

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)	Sensitivity
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	

Summary for dataset: A2/TransAlign_quins.stats

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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)	Sensitivity
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			

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)	Sensitivity
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	0.893617	0.69783	1				
R1_62	0.70354	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			

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	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	

Summary for dataset: B2/TransAlign_quins.stats

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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		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			

Summary for dataset: B3/TransAlign_quins.stats

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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

TransQuin Expression (Gene)

Expression summary statistics for: A1

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

Experiment: 60570 gene
Synthetic: 75 gene

Reference: 76 gene
Detected: 4.39067 gene

*** Detection Limits

Break: 3.77655 (R1_62)

Left: $4.39067 + 0.0805742x$ ($R^2 = 0.0567335$)

Right: $2.0794 + 1.00352x$ ($R^2 = 0.922502$)

*** 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.fpk_tracking

Experiment: 60570 gene

Synthetic: 75 gene

Reference: 76 gene

Detected: 4.62321 gene

*** Detection Limits

Break: 3.77655 (R1_62)

Left: $4.62321 + 0.0227324x$ ($R^2 = 0.00360572$)

Right: $2.20463 + 0.990951x$ ($R^2 = 0.91596$)

*** 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.fpk_tracking

Experiment: 60569 gene

Synthetic: 75 gene

Reference: 76 gene

Detected: 5.25776 gene

*** Detection Limits

Break: 15.1062 (R1_101)

Left: $5.25776 + 0.16804x$ ($R^2 = 0.139073$)

Right: $1.51144 + 1.05768x$ ($R^2 = 0.903529$)

*** 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.fpk_tracking

Experiment: 60570 gene

Synthetic: 75 gene

Reference: 76 gene

Detected: 4.39067 gene

*** Detection Limits

Break: 3.77655 (R1_62)

Left: $4.39067 + 0.0805742x$ ($R^2 = 0.0567335$)

Right: $2.0794 + 1.00352x$ ($R^2 = 0.922502$)

*** 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.fpk_tracking

Experiment: 60570 gene

Synthetic: 75 gene

Reference: 76 gene

Detected: 4.62321 gene

*** Detection Limits

Break: 3.77655 (R1_62)

Left: $4.62321 + 0.0227324x$ ($R^2 = 0.00360572$)

Right: $2.20463 + 0.990951x$ ($R^2 = 0.91596$)

*** 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.fpk_tracking

Experiment: 60569 gene

Synthetic: 75 gene

Reference: 76 gene

Detected: 5.25776 gene

*** Detection Limits

Break: 15.1062 (R1_101)

Left: $5.25776 + 0.16804x$ ($R^2 = 0.139073$)

Right: $1.51144 + 1.05768x$ ($R^2 = 0.903529$)

