_150	0.835832	1	0.996781	1	0.569783	0.835832	0.996334
R2_151	0.588364	1	0.990961	1	0.00205912	0.588364	0.997035
R2_152	0.605321	1	0.998972	1	0.0178198	0.605321	0.997586
R2_153	0.684902	1	0.995235	1	0.998407	0.684902	0.998663
R2_154	0.855658	1	0.988085	1	0.643553	0.855658	0.994631
R2_18	0.628326	1	0.98154 1	0.932426	0.628326	0.986486
R2_19	0.811493	1	0.990813	1	0.706767	0.811493	0.99829
R2_20	0.733948	1	0.998507	1	0.998241	0.733948	0.996347
R2_24	0.586594	0.979592	0.9931	0.957447	1	0.586594	0.998743
R2_26	0.916294	1	0.995585	1	0.994024	0.916294	0.997754
R2_27	0.755952	1	0.995752	1	1	0.755952	0.998035

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R2_28   0.689639    1   0.998662    1   1   0.689639    0.980137
R2_32   0.671486    1   0.991023    1   1   0.671486    0.998171
R2_33   0.961131    1   0.916667    1   1   0.961131    0.992701
R2_37   0.727623    1   0.994605    1   0.997226    0.727623    0.997515
R2_38   0.398484    1   0.99778 1   1   0.398484    0.998348
R2_41   0.839171    1   0.993471    1   0.99638 0.839171    0.968247
R2_42   0.884884    1   0.99882 1   1   0.884884    0.949667
R2_45   0.464384    1   0.99941 1   0.999372    0.464384    0.999067
R2_46   0.719784    1   0.992964    1   1   0.719784    0.967664
R2_47   0.888714    1   0.996164    1   0.869457    0.888714    0.998456
R2_53   0.391647    1   0.996204    1   0.995389    0.391647    0.997262
R2_54   0.864703    1   0.992777    1   0.996222    0.864703    0.997446
R2_55   0.880804    1   0.990786    1   0.84464 0.880804    0.988336
R2_57   0.661135    1   0.997049    1   0.00967222  0.661135    0.99767
R2_59   0.592539    1   0.996507    1   0.997951    0.592539    0.998639
R2_6    0.700096    1   0.996782    1   0.996937    0.700096    0.995885
R2_60   0.605759    1   0.998467    1   0.0137983   0.605759    0.998243
R2_63   0.884363    1   0.986952    1   0.981729    0.884363    0.997037
R2_65   1   1   --  --  0.994493    1   0.994493
R2_66   0.529254    1   0.99313 1   0.998672    0.529254    0.985015
R2_67   0.971319    1   1   1   1   0.971319    1
R2_68   0.717828    1   0.996276    1   0.997953    0.717828    0.999378
R2_7    0.76132 1   0.997977    1   0.999136    0.76132 0.996124
R2_71   0.916444    1   0.991426    1   0.989924    0.916444    0.998543
R2_72   0.347439    0.866667    0.992315    0.727273    1   0.347439    0.997017
R2_73   0.928328    1   0.996213    1   0.995682    0.928328    0.998776
R2_76   0.473551    1   0.996066    1   1   0.473551    0.998472
```

Alignment sequin statistics for: B1

Summary for dataset: B1/TransAlign_quins.stats

ID	Covered	Sensitivity (Exon)	Specificity (Exon)	Sensitivity (Intron)	Specificity (Intron)	Sens
R1_101	0.798085	1	0.996503	1	1	0.798085	0.998911	
R1_102	0.719144	1	0.994911	1	0.0477612	0.719144	0.998054	
R1_103	0.627978	1	0.992949	1	0.877408	0.627978	0.996046	
R1_11	0.644489	1	1	1	0.0383237	0.644489	1	
R1_12	0.570194	1	0.993312	1	0.994968	0.570194	0.998184	
R1_13	0.921152	1	0.988876	0.909091	0.986406	0.921152	0.993865	
R1_14	1	0.999785	--	--	0.998494	0.996992	0.998494	
R1_21	0.630945	1	0.997942	1	0.922412	0.630945	0.942446	
R1_22	0.525339	1	1	1	0.00512173	0.525339	1	
R1_23	0.609892	1	0.990422	1	0.00775832	0.609892	0.996585	
R1_24	0.999782	1	0.997355	1	0.99911	0.999782	0.997819	
R1_31	0.688764	1	0.993387	1	0.997399	0.688764	0.991875	
R1_32	0.541401	1	1	1	1	0.541401	1	
R1_33	0.901271	1	0.996101	1	1	0.901271	0.999017	
R1_41	0.78125	1	0.999389	1	0.975044	0.78125	0.996457	
R1_42	0.617479	1	0.992588	1	0.880227	0.617479	0.990854	
R1_43	0.52643	0.975	0.992495	0.973684	0.701694	0.52643	0.994868	
R1_51	0.604848	1	0.998724	1	0.341777	0.604848	0.996286	
R1_52	0.622807	1	0.994452	1	0.996778	0.622807	0.998166	
R1_53	0.998489	1	0.996504	1	0.186155	0.998489	0.996482	
R1_61	0.69783	1	1	1	0.893617	0.69783	1	
R1_62	0.70354	1	1	1	0.855072	0.70354	1	
R1_63	0.670484	1	0.997312	1	0.942241	0.670484	0.995363	
R1_71	0.740968	1	0.98966	1	0.969902	0.740968	0.986694	
R1_72	0.578781	1	1	1	0.777778	0.578781	1	
R1_73	0.731325	1	0.99004	0.96	0.996528	0.731325	0.997432	
R1_81	0.747244	1	0.996751	1	0.992513	0.747244	0.997897	
R1_82	0.587741	1	0.993087	1	0.988905	0.587741	0.991501	
R1_83	0.647898	1	0.997868	1	0.99442	0.647898	0.998217	
R1_91	0.682489	1	1	1	1	0.682489	1	
R1_92	0.777073	1	0.989744	1	0.997185	0.777073	0.996204	
R1_93	0.625431	1	0.997054	1	0.997791	0.625431	0.996705	
R2_1	1	1	--	--	0.992965	1	0.992965	
R2_105	1	0.985507	--	--	0.706667	0.992509	0.706667	
R2_115	0.840674	1	0.991763	1	0.991845	0.840674	0.922985	
R2_116	0.512172	1	0.996177	1	1	0.512172	0.999069	
R2_117	0.711578	1	0.996356	1	0.996453	0.711578	0.994986	
R2_14	0.719569	1	0.982878	1	0.916738	0.719569	0.991507	
R2_150	0.832372	1	0.9986	1	0.130011	0.832372	0.997696	
R2_151	0.549869	1	0.991817	1	0.00119505	0.549869	0.999205	
R2_152	0.603856	1	0.997347	1	0.0157253	0.603856	0.998789	
R2_153	0.680012	1	0.991903	1	1	0.680012	0.988011	
R2_154	0.855081	1	0.988127	1	0.451182	0.855081	0.994627	
R2_18	0.628326	1	0.984865	1	0.925924	0.628326	0.986486	
R2_19	0.811146	1	0.994538	1	0.821059	0.811146	0.999144	
R2_20	0.732795	1	0.998868	1	0.999023	0.732795	0.998952	
R2_24	0.576259	0.979592	0.99326	0.957447	1	0.576259	0.998721	
R2_26	0.916638	1	0.993005	1	0.94618	0.916638	0.997195	
R2_27	0.752976	1	0.990885	1	1	0.752976	0.99921	

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R2_28   0.684578    1   1   1   1   0.684578    1
R2_32   0.669333    1   0.994737    1   0.997678    0.669333    0.998165
R2_33   0.441696    0.5 1   0   nan 0.441696    1
R2_37   0.716293    1   0.997416    1   1   0.716293    0.999684
R2_38   0.380686    1   0.991424    1   0.967742    0.380686    0.998271
R2_41   0.838099    1   0.994207    1   0.993615    0.838099    0.990287
R2_42   0.831008    1   0.997712    1   1   0.831008    0.999534
R2_45   0.46395 1   1   1   1   0.46395 1
R2_46   0.709561    1   0.992042    1   1   0.709561    0.998308
R2_47   0.888911    1   0.996396    1   0.986294    0.888911    0.997797
R2_53   0.389317    1   0.993598    1   0.991416    0.389317    0.99908
R2_54   0.864703    1   0.991482    1   0.994474    0.864703    0.997446
R2_55   0.880804    1   0.981805    1   0.997933    0.880804    0.99142
R2_57   0.64917 1   0.99569 1   0.0158003   0.64917 0.998812
R2_59   0.580426    1   0.997258    1   0.994024    0.580426    0.999722
R2_6    0.702989    1   0.996508    1   1   0.702989    0.990489
R2_60   0.608603    1   0.997788    1   0.354215    0.608603    0.997088
R2_63   0.886991    1   0.999101    1   0.99974 0.886991    0.997046
R2_65   1   1   --  --  0.993392    1   0.993392
R2_66   0.528717    1   0.999688    1   0.999066    0.528717    0.987964
R2_67   0.957935    1   1   1   1   0.957935    1
R2_68   0.569258    0.846154    0.996355    0.833333    0.996273    0.569258    0.998824
R2_7    0.76132 1   0.998103    1   0.999407    0.76132 0.996124
R2_71   0.779412    1   0.978   1   0.975352    0.779412    0.998288
R2_72   0.327246    0.866667    0.986853    0.727273    1   0.327246    0.998188
R2_73   0.944027    1   0.996729    0.952381    0.998051    0.944027    0.999037
R2_76   0.463043    1   0.996047    1   1   0.463043    0.999218
```

