

Anaquin: TransQuin Report

Contents

TransQuin Alignment	3
Summary statistics for: A1	3
Sequin statistics for: A1	5
Summary statistics for: A2	7
Sequin statistics for: A2	8
Summary statistics for: A3	10
Sequin statistics for: A3	11
Summary statistics for: B1	13
Sequin statistics for: B1	14
Summary statistics for: B2	16
Sequin statistics for: B2	17
Summary statistics for: B3	19
Sequin statistics for: B3	20
TransQuin Assembly	22
Summary statistics for: A1	22
Summary statistics for: A2	23
Summary statistics for: A3	24
Summary statistics for: B1	25
Summary statistics for: B2	26
Summary statistics for: B3	27
TransQuin Expression (Gene)	28
Expression summary statistics for: A1	28
Expression scatter plot for: A1	29
Expression summary statistics for: A2	30
Expression scatter plot for: A2	31
Expression summary statistics for: A3	32
Expression scatter plot for: A3	33
Expression summary statistics for: B1	34
Expression scatter plot for: B1	35
Expression summary statistics for: B2	36
Expression scatter plot for: B2	37
Expression summary statistics for: B3	38
Expression scatter plot for: B3	39

TransQuin Expression (Isoform)	40
Expression summary statistics for: A1	40
Expression scatter plot for: A1	41
Expression summary statistics for: A2	42
Expression scatter plot for: A2	43
Expression summary statistics for: A3	44
Expression scatter plot for: A3	45
Expression summary statistics for: B1	46
Expression scatter plot for: B1	47
Expression summary statistics for: B2	48
Expression scatter plot for: B2	49
Expression summary statistics for: B3	50
Expression scatter plot for: B3	51
Minor/Major plot	52
 TransQuin Differential	 53
Differential summary statistics	53
ROC plot	54
MA plot	55
LODR plot	56

TransQuin Alignment

Summary statistics for: A1

Summary for file: K_RMxA1v2.accepted_hits.bam

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

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

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

Dilution: 0.761291

*** The following statistics are computed at the exon, intron and base level.

*** Exon level is defined by performance per exon. An alignment that
*** is not mapped entirely within an exon is considered as a FP. The
*** intron level is similar.

*** Base level is defined by performance per nucleotide. A partial
*** mapped read will have FP and TP.

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

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

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

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

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

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

----- Undetected -----

Exon: 0.002521
Intron: 0.006809
Gene: 0.026316

Sequin statistics for: A1

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

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

Summary statistics for: A2

Summary for file: K_RMxA2v2.accepted_hits.bam

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

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

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

Dilution: 0.766192

*** The following statistics are computed at the exon, intron and base level.

*** Exon level is defined by performance per exon. An alignment that
*** is not mapped entirely within an exon is considered as a FP. The
*** intron level is similar.

*** Base level is defined by performance per nucleotide. A partial
*** mapped read will have FP and TP.

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

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

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

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

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

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

----- Undetected -----

Exon: 0.002521
Intron: 0.013619
Gene: 0.026316

ID	Covered Sensitivity			Specificity (Exon)			Sensitivity (Intron)		Specificity (Intron)		Sensitivity
R1_101	0.843342	1	0.997495	1	0.995816	0.843342	0.995889				
R1_102	0.721599	1	0.995219	1	0.00552418	0.721599	0.998544				
R1_103	0.628532	1	0.995586	1	0.185487	0.628532	0.995612				
R1_11	0.647177	1	0.999245	1	0.0529042	0.647177	0.997927				
R1_12	0.590595	1	0.9933	0.956522	1	0.590595	0.998247				
R1_13	0.920394	1	0.988579	0.909091	0.661924	0.920394	0.995082				
R1_14	1	0.999844	--	--	1	0.991045	1				
R1_21	0.630945	1	0.994394	1	0.942939	0.630945	0.942446				
R1_22	0.527602	1	0.998493	1	0.101617	0.527602	0.994032				
R1_23	0.604667	1	0.989406	1	0.0153541	0.604667	0.997701				
R1_24	1	1	0.995351	1	0.995767	1	0.99782				
R1_31	0.687823	1	0.994739	1	0.998694	0.687823	0.995916				
R1_32	0.545455	1	0.998386	1	1	0.545455	0.995772				
R1_33	0.911321	1	0.998728	1	0.99726	0.911321	0.999676				
R1_41	0.78125	1	0.996939	1	0.932387	0.78125	0.994695				
R1_42	0.617479	1	0.981914	1	0.891942	0.617479	0.986842				
R1_43	0.541274	1	0.990613	0.973684	0.989699	0.541274	0.996335				
R1_51	0.607103	1	0.995118	1	0.988762	0.607103	0.99446				
R1_52	0.623188	1	0.979032	1	0.992218	0.623188	0.977858				
R1_53	0.998489	1	0.995792	1	0.726932	0.998489	0.996983				
R1_61	0.676962	1	0.99811	1	0.00262261	0.676962	0.998768				
R1_62	0.767383	1	0.992147	1	0.00112939	0.767383	0.999177				
R1_63	0.669964	1	0.995761	1	0.964477	0.669964	0.995745				
R1_71	0.740968	1	0.993449	1	0.964899	0.740968	0.987705				
R1_72	0.600451	1	1	1	0.000569401	0.600451	1				
R1_73	0.732371	1	0.989559	0.96	0.531614	0.732371	0.996583				
R1_81	0.747244	1	0.998029	1	0.994022	0.747244	0.996849				
R1_82	0.587741	1	0.992549	1	0.995822	0.587741	0.991501				
R1_83	0.645199	1	0.999418	1	0.999628	0.645199	0.99702				
R1_91	0.685696	1	1	1	1	0.685696	1				
R1_92	0.781726	1	0.980355	1	0.995561	0.781726	0.995153				
R1_93	0.625086	1	0.996684	1	0.998378	0.625086	0.996156				
R2_1	1	1	--	--	0.98995	1	0.98995				
R2_105	1	1	--	--	0.68	1	0.68				
R2_115	0.840131	1	0.989271	1	0.996256	0.840131	0.99549				
R2_116	0.524582	1	0.996665	1	1	0.524582	0.998183				
R2_117	0.710041	1	0.999708	1	0.999328	0.710041	0.997122				
R2_14	0.719569	1	0.988161	1	0.737964	0.719569	0.991507				
R2_150	0.835448	1	0.998619	1	0.673702	0.835448	0.991785				
R2_151	0.565179	1	0.981308	0.85	0.00120631	0.565179	0.998454				

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

Summary statistics for: A3

Summary for file: K_RMxA3v2.accepted_hits.bam

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

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

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

Dilution: 0.772589

*** The following statistics are computed at the exon, intron and base level.

*** Exon level is defined by performance per exon. An alignment that
*** is not mapped entirely within an exon is considered as a FP. The
*** intron level is similar.

*** Base level is defined by performance per nucleotide. A partial
*** mapped read will have FP and TP.

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

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

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

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

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

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

----- Undetected -----

Exon: 0.002521
Intron: 0.007782
Gene: 0.026316

ID	Covered Sensitivity			Specificity (Exon)			Sensitivity (Intron)		Specificity (Intron)		Sensitivity
R1_101	0.844212	1	0.999087	1	1	0.844212	0.99897				
R1_102	0.723352	1	0.995112	1	0.0284201	0.723352	0.998065				
R1_103	0.629086	1	0.995227	1	0.535702	0.629086	0.99518				
R1_11	0.646505	1	0.998816	1	0.0505829	0.646505	0.997925				
R1_12	0.591978	1	0.993087	1	0.999141	0.591978	0.997669				
R1_13	0.920394	1	0.988092	0.909091	0.909266	0.920394	0.995082				
R1_14	1	0.999779	--	--	1	0.995502	1				
R1_21	0.630945	1	0.993913	1	0.951111	0.630945	0.941599				
R1_22	0.528054	1	0.998712	1	0.201023	0.528054	0.994037				
R1_23	0.610589	1	0.987265	1	0.0338936	0.610589	0.997156				
R1_24	1	1	0.995487	1	0.998898	1	0.99782				
R1_31	0.687823	1	0.994534	1	0.998714	0.687823	0.995916				
R1_32	0.544876	1	0.997818	1	1	0.544876	0.995767				
R1_33	0.912504	1	0.997554	1	0.996416	0.912504	0.998706				
R1_41	0.78125	1	0.99667	1	0.999697	0.78125	0.996457				
R1_42	0.617479	1	0.980701	1	0.897666	0.617479	0.985844				
R1_43	0.540731	1	0.99053	0.973684	0.984815	0.540731	0.996331				
R1_51	0.607103	1	0.996042	1	0.992969	0.607103	0.993542				
R1_52	0.623951	1	0.989971	1	1	0.623951	0.969769				
R1_53	0.998489	1	0.998404	1	0.973515	0.998489	0.996983				
R1_61	0.709516	1	0.993926	1	1	0.709516	0.998825				
R1_62	0.776233	1	1	1	1	0.776233	1				
R1_63	0.669703	1	0.995554	1	0.974728	0.669703	0.995743				
R1_71	0.740968	1	0.993971	1	0.988434	0.740968	0.985685				
R1_72	0.604966	1	1	1	1	0.604966	1				
R1_73	0.731743	1	0.983855	0.96	0.986432	0.731743	0.996864				
R1_81	0.747638	1	0.996786	1	0.994027	0.747638	0.99685				
R1_82	0.587741	1	0.992415	1	0.997628	0.587741	0.993612				
R1_83	0.644427	1	0.997372	1	0.996722	0.644427	0.998208				
R1_91	0.684413	1	0.998495	1	1	0.684413	0.998129				
R1_92	0.778765	1	0.980597	1	0.995994	0.778765	0.995135				
R1_93	0.625086	1	0.995437	1	0.998834	0.625086	0.996703				
R2_1	1	1	--	--	0.994975	1	0.994975				
R2_105	1	0.979167	--	--	0.981333	0.994595	0.981333				
R2_115	0.837955	1	0.989482	1	0.997475	0.837955	0.923861				
R2_116	0.583771	1	0.988752	1	1	0.583771	0.997553				
R2_117	0.709016	1	0.999618	1	0.99934	0.709016	0.9964				
R2_14	0.719569	1	0.989328	1	0.838494	0.719569	0.991507				
R2_150	0.835832	1	0.997978	1	0.821556						

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

Summary statistics for: B1

Summary for file: G_RMXB1v2.accepted_hits.bam

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

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

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

Dilution: 0.842494

*** The following statistics are computed at the exon, intron and base level.

*** Exon level is defined by performance per exon. An alignment that
*** is not mapped entirely within an exon is considered as a FP. The
*** intron level is similar.