*** 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

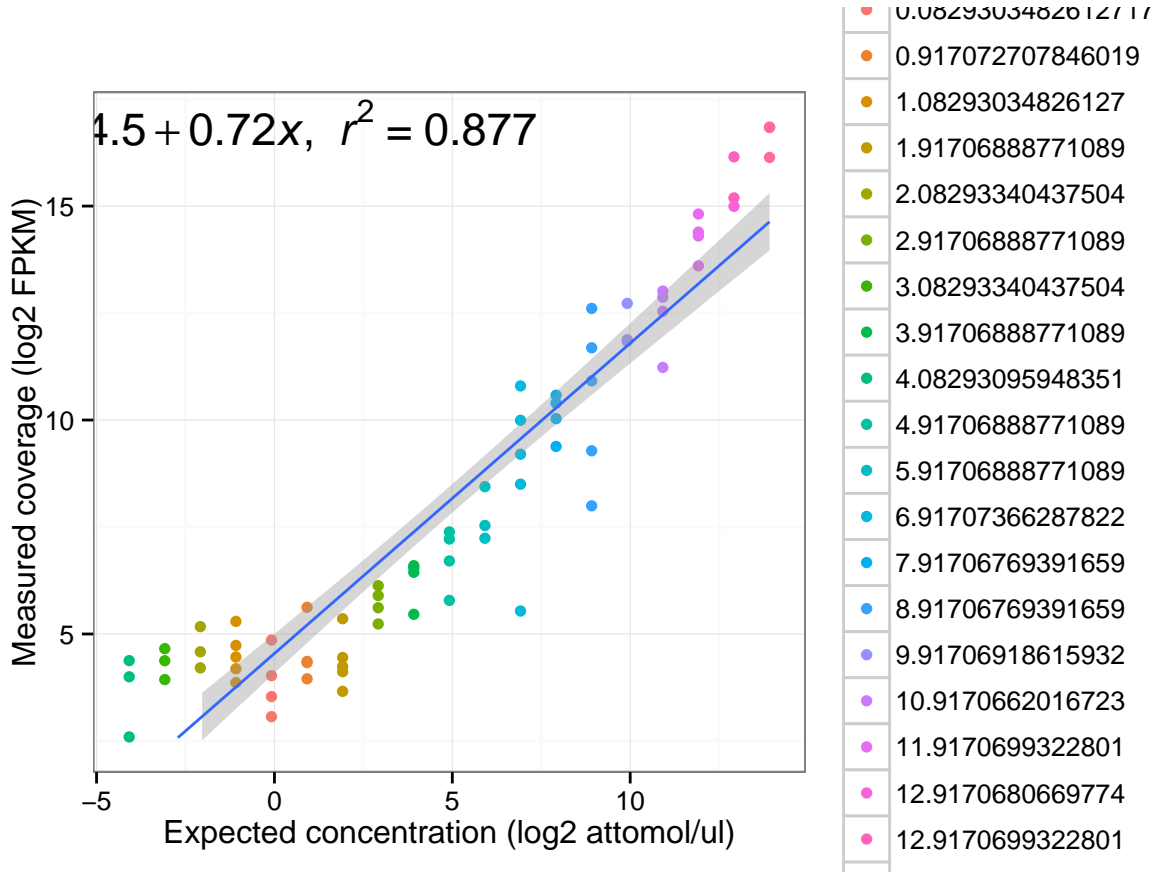
P-value: 0

