

Additional File S4:

Concordance with the Illumina BovineHD BeadChip® (n=48)

a) Non-reference sensitivity (NRS) for single nucleotide variants identified using Platypus, Samtools, UnifiedGenotyper and Haplotype Caller (single and multi sample variant identification) using variants identified with the Illumina BovineHD BeadChip® as a gold standard (BTA1-BTA29)

Animal	Single sample variant identification												Multi sample variant identification				
	Platypus			Platypus (Primitives)			Samtools			UnifiedGenotyper			Haplotype Caller	Platypus	Platypus (Primitives)	Samtools	Unified Genotyper
	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR+BQSR	IR+BQSR	IR+BQSR	IR+BQSR
HD_1	0.909	0.914	0.914	0.919	0.978	0.978	0.972	0.973	0.983	0.979	0.985	0.985	0.981	0.934	0.949	0.974	0.981
HD_2	0.852	0.866	0.866	0.911	0.925	0.925	0.945	0.948	0.948	0.920	0.945	0.945	0.976	0.930	0.950	0.974	0.976
HD_3	0.853	0.869	0.869	0.912	0.928	0.928	0.947	0.952	0.952	0.921	0.948	0.948	0.977	0.930	0.950	0.975	0.977
HD_4	0.844	0.859	0.859	0.902	0.917	0.917	0.939	0.943	0.943	0.913	0.938	0.938	0.975	0.929	0.949	0.974	0.975
HD_5	0.840	0.859	0.859	0.898	0.916	0.916	0.947	0.953	0.953	0.921	0.945	0.945	0.977	0.930	0.950	0.975	0.977
HD_6	0.863	0.876	0.876	0.922	0.936	0.936	0.948	0.952	0.952	0.932	0.952	0.952	0.977	0.931	0.950	0.975	0.977
HD_7	0.817	0.842	0.842	0.870	0.897	0.897	0.916	0.925	0.925	0.883	0.922	0.922	0.969	0.925	0.945	0.968	0.969
HD_8	0.860	0.877	0.877	0.919	0.937	0.937	0.951	0.956	0.956	0.928	0.953	0.953	0.977	0.930	0.950	0.975	0.977
HD_9	0.860	0.875	0.875	0.919	0.935	0.935	0.957	0.961	0.961	0.937	0.955	0.955	0.978	0.931	0.951	0.976	0.978
HD_10	0.885	0.898	0.898	0.947	0.959	0.959	0.969	0.972	0.972	0.959	0.971	0.972	0.980	0.932	0.952	0.978	0.980
HD_11	0.856	0.874	0.874	0.915	0.934	0.934	0.951	0.956	0.956	0.927	0.952	0.952	0.977	0.931	0.950	0.976	0.977
HD_12	0.880	0.894	0.894	0.941	0.955	0.955	0.965	0.969	0.969	0.953	0.968	0.968	0.978	0.932	0.952	0.978	0.979
HD_13	0.868	0.886	0.886	0.928	0.946	0.946	0.957	0.962	0.962	0.940	0.961	0.961	0.978	0.932	0.951	0.977	0.978
HD_14	0.876	0.890	0.890	0.936	0.951	0.951	0.962	0.966	0.966	0.947	0.965	0.965	0.979	0.932	0.951	0.978	0.979
HD_15	0.877	0.892	0.892	0.938	0.953	0.953	0.963	0.967	0.967	0.949	0.966	0.966	0.980	0.932	0.952	0.978	0.980
HD_16	0.860	0.876	0.876	0.919	0.935	0.935	0.954	0.959	0.959	0.934	0.954	0.954	0.978	0.931	0.951	0.977	0.979
HD_17	0.843	0.863	0.863	0.901	0.921	0.921	0.944	0.950	0.950	0.916	0.944	0.944	0.976	0.930	0.949	0.975	0.976
HD_18	0.843	0.861	0.861	0.900	0.919	0.919	0.942	0.947	0.947	0.915	0.943	0.943	0.977	0.929	0.949	0.975	0.977
HD_19	0.845	0.863	0.863	0.903	0.922	0.922	0.943	0.948	0.948	0.917	0.944	0.944	0.976	0.930	0.949	0.975	0.976
HD_20	0.866	0.880	0.880	0.925	0.940	0.940	0.958	0.963	0.963	0.940	0.959	0.959	0.978	0.931	0.951	0.977	0.979
HD_21	0.888	0.893	0.893	0.949	0.954	0.954	0.967	0.970	0.971	0.955	0.968	0.968	0.980	0.933	0.952	0.979	0.980
HD_22	0.886	0.895	0.895	0.947	0.956	0.956	0.970	0.972	0.972	0.960	0.971	0.971	0.980	0.933	0.952	0.979	0.980
HD_23	0.840	0.859	0.859	0.897	0.916	0.916	0.940	0.945	0.945	0.911	0.940	0.940	0.975	0.930	0.949	0.974	0.976
HD_24	0.883	0.892	0.892	0.942	0.952	0.952	0.967	0.971	0.971	0.956	0.968	0.968	0.978	0.932	0.951	0.977	0.979
HD_25	0.883	0.893	0.893	0.944	0.954	0.954	0.968	0.972	0.972	0.957	0.969	0.969	0.980	0.933	0.952	0.979	0.981
HD_26	0.882	0.893	0.893	0.943	0.955	0.955	0.967	0.971	0.971	0.954	0.968	0.968	0.979	0.933	0.952	0.978	0.979
HD_27	0.856	0.871	0.871	0.914	0.929	0.929	0.950	0.956	0.956	0.927	0.949	0.949	0.975	0.929	0.948	0.974	0.975
HD_28	0.882	0.892	0.892	0.942	0.952	0.952	0.968	0.971	0.971	0.955	0.967	0.967	0.980	0.932	0.952	0.978	0.980
HD_29	0.847	0.863	0.863	0.904	0.920	0.920	0.941	0.946	0.946	0.915	0.942	0.942	0.973	0.929	0.948	0.972	0.974
HD_30	0.854	0.872	0.872	0.913	0.931	0.931	0.949	0.954	0.954	0.923	0.950	0.951	0.978	0.931	0.950	0.975	0.978
HD_31	0.864	0.880	0.880	0.923	0.940	0.940	0.955	0.959	0.959	0.934	0.957	0.957	0.978	0.931	0.951	0.977	0.979
HD_32	0.862	0.879	0.879	0.921	0.939	0.939	0.953	0.959	0.959	0.933	0.956	0.956	0.979	0.932	0.952	0.977	0.979
HD_33	0.860	0.879	0.879	0.920	0.939	0.939	0.954	0.959	0.959	0.932	0.956	0.956	0.978	0.931	0.951	0.976	0.978
HD_34	0.859	0.878	0.878	0.917	0.937	0.937	0.952	0.958	0.958	0.930	0.954	0.954	0.975	0.930	0.949	0.975	0.976
HD_35	0.862	0.879	0.879	0.921	0.939	0.939	0.953	0.958	0.958	0.933	0.955	0.956	0.978	0.931	0.950	0.976	0.978
HD_36	0.862	0.878	0.878	0.922	0.938	0.938	0.953	0.957	0.957	0.934	0.955	0.955	0.978	0.931	0.951	0.977	0.978
HD_37	0.855	0.873	0.873	0.914	0.932	0.932	0.950	0.954	0.954	0.926	0.951	0.951	0.978	0.931	0.951	0.976	0.978
HD_38	0.870	0.886	0.886	0.930	0.946	0.946	0.959	0.963	0.963	0.942	0.961	0.961	0.978	0.932	0.951	0.977	0.979
HD_39	0.877	0.890	0.890	0.936	0.949	0.949	0.962	0.967	0.967	0.947	0.963	0.963	0.977	0.932	0.951	0.976	0.978
HD_40	0.859	0.876	0.876	0.919	0.936	0.936	0.954	0.959	0.959	0.933	0.954	0.954	0.978	0.932	0.951	0.976	0.979
HD_41	0.868	0.883	0.883	0.927	0.943	0.943	0.959	0.964	0.964	0.940	0.959	0.959	0.978	0.932	0.952	0.977	0.979
HD_42	0.872	0.885	0.885	0.933	0.946	0.946	0.962	0.966	0.966	0.946	0.962	0.962	0.978	0.932	0.952	0.977	0.979
HD_43	0.856	0.871	0.871	0.915	0.930	0.930	0.951	0.955	0.955	0.929	0.950	0.950	0.976	0.930	0.950	0.975	0.977
HD_44	0.858	0.876	0.876	0.918	0.935	0.935	0.952	0.957	0.957	0.928	0.952	0.952	0.977	0.931	0.950	0.976	0.977
HD_45	0.872	0.886	0.886	0.932	0.946	0.946	0.960	0.964	0.964	0.942	0.961	0.961	0.978	0.932	0.952	0.977	0.979
HD_46	0.859	0.875	0.875	0.919	0.935	0.935	0.951	0.956	0.955	0.930	0.951	0.952	0.977	0.930	0.950	0.975	0.977
HD_47	0.831	0.848	0.848	0.889	0.906	0.906	0.930	0.934	0.934	0.899	0.929	0.929	0.973	0.928	0.948	0.972	0.973
HD_48	0.841	0.860	0.860	0.899	0.919	0.919	0.938	0.942	0.942	0.909	0.941	0.941	0.975	0.928	0.948	0.973	0.975
Average	0.862	0.877	0.878	0.920	0.937	0.937	0.953	0.958	0.958	0.934	0.955	0.955	0.977	0.931	0.950	0.976	0.978