*** Base level is defined by performance per nucleotide. A partial
*** mapped read will have FP and TP.

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

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

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

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

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

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

----- Undetected -----

Exon: 0.006723
Intron: 0.015564
Gene: 0.052632

ID	Covered Sensitivity			Specificity (Exon)			Sensitivity (Intron)		Specificity (Intron)		Sensitivity
R1_101	0.787641	1	0.996774	1	1	0.787641	0.998896				
R1_102	0.721248	1	0.98946	1	0.108223	0.721248	0.999514				
R1_103	0.627978	1	0.992978	1	0.959322	0.627978	0.996484				
R1_11	0.644489	1	0.989534	1	1	0.644489	0.997919				
R1_12	0.569848	1	0.992637	1	0.991467	0.569848	0.998788				
R1_13	0.920394	1	0.988299		0.909091	0.983353	0.920394	0.995082			
R1_14	1	0.999917	--	--	0.996988	0.996988	0.996988				
R1_21	0.630945	1	0.993465	1	0.902076	0.630945	0.941599				
R1_22	0.526697	1	0.999028	1	0.0033303	0.526697	0.997429				
R1_23	0.609892	1	0.983464	1	0.00570884	0.609892	0.997153				
R1_24	0.999345	1	0.995356	1	0.998841	0.999345	0.998472				
R1_31	0.688764	1	0.99394	1	0.997605	0.688764	0.992547				
R1_32	0.541401	1	1	1	1	0.541401	1				
R1_33	0.88324	1	0.997831	1	1	0.88324	0.999331				
R1_41	0.78125	1	0.99979	1	0.997007	0.78125	0.995575				
R1_42	0.617479	1	0.989977	1	0.975927	0.617479	0.990854				
R1_43	0.541999	1	0.986484		0.973684	0.348855	0.541999	0.996339			
R1_51	0.603157	1	0.995454	1	0.855858	0.603157	0.995349				
R1_52	0.622807	1	0.994252	1	1	0.622807	0.998166				
R1_53	0.998993	1	0.997143	1	0.718094	0.998993	0.996985				
R1_61	0.718698	1	1	1	1	0.718698	1				
R1_62	0.697219	1	1	1	1	0.697219	1				
R1_63	0.670484	1	0.994539	1	0.857561	0.670484	0.995748				
R1_71	0.740968	1	0.99358	1	0.848788	0.740968	0.986694				
R1_72	0.544921	1	1	1	1	0.544921	1				
R1_73	0.731115	1	0.991175		0.96	0.993206	0.731115	0.997431			
R1_81	0.747244	1	0.996891	1	0.991853	0.747244	0.996325				
R1_82	0.587741	1	0.999352	1	0.987979	0.587741	0.992908				
R1_83	0.647513	1	0.998826	1	0.998681	0.647513	0.998216				
R1_91	0.66517	1	1	1	0.66517	1					
R1_92	0.778765	1	0.980861	1	0.995714	0.778765	0.995135				
R1_93	0.625086	1	0.996681	1	0.99831	0.625086	0.996156				
R2_1	1	1	--	--	0.994975	1	0.994975				
R2_105	1	0.992857	--	--	0.946667	0.994398	0.946667				
R2_115	0.842849	1	0.991243	1	0.99245	0.842849	0.923719				
R2_116	0.573747	1	0.984551	1	1	0.573747	0.999169				
R2_117	0.71209	1	0.998192	1	0.997355	0.71209	0.994989				
R2_14	0.719569	1	0.984461	1	0.904376	0.719569	0.991507				
R2_150	0.831603	1	0.999201	1	0.0928247	0.831603	0.997694				

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

Summary statistics for: B2

Summary for file: G_RMXB2v2.accepted_hits.bam

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

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

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

Dilution: 0.839848

*** The following statistics are computed at the exon, intron and base level.

*** Exon level is defined by performance per exon. An alignment that
*** is not mapped entirely within an exon is considered as a FP. The
*** intron level is similar.

*** Base level is defined by performance per nucleotide. A partial
*** mapped read will have FP and TP.

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

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

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

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

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

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

----- Undetected -----

Exon: 0.005882
Intron: 0.013619
Gene: 0.039474

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

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

Summary statistics for: B3

Summary for file: G_RMXB3v2.accepted_hits.bam

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

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

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

Dilution: 0.828492

*** The following statistics are computed at the exon, intron and base level.

*** Exon level is defined by performance per exon. An alignment that
*** is not mapped entirely within an exon is considered as a FP. The
*** intron level is similar.

*** Base level is defined by performance per nucleotide. A partial
*** mapped read will have FP and TP.

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

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

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

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

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

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

----- Undetected -----

Exon: 0.005042
Intron: 0.016537
Gene: 0.052632

ID	Covered	Sensitivity	Specificity (Exon)	Sensitivity (Intron)	Specificity (Intron)	Sensitivity	Specificity
R1_101	0.841601	1	0.99403	1	0.841601	0.998967	
R1_102	0.717742	1	0.980746	1	0.0221654	0.717742	0.999024
R1_103	0.627978	1	0.992148	1	0.835009	0.627978	0.996922
R1_11	0.645161	1	0.999461	1	1	0.645161	0.998959
R1_12	0.590595	1	0.991325	1	0.99781	0.590595	0.99883
R1_13	0.920394	1	0.988254	0.909091	0.987014	0.920394	0.995898
R1_14	1	0.999656	--	--	1	0.989568	1
R1_21	0.630945	1	0.993922	1	0.822178	0.630945	0.942446
R1_22	0.525792	1	1	1	0.00123868	0.525792	1
R1_23	0.60815	1	0.98571	1	0.00229028	0.60815	0.997714
R1_24	0.999563	1	0.995155	1	0.998935	0.999563	0.997819
R1_31	0.689234	1	0.991529	1	0.983869	0.689234	0.991881
R1_32	0.544296	1	1	1	1	0.544296	1
R1_33	0.890038	1	0.996205	1	1	0.890038	0.999005
R1_41	0.78125	1	0.999946	1	0.996632	0.78125	0.998225
R1_42	0.617479	1	0.991638	1	0.949859	0.617479	0.992872
R1_43	0.541818	1	0.986158	0.973684	0.604672	0.541818	0.996007
R1_51	0.60372	1	0.995606	1	0.831258	0.60372	0.996279
R1_52	0.62357	1	0.993546	1	0.999107	0.62357	0.997559
R1_53	0.998489	1	0.99506	1	0.72554	0.998489	0.995982
R1_61	0.686144	1	1	1	0.911765	0.686144	1
R1_62	0.716182	1	1	1	0.842105	0.716182	1
R1_63	0.670484	1	0.9934	1	0.879043	0.670484	0.995363
R1_71	0.740968	1	0.991256	1	0.984353	0.740968	0.987705
R1_72	0.586456	1	1	1	0.666667	0.586456	1
R1_73	0.731325	1	0.99045	0.96	0.991894	0.731325	0.997432
R1_81	0.749606	1	0.997294	1	0.989216	0.749606	0.996337
R1_82	0.587741	1	0.995803	1	0.987377	0.587741	0.991501
R1_83	0.644813	1	0.998136	1	0.995882	0.644813	0.998209
R1_91	0.679282	1	1	1	1	0.679282	1
R1_92	0.77665	1	0.97995	1	0.996986	0.77665	0.995122
R1_93	0.625086	1	0.996497	1	0.998423	0.625086	0.996156
R2_1	1	1	--	--	0.988945	1	0.988945
R2_105	1	0.983471	--	--	0.984	0.994609	0.984
R2_115	0.842849	1	0.989942	1	0.993289	0.842849	0.92427
R2_116	0.521718	1	0.996266	1	1	0.521718	0.998174
R2_117	0.711066	1	0.999352	1	0.997792	0.711066	0.997126
R2_14	0.719569	1	0.984373	1	0.944812	0.719569	0.991507
R2_150	0.833141	1	0.999017	1	0.0395501	0.833141	0.997698
R2_151	0.584864	1	0.997917	1	0.000290904	0.584864	0.999253
R2_152	0.603856	1	0.997058	1	0.00392735	0.603856	0.998386
R2_153	0.668093	1	0.997268	0.95	1	0.668093	0.99863
R2_154	0.855658	1	0.991371	1	0.158151	0.855658	0.994631
R2_18	0.628326	1	0.985099	1	0.89836	0.628326	0.986486
R2_19	0.811146	1	0.996027	1	0.769173	0.811146	0.998716
R2_20	0.732795	1	0.998371	1	0.998409	0.732795	0.997906
R2_24	0.586151	0.979592	0.988855	0.957447	0.		