SSM: 879.802, DF: 1

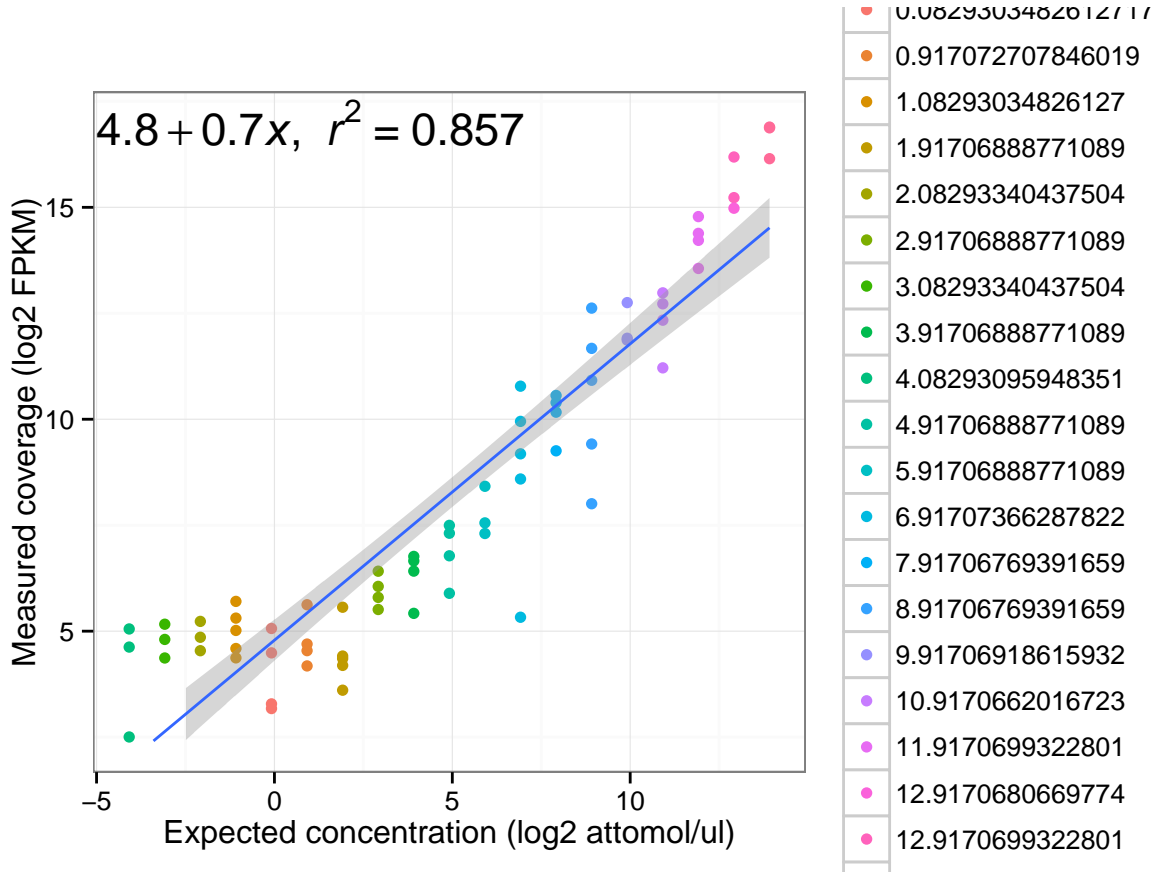
SSE: 171.015, DF: 71

SST: 1050.82, DF: 72

