Genomics Track results, categorization task — The Chinese University of Hong Kong

allele subtask

Run	TP	FP	FN	Precision	Recall	F beta	Utility Factor	Raw	Max	Normalized
cuhkrun1	311	644	21	0.3257	0.9367	0.4833	17.00	4643	5644	0.8226
cuhkrun2A	318	641	14	0.3316	0.9578	0.4926	17.00	4765	5644	0.8443
cuhkrun3A	317	604	15	0.3442	0.9548	0.5060	17.00	4785	5644	0.8478

expression subtask

Run	TP	FP	FN	Precision	Recall	F beta	Utility Factor	Raw	Max	Normalized
cuhkrun1E	96	762	9	0.1119	0.9143	0.1994	64.00	5382	6720	0.8009
cuhkrun2E	98	680	7	0.1260	0.9333	0.2220	64.00	5592	6720	0.8321
cuhkrun3E	96	552	9	0.1481	0.9143	0.2550	64.00	5592	6720	0.8321

go subtask

Run	TP	FP	FN	Precision	Recall	F beta	Utility Factor	Raw	Max	Normalized
cuhkrun1G	318	857	200	0.2706	0.6139	0.3757	11.00	2641	5698	0.4635
cuhkrun2G	337	1261	181	0.2109	0.6506	0.3185	11.00	2446	5698	0.4293
cuhkrun3G	292	1477	226	0.1651	0.5637	0.2554	11.00	1735	5698	0.3045

tumor subtask

Run	TP	FP	FN	Precision	Recall	F beta	Utility Factor	Raw	Max	Normalized
cuhkrun1T	18	216	2	0.0769	0.9000	0.1417	231.00	3942	4620	0.8532
cuhkrun2T	8	290	12	0.0268	0.4000	0.0503	231.00	1558	4620	0.3372
cuhkrun3T	20	449	0	0.0426	1.0000	0.0818	231.00	4171	4620	0.9028