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

TransQuin Assembly

Summary statistics for: A1

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

Experiment: 156131 features
Synthetic: 1955 features

Reference: 162 exons
Reference: 1028 introns

*** The following statistics are computed for exact and fuzzy.

*** The fuzzy level is 10 nucleotides.

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

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

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

Sensitivity: 0.996032 (0.996032)
Specificity: 0.996032 (0.996032)

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

Sensitivity: 1
Specificity: 1

----- Intron Chain level -----

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

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

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

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

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

Summary statistics for: A2

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

Experiment: 144223 features

Synthetic: 1928 features

Reference: 162 exons

Reference: 1028 introns

*** The following statistics are computed for exact and fuzzy.

*** The fuzzy level is 10 nucleotides.

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

Sensitivity: 1 (1)

Specificity: 1 (1)

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

Sensitivity: 0.996032 (0.996032)

Specificity: 0.996032 (0.996032)

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

Sensitivity: 1

Specificity: 1

----- Intron Chain level -----

Sensitivity: 1 (1)

Specificity: 1 (1)

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

Sensitivity: 1 (0.993939)

Specificity: 1 (0.993939)

Missing exons: 0/872 (0)

Missing introns: 3/756 (0.00396825)

Novel exons: 0/872 (0)

Novel introns: 0/756 (0)

Summary statistics for: A3

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

Experiment: 147191 features

Synthetic: 2037 features

Reference: 162 exons

Reference: 1028 introns

*** The following statistics are computed for exact and fuzzy.

*** The fuzzy level is 10 nucleotides.

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

Sensitivity: 1 (1)

Specificity: 1 (1)

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

Sensitivity: 0.996032 (0.996032)

Specificity: 0.996032 (0.996032)

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

Sensitivity: 1

Specificity: 1

----- Intron Chain level -----

Sensitivity: 1 (1)

Specificity: 1 (1)

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

Sensitivity: 1 (0.993939)

Specificity: 1 (0.993939)

Missing exons: 0/872 (0)

Missing introns: 3/756 (0.00396825)

Novel exons: 0/872 (0)

Novel introns: 0/756 (0)

Summary statistics for: B1

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

Experiment: 108316 features

Synthetic: 1691 features

Reference: 162 exons

Reference: 1028 introns

*** The following statistics are computed for exact and fuzzy.

*** The fuzzy level is 10 nucleotides.

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

Sensitivity: 1 (1)

Specificity: 1 (1)

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

Sensitivity: 0.996032 (0.996032)

Specificity: 0.996032 (0.996032)

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

Sensitivity: 1

Specificity: 1

----- Intron Chain level -----

Sensitivity: 1 (1)

Specificity: 1 (1)

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

Sensitivity: 1 (0.993939)

Specificity: 1 (0.993939)

Missing exons: 0/872 (0)

Missing introns: 3/756 (0.00396825)

Novel exons: 0/872 (0)

Novel introns: 0/756 (0)

Summary statistics for: B2

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

Experiment: 107544 features

Synthetic: 1616 features

Reference: 162 exons

Reference: 1028 introns

*** The following statistics are computed for exact and fuzzy.

*** The fuzzy level is 10 nucleotides.

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

Sensitivity: 1 (1)

Specificity: 1 (1)

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

Sensitivity: 0.996032 (0.996032)

Specificity: 0.996032 (0.996032)

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

Sensitivity: 1

Specificity: 1

----- Intron Chain level -----

Sensitivity: 1 (1)

Specificity: 1 (1)

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

Sensitivity: 1 (0.993939)

Specificity: 1 (0.993939)

Missing exons: 0/872 (0)

Missing introns: 3/756 (0.00396825)

Novel exons: 0/872 (0)

Novel introns: 0/756 (0)

Summary statistics for: B3

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

Experiment: 107544 features
Synthetic: 1616 features

Reference: 162 exons
Reference: 1028 introns

*** The following statistics are computed for exact and fuzzy.

*** The fuzzy level is 10 nucleotides.

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

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

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

Sensitivity: 0.996032 (0.996032)
Specificity: 0.996032 (0.996032)

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

Sensitivity: 1
Specificity: 1

----- Intron Chain level -----

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

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

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

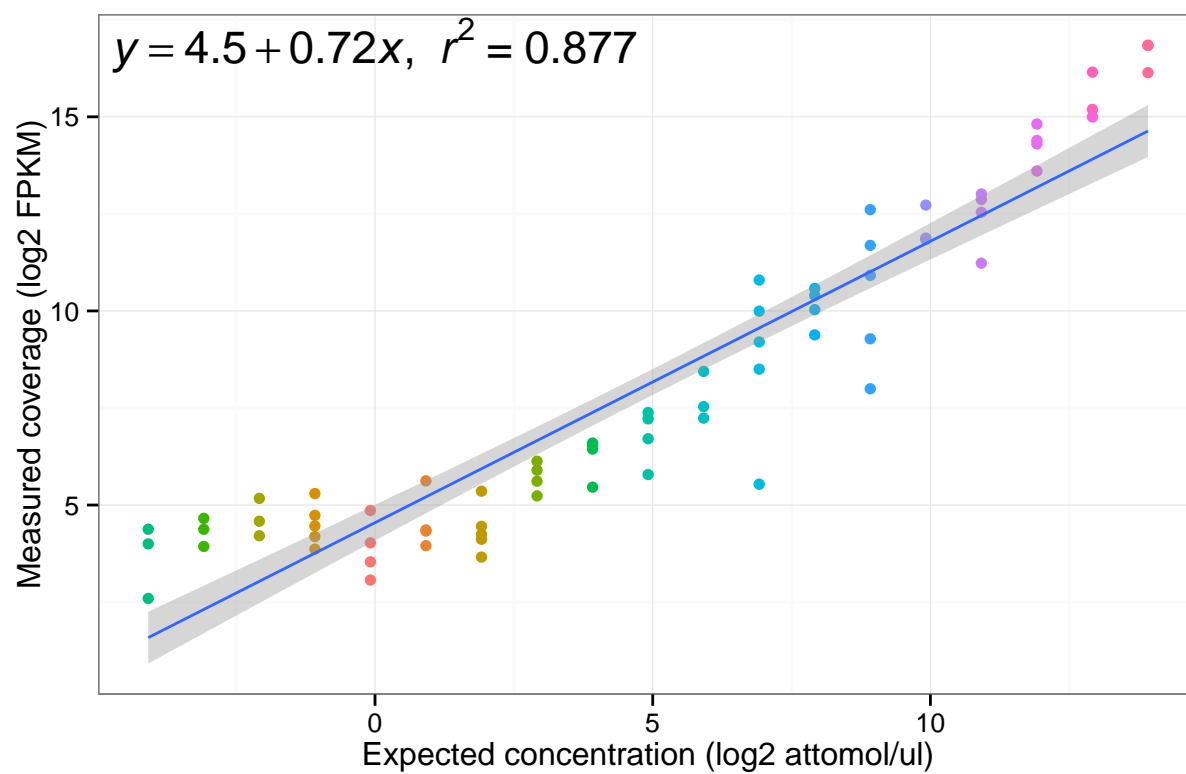
Missing exons: 0/872 (0)
Missing introns: 3/756 (0.00396825)

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

TransQuin Expression (Gene)