b) Non-reference discrepancy (NRD) for single nucleotide variants identified using Platypus, Samtools, UnifiedGenotyper and Haplotype Caller (single and multi sample variant identification) using variants identified with the Illumina BovineHD BeadChip® as a gold standard (BTA1-BTA29)

Animal	Single sampe variant identification												Multi sample variant identification				
	Platypus			Platypus (Primitives)			Samtools			UnifiedGenotyper			Haplotype Caller	Platypus	Platypus (Primitives)	Samtools	Unified Genotyper
	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR+BQSR	IR+BQSR	IR+BQSR	IR+BQSR
HD_1	0.003	0.003	0.003	0.008	0.004	0.004	0.003	0.003	0.003	0.004	0.004	0.004	0.007	0.005	0.007	0.023	0.006
HD_2	0.008	0.007	0.007	0.009	0.008	0.008	0.008	0.007	0.007	0.008	0.008	0.008	0.012	0.009	0.010	0.013	0.011
HD_3	0.007	0.007	0.007	0.008	0.008	0.008	0.007	0.007	0.007	0.008	0.007	0.007	0.011	0.009	0.010	0.012	0.011
HD_4	0.008	0.008	0.008	0.009	0.009	0.009	0.008	0.008	0.008	0.008	0.008	0.008	0.013	0.009	0.010	0.014	0.012
HD_5	0.010	0.009	0.009	0.011	0.010	0.010	0.008	0.008	0.008	0.008	0.008	0.008	0.012	0.009	0.010	0.011	0.011
HD_6	0.007	0.007	0.007	0.008	0.008	0.008	0.008	0.008	0.008	0.008	0.008	0.008	0.012	0.009	0.010	0.013	0.012
HD_7	0.019	0.019	0.019	0.021	0.021	0.021	0.021	0.019	0.019	0.021	0.021	0.021	0.026	0.020	0.021	0.028	0.025
HD_8	0.008	0.008	0.008	0.009	0.009	0.009	0.008	0.008	0.008	0.009	0.009	0.009	0.013	0.010	0.010	0.012	0.012
HD_9	0.007	0.007	0.007	0.008	0.008	0.008	0.006	0.006	0.006	0.006	0.006	0.006	0.010	0.008	0.008	0.009	0.009
HD_10	0.006	0.007	0.007	0.007	0.008	0.008	0.006	0.006	0.007	0.006	0.007	0.007	0.010	0.008	0.009	0.009	0.009
HD_11	0.007	0.007	0.007	0.008	0.008	0.007	0.007	0.006	0.006	0.007	0.007	0.007	0.011	0.008	0.009	0.011	0.010
HD_12	0.005	0.004	0.004	0.006	0.005	0.005	0.005	0.004	0.004	0.005	0.005	0.005	0.008	0.006	0.007	0.008	0.008
HD_13	0.006	0.005	0.005	0.007	0.006	0.006	0.006	0.005	0.005	0.006	0.006	0.006	0.010	0.007	0.008	0.010	0.009
HD_14	0.005	0.005	0.005	0.006	0.006	0.006	0.006	0.005	0.005	0.006	0.006	0.006	0.009	0.007	0.008	0.008	0.008
HD_15	0.005	0.004	0.004	0.006	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.008	0.007	0.007	0.008	0.008
HD_16	0.007	0.007	0.007	0.008	0.008	0.008	0.007	0.006	0.006	0.007	0.007	0.007	0.011	0.008	0.009	0.011	0.010
HD_17	0.008	0.008	0.008	0.009	0.009	0.009	0.008	0.007	0.007	0.008	0.008	0.008	0.012	0.010	0.010	0.013	0.011
HD_18	0.008	0.008	0.008	0.009	0.009	0.009	0.008	0.008	0.008	0.009	0.009	0.009	0.012	0.010	0.011	0.013	0.012
HD_19	0.008	0.008	0.008	0.009	0.009	0.009	0.009	0.008	0.008	0.009	0.009	0.009	0.012	0.009	0.010	0.013	0.012
HD_20	0.007	0.007	0.007	0.008	0.008	0.008	0.007	0.006	0.006	0.007	0.007	0.007	0.011	0.008	0.009	0.010	0.010
HD_21	0.004	0.005	0.005	0.005	0.006	0.006	0.005	0.005	0.005	0.005	0.005	0.006	0.009	0.007	0.008	0.009	0.008
HD_22	0.005	0.006	0.006	0.006	0.007	0.007	0.005	0.005	0.005	0.006	0.006	0.006	0.010	0.007	0.008	0.008	0.008
HD_23	0.009	0.009	0.009	0.010	0.010	0.010	0.009	0.008	0.008	0.009	0.009	0.009	0.013	0.010	0.011	0.014	0.013
HD_24	0.012	0.012	0.012	0.013	0.013	0.013	0.012	0.011	0.011	0.012	0.012	0.013	0.015	0.013	0.014	0.014	0.014
HD_25	0.005	0.005	0.005	0.006	0.006	0.006	0.005	0.005	0.005	0.005	0.005	0.006	0.009	0.007	0.008	0.008	0.008
HD_26	0.005	0.005	0.005	0.006	0.006	0.006	0.006	0.005	0.005	0.006	0.006	0.006	0.009	0.007	0.008	0.008	0.008
HD_27	0.015	0.014	0.014	0.016	0.016	0.016	0.015	0.014	0.014	0.015	0.015	0.015	0.018	0.015	0.016	0.018	0.017
HD_28	0.005	0.005	0.005	0.006	0.005	0.005	0.005	0.004	0.004	0.005	0.005	0.005	0.009	0.007	0.007	0.008	0.008
HD_29	0.016	0.016	0.016	0.018	0.017	0.017	0.017	0.016	0.015	0.017	0.017	0.017	0.020	0.017	0.017	0.021	0.019
HD_30	0.007	0.007	0.007	0.009	0.008	0.008	0.008	0.007	0.007	0.008	0.007	0.007	0.011	0.009	0.009	0.011	0.010
HD_31	0.006	0.006	0.006	0.007	0.007	0.007	0.007	0.006	0.006	0.007	0.007	0.007	0.011	0.008	0.009	0.011	0.010
HD_32	0.007	0.007	0.007	0.008	0.008	0.008	0.007	0.007	0.007	0.007	0.008	0.008	0.012	0.008	0.009	0.011	0.010
HD_33	0.007	0.007	0.007	0.009	0.009	0.009	0.008	0.008	0.008	0.008	0.008	0.008	0.013	0.010	0.010	0.012	0.011
HD_34	0.014	0.014	0.014	0.015	0.015	0.015	0.014	0.013	0.013	0.014	0.014	0.014	0.017	0.015	0.015	0.017	0.017
HD_35	0.006	0.006	0.006	0.007	0.007	0.007	0.007	0.006	0.006	0.007	0.007	0.007	0.011	0.009	0.009	0.011	0.010
HD_36	0.007	0.006	0.006	0.007	0.007	0.007	0.007	0.006	0.006	0.007	0.007	0.007	0.011	0.008	0.009	0.011	0.010
HD_37	0.009	0.010	0.010	0.010	0.011	0.011	0.009	0.009	0.009	0.009	0.010	0.011	0.015	0.011	0.012	0.014	0.013
HD_38	0.007	0.006	0.006	0.008	0.007	0.007	0.007	0.006	0.006	0.007	0.007	0.007	0.010	0.008	0.008	0.010	0.009
HD_39	0.012	0.011	0.011	0.013	0.013	0.013	0.012	0.011	0.011	0.012	0.012	0.012	0.015	0.013	0.014	0.015	0.014
HD_40	0.007	0.006	0.006	0.008	0.007	0.007	0.007	0.006	0.006	0.007	0.007	0.007	0.010	0.008	0.009	0.010	0.010
HD_41	0.006	0.006	0.006	0.007	0.007	0.007	0.006	0.006	0.006	0.006	0.006	0.006	0.010	0.007	0.008	0.009	0.008
HD_42	0.006	0.006	0.006	0.007	0.007	0.007	0.006	0.005	0.005	0.006	0.006	0.006	0.010	0.007	0.008	0.009	0.008
HD_43	0.007	0.007	0.007	0.008	0.008	0.008	0.007	0.007	0.007	0.008	0.007	0.008	0.012	0.009	0.010	0.012	0.011
HD_44	0.007	0.007	0.007	0.008	0.008	0.008	0.007	0.007	0.007	0.007	0.007	0.008	0.011	0.009	0.009	0.011	0.010
HD_45	0.006	0.006	0.006	0.007	0.007	0.007	0.006	0.006	0.006	0.006	0.007	0.007	0.011	0.008	0.009	0.010	0.009
HD_46	0.008	0.008	0.008	0.009	0.009	0.009	0.008	0.008	0.008	0.008	0.009	0.009	0.013	0.010	0.010	0.013	0.012
HD_47	0.011	0.011	0.011	0.012	0.012	0.012	0.011	0.011	0.011	0.011	0.012	0.012	0.017	0.013	0.014	0.021	0.016
HD_48	0.009	0.008	0.008	0.010	0.009	0.009	0.009	0.008	0.008	0.009	0.009	0.009	0.013	0.011	0.011	0.014	0.012
Average	0.008	0.008	0.008	0.009	0.009	0.009	0.008	0.007	0.007	0.008	0.008	0.008	0.012	0.009	0.010	0.012	0.011