Alignment sequin statistics for: B2

Summary for dataset: B2/TransAlign_quins.stats

ID	Covered	Sensitivity (Exon)	Specificity (Exon)	Sensitivity (Intron)	Specificity (Intron)	Sens
R1_101	0.833768	1	1	1	1	0.833768	1
R1_102	0.719495	1	0.987047	1	0.00176159	0.719495	0.99854
R1_103	0.627701	1	0.992816	1	0.207487	0.627701	0.995169
R1_11	0.644489	1	1	1	0.0448018	0.644489	1
R1_12	0.583333	1	0.99528 1	0.99734 0.583333	0.998225		
R1_13	0.920773	1	0.995253	0.909091	0.780182	0.920773	0.993863
R1_14	1	0.999648	--	--	1	0.995502	1
R1_21	0.630945	1	0.997868	1	0.894799	0.630945	0.942446
R1_22	0.527149	1	0.997019	1	0.00852348	0.527149	0.998286
R1_23	0.61024 1	0.993084	1	0.015077	0.61024 0.998291		
R1_24	1	1	0.996884	1	0.997909	1	0.998473
R1_31	0.689234	1	0.992408	1	0.99621 0.689234	0.991881	
R1_32	0.540822	1	1	1	1	0.540822	1
R1_33	0.880579	1	1	0.96	1	0.880579	1
R1_41	0.78125 1	0.999422	1	0.887919	0.78125 0.993816		
R1_42	0.617479	1	0.993277	1	0.891905	0.617479	0.993884
R1_43	0.526249	0.975	0.991493	0.973684	0.720085	0.526249	0.994867
R1_51	0.603157	1	0.995285	1	0.0946672	0.603157	0.997204
R1_52	0.6209 1	0.993337	1	0.998695	0.6209 0.970203		
R1_53	0.998489	1	0.996715	1	0.0428192	0.998489	0.996983
R1_61	0.689482	1	1	1	0.00220526	0.689482	1
R1_62	0.774968	1	1	1	0.000468596	0.774968	1
R1_63	0.670484	1	0.997277	1	0.87543 0.670484	0.995363	
R1_71	0.740968	1	0.992827	1	0.949823	0.740968	0.983673
R1_72	0.607223	1	1	1	0.00092004	0.607223	1
R1_73	0.731743	1	0.991638	0.96	0.0932937	0.731743	0.996864
R1_81	0.748031	1	0.997098	1	0.04424 0.748031	0.996329	
R1_82	0.587741	1	0.99522 1	0.73257 0.587741	0.993612		
R1_83	0.647513	1	0.998545	1	0.997938	0.647513	0.998216
R1_91	0.676716	1	0.996396	1	0.989189	0.676716	0.999053
R1_92	0.777496	1	0.989192	1	0.997857	0.777496	0.995127
R1_93	0.62612 1	0.996901	1	0.996568	0.62612 0.995616		
R2_1	1	1	--	--	0.99397 1	0.99397	
R2_105	1	0.975904	--	--	0.874667	0.993939	0.874667
R2_115	0.838499	1	0.993517	1	0.991845	0.838499	0.922801
R2_116	0.57136 1	0.991803	1	1	0.57136 0.9975		
R2_117	0.711066	1	0.997246	1	0.99467 0.711066	0.994982	
R2_14	0.719569	1	0.983698	1	0.932459	0.719569	0.991507
R2_150	0.83391 1	0.998194	1	0.214306	0.83391 0.9977		
R2_151	0.568241	1	0.982484	1	0.00243339	0.568241	0.997696
R2_152	0.603124	1	0.998362	1	0.0300802	0.603124	0.997981
R2_153	0.671149	1	0.99501 1	1	0.671149	0.987854	
R2_154	0.855658	1	0.987492	1	0.600748	0.855658	0.993964
R2_18	0.628326	1	0.984022	1	0.991925	0.628326	0.986486
R2_19	0.811378	1	0.996101	1	0.141851	0.811378	0.999001
R2_20	0.734333	1	0.996728	1	0.996232	0.734333	0.995829
R2_24	0.585856	0.979592	0.992486	0.957447	1	0.585856	0.997988
R2_26	0.916638	1	0.993025	1	0.787821	0.916638	0.997568
R2_27	0.75625 1	0.99559 1	1	0.75625 0.999607			

```
R2_28   0.688434    1   1   1   1   0.688434    1
R2_32   0.66964 1   0.994642    1   1   0.66964 0.989545
R2_33   0.897527    1   1   1   1   0.897527    1
R2_37   0.722184    1   0.987135    0.888889    0.996283    0.722184    0.998434
R2_38   0.378378    1   0.965649    1   1   0.378378    0.998261
R2_41   0.837026    1   0.994549    1   0.997638    0.837026    0.99702
R2_42   0.865891    1   1   1   1   0.865891    1
R2_45   0.463083    1   0.999771    1   1   0.463083    0.999688
R2_46   0.705352    1   1   1   1   0.705352    1
R2_47   0.889107    1   0.996018    1   0.984317    0.889107    0.998017
R2_53   0.389496    1   0.998159    1   1   0.389496    0.99908
R2_54   0.864703    1   0.992218    1   0.997733    0.864703    0.997191
R2_55   0.880804    1   0.981264    1   0.998791    0.880804    0.990647
R2_57   0.624083    1   0.995   0.941176    0.0127108   0.624083    0.998765
R2_59   0.57655 1   1   1   1   0.57655 1
R2_6    0.702025    1   0.995867    1   1   0.702025    0.98913
R2_60   0.608603    1   0.99745 1   0.370078    0.608603    0.996508
R2_63   0.886991    1   0.998516    1   0.999484    0.886991    0.996555
R2_65   1   1   --  --  0.995595    1   0.995595
R2_66   0.527107    1   0.999693    1   0.998859    0.527107    0.987928
R2_67   0.944551    1   1   1   1   0.944551    1
R2_68   0.596738    0.884615    0.996294    0.833333    0.996175    0.596738    0.998878
R2_7    0.76132 1   0.998123    1   0.998683    0.76132 0.995573
R2_71   0.669118    1   0.996303    1   1   0.669118    0.999002
R2_72   0.341203    0.866667    0.987028    0.727273    1   0.341203    0.998696
R2_73   0.929693    1   0.996043    1   0.999042    0.929693    0.999511
R2_76   0.476449    1   0.99776 1   1   0.476449    0.99924
```

Alignment sequin statistics for: B3

Summary for dataset: B3/TransAlign_quins.stats

ID	Covered	Sensitivity (Exon)	Specificity (Exon)	Sensitivity (Intron)	Specificity (Intron)	Sens
R1_101	0.845953	1	1	1	1	0.845953	1	
R1_102	0.709327	1	0.986618	1	0.0102989	0.709327	0.998519	
R1_103	0.627978	1	0.992584	1	0.632425	0.627978	0.995608	
R1_11	0.626344	1	0.998551	1	0.037669	0.626344	0.995726	
R1_12	0.590941	1	0.99219 1	0.994792	0.590941	0.998248		
R1_13	0.920015	1	0.98925 0.909091	0.951455	0.920015	0.994672		
R1_14	1	0.999485	-- --	1	0.989568	1		
R1_21	0.630945	1	0.998002	1	0.797785	0.630945	0.940754	
R1_22	0.527149	1	0.998893	1	0.00177882	0.527149	0.996578	
R1_23	0.609544	1	0.993163	1	0.00284772	0.609544	0.997719	
R1_24	0.999563	1	0.996226	1	0.998971	0.999563	0.998037	
R1_31	0.689234	1	0.988055	1	0.98054 0.689234	0.992552		
R1_32	0.543717	1	1	1	1	0.543717	1	
R1_33	0.903045	1	0.996546	1	1	0.903045	0.999019	
R1_41	0.78125 1	0.999615	1	0.973023	0.78125 0.996457			
R1_42	0.617479	1	0.993761	1	0.876575	0.617479	0.991862	
R1_43	0.52643 0.975	0.992023	0.973684	0.491409	0.52643 0.994868			
R1_51	0.604284	1	0.996424	1	0.331359	0.604284	0.996283	
R1_52	0.625095	1	0.992522	1	0.998908	0.625095	0.996353	
R1_53	0.998489	1	0.996255	1	0.207714	0.998489	0.996983	
R1_61	0.686978	1	1	1	0.0155595	0.686978	1	
R1_62	0.771176	1	1	1	0.00775528	0.771176	1	
R1_63	0.670484	1	0.997669	1	0.87759 0.670484	0.994595		
R1_71	0.740968	1	0.990145	1	0.965978	0.740968	0.986694	
R1_72	0.588713	1	1	1	0.00389273	0.588713	1	
R1_73	0.730906	1	0.991228	1	0.395113	0.730906	0.99743	
R1_81	0.748425	1	0.996473	1	0.206774	0.748425	0.995809	
R1_82	0.587741	1	0.993872	1	0.997645	0.587741	0.994318	
R1_83	0.645584	1	0.998169	1	0.998138	0.645584	0.997616	
R1_91	0.679923	1	0.998533	1	0.995893	0.679923	0.999057	
R1_92	0.776227	1	0.989358	1	0.997596	0.776227	0.995119	
R1_93	0.625086	1	0.996451	1	0.997744	0.625086	0.994518	
R2_1	1	1	-- --	0.994975	1	0.994975		
R2_105	1	0.963855	-- --	0.984	0.994609	0.984		
R2_115	0.841218	1	0.993299	1	0.992553	0.841218	0.923031	
R2_116	0.518854	1	0.997216	1	1	0.518854	0.999081	
R2_117	0.711066	1	0.998624	1	0.998808	0.711066	0.995696	
R2_14	0.719569	1	0.983239	1	0.944448	0.719569	0.991507	
R2_150	0.833526	1	0.998103	1	0.0494174	0.833526	0.997699	
R2_151	0.550744	1	0.991131	1	0.000491875	0.550744	0.998414	
R2_152	0.603368	1	0.997909	1	0.00507309	0.603368	0.998384	
R2_153	0.683374	1	0.997373	1	0.980994	0.683374	0.999553	
R2_154	0.855658	1	0.993276	1	0.208654	0.855658	0.994631	
R2_18	0.628326	1	0.982681	1	0.921885	0.628326	0.986486	
R2_19	0.811146	1	0.993283	1	0.517208	0.811146	0.998574	
R2_20	0.73318 1	0.999189	1	0.878936	0.73318 0.997907			
R2_24	0.586003	0.979592	0.992228	0.957447	1	0.586003	0.998239	
R2_26	0.916294	1	0.993199	1	0.943673	0.916294	0.997567	
R2_27	0.746429	1	0.995575	1	1	0.746429	0.998805	

```
R2_28   0.688675    1   1   1   1   0.688675    1
R2_32   0.667795    1   0.994107    1   0.998188    0.667795    0.99862
R2_33   0.551237    1   1   1   0.00267738  0.551237    1
R2_37   0.719692    1   0.996328    1   1   0.719692    0.999371
R2_38   0.395517    1   0.985272    1   1   0.395517    0.997506
R2_41   0.838456    1   0.993427    1   0.657222    0.838456    0.989873
R2_42   0.866667    1   1   1   1   0.866667    1
R2_45   0.457304    1   0.998857    1   0.338757    0.457304    0.998423
R2_46   0.708358    1   1   1   1   0.708358    1
R2_47   0.889107    1   0.996537    1   0.994835    0.889107    0.997578
R2_53   0.387345    1   0.996615    1   0.994531    0.387345    0.999075
R2_54   0.864703    1   0.99145 1   0.990187    0.864703    0.997191
R2_55   0.880804    1   0.981338    1   0.981419    0.880804    0.990647
R2_57   0.641837    1   0.993761    0.941176    0.0167529   0.641837    0.998199
R2_59   0.59593 1   0.997914    1   1   0.59593 0.999729
R2_6    0.702025    1   0.996081    1   1   0.702025    0.990476
R2_60   0.608603    1   0.997823    1   0.372401    0.608603    0.995928
R2_63   0.886991    1   0.998307    1   0.998181    0.886991    0.995575
R2_65   1   1   --  --  0.995595    1   0.995595
R2_66   0.527107    1   0.999681    1   0.998892    0.527107    0.992922
R2_67   0.967495    1   1   1   1   0.967495    1
R2_68   0.598525    0.923077    0.996258    0.875   0.998003    0.598525    0.95508
R2_7    0.76132 1   0.998201    1   0.999497    0.76132 0.994472
R2_71   0.780749    1   0.994604    1   1   0.780749    0.999145
R2_72   0.318634    0.866667    0.991273    0.454545    1   0.318634    0.998604
R2_73   0.949033    1   0.996016    1   0.997414    0.949033    0.998803
R2_76   0.473913    1   0.991788    1   1   0.473913    0.999236
```

Transcriptome Analysis

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)
   Detection:   0.014305 (R1_91_1)

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

   Sensitivity: 0.996032 (0.996032)
   Specificity: 0.996032 (0.996032)
   Detection:   0.015736 (R2_72_1)

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

   Sensitivity: 1
   Specificity: 1
   Detection:   - ()

   -------------------- 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)
```

Assembly 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)
   Detection:   0.014305 (R1_91_1)

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

   Sensitivity: 0.996032 (0.996032)
   Specificity: 0.996032 (0.996032)
   Detection:   0.015736 (R2_72_1)

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

   Sensitivity: 1
   Specificity: 1
   Detection:   - ()

   -------------------- 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)
```

Assembly 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)
   Detection:   0.014305 (R1_91_1)

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

   Sensitivity: 0.996032 (0.996032)
   Specificity: 0.996032 (0.996032)
   Detection:   0.015736 (R2_72_1)

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

   Sensitivity: 1
   Specificity: 1
   Detection:   - ()

   -------------------- 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)
```

Assembly 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)
   Detection:   0.014305 (R1_91_1)

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

   Sensitivity: 0.996032 (0.996032)
   Specificity: 0.996032 (0.996032)
   Detection:   0.015736 (R2_72_1)

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

   Sensitivity: 1
   Specificity: 1
   Detection:   - ()

   -------------------- 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)
```

Assembly 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)
   Detection:   0.033719 (R2_46_2)