Expression summary statistics for: A1

Expression scatter plot for: A1



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

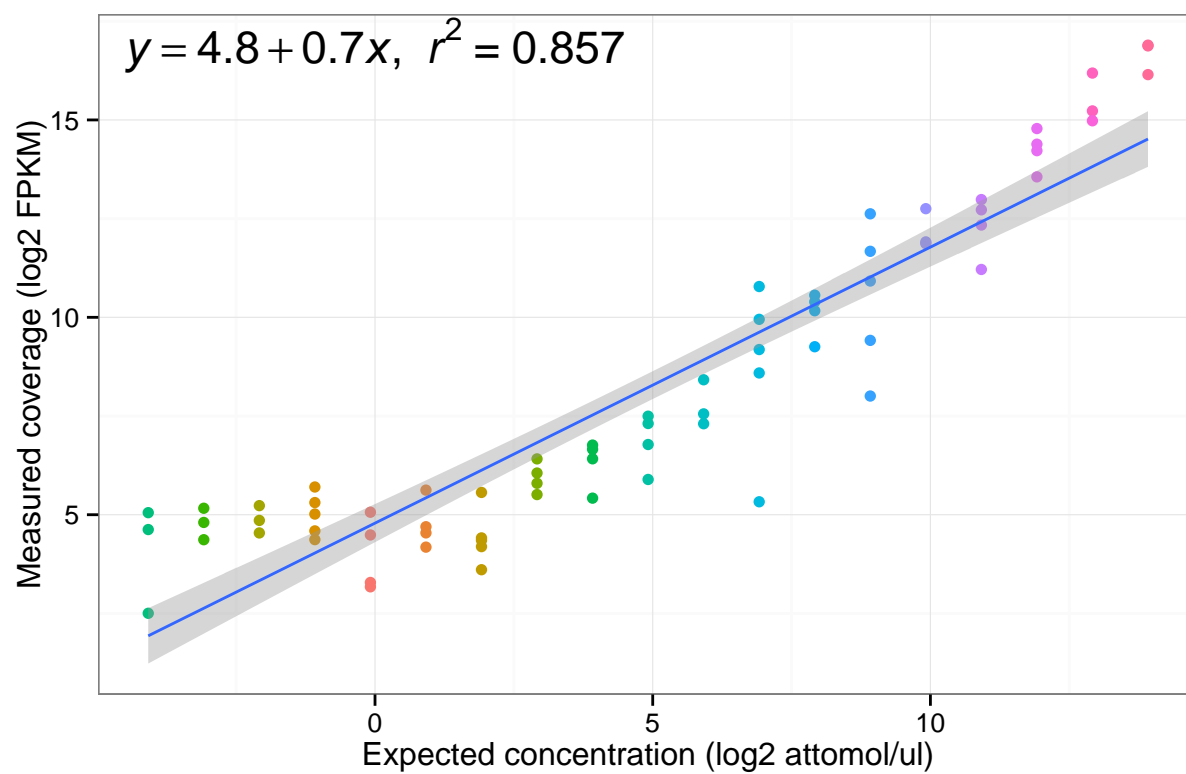
P-value: 0

SSM: 967.772, DF: 1

SSE: 161.616, DF: 71

SST: 1129.39, DF: 72

Expression scatter plot for: A2



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

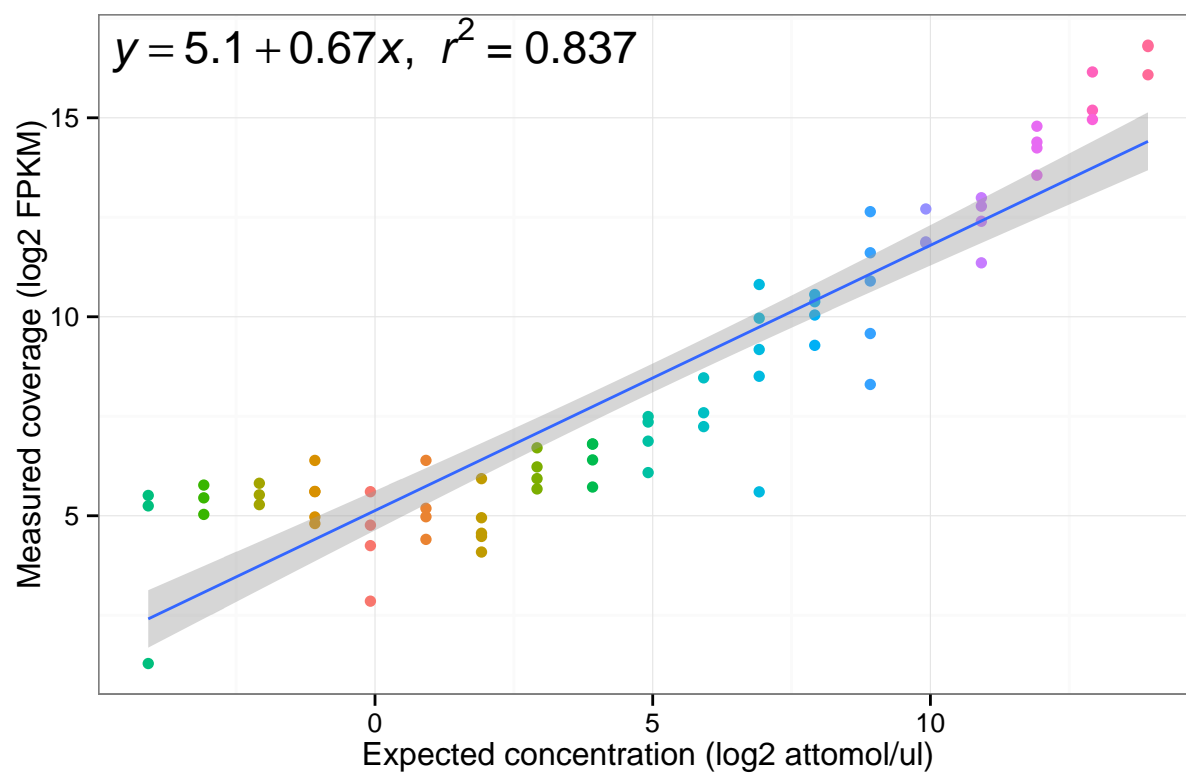
P-value: 0

SSM: 879.802, DF: 1

SSE: 171.015, DF: 71

SST: 1050.82, DF: 72

Expression scatter plot for: A3



Expression summary statistics for: B1

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

Experiment: 60568 gene

Synthetic: 74 gene

Reference: 76 gene

Detected: 5.19759 gene

*** Detection Limits

Break: 1.88828 (R1_72)

Left: $5.19759 + 0.42932x$ ($R^2 = 0.278885$)

Right: $2.76376 + 0.857773x$ ($R^2 = 0.701784$)

*** Statistics for linear regression

Correlation: 0.87057

Slope: 3.70819

R2: 0.757893

F-statistic: 219.128

P-value: 0

SSM: $3.24184e+10$, DF: 1

SSE: $1.0356e+10$, DF: 70

SST: $4.27744e+10$, DF: 71

*** Statistics for linear regression (log2 scale)

Correlation: 0.84233

Slope: 0.652163

R2: 0.709519

F-statistic: 170.98

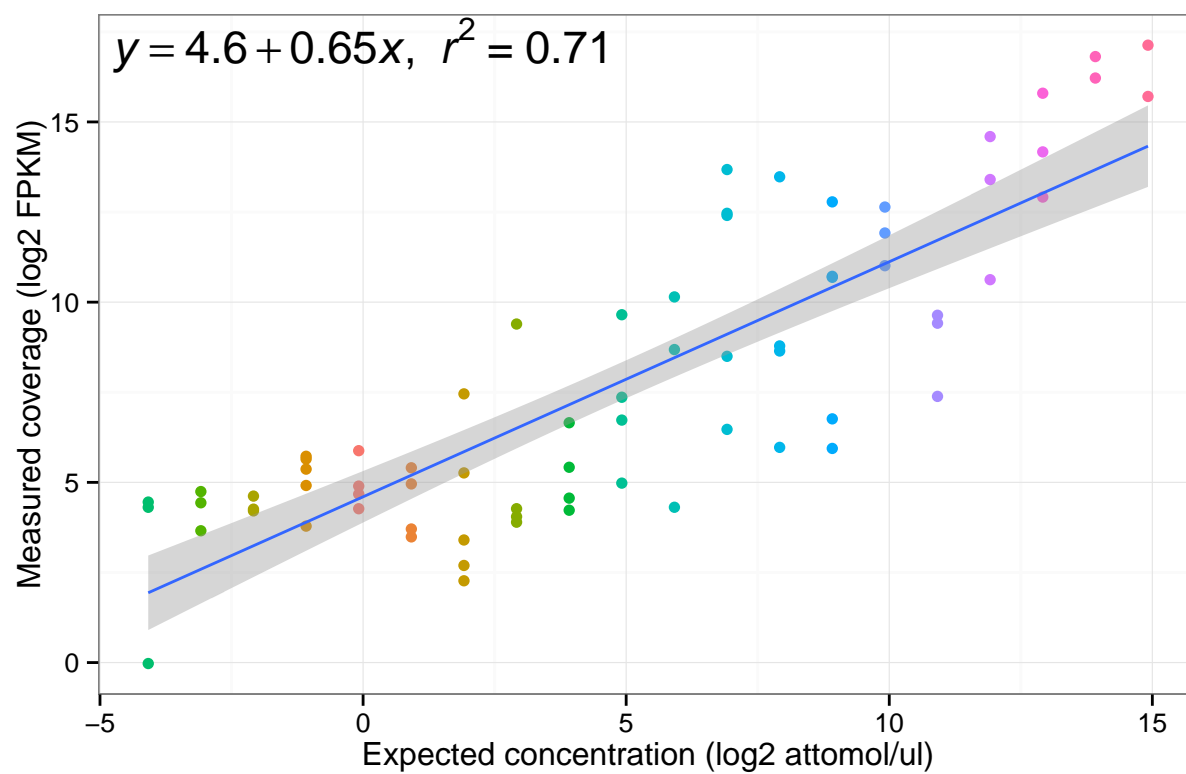
P-value: 0

SSM: 856.494, DF: 1

SSE: 350.653, DF: 70

SST: 1207.15, DF: 71

Expression scatter plot for: B1



Expression summary statistics for: B2

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

Experiment: 60570 gene

Synthetic: 74 gene

Reference: 76 gene

Detected: 5.22081 gene

*** Detection Limits

Break: 1.88828 (R1_72)

Left: $5.22081 + 0.303379x$ ($R^2 = 0.28516$)

Right: $2.85593 + 0.848121x$ ($R^2 = 0.700146$)

*** Statistics for linear regression

Correlation: 0.866031

Slope: 3.64019

R2: 0.750009

F-statistic: 210.01

P-value: 0

SSM: $3.12402e+10$, DF: 1

SSE: $1.04129e+10$, DF: 70

SST: $4.16532e+10$, DF: 71

*** Statistics for linear regression (log2 scale)

Correlation: 0.836934

Slope: 0.63197

R2: 0.700459

F-statistic: 163.691

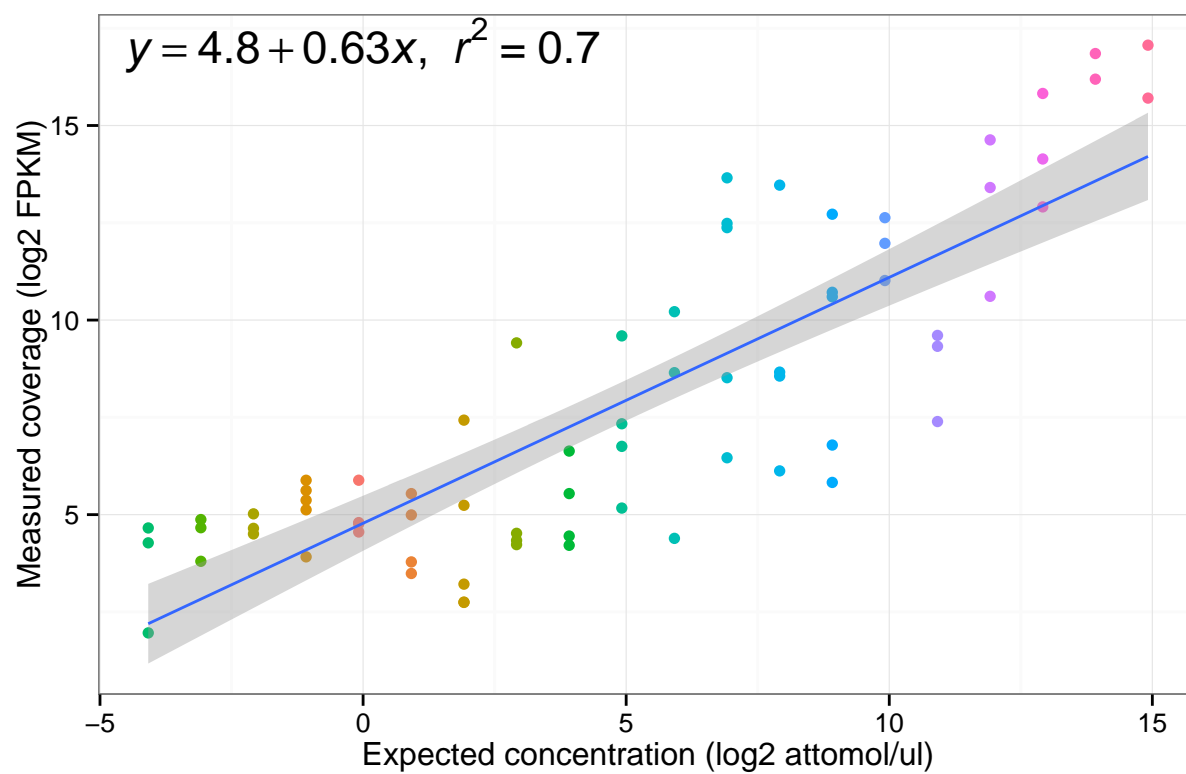
P-value: 0

SSM: 804.275, DF: 1

SSE: 343.936, DF: 70

SST: 1148.21, DF: 71

Expression scatter plot for: B2



Expression summary statistics for: B3

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

Experiment: 60570 gene

Synthetic: 74 gene

Reference: 76 gene

Detected: 5.22081 gene

*** Detection Limits

Break: 1.88828 (R1_72)

Left: $5.22081 + 0.303379x$ ($R^2 = 0.28516$)

Right: $2.85593 + 0.848121x$ ($R^2 = 0.700146$)

*** Statistics for linear regression

Correlation: 0.866031

Slope: 3.64019

R2: 0.750009

F-statistic: 210.01

P-value: 0

SSM: $3.12402e+10$, DF: 1

SSE: $1.04129e+10$, DF: 70

SST: $4.16532e+10$, DF: 71

*** Statistics for linear regression (log2 scale)

Correlation: 0.836934

Slope: 0.63197

R2: 0.700459

F-statistic: 163.691

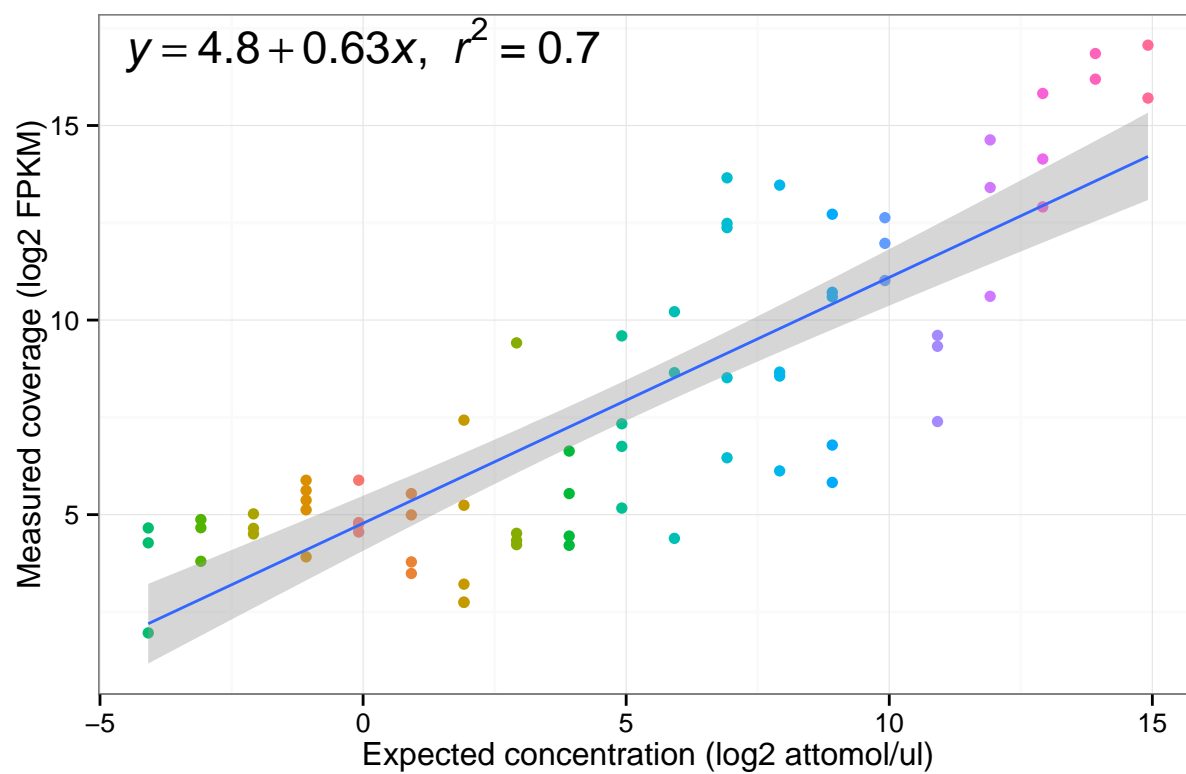
P-value: 0

SSM: 804.275, DF: 1

SSE: 343.936, DF: 70

SST: 1148.21, DF: 71

Expression scatter plot for: B3



TransQuin Expression (Isoform)

Expression summary statistics for: A1

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

Experiment: 100769 isoform
Synthetic: 164 isoform

Reference: 162 isoform
Detected: 1.25307 isoform

*** Detection Limits

Break: 3.5544 (R1_32_1)

Left: $1.25307 + 0.157653x$ ($R^2 = 0.0887965$)
Right: $0.825739 + 1.06985x$ ($R^2 = 0.865753$)