c) Single nucleotide variant concordance identified using Platypus, Samtools, UnifiedGenotyper and Haplotype Caller (single vs. multi sample variant identification) using variants identified with the Illumina BovineHD BeadChip® as a gold standard. (BTA1-BTA29)

Animal	Single sampe variant identification												Multi sample variant identification					
	Platypus			Platypus (Primitives)			Samtools			UnifiedGenotyper			Haplotype Caller	Platypus	Platypus (Primitives)	Samtools	Unified Genotyper	
	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR+BQSR	IR+BQSR	IR+BQSR	IR+BQSR	
HD_1	0.552	0.555	0.555	0.572	0.593	0.593	0.592	0.593	0.597	0.595	0.598	0.598	0.881	0.839	0.857	0.879	0.882	
HD_2	0.542	0.552	0.552	0.580	0.589	0.589	0.602	0.604	0.604	0.587	0.602	0.602	0.881	0.838	0.857	0.879	0.882	
HD_3	0.529	0.539	0.539	0.565	0.575	0.575	0.588	0.590	0.590	0.571	0.588	0.588	0.881	0.838	0.858	0.879	0.882	
HD_4	0.535	0.545	0.545	0.572	0.581	0.581	0.596	0.599	0.599	0.580	0.596	0.596	0.880	0.837	0.857	0.879	0.882	
HD_5	0.536	0.548	0.548	0.572	0.584	0.584	0.605	0.609	0.609	0.588	0.603	0.603	0.881	0.838	0.858	0.879	0.882	
HD_6	0.550	0.559	0.559	0.588	0.597	0.597	0.606	0.608	0.608	0.595	0.608	0.608	0.881	0.838	0.857	0.879	0.882	
HD_7	0.517	0.533	0.533	0.551	0.567	0.567	0.580	0.585	0.585	0.559	0.584	0.584	0.878	0.834	0.853	0.877	0.879	
HD_8	0.542	0.554	0.554	0.580	0.591	0.591	0.600	0.603	0.603	0.586	0.602	0.602	0.881	0.838	0.858	0.879	0.882	
HD_9	0.551	0.561	0.561	0.589	0.599	0.599	0.614	0.617	0.617	0.601	0.613	0.613	0.881	0.839	0.858	0.879	0.882	
HD_10	0.560	0.568	0.568	0.599	0.607	0.607	0.614	0.616	0.616	0.607	0.615	0.615	0.881	0.839	0.858	0.879	0.882	
HD_11	0.538	0.549	0.549	0.575	0.586	0.586	0.598	0.601	0.601	0.583	0.599	0.599	0.881	0.839	0.858	0.879	0.882	
HD_12	0.564	0.573	0.573	0.602	0.611	0.611	0.618	0.621	0.621	0.611	0.621	0.621	0.881	0.839	0.858	0.879	0.882	
HD_13	0.541	0.552	0.552	0.578	0.589	0.589	0.597	0.600	0.600	0.587	0.600	0.600	0.881	0.838	0.858	0.879	0.882	
HD_14	0.543	0.553	0.553	0.581	0.590	0.590	0.597	0.600	0.600	0.588	0.599	0.599	0.881	0.839	0.858	0.879	0.882	
HD_15	0.542	0.551	0.551	0.579	0.588	0.588	0.596	0.598	0.598	0.587	0.597	0.597	0.881	0.839	0.858	0.879	0.882	
HD_16	0.528	0.538	0.538	0.564	0.574	0.574	0.586	0.589	0.589	0.574	0.587	0.587	0.881	0.838	0.858	0.879	0.882	
HD_17	0.528	0.541	0.541	0.565	0.577	0.577	0.592	0.596	0.596	0.575	0.592	0.593	0.881	0.838	0.858	0.879	0.882	
HD_18	0.515	0.527	0.527	0.551	0.562	0.562	0.577	0.580	0.580	0.560	0.578	0.578	0.881	0.838	0.857	0.879	0.882	
HD_19	0.525	0.536	0.536	0.560	0.572	0.572	0.586	0.589	0.589	0.570	0.587	0.587	0.881	0.838	0.857	0.879	0.882	
HD_20	0.548	0.557	0.557	0.585	0.595	0.595	0.607	0.610	0.610	0.595	0.607	0.607	0.881	0.838	0.858	0.879	0.882	
HD_21	0.535	0.538	0.538	0.572	0.575	0.575	0.584	0.585	0.585	0.576	0.584	0.584	0.881	0.839	0.858	0.879	0.882	
HD_22	0.541	0.547	0.547	0.578	0.584	0.584	0.593	0.595	0.595	0.587	0.594	0.594	0.881	0.839	0.858	0.879	0.882	
HD_23	0.526	0.537	0.537	0.562	0.573	0.573	0.589	0.592	0.592	0.571	0.589	0.589	0.881	0.838	0.857	0.879	0.882	
HD_24	0.552	0.557	0.557	0.589	0.594	0.594	0.605	0.607	0.607	0.598	0.605	0.605	0.879	0.838	0.857	0.878	0.880	
HD_25	0.552	0.558	0.558	0.590	0.596	0.596	0.606	0.608	0.608	0.599	0.607	0.607	0.881	0.839	0.858	0.879	0.882	
HD_26	0.561	0.569	0.569	0.600	0.607	0.607	0.616	0.618	0.618	0.608	0.616	0.617	0.881	0.839	0.858	0.879	0.882	
HD_27	0.534	0.544	0.544	0.570	0.579	0.579	0.594	0.596	0.596	0.579	0.593	0.593	0.879	0.837	0.856	0.878	0.880	
HD_28	0.551	0.558	0.558	0.589	0.595	0.595	0.606	0.608	0.608	0.598	0.606	0.606	0.881	0.839	0.858	0.879	0.882	
HD_29	0.546	0.556	0.556	0.583	0.593	0.593	0.607	0.610	0.610	0.590	0.608	0.608	0.879	0.836	0.855	0.877	0.880	
HD_30	0.552	0.564	0.564	0.590	0.602	0.601	0.614	0.617	0.617	0.597	0.615	0.615	0.881	0.838	0.858	0.879	0.882	
HD_31	0.540	0.550	0.550	0.577	0.587	0.587	0.597	0.600	0.600	0.584	0.598	0.598	0.881	0.839	0.858	0.879	0.882	
HD_32	0.555	0.566	0.566	0.593	0.605	0.605	0.615	0.618	0.618	0.601	0.617	0.617	0.881	0.838	0.858	0.879	0.882	
HD_33	0.551	0.563	0.563	0.589	0.601	0.601	0.611	0.614	0.614	0.597	0.613	0.613	0.881	0.838	0.858	0.879	0.882	
HD_34	0.548	0.560	0.560	0.585	0.597	0.597	0.607	0.611	0.611	0.593	0.609	0.609	0.879	0.837	0.856	0.878	0.880	
HD_35	0.539	0.550	0.550	0.576	0.587	0.587	0.597	0.600	0.600	0.585	0.599	0.599	0.881	0.838	0.858	0.879	0.882	
HD_36	0.540	0.550	0.550	0.577	0.587	0.587	0.598	0.600	0.600	0.586	0.599	0.599	0.881	0.838	0.858	0.879	0.882	
HD_37	0.548	0.559	0.559	0.585	0.597	0.597	0.609	0.612	0.612	0.594	0.610	0.610	0.881	0.838	0.858	0.879	0.882	
HD_38	0.560	0.570	0.570	0.599	0.609	0.609	0.618	0.621	0.621	0.607	0.619	0.619	0.881	0.839	0.858	0.879	0.883	
HD_39	0.544	0.552	0.552	0.580	0.588	0.588	0.597	0.600	0.600	0.588	0.598	0.598	0.879	0.838	0.857	0.878	0.880	
HD_40	0.552	0.563	0.563	0.590	0.600	0.600	0.613	0.616	0.616	0.599	0.613	0.613	0.881	0.838	0.858	0.879	0.882	
HD_41	0.554	0.564	0.564	0.592	0.602	0.602	0.613	0.616	0.616	0.601	0.613	0.613	0.881	0.839	0.858	0.879	0.882	
HD_42	0.556	0.564	0.564	0.594	0.602	0.602	0.614	0.616	0.616	0.604	0.614	0.614	0.881	0.839	0.858	0.879	0.882	
HD_43	0.540	0.549	0.549	0.576	0.586	0.586	0.600	0.602	0.602	0.586	0.599	0.600	0.881	0.838	0.858	0.879	0.882	
HD_44	0.548	0.560	0.560	0.586	0.597	0.597	0.609	0.612	0.612	0.593	0.609	0.609	0.881	0.839	0.858	0.879	0.882	
HD_45	0.532	0.541	0.541	0.569	0.577	0.577	0.586	0.589	0.589	0.576	0.587	0.587	0.881	0.839	0.858	0.879	0.882	
HD_46	0.538	0.548	0.548	0.575	0.585	0.585	0.596	0.599	0.599	0.583	0.596	0.596	0.881	0.838	0.857	0.879	0.882	
HD_47	0.522	0.533	0.533	0.558	0.569	0.569	0.585	0.587	0.587	0.565	0.584	0.584	0.880	0.837	0.856	0.879	0.882	
HD_48	0.527	0.539	0.539	0.564	0.576	0.576	0.589	0.591	0.591	0.571	0.591	0.591	0.881	0.838	0.857	0.879	0.882	
Average	0.542	0.552	0.552	0.579	0.589	0.589	0.600	0.603	0.603	0.588	0.601	0.601	0.881	0.838	0.857	0.879	0.882	