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

   Sensitivity: 0.996032 (0.996032)
   Specificity: 0.996032 (0.996032)
   Detection:   0.015736 (R2_72_1)

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

   Sensitivity: 1
   Specificity: 1
   Detection:   - ()

   -------------------- 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)
```

Assembly 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)
   Detection:   0.033719 (R2_46_2)

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

   Sensitivity: 0.996032 (0.996032)
   Specificity: 0.996032 (0.996032)
   Detection:   0.015736 (R2_72_1)

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

   Sensitivity: 1
   Specificity: 1
   Detection:   - ()

   -------------------- 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)
```

Assembly sequin statistics for: A1

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

ID	Exon	Intron	Transcript
R1_101_1	2	2	2
R1_101_2	0	1	0
R1_102_1	4	5	3
R1_102_2	5	6	0
R1_103_1	23	21	3
R1_103_2	17	22	0
R1_11_1	0	1	4
R1_11_2	2	3	0
R1_12_1	24	18	5
R1_12_2	14	24	0
R1_13_1	6	8	7
R1_13_2	1	2	0
R1_14_1	0	0	2
R1_21_1	3	4	4
R1_21_2	0	1	0
R1_22_1	14	14	4
R1_22_2	3	6	0
R1_23_1	8	11	2
R1_23_2	8	5	0
R1_24_1	54	56	9
R1_31_1	6	5	4
R1_31_2	10	14	0
R1_32_1	3	2	3
R1_32_2	2	3	0
R1_33_1	21	24	2
R1_33_2	2	1	0
R1_41_1	2	4	3
R1_41_2	0	0	0
R1_42_1	2	5	4
R1_42_2	4	3	0
R1_43_1	15	19	5
R1_43_2	23	22	0
R1_51_1	1	4	3
R1_51_2	4	3	0
R1_52_1	14	17	4
R1_52_2	14	16	0
R1_53_1	8	8	1
R1_61_1	3	3	2
R1_61_2	0	2	0
R1_62_1	3	3	2
R1_62_2	0	2	0
R1_63_1	37	46	4
R1_63_2	21	15	0
R1_71_1	4	6	6
R1_71_2	5	6	0
R1_72_1	1	1	1
R1_72_2	0	0	0
R1_73_1	28	21	8
R1_73_2	25	37	1

```
R1_81_1 4   2   6
R1_81_2 3   8   0
R1_82_1 9   6   4
R1_82_2 0   3   0
R1_83_1 4   7   5
R1_83_2 6   6   0
R1_91_1 1   3   2
R1_91_2 2   2   0
R1_92_1 38  43  10
R1_92_2 11  11  0
R1_93_1 13  17  4
R1_93_2 8   4   0
R2_105_1    0   0   1
R2_115_1    9   9   4
R2_115_2    4   9   0
R2_116_1    9   6   6
R2_116_2    5   9   0
R2_116_3    9   14  0
R2_117_1    1   4   3
R2_117_3    3   2   0
R2_14_1 2   3   5
R2_14_2 4   5   0
R2_14_3 0   1   0
R2_150_1    2   3   2
R2_150_2    4   5   0
R2_151_1    5   5   2
R2_151_2    4   7   0
R2_151_3    2   1   0
R2_152_1    26  22  3
R2_152_2    16  23  0
R2_153_1    4   1   4
R2_153_2    8   4   0
R2_153_3    13  22  0
R2_154_1    2   4   5
R2_154_2    0   2   0
R2_18_1 8   5   2
R2_18_2 0   5   0
R2_19_1 15  12  8
R2_19_2 5   11  0
R2_1_1  0   0   1
R2_20_1 15  14  3
R2_20_2 5   6   0
R2_24_1 36  29  0
R2_24_2 20  28  0
R2_26_1 33  33  10
R2_26_2 0   4   0
R2_27_1 13  7   3
R2_27_2 4   10  0
R2_28_1 1   1   2
R2_28_2 0   0   0
R2_28_3 0   1   0
R2_32_1 4   7   3
R2_32_2 5   9   0
R2_32_3 6   2   0
```

R2_33_1	0	1	1
R2_37_1	0	3	3
R2_37_2	19	15	0
R2_37_3	1	5	0
R2_38_1	0	4	3
R2_38_2	0	0	0
R2_38_3	1	3	0
R2_38_4	4	1	0
R2_41_1	14	23	5
R2_41_2	9	3	0
R2_42_1	6	7	2
R2_42_2	2	1	0
R2_42_3	0	1	0
R2_45_1	0	20	7
R2_45_2	32	23	0
R2_45_3	17	22	0
R2_45_4	14	5	0
R2_46_1	5	7	2
R2_46_2	1	1	0
R2_46_3	0	0	0
R2_47_1	47	51	6
R2_47_2	4	4	0
R2_53_1	4	15	3
R2_53_2	8	7	0
R2_53_3	15	8	0
R2_54_1	18	19	4
R2_54_2	4	5	0
R2_55_2	1	2	4
R2_55_3	3	4	1
R2_57_1	6	12	3
R2_57_2	16	13	0
R2_59_1	4	14	3
R2_59_2	7	7	0
R2_59_3	11	4	0
R2_60_1	2	2	2
R2_60_2	14	16	0
R2_63_1	0	0	1
R2_63_3	1	2	1
R2_65_1	0	0	1
R2_66_1	1	2	3
R2_66_2	1	1	0
R2_67_1	0	1	1
R2_68_1	7	14	2
R2_68_2	17	12	0
R2_6_1	3	5	0
R2_6_2	0	0	0
R2_71_1	7	7	3
R2_71_2	2	5	0
R2_72_1	0	1	4
R2_72_2	0	3	0
R2_72_3	3	3	0
R2_72_4	1	0	0
R2_73_1	1	3	2
R2_73_2	18	18	0

```
R2_76_1 2   3   3
R2_76_2 6   7   0
R2_76_3 3   4   0
R2_7_1  0   1   3
R2_7_2  6   7   1
```

Assembly sequin statistics for: A2

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

ID	Exon	Intron	Transcript
R1_101_1	1	2	2
R1_101_2	0	1	0
R1_102_1	4	5	4
R1_102_2	6	6	0
R1_103_1	26	24	4
R1_103_2	18	24	0
R1_11_1	0	1	3
R1_11_2	2	3	0
R1_12_1	13	9	3
R1_12_2	7	13	0
R1_13_1	12	16	9
R1_13_2	1	3	0
R1_14_1	0	0	2
R1_21_1	4	6	4
R1_21_2	0	1	0
R1_22_1	14	14	4
R1_22_2	3	6	0
R1_23_1	8	11	2
R1_23_2	8	5	0
R1_24_1	35	35	7
R1_31_1	6	6	4
R1_31_2	12	15	0
R1_32_1	1	2	3
R1_32_2	2	3	0
R1_33_1	21	24	2
R1_33_2	2	1	0
R1_41_1	2	4	3
R1_41_2	0	0	0
R1_42_1	2	6	4
R1_42_2	5	4	0
R1_43_1	15	19	5
R1_43_2	26	22	0
R1_51_1	1	5	4
R1_51_2	5	4	0
R1_52_1	14	16	3
R1_52_2	12	14	0
R1_53_1	7	8	3
R1_61_1	4	4	3
R1_61_2	0	3	0
R1_62_1	3	3	2
R1_62_2	0	2	0
R1_63_1	52	62	5
R1_63_2	26	20	0
R1_71_1	4	7	7
R1_71_2	5	6	0
R1_72_1	1	1	1
R1_72_2	0	0	0
R1_73_1	20	15	6
R1_73_2	17	23	0

R1_81_1 4 2 6
R1_81_2 3 8 0
R1_82_1 7 6 4
R1_82_2 0 3 0
R1_83_1 4 7 4
R1_83_2 6 6 0
R1_91_1 1 3 2
R1_91_2 2 2 0
R1_92_1 38 43 11
R1_92_2 11 11 0
R1_93_1 17 22 4
R1_93_2 10 5 0
R2_105_1 0 0 1
R2_115_1 9 9 4
R2_115_2 7 9 0
R2_116_1 5 4 3
R2_116_2 3 5 0
R2_116_3 4 6 0
R2_117_1 1 4 3
R2_117_3 3 2 0
R2_14_1 2 3 5
R2_14_2 4 5 0
R2_14_3 0 1 0
R2_150_1 2 3 5
R2_150_2 4 5 0
R2_151_1 4 6 3
R2_151_2 3 4 0
R2_151_3 1 1 0
R2_152_1 25 21 3
R2_152_2 18 24 0
R2_153_1 3 1 3
R2_153_2 7 5 0
R2_153_3 7 14 0
R2_154_1 2 4 7
R2_154_2 0 2 0
R2_18_1 8 5 2
R2_18_2 0 5 0
R2_19_1 15 12 11
R2_19_2 5 11 0
R2_1_1 0 0 1
R2_20_1 9 9 2
R2_20_2 2 3 0
R2_24_1 45 43 0
R2_24_2 21 26 0
R2_26_1 32 32 12
R2_26_2 0 4 0
R2_27_1 11 8 3
R2_27_2 5 11 0
R2_28_1 0 1 2
R2_28_2 0 0 0
R2_28_3 0 1 0
R2_32_1 4 7 3
R2_32_2 6 9 0
R2_32_3 6 2 0

R2_33_1	0	1	1
R2_37_1	0	3	3
R2_37_2	21	15	0
R2_37_3	1	5	0
R2_38_1	0	4	4
R2_38_2	0	0	0
R2_38_3	4	9	0
R2_38_4	7	2	0
R2_41_1	17	23	6
R2_41_2	9	3	0
R2_42_1	5	7	2
R2_42_2	3	1	0
R2_42_3	0	1	0
R2_45_1	0	13	5
R2_45_2	24	19	0
R2_45_3	14	17	0
R2_45_4	10	4	0
R2_46_1	6	8	3
R2_46_2	2	3	0
R2_46_3	0	0	0
R2_47_1	31	34	5
R2_47_2	3	3	0
R2_53_1	5	18	3
R2_53_2	7	5	0
R2_53_3	15	7	0
R2_54_1	18	19	4
R2_54_2	4	5	1
R2_55_2	1	2	4
R2_55_3	3	4	1
R2_57_1	0	0	0
R2_57_2	0	0	0
R2_59_1	4	14	3
R2_59_2	7	7	0
R2_59_3	11	4	0
R2_60_1	3	3	3
R2_60_2	22	25	0
R2_63_1	0	0	2
R2_63_3	1	3	1
R2_65_1	0	0	1
R2_66_1	1	2	3
R2_66_2	0	1	0
R2_67_1	1	1	1
R2_68_1	7	14	2
R2_68_2	17	12	0
R2_6_1	3	5	0
R2_6_2	0	0	0
R2_71_1	8	8	4
R2_71_2	2	6	0
R2_72_1	0	1	3
R2_72_2	2	3	0
R2_72_3	3	2	0
R2_72_4	0	0	0
R2_73_1	2	5	3
R2_73_2	35	35	0

```
R2_76_1 2   3   3
R2_76_2 9   7   0
R2_76_3 3   4   0
R2_7_1  0   1   3
R2_7_2  6   7   1
```

