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Overview of BioCreative II gene normalization

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Scores from all gene normalization runs

Team_Run	Micro-Average			True Positive	False Positive	False Negative	Macro-Average		
	Recall	Precision	F-measure				Recall	Precision	F-measure
Maximum	0.875	0.841	0.810	687	840	541	0.876	0.898	0.811
Top									
Quartile	0.767	0.782	0.770	602	271	282	0.817	0.807	0.754
Median	0.750	0.797	0.773	582	149	227	0.832	0.784	0.759
3rd									
Quartile	0.732	0.735	0.717	575	198	211	0.775	0.773	0.700
Minimum	0.311	0.361	0.370	244	102	98	0.474	0.316	0.342
T004_1	0.734	0.841	0.784	576	109	209	0.876	0.776	0.775
T004_2	0.743	0.829	0.784	583	120	202	0.865	0.784	0.777
T004_3	0.748	0.820	0.782	587	129	198	0.854	0.787	0.772
T006_1	0.601	0.767	0.674	472	143	313	0.794	0.700	0.686
T006_2	0.606	0.767	0.677	476	145	309	0.787	0.705	0.685
T006_3	0.782	0.597	0.677	614	414	171	0.629	0.808	0.666
T007_1	0.707	0.731	0.719	555	204	230	0.755	0.728	0.687
T007_2	0.703	0.746	0.724	552	188	233	0.770	0.725	0.694
T007_3	0.699	0.749	0.723	549	184	236	0.770	0.717	0.688
T013_1	0.768	0.833	0.799	603	121	182	0.848	0.803	0.779
T013_2	0.730	0.835	0.779	573	113	212	0.856	0.770	0.749
T013_3	0.803	0.779	0.790	630	179	155	0.816	0.829	0.773
T014_1	0.485	0.762	0.593	381	119	404	0.783	0.575	0.584
T014_2	0.483	0.471	0.477	379	425	406	0.474	0.517	0.419
T014_3	0.655	0.479	0.553	514	559	271	0.543	0.701	0.555
T017_1	0.708	0.720	0.714	556	216	229	0.764	0.754	0.709
T017_2	0.641	0.806	0.714	503	121	282	0.845	0.701	0.710
T017_3	0.757	0.631	0.688	594	348	191	0.671	0.804	0.688
T030_1	0.661	0.716	0.687	519	206	266	0.736	0.695	0.649
T030_2	0.666	0.702	0.684	523	222	262	0.729	0.698	0.645
T030_3	0.707	0.580	0.637	555	402	230	0.616	0.737	0.617
T034_1	0.815	0.792	0.804	640	168	145	0.815	0.841	0.782

T034_2	0.847	0.723	0.780	665	255	120	0.736	0.870	0.758
T034_3	0.789	0.739	0.763	619	219	166	0.754	0.821	0.740
T036_1	0.713	0.520	0.602	560	516	225	0.562	0.764	0.595
T042_1	0.833	0.789	0.810	654	175	131	0.836	0.866	0.811
T042_2	0.875	0.496	0.633	687	699	98	0.567	0.898	0.649
T042_3	0.725	0.707	0.716	569	236	216	0.732	0.760	0.706
T058_1	0.429	0.361	0.392	337	596	448	0.570	0.476	0.382
T058_2	0.415	0.375	0.394	326	543	459	0.611	0.475	0.398
T058_3	0.331	0.419	0.370	260	361	525	0.671	0.371	0.342
T101_1	0.762	0.751	0.756	598	198	187	0.771	0.808	0.741
T101_2	0.743	0.801	0.771	583	145	202	0.820	0.789	0.755
T101_3	0.734	0.804	0.767	576	140	209	0.820	0.779	0.749
T102_1	0.415	0.585	0.486	326	231	459	0.660	0.420	0.431
T102_2	0.521	0.552	0.536	409	332	376	0.619	0.535	0.494
T102_3	0.790	0.425	0.552	620	840	165	0.483	0.814	0.559
T104_1	0.743	0.807	0.774	583	139	202	0.840	0.785	0.773
T104_2	0.758	0.779	0.768	595	169	190	0.804	0.803	0.763
T107_1	0.740	0.784	0.761	581	160	204	0.818	0.776	0.739
T108_1	0.796	0.655	0.719	625	329	160	0.685	0.826	0.708
T108_2	0.782	0.690	0.733	614	276	171	0.723	0.814	0.720
T108_3	0.749	0.726	0.737	588	222	197	0.761	0.785	0.724
T109_1	0.824	0.743	0.781	647	224	138	0.780	0.848	0.775
T109_2	0.792	0.764	0.778	622	192	163	0.806	0.815	0.767
T109_3	0.769	0.790	0.779	604	161	181	0.817	0.806	0.764
T110_1	0.629	0.783	0.698	494	137	291	0.830	0.691	0.685
T110_2	0.641	0.738	0.686	503	179	282	0.794	0.708	0.674
T110_3	0.622	0.732	0.672	488	179	297	0.785	0.698	0.669
T111_1	0.327	0.652	0.436	257	137	528	0.790	0.331	0.362
T111_2	0.311	0.705	0.431	244	102	541	0.828	0.316	0.357
T111_3	0.664	0.717	0.689	521	206	264	0.731	0.706	0.664
T113_1	0.745	0.723	0.734	585	224	200	0.779	0.795	0.733
T113_2	0.761	0.752	0.756	597	197	188	0.782	0.810	0.745