d) Single nucleotide variant concordance by genotypes identified using Platypus, Samtools, UnifiedGenotyper and Haplotype Caller (single vs. multi sample variant identification) using variants identified with the Illumina BovineHD BeadChip® as a gold standard (BTA1-BTA29)

Animal	Single sampe variant identification												Multi sample variant identification				
	Platypus			Platypus (Primitives)			Samtools			UnifiedGenotyper			Haplotype	Platypus			Unified
	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	Caller	Platypus	(Primitives)	Samtools	Genotyper
HD_1	0.997	0.997	0.997	0.989	0.996	0.996	0.997	0.997	0.997	0.996	0.996	0.996	0.995	0.997	0.993	0.984	0.996
HD_2	0.992	0.993	0.993	0.991	0.992	0.992	0.992	0.993	0.993	0.992	0.992	0.992	0.992	0.994	0.993	0.991	0.992
HD_3	0.993	0.993	0.993	0.992	0.992	0.992	0.993	0.993	0.993	0.992	0.993	0.993	0.992	0.994	0.993	0.991	0.993
HD_4	0.992	0.992	0.992	0.991	0.991	0.991	0.992	0.992	0.992	0.992	0.992	0.992	0.992	0.991	0.994	0.993	0.990
HD_5	0.990	0.991	0.991	0.989	0.990	0.990	0.992	0.992	0.992	0.992	0.992	0.992	0.992	0.993	0.993	0.992	0.992
HD_6	0.993	0.993	0.993	0.992	0.992	0.992	0.992	0.992	0.992	0.992	0.992	0.992	0.992	0.991	0.994	0.993	0.991
HD_7	0.981	0.981	0.981	0.979	0.979	0.979	0.979	0.981	0.981	0.979	0.981	0.979	0.979	0.982	0.986	0.985	0.980
HD_8	0.992	0.992	0.992	0.991	0.991	0.991	0.992	0.992	0.992	0.991	0.991	0.991	0.991	0.993	0.993	0.991	0.992
HD_9	0.993	0.993	0.993	0.992	0.992	0.992	0.994	0.994	0.994	0.994	0.994	0.994	0.993	0.995	0.994	0.993	0.994
HD_10	0.994	0.993	0.993	0.993	0.992	0.992	0.994	0.994	0.993	0.994	0.993	0.993	0.993	0.994	0.994	0.994	0.994
HD_11	0.993	0.993	0.993	0.992	0.992	0.993	0.993	0.994	0.994	0.993	0.993	0.993	0.993	0.994	0.994	0.992	0.993
HD_12	0.995	0.996	0.996	0.994	0.995	0.995	0.995	0.996	0.996	0.995	0.995	0.995	0.994	0.995	0.995	0.994	0.995
HD_13	0.994	0.995	0.995	0.993	0.994	0.994	0.994	0.995	0.995	0.994	0.994	0.994	0.993	0.995	0.995	0.993	0.994
HD_14	0.995	0.995	0.995	0.994	0.994	0.994	0.994	0.995	0.995	0.994	0.994	0.994	0.994	0.995	0.995	0.994	0.994
HD_15	0.995	0.996	0.996	0.994	0.995	0.995	0.995	0.995	0.995	0.995	0.995	0.995	0.994	0.995	0.995	0.994	0.995
HD_16	0.993	0.993	0.993	0.992	0.992	0.992	0.993	0.994	0.994	0.993	0.993	0.993	0.993	0.994	0.994	0.993	0.993
HD_17	0.992	0.992	0.992	0.991	0.991	0.991	0.992	0.993	0.993	0.992	0.992	0.992	0.991	0.993	0.993	0.991	0.992
HD_18	0.992	0.992	0.992	0.991	0.991	0.991	0.992	0.992	0.992	0.991	0.991	0.991	0.992	0.993	0.993	0.991	0.992
HD_19	0.992	0.992	0.992	0.991	0.991	0.991	0.991	0.992	0.992	0.991	0.991	0.991	0.992	0.994	0.993	0.991	0.992
HD_20	0.993	0.993	0.993	0.992	0.992	0.992	0.993	0.994	0.994	0.993	0.993	0.993	0.992	0.994	0.994	0.993	0.993
HD_21	0.996	0.995	0.995	0.995	0.994	0.994	0.995	0.995	0.995	0.995	0.995	0.995	0.994	0.995	0.995	0.994	0.995
HD_22	0.995	0.994	0.994	0.994	0.993	0.993	0.995	0.995	0.995	0.994	0.994	0.994	0.993	0.995	0.995	0.994	0.994
HD_23	0.991	0.991	0.991	0.990	0.990	0.990	0.991	0.992	0.992	0.991	0.991	0.991	0.991	0.993	0.993	0.990	0.991