Assembly sequin statistics for: A3

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

ID	Exon	Intron	Transcript
R1_101_1	1	2	2
R1_101_2	0	1	0
R1_102_1	5	8	3
R1_102_2	7	7	0
R1_103_1	31	29	4
R1_103_2	23	29	0
R1_11_1	0	1	4
R1_11_2	4	6	0
R1_12_1	21	17	3
R1_12_2	10	17	0
R1_13_1	6	9	7
R1_13_2	1	2	0
R1_14_1	0	0	2
R1_21_1	4	6	5
R1_21_2	0	1	0
R1_22_1	14	14	4
R1_22_2	3	6	0
R1_23_1	8	11	2
R1_23_2	6	5	0
R1_24_1	35	35	7
R1_31_1	9	6	4
R1_31_2	12	15	0
R1_32_1	1	2	3
R1_32_2	2	3	0
R1_33_1	21	24	3
R1_33_2	2	1	0
R1_41_1	2	4	3
R1_41_2	0	0	0
R1_42_1	2	6	4
R1_42_2	5	4	0
R1_43_1	14	20	5
R1_43_2	22	17	0
R1_51_1	1	5	4
R1_51_2	5	4	0
R1_52_1	20	23	5
R1_52_2	18	21	0
R1_53_1	7	8	2
R1_61_1	7	4	3
R1_61_2	0	3	0
R1_62_1	3	3	3
R1_62_2	0	2	0
R1_63_1	24	31	3
R1_63_2	16	11	0
R1_71_1	4	7	7
R1_71_2	7	6	0
R1_72_1	1	1	2
R1_72_2	0	0	0
R1_73_1	35	27	13
R1_73_2	26	45	0

```
R1_81_1 4   2   6
R1_81_2 3   8   0
R1_82_1 9   6   4
R1_82_2 1   3   0
R1_83_1 4   7   6
R1_83_2 6   6   0
R1_91_1 1   3   3
R1_91_2 2   2   0
R1_92_1 38  43  10
R1_92_2 11  11  0
R1_93_1 15  21  5
R1_93_2 6   5   0
R2_105_1    0   0   1
R2_115_1    9   9   4
R2_115_2    4   9   0
R2_116_1    7   4   5
R2_116_2    3   6   0
R2_116_3    8   13  0
R2_117_1    1   4   3
R2_117_3    3   2   0
R2_14_1 2   3   5
R2_14_2 4   5   0
R2_14_3 0   1   0
R2_150_1    2   3   5
R2_150_2    4   5   0
R2_151_1    11  8   3
R2_151_2    6   11  0
R2_151_3    2   1   0
R2_152_1    26  22  3
R2_152_2    16  23  0
R2_153_1    4   2   4
R2_153_2    10  5   0
R2_153_3    8   17  0
R2_154_1    2   4   7
R2_154_2    0   2   0
R2_18_1 8   5   2
R2_18_2 0   5   0
R2_19_1 15  12  9
R2_19_2 5   11  0
R2_1_1  0   0   1
R2_20_1 8   9   2
R2_20_2 2   3   0
R2_24_1 47  39  0
R2_24_2 22  33  0
R2_26_1 36  33  11
R2_26_2 0   4   0
R2_27_1 11  8   3
R2_27_2 5   11  0
R2_28_1 0   2   3
R2_28_2 0   0   0
R2_28_3 1   2   0
R2_32_1 4   7   3
R2_32_2 5   9   0
R2_32_3 6   2   0
```

R2_33_1	0	1	1
R2_37_1	0	3	4
R2_37_2	29	21	0
R2_37_3	2	8	0
R2_38_1	0	3	3
R2_38_2	0	0	0
R2_38_3	2	5	0
R2_38_4	5	2	0
R2_41_1	14	23	6
R2_41_2	9	3	0
R2_42_1	5	7	2
R2_42_2	2	1	0
R2_42_3	0	1	0
R2_45_1	0	16	7
R2_45_2	24	18	0
R2_45_3	15	18	0
R2_45_4	12	5	0
R2_46_1	4	7	3
R2_46_2	1	2	0
R2_46_3	0	0	0
R2_47_1	47	51	6
R2_47_2	4	4	0
R2_53_1	3	11	2
R2_53_2	5	4	0
R2_53_3	10	5	0
R2_54_1	18	19	4
R2_54_2	4	5	1
R2_55_2	1	2	4
R2_55_3	3	4	1
R2_57_1	0	0	0
R2_57_2	0	0	0
R2_59_1	4	14	3
R2_59_2	7	7	0
R2_59_3	11	4	0
R2_60_1	3	3	3
R2_60_2	22	25	0
R2_63_1	0	0	2
R2_63_3	1	3	1
R2_65_1	0	0	1
R2_66_1	4	3	4
R2_66_2	0	1	0
R2_67_1	0	1	1
R2_68_1	12	23	3
R2_68_2	23	15	0
R2_6_1	3	5	0
R2_6_2	0	0	0
R2_71_1	7	7	3
R2_71_2	2	5	0
R2_72_1	0	1	3
R2_72_2	0	3	0
R2_72_3	3	3	0
R2_72_4	1	0	0
R2_73_1	2	5	3
R2_73_2	37	35	0

```
R2_76_1 2   3   3
R2_76_2 9   7   0
R2_76_3 3   4   0
R2_7_1  0   1   3
R2_7_2  8   7   1
```

Assembly sequin statistics for: B1

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

ID	Exon	Intron	Transcript
R1_101_1	2	2	2
R1_101_2	0	1	0
R1_102_1	4	5	2
R1_102_2	5	6	0
R1_103_1	23	22	4
R1_103_2	20	21	0
R1_11_1	0	1	3
R1_11_2	2	3	0
R1_12_1	21	16	4
R1_12_2	11	19	0
R1_13_1	6	8	6
R1_13_2	1	2	0
R1_14_1	0	0	2
R1_21_1	3	4	3
R1_21_2	0	1	0
R1_22_1	14	14	3
R1_22_2	3	6	0
R1_23_1	8	11	2
R1_23_2	6	5	0
R1_24_1	34	35	1
R1_31_1	6	6	4
R1_31_2	12	15	0
R1_32_1	1	2	2
R1_32_2	2	3	0
R1_33_1	21	24	2
R1_33_2	2	1	0
R1_41_1	2	4	4
R1_41_2	0	0	0
R1_42_1	2	5	3
R1_42_2	4	3	0
R1_43_1	12	15	4
R1_43_2	17	16	0
R1_51_1	1	4	2
R1_51_2	4	3	0
R1_52_1	14	16	3
R1_52_2	13	15	0
R1_53_1	8	8	5
R1_61_1	3	3	2
R1_61_2	0	2	0
R1_62_1	1	1	1
R1_62_2	0	1	0
R1_63_1	44	54	5
R1_63_2	24	16	0
R1_71_1	4	6	6
R1_71_2	7	6	0
R1_72_1	0	1	2
R1_72_2	0	0	0
R1_73_1	10	8	6
R1_73_2	10	16	0

```
R1_81_1 4   2   6
R1_81_2 3   8   0
R1_82_1 7   6   4
R1_82_2 0   3   0
R1_83_1 4   7   4
R1_83_2 6   6   0
R1_91_1 1   3   2
R1_91_2 2   2   0
R1_92_1 16  17  10
R1_92_2 8   9   0
R1_93_1 14  19  4
R1_93_2 9   5   0
R2_105_1    0   0   1
R2_115_1    7   7   4
R2_115_2    5   6   1
R2_116_1    9   8   5
R2_116_2    5   9   0
R2_116_3    4   6   0
R2_117_1    0   2   2
R2_117_3    2   2   0
R2_14_1 2   3   7
R2_14_2 4   5   0
R2_14_3 0   1   0
R2_150_1    2   3   4
R2_150_2    4   5   0
R2_151_1    0   0   0
R2_151_2    0   0   0
R2_151_3    0   0   0
R2_152_1    26  22  3
R2_152_2    16  23  0
R2_153_1    5   2   5
R2_153_2    11  8   0
R2_153_3    13  24  0
R2_154_1    2   3   4
R2_154_2    0   1   0
R2_18_1 8   5   2
R2_18_2 0   5   0
R2_19_1 15  12  8
R2_19_2 5   11  0
R2_1_1  0   0   1
R2_20_1 8   9   2
R2_20_2 2   3   0
R2_24_1 40  32  0
R2_24_2 21  33  0
R2_26_1 2   2   8
R2_26_2 0   2   0
R2_27_1 7   5   2
R2_27_2 3   7   0
R2_28_1 1   2   4
R2_28_2 0   0   0
R2_28_3 1   2   0
R2_32_1 3   5   2
R2_32_2 4   7   0
R2_32_3 4   1   0
```

R2_33_1	0	0	0
R2_37_1	0	3	3
R2_37_2	19	15	0
R2_37_3	1	5	0
R2_38_1	0	3	3
R2_38_2	0	0	0
R2_38_3	2	5	0
R2_38_4	5	2	0
R2_41_1	14	23	3
R2_41_2	9	3	0
R2_42_1	5	7	3
R2_42_2	2	1	0
R2_42_3	0	2	0
R2_45_1	0	10	4
R2_45_2	17	12	0
R2_45_3	10	13	0
R2_45_4	7	3	0
R2_46_1	5	8	3
R2_46_2	1	1	0
R2_46_3	0	0	0
R2_47_1	31	34	7
R2_47_2	3	3	0
R2_53_1	5	18	3
R2_53_2	7	5	0
R2_53_3	15	7	0
R2_54_1	18	19	3
R2_54_2	4	5	1
R2_55_2	1	2	5
R2_55_3	3	4	1
R2_57_1	4	8	3
R2_57_2	9	8	0
R2_59_1	2	6	2
R2_59_2	2	2	0
R2_59_3	4	1	0
R2_60_1	3	3	3
R2_60_2	22	25	0
R2_63_1	0	1	4
R2_63_3	1	3	0
R2_65_1	0	0	1
R2_66_1	1	2	3
R2_66_2	1	1	0
R2_67_1	0	1	1
R2_68_1	6	9	2
R2_68_2	6	3	0
R2_6_1	3	5	0
R2_6_2	0	0	0
R2_71_1	4	3	2
R2_71_2	2	5	0
R2_72_1	0	1	5
R2_72_2	0	3	0
R2_72_3	2	2	0
R2_72_4	0	0	0
R2_73_1	1	3	2
R2_73_2	28	29	1

```
R2_76_1 2   3   3
R2_76_2 6   7   0
R2_76_3 3   4   0
R2_7_1  0   1   3
R2_7_2  6   7   1
```

Assembly sequin statistics for: B2

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

ID	Exon	Intron	Transcript
R1_101_1	1	2	2
R1_101_2	0	1	0
R1_102_1	6	7	3
R1_102_2	7	9	0
R1_103_1	23	22	4
R1_103_2	20	21	0
R1_11_1	0	1	3
R1_11_2	2	3	0
R1_12_1	20	15	3
R1_12_2	10	18	0
R1_13_1	6	8	6
R1_13_2	1	2	0
R1_14_1	0	0	2
R1_21_1	3	4	4
R1_21_2	0	1	0
R1_22_1	9	9	2
R1_22_2	4	4	0
R1_23_1	8	11	2
R1_23_2	8	5	0
R1_24_1	35	35	3
R1_31_1	6	6	4
R1_31_2	12	15	0
R1_32_1	1	2	2
R1_32_2	2	3	0
R1_33_1	21	24	2
R1_33_2	2	1	0
R1_41_1	2	4	3
R1_41_2	0	0	0
R1_42_1	2	5	3
R1_42_2	4	3	0
R1_43_1	21	27	6
R1_43_2	26	24	0
R1_51_1	1	4	3
R1_51_2	4	3	0
R1_52_1	15	16	3
R1_52_2	12	14	0
R1_53_1	7	8	3
R1_61_1	4	4	3
R1_61_2	0	3	0
R1_62_1	1	1	1
R1_62_2	0	1	0
R1_63_1	25	33	4
R1_63_2	16	11	0
R1_71_1	4	7	7
R1_71_2	7	6	0
R1_72_1	0	1	2
R1_72_2	0	0	0
R1_73_1	11	8	5
R1_73_2	9	16	0

```
R1_81_1 4   2   6
R1_81_2 3   8   0
R1_82_1 7   6   4
R1_82_2 0   3   0
R1_83_1 4   7   4
R1_83_2 6   6   0
R1_91_1 2   3   2
R1_91_2 3   2   0
R1_92_1 25  30  9
R1_92_2 7   6   0
R1_93_1 10  13  3
R1_93_2 4   3   0
R2_105_1    0   0   1
R2_115_1    7   7   4
R2_115_2    3   6   1
R2_116_1    7   6   4
R2_116_2    4   7   0
R2_116_3    4   6   0
R2_117_1    1   4   3
R2_117_3    3   2   0
R2_14_1 3   5   7
R2_14_2 5   6   0
R2_14_3 0   1   0
R2_150_1    0   0   3
R2_150_2    4   5   0
R2_151_1    0   0   0
R2_151_2    0   0   0
R2_151_3    0   0   0
R2_152_1    26  22  3
R2_152_2    17  23  0
R2_153_1    4   1   4
R2_153_2    10  6   0
R2_153_3    16  25  0
R2_154_1    2   4   5
R2_154_2    0   2   0
R2_18_1 8   5   2
R2_18_2 0   5   0
R2_19_1 15  12  7
R2_19_2 5   11  0
R2_1_1  0   0   1
R2_20_1 8   9   2
R2_20_2 2   3   0
R2_24_1 30  23  0
R2_24_2 14  23  0
R2_26_1 2   2   8
R2_26_2 0   2   0
R2_27_1 7   5   2
R2_27_2 3   7   0
R2_28_1 0   2   3
R2_28_2 0   0   0
R2_28_3 1   1   0
R2_32_1 3   5   2
R2_32_2 4   7   0
R2_32_3 4   1   0
```