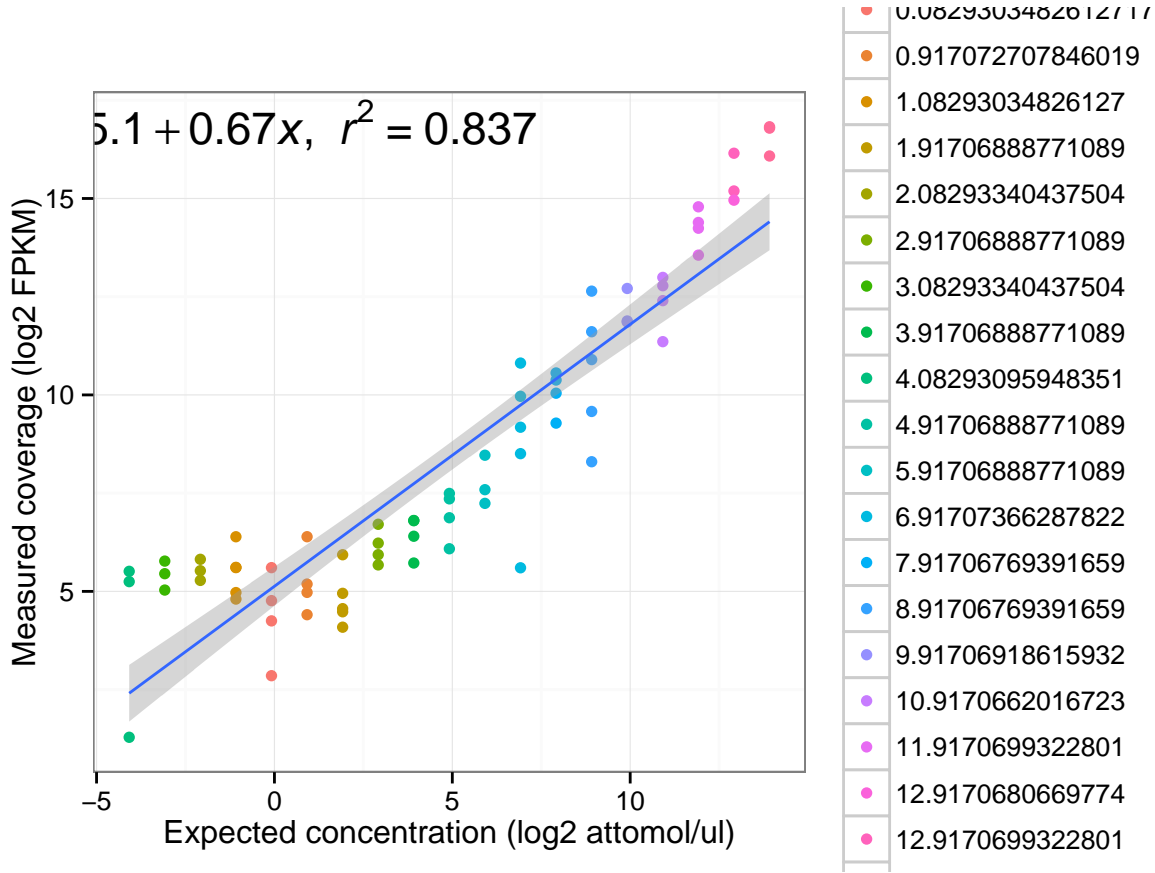
Expression scatter plot for: A1



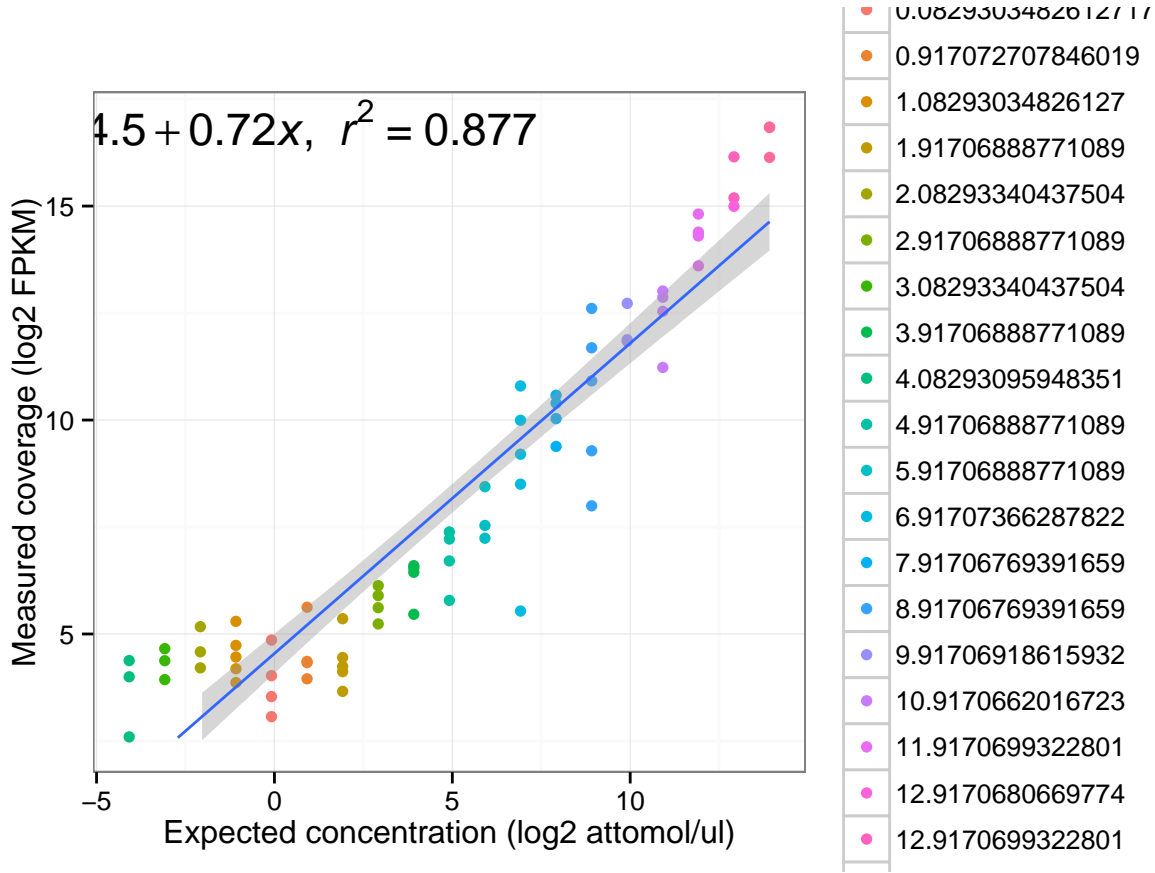