HD_24	0.988	0.988	0.988	0.987	0.987	0.987	0.988	0.989	0.989	0.988	0.988	0.987	0.990	0.991	0.991	0.990	0.990
HD_25	0.995	0.995	0.995	0.994	0.994	0.994	0.995	0.995	0.995	0.995	0.995	0.994	0.994	0.995	0.995	0.994	0.994
HD_26	0.995	0.995	0.995	0.994	0.994	0.994	0.994	0.995	0.995	0.994	0.994	0.994	0.993	0.995	0.995	0.994	0.994
HD_27	0.985	0.986	0.986	0.984	0.984	0.984	0.985	0.986	0.986	0.985	0.985	0.985	0.988	0.990	0.989	0.988	0.988
HD_28	0.995	0.995	0.995	0.994	0.995	0.995	0.995	0.996	0.996	0.995	0.995	0.995	0.994	0.995	0.995	0.994	0.995
HD_29	0.984	0.984	0.984	0.982	0.983	0.983	0.983	0.984	0.985	0.983	0.983	0.983	0.986	0.988	0.988	0.985	0.986
HD_30	0.993	0.993	0.993	0.991	0.992	0.992	0.992	0.993	0.993	0.992	0.993	0.993	0.992	0.994	0.993	0.992	0.993
HD_31	0.994	0.994	0.994	0.993	0.993	0.993	0.993	0.994	0.994	0.993	0.993	0.993	0.993	0.994	0.994	0.993	0.993
HD_32	0.993	0.993	0.993	0.992	0.992	0.992	0.993	0.993	0.993	0.993	0.992	0.992	0.992	0.994	0.994	0.992	0.992
HD_33	0.993	0.993	0.993	0.991	0.991	0.991	0.992	0.992	0.992	0.992	0.992	0.992	0.991	0.993	0.993	0.991	0.992
HD_34	0.986	0.986	0.986	0.985	0.985	0.985	0.986	0.987	0.987	0.986	0.986	0.986	0.988	0.990	0.989	0.988	0.988
HD_35	0.994	0.994	0.994	0.993	0.993	0.993	0.993	0.994	0.994	0.993	0.993	0.993	0.992	0.994	0.994	0.992	0.993
HD_36	0.993	0.994	0.994	0.993	0.993	0.993	0.993	0.994	0.994	0.993	0.993	0.993	0.993	0.994	0.994	0.992	0.993
HD_37	0.991	0.990	0.990	0.990	0.989	0.989	0.991	0.991	0.991	0.991	0.990	0.989	0.989	0.992	0.992	0.990	0.990
HD_38	0.993	0.994	0.994	0.992	0.993	0.993	0.993	0.994	0.994	0.993	0.993	0.993	0.993	0.994	0.994	0.993	0.993
HD_39	0.988	0.989	0.989	0.987	0.987	0.987	0.988	0.989	0.989	0.988	0.988	0.988	0.989	0.991	0.991	0.989	0.990
HD_40	0.993	0.994	0.994	0.992	0.993	0.993	0.993	0.994	0.994	0.993	0.993	0.993	0.992	0.994	0.994	0.993	0.993
HD_41	0.994	0.994	0.994	0.993	0.993	0.993	0.994	0.994	0.994	0.994	0.994	0.994	0.993	0.995	0.994	0.994	0.994
HD_42	0.994	0.994	0.994	0.993	0.993	0.993	0.994	0.995	0.995	0.994	0.994	0.994	0.993	0.995	0.995	0.994	0.994
HD_43	0.993	0.993	0.993	0.992	0.992	0.992	0.993	0.993	0.993	0.992	0.993	0.992	0.992	0.994	0.993	0.991	0.992
HD_44	0.993	0.993	0.993	0.992	0.992	0.992	0.993	0.993	0.993	0.993	0.993	0.992	0.992	0.994	0.994	0.992	0.993
HD_45	0.994	0.994	0.994	0.993	0.993	0.993	0.994	0.994	0.994	0.994	0.993	0.993	0.993	0.994	0.994	0.993	0.994
HD_46	0.992	0.992	0.992	0.991	0.991	0.991	0.992	0.992	0.992	0.992	0.991	0.991	0.991	0.993	0.993	0.991	0.992
HD_47	0.989	0.989	0.989	0.988	0.988	0.988	0.989	0.989	0.989	0.989	0.988	0.988	0.988	0.991	0.990	0.986	0.989
HD_48	0.991	0.992	0.992	0.990	0.991	0.991	0.991	0.992	0.992	0.991	0.991	0.991	0.991	0.993	0.992	0.990	0.991
Average	0.992	0.992	0.992	0.991	0.991	0.991	0.992	0.993	0.993	0.992	0.992	0.992	0.992	0.993	0.993	0.991	0.992

e) Concordance for homozygous reference genotypes identified using Platypus, Samtools, UnifiedGenotyper and Haplotype Caller (single and multi sample variant identification) using variants identified with the Illumina BovineHD BeadChip® as a gold standard (BTA1-BTA29)