R2_33_1	1	1	1
R2_37_1	0	3	2
R2_37_2	10	8	0
R2_37_3	1	2	0
R2_38_1	0	2	3
R2_38_2	0	0	0
R2_38_3	2	4	0
R2_38_4	4	3	0
R2_41_1	13	21	3
R2_41_2	9	4	0
R2_42_1	5	7	3
R2_42_2	5	2	0
R2_42_3	0	2	0
R2_45_1	0	7	3
R2_45_2	14	11	0
R2_45_3	8	10	0
R2_45_4	6	3	0
R2_46_1	5	7	2
R2_46_2	1	1	0
R2_46_3	0	0	0
R2_47_1	31	34	7
R2_47_2	4	3	0
R2_53_1	3	11	2
R2_53_2	7	4	0
R2_53_3	10	5	0
R2_54_1	18	19	4
R2_54_2	4	5	1
R2_55_2	2	3	5
R2_55_3	3	4	1
R2_57_1	2	5	2
R2_57_2	10	9	0
R2_59_1	3	9	2
R2_59_2	4	5	0
R2_59_3	8	3	0
R2_60_1	2	2	3
R2_60_2	14	16	0
R2_63_1	0	1	4
R2_63_3	1	3	0
R2_65_1	0	0	1
R2_66_1	1	2	3
R2_66_2	0	1	0
R2_67_1	0	1	1
R2_68_1	5	9	2
R2_68_2	6	3	0
R2_6_1	3	5	0
R2_6_2	0	0	0
R2_71_1	7	7	3
R2_71_2	2	5	0
R2_72_1	0	1	4
R2_72_2	0	3	0
R2_72_3	2	3	0
R2_72_4	1	0	0
R2_73_1	1	3	2
R2_73_2	18	18	0

```
R2_76_1 2   3   3
R2_76_2 6   7   0
R2_76_3 3   4   0
R2_7_1  0   1   3
R2_7_2  6   7   1
```

Assembly sequin statistics for: B3

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

ID	Exon	Intron	Transcript
R1_101_1	1	2	2
R1_101_2	0	1	0
R1_102_1	6	7	3
R1_102_2	7	9	0
R1_103_1	23	22	4
R1_103_2	20	21	0
R1_11_1	0	1	3
R1_11_2	2	3	0
R1_12_1	20	15	3
R1_12_2	10	18	0
R1_13_1	6	8	6
R1_13_2	1	2	0
R1_14_1	0	0	2
R1_21_1	3	4	4
R1_21_2	0	1	0
R1_22_1	9	9	2
R1_22_2	4	4	0
R1_23_1	8	11	2
R1_23_2	8	5	0
R1_24_1	35	35	3
R1_31_1	6	6	4
R1_31_2	12	15	0
R1_32_1	1	2	2
R1_32_2	2	3	0
R1_33_1	21	24	2
R1_33_2	2	1	0
R1_41_1	2	4	3
R1_41_2	0	0	0
R1_42_1	2	5	3
R1_42_2	4	3	0
R1_43_1	21	27	6
R1_43_2	26	24	0
R1_51_1	1	4	3
R1_51_2	4	3	0
R1_52_1	15	16	3
R1_52_2	12	14	0
R1_53_1	7	8	3
R1_61_1	4	4	3
R1_61_2	0	3	0
R1_62_1	1	1	1
R1_62_2	0	1	0
R1_63_1	25	33	4
R1_63_2	16	11	0
R1_71_1	4	7	7
R1_71_2	7	6	0
R1_72_1	0	1	2
R1_72_2	0	0	0
R1_73_1	11	8	5
R1_73_2	9	16	0

```
R1_81_1 4   2   6
R1_81_2 3   8   0
R1_82_1 7   6   4
R1_82_2 0   3   0
R1_83_1 4   7   4
R1_83_2 6   6   0
R1_91_1 2   3   2
R1_91_2 3   2   0
R1_92_1 25  30  9
R1_92_2 7   6   0
R1_93_1 10  13  3
R1_93_2 4   3   0
R2_105_1    0   0   1
R2_115_1    7   7   4
R2_115_2    3   6   1
R2_116_1    7   6   4
R2_116_2    4   7   0
R2_116_3    4   6   0
R2_117_1    1   4   3
R2_117_3    3   2   0
R2_14_1 3   5   7
R2_14_2 5   6   0
R2_14_3 0   1   0
R2_150_1    0   0   3
R2_150_2    4   5   0
R2_151_1    0   0   0
R2_151_2    0   0   0
R2_151_3    0   0   0
R2_152_1    26  22  3
R2_152_2    17  23  0
R2_153_1    4   1   4
R2_153_2    10  6   0
R2_153_3    16  25  0
R2_154_1    2   4   5
R2_154_2    0   2   0
R2_18_1 8   5   2
R2_18_2 0   5   0
R2_19_1 15  12  7
R2_19_2 5   11  0
R2_1_1  0   0   1
R2_20_1 8   9   2
R2_20_2 2   3   0
R2_24_1 30  23  0
R2_24_2 14  23  0
R2_26_1 2   2   8
R2_26_2 0   2   0
R2_27_1 7   5   2
R2_27_2 3   7   0
R2_28_1 0   2   3
R2_28_2 0   0   0
R2_28_3 1   1   0
R2_32_1 3   5   2
R2_32_2 4   7   0
R2_32_3 4   1   0
```

R2_33_1	1	1	1
R2_37_1	0	3	2
R2_37_2	10	8	0
R2_37_3	1	2	0
R2_38_1	0	2	3
R2_38_2	0	0	0
R2_38_3	2	4	0
R2_38_4	4	3	0
R2_41_1	13	21	3
R2_41_2	9	4	0
R2_42_1	5	7	3
R2_42_2	5	2	0
R2_42_3	0	2	0
R2_45_1	0	7	3
R2_45_2	14	11	0
R2_45_3	8	10	0
R2_45_4	6	3	0
R2_46_1	5	7	2
R2_46_2	1	1	0
R2_46_3	0	0	0
R2_47_1	31	34	7
R2_47_2	4	3	0
R2_53_1	3	11	2
R2_53_2	7	4	0
R2_53_3	10	5	0
R2_54_1	18	19	4
R2_54_2	4	5	1
R2_55_2	2	3	5
R2_55_3	3	4	1
R2_57_1	2	5	2
R2_57_2	10	9	0
R2_59_1	3	9	2
R2_59_2	4	5	0
R2_59_3	8	3	0
R2_60_1	2	2	3
R2_60_2	14	16	0
R2_63_1	0	1	4
R2_63_3	1	3	0
R2_65_1	0	0	1
R2_66_1	1	2	3
R2_66_2	0	1	0
R2_67_1	0	1	1
R2_68_1	5	9	2
R2_68_2	6	3	0
R2_6_1	3	5	0
R2_6_2	0	0	0
R2_71_1	7	7	3
R2_71_2	2	5	0
R2_72_1	0	1	4
R2_72_2	0	3	0
R2_72_3	2	3	0
R2_72_4	1	0	0
R2_73_1	1	3	2
R2_73_2	18	18	0

```
R2_76_1 2   3   3
R2_76_2 6   7   0
R2_76_3 3   4   0
R2_7_1  0   1   3
R2_7_2  6   7   1
```

TransQuin Expression (Gene)

Expression summary statistics for: A1

```
Summary for dataset: /Users/tedwong/Desktop/K_562/Cufflinks/A1/genes.fpkm_tracking

   Experiment:  60570 gene
   Synthetic:   75 gene

   Reference:   76 gene
   Detected:    4.39067 gene

   ***
   *** Detection Limits
   ***

   Break: 3.77655 (R1_62)

   Left:  4.39067 + 0.0805742x (R2 = 0.0567335)
   Right: 2.0794 + 1.00352x (R2 = 0.922502)

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

   Correlation: 0.962825
   Slope:       6.46625
   R2:          0.927032
   F-statistic: 902.032
   P-value:     0
   SSM:         3.50824e+10, DF: 1
   SSE:         2.76138e+09, DF: 71
   SST:         3.78438e+10, DF: 72

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

   Correlation: 0.936306
   Slope:       0.724913
   R2:          0.876669
   F-statistic: 504.686
   P-value:     0
   SSM:         1040.46, DF: 1
   SSE:         146.373, DF: 71
   SST:         1186.83, DF: 72
```

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 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 summary statistics for: B1

```
Summary for dataset: /Users/tedwong/Desktop/K_562/Cufflinks/A1/genes.fpkm_tracking

   Experiment:  60570 gene
   Synthetic:   75 gene

   Reference:   76 gene
   Detected:    4.39067 gene

   ***
   *** Detection Limits
   ***

   Break: 3.77655 (R1_62)

   Left:  4.39067 + 0.0805742x (R2 = 0.0567335)
   Right: 2.0794 + 1.00352x (R2 = 0.922502)

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

   Correlation: 0.962825
   Slope:       6.46625
   R2:          0.927032
   F-statistic: 902.032
   P-value:     0
   SSM:         3.50824e+10, DF: 1
   SSE:         2.76138e+09, DF: 71
   SST:         3.78438e+10, DF: 72

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

   Correlation: 0.936306
   Slope:       0.724913
   R2:          0.876669
   F-statistic: 504.686
   P-value:     0
   SSM:         1040.46, DF: 1
   SSE:         146.373, DF: 71
   SST:         1186.83, DF: 72
```