Expression scatter plot for: A2



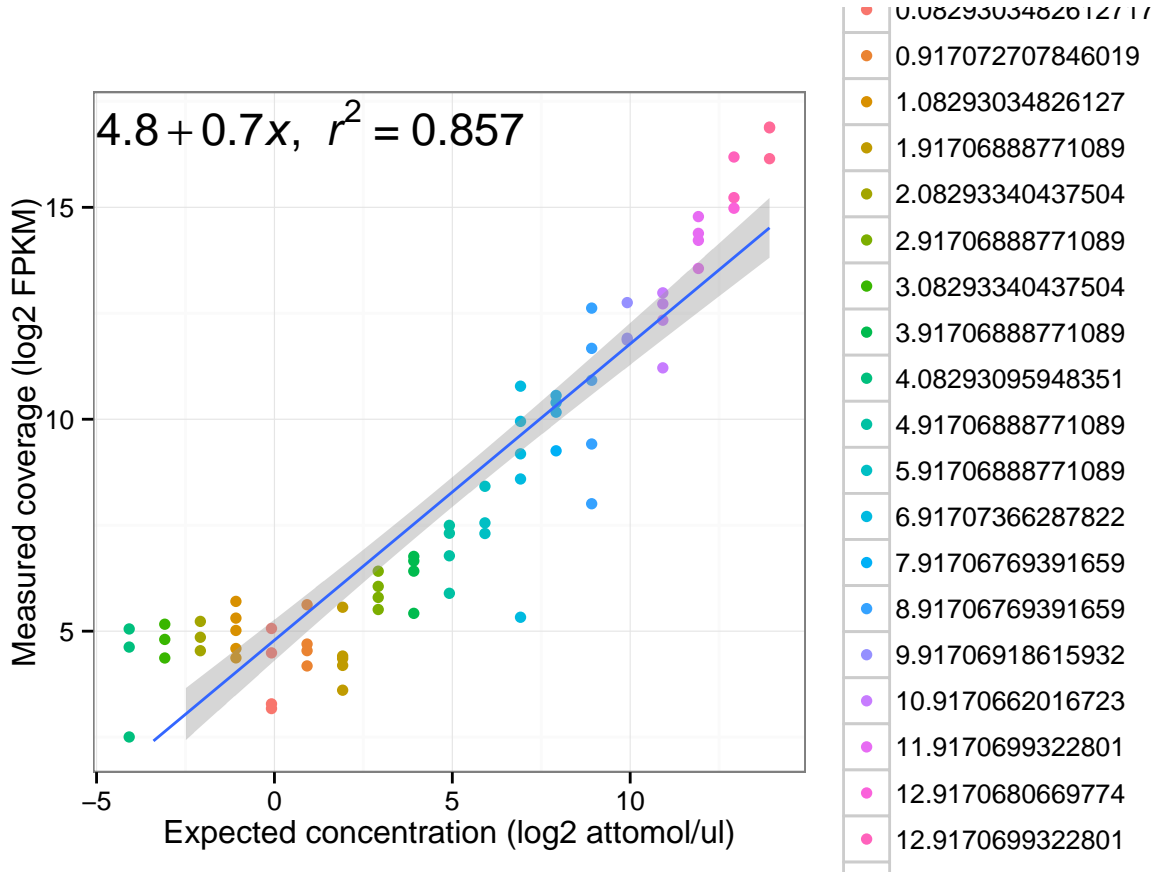
Expression scatter plot for: A3