Animal	Single sampe variant identification												Multi sample variant identification				
	Platypus			Platypus (Primitives)			Samtools			UnifiedGenotyper			Haplotype	Platypus			Unified
	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	Caller	Platypus	(Primitives)	Samtools	Genotyper
HD_1	0.001	0.002	0.002	0.002	0.003	0.003	0.002	0.002	0.002	0.003	0.003	0.003	0.732	0.702	0.706	0.728	0.734
HD_2	0.001	0.001	0.001	0.003	0.003	0.003	0.003	0.002	0.002	0.003	0.003	0.003	0.713	0.682	0.701	0.709	0.715
HD_3	0.001	0.001	0.001	0.003	0.003	0.003	0.002	0.002	0.002	0.002	0.002	0.003	0.724	0.694	0.712	0.720	0.726
HD_4	0.001	0.001	0.001	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.714	0.683	0.702	0.710	0.716
HD_5	0.001	0.001	0.001	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.713	0.684	0.702	0.709	0.715
HD_6	0.001	0.001	0.001	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.712	0.681	0.700	0.708	0.714
HD_7	0.008	0.009	0.009	0.011	0.011	0.011	0.011	0.009	0.009	0.010	0.011	0.011	0.712	0.680	0.699	0.711	0.715
HD_8	0.001	0.001	0.001	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.719	0.688	0.706	0.713	0.721
HD_9	0.001	0.001	0.001	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.710	0.681	0.699	0.706	0.712
HD_10	0.001	0.001	0.001	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.715	0.687	0.705	0.711	0.717
HD_11	0.001	0.001	0.001	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.719	0.689	0.708	0.714	0.721
HD_12	0.001	0.001	0.001	0.003	0.003	0.003	0.002	0.002	0.002	0.002	0.002	0.002	0.712	0.681	0.700	0.706	0.714
HD_13	0.001	0.001	0.001	0.002	0.003	0.003	0.002	0.002	0.002	0.002	0.002	0.002	0.723	0.692	0.711	0.719	0.725
HD_14	0.001	0.001	0.001	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.724	0.694	0.712	0.719	0.726
HD_15	0.001	0.001	0.001	0.003	0.003	0.003	0.002	0.002	0.002	0.002	0.003	0.003	0.725	0.695	0.714	0.721	0.727
HD_16	0.001	0.001	0.001	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.726	0.696	0.715	0.723	0.728
HD_17	0.001	0.001	0.001	0.003	0.003	0.003	0.002	0.002	0.002	0.002	0.003	0.003	0.720	0.690	0.709	0.716	0.722
HD_18	0.001	0.001	0.001	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.727	0.697	0.716	0.724	0.729
HD_19	0.001	0.001	0.001	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.723	0.693	0.711	0.718	0.725
HD_20	0.001	0.001	0.001	0.003	0.003	0.003	0.002	0.002	0.002	0.003	0.003	0.003	0.717	0.688	0.706	0.713	0.719
HD_21	0.001	0.001	0.001	0.003	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.733	0.702	0.721	0.729	0.735
HD_22	0.001	0.001	0.001	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.729	0.699	0.718	0.724	0.731
HD_23	0.001	0.001	0.001	0.003	0.003	0.003	0.002	0.002	0.002	0.003	0.003	0.003	0.720	0.689	0.708	0.716	0.722
HD_24	0.008	0.008	0.008	0.010	0.010	0.010	0.009	0.009	0.009	0.010	0.010	0.010	0.718	0.689	0.708	0.715	0.720
HD_25	0.002	0.002	0.002	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.720	0.691	0.710	0.716	0.722
HD_26	0.001	0.001	0.001	0.003	0.003	0.003	0.002	0.002	0.002	0.002	0.002	0.003	0.714	0.684	0.702	0.709	0.716
HD_27	0.007	0.008	0.008	0.009	0.009	0.009	0.009	0.008	0.008	0.009	0.009	0.010	0.720	0.690	0.709	0.716	0.722
HD_28	0.001	0.001	0.001	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.718	0.689	0.707	0.714	0.720
HD_29	0.009	0.010	0.010	0.012	0.012	0.012	0.012	0.011	0.011	0.012	0.012	0.012	0.705	0.675	0.694	0.701	0.707
HD_30	0.002	0.002	0.002	0.003	0.003	0.003	0.003	0.002	0.002	0.003	0.003	0.003	0.706	0.677	0.695	0.702	0.708
HD_31	0.002	0.002	0.002	0.003	0.003	0.003	0.003	0.002	0.002	0.003	0.003	0.003	0.721	0.692	0.710	0.717	0.723
HD_32	0.001	0.001	0.001	0.003	0.003	0.003	0.003	0.002	0.002	0.003	0.003	0.003	0.706	0.678	0.696	0.703	0.709
HD_33	0.002	0.002	0.002	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.710	0.680	0.699	0.706	0.712
HD_34	0.008	0.008	0.008	0.010	0.010	0.010	0.010	0.009	0.009	0.010	0.010	0.010	0.712	0.681	0.700	0.707	0.714
HD_35	0.001	0.001	0.001	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.721	0.690	0.709	0.717	0.723
HD_36	0.001	0.001	0.001	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.719	0.690	0.708	0.715	0.722
HD_37	0.001	0.001	0.001	0.003	0.003	0.003	0.002	0.002	0.002	0.003	0.003	0.003	0.710	0.679	0.698	0.706	0.712
HD_38	0.001	0.001	0.001	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.708	0.679	0.697	0.704	0.710
HD_39	0.008	0.008	0.008	0.010	0.010	0.010	0.009	0.009	0.009	0.010	0.010	0.010	0.723	0.692	0.711	0.719	0.725
HD_40	0.002	0.002	0.002	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.708	0.679	0.698	0.705	0.710
HD_41	0.001	0.001	0.001	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.712	0.681	0.700	0.707	0.714
HD_42	0.001	0.001	0.001	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.713	0.683	0.701	0.708	0.715
HD_43	0.001	0.001	0.001	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.718	0.687	0.705	0.713	0.720
HD_44	0.001	0.001	0.001	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.713	0.683	0.701	0.709	0.715
HD_45	0.001	0.001	0.001	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.730	0.698	0.717	0.725	0.732
HD_46	0.001	0.001	0.001	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.721	0.691	0.709	0.717	0.723
HD_47	0.001	0.001	0.001	0.003	0.003	0.003	0.003	0.002	0.002	0.003	0.003	0.003	0.718	0.685	0.703	0.714	0.720
HD_48	0.001	0.001	0.001	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.002	0.719	0.690	0.708	0.715	0.722
Average	0.002	0.002	0.002	0.003	0.004	0.003	0.003	0.003	0.003	0.003	0.003	0.003	0.718	0.687	0.706	0.713	0.720

f) Concordance for heterozygous genotypes identified using Platypus, Samtools, UnifiedGenotyper and Haplotype Caller (single and multi sample variant identification) using variants identified with the Illumina BovineHD BeadChip® as a gold standard (BTA1-BTA29)