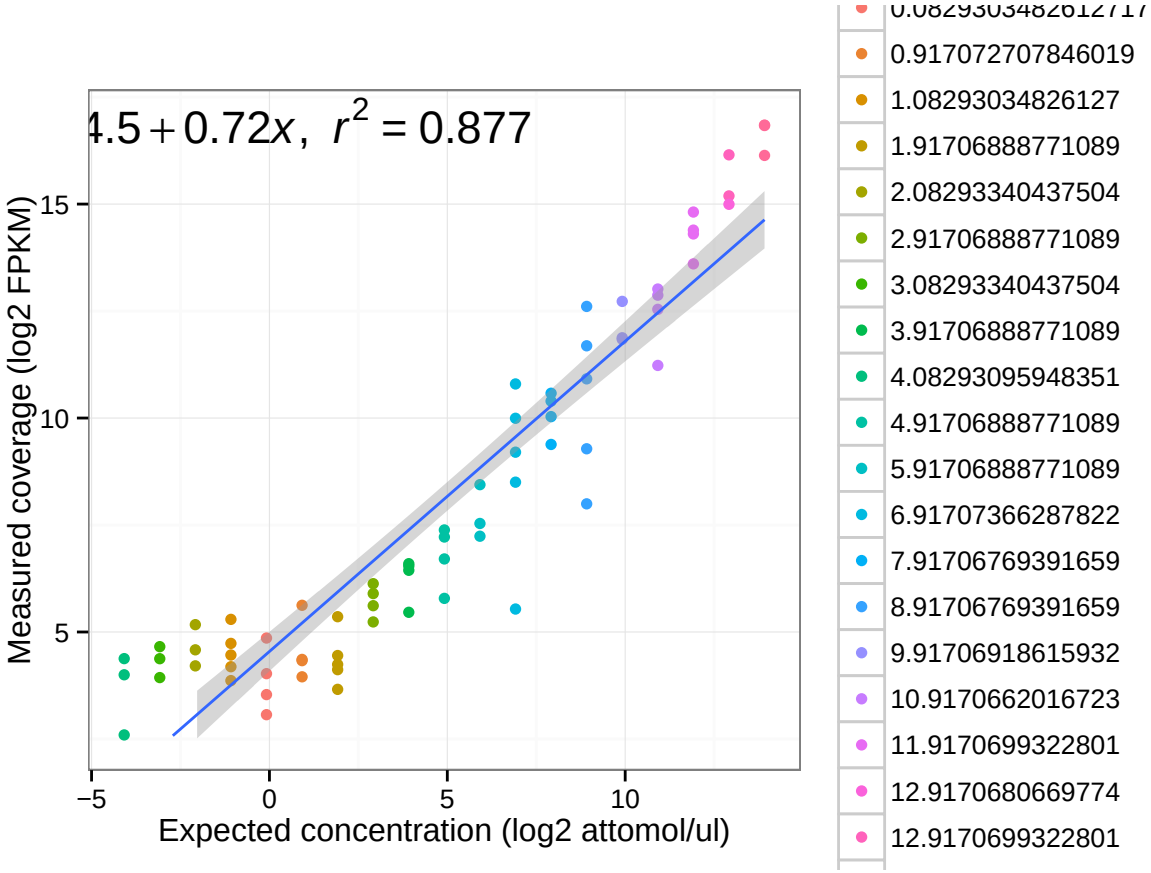
Expression summary statistics for: B2

```
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
```

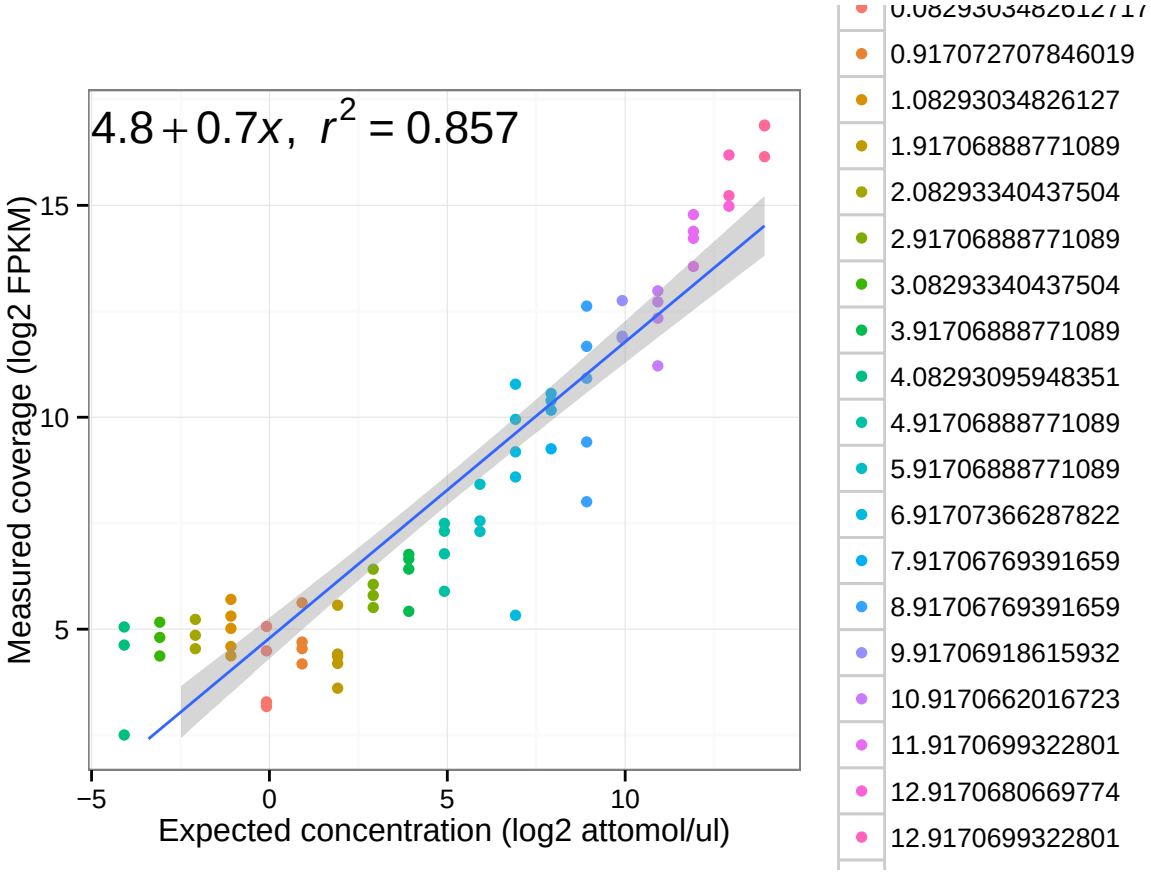
Expression summary statistics for: B3

```
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
```