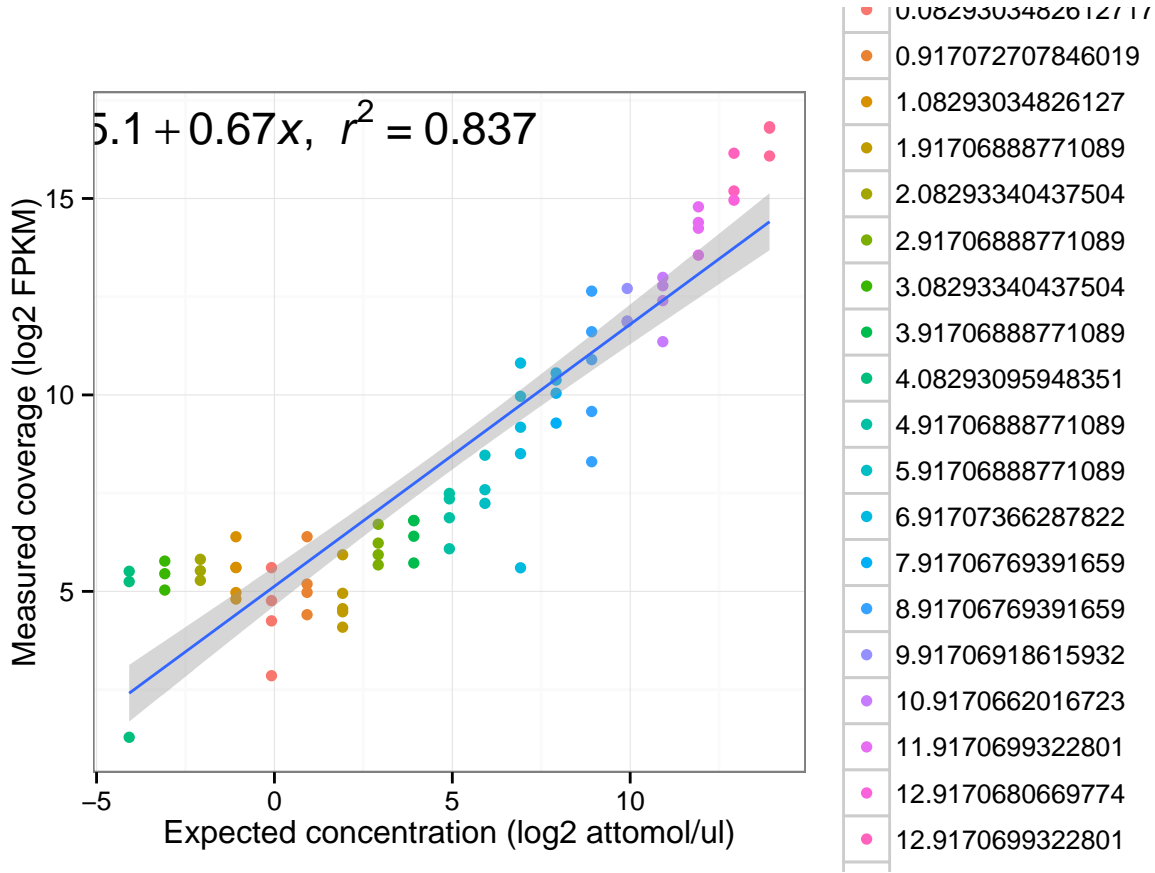
Expression scatter plot for: B1



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)

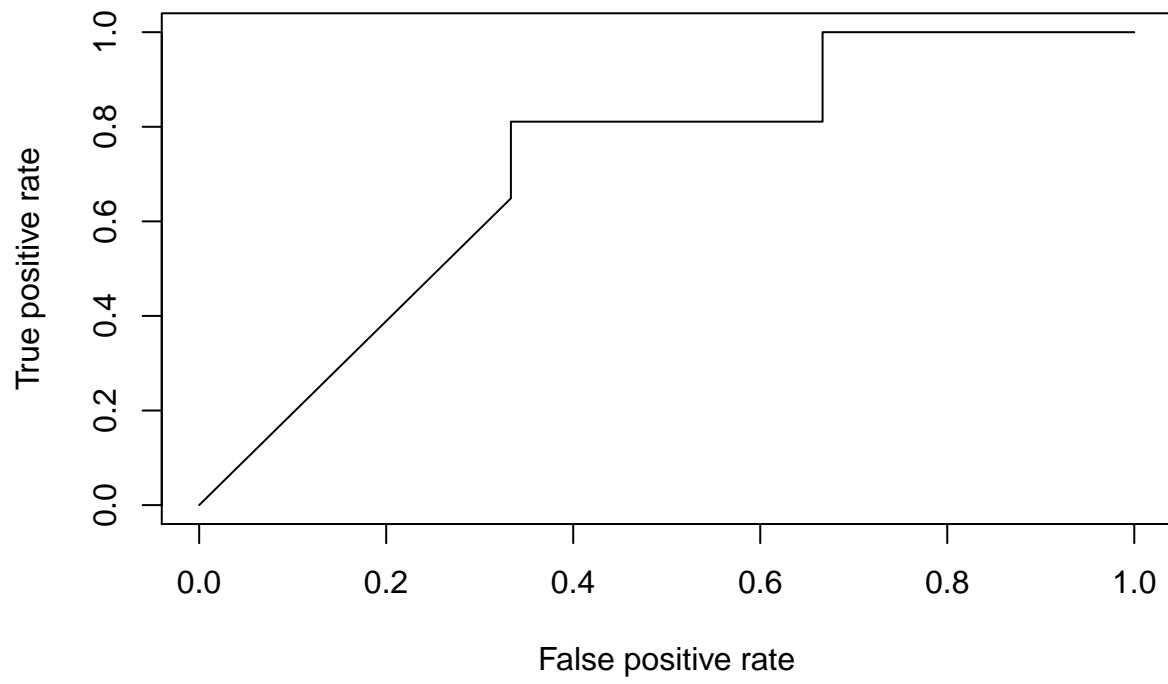
*** Statistics for linear regression

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

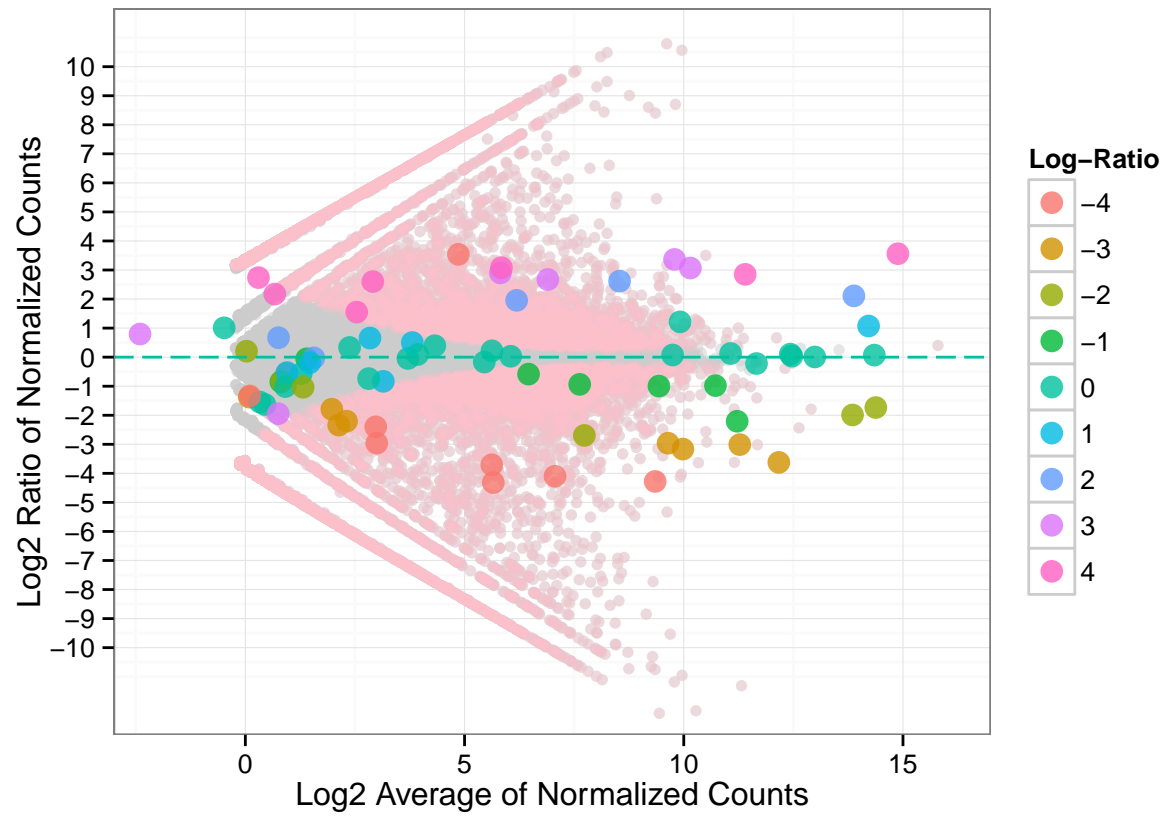
*** Statistics for linear regression (log2 scale)