Animal	Single sampe variant identification												Multi sample variant identification				
	Platypus			Platypus (Primitives)			Samtools			UnifiedGenotyper			Haplotype	Platypus			Unified
	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	Caller	Platypus	(Primitives)	Samtools	Genotyper
HD_1	0.886	0.899	0.899	0.870	0.963	0.963	0.958	0.961	0.971	0.959	0.972	0.972	0.980	0.939	0.959	0.980	0.981
HD_2	0.787	0.817	0.817	0.845	0.875	0.875	0.901	0.911	0.911	0.851	0.900	0.900	0.984	0.938	0.960	0.981	0.985
HD_3	0.774	0.811	0.811	0.831	0.868	0.868	0.897	0.910	0.910	0.838	0.896	0.896	0.983	0.938	0.960	0.980	0.983
HD_4	0.776	0.807	0.807	0.834	0.865	0.865	0.894	0.905	0.905	0.843	0.891	0.891	0.983	0.936	0.959	0.981	0.984
HD_5	0.760	0.799	0.799	0.815	0.855	0.855	0.902	0.917	0.917	0.849	0.895	0.895	0.984	0.938	0.960	0.980	0.985
HD_6	0.815	0.843	0.843	0.875	0.902	0.902	0.915	0.925	0.925	0.882	0.920	0.920	0.985	0.936	0.959	0.980	0.985
HD_7	0.737	0.785	0.785	0.787	0.837	0.837	0.859	0.880	0.880	0.794	0.869	0.869	0.984	0.936	0.958	0.978	0.985
HD_8	0.791	0.830	0.830	0.849	0.887	0.887	0.905	0.920	0.920	0.856	0.909	0.909	0.982	0.938	0.959	0.980	0.983
HD_9	0.800	0.831	0.831	0.859	0.890	0.890	0.922	0.934	0.934	0.883	0.919	0.919	0.986	0.938	0.960	0.980	0.986
HD_10	0.844	0.870	0.870	0.906	0.932	0.932	0.944	0.952	0.952	0.922	0.947	0.947	0.985	0.937	0.959	0.980	0.986
HD_11	0.784	0.823	0.823	0.842	0.881	0.881	0.906	0.920	0.920	0.855	0.907	0.907	0.982	0.939	0.960	0.980	0.983
HD_12	0.839	0.866	0.866	0.900	0.928	0.928	0.938	0.948	0.948	0.913	0.943	0.944	0.985	0.938	0.959	0.980	0.986
HD_13	0.812	0.849	0.849	0.870	0.908	0.908	0.921	0.935	0.935	0.884	0.928	0.928	0.983	0.939	0.960	0.980	0.984
HD_14	0.820	0.852	0.852	0.880	0.913	0.913	0.926	0.939	0.939	0.894	0.932	0.932	0.984	0.937	0.959	0.980	0.985
HD_15	0.823	0.855	0.855	0.883	0.915	0.915	0.929	0.941	0.941	0.896	0.933	0.933	0.985	0.938	0.960	0.980	0.986
HD_16	0.787	0.823	0.823	0.845	0.881	0.881	0.908	0.923	0.923	0.862	0.907	0.907	0.985	0.938	0.960	0.980	0.985
HD_17	0.762	0.803	0.803	0.818	0.859	0.859	0.893	0.908	0.908	0.833	0.891	0.891	0.983	0.938	0.960	0.980	0.983
HD_18	0.755	0.796	0.796	0.811	0.852	0.852	0.886	0.901	0.901	0.825	0.886	0.886	0.986	0.937	0.959	0.980	0.986
HD_19	0.766	0.805	0.805	0.822	0.861	0.861	0.891	0.905	0.905	0.836	0.892	0.892	0.983	0.937	0.959	0.981	0.984
HD_20	0.805	0.837	0.837	0.864	0.895	0.895	0.922	0.934	0.934	0.882	0.921	0.921	0.983	0.938	0.960	0.980	0.984
HD_21	0.833	0.849	0.849	0.894	0.909	0.909	0.931	0.942	0.942	0.899	0.931	0.931	0.984	0.938	0.960	0.981	0.985
HD_22	0.839	0.861	0.861	0.900	0.921	0.922	0.942	0.950	0.950	0.918	0.943	0.943	0.982	0.938	0.960	0.980	0.983
HD_23	0.760	0.799	0.799	0.815	0.854	0.854	0.888	0.902	0.902	0.827	0.886	0.886	0.985	0.938	0.960	0.981	0.986
HD_24	0.838	0.859	0.859	0.897	0.918	0.918	0.940	0.950	0.950	0.916	0.940	0.940	0.984	0.938	0.960	0.980	0.984
HD_25	0.839	0.861	0.861	0.899	0.921	0.921	0.942	0.951	0.951	0.918	0.942	0.943	0.984	0.938	0.960	0.981	0.985
HD_26	0.839	0.863	0.863	0.900	0.924	0.924	0.940	0.950	0.950	0.913	0.940	0.941	0.984	0.938	0.959	0.981	0.984
HD_27	0.787	0.819	0.819	0.842	0.875	0.875	0.906	0.920	0.919	0.857	0.902	0.902	0.982	0.937	0.959	0.980	0.983
HD_28	0.830	0.853	0.853	0.890	0.913	0.913	0.937	0.945	0.945	0.909	0.935	0.935	0.983	0.937	0.960	0.981	0.984
HD_29	0.785	0.817	0.817	0.841	0.873	0.873	0.899	0.911	0.911	0.848	0.900	0.900	0.984	0.938	0.960	0.980	0.985
HD_30	0.792	0.828	0.828	0.849	0.886	0.886	0.909	0.922	0.922	0.858	0.911	0.911	0.984	0.939	0.960	0.981	0.985
HD_31	0.797	0.833	0.833	0.856	0.892	0.892	0.913	0.926	0.926	0.866	0.915	0.915	0.984	0.938	0.960	0.981	0.985
HD_32	0.806	0.840	0.840	0.865	0.900	0.900	0.917	0.930	0.930	0.876	0.922	0.922	0.985	0.938	0.960	0.981	0.986
HD_33	0.797	0.836	0.836	0.855	0.894	0.894	0.914	0.927	0.927	0.869	0.917	0.917	0.985	0.939	0.960	0.980	0.985
HD_34	0.800	0.837	0.837	0.856	0.894	0.894	0.913	0.928	0.928	0.870	0.917	0.917	0.983	0.938	0.959	0.980	0.984
HD_35	0.797	0.834	0.834	0.856	0.893	0.893	0.912	0.925	0.925	0.869	0.916	0.916	0.984	0.938	0.959	0.980	0.985
HD_36	0.802	0.835	0.835	0.861	0.895	0.895	0.914	0.925	0.925	0.873	0.917	0.917	0.985	0.938	0.960	0.982	0.986
HD_37	0.792	0.827	0.827	0.849	0.885	0.885	0.910	0.921	0.921	0.861	0.911	0.911	0.984	0.939	0.960	0.981	0.985
HD_38	0.818	0.849	0.849	0.877	0.909	0.909	0.927	0.937	0.937	0.891	0.928	0.928	0.984	0.938	0.959	0.981	0.985
HD_39	0.824	0.852	0.852	0.882	0.910	0.910	0.928	0.940	0.940	0.896	0.930	0.930	0.983	0.939	0.959	0.981	0.984
HD_40	0.798	0.833	0.833	0.856	0.891	0.891	0.917	0.929	0.929	0.874	0.916	0.916	0.985	0.938	0.960	0.981	0.986
HD_41	0.807	0.839	0.839	0.865	0.898	0.898	0.923	0.935	0.935	0.882	0.921	0.921	0.984	0.939	0.960	0.981	0.985
HD_42	0.821	0.848	0.848	0.880	0.907	0.907	0.930	0.940	0.941	0.898	0.929	0.929	0.983	0.937	0.959	0.980	0.984
HD_43	0.789	0.823	0.823	0.845	0.879	0.879	0.907	0.919	0.919	0.860	0.905	0.905	0.984	0.939	0.960	0.980	0.985
HD_44	0.794	0.830	0.830	0.851	0.888	0.887	0.911	0.924	0.924	0.862	0.910	0.910	0.983	0.938	0.959	0.981	0.984
HD_45	0.807	0.839	0.839	0.865	0.897	0.897	0.917	0.931	0.931	0.876	0.918	0.918	0.983	0.939	0.960	0.980	0.983
HD_46	0.794	0.827	0.827	0.852	0.886	0.886	0.909	0.921	0.921	0.863	0.908	0.908	0.983	0.937	0.960	0.980	0.984
HD_47	0.742	0.780	0.780	0.797	0.836	0.836	0.870	0.882	0.882	0.801	0.865	0.865	0.980	0.935	0.958	0.981	0.982
HD_48	0.763	0.803	0.803	0.818	0.858	0.858	0.884	0.898	0.898	0.823	0.889	0.889	0.982	0.937	0.960	0.981	0.983
Average	0.800	0.833	0.833	0.857	0.891	0.891	0.914	0.926	0.926	0.871	0.915	0.915	0.984	0.938	0.960	0.980	0.984

g) Concordance for homozygous alternative genotypes identified using Platypus, Samtools, UnifiedGenotyper and Haplotype Caller (single and multi sample variant identification) using variants identified with the Illumina BovineHD BeadChip® as a gold standard (BTA1-BTA29)