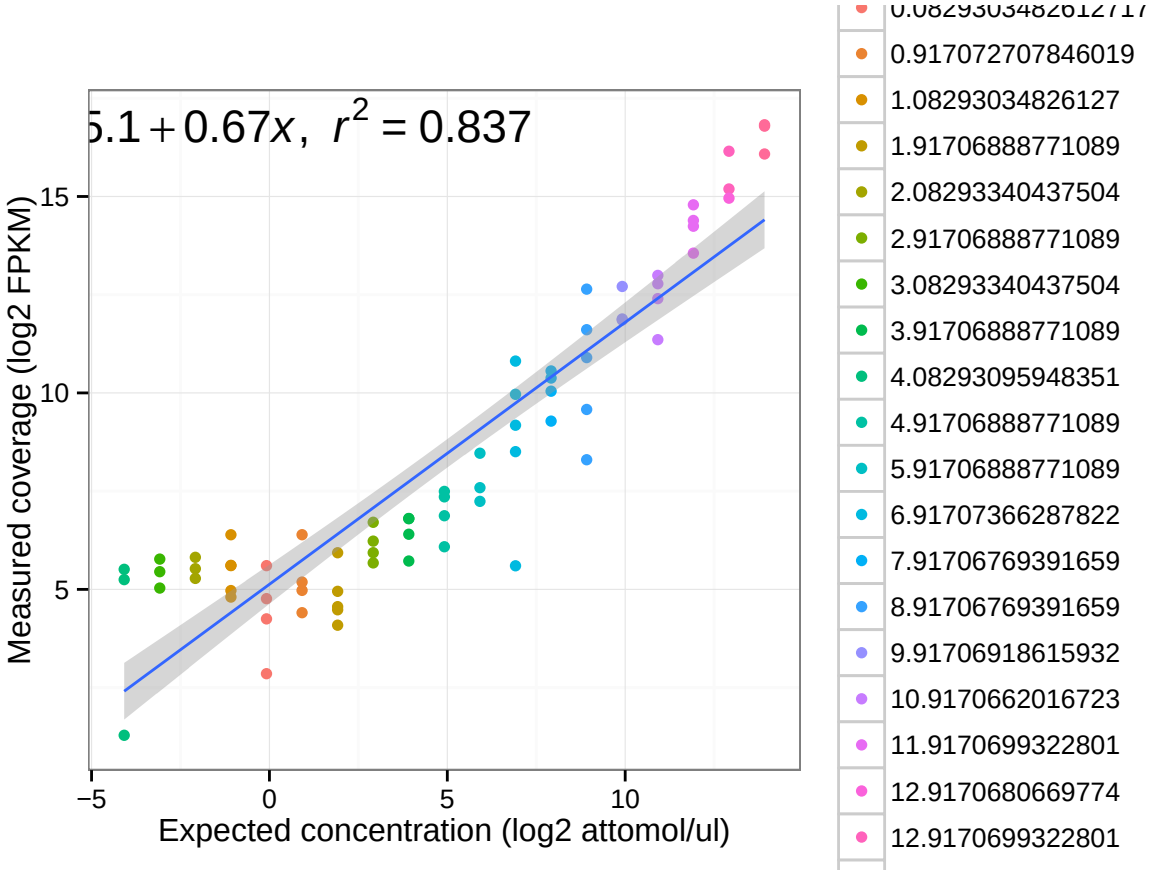
Expression scatter plot for: A1



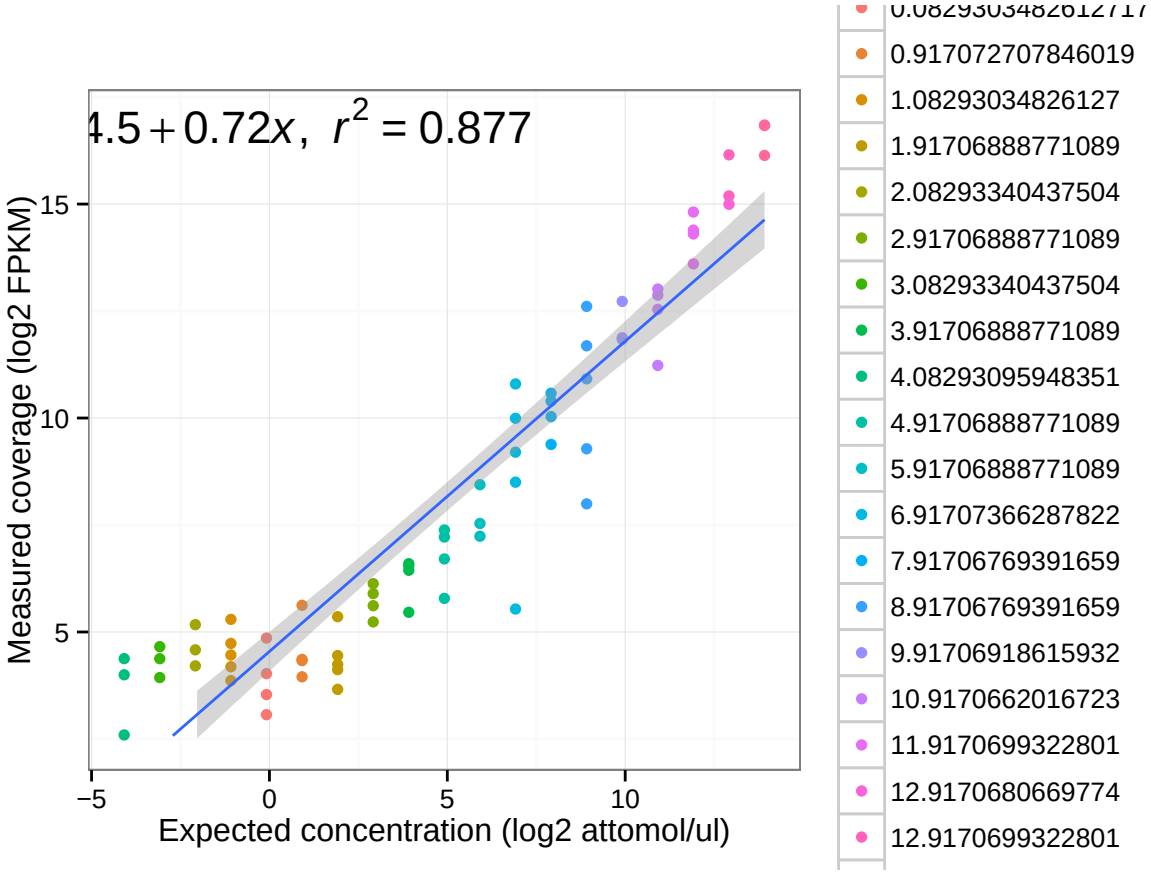
Expression scatter plot for: A2



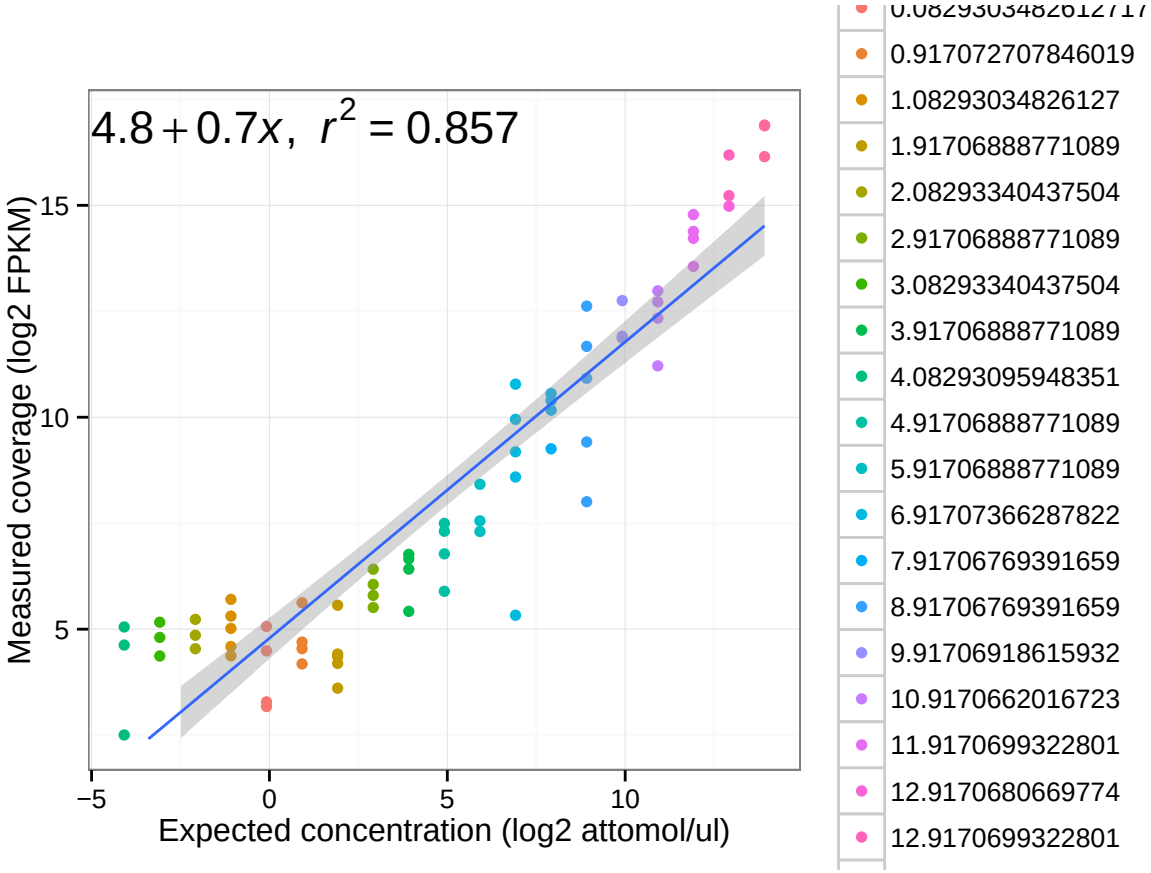
Expression scatter plot for: A3



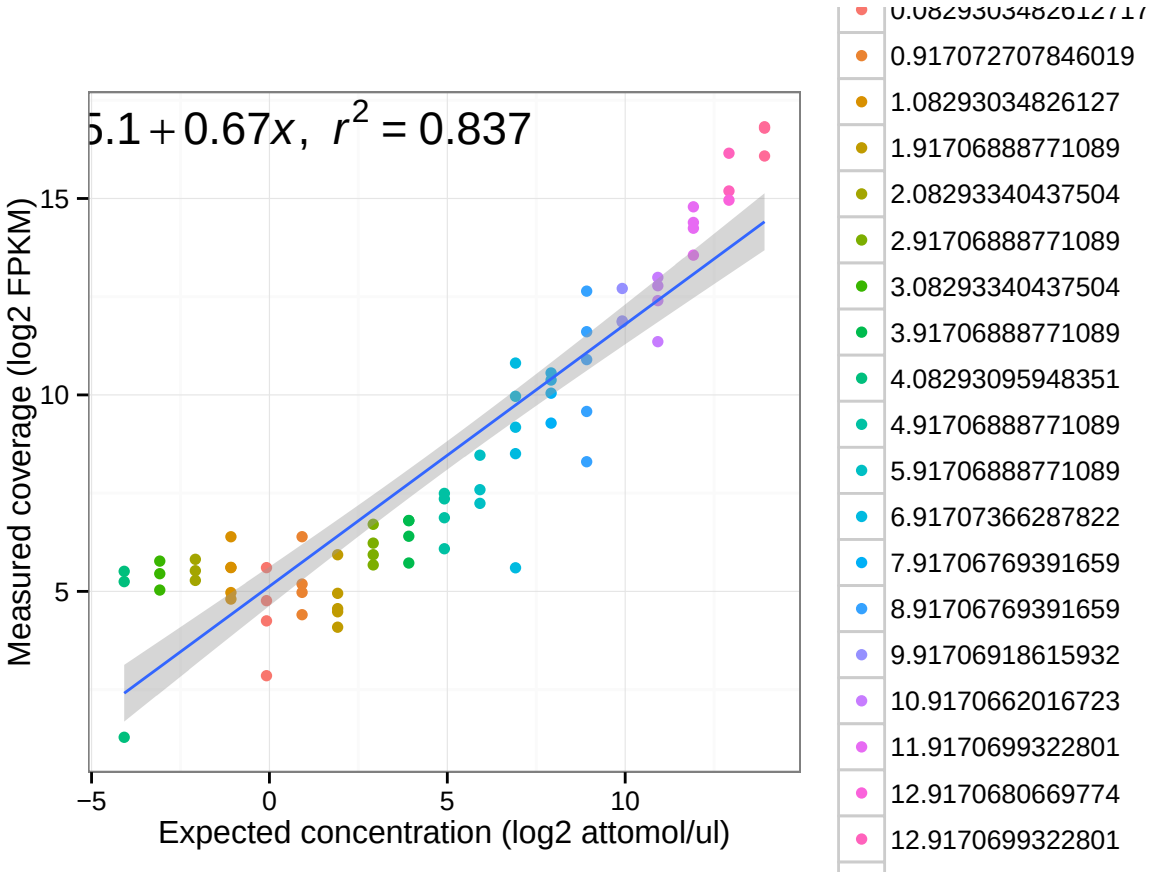
Expression scatter plot for: B1



Expression scatter plot for: B2



Expression scatter plot for: B3



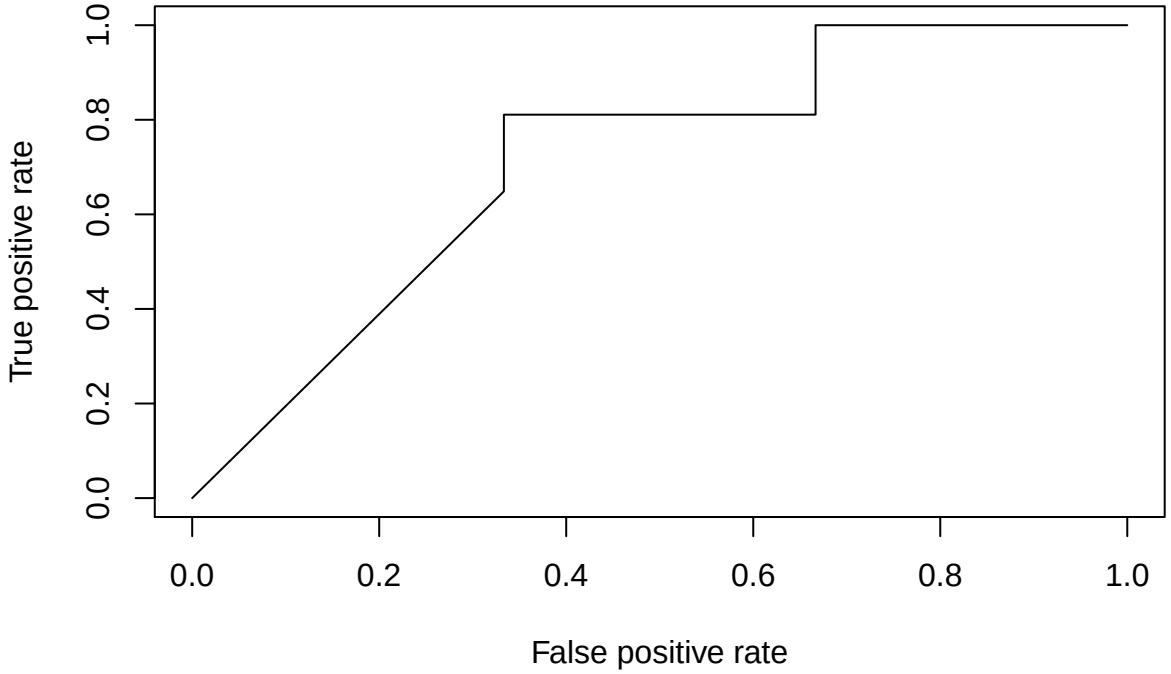
TransQuin Expression (Isoform)

TransQuin Differential

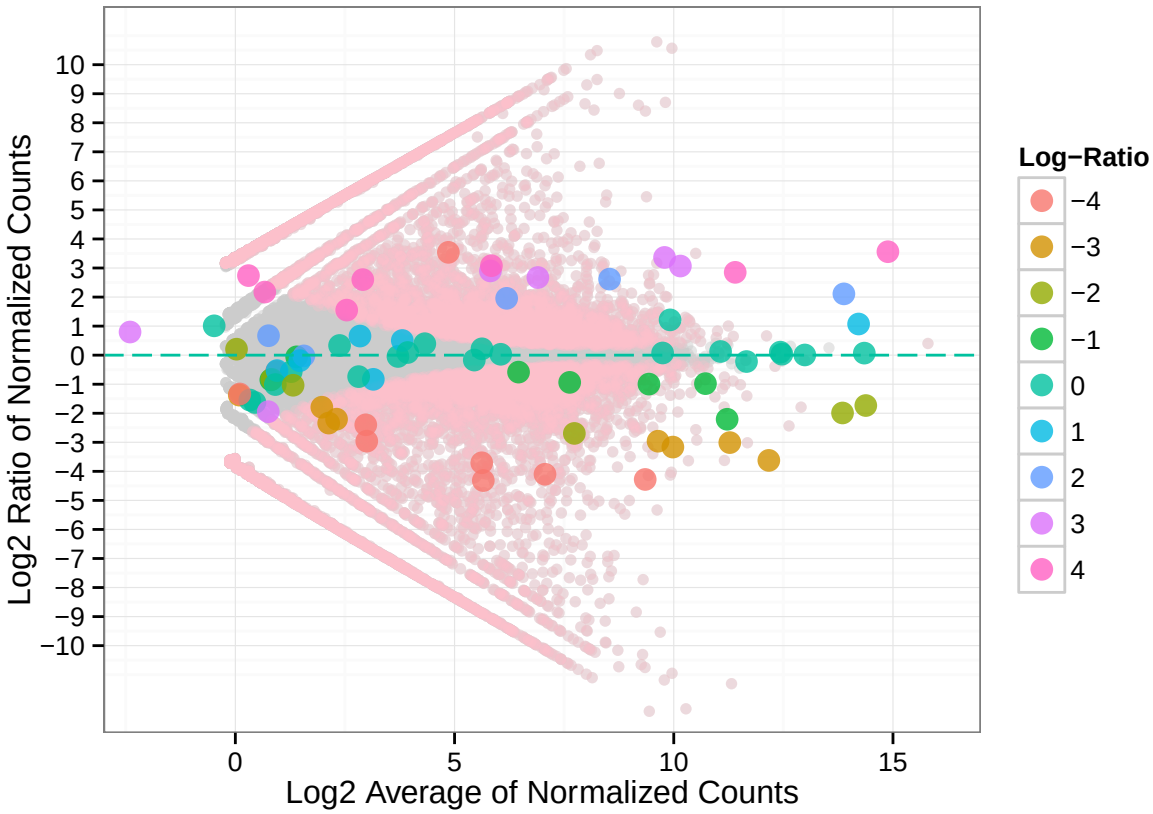
Differential summary statistics

```
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
```