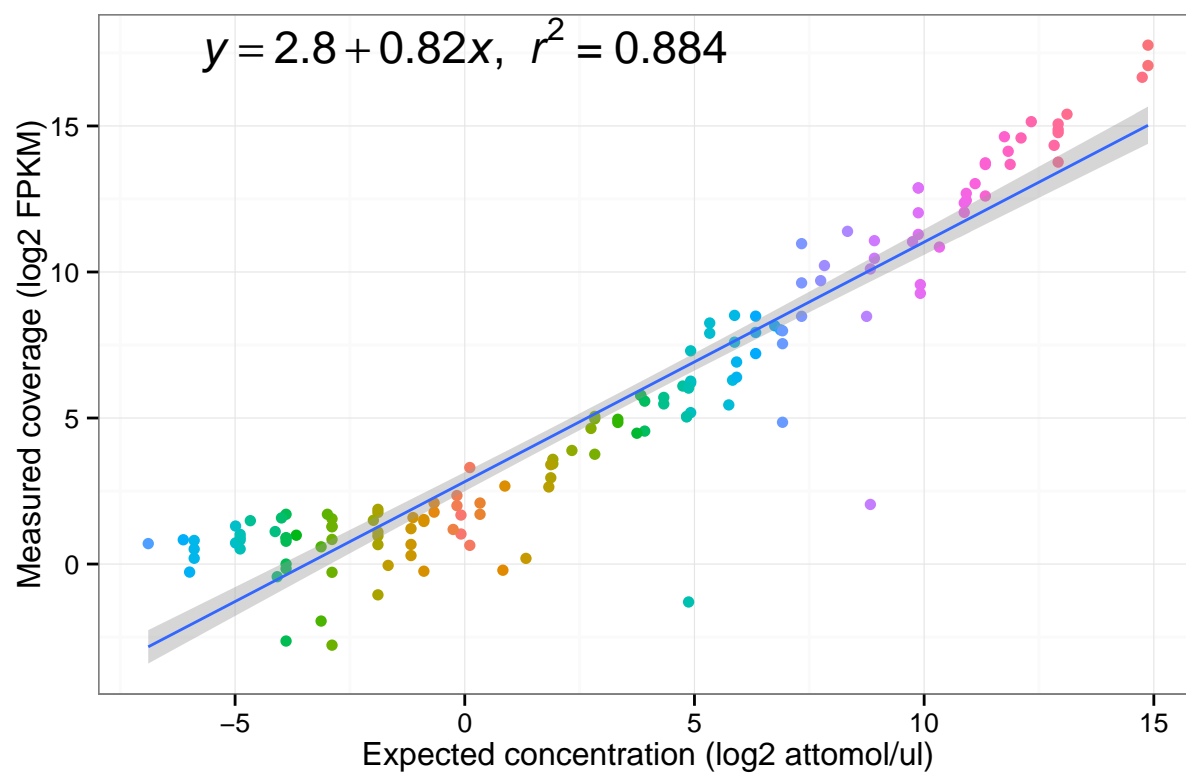
*** Statistics for linear regression

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

*** Statistics for linear regression (log2 scale)

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

Expression scatter plot for: A1



Expression summary statistics for: A2

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

Experiment: 100769 isoform
Synthetic: 164 isoform

Reference: 162 isoform
Detected: 1.25307 isoform

*** Detection Limits

Break: 3.5544 (R1_32_1)

Left: $1.25307 + 0.157653x$ ($R^2 = 0.0887965$)
Right: $0.825739 + 1.06985x$ ($R^2 = 0.865753$)

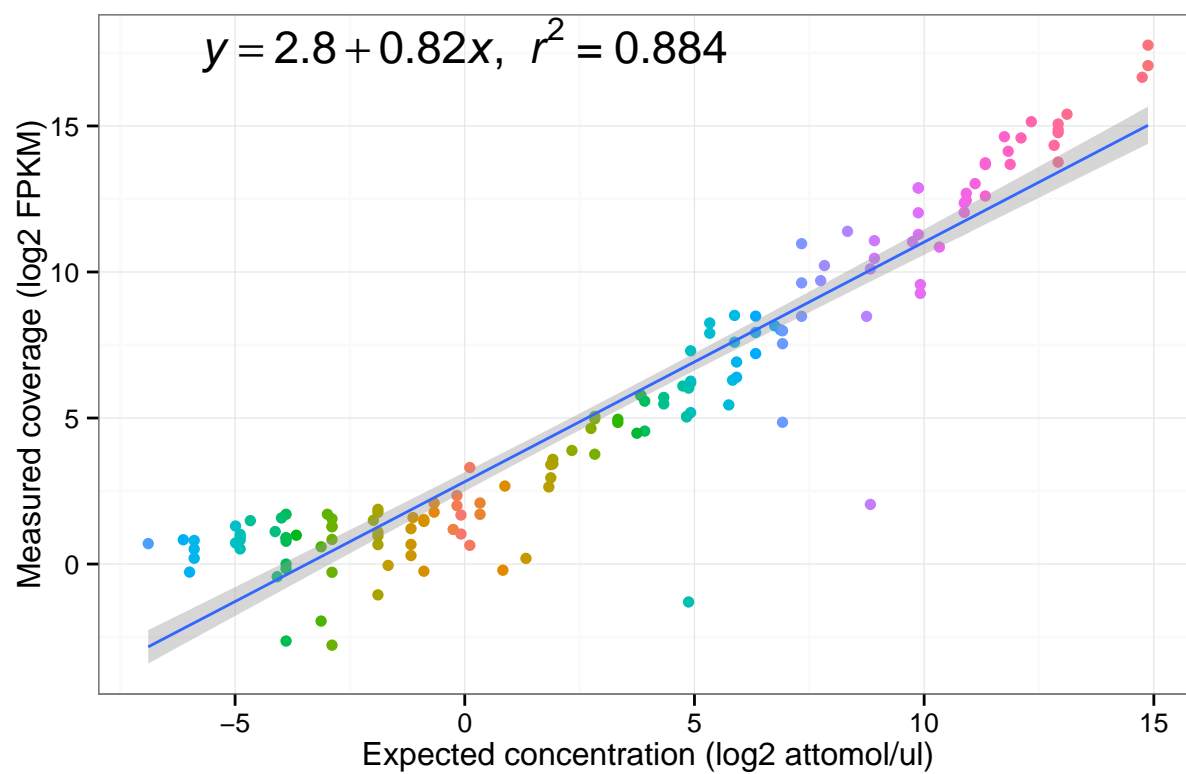
*** Statistics for linear regression

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

*** Statistics for linear regression (log2 scale)

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

Expression scatter plot for: A2



Expression summary statistics for: A3

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

Experiment: 100769 isoform
Synthetic: 164 isoform

Reference: 162 isoform
Detected: 1.25307 isoform

*** Detection Limits

Break: 3.5544 (R1_32_1)

Left: $1.25307 + 0.157653x$ ($R^2 = 0.0887965$)
Right: $0.825739 + 1.06985x$ ($R^2 = 0.865753$)

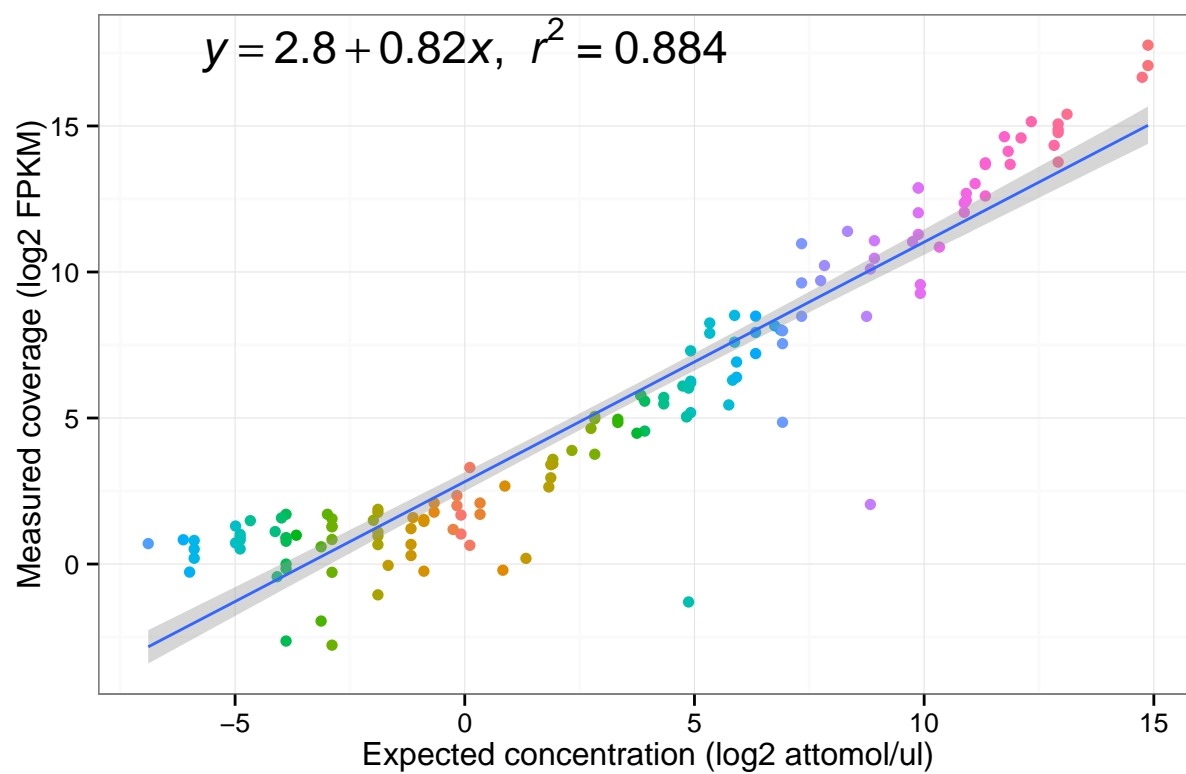
*** Statistics for linear regression

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

*** Statistics for linear regression (log2 scale)

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

Expression scatter plot for: A3



Expression summary statistics for: B1

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

Experiment: 100769 isoform
Synthetic: 164 isoform

Reference: 162 isoform
Detected: 1.25307 isoform

*** Detection Limits

Break: 3.5544 (R1_32_1)

Left: $1.25307 + 0.157653x$ ($R^2 = 0.0887965$)

Right: $0.825739 + 1.06985x$ ($R^2 = 0.865753$)

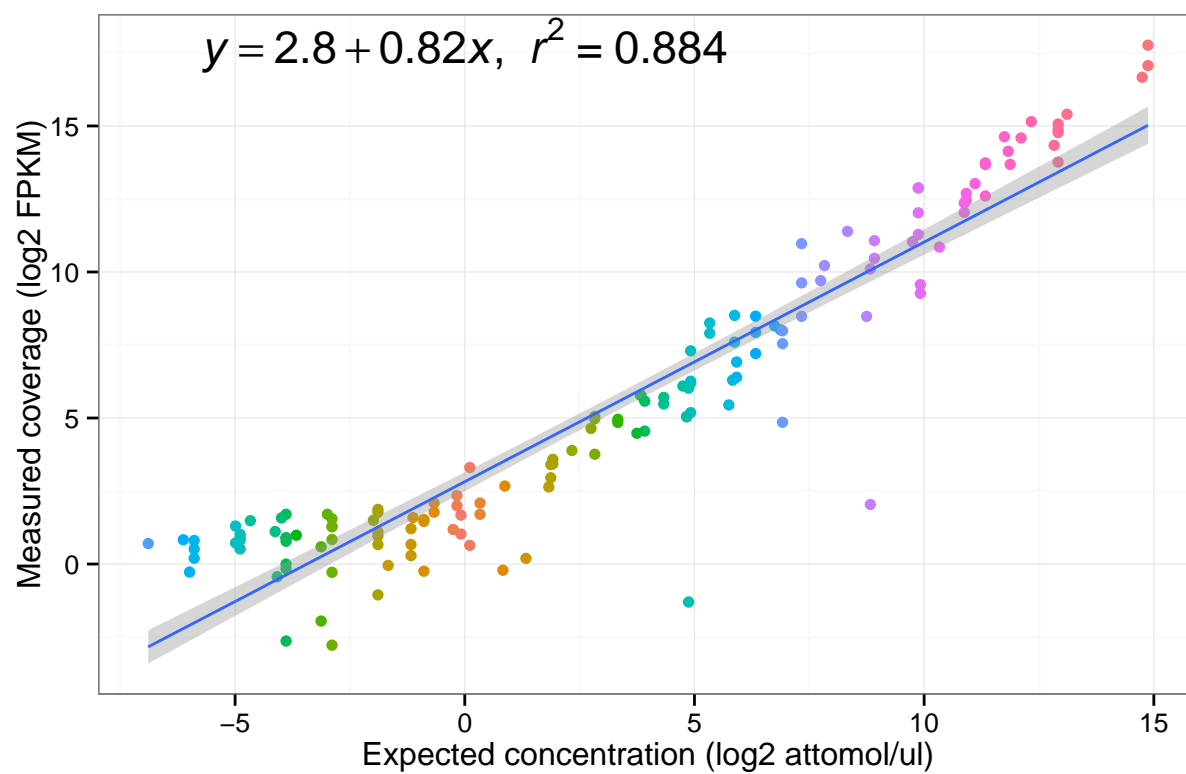
*** Statistics for linear regression

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

*** Statistics for linear regression (log2 scale)

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

Expression scatter plot for: B1



Expression summary statistics for: B2

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

Experiment: 100769 isoform
Synthetic: 164 isoform

Reference: 162 isoform
Detected: 1.25307 isoform

*** Detection Limits

Break: 3.5544 (R1_32_1)

Left: $1.25307 + 0.157653x$ ($R^2 = 0.0887965$)

Right: $0.825739 + 1.06985x$ ($R^2 = 0.865753$)

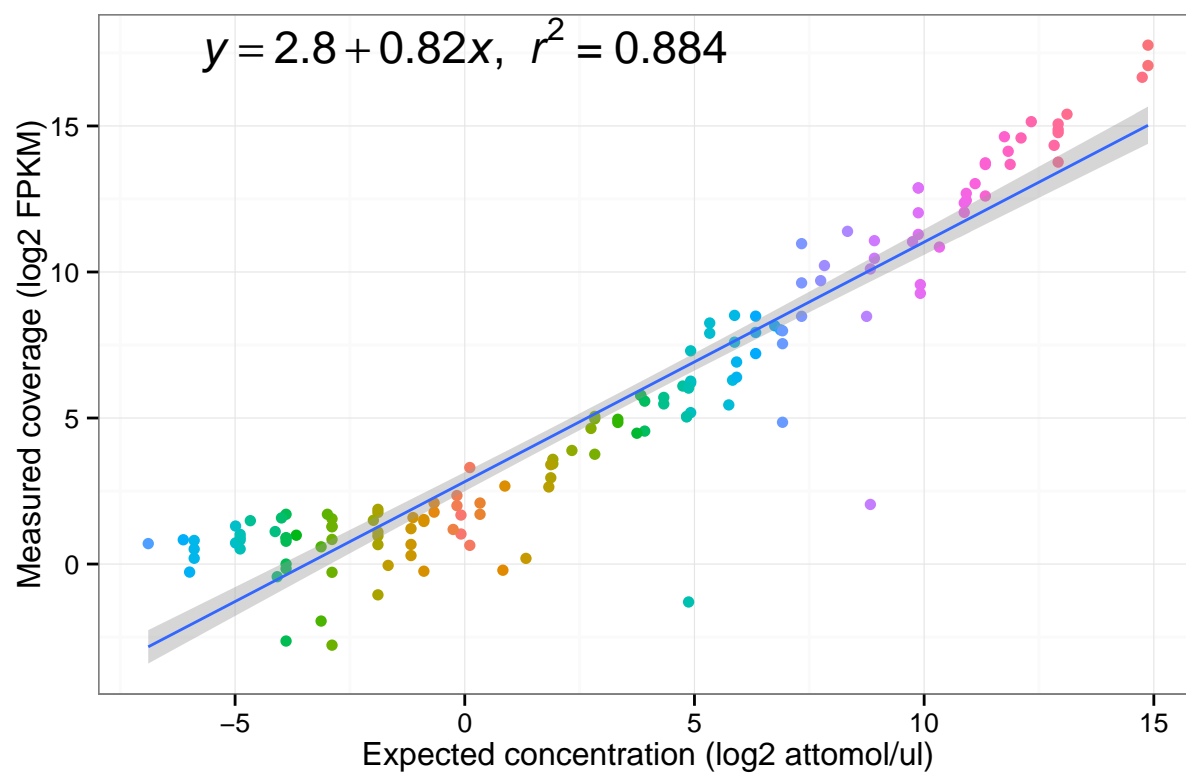
*** Statistics for linear regression

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

*** Statistics for linear regression (log2 scale)

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

Expression scatter plot for: B2



Expression summary statistics for: B3

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

Experiment: 100769 isoform
Synthetic: 164 isoform

Reference: 162 isoform
Detected: 1.25307 isoform

*** Detection Limits

Break: 3.5544 (R1_32_1)

Left: $1.25307 + 0.157653x$ ($R^2 = 0.0887965$)
Right: $0.825739 + 1.06985x$ ($R^2 = 0.865753$)