Animal	Single sampe variant identification												Multi sample variant identification				
	Platypus			Platypus (Primitives)			Samtools		UnifiedGenotyper				Haplotype Caller	Platypus	Platypus (Primitives)	Samtools	Unified Genotyper
	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR+BQSR	IR+BQSR	IR+BQSR	IR+BQSR
HD_1	0.886	0.899	0.899	0.870	0.963	0.963	0.958	0.961	0.971	0.959	0.972	0.972	0.980	0.939	0.959	0.980	0.981
HD_2	0.787	0.817	0.817	0.845	0.875	0.875	0.901	0.911	0.911	0.851	0.900	0.900	0.984	0.938	0.960	0.981	0.985
HD_3	0.774	0.811	0.811	0.831	0.868	0.868	0.897	0.910	0.910	0.838	0.896	0.896	0.983	0.938	0.960	0.980	0.983
HD_4	0.776	0.807	0.807	0.834	0.865	0.865	0.894	0.905	0.905	0.843	0.891	0.891	0.983	0.936	0.959	0.981	0.984
HD_5	0.760	0.799	0.799	0.815	0.855	0.855	0.902	0.917	0.917	0.849	0.895	0.895	0.984	0.938	0.960	0.980	0.985
HD_6	0.815	0.843	0.843	0.875	0.902	0.902	0.915	0.925	0.925	0.882	0.920	0.920	0.985	0.936	0.959	0.980	0.985
HD_7	0.737	0.785	0.785	0.787	0.837	0.837	0.859	0.880	0.880	0.794	0.869	0.869	0.984	0.936	0.958	0.978	0.985
HD_8	0.791	0.830	0.830	0.849	0.887	0.887	0.905	0.920	0.920	0.856	0.909	0.909	0.982	0.938	0.959	0.980	0.983
HD_9	0.800	0.831	0.831	0.859	0.890	0.890	0.922	0.934	0.934	0.883	0.919	0.919	0.986	0.938	0.960	0.980	0.986
HD_10	0.844	0.870	0.870	0.906	0.932	0.932	0.944	0.952	0.952	0.922	0.947	0.947	0.985	0.937	0.959	0.980	0.986
HD_11	0.784	0.823	0.823	0.842	0.881	0.881	0.906	0.920	0.920	0.855	0.907	0.907	0.982	0.939	0.960	0.980	0.983
HD_12	0.839	0.866	0.866	0.900	0.928	0.928	0.938	0.948	0.948	0.913	0.943	0.944	0.985	0.938	0.959	0.980	0.986
HD_13	0.812	0.849	0.849	0.870	0.908	0.908	0.921	0.935	0.935	0.884	0.928	0.928	0.983	0.939	0.960	0.980	0.984
HD_14	0.820	0.852	0.852	0.880	0.913	0.913	0.926	0.939	0.939	0.894	0.932	0.932	0.984	0.937	0.959	0.980	0.985
HD_15	0.823	0.855	0.855	0.883	0.915	0.915	0.929	0.941	0.941	0.896	0.933	0.933	0.985	0.938	0.960	0.980	0.986
HD_16	0.787	0.823	0.823	0.845	0.881	0.881	0.908	0.923	0.923	0.862	0.907	0.907	0.985	0.938	0.960	0.980	0.985
HD_17	0.762	0.803	0.803	0.818	0.859	0.859	0.893	0.908	0.908	0.833	0.891	0.891	0.983	0.938	0.960	0.980	0.983
HD_18	0.755	0.796	0.796	0.811	0.852	0.852	0.886	0.901	0.901	0.825	0.886	0.886	0.986	0.937	0.959	0.980	0.986
HD_19	0.766	0.805	0.805	0.822	0.861	0.861	0.891	0.905	0.905	0.836	0.892	0.892	0.983	0.937	0.959	0.981	0.984
HD_20	0.805	0.837	0.837	0.864	0.895	0.895	0.922	0.934	0.934	0.882	0.921	0.921	0.983	0.938	0.960	0.980	0.984
HD_21	0.833	0.849	0.849	0.894	0.909	0.909	0.931	0.942	0.942	0.899	0.931	0.931	0.984	0.938	0.960	0.981	0.985
HD_22	0.839	0.861	0.861	0.900	0.921	0.922	0.942	0.950	0.950	0.918	0.943	0.943	0.982	0.938	0.960	0.980	0.983
HD_23	0.760	0.799	0.799	0.815	0.854	0.854	0.888	0.902	0.902	0.827	0.886	0.886	0.985	0.938	0.960	0.981	0.986
HD_24	0.838	0.859	0.859	0.897	0.918	0.918	0.940	0.950	0.950	0.916	0.940	0.940	0.984	0.938	0.960	0.980	0.984
HD_25	0.839	0.861	0.861	0.899	0.921	0.921	0.942	0.951	0.951	0.918	0.942	0.943	0.984	0.938	0.960	0.981	0.985
HD_26	0.839	0.863	0.863	0.900	0.924	0.924	0.940	0.950	0.950	0.913	0.940	0.941	0.984	0.938	0.959	0.981	0.984
HD_27	0.787	0.819	0.819	0.842	0.875	0.875	0.906	0.920	0.919	0.857	0.902	0.902	0.982	0.937	0.959	0.980	0.983
HD_28	0.830	0.853	0.853	0.890	0.913	0.913	0.937	0.945	0.945	0.909	0.935	0.935	0.983	0.937	0.960	0.981	0.984
HD_29	0.785	0.817	0.817	0.841	0.873	0.873	0.899	0.911	0.911	0.848	0.900	0.900	0.984	0.938	0.960	0.980	0.985
HD_30	0.792	0.828	0.828	0.849	0.886	0.886	0.909	0.922	0.922	0.858	0.911	0.911	0.984	0.939	0.960	0.981	0.985
HD_31	0.797	0.833	0.833	0.856	0.892	0.892	0.913	0.926	0.926	0.866	0.915	0.915	0.984	0.938	0.960	0.981	0.985
HD_32	0.806	0.840	0.840	0.865	0.900	0.900	0.917	0.930	0.930	0.876	0.922	0.922	0.985	0.938	0.960	0.981	0.986
HD_33	0.797	0.836	0.836	0.855	0.894	0.894	0.914	0.927	0.927	0.869	0.917	0.917	0.985	0.939	0.960	0.980	0.985
HD_34	0.800	0.837	0.837	0.856	0.894	0.894	0.913	0.928	0.928	0.870	0.917	0.917	0.983	0.938	0.959	0.980	0.984
HD_35	0.797	0.834	0.834	0.856	0.893	0.893	0.912	0.925	0.925	0.869	0.916	0.916	0.984	0.938	0.959	0.980	0.985
HD_36	0.802	0.835	0.835	0.861	0.895	0.895	0.914	0.925	0.925	0.873	0.917	0.917	0.985	0.938	0.960	0.982	0.986
HD_37	0.792	0.827	0.827	0.849	0.885	0.885	0.910	0.921	0.921	0.861	0.911	0.911	0.984	0.939	0.960	0.981	0.985
HD_38	0.818	0.849	0.849	0.877	0.909	0.909	0.927	0.937	0.937	0.891	0.928	0.928	0.984	0.938	0.959	0.981	0.985
HD_39	0.824	0.852	0.852	0.882	0.910	0.910	0.928	0.940	0.940	0.896	0.930	0.930	0.983	0.939	0.959	0.981	0.984
HD_40	0.798	0.833	0.833	0.856	0.891	0.891	0.917	0.929	0.929	0.874	0.916	0.916	0.985	0.938	0.960	0.981	0.986
HD_41	0.807	0.839	0.839	0.865	0.898	0.898	0.923	0.935	0.935	0.882	0.921	0.921	0.984	0.939	0.960	0.981	0.985
HD_42	0.821	0.848	0.848	0.880	0.907	0.907	0.930	0.940	0.941	0.898	0.929	0.929	0.983	0.937	0.959	0.980	0.984
HD_43	0.789	0.823	0.823	0.845	0.879	0.879	0.907	0.919	0.919	0.860	0.905	0.905	0.984	0.939	0.960	0.980	0.985
HD_44	0.794	0.830	0.830	0.851	0.888	0.887	0.911	0.924	0.924	0.862	0.910	0.910	0.983	0.938	0.959	0.981	0.984
HD_45	0.807	0.839	0.839	0.865	0.897	0.897	0.917	0.931	0.931	0.876	0.918	0.918	0.983	0.939	0.960	0.980	0.983
HD_46	0.794	0.827	0.827	0.852	0.886	0.886	0.909	0.921	0.921	0.863	0.908	0.908	0.983	0.937	0.960	0.980	0.984
HD_47	0.742	0.780	0.780	0.797	0.836	0.836	0.870	0.882	0.882	0.801	0.865	0.865	0.980	0.935	0.958	0.981	0.982
HD_48	0.763	0.803	0.803	0.818	0.858	0.858	0.884	0.898	0.898	0.823	0.889	0.889	0.982	0.937	0.960	0.981	0.983
Average	0.800	0.833	0.833	0.857	0.891	0.891	0.914	0.926	0.926	0.871	0.915	0.915	0.984	0.938	0.960	0.980	0.984

Raw= no InDel realignment or base quality score recalibration

IR= InDel realignment

IR+BQSR= InDel realignment followed by base quality score recalibration