Appendix 1.

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| **Welcome to PHASE\_KEY, PATIENTS Module** |
| Haplotype Segregation Software, v. 1.0 |
| Institute of Haematology and Transfusion Medicine, Warsaw, Poland |
| http://www.ihit.waw.pl |
|  |
| SUMMARY RESULTS OF HAPLOTYPE SEGREGATION |
|  |
| Patient1: Chory 1 |
| A\_1 | Cw\_1 | B\_1 | DRB1\_1 | DQB1\_1 | HF | A\_1 | Cw\_1 | B\_1 | DRB1\_1 | DQB1\_1 | HF | P |
| 2501 | **0704** | **4427** | 0701 | 0202 | 0,0011 | 2902 | 1601 | 4403 | 0401 | 0302 | 0,002229 | 0,43 |
|  |  |  |  |  |  |  |  |  |  |  |  |  |
| Patient2: Dawca I i II |
| A\_1 | Cw\_1 | B\_1 | DRB1\_1 | DQB1\_1 | HF | A\_1 | Cw\_1 | B\_1 | DRB1\_1 | DQB1\_1 | HF | P |
| 2501 | **0501** | **4402** | 0701 | 0202 | 0,001129 | 2902 | 1601 | 4403 | 0401 | 0302 | 0,002229 | 0,49 |
|  |
| Population details: |
| Sample size:  | 200 | Country: | Poland |
| Race: | Caucasian/White | Region: | Whole country |
| Ethnicity: | Polish | Bias: | Unbiased healthy voluntears |
|  |
|  |
| DETAILED RESULTS OF HAPLOTYPE SEGREGATION |
|  |
| Patient1: Chory 1 |
| A\_1 | Cw\_1 | B\_1 | DRB1\_1 | DQB1\_1 | HF | A\_1 | Cw\_1 | B\_1 | DRB1\_1 | DQB1\_1 | HF | P |
| 2501 | **0704** | **4427** | 0701 | 0202 | 0,0011 | 2902 | 1601 | 4403 | 0401 | 0302 | 0,002229 | 0,43 |
| 2501 | **0704** | **4427** | 0701 | 0302 | 0,000694 | 2902 | 1601 | 4403 | 0401 | 0202 | 0,001274 | 0,301 |
| 2501 | **0704** | **4427** | 0401 | 0302 | 0,000272 | 2902 | 1601 | 4403 | 0701 | 0202 | 0,000557 | 0,105 |
| 2501 | 1601 | 4403 | 0701 | 0202 | 0,002871 | 2902 | **0704** | **4427** | 0401 | 0302 | 0,00026 | 0,101 |
| 2501 | **0704** | **4427** | 0401 | 0202 | 0,000037 | 2902 | 1601 | 4403 | 0701 | 0302 | 0,000099 | 0,023 |
| 2501 | 1601 | 4403 | 0401 | 0202 | 0,000111 | 2902 | **0704** | **4427** | 0701 | 0302 | 0,000074 | 0,022 |
| 2501 | 1601 | 4403 | 0401 | 0302 | 0,000074 | 2902 | **0704** | **4427** | 0701 | 0202 | 0,000037 | 0,013 |
| Patient2: Dawca I i II |
| A\_1 | Cw\_1 | B\_1 | DRB1\_1 | DQB1\_1 | HF | A\_1 | Cw\_1 | B\_1 | DRB1\_1 | DQB1\_1 | HF | P |
| 2501 | **0501** | **4402** | 0701 | 0202 | 0,001129 | 2902 | 1601 | 4403 | 0401 | 0302 | 0,002229 | 0,49 |
| 2501 | **0501** | **4402** | 0701 | 0302 | 0,000579 | 2902 | 1601 | 4403 | 0401 | 0202 | 0,001274 | 0,202 |
| 2501 | 1601 | 4403 | 0701 | 0202 | 0,002871 | 2902 | **0501** | **4402** | 0401 | 0302 | 0,000334 | 0,139 |
| 2501 | **0501** | **4402** | 0401 | 0302 | 0,000285 | 2902 | 1601 | 4403 | 0701 | 0202 | 0,000557 | 0,132 |
| 2501 | **0501** | **4402** | 0401 | 0202 | 0,000062 | 2902 | 1601 | 4403 | 0701 | 0302 | 0,000099 | 0,015 |
| 2501 | 1601 | 4403 | 0401 | 0302 | 0,000074 | 2902 | **0501** | **4402** | 0701 | 0202 | 0,000037 | 0,011 |
| Opinion: The level of mismatching: 2 alleles/antigens per 10 alleles tested (compatibility 8/10). Haplotype analysis indicated that 2 mismatched alleles/antigens are located within the same haplotype and the second haplotype is matched. It is favorable condition as compared to 2 haplotype mismatch [4.3, 4.4, 4.5].  |