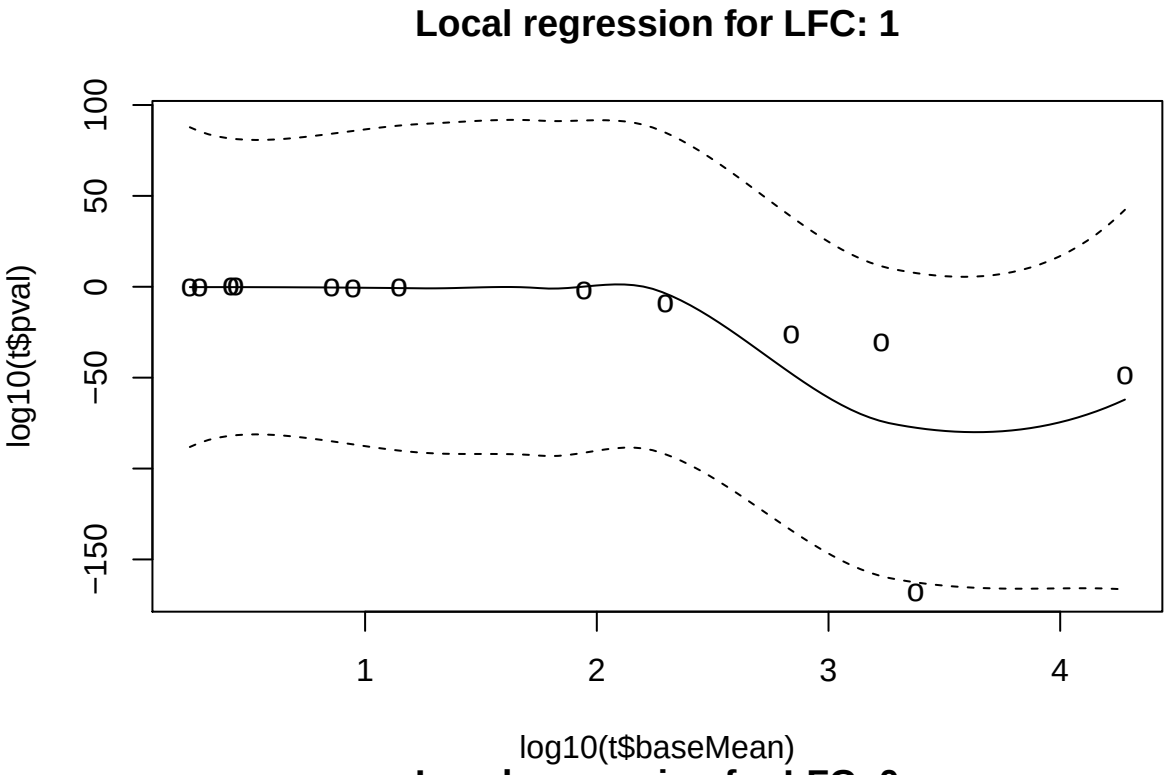
ROC plot

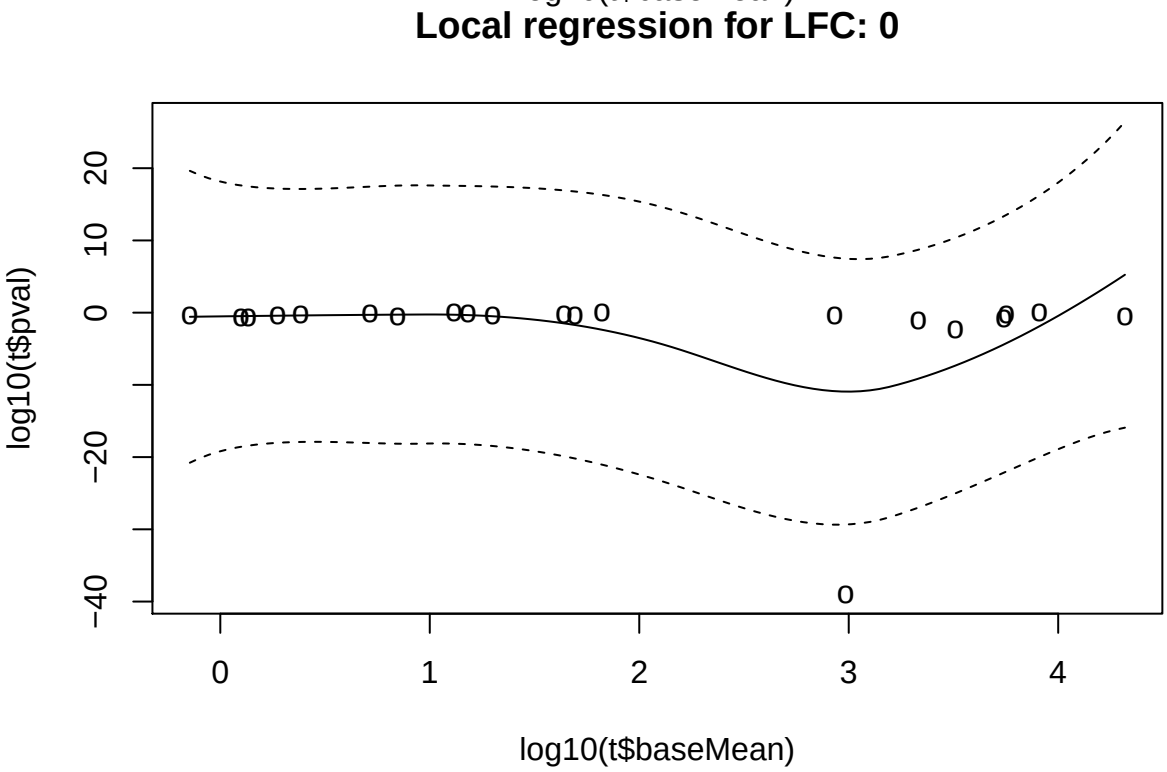

True positive rate
0.0
0.2
0.4
0.6
0.8
1.0
0.0
0.2
0.4
0.6
0.8
1.0
False positive rate

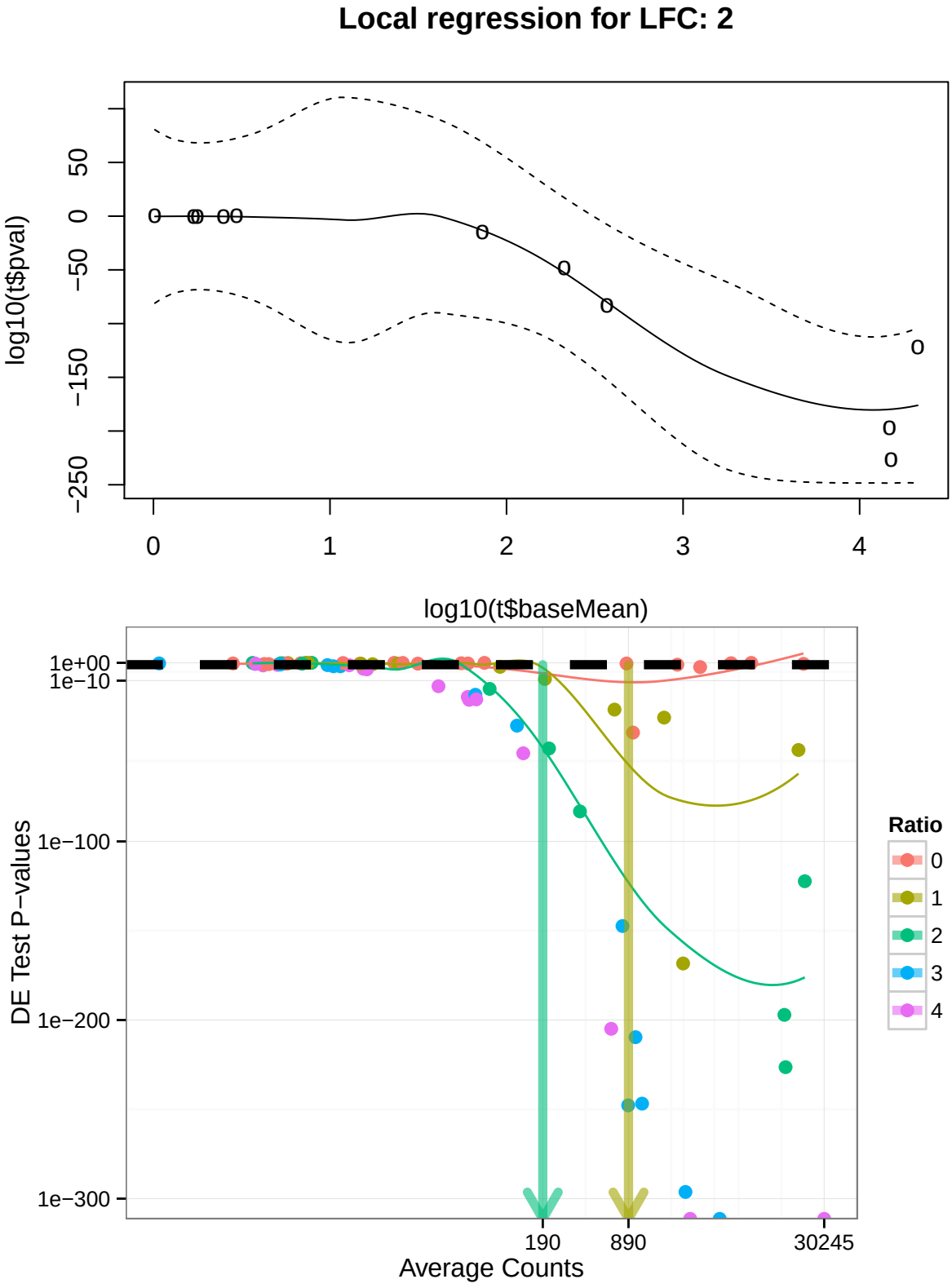
MA plot


Log2 Ratio of Normalized Counts
10
9
8
7
6
5
4
3
2
1
0
−1
−2
−3
−4
−5
−6
−7
−8
−9
−10
0
5
10
15
Log2 Average of Normalized Counts
Log−Ratio
−4
−3
−2
−1
0
1
2
3
4

LODR plot


Local regression for LFC: 1
log10(t$pval)
100
50
0
−50
−150
1
2
3
4
log10(t$baseMean)


Local regression for LFC: 0
log10(t$pval)
20
10
0
−20
−40
0
1
2
3
4
log10(t$baseMean)


Local regression for LFC: 2
log10(t$pval)
50
0
−50
−150
−250
0
1
2
3
4
log10(t$baseMean)
DE Test P−values
1e+00
1e−10
1e−100
1e−200
1e−300
190
890
30245
Average Counts
Ratio
0
1
2
3
4