Genomics Track results, categorization task — University of Wisconsin

allele subtask

Run	TP	FP	FN	Precision	Recall	F beta	Utility Factor	Raw	Max	Normalized
Afull	293	785	39	0.2718	0.8825	0.4156	17.00	4196	5644	0.7434
Ameta	297	683	35	0.3031	0.8946	0.4527	17.00	4366	5644	0.7736
Apars	308	876	24	0.2601	0.9277	0.4063	17.00	4360	5644	0.7725

expression subtask

Run	TP	FP	FN	Precision	Recall	F beta	Utility Factor	Raw	Max	Normalized
Efull	82	1208	23	0.0636	0.7810	0.1176	64.00	4040	6720	0.6012
Emeta	77	528	28	0.1273	0.7333	0.2169	64.00	4400	6720	0.6548
Epars	93	1044	12	0.0818	0.8857	0.1498	64.00	4908	6720	0.7304

go subtask

Run	TP	FP	FN	Precision	Recall	F beta	Utility Factor	Raw	Max	Normalized
Gfull	362	1539	156	0.1904	0.6988	0.2993	11.00	2443	5698	0.4287
Gmeta	411	2022	107	0.1689	0.7934	0.2785	11.00	2499	5698	0.4386
Gpars	393	1718	125	0.1862	0.7587	0.2990	11.00	2605	5698	0.4572

tumor subtask

Run	TP	FP	FN	Precision	Recall	F beta	Utility Factor	Raw	Max	Normalized
Tfull	18	388	2	0.0443	0.9000	0.0845	231.00	3770	4620	0.8160
Tmeta	17	308	3	0.0523	0.8500	0.0986	231.00	3619	4620	0.7833
Tpars	19	581	1	0.0317	0.9500	0.0613	231.00	3808	4620	0.8242