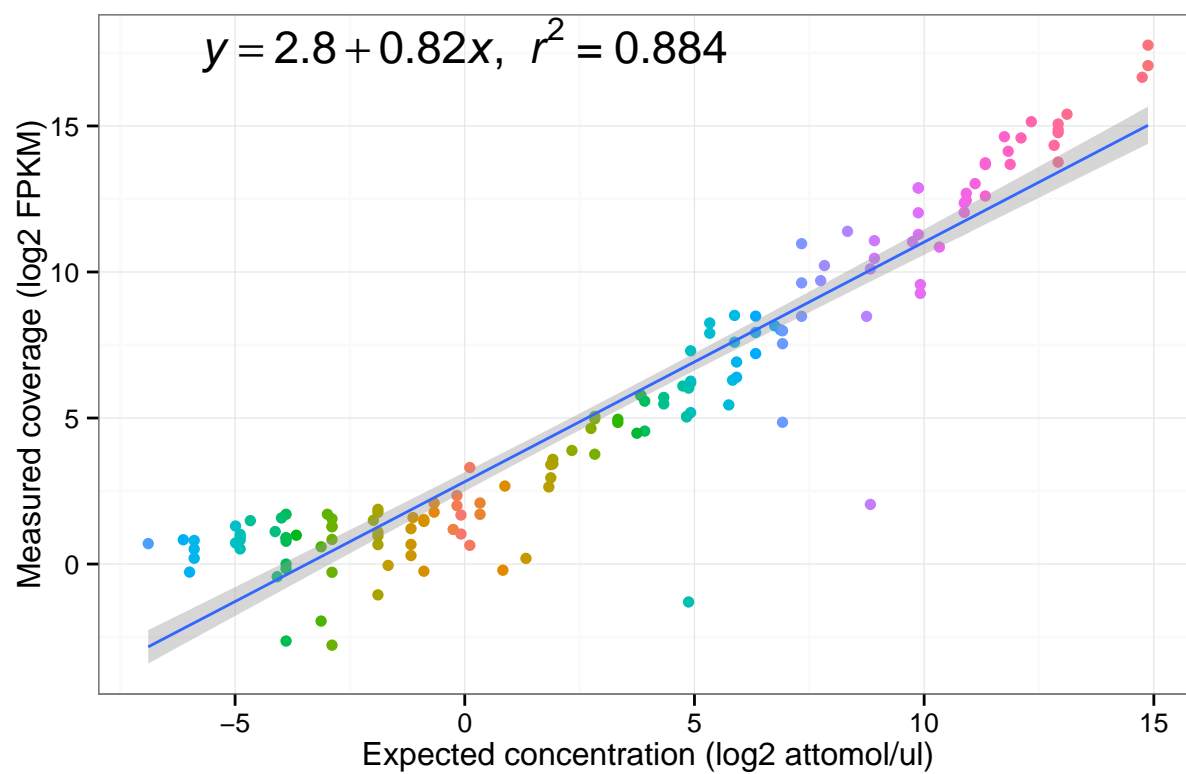
*** Statistics for linear regression

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

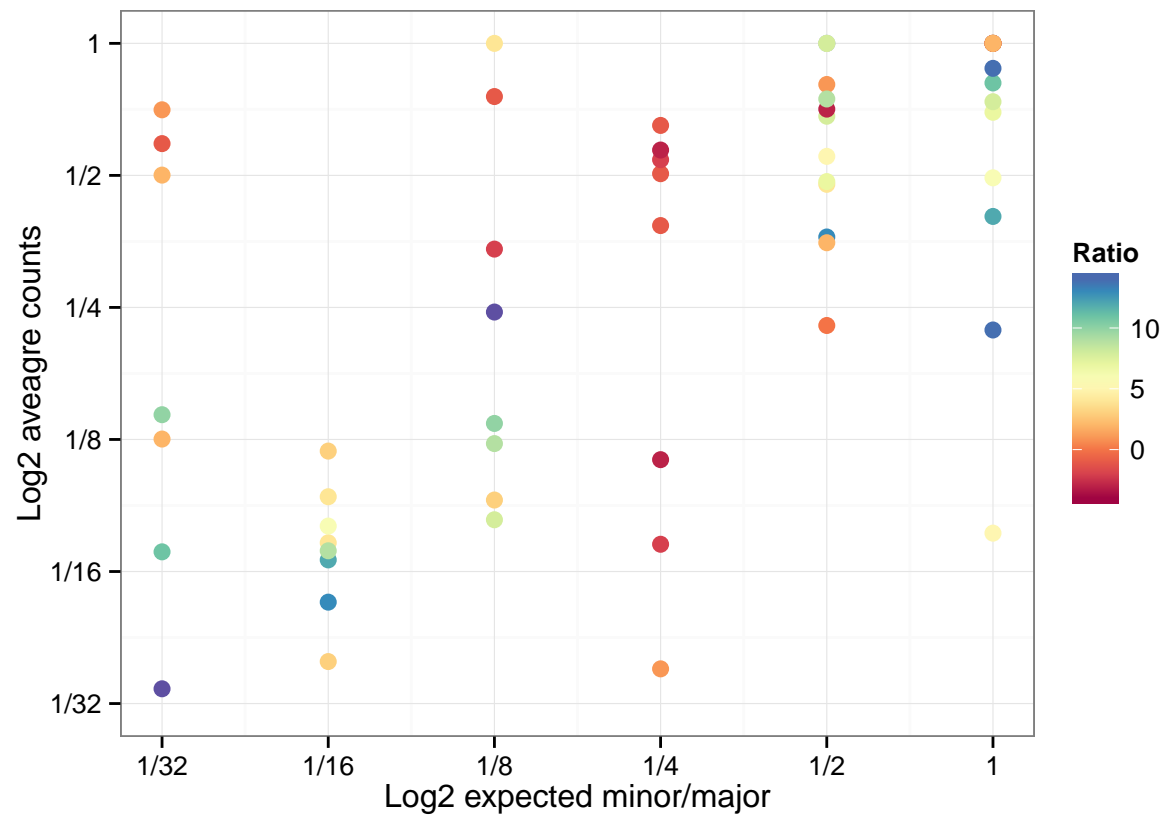
*** Statistics for linear regression (log2 scale)

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

Expression scatter plot for: B3



Minor/Major plot



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)

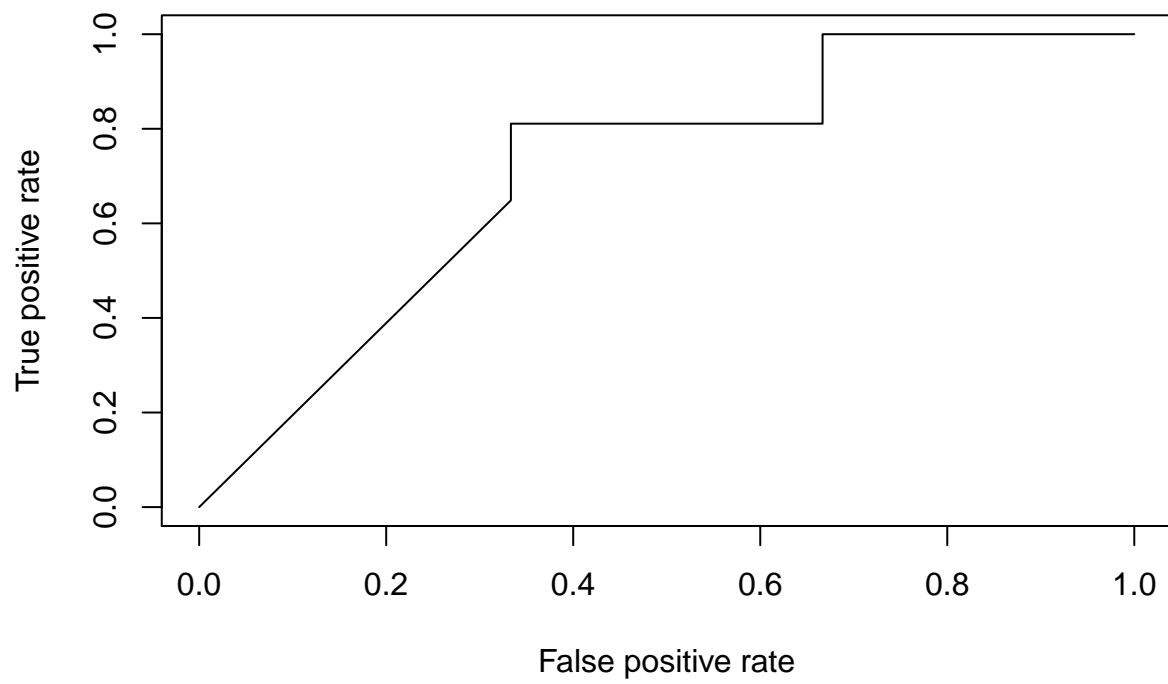
*** Statistics for linear regression

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

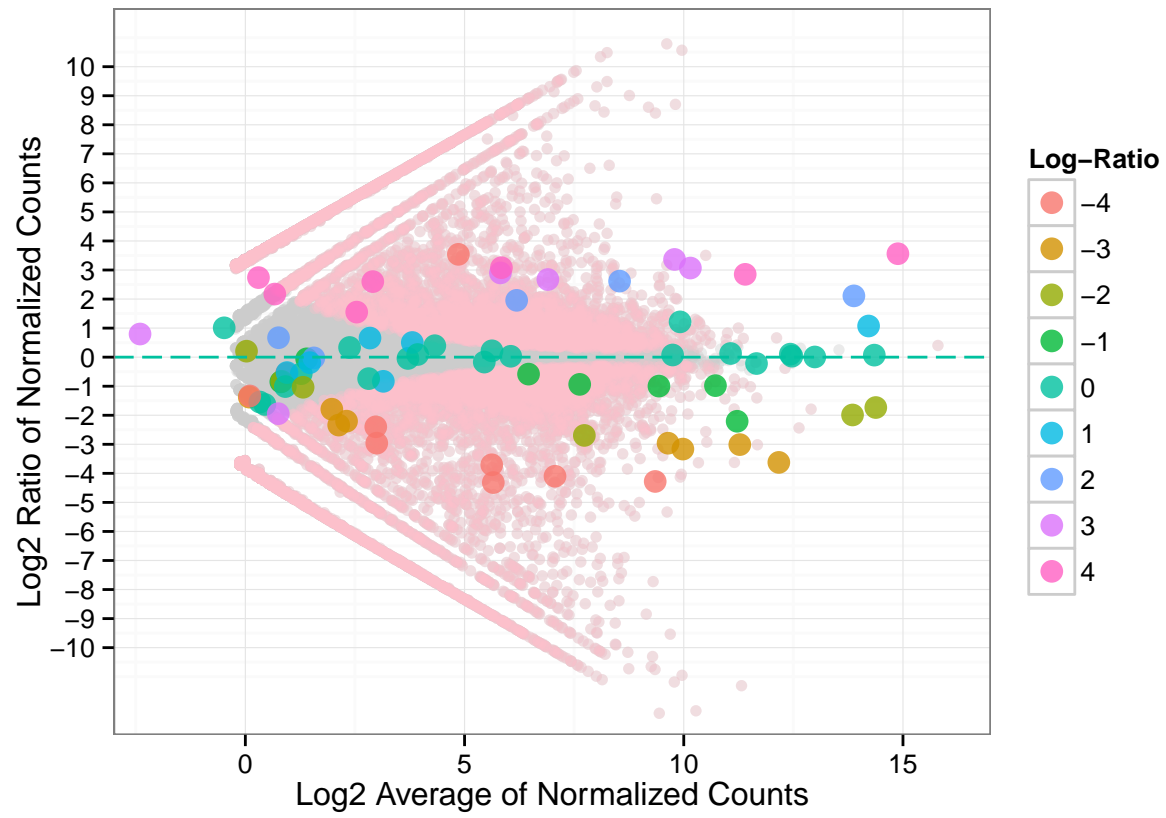
*** Statistics for linear regression (log2 scale)

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