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

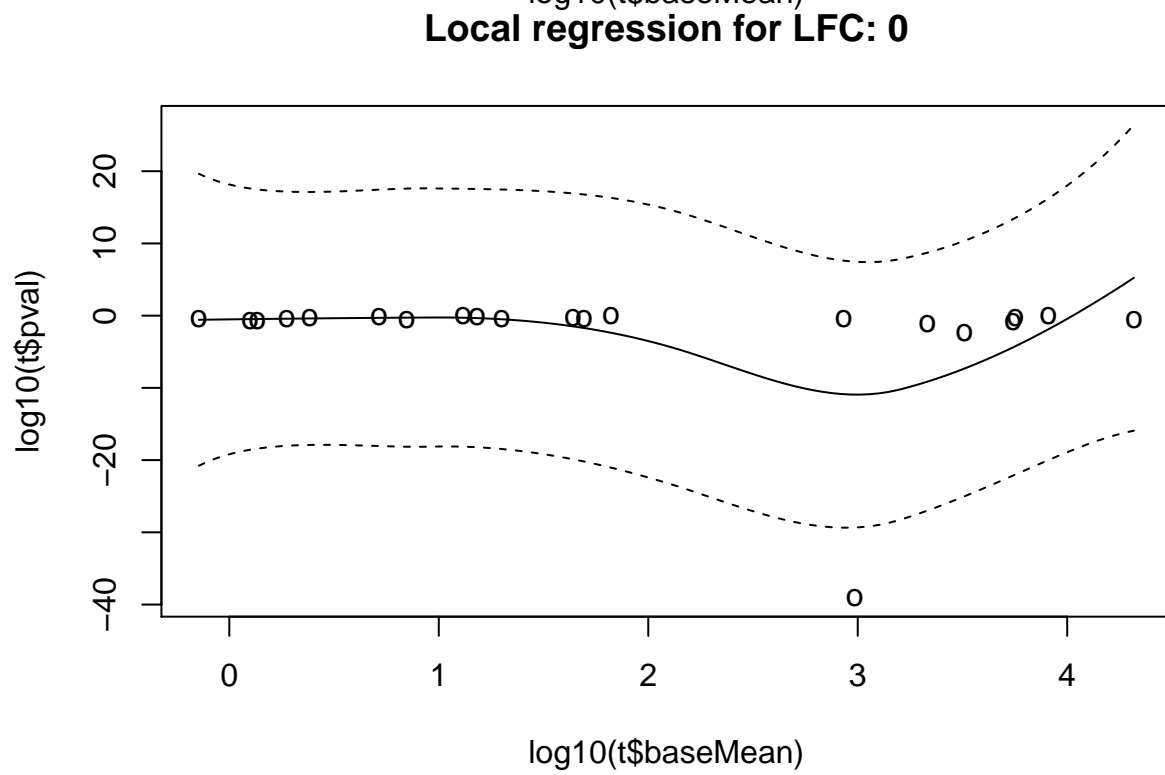
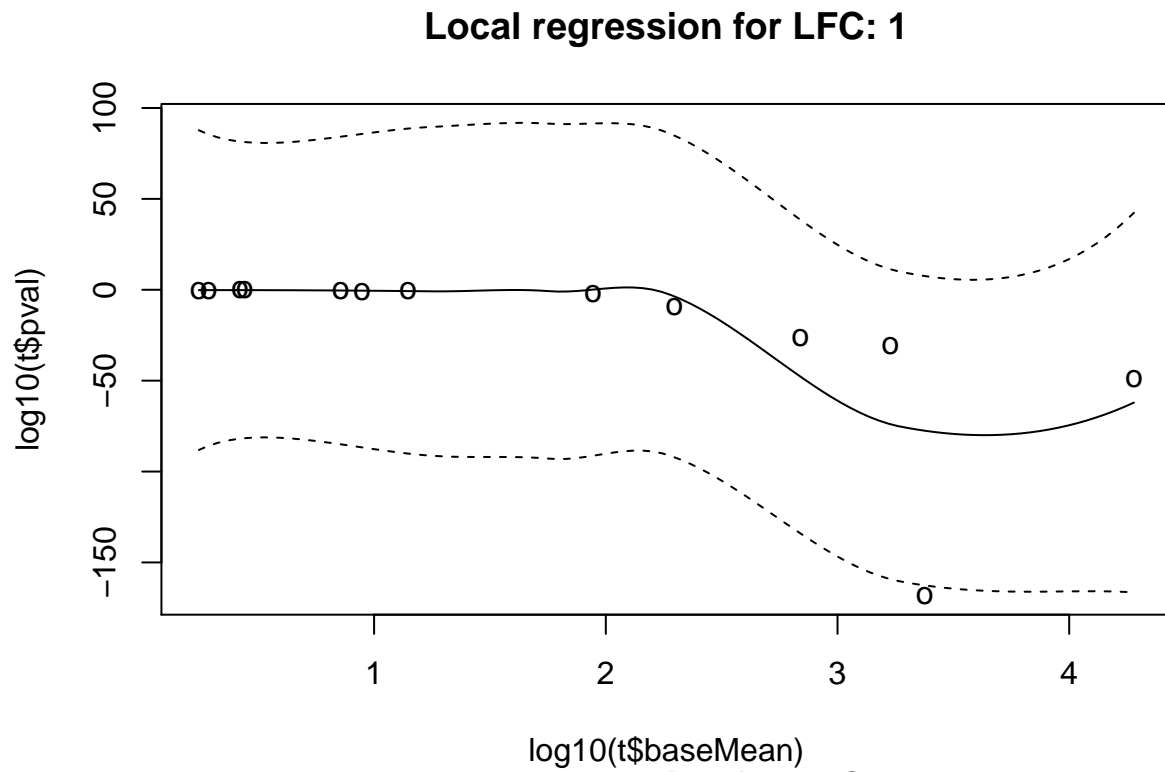
ROC plot



MA plot



LODR plot



Local regression for LFC